



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 06:33 PM UTC

PDB ID : 8WIB / pdb_00008wib
EMDB ID : EMD-37562
Title : Cryo- EM structure of Mycobacterium smegmatis 70S ribosome, E- tRNA and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

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:

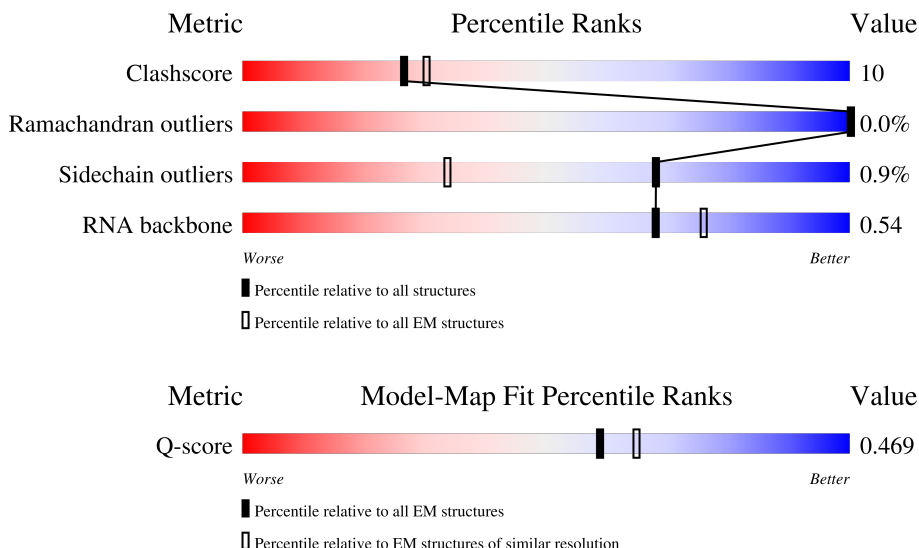
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.50 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	13950 (3.00 - 4.00)

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	
2	F	217	
3	G	215	

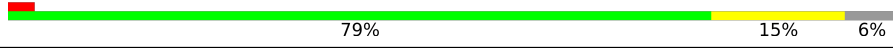
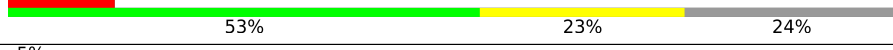
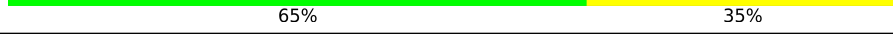
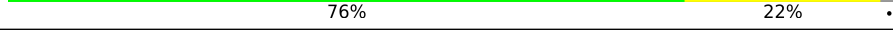
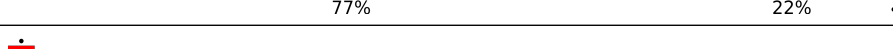
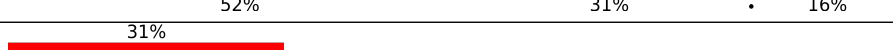
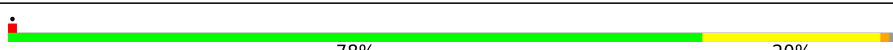
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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75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

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Mol	Chain	Length	Quality of chain
29	C	76	
30	a	1528	
31	v	33	
32	d	275	
33	e	201	
34	f	214	
35	g	96	
36	h	156	
37	i	132	
38	j	150	
39	k	101	
40	l	138	
41	m	124	
42	n	124	
43	o	101	
44	p	89	
45	q	156	
46	r	98	
47	s	84	
48	t	93	
49	u	86	
50	w	264	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 142247 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	209	Total	C	N	O	S	0	0
			1563	969	305	285	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	208	Total	C	N	O	S	0	0
			1562	965	294	301	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	180	Total	C	N	O	S	0	0
			1428	897	267	258	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	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	125	Total	C	N	O	0	0
			951	583	198	170		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
12	S	111	Total	C	N	O	0	0
			888	559	166	163		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	123	Total	C	N	O	0	0
			982	610	202	170		

- 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	96	Total	C	N	O	0	0
			751	476	137	138		

- 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
			706	441	132	131	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	62	Total	C	N	O	S	0	0
			465	280	102	79	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	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	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	59	Total	C	N	O	S	0	0
			458	284	84	85	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3022	Total	C	N	O	P	0	0
			64906	28929	11938	21017	3022		

- 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 E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	C	76	Total	C	N	O	P	0	0
			1622	723	294	529	76		

- Molecule 30 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	1515	Total	C	N	O	P	0	0
			32521	14485	5944	10577	1515		

- Molecule 31 is a protein called 30S ribosomal protein S22.

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

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 33 is a protein called 30S ribosomal protein S4.

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

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	166	Total	C	N	O	S	0	0
			1208	761	228	215	4		

- Molecule 35 is a protein called 30S ribosomal protein S6.

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

- Molecule 36 is a protein called 30S ribosomal protein S7.

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

- Molecule 37 is a protein called 30S ribosomal protein S8.

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

- Molecule 38 is a protein called 30S ribosomal protein S9.

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

- Molecule 39 is a protein called 30S ribosomal protein S10.

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

- Molecule 40 is a protein called 30S ribosomal protein S11.

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

- Molecule 41 is a protein called 30S ribosomal protein S12.

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

- Molecule 42 is a protein called 30S ribosomal protein S13.

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

- Molecule 43 is a protein called 30S ribosomal protein S14A.

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

- Molecule 44 is a protein called 30S ribosomal protein S15.

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

- Molecule 45 is a protein called 30S ribosomal protein S16.

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

- Molecule 46 is a protein called 30S ribosomal protein S17.

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

- Molecule 47 is a protein called 30S ribosomal protein S18B.

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

- Molecule 48 is a protein called 30S ribosomal protein S19.

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

- Molecule 49 is a protein called 30S ribosomal protein S20.

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

- 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:

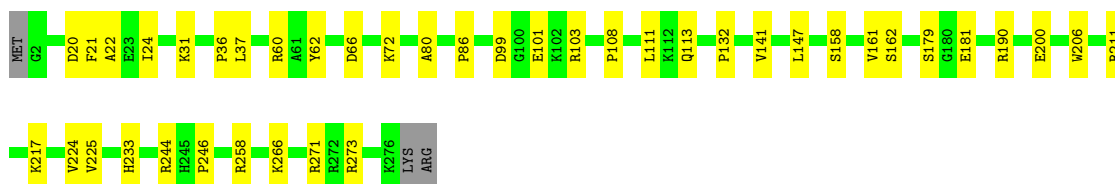
Chain	Residue	Modelled	Actual	Comment	Reference
w	259	HIS	-	expression tag	UNP A0QZ86
w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

3 Residue-property plots

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.

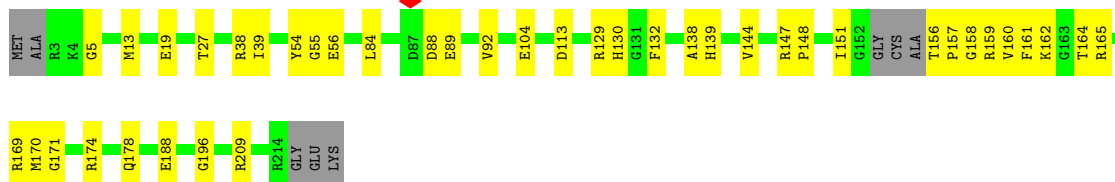
• Molecule 1: 50S ribosomal protein L2

Chain E: 



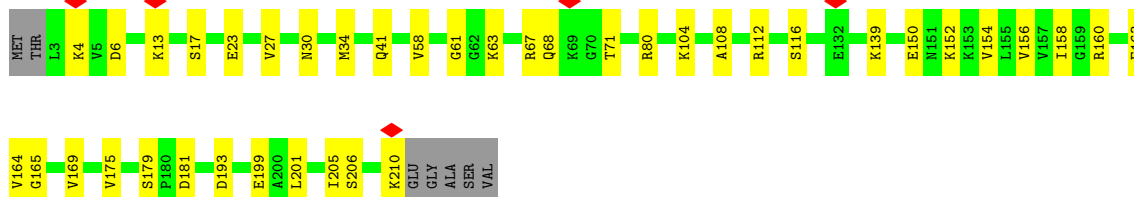
• Molecule 2: 50S ribosomal protein L3

Chain F: 



• Molecule 3: 50S ribosomal protein L4

Chain G: 

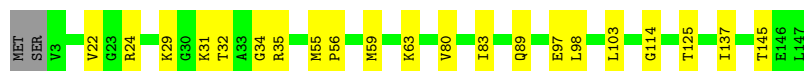


• Molecule 4: 50S ribosomal protein L5

Chain H: 

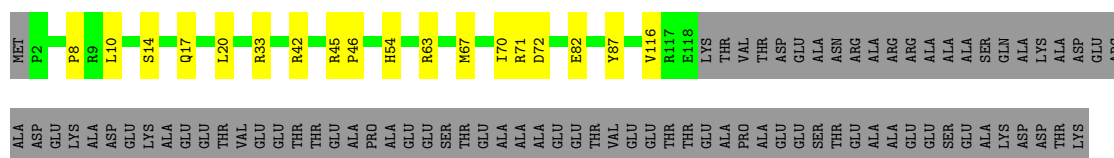


Chain O:  84% 14%



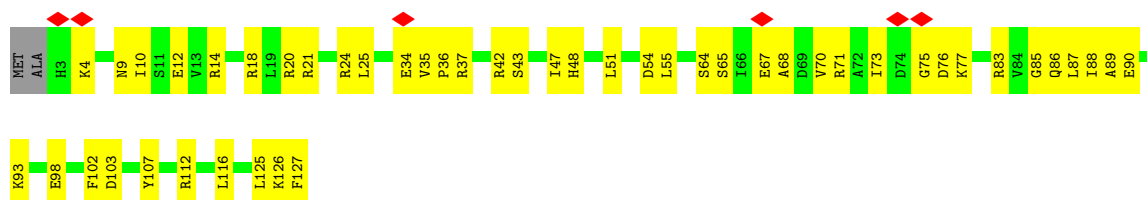
- Molecule 10: 50S ribosomal protein L17

Chain Q:  50% 9% 41%



- Molecule 11: 50S ribosomal protein L18

Chain R:  5% 61% 38%



- Molecule 12: 50S ribosomal protein L19

Chain S:  79% 19%



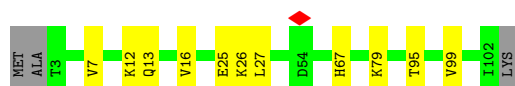
- Molecule 13: 50S ribosomal protein L20

Chain T:  76% 19% 5%



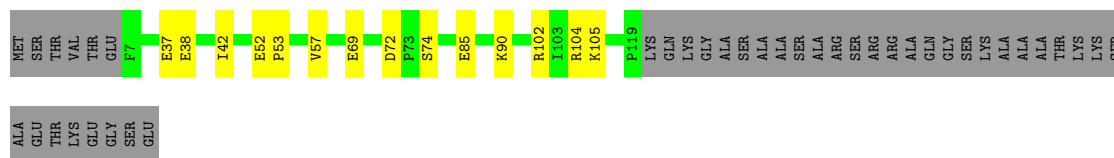
- Molecule 14: 50S ribosomal protein L21

Chain U:  86% 11%



- Molecule 15: 50S ribosomal protein L22

Chain V:  65% 9% 26%



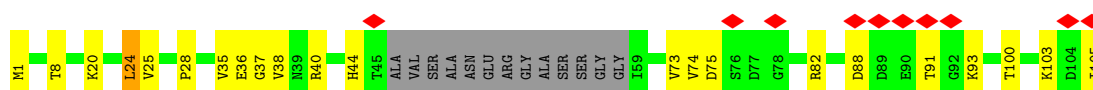
- Molecule 16: 50S ribosomal protein L23

Chain W:  84% 12%



- Molecule 17: 50S ribosomal protein L24

Chain X:  10% 67% 20% 12%



- Molecule 18: 50S ribosomal protein L27

Chain Z:  73% 15% 13%



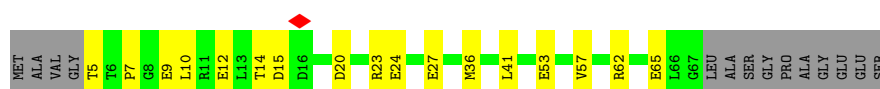
- Molecule 19: 50S ribosomal protein L28

Chain 1:  59% 34%



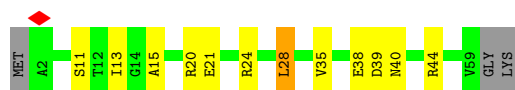
- Molecule 20: 50S ribosomal protein L29

Chain 2:  60% 22% 18%

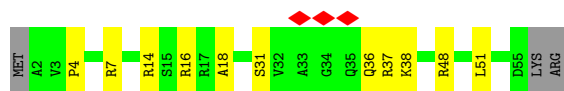
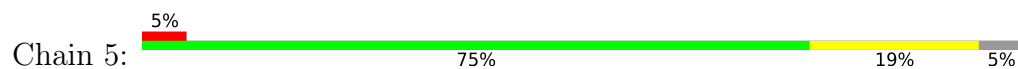


- Molecule 21: 50S ribosomal protein L30

Chain 3:  75% 18% 5%



- Molecule 22: 50S ribosomal protein L32



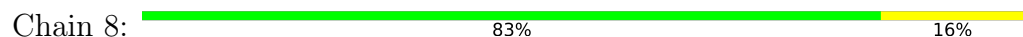
- Molecule 23: 50S ribosomal protein L33A



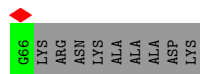
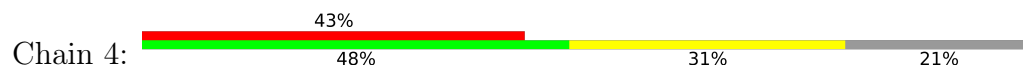
- Molecule 24: 50S ribosomal protein L34



- Molecule 25: 50S ribosomal protein L35



- Molecule 26: 50S ribosomal protein L31

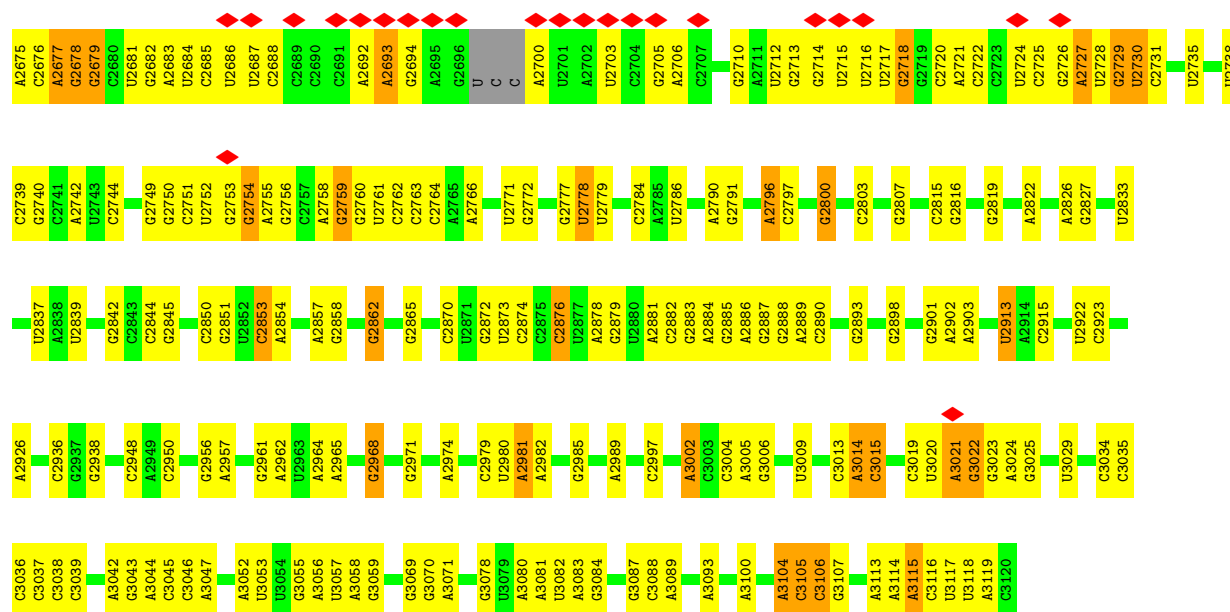


- Molecule 27: 23S rRNA



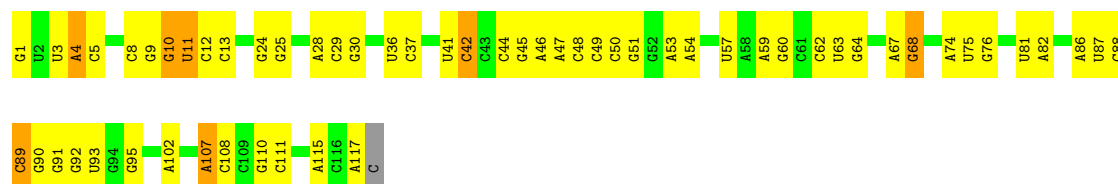


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A2584	U2411	U2264	U2265	G2153	C2033	A1896	G1738	C1648	U1523	A1416
A2585	G2413	A2266	C2267	G2154	U2033	A1897	A1739	G1650	G1524	
A2593								C1651		G1424
G2599	C2417	U2353	A2276	A2160	C2043	C1900	G1754	A1652	G1528	G1426
A2600	U2418	U2355	G2276	A2161	A2046	C1901	A1756	G1653	U1529	
A2601	C2419	U2356		A2162		G1922	G1757	G1654	G1530	
A2602	U2420	G2356	C2279	U2163	G2056	G1917	U1757	A1655	C1531	U1430
G2603	A2421	A2357	G2280	U2170		G1921	G1758	G1656	G1532	C1431
U2604	A2422	A2358		C2171	U2061	G1922	A1759	G1657	U1533	
C2605		G2359	A2284	A2176	G2062	G1923	U1767	G1658	C1534	C1435
G2606	U2425	C2360	A2285	U2195	G2063	G1927	G1786	U1659	C1535	C1436
G2607	C2426	U2361	A2286	G2196	A2064	G1928	A1787	A1660	A1536	A1437
G2608	G2427	C2362	C2287	U2179	A2065	C1927	G1788	G1670	U1537	G1438
A2609	C2431	A2363	C2288	G2188	A2070	G1933	A1789		A1538	U1444
G2613	A2434	A2364	C2289	C2191	A2071	U1937	A1790	G1673	G1541	C1448
U2614	U2435	A2365		C2192		G1938	A1791	G1674	A1542	C1449
G2615	A2436	C2366	A2294	C2193	G2074	U1939	A1792	G1675	A1543	
A2616		C2367	C2295	A2194	G2075			G1676	U1544	G1452
U2617	U2443	C2368	C2299	U2195		U1946	U1798	G1677		
C2618	C2444	A2370		G2196	A2084	U1947		A1678	C1545	U1455
	G2447	U2372	G3311	G2212	C2085	U1948	A1803	A1680	A1546	G1456
C2622	U2448	G2373	G2316	C2211	U2086	A1948	G1804	U1681	C1547	C1465
A2623	G2449	U2374	G2317	A2212	C2087	G1949	G1805	G1682	G1548	U1466
U2626	A2449	U2375	G2318	U2215	C2088	G1950	A1806	G1684	G1549	C1467
C2627		G2376	U2319	U2216	C2089		C1807	G1685	G1550	A1468
	U2457	G2377	C2320	U2217	U2090	A1985	G1815	A1690	U1551	A1469
A2630	G2458	G2378	U2321	A2221	U2091	C1973	C1825	A1691	A1552	G1470
	G2462	G2379	G2322	C2224	U2092	A1974	A1826	G1703	C1553	C1472
G2642	U2463	G2380	G2323	G2224	G2093	A1975	C1830	U1704	A1554	G1476
U2643	U2464	A2381	A2324	G2236	G2094	U1981	G1840	A1705	U1555	C1477
C2644	A2465	C2382	U2325	A2237	G2095	A1990	U1854	G1707	A1556	C1478
	G2466	U2383	G2326	A2238	G2096	C1991	A1855	G1710	C1557	G1479
U2647	U2467	C2384	C2327	A2239	G2097	U1992	C1866	A1480	A1558	
C2648	U2468	U2385	G2328	U2240	U2098	U1996	G1870	C1626	U1560	C1485
A2649	U2469	G2386	U2329	A2244	G2099	U1997	A1859	G1627	C1561	U1486
A2650	A2470	U2387	U2330	C2245	A2106	U1998	G1860	U1624	A1493	U1494
C2651	A2471	U2388	U2331	U2246	G2107	A2001	U1864	G1825	A1499	
G2652	C2472	U2389	G2332	C2247	A2108	A2002	A1865	G1626	A1500	A1500
A2654	G2474	U2390	G2333	C2248	A2109	A2003	C1866	G1627	C1501	G1502
U2655		G2391	U2334	G2249	A2113	A2004	U1870	U1627	A1499	
G2656	U2482	A2392	U2335	G2250	A2114	C2005	G1871	G1628	A1500	
A2657		A2393	U2336	G2251	G2130	C2006	C1872	G1629	C1501	
C2658	C2488	U2394	G2337	U2252	A2137	C2007	U1872	U1630	G1502	
A2659	U2489	A2395	U2338	A2253	A2137	G2016	A1876	A1631	G1507	
	A2490	U2396	U2339	A2254	U2141	C2017	U1728	G1632	A1508	
C2665	A2491	A2396	A2340	A2255	A2142	G2018	U1729	U1633	U1509	
C2666	U2492	C2397	A2341	A2256	A2143	A2019	U1730	C1634	A1510	
C2667	A2493	C2398	G2342	A2257	A2144	A2020	U1731	G1639	U1510	
	U2494	U2399	G2343	A2258	C2144			A1640	C1642	
G2671	G2495	C2400	U2345	U2259	U2147			U1641	A1642	
U2672		U2401	G2346	U2261				G1645		
U2673	G2503	C2402	G2347							
A2674	G2504	U2403	G2348							
		G2404								
		A2405								
		U2406								
		C2407								
		G2408								



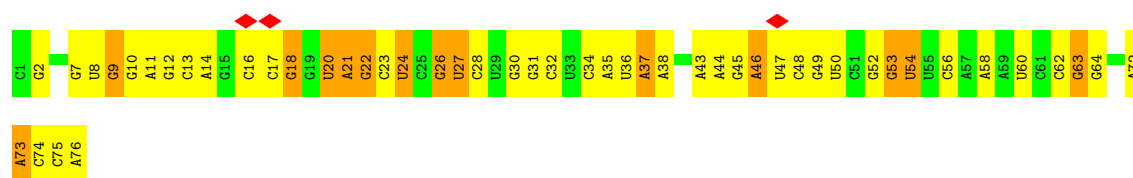
• Molecule 28: 5S rRNA

Chain B: 50% 43% 6%



• Molecule 29: E-tRNA

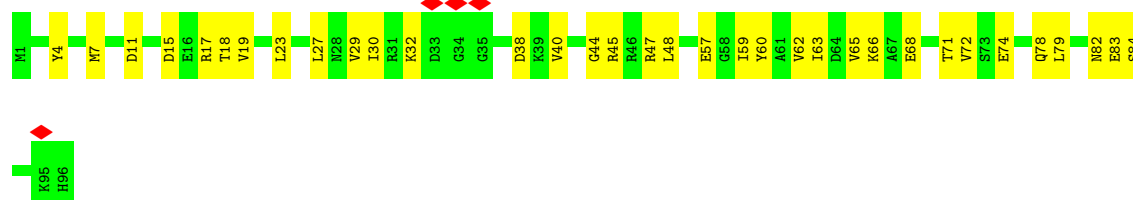
Chain C: 34% 47% 18%



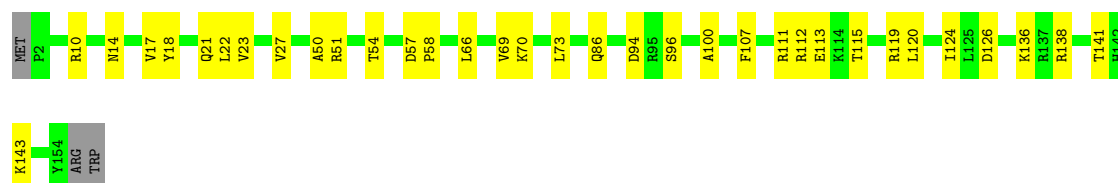
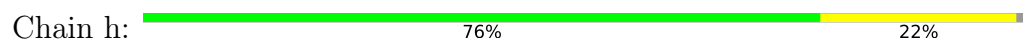




- Molecule 35: 30S ribosomal protein S6



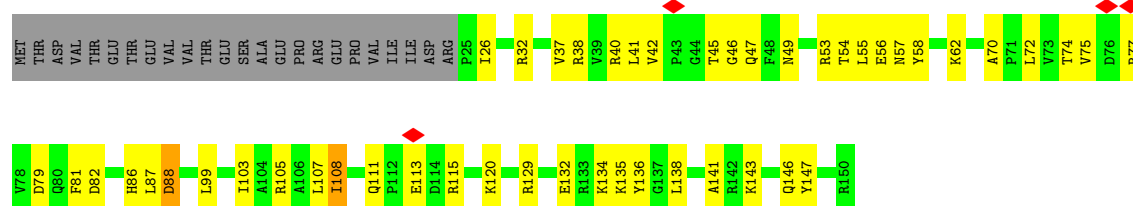
- Molecule 36: 30S ribosomal protein S7



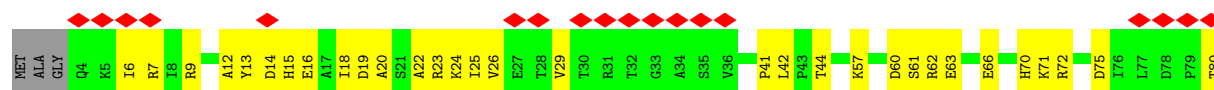
- Molecule 37: 30S ribosomal protein S8

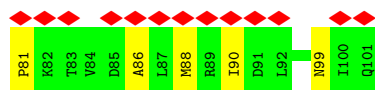


- Molecule 38: 30S ribosomal protein S9



- Molecule 39: 30S ribosomal protein S10





- Molecule 40: 30S ribosomal protein S11

Chain l: 57% 25% 17%



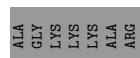
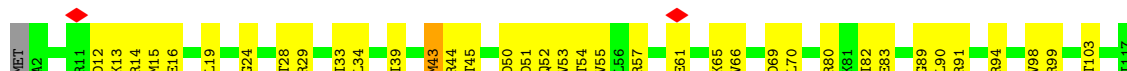
- Molecule 41: 30S ribosomal protein S12

Chain m: 78% 20%



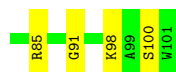
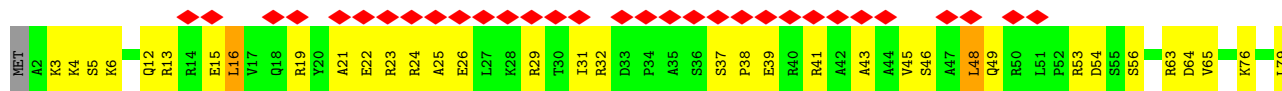
- Molecule 42: 30S ribosomal protein S13

Chain n: 64% 29% 6%



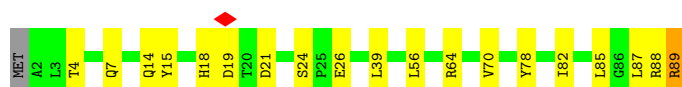
- Molecule 43: 30S ribosomal protein S14A

Chain o: 31% 60% 37% 2%

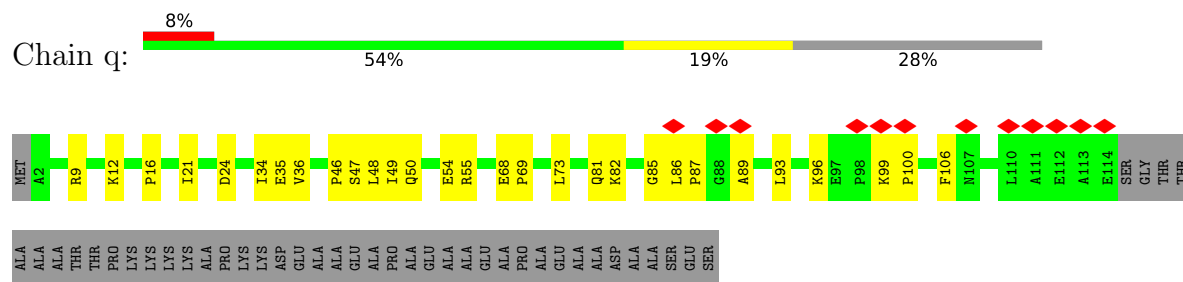


- Molecule 44: 30S ribosomal protein S15

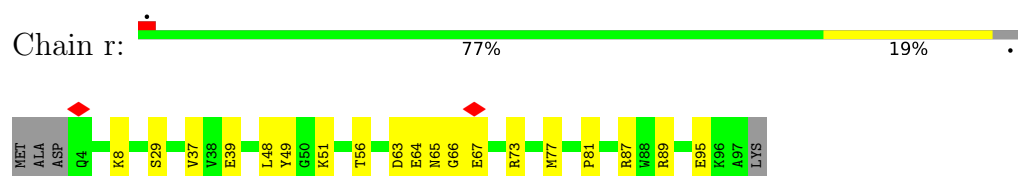
Chain p: 78% 20% 2%



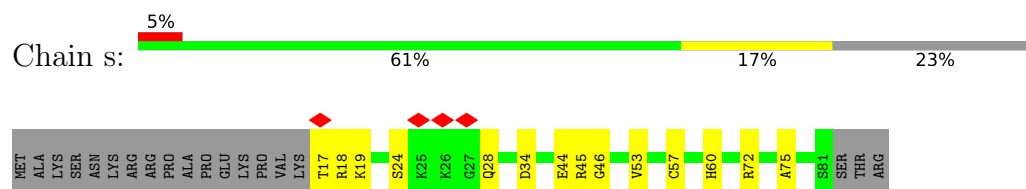
- Molecule 45: 30S ribosomal protein S16



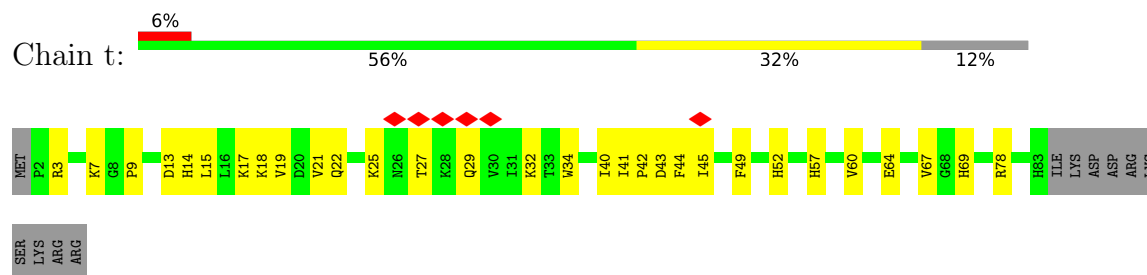
- Molecule 46: 30S ribosomal protein S17



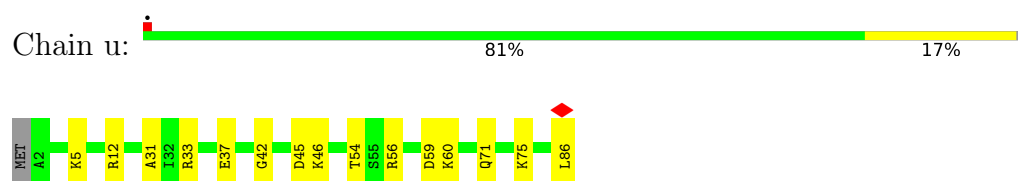
- Molecule 47: 30S ribosomal protein S18B



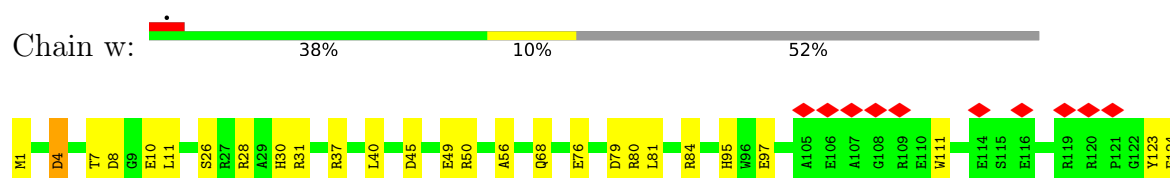
- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20



- Molecule 50: Ribosome hibernation promotion factor RafH



P125																												
	R126	PRO	GLU	GLU	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG	ARG
VAL	LEU	VAL	ILE	VAL	PRO	TYR	GLY	PRO	ALA	ASP	GLU	THR	PRO	ALA	ASP	GLY	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU	LEU
ARG	TYR	ASP	GLY	HIS	TYR	GLY	ILE	THR	PRO	ALA	ASP	GLY	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS	HIS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44299	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE; CTF correction in Relion3.1.4	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	0.221	Depositor
Minimum map value	-0.033	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	0.32	0/2153	0.34	0/2895
2	F	0.32	0/1584	0.46	1/2130 (0.0%)
3	G	0.33	0/1585	0.47	0/2143
4	H	0.23	0/1450	0.40	0/1951
5	I	0.18	0/1281	0.45	0/1733
6	J	0.31	0/311	0.49	0/419
7	M	0.31	0/1157	0.35	0/1567
8	N	0.30	0/946	0.37	0/1268
9	O	0.29	0/1091	0.39	0/1457
10	Q	0.31	0/936	0.42	0/1256
11	R	0.27	0/961	0.53	0/1291
12	S	0.30	0/902	0.44	0/1212
13	T	0.33	0/994	0.38	0/1333
14	U	0.31	0/764	0.36	0/1030
15	V	0.30	0/878	0.38	0/1192
16	W	0.31	0/761	0.37	0/1023
17	X	0.27	0/712	0.45	0/952
18	Z	0.30	0/583	0.34	0/782
19	1	0.32	0/473	0.52	0/634
20	2	0.28	0/530	0.48	0/708
21	3	0.36	0/473	0.43	0/635
22	5	0.23	0/427	0.32	0/572
23	6	0.38	0/405	0.84	1/542 (0.2%)
24	7	0.35	0/380	0.38	0/500
25	8	0.26	0/507	0.31	0/672
26	4	0.22	0/467	0.45	0/626
27	A	0.31	0/72677	0.32	0/113395
28	B	0.28	0/2799	0.33	0/4362
29	C	0.16	0/1812	0.35	0/2821
30	a	0.18	0/36400	0.27	0/56798
31	v	0.12	0/271	0.26	0/348
32	d	0.16	0/1684	0.36	0/2261
33	e	0.16	0/1672	0.32	0/2251
34	f	0.16	0/1224	0.33	0/1653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.20	0/782	0.42	0/1059
36	h	0.18	0/1225	0.40	0/1653
37	i	0.19	0/1025	0.32	0/1385
38	j	0.20	0/1012	0.44	0/1362
39	k	0.21	0/798	0.48	0/1081
40	l	0.17	0/873	0.36	0/1180
41	m	0.19	0/969	0.34	0/1294
42	n	0.20	0/942	0.50	0/1260
43	o	0.26	0/830	0.45	0/1106
44	p	0.24	0/729	0.51	0/977
45	q	0.19	0/908	0.38	0/1226
46	r	0.18	0/759	0.39	0/1016
47	s	0.20	0/518	0.41	0/693
48	t	0.21	0/680	0.45	0/915
49	u	0.20	0/663	0.39	0/882
50	w	0.18	0/1023	0.36	0/1381
All	All	0.27	0/154986	0.33	2/232882 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	6	50	PRO	CA-N-CD	-9.62	98.53	112.00
2	F	151	ILE	N-CA-C	-6.84	106.83	113.53

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	32	0
2	F	1563	0	1608	31	0
3	G	1562	0	1600	32	0
4	H	1428	0	1457	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	1260	0	1300	59	0
6	J	308	0	323	12	0
7	M	1130	0	1167	21	0
8	N	938	0	1000	11	0
9	O	1078	0	1151	14	0
10	Q	919	0	959	13	0
11	R	951	0	986	43	0
12	S	888	0	913	18	0
13	T	982	0	1033	20	0
14	U	754	0	802	9	0
15	V	864	0	903	11	0
16	W	751	0	797	9	0
17	X	706	0	757	16	0
18	Z	574	0	591	10	0
19	1	465	0	479	21	0
20	2	527	0	538	11	0
21	3	470	0	497	11	0
22	5	423	0	463	11	0
23	6	397	0	407	18	0
24	7	377	0	411	12	0
25	8	502	0	541	7	0
26	4	458	0	447	36	0
27	A	64906	0	32655	926	0
28	B	2502	0	1274	42	0
29	C	1622	0	825	48	0
30	a	32521	0	16365	492	0
31	v	271	0	329	5	0
32	d	1660	0	1707	44	0
33	e	1641	0	1668	34	0
34	f	1208	0	1276	34	0
35	g	771	0	797	38	0
36	h	1207	0	1259	26	0
37	i	1010	0	1046	24	0
38	j	994	0	1050	43	0
39	k	784	0	816	41	0
40	l	855	0	863	26	0
41	m	958	0	1045	21	0
42	n	935	0	985	41	0
43	o	819	0	866	39	0
44	p	720	0	760	15	0
45	q	891	0	935	20	0
46	r	748	0	795	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	s	513	0	540	11	0
48	t	662	0	677	27	0
49	u	660	0	712	10	0
50	w	1004	0	991	34	0
All	All	142247	0	93531	2300	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 (2300) 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)
29:C:34:C:O2	50:w:31:ARG:NE	1.61	1.34
27:A:1611:A:H2	35:g:17:ARG:NH2	1.29	1.30
29:C:34:C:O2	50:w:31:ARG:CZ	1.94	1.15
29:C:34:C:O2	50:w:31:ARG:NH2	1.80	1.13
27:A:1611:A:C2	35:g:17:ARG:NH2	2.17	1.12
30:a:1299:C:N3	43:o:53:ARG:NH1	2.02	1.07
29:C:32:C:H4'	36:h:86:GLN:HE22	1.14	1.05
27:A:2971:G:H21	27:A:2981:A:N6	1.55	1.04
27:A:1550:G:H1	27:A:1620:U:H3	1.04	1.04
29:C:34:C:C2	50:w:31:ARG:NH2	2.28	1.01
30:a:957:A:N6	39:k:62:ARG:HH21	1.58	1.00
27:A:1560:U:H1'	35:g:17:ARG:HD3	1.44	0.97
27:A:2086:U:H3	27:A:2096:G:H1	1.01	0.97
27:A:1754:G:H1	27:A:1759:A:H61	1.13	0.97
27:A:2971:G:N2	27:A:2981:A:H62	1.61	0.96
27:A:1754:G:H1	27:A:1759:A:N6	1.63	0.96
30:a:1010:C:N4	30:a:1014:U:H3	1.63	0.95
30:a:957:A:N1	39:k:62:ARG:NH2	2.13	0.95
26:4:36:GLU:OE1	42:n:54:THR:N	2.00	0.95
27:A:1611:A:H2	35:g:17:ARG:HH21	1.11	0.95
27:A:337:U:H3	27:A:344:G:H1	0.99	0.93
26:4:36:GLU:OE1	42:n:54:THR:HG22	1.68	0.93
27:A:1754:G:N2	27:A:1759:A:N1	2.17	0.92
30:a:1133:G:OP1	39:k:70:HIS:ND1	2.02	0.92
30:a:1010:C:H42	30:a:1014:U:H3	0.99	0.91
27:A:334:G:H1	27:A:347:U:H3	1.14	0.91
30:a:826:U:H4'	47:s:19:LYS:HE2	1.52	0.90
26:4:36:GLU:OE1	42:n:54:THR:CG2	2.19	0.89
27:A:2971:G:H21	27:A:2981:A:H62	0.94	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1232:A:H62	30:a:1268:C:H42	1.24	0.86
27:A:2674:A:N6	27:A:2725:C:O2	2.10	0.85
29:C:32:C:H4'	36:h:86:GLN:NE2	1.90	0.85
26:4:36:GLU:CD	42:n:53:VAL:HB	2.01	0.85
4:H:87:ARG:H	4:H:90:MET:HE2	1.42	0.85
30:a:82:U:H3	30:a:87:G:H1	0.85	0.84
29:C:50:U:H3	29:C:64:G:H1	1.26	0.84
38:j:136:TYR:HD2	39:k:60:ASP:O	1.61	0.84
30:a:957:A:C6	39:k:62:ARG:NH2	2.46	0.83
1:E:244:ARG:NH2	27:A:2463:G:OP1	2.10	0.83
26:4:36:GLU:HB2	42:n:57:ARG:NH2	1.93	0.83
26:4:60:ARG:NH2	30:a:1293:G:OP1	2.12	0.83
43:o:6:LYS:HB3	43:o:63:ARG:HH12	1.43	0.83
47:s:17:THR:HG22	47:s:18:ARG:HD2	1.60	0.83
30:a:728:A:O2'	30:a:729:A:N7	2.11	0.83
2:F:139:HIS:NE2	27:A:1888:C:O2	2.11	0.83
27:A:1540:U:H3	27:A:1632:G:H1	1.26	0.82
27:A:1560:U:C2'	35:g:17:ARG:HH11	1.92	0.82
12:S:38:ARG:NH2	30:a:346:G:OP1	2.12	0.82
30:a:1517:C:H1'	50:w:111:TRP:HB3	1.63	0.81
2:F:160:VAL:HG21	27:A:2842:G:H21	1.45	0.81
26:4:36:GLU:HB2	42:n:57:ARG:HH21	1.46	0.81
30:a:989:G:H1	30:a:1006:U:H3	1.27	0.81
30:a:598:C:O2	45:q:12:LYS:NZ	2.13	0.80
26:4:36:GLU:CB	42:n:57:ARG:NH2	2.45	0.80
38:j:136:TYR:CD2	39:k:60:ASP:O	2.35	0.80
27:A:337:U:O2	27:A:344:G:N2	2.15	0.80
27:A:1755:A:O2'	27:A:1758:G:N2	2.16	0.79
26:4:36:GLU:OE2	42:n:53:VAL:HB	1.81	0.79
27:A:1542:A:H61	27:A:1628:A:H1'	1.46	0.78
5:I:90:ILE:HD13	5:I:95:TYR:HB2	1.65	0.78
27:A:329:U:O2	27:A:446:G:O6	2.01	0.78
30:a:957:A:N6	39:k:62:ARG:NH2	2.32	0.78
27:A:2681:U:H3	27:A:2718:G:H1	1.31	0.78
4:H:83:GLN:OE1	4:H:83:GLN:N	2.17	0.78
23:6:14:ALA:HB2	23:6:21:ARG:HE	1.47	0.78
5:I:88:MET:HE3	5:I:89:GLU:H	1.47	0.78
27:A:2386:U:OP1	27:A:2393:A:O2'	2.01	0.78
5:I:57:ASP:OD1	5:I:58:ASP:N	2.18	0.77
27:A:1147:A:N6	27:A:1243:G:O2'	2.17	0.77
27:A:326:A:H61	27:A:449:G:H1	1.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:365:U:H3	27:A:437:G:H1	1.31	0.77
40:l:28:GLY:HA2	40:l:46:PRO:HD3	1.64	0.77
27:A:747:A:N6	27:A:768:G:O2'	2.18	0.76
20:2:62:ARG:NH1	20:2:65:GLU:OE2	2.19	0.76
27:A:1996:U:OP2	27:A:2001:A:N6	2.18	0.76
30:a:957:A:H61	39:k:62:ARG:HH21	1.30	0.76
3:G:41:GLN:HG2	27:A:709:U:H1'	1.66	0.76
27:A:324:C:N4	27:A:451:U:O4	2.19	0.76
27:A:2756:G:O2'	27:A:2881:A:N1	2.18	0.75
30:a:472:C:H2'	30:a:473:A:C8	2.21	0.75
10:Q:10:LEU:HB2	10:Q:17:GLN:HG3	1.67	0.75
21:3:38:GLU:OE1	21:3:38:GLU:N	2.18	0.75
30:a:644:G:H22	30:a:721:G:H1	1.35	0.75
1:E:72:LYS:NZ	1:E:101:GLU:OE1	2.18	0.75
27:A:279:U:H3	27:A:307:G:H1	1.34	0.75
27:A:1547:G:H1	27:A:1623:U:H3	0.79	0.75
27:A:2674:A:OP1	27:A:2721:A:O2'	2.04	0.75
27:A:1710:A:N6	27:A:1716:A:OP2	2.20	0.75
27:A:1560:U:H1'	35:g:17:ARG:CD	2.18	0.74
30:a:83:U:O2	30:a:86:G:O6	2.05	0.74
30:a:593:C:OP1	33:e:76:ARG:NH1	2.15	0.74
49:u:45:ASP:OD1	49:u:46:LYS:N	2.20	0.74
5:I:96:ARG:HH22	5:I:98:GLN:HB3	1.52	0.74
24:7:38:ARG:HG3	24:7:45:LEU:HD21	1.70	0.74
27:A:1530:G:H21	27:A:1805:G:H22	1.35	0.74
27:A:1540:U:O4	27:A:1632:G:O6	2.05	0.74
27:A:1533:U:OP2	27:A:1535:C:N4	2.20	0.73
27:A:1556:A:N1	27:A:1615:G:O6	2.22	0.73
30:a:82:U:O2	30:a:87:G:N2	2.17	0.73
30:a:241:C:H5''	41:m:13:ARG:HH22	1.54	0.73
12:S:38:ARG:NH1	30:a:346:G:OP1	2.22	0.73
27:A:1530:G:N2	27:A:1805:G:H1	1.87	0.73
27:A:2470:A:H2'	27:A:2471:A:H8	1.53	0.73
50:w:49:GLU:HG2	50:w:50:ARG:HG2	1.70	0.73
5:I:104:LEU:HD21	5:I:132:PHE:HE2	1.53	0.73
9:O:89:GLN:OE1	9:O:89:GLN:N	2.21	0.72
30:a:975:G:O2'	30:a:976:A:N7	2.22	0.72
10:Q:42:ARG:NH2	27:A:3038:C:OP1	2.22	0.72
30:a:1133:G:OP1	39:k:70:HIS:CE1	2.42	0.72
27:A:499:G:OP2	27:A:2630:A:O2'	2.08	0.72
27:A:736:G:N2	27:A:739:U:OP2	2.18	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1532:G:O2'	27:A:1803:A:N1	2.21	0.72
27:A:1560:U:C1'	35:g:17:ARG:HD3	2.19	0.72
30:a:772:A:O2'	30:a:774:A:N7	2.22	0.72
19:1:47:GLN:N	19:1:47:GLN:OE1	2.23	0.72
27:A:217:G:H22	27:A:235:U:H4'	1.54	0.72
27:A:334:G:N2	27:A:347:U:O2	2.20	0.72
27:A:2357:A:N7	27:A:2379:G:N2	2.38	0.71
27:A:1530:G:H22	27:A:1805:G:H1	1.37	0.71
27:A:2339:G:H1	27:A:2387:U:H3	1.37	0.71
3:G:150:GLU:N	3:G:150:GLU:OE1	2.23	0.71
27:A:2883:G:N2	27:A:2886:A:OP2	2.17	0.71
23:6:18:CYS:SG	23:6:20:HIS:NE2	2.64	0.71
1:E:271:ARG:NH2	27:A:2016:G:OP2	2.24	0.71
20:2:9:GLU:OE1	20:2:9:GLU:N	2.22	0.71
25:8:47:ARG:NH2	27:A:724:G:OP1	2.23	0.71
27:A:830:A:C2	44:p:56:LEU:HD21	2.26	0.71
30:a:1034:C:O2'	50:w:45:ASP:OD2	2.09	0.71
4:H:57:ILE:HG13	4:H:91:PRO:HB2	1.73	0.70
30:a:229:U:O2'	45:q:24:ASP:OD2	2.09	0.70
39:k:63:GLU:OE1	43:o:85:ARG:NH1	2.24	0.70
27:A:1018:U:O2	27:A:1019:C:N4	2.24	0.70
33:e:49:GLN:HB3	33:e:198:LEU:HB2	1.72	0.70
48:t:25:LYS:HE2	48:t:27:THR:HB	1.74	0.70
27:A:1554:U:H2'	27:A:1555:A:C8	2.26	0.70
24:7:7:THR:O	27:A:801:U:O2'	2.09	0.70
29:C:34:C:H2'	50:w:31:ARG:NH2	2.06	0.70
16:W:18:GLU:OE2	16:W:18:GLU:N	2.22	0.70
27:A:2343:G:H2'	27:A:2344:G:C8	2.25	0.70
27:A:2372:U:H2'	27:A:2373:G:C8	2.27	0.70
30:a:947:U:O2'	50:w:37:ARG:NH2	2.25	0.70
37:i:71:GLU:OE1	37:i:71:GLU:N	2.25	0.70
24:7:37:ARG:NH1	24:7:44:ALA:O	2.25	0.70
27:A:2674:A:N6	27:A:2725:C:C2	2.58	0.70
32:d:104:GLU:OE1	32:d:105:VAL:N	2.24	0.70
27:A:1560:U:H2'	35:g:17:ARG:NH1	2.07	0.69
30:a:8:U:OP1	30:a:9:U:C5	2.45	0.69
33:e:176:LEU:HB3	45:q:106:PHE:HE1	1.57	0.69
27:A:2371:G:H2'	27:A:2372:U:C6	2.27	0.69
30:a:957:A:H61	39:k:62:ARG:NH2	1.90	0.69
30:a:1329:G:H5''	38:j:129:ARG:HG2	1.74	0.69
30:a:654:G:H2'	30:a:655:A:H8	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:q:35:GLU:OE2	45:q:55:ARG:NH2	2.25	0.69
8:N:93:PRO:HG3	8:N:114:ILE:HG12	1.75	0.69
30:a:666:U:H1'	40:l:53:TRP:HE1	1.58	0.69
5:I:35:LEU:HB2	5:I:76:LEU:HD13	1.74	0.69
27:A:2681:U:O4	27:A:2718:G:O6	2.11	0.69
5:I:88:MET:HE2	5:I:163:VAL:HB	1.74	0.69
27:A:1541:G:OP2	27:A:1629:G:N2	2.26	0.68
27:A:990:G:O6	27:A:1018:U:O4	2.10	0.68
27:A:2342:A:N6	27:A:2390:U:O2'	2.26	0.68
30:a:693:G:H2'	30:a:694:G:C8	2.28	0.68
5:I:58:ASP:O	5:I:63:ARG:NH1	2.26	0.68
7:M:141:GLU:N	7:M:141:GLU:OE2	2.25	0.68
27:A:1552:A:N6	27:A:1616:A:OP2	2.26	0.68
4:H:20:ARG:HG2	4:H:35:ILE:HG21	1.74	0.68
27:A:1547:G:O6	27:A:1623:U:O4	2.11	0.68
30:a:9:U:H3'	30:a:10:G:N2	2.09	0.68
35:g:74:GLU:OE1	35:g:78:GLN:NE2	2.27	0.68
27:A:664:A:H3'	27:A:665:G:H8	1.56	0.68
30:a:1359:U:O4	36:h:10:ARG:NH1	2.26	0.68
36:h:51:ARG:HB2	36:h:58:PRO:HG3	1.76	0.68
27:A:1541:G:H2'	27:A:1542:A:H8	1.59	0.68
34:f:101:LEU:HD21	34:f:145:VAL:HG22	1.75	0.68
5:I:108:LEU:HD11	5:I:153:ARG:HB2	1.76	0.68
5:I:150:ARG:HD2	5:I:163:VAL:HG23	1.75	0.68
27:A:2470:A:H2'	27:A:2471:A:C8	2.29	0.68
30:a:485:G:H2'	30:a:486:G:C8	2.29	0.68
32:d:12:LEU:HD21	43:o:91:GLY:HA2	1.76	0.67
13:T:73:ASP:O	13:T:114:ARG:NH2	2.27	0.67
29:C:62:C:H2'	29:C:63:G:H8	1.59	0.67
30:a:1094:C:H1'	43:o:100:SER:HB2	1.76	0.67
27:A:567:A:H4'	27:A:568:A:H5'	1.76	0.67
9:O:97:GLU:N	9:O:97:GLU:OE2	2.27	0.67
8:N:112:MET:HA	8:N:112:MET:HE3	1.77	0.67
20:2:9:GLU:HA	20:2:12:GLU:HG2	1.75	0.67
12:S:48:ARG:NH1	12:S:97:TYR:OH	2.26	0.67
30:a:1133:G:H4'	39:k:15:HIS:CE1	2.30	0.67
30:a:1159:G:N2	30:a:1162:G:OP2	2.28	0.67
30:a:1231:A:H2'	30:a:1232:A:C8	2.30	0.67
27:A:994:A:OP2	27:A:1014:G:N2	2.21	0.67
18:Z:49:VAL:HG22	18:Z:79:ASN:HB3	1.77	0.67
30:a:1338:G:H2'	30:a:1339:A:H8	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:d:33:LYS:HD3	43:o:65:VAL:CG2	2.25	0.67
45:q:86:LEU:HB2	45:q:87:PRO:HD3	1.77	0.67
2:F:148:PRO:O	27:A:2735:U:O2'	2.14	0.66
39:k:7:ARG:NH1	39:k:75:ASP:OD2	2.28	0.66
43:o:53:ARG:O	43:o:56:SER:OG	2.13	0.66
15:V:37:GLU:OE1	15:V:37:GLU:N	2.23	0.66
19:1:41:ARG:HG2	19:1:43:GLY:H	1.59	0.66
30:a:461:G:O2'	30:a:463:C:N4	2.27	0.66
30:a:653:G:H2'	30:a:654:G:C8	2.30	0.66
44:p:24:SER:OG	44:p:26:GLU:OE2	2.13	0.66
26:4:37:VAL:N	42:n:57:ARG:HH22	1.93	0.66
26:4:65:TYR:CG	48:t:9:PRO:HD3	2.31	0.66
27:A:2323:G:H1	27:A:2412:U:H3	1.42	0.66
5:I:98:GLN:HA	5:I:126:VAL:HG11	1.76	0.66
29:C:36:U:H3'	29:C:37:A:H5''	1.76	0.66
30:a:1338:G:H2'	30:a:1339:A:C8	2.29	0.66
30:a:1014:U:H2'	30:a:1015:G:C8	2.31	0.66
30:a:1298:G:N1	30:a:1301:A:OP2	2.27	0.66
27:A:1165:G:HO2'	27:A:1228:A:H61	1.40	0.66
27:A:3078:G:N2	27:A:3081:A:OP2	2.25	0.66
30:a:411:A:C4	30:a:413:G:H1'	2.31	0.66
42:n:13:LYS:H	42:n:45:THR:HG23	1.59	0.66
5:I:120:GLU:OE1	5:I:120:GLU:N	2.24	0.66
27:A:2333:G:O2'	27:A:2343:G:OP2	2.13	0.66
27:A:470:G:N2	27:A:481:C:N3	2.44	0.66
27:A:987:A:H2	27:A:1021:G:H22	1.44	0.66
31:v:27:GLN:OE1	31:v:27:GLN:N	2.27	0.66
11:R:126:LYS:HE2	11:R:126:LYS:N	2.11	0.66
17:X:44:HIS:HB3	27:A:571:A:H1'	1.78	0.66
30:a:1017:C:H2'	30:a:1018:C:C6	2.30	0.66
30:a:1051:C:H2'	30:a:1052:G:H8	1.61	0.66
30:a:1133:G:H4'	39:k:15:HIS:NE2	2.10	0.66
37:i:50:ARG:HH12	37:i:63:GLN:HE22	1.42	0.66
34:f:70:MET:HG2	34:f:96:PHE:HD1	1.60	0.65
30:a:1066:U:H3	30:a:1079:G:H22	1.43	0.65
38:j:99:LEU:O	38:j:103:ILE:HD12	1.96	0.65
19:1:40:THR:OG1	19:1:47:GLN:NE2	2.30	0.65
30:a:1018:C:H2'	30:a:1019:U:C6	2.32	0.65
14:U:26:LYS:HA	14:U:95:THR:HG23	1.77	0.65
27:A:137:G:H21	27:A:1524:G:H1'	1.61	0.65
33:e:7:PRO:HB2	33:e:10:ARG:HG3	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:R:34:GLU:OE1	11:R:34:GLU:N	2.20	0.65
30:a:437:U:O2'	33:e:115:HIS:ND1	2.27	0.65
39:k:16:GLU:OE2	39:k:16:GLU:N	2.24	0.65
3:G:199:GLU:OE1	3:G:199:GLU:N	2.21	0.65
26:4:1:MET:HA	26:4:1:MET:HE3	1.77	0.65
32:d:20:SER:OG	32:d:22:TRP:NE1	2.30	0.65
49:u:31:ALA:HB1	49:u:54:THR:HG22	1.79	0.65
27:A:1018:U:H1'	27:A:1019:C:H41	1.62	0.65
27:A:2364:C:H2'	27:A:2365:A:C8	2.32	0.65
27:A:2878:A:N6	27:A:2890:C:OP2	2.29	0.65
43:o:23:ARG:HD2	43:o:24:ARG:HG2	1.78	0.65
1:E:60:ARG:HA	27:A:1788:G:H5'	1.79	0.65
27:A:724:G:N2	27:A:727:A:OP2	2.26	0.64
27:A:2323:G:N2	27:A:2412:U:O2	2.22	0.64
27:A:2862:G:O2'	27:A:3002:A:N6	2.30	0.64
48:t:19:VAL:HG21	48:t:44:PHE:HE1	1.62	0.64
5:I:108:LEU:HD21	5:I:153:ARG:HD2	1.79	0.64
27:A:1009:U:H2'	27:A:1010:U:C6	2.31	0.64
27:A:2677:A:O2'	27:A:2796:A:N3	2.31	0.64
1:E:179:SER:OG	27:A:2016:G:N7	2.30	0.64
38:j:47:GLN:HE22	38:j:49:ASN:HB2	1.63	0.64
48:t:34:TRP:HD1	48:t:52:HIS:HB2	1.63	0.64
26:4:36:GLU:CD	42:n:54:THR:CG2	2.71	0.64
30:a:438:U:O2'	30:a:439:U:O2	2.11	0.64
26:4:58:VAL:HG23	48:t:64:GLU:HG2	1.80	0.64
27:A:308:U:H2'	27:A:309:G:H8	1.61	0.64
27:A:1544:U:O4	27:A:1626:G:O6	2.16	0.64
26:4:16:CYS:SG	26:4:17:GLY:N	2.71	0.64
27:A:326:A:N6	27:A:449:G:H1	1.96	0.64
27:A:989:G:O6	27:A:990:G:N2	2.31	0.64
27:A:2759:G:H2'	27:A:2760:G:H8	1.63	0.64
33:e:176:LEU:HB3	45:q:106:PHE:CE1	2.33	0.64
47:s:57:CYS:SG	47:s:60:HIS:ND1	2.71	0.64
1:E:80:ALA:O	1:E:113:GLN:NE2	2.19	0.63
22:5:4:PRO:HA	27:A:2839:U:C2	2.33	0.63
27:A:666:A:N6	27:A:2258:U:OP1	2.31	0.63
27:A:1165:G:O2'	27:A:1228:A:N6	2.25	0.63
27:A:1426:G:OP2	27:A:1426:G:N2	2.30	0.63
30:a:297:G:N2	30:a:300:A:OP2	2.25	0.63
27:A:3014:A:O2'	27:A:3015:C:H5''	1.98	0.63
26:4:36:GLU:CD	42:n:54:THR:HG22	2.23	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:532:U:H2'	30:a:533:G:H8	1.62	0.63
35:g:82:ASN:OD1	35:g:84:SER:OG	2.16	0.63
37:i:50:ARG:NE	37:i:52:GLU:OE2	2.28	0.63
46:r:67:GLU:N	46:r:67:GLU:OE1	2.31	0.63
27:A:1229:A:H8	27:A:1230:G:H1'	1.64	0.63
27:A:1754:G:N1	27:A:1759:A:N6	2.27	0.63
30:a:82:U:O4	30:a:87:G:O6	2.17	0.63
34:f:70:MET:HG2	34:f:96:PHE:CD1	2.32	0.63
15:V:52:GLU:N	15:V:52:GLU:OE2	2.31	0.63
30:a:1160:A:OP2	38:j:115:ARG:NH2	2.32	0.63
34:f:61:LEU:HD22	34:f:159:ILE:HG22	1.79	0.63
29:C:32:C:C4'	36:h:86:GLN:HE22	2.02	0.63
3:G:139:LYS:NZ	27:A:401:C:OP2	2.26	0.62
30:a:1120:G:H4'	30:a:1121:G:H5'	1.81	0.62
30:a:1516:U:H2'	30:a:1517:C:C6	2.34	0.62
10:Q:70:ILE:HG22	10:Q:72:ASP:H	1.64	0.62
27:A:1543:A:N1	27:A:1628:A:O2'	2.29	0.62
30:a:9:U:H3'	30:a:10:G:H21	1.62	0.62
30:a:872:G:O2'	30:a:888:A:N6	2.32	0.62
33:e:182:GLU:H	33:e:185:GLN:HE21	1.46	0.62
27:A:933:G:N1	27:A:1303:U:OP2	2.26	0.62
30:a:1014:U:H2'	30:a:1015:G:H8	1.65	0.62
30:a:1207:C:OP2	42:n:103:THR:OG1	2.15	0.62
27:A:2482:U:O2'	27:A:2651:C:OP2	2.17	0.62
39:k:19:ASP:OD1	39:k:72:ARG:NH1	2.32	0.62
27:A:2344:G:O3'	27:A:2391:G:N2	2.33	0.62
22:5:14:ARG:HB3	27:A:13:G:H5''	1.80	0.62
27:A:2407:C:N4	27:A:2408:G:O6	2.32	0.62
30:a:694:G:H2'	30:a:695:A:C8	2.34	0.62
27:A:1223:U:H2'	27:A:1224:G:H8	1.64	0.62
29:C:10:G:H2'	29:C:11:A:C8	2.34	0.62
43:o:32:ARG:HA	43:o:39:GLU:HG2	1.80	0.62
27:A:664:A:H3'	27:A:665:G:C8	2.35	0.62
30:a:517:G:OP1	41:m:110:ARG:NH2	2.33	0.62
27:A:1560:U:C2'	35:g:17:ARG:NH1	2.62	0.62
27:A:2329:G:O6	27:A:2406:U:O4	2.18	0.62
30:a:1003:C:H2'	30:a:1004:G:H8	1.64	0.62
30:a:1265:U:OP2	30:a:1266:U:O2'	2.17	0.62
30:a:1410:C:H2'	30:a:1411:A:H8	1.65	0.62
48:t:34:TRP:CD1	48:t:52:HIS:HB2	2.35	0.62
27:A:256:A:H2'	27:A:257:A:H8	1.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:640:G:O2'	27:A:642:G:OP2	2.15	0.61
27:A:993:G:N1	27:A:1015:A:OP2	2.22	0.61
30:a:863:G:OP2	41:m:6:GLN:NE2	2.30	0.61
8:N:108:GLU:H	8:N:108:GLU:CD	2.08	0.61
11:R:90:GLU:HA	11:R:93:LYS:HG2	1.82	0.61
12:S:52:GLY:H	12:S:56:GLU:HG2	1.64	0.61
27:A:2106:A:H3'	27:A:2107:G:H5''	1.82	0.61
27:A:2599:G:N2	27:A:2602:A:OP2	2.31	0.61
30:a:1299:C:OP1	43:o:56:SER:HB3	2.00	0.61
35:g:83:GLU:OE1	35:g:83:GLU:N	2.31	0.61
2:F:5:GLY:HA3	2:F:84:LEU:HD21	1.83	0.61
27:A:551:G:N2	27:A:554:A:OP2	2.33	0.61
27:A:2552:A:H2'	27:A:2553:G:C8	2.36	0.61
50:w:68:GLN:O	50:w:84:ARG:NH1	2.33	0.61
4:H:130:ASP:HB3	27:A:2527:G:O4'	1.99	0.61
35:g:66:LYS:HB2	35:g:66:LYS:HZ2	1.65	0.61
47:s:18:ARG:NH1	47:s:53:VAL:O	2.33	0.61
10:Q:14:SER:OG	27:A:2913:U:O2'	2.15	0.61
27:A:2254:A:H4'	27:A:2255:A:C8	2.36	0.61
27:A:663:A:C5	27:A:2254:A:C6	2.88	0.61
27:A:2329:G:N1	27:A:2406:U:N3	2.48	0.61
27:A:2356:G:H2'	27:A:2380:G:H1	1.64	0.61
30:a:25:G:H2'	30:a:26:G:C8	2.36	0.61
30:a:241:C:H5''	41:m:13:ARG:NH2	2.14	0.61
23:6:38:ILE:O	23:6:51:HIS:N	2.29	0.61
30:a:92:A:O2'	30:a:93:C:O5'	2.19	0.61
4:H:99:ARG:HD2	28:B:44:C:O2'	2.01	0.61
27:A:2363:A:H2'	27:A:2364:C:C6	2.36	0.61
30:a:1015:G:H2'	30:a:1016:G:H8	1.66	0.61
27:A:1165:G:H4'	27:A:1166:A:H5'	1.83	0.60
11:R:77:LYS:HB3	11:R:112:ARG:HD3	1.83	0.60
30:a:983:C:H2'	30:a:984:A:C8	2.36	0.60
30:a:819:U:H3	30:a:829:G:H1	1.49	0.60
32:d:35:ASP:OD1	32:d:58:ARG:NH2	2.31	0.60
32:d:60:ARG:HH11	32:d:60:ARG:HA	1.66	0.60
38:j:37:VAL:HG22	38:j:87:LEU:HD22	1.83	0.60
40:l:52:ALA:HB1	40:l:82:LYS:HB3	1.82	0.60
27:A:1073:G:O2'	27:A:1076:A:N6	2.34	0.60
45:q:68:GLU:H	45:q:68:GLU:CD	2.09	0.60
30:a:407:A:H2'	30:a:408:G:H8	1.67	0.60
42:n:19:LEU:HD23	42:n:33:ILE:HD11	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:O:80:VAL:HA	9:O:83:ILE:HD12	1.83	0.60
27:A:681:C:H2'	27:A:682:A:H8	1.66	0.60
40:I:27:HIS:CE1	40:I:90:LYS:HD2	2.37	0.60
4:H:168:THR:OG1	4:H:169:ASN:OD1	2.18	0.60
30:a:1407:U:H2'	30:a:1408:A:C8	2.37	0.60
43:o:21:ALA:HA	43:o:25:ALA:HB3	1.84	0.60
42:n:57:ARG:O	42:n:61:GLU:HG2	2.01	0.60
15:V:53:PRO:O	15:V:57:VAL:HG23	2.02	0.59
20:2:36:MET:HE2	20:2:41:LEU:HD21	1.84	0.59
27:A:2065:A:H5'	30:a:682:A:H5'	1.84	0.59
27:A:2902:A:H2'	27:A:2903:A:C8	2.36	0.59
36:h:14:ASN:OD1	36:h:21:GLN:NE2	2.34	0.59
9:O:98:LEU:HD22	9:O:103:LEU:HD12	1.84	0.59
30:a:1057:G:N2	30:a:1060:A:OP2	2.32	0.59
41:m:73:ASN:HD21	41:m:105:GLN:HG3	1.67	0.59
27:A:271:A:OP2	27:A:314:G:N2	2.33	0.59
29:C:62:C:H2'	29:C:63:G:C8	2.36	0.59
32:d:60:ARG:HA	32:d:60:ARG:NH1	2.18	0.59
6:J:23:ASP:OD1	6:J:23:ASP:N	2.34	0.59
2:F:88:ASP:N	2:F:88:ASP:OD1	2.34	0.59
13:T:25:ARG:NH1	27:A:2245:C:OP1	2.35	0.59
18:Z:32:LYS:HB3	27:A:759:G:C6	2.38	0.59
27:A:2211:C:H2'	27:A:2212:A:H8	1.66	0.59
27:A:2279:C:N4	27:A:2724:U:H1'	2.18	0.59
34:f:70:MET:HE3	34:f:98:ARG:HD2	1.83	0.59
4:H:15:TYR:HA	4:H:19:ILE:HB	1.84	0.59
5:I:39:GLU:OE1	5:I:39:GLU:N	2.35	0.59
27:A:2381:A:H4'	27:A:2382:G:O5'	2.02	0.59
30:a:390:U:H2'	30:a:391:G:H8	1.68	0.59
23:6:9:PRO:HD2	23:6:27:LYS:O	2.03	0.59
27:A:2538:A:H2'	27:A:2539:G:H8	1.68	0.59
1:E:200:GLU:OE1	1:E:200:GLU:N	2.31	0.59
4:H:55:LYS:HD2	4:H:55:LYS:O	2.03	0.59
10:Q:8:PRO:HG2	27:A:1870:U:C5	2.38	0.59
11:R:71:ARG:NH2	28:B:28:A:OP1	2.36	0.59
27:A:994:A:H5''	27:A:1014:G:H21	1.68	0.59
30:a:12:A:C6	33:e:201:LYS:HG3	2.38	0.59
30:a:1159:G:OP1	38:j:115:ARG:NH1	2.35	0.59
27:A:176:G:OP2	27:A:176:G:N2	2.26	0.58
27:A:543:U:H3'	27:A:544:U:H5''	1.83	0.58
2:F:157:PRO:HB3	27:A:1248:U:H3	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:j:88:ASP:OD1	38:j:88:ASP:N	2.35	0.58
2:F:138:ALA:HB3	27:A:2217:U:H4'	1.86	0.58
30:a:1197:U:OP1	43:o:3:LYS:HE3	2.04	0.58
43:o:22:GLU:HB3	43:o:23:ARG:CZ	2.33	0.58
11:R:68:ALA:HA	11:R:71:ARG:HB2	1.86	0.58
13:T:83:LEU:HD22	13:T:88:VAL:HG11	1.85	0.58
18:Z:64:PRO:HB3	27:A:759:G:H1	1.68	0.58
11:R:127:PHE:O	27:A:2601:A:O2'	2.19	0.58
12:S:38:ARG:CZ	30:a:346:G:OP1	2.51	0.58
27:A:543:U:H5	27:A:561:G:H5'	1.69	0.58
32:d:23:TYR:CD2	39:k:13:TYR:CE2	2.91	0.58
2:F:19:GLU:N	2:F:19:GLU:OE2	2.35	0.58
4:H:126:PRO:HB2	4:H:174:ARG:NH1	2.18	0.58
4:H:126:PRO:HB2	4:H:174:ARG:HH12	1.68	0.58
29:C:23:C:H2'	29:C:24:U:C6	2.38	0.58
9:O:56:PRO:HD2	9:O:59:MET:HE3	1.83	0.58
10:Q:82:GLU:N	10:Q:82:GLU:OE2	2.36	0.58
21:3:13:ILE:HG21	27:A:1106:A:N7	2.19	0.58
27:A:242:G:O2'	27:A:254:G:O6	2.22	0.58
27:A:2902:A:H2'	27:A:2903:A:H8	1.68	0.58
17:X:24:LEU:HD12	17:X:25:VAL:HG23	1.85	0.58
23:6:37:GLU:HG2	23:6:52:LYS:HD2	1.86	0.58
26:4:36:GLU:HB3	42:n:57:ARG:NH2	2.19	0.58
27:A:1033:A:H5''	28:B:95:G:O2'	2.03	0.58
27:A:1560:U:C1'	35:g:17:ARG:HH11	2.16	0.58
27:A:3055:G:H2'	27:A:3100:A:H61	1.68	0.58
30:a:8:U:H3'	30:a:9:U:C6	2.38	0.58
30:a:669:C:OP1	40:l:55:SER:OG	2.22	0.58
7:M:3:THR:HG22	13:T:64:ARG:NH1	2.19	0.58
26:4:58:VAL:CG2	48:t:64:GLU:HG2	2.33	0.58
27:A:90:C:H2'	27:A:91:C:O4'	2.04	0.58
27:A:284:G:H1'	27:A:303:G:C2	2.38	0.58
27:A:718:C:O2'	27:A:772:U:OP1	2.20	0.58
27:A:1758:G:H2'	27:A:1759:A:C8	2.39	0.58
30:a:936:G:H21	30:a:1208:A:H62	1.51	0.58
33:e:94:ASP:OD1	33:e:95:ASN:N	2.35	0.58
40:l:37:ASN:HA	40:l:67:SER:HB3	1.85	0.58
5:I:96:ARG:NH1	5:I:98:GLN:OE1	2.37	0.58
30:a:324:G:N1	30:a:327:A:OP2	2.37	0.58
30:a:413:G:O2'	30:a:428:G:N2	2.37	0.58
30:a:485:G:H2'	30:a:486:G:H8	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1337:A:H2'	30:a:1338:G:H8	1.68	0.58
40:l:85:GLU:N	40:l:85:GLU:OE2	2.37	0.58
45:q:48:LEU:HD11	45:q:50:GLN:HE21	1.68	0.58
27:A:329:U:O2	27:A:446:G:C6	2.57	0.57
27:A:2249:G:H2'	27:A:2250:A:C8	2.39	0.57
30:a:1418:G:H2'	30:a:1419:C:C6	2.38	0.57
1:E:225:VAL:HG11	27:A:2005:C:H5''	1.86	0.57
27:A:2394:A:O2'	27:A:2396:A:OP1	2.11	0.57
29:C:32:C:C4'	36:h:86:GLN:NE2	2.65	0.57
30:a:632:U:O4	30:a:732:G:O2'	2.22	0.57
30:a:1199:C:H2'	30:a:1200:A:C8	2.38	0.57
30:a:1299:C:C2	43:o:53:ARG:NH1	2.71	0.57
39:k:9:ARG:HB3	39:k:99:ASN:HB3	1.85	0.57
39:k:63:GLU:OE2	43:o:98:LYS:NZ	2.36	0.57
42:n:24:GLY:HA3	42:n:66:VAL:HG12	1.85	0.57
5:I:39:GLU:OE1	5:I:40:PRO:HD3	2.04	0.57
7:M:3:THR:HG22	13:T:64:ARG:HH12	1.69	0.57
7:M:13:ARG:NH1	7:M:49:ASP:O	2.37	0.57
27:A:138:A:H2'	27:A:139:U:O2	2.03	0.57
27:A:1500:A:O2'	27:A:1511:U:O2	2.22	0.57
27:A:2465:A:H2'	27:A:2466:G:C8	2.39	0.57
28:B:67:A:H4'	28:B:68:G:H5'	1.85	0.57
30:a:21:U:H2'	30:a:22:C:C6	2.38	0.57
30:a:401:C:O2'	30:a:601:A:N3	2.35	0.57
30:a:1266:U:O2'	30:a:1267:U:OP1	2.22	0.57
37:i:10:PHE:HD2	37:i:36:ILE:HD11	1.68	0.57
42:n:65:LYS:NZ	42:n:69:ASP:OD1	2.35	0.57
27:A:72:G:H22	27:A:108:A:H2	1.51	0.57
27:A:1381:G:O2'	27:A:2236:G:O6	2.22	0.57
27:A:1710:A:H61	27:A:1716:A:H5''	1.69	0.57
29:C:10:G:H2'	29:C:11:A:H8	1.70	0.57
30:a:928:A:H2'	30:a:929:G:C8	2.38	0.57
50:w:56:ALA:HB2	50:w:81:LEU:HD21	1.87	0.57
4:H:78:ARG:HG2	27:A:2536:U:OP1	2.04	0.57
5:I:119:PRO:HD2	5:I:122:ILE:HD11	1.87	0.57
15:V:104:ARG:NH1	27:A:2237:A:H5'	2.20	0.57
22:5:16:ARG:NH2	27:A:1379:G:OP1	2.27	0.57
27:A:2764:C:O2'	27:A:2964:A:N3	2.31	0.57
30:a:207:G:O2'	49:u:59:ASP:OD2	2.22	0.57
30:a:390:U:H2'	30:a:391:G:C8	2.40	0.57
27:A:654:U:H1'	27:A:664:A:H1'	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1675:U:O2'	27:A:1676:G:N7	2.36	0.57
27:A:2751:C:H2'	27:A:2752:U:O4'	2.05	0.57
19:1:28:ARG:NH1	19:1:30:ASN:OD1	2.37	0.57
27:A:857:U:H2'	27:A:858:A:C8	2.39	0.57
30:a:695:A:H2'	30:a:696:A:C8	2.40	0.57
2:F:158:GLY:HA2	27:A:2276:G:O2'	2.04	0.57
27:A:2671:G:O4'	27:A:2725:C:N4	2.37	0.57
30:a:144:G:H2'	30:a:145:G:C8	2.39	0.57
30:a:1375:G:N2	30:a:1486:A:H8	2.01	0.57
41:m:74:LEU:HD21	41:m:104:THR:HB	1.85	0.57
45:q:81:GLN:O	45:q:85:GLY:N	2.38	0.57
27:A:339:U:H2'	27:A:340:A:C8	2.40	0.57
29:C:34:C:C2	50:w:31:ARG:NE	2.63	0.57
30:a:269:U:H2'	30:a:270:A:C8	2.40	0.57
30:a:1477:A:O2'	50:w:79:ASP:OD2	2.22	0.57
48:t:32:LYS:HE3	48:t:57:HIS:CE1	2.40	0.57
7:M:34:THR:HG23	7:M:39:LYS:HB2	1.86	0.57
24:7:27:THR:HG23	24:7:30:GLY:H	1.70	0.57
27:A:1640:A:H2'	27:A:1642:G:N7	2.20	0.57
33:e:142:GLU:OE2	33:e:172:ARG:NH2	2.30	0.57
33:e:189:PRO:O	33:e:190:LEU:HG	2.05	0.57
48:t:27:THR:HG22	48:t:29:GLN:HE21	1.70	0.57
3:G:58:VAL:HG21	3:G:80:ARG:HB3	1.85	0.56
19:1:57:LYS:NZ	27:A:488:G:N7	2.45	0.56
21:3:39:ASP:OD1	21:3:44:ARG:HD3	2.05	0.56
27:A:789:G:H2'	27:A:919:A:H61	1.70	0.56
27:A:1105:C:O2'	27:A:1118:A:N3	2.35	0.56
27:A:2224:C:O2'	27:A:2913:U:OP2	2.22	0.56
27:A:2682:G:H21	27:A:2683:A:H61	1.53	0.56
30:a:1130:C:H2'	30:a:1131:G:C8	2.40	0.56
15:V:69:GLU:N	15:V:69:GLU:OE2	2.38	0.56
18:Z:18:ALA:HB1	27:A:2495:G:OP1	2.05	0.56
27:A:191:G:OP2	27:A:191:G:N2	2.28	0.56
27:A:389:G:N1	27:A:392:A:OP2	2.35	0.56
27:A:1025:A:N3	27:A:2488:C:O2'	2.34	0.56
30:a:664:U:O2'	40:l:50:VAL:O	2.19	0.56
30:a:949:C:H4'	38:j:147:TYR:CE1	2.40	0.56
30:a:997:A:H5''	48:t:14:HIS:CD2	2.41	0.56
30:a:1232:A:H62	30:a:1268:C:N4	1.99	0.56
4:H:128:GLN:O	27:A:2527:G:O2'	2.22	0.56
27:A:990:G:N2	27:A:1018:U:O2	2.28	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2286:A:N7	27:A:2727:A:N6	2.52	0.56
38:j:111:GLN:HE22	38:j:113:GLU:HB3	1.71	0.56
40:l:43:ILE:HG13	40:l:83:ALA:HB2	1.87	0.56
27:A:935:A:H4'	27:A:951:G:N2	2.20	0.56
27:A:1705:C:H2'	27:A:1706:A:H8	1.69	0.56
29:C:35:A:H2'	29:C:36:U:C6	2.41	0.56
30:a:209:A:N3	30:a:222:U:O2'	2.36	0.56
30:a:337:G:H2'	30:a:338:A:H8	1.69	0.56
32:d:153:CYS:HB3	32:d:198:VAL:HG13	1.86	0.56
1:E:108:PRO:HD2	1:E:111:LEU:HD22	1.86	0.56
4:H:76:ARG:NH2	28:B:42:C:N3	2.51	0.56
7:M:98:THR:HB	7:M:124:VAL:HG23	1.88	0.56
18:Z:11:ARG:O	18:Z:14:ARG:NH1	2.38	0.56
27:A:357:U:H4'	27:A:358:G:O5'	2.06	0.56
27:A:857:U:H2'	27:A:858:A:H8	1.70	0.56
27:A:1614:G:H2'	27:A:1615:G:H8	1.69	0.56
27:A:2366:C:H2'	27:A:2367:G:O4'	2.05	0.56
27:A:2686:U:H2'	27:A:2687:U:C6	2.40	0.56
3:G:63:LYS:HB3	27:A:912:C:OP1	2.05	0.56
27:A:1396:G:H2'	27:A:1397:U:C6	2.39	0.56
27:A:2467:U:H2'	27:A:2468:U:C6	2.41	0.56
29:C:9:G:O2'	29:C:10:G:N7	2.37	0.56
30:a:1310:C:H5''	42:n:28:THR:HG21	1.87	0.56
39:k:20:ALA:HA	39:k:23:ARG:HH12	1.71	0.56
27:A:986:G:C2	27:A:987:A:H1'	2.39	0.56
30:a:272:C:H2'	30:a:273:A:H8	1.70	0.56
30:a:402:G:OP1	33:e:66:GLN:NE2	2.38	0.56
38:j:26:ILE:HD11	38:j:41:LEU:HB3	1.86	0.56
43:o:32:ARG:HH21	48:t:7:LYS:HE2	1.70	0.56
4:H:67:ILE:O	4:H:109:ARG:NH2	2.38	0.56
8:N:48:PRO:O	30:a:1405:G:OP1	2.24	0.56
24:7:10:PRO:HG2	27:A:1424:G:H4'	1.86	0.56
32:d:39:ARG:NH1	32:d:54:VAL:O	2.38	0.56
42:n:39:ILE:HD12	42:n:39:ILE:H	1.71	0.56
21:3:21:GLU:OE1	21:3:24:ARG:NH1	2.39	0.56
27:A:1476:G:H2'	27:A:1477:C:C6	2.40	0.56
28:B:41:U:N3	28:B:45:G:OP2	2.37	0.56
29:C:43:A:H2'	29:C:44:A:C8	2.41	0.56
38:j:54:THR:HG23	38:j:56:GLU:H	1.71	0.56
30:a:1303:U:O2'	48:t:78:ARG:NH2	2.40	0.55
44:p:85:LEU:HB3	44:p:87:LEU:HG	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:36:GLU:C	42:n:57:ARG:HH22	2.14	0.55
27:A:586:U:H2'	27:A:587:G:O4'	2.06	0.55
27:A:1122:C:H2'	27:A:1129:G:H2'	1.88	0.55
27:A:2384:C:H5''	27:A:2387:U:O4	2.06	0.55
27:A:2386:U:OP1	27:A:2394:A:H5''	2.07	0.55
29:C:21:A:O2'	29:C:46:A:N6	2.38	0.55
30:a:358:U:H2'	30:a:359:G:H8	1.71	0.55
30:a:1410:C:H2'	30:a:1411:A:C8	2.41	0.55
15:V:90:LYS:HB3	15:V:102:ARG:HD2	1.88	0.55
30:a:816:G:O6	30:a:833:C:N4	2.39	0.55
30:a:819:U:H3	30:a:829:G:H22	1.54	0.55
30:a:1296:C:H2'	30:a:1297:U:C6	2.41	0.55
3:G:179:SER:OG	3:G:181:ASP:OD1	2.21	0.55
27:A:2343:G:H1	27:A:2401:U:H3	1.53	0.55
27:A:2457:U:H2'	27:A:2458:G:H8	1.70	0.55
30:a:973:U:O4	30:a:1193:U:O2'	2.22	0.55
48:t:15:LEU:HA	48:t:18:LYS:HB2	1.87	0.55
3:G:4:LYS:NZ	3:G:17:SER:HB3	2.22	0.55
5:I:57:ASP:OD1	5:I:59:GLU:N	2.38	0.55
16:W:68:ARG:NH2	27:A:1449:C:OP1	2.39	0.55
33:e:164:SER:OG	33:e:185:GLN:OE1	2.25	0.55
36:h:69:VAL:HG23	36:h:100:ALA:HB1	1.87	0.55
41:m:35:THR:N	41:m:54:ARG:O	2.39	0.55
43:o:43:ALA:HB1	43:o:46:SER:HB2	1.88	0.55
1:E:86:PRO:HG3	27:A:1787:A:H2'	1.88	0.55
13:T:33:ARG:NH2	27:A:672:C:OP1	2.40	0.55
27:A:1706:A:H2'	27:A:1707:G:H8	1.72	0.55
34:f:93:ARG:HA	34:f:96:PHE:HE2	1.70	0.55
27:A:2385:G:OP2	27:A:2387:U:N3	2.38	0.55
27:A:2922:U:H2'	27:A:2923:C:C6	2.42	0.55
30:a:8:U:OP1	30:a:9:U:H5	1.89	0.55
30:a:1476:A:O2'	50:w:80:ARG:NH2	2.38	0.55
33:e:83:ASP:N	33:e:83:ASP:OD1	2.40	0.55
36:h:113:GLU:HB2	36:h:119:ARG:HG2	1.89	0.55
42:n:50:ASP:OD1	42:n:51:ASP:N	2.40	0.55
27:A:1690:A:H2'	27:A:1691:A:C8	2.42	0.55
30:a:32:G:O2'	30:a:296:U:OP1	2.24	0.55
30:a:49:U:H2'	30:a:50:G:C8	2.42	0.55
9:O:32:THR:HG22	9:O:35:ARG:H	1.70	0.55
23:6:24:ILE:HD13	27:A:2643:U:H4'	1.87	0.55
27:A:1561:C:C1'	35:g:17:ARG:HH12	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1729:A:H2'	27:A:1731:A:C8	2.42	0.55
28:B:10:G:O2'	28:B:11:U:OP1	2.21	0.55
30:a:823:U:O4	30:a:826:U:N3	2.35	0.55
30:a:826:U:H2'	30:a:828:G:H5'	1.87	0.55
35:g:32:LYS:HD2	35:g:32:LYS:C	2.32	0.55
27:A:1612:U:H2'	27:A:1613:G:H8	1.71	0.55
27:A:1758:G:H2'	27:A:1759:A:H8	1.71	0.55
27:A:2870:C:OP2	27:A:2956:G:O2'	2.23	0.55
30:a:1104:G:N2	30:a:1105:U:O4	2.37	0.55
26:4:65:TYR:CD1	48:t:9:PRO:HD3	2.42	0.54
27:A:3022:G:H2'	27:A:3023:G:O4'	2.06	0.54
27:A:3071:A:N7	27:A:3089:A:O2'	2.39	0.54
30:a:504:G:H2'	30:a:505:C:C6	2.42	0.54
30:a:1040:U:OP1	43:o:85:ARG:NH2	2.40	0.54
38:j:45:THR:OG1	38:j:46:GLY:N	2.40	0.54
11:R:102:PHE:HD2	27:A:2600:A:N1	2.05	0.54
18:Z:11:ARG:NH2	18:Z:12:ASN:OD1	2.41	0.54
27:A:858:A:O2'	27:A:1877:U:OP1	2.25	0.54
27:A:1236:G:H2'	27:A:1237:U:O4'	2.06	0.54
30:a:83:U:O2	30:a:86:G:C6	2.60	0.54
30:a:905:A:O2'	30:a:1382:C:OP2	2.24	0.54
32:d:53:ASP:OD1	32:d:54:VAL:N	2.39	0.54
36:h:70:LYS:HG2	36:h:96:SER:HB2	1.88	0.54
5:I:128:SER:HB2	5:I:131:LYS:HG2	1.88	0.54
27:A:265:A:N1	27:A:515:U:O2'	2.35	0.54
29:C:18:G:H5''	29:C:58:A:H2	1.71	0.54
30:a:1138:A:H62	30:a:1159:G:H21	1.54	0.54
5:I:104:LEU:HD21	5:I:132:PHE:CE2	2.40	0.54
27:A:1087:G:H2'	27:A:1088:U:C6	2.41	0.54
27:A:2356:G:H2'	27:A:2380:G:H22	1.73	0.54
27:A:2528:G:H22	27:A:2536:U:H3	1.54	0.54
30:a:335:C:H2'	30:a:336:A:H8	1.72	0.54
2:F:89:GLU:HA	2:F:92:VAL:HG12	1.90	0.54
4:H:45:MET:HE1	4:H:157:ARG:HD2	1.89	0.54
4:H:81:ILE:O	4:H:86:LEU:N	2.40	0.54
27:A:2088:C:H2'	27:A:2089:C:C6	2.43	0.54
30:a:979:U:H2'	30:a:980:G:H8	1.71	0.54
42:n:50:ASP:O	42:n:54:THR:HG23	2.07	0.54
3:G:206:SER:O	3:G:210:LYS:HB3	2.06	0.54
27:A:830:A:OP1	44:p:64:ARG:NH1	2.39	0.54
27:A:920:G:N2	27:A:944:A:OP1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1099:A:OP2	27:A:1100:C:N4	2.34	0.54
27:A:1684:C:H2'	27:A:1685:G:H8	1.73	0.54
27:A:2682:G:O2'	27:A:2684:U:O4	2.25	0.54
28:B:81:U:H2'	28:B:82:A:C8	2.43	0.54
29:C:44:A:H2'	29:C:45:G:O4'	2.07	0.54
30:a:21:U:H2'	30:a:22:C:H6	1.73	0.54
30:a:1232:A:N6	30:a:1268:C:H42	2.00	0.54
11:R:90:GLU:OE1	11:R:90:GLU:N	2.37	0.54
27:A:81:A:N1	27:A:96:G:O2'	2.37	0.54
27:A:1534:C:H3'	27:A:1535:C:O2	2.08	0.54
27:A:3020:U:H1'	27:A:3022:G:O6	2.08	0.54
27:A:3034:C:H2'	27:A:3035:C:H6	1.73	0.54
30:a:928:A:H2'	30:a:929:G:H8	1.72	0.54
2:F:188:GLU:H	2:F:188:GLU:CD	2.14	0.54
20:2:7:PRO:HA	20:2:10:LEU:HB3	1.90	0.54
24:7:28:ARG:HH12	27:A:210:G:P	2.30	0.54
27:A:337:U:O4	27:A:344:G:O6	2.26	0.54
27:A:444:U:H5'	27:A:446:G:H4'	1.89	0.54
30:a:235:C:H2'	30:a:236:G:H8	1.73	0.54
3:G:23:GLU:OE1	3:G:23:GLU:N	2.28	0.54
23:6:8:ARG:HA	23:6:27:LYS:O	2.08	0.54
26:4:57:ARG:HA	26:4:60:ARG:HG3	1.90	0.54
40:l:29:ALA:O	40:l:44:THR:N	2.34	0.54
43:o:32:ARG:NH1	43:o:48:LEU:HD22	2.22	0.54
27:A:1146:A:N3	27:A:2710:G:O2'	2.41	0.53
27:A:1553:C:H5'	27:A:1554:U:C5	2.44	0.53
27:A:2457:U:H2'	27:A:2458:G:C8	2.44	0.53
27:A:2675:A:OP1	27:A:2721:A:N6	2.41	0.53
29:C:11:A:H2'	29:C:12:G:C8	2.43	0.53
30:a:498:C:H4'	30:a:499:C:O5'	2.08	0.53
34:f:93:ARG:HA	34:f:96:PHE:CE2	2.43	0.53
50:w:4:ASP:OD1	50:w:4:ASP:N	2.33	0.53
26:4:14:VAL:HB	26:4:22:PHE:HB3	1.89	0.53
27:A:1284:A:H2'	27:A:1285:G:H8	1.72	0.53
27:A:1611:A:H2'	27:A:1612:U:C6	2.43	0.53
27:A:2465:A:H2'	27:A:2466:G:H8	1.73	0.53
28:B:86:A:H2'	28:B:88:C:OP2	2.08	0.53
29:C:34:C:C2	50:w:31:ARG:CZ	2.79	0.53
30:a:362:G:N2	30:a:365:U:OP2	2.39	0.53
45:q:82:LYS:HB2	45:q:89:ALA:HB2	1.90	0.53
4:H:76:ARG:HE	28:B:42:C:H42	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:4:36:GLU:OE1	42:n:54:THR:CA	2.56	0.53
27:A:1612:U:O2	35:g:17:ARG:NE	2.41	0.53
27:A:2086:U:H2'	27:A:2087:C:C6	2.43	0.53
27:A:2248:C:H2'	27:A:2249:G:H8	1.74	0.53
30:a:1110:A:H4'	38:j:40:ARG:NH1	2.22	0.53
30:a:1248:U:O2'	30:a:1249:G:O5'	2.26	0.53
35:g:15:ASP:OD1	35:g:18:THR:HG22	2.08	0.53
9:O:125:THR:HG23	9:O:145:THR:HG23	1.90	0.53
12:S:38:ARG:NH1	30:a:345:C:H5'	2.24	0.53
27:A:1703:G:H2'	27:A:1704:U:C6	2.43	0.53
27:A:1804:G:H2'	27:A:1805:G:C8	2.43	0.53
30:a:544:C:C4	46:r:48:LEU:HD11	2.44	0.53
34:f:108:HIS:CD2	37:i:101:LEU:HD12	2.43	0.53
1:E:66:ASP:OD2	1:E:103:ARG:NH1	2.42	0.53
13:T:26:GLY:O	13:T:30:ARG:NH1	2.41	0.53
27:A:997:G:H2'	27:A:998:G:C8	2.44	0.53
27:A:2474:G:O2'	27:A:2720:C:OP1	2.21	0.53
30:a:1132:U:H5''	39:k:44:THR:OG1	2.09	0.53
30:a:1149:C:O2'	30:a:1150:A:OP2	2.24	0.53
36:h:17:VAL:HG23	36:h:18:TYR:HD1	1.73	0.53
44:p:88:ARG:HG2	44:p:89:ARG:HD2	1.90	0.53
27:A:2729:G:H2'	27:A:2800:G:N1	2.23	0.53
27:A:2815:C:H2'	27:A:2816:G:H8	1.72	0.53
30:a:60:U:H2'	30:a:61:G:H8	1.73	0.53
30:a:725:A:OP1	30:a:833:C:O2'	2.27	0.53
46:r:73:ARG:HB2	46:r:95:GLU:HG3	1.90	0.53
13:T:97:GLU:OE2	13:T:101:SER:OG	2.27	0.53
27:A:298:G:O2'	27:A:299:G:O4'	2.20	0.53
27:A:625:A:N6	27:A:647:G:O2'	2.41	0.53
30:a:407:A:H2'	30:a:408:G:C8	2.44	0.53
30:a:1003:C:H2'	30:a:1004:G:C8	2.43	0.53
30:a:1265:U:H5''	30:a:1266:U:H4'	1.90	0.53
8:N:17:LYS:HE3	8:N:47:ILE:HG13	1.89	0.53
27:A:1560:U:H1'	35:g:17:ARG:CG	2.38	0.53
30:a:436:C:H2'	30:a:437:U:C6	2.44	0.53
42:n:80:ARG:HA	42:n:83:GLU:HG3	1.90	0.53
5:I:150:ARG:NE	5:I:163:VAL:O	2.42	0.53
19:1:60:LYS:HE2	19:1:60:LYS:HA	1.89	0.53
27:A:351:G:O6	27:A:444:U:O2	2.27	0.53
27:A:994:A:H5''	27:A:1014:G:N2	2.23	0.53
27:A:1922:G:H2'	27:A:1923:G:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:C:14:A:C6	29:C:22:G:C5	2.97	0.53
11:R:73:ILE:H	11:R:73:ILE:HD12	1.73	0.53
26:4:13:THR:HA	26:4:22:PHE:O	2.09	0.53
27:A:1704:U:H2'	27:A:1705:C:C6	2.44	0.53
27:A:2074:G:O6	27:A:2075:G:N1	2.41	0.53
30:a:399:G:H2'	30:a:400:C:C6	2.44	0.53
30:a:481:G:H2'	30:a:482:A:H8	1.74	0.53
1:E:132:PRO:HA	1:E:190:ARG:HA	1.91	0.52
27:A:2879:G:O2'	27:A:2888:G:O6	2.22	0.52
4:H:149:ASP:O	4:H:153:ILE:HG23	2.08	0.52
9:O:34:GLY:HA2	27:A:1305:G:H5''	1.91	0.52
11:R:48:HIS:ND1	11:R:64:SER:OG	2.33	0.52
27:A:316:U:O2'	27:A:317:G:OP1	2.26	0.52
27:A:883:G:H22	27:A:1494:U:H1'	1.74	0.52
27:A:928:U:H2'	27:A:929:C:C6	2.45	0.52
27:A:1673:A:H5''	27:A:1674:G:H5''	1.92	0.52
43:o:45:VAL:O	43:o:49:GLN:HG3	2.09	0.52
17:X:24:LEU:HD23	17:X:36:GLU:HG2	1.90	0.52
27:A:1001:C:C5	27:A:1002:C:H1'	2.44	0.52
27:A:1541:G:H1	27:A:1631:A:H62	1.58	0.52
27:A:2515:U:H2'	27:A:2516:U:C6	2.44	0.52
27:A:2819:G:N2	27:A:2822:A:OP2	2.32	0.52
32:d:90:LEU:HB3	32:d:98:VAL:HG11	1.91	0.52
37:i:5:ASP:OD2	37:i:79:ARG:NE	2.37	0.52
3:G:163:GLU:OE1	3:G:164:VAL:N	2.41	0.52
13:T:37:GLU:OE2	27:A:1367:G:N1	2.36	0.52
27:A:247:G:OP2	27:A:249:C:N4	2.39	0.52
27:A:2137:A:C2	30:a:1477:A:C5	2.96	0.52
27:A:2750:G:H2'	27:A:2751:C:C6	2.45	0.52
29:C:35:A:C5	50:w:31:ARG:NH2	2.78	0.52
30:a:498:C:H5''	30:a:499:C:C6	2.44	0.52
33:e:197:GLU:OE2	34:f:130:VAL:HB	2.10	0.52
27:A:1921:G:H2'	27:A:1922:G:H8	1.74	0.52
27:A:2376:G:H2'	27:A:2377:G:H8	1.75	0.52
28:B:50:C:H2'	28:B:51:G:H8	1.75	0.52
37:i:10:PHE:CD2	37:i:36:ILE:HD11	2.45	0.52
6:J:8:GLU:OE1	6:J:14:ALA:HA	2.09	0.52
11:R:21:ARG:HD3	27:A:2518:C:OP1	2.10	0.52
13:T:119:GLU:OE1	13:T:119:GLU:N	2.33	0.52
27:A:296:A:N1	27:A:340:A:N6	2.58	0.52
27:A:2374:U:H2'	27:A:2375:G:H8	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:481:G:H2'	30:a:482:A:C8	2.44	0.52
4:H:61:ILE:HD12	4:H:72:PRO:HG2	1.92	0.52
10:Q:20:LEU:HD11	27:A:1392:G:H4'	1.92	0.52
20:2:5:THR:OG1	20:2:9:GLU:OE2	2.23	0.52
23:6:36:LEU:HD23	23:6:37:GLU:N	2.25	0.52
27:A:114:G:OP2	27:A:116:A:O2'	2.24	0.52
33:e:139:ASP:OD1	33:e:140:VAL:N	2.43	0.52
6:J:12:LEU:HD12	6:J:19:VAL:HG11	1.92	0.52
23:6:20:HIS:HB2	23:6:22:ASN:OD1	2.09	0.52
27:A:1621:C:H2'	27:A:1622:G:H8	1.74	0.52
27:A:2378:U:H2'	27:A:2379:G:H8	1.75	0.52
30:a:1242:A:OP2	30:a:1255:G:N2	2.42	0.52
37:i:38:GLU:OE2	37:i:42:ARG:NH2	2.41	0.52
47:s:44:GLU:OE1	47:s:44:GLU:N	2.41	0.52
27:A:351:G:O6	27:A:444:U:C2	2.63	0.52
27:A:392:A:C4	27:A:394:G:C8	2.98	0.52
27:A:1559:A:H2'	27:A:1560:U:C6	2.45	0.52
27:A:1756:G:H1'	27:A:1758:G:C6	2.45	0.52
27:A:1790:A:H2'	27:A:1791:A:C8	2.44	0.52
28:B:5:C:OP1	28:B:62:C:O2'	2.27	0.52
30:a:294:C:OP1	30:a:590:A:O2'	2.24	0.52
30:a:1367:C:H2'	30:a:1368:G:H8	1.75	0.52
46:r:77:MET:SD	46:r:89:ARG:NH2	2.83	0.52
5:I:117:GLU:OE2	5:I:118:ALA:N	2.43	0.52
17:X:75:ASP:OD2	17:X:100:THR:OG1	2.26	0.52
27:A:782:U:H2'	27:A:783:G:O4'	2.09	0.52
27:A:1076:A:O2'	27:A:2681:U:O2'	2.21	0.52
27:A:2872:G:H2'	27:A:2873:U:C6	2.45	0.52
30:a:337:G:H2'	30:a:338:A:C8	2.45	0.52
30:a:642:C:H2'	30:a:643:A:C8	2.45	0.52
30:a:943:U:OP2	30:a:1204:C:O2'	2.20	0.52
30:a:987:A:H2'	30:a:988:C:C6	2.44	0.52
41:m:54:ARG:HG3	41:m:62:GLU:OE2	2.10	0.52
27:A:256:A:H2'	27:A:257:A:C8	2.43	0.51
27:A:639:C:O2'	27:A:640:G:H8	1.93	0.51
27:A:3020:U:O2'	27:A:3021:A:O5'	2.24	0.51
30:a:470:U:H2'	30:a:471:G:H8	1.75	0.51
30:a:1296:C:H2'	30:a:1297:U:H6	1.75	0.51
30:a:1337:A:H2'	30:a:1338:G:C8	2.44	0.51
33:e:132:VAL:HG11	33:e:177:VAL:HG21	1.92	0.51
19:1:24:ARG:NH1	27:A:469:G:OP1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:636:U:H5''	27:A:637:G:C4	2.45	0.51
27:A:681:C:H2'	27:A:682:A:C8	2.45	0.51
27:A:1165:G:HO2'	27:A:1228:A:N6	2.02	0.51
27:A:1621:C:H2'	27:A:1622:G:C8	2.45	0.51
27:A:2096:G:H2'	27:A:2097:G:H8	1.75	0.51
30:a:654:G:H2'	30:a:655:A:C8	2.40	0.51
30:a:1497:A:H2'	30:a:1498:C:C6	2.45	0.51
35:g:68:GLU:N	35:g:68:GLU:OE2	2.43	0.51
36:h:17:VAL:HG23	36:h:18:TYR:CD1	2.45	0.51
9:O:63:LYS:NZ	27:A:249:C:O2	2.38	0.51
27:A:30:U:O4	27:A:534:G:O2'	2.22	0.51
27:A:2137:A:C2	30:a:1477:A:C4	2.98	0.51
30:a:770:A:OP1	50:w:30:HIS:ND1	2.33	0.51
30:a:1199:C:H2'	30:a:1200:A:H8	1.74	0.51
7:M:71:LYS:NZ	27:A:1140:G:OP1	2.44	0.51
27:A:27:G:H2'	27:A:28:C:C6	2.46	0.51
27:A:974:G:H4'	27:A:975:U:O5'	2.11	0.51
27:A:1540:U:C4	27:A:1632:G:O6	2.63	0.51
27:A:1544:U:C4	27:A:1626:G:O6	2.63	0.51
27:A:1624:U:O2'	27:A:1625:G:N7	2.40	0.51
30:a:60:U:H2'	30:a:61:G:C8	2.46	0.51
30:a:122:G:OP1	30:a:585:U:O2'	2.26	0.51
30:a:895:A:H4'	30:a:896:A:O5'	2.11	0.51
30:a:1457:G:H2'	30:a:1458:G:C8	2.45	0.51
37:i:12:THR:HG22	37:i:15:ARG:HH12	1.74	0.51
43:o:32:ARG:HH12	43:o:48:LEU:HD22	1.76	0.51
11:R:37:ARG:NH2	11:R:54:ASP:OD1	2.42	0.51
27:A:1529:U:H3'	27:A:1530:G:C8	2.46	0.51
27:A:1609:G:H2'	27:A:1610:C:C6	2.45	0.51
27:A:3019:C:H2'	27:A:3020:U:O4'	2.11	0.51
34:f:135:ALA:HB1	34:f:162:VAL:HG23	1.93	0.51
38:j:38:ARG:HB2	38:j:86:HIS:HB2	1.92	0.51
39:k:88:MET:N	39:k:88:MET:HE2	2.25	0.51
5:I:5:GLY:HA2	5:I:70:ARG:HB2	1.92	0.51
25:8:59:ASN:O	25:8:63:ASN:ND2	2.43	0.51
27:A:966:U:H2'	27:A:967:G:H8	1.75	0.51
27:A:1435:C:C5	27:A:1444:U:H5''	2.45	0.51
40:l:47:GLN:OE1	40:l:47:GLN:N	2.43	0.51
43:o:19:ARG:O	43:o:23:ARG:NH1	2.44	0.51
50:w:7:THR:OG1	50:w:8:ASP:N	2.43	0.51
16:W:95:LEU:O	16:W:95:LEU:HD12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1127:A:N3	27:A:1272:C:O2'	2.42	0.51
27:A:2176:A:N3	27:A:2784:C:O2'	2.37	0.51
28:B:10:G:O2'	28:B:11:U:H5'	2.11	0.51
16:W:40:THR:HG22	27:A:1815:G:OP1	2.11	0.51
27:A:747:A:H2'	27:A:748:U:O4'	2.11	0.51
27:A:1294:U:H2'	27:A:1295:U:C6	2.46	0.51
28:B:37:C:N4	28:B:50:C:O2	2.43	0.51
30:a:708:A:H2'	30:a:709:A:C8	2.46	0.51
30:a:953:G:N2	30:a:1346:A:OP1	2.30	0.51
30:a:1490:U:O2	40:l:137:ARG:NH1	2.43	0.51
11:R:24:ARG:HB2	27:A:2559:A:OP1	2.10	0.51
14:U:12:LYS:NZ	27:A:1112:C:O2	2.43	0.51
18:Z:75:ARG:HD2	27:A:2558:C:N4	2.25	0.51
27:A:362:A:H2'	27:A:363:A:H8	1.75	0.51
27:A:473:C:O2'	27:A:476:G:N2	2.43	0.51
48:t:22:GLN:HA	48:t:25:LYS:HZ2	1.76	0.51
5:I:97:VAL:HG22	5:I:106:PHE:HD2	1.76	0.51
30:a:191:C:H2'	30:a:192:G:O4'	2.11	0.51
30:a:716:U:H2'	30:a:717:C:C6	2.45	0.51
38:j:105:ARG:O	38:j:108:ILE:HG22	2.11	0.51
42:n:90:LEU:HD23	42:n:90:LEU:H	1.76	0.51
45:q:99:LYS:HE3	45:q:100:PRO:HD2	1.93	0.51
46:r:64:GLU:OE1	46:r:64:GLU:HA	2.11	0.51
5:I:46:ALA:HB2	5:I:52:VAL:HG23	1.93	0.50
27:A:277:U:H2'	27:A:278:A:C8	2.46	0.50
27:A:326:A:N1	27:A:449:G:N2	2.57	0.50
27:A:996:G:H2'	27:A:997:G:C8	2.46	0.50
27:A:2170:U:H2'	27:A:2171:C:C6	2.46	0.50
27:A:3005:A:H5''	27:A:3006:G:H5'	1.93	0.50
12:S:105:LYS:HG3	30:a:1415:G:OP1	2.11	0.50
27:A:347:U:H2'	27:A:348:G:H8	1.77	0.50
27:A:356:G:H5''	27:A:357:U:OP1	2.12	0.50
27:A:991:C:H2'	27:A:992:C:C6	2.47	0.50
32:d:33:LYS:HD3	43:o:65:VAL:HG21	1.93	0.50
32:d:87:ARG:O	32:d:91:GLU:HG2	2.12	0.50
7:M:27:ARG:NH2	27:A:1260:C:O2'	2.28	0.50
27:A:429:A:H2'	27:A:430:A:C8	2.46	0.50
30:a:1115:G:H1'	30:a:1121:G:N2	2.27	0.50
32:d:48:ARG:H	32:d:48:ARG:HD2	1.76	0.50
38:j:136:TYR:HE2	39:k:61:SER:HA	1.75	0.50
45:q:49:ILE:HB	45:q:93:LEU:HD11	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:1:36:VAL:HG22	19:1:63:ARG:HH21	1.76	0.50
27:A:363:A:H2'	27:A:364:A:O4'	2.11	0.50
27:A:1076:A:H2'	27:A:1077:A:C8	2.46	0.50
27:A:2093:G:HO2'	27:A:2094:G:H8	1.60	0.50
30:a:1396:A:H2	30:a:1471:G:H22	1.58	0.50
30:a:1506:U:H2'	30:a:1507:G:H8	1.75	0.50
46:r:39:GLU:OE2	46:r:56:THR:HB	2.12	0.50
30:a:698:A:H5'	40:l:128:ASN:HB2	1.94	0.50
26:4:36:GLU:CD	42:n:54:THR:HG23	2.35	0.50
27:A:1148:G:O6	27:A:1243:G:N2	2.45	0.50
27:A:1938:G:N1	27:A:1955:A:OP2	2.38	0.50
30:a:985:G:H2'	30:a:986:G:C8	2.47	0.50
30:a:1329:G:O6	38:j:32:ARG:NH2	2.45	0.50
32:d:40:LYS:O	32:d:44:THR:HG22	2.11	0.50
44:p:26:GLU:OE2	44:p:26:GLU:N	2.30	0.50
47:s:46:GLY:O	47:s:72:ARG:NH2	2.44	0.50
1:E:181:GLU:HG3	1:E:271:ARG:HA	1.94	0.50
3:G:30:ASN:O	3:G:34:MET:HG3	2.12	0.50
11:R:34:GLU:HG2	11:R:35:VAL:HG23	1.93	0.50
20:2:14:THR:OG1	20:2:15:ASP:N	2.44	0.50
27:A:1551:U:H3'	27:A:1552:A:C8	2.46	0.50
27:A:2603:G:H2'	27:A:2604:U:C6	2.47	0.50
27:A:2671:G:C8	27:A:2724:U:H3'	2.47	0.50
30:a:468:U:H2'	30:a:469:G:H8	1.77	0.50
30:a:1297:U:O2'	30:a:1342:A:N3	2.44	0.50
32:d:49:ALA:HA	32:d:71:ARG:HD3	1.93	0.50
6:J:4:ILE:HD11	6:J:16:GLY:HA2	1.94	0.50
25:8:45:ASP:OD1	25:8:46:GLY:N	2.45	0.50
27:A:217:G:N2	27:A:235:U:H4'	2.26	0.50
27:A:665:G:N2	27:A:2255:A:OP1	2.45	0.50
30:a:1491:A:H2'	30:a:1492:G:C8	2.47	0.50
12:S:19:PHE:O	12:S:49:ARG:NH1	2.45	0.50
18:Z:41:ARG:NE	18:Z:41:ARG:HA	2.27	0.50
27:A:1556:A:N1	27:A:1615:G:C6	2.80	0.50
27:A:2342:A:C2	27:A:2392:A:H2'	2.47	0.50
30:a:23:C:H2'	30:a:24:U:C6	2.47	0.50
30:a:891:A:N3	30:a:1396:A:O2'	2.44	0.50
30:a:1181:C:H4'	30:a:1182:A:H5'	1.94	0.50
30:a:1351:G:OP2	38:j:134:LYS:HD3	2.12	0.50
30:a:1458:G:H2'	30:a:1459:G:O4'	2.12	0.50
5:I:19:ILE:HG12	5:I:24:LEU:HG	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2:A:H2'	27:A:3:A:C8	2.47	0.49
27:A:2275:A:H8	27:A:2275:A:OP2	1.94	0.49
27:A:2279:C:H41	27:A:2724:U:H1'	1.77	0.49
27:A:2752:U:O2'	27:A:2754:G:OP1	2.24	0.49
32:d:168:TYR:OH	34:f:80:GLU:OE2	2.22	0.49
34:f:196:LYS:HZ2	34:f:199:ARG:HE	1.60	0.49
5:I:92:GLY:HA3	5:I:95:TYR:HE2	1.78	0.49
9:O:80:VAL:HG22	9:O:114:GLY:HA2	1.94	0.49
14:U:27:LEU:H	14:U:95:THR:HG21	1.77	0.49
19:1:36:VAL:HG13	19:1:63:ARG:HE	1.77	0.49
19:1:48:ARG:HB2	19:1:48:ARG:NH1	2.27	0.49
25:8:50:VAL:HG11	25:8:58:ILE:HD12	1.93	0.49
27:A:139:U:H2'	27:A:140:G:O4'	2.11	0.49
27:A:502:C:H2'	27:A:503:A:H8	1.76	0.49
27:A:2029:A:H2'	27:A:2030:C:C6	2.47	0.49
27:A:2366:C:H3'	27:A:2367:G:C8	2.47	0.49
30:a:81:C:H3'	30:a:82:U:H5''	1.93	0.49
30:a:850:C:H2'	30:a:851:A:O4'	2.13	0.49
36:h:23:VAL:O	36:h:27:VAL:HG13	2.12	0.49
40:l:99:GLY:HA2	40:l:102:ARG:HD3	1.93	0.49
48:t:40:ILE:HG12	48:t:69:HIS:O	2.13	0.49
5:I:5:GLY:HA2	5:I:70:ARG:CB	2.42	0.49
5:I:46:ALA:N	5:I:50:ALA:O	2.46	0.49
27:A:356:G:H4'	27:A:358:G:C5	2.47	0.49
27:A:380:A:N1	27:A:404:A:O2'	2.39	0.49
28:B:46:A:C4	28:B:47:A:C8	3.00	0.49
30:a:900:A:H2'	30:a:901:A:C8	2.47	0.49
30:a:927:G:C2	30:a:928:A:C8	3.00	0.49
30:a:1414:C:H2'	30:a:1415:G:O4'	2.11	0.49
33:e:87:ARG:O	33:e:91:SER:OG	2.26	0.49
40:l:61:PHE:HE2	40:l:74:LEU:HD12	1.77	0.49
27:A:543:U:C5	27:A:561:G:H5'	2.47	0.49
27:A:564:G:N1	27:A:567:A:OP2	2.44	0.49
27:A:971:G:H2'	27:A:972:A:C8	2.47	0.49
27:A:1146:A:OP2	27:A:1244:A:N6	2.28	0.49
2:F:13:MET:HG2	2:F:27:THR:HG23	1.93	0.49
27:A:1003:A:OP1	27:A:1003:A:H2'	2.12	0.49
27:A:1609:G:H2'	27:A:1610:C:H6	1.75	0.49
27:A:2420:U:H1'	27:A:2421:A:C8	2.47	0.49
27:A:2738:U:H2'	27:A:2739:C:C6	2.47	0.49
27:A:2752:U:H3'	27:A:2754:G:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2873:U:H2'	27:A:2874:C:C6	2.48	0.49
30:a:485:G:H5''	30:a:514:U:C2	2.47	0.49
30:a:1374:U:H2'	30:a:1375:G:C8	2.47	0.49
41:m:4:ILE:HG21	46:r:51:LYS:HB2	1.95	0.49
13:T:68:ALA:O	13:T:72:ASN:ND2	2.44	0.49
17:X:35:VAL:HB	17:X:38:VAL:HG22	1.94	0.49
24:7:28:ARG:NH2	27:A:210:G:OP1	2.39	0.49
27:A:298:G:H22	27:A:338:C:N4	2.10	0.49
27:A:2654:A:H5'	27:A:2655:U:OP2	2.13	0.49
30:a:320:G:H2'	30:a:321:A:C8	2.48	0.49
30:a:612:U:H5'	30:a:613:G:C8	2.48	0.49
1:E:273:ARG:CZ	1:E:273:ARG:HB3	2.43	0.49
27:A:285:U:H3'	27:A:286:G:H4'	1.94	0.49
27:A:987:A:H2'	27:A:988:U:H5'	1.94	0.49
27:A:2144:C:OP1	30:a:1501:G:C8	2.65	0.49
27:A:2327:C:H2'	27:A:2328:G:C8	2.47	0.49
30:a:9:U:C4	30:a:10:G:C5	3.00	0.49
30:a:200:U:O4	46:r:8:LYS:HE3	2.13	0.49
30:a:522:G:H2'	30:a:523:U:C6	2.47	0.49
33:e:90:GLU:HG3	33:e:95:ASN:HD21	1.78	0.49
5:I:22:GLN:NE2	5:I:38:ALA:O	2.46	0.49
27:A:270:U:C2'	27:A:271:A:H5'	2.42	0.49
27:A:362:A:H2'	27:A:363:A:C8	2.48	0.49
27:A:1690:A:H2'	27:A:1691:A:H8	1.78	0.49
27:A:1791:A:H2'	27:A:1792:A:C8	2.48	0.49
27:A:2364:C:H2'	27:A:2365:A:H8	1.78	0.49
29:C:53:G:O2'	29:C:54:U:O5'	2.22	0.49
30:a:38:C:H2'	30:a:39:G:H8	1.78	0.49
30:a:716:U:H2'	30:a:717:C:H6	1.77	0.49
38:j:136:TYR:CE2	39:k:61:SER:HA	2.48	0.49
5:I:104:LEU:HD22	5:I:124:PHE:CG	2.48	0.49
19:1:2:ALA:HB2	27:A:1479:G:OP1	2.13	0.49
21:3:28:LEU:HD23	21:3:35:VAL:HG22	1.94	0.49
27:A:1224:G:H2'	27:A:1225:G:H8	1.77	0.49
27:A:2777:G:C2	27:A:2807:G:H1'	2.47	0.49
27:A:2800:G:O2'	27:A:2803:C:OP2	2.22	0.49
29:C:63:G:H2'	29:C:64:G:C8	2.47	0.49
30:a:263:A:H2'	30:a:264:U:C6	2.47	0.49
32:d:177:THR:HG22	32:d:180:ALA:H	1.78	0.49
37:i:40:LEU:HD21	37:i:131:VAL:HG21	1.95	0.49
48:t:41:ILE:HG22	48:t:43:ASP:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:w:10:GLU:OE1	50:w:10:GLU:N	2.44	0.49
15:V:72:ASP:OD1	15:V:74:SER:OG	2.27	0.49
27:A:349:G:H2'	27:A:350:A:H8	1.78	0.49
27:A:2255:A:N3	27:A:2679:G:H1'	2.28	0.49
27:A:2288:C:H2'	27:A:2289:C:H6	1.78	0.49
27:A:3023:G:H2'	27:A:3024:A:O4'	2.12	0.49
30:a:493:A:H2'	30:a:494:C:C6	2.48	0.49
30:a:993:G:H1	30:a:1002:U:H3	1.61	0.49
30:a:1156:G:H2'	30:a:1157:A:H8	1.78	0.49
30:a:1517:C:H5'	30:a:1518:A:H5'	1.95	0.49
1:E:141:VAL:HG13	1:E:162:SER:HB2	1.94	0.48
12:S:13:ARG:NH1	12:S:80:ILE:O	2.44	0.48
23:6:39:LYS:HA	23:6:50:PRO:HA	1.96	0.48
27:A:61:G:H2'	27:A:62:G:H8	1.78	0.48
27:A:1610:C:H2'	27:A:1611:A:C8	2.48	0.48
27:A:2088:C:H2'	27:A:2089:C:C5	2.47	0.48
27:A:2759:G:H2'	27:A:2760:G:C8	2.46	0.48
27:A:2761:U:H2'	27:A:2762:C:O4'	2.13	0.48
29:C:20:U:H2'	29:C:20:U:OP2	2.13	0.48
30:a:456:C:H1'	30:a:457:A:C4	2.48	0.48
11:R:9:ASN:ND2	28:B:59:A:N3	2.60	0.48
27:A:1158:U:H2'	27:A:1159:C:C6	2.47	0.48
27:A:1537:U:H2'	27:A:1538:G:C8	2.48	0.48
27:A:1622:G:C2	27:A:1623:U:C5	3.01	0.48
27:A:2672:A:H5'	27:A:2673:U:H2'	1.94	0.48
27:A:2778:U:H2'	27:A:2779:U:C6	2.47	0.48
30:a:1168:G:OP1	38:j:135:LYS:HE3	2.14	0.48
27:A:282:A:C6	27:A:305:G:C6	3.02	0.48
30:a:246:A:C2	30:a:282:A:C5	3.01	0.48
30:a:580:G:C6	30:a:619:G:C6	3.01	0.48
30:a:997:A:H2'	30:a:998:G:C8	2.48	0.48
30:a:1100:U:H2'	30:a:1101:C:C6	2.48	0.48
34:f:108:HIS:HD2	37:i:101:LEU:HD12	1.77	0.48
15:V:104:ARG:HH11	27:A:2237:A:H5'	1.78	0.48
27:A:1002:C:H2'	27:A:1003:A:H3'	1.96	0.48
27:A:2294:A:H2'	27:A:2295:C:C6	2.49	0.48
30:a:382:A:H2'	30:a:383:A:C8	2.48	0.48
5:I:104:LEU:HD22	5:I:124:PHE:CD2	2.49	0.48
13:T:36:LYS:NZ	27:A:1367:G:N7	2.61	0.48
27:A:2043:C:O2'	27:A:2195:U:OP2	2.32	0.48
27:A:2336:U:N3	27:A:2337:A:N7	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:92:A:H1'	30:a:93:C:H5	1.77	0.48
30:a:1206:U:O2	30:a:1206:U:H2'	2.13	0.48
45:q:9:ARG:CZ	45:q:16:PRO:HB3	2.44	0.48
45:q:21:ILE:HG22	45:q:36:VAL:HG22	1.95	0.48
50:w:30:HIS:CE1	50:w:95:HIS:HE1	2.32	0.48
16:W:10:ILE:HD12	16:W:37:SER:HB3	1.94	0.48
27:A:88:A:H1'	27:A:89:A:C8	2.47	0.48
27:A:539:C:N4	27:A:542:A:OP2	2.32	0.48
27:A:801:U:H2'	27:A:903:A:N1	2.29	0.48
27:A:1076:A:HO2'	27:A:2681:U:HO2'	1.55	0.48
27:A:1398:G:N2	27:A:1401:A:OP2	2.46	0.48
27:A:2387:U:H3'	27:A:2388:G:C8	2.49	0.48
27:A:2388:G:C2	27:A:2389:U:H1'	2.49	0.48
27:A:2682:G:H21	27:A:2683:A:N6	2.11	0.48
30:a:902:U:H2'	30:a:903:U:C6	2.49	0.48
30:a:1387:C:H2'	30:a:1388:G:C8	2.49	0.48
41:m:50:ARG:NH1	41:m:89:ASP:OD2	2.34	0.48
2:F:38:ARG:C	2:F:39:ILE:HD13	2.39	0.48
26:4:26:SER:OG	26:4:27:THR:N	2.46	0.48
27:A:1476:G:H2'	27:A:1477:C:H6	1.78	0.48
27:A:1535:C:H2'	27:A:1536:A:O4'	2.13	0.48
30:a:522:G:H2'	30:a:523:U:H6	1.79	0.48
30:a:858:A:H1'	37:i:12:THR:HG21	1.95	0.48
30:a:1051:C:H2'	30:a:1052:G:C8	2.45	0.48
30:a:1440:A:H3'	30:a:1441:G:H8	1.79	0.48
40:l:35:THR:OG1	40:l:36:PHE:N	2.47	0.48
27:A:89:A:O2'	27:A:90:C:OP1	2.28	0.48
27:A:294:G:O6	27:A:342:C:N4	2.42	0.48
27:A:988:U:O2'	27:A:990:G:O4'	2.32	0.48
27:A:990:G:H1	27:A:1018:U:H3	0.69	0.48
27:A:1150:A:H2	27:A:1240:G:H1	1.62	0.48
27:A:1612:U:H2'	27:A:1613:G:C8	2.48	0.48
30:a:1213:U:OP1	38:j:146:GLN:NE2	2.40	0.48
39:k:66:GLU:OE1	39:k:66:GLU:N	2.46	0.48
7:M:94:GLU:OE1	7:M:95:LYS:NZ	2.45	0.48
10:Q:33:ARG:HH12	22:5:51:LEU:HD21	1.78	0.48
27:A:188:G:O6	27:A:204:G:O2'	2.29	0.48
27:A:1002:C:H2'	27:A:1003:A:H5''	1.95	0.48
27:A:1500:A:C4	27:A:1518:A:C2	3.02	0.48
27:A:1528:G:H2'	27:A:1529:U:C6	2.49	0.48
27:A:2361:U:H3	27:A:2376:G:H1	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1017:C:O2'	30:a:1018:C:O4'	2.21	0.48
43:o:76:LYS:O	43:o:76:LYS:HD3	2.14	0.48
2:F:130:HIS:HB3	2:F:165:ARG:NH1	2.28	0.48
17:X:91:THR:OG1	17:X:93:LYS:HG2	2.14	0.48
27:A:1332:G:C6	27:A:1347:G:C6	3.02	0.48
27:A:2265:U:H2'	27:A:2266:A:C8	2.49	0.48
27:A:2703:U:OP1	27:A:2761:U:O2'	2.31	0.48
29:C:58:A:O2'	29:C:60:U:OP2	2.30	0.48
32:d:58:ARG:HG3	32:d:63:VAL:HG22	1.95	0.48
4:H:100:GLY:H	4:H:103:MET:HE2	1.79	0.47
19:1:22:HIS:HB3	27:A:199:U:H4'	1.96	0.47
27:A:563:U:H4'	27:A:597:C:H5'	1.95	0.47
27:A:735:U:H2'	27:A:736:G:O4'	2.14	0.47
27:A:1015:A:H2'	27:A:1016:C:O4'	2.12	0.47
27:A:2075:G:HO2'	27:A:2107:G:H1	0.62	0.47
27:A:2363:A:N6	27:A:2375:G:O6	2.47	0.47
28:B:107:A:H2'	28:B:108:C:C6	2.49	0.47
30:a:1011:U:O2'	30:a:1012:U:O5'	2.32	0.47
47:s:28:GLN:H	47:s:28:GLN:CD	2.22	0.47
19:1:21:SER:HB2	27:A:2657:A:C2	2.49	0.47
27:A:263:G:H2'	27:A:264:G:O4'	2.14	0.47
27:A:601:A:H2'	27:A:602:A:H8	1.78	0.47
27:A:671:G:C2	27:A:1377:A:C5	3.02	0.47
27:A:1541:G:H1	27:A:1631:A:N6	2.11	0.47
27:A:1656:A:H2'	27:A:1657:G:H8	1.79	0.47
27:A:2738:U:H2'	27:A:2739:C:H6	1.79	0.47
27:A:3117:U:H2'	27:A:3118:U:C6	2.49	0.47
30:a:1220:A:H62	30:a:1281:A:N6	2.12	0.47
30:a:1488:G:OP1	30:a:1491:A:H4'	2.14	0.47
35:g:19:VAL:O	35:g:23:LEU:HG	2.14	0.47
43:o:13:ARG:HG2	43:o:54:ASP:OD2	2.14	0.47
4:H:130:ASP:HB3	27:A:2527:G:C1'	2.45	0.47
11:R:98:GLU:OE2	11:R:98:GLU:HA	2.14	0.47
27:A:678:A:N1	27:A:924:G:O2'	2.40	0.47
27:A:738:A:O2'	27:A:740:A:OP1	2.32	0.47
27:A:998:G:N2	27:A:1010:U:H3	2.11	0.47
27:A:2107:G:H4'	27:A:2107:G:OP1	2.14	0.47
27:A:2170:U:H2'	27:A:2171:C:H6	1.78	0.47
27:A:2353:U:N3	27:A:2354:G:O6	2.46	0.47
27:A:2622:C:H2'	27:A:2623:A:H8	1.80	0.47
27:A:2968:G:N7	27:A:2979:C:H1'	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:109:G:H2'	30:a:110:U:C6	2.49	0.47
48:t:34:TRP:NE1	48:t:57:HIS:HE2	2.13	0.47
3:G:210:LYS:HB2	3:G:210:LYS:HE2	1.74	0.47
20:2:23:ARG:O	20:2:27:GLU:HG3	2.15	0.47
24:7:11:ASN:ND2	27:A:885:G:OP1	2.46	0.47
27:A:376:G:C5	27:A:426:G:C2	3.02	0.47
27:A:502:C:H2'	27:A:503:A:C8	2.49	0.47
27:A:979:G:H2'	27:A:980:C:C6	2.49	0.47
27:A:993:G:N2	27:A:1015:A:O5'	2.44	0.47
27:A:1377:A:C6	27:A:1378:U:C4	3.02	0.47
27:A:1533:U:O2	27:A:1803:A:O2'	2.23	0.47
27:A:1541:G:H22	27:A:1631:A:N6	2.12	0.47
27:A:2351:A:N3	27:A:2396:A:O2'	2.47	0.47
30:a:422:C:H4'	30:a:423:G:O5'	2.14	0.47
33:e:55:LYS:O	33:e:59:SER:OG	2.24	0.47
38:j:62:LYS:HD3	38:j:62:LYS:HA	1.61	0.47
5:I:89:GLU:HA	5:I:131:LYS:HA	1.97	0.47
27:A:1229:A:C8	27:A:1230:G:H1'	2.48	0.47
27:A:2752:U:H3'	27:A:2754:G:H8	1.79	0.47
30:a:145:G:O2'	30:a:1429:A:N3	2.36	0.47
30:a:269:U:H2'	30:a:270:A:H8	1.79	0.47
32:d:23:TYR:CE2	39:k:13:TYR:CZ	3.03	0.47
32:d:189:ALA:HB3	32:d:196:ILE:HB	1.95	0.47
35:g:11:ASP:N	35:g:11:ASP:OD1	2.47	0.47
30:a:39:G:H2'	30:a:40:C:C6	2.50	0.47
30:a:859:C:OP1	37:i:82:LYS:NZ	2.33	0.47
30:a:1269:A:H2'	30:a:1270:A:C8	2.49	0.47
33:e:163:PRO:HG2	33:e:166:LEU:HD12	1.95	0.47
37:i:43:GLU:HA	37:i:43:GLU:OE2	2.14	0.47
38:j:72:LEU:HD23	38:j:107:LEU:HD11	1.97	0.47
40:l:95:VAL:HG11	40:l:106:ILE:HD11	1.95	0.47
47:s:19:LYS:HA	47:s:19:LYS:HE3	1.96	0.47
2:F:56:GLU:HA	2:F:56:GLU:OE2	2.15	0.47
11:R:12:GLU:CD	28:B:60:G:H4'	2.40	0.47
12:S:94:ALA:HB2	27:A:3069:G:C8	2.49	0.47
17:X:82:ARG:NH2	27:A:382:A:OP2	2.47	0.47
18:Z:15:ASP:OD1	18:Z:16:SER:N	2.45	0.47
19:1:41:ARG:HG3	19:1:42:PRO:HD2	1.96	0.47
21:3:11:SER:HB3	27:A:1106:A:P	2.55	0.47
27:A:1523:U:H2'	27:A:1524:G:C8	2.50	0.47
27:A:2299:C:OP2	27:A:2462:G:N2	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2351:A:H2'	27:A:2352:C:C6	2.49	0.47
27:A:2739:C:H2'	27:A:2740:G:H8	1.79	0.47
27:A:2750:G:H1	27:A:2761:U:H3	1.63	0.47
27:A:3057:U:H2'	27:A:3058:A:C8	2.50	0.47
29:C:34:C:H2'	29:C:35:A:C8	2.49	0.47
30:a:9:U:H2'	30:a:10:G:O4'	2.13	0.47
30:a:25:G:H2'	30:a:26:G:H8	1.78	0.47
30:a:1219:A:H5'	30:a:1318:C:H41	1.80	0.47
32:d:129:PHE:O	32:d:133:MET:HG3	2.15	0.47
34:f:130:VAL:O	34:f:137:ARG:NH2	2.48	0.47
34:f:132:ALA:O	34:f:137:ARG:NH1	2.47	0.47
38:j:132:GLU:HG2	38:j:141:ALA:HB1	1.96	0.47
39:k:22:ALA:O	39:k:26:VAL:HG12	2.14	0.47
41:m:110:ARG:NH1	41:m:112:GLN:O	2.40	0.47
44:p:18:HIS:CE1	44:p:21:ASP:HB2	2.50	0.47
45:q:54:GLU:OE2	45:q:55:ARG:HD2	2.15	0.47
11:R:14:ARG:NH1	28:B:48:C:OP2	2.48	0.47
19:1:45:ASN:OD1	19:1:45:ASN:N	2.47	0.47
20:2:53:GLU:O	20:2:57:VAL:HG23	2.15	0.47
27:A:2096:G:H2'	27:A:2097:G:C8	2.49	0.47
30:a:492:U:H2'	30:a:493:A:H8	1.79	0.47
30:a:535:C:H2'	30:a:536:C:C6	2.50	0.47
30:a:824:C:O2'	30:a:826:U:O4	2.33	0.47
35:g:44:GLY:HA2	35:g:60:TYR:H	1.79	0.47
47:s:45:ARG:HG3	47:s:45:ARG:HH11	1.80	0.47
1:E:99:ASP:O	27:A:1720:G:N2	2.45	0.47
27:A:159:A:N3	27:A:2431:C:O2'	2.46	0.47
27:A:279:U:H2'	27:A:280:G:H8	1.80	0.47
27:A:429:A:H2'	27:A:430:A:H8	1.79	0.47
27:A:2070:A:H2'	27:A:2071:A:C8	2.49	0.47
30:a:669:C:C2	30:a:670:G:C8	3.03	0.47
30:a:692:A:H2'	30:a:693:G:C8	2.50	0.47
30:a:1010:C:N3	30:a:1014:U:O2	2.48	0.47
30:a:1059:G:H2'	30:a:1060:A:C8	2.50	0.47
30:a:1143:C:H2'	30:a:1144:G:H8	1.79	0.47
30:a:1515:A:H2'	30:a:1516:U:C6	2.50	0.47
36:h:50:ALA:O	36:h:54:THR:HG23	2.15	0.47
37:i:115:ASP:N	37:i:115:ASP:OD1	2.45	0.47
38:j:26:ILE:HD12	38:j:26:ILE:O	2.14	0.47
49:u:42:GLY:HA2	49:u:86:LEU:HD11	1.97	0.47
5:I:153:ARG:HE	5:I:154:ARG:H	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:49:ASP:OD1	7:M:49:ASP:N	2.37	0.47
27:A:543:U:H3'	27:A:544:U:C5'	2.45	0.47
27:A:1337:G:N2	27:A:1340:A:OP2	2.44	0.47
30:a:488:C:H1'	30:a:489:A:C2	2.50	0.47
30:a:688:C:H2'	30:a:689:A:H8	1.80	0.47
30:a:1367:C:H2'	30:a:1368:G:C8	2.50	0.47
34:f:87:LYS:O	34:f:90:GLU:HG3	2.14	0.47
3:G:108:ALA:HB1	3:G:112:ARG:NH1	2.29	0.46
3:G:154:VAL:HG23	3:G:193:ASP:HB2	1.95	0.46
5:I:126:VAL:HG22	5:I:132:PHE:HB2	1.97	0.46
11:R:36:PRO:HG2	11:R:51:LEU:HD12	1.97	0.46
27:A:990:G:O2'	27:A:991:C:OP2	2.29	0.46
27:A:1630:U:H2'	27:A:1631:A:H8	1.80	0.46
27:A:1630:U:H2'	27:A:1631:A:C8	2.50	0.46
27:A:3057:U:H2'	27:A:3058:A:H8	1.80	0.46
29:C:26:G:HO2'	29:C:27:U:P	2.38	0.46
30:a:749:G:H4'	30:a:1497:A:H4'	1.95	0.46
30:a:1042:U:H2'	30:a:1043:C:C6	2.49	0.46
30:a:1269:A:H2	30:a:1335:G:H1'	1.79	0.46
30:a:1299:C:OP1	43:o:56:SER:CB	2.63	0.46
30:a:1334:C:H2'	30:a:1335:G:C8	2.51	0.46
30:a:1407:U:H2'	30:a:1408:A:H8	1.77	0.46
35:g:66:LYS:HB2	35:g:66:LYS:NZ	2.30	0.46
38:j:79:ASP:CG	38:j:79:ASP:O	2.58	0.46
18:Z:73:ARG:NH1	27:A:2558:C:C4	2.83	0.46
27:A:277:U:H2'	27:A:278:A:H8	1.79	0.46
27:A:1119:A:H2'	27:A:1120:G:O4'	2.15	0.46
27:A:1806:A:H2'	27:A:1807:C:C6	2.50	0.46
27:A:1885:G:N2	27:A:2216:G:OP2	2.42	0.46
27:A:2363:A:C6	27:A:2375:G:C6	3.04	0.46
27:A:2673:U:O3'	27:A:2674:A:H8	1.98	0.46
30:a:488:C:H1'	30:a:489:A:H2	1.78	0.46
30:a:768:U:O2'	50:w:97:GLU:HG2	2.15	0.46
30:a:907:G:C2	30:a:909:G:C8	3.03	0.46
30:a:1001:G:H2'	30:a:1002:U:C6	2.49	0.46
30:a:1067:G:H2'	30:a:1068:G:H8	1.79	0.46
30:a:1351:G:H5''	38:j:134:LYS:HB3	1.97	0.46
32:d:48:ARG:HD2	32:d:48:ARG:N	2.30	0.46
33:e:165:TRP:CD1	33:e:181:PRO:HB3	2.51	0.46
42:n:16:GLU:N	42:n:16:GLU:OE1	2.48	0.46
5:I:84:TYR:N	5:I:136:GLY:O	2.35	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:R:42:ARG:HA	11:R:47:ILE:HG13	1.96	0.46
11:R:43:SER:O	11:R:112:ARG:NH2	2.37	0.46
11:R:83:ARG:O	11:R:87:LEU:HD13	2.15	0.46
11:R:102:PHE:CD2	27:A:2600:A:N1	2.83	0.46
19:1:7:ILE:HG21	19:1:60:LYS:HG3	1.97	0.46
27:A:487:U:H2'	27:A:488:G:O4'	2.15	0.46
27:A:643:G:O2'	27:A:644:G:OP1	2.30	0.46
27:A:844:G:O2'	27:A:878:G:H4'	2.15	0.46
27:A:929:C:H1'	27:A:1339:G:N2	2.31	0.46
27:A:977:G:H2'	27:A:978:A:O4'	2.15	0.46
27:A:2329:G:H2'	27:A:2330:U:C6	2.51	0.46
27:A:2330:U:H3'	27:A:2331:U:C5	2.51	0.46
27:A:2363:A:H2'	27:A:2364:C:H6	1.77	0.46
30:a:480:G:H2'	30:a:481:G:H8	1.80	0.46
34:f:36:TYR:HE1	34:f:66:ASP:HB3	1.81	0.46
35:g:29:VAL:HG13	35:g:30:ILE:HG23	1.97	0.46
38:j:70:ALA:O	38:j:74:THR:HG22	2.15	0.46
2:F:188:GLU:OE1	2:F:188:GLU:N	2.29	0.46
7:M:91:GLU:HA	7:M:94:GLU:HG2	1.95	0.46
10:Q:87:TYR:OH	10:Q:116:VAL:O	2.33	0.46
12:S:14:ASP:OD1	12:S:15:ASP:N	2.49	0.46
27:A:1536:A:H2'	27:A:1537:U:C6	2.49	0.46
27:A:2552:A:H2'	27:A:2553:G:H8	1.77	0.46
27:A:2580:G:H2'	27:A:2581:G:O4'	2.15	0.46
29:C:34:C:H2'	50:w:31:ARG:HH21	1.79	0.46
30:a:1375:G:H21	30:a:1486:A:H8	1.63	0.46
40:l:92:ASP:OD1	40:l:92:ASP:N	2.48	0.46
45:q:46:PRO:HG3	45:q:96:LYS:HD3	1.98	0.46
27:A:278:A:H2'	27:A:279:U:O4'	2.16	0.46
27:A:1509:U:H2'	27:A:1510:A:O4'	2.15	0.46
27:A:2019:A:H2'	27:A:2020:A:C8	2.50	0.46
28:B:63:U:H2'	28:B:64:G:H8	1.81	0.46
30:a:452:A:C2	45:q:47:SER:HB3	2.50	0.46
30:a:534:U:H2'	30:a:535:C:C6	2.50	0.46
42:n:91:ARG:HB3	42:n:98:VAL:HG12	1.96	0.46
2:F:144:VAL:HA	2:F:147:ARG:HD3	1.97	0.46
11:R:20:ARG:NH1	27:A:2520:U:C5	2.84	0.46
12:S:82:HIS:CE1	12:S:84:ASP:HB2	2.50	0.46
27:A:1167:C:H1'	27:A:1231:U:H4'	1.97	0.46
27:A:1825:C:N4	27:A:1840:G:OP2	2.29	0.46
27:A:2085:C:O2'	27:A:2086:U:O4'	2.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:3043:G:H2'	27:A:3044:A:H5''	1.96	0.46
43:o:4:LYS:HE3	43:o:4:LYS:HB2	1.81	0.46
43:o:22:GLU:HB3	43:o:23:ARG:NH1	2.31	0.46
27:A:166:A:H2'	27:A:167:G:O4'	2.15	0.46
27:A:587:G:N1	27:A:590:A:OP2	2.42	0.46
27:A:967:G:H2'	27:A:968:C:H6	1.81	0.46
27:A:1244:A:H4'	27:A:1245:U:O4'	2.15	0.46
27:A:1523:U:H2'	27:A:1524:G:H8	1.80	0.46
27:A:1922:G:H2'	27:A:1923:G:C8	2.50	0.46
27:A:2417:C:H2'	27:A:2418:U:O4'	2.16	0.46
27:A:2901:G:H2'	27:A:2902:A:H8	1.80	0.46
30:a:920:A:N3	30:a:1359:U:O2'	2.38	0.46
35:g:44:GLY:HA3	35:g:59:ILE:HG23	1.97	0.46
37:i:94:LEU:HD22	37:i:106:ILE:HD13	1.98	0.46
43:o:22:GLU:HB3	43:o:23:ARG:NH2	2.31	0.46
48:t:42:PRO:O	48:t:45:ILE:HG12	2.16	0.46
2:F:170:MET:HG2	2:F:171:GLY:N	2.30	0.46
27:A:220:A:H2	27:A:266:U:H5''	1.81	0.46
27:A:1705:C:H2'	27:A:1706:A:C8	2.50	0.46
27:A:2538:A:H2'	27:A:2539:G:C8	2.49	0.46
27:A:2815:C:N4	27:A:2816:G:O6	2.48	0.46
28:B:24:G:H2'	28:B:25:G:C8	2.50	0.46
30:a:82:U:N3	30:a:87:G:N1	2.28	0.46
30:a:995:A:N6	30:a:1001:G:O6	2.49	0.46
30:a:1242:A:N6	30:a:1255:G:H1'	2.31	0.46
33:e:151:GLN:O	33:e:155:GLU:HG3	2.15	0.46
39:k:42:LEU:HB2	39:k:71:LYS:HB2	1.96	0.46
49:u:33:ARG:O	49:u:37:GLU:HG3	2.15	0.46
4:H:80:SER:N	4:H:88:GLU:OE2	2.49	0.46
17:X:73:VAL:HG11	17:X:105:ILE:HD13	1.97	0.46
27:A:308:U:H2'	27:A:309:G:C8	2.46	0.46
27:A:844:G:H4'	27:A:878:G:H5'	1.96	0.46
27:A:2678:G:H2'	27:A:2678:G:N3	2.31	0.46
29:C:37:A:H4'	29:C:37:A:OP1	2.16	0.46
30:a:321:A:H2'	30:a:322:C:H6	1.80	0.46
30:a:774:A:H2'	30:a:775:C:C6	2.50	0.46
49:u:5:LYS:HE2	49:u:5:LYS:HB3	1.76	0.46
5:I:126:VAL:HA	5:I:132:PHE:HB2	1.98	0.46
27:A:34:C:H2'	27:A:35:A:C8	2.50	0.46
27:A:443:C:H2'	27:A:444:U:O4'	2.16	0.46
27:A:621:U:H2'	27:A:622:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:998:G:H2'	27:A:999:C:C6	2.51	0.46
27:A:1100:C:H5''	27:A:1101:A:OP1	2.17	0.46
27:A:1659:U:H2'	27:A:1660:A:H8	1.81	0.46
27:A:2330:U:H3'	27:A:2331:U:C6	2.50	0.46
27:A:2532:G:O2'	27:A:2534:A:N7	2.45	0.46
27:A:2888:G:O5'	27:A:2888:G:H8	1.99	0.46
30:a:1013:G:H2'	30:a:1014:U:O4'	2.15	0.46
30:a:1418:G:H2'	30:a:1419:C:H6	1.81	0.46
37:i:50:ARG:HH12	37:i:63:GLN:NE2	2.12	0.46
50:w:111:TRP:CD1	50:w:111:TRP:C	2.93	0.46
17:X:37:GLY:HA2	17:X:40:ARG:NH2	2.30	0.45
22:5:18:ALA:CB	27:A:12:G:H4'	2.45	0.45
27:A:264:G:H4'	27:A:516:G:H22	1.81	0.45
27:A:1284:A:H2'	27:A:1285:G:C8	2.50	0.45
27:A:1437:A:N1	27:A:1448:C:O2'	2.44	0.45
27:A:1529:U:H3'	27:A:1530:G:H8	1.81	0.45
27:A:3118:U:H2'	27:A:3119:A:C8	2.51	0.45
30:a:252:U:H2'	30:a:253:U:C6	2.51	0.45
30:a:489:A:H8	30:a:523:U:O2'	1.99	0.45
30:a:1002:U:H2'	30:a:1003:C:C6	2.51	0.45
32:d:15:THR:HG21	32:d:181:ASP:HB3	1.97	0.45
34:f:70:MET:CG	34:f:96:PHE:HD1	2.29	0.45
5:I:47:GLU:OE1	5:I:47:GLU:N	2.25	0.45
9:O:31:LYS:HG2	9:O:31:LYS:O	2.15	0.45
15:V:38:GLU:O	15:V:42:ILE:HG13	2.16	0.45
26:4:36:GLU:OE1	42:n:54:THR:HG23	2.08	0.45
27:A:546:G:O2'	27:A:557:G:O6	2.34	0.45
27:A:995:U:H2'	27:A:996:G:C8	2.51	0.45
27:A:1639:G:H5'	27:A:1640:A:OP1	2.16	0.45
27:A:1679:A:OP1	27:A:1679:A:H4'	2.16	0.45
27:A:2758:A:H2'	27:A:2759:G:O4'	2.16	0.45
28:B:63:U:H2'	28:B:64:G:C8	2.52	0.45
30:a:698:A:C8	40:l:127:HIS:HB3	2.51	0.45
30:a:1278:C:H4'	30:a:1284:U:O4	2.16	0.45
33:e:90:GLU:O	33:e:95:ASN:ND2	2.47	0.45
41:m:7:LEU:HB3	46:r:49:TYR:CE2	2.52	0.45
11:R:76:ASP:OD1	11:R:77:LYS:N	2.42	0.45
19:1:14:PHE:HZ	27:A:1480:A:N7	2.13	0.45
21:3:13:ILE:HD11	27:A:1107:G:C8	2.51	0.45
27:A:947:U:H2'	27:A:948:G:C8	2.51	0.45
27:A:1611:A:H2'	27:A:1612:U:H6	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1630:U:O4	27:A:1631:A:N6	2.49	0.45
27:A:2084:A:H2'	27:A:2085:C:O4'	2.16	0.45
27:A:2374:U:H2'	27:A:2375:G:C8	2.51	0.45
29:C:11:A:H2'	29:C:12:G:H8	1.81	0.45
30:a:449:C:H2'	30:a:450:G:O4'	2.17	0.45
30:a:468:U:H2'	30:a:469:G:C8	2.50	0.45
31:v:27:GLN:HA	31:v:30:LYS:HD3	1.97	0.45
34:f:126:PRO:HA	34:f:147:ASP:OD2	2.17	0.45
41:m:49:LEU:HD23	41:m:49:LEU:HA	1.81	0.45
1:E:233:HIS:NE2	1:E:246:PRO:HA	2.32	0.45
2:F:27:THR:OG1	2:F:196:GLY:O	2.28	0.45
11:R:55:LEU:HD12	11:R:55:LEU:H	1.82	0.45
17:X:37:GLY:HA2	17:X:40:ARG:HH21	1.81	0.45
19:1:33:ILE:CG2	19:1:50:ASN:HB3	2.46	0.45
19:1:48:ARG:HB2	19:1:48:ARG:HH11	1.80	0.45
27:A:5:U:C2	27:A:6:G:C8	3.04	0.45
27:A:655:G:H22	27:A:670:A:H2	1.63	0.45
27:A:929:C:H1'	27:A:1339:G:H21	1.82	0.45
27:A:1008:G:C2	27:A:1009:U:C4	3.03	0.45
27:A:1650:G:H2'	27:A:1651:C:C6	2.51	0.45
27:A:2065:A:H5'	30:a:682:A:C4'	2.46	0.45
27:A:2712:U:H2'	27:A:2713:G:C8	2.51	0.45
29:C:26:G:H1	29:C:45:G:H21	1.64	0.45
30:a:214:U:H1'	30:a:218:G:N2	2.31	0.45
30:a:684:A:C5	30:a:685:U:C5	3.05	0.45
30:a:1251:G:H2'	30:a:1252:G:H8	1.81	0.45
30:a:1287:G:H22	30:a:1313:G:H1'	1.81	0.45
32:d:130:ARG:HD2	34:f:80:GLU:OE2	2.16	0.45
43:o:26:GLU:HA	43:o:29:ARG:HG3	1.98	0.45
46:r:65:ASN:N	46:r:65:ASN:OD1	2.48	0.45
4:H:76:ARG:HH21	28:B:42:C:H42	1.64	0.45
6:J:27:ARG:HG2	6:J:28:ASN:OD1	2.17	0.45
12:S:48:ARG:HB2	12:S:95:LYS:HG2	1.99	0.45
13:T:12:LYS:O	13:T:16:THR:HG23	2.16	0.45
14:U:25:GLU:OE2	27:A:1111:G:N2	2.47	0.45
27:A:388:U:H2'	27:A:389:G:O4'	2.17	0.45
27:A:1468:A:H2'	27:A:1469:A:C8	2.52	0.45
27:A:2086:U:H2'	27:A:2087:C:H6	1.81	0.45
27:A:2366:C:H3'	27:A:2367:G:H8	1.82	0.45
30:a:737:U:OP1	30:a:802:G:O2'	2.35	0.45
30:a:890:A:H2'	30:a:891:A:H8	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1044:G:O2'	30:a:1171:G:N2	2.49	0.45
32:d:6:ASN:OD1	32:d:9:GLY:N	2.42	0.45
32:d:80:GLY:O	32:d:84:ASP:N	2.35	0.45
39:k:72:ARG:HD3	39:k:72:ARG:HA	1.65	0.45
3:G:165:GLY:O	3:G:169:VAL:HG22	2.17	0.45
4:H:111:ILE:HD13	4:H:115:LEU:HD12	1.98	0.45
27:A:307:G:H2'	27:A:308:U:C6	2.52	0.45
27:A:789:G:C4	27:A:919:A:N6	2.84	0.45
27:A:2510:A:H4'	27:A:2511:A:O4'	2.16	0.45
27:A:2545:G:H5'	27:A:2546:A:OP2	2.16	0.45
27:A:2729:G:H2'	27:A:2800:G:H1	1.82	0.45
30:a:589:A:C5	30:a:590:A:C8	3.05	0.45
30:a:976:A:C2	43:o:5:SER:HB3	2.52	0.45
30:a:1124:G:H2'	30:a:1125:G:H8	1.80	0.45
30:a:1157:A:H2'	30:a:1158:G:C8	2.52	0.45
30:a:1390:C:C2	30:a:1391:A:C8	3.05	0.45
30:a:1411:A:H2'	30:a:1412:C:C6	2.52	0.45
36:h:138:ARG:HA	36:h:141:THR:HG22	1.99	0.45
41:m:59:SER:C	41:m:60:GLN:OE1	2.60	0.45
42:n:82:ILE:HA	42:n:89:GLY:HA2	1.98	0.45
6:J:10:GLU:HG3	6:J:11:HIS:ND1	2.31	0.45
7:M:91:GLU:OE1	7:M:91:GLU:N	2.49	0.45
11:R:73:ILE:HG22	11:R:75:GLY:H	1.81	0.45
16:W:69:THR:N	16:W:72:GLY:O	2.45	0.45
26:4:34:VAL:HG11	42:n:50:ASP:OD2	2.16	0.45
27:A:577:G:C5	27:A:1399:A:C2	3.05	0.45
27:A:690:G:C6	27:A:776:G:C6	3.05	0.45
27:A:736:G:N2	27:A:738:A:H3'	2.32	0.45
27:A:1250:U:H3'	27:A:1251:A:H5''	1.97	0.45
27:A:1377:A:C4	27:A:1378:U:C5	3.04	0.45
27:A:1554:U:H2'	27:A:1555:A:H8	1.77	0.45
27:A:1854:U:H2'	27:A:1855:A:H8	1.81	0.45
27:A:2074:G:N2	27:A:2110:U:O4	2.50	0.45
27:A:2356:G:H21	27:A:2381:A:N6	2.14	0.45
30:a:360:G:H2'	30:a:361:G:C8	2.52	0.45
30:a:1138:A:H1'	30:a:1162:G:N2	2.32	0.45
30:a:1281:A:H2'	30:a:1281:A:N3	2.32	0.45
43:o:12:GLN:O	43:o:15:GLU:HG3	2.17	0.45
3:G:108:ALA:HB1	3:G:112:ARG:HH11	1.81	0.45
4:H:128:GLN:HB2	4:H:135:TYR:CE1	2.51	0.45
5:I:127:GLU:OE1	5:I:127:GLU:N	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:7:LYS:H	7:M:10:ASP:CG	2.24	0.45
11:R:83:ARG:HA	11:R:86:GLN:OE1	2.16	0.45
15:V:105:LYS:HD3	27:A:2236:G:OP1	2.17	0.45
16:W:24:ILE:HD11	16:W:96:PHE:CD2	2.52	0.45
27:A:89:A:HO2'	27:A:90:C:P	2.38	0.45
27:A:290:C:N4	27:A:300:G:H21	2.15	0.45
27:A:672:C:H2'	27:A:673:C:C6	2.51	0.45
27:A:818:U:H2'	27:A:819:G:O4'	2.17	0.45
27:A:3024:A:H2'	27:A:3025:G:H8	1.81	0.45
48:t:13:ASP:O	48:t:17:LYS:HG2	2.17	0.45
1:E:206:TRP:HE3	1:E:211:ARG:HE	1.64	0.45
3:G:67:ARG:HH21	3:G:71:THR:HA	1.82	0.45
5:I:45:ARG:HA	5:I:51:ILE:HG22	1.98	0.45
14:U:79:LYS:NZ	27:A:1108:A:N1	2.65	0.45
27:A:460:G:O2'	27:A:488:G:O6	2.29	0.45
27:A:740:A:O2'	27:A:741:G:OP2	2.27	0.45
27:A:1487:U:O2'	27:A:2436:A:N3	2.49	0.45
27:A:2771:U:H2'	27:A:2772:G:H8	1.82	0.45
30:a:1109:C:O2'	30:a:1110:A:N7	2.36	0.45
35:g:7:MET:HE3	35:g:7:MET:HB2	1.83	0.45
35:g:45:ARG:HD3	35:g:45:ARG:HA	1.70	0.45
35:g:79:LEU:HD23	35:g:79:LEU:HA	1.86	0.45
5:I:3:ARG:O	5:I:6:LYS:HG2	2.17	0.45
7:M:120:LYS:HD3	27:A:3004:C:OP2	2.18	0.45
27:A:356:G:H4'	27:A:358:G:C6	2.52	0.45
27:A:988:U:H4'	27:A:989:G:OP1	2.17	0.45
27:A:2094:G:O2'	27:A:2095:G:H8	2.00	0.45
27:A:3014:A:N6	27:A:3113:A:OP2	2.49	0.45
30:a:884:G:H2'	30:a:885:G:H8	1.82	0.45
32:d:123:LEU:HD11	32:d:129:PHE:HA	1.98	0.45
40:l:29:ALA:HB1	40:l:94:PHE:HE2	1.82	0.45
22:5:4:PRO:HG2	27:A:2240:U:O2	2.17	0.44
27:A:1937:U:H2'	27:A:1938:G:O4'	2.17	0.44
27:A:2563:G:H2'	27:A:2564:A:H8	1.82	0.44
27:A:2581:G:OP2	27:A:2581:G:H8	1.99	0.44
27:A:2693:A:C6	27:A:2706:A:C8	3.05	0.44
27:A:2857:A:H2'	27:A:2858:G:H8	1.82	0.44
30:a:413:G:H5''	30:a:414:A:H5''	1.98	0.44
30:a:474:G:O2'	30:a:476:A:H1'	2.17	0.44
30:a:997:A:C2	30:a:1200:A:H1'	2.52	0.44
30:a:1118:A:OP1	30:a:1118:A:H2'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1131:G:N2	39:k:41:PRO:HG2	2.32	0.44
39:k:12:ALA:HB3	39:k:18:ILE:HB	1.98	0.44
39:k:16:GLU:H	39:k:16:GLU:CD	2.11	0.44
5:I:30:LYS:HG2	5:I:81:THR:O	2.17	0.44
26:4:57:ARG:CD	48:t:67:VAL:O	2.65	0.44
27:A:218:A:N3	27:A:234:U:O2'	2.38	0.44
27:A:1628:A:H2	27:A:1631:A:C2	2.35	0.44
27:A:1656:A:H2'	27:A:1657:G:C8	2.52	0.44
27:A:2338:G:H4'	27:A:2388:G:H22	1.82	0.44
27:A:2548:U:H5''	27:A:2549:G:H5''	2.00	0.44
27:A:3045:C:H2'	27:A:3046:C:O4'	2.17	0.44
30:a:481:G:OP1	41:m:114:ARG:NH2	2.48	0.44
30:a:1163:G:H4'	30:a:1164:U:H5'	2.00	0.44
30:a:1232:A:H2'	30:a:1233:A:C8	2.52	0.44
34:f:91:GLU:OE1	34:f:95:ASN:ND2	2.50	0.44
43:o:31:ILE:O	43:o:37:SER:OG	2.33	0.44
43:o:32:ARG:NH2	48:t:7:LYS:HE2	2.32	0.44
44:p:19:ASP:OD1	44:p:19:ASP:C	2.60	0.44
4:H:132:THR:HG22	4:H:132:THR:O	2.18	0.44
7:M:45:THR:HG22	7:M:47:ASN:H	1.82	0.44
27:A:301:U:C2	27:A:338:C:H5'	2.53	0.44
27:A:978:A:H2'	27:A:979:G:H8	1.81	0.44
27:A:1154:G:C6	27:A:1238:G:C6	3.06	0.44
27:A:2681:U:C4	27:A:2718:G:O6	2.70	0.44
28:B:47:A:C5	28:B:48:C:C5	3.06	0.44
29:C:32:C:C5'	36:h:86:GLN:NE2	2.80	0.44
30:a:826:U:H5'	30:a:827:U:OP1	2.17	0.44
30:a:1447:C:H2'	30:a:1448:G:H8	1.81	0.44
32:d:59:THR:OG1	32:d:62:ARG:NH2	2.50	0.44
35:g:40:VAL:HG23	35:g:63:ILE:HG13	1.99	0.44
44:p:78:TYR:O	44:p:82:ILE:HG12	2.18	0.44
3:G:156:VAL:HG12	3:G:158:ILE:HG23	1.99	0.44
5:I:97:VAL:O	5:I:129:PRO:HA	2.18	0.44
13:T:119:GLU:H	13:T:119:GLU:CD	2.24	0.44
27:A:636:U:H5''	27:A:637:G:N9	2.33	0.44
27:A:935:A:H4'	27:A:951:G:H22	1.82	0.44
27:A:967:G:H2'	27:A:968:C:C6	2.53	0.44
27:A:984:U:C2	27:A:985:G:C8	3.06	0.44
27:A:2288:C:H2'	27:A:2289:C:C6	2.53	0.44
28:B:92:G:H2'	28:B:93:U:C6	2.52	0.44
30:a:10:G:O6	34:f:124:ALA:HA	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:323:U:H2'	30:a:324:G:O4'	2.17	0.44
30:a:964:U:H4'	30:a:965:A:O4'	2.16	0.44
34:f:196:LYS:O	34:f:200:GLU:HG2	2.16	0.44
36:h:143:LYS:HE2	36:h:143:LYS:HB2	1.89	0.44
3:G:61:GLY:HA3	3:G:80:ARG:HG2	2.00	0.44
4:H:12:LYS:HE3	4:H:104:TRP:NE1	2.32	0.44
27:A:248:G:H5'	27:A:250:G:N7	2.33	0.44
27:A:662:G:C5	27:A:2254:A:N6	2.86	0.44
27:A:1016:C:H2'	27:A:1017:G:O4'	2.17	0.44
27:A:1550:G:O6	27:A:1620:U:O4	2.36	0.44
27:A:2471:A:H2'	27:A:2472:C:H6	1.82	0.44
27:A:2844:C:C4	27:A:2845:G:N7	2.86	0.44
30:a:45:G:H2'	30:a:46:G:H8	1.83	0.44
30:a:1043:C:OP2	30:a:1044:G:O2'	2.33	0.44
38:j:53:ARG:NE	38:j:57:ASN:OD1	2.46	0.44
43:o:64:ASP:OD1	43:o:79:LEU:HD23	2.17	0.44
4:H:171:ALA:O	4:H:174:ARG:HG2	2.18	0.44
5:I:142:VAL:O	5:I:146:SER:OG	2.29	0.44
11:R:125:LEU:HD23	11:R:125:LEU:HA	1.71	0.44
21:3:40:ASN:O	21:3:44:ARG:HG2	2.17	0.44
27:A:324:C:O2	27:A:452:G:N2	2.51	0.44
27:A:947:U:H2'	27:A:948:G:H8	1.81	0.44
27:A:1018:U:H1'	27:A:1019:C:N4	2.29	0.44
27:A:1549:G:O2'	27:A:1550:G:O5'	2.35	0.44
29:C:63:G:H2'	29:C:64:G:H8	1.83	0.44
30:a:1383:C:H1'	50:w:84:ARG:HD3	1.98	0.44
31:v:27:GLN:O	31:v:30:LYS:HG2	2.18	0.44
46:r:63:ASP:OD1	46:r:63:ASP:N	2.51	0.44
2:F:157:PRO:HG2	2:F:159:ARG:HG2	1.99	0.44
6:J:5:LEU:HD22	6:J:9:VAL:HG11	2.00	0.44
11:R:25:LEU:HD11	11:R:103:ASP:OD1	2.17	0.44
14:U:7:VAL:O	14:U:13:GLN:HA	2.18	0.44
15:V:85:GLU:O	27:A:21:G:O2'	2.33	0.44
27:A:215:A:C8	27:A:520:A:N6	2.86	0.44
27:A:298:G:H22	27:A:338:C:H42	1.65	0.44
27:A:934:A:OP2	27:A:1302:G:N2	2.38	0.44
27:A:1074:A:H2	27:A:2682:G:H4'	1.82	0.44
27:A:2344:G:H4'	27:A:2391:G:H22	1.82	0.44
27:A:2581:G:H2'	27:A:2583:C:OP2	2.18	0.44
28:B:29:C:O2'	28:B:60:G:N2	2.50	0.44
28:B:45:G:N2	28:B:49:C:C2	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:470:U:C2	30:a:471:G:C8	3.06	0.44
30:a:743:G:H2'	30:a:744:C:C6	2.52	0.44
30:a:1271:A:H2'	30:a:1272:G:H5'	1.99	0.44
32:d:72:PRO:HG3	32:d:104:GLU:HB2	2.00	0.44
2:F:104:GLU:H	2:F:104:GLU:CD	2.25	0.44
2:F:104:GLU:OE1	2:F:104:GLU:N	2.35	0.44
3:G:152:LYS:HE3	3:G:152:LYS:HB2	1.83	0.44
21:3:13:ILE:HG21	27:A:1106:A:C5	2.52	0.44
24:7:6:ARG:HB2	27:A:1830:C:O2'	2.18	0.44
27:A:1326:G:H1'	27:A:1352:A:N6	2.33	0.44
27:A:2531:G:H5'	27:A:2532:G:C8	2.53	0.44
27:A:2569:G:N3	27:A:2605:C:H2'	2.32	0.44
27:A:2613:G:H5''	27:A:2614:U:O4'	2.18	0.44
27:A:2876:C:N3	27:A:2893:G:N1	2.65	0.44
30:a:255:G:H2'	30:a:256:U:C6	2.52	0.44
39:k:25:ILE:O	39:k:29:VAL:HG22	2.18	0.44
41:m:4:ILE:HG22	46:r:51:LYS:HD2	2.00	0.44
42:n:15:MET:HG2	42:n:43:MET:O	2.18	0.44
48:t:17:LYS:O	48:t:21:VAL:HG13	2.17	0.44
2:F:132:PHE:HE1	2:F:165:ARG:CZ	2.31	0.44
3:G:6:ASP:OD1	3:G:6:ASP:N	2.36	0.44
3:G:104:LYS:NZ	27:A:713:G:N7	2.63	0.44
5:I:39:GLU:CD	5:I:40:PRO:HD3	2.43	0.44
10:Q:45:ARG:HB2	10:Q:46:PRO:HD3	2.00	0.44
12:S:51:GLY:HA2	12:S:56:GLU:CD	2.43	0.44
17:X:88:ASP:OD1	17:X:93:LYS:N	2.51	0.44
27:A:72:G:H2'	27:A:72:G:N3	2.32	0.44
27:A:685:G:N3	27:A:685:G:H2'	2.33	0.44
27:A:2249:G:H2'	27:A:2250:A:H8	1.80	0.44
27:A:2443:U:H2'	27:A:2444:C:C6	2.53	0.44
27:A:2729:G:O2'	27:A:2730:U:O5'	2.35	0.44
27:A:2815:C:H2'	27:A:2816:G:C8	2.51	0.44
27:A:2878:A:N1	27:A:2889:A:H5''	2.33	0.44
28:B:75:U:C2	28:B:76:G:C8	3.06	0.44
30:a:11:G:H1	34:f:122:ARG:HH11	1.66	0.44
30:a:581:U:H2'	30:a:582:U:C6	2.53	0.44
30:a:1301:A:OP1	48:t:3:ARG:HB2	2.18	0.44
32:d:29:LYS:HB3	32:d:29:LYS:HE3	1.70	0.44
38:j:108:ILE:HD12	38:j:108:ILE:HA	1.75	0.44
2:F:113:ASP:OD1	2:F:178:GLN:HA	2.18	0.43
4:H:126:PRO:O	4:H:174:ARG:NH1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:16:VAL:HB	14:U:99:VAL:HG21	2.00	0.43
27:A:306:U:H2'	27:A:307:G:H8	1.83	0.43
27:A:751:A:H2'	27:A:752:C:C6	2.53	0.43
27:A:1001:C:C6	27:A:1002:C:H1'	2.53	0.43
27:A:1013:U:N3	27:A:1014:G:H1'	2.33	0.43
27:A:1295:U:H2'	27:A:1296:G:H8	1.82	0.43
27:A:1738:G:C2	27:A:1739:A:C8	3.06	0.43
27:A:3036:C:C4	27:A:3037:C:C5	3.06	0.43
27:A:3053:U:O4	27:A:3104:A:H5''	2.18	0.43
28:B:1:G:C6	28:B:117:A:N1	2.86	0.43
30:a:318:G:C6	30:a:336:A:C6	3.06	0.43
30:a:411:A:C5	30:a:413:G:H1'	2.53	0.43
35:g:4:TYR:CD2	35:g:72:VAL:HG21	2.52	0.43
42:n:29:ARG:O	42:n:33:ILE:HG23	2.18	0.43
43:o:38:PRO:HB2	43:o:41:ARG:HD3	1.99	0.43
50:w:11:LEU:HD13	50:w:40:LEU:HB3	2.00	0.43
1:E:258:ARG:HD2	27:A:2016:G:OP1	2.18	0.43
4:H:40:LYS:HD2	4:H:99:ARG:NH2	2.33	0.43
4:H:75:ARG:HH21	4:H:78:ARG:HH22	1.66	0.43
5:I:35:LEU:HD22	5:I:36:ASP:H	1.82	0.43
27:A:150:C:H2'	27:A:151:A:H8	1.82	0.43
27:A:978:A:H2'	27:A:979:G:C8	2.53	0.43
27:A:996:G:H2'	27:A:997:G:H8	1.82	0.43
27:A:1645:G:H2'	27:A:1646:U:C6	2.53	0.43
27:A:2755:A:H2	27:A:2882:C:O2	2.01	0.43
27:A:3070:G:O2'	27:A:3087:G:N2	2.51	0.43
29:C:2:G:C2	29:C:72:A:C2	3.06	0.43
30:a:99:U:OP1	49:u:12:ARG:NH1	2.52	0.43
30:a:254:G:C6	30:a:273:A:C6	3.07	0.43
30:a:1035:A:C6	30:a:1187:G:C5	3.06	0.43
30:a:1222:G:H2'	30:a:1223:G:H8	1.82	0.43
30:a:1481:G:OP2	50:w:28:ARG:NH2	2.51	0.43
34:f:117:GLY:HA2	34:f:155:SER:HB3	2.00	0.43
37:i:101:LEU:HD23	37:i:101:LEU:HA	1.82	0.43
39:k:20:ALA:HA	39:k:23:ARG:NH1	2.32	0.43
42:n:69:ASP:OD1	42:n:70:LEU:N	2.51	0.43
47:s:34:ASP:OD1	47:s:34:ASP:O	2.35	0.43
2:F:174:ARG:NE	27:A:2997:C:OP1	2.51	0.43
4:H:110:LEU:HD12	4:H:114:ALA:HB3	2.00	0.43
11:R:18:ARG:NH2	28:B:8:C:OP1	2.48	0.43
22:5:7:ARG:NH1	27:A:671:G:O2'	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:8:12:LYS:NZ	27:A:246:U:O4	2.45	0.43
27:A:222:A:O2'	27:A:508:G:N3	2.41	0.43
27:A:580:G:H2'	27:A:581:G:O4'	2.19	0.43
27:A:666:A:N6	27:A:2257:A:H4'	2.34	0.43
27:A:844:G:H5'	27:A:845:C:H5''	2.00	0.43
27:A:1640:A:O2'	27:A:1641:U:OP1	2.36	0.43
27:A:2777:G:N3	27:A:2807:G:H1'	2.33	0.43
30:a:686:A:C6	30:a:687:U:C4	3.06	0.43
30:a:918:C:C2	30:a:919:A:C8	3.05	0.43
30:a:996:G:N2	30:a:999:A:OP2	2.36	0.43
39:k:14:ASP:O	39:k:18:ILE:HG22	2.18	0.43
40:l:74:LEU:O	40:l:77:GLU:HG3	2.18	0.43
42:n:15:MET:HB3	42:n:34:LEU:HD11	2.00	0.43
48:t:49:PHE:O	48:t:60:VAL:N	2.45	0.43
1:E:37:LEU:HD13	1:E:62:TYR:HB2	2.00	0.43
8:N:63:VAL:HG23	8:N:64:ARG:HG3	2.00	0.43
11:R:85:GLY:O	11:R:88:ILE:HG22	2.19	0.43
24:7:21:PHE:HB2	24:7:46:THR:HG21	2.01	0.43
27:A:356:G:H4'	27:A:358:G:C4	2.53	0.43
27:A:790:A:N3	27:A:2667:C:O2'	2.42	0.43
27:A:1025:A:H2'	27:A:1026:A:C8	2.53	0.43
27:A:1706:A:H2'	27:A:1707:G:C8	2.52	0.43
27:A:2759:G:N3	27:A:2760:G:C8	2.87	0.43
27:A:2964:A:H2'	27:A:2965:A:C8	2.53	0.43
30:a:30:A:H61	30:a:538:G:H1'	1.83	0.43
30:a:371:A:H2'	30:a:372:C:O4'	2.18	0.43
30:a:918:C:C4	30:a:919:A:N7	2.86	0.43
30:a:1116:U:H1'	30:a:1117:U:C2	2.53	0.43
32:d:47:GLU:HB2	32:d:48:ARG:HH11	1.83	0.43
32:d:130:ARG:H	32:d:130:ARG:HG2	1.50	0.43
38:j:55:LEU:O	38:j:55:LEU:HD13	2.18	0.43
42:n:90:LEU:O	42:n:94:ARG:HG2	2.17	0.43
44:p:39:LEU:HD12	44:p:39:LEU:HA	1.80	0.43
46:r:63:ASP:OD2	46:r:66:GLY:HA2	2.18	0.43
1:E:273:ARG:HB3	1:E:273:ARG:NH1	2.32	0.43
4:H:158:GLY:C	4:H:159:MET:HG3	2.42	0.43
5:I:147:ALA:O	5:I:151:ARG:HG3	2.17	0.43
11:R:9:ASN:OD1	11:R:10:ILE:N	2.51	0.43
27:A:6:G:H2'	27:A:2853:C:H42	1.83	0.43
27:A:270:U:H1'	27:A:512:G:N2	2.33	0.43
27:A:347:U:H2'	27:A:348:G:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:583:G:C5	27:A:584:A:C8	3.06	0.43
27:A:639:C:O2'	27:A:640:G:O5'	2.34	0.43
27:A:668:U:H2'	27:A:669:G:C8	2.52	0.43
27:A:813:C:O2'	27:A:849:A:N6	2.49	0.43
27:A:1528:G:H2'	27:A:1529:U:H6	1.83	0.43
27:A:1556:A:C2	27:A:1615:G:N1	2.86	0.43
27:A:1733:C:H2'	27:A:1734:C:H6	1.83	0.43
27:A:2254:A:H4'	27:A:2255:A:N7	2.33	0.43
27:A:2357:A:H2	27:A:2382:G:O4'	2.01	0.43
30:a:21:U:O2'	30:a:1059:G:H1'	2.18	0.43
30:a:494:C:H2'	30:a:495:G:H8	1.84	0.43
30:a:614:C:H2'	30:a:615:G:H8	1.83	0.43
44:p:14:GLN:OE1	44:p:15:TYR:HD1	2.02	0.43
11:R:47:ILE:HD13	11:R:116:LEU:HD23	2.01	0.43
24:7:18:VAL:O	24:7:23:LEU:HD22	2.18	0.43
27:A:273:A:H62	27:A:313:G:H21	1.67	0.43
27:A:356:G:N2	27:A:357:U:O4	2.51	0.43
27:A:2394:A:H5'	27:A:2396:A:N7	2.34	0.43
27:A:2692:A:P	27:A:2700:A:H61	2.42	0.43
28:B:4:A:H4'	28:B:63:U:H4'	2.01	0.43
28:B:50:C:H2'	28:B:51:G:C8	2.53	0.43
30:a:631:C:H2'	30:a:632:U:C6	2.53	0.43
30:a:995:A:C6	30:a:1001:G:C6	3.07	0.43
30:a:1177:A:O2'	30:a:1178:A:OP1	2.25	0.43
30:a:1290:C:OP2	42:n:99:ARG:HG3	2.19	0.43
1:E:31:LYS:NZ	27:A:1647:G:N7	2.59	0.43
2:F:113:ASP:N	2:F:209:ARG:O	2.48	0.43
5:I:91:PHE:CE1	5:I:164:ARG:HB2	2.54	0.43
6:J:31:LEU:N	6:J:32:PRO:HD2	2.33	0.43
27:A:161:U:H4'	27:A:162:A:OP1	2.18	0.43
27:A:663:A:C6	27:A:2254:A:C6	3.07	0.43
27:A:1378:U:C4	27:A:1379:G:C6	3.06	0.43
27:A:2471:A:H2'	27:A:2472:C:C6	2.54	0.43
29:C:72:A:H3'	29:C:73:A:H5''	2.01	0.43
30:a:10:G:C5	34:f:149:LEU:HD11	2.53	0.43
30:a:384:G:H2'	30:a:385:C:C6	2.53	0.43
30:a:805:A:H2'	30:a:806:C:C6	2.53	0.43
30:a:905:A:H2'	30:a:906:C:C6	2.54	0.43
34:f:195:LEU:O	34:f:199:ARG:HG3	2.17	0.43
36:h:73:LEU:HD12	36:h:73:LEU:HA	1.79	0.43
40:l:65:ARG:HD3	40:l:65:ARG:HA	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:68:GLN:HE22	27:A:790:A:H4'	1.84	0.43
4:H:182:PHE:HA	4:H:183:PRO:HD3	1.83	0.43
5:I:9:VAL:HG11	5:I:74:ALA:HB2	2.00	0.43
10:Q:8:PRO:HG2	27:A:1870:U:C4	2.54	0.43
13:T:49:ASP:OD2	27:A:621:U:O2'	2.26	0.43
19:1:14:PHE:HZ	27:A:1480:A:C8	2.37	0.43
27:A:361:A:N1	27:A:440:U:O2'	2.49	0.43
27:A:1471:G:H2'	27:A:1472:C:C6	2.53	0.43
27:A:1485:C:H2'	27:A:1486:G:O4'	2.19	0.43
27:A:2385:G:O2'	27:A:2387:U:O4'	2.34	0.43
27:A:3115:A:C2	27:A:3116:C:C2	3.07	0.43
30:a:337:G:C2	30:a:338:A:C5	3.07	0.43
30:a:384:G:H2'	30:a:385:C:H6	1.83	0.43
30:a:493:A:H2'	30:a:494:C:H6	1.84	0.43
30:a:580:G:H2'	30:a:581:U:C6	2.54	0.43
30:a:658:U:H2'	30:a:659:C:H6	1.83	0.43
30:a:1098:U:H2'	30:a:1099:C:H6	1.84	0.43
30:a:1389:U:C4	30:a:1390:C:C5	3.07	0.43
33:e:75:ASN:C	33:e:75:ASN:HD22	2.26	0.43
44:p:85:LEU:CB	44:p:87:LEU:HG	2.49	0.43
25:8:31:HIS:NE2	27:A:2616:A:OP2	2.36	0.43
25:8:34:GLU:HB2	27:A:2644:C:OP1	2.18	0.43
27:A:764:U:H2'	27:A:765:G:C8	2.54	0.43
27:A:1302:G:H8	27:A:1302:G:O5'	2.01	0.43
27:A:1703:G:H2'	27:A:1704:U:H6	1.83	0.43
27:A:1896:A:C4	27:A:1897:A:C8	3.07	0.43
27:A:1939:U:H3	27:A:1955:A:H62	1.66	0.43
27:A:2074:G:H21	27:A:2109:A:H62	1.65	0.43
27:A:2338:G:H4'	27:A:2388:G:N2	2.33	0.43
27:A:2971:G:O6	27:A:2979:C:H5''	2.19	0.43
29:C:34:C:C2'	50:w:31:ARG:NH2	2.80	0.43
30:a:24:U:H2'	30:a:25:G:O4'	2.19	0.43
30:a:280:C:H42	46:r:56:THR:HG23	1.83	0.43
30:a:473:A:H2'	30:a:474:G:C8	2.54	0.43
30:a:1098:U:H2'	30:a:1099:C:C6	2.54	0.43
33:e:104:ARG:H	33:e:108:MET:HE3	1.84	0.43
35:g:30:ILE:HD11	35:g:38:ASP:OD1	2.18	0.43
38:j:136:TYR:CE2	39:k:60:ASP:O	2.70	0.43
41:m:31:ARG:HH21	41:m:58:THR:HG21	1.83	0.43
1:E:36:PRO:HB3	27:A:1790:A:H5'	2.01	0.43
1:E:158:SER:HB3	1:E:161:VAL:HG21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:30:LYS:HA	5:I:30:LYS:HD2	1.58	0.43
11:R:73:ILE:HD12	11:R:73:ILE:N	2.33	0.43
17:X:44:HIS:HB3	27:A:571:A:C1'	2.47	0.43
27:A:1223:U:H2'	27:A:1224:G:C8	2.49	0.43
27:A:2003:A:H1'	27:A:2162:A:N6	2.34	0.43
27:A:2188:G:O2'	27:A:2191:C:OP2	2.20	0.43
27:A:2328:G:C6	27:A:2408:G:N1	2.86	0.43
27:A:2373:G:H2'	27:A:2374:U:C6	2.53	0.43
27:A:2716:U:H2'	27:A:2717:U:C6	2.54	0.43
27:A:2968:G:OP2	27:A:2979:C:N4	2.52	0.43
30:a:335:C:H2'	30:a:336:A:C8	2.54	0.43
30:a:425:G:H2'	30:a:426:U:C6	2.53	0.43
30:a:492:U:H2'	30:a:493:A:C8	2.54	0.43
30:a:1219:A:H2	30:a:1222:G:N3	2.16	0.43
30:a:1220:A:H62	30:a:1281:A:H61	1.66	0.43
30:a:1359:U:H2'	30:a:1360:A:C8	2.54	0.43
34:f:132:ALA:HB2	34:f:150:ALA:HB3	1.99	0.43
35:g:4:TYR:N	35:g:65:VAL:O	2.32	0.43
50:w:76:GLU:OE2	50:w:80:ARG:NE	2.50	0.43
3:G:4:LYS:HZ3	3:G:17:SER:HB3	1.82	0.42
4:H:8:LEU:HB3	4:H:13:GLN:HE21	1.83	0.42
5:I:77:VAL:HA	5:I:80:VAL:HG22	2.01	0.42
5:I:81:THR:HG1	5:I:82:GLU:CD	2.19	0.42
5:I:88:MET:HB3	5:I:132:PHE:CE1	2.54	0.42
7:M:36:LEU:O	7:M:51:GLY:HA3	2.19	0.42
16:W:48:LYS:HE2	16:W:48:LYS:HB2	1.74	0.42
17:X:8:THR:O	17:X:74:VAL:HG12	2.17	0.42
27:A:2425:U:O2'	27:A:2427:G:OP1	2.29	0.42
27:A:2622:C:H2'	27:A:2623:A:C8	2.54	0.42
27:A:2873:U:H2'	27:A:2874:C:H6	1.83	0.42
29:C:72:A:H2'	29:C:73:A:O4'	2.19	0.42
30:a:229:U:H5''	45:q:34:ILE:HD13	2.00	0.42
30:a:318:G:O6	30:a:336:A:N6	2.53	0.42
30:a:1508:C:H2'	30:a:1509:G:C8	2.54	0.42
34:f:59:THR:HG22	34:f:77:LYS:HB3	2.01	0.42
35:g:30:ILE:HG22	35:g:71:THR:HG22	2.01	0.42
37:i:22:HIS:O	37:i:66:TYR:OH	2.32	0.42
39:k:88:MET:HE2	39:k:88:MET:H	1.83	0.42
6:J:25:TYR:HE2	6:J:30:LEU:HD21	1.84	0.42
8:N:24:VAL:HG12	8:N:30:ARG:HD3	2.00	0.42
9:O:55:MET:HE2	9:O:55:MET:HB2	1.92	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:U:67:HIS:ND1	14:U:95:THR:HG22	2.34	0.42
21:3:15:ALA:O	21:3:20:ARG:NH1	2.53	0.42
27:A:21:G:H2'	27:A:22:U:C6	2.55	0.42
27:A:1118:A:H2'	27:A:1119:A:C8	2.54	0.42
30:a:92:A:HO2'	30:a:93:C:H6	1.64	0.42
30:a:309:G:O2'	30:a:587:A:N1	2.52	0.42
30:a:309:G:H2'	30:a:310:G:H8	1.85	0.42
30:a:452:A:H2	45:q:47:SER:HB3	1.83	0.42
34:f:48:LYS:HB2	34:f:48:LYS:HE2	1.82	0.42
34:f:137:ARG:O	34:f:141:GLU:HG3	2.19	0.42
48:t:34:TRP:HE1	48:t:52:HIS:CD2	2.37	0.42
1:E:86:PRO:HG3	27:A:1787:A:C2'	2.49	0.42
13:T:77:ASN:OD1	13:T:78:ARG:N	2.52	0.42
17:X:1:MET:SD	17:X:28:PRO:HA	2.60	0.42
22:5:31:SER:HB2	22:5:36:GLN:OE1	2.19	0.42
27:A:453:U:H2'	27:A:454:U:C6	2.54	0.42
27:A:660:U:N3	27:A:663:A:OP2	2.33	0.42
27:A:1233:A:H2'	27:A:1234:U:O4'	2.18	0.42
27:A:1900:C:OP2	27:A:1917:G:N2	2.41	0.42
27:A:2065:A:H5'	30:a:682:A:C5'	2.49	0.42
30:a:136:G:C6	30:a:225:G:C5	3.07	0.42
30:a:380:G:N2	30:a:383:A:OP2	2.46	0.42
30:a:1020:G:H2'	30:a:1021:U:C6	2.54	0.42
41:m:99:ARG:NH1	41:m:105:GLN:O	2.44	0.42
1:E:217:LYS:HE3	1:E:217:LYS:HB3	1.69	0.42
11:R:67:GLU:OE2	11:R:67:GLU:N	2.50	0.42
13:T:89:GLU:HA	13:T:89:GLU:OE2	2.20	0.42
27:A:2394:A:H3'	27:A:2396:A:C8	2.53	0.42
27:A:2401:U:H2'	27:A:2402:C:C6	2.55	0.42
27:A:3052:A:O2'	27:A:3105:C:OP1	2.29	0.42
30:a:49:U:OP1	30:a:307:C:O2'	2.34	0.42
30:a:322:C:H2'	30:a:323:U:C6	2.54	0.42
30:a:1249:G:H2'	30:a:1250:A:C8	2.54	0.42
8:N:110:LYS:HA	8:N:110:LYS:HD2	1.75	0.42
26:4:61:PHE:CZ	48:t:41:ILE:HD12	2.54	0.42
27:A:639:C:HO2'	27:A:640:G:C5'	2.31	0.42
27:A:680:U:H2'	27:A:681:C:C6	2.55	0.42
27:A:692:C:H2'	27:A:693:G:H8	1.85	0.42
27:A:2098:U:H2'	27:A:2099:G:O4'	2.20	0.42
27:A:2211:C:H2'	27:A:2212:A:C8	2.52	0.42
30:a:281:G:H8	30:a:281:G:OP2	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:i:31:LYS:HE3	37:i:31:LYS:HB2	1.74	0.42
3:G:13:LYS:HD2	3:G:13:LYS:C	2.45	0.42
3:G:201:LEU:O	3:G:205:ILE:HG12	2.19	0.42
23:6:11:ILE:HD12	23:6:11:ILE:O	2.20	0.42
23:6:15:CYS:SG	23:6:16:GLU:N	2.93	0.42
26:4:15:GLN:HA	26:4:20:HIS:O	2.20	0.42
27:A:27:G:H2'	27:A:28:C:H6	1.84	0.42
27:A:175:G:H3'	27:A:176:G:N2	2.34	0.42
27:A:249:C:OP2	27:A:2618:C:O2'	2.28	0.42
27:A:618:C:OP1	27:A:653:G:N1	2.51	0.42
27:A:646:U:H2'	27:A:647:G:O4'	2.19	0.42
27:A:828:G:H2'	27:A:829:U:C6	2.54	0.42
27:A:1077:A:O5'	27:A:1077:A:H8	2.02	0.42
27:A:1158:U:H2'	27:A:1159:C:H6	1.84	0.42
27:A:1311:C:H2'	27:A:1312:G:H8	1.85	0.42
27:A:1501:C:H2'	27:A:1502:G:C8	2.54	0.42
27:A:2238:A:H2'	27:A:2239:A:C8	2.54	0.42
27:A:2562:G:C2	27:A:2563:G:C8	3.07	0.42
27:A:2851:G:O2'	27:A:3005:A:N1	2.37	0.42
27:A:2901:G:H2'	27:A:2902:A:C8	2.54	0.42
30:a:424:G:H2'	30:a:425:G:H8	1.84	0.42
30:a:614:C:H2'	30:a:615:G:C8	2.55	0.42
30:a:761:A:OP2	30:a:780:G:N1	2.35	0.42
30:a:804:U:H2'	30:a:805:A:H8	1.84	0.42
30:a:808:A:H2'	30:a:809:G:O4'	2.19	0.42
30:a:821:C:N4	30:a:822:U:O2	2.52	0.42
30:a:930:C:H2'	30:a:931:A:H8	1.85	0.42
32:d:147:LYS:HB3	32:d:203:TYR:CD2	2.55	0.42
33:e:86:LEU:HD23	33:e:86:LEU:HA	1.88	0.42
41:m:18:LYS:HD3	41:m:18:LYS:HA	1.75	0.42
50:w:8:ASP:C	50:w:8:ASP:OD1	2.62	0.42
4:H:92:ILE:HD13	4:H:92:ILE:HA	1.92	0.42
5:I:120:GLU:H	5:I:120:GLU:CD	2.22	0.42
8:N:108:GLU:CD	8:N:108:GLU:N	2.76	0.42
12:S:51:GLY:HA2	12:S:56:GLU:HG2	2.02	0.42
23:6:37:GLU:OE2	23:6:50:PRO:HB3	2.20	0.42
27:A:216:A:H2'	27:A:217:G:C8	2.54	0.42
27:A:1296:G:H2'	27:A:1297:G:C8	2.54	0.42
27:A:1437:A:C2	27:A:1438:G:C8	3.08	0.42
27:A:1538:G:H2'	27:A:1539:A:C8	2.55	0.42
27:A:1614:G:H2'	27:A:1615:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1791:A:H2'	27:A:1792:A:H8	1.84	0.42
27:A:2152:A:H2'	27:A:2153:G:O4'	2.18	0.42
27:A:2351:A:H1'	27:A:2396:A:O2'	2.20	0.42
27:A:2359:G:N1	27:A:2379:G:H1'	2.35	0.42
27:A:3083:A:H2'	27:A:3084:G:H8	1.83	0.42
28:B:91:G:H2'	28:B:92:G:H8	1.83	0.42
28:B:110:G:H2'	28:B:111:C:C6	2.55	0.42
30:a:266:G:H2'	30:a:266:G:N3	2.33	0.42
30:a:481:G:H1'	30:a:529:C:H1'	2.01	0.42
30:a:590:A:C5	30:a:591:C:C5	3.08	0.42
30:a:1480:C:H2'	30:a:1481:G:O4'	2.20	0.42
38:j:108:ILE:HD11	38:j:115:ARG:HB2	2.00	0.42
39:k:6:ILE:HD12	39:k:6:ILE:O	2.20	0.42
42:n:14:ARG:NH2	42:n:16:GLU:OE2	2.52	0.42
1:E:147:LEU:HA	1:E:147:LEU:HD23	1.84	0.42
4:H:57:ILE:O	4:H:61:ILE:HG12	2.19	0.42
6:J:25:TYR:HD2	6:J:30:LEU:HD11	1.84	0.42
11:R:67:GLU:CD	11:R:67:GLU:H	2.25	0.42
23:6:10:LYS:HE2	23:6:10:LYS:HB2	1.79	0.42
24:7:13:ARG:NH1	27:A:1493:A:OP1	2.52	0.42
27:A:601:A:H2'	27:A:602:A:C8	2.54	0.42
27:A:911:U:H2'	27:A:912:C:C6	2.55	0.42
27:A:1132:U:N3	27:A:1133:G:N7	2.67	0.42
27:A:1157:G:H1	27:A:1234:U:H3	1.68	0.42
27:A:2961:G:H2'	27:A:2962:A:C8	2.54	0.42
30:a:49:U:H2'	30:a:50:G:H8	1.81	0.42
30:a:119:C:OP1	30:a:311:C:O2'	2.36	0.42
30:a:264:U:H2'	30:a:265:G:O4'	2.20	0.42
30:a:657:U:H3	30:a:693:G:H22	1.68	0.42
32:d:34:GLU:OE2	32:d:58:ARG:NE	2.53	0.42
35:g:47:ARG:HA	35:g:57:GLU:HA	2.02	0.42
2:F:129:ARG:NH2	2:F:169:ARG:O	2.52	0.42
4:H:31:ASN:OD1	4:H:33:MET:HG3	2.20	0.42
6:J:10:GLU:HG3	6:J:11:HIS:CE1	2.55	0.42
8:N:2:ILE:HD13	8:N:2:ILE:HA	1.85	0.42
21:3:11:SER:OG	27:A:1107:G:OP2	2.29	0.42
27:A:290:C:N4	27:A:299:G:H22	2.18	0.42
27:A:479:A:H1'	27:A:499:G:O4'	2.20	0.42
27:A:990:G:O2'	27:A:991:C:H5	2.02	0.42
27:A:1234:U:H2'	27:A:1235:U:H6	1.85	0.42
27:A:2318:U:C4	27:A:2319:G:N7	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2325:U:H2'	27:A:2326:A:H8	1.83	0.42
27:A:2326:A:C6	27:A:2410:A:C5	3.08	0.42
27:A:2642:G:H2'	27:A:2643:U:O4'	2.19	0.42
27:A:2717:U:C4	27:A:2718:G:C8	3.08	0.42
27:A:2885:G:H2'	27:A:2886:A:C8	2.54	0.42
29:C:26:G:O2'	29:C:27:U:O5'	2.32	0.42
30:a:9:U:H3'	30:a:10:G:C2	2.55	0.42
30:a:397:A:H5'	30:a:398:C:OP1	2.20	0.42
30:a:1382:C:C2	30:a:1486:A:N6	2.88	0.42
32:d:71:ARG:HB3	32:d:74:ILE:HG13	2.01	0.42
32:d:206:ASP:N	32:d:206:ASP:OD1	2.51	0.42
27:A:1407:G:H2'	27:A:1408:C:C6	2.55	0.42
27:A:1859:A:H2'	27:A:1860:G:O4'	2.20	0.42
27:A:2324:A:N1	27:A:2412:U:C2	2.87	0.42
30:a:619:G:O6	30:a:620:A:N6	2.53	0.42
30:a:847:A:H2'	30:a:848:C:C6	2.55	0.42
30:a:1087:C:C4	30:a:1088:G:C8	3.07	0.42
32:d:11:ARG:NH2	32:d:175:LEU:O	2.52	0.42
36:h:115:THR:O	36:h:119:ARG:HG3	2.20	0.42
37:i:54:ALA:HB2	37:i:59:SER:OG	2.20	0.42
46:r:29:SER:HB3	46:r:37:VAL:HB	2.01	0.42
49:u:56:ARG:O	49:u:60:LYS:HB3	2.20	0.42
11:R:4:LYS:HA	11:R:4:LYS:HD3	1.83	0.41
26:4:12:THR:HG21	26:4:26:SER:HB3	2.02	0.41
27:A:1035:G:H21	27:A:2493:A:H8	1.67	0.41
27:A:1378:U:H2'	27:A:1379:G:C8	2.54	0.41
27:A:1927:C:O2'	27:A:3080:A:N3	2.47	0.41
27:A:1992:U:O4	27:A:2006:A:H2	2.02	0.41
27:A:2261:U:H2'	27:A:2262:C:C6	2.55	0.41
27:A:2421:A:O2'	27:A:2422:A:H8	2.03	0.41
27:A:2443:U:H2'	27:A:2444:C:H6	1.85	0.41
30:a:39:G:H2'	30:a:40:C:H6	1.85	0.41
30:a:562:U:OP2	30:a:738:G:N1	2.45	0.41
30:a:724:C:H2'	30:a:725:A:H8	1.85	0.41
30:a:806:C:O2	37:i:16:ASN:ND2	2.53	0.41
31:v:5:ILE:O	31:v:9:ARG:HG3	2.20	0.41
32:d:65:VAL:O	32:d:100:LEU:HD12	2.20	0.41
36:h:120:LEU:O	36:h:124:ILE:HG13	2.19	0.41
37:i:11:LEU:HD22	37:i:77:LEU:HD22	2.01	0.41
38:j:77:ARG:HB3	38:j:81:PHE:HE2	1.85	0.41
38:j:120:LYS:HA	38:j:120:LYS:HE3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:u:59:ASP:OD1	49:u:59:ASP:N	2.53	0.41
7:M:113:LYS:HE2	27:A:616:A:OP1	2.19	0.41
27:A:9:U:O2	27:A:2850:C:H4'	2.21	0.41
27:A:33:G:C6	27:A:34:C:C4	3.08	0.41
27:A:81:A:C2	27:A:100:A:C5	3.08	0.41
27:A:2676:C:H42	27:A:2728:U:H3	1.68	0.41
27:A:2882:C:H2'	27:A:2883:G:O4'	2.20	0.41
28:B:88:C:H3'	28:B:89:C:C6	2.55	0.41
28:B:110:G:H2'	28:B:111:C:H6	1.84	0.41
30:a:315:A:N7	30:a:328:U:H5	2.18	0.41
30:a:907:G:O2'	30:a:909:G:OP1	2.36	0.41
30:a:982:A:H2'	30:a:983:C:C6	2.54	0.41
30:a:1390:C:N3	30:a:1391:A:N7	2.67	0.41
30:a:1425:G:H5''	30:a:1426:C:H5	1.84	0.41
1:E:266:LYS:HE3	27:A:2447:G:O3'	2.21	0.41
4:H:16:ARG:HE	4:H:16:ARG:HB2	1.60	0.41
9:O:22:VAL:HG12	9:O:29:LYS:HD2	2.02	0.41
27:A:41:A:H2'	27:A:42:G:O4'	2.20	0.41
27:A:1152:G:H2'	27:A:1153:U:C6	2.56	0.41
27:A:1529:U:H2'	27:A:1530:G:O4'	2.21	0.41
27:A:1533:U:H5''	27:A:1535:C:H42	1.85	0.41
27:A:1547:G:N2	27:A:1623:U:O2	2.35	0.41
27:A:1728:U:H4'	27:A:1729:A:O4'	2.21	0.41
27:A:1733:C:H2'	27:A:1734:C:C6	2.55	0.41
29:C:34:C:C2'	50:w:31:ARG:HH21	2.32	0.41
30:a:430:A:OP1	33:e:7:PRO:HA	2.20	0.41
30:a:543:A:H2'	30:a:547:G:C8	2.55	0.41
30:a:813:U:H2'	30:a:814:G:H8	1.86	0.41
30:a:976:A:N3	43:o:5:SER:HB3	2.36	0.41
30:a:982:A:N6	30:a:1022:G:C6	2.88	0.41
34:f:50:VAL:HG22	34:f:51:LYS:H	1.85	0.41
35:g:27:LEU:O	35:g:30:ILE:HG13	2.20	0.41
41:m:4:ILE:O	41:m:8:VAL:HG13	2.20	0.41
4:H:36:PRO:HB3	4:H:167:ALA:HA	2.02	0.41
8:N:30:ARG:HG3	27:A:2898:G:H4'	2.02	0.41
16:W:62:ARG:NH2	27:A:1455:U:OP2	2.49	0.41
23:6:7:VAL:O	23:6:8:ARG:C	2.64	0.41
27:A:4:G:H2'	27:A:5:U:H6	1.85	0.41
27:A:307:G:C2	27:A:308:U:C2	3.08	0.41
27:A:737:A:N1	27:A:2593:A:O2'	2.49	0.41
27:A:1074:A:N1	27:A:2683:A:C8	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2394:A:H3'	27:A:2396:A:N7	2.36	0.41
27:A:2887:G:H2'	27:A:2888:G:O4'	2.20	0.41
28:B:37:C:N3	28:B:50:C:O2'	2.47	0.41
30:a:321:A:H2'	30:a:322:C:C6	2.55	0.41
30:a:658:U:H2'	30:a:659:C:C6	2.55	0.41
30:a:1249:G:O2'	30:a:1250:A:O4'	2.34	0.41
30:a:1450:C:H2'	30:a:1451:G:O4'	2.20	0.41
38:j:58:TYR:CZ	38:j:87:LEU:HD12	2.55	0.41
50:w:1:MET:HB2	50:w:26:SER:HB2	2.00	0.41
4:H:101:ASP:OD1	4:H:102:ARG:N	2.54	0.41
4:H:130:ASP:O	4:H:132:THR:N	2.45	0.41
6:J:25:TYR:CE2	6:J:30:LEU:HD21	2.55	0.41
10:Q:70:ILE:O	10:Q:71:ARG:HB3	2.21	0.41
20:2:12:GLU:HA	20:2:12:GLU:OE1	2.20	0.41
23:6:37:GLU:C	23:6:37:GLU:OE1	2.64	0.41
27:A:296:A:C6	27:A:340:A:N6	2.87	0.41
27:A:419:G:C5	27:A:420:G:H1'	2.56	0.41
27:A:851:C:H2'	27:A:852:C:H6	1.85	0.41
27:A:979:G:H2'	27:A:980:C:H6	1.84	0.41
27:A:1137:U:O2'	27:A:1139:A:N7	2.40	0.41
27:A:2553:G:H2'	27:A:2554:U:C6	2.55	0.41
27:A:3021:A:H4'	27:A:3022:G:N7	2.36	0.41
27:A:3058:A:H2'	27:A:3059:G:H8	1.85	0.41
28:B:88:C:H2'	28:B:89:C:O4'	2.21	0.41
29:C:34:C:C1'	50:w:31:ARG:HH21	2.34	0.41
30:a:1050:U:H2'	30:a:1051:C:C6	2.56	0.41
30:a:1422:G:H2'	30:a:1423:U:C6	2.55	0.41
30:a:1487:A:N6	30:a:1516:U:H1'	2.35	0.41
32:d:37:ALA:O	32:d:40:LYS:HG2	2.20	0.41
3:G:160:ARG:NH2	27:A:706:G:O2'	2.54	0.41
4:H:59:GLY:HA3	4:H:157:ARG:HH12	1.85	0.41
11:R:89:ALA:O	11:R:93:LYS:HG2	2.21	0.41
13:T:119:GLU:N	13:T:119:GLU:CD	2.79	0.41
14:U:26:LYS:HB3	14:U:26:LYS:HE2	1.77	0.41
27:A:98:U:H3'	27:A:99:G:H5'	2.03	0.41
27:A:673:C:H2'	27:A:674:U:C6	2.55	0.41
27:A:694:C:H2'	27:A:695:G:O4'	2.20	0.41
27:A:750:C:H2'	27:A:751:A:C8	2.56	0.41
27:A:994:A:N7	27:A:1014:G:O2'	2.52	0.41
27:A:2253:A:C2'	27:A:2254:A:H5'	2.50	0.41
27:A:2350:G:H4'	27:A:2351:A:OP1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2376:G:H2'	27:A:2377:G:C8	2.54	0.41
27:A:2685:C:H2'	27:A:2686:U:C6	2.56	0.41
27:A:2876:C:N4	27:A:2893:G:O6	2.51	0.41
28:B:89:C:H2'	28:B:90:G:O4'	2.21	0.41
30:a:298:A:H2'	30:a:299:G:C8	2.55	0.41
30:a:489:A:C8	30:a:523:U:O2'	2.74	0.41
30:a:702:G:H2'	30:a:702:G:N3	2.36	0.41
30:a:980:G:C6	30:a:1024:G:C6	3.09	0.41
30:a:984:A:N6	30:a:1020:G:O6	2.54	0.41
30:a:1324:C:H2'	30:a:1325:G:C8	2.56	0.41
33:e:185:GLN:H	33:e:185:GLN:HG2	1.68	0.41
34:f:140:LEU:HD13	34:f:148:ILE:HG21	2.01	0.41
35:g:48:LEU:HB3	47:s:75:ALA:HB1	2.03	0.41
36:h:57:ASP:HA	36:h:58:PRO:HD3	1.95	0.41
1:E:20:ASP:O	1:E:22:ALA:N	2.53	0.41
2:F:104:GLU:CD	2:F:104:GLU:N	2.79	0.41
3:G:169:VAL:HB	3:G:175:VAL:HG11	2.03	0.41
4:H:57:ILE:HD13	4:H:57:ILE:HA	1.97	0.41
4:H:76:ARG:HH21	28:B:42:C:N4	2.18	0.41
23:6:40:LYS:NZ	27:A:2571:C:OP1	2.54	0.41
27:A:736:G:H1'	27:A:740:A:N6	2.36	0.41
27:A:739:U:O3'	27:A:740:A:H2'	2.20	0.41
27:A:1288:A:H2'	27:A:1289:A:C8	2.55	0.41
27:A:1633:U:H2'	27:A:1634:C:C6	2.56	0.41
27:A:1677:G:H2'	27:A:1678:U:O4'	2.21	0.41
27:A:2056:G:N3	27:A:2056:G:H2'	2.36	0.41
27:A:2758:A:C6	27:A:2759:G:C5	3.08	0.41
30:a:109:G:H1'	30:a:354:G:H5'	2.02	0.41
30:a:456:C:H1'	30:a:457:A:C5	2.55	0.41
30:a:932:U:H2'	30:a:933:G:H8	1.85	0.41
30:a:1253:U:H2'	30:a:1254:G:O4'	2.21	0.41
30:a:1432:C:H2'	30:a:1433:C:C6	2.56	0.41
33:e:188:VAL:HG13	33:e:189:PRO:O	2.21	0.41
40:l:37:ASN:OD1	40:l:37:ASN:N	2.53	0.41
44:p:26:GLU:H	44:p:26:GLU:CD	2.25	0.41
4:H:44:ASN:OD1	4:H:45:MET:N	2.53	0.41
5:I:82:GLU:N	5:I:82:GLU:OE2	2.54	0.41
12:S:61:ARG:NH1	12:S:70:GLU:OE1	2.54	0.41
26:4:28:LYS:HB2	26:4:33:ILE:HD11	2.03	0.41
27:A:311:G:C4	27:A:312:G:C8	3.08	0.41
27:A:1234:U:H2'	27:A:1235:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:2074:G:N2	27:A:2109:A:H62	2.18	0.41
30:a:518:U:H2'	30:a:519:A:H8	1.86	0.41
30:a:538:G:OP2	30:a:539:A:O2'	2.28	0.41
30:a:1385:C:H2'	30:a:1386:C:O4'	2.20	0.41
33:e:73:GLU:OE1	33:e:76:ARG:NH2	2.44	0.41
36:h:112:ARG:HE	36:h:112:ARG:HB3	1.58	0.41
38:j:42:VAL:HG23	38:j:82:ASP:HB2	2.02	0.41
39:k:80:THR:OG1	39:k:81:PRO:HD2	2.21	0.41
1:E:21:PHE:HB3	1:E:24:ILE:HG12	2.03	0.41
7:M:72:LYS:NZ	27:A:1257:G:H5''	2.35	0.41
7:M:98:THR:HB	7:M:124:VAL:CG2	2.51	0.41
12:S:12:LEU:HA	12:S:12:LEU:HD12	1.78	0.41
13:T:95:LEU:HD23	13:T:95:LEU:HA	1.97	0.41
22:5:48:ARG:HD3	27:A:3106:C:N4	2.35	0.41
26:4:38:CYS:SG	26:4:39:SER:N	2.93	0.41
26:4:61:PHE:CD1	26:4:61:PHE:C	2.99	0.41
27:A:362:A:O2'	27:A:363:A:O4'	2.27	0.41
27:A:662:G:C5	27:A:2254:A:C6	3.09	0.41
27:A:780:U:H2'	27:A:781:C:H6	1.86	0.41
27:A:986:G:N3	27:A:987:A:H1'	2.36	0.41
27:A:1396:G:H2'	27:A:1397:U:H6	1.81	0.41
27:A:1533:U:H3'	27:A:1534:C:H5''	2.03	0.41
27:A:2142:A:O2'	27:A:2144:C:N4	2.53	0.41
27:A:2265:U:H2'	27:A:2266:A:H8	1.86	0.41
27:A:2515:U:H2'	27:A:2516:U:H6	1.84	0.41
27:A:2673:U:O2'	27:A:2725:C:N4	2.54	0.41
27:A:2884:A:H3'	27:A:2885:G:C8	2.56	0.41
28:B:59:A:C5	28:B:60:G:C8	3.08	0.41
28:B:74:A:C8	28:B:102:A:C6	3.09	0.41
30:a:23:C:H2'	30:a:24:U:H6	1.86	0.41
30:a:30:A:N6	30:a:538:G:H1'	2.35	0.41
30:a:157:A:H2'	30:a:158:A:O4'	2.20	0.41
30:a:184:U:H2'	30:a:185:G:H8	1.86	0.41
30:a:190:U:H2'	30:a:191:C:C6	2.56	0.41
30:a:356:A:N3	30:a:368:U:O2'	2.38	0.41
30:a:358:U:H2'	30:a:359:G:C8	2.53	0.41
30:a:960:A:C4	30:a:1301:A:C2	3.09	0.41
30:a:1105:U:C2	30:a:1107:G:C8	3.09	0.41
30:a:1136:A:H2'	30:a:1137:G:O4'	2.21	0.41
32:d:192:THR:HG23	32:d:193:PHE:CD1	2.56	0.41
36:h:22:LEU:HD11	36:h:66:LEU:HG	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:j:42:VAL:O	38:j:82:ASP:N	2.54	0.41
38:j:72:LEU:HA	38:j:75:VAL:HG12	2.03	0.41
40:l:81:ARG:NH1	40:l:81:ARG:HB3	2.35	0.41
44:p:4:THR:HG23	44:p:7:GLN:OE1	2.21	0.41
50:w:123:TYR:HD1	50:w:124:PHE:H	1.68	0.41
1:E:21:PHE:HB3	1:E:24:ILE:CG1	2.51	0.41
3:G:27:VAL:HG22	3:G:116:SER:OG	2.21	0.41
4:H:36:PRO:HA	4:H:166:THR:HB	2.02	0.41
7:M:55:ILE:HA	7:M:123:LYS:O	2.21	0.41
13:T:109:LEU:HD23	13:T:109:LEU:HA	1.90	0.41
22:5:38:LYS:HA	22:5:38:LYS:HD3	1.81	0.41
26:4:60:ARG:NH2	30:a:1293:G:P	2.94	0.41
27:A:747:A:H2	27:A:768:G:H21	1.66	0.41
27:A:829:U:H5	44:p:88:ARG:CZ	2.34	0.41
27:A:1007:G:C2	27:A:1008:G:C5	3.08	0.41
27:A:1501:C:H2'	27:A:1502:G:H8	1.85	0.41
27:A:1876:A:O2'	27:A:1877:U:H5'	2.21	0.41
27:A:2061:U:C2	27:A:2062:G:C8	3.09	0.41
27:A:2071:A:H2	27:A:2311:G:O4'	2.04	0.41
27:A:2113:A:H2'	27:A:2114:A:C8	2.55	0.41
27:A:2147:U:H2'	27:A:2148:C:C6	2.55	0.41
30:a:458:A:OP1	30:a:459:G:H1'	2.21	0.41
30:a:980:G:H1	30:a:1023:U:H3	1.68	0.41
30:a:1200:A:H2'	30:a:1201:G:H8	1.86	0.41
30:a:1295:U:H2'	30:a:1296:C:C6	2.55	0.41
30:a:1350:U:OP2	38:j:134:LYS:NZ	2.41	0.41
30:a:1429:A:O2'	30:a:1430:A:H5'	2.20	0.41
33:e:18:ASP:HB2	33:e:26:PHE:CD2	2.57	0.41
39:k:26:VAL:HA	39:k:29:VAL:HG22	2.03	0.41
39:k:86:ALA:O	39:k:90:ILE:HG13	2.21	0.41
40:l:76:ALA:HB3	40:l:108:SER:HB2	2.03	0.41
49:u:71:GLN:O	49:u:75:LYS:HG2	2.21	0.41
3:G:63:LYS:HB3	27:A:912:C:P	2.62	0.40
5:I:12:PRO:HB2	5:I:15:VAL:HG12	2.02	0.40
11:R:18:ARG:HD2	11:R:107:TYR:CZ	2.57	0.40
17:X:40:ARG:H	17:X:40:ARG:HG2	1.71	0.40
17:X:103:LYS:NZ	17:X:103:LYS:HB3	2.36	0.40
27:A:7:U:H3'	27:A:8:U:C6	2.56	0.40
27:A:919:A:H5'	27:A:920:G:P	2.61	0.40
27:A:1431:U:C2	27:A:1452:G:N2	2.89	0.40
27:A:1756:G:H1'	27:A:1758:G:N1	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1900:C:H2'	27:A:1901:C:C6	2.56	0.40
27:A:2329:G:O6	27:A:2406:U:C4	2.74	0.40
27:A:2341:U:H5'	27:A:2342:A:OP1	2.20	0.40
30:a:96:G:C4	30:a:97:A:C8	3.08	0.40
30:a:1200:A:H2'	30:a:1201:G:C8	2.56	0.40
30:a:1301:A:C8	30:a:1305:G:C5	3.08	0.40
30:a:1409:A:H2'	30:a:1410:C:H6	1.86	0.40
32:d:32:VAL:O	32:d:36:VAL:HG13	2.20	0.40
33:e:183:ARG:HD2	33:e:183:ARG:HA	1.87	0.40
34:f:192:ALA:O	34:f:196:LYS:HG2	2.20	0.40
38:j:138:LEU:HB3	38:j:143:LYS:O	2.21	0.40
43:o:38:PRO:HB2	43:o:41:ARG:CD	2.51	0.40
1:E:224:VAL:HG13	27:A:2043:C:OP1	2.21	0.40
2:F:129:ARG:HD3	2:F:130:HIS:NE2	2.36	0.40
4:H:80:SER:HB2	4:H:87:ARG:NH1	2.36	0.40
4:H:100:GLY:N	4:H:103:MET:HE2	2.36	0.40
5:I:22:GLN:HE21	5:I:39:GLU:HA	1.86	0.40
7:M:56:VAL:HB	7:M:124:VAL:HG12	2.02	0.40
27:A:814:A:H2'	27:A:815:G:O4'	2.22	0.40
27:A:1560:U:H2'	27:A:1561:C:C6	2.56	0.40
27:A:1725:G:H2'	27:A:1726:C:O4'	2.20	0.40
27:A:3055:G:H2'	27:A:3100:A:N6	2.35	0.40
29:C:18:G:C6	29:C:58:A:C6	3.08	0.40
30:a:1276:G:H2'	30:a:1277:U:C6	2.57	0.40
36:h:136:LYS:HE3	36:h:136:LYS:HB3	1.75	0.40
41:m:99:ARG:CZ	41:m:107:VAL:HG12	2.52	0.40
42:n:12:ASP:OD1	42:n:44:ARG:NE	2.54	0.40
42:n:52:GLN:HA	42:n:55:VAL:HG12	2.02	0.40
2:F:54:TYR:CG	2:F:55:GLY:N	2.89	0.40
3:G:13:LYS:HD2	3:G:13:LYS:O	2.21	0.40
5:I:82:GLU:CD	5:I:82:GLU:N	2.79	0.40
20:2:20:ASP:O	20:2:24:GLU:HG3	2.21	0.40
22:5:4:PRO:HA	27:A:2839:U:N1	2.36	0.40
27:A:227:A:N1	27:A:505:C:O2'	2.50	0.40
27:A:289:A:C5	27:A:290:C:H5	2.40	0.40
27:A:632:G:C6	27:A:640:G:C6	3.09	0.40
27:A:1000:C:H3'	27:A:1001:C:H5''	2.03	0.40
27:A:2375:G:H2'	27:A:2376:G:C8	2.56	0.40
27:A:2541:U:H2'	27:A:2542:G:O4'	2.21	0.40
27:A:2573:G:C6	27:A:2593:A:C6	3.09	0.40
30:a:215:U:H4'	30:a:216:U:H5'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1100:U:H2'	30:a:1101:C:H6	1.87	0.40
30:a:1115:G:H1'	30:a:1121:G:H22	1.86	0.40
30:a:1231:A:C5	30:a:1269:A:C5	3.09	0.40
31:v:16:LYS:HA	31:v:16:LYS:HD2	1.87	0.40
43:o:16:LEU:HD22	43:o:19:ARG:HH12	1.85	0.40
4:H:8:LEU:HD12	4:H:8:LEU:HA	1.91	0.40
4:H:40:LYS:HG2	4:H:164:VAL:CG1	2.52	0.40
5:I:86:GLN:OE1	5:I:86:GLN:HA	2.22	0.40
9:O:24:ARG:HA	27:A:926:U:H2'	2.03	0.40
11:R:65:SER:HA	11:R:70:VAL:HG11	2.04	0.40
11:R:87:LEU:HA	11:R:90:GLU:OE2	2.22	0.40
12:S:34:GLY:O	12:S:36:LYS:NZ	2.42	0.40
27:A:618:C:OP1	27:A:653:G:N2	2.54	0.40
27:A:1259:U:H1'	27:A:1261:A:C6	2.56	0.40
27:A:1348:G:C6	27:A:1349:U:C4	3.09	0.40
27:A:2088:C:N3	27:A:2095:G:C6	2.89	0.40
27:A:2342:A:N6	27:A:2390:U:H1'	2.36	0.40
27:A:2490:A:H4'	27:A:2491:A:N3	2.36	0.40
27:A:3034:C:H2'	27:A:3035:C:C6	2.54	0.40
29:C:30:G:C4	29:C:31:G:C8	3.10	0.40
30:a:222:U:H2'	30:a:223:G:C8	2.57	0.40
30:a:962:C:H2'	30:a:963:U:O4'	2.22	0.40
30:a:1320:G:H2'	30:a:1321:A:C8	2.57	0.40
32:d:107:ASN:HB3	32:d:110:SER:HB3	2.03	0.40
33:e:126:ASP:O	33:e:127:ILE:HG12	2.22	0.40
37:i:67:GLY:HA3	37:i:71:GLU:OE2	2.22	0.40
2:F:130:HIS:ND1	2:F:165:ARG:HD2	2.36	0.40
4:H:142:GLN:HG3	4:H:148:ILE:HD13	2.02	0.40
10:Q:63:ARG:O	10:Q:67:MET:HG3	2.22	0.40
19:1:3:ALA:HB1	19:1:12:PRO:HD3	2.04	0.40
23:6:44:ASN:OD1	23:6:44:ASN:N	2.54	0.40
27:A:24:G:O2'	27:A:25:A:OP2	2.36	0.40
27:A:1074:A:C6	27:A:2683:A:C8	3.09	0.40
27:A:1102:G:H2'	27:A:1102:G:N3	2.36	0.40
27:A:1430:C:H2'	27:A:1431:U:C6	2.56	0.40
27:A:1653:G:H2'	27:A:1654:G:O4'	2.22	0.40
27:A:2247:A:H2'	27:A:2248:C:C6	2.57	0.40
27:A:2378:U:H2'	27:A:2379:G:C8	2.55	0.40
27:A:2551:A:H2'	27:A:2552:A:C8	2.56	0.40
27:A:2563:G:C2	27:A:2564:A:C5	3.09	0.40
27:A:3020:U:O2'	27:A:3021:A:N3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:3046:C:H2'	27:A:3047:A:O4'	2.22	0.40
30:a:45:G:H2'	30:a:46:G:C8	2.56	0.40
30:a:256:U:H2'	30:a:257:G:H8	1.87	0.40
30:a:418:C:H2'	30:a:419:C:C6	2.56	0.40
30:a:539:A:H4'	30:a:540:A:H3'	2.04	0.40
30:a:670:G:H2'	30:a:671:G:C8	2.57	0.40
30:a:672:U:O2'	30:a:674:G:N7	2.51	0.40
30:a:1111:G:C6	30:a:1112:C:C5	3.09	0.40
30:a:1177:A:H4'	30:a:1177:A:OP1	2.21	0.40
30:a:1515:A:H2'	30:a:1516:U:H6	1.86	0.40
35:g:62:VAL:C	35:g:63:ILE:HD12	2.47	0.40
36:h:107:PHE:O	36:h:111:ARG:HG2	2.22	0.40
36:h:126:ASP:OD1	36:h:126:ASP:N	2.52	0.40
40:l:96:LYS:HD2	40:l:124:PRO:HD3	2.03	0.40
45:q:69:PRO:O	45:q:73:LEU:HG	2.22	0.40
46:r:81:PRO:HB3	46:r:87:ARG:CZ	2.52	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%)	267 (98%)	6 (2%)	0	100	100
2	F	205/217 (94%)	200 (98%)	5 (2%)	0	100	100
3	G	206/215 (96%)	199 (97%)	7 (3%)	0	100	100
4	H	178/187 (95%)	173 (97%)	5 (3%)	0	100	100
5	I	163/179 (91%)	159 (98%)	4 (2%)	0	100	100
6	J	39/151 (26%)	37 (95%)	2 (5%)	0	100	100
7	M	144/147 (98%)	143 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
10	Q	115/199 (58%)	112 (97%)	3 (3%)	0	100	100
11	R	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
12	S	109/113 (96%)	103 (94%)	6 (6%)	0	100	100
13	T	121/129 (94%)	120 (99%)	1 (1%)	0	100	100
14	U	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
15	V	111/153 (72%)	109 (98%)	2 (2%)	0	100	100
16	W	94/100 (94%)	93 (99%)	1 (1%)	0	100	100
17	X	88/105 (84%)	86 (98%)	2 (2%)	0	100	100
18	Z	75/88 (85%)	71 (95%)	4 (5%)	0	100	100
19	1	60/64 (94%)	56 (93%)	4 (7%)	0	100	100
20	2	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
21	3	56/61 (92%)	54 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	52 (100%)	0	0	100	100
23	6	46/55 (84%)	43 (94%)	3 (6%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
26	4	55/75 (73%)	54 (98%)	1 (2%)	0	100	100
31	v	29/33 (88%)	29 (100%)	0	0	100	100
32	d	206/275 (75%)	197 (96%)	9 (4%)	0	100	100
33	e	198/201 (98%)	192 (97%)	6 (3%)	0	100	100
34	f	164/214 (77%)	159 (97%)	5 (3%)	0	100	100
35	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
36	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
37	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
38	j	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
39	k	96/101 (95%)	91 (95%)	4 (4%)	1 (1%)	12	44
40	l	113/138 (82%)	109 (96%)	4 (4%)	0	100	100
41	m	120/124 (97%)	113 (94%)	7 (6%)	0	100	100
42	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	o	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
44	p	86/89 (97%)	86 (100%)	0	0	100	100
45	q	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
46	r	92/98 (94%)	87 (95%)	5 (5%)	0	100	100
47	s	63/84 (75%)	62 (98%)	1 (2%)	0	100	100
48	t	80/93 (86%)	76 (95%)	4 (5%)	0	100	100
49	u	83/86 (96%)	83 (100%)	0	0	100	100
50	w	124/264 (47%)	119 (96%)	5 (4%)	0	100	100
All	All	5115/5975 (86%)	4956 (97%)	158 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	k	57	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	215/218 (99%)	215 (100%)	0	100	100
2	F	159/163 (98%)	155 (98%)	4 (2%)	42	63
3	G	168/173 (97%)	168 (100%)	0	100	100
4	H	149/156 (96%)	147 (99%)	2 (1%)	61	72
5	I	139/150 (93%)	137 (99%)	2 (1%)	59	71
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	117 (98%)	2 (2%)	53	70
8	N	100/100 (100%)	99 (99%)	1 (1%)	68	75
9	O	112/114 (98%)	111 (99%)	1 (1%)	70	76
10	Q	96/158 (61%)	95 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	98/100 (98%)	98 (100%)	0	100	100
13	T	96/99 (97%)	95 (99%)	1 (1%)	68	75
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	89/117 (76%)	89 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	77 (98%)	2 (2%)	42	63
18	Z	56/63 (89%)	56 (100%)	0	100	100
19	1	50/51 (98%)	47 (94%)	3 (6%)	17	44
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	51 (98%)	1 (2%)	50	68
22	5	43/46 (94%)	42 (98%)	1 (2%)	44	64
23	6	46/52 (88%)	46 (100%)	0	100	100
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	51/63 (81%)	51 (100%)	0	100	100
31	v	29/31 (94%)	29 (100%)	0	100	100
32	d	170/212 (80%)	169 (99%)	1 (1%)	78	79
33	e	175/176 (99%)	174 (99%)	1 (1%)	78	79
34	f	121/147 (82%)	120 (99%)	1 (1%)	73	77
35	g	85/85 (100%)	85 (100%)	0	100	100
36	h	129/132 (98%)	128 (99%)	1 (1%)	73	77
37	i	107/108 (99%)	107 (100%)	0	100	100
38	j	102/125 (82%)	100 (98%)	2 (2%)	48	67
39	k	89/90 (99%)	88 (99%)	1 (1%)	65	74
40	l	89/105 (85%)	87 (98%)	2 (2%)	45	65
41	m	103/105 (98%)	103 (100%)	0	100	100
42	n	99/104 (95%)	98 (99%)	1 (1%)	68	75
43	o	85/86 (99%)	83 (98%)	2 (2%)	43	64
44	p	76/77 (99%)	74 (97%)	2 (3%)	40	62
45	q	92/118 (78%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	r	80/83 (96%)	80 (100%)	0	100	100
47	s	55/72 (76%)	54 (98%)	1 (2%)	51	69
48	t	73/84 (87%)	73 (100%)	0	100	100
49	u	69/70 (99%)	69 (100%)	0	100	100
50	w	98/215 (46%)	97 (99%)	1 (1%)	68	75
All	All	4277/4842 (88%)	4240 (99%)	37 (1%)	68	76

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	156	THR
2	F	161	PHE
2	F	162	LYS
2	F	164	THR
4	H	58	ASN
4	H	81	ILE
5	I	103	ASN
5	I	117	GLU
7	M	94	GLU
7	M	138	ILE
8	N	94	ARG
9	O	137	ILE
10	Q	54	HIS
13	T	59	LYS
17	X	20	LYS
17	X	24	LEU
19	1	45	ASN
19	1	60	LYS
19	1	61	VAL
21	3	28	LEU
22	5	37	ARG
32	d	89	ASP
33	e	75	ASN
34	f	77	LYS
36	h	94	ASP
38	j	88	ASP
38	j	108	ILE
39	k	24	LYS
40	l	35	THR
40	l	128	ASN

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Mol	Chain	Res	Type
42	n	43	MET
43	o	16	LEU
43	o	48	LEU
44	p	70	VAL
44	p	89	ARG
47	s	24	SER
50	w	4	ASP

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

Mol	Chain	Res	Type
2	F	183	HIS
3	G	41	GLN
3	G	91	HIS
3	G	151	ASN
3	G	184	ASN
3	G	202	ASN
4	H	142	GLN
5	I	66	HIS
8	N	3	GLN
9	O	54	GLN
10	Q	54	HIS
10	Q	62	ASN
11	R	53	ASN
13	T	27	GLN
20	2	44	ASN
22	5	12	ASN
23	6	28	ASN
23	6	31	ASN
25	8	25	GLN
32	d	152	GLN
33	e	75	ASN
33	e	95	ASN
33	e	167	GLN
33	e	179	GLN
36	h	86	GLN
38	j	47	GLN
40	l	27	HIS
40	l	31	HIS
40	l	84	GLN
48	t	14	HIS
48	t	29	GLN

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Mol	Chain	Res	Type
48	t	52	HIS
49	u	3	ASN
49	u	7	GLN
50	w	95	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3018/3119 (96%)	552 (18%)	16 (0%)
28	B	116/118 (98%)	17 (14%)	1 (0%)
29	C	75/76 (98%)	29 (38%)	3 (4%)
30	a	1514/1528 (99%)	265 (17%)	0
All	All	4723/4841 (97%)	863 (18%)	20 (0%)

All (863) 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	29	C
27	A	32	G
27	A	33	G
27	A	55	G
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	117	U
27	A	125	C
27	A	148	A
27	A	164	A
27	A	195	A

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Mol	Chain	Res	Type
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	231	U
27	A	248	G
27	A	265	A
27	A	271	A
27	A	272	A
27	A	275	C
27	A	279	U
27	A	283	U
27	A	285	U
27	A	286	G
27	A	290	C
27	A	292	G
27	A	297	G
27	A	298	G
27	A	299	G
27	A	300	G
27	A	301	U
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	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

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Mol	Chain	Res	Type
27	A	346	C
27	A	350	A
27	A	351	G
27	A	352	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	434	G
27	A	437	G
27	A	444	U
27	A	445	U
27	A	446	G
27	A	447	A
27	A	450	G
27	A	452	G
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	505	C
27	A	509	U
27	A	512	G
27	A	523	U
27	A	543	U
27	A	544	U
27	A	555	G
27	A	566	A
27	A	568	A
27	A	569	G
27	A	578	G

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Mol	Chain	Res	Type
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	597	C
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	667	A
27	A	679	G
27	A	684	G
27	A	685	G
27	A	696	A
27	A	706	G
27	A	707	G
27	A	708	G
27	A	721	A
27	A	728	G
27	A	731	A
27	A	738	A
27	A	740	A
27	A	747	A
27	A	754	C
27	A	756	A
27	A	758	A
27	A	759	G
27	A	760	U
27	A	764	U
27	A	765	G

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Mol	Chain	Res	Type
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	839	U
27	A	845	C
27	A	862	U
27	A	863	G
27	A	868	C
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	920	G
27	A	927	C
27	A	942	U
27	A	944	A
27	A	960	G
27	A	961	U
27	A	972	A
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

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Mol	Chain	Res	Type
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	1015	A
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	1069	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
27	A	1158	U
27	A	1164	A
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	1244	A
27	A	1245	U
27	A	1248	U
27	A	1250	U
27	A	1251	A

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Mol	Chain	Res	Type
27	A	1252	G
27	A	1253	C
27	A	1254	G
27	A	1260	C
27	A	1261	A
27	A	1292	U
27	A	1293	G
27	A	1298	C
27	A	1335	G
27	A	1344	A
27	A	1353	G
27	A	1359	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	1436	C
27	A	1456	G
27	A	1465	C
27	A	1467	U
27	A	1480	A
27	A	1493	A
27	A	1494	U
27	A	1499	A
27	A	1507	G
27	A	1508	A
27	A	1510	A
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	1550	G
27	A	1551	U
27	A	1552	A
27	A	1553	C
27	A	1554	U

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Mol	Chain	Res	Type
27	A	1625	G
27	A	1627	U
27	A	1628	A
27	A	1629	G
27	A	1630	U
27	A	1632	G
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	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
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	1758	G
27	A	1767	U
27	A	1786	G
27	A	1789	A
27	A	1798	U
27	A	1803	A
27	A	1826	A
27	A	1864	U
27	A	1866	C
27	A	1871	G
27	A	1872	A

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Mol	Chain	Res	Type
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	1973	C
27	A	1975	A
27	A	1981	U
27	A	1990	A
27	A	2003	A
27	A	2004	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
27	A	2075	G
27	A	2085	C
27	A	2086	U
27	A	2087	C
27	A	2088	C
27	A	2089	C
27	A	2090	U
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	2107	G
27	A	2130	G
27	A	2137	A
27	A	2141	U
27	A	2153	G
27	A	2154	G
27	A	2160	A

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Mol	Chain	Res	Type
27	A	2161	A
27	A	2162	A
27	A	2163	U
27	A	2179	U
27	A	2188	G
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	2244	A
27	A	2247	A
27	A	2251	G
27	A	2254	A
27	A	2255	A
27	A	2256	G
27	A	2257	A
27	A	2263	G
27	A	2267	C
27	A	2279	C
27	A	2280	G
27	A	2284	A
27	A	2285	G
27	A	2286	A
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	2333	G
27	A	2334	U
27	A	2335	G
27	A	2338	G
27	A	2339	G
27	A	2340	A

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Mol	Chain	Res	Type
27	A	2341	U
27	A	2342	A
27	A	2343	G
27	A	2351	A
27	A	2353	U
27	A	2354	G
27	A	2355	U
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	2382	G
27	A	2384	C
27	A	2386	U
27	A	2387	U
27	A	2388	G
27	A	2389	U
27	A	2390	U
27	A	2393	A
27	A	2394	A
27	A	2395	U
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	2405	A
27	A	2407	C
27	A	2408	G
27	A	2410	A
27	A	2413	G
27	A	2421	A
27	A	2422	A
27	A	2427	G
27	A	2434	A
27	A	2436	A
27	A	2447	G
27	A	2449	A
27	A	2462	G

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Mol	Chain	Res	Type
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	2582	A
27	A	2585	U
27	A	2607	G
27	A	2609	A
27	A	2626	U
27	A	2627	C
27	A	2647	U
27	A	2649	A
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

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Mol	Chain	Res	Type
27	A	2718	G
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	2754	G
27	A	2759	G
27	A	2763	C
27	A	2766	A
27	A	2778	U
27	A	2786	U
27	A	2790	A
27	A	2791	G
27	A	2796	A
27	A	2797	C
27	A	2800	G
27	A	2826	A
27	A	2827	G
27	A	2833	U
27	A	2837	U
27	A	2853	C
27	A	2854	A
27	A	2862	G
27	A	2865	G
27	A	2876	C
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	2980	U

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Mol	Chain	Res	Type
27	A	2981	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	3015	C
27	A	3021	A
27	A	3022	G
27	A	3029	U
27	A	3039	C
27	A	3042	A
27	A	3056	A
27	A	3082	U
27	A	3088	C
27	A	3093	A
27	A	3104	A
27	A	3105	C
27	A	3106	C
27	A	3107	G
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
28	B	13	C
28	B	30	G
28	B	36	U
28	B	42	C
28	B	53	A
28	B	54	A
28	B	57	U
28	B	68	G
28	B	87	U
28	B	89	C
28	B	107	A
28	B	115	A
29	C	7	G

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Mol	Chain	Res	Type
29	C	8	U
29	C	9	G
29	C	13	C
29	C	16	C
29	C	17	C
29	C	18	G
29	C	20	U
29	C	21	A
29	C	22	G
29	C	24	U
29	C	26	G
29	C	27	U
29	C	28	C
29	C	37	A
29	C	38	A
29	C	46	A
29	C	47	U
29	C	48	C
29	C	49	G
29	C	52	G
29	C	53	G
29	C	54	U
29	C	56	C
29	C	63	G
29	C	73	A
29	C	74	C
29	C	75	C
29	C	76	A
30	a	9	U
30	a	12	A
30	a	13	G
30	a	36	A
30	a	43	G
30	a	51	C
30	a	52	U
30	a	55	A
30	a	58	C
30	a	59	A
30	a	82	U
30	a	84	U
30	a	86	G
30	a	87	G

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Mol	Chain	Res	Type
30	a	93	C
30	a	116	A
30	a	117	C
30	a	126	G
30	a	128	U
30	a	141	U
30	a	160	C
30	a	192	G
30	a	193	C
30	a	196	G
30	a	200	U
30	a	210	A
30	a	211	A
30	a	216	U
30	a	217	U
30	a	218	G
30	a	220	G
30	a	243	A
30	a	245	C
30	a	247	G
30	a	251	G
30	a	252	U
30	a	266	G
30	a	267	C
30	a	279	A
30	a	280	C
30	a	281	G
30	a	289	G
30	a	321	A
30	a	329	A
30	a	330	C
30	a	332	G
30	a	344	A
30	a	345	C
30	a	347	G
30	a	351	G
30	a	352	C
30	a	353	A
30	a	354	G
30	a	367	U
30	a	372	C
30	a	390	U

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Mol	Chain	Res	Type
30	a	392	C
30	a	397	A
30	a	398	C
30	a	406	G
30	a	414	A
30	a	421	U
30	a	422	C
30	a	423	G
30	a	424	G
30	a	426	U
30	a	428	G
30	a	429	U
30	a	430	A
30	a	433	C
30	a	434	C
30	a	452	A
30	a	453	G
30	a	456	C
30	a	457	A
30	a	458	A
30	a	459	G
30	a	461	G
30	a	465	G
30	a	466	U
30	a	475	A
30	a	476	A
30	a	477	G
30	a	478	A
30	a	485	G
30	a	486	G
30	a	491	C
30	a	497	G
30	a	498	C
30	a	499	C
30	a	501	G
30	a	507	G
30	a	509	G
30	a	511	U
30	a	512	A
30	a	513	A
30	a	515	A
30	a	519	A

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Mol	Chain	Res	Type
30	a	527	A
30	a	542	U
30	a	544	C
30	a	552	A
30	a	553	A
30	a	556	A
30	a	557	G
30	a	576	C
30	a	612	U
30	a	613	G
30	a	633	A
30	a	645	G
30	a	666	U
30	a	668	G
30	a	683	G
30	a	701	G
30	a	702	G
30	a	703	U
30	a	711	G
30	a	729	A
30	a	735	G
30	a	757	A
30	a	761	A
30	a	765	G
30	a	772	A
30	a	773	U
30	a	774	A
30	a	782	A
30	a	792	G
30	a	793	U
30	a	794	A
30	a	795	A
30	a	796	A
30	a	797	C
30	a	801	G
30	a	808	A
30	a	822	U
30	a	823	U
30	a	824	C
30	a	826	U
30	a	827	U
30	a	828	G

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Mol	Chain	Res	Type
30	a	829	G
30	a	841	U
30	a	884	G
30	a	896	A
30	a	908	G
30	a	909	G
30	a	913	C
30	a	914	C
30	a	916	C
30	a	917	A
30	a	942	U
30	a	943	U
30	a	950	A
30	a	951	A
30	a	953	G
30	a	956	A
30	a	957	A
30	a	958	G
30	a	959	A
30	a	973	U
30	a	974	U
30	a	975	G
30	a	976	A
30	a	981	C
30	a	982	A
30	a	985	G
30	a	986	G
30	a	988	C
30	a	990	C
30	a	1007	U
30	a	1008	C
30	a	1011	U
30	a	1012	U
30	a	1013	G
30	a	1014	U
30	a	1020	G
30	a	1021	U
30	a	1022	G
30	a	1025	C
30	a	1033	G
30	a	1034	C
30	a	1035	A

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Mol	Chain	Res	Type
30	a	1045	U
30	a	1074	G
30	a	1075	U
30	a	1081	A
30	a	1088	G
30	a	1104	G
30	a	1108	C
30	a	1110	A
30	a	1112	C
30	a	1113	A
30	a	1115	G
30	a	1116	U
30	a	1117	U
30	a	1118	A
30	a	1119	U
30	a	1120	G
30	a	1123	G
30	a	1138	A
30	a	1140	U
30	a	1147	G
30	a	1148	U
30	a	1149	C
30	a	1150	A
30	a	1151	A
30	a	1162	G
30	a	1165	G
30	a	1171	G
30	a	1176	C
30	a	1177	A
30	a	1178	A
30	a	1181	C
30	a	1182	A
30	a	1193	U
30	a	1194	A
30	a	1195	U
30	a	1217	A
30	a	1219	A
30	a	1231	A
30	a	1238	U
30	a	1241	G
30	a	1249	G
30	a	1251	G

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Mol	Chain	Res	Type
30	a	1261	A
30	a	1266	U
30	a	1267	U
30	a	1268	C
30	a	1283	U
30	a	1284	U
30	a	1285	C
30	a	1287	G
30	a	1302	C
30	a	1328	A
30	a	1329	G
30	a	1343	G
30	a	1344	C
30	a	1346	A
30	a	1347	C
30	a	1351	G
30	a	1353	G
30	a	1357	A
30	a	1364	U
30	a	1380	C
30	a	1405	G
30	a	1424	G
30	a	1426	C
30	a	1429	A
30	a	1433	C
30	a	1434	U
30	a	1435	U
30	a	1436	G
30	a	1440	A
30	a	1463	G
30	a	1476	A
30	a	1481	G
30	a	1483	A
30	a	1486	A
30	a	1488	G
30	a	1490	U
30	a	1501	G
30	a	1504	G
30	a	1513	G
30	a	1514	G
30	a	1522	C

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	89	A
27	A	97	U
27	A	316	U
27	A	335	G
27	A	357	U
27	A	445	U
27	A	643	G
27	A	974	G
27	A	1002	C
27	A	1004	C
27	A	1084	U
27	A	1117	U
27	A	2094	G
27	A	2350	G
27	A	2381	A
27	A	2729	G
28	B	10	G
29	C	17	C
29	C	20	U
29	C	53	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.

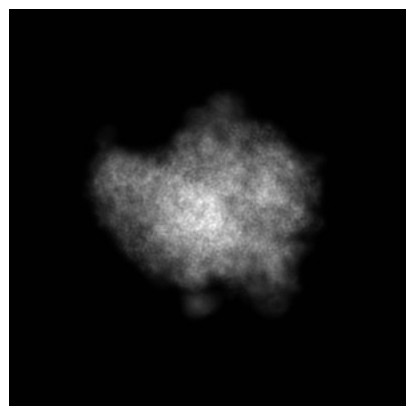
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37562. These allow visual inspection of the internal detail of the map and identification of artifacts.

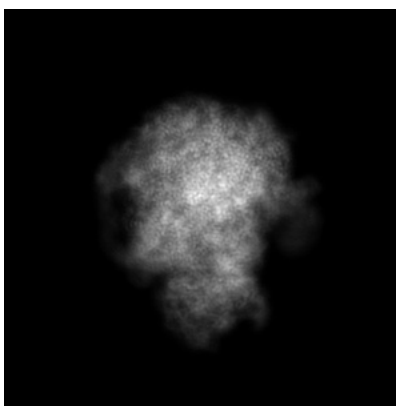
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

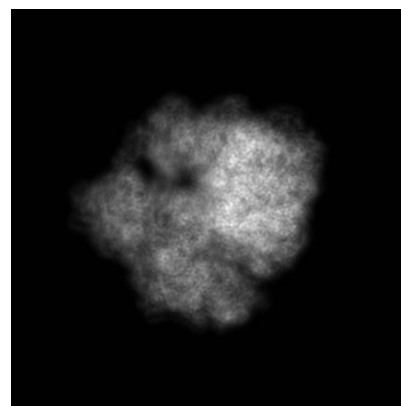
6.1.1 Primary map



X

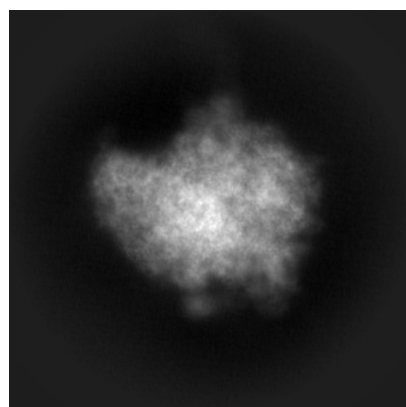


Y

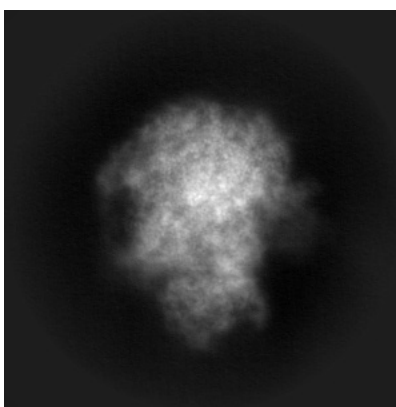


Z

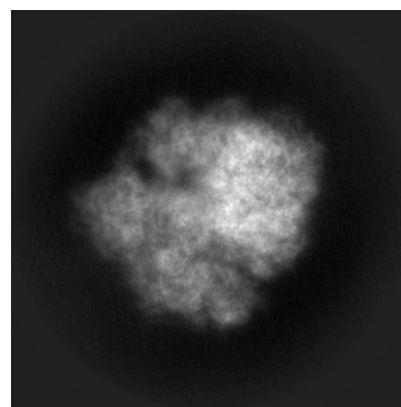
6.1.2 Raw map



X



Y

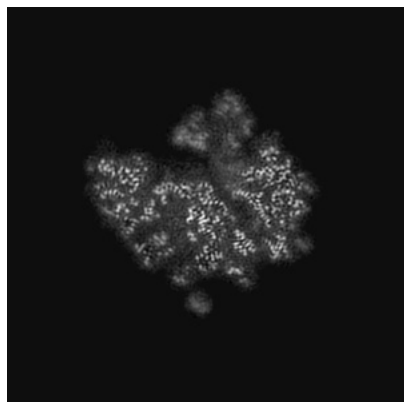


Z

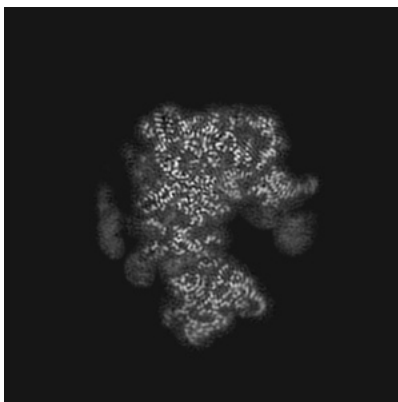
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

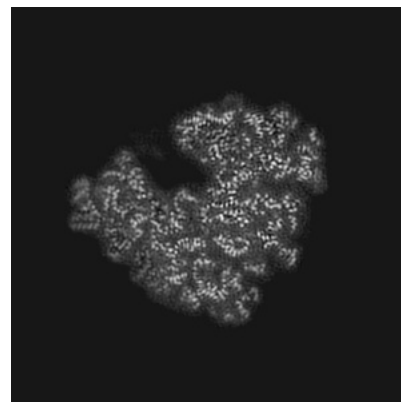
6.2.1 Primary map



X Index: 190

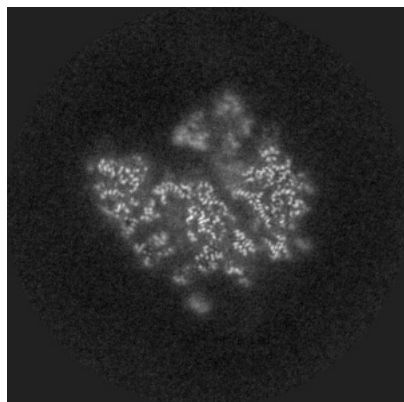


Y Index: 190

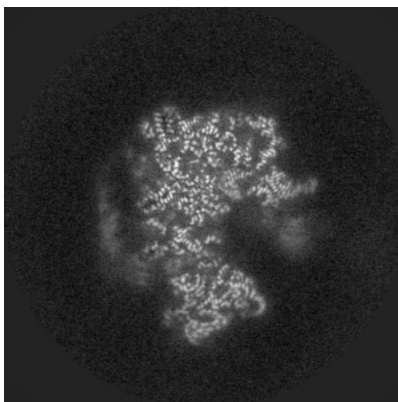


Z Index: 190

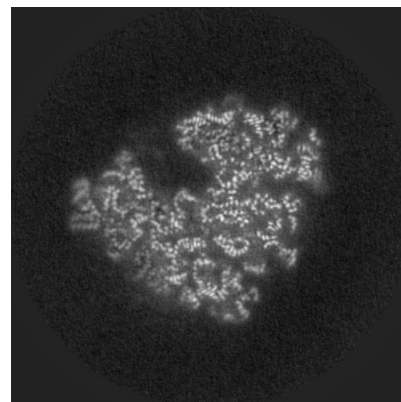
6.2.2 Raw map



X Index: 190



Y Index: 190

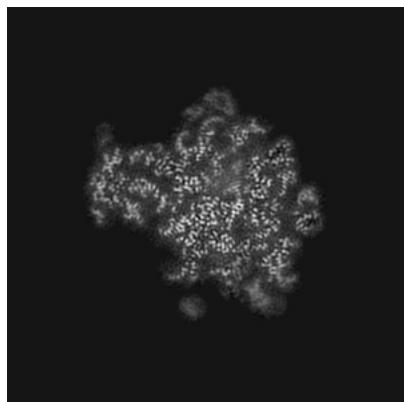


Z Index: 190

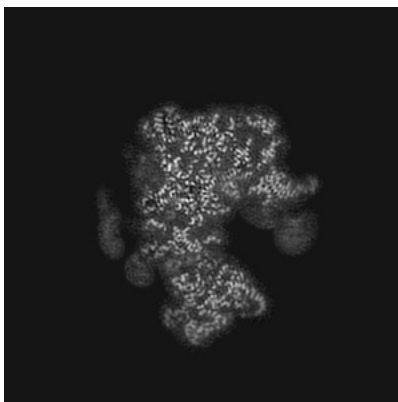
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

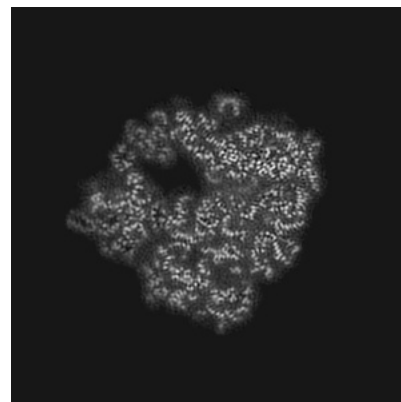
6.3.1 Primary map



X Index: 213

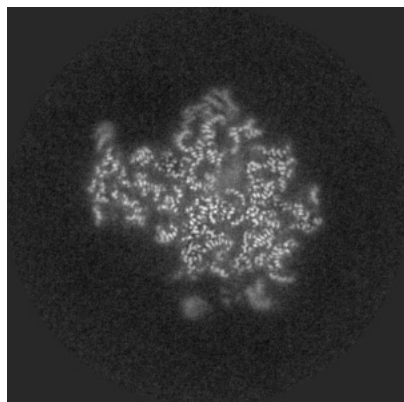


Y Index: 191

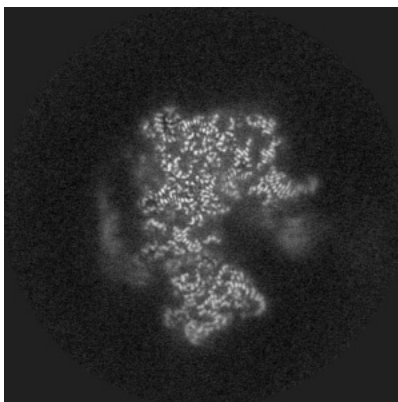


Z Index: 200

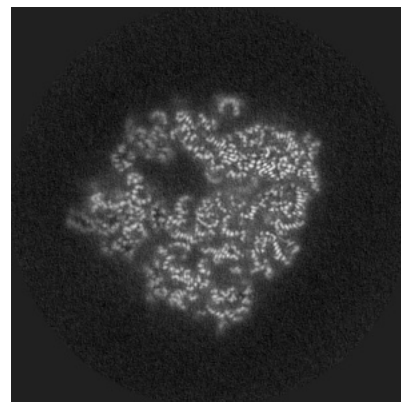
6.3.2 Raw map



X Index: 209



Y Index: 191

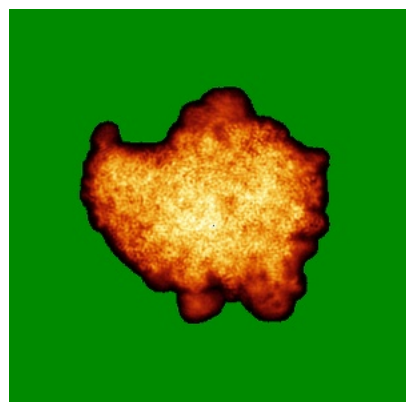


Z Index: 200

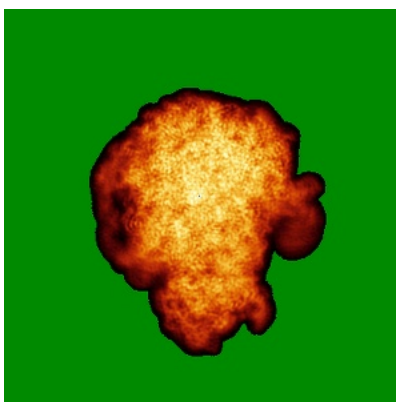
The images above show the largest variance slices of the map in three orthogonal directions.

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

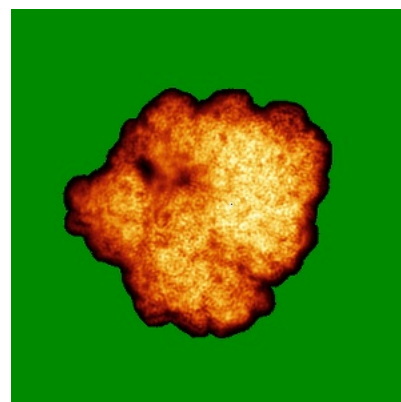
6.4.1 Primary map



X

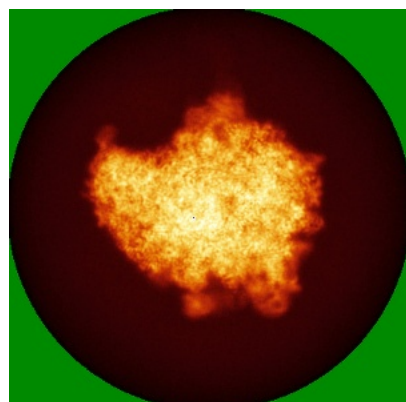


Y

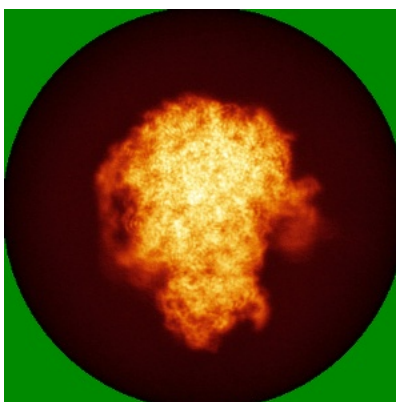


Z

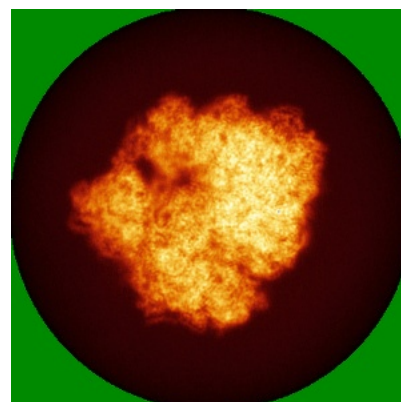
6.4.2 Raw map



X



Y

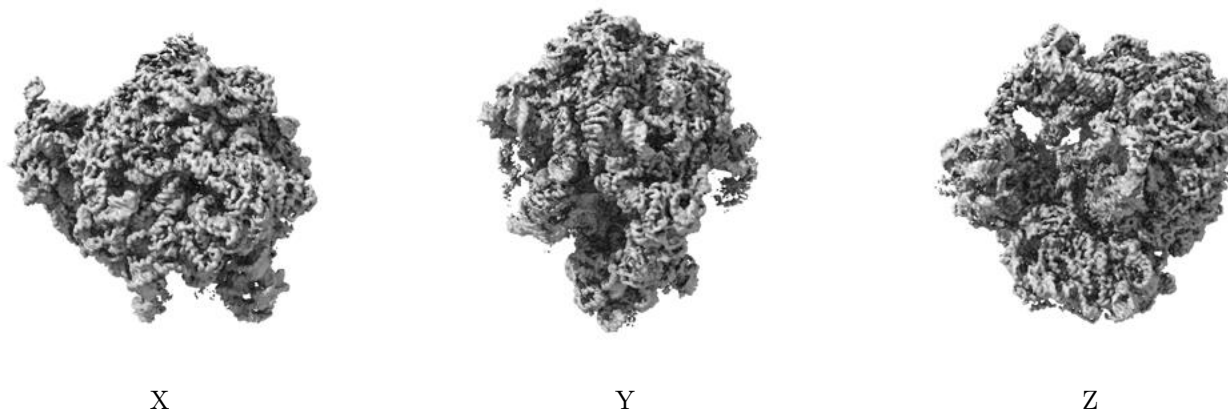


Z

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.

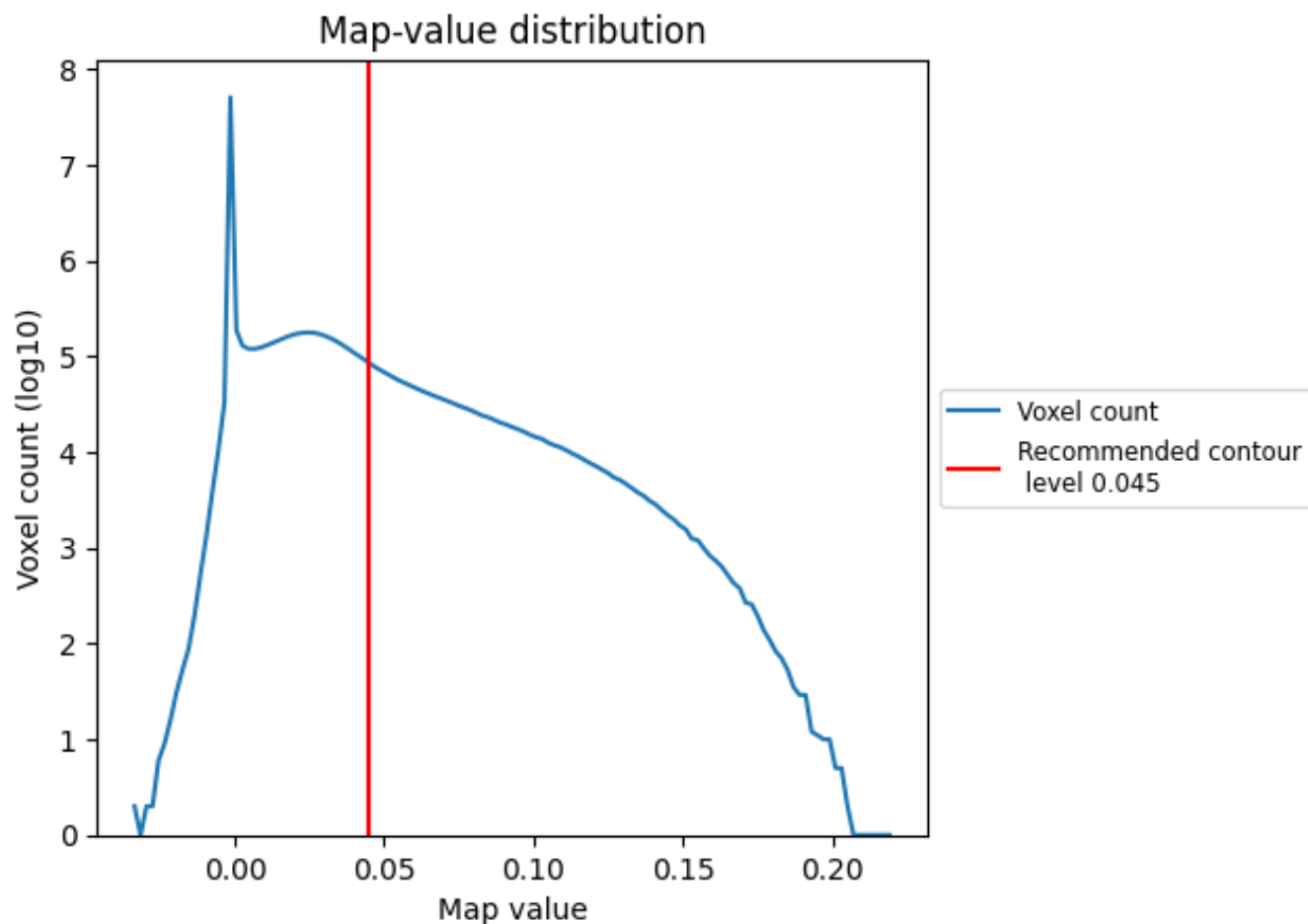
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

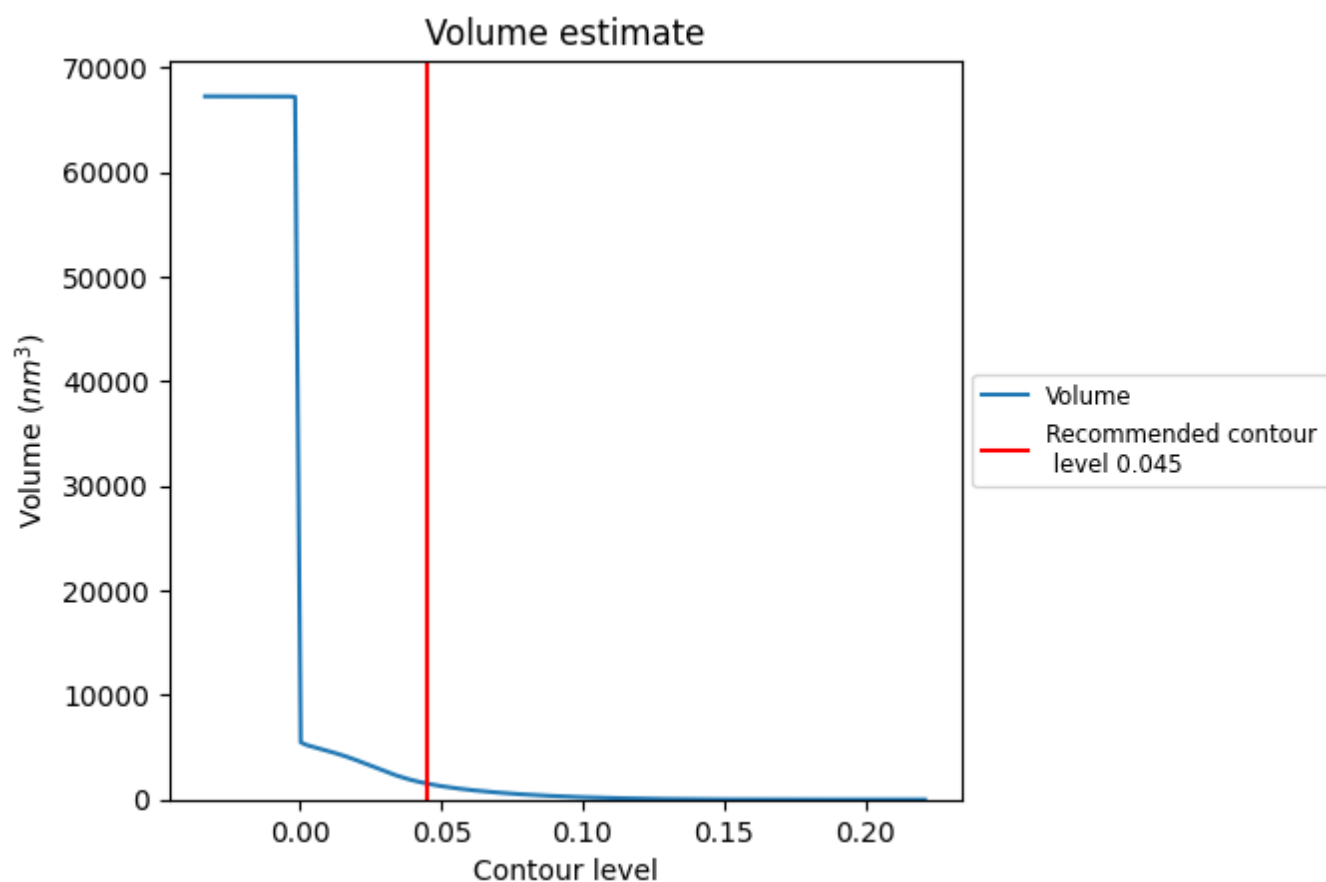
This section contains the results of statistical analysis of the map.

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.

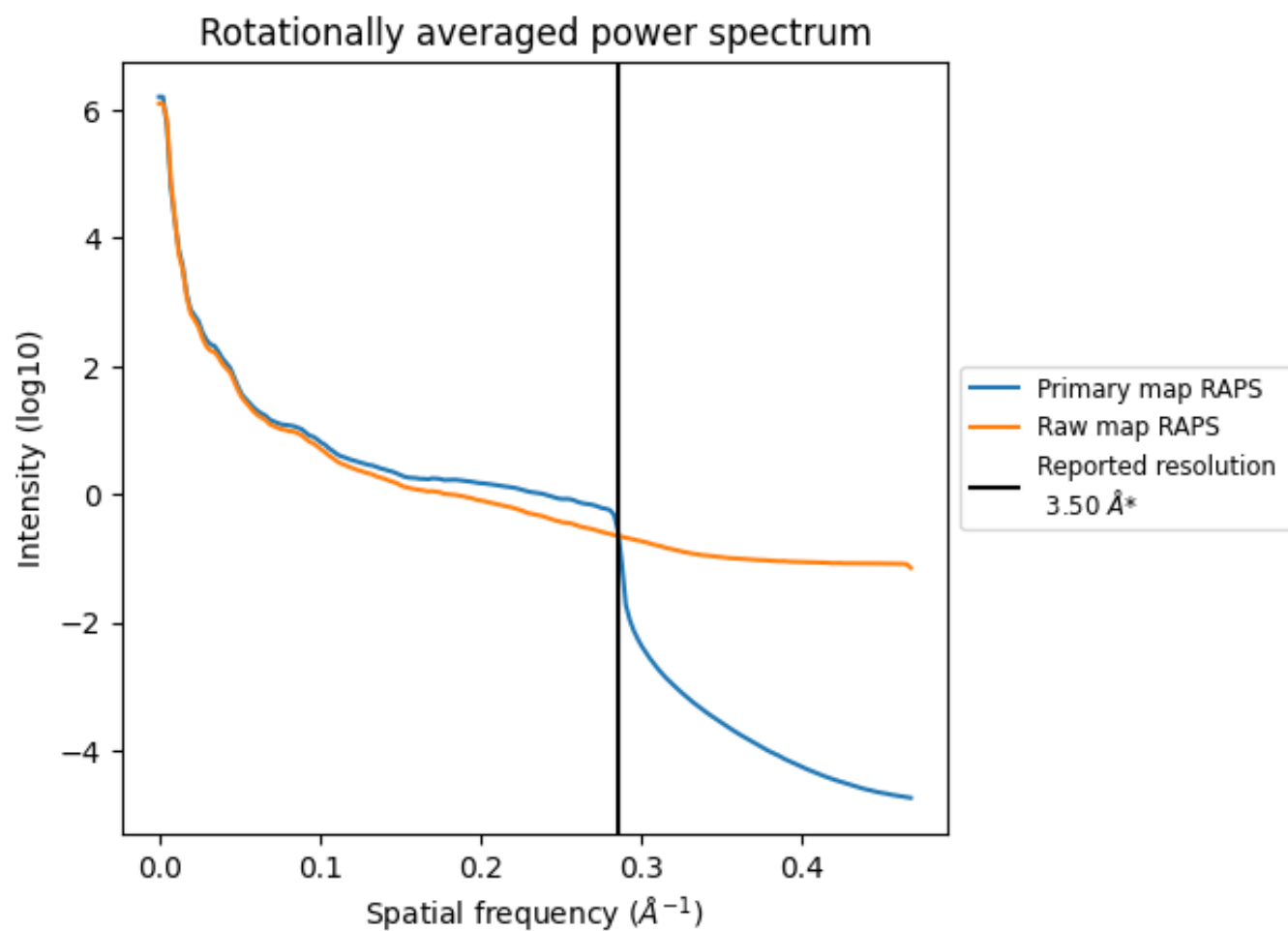
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1530 nm³; this corresponds to an approximate mass of 1382 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 ⓘ

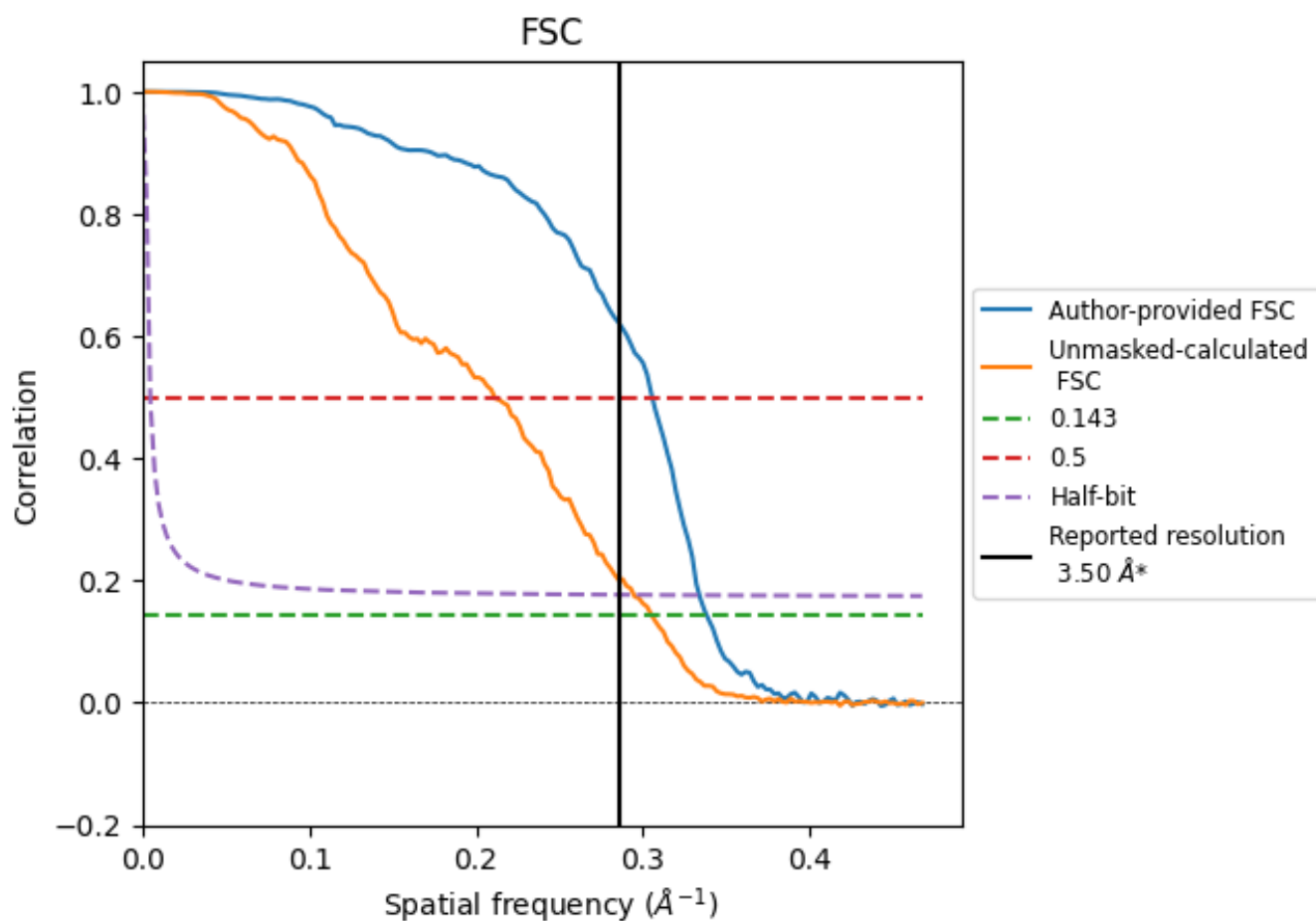


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

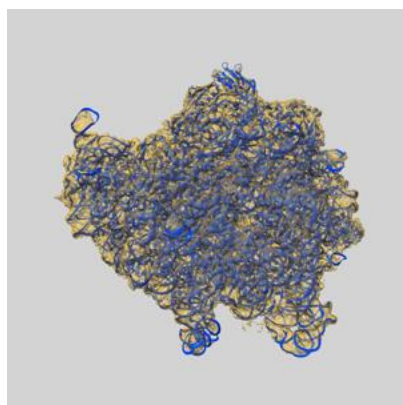
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.50
Author-provided FSC curve	2.96	3.27	2.99	-
Unmasked-calculated*	3.28	4.73	3.39	-

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

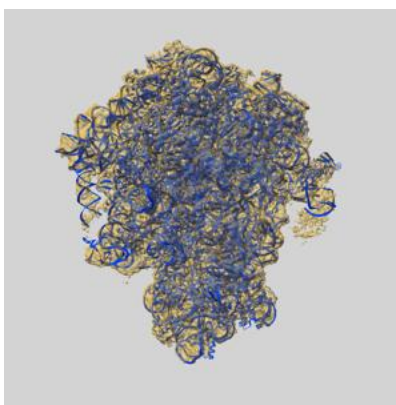
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37562 and PDB model 8WIB. Per-residue inclusion information can be found in section 3 on page 13.

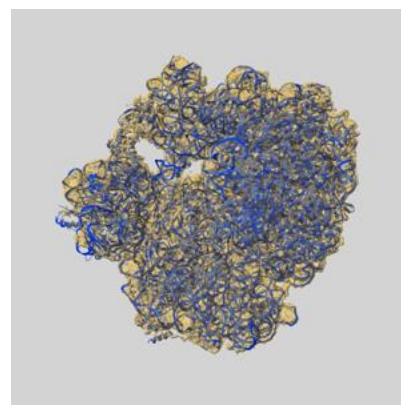
9.1 Map-model overlay [i](#)



X



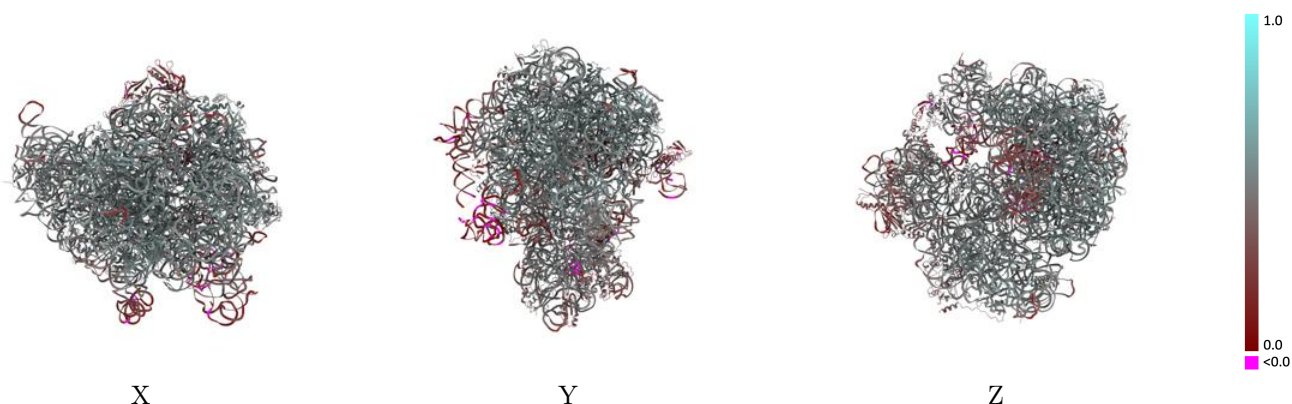
Y



Z

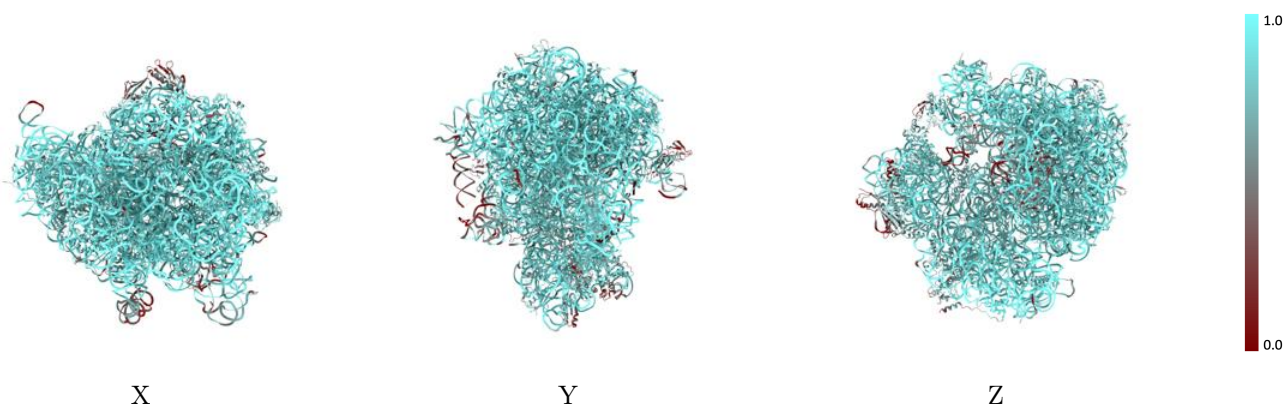
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



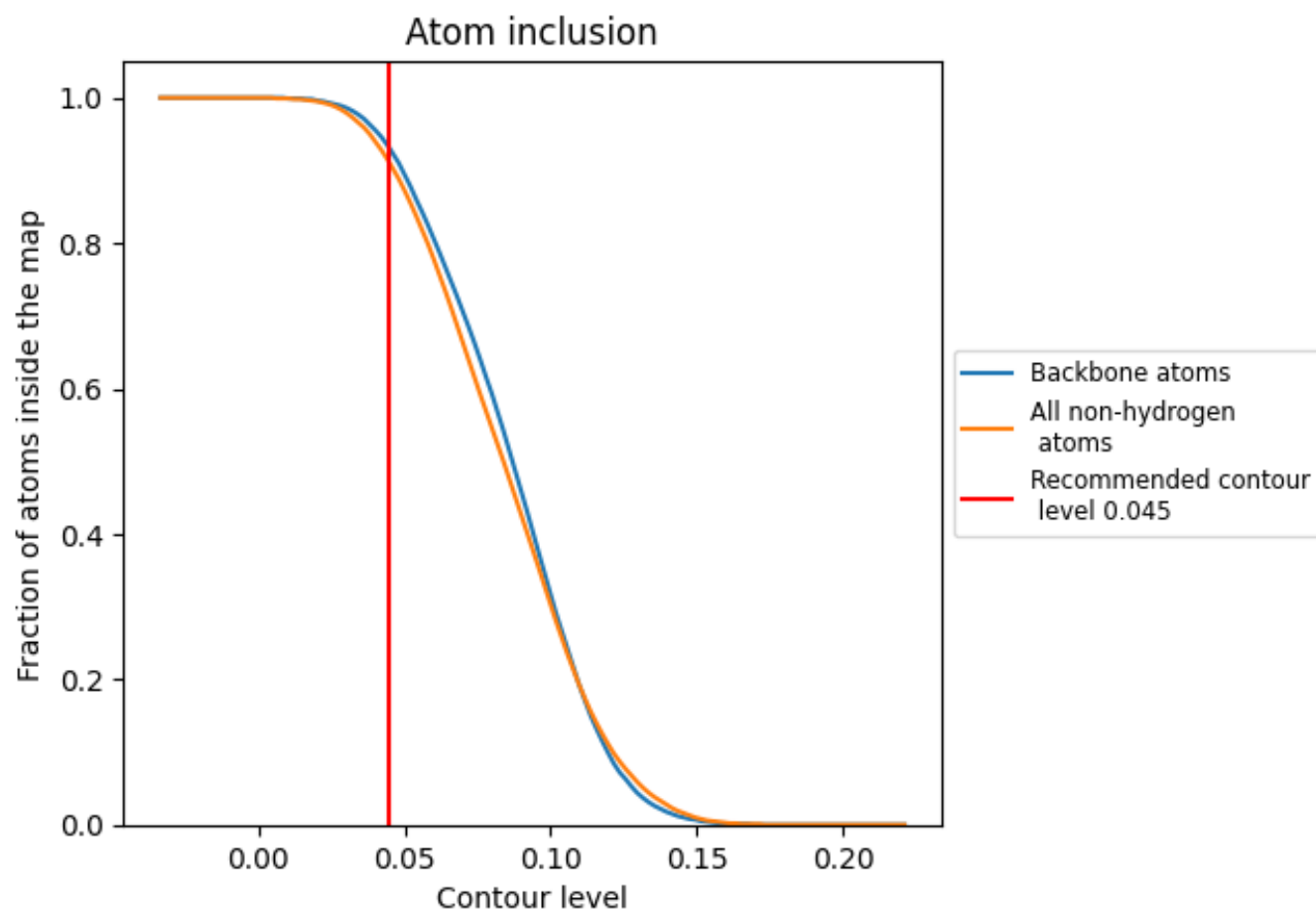
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 91% 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	 0.9100	 0.4690
1	 0.9260	 0.4990
2	 0.8520	 0.4820
3	 0.8990	 0.5140
4	 0.3920	 0.1710
5	 0.8680	 0.5320
6	 0.8160	 0.4510
7	 0.9890	 0.5160
8	 0.9400	 0.5290
A	 0.9330	 0.4690
B	 0.9650	 0.4610
C	 0.8510	 0.2860
E	 0.9610	 0.5460
F	 0.9090	 0.5210
G	 0.8680	 0.5040
H	 0.8000	 0.4400
I	 0.4440	 0.2230
J	 0.5170	 0.2470
M	 0.9160	 0.5140
N	 0.9210	 0.5290
O	 0.8980	 0.5190
Q	 0.9590	 0.5400
R	 0.8390	 0.4630
S	 0.8910	 0.5100
T	 0.9470	 0.5350
U	 0.8850	 0.5460
V	 0.9500	 0.5420
W	 0.8920	 0.5230
X	 0.7780	 0.4700
Z	 0.9210	 0.5190
a	 0.9690	 0.4820
d	 0.6600	 0.3720
e	 0.7670	 0.4320
f	 0.5970	 0.4420
g	 0.8180	 0.4760



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Chain	Atom inclusion	Q-score
h	 0.8240	 0.4440
i	 0.8950	 0.5090
j	 0.8050	 0.4460
k	 0.5410	 0.3550
l	 0.8570	 0.4800
m	 0.8670	 0.4990
n	 0.8150	 0.4220
o	 0.5800	 0.3510
p	 0.8750	 0.4770
q	 0.8210	 0.4730
r	 0.8880	 0.5070
s	 0.8300	 0.4530
t	 0.7820	 0.4260
u	 0.8940	 0.4880
v	 0.9090	 0.4830
w	 0.8260	 0.4510