



Full wwPDB EM Validation Report ⓘ

Mar 4, 2026 – 11:57 PM UTC

PDB ID : 9NKL / pdb_00009nkl
EMDB ID : EMD-40932
Title : E. coli 70S initiation complex
Authors : Singh, S.; Hunt, J.F.
Deposited on : 2025-03-01
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

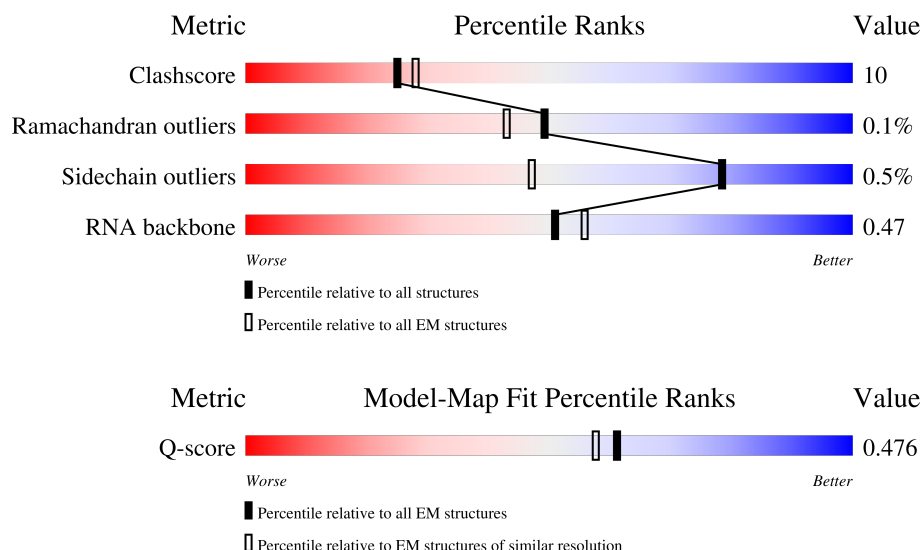
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	13	142	
2	14	122	
3	15	144	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	16	136	
5	17	120	
6	18	116	
7	19	114	
8	2	271	
9	20	117	
10	21	103	
11	22	110	
12	23	93	
13	24	102	
14	25	94	
15	27	76	
16	28	77	
17	29	63	
18	3	209	
19	30	58	
20	31	66	
21	32	56	
22	34	46	
23	35	64	
24	36	38	
25	4	201	
26	5	177	
27	6	176	
28	9	149	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	M	9	
30	R1	2903	
31	R2	119	
32	R3	1531	
33	sb	218	
34	sc	206	
35	sd	205	
36	se	157	
37	sf	100	
38	sg	151	
39	sh	129	
40	si	127	
41	sj	98	
42	sk	116	
43	sl	123	
44	sm	114	
45	sn	100	
46	so	88	
47	sp	82	
48	sq	80	
49	sr	65	
50	ss	79	
51	st	85	
52	su	65	
53	T	78	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	33	50	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
53	H2U	T	20	X	-	-	-
53	4OC	T	32	X	-	-	-
53	MUM	T	54	X	-	-	-
53	4SU	T	8	X	-	-	-

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 144154 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	13	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 2 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	14	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 3 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	15	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 4 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	16	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 5 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	17	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 6 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	18	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 7 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	19	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 8 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	2	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 9 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	20	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 10 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	21	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 11 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	22	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 12 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	23	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 13 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	24	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 14 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	25	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 15 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	27	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 16 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	28	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 17 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	29	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 18 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	3	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 19 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	30	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 20 is a protein called Large ribosomal subunit protein bL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	31	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	32	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 22 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	34	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 23 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	35	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 24 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	36	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 25 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	4	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 26 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	5	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 27 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	6	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 28 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	9	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 29 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	M	9	Total	C	N	O	P	0	0
			195	88	40	58	9		

- Molecule 30 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	R1	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

- Molecule 31 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	R2	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R3	1531	Total	C	N	O	P	0	0
			32850	14652	6028	10640	1530		

- Molecule 33 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	sb	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 34 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	sc	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 35 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	sd	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 36 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	se	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 37 is a protein called 30S ribosomal protein S6, non-modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	sf	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 38 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	sg	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 39 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	sh	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 40 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	si	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 41 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	sj	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 42 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	sk	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 43 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	sl	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 44 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	sm	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 45 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	sn	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 46 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	so	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 47 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	sp	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 48 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	sq	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	sr	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ss	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	st	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 52 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	su	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 53 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	T	78	Total	C	N	O	P S	0	0
			1649	740	295	536	76 2		

- Molecule 54 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	33	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 55 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	3	1	Total	Mg	0
			1	1	
55	32	1	Total	Mg	0
			1	1	
55	R1	126	Total	Mg	0
			126	126	

Continued on next page...

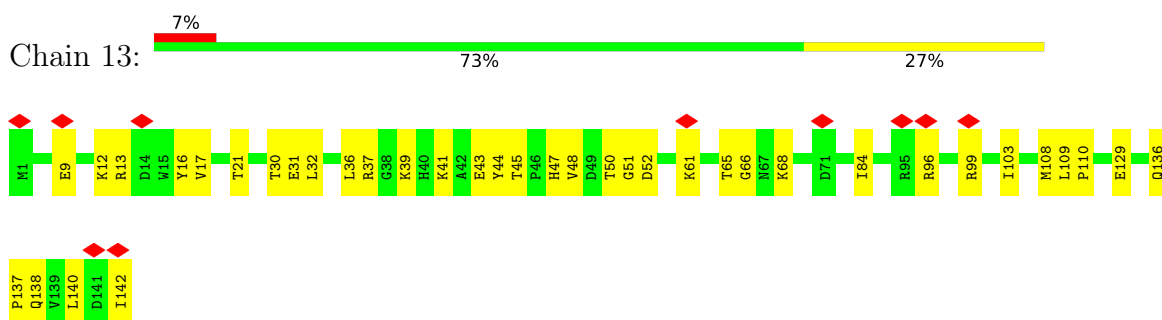
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
55	R3	33	Total	Mg	0
			33	33	

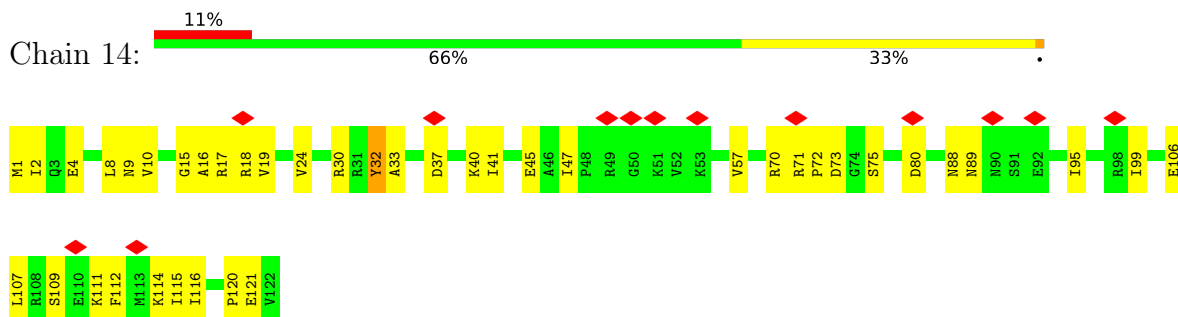
3 Residue-property plots [i](#)

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

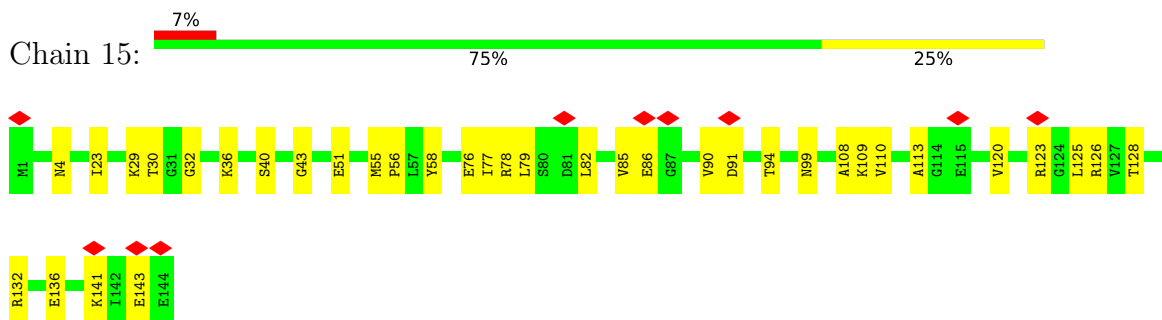
- Molecule 1: Large ribosomal subunit protein uL13



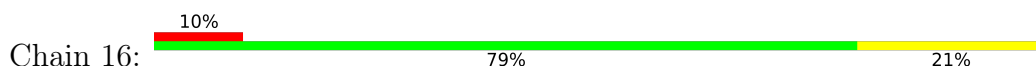
- Molecule 2: 50S ribosomal protein L14



- Molecule 3: Large ribosomal subunit protein uL15

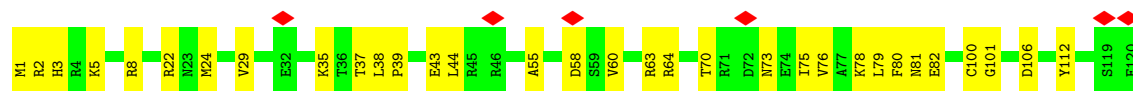
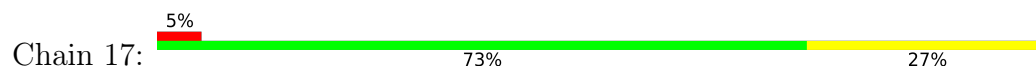


- Molecule 4: 50S ribosomal protein L16

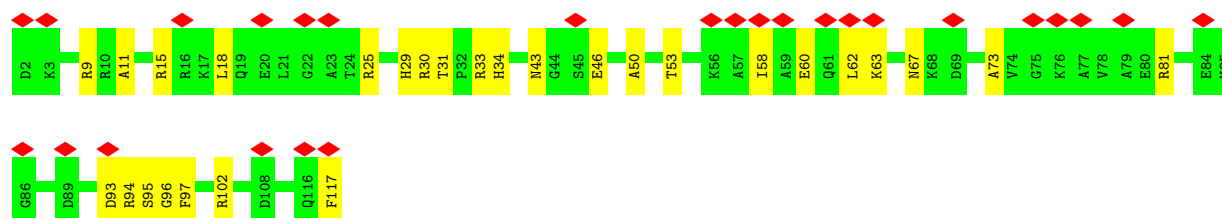
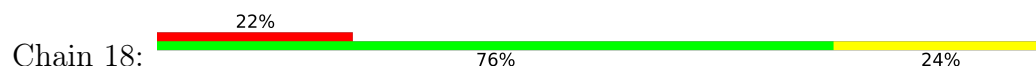




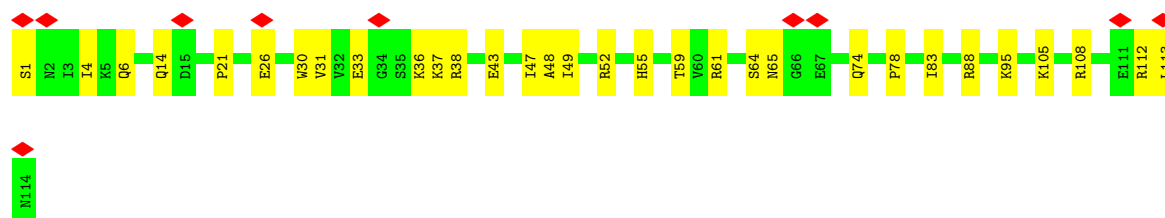
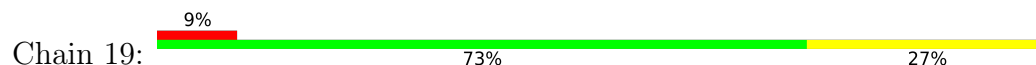
- Molecule 5: Large ribosomal subunit protein bL17



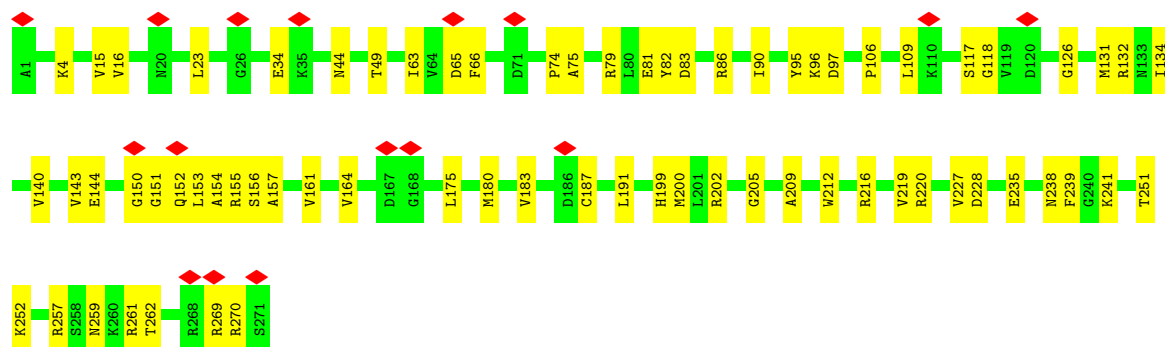
- Molecule 6: Large ribosomal subunit protein uL18



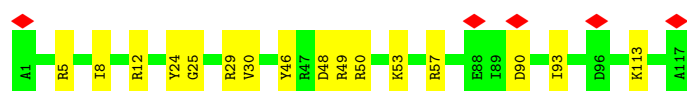
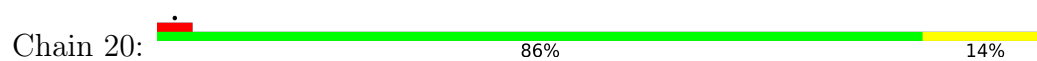
- Molecule 7: 50S ribosomal protein L19



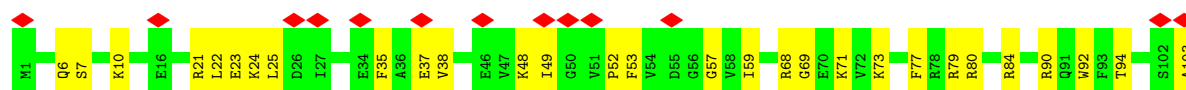
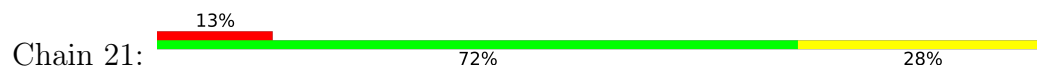
- Molecule 8: 50S ribosomal protein L2



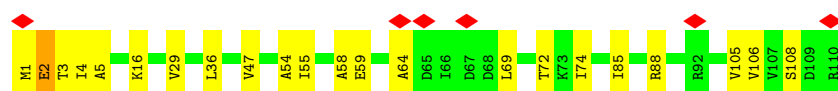
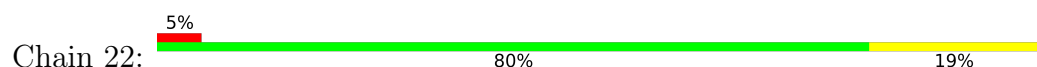
- Molecule 9: Large ribosomal subunit protein bL20



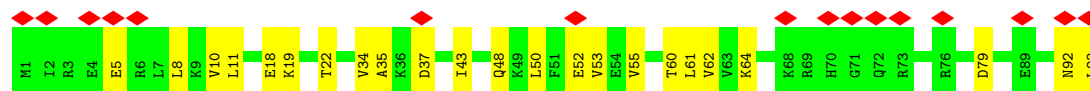
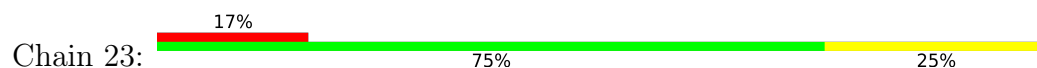
- Molecule 10: Large ribosomal subunit protein bL21



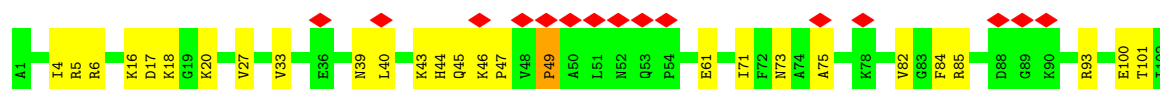
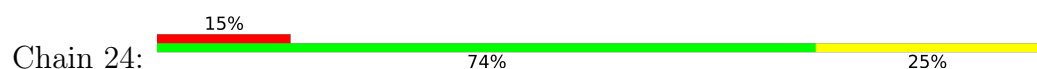
- Molecule 11: Large ribosomal subunit protein uL22



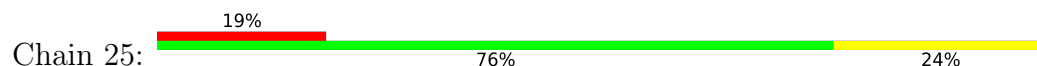
- Molecule 12: Large ribosomal subunit protein uL23



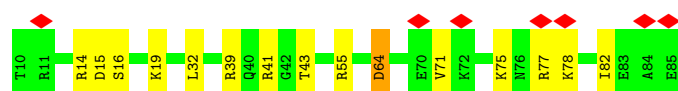
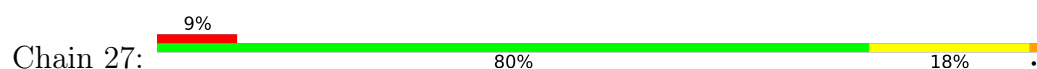
- Molecule 13: Large ribosomal subunit protein uL24



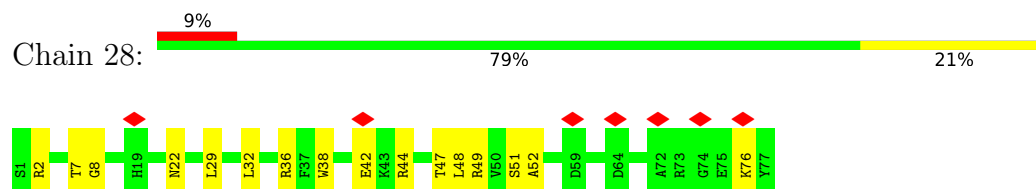
- Molecule 14: Large ribosomal subunit protein bL25



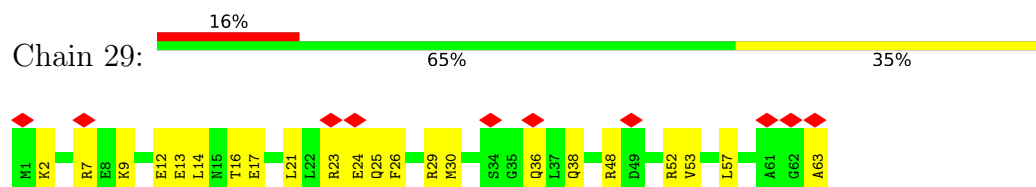
- Molecule 15: Large ribosomal subunit protein bL27



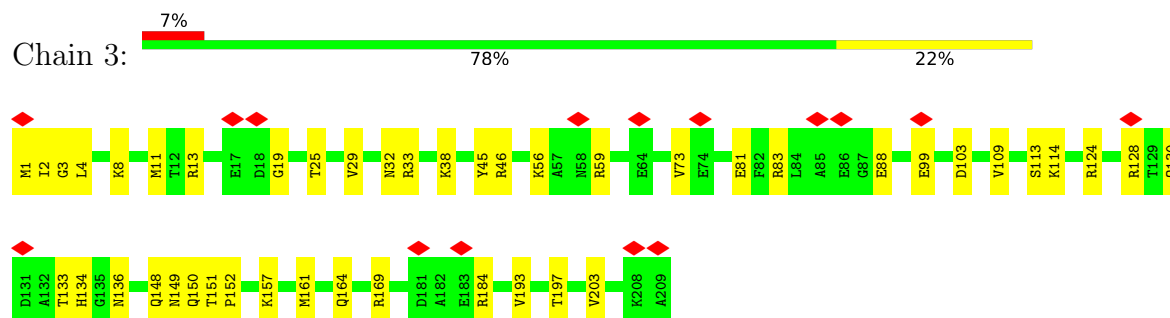
- Molecule 16: 50S ribosomal protein L28



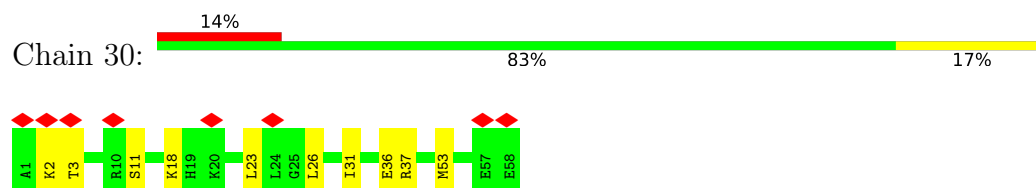
- Molecule 17: Large ribosomal subunit protein uL29



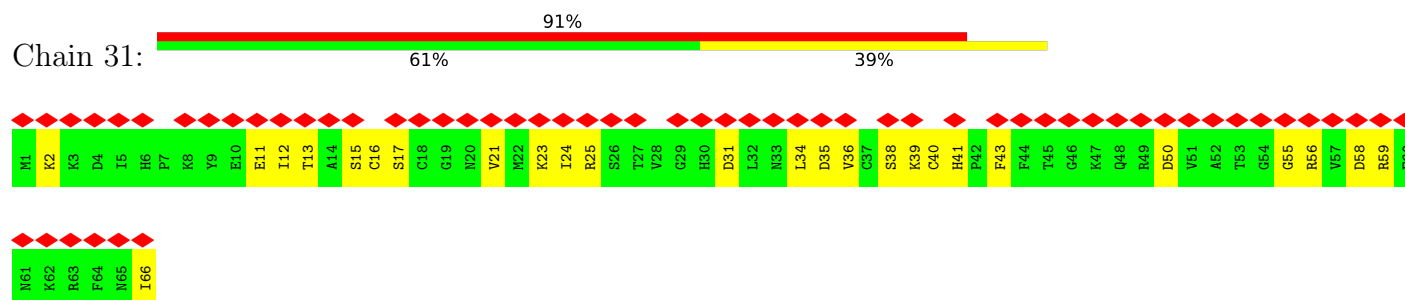
- Molecule 18: 50S ribosomal protein L3



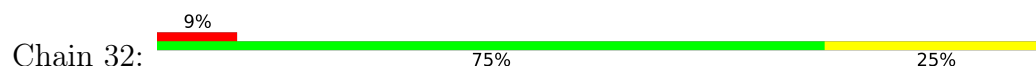
- Molecule 19: 50S ribosomal protein L30

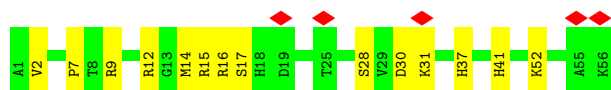


- Molecule 20: Large ribosomal subunit protein bL31

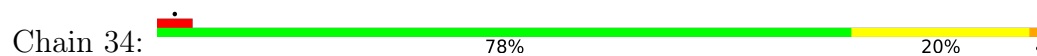


- Molecule 21: 50S ribosomal protein L32

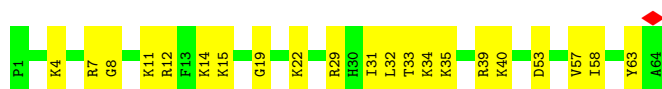




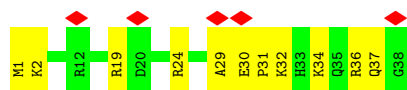
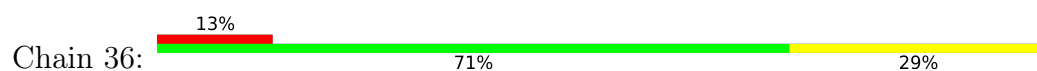
- Molecule 22: 50S ribosomal protein L34



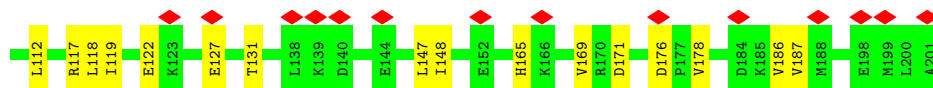
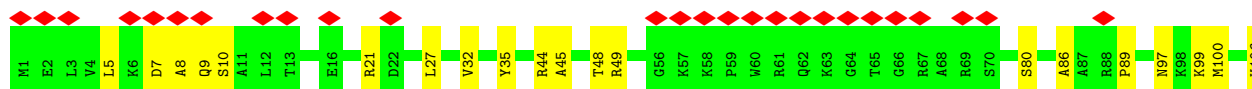
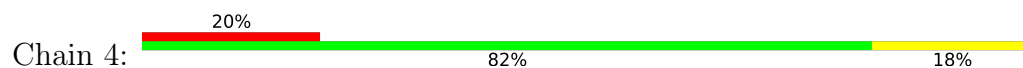
- Molecule 23: Large ribosomal subunit protein bL35



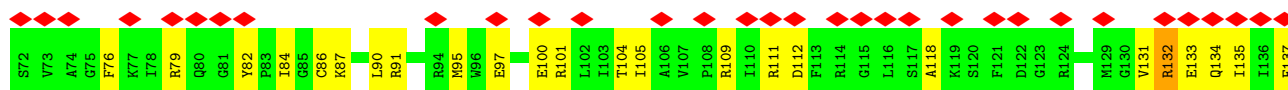
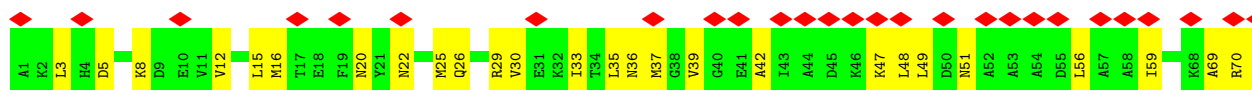
- Molecule 24: 50S ribosomal protein L36

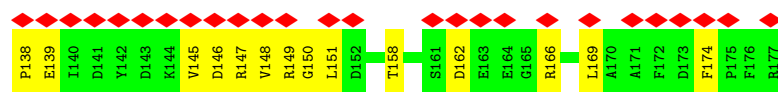


- Molecule 25: Large ribosomal subunit protein uL4

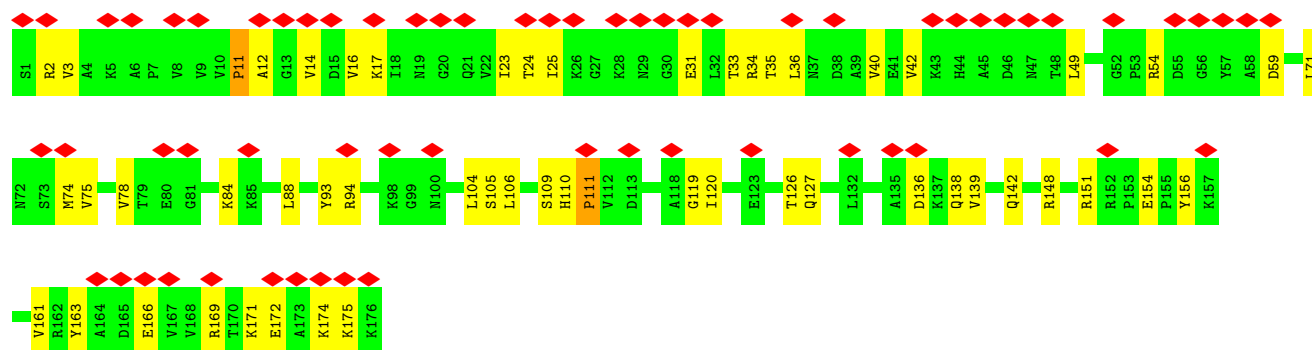


- Molecule 26: 50S ribosomal protein L5

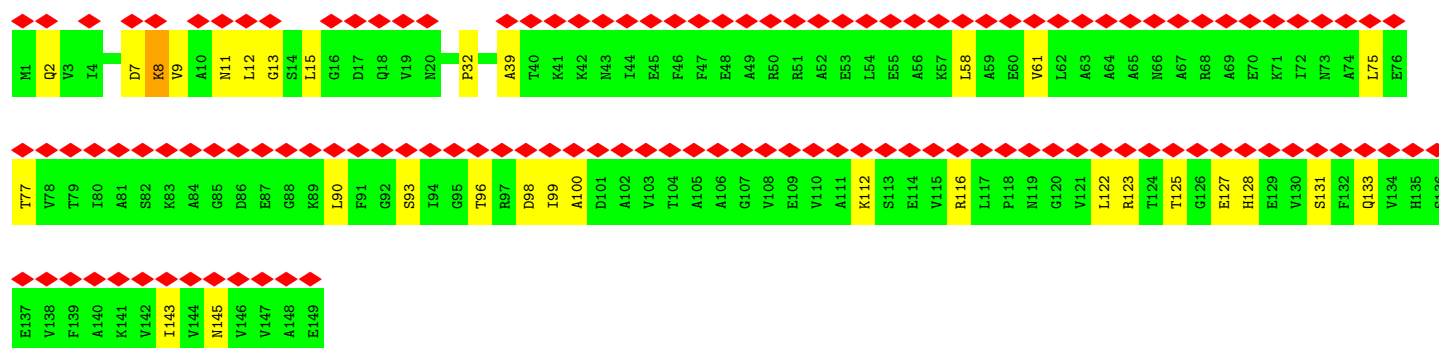
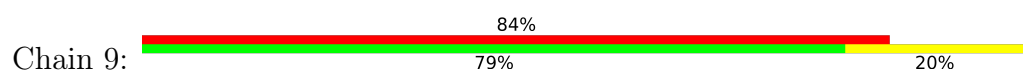




- Molecule 27: Large ribosomal subunit protein uL6



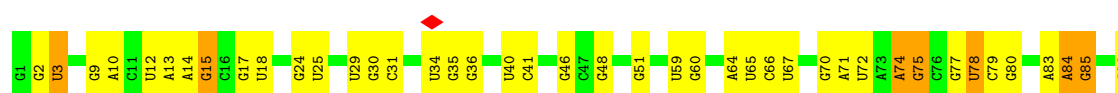
- Molecule 28: Large ribosomal subunit protein bL9

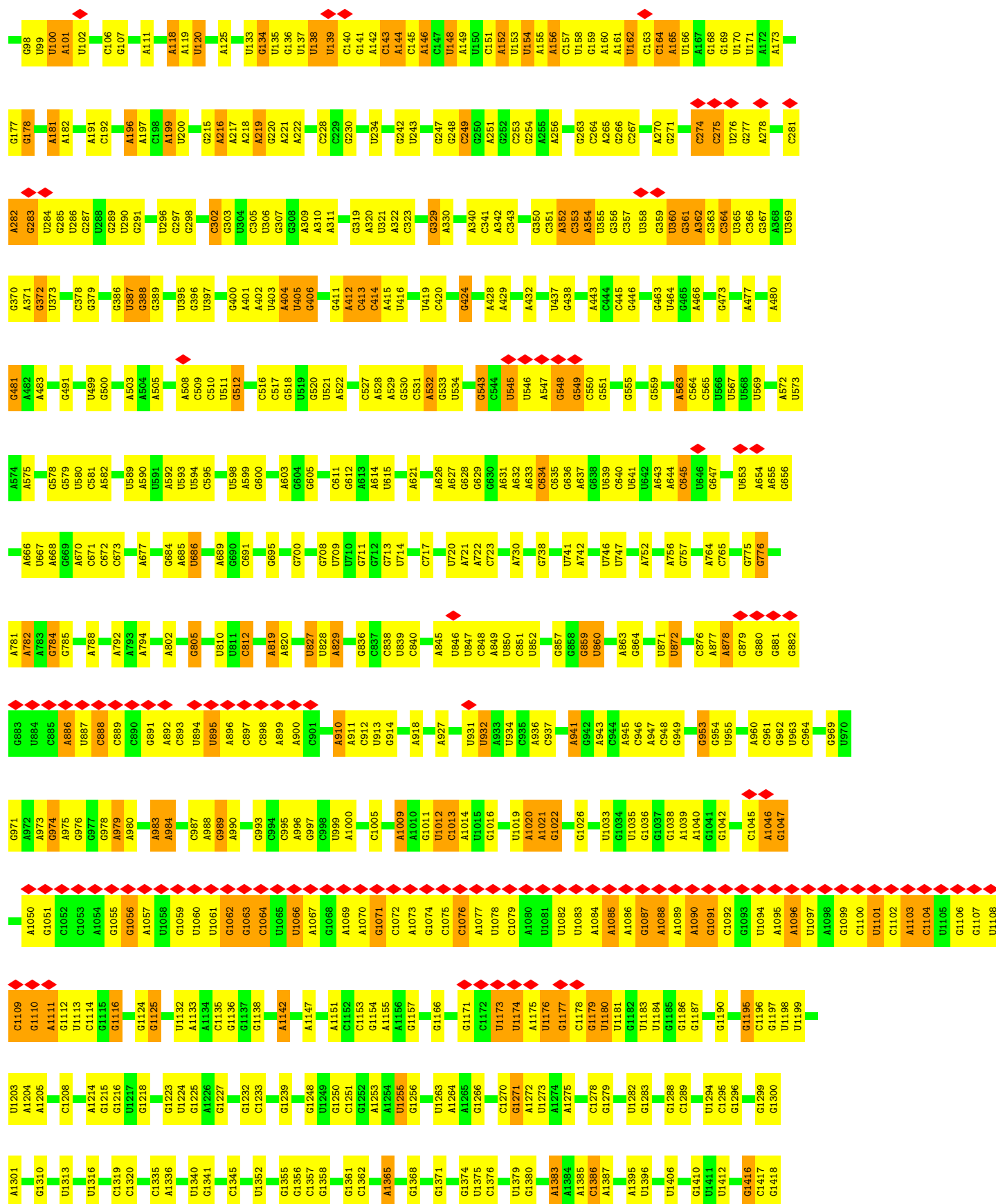


- Molecule 29: mRNA

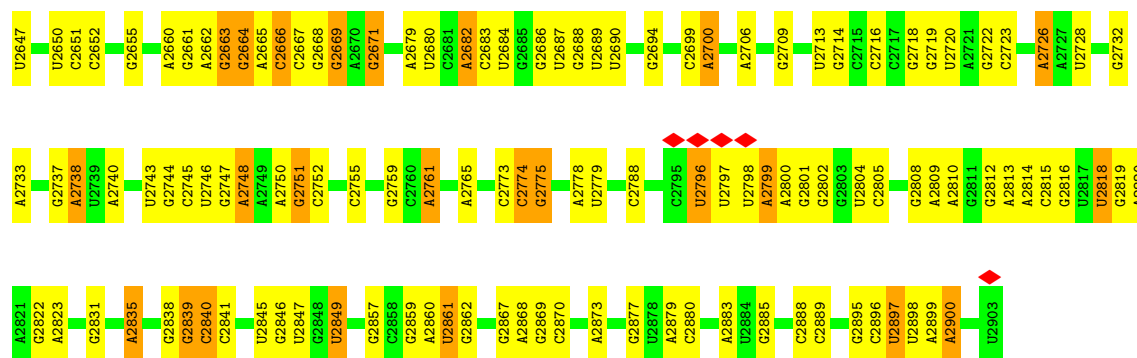


- Molecule 30: 23S ribosomal RNA

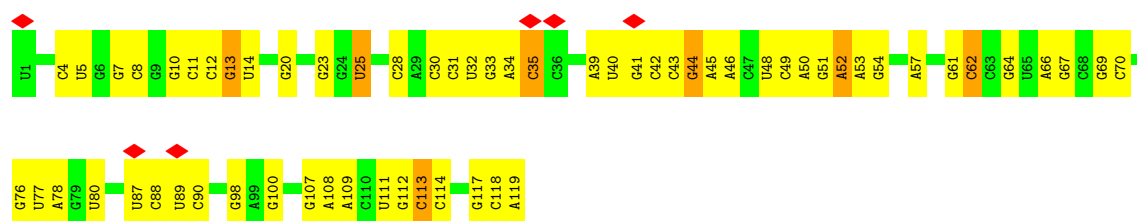




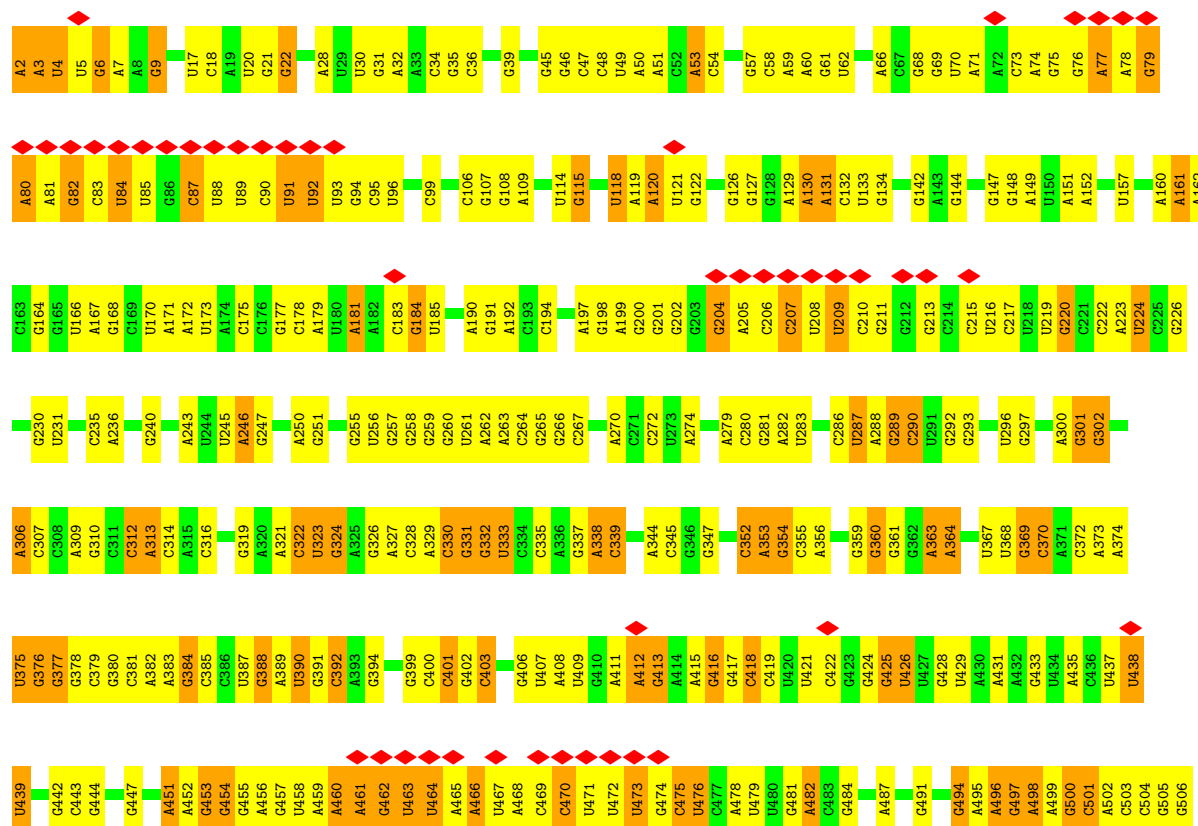
C2462	A2469	G2470	U2473	U2474	C2475	A2476	A2477	A2478	G2481	G2487	G2488	G2494	G2495	C2496	A2497	C2498	C2499	U2500	C2501	G2502	A2503	U2504	G2505	U2506	C2507	G2508	A2513	U2514	C2515	A2516	C2517	U2518	U2519	C2520	C2521	U2522	A2530	C2535	C2536	U2537	C2538	C2539	C2540	G2545	U2546	A2547	A2548	G2549	C2550										
G2260	G2261	G2262	C2263	C2264	C2268	A2269	G2270	G2271	A2277	A2281	G2282	G2283	U2284	C2285	A2286	U2287	U2290	G2299	U2402	C2403	G2410	A2411	A2412	G2413	G2414	G2415	A2418	U2419	U2423	C2427	G2428	G2429	A2430	A2434	A2435	G2436	A2439	C2440	U2441	G2447	A2448	G2455	C2456	A2461															
G2269	G2279	C2283	G2286	A2287	A2288	G2289	G2290	U2291	U2292	U2296	A2297	A2298	U2302	G2303	G2304	C2305	G2306	G2307	G2308	A2309	C2310	A2311	U2312	C2313	A2314	G2315	A2317	G2318	G2319	A2322	G2323	U2324	G2325	C2326	A2327	A2328	U2329	G2330	G2331	A2332	U2333	U2334	A2335	A2336	G2345	A2346	C2347	U2348	G2349	C2359									
C2175	A2176	C2177	C2178	C2179	U2180	U2181	U2182	A2183	A2184	U2185	G2186	U2187	U2188	U2189	G2190	A2191	U2192	G2193	U2194	U2195	G2204	A2211	A2212	U2213	C2214	A2225	C2226	U2229	G2230	U2231	C2232	U2233	G2234	G2238	G2239	U2240	A2241	G2242	U2243	U2244	U2245	G2246	A2247	C2248	U2249	G2250	C2258	U2262	C2263	A2266									
G2115	G2116	A2117	U2118	A2119	G2120	G2121	U2122	G2123	G2124	G2125	A2126	G2127	G2128	C2129	U2130	U2131	U2132	G2133	A2134	A2135	G2136	U2137	G2138	U2139	G2140	G2141	A2142	G2143	G2144	C2145	C2146	A2147	G2148	U2149	C2150	U2151	G2152	C2153	A2154	U2155	G2156	G2157	A2158	G2159	C2160	C2161	G2162	A2163	C2164	C2165	U2166	U2167	G2168	A2169	A2170	A2171	U2172	A2173	C2174
A2033	U2034	G2035	C2036	A2037	G2038	U2039	G2040	U2041	A2042	C2043	A2052	C2055	G2056	A2059	A2060	A2062	G2067	U2068	G2069	A2070	A2071	C2072	C2073	U2074	U2075	U2076	A2077	A2080	U2081	A2082	A2090	A2095	C2096	A2097	U2098	U2099	G2100	A2101	G2102	C2103	C2104	U2105	U2106	G2107	A2108	U2109	G2110	U2111	U2112	U2113	A2114								
C1914	U1915	A1919	C1920	G1921	G1929	A1930	A1936	A1937	A1938	U1943	G1954	U1955	U1956	A1966	C1967	A1970	U1971	G1972	G1983	U1991	G1992	U1993	C1994	U1995	C1996	C1997	G2004	A2005	C2006	U2011	G2012	A2013	A2014	A2015	A2020	C2021	U2022	C2023	G2024	C2025	U2026	G2027	U2028	G2029	A2030	A2031	G2032												
G1811	U1812	G1813	C1816	G1817	U1818	A1819	U1820	G1823	U1827	G1828	A1829	G1831	C1832	C1843	C1844	G1845	G1846	A1847	A1848	A1853	A1854	G1862	G1863	U1864	U1865	A1866	G1869	C1870	A1871	A1872	G1873	C1874	C1879	U1880	G1881	G1884	A1889	U1897	A1900	A1901	G1906	G1910	A1913																
C1728	U1729	G1732	G1733	U1736	G1737	G1738	A1739	G1740	A1744	A1745	A1746	U1747	G1750	U1751	C1752	A1755	G1756	A1757	U1758	A1759	C1760	G1764	U1769	G1770	U1771	G1772	A1773	G1776	A1779	A1780	G1781	A1784	A1785	A1789	G1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803	A1808	A1809	A1810													
A1509	G1510	C1511	C1512	A1515	G1516	A1519	G1532	U1523	A1528	G1529	G1530	C1531	A1532	C1533	U1534	A1535	C1536	G1537	G1538	U1539	G1540	C1541	U1542	G1543	A1544	U1545	G1546	A1549	C1550	C1558	U1559	G1560	A1566	A1569	U1578	A1583	U1584	C1585	A1586	G1587	U1588	U1589	A1590	A1591	C1592	A1593	U1594	C1595											
A1419	A1420	G1424	G1425	C1428	A1431	G1432	A1433	A1434	C1437	G1441	U1442	U1443	G1444	C1447	G1448	G1452	A1453	G1459	U1460	C1463	G1464	A1465	U1466	A1469	A1470	G1471	C1472	G1473	U1474	G1475	G1478	U1481	G1482	G1483	A1490	C1493	A1494	A1495	A1496	A1504	A1505	U1506	C1507	A1508															

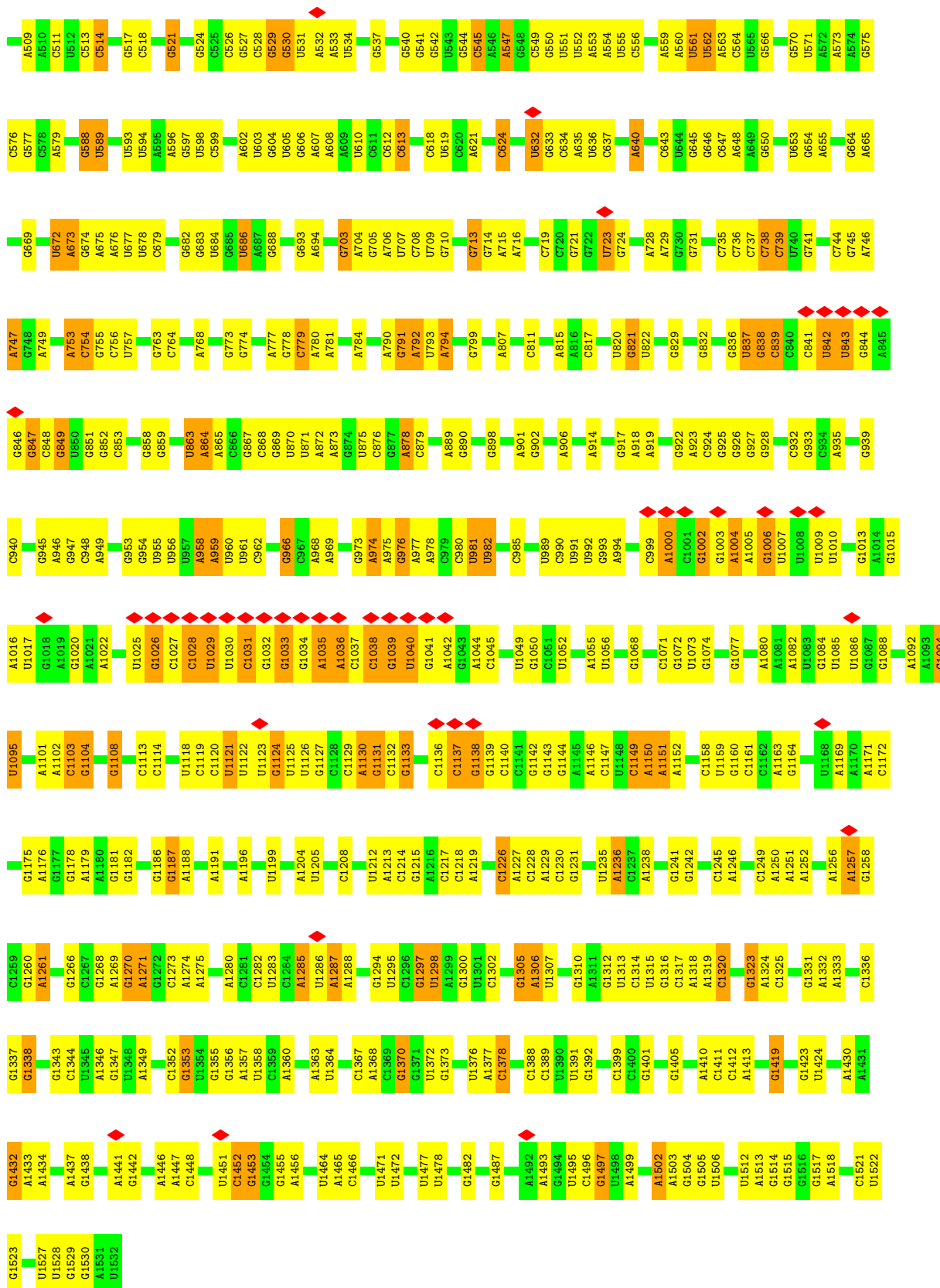


• Molecule 31: 5S ribosomal RNA

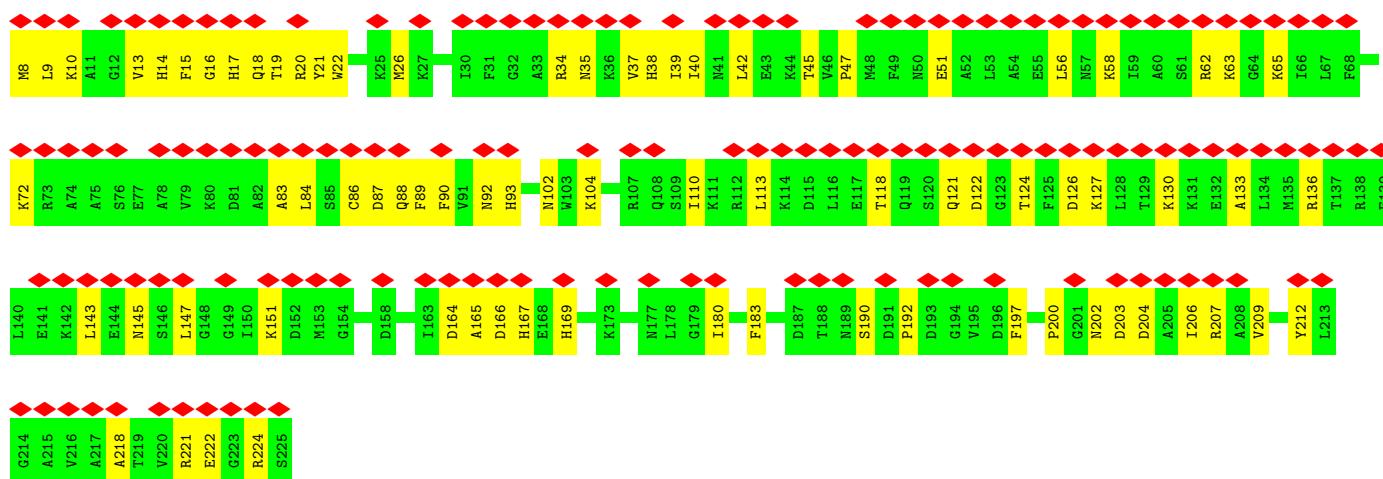


• Molecule 32: 16S ribosomal RNA

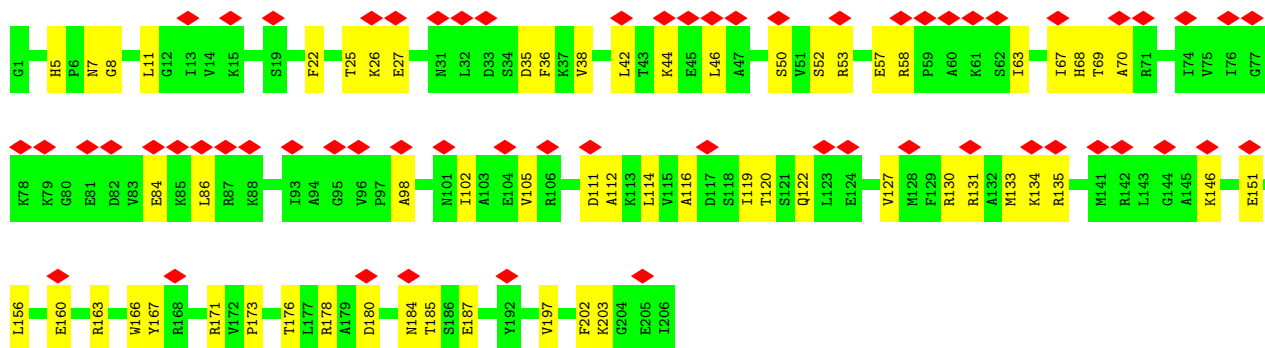




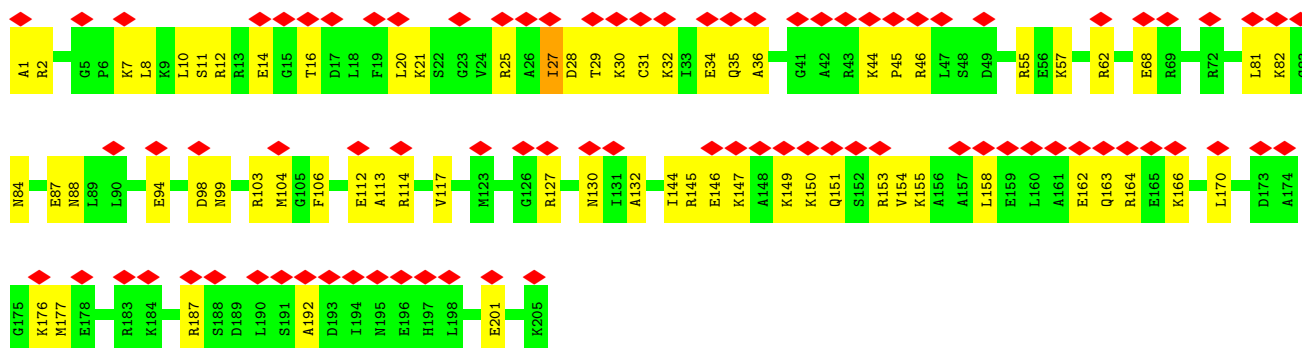
- Molecule 33: Small ribosomal subunit protein uS2



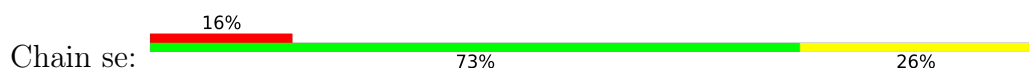
• Molecule 34: Small ribosomal subunit protein uS3

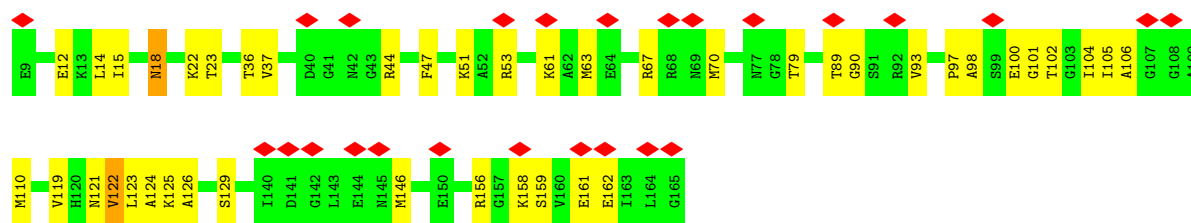


• Molecule 35: 30S ribosomal protein S4

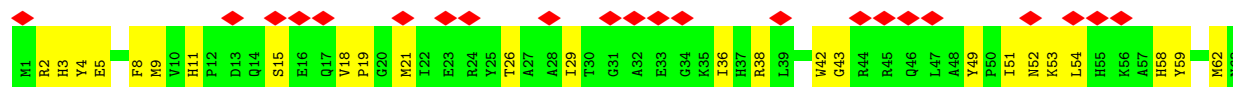


• Molecule 36: Small ribosomal subunit protein uS5

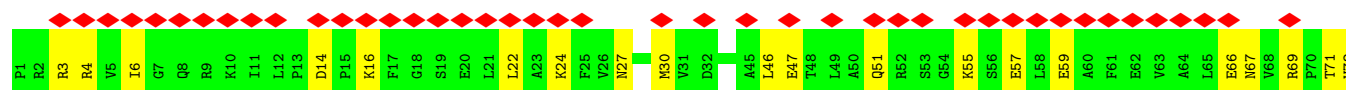
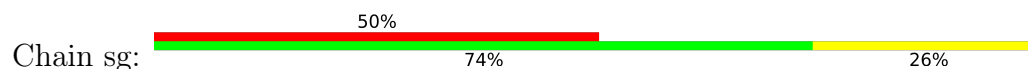




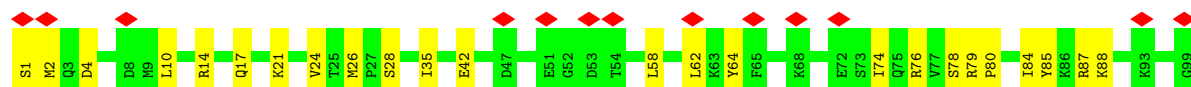
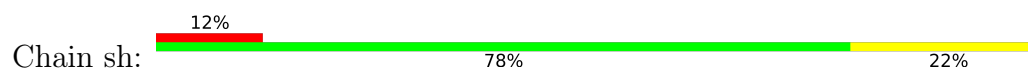
- Molecule 37: 30S ribosomal protein S6, non-modified isoform



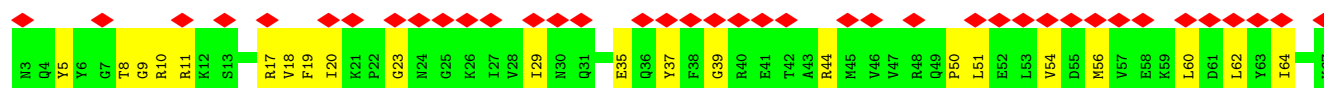
- Molecule 38: 30S ribosomal protein S7

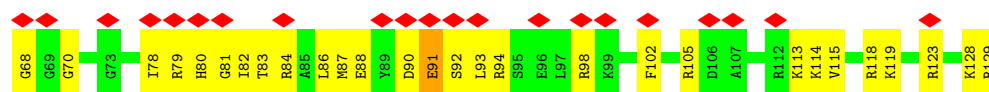


- Molecule 39: 30S ribosomal protein S8

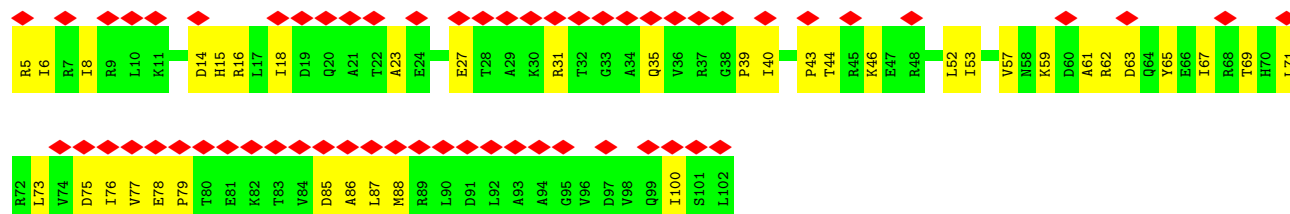


- Molecule 40: Small ribosomal subunit protein uS9

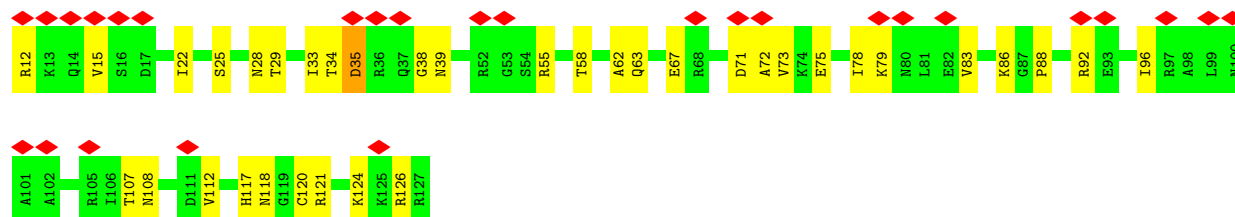




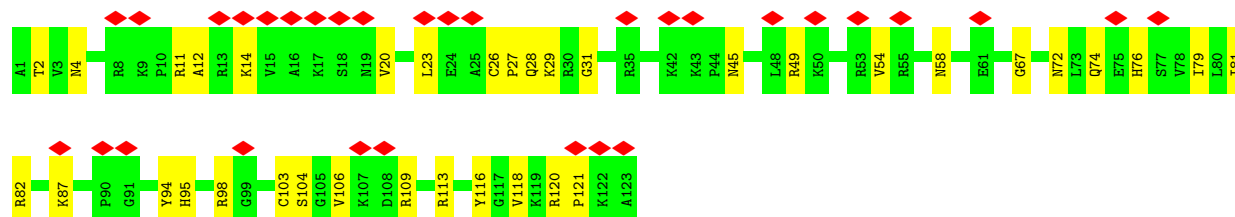
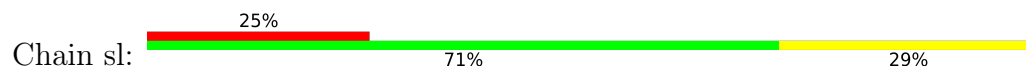
- Molecule 41: 30S ribosomal protein S10



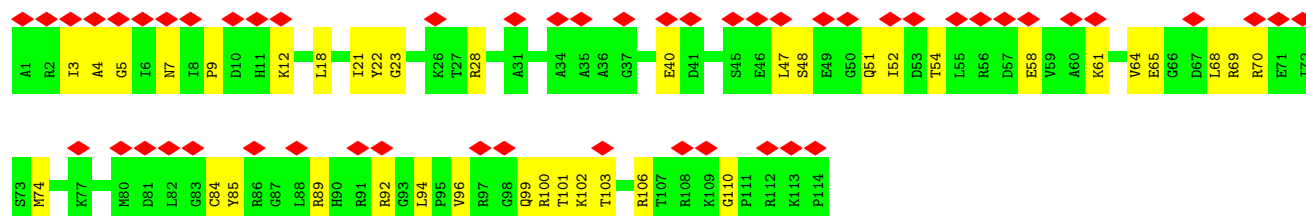
- Molecule 42: Small ribosomal subunit protein uS11



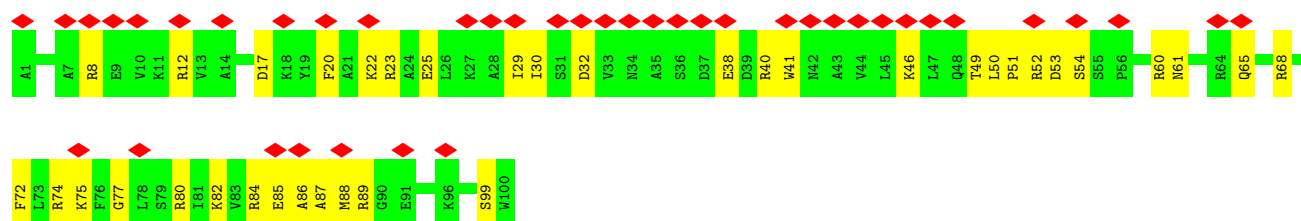
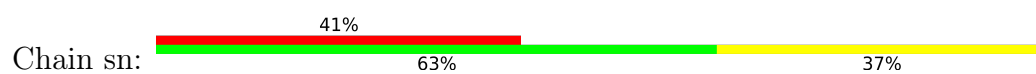
- Molecule 43: Small ribosomal subunit protein uS12



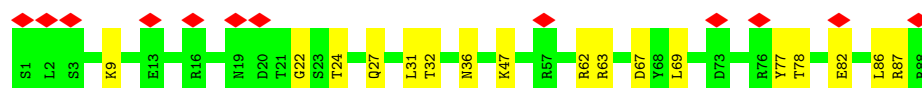
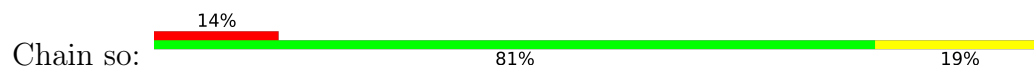
- Molecule 44: 30S ribosomal protein S13



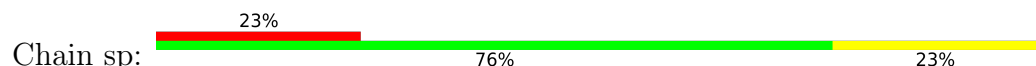
- Molecule 45: Small ribosomal subunit protein uS14



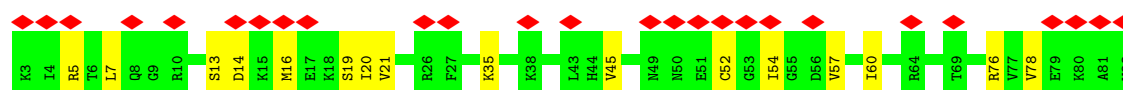
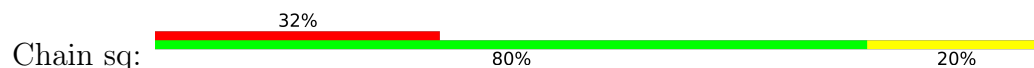
- Molecule 46: Small ribosomal subunit protein uS15



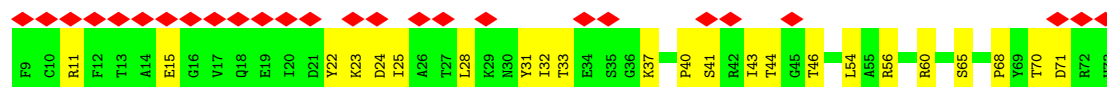
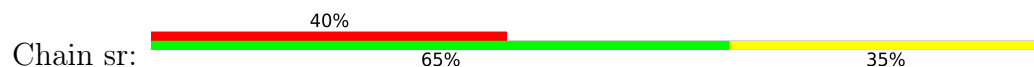
- Molecule 47: Small ribosomal subunit protein bS16



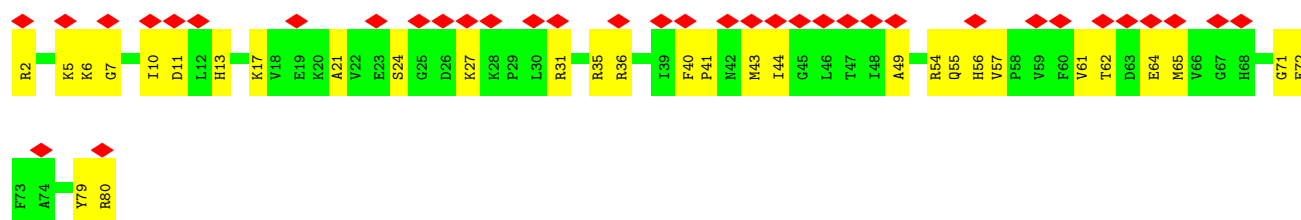
- Molecule 48: Small ribosomal subunit protein uS17



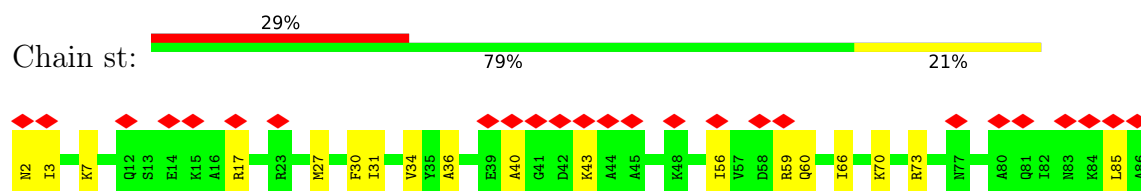
- Molecule 49: 30S ribosomal protein S18



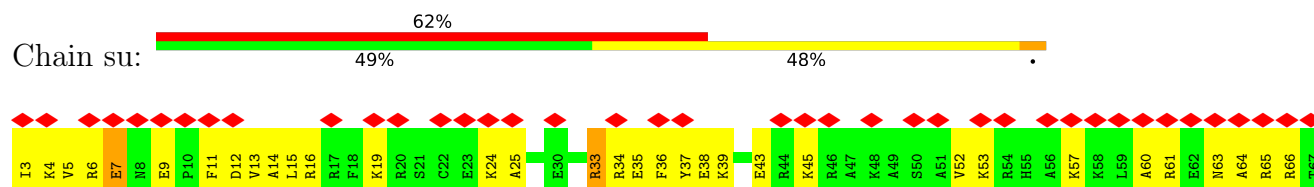
- Molecule 50: 30S ribosomal protein S19



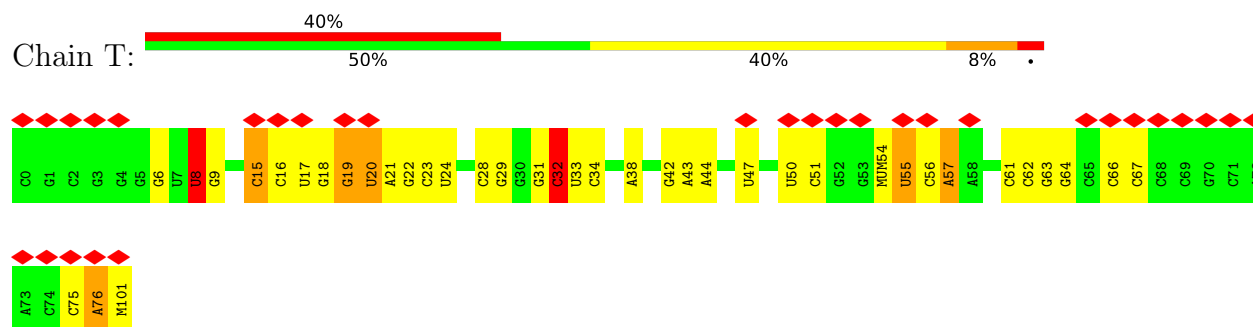
- Molecule 51: 30S ribosomal protein S20



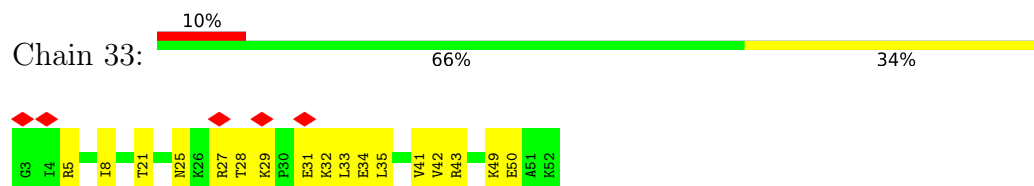
- Molecule 52: Small ribosomal subunit protein bS21



- Molecule 53: tRNA



- Molecule 54: Large ribosomal subunit protein bL33



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	146197	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	64	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.767	Depositor
Minimum map value	-1.785	Depositor
Average map value	0.007	Depositor
Map value standard deviation	0.137	Depositor
Recommended contour level	0.55	Depositor
Map size (Å)	380.0, 380.0, 380.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.95, 0.95, 0.95	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4SU, FME, H2U, PSU, MUM, MG, 4OC

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	13	0.26	0/1152	0.35	0/1551
2	14	0.31	0/947	0.46	0/1268
3	15	0.28	0/1062	0.42	0/1413
4	16	0.26	0/1093	0.39	0/1460
5	17	0.28	0/973	0.39	0/1301
6	18	0.21	0/902	0.40	0/1209
7	19	0.28	0/929	0.39	0/1242
8	2	0.31	0/2121	0.41	0/2852
9	20	0.31	0/960	0.36	0/1278
10	21	0.26	0/829	0.42	0/1107
11	22	0.28	0/864	0.38	0/1156
12	23	0.26	0/744	0.39	0/994
13	24	0.84	4/787 (0.5%)	0.86	4/1051 (0.4%)
14	25	0.22	0/766	0.35	0/1025
15	27	0.27	0/589	0.36	0/779
16	28	0.29	0/635	0.38	0/848
17	29	0.22	0/510	0.34	0/677
18	3	0.28	0/1586	0.40	0/2134
19	30	0.26	0/453	0.37	0/605
20	31	0.17	0/531	0.42	0/709
21	32	0.28	0/450	0.42	0/599
22	34	0.32	0/380	0.42	0/498
23	35	0.29	0/513	0.40	0/676
24	36	0.30	0/303	0.49	0/397
25	4	0.26	0/1571	0.36	0/2113
26	5	0.21	0/1434	0.43	0/1926
27	6	0.24	0/1343	0.60	2/1816 (0.1%)
28	9	0.17	0/1122	0.52	0/1515
29	M	0.22	0/219	0.25	0/339
30	R1	0.30	0/69792	0.33	0/108870
31	R2	0.23	0/2847	0.29	0/4440
32	R3	0.26	0/36782	0.33	0/57377

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	sb	0.18	0/1735	0.42	0/2338
34	sc	0.22	0/1651	0.41	0/2225
35	sd	0.22	0/1665	0.43	0/2227
36	se	0.25	0/1169	0.49	0/1573
37	sf	0.22	0/835	0.50	0/1128
38	sg	0.18	0/1195	0.36	0/1602
39	sh	0.23	0/989	0.33	0/1326
40	si	0.20	0/1034	0.48	0/1375
41	sj	0.21	0/796	0.44	0/1077
42	sk	0.26	0/885	0.47	0/1195
43	sl	0.26	0/969	0.49	0/1300
44	sm	0.20	0/892	0.41	0/1193
45	sn	0.24	0/817	0.48	0/1088
46	so	0.21	0/722	0.32	0/964
47	sp	0.21	0/659	0.38	0/884
48	sq	0.23	0/657	0.47	0/881
49	sr	0.19	0/544	0.35	0/731
50	ss	0.21	0/652	0.44	0/877
51	st	0.20	0/671	0.34	0/888
52	su	0.26	0/550	0.68	0/728
53	T	0.23	0/1716	0.30	0/2672
54	33	0.29	0/416	0.50	0/554
All	All	0.28	4/156408 (0.0%)	0.36	6/234051 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
26	5	0	1
28	9	0	1
35	sd	0	1
45	sn	0	1
52	su	0	2
53	T	6	0
All	All	6	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	24	49	PRO	CG-CD	-17.74	0.90	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	24	49	PRO	N-CD	10.38	1.62	1.47
13	24	49	PRO	CB-CG	6.66	1.82	1.49
13	24	49	PRO	N-CA	-5.26	1.41	1.47

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	24	49	PRO	N-CD-CG	-16.14	78.99	103.20
13	24	49	PRO	CA-N-CD	-11.41	96.02	112.00
27	6	111	PRO	CA-N-CD	-10.21	97.71	112.00
27	6	11	PRO	CA-N-CD	-8.93	99.50	112.00
13	24	49	PRO	CA-CB-CG	-8.90	87.59	104.50
13	24	49	PRO	N-CA-CB	-5.65	95.99	102.60

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
53	T	8	4SU	C2',C3'
53	T	20	H2U	C2',C1'
53	T	32	4OC	C2'
53	T	54	MUM	C5

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
26	5	132	ARG	Sidechain
28	9	8	LYS	Peptide
35	sd	27	ILE	Peptide
45	sn	86	ALA	Peptide
52	su	33	ARG	Peptide
52	su	7	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	13	1129	0	1162	28	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	14	938	0	1012	30	0
3	15	1053	0	1129	30	0
4	16	1074	0	1157	20	0
5	17	960	0	1000	20	0
6	18	892	0	923	28	0
7	19	917	0	965	21	0
8	2	2082	0	2157	54	0
9	20	947	0	1022	15	0
10	21	816	0	839	23	0
11	22	857	0	922	13	0
12	23	738	0	807	17	0
13	24	779	0	834	29	0
14	25	753	0	780	14	0
15	27	582	0	599	16	0
16	28	625	0	655	11	0
17	29	509	0	543	19	0
18	3	1565	0	1616	39	0
19	30	449	0	491	8	0
20	31	522	0	524	23	0
21	32	444	0	461	14	0
22	34	377	0	418	6	0
23	35	504	0	574	21	0
24	36	302	0	343	10	0
25	4	1552	0	1619	26	0
26	5	1410	0	1447	66	0
27	6	1323	0	1374	44	0
28	9	1111	0	1148	24	0
29	M	195	0	99	0	0
30	R1	62318	0	31350	816	0
31	R2	2546	0	1292	51	0
32	R3	32850	0	16534	561	0
33	sb	1704	0	1732	63	0
34	sc	1624	0	1699	44	0
35	sd	1643	0	1710	56	0
36	se	1156	0	1199	33	0
37	sf	817	0	808	34	0
38	sg	1181	0	1240	29	0
39	sh	979	0	1034	17	0
40	si	1022	0	1070	55	0
41	sj	786	0	828	26	0
42	sk	869	0	878	30	0
43	sl	955	0	1019	29	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	sm	883	0	944	30	0
45	sn	805	0	847	38	0
46	so	714	0	737	14	0
47	sp	649	0	666	16	0
48	sq	648	0	691	10	0
49	sr	535	0	552	15	0
50	ss	637	0	665	29	0
51	st	665	0	714	16	0
52	su	544	0	579	40	0
53	T	1649	0	841	21	0
54	33	409	0	440	16	0
55	3	1	0	0	0	0
55	32	1	0	0	0	0
55	R1	126	0	0	0	0
55	R3	33	0	0	0	0
All	All	144154	0	96689	2463	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 (2463) 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)
13:24:49:PRO:CB	13:24:49:PRO:CG	1.82	1.50
13:24:49:PRO:CG	13:24:49:PRO:N	1.69	1.44
13:24:49:PRO:CG	13:24:49:PRO:HD2	1.60	1.11
13:24:49:PRO:CG	13:24:49:PRO:CA	2.31	1.08
13:24:49:PRO:CG	13:24:49:PRO:HD3	1.60	1.06
13:24:49:PRO:CD	13:24:49:PRO:HG3	1.55	1.05
13:24:49:PRO:CD	13:24:49:PRO:HG2	1.55	1.04
13:24:49:PRO:N	13:24:49:PRO:HG3	1.55	1.03
30:R1:2545:G:H21	30:R1:2565:A:H8	1.14	0.96
30:R1:2107:G:H1	30:R1:2182:U:H3	0.92	0.91
32:R3:359:G:HO2'	32:R3:360:G:H8	0.97	0.91
30:R1:156:A:H2	30:R1:169:G:H1	1.19	0.90
13:24:49:PRO:CG	13:24:49:PRO:CD	0.90	0.89
32:R3:1151:A:N6	32:R3:1152:A:N6	2.20	0.88
34:sc:133:MET:HE3	34:sc:167:TYR:HB2	1.56	0.88
30:R1:1270:C:H5''	30:R1:1271:G:H5'	1.56	0.86
30:R1:156:A:C2	30:R1:169:G:N1	2.44	0.86
30:R1:287:G:N2	30:R1:353:C:N3	2.23	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
52:su:33:ARG:HB3	52:su:34:ARG:HE	1.40	0.83
32:R3:1356:G:H2'	32:R3:1357:A:H8	1.43	0.83
27:6:172:GLU:HG2	27:6:174:LYS:H	1.43	0.83
30:R1:545:U:HO2'	30:R1:548:G:H1	1.20	0.83
28:9:9:VAL:HG12	28:9:11:ASN:H	1.44	0.83
30:R1:1410:G:N2	30:R1:1592:C:O2	2.10	0.83
53:T:32:4OC:O2'	53:T:32:4OC:O2	1.96	0.83
30:R1:880:G:N2	30:R1:897:C:N3	2.27	0.82
2:14:99:ILE:HD11	2:14:115:ILE:HD12	1.60	0.82
28:9:127:GLU:OE1	28:9:145:ASN:ND2	2.12	0.82
30:R1:1410:G:N1	30:R1:1592:C:N3	2.26	0.81
5:17:37:THR:HG22	5:17:39:PRO:HD2	1.61	0.81
26:5:132:ARG:NH2	30:R1:2305:U:H1'	1.96	0.81
30:R1:358:U:H2'	30:R1:359:G:H8	1.46	0.81
26:5:70:ARG:NH2	30:R1:2298:A:OP1	2.12	0.81
16:28:76:LYS:NZ	30:R1:152:A:OP1	2.13	0.81
31:R2:30:C:H1'	31:R2:57:A:H61	1.44	0.80
21:32:15:ARG:NH2	30:R1:1264:A:OP1	2.13	0.80
24:36:2:LYS:NZ	30:R1:2478:A:OP2	2.14	0.80
32:R3:1027:C:N3	32:R3:1034:G:N1	2.29	0.80
32:R3:1002:G:H1	32:R3:1038:C:HO2'	1.21	0.80
23:35:39:ARG:NH1	30:R1:2362:C:OP1	2.15	0.80
30:R1:2097:A:N6	30:R1:2098:U:O2	2.15	0.80
35:sd:27:ILE:HG13	35:sd:28:ASP:H	1.47	0.79
18:3:4:LEU:HD13	18:3:29:VAL:HG11	1.64	0.79
32:R3:58:C:O2'	32:R3:388:G:N2	2.16	0.79
52:su:35:GLU:HG2	52:su:36:PHE:H	1.47	0.79
8:2:216:ARG:NH2	30:R1:781:A:OP1	2.16	0.79
45:sn:75:LYS:HA	45:sn:75:LYS:HE2	1.64	0.79
42:sk:12:ARG:N	42:sk:75:GLU:OE2	2.15	0.79
50:ss:24:SER:HB2	50:ss:27:LYS:HZ2	1.48	0.79
20:31:24:ILE:HD11	26:5:101:ARG:HG2	1.65	0.79
47:sp:4:ILE:HG12	47:sp:21:VAL:HG22	1.65	0.78
8:2:270:ARG:NH2	30:R1:1798:U:OP2	2.16	0.78
20:31:2:LYS:NZ	31:R2:43:C:OP2	2.15	0.78
32:R3:207:C:H2'	32:R3:213:G:H1	1.49	0.78
32:R3:1323:G:N7	50:ss:2:ARG:NH2	2.32	0.78
27:6:138:GLN:NE2	30:R1:2745:C:O2	2.18	0.77
18:3:59:ARG:NH2	30:R1:2831:G:OP2	2.17	0.76
32:R3:673:A:H2'	32:R3:674:G:C8	2.20	0.76
10:21:6:GLN:OE1	10:21:6:GLN:N	2.18	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:597:G:N2	32:R3:643:C:O2	2.18	0.76
32:R3:693:G:OP1	42:sk:126:ARG:NH2	2.19	0.76
30:R1:1668:A:N3	30:R1:1670:C:N4	2.34	0.76
16:28:42:GLU:OE1	16:28:44:ARG:NH2	2.19	0.76
26:5:3:LEU:HD11	26:5:100:GLU:HB2	1.66	0.76
32:R3:939:G:OP1	38:sg:101:ARG:NH2	2.18	0.76
26:5:147:ARG:HG2	26:5:148:VAL:H	1.51	0.75
32:R3:619:U:H4'	35:sd:127:ARG:HH22	1.49	0.75
46:so:32:THR:HG22	46:so:62:ARG:HH11	1.51	0.75
30:R1:880:G:H22	30:R1:895:U:H3	1.33	0.75
32:R3:1257:A:OP1	34:sc:26:LYS:NZ	2.18	0.75
3:15:76:GLU:OE1	30:R1:636:G:N1	2.16	0.75
32:R3:297:G:N2	32:R3:300:A:OP2	2.18	0.75
28:9:2:GLN:HE22	28:9:39:ALA:HB3	1.50	0.75
32:R3:424:G:H2'	32:R3:425:G:C8	2.22	0.75
42:sk:83:VAL:HG11	42:sk:96:ILE:HD12	1.67	0.75
30:R1:2324:U:H3'	30:R1:2325:G:H5''	1.69	0.75
32:R3:57:G:N2	32:R3:388:G:O6	2.20	0.75
38:sg:149:ALA:HB1	42:sk:58:THR:HG21	1.69	0.75
28:9:8:LYS:HG2	28:9:15:LEU:HB2	1.67	0.74
6:18:63:LYS:NZ	31:R2:51:G:OP1	2.20	0.74
30:R1:284:U:O2	30:R1:356:G:N2	2.20	0.74
30:R1:2668:G:O2'	30:R1:2669:G:O5'	2.04	0.74
4:16:35:ALA:HB2	4:16:102:LEU:HD11	1.69	0.74
6:18:9:ARG:NH2	30:R1:2296:U:OP2	2.21	0.74
32:R3:292:G:H21	32:R3:608:A:H61	1.33	0.74
43:sl:54:VAL:HG21	43:sl:81:ILE:HD11	1.70	0.74
12:23:19:LYS:NZ	30:R1:1340:U:OP1	2.21	0.74
30:R1:2469:A:N6	30:R1:2481:G:O2'	2.21	0.74
53:T:6:G:N1	53:T:66:C:N3	2.32	0.74
19:30:36:GLU:O	19:30:37:ARG:NH1	2.20	0.74
30:R1:2162:G:O4'	30:R1:2173:A:N6	2.20	0.74
39:sh:10:LEU:HD22	39:sh:74:ILE:HD11	1.70	0.74
49:sr:56:ARG:HD2	49:sr:60:ARG:HH21	1.53	0.74
53:T:31:G:H2'	53:T:32:4OC:H6	1.69	0.74
18:3:38:LYS:NZ	18:3:81:GLU:OE1	2.21	0.73
34:sc:184:ASN:OD1	34:sc:185:THR:N	2.21	0.73
44:sm:3:ILE:HG22	44:sm:4:ALA:H	1.52	0.73
24:36:1:MET:HE2	24:36:36:ARG:HB2	1.67	0.73
32:R3:1522:U:H2'	32:R3:1523:G:H8	1.54	0.73
1:13:96:ARG:NH2	30:R1:2639:A:O3'	2.19	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:si:23:GLY:H	40:si:60:LEU:HA	1.53	0.73
23:35:33:THR:HG1	54:33:21:THR:HG1	1.30	0.73
42:sk:71:ASP:OD1	42:sk:72:ALA:N	2.22	0.73
30:R1:2107:G:O6	30:R1:2182:U:O4	2.07	0.73
32:R3:1367:C:OP2	40:si:113:LYS:NZ	2.21	0.73
48:sq:76:ARG:HH12	48:sq:78:VAL:HG12	1.53	0.73
9:20:57:ARG:NH1	30:R1:1154:G:OP2	2.21	0.73
20:31:56:ARG:HG2	20:31:59:ARG:HE	1.52	0.73
32:R3:890:G:O2'	32:R3:906:A:N6	2.22	0.73
32:R3:981:U:H1'	45:sn:60:ARG:HH22	1.54	0.73
53:T:6:G:N2	53:T:66:C:O2	2.17	0.73
11:22:4:ILE:HG22	11:22:106:VAL:HG22	1.69	0.72
31:R2:112:G:O2'	31:R2:113:C:O2	2.06	0.72
3:15:99:ASN:ND2	30:R1:621:A:OP2	2.22	0.72
47:sp:46:LYS:HG2	47:sp:47:GLU:H	1.53	0.72
43:sl:4:ASN:OD1	48:sq:35:LYS:NZ	2.20	0.72
47:sp:46:LYS:HG2	47:sp:47:GLU:N	2.03	0.72
30:R1:500:G:H22	30:R1:503:A:H5'	1.54	0.72
8:2:269:ARG:NH2	30:R1:1799:G:OP2	2.23	0.72
32:R3:411:A:O2'	35:sd:30:LYS:NZ	2.20	0.72
8:2:79:ARG:NH1	8:2:81:GLU:OE1	2.23	0.72
32:R3:674:G:H2'	32:R3:675:A:H8	1.55	0.72
32:R3:1028:C:O2	32:R3:1033:G:N2	2.23	0.71
37:sf:11:HIS:HB2	37:sf:54:LEU:HD22	1.72	0.71
32:R3:77:A:N6	32:R3:91:U:O4	2.23	0.71
22:34:43:THR:OG1	22:34:44:VAL:N	2.22	0.71
32:R3:1005:A:H2'	32:R3:1006:G:C4	2.25	0.71
40:si:39:GLY:O	40:si:44:ARG:NH1	2.23	0.71
30:R1:13:A:O2'	30:R1:15:G:N7	2.23	0.71
32:R3:80:A:N6	32:R3:89:U:O4	2.23	0.71
28:9:116:ARG:HB2	28:9:131:SER:HB2	1.72	0.71
32:R3:1092:A:H5''	38:sg:3:ARG:HH21	1.56	0.71
8:2:143:VAL:HB	8:2:153:LEU:HB2	1.73	0.71
13:24:6:ARG:NH2	30:R1:99:U:O2	2.24	0.71
37:sf:29:ILE:HD13	37:sf:64:VAL:HG21	1.73	0.71
44:sm:64:VAL:HG22	44:sm:65:GLU:H	1.56	0.71
1:13:21:THR:HG22	1:13:61:LYS:HD2	1.73	0.71
30:R1:135:U:H3	30:R1:143:C:H42	1.39	0.71
32:R3:723:U:O2	52:su:45:LYS:NZ	2.23	0.71
30:R1:918:A:N3	31:R2:80:U:O2'	2.24	0.70
30:R1:2699:C:O2'	30:R1:2700:A:O5'	2.09	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:805:G:N2	30:R1:829:A:OP1	2.24	0.70
32:R3:1038:C:O2'	32:R3:1039:G:N2	2.24	0.70
38:sg:4:ARG:HH12	38:sg:6:ILE:HG12	1.57	0.70
42:sk:126:ARG:O	52:su:33:ARG:NH1	2.15	0.70
24:36:37:GLN:NE2	30:R1:1124:G:O2'	2.25	0.70
32:R3:1071:C:OP1	36:se:53:ARG:NH2	2.24	0.70
32:R3:1405:G:H21	32:R3:1518:A:H8	1.38	0.70
39:sh:17:GLN:HG2	39:sh:62:LEU:HD13	1.72	0.70
18:3:128:ARG:NH2	30:R1:1995:U:OP1	2.25	0.70
30:R1:163:C:H2'	30:R1:164:C:H4'	1.74	0.69
32:R3:1316:G:N2	32:R3:1319:A:OP2	2.25	0.69
35:sd:106:PHE:HE1	35:sd:177:MET:HB2	1.56	0.69
52:su:6:ARG:NH1	52:su:6:ARG:HA	2.07	0.69
1:13:31:GLU:HG2	1:13:142:ILE:HD11	1.74	0.69
6:18:31:THR:HG23	6:18:34:HIS:H	1.56	0.69
23:35:31:ILE:O	23:35:35:LYS:NZ	2.24	0.69
30:R1:1936:A:H2	30:R1:1943:U:H3	1.40	0.69
43:sl:113:ARG:HB2	43:sl:118:VAL:HB	1.75	0.69
2:14:70:ARG:NH1	30:R1:2684:U:O4'	2.26	0.69
40:si:39:GLY:HA2	40:si:44:ARG:HD3	1.75	0.69
30:R1:356:G:H2'	30:R1:357:C:C6	2.28	0.69
32:R3:147:G:H2'	32:R3:148:G:C8	2.28	0.69
40:si:91:GLU:HA	40:si:94:ARG:HB2	1.74	0.69
52:su:39:LYS:O	52:su:43:GLU:N	2.20	0.69
17:29:2:LYS:NZ	30:R1:78:U:OP1	2.19	0.69
30:R1:1178:C:N3	30:R1:1179:G:O2'	2.26	0.69
30:R1:2107:G:N2	30:R1:2182:U:O2	2.23	0.69
30:R1:2128:G:H1	30:R1:2160:C:H42	1.39	0.69
37:sf:52:ASN:O	37:sf:52:ASN:ND2	2.25	0.69
40:si:86:LEU:O	40:si:94:ARG:NH2	2.26	0.69
1:13:43:GLU:N	1:13:43:GLU:OE2	2.25	0.69
4:16:69:PRO:HA	4:16:94:ALA:HB2	1.74	0.69
30:R1:677:A:HO2'	30:R1:2070:A:HO2'	1.38	0.69
30:R1:1094:U:N3	30:R1:1097:U:OP2	2.26	0.69
40:si:79:ARG:HG2	40:si:79:ARG:HH11	1.58	0.69
30:R1:84:A:N1	30:R1:98:G:O2'	2.25	0.68
28:9:8:LYS:O	28:9:9:VAL:HG23	1.93	0.68
8:2:4:LYS:HG2	8:2:16:VAL:HG22	1.74	0.68
27:6:16:VAL:HG11	27:6:49:LEU:HD11	1.75	0.68
35:sd:155:LYS:NZ	35:sd:155:LYS:O	2.26	0.68
5:17:29:VAL:O	5:17:78:LYS:NZ	2.26	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:4:49:ARG:NH1	30:R1:673:C:OP1	2.27	0.68
44:sm:40:GLU:OE2	44:sm:40:GLU:N	2.23	0.68
30:R1:199:A:O2'	30:R1:200:U:O2	2.12	0.68
30:R1:1872:A:O2'	30:R1:1873:G:O4'	2.11	0.68
30:R1:2096:C:H42	30:R1:2193:G:H1	1.40	0.68
32:R3:115:G:H8	32:R3:115:G:OP1	1.77	0.68
32:R3:811:C:O2'	32:R3:901:A:N1	2.27	0.68
49:sr:11:ARG:HH11	49:sr:15:GLU:HG3	1.59	0.68
4:16:66:ARG:NH1	4:16:104:GLU:OE2	2.26	0.68
11:22:36:LEU:HD21	11:22:47:VAL:HG13	1.74	0.68
30:R1:848:C:H2'	30:R1:849:A:H8	1.57	0.68
49:sr:44:THR:HG23	49:sr:46:THR:HG23	1.76	0.68
32:R3:409:U:H3	32:R3:433:G:H1	1.39	0.68
13:24:27:VAL:HG12	13:24:33:VAL:HG12	1.74	0.68
32:R3:148:G:N2	32:R3:175:C:O2	2.27	0.68
32:R3:58:C:H2'	32:R3:59:A:H8	1.59	0.67
24:36:29:ALA:O	27:6:169:ARG:NH1	2.25	0.67
30:R1:59:U:O2'	30:R1:74:A:OP2	2.11	0.67
30:R1:2328:A:H2'	30:R1:2329:U:C6	2.29	0.67
32:R3:380:G:N2	32:R3:383:A:OP2	2.27	0.67
25:4:44:ARG:NH2	30:R1:1248:G:OP1	2.25	0.67
26:5:91:ARG:NH1	31:R2:43:C:O2	2.27	0.67
30:R1:1056:G:N1	30:R1:1102:C:OP2	2.27	0.67
32:R3:1002:G:N2	32:R3:1039:G:H2'	2.10	0.67
32:R3:1377:A:H5''	32:R3:1378:C:H5'	1.76	0.67
30:R1:2099:U:N3	30:R1:2100:G:O6	2.28	0.67
32:R3:1447:A:H5''	32:R3:1448:C:H5	1.59	0.67
35:sd:25:ARG:NH1	35:sd:28:ASP:O	2.27	0.67
30:R1:351:C:H2'	30:R1:352:A:C8	2.30	0.67
33:sb:166:ASP:O	33:sb:169:HIS:ND1	2.28	0.67
30:R1:157:C:H2'	30:R1:158:U:H5''	1.77	0.67
30:R1:932:U:O2'	30:R1:934:U:O4	2.12	0.67
30:R1:1629:U:O4	30:R1:1630:A:N6	2.28	0.67
30:R1:2189:U:H2'	30:R1:2190:G:C8	2.30	0.66
32:R3:1077:G:N2	32:R3:1080:A:OP2	2.27	0.66
35:sd:32:LYS:HE2	35:sd:36:ALA:HB2	1.76	0.66
51:st:66:ILE:HG23	51:st:70:LYS:HD3	1.76	0.66
31:R2:14:U:OP2	31:R2:70:C:O2'	2.12	0.66
32:R3:324:G:N1	32:R3:327:A:OP2	2.28	0.66
32:R3:673:A:O3'	37:sf:86:ARG:NH2	2.28	0.66
37:sf:5:GLU:OE2	49:sr:23:LYS:NZ	2.29	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:sg:110:ARG:NH1	38:sg:122:GLU:OE1	2.24	0.66
43:sl:67:GLY:O	43:sl:98:ARG:NH1	2.28	0.66
30:R1:2651:C:C4	30:R1:2652:C:N4	2.64	0.66
4:16:82:MET:HE3	30:R1:960:A:H61	1.61	0.66
32:R3:1149:C:OP2	40:si:10:ARG:NH2	2.29	0.66
35:sd:34:GLU:HG2	35:sd:35:GLN:H	1.60	0.66
44:sm:23:GLY:O	44:sm:28:ARG:NH1	2.28	0.66
32:R3:1307:U:OP1	44:sm:99:GLN:NE2	2.28	0.66
2:14:80:ASP:OD2	7:19:61:ARG:NH2	2.29	0.66
32:R3:1317:C:OP1	45:sn:54:SER:OG	2.14	0.66
26:5:79:ARG:HB2	26:5:82:TYR:HE1	1.61	0.66
27:6:40:VAL:O	27:6:54:ARG:NH2	2.29	0.66
28:9:7:ASP:OD1	28:9:8:LYS:N	2.29	0.66
30:R1:284:U:N3	30:R1:356:G:N1	2.43	0.66
32:R3:1360:A:OP2	45:sn:74:ARG:NH2	2.29	0.66
44:sm:47:LEU:HD23	44:sm:52:ILE:HG12	1.77	0.66
30:R1:1079:C:H41	30:R1:1088:A:H5''	1.61	0.65
14:25:35:GLU:OE1	14:25:35:GLU:N	2.29	0.65
30:R1:2104:C:H41	30:R1:2185:U:H3	1.42	0.65
32:R3:1137:C:O2	32:R3:1138:G:N2	2.29	0.65
2:14:2:ILE:HD13	2:14:8:LEU:HD21	1.79	0.65
30:R1:2328:A:H2'	30:R1:2329:U:H6	1.60	0.65
32:R3:1313:U:OP2	50:ss:5:LYS:NZ	2.29	0.65
32:R3:1452:C:O2'	32:R3:1453:G:N2	2.29	0.65
30:R1:1019:U:OP1	30:R1:1035:U:O2'	2.14	0.65
30:R1:1071:G:H1'	30:R1:1089:A:C5	2.31	0.65
30:R1:285:G:O6	30:R1:355:U:C2	2.49	0.65
3:15:109:LYS:HE2	3:15:128:THR:HG22	1.77	0.65
28:9:12:LEU:HG	28:9:13:GLY:H	1.62	0.65
33:sb:84:LEU:HB2	33:sb:90:PHE:HE2	1.61	0.65
27:6:111:PRO:HD2	27:6:111:PRO:O	1.97	0.65
30:R1:156:A:H2	30:R1:169:G:N1	1.88	0.65
30:R1:1069:A:H1'	30:R1:1096:A:H4'	1.78	0.65
30:R1:2316:G:H2'	30:R1:2317:A:H8	1.62	0.65
32:R3:1344:C:OP1	40:si:123:ARG:NH1	2.30	0.65
40:si:10:ARG:O	40:si:105:ARG:NH1	2.30	0.65
13:24:5:ARG:NH1	30:R1:84:A:OP1	2.30	0.65
32:R3:1261:A:N6	32:R3:1274:A:O2'	2.29	0.65
54:33:34:GLU:N	54:33:34:GLU:OE2	2.30	0.65
21:32:12:ARG:NH2	30:R1:517:C:OP1	2.30	0.64
32:R3:7:A:H2'	36:se:123:LEU:HD12	1.79	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:134:G:O6	47:sp:25:ARG:NH1	2.30	0.64
32:R3:1114:C:H1'	45:sn:99:SER:HB3	1.78	0.64
30:R1:1779:U:OP2	30:R1:1784:A:N6	2.29	0.64
30:R1:1102:C:H2'	30:R1:1103:A:H8	1.62	0.64
34:sc:84:GLU:OE1	34:sc:84:GLU:N	2.30	0.64
25:4:147:LEU:HB3	25:4:186:VAL:HG12	1.80	0.64
32:R3:1297:G:N3	38:sg:113:LYS:NZ	2.45	0.64
15:27:77:ARG:NH2	30:R1:2332:C:OP1	2.30	0.64
9:20:49:ARG:O	9:20:53:LYS:NZ	2.30	0.64
15:27:64:ASP:N	15:27:64:ASP:OD1	2.30	0.64
30:R1:2774:C:O2'	30:R1:2775:G:O5'	2.15	0.64
33:sb:87:ASP:OD2	33:sb:224:ARG:NH1	2.30	0.64
54:33:32:LYS:HZ2	54:33:49:LYS:HB3	1.62	0.64
32:R3:1151:A:C6	32:R3:1152:A:N6	2.65	0.64
6:18:30:ARG:NH2	31:R2:48:U:OP1	2.31	0.64
7:19:88:ARG:HB2	7:19:112:ARG:HB2	1.81	0.64
15:27:55:ARG:NH1	30:R1:2364:C:OP1	2.30	0.64
18:3:4:LEU:HD22	18:3:32:ASN:HD22	1.62	0.64
30:R1:1062:G:N2	30:R1:1076:C:O2	2.23	0.63
30:R1:2121:G:N2	30:R1:2122:U:O4	2.30	0.63
30:R1:2258:C:O2'	30:R1:2427:C:OP2	2.16	0.63
30:R1:2651:C:N4	30:R1:2652:C:N4	2.47	0.63
2:14:120:PRO:HB2	2:14:121:GLU:OE1	1.99	0.63
4:16:86:LYS:NZ	30:R1:955:U:OP1	2.31	0.63
6:18:60:GLU:OE1	6:18:60:GLU:N	2.29	0.63
22:34:1:MET:SD	22:34:1:MET:N	2.62	0.63
23:35:14:LYS:HB2	23:35:22:LYS:HE3	1.81	0.63
32:R3:292:G:N2	32:R3:608:A:H61	1.96	0.63
14:25:48:MET:HE1	14:25:51:GLN:HE21	1.62	0.63
34:sc:35:ASP:OD1	34:sc:58:ARG:NH2	2.29	0.63
5:17:22:ARG:HG3	5:17:70:THR:HA	1.79	0.63
18:3:151:THR:OG1	30:R1:2032:G:N2	2.31	0.63
32:R3:1009:U:H3	32:R3:1020:G:H1	1.45	0.63
37:sf:38:ARG:HH21	37:sf:95:ALA:HB1	1.64	0.63
2:14:106:GLU:N	2:14:106:GLU:OE2	2.32	0.63
7:19:14:GLN:OE1	7:19:14:GLN:N	2.31	0.63
30:R1:979:A:H5'	30:R1:980:A:H5''	1.80	0.63
32:R3:962:C:H5	32:R3:973:G:H1	1.45	0.63
41:sj:6:ILE:HD11	41:sj:76:ILE:HB	1.81	0.63
34:sc:116:ALA:O	34:sc:120:THR:OG1	2.16	0.63
27:6:175:LYS:HA	27:6:175:LYS:HE3	1.80	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:1273:C:H2'	32:R3:1274:A:O4'	1.99	0.62
40:si:129:ARG:NH2	53:T:33:U:OP2	2.32	0.62
35:sd:28:ASP:OD1	35:sd:31:CYS:N	2.31	0.62
40:si:62:LEU:HB3	40:si:64:ILE:HD11	1.81	0.62
17:29:36:GLN:O	17:29:38:GLN:NE2	2.33	0.62
30:R1:1019:U:H3	30:R1:1142:A:H62	1.47	0.62
30:R1:1528:A:OP2	30:R1:1543:G:N2	2.29	0.62
32:R3:1036:A:H2'	32:R3:1037:C:C6	2.34	0.62
34:sc:57:GLU:OE2	34:sc:57:GLU:N	2.32	0.62
27:6:23:ILE:HD11	27:6:42:VAL:HG21	1.80	0.62
30:R1:2246:G:H2'	30:R1:2247:A:H8	1.65	0.62
18:3:109:VAL:HG22	18:3:203:VAL:HG22	1.81	0.62
30:R1:2102:G:N1	30:R1:2188:U:O4	2.31	0.62
26:5:132:ARG:NH2	30:R1:2305:U:O2	2.31	0.62
32:R3:745:G:H2'	32:R3:746:A:H8	1.63	0.62
48:sq:16:MET:HG3	48:sq:19:SER:HB2	1.81	0.62
30:R1:2487:G:H2'	30:R1:2488:G:H8	1.65	0.62
32:R3:1073:U:O2	33:sb:102:ASN:ND2	2.28	0.62
33:sb:180:ILE:H	33:sb:180:ILE:HD12	1.64	0.62
30:R1:547:A:H5''	30:R1:548:G:N7	2.13	0.62
32:R3:1009:U:O2	32:R3:1020:G:N2	2.29	0.62
33:sb:13:VAL:HB	33:sb:207:ARG:HH11	1.65	0.62
36:se:156:ARG:NH1	39:sh:42:GLU:OE1	2.33	0.62
41:sj:5:ARG:HD2	41:sj:79:PRO:HB3	1.82	0.62
30:R1:1091:G:H2'	30:R1:1092:C:C6	2.34	0.61
33:sb:92:ASN:OD1	33:sb:93:HIS:ND1	2.33	0.61
1:13:44:TYR:HD1	1:13:45:THR:N	1.97	0.61
30:R1:1047:G:N2	30:R1:1110:G:N3	2.48	0.61
32:R3:447:G:O2'	32:R3:487:A:N6	2.33	0.61
44:sm:89:ARG:HB2	44:sm:96:VAL:HG12	1.82	0.61
26:5:132:ARG:HA	26:5:132:ARG:NE	2.14	0.61
30:R1:1064:C:OP1	30:R1:1066:U:O2'	2.17	0.61
7:19:64:SER:OG	7:19:65:ASN:N	2.28	0.61
30:R1:387:U:H4'	30:R1:388:G:H5'	1.82	0.61
30:R1:1590:A:H2'	30:R1:1591:A:H8	1.64	0.61
32:R3:744:C:H2'	32:R3:745:G:H8	1.65	0.61
41:sj:53:ILE:HD11	45:sn:84:ARG:CZ	2.31	0.61
13:24:100:GLU:OE1	13:24:100:GLU:N	2.31	0.61
30:R1:1045:C:O4'	30:R1:1111:A:N6	2.34	0.61
32:R3:673:A:H2'	32:R3:674:G:H8	1.66	0.61
32:R3:1179:A:OP2	40:si:98:ARG:NH2	2.33	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:1405:G:O2'	32:R3:1518:A:O2'	2.10	0.61
42:sk:63:GLN:NE2	42:sk:67:GLU:OE2	2.33	0.61
6:18:117:PHE:O	30:R1:2377:A:O2'	2.18	0.61
30:R1:1057:A:H62	30:R1:1087:G:H8	1.46	0.61
32:R3:669:G:OP1	46:so:47:LYS:NZ	2.33	0.61
40:si:56:MET:HE3	40:si:60:LEU:HD22	1.82	0.61
11:22:3:THR:HG21	11:22:58:ALA:HA	1.82	0.61
27:6:31:GLU:OE2	27:6:33:THR:OG1	2.18	0.61
32:R3:1218:C:H2'	32:R3:1219:A:C8	2.36	0.61
34:sc:26:LYS:HB3	34:sc:27:GLU:OE2	2.00	0.61
12:23:18:GLU:OE1	12:23:18:GLU:N	2.31	0.61
15:27:41:ARG:NH2	30:R1:2387:U:O2'	2.28	0.61
23:35:35:LYS:HG2	23:35:39:ARG:HH21	1.65	0.61
4:16:105:MET:HE2	4:16:108:VAL:HG21	1.82	0.61
25:4:48:THR:HG22	25:4:86:ALA:HB3	1.83	0.61
30:R1:197:A:N6	30:R1:2430:A:O2'	2.33	0.61
30:R1:351:C:H2'	30:R1:352:A:H8	1.63	0.61
32:R3:413:G:O2'	32:R3:428:G:N2	2.34	0.61
32:R3:928:G:H1	32:R3:1389:C:H5	1.49	0.61
49:sr:25:ILE:H	49:sr:25:ILE:HD12	1.66	0.61
30:R1:413:C:O2'	30:R1:414:C:O2	2.18	0.60
32:R3:674:G:H21	42:sk:117:HIS:HB2	1.66	0.60
33:sb:13:VAL:O	33:sb:207:ARG:NH1	2.34	0.60
40:si:29:ILE:HG22	40:si:37:TYR:HD2	1.66	0.60
23:35:7:ARG:NH1	30:R1:243:U:OP2	2.34	0.60
26:5:104:THR:HG22	26:5:105:ILE:HG23	1.83	0.60
11:22:74:ILE:HD12	11:22:105:VAL:HG22	1.83	0.60
20:31:66:ILE:HG21	50:ss:7:GLY:H	1.65	0.60
30:R1:1103:A:H5'	30:R1:1104:C:H5	1.66	0.60
30:R1:2508:G:H1	30:R1:2580:U:H5	1.47	0.60
30:R1:1844:C:C2	30:R1:1897:G:N2	2.69	0.60
30:R1:2073:C:H5	30:R1:2436:G:H1	1.47	0.60
32:R3:501:C:H2'	32:R3:502:A:C8	2.36	0.60
14:25:8:VAL:O	14:25:10:LYS:NZ	2.34	0.60
19:30:23:LEU:HD11	19:30:53:MET:HE1	1.83	0.60
27:6:24:THR:HG22	27:6:33:THR:HG23	1.84	0.60
30:R1:631:A:N3	30:R1:2415:G:O2'	2.33	0.60
32:R3:593:U:H2'	32:R3:594:U:C6	2.36	0.60
25:4:35:TYR:OH	25:4:176:ASP:OD2	2.18	0.60
30:R1:281:C:H5	30:R1:359:G:H1	1.47	0.60
32:R3:537:G:OP1	43:sl:109:ARG:NH2	2.30	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:sb:113:LEU:HB2	33:sb:143:LEU:HD21	1.83	0.60
22:34:31:LEU:HD22	22:34:42:LEU:HD23	1.83	0.60
27:6:106:LEU:HD11	27:6:151:ARG:HB2	1.83	0.60
30:R1:2122:U:H2'	30:R1:2123:G:H4'	1.84	0.60
40:si:51:LEU:HD21	40:si:82:ILE:HD11	1.82	0.60
10:21:79:ARG:NH2	30:R1:563:A:OP2	2.34	0.60
24:36:37:GLN:NE2	30:R1:1125:G:H5'	2.16	0.60
26:5:56:LEU:HD22	26:5:86:CYS:SG	2.42	0.60
30:R1:1466:U:HO2'	30:R1:1546:G:HO2'	1.45	0.60
30:R1:2688:G:N1	30:R1:2720:U:OP2	2.24	0.60
32:R3:71:A:N6	32:R3:99:C:O2'	2.35	0.60
8:2:97:ASP:OD1	8:2:97:ASP:N	2.34	0.60
12:23:62:VAL:O	12:23:64:LYS:NZ	2.35	0.60
32:R3:115:G:O2'	32:R3:289:G:H5'	2.01	0.60
33:sb:45:THR:HG22	33:sb:200:PRO:HG2	1.83	0.60
38:sg:73:GLU:OE1	38:sg:73:GLU:N	2.34	0.60
30:R1:2839:G:H2'	30:R1:2840:C:H6	1.66	0.60
32:R3:1129:C:H5	32:R3:1143:G:H1	1.48	0.60
42:sk:107:THR:OG1	42:sk:108:ASN:OD1	2.15	0.60
52:su:33:ARG:HG2	52:su:34:ARG:H	1.67	0.60
26:5:59:ILE:O	26:5:101:ARG:NH2	2.34	0.59
30:R1:1179:G:H5''	30:R1:1180:U:H6	1.66	0.59
30:R1:1597:A:H5''	30:R1:1598:A:H5'	1.85	0.59
30:R1:2751:G:OP1	30:R1:2751:G:N2	2.35	0.59
30:R1:2041:U:H2'	30:R1:2042:A:H8	1.67	0.59
30:R1:2246:G:H2'	30:R1:2247:A:C8	2.37	0.59
39:sh:1:SER:OG	39:sh:2:MET:N	2.32	0.59
50:ss:49:ALA:HB1	50:ss:56:HIS:HB3	1.82	0.59
32:R3:1266:G:N2	32:R3:1269:A:OP2	2.20	0.59
1:13:16:TYR:HD2	1:13:140:LEU:HB2	1.65	0.59
26:5:79:ARG:NH1	53:T:56:C:N3	2.50	0.59
30:R1:1386:C:H2'	30:R1:1387:A:H8	1.66	0.59
30:R1:2595:G:N2	30:R1:2598:A:OP2	2.24	0.59
13:24:71:ILE:HD11	13:24:82:VAL:HG22	1.84	0.59
30:R1:1216:G:N2	30:R1:1233:C:O2	2.19	0.59
31:R2:32:U:N3	31:R2:33:G:N7	2.50	0.59
32:R3:359:G:O2'	32:R3:360:G:O5'	2.20	0.59
32:R3:494:G:H2'	32:R3:496:A:H8	1.67	0.59
41:sj:5:ARG:N	41:sj:77:VAL:HA	2.17	0.59
17:29:52:ARG:NH1	30:R1:77:G:OP1	2.35	0.59
25:4:32:VAL:HG23	25:4:178:VAL:HG12	1.83	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:126:G:OP1	32:R3:605:U:O2'	2.16	0.59
32:R3:377:G:C2	32:R3:387:U:O2	2.55	0.59
32:R3:461:A:H5''	32:R3:463:U:C4	2.38	0.59
40:si:83:THR:O	40:si:94:ARG:NH1	2.35	0.59
30:R1:415:A:O2'	30:R1:1866:A:OP1	2.19	0.59
32:R3:6:G:H1	36:se:101:GLY:HA2	1.68	0.59
32:R3:75:G:N2	32:R3:77:A:OP1	2.36	0.59
54:33:32:LYS:NZ	54:33:49:LYS:HB3	2.18	0.59
7:19:78:PRO:HG2	18:3:19:GLY:HA2	1.85	0.59
20:31:34:LEU:HD11	26:5:109:ARG:HD2	1.84	0.59
26:5:162:ASP:OD1	26:5:162:ASP:N	2.33	0.59
27:6:171:LYS:NZ	30:R1:2530:A:N7	2.51	0.59
30:R1:154:U:O4	30:R1:155:A:N6	2.35	0.59
30:R1:1482:G:H2'	30:R1:1483:G:H8	1.65	0.59
33:sb:8:MET:N	33:sb:8:MET:SD	2.75	0.59
43:sl:72:ASN:ND2	43:sl:104:SER:OG	2.36	0.59
32:R3:333:U:OP1	51:st:2:ASN:N	2.36	0.59
32:R3:352:C:O2'	32:R3:354:G:OP1	2.19	0.59
32:R3:954:G:H2'	32:R3:955:U:C6	2.38	0.59
32:R3:999:C:C4	32:R3:1000:A:H1'	2.38	0.59
32:R3:1218:C:H2'	32:R3:1219:A:H8	1.67	0.59
34:sc:27:GLU:OE2	34:sc:27:GLU:N	2.36	0.59
30:R1:819:A:OP2	30:R1:1187:G:N2	2.29	0.59
30:R1:1636:U:O2'	30:R1:1760:C:O2	2.16	0.59
30:R1:1725:U:H2'	30:R1:1726:C:C6	2.38	0.59
32:R3:624:C:H4'	47:sp:10:GLY:HA2	1.83	0.59
35:sd:7:LYS:HB3	35:sd:20:LEU:HD21	1.85	0.59
8:2:154:ALA:HB2	8:2:161:VAL:HG23	1.85	0.58
12:23:18:GLU:CD	12:23:18:GLU:H	2.11	0.58
30:R1:971:G:O2'	30:R1:983:A:N3	2.35	0.58
32:R3:1005:A:N6	32:R3:1025:U:O2'	2.30	0.58
32:R3:1367:C:H5''	40:si:115:VAL:HG23	1.84	0.58
10:21:38:VAL:HG11	10:21:57:GLY:HA3	1.85	0.58
23:35:32:LEU:HD22	23:35:40:LYS:HD3	1.86	0.58
32:R3:838:G:O2'	32:R3:839:C:O5'	2.20	0.58
32:R3:1347:G:O6	40:si:11:ARG:NH2	2.36	0.58
37:sf:69:GLU:CD	37:sf:69:GLU:H	2.11	0.58
4:16:134:THR:OG1	4:16:135:VAL:N	2.37	0.58
8:2:156:SER:OG	8:2:157:ALA:N	2.35	0.58
8:2:257:ARG:NH1	30:R1:1799:G:OP1	2.35	0.58
26:5:76:PHE:HE2	30:R1:2310:C:H2'	1.69	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:370:G:O2'	30:R1:424:G:OP1	2.22	0.58
36:se:79:THR:HB	36:se:121:ASN:HD22	1.67	0.58
40:si:8:THR:H	40:si:84:ARG:HD2	1.67	0.58
8:2:117:SER:OG	8:2:118:GLY:N	2.33	0.58
30:R1:358:U:H2'	30:R1:359:G:C8	2.33	0.58
32:R3:82:G:C2	32:R3:84:U:H5'	2.38	0.58
32:R3:981:U:C1'	45:sn:60:ARG:HH22	2.16	0.58
33:sb:110:ILE:HD11	33:sb:151:LYS:HA	1.85	0.58
10:21:68:ARG:HD3	10:21:92:TRP:CE2	2.39	0.58
30:R1:989:G:OP1	30:R1:1157:G:O2'	2.21	0.58
30:R1:1386:C:H2'	30:R1:1387:A:C8	2.39	0.58
32:R3:1088:G:H4'	52:su:65:ARG:CZ	2.34	0.58
25:4:122:GLU:OE1	25:4:122:GLU:N	2.36	0.58
30:R1:134:G:H22	30:R1:144:A:H2	1.52	0.58
30:R1:1022:G:H22	30:R1:1142:A:H2	1.51	0.58
30:R1:1583:A:H4'	30:R1:1584:U:H5	1.68	0.58
32:R3:1027:C:N4	32:R3:1034:G:O6	2.20	0.58
37:sf:8:PHE:HE2	37:sf:62:MET:HE3	1.68	0.58
32:R3:1000:A:N6	32:R3:1002:G:N7	2.52	0.58
32:R3:1121:U:H2'	32:R3:1122:U:C6	2.38	0.58
33:sb:87:ASP:OD1	33:sb:87:ASP:N	2.35	0.58
42:sk:33:ILE:HG21	42:sk:73:VAL:HG11	1.84	0.58
17:29:24:GLU:N	17:29:24:GLU:OE2	2.37	0.58
30:R1:820:A:H4'	30:R1:836:G:H22	1.69	0.58
30:R1:2788:C:O2'	30:R1:2809:A:N3	2.34	0.58
41:sj:73:LEU:HD21	41:sj:75:ASP:HB2	1.86	0.58
32:R3:313:A:H2'	32:R3:314:C:C6	2.39	0.58
32:R3:1002:G:N2	32:R3:1039:G:N3	2.52	0.58
33:sb:17:HIS:O	33:sb:19:THR:N	2.37	0.58
30:R1:1594:U:H2'	30:R1:1595:C:C6	2.39	0.57
38:sg:112:ASP:OD1	38:sg:113:LYS:N	2.36	0.57
42:sk:25:SER:OG	42:sk:28:ASN:O	2.17	0.57
32:R3:1029:U:O2'	32:R3:1031:C:O2	2.20	0.57
40:si:18:VAL:HG12	40:si:64:ILE:HG12	1.86	0.57
41:sj:88:MET:N	41:sj:88:MET:SD	2.77	0.57
30:R1:2134:A:O5'	30:R1:2157:G:O2'	2.22	0.57
36:se:44:ARG:HB3	36:se:70:MET:HE3	1.86	0.57
36:se:161:GLU:OE2	36:se:161:GLU:N	2.27	0.57
37:sf:82:ASP:OD1	37:sf:82:ASP:N	2.38	0.57
11:22:16:LYS:NZ	30:R1:2011:U:OP2	2.33	0.57
18:3:164:GLN:NE2	30:R1:2822:G:OP1	2.36	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2718:G:O2'	30:R1:2847:U:OP1	2.22	0.57
32:R3:1391:U:H2'	32:R3:1392:G:C8	2.40	0.57
36:se:104:ILE:HD11	36:se:119:VAL:O	2.04	0.57
30:R1:2505:G:H2'	30:R1:2576:G:H1	1.70	0.57
32:R3:53:A:N6	32:R3:359:G:O6	2.37	0.57
32:R3:377:G:N1	32:R3:387:U:C2	2.73	0.57
33:sb:58:LYS:HE2	33:sb:62:ARG:HH22	1.70	0.57
33:sb:124:THR:O	33:sb:136:ARG:NH2	2.36	0.57
35:sd:113:ALA:O	35:sd:117:VAL:HG12	2.05	0.57
1:13:30:THR:HG21	30:R1:1012:U:O4	2.04	0.57
8:2:220:ARG:NH1	30:R1:1789:A:OP2	2.37	0.57
30:R1:2077:A:N3	30:R1:2434:A:O2'	2.35	0.57
30:R1:2626:C:H2'	30:R1:2627:G:C8	2.40	0.57
32:R3:1130:A:O2'	32:R3:1131:G:H8	1.87	0.57
34:sc:122:GLN:HG2	34:sc:127:VAL:HG11	1.87	0.57
44:sm:100:ARG:HH21	44:sm:103:THR:HG22	1.70	0.57
47:sp:6:LEU:HB3	47:sp:17:TYR:HB3	1.85	0.57
26:5:51:ASN:HB2	26:5:149:ARG:HH12	1.70	0.57
28:9:122:LEU:HB3	28:9:128:HIS:ND1	2.20	0.57
32:R3:1249:C:O2'	40:si:70:GLY:O	2.20	0.57
8:2:75:ALA:HB2	8:2:95:TYR:CD1	2.39	0.57
13:24:6:ARG:NH1	30:R1:84:A:O3'	2.37	0.57
32:R3:674:G:H2'	32:R3:675:A:C8	2.39	0.57
32:R3:1270:G:O2'	32:R3:1271:A:OP1	2.19	0.57
32:R3:1401:G:O6	32:R3:1504:G:N2	2.37	0.57
25:4:148:ILE:HB	25:4:169:VAL:HG22	1.86	0.57
27:6:12:ALA:O	27:6:14:VAL:N	2.36	0.57
30:R1:372:G:O2'	30:R1:400:G:O6	2.14	0.57
30:R1:1083:U:O2'	30:R1:1085:A:OP2	2.10	0.57
32:R3:981:U:H2'	32:R3:982:U:C5	2.40	0.57
33:sb:86:CYS:SG	33:sb:221:ARG:NH1	2.78	0.57
40:si:83:THR:HG21	40:si:102:PHE:HB3	1.86	0.57
42:sk:126:ARG:HB2	52:su:33:ARG:HH11	1.70	0.57
30:R1:247:G:OP2	30:R1:249:C:N4	2.37	0.57
30:R1:2747:G:O6	30:R1:2755:C:H5''	2.04	0.57
34:sc:5:HIS:CE1	34:sc:7:ASN:HB3	2.40	0.57
3:15:82:LEU:HD13	3:15:90:VAL:HG21	1.87	0.56
5:17:100:CYS:SG	5:17:101:GLY:N	2.77	0.56
8:2:200:MET:HE2	30:R1:1820:U:N3	2.20	0.56
11:22:2:GLU:N	11:22:2:GLU:OE2	2.38	0.56
2:14:112:PHE:HB3	2:14:115:ILE:CG2	2.34	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:152:A:H61	30:R1:173:A:H61	1.53	0.56
30:R1:357:C:H2'	30:R1:358:U:C6	2.40	0.56
30:R1:1529:G:H2'	30:R1:1530:G:H8	1.68	0.56
32:R3:550:G:H2'	32:R3:551:U:H6	1.70	0.56
32:R3:1317:C:H42	45:sn:52:ARG:HH21	1.51	0.56
3:15:23:ILE:H	3:15:23:ILE:HD12	1.71	0.56
27:6:11:PRO:HG3	27:6:75:VAL:HG13	1.86	0.56
30:R1:871:U:H2'	30:R1:872:U:C6	2.40	0.56
30:R1:1590:A:H2'	30:R1:1591:A:C8	2.40	0.56
30:R1:1682:G:H2'	30:R1:1683:U:C6	2.40	0.56
30:R1:2154:A:H2'	30:R1:2155:U:H6	1.70	0.56
32:R3:1513:A:H2'	32:R3:1514:G:H8	1.69	0.56
34:sc:130:ARG:HB3	34:sc:134:LYS:NZ	2.21	0.56
40:si:35:GLU:HA	40:si:39:GLY:HA3	1.86	0.56
30:R1:2663:G:H2'	30:R1:2664:G:O4'	2.05	0.56
30:R1:2812:G:H2'	30:R1:2813:A:C8	2.41	0.56
38:sg:27:ASN:HA	38:sg:30:MET:HE2	1.88	0.56
40:si:78:ILE:H	40:si:78:ILE:HD12	1.70	0.56
44:sm:3:ILE:HG12	44:sm:7:ASN:HB2	1.88	0.56
44:sm:84:CYS:SG	44:sm:85:TYR:N	2.78	0.56
14:25:11:GLU:HG2	14:25:16:ALA:HB2	1.87	0.56
26:5:12:VAL:O	26:5:16:MET:HG2	2.05	0.56
30:R1:2626:C:H2'	30:R1:2627:G:H8	1.69	0.56
32:R3:847:G:H2'	32:R3:848:C:C6	2.41	0.56
32:R3:875:U:O2'	39:sh:14:ARG:NH1	2.39	0.56
32:R3:974:A:OP1	45:sn:68:ARG:NH2	2.37	0.56
32:R3:1150:A:O2'	32:R3:1151:A:O4'	2.24	0.56
34:sc:151:GLU:HG3	34:sc:166:TRP:HB3	1.87	0.56
26:5:111:ARG:NH2	44:sm:4:ALA:O	2.39	0.56
30:R1:136:G:H1	30:R1:142:A:H2	1.45	0.56
31:R2:25:U:O2	31:R2:117:G:O2'	2.22	0.56
32:R3:73:C:H2'	32:R3:74:A:C8	2.41	0.56
32:R3:714:G:H2'	32:R3:715:A:C8	2.41	0.56
39:sh:21:LYS:O	39:sh:64:TYR:OH	2.21	0.56
21:32:12:ARG:HD2	21:32:16:ARG:HH22	1.69	0.56
30:R1:877:A:H1'	30:R1:900:A:N6	2.20	0.56
30:R1:2545:G:N2	30:R1:2565:A:H8	1.95	0.56
31:R2:7:G:H1	31:R2:113:C:H5	1.53	0.56
52:su:33:ARG:HG2	52:su:34:ARG:N	2.20	0.56
53:T:6:G:OP1	53:T:15:C:N4	2.38	0.56
1:13:129:GLU:N	1:13:129:GLU:OE2	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:18:29:HIS:CE1	31:R2:7:G:H5'	2.41	0.56
26:5:29:ARG:HE	26:5:158:THR:HG21	1.71	0.56
30:R1:878:A:H3'	30:R1:879:G:H8	1.70	0.56
30:R1:1437:C:HO2'	30:R1:1516:G:HO2'	1.48	0.56
16:28:2:ARG:NH1	30:R1:1365:A:OP1	2.39	0.56
30:R1:2105:U:O2'	30:R1:2106:U:OP1	2.23	0.56
32:R3:597:G:N1	32:R3:643:C:N3	2.46	0.56
32:R3:686:U:O4	32:R3:703:G:O2'	2.20	0.56
35:sd:57:LYS:NZ	35:sd:68:GLU:OE1	2.34	0.56
4:16:4:PRO:HG3	4:16:68:PHE:HE2	1.71	0.56
7:19:30:TRP:CE3	7:19:37:LYS:HG2	2.40	0.56
30:R1:1013:C:H2'	30:R1:1014:A:H8	1.71	0.56
32:R3:1270:G:H2'	32:R3:1271:A:C8	2.41	0.56
32:R3:672:U:H2'	32:R3:673:A:C8	2.41	0.55
32:R3:1030:U:O4	32:R3:1033:G:N2	2.39	0.55
35:sd:162:GLU:OE1	35:sd:162:GLU:N	2.39	0.55
18:3:45:TYR:OH	30:R1:2636:C:O2'	2.20	0.55
32:R3:114:U:H1'	32:R3:353:A:H1'	1.88	0.55
32:R3:501:C:H2'	32:R3:502:A:H8	1.72	0.55
33:sb:130:LYS:HA	33:sb:133:ALA:HB3	1.87	0.55
44:sm:64:VAL:CG2	44:sm:65:GLU:H	2.19	0.55
26:5:111:ARG:CZ	44:sm:5:GLY:HA2	2.37	0.55
32:R3:257:G:H2'	32:R3:258:G:H8	1.71	0.55
32:R3:619:U:H5	35:sd:130:ASN:HB3	1.72	0.55
32:R3:867:G:O2'	32:R3:873:A:N1	2.32	0.55
32:R3:1287:A:H2'	32:R3:1288:A:C8	2.41	0.55
36:se:12:GLU:OE1	36:se:63:MET:HE2	2.07	0.55
37:sf:53:LYS:HA	37:sf:53:LYS:HE2	1.88	0.55
42:sk:92:ARG:HH12	52:su:19:LYS:HD2	1.71	0.55
1:13:41:LYS:NZ	1:13:50:THR:O	2.25	0.55
7:19:47:ILE:HG22	7:19:59:THR:OG1	2.07	0.55
30:R1:1063:G:N2	30:R1:1076:C:OP1	2.35	0.55
30:R1:1746:A:H2'	30:R1:1747:U:C6	2.41	0.55
32:R3:1305:G:H4'	32:R3:1306:A:O5'	2.05	0.55
35:sd:146:GLU:OE1	35:sd:146:GLU:N	2.37	0.55
40:si:29:ILE:HD13	40:si:64:ILE:HB	1.89	0.55
41:sj:65:TYR:OH	45:sn:84:ARG:HG3	2.06	0.55
23:35:4:LYS:NZ	30:R1:253:C:OP2	2.39	0.55
23:35:32:LEU:HD23	23:35:35:LYS:HD2	1.89	0.55
32:R3:57:G:N1	32:R3:356:A:C2	2.75	0.55
45:sn:22:LYS:HG3	45:sn:23:ARG:HD3	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:720:U:H2'	30:R1:721:A:H8	1.72	0.55
32:R3:1513:A:H2'	32:R3:1514:G:C8	2.41	0.55
38:sg:55:LYS:HB3	38:sg:59:GLU:HG2	1.89	0.55
1:13:109:LEU:HD23	1:13:110:PRO:HD2	1.89	0.55
6:18:25:ARG:NH2	31:R2:8:C:O3'	2.39	0.55
18:3:148:GLN:HB2	18:3:152:PRO:HG2	1.88	0.55
30:R1:191:A:H2'	30:R1:192:C:H6	1.70	0.55
30:R1:282:A:H2'	30:R1:283:G:C8	2.42	0.55
30:R1:2327:A:H2'	30:R1:2328:A:C8	2.42	0.55
30:R1:2812:G:H2'	30:R1:2813:A:H8	1.71	0.55
32:R3:9:G:OP2	36:se:125:LYS:NZ	2.34	0.55
45:sn:72:PHE:CZ	45:sn:77:GLY:HA2	2.42	0.55
25:4:119:ILE:O	25:4:187:VAL:HA	2.06	0.55
30:R1:1504:A:H2'	30:R1:1505:A:C8	2.42	0.55
32:R3:1323:G:H2'	32:R3:1324:A:C8	2.41	0.55
46:so:86:LEU:HD12	46:so:87:ARG:HG2	1.88	0.55
50:ss:21:ALA:HA	50:ss:27:LYS:HZ1	1.72	0.55
54:33:28:THR:HG23	54:33:29:LYS:HG2	1.87	0.55
3:15:29:LYS:O	3:15:30:THR:OG1	2.18	0.55
5:17:106:ASP:OD1	30:R1:1649:G:O2'	2.23	0.55
18:3:149:ASN:OD1	18:3:150:GLN:N	2.38	0.55
23:35:15:LYS:HZ2	23:35:19:GLY:HA2	1.71	0.55
27:6:2:ARG:NH1	30:R1:2751:G:OP2	2.39	0.55
31:R2:13:G:H8	31:R2:69:G:H21	1.53	0.55
32:R3:1034:G:H2'	32:R3:1035:A:H8	1.71	0.55
53:T:6:G:O6	53:T:66:C:N4	2.33	0.55
12:23:8:LEU:O	17:29:29:ARG:NH2	2.40	0.54
20:31:58:ASP:N	20:31:58:ASP:OD1	2.37	0.54
27:6:154:GLU:HG3	27:6:156:TYR:H	1.73	0.54
30:R1:528:A:H2	30:R1:2043:C:H4'	1.72	0.54
31:R2:31:C:H1'	31:R2:53:A:H61	1.72	0.54
31:R2:117:G:OP2	31:R2:117:G:N2	2.37	0.54
32:R3:745:G:H2'	32:R3:746:A:C8	2.42	0.54
32:R3:1151:A:N6	32:R3:1152:A:H62	2.01	0.54
42:sk:35:ASP:OD1	42:sk:39:ASN:HB2	2.07	0.54
8:2:144:GLU:HA	8:2:151:GLY:HA2	1.88	0.54
20:31:11:GLU:HA	20:31:25:ARG:HA	1.90	0.54
30:R1:1900:A:H1'	30:R1:1970:A:H2'	1.89	0.54
30:R1:2164:C:H2'	30:R1:2165:C:H4'	1.88	0.54
31:R2:39:A:H2'	31:R2:40:U:C6	2.43	0.54
32:R3:1144:G:H21	32:R3:1146:A:H62	1.55	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:22:59:GLU:HA	11:22:64:ALA:HA	1.89	0.54
30:R1:720:U:H2'	30:R1:721:A:C8	2.43	0.54
32:R3:1009:U:H2'	32:R3:1010:U:C6	2.42	0.54
34:sc:111:ASP:HB3	34:sc:114:LEU:HB2	1.89	0.54
35:sd:55:ARG:NH2	35:sd:62:ARG:HH22	2.05	0.54
42:sk:79:LYS:HE2	42:sk:79:LYS:HA	1.88	0.54
47:sp:67:ILE:HD12	47:sp:67:ILE:H	1.73	0.54
30:R1:64:A:H2'	30:R1:65:U:C6	2.43	0.54
30:R1:1873:G:H2'	30:R1:1874:C:C6	2.42	0.54
18:3:169:ARG:HD3	30:R1:2773:C:H5'	1.89	0.54
30:R1:151:C:H2'	30:R1:152:A:C8	2.43	0.54
30:R1:285:G:H1	30:R1:355:U:H2'	1.72	0.54
30:R1:1585:C:H3'	30:R1:1586:A:H8	1.72	0.54
32:R3:127:G:O3'	48:sq:5:ARG:NH2	2.40	0.54
8:2:144:GLU:HB2	8:2:187:CYS:HB3	1.89	0.54
27:6:126:THR:HG22	27:6:127:GLN:H	1.73	0.54
30:R1:851:C:H2'	30:R1:852:U:C6	2.43	0.54
32:R3:392:C:OP2	47:sp:8:ARG:NH2	2.40	0.54
32:R3:716:A:O2'	42:sk:118:ASN:OD1	2.23	0.54
33:sb:17:HIS:C	33:sb:19:THR:H	2.16	0.54
35:sd:2:ARG:HD2	35:sd:114:ARG:HH21	1.71	0.54
47:sp:68:SER:OG	47:sp:69:ASP:N	2.40	0.54
52:su:5:VAL:HG21	52:su:16:ARG:HG2	1.88	0.54
2:14:114:LYS:O	2:14:114:LYS:HD3	2.07	0.54
32:R3:200:G:H2'	32:R3:201:G:C8	2.42	0.54
32:R3:1250:A:H2'	32:R3:1251:A:C8	2.43	0.54
32:R3:1323:G:H2'	32:R3:1324:A:H8	1.72	0.54
44:sm:64:VAL:HG22	44:sm:65:GLU:N	2.22	0.54
47:sp:79:ASN:OD1	47:sp:79:ASN:N	2.41	0.54
28:9:93:SER:OG	28:9:123:ARG:NH2	2.39	0.54
30:R1:72:U:O2'	30:R1:75:G:N2	2.41	0.54
30:R1:136:G:N1	30:R1:142:A:C2	2.67	0.54
30:R1:881:G:H2'	30:R1:882:G:C8	2.43	0.54
30:R1:1174:U:O2'	30:R1:1176:U:OP2	2.18	0.54
32:R3:332:G:O2'	32:R3:333:U:H5'	2.07	0.54
38:sg:104:VAL:HG12	38:sg:108:ARG:HE	1.73	0.54
17:29:7:ARG:NH1	17:29:7:ARG:HB2	2.23	0.54
18:3:2:ILE:HG13	18:3:3:GLY:H	1.73	0.54
30:R1:414:C:OP1	30:R1:1879:C:O2'	2.21	0.54
31:R2:51:G:H2'	31:R2:52:A:O4'	2.07	0.54
32:R3:75:G:H3'	32:R3:76:G:C8	2.43	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:1315:U:O2'	32:R3:1360:A:N3	2.37	0.54
34:sc:53:ARG:HB3	34:sc:68:HIS:HD2	1.73	0.54
35:sd:146:GLU:HA	35:sd:149:LYS:HB2	1.89	0.54
41:sj:14:ASP:N	41:sj:14:ASP:OD1	2.41	0.54
45:sn:20:PHE:CE1	45:sn:54:SER:HA	2.42	0.54
6:18:46:GLU:OE1	6:18:46:GLU:N	2.41	0.54
22:34:24:THR:HG23	22:34:27:GLY:H	1.72	0.54
26:5:118:ALA:O	26:5:166:ARG:NH2	2.36	0.54
35:sd:94:GLU:HA	35:sd:99:ASN:ND2	2.23	0.54
7:19:6:GLN:OE1	18:3:184:ARG:NH1	2.41	0.53
19:30:11:SER:HB2	30:R1:988:A:H5''	1.90	0.53
30:R1:285:G:O6	30:R1:355:U:O2	2.26	0.53
30:R1:1853:A:H2'	30:R1:1854:A:C8	2.43	0.53
32:R3:500:G:O2'	32:R3:501:C:OP1	2.24	0.53
37:sf:90:MET:HE1	49:sr:22:TYR:CZ	2.43	0.53
2:14:1:MET:HE2	2:14:1:MET:N	2.23	0.53
8:2:49:THR:OG1	30:R1:1813:G:N3	2.39	0.53
13:24:84:PHE:HE1	13:24:93:ARG:HG2	1.72	0.53
20:31:56:ARG:NH1	50:ss:64:GLU:O	2.36	0.53
21:32:14:MET:O	21:32:17:SER:OG	2.20	0.53
32:R3:401:C:O2'	32:R3:621:A:N3	2.37	0.53
37:sf:42:TRP:HB2	37:sf:59:TYR:HB2	1.90	0.53
50:ss:6:LYS:HD3	50:ss:6:LYS:H	1.73	0.53
30:R1:1589:U:H2'	30:R1:1590:A:H8	1.72	0.53
32:R3:1033:G:H2'	32:R3:1034:G:C8	2.43	0.53
7:19:105:LYS:HB2	32:R3:1432:G:H5'	1.91	0.53
12:23:5:GLU:N	12:23:5:GLU:OE2	2.42	0.53
17:29:23:ARG:HB3	17:29:24:GLU:OE2	2.09	0.53
26:5:5:ASP:OD1	26:5:5:ASP:N	2.40	0.53
32:R3:925:G:C2	32:R3:927:G:C8	2.96	0.53
33:sb:9:LEU:HD23	33:sb:9:LEU:O	2.08	0.53
33:sb:40:ILE:HD11	33:sb:200:PRO:HB2	1.89	0.53
44:sm:9:PRO:HB2	44:sm:12:LYS:HE2	1.90	0.53
2:14:4:GLU:OE1	2:14:4:GLU:N	2.42	0.53
12:23:52:GLU:N	12:23:52:GLU:OE2	2.42	0.53
15:27:43:THR:HG21	30:R1:2336:A:H61	1.73	0.53
26:5:20:ASN:ND2	26:5:20:ASN:O	2.41	0.53
30:R1:1808:A:H3'	30:R1:1809:A:C8	2.43	0.53
33:sb:206:ILE:HD12	33:sb:206:ILE:H	1.73	0.53
43:sl:106:VAL:HG12	43:sl:116:TYR:HB3	1.90	0.53
1:13:17:VAL:HG23	1:13:137:PRO:HB2	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:17:2:ARG:HA	5:17:5:LYS:HD2	1.90	0.53
3:15:55:MET:HE3	30:R1:2429:G:N7	2.24	0.53
5:17:24:MET:HE3	5:17:44:LEU:HD22	1.91	0.53
10:21:24:LYS:HA	10:21:94:THR:HG23	1.90	0.53
23:35:11:LYS:NZ	30:R1:247:G:O6	2.41	0.53
30:R1:361:G:O2'	30:R1:362:A:O4'	2.26	0.53
30:R1:1441:G:H2'	30:R1:1442:U:C6	2.44	0.53
30:R1:1482:G:H2'	30:R1:1483:G:C8	2.44	0.53
32:R3:191:G:H2'	32:R3:192:A:H8	1.72	0.53
32:R3:292:G:H21	32:R3:608:A:N6	2.03	0.53
35:sd:164:ARG:HG3	35:sd:166:LYS:H	1.73	0.53
50:ss:62:THR:H	50:ss:65:MET:HE3	1.73	0.53
54:33:31:GLU:OE1	54:33:31:GLU:N	2.42	0.53
24:36:19:ARG:HD2	24:36:24:ARG:HD2	1.90	0.53
28:9:58:LEU:HA	28:9:61:VAL:HG22	1.91	0.53
30:R1:463:G:N2	30:R1:466:A:OP2	2.40	0.53
30:R1:1107:G:H2'	30:R1:1108:U:C6	2.44	0.53
32:R3:746:A:H2'	32:R3:747:A:C8	2.44	0.53
5:17:58:ASP:OD1	5:17:63:ARG:NE	2.32	0.53
8:2:200:MET:HE2	30:R1:1820:U:C2	2.44	0.53
26:5:69:ALA:HB2	26:5:84:ILE:HD11	1.90	0.53
32:R3:289:G:O2'	32:R3:290:C:O5'	2.26	0.53
32:R3:1270:G:H2'	32:R3:1271:A:H8	1.73	0.53
52:su:35:GLU:OE1	52:su:35:GLU:N	2.24	0.53
10:21:49:ILE:HB	10:21:52:PRO:HA	1.91	0.53
26:5:137:PHE:HB3	26:5:139:GLU:OE1	2.09	0.53
30:R1:274:C:H41	30:R1:363:G:N2	2.07	0.53
30:R1:1176:U:O2'	30:R1:1177:G:N7	2.39	0.53
30:R1:1183:U:H2'	30:R1:1184:U:C6	2.43	0.53
30:R1:1218:G:C2	30:R1:1232:G:C5	2.97	0.53
27:6:23:ILE:HG21	27:6:71:LEU:HD11	1.91	0.52
30:R1:1357:C:H2'	30:R1:1358:G:O4'	2.09	0.52
32:R3:470:C:H1'	32:R3:471:U:C6	2.44	0.52
32:R3:738:C:HO2'	32:R3:739:C:H6	1.56	0.52
34:sc:156:LEU:HD12	34:sc:163:ARG:HG3	1.91	0.52
30:R1:242:G:O2'	30:R1:254:G:O6	2.27	0.52
30:R1:849:A:H2'	30:R1:850:U:H6	1.74	0.52
30:R1:1009:A:N3	30:R1:1153:C:O2'	2.40	0.52
30:R1:1770:G:C6	30:R1:1983:G:C6	2.97	0.52
32:R3:1068:G:N2	32:R3:1191:A:N3	2.50	0.52
32:R3:1250:A:H4'	40:si:68:GLY:HA2	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:sf:18:VAL:HA	37:sf:21:MET:HG3	1.91	0.52
40:si:78:ILE:O	40:si:82:ILE:HG22	2.09	0.52
18:3:136:ASN:OD1	30:R1:2579:C:O2'	2.28	0.52
26:5:87:LYS:NZ	30:R1:2314:A:OP1	2.38	0.52
30:R1:161:A:H1'	30:R1:162:U:H5''	1.89	0.52
30:R1:1099:G:H2'	30:R1:1100:C:C6	2.45	0.52
32:R3:707:U:H2'	32:R3:708:C:C6	2.44	0.52
40:si:90:ASP:O	40:si:92:SER:N	2.41	0.52
48:sq:14:ASP:HB3	48:sq:54:ILE:HG12	1.90	0.52
21:32:28:SER:OG	21:32:37:HIS:NE2	2.42	0.52
30:R1:695:G:H5''	30:R1:1380:G:H4'	1.90	0.52
30:R1:2134:A:C8	30:R1:2157:G:H4'	2.44	0.52
30:R1:2291:U:H2'	30:R1:2292:U:C6	2.45	0.52
30:R1:2774:C:HO2'	30:R1:2775:G:H8	1.53	0.52
31:R2:31:C:H2'	31:R2:32:U:H6	1.74	0.52
32:R3:161:A:H2'	32:R3:162:A:C8	2.45	0.52
34:sc:119:ILE:HD11	34:sc:197:VAL:HG11	1.91	0.52
6:18:33:ARG:HG2	6:18:34:HIS:CD2	2.45	0.52
30:R1:578:G:OP1	30:R1:1255:U:O2'	2.28	0.52
30:R1:1082:U:H3	30:R1:1086:A:N6	2.08	0.52
32:R3:160:A:H2'	32:R3:161:A:C8	2.44	0.52
32:R3:178:C:OP2	51:st:59:ARG:NH2	2.42	0.52
46:so:24:THR:HG21	46:so:69:LEU:HG	1.90	0.52
2:14:71:ARG:HG3	2:14:72:PRO:HD2	1.91	0.52
14:25:48:MET:O	14:25:48:MET:HE3	2.10	0.52
23:35:40:LYS:NZ	30:R1:2419:U:OP1	2.43	0.52
30:R1:378:C:N4	30:R1:379:G:O6	2.42	0.52
30:R1:2230:G:H2'	30:R1:2231:U:C6	2.45	0.52
30:R1:2461:A:H2'	30:R1:2462:C:C6	2.45	0.52
32:R3:91:U:H3'	32:R3:92:U:H5''	1.91	0.52
32:R3:363:A:N6	43:sl:26:CYS:SG	2.83	0.52
32:R3:705:G:C5	32:R3:706:A:C8	2.98	0.52
49:sr:40:PRO:HG2	49:sr:43:ILE:HG12	1.92	0.52
1:13:9:GLU:OE2	1:13:9:GLU:N	2.41	0.52
8:2:251:THR:OG1	8:2:252:LYS:N	2.43	0.52
27:6:59:ASP:OD1	27:6:59:ASP:N	2.39	0.52
30:R1:863:A:H2'	30:R1:864:G:H8	1.74	0.52
30:R1:1589:U:H2'	30:R1:1590:A:C8	2.45	0.52
32:R3:191:G:H2'	32:R3:192:A:C8	2.45	0.52
32:R3:1343:G:H2'	32:R3:1344:C:C6	2.44	0.52
33:sb:204:ASP:OD1	33:sb:204:ASP:N	2.36	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:108:MET:HE2	30:R1:1138:G:H21	1.75	0.52
7:19:105:LYS:O	7:19:108:ARG:NH1	2.34	0.52
30:R1:1679:A:H2'	30:R1:1680:U:C6	2.45	0.52
30:R1:2229:U:H2'	30:R1:2230:G:H8	1.74	0.52
30:R1:2287:A:N7	30:R1:2289:G:C8	2.78	0.52
37:sf:18:VAL:HG13	37:sf:19:PRO:HD3	1.91	0.52
44:sm:92:ARG:HD3	44:sm:94:LEU:HD12	1.90	0.52
46:so:32:THR:O	46:so:36:ASN:ND2	2.43	0.52
30:R1:100:U:H4'	30:R1:101:A:O4'	2.10	0.52
30:R1:2144:G:N3	30:R1:2146:C:H1'	2.25	0.52
30:R1:2189:U:O2'	30:R1:2190:G:OP1	2.25	0.52
30:R1:2591:C:H2'	30:R1:2592:G:H8	1.75	0.52
32:R3:20:U:H2'	32:R3:21:G:O4'	2.09	0.52
32:R3:1026:G:N1	32:R3:1036:A:C6	2.77	0.52
32:R3:1144:G:N2	32:R3:1146:A:H62	2.08	0.52
35:sd:8:LEU:HB2	35:sd:21:LYS:HZ1	1.75	0.52
42:sk:88:PRO:HA	42:sk:92:ARG:HD2	1.92	0.52
52:su:24:LYS:HG2	52:su:25:ALA:N	2.25	0.52
25:4:119:ILE:HB	25:4:187:VAL:HG12	1.91	0.52
32:R3:235:C:H2'	32:R3:236:A:H8	1.75	0.52
44:sm:51:GLN:O	44:sm:54:THR:OG1	2.23	0.52
52:su:45:LYS:HA	52:su:45:LYS:HE2	1.90	0.52
8:2:44:ASN:ND2	30:R1:1371:G:OP1	2.44	0.51
30:R1:1853:A:N7	30:R1:1889:A:N6	2.58	0.51
30:R1:2849:U:H4'	30:R1:2868:A:C2	2.46	0.51
32:R3:966:G:N2	53:T:34:C:H5'	2.24	0.51
33:sb:16:GLY:O	33:sb:17:HIS:HB2	2.10	0.51
42:sk:29:THR:HG21	42:sk:62:ALA:HB2	1.93	0.51
11:22:29:VAL:HG21	11:22:55:ILE:HD11	1.92	0.51
27:6:106:LEU:O	27:6:106:LEU:HD23	2.10	0.51
30:R1:1103:A:H5''	30:R1:1104:C:C5	2.44	0.51
30:R1:1176:U:O2'	30:R1:1178:C:N4	2.43	0.51
30:R1:1862:G:O6	30:R1:1881:C:N4	2.43	0.51
30:R1:2839:G:H2'	30:R1:2840:C:C6	2.46	0.51
32:R3:35:G:H2'	32:R3:36:C:C6	2.45	0.51
32:R3:946:A:H2'	32:R3:947:G:C8	2.45	0.51
32:R3:1186:G:O3'	40:si:114:LYS:NZ	2.43	0.51
26:5:147:ARG:HB3	26:5:149:ARG:HG3	1.92	0.51
28:9:90:LEU:HG	28:9:125:THR:HG22	1.93	0.51
30:R1:136:G:H22	30:R1:142:A:H2	1.57	0.51
30:R1:976:G:O2'	30:R1:1155:A:O2'	2.17	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:R2:4:C:H2'	31:R2:5:U:H6	1.76	0.51
32:R3:416:G:O6	32:R3:417:G:O6	2.28	0.51
44:sm:106:ARG:NH1	44:sm:110:GLY:O	2.44	0.51
49:sr:31:TYR:CG	49:sr:54:LEU:HD11	2.46	0.51
17:29:17:GLU:HB2	17:29:53:VAL:HG11	1.93	0.51
26:5:16:MET:HE3	26:5:16:MET:HA	1.91	0.51
30:R1:270:A:N1	30:R1:369:U:O2'	2.43	0.51
30:R1:1424:G:C6	30:R1:1425:G:C2	2.98	0.51
37:sf:26:THR:HG22	37:sf:36:ILE:HD13	1.91	0.51
7:19:83:ILE:O	7:19:83:ILE:HG22	2.11	0.51
30:R1:419:U:H2'	30:R1:420:C:H6	1.76	0.51
30:R1:877:A:H1'	30:R1:900:A:H62	1.75	0.51
32:R3:335:C:O2'	32:R3:1433:A:N3	2.37	0.51
32:R3:382:A:H2'	32:R3:383:A:C8	2.46	0.51
32:R3:603:U:H2'	32:R3:604:G:H8	1.75	0.51
32:R3:768:A:N3	32:R3:1512:U:O2'	2.44	0.51
32:R3:1226:C:N4	44:sm:102:LYS:HG3	2.26	0.51
36:se:23:THR:HG23	36:se:23:THR:O	2.10	0.51
3:15:82:LEU:HD12	3:15:120:VAL:HG11	1.91	0.51
18:3:103:ASP:OD1	18:3:103:ASP:N	2.43	0.51
30:R1:286:U:H3	30:R1:354:A:N6	2.08	0.51
30:R1:974:G:H1'	30:R1:975:A:C8	2.46	0.51
30:R1:1057:A:OP2	30:R1:1089:A:N6	2.43	0.51
30:R1:1361:G:H2'	30:R1:1362:C:C6	2.45	0.51
30:R1:2247:A:H2'	30:R1:2248:C:H6	1.75	0.51
32:R3:723:U:H5	52:su:52:VAL:HG21	1.76	0.51
37:sf:3:HIS:HB2	37:sf:92:THR:HA	1.93	0.51
38:sg:66:GLU:HA	38:sg:69:ARG:HD3	1.91	0.51
26:5:33:ILE:HG23	26:5:90:LEU:HB2	1.92	0.51
30:R1:598:U:H2'	30:R1:599:A:H8	1.75	0.51
30:R1:936:A:H2'	30:R1:937:C:C6	2.46	0.51
32:R3:57:G:O6	32:R3:356:A:C6	2.64	0.51
32:R3:108:G:H5'	32:R3:109:A:H5''	1.92	0.51
32:R3:553:A:H2'	32:R3:554:A:H8	1.74	0.51
21:32:15:ARG:NH1	30:R1:1266:G:OP2	2.44	0.51
30:R1:191:A:H2'	30:R1:192:C:C6	2.46	0.51
30:R1:1047:G:H21	30:R1:1110:G:H21	1.58	0.51
30:R1:2098:U:O2'	30:R1:2099:U:O5'	2.28	0.51
32:R3:505:G:H2'	32:R3:506:G:H8	1.76	0.51
32:R3:1124:G:O2'	32:R3:1127:G:O6	2.29	0.51
35:sd:44:LYS:HD3	35:sd:45:PRO:HD2	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:21:10:LYS:NZ	10:21:23:GLU:OE2	2.32	0.51
27:6:163:TYR:HB2	27:6:166:GLU:HB3	1.92	0.51
30:R1:511:U:H2'	30:R1:512:G:H5'	1.93	0.51
30:R1:1299:G:N1	30:R1:1640:A:OP2	2.32	0.51
30:R1:2141:G:H2'	30:R1:2142:A:O4'	2.11	0.51
30:R1:2660:A:H8	30:R1:2660:A:OP1	1.94	0.51
32:R3:82:G:N1	32:R3:87:C:O2'	2.34	0.51
32:R3:744:C:H2'	32:R3:745:G:C8	2.46	0.51
14:25:34:LYS:HB2	14:25:35:GLU:OE1	2.11	0.51
20:31:11:GLU:O	20:31:23:LYS:NZ	2.44	0.51
30:R1:48:G:N2	30:R1:177:G:OP2	2.38	0.51
30:R1:100:U:H5''	30:R1:101:A:OP1	2.10	0.51
30:R1:643:A:C4	54:33:43:ARG:NH2	2.77	0.51
30:R1:955:U:H5	30:R1:962:G:H1	1.58	0.51
30:R1:2061:G:N2	30:R1:2062:A:N7	2.58	0.51
30:R1:2127:G:H2'	30:R1:2128:G:C8	2.46	0.51
45:sn:46:LYS:O	45:sn:49:THR:HG22	2.11	0.51
2:14:17:ARG:HB3	2:14:45:GLU:HG2	1.92	0.50
6:18:31:THR:O	6:18:102:ARG:NH2	2.42	0.50
12:23:53:VAL:HG12	12:23:92:ASN:HB2	1.94	0.50
18:3:4:LEU:HD22	18:3:32:ASN:ND2	2.24	0.50
28:9:9:VAL:HB	28:9:12:LEU:O	2.10	0.50
30:R1:880:G:H2'	30:R1:881:G:C8	2.46	0.50
30:R1:1802:A:H2'	30:R1:1803:A:C8	2.46	0.50
32:R3:21:G:H2'	32:R3:22:G:C8	2.46	0.50
32:R3:321:A:H2'	32:R3:322:C:H5'	1.93	0.50
52:su:64:ALA:C	52:su:66:ARG:H	2.19	0.50
6:18:15:ARG:HG3	6:18:25:ARG:HH12	1.76	0.50
11:22:5:ALA:HB2	11:22:54:ALA:HB2	1.93	0.50
13:24:43:LYS:NZ	30:R1:481:G:O5'	2.44	0.50
14:25:4:ILE:HG21	14:25:42:LEU:HD12	1.93	0.50
30:R1:306:U:H3	30:R1:310:A:H62	1.58	0.50
30:R1:1056:G:O6	30:R1:1101:U:H3'	2.12	0.50
30:R1:1266:G:O2'	30:R1:2012:G:O6	2.29	0.50
30:R1:1383:A:H2	30:R1:1406:U:H1'	1.77	0.50
30:R1:1538:G:H2'	30:R1:1539:U:C6	2.46	0.50
30:R1:1746:A:H2'	30:R1:1747:U:H6	1.76	0.50
32:R3:588:G:O2'	32:R3:589:U:OP1	2.28	0.50
32:R3:683:G:N2	42:sk:38:GLY:O	2.44	0.50
32:R3:898:G:N2	32:R3:901:A:OP2	2.44	0.50
32:R3:981:U:O2'	45:sn:60:ARG:NH1	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:1269:A:N1	32:R3:1312:G:O2'	2.40	0.50
53:T:28:C:H2'	53:T:29:G:H8	1.76	0.50
54:33:27:ARG:HG2	54:33:27:ARG:HH11	1.75	0.50
4:16:71:LYS:HB3	4:16:93:VAL:O	2.11	0.50
25:4:21:ARG:HD2	25:4:106:LYS:HB3	1.93	0.50
26:5:79:ARG:HB2	26:5:82:TYR:CE1	2.43	0.50
30:R1:600:G:N2	30:R1:605:G:O3'	2.44	0.50
30:R1:878:A:H3'	30:R1:879:G:C8	2.46	0.50
30:R1:978:G:H3'	30:R1:979:A:H5''	1.92	0.50
30:R1:1534:U:H2'	30:R1:1536:C:H1'	1.92	0.50
32:R3:978:A:C4	32:R3:1319:A:C2	2.99	0.50
37:sf:75:GLU:OE2	37:sf:89:VAL:HG21	2.11	0.50
9:20:90:ASP:OD1	9:20:90:ASP:N	2.31	0.50
25:4:8:ALA:O	25:4:9:GLN:HG3	2.12	0.50
26:5:132:ARG:NH1	30:R1:2305:U:O2'	2.44	0.50
30:R1:886:A:N6	30:R1:889:C:OP2	2.44	0.50
30:R1:1047:G:H21	30:R1:1110:G:N2	2.09	0.50
30:R1:2186:G:H2'	30:R1:2187:U:C5	2.45	0.50
30:R1:2651:C:C4	30:R1:2652:C:C4	2.99	0.50
32:R3:1316:G:N2	32:R3:1318:A:H3'	2.27	0.50
33:sb:126:ASP:OD2	33:sb:127:LYS:NZ	2.44	0.50
35:sd:145:ARG:HG2	35:sd:147:LYS:HG2	1.94	0.50
38:sg:14:ASP:OD2	38:sg:16:LYS:N	2.37	0.50
8:2:86:ARG:NH2	30:R1:1817:G:OP1	2.44	0.50
12:23:48:GLN:HG3	12:23:55:VAL:HG12	1.92	0.50
27:6:104:LEU:HD23	27:6:106:LEU:HB2	1.94	0.50
30:R1:849:A:H2'	30:R1:850:U:C6	2.47	0.50
30:R1:1173:U:O2'	30:R1:1174:U:O3'	2.17	0.50
30:R1:2430:A:H2'	30:R1:2430:A:N3	2.27	0.50
35:sd:187:ARG:HH22	35:sd:192:ALA:HA	1.74	0.50
16:28:32:LEU:HD22	16:28:49:ARG:HG3	1.93	0.50
23:35:34:LYS:NZ	30:R1:2390:U:O5'	2.40	0.50
25:4:27:LEU:CD1	25:4:100:MET:HG2	2.42	0.50
30:R1:848:C:H2'	30:R1:849:A:C8	2.43	0.50
30:R1:1038:G:H2'	30:R1:1039:A:C8	2.47	0.50
30:R1:2004:G:C5	30:R1:2005:A:C8	3.00	0.50
32:R3:1179:A:H5''	40:si:98:ARG:HH22	1.76	0.50
41:sj:27:GLU:O	41:sj:31:ARG:HB3	2.12	0.50
28:9:9:VAL:HB	28:9:12:LEU:H	1.77	0.50
30:R1:319:G:H1	30:R1:323:C:H5	1.58	0.50
31:R2:40:U:H1'	31:R2:45:A:H61	1.77	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:263:A:OP1	51:st:73:ARG:NH2	2.44	0.50
32:R3:632:U:H5''	32:R3:633:G:C8	2.47	0.50
32:R3:753:A:H4'	32:R3:754:C:O5'	2.10	0.50
32:R3:932:C:H5'	38:sg:3:ARG:HH11	1.77	0.50
32:R3:1294:G:H2'	32:R3:1295:U:C6	2.47	0.50
32:R3:1447:A:H5''	32:R3:1448:C:C5	2.45	0.50
2:14:30:ARG:NH2	2:14:37:ASP:OD2	2.44	0.50
30:R1:404:A:O2'	30:R1:405:U:OP2	2.29	0.50
32:R3:461:A:O2'	32:R3:462:G:OP1	2.21	0.50
32:R3:1055:A:O2'	34:sc:160:GLU:O	2.28	0.50
34:sc:180:ASP:OD1	34:sc:203:LYS:HB2	2.12	0.50
52:su:53:LYS:HB3	52:su:57:LYS:HZ2	1.77	0.50
26:5:42:ALA:HB2	26:5:48:LEU:HD22	1.92	0.50
32:R3:672:U:H2'	32:R3:673:A:H8	1.75	0.50
42:sk:34:THR:OG1	42:sk:35:ASP:N	2.44	0.50
43:sl:23:LEU:HD22	43:sl:58:ASN:ND2	2.26	0.50
47:sp:69:ASP:OD1	47:sp:70:ARG:N	2.45	0.50
52:su:24:LYS:HG2	52:su:25:ALA:H	1.77	0.50
6:18:58:ILE:HD11	6:18:73:ALA:HB1	1.93	0.49
17:29:21:LEU:HA	17:29:25:GLN:HB3	1.93	0.49
18:3:99:GLU:OE1	18:3:99:GLU:HA	2.12	0.49
26:5:131:VAL:HG23	26:5:133:GLU:H	1.77	0.49
30:R1:1723:G:C5	30:R1:1724:G:C8	2.99	0.49
32:R3:878:A:H2'	32:R3:879:C:H6	1.76	0.49
32:R3:1412:C:H2'	32:R3:1413:A:C8	2.47	0.49
50:ss:10:ILE:HD13	50:ss:40:PHE:HE2	1.76	0.49
18:3:113:SER:OG	18:3:114:LYS:N	2.45	0.49
21:32:37:HIS:ND1	21:32:41:HIS:O	2.44	0.49
25:4:7:ASP:HB2	25:4:122:GLU:OE2	2.12	0.49
27:6:142:GLN:NE2	30:R1:2761:A:H1'	2.27	0.49
30:R1:1463:C:H2'	30:R1:1464:G:H8	1.76	0.49
30:R1:2549:G:C2	30:R1:2550:G:N7	2.80	0.49
30:R1:2745:C:H2'	30:R1:2746:U:C6	2.47	0.49
31:R2:61:G:H2'	31:R2:62:C:C6	2.47	0.49
32:R3:778:G:H2'	32:R3:779:C:C6	2.46	0.49
33:sb:110:ILE:HG13	33:sb:147:LEU:HD21	1.94	0.49
34:sc:50:SER:O	34:sc:69:THR:OG1	2.27	0.49
36:se:18:ASN:N	36:se:18:ASN:OD1	2.43	0.49
50:ss:79:TYR:CD1	50:ss:80:ARG:HG2	2.47	0.49
9:20:48:ASP:OD1	30:R1:534:U:O2'	2.27	0.49
27:6:88:LEU:HD23	27:6:93:TYR:HB3	1.94	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:6:94:ARG:HB3	27:6:105:SER:HB3	1.94	0.49
30:R1:305:C:H2'	30:R1:306:U:C6	2.47	0.49
30:R1:1494:A:H2'	30:R1:1495:A:C8	2.46	0.49
30:R1:2131:U:H4'	30:R1:2133:G:H1'	1.94	0.49
30:R1:2773:C:N4	30:R1:2774:C:H41	2.10	0.49
30:R1:2822:G:H2'	30:R1:2823:A:H5''	1.94	0.49
32:R3:73:C:H2'	32:R3:74:A:H8	1.76	0.49
32:R3:1034:G:H2'	32:R3:1035:A:C8	2.46	0.49
35:sd:11:SER:OG	35:sd:16:THR:O	2.25	0.49
40:si:54:VAL:HG23	40:si:56:MET:HB2	1.94	0.49
40:si:115:VAL:HG21	41:sj:62:ARG:HG3	1.94	0.49
45:sn:25:GLU:O	45:sn:29:ILE:N	2.41	0.49
1:13:108:MET:HE2	30:R1:1138:G:N2	2.28	0.49
1:13:109:LEU:CD2	1:13:110:PRO:HD2	2.43	0.49
4:16:102:LEU:H	4:16:102:LEU:HD12	1.77	0.49
30:R1:464:U:H1'	30:R1:686:U:H5	1.77	0.49
30:R1:1047:G:N2	30:R1:1110:G:H2'	2.28	0.49
30:R1:1124:G:H2'	30:R1:1125:G:O4'	2.13	0.49
30:R1:1447:C:H2'	30:R1:1448:G:H8	1.78	0.49
32:R3:842:U:O2'	32:R3:843:U:H4'	2.12	0.49
40:si:5:TYR:CE2	40:si:88:GLU:HB3	2.48	0.49
54:33:8:ILE:HD12	54:33:50:GLU:HG2	1.93	0.49
28:9:75:LEU:HD23	28:9:75:LEU:H	1.76	0.49
30:R1:569:U:O2'	30:R1:983:A:N1	2.41	0.49
30:R1:611:C:H2'	30:R1:612:G:O4'	2.12	0.49
32:R3:363:A:O2'	32:R3:364:A:OP1	2.27	0.49
32:R3:464:U:C5	32:R3:466:A:H5'	2.48	0.49
33:sb:209:VAL:HA	33:sb:212:TYR:HD2	1.76	0.49
42:sk:15:VAL:HG13	42:sk:78:ILE:HG12	1.95	0.49
47:sp:37:GLY:HA3	47:sp:52:LEU:HA	1.93	0.49
10:21:37:GLU:HG2	10:21:53:PHE:HE2	1.78	0.49
30:R1:700:G:O2'	30:R1:1632:A:N3	2.34	0.49
30:R1:1071:G:N1	30:R1:1091:G:O6	2.18	0.49
30:R1:1469:A:H2'	30:R1:1470:A:C8	2.47	0.49
30:R1:2796:U:H3	30:R1:2799:A:H61	1.61	0.49
30:R1:2898:U:H2'	30:R1:2899:A:C8	2.48	0.49
32:R3:77:A:N3	32:R3:93:U:H2'	2.28	0.49
32:R3:384:G:H2'	32:R3:385:C:C6	2.47	0.49
32:R3:537:G:H5''	43:sl:109:ARG:HH12	1.77	0.49
32:R3:559:A:H4'	32:R3:560:A:H3'	1.95	0.49
32:R3:1009:U:H2'	32:R3:1010:U:H6	1.75	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:si:20:ILE:HG23	40:si:60:LEU:HD12	1.94	0.49
53:T:63:G:H2'	53:T:64:G:H8	1.78	0.49
26:5:30:VAL:HG23	26:5:95:MET:HE1	1.94	0.49
30:R1:1474:U:O4	30:R1:1475:G:N2	2.45	0.49
30:R1:2304:G:H22	30:R1:2312:U:H3	1.59	0.49
30:R1:2722:G:H2'	30:R1:2723:C:C6	2.47	0.49
33:sb:17:HIS:NE2	33:sb:39:ILE:HA	2.27	0.49
34:sc:25:THR:HG23	45:sn:75:LYS:NZ	2.27	0.49
6:18:46:GLU:HA	31:R2:113:C:H1'	1.94	0.49
21:32:9:ARG:NH2	30:R1:516:C:OP1	2.45	0.49
30:R1:302:C:H2'	30:R1:303:G:H8	1.76	0.49
30:R1:1721:G:N2	30:R1:1740:G:O6	2.46	0.49
30:R1:2682:A:H61	30:R1:2728:U:H1'	1.78	0.49
32:R3:1151:A:OP1	41:sj:44:THR:HG23	2.12	0.49
39:sh:88:LYS:HE2	39:sh:119:GLY:HA2	1.95	0.49
40:si:54:VAL:HG11	40:si:93:LEU:HD21	1.93	0.49
42:sk:108:ASN:HB3	52:su:6:ARG:NH1	2.28	0.49
6:18:67:ASN:HB2	31:R2:50:A:OP1	2.12	0.49
8:2:235:GLU:OE1	8:2:235:GLU:HA	2.13	0.49
21:32:2:VAL:HG13	30:R1:2015:A:C6	2.48	0.49
27:6:110:HIS:HB2	27:6:111:PRO:HD3	1.95	0.49
30:R1:151:C:H2'	30:R1:152:A:H8	1.77	0.49
30:R1:639:U:H2'	30:R1:640:C:C6	2.48	0.49
30:R1:1101:U:H2'	30:R1:1102:C:C6	2.47	0.49
30:R1:1779:U:H5	30:R1:1784:A:N7	2.10	0.49
30:R1:2774:C:O2'	30:R1:2775:G:H8	1.95	0.49
32:R3:821:G:H2'	32:R3:822:U:H6	1.77	0.49
32:R3:918:A:H2'	32:R3:919:A:C8	2.47	0.49
32:R3:1146:A:H2'	32:R3:1147:C:O4'	2.13	0.49
15:27:43:THR:H	30:R1:2331:G:H4'	1.78	0.49
30:R1:1089:A:H2	30:R1:1090:A:H62	1.59	0.49
32:R3:868:C:H2'	32:R3:869:G:O4'	2.13	0.49
32:R3:923:A:O2'	32:R3:1399:C:OP2	2.31	0.49
36:se:79:THR:OG1	36:se:97:PRO:O	2.29	0.49
41:sj:15:HIS:CE1	41:sj:16:ARG:HG2	2.48	0.49
43:sl:54:VAL:HG22	43:sl:79:ILE:HD11	1.94	0.49
49:sr:70:THR:OG1	49:sr:71:ASP:N	2.46	0.49
30:R1:165:A:O2'	30:R1:166:U:O4'	2.31	0.48
32:R3:736:C:H2'	32:R3:737:C:H6	1.77	0.48
32:R3:1120:C:C2	32:R3:1121:U:C5	3.00	0.48
32:R3:1138:G:O2'	32:R3:1140:C:OP1	2.29	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:1377:A:C6	38:sg:6:ILE:HD13	2.48	0.48
33:sb:20:ARG:HG3	33:sb:21:TYR:N	2.28	0.48
35:sd:28:ASP:O	35:sd:29:THR:OG1	2.28	0.48
35:sd:201:GLU:OE2	36:se:104:ILE:N	2.46	0.48
42:sk:86:LYS:HG3	42:sk:112:VAL:O	2.13	0.48
43:sl:82:ARG:O	43:sl:95:HIS:N	2.45	0.48
44:sm:3:ILE:HG22	44:sm:4:ALA:N	2.25	0.48
7:19:33:GLU:HG3	7:19:36:LYS:HG3	1.93	0.48
12:23:60:THR:OG1	12:23:61:LEU:N	2.46	0.48
27:6:74:MET:O	27:6:78:VAL:HG22	2.13	0.48
30:R1:1869:G:H3'	30:R1:1870:C:H4'	1.95	0.48
30:R1:1873:G:H2'	30:R1:1874:C:H6	1.76	0.48
32:R3:1419:G:C6	32:R3:1482:G:C2	3.00	0.48
34:sc:187:GLU:N	34:sc:187:GLU:OE1	2.46	0.48
35:sd:8:LEU:HB2	35:sd:21:LYS:NZ	2.28	0.48
38:sg:111:GLY:HA2	38:sg:118:ARG:HH11	1.79	0.48
48:sq:45:VAL:HG21	48:sq:60:ILE:HG21	1.95	0.48
50:ss:24:SER:HB2	50:ss:27:LYS:NZ	2.22	0.48
3:15:58:TYR:OH	30:R1:251:A:OP1	2.28	0.48
32:R3:1391:U:H2'	32:R3:1392:G:H8	1.77	0.48
37:sf:51:ILE:C	37:sf:53:LYS:H	2.20	0.48
42:sk:55:ARG:O	42:sk:58:THR:HG22	2.13	0.48
11:22:72:THR:OG1	11:22:108:SER:OG	2.24	0.48
26:5:111:ARG:HD3	26:5:112:ASP:H	1.77	0.48
26:5:133:GLU:OE2	26:5:134:GLN:N	2.47	0.48
30:R1:1335:C:H2'	30:R1:1336:A:H8	1.79	0.48
30:R1:1532:A:H2'	30:R1:1533:C:C6	2.48	0.48
30:R1:2315:G:O2'	30:R1:2316:G:H8	1.96	0.48
32:R3:416:G:C6	32:R3:417:G:O6	2.65	0.48
33:sb:83:ALA:O	33:sb:88:GLN:N	2.46	0.48
35:sd:106:PHE:CE1	35:sd:177:MET:HB2	2.43	0.48
36:se:110:MET:HE1	36:se:124:ALA:HB1	1.96	0.48
30:R1:2537:U:H2'	30:R1:2538:C:H6	1.77	0.48
32:R3:1130:A:C6	32:R3:1146:A:C6	3.02	0.48
32:R3:1178:G:N2	32:R3:1181:G:OP2	2.42	0.48
8:2:106:PRO:HD2	8:2:109:LEU:HD12	1.96	0.48
8:2:200:MET:O	8:2:202:ARG:N	2.46	0.48
17:29:14:LEU:HG	17:29:57:LEU:HD21	1.95	0.48
30:R1:1020:A:H4'	30:R1:1021:A:O5'	2.14	0.48
30:R1:1039:A:H2	30:R1:1116:G:H22	1.59	0.48
30:R1:2025:C:H2'	30:R1:2026:U:C6	2.48	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:sc:25:THR:HG23	45:sn:75:LYS:HZ1	1.77	0.48
4:16:57:VAL:C	4:16:58:LYS:HG3	2.39	0.48
10:21:57:GLY:N	10:21:103:ALA:O	2.39	0.48
30:R1:156:A:H2	30:R1:169:G:H22	1.62	0.48
30:R1:365:U:H2'	30:R1:366:C:C6	2.48	0.48
30:R1:987:C:O2'	30:R1:1000:A:N3	2.39	0.48
30:R1:1593:A:H2'	30:R1:1594:U:C6	2.49	0.48
30:R1:2029:G:N1	30:R1:2033:A:OP2	2.34	0.48
30:R1:2061:G:H22	53:T:101:FME:HE3	1.78	0.48
30:R1:2163:A:H5''	30:R1:2164:C:OP2	2.13	0.48
32:R3:204:G:N3	32:R3:204:G:H2'	2.28	0.48
32:R3:1356:G:H2'	32:R3:1357:A:C8	2.35	0.48
32:R3:1388:C:H2'	32:R3:1389:C:O2	2.13	0.48
37:sf:74:LEU:HD11	37:sf:78:PHE:CZ	2.49	0.48
1:13:99:ARG:O	1:13:103:ILE:HG12	2.13	0.48
6:18:93:ASP:OD1	6:18:95:SER:N	2.47	0.48
7:19:74:GLN:HG3	18:3:13:ARG:HH22	1.78	0.48
15:27:71:VAL:O	15:27:71:VAL:HG22	2.14	0.48
30:R1:282:A:C6	30:R1:359:G:C6	3.02	0.48
30:R1:632:A:H2'	30:R1:633:A:C8	2.48	0.48
30:R1:1594:U:H2'	30:R1:1595:C:H6	1.78	0.48
30:R1:2181:U:H3'	30:R1:2182:U:H5''	1.96	0.48
32:R3:878:A:OP1	39:sh:79:ARG:NH1	2.43	0.48
32:R3:1004:A:N6	32:R3:1025:U:O2'	2.47	0.48
32:R3:1260:G:H4'	32:R3:1283:U:O2'	2.14	0.48
32:R3:1355:G:H2'	32:R3:1356:G:H8	1.79	0.48
34:sc:111:ASP:OD2	34:sc:112:ALA:N	2.47	0.48
43:sl:2:THR:HG22	43:sl:4:ASN:H	1.79	0.48
43:sl:20:VAL:HB	43:sl:94:TYR:CE1	2.48	0.48
54:33:5:ARG:HG2	54:33:25:ASN:HB2	1.96	0.48
5:17:82:GLU:N	5:17:82:GLU:OE2	2.46	0.48
7:19:112:ARG:O	7:19:113:LEU:HG	2.14	0.48
30:R1:947:A:H2'	30:R1:948:C:C6	2.48	0.48
30:R1:1744:A:H3'	30:R1:1745:A:H8	1.78	0.48
30:R1:2004:G:C4	30:R1:2005:A:C8	3.02	0.48
32:R3:286:C:H2'	32:R3:287:U:C6	2.48	0.48
32:R3:737:C:C2'	32:R3:738:C:H5'	2.44	0.48
32:R3:981:U:H4'	45:sn:60:ARG:NH1	2.29	0.48
32:R3:1405:G:N2	32:R3:1518:A:H8	2.08	0.48
33:sb:19:THR:OG1	33:sb:20:ARG:N	2.47	0.48
35:sd:176:LYS:C	35:sd:177:MET:HG2	2.39	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:sj:46:LYS:HA	41:sj:67:ILE:O	2.13	0.48
10:21:48:LYS:HB2	10:21:48:LYS:HE3	1.46	0.48
30:R1:30:G:O2'	30:R1:1214:A:N3	2.39	0.48
30:R1:271:G:N3	30:R1:367:G:N2	2.62	0.48
30:R1:639:U:H2'	30:R1:640:C:H6	1.77	0.48
30:R1:1670:C:O5'	30:R1:1670:C:H6	1.97	0.48
30:R1:2102:G:H2'	30:R1:2103:C:C6	2.48	0.48
32:R3:166:U:H2'	32:R3:167:A:H8	1.77	0.48
32:R3:375:U:H2'	32:R3:376:G:O4'	2.13	0.48
32:R3:1095:U:P	32:R3:1108:G:H1	2.36	0.48
35:sd:12:ARG:NH1	35:sd:36:ALA:O	2.33	0.48
35:sd:27:ILE:HG13	35:sd:28:ASP:N	2.24	0.48
23:35:31:ILE:O	23:35:31:ILE:HG22	2.14	0.47
27:6:16:VAL:HG22	27:6:25:ILE:HD12	1.96	0.47
30:R1:2135:A:H5''	30:R1:2136:G:H8	1.79	0.47
32:R3:958:A:H8	32:R3:985:C:O2'	1.97	0.47
32:R3:1288:A:N3	32:R3:1352:C:O2'	2.38	0.47
35:sd:98:ASP:OD2	35:sd:114:ARG:HA	2.14	0.47
36:se:98:ALA:HB2	36:se:123:LEU:HD23	1.96	0.47
36:se:121:ASN:O	36:se:122:VAL:HB	2.14	0.47
39:sh:87:ARG:NH1	39:sh:87:ARG:HB2	2.29	0.47
50:ss:6:LYS:HD3	50:ss:6:LYS:N	2.28	0.47
2:14:19:VAL:HB	2:14:41:ILE:HD12	1.96	0.47
7:19:55:HIS:HA	18:3:13:ARG:HH21	1.79	0.47
8:2:252:LYS:NZ	30:R1:1795:C:O2	2.47	0.47
20:31:55:GLY:O	20:31:59:ARG:NH2	2.47	0.47
26:5:105:ILE:HD12	26:5:138:PRO:HG3	1.96	0.47
30:R1:863:A:O3'	31:R2:100:G:N2	2.47	0.47
30:R1:1511:G:H2'	30:R1:1512:C:H6	1.79	0.47
32:R3:184:G:H2'	32:R3:185:U:C6	2.49	0.47
32:R3:647:C:H2'	32:R3:648:A:H8	1.79	0.47
34:sc:38:VAL:O	34:sc:42:LEU:HD23	2.14	0.47
49:sr:24:ASP:O	49:sr:28:LEU:HD23	2.13	0.47
49:sr:32:ILE:HG13	49:sr:33:THR:O	2.14	0.47
52:su:15:LEU:HD23	52:su:15:LEU:O	2.14	0.47
27:6:17:LYS:HB2	27:6:24:THR:OG1	2.14	0.47
30:R1:219:A:N3	30:R1:234:U:O2'	2.44	0.47
30:R1:910:A:H2'	30:R1:911:A:C8	2.50	0.47
30:R1:2737:G:H2'	30:R1:2738:A:C8	2.49	0.47
31:R2:10:G:H2'	31:R2:11:C:O4'	2.13	0.47
32:R3:144:G:C6	32:R3:179:A:C6	3.02	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:821:G:H2'	32:R3:822:U:C6	2.49	0.47
32:R3:859:G:OP2	32:R3:869:G:N1	2.31	0.47
1:13:99:ARG:HE	1:13:103:ILE:HD11	1.78	0.47
2:14:121:GLU:OE1	2:14:121:GLU:N	2.46	0.47
6:18:102:ARG:HG2	31:R2:49:C:OP1	2.14	0.47
10:21:80:ARG:NH2	30:R1:572:A:OP2	2.47	0.47
25:4:97:ASN:OD1	25:4:97:ASN:N	2.47	0.47
28:9:99:ILE:HG13	28:9:100:ALA:N	2.28	0.47
28:9:125:THR:O	28:9:125:THR:OG1	2.32	0.47
30:R1:820:A:C2	30:R1:943:A:H4'	2.50	0.47
30:R1:949:G:C4	30:R1:969:G:N2	2.82	0.47
31:R2:33:G:C6	31:R2:34:A:C5	3.02	0.47
31:R2:34:A:C5	31:R2:44:G:N7	2.82	0.47
32:R3:338:A:H3'	32:R3:339:C:H5''	1.96	0.47
32:R3:464:U:C6	32:R3:466:A:H5'	2.50	0.47
32:R3:1187:G:H2'	32:R3:1188:A:H8	1.79	0.47
32:R3:1324:A:H2'	32:R3:1325:C:H6	1.80	0.47
33:sb:169:HIS:HD1	33:sb:169:HIS:H	1.60	0.47
34:sc:46:LEU:HD11	34:sc:86:LEU:HD11	1.97	0.47
45:sn:12:ARG:HG2	45:sn:53:ASP:OD2	2.15	0.47
52:su:14:ALA:C	52:su:16:ARG:H	2.22	0.47
3:15:108:ALA:HB3	3:15:125:LEU:HD22	1.97	0.47
16:28:38:TRP:CD1	28:9:32:PRO:HA	2.48	0.47
16:28:47:THR:C	16:28:48:LEU:HD12	2.40	0.47
17:29:63:ALA:HB1	30:R1:111:A:H5''	1.96	0.47
18:3:149:ASN:HB3	30:R1:2572:A:OP2	2.12	0.47
30:R1:1709:U:H2'	30:R1:1710:G:H8	1.80	0.47
30:R1:2105:U:H2'	30:R1:2106:U:C6	2.49	0.47
32:R3:588:G:HO2'	32:R3:589:U:P	2.36	0.47
32:R3:1032:G:H21	32:R3:1033:G:H5'	1.79	0.47
32:R3:1151:A:C6	32:R3:1152:A:C6	3.02	0.47
36:se:98:ALA:HB3	36:se:122:VAL:H	1.79	0.47
13:24:18:LYS:NZ	30:R1:310:A:OP1	2.36	0.47
25:4:148:ILE:HD13	25:4:187:VAL:CG2	2.45	0.47
30:R1:2:G:H2'	30:R1:3:U:H6	1.79	0.47
30:R1:1726:C:H2'	30:R1:1727:C:C6	2.50	0.47
30:R1:2667:C:H2'	30:R1:2668:G:H5'	1.96	0.47
32:R3:603:U:H2'	32:R3:604:G:C8	2.49	0.47
32:R3:640:A:HO2'	39:sh:106:SER:HG	1.53	0.47
1:13:12:LYS:HD3	1:13:12:LYS:HA	1.73	0.47
6:18:11:ALA:HB2	6:18:96:GLY:N	2.30	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:2:23:LEU:HD13	8:2:82:TYR:HB2	1.96	0.47
8:2:259:ASN:ND2	8:2:262:THR:OG1	2.39	0.47
17:29:48:ARG:HH11	17:29:48:ARG:HG3	1.79	0.47
20:31:15:SER:HA	20:31:21:VAL:HG22	1.96	0.47
30:R1:592:A:H2'	30:R1:593:U:C6	2.50	0.47
30:R1:1090:A:N6	30:R1:1102:C:H42	2.12	0.47
30:R1:1355:G:H2'	30:R1:1356:G:H8	1.79	0.47
30:R1:1670:C:H2'	30:R1:1671:U:O4'	2.14	0.47
30:R1:2134:A:H1'	30:R1:2158:A:H5'	1.97	0.47
31:R2:31:C:H2'	31:R2:32:U:C6	2.50	0.47
32:R3:473:U:O2	32:R3:474:G:N1	2.47	0.47
32:R3:674:G:N2	42:sk:117:HIS:HB2	2.30	0.47
32:R3:790:A:OP1	53:T:38:A:O2'	2.33	0.47
32:R3:1102:A:O2'	32:R3:1103:C:H5'	2.14	0.47
32:R3:1129:C:H1'	32:R3:1130:A:C2	2.49	0.47
32:R3:1175:G:C2	32:R3:1176:A:C8	3.03	0.47
32:R3:1455:G:H2'	32:R3:1456:A:H8	1.79	0.47
33:sb:14:HIS:O	33:sb:14:HIS:ND1	2.47	0.47
33:sb:121:GLN:NE2	33:sb:122:ASP:HB2	2.29	0.47
43:sl:31:GLY:HA3	43:sl:54:VAL:HG13	1.97	0.47
48:sq:20:ILE:HG21	48:sq:52:CYS:SG	2.55	0.47
52:su:36:PHE:O	52:su:38:GLU:N	2.48	0.47
4:16:59:ARG:HB3	4:16:60:GLN:NE2	2.30	0.47
5:17:73:ASN:HA	5:17:76:VAL:HG22	1.97	0.47
9:20:25:GLY:O	9:20:29:ARG:NH1	2.46	0.47
15:27:15:ASP:OD1	15:27:16:SER:N	2.44	0.47
15:27:78:LYS:HE2	15:27:78:LYS:HB2	1.71	0.47
24:36:30:GLU:C	24:36:32:LYS:H	2.21	0.47
30:R1:1278:C:H2'	30:R1:1279:G:H8	1.80	0.47
30:R1:2507:C:H5''	30:R1:2573:C:H5	1.79	0.47
32:R3:321:A:C2'	32:R3:322:C:H5'	2.45	0.47
32:R3:363:A:HO2'	32:R3:364:A:P	2.36	0.47
32:R3:407:U:O2'	35:sd:112:GLU:OE1	2.15	0.47
39:sh:28:SER:HB2	39:sh:58:LEU:HB2	1.96	0.47
1:13:37:ARG:NH2	1:13:44:TYR:OH	2.48	0.47
4:16:53:MET:HE2	4:16:117:PHE:CE1	2.50	0.47
20:31:41:HIS:HB3	20:31:43:PHE:CD1	2.50	0.47
30:R1:119:A:H4'	30:R1:120:U:H5'	1.97	0.47
30:R1:350:G:H2'	30:R1:351:C:C6	2.50	0.47
30:R1:741:U:H2'	30:R1:742:A:H8	1.79	0.47
30:R1:1709:U:C2	30:R1:1750:G:N2	2.82	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:181:A:H61	32:R3:194:C:H3'	1.79	0.47
32:R3:502:A:H2'	32:R3:503:C:H6	1.80	0.47
32:R3:561:U:O2'	32:R3:562:U:OP1	2.29	0.47
32:R3:673:A:H5''	37:sf:86:ARG:NH1	2.29	0.47
33:sb:218:ALA:O	33:sb:222:GLU:HG3	2.15	0.47
34:sc:130:ARG:HB3	34:sc:134:LYS:HZ1	1.79	0.47
47:sp:8:ARG:HB3	47:sp:28:ARG:NH1	2.30	0.47
13:24:84:PHE:CE1	13:24:93:ARG:HG2	2.49	0.47
17:29:2:LYS:HZ1	30:R1:78:U:P	2.33	0.47
30:R1:306:U:H2'	30:R1:307:G:O4'	2.14	0.47
30:R1:2804:U:H2'	30:R1:2805:C:C6	2.49	0.47
31:R2:4:C:H2'	31:R2:5:U:C6	2.50	0.47
31:R2:30:C:H1'	31:R2:57:A:N6	2.23	0.47
32:R3:167:A:H2'	32:R3:168:G:C8	2.50	0.47
32:R3:563:A:O2'	32:R3:566:G:O2'	2.28	0.47
32:R3:946:A:H2'	32:R3:947:G:H8	1.78	0.47
32:R3:1092:A:H5''	38:sg:3:ARG:NH2	2.27	0.47
38:sg:55:LYS:HD2	38:sg:59:GLU:HG3	1.97	0.47
38:sg:136:LYS:HE2	38:sg:136:LYS:HB2	1.77	0.47
40:si:113:LYS:HE2	40:si:118:ARG:O	2.16	0.47
2:14:15:GLY:O	2:14:47:ILE:HG12	2.15	0.46
28:9:2:GLN:NE2	28:9:2:GLN:O	2.49	0.46
30:R1:594:U:H2'	30:R1:595:C:C6	2.50	0.46
30:R1:2168:G:N3	30:R1:2168:G:H2'	2.30	0.46
32:R3:246:A:C2	32:R3:282:A:C5	3.03	0.46
32:R3:377:G:N1	32:R3:387:U:N3	2.62	0.46
32:R3:400:C:H2'	32:R3:401:C:C6	2.50	0.46
32:R3:528:C:N4	43:sl:45:ASN:OD1	2.46	0.46
33:sb:58:LYS:C	33:sb:58:LYS:HD3	2.40	0.46
43:sl:27:PRO:HB2	43:sl:28:GLN:OE1	2.15	0.46
8:2:155:ARG:NH2	30:R1:1818:U:OP2	2.45	0.46
28:9:96:THR:O	28:9:96:THR:OG1	2.31	0.46
30:R1:106:C:H2'	30:R1:107:G:H8	1.80	0.46
30:R1:271:G:C4	30:R1:367:G:N2	2.83	0.46
30:R1:1470:A:H2'	30:R1:1471:G:O4'	2.15	0.46
30:R1:2121:G:N3	30:R1:2121:G:H2'	2.30	0.46
30:R1:2184:A:H2'	30:R1:2185:U:C6	2.51	0.46
30:R1:2303:G:C4	30:R1:2304:G:C8	3.03	0.46
32:R3:219:U:H2'	32:R3:220:G:O4'	2.16	0.46
32:R3:323:U:OP1	51:st:17:ARG:HA	2.15	0.46
32:R3:356:A:HO2'	32:R3:368:U:HO2'	1.61	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:792:A:H1'	32:R3:794:A:N7	2.30	0.46
32:R3:1252:A:H61	32:R3:1285:A:H62	1.63	0.46
32:R3:1356:G:N3	32:R3:1357:A:C8	2.83	0.46
47:sp:4:ILE:HD13	47:sp:57:ILE:HD13	1.98	0.46
50:ss:40:PHE:O	50:ss:43:MET:HG3	2.15	0.46
52:su:35:GLU:C	52:su:37:TYR:H	2.23	0.46
53:T:23:C:H2'	53:T:24:U:C6	2.50	0.46
10:21:52:PRO:HB2	10:21:53:PHE:HD1	1.81	0.46
18:3:133:THR:HG22	18:3:134:HIS:N	2.30	0.46
20:31:11:GLU:OE1	20:31:11:GLU:N	2.48	0.46
20:31:34:LEU:HD23	20:31:35:ASP:O	2.15	0.46
30:R1:886:A:H2'	30:R1:888:C:H5	1.79	0.46
30:R1:1482:G:C2	30:R1:1508:A:N7	2.83	0.46
30:R1:1522:A:H4'	30:R1:1523:U:H5'	1.98	0.46
30:R1:2024:G:C5	30:R1:2040:G:C2	3.04	0.46
30:R1:2107:G:N1	30:R1:2182:U:N3	2.29	0.46
30:R1:2193:G:H2'	30:R1:2194:U:O4'	2.15	0.46
32:R3:309:A:H2'	32:R3:310:G:H8	1.80	0.46
32:R3:547:A:OP2	35:sd:1:ALA:N	2.39	0.46
32:R3:864:A:H5''	36:se:89:THR:HG23	1.97	0.46
39:sh:35:ILE:HD12	39:sh:125:ILE:HG21	1.96	0.46
3:15:78:ARG:HD2	3:15:113:ALA:HB3	1.97	0.46
15:27:41:ARG:HD2	15:27:41:ARG:HA	1.74	0.46
30:R1:263:G:O2'	30:R1:429:A:N3	2.40	0.46
30:R1:437:U:H2'	30:R1:438:G:C8	2.51	0.46
30:R1:579:G:H2'	30:R1:580:U:C6	2.50	0.46
30:R1:589:U:O2'	30:R1:590:A:H5'	2.15	0.46
30:R1:1463:C:H2'	30:R1:1464:G:C8	2.51	0.46
30:R1:1936:A:H2	30:R1:1943:U:N3	2.11	0.46
30:R1:2247:A:H2'	30:R1:2248:C:C6	2.51	0.46
32:R3:451:A:H1'	32:R3:452:A:C2	2.49	0.46
32:R3:517:G:N2	32:R3:530:G:OP1	2.33	0.46
32:R3:533:A:O2'	32:R3:534:U:H5''	2.15	0.46
32:R3:645:G:C2	32:R3:646:G:C8	3.03	0.46
32:R3:1320:C:H1'	50:ss:72:GLU:HB3	1.98	0.46
34:sc:131:ARG:HD3	34:sc:135:ARG:HH22	1.80	0.46
36:se:100:GLU:OE1	36:se:102:THR:OG1	2.20	0.46
3:15:51:GLU:OE1	3:15:56:PRO:HA	2.15	0.46
5:17:38:LEU:HB3	5:17:39:PRO:HD3	1.97	0.46
16:28:2:ARG:HD2	16:28:29:LEU:HD23	1.97	0.46
30:R1:289:G:H2'	30:R1:290:U:O4'	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:1504:A:H2'	30:R1:1505:A:H8	1.79	0.46
30:R1:1736:U:H2'	30:R1:1737:G:O4'	2.15	0.46
30:R1:2028:U:H2'	30:R1:2029:G:C8	2.50	0.46
31:R2:33:G:H2'	31:R2:34:A:O4'	2.16	0.46
32:R3:74:A:C2	32:R3:75:G:C8	3.03	0.46
32:R3:337:G:C2	32:R3:338:A:C5	3.03	0.46
32:R3:605:U:H2'	32:R3:606:G:H8	1.80	0.46
32:R3:737:C:O2'	32:R3:738:C:H5'	2.15	0.46
32:R3:923:A:H2'	32:R3:924:C:C6	2.50	0.46
32:R3:1230:C:H2'	32:R3:1231:G:H8	1.79	0.46
33:sb:93:HIS:CE1	33:sb:145:ASN:HD22	2.32	0.46
37:sf:15:SER:O	37:sf:18:VAL:HG12	2.15	0.46
38:sg:72:VAL:HG12	38:sg:89:GLU:HA	1.97	0.46
52:su:60:ALA:O	52:su:63:ASN:ND2	2.49	0.46
2:14:40:LYS:HE3	2:14:57:VAL:HG12	1.97	0.46
3:15:85:VAL:HG23	3:15:86:GLU:H	1.80	0.46
30:R1:145:C:H2'	30:R1:146:A:N3	2.30	0.46
30:R1:282:A:N6	30:R1:359:G:O6	2.48	0.46
30:R1:419:U:H2'	30:R1:420:C:C6	2.50	0.46
30:R1:1494:A:H2'	30:R1:1495:A:H8	1.79	0.46
32:R3:981:U:O2'	45:sn:60:ARG:NH2	2.49	0.46
46:so:22:GLY:O	46:so:27:GLN:NE2	2.33	0.46
46:so:63:ARG:HD2	46:so:63:ARG:HA	1.73	0.46
1:13:45:THR:HB	1:13:48:VAL:HG22	1.97	0.46
8:2:109:LEU:HD23	8:2:109:LEU:HA	1.71	0.46
8:2:259:ASN:C	8:2:261:ARG:H	2.24	0.46
30:R1:1919:A:N1	32:R3:1495:U:O2'	2.38	0.46
30:R1:2006:C:O2'	30:R1:2823:A:N3	2.49	0.46
31:R2:23:G:N2	31:R2:61:G:N3	2.63	0.46
32:R3:151:A:C5	32:R3:152:A:C8	3.04	0.46
32:R3:157:U:H3	32:R3:164:G:H1	1.62	0.46
32:R3:412:A:H62	32:R3:431:A:H61	1.62	0.46
32:R3:474:G:C8	32:R3:475:C:C5	3.03	0.46
32:R3:1217:C:H2'	32:R3:1218:C:H6	1.81	0.46
32:R3:1319:A:C8	32:R3:1323:G:C5	3.03	0.46
44:sm:22:TYR:CD1	44:sm:68:LEU:HD23	2.50	0.46
8:2:131:MET:HA	8:2:134:ILE:HB	1.96	0.46
15:27:39:ARG:HH11	15:27:39:ARG:HG3	1.79	0.46
30:R1:156:A:H2'	30:R1:157:C:O4'	2.15	0.46
32:R3:560:A:H5''	32:R3:561:U:H3'	1.97	0.46
32:R3:939:G:H2'	32:R3:940:C:C6	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:1226:C:H2'	44:sm:101:THR:CG2	2.46	0.46
32:R3:1305:G:N2	32:R3:1331:G:H1'	2.31	0.46
33:sb:56:LEU:HD23	33:sb:56:LEU:HA	1.71	0.46
41:sj:69:THR:O	41:sj:69:THR:OG1	2.30	0.46
52:su:7:GLU:HB3	52:su:11:PHE:HB3	1.97	0.46
53:T:43:A:H2'	53:T:44:A:C8	2.50	0.46
8:2:209:ALA:HA	8:2:212:TRP:NE1	2.31	0.46
12:23:10:VAL:HG12	12:23:11:LEU:HD12	1.97	0.46
15:27:14:ARG:NH1	30:R1:2279:G:N7	2.63	0.46
30:R1:177:G:H3'	30:R1:178:G:H8	1.80	0.46
30:R1:644:A:H2'	30:R1:645:C:O4'	2.15	0.46
30:R1:1042:G:H1	30:R1:1113:U:H3	1.63	0.46
30:R1:2081:U:H2'	30:R1:2082:A:H8	1.81	0.46
32:R3:279:A:H5''	32:R3:280:C:H3'	1.96	0.46
32:R3:1287:A:H2	32:R3:1353:G:H1'	1.81	0.46
35:sd:82:LYS:O	35:sd:88:ASN:ND2	2.42	0.46
37:sf:38:ARG:HG3	37:sf:96:VAL:O	2.16	0.46
41:sj:8:ILE:HD12	41:sj:100:ILE:HG12	1.98	0.46
46:so:63:ARG:NH2	46:so:67:ASP:OD1	2.48	0.46
53:T:50:U:H2'	53:T:51:C:C6	2.51	0.46
30:R1:1751:U:H2'	30:R1:1752:C:C6	2.51	0.46
30:R1:2113:U:H3'	30:R1:2114:A:C8	2.51	0.46
30:R1:2845:U:H2'	30:R1:2846:G:H8	1.81	0.46
32:R3:555:U:H2'	32:R3:556:C:C6	2.51	0.46
8:2:209:ALA:HA	8:2:212:TRP:CE2	2.50	0.45
25:4:171:ASP:C	25:4:171:ASP:OD1	2.58	0.45
30:R1:2651:C:N3	30:R1:2652:C:C4	2.84	0.45
30:R1:2668:G:O2'	30:R1:2669:G:H8	1.99	0.45
31:R2:32:U:C2	31:R2:51:G:N2	2.84	0.45
32:R3:922:G:H2'	32:R3:923:A:C8	2.51	0.45
32:R3:1151:A:P	41:sj:43:PRO:HA	2.56	0.45
32:R3:1319:A:C8	32:R3:1323:G:C6	3.04	0.45
32:R3:1372:U:H2'	32:R3:1373:G:O4'	2.16	0.45
34:sc:52:SER:HB2	34:sc:114:LEU:CD2	2.46	0.45
43:sl:120:ARG:HG3	43:sl:121:PRO:HD2	1.97	0.45
51:st:27:MET:O	51:st:31:ILE:HD12	2.17	0.45
5:17:44:LEU:HD12	5:17:44:LEU:HA	1.77	0.45
7:19:21:PRO:HG3	7:19:49:ILE:HD12	1.97	0.45
27:6:148:ARG:HA	27:6:161:VAL:HG13	1.97	0.45
30:R1:2243:U:H2'	30:R1:2244:U:C6	2.50	0.45
30:R1:2679:A:H2'	30:R1:2680:U:C6	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:129:A:H1'	32:R3:130:A:C8	2.51	0.45
32:R3:719:C:H1'	49:sr:37:LYS:HB3	1.98	0.45
32:R3:878:A:H5''	39:sh:80:PRO:HG2	1.96	0.45
36:se:14:LEU:HD12	36:se:15:ILE:H	1.81	0.45
9:20:12:ARG:NH1	30:R1:812:C:OP1	2.50	0.45
13:24:16:LYS:HG3	13:24:17:ASP:OD1	2.17	0.45
30:R1:1186:G:H2'	30:R1:1187:G:O4'	2.17	0.45
30:R1:1797:G:C6	30:R1:1798:U:C4	3.03	0.45
30:R1:2399:G:C6	30:R1:2418:A:C6	3.04	0.45
32:R3:791:G:H2'	32:R3:792:A:H5'	1.98	0.45
32:R3:1410:A:H2'	32:R3:1411:C:C6	2.52	0.45
44:sm:58:GLU:O	44:sm:61:LYS:HG2	2.16	0.45
2:14:114:LYS:HD3	2:14:114:LYS:C	2.41	0.45
5:17:60:VAL:O	5:17:64:ARG:HG2	2.17	0.45
8:2:131:MET:HE1	8:2:183:VAL:HG21	1.98	0.45
8:2:227:VAL:HG13	8:2:228:ASP:OD1	2.17	0.45
18:3:8:LYS:HD3	18:3:197:THR:HA	1.99	0.45
30:R1:29:U:O2	30:R1:1215:G:O2'	2.35	0.45
30:R1:2514:U:H2'	30:R1:2515:C:C6	2.52	0.45
45:sn:17:ASP:OD1	45:sn:17:ASP:N	2.41	0.45
46:so:9:LYS:HA	46:so:9:LYS:HD2	1.83	0.45
53:T:63:G:H2'	53:T:64:G:C8	2.52	0.45
8:2:152:GLN:HG2	30:R1:1818:U:O4	2.17	0.45
9:20:29:ARG:HH22	30:R1:18:U:P	2.40	0.45
26:5:8:LYS:HB2	26:5:8:LYS:HE3	1.74	0.45
26:5:70:ARG:NH1	26:5:71:LYS:HB2	2.31	0.45
30:R1:686:U:H2'	30:R1:788:A:N1	2.32	0.45
30:R1:2324:U:C3'	30:R1:2325:G:H5''	2.40	0.45
30:R1:2330:G:C2	30:R1:2386:A:C2	3.05	0.45
30:R1:2639:A:H2'	30:R1:2640:G:O4'	2.17	0.45
32:R3:264:C:H2'	32:R3:265:G:O4'	2.16	0.45
51:st:2:ASN:CG	51:st:3:ILE:H	2.24	0.45
54:33:33:LEU:HD22	54:33:35:LEU:HD21	1.99	0.45
30:R1:84:A:H4'	30:R1:85:G:H5'	1.98	0.45
30:R1:404:A:C8	30:R1:406:G:C6	3.05	0.45
30:R1:520:G:H2'	30:R1:521:U:C6	2.52	0.45
30:R1:2368:C:H2'	30:R1:2369:A:H8	1.82	0.45
30:R1:2473:U:O2'	30:R1:2474:U:O5'	2.34	0.45
30:R1:2500:U:H5''	30:R1:2501:C:OP2	2.16	0.45
30:R1:2655:G:O2'	30:R1:2664:G:O6	2.21	0.45
30:R1:2774:C:O2'	30:R1:2775:G:C8	2.67	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:382:A:H2'	32:R3:383:A:H8	1.81	0.45
32:R3:456:A:H62	32:R3:476:U:H3	1.64	0.45
32:R3:976:G:OP2	32:R3:1358:U:O2'	2.33	0.45
32:R3:1013:G:N2	32:R3:1016:A:OP2	2.49	0.45
33:sb:126:ASP:OD1	33:sb:126:ASP:N	2.47	0.45
40:si:84:ARG:HH11	40:si:84:ARG:HG3	1.81	0.45
9:20:5:ARG:NH1	30:R1:1251:C:OP2	2.48	0.45
21:32:7:PRO:HD2	30:R1:1263:U:O2'	2.16	0.45
28:9:77:THR:HA	28:9:143:ILE:O	2.17	0.45
30:R1:24:G:H2'	30:R1:25:U:C6	2.52	0.45
30:R1:2115:G:H1'	30:R1:2117:A:N7	2.31	0.45
30:R1:2134:A:H2'	30:R1:2135:A:O4'	2.17	0.45
30:R1:2412:A:H2'	30:R1:2413:G:O4'	2.17	0.45
30:R1:2650:U:C2	30:R1:2671:G:N2	2.85	0.45
30:R1:2751:G:H3'	30:R1:2752:C:H6	1.81	0.45
32:R3:482:A:H8	32:R3:482:A:O5'	2.00	0.45
32:R3:1082:A:OP2	36:se:22:LYS:NZ	2.50	0.45
32:R3:1399:C:O2	32:R3:1502:A:N6	2.49	0.45
35:sd:103:ARG:HA	35:sd:103:ARG:HD2	1.79	0.45
3:15:91:ASP:H	3:15:94:THR:HG1	1.62	0.45
8:2:15:VAL:HG22	8:2:205:GLY:HA3	1.99	0.45
10:21:25:LEU:HD23	10:21:25:LEU:H	1.81	0.45
19:30:26:LEU:HD23	19:30:26:LEU:HA	1.84	0.45
30:R1:9:G:C2	30:R1:2895:G:C6	3.04	0.45
30:R1:412:A:H2'	30:R1:413:C:H5'	1.99	0.45
30:R1:640:C:H2'	30:R1:641:U:C6	2.52	0.45
30:R1:863:A:H2'	30:R1:864:G:C8	2.51	0.45
30:R1:2038:G:H2'	30:R1:2039:U:O4'	2.17	0.45
32:R3:330:C:O2'	32:R3:331:G:OP2	2.32	0.45
32:R3:513:C:H2'	32:R3:514:C:C6	2.51	0.45
32:R3:981:U:C3'	45:sn:60:ARG:HH12	2.29	0.45
45:sn:38:GLU:HA	45:sn:41:TRP:HB3	1.98	0.45
10:21:7:SER:HB3	10:21:22:LEU:HD22	1.98	0.45
30:R1:156:A:N1	30:R1:169:G:O6	2.50	0.45
30:R1:722:A:H2'	30:R1:723:C:C6	2.52	0.45
30:R1:963:U:C2	30:R1:964:C:C5	3.05	0.45
30:R1:1196:C:C2	30:R1:1197:G:C8	3.04	0.45
30:R1:1419:A:C8	30:R1:1579:A:N6	2.85	0.45
30:R1:1812:U:H2'	30:R1:1813:G:H8	1.80	0.45
31:R2:76:G:H2'	31:R2:77:U:H6	1.82	0.45
32:R3:2:A:O2'	32:R3:3:A:OP1	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:598:U:H2'	32:R3:599:C:C6	2.52	0.45
32:R3:715:A:H2'	32:R3:716:A:C8	2.51	0.45
32:R3:1455:G:H2'	32:R3:1456:A:C8	2.52	0.45
45:sn:50:LEU:HD22	45:sn:51:PRO:HD2	1.98	0.45
9:20:30:VAL:HG13	30:R1:581:C:H5'	1.99	0.45
10:21:35:PHE:HB2	10:21:59:ILE:HB	1.98	0.45
21:32:31:LYS:HG3	30:R1:2885:G:N2	2.32	0.45
23:35:15:LYS:NZ	23:35:19:GLY:HA2	2.31	0.45
26:5:131:VAL:HG22	26:5:151:LEU:H	1.82	0.45
26:5:169:LEU:O	26:5:174:PHE:HB2	2.17	0.45
30:R1:1443:U:H2'	30:R1:1444:G:H8	1.82	0.45
30:R1:2686:G:H2'	30:R1:2687:U:C6	2.52	0.45
32:R3:417:G:O2'	32:R3:418:C:H5'	2.17	0.45
32:R3:1226:C:H6	44:sm:101:THR:HG22	1.80	0.45
34:sc:53:ARG:HB3	34:sc:68:HIS:CD2	2.52	0.45
40:si:9:GLY:HA2	40:si:80:HIS:CD2	2.52	0.45
2:14:88:ASN:OD1	2:14:89:ASN:N	2.50	0.44
8:2:66:PHE:HB3	8:2:150:GLY:O	2.17	0.44
18:3:33:ARG:HE	18:3:73:VAL:HG12	1.83	0.44
25:4:5:LEU:HD13	25:4:10:SER:HB2	1.99	0.44
26:5:39:VAL:HG21	26:5:49:LEU:HD13	1.98	0.44
30:R1:153:U:H2'	30:R1:154:U:O4'	2.17	0.44
30:R1:876:C:H2'	30:R1:877:A:C8	2.52	0.44
30:R1:1447:C:O2'	30:R1:1544:A:N3	2.44	0.44
30:R1:2857:G:N2	30:R1:2860:A:OP2	2.48	0.44
32:R3:1324:A:H2'	32:R3:1325:C:C6	2.52	0.44
35:sd:98:ASP:HB2	35:sd:132:ALA:O	2.16	0.44
51:st:7:LYS:HB3	51:st:7:LYS:HE2	1.67	0.44
3:15:32:GLY:HA2	30:R1:1190:G:H5''	1.99	0.44
3:15:40:SER:O	3:15:40:SER:OG	2.33	0.44
26:5:135:ILE:HD13	26:5:145:VAL:HG11	2.00	0.44
27:6:34:ARG:HG3	27:6:35:THR:O	2.17	0.44
28:9:116:ARG:HE	28:9:133:GLN:HG3	1.80	0.44
30:R1:1910:G:N2	30:R1:1921:G:C4	2.85	0.44
32:R3:4:U:H2'	32:R3:4:U:O2	2.17	0.44
32:R3:79:G:OP1	32:R3:80:A:H8	1.99	0.44
32:R3:109:A:C6	32:R3:326:G:C6	3.06	0.44
32:R3:478:A:H2'	32:R3:479:U:O4'	2.17	0.44
33:sb:72:LYS:HB3	33:sb:72:LYS:HE2	1.60	0.44
34:sc:70:ALA:HA	34:sc:105:VAL:HB	1.98	0.44
41:sj:53:ILE:HG22	41:sj:61:ALA:O	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:sn:32:ASP:O	45:sn:40:ARG:NH1	2.50	0.44
52:su:35:GLU:CG	52:su:36:PHE:H	2.23	0.44
27:6:119:GLY:C	27:6:120:ILE:HD13	2.41	0.44
30:R1:66:C:C4	30:R1:67:U:C5	3.05	0.44
30:R1:364:C:H2'	30:R1:365:U:C6	2.52	0.44
30:R1:897:C:H41	30:R1:899:A:N6	2.16	0.44
30:R1:1469:A:H2'	30:R1:1470:A:H8	1.82	0.44
30:R1:1679:A:H2'	30:R1:1680:U:H6	1.83	0.44
30:R1:2841:C:C2	30:R1:2877:G:N2	2.84	0.44
32:R3:57:G:C6	32:R3:356:A:N1	2.84	0.44
32:R3:425:G:H2'	32:R3:426:U:H6	1.81	0.44
32:R3:1039:G:O2'	32:R3:1040:U:O4'	2.35	0.44
35:sd:34:GLU:HG2	35:sd:35:GLN:N	2.29	0.44
39:sh:85:TYR:CE1	39:sh:123:GLU:HB2	2.53	0.44
48:sq:13:SER:HB2	48:sq:21:VAL:HB	1.98	0.44
51:st:43:LYS:HZ1	51:st:85:LEU:C	2.25	0.44
2:14:1:MET:HE2	2:14:1:MET:H1	1.81	0.44
10:21:57:GLY:H	10:21:103:ALA:C	2.22	0.44
18:3:56:LYS:NZ	30:R1:2835:A:OP1	2.45	0.44
19:30:2:LYS:HE2	19:30:2:LYS:HB3	1.79	0.44
19:30:2:LYS:HG2	19:30:3:THR:H	1.81	0.44
20:31:36:VAL:HB	20:31:40:CYS:HB2	1.98	0.44
30:R1:156:A:N1	30:R1:169:G:C6	2.86	0.44
30:R1:1035:U:H2'	30:R1:1036:G:H8	1.82	0.44
30:R1:1432:G:H2'	30:R1:1433:A:C8	2.53	0.44
30:R1:2071:A:H2'	30:R1:2072:C:C6	2.52	0.44
30:R1:2818:U:H2'	30:R1:2819:G:H8	1.82	0.44
30:R1:2845:U:H2'	30:R1:2846:G:C8	2.53	0.44
31:R2:33:G:C4	31:R2:34:A:C8	3.05	0.44
32:R3:34:C:H2'	32:R3:35:G:H8	1.81	0.44
32:R3:222:C:H2'	32:R3:223:A:H8	1.82	0.44
32:R3:230:G:H2'	32:R3:231:U:O4'	2.18	0.44
32:R3:363:A:N1	43:sl:27:PRO:HD2	2.33	0.44
32:R3:634:C:H2'	32:R3:635:A:C8	2.52	0.44
32:R3:864:A:H2'	32:R3:865:A:C8	2.53	0.44
32:R3:1320:C:H42	50:ss:35:ARG:HB2	1.82	0.44
35:sd:154:VAL:O	35:sd:158:LEU:HB2	2.18	0.44
39:sh:24:VAL:HG23	39:sh:26:MET:HE1	2.00	0.44
43:sl:26:CYS:SG	43:sl:29:LYS:HD3	2.57	0.44
45:sn:87:ALA:C	45:sn:89:ARG:H	2.26	0.44
50:ss:54:ARG:HG3	50:ss:55:GLN:N	2.31	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:T:75:C:H5''	53:T:76:A:OP2	2.17	0.44
1:13:32:LEU:O	1:13:36:LEU:HG	2.18	0.44
2:14:112:PHE:HB3	2:14:115:ILE:HG21	1.99	0.44
5:17:8:ARG:NE	5:17:43:GLU:OE2	2.41	0.44
8:2:239:PHE:O	8:2:241:LYS:HG3	2.18	0.44
30:R1:275:C:O2	30:R1:363:G:N1	2.29	0.44
30:R1:283:G:H2'	30:R1:284:U:O4'	2.18	0.44
30:R1:296:U:H2'	30:R1:297:G:H8	1.82	0.44
30:R1:851:C:H2'	30:R1:852:U:H6	1.81	0.44
30:R1:2801:G:H2'	30:R1:2802:G:H8	1.83	0.44
32:R3:77:A:C2	32:R3:93:U:H2'	2.52	0.44
32:R3:296:U:O2'	32:R3:556:C:O2	2.35	0.44
32:R3:878:A:H2'	32:R3:879:C:C6	2.51	0.44
32:R3:1002:G:H21	32:R3:1039:G:H2'	1.82	0.44
37:sf:49:TYR:HE1	49:sr:65:SER:HA	1.83	0.44
37:sf:71:ILE:O	37:sf:75:GLU:HG2	2.16	0.44
1:13:136:GLN:HE21	30:R1:2899:A:H5'	1.83	0.44
6:18:93:ASP:OD1	6:18:93:ASP:C	2.61	0.44
7:19:52:ARG:HD3	7:19:52:ARG:HA	1.86	0.44
26:5:29:ARG:H	26:5:158:THR:HG22	1.83	0.44
30:R1:216:A:C8	30:R1:432:A:C6	3.05	0.44
30:R1:1511:G:H2'	30:R1:1512:C:C6	2.53	0.44
30:R1:2104:C:N4	30:R1:2185:U:H3	2.14	0.44
32:R3:664:G:H22	32:R3:741:G:H1	1.65	0.44
32:R3:848:C:H2'	32:R3:849:G:O4'	2.17	0.44
32:R3:1217:C:OP2	45:sn:8:ARG:NH2	2.51	0.44
33:sb:65:LYS:HD2	33:sb:89:PHE:CE2	2.53	0.44
37:sf:9:MET:HG2	37:sf:59:TYR:CE1	2.52	0.44
38:sg:67:ASN:O	38:sg:137:ARG:NH1	2.48	0.44
43:sl:20:VAL:HB	43:sl:94:TYR:HE1	1.83	0.44
54:33:32:LYS:HD2	54:33:50:GLU:HB3	2.00	0.44
7:19:31:VAL:HG13	7:19:38:ARG:HB3	1.99	0.44
9:20:49:ARG:HD2	30:R1:993:G:OP1	2.17	0.44
10:21:77:PHE:HD1	10:21:84:ARG:HD3	1.82	0.44
14:25:75:GLN:HB2	14:25:92:VAL:HG23	1.99	0.44
26:5:26:GLN:OE1	31:R2:57:A:O2'	2.22	0.44
30:R1:677:A:C6	30:R1:802:A:C6	3.05	0.44
30:R1:708:G:H2'	30:R1:709:U:C6	2.53	0.44
30:R1:1473:G:C6	30:R1:1519:G:C6	3.06	0.44
30:R1:1847:G:O2'	30:R1:1848:A:H8	2.01	0.44
30:R1:1954:G:O2'	30:R1:1956:U:O4	2.33	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2241:A:N6	30:R1:2242:G:O6	2.51	0.44
30:R1:2414:G:C2	30:R1:2415:G:C8	3.05	0.44
32:R3:115:G:P	32:R3:115:G:O4'	2.76	0.44
32:R3:632:U:H5''	32:R3:633:G:H8	1.83	0.44
32:R3:820:U:H4'	32:R3:821:G:OP2	2.17	0.44
32:R3:1282:C:H2'	32:R3:1283:U:C6	2.53	0.44
33:sb:130:LYS:HB3	33:sb:130:LYS:HE2	1.82	0.44
34:sc:114:LEU:HD13	34:sc:114:LEU:HA	1.85	0.44
35:sd:163:GLN:OE1	35:sd:163:GLN:N	2.50	0.44
35:sd:187:ARG:HA	35:sd:187:ARG:HH11	1.82	0.44
40:si:5:TYR:O	40:si:19:PHE:HA	2.18	0.44
40:si:29:ILE:CD1	40:si:64:ILE:HB	2.48	0.44
42:sk:126:ARG:C	52:su:33:ARG:HH12	2.15	0.44
52:su:35:GLU:H	52:su:35:GLU:CD	2.19	0.44
1:13:68:LYS:NZ	30:R1:1022:G:O6	2.43	0.44
6:18:62:LEU:HD23	6:18:62:LEU:HA	1.77	0.44
8:2:83:ASP:HB2	8:2:90:ILE:HG12	2.00	0.44
18:3:157:LYS:HB2	18:3:157:LYS:HE2	1.73	0.44
26:5:22:ASN:OD1	26:5:22:ASN:N	2.43	0.44
30:R1:156:A:H2	30:R1:169:G:C2	2.36	0.44
30:R1:278:A:N6	30:R1:361:G:C8	2.86	0.44
30:R1:640:C:H2'	30:R1:641:U:H6	1.82	0.44
30:R1:1076:C:H2'	30:R1:1077:A:O4'	2.17	0.44
30:R1:1335:C:H2'	30:R1:1336:A:C8	2.52	0.44
30:R1:1418:G:N2	30:R1:1579:A:N7	2.65	0.44
30:R1:2290:G:H2'	30:R1:2291:U:C6	2.52	0.44
30:R1:2813:A:C4	30:R1:2814:A:C8	3.06	0.44
30:R1:2897:U:H2'	30:R1:2898:U:C6	2.53	0.44
32:R3:444:G:C6	32:R3:491:G:C6	3.06	0.44
32:R3:1514:G:H2'	32:R3:1515:G:H8	1.83	0.44
37:sf:2:ARG:HD2	37:sf:91:ARG:NH1	2.33	0.44
45:sn:82:LYS:HD3	45:sn:85:GLU:HB3	1.99	0.44
11:22:69:LEU:HD23	11:22:69:LEU:HA	1.79	0.44
12:23:50:LEU:HD12	17:29:26:PHE:CZ	2.52	0.44
24:36:31:PRO:HD2	27:6:169:ARG:HH22	1.83	0.44
25:4:118:LEU:HD13	25:4:186:VAL:HG23	1.98	0.44
26:5:25:MET:HB2	26:5:29:ARG:HH12	1.83	0.44
26:5:29:ARG:H	26:5:158:THR:CG2	2.31	0.44
30:R1:880:G:H2'	30:R1:881:G:H8	1.83	0.44
30:R1:886:A:H3'	30:R1:886:A:N3	2.33	0.44
30:R1:1056:G:H4'	30:R1:1057:A:O4'	2.18	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:R2:78:A:H62	31:R2:98:G:H21	1.64	0.44
32:R3:359:G:C4	32:R3:360:G:C8	3.06	0.44
32:R3:453:G:C4	32:R3:454:G:C8	3.06	0.44
32:R3:529:G:H5''	32:R3:530:G:OP2	2.18	0.44
32:R3:981:U:H4'	45:sn:60:ARG:HH12	1.82	0.44
32:R3:1027:C:O2	32:R3:1034:G:N2	2.23	0.44
32:R3:1187:G:H2'	32:R3:1188:A:C8	2.53	0.44
38:sg:98:LEU:HD12	38:sg:98:LEU:HA	1.81	0.44
40:si:17:ARG:O	40:si:64:ILE:HA	2.18	0.44
42:sk:120:CYS:SG	42:sk:121:ARG:N	2.91	0.44
44:sm:48:SER:O	44:sm:52:ILE:HG13	2.17	0.44
46:so:69:LEU:HD23	46:so:69:LEU:HA	1.80	0.44
2:14:109:SER:C	2:14:111:LYS:H	2.26	0.43
3:15:79:LEU:HD23	3:15:79:LEU:HA	1.86	0.43
14:25:40:ILE:HD11	14:25:63:ILE:HG21	1.99	0.43
14:25:80:HIS:ND1	14:25:81:PRO:HD2	2.33	0.43
30:R1:138:U:O2'	30:R1:139:U:H5'	2.18	0.43
30:R1:168:G:H2'	30:R1:169:G:H8	1.82	0.43
30:R1:2515:C:H2'	30:R1:2516:A:H8	1.82	0.43
30:R1:2861:U:H2'	30:R1:2862:G:H8	1.82	0.43
32:R3:161:A:C6	32:R3:162:A:C6	3.06	0.43
32:R3:413:G:N7	35:sd:30:LYS:HE2	2.34	0.43
32:R3:502:A:N6	32:R3:544:G:O6	2.50	0.43
32:R3:544:G:H2'	32:R3:545:C:C6	2.53	0.43
32:R3:636:U:H2'	32:R3:637:C:C6	2.52	0.43
32:R3:676:A:H2'	32:R3:677:U:H6	1.82	0.43
32:R3:958:A:O2'	32:R3:959:A:O5'	2.25	0.43
32:R3:1378:C:H1'	38:sg:91:ARG:HH22	1.82	0.43
32:R3:1465:A:H2'	32:R3:1466:C:C6	2.53	0.43
35:sd:94:GLU:CD	35:sd:99:ASN:HD21	2.24	0.43
35:sd:151:GLN:C	35:sd:153:ARG:H	2.25	0.43
40:si:5:TYR:HD1	40:si:87:MET:HE2	1.83	0.43
8:2:238:ASN:ND2	30:R1:2595:G:O6	2.51	0.43
9:20:93:ILE:HD13	9:20:93:ILE:HA	1.89	0.43
12:23:92:ASN:O	12:23:93:LEU:HD23	2.18	0.43
18:3:46:ARG:NH2	18:3:88:GLU:O	2.30	0.43
20:31:16:CYS:SG	20:31:17:SER:N	2.90	0.43
28:9:122:LEU:HB3	28:9:128:HIS:CE1	2.53	0.43
30:R1:309:A:N3	30:R1:329:G:O2'	2.49	0.43
30:R1:1208:C:C2	30:R1:1239:G:N2	2.87	0.43
30:R1:1416:G:H2'	30:R1:1417:C:H6	1.82	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2118:U:O2'	30:R1:2119:A:H5''	2.18	0.43
30:R1:2302:U:C2	30:R1:2303:G:C8	3.07	0.43
30:R1:2540:C:O2'	30:R1:2740:A:N3	2.42	0.43
31:R2:53:A:H2'	31:R2:54:G:O4'	2.18	0.43
32:R3:953:G:C6	32:R3:1229:A:C6	3.05	0.43
32:R3:1133:G:H22	32:R3:1143:G:H1'	1.83	0.43
33:sb:164:ASP:CG	33:sb:167:HIS:HB3	2.43	0.43
34:sc:36:PHE:C	34:sc:36:PHE:CD2	2.94	0.43
36:se:14:LEU:HD13	36:se:36:THR:HG22	1.99	0.43
39:sh:4:ASP:HB2	39:sh:80:PRO:HG3	2.01	0.43
48:sq:57:VAL:O	48:sq:78:VAL:HG22	2.19	0.43
9:20:113:LYS:HE3	9:20:113:LYS:HB2	1.75	0.43
18:3:25:THR:HG21	18:3:193:VAL:HG22	2.00	0.43
26:5:134:GLN:HG2	26:5:135:ILE:N	2.33	0.43
30:R1:30:G:H2'	30:R1:31:C:C6	2.53	0.43
30:R1:581:C:H2'	30:R1:582:A:H8	1.83	0.43
30:R1:2349:G:O6	30:R1:2369:A:N6	2.50	0.43
30:R1:2666:C:H2'	30:R1:2667:C:O4'	2.17	0.43
32:R3:279:A:H5'	32:R3:281:G:O4'	2.18	0.43
32:R3:553:A:H2'	32:R3:554:A:C8	2.52	0.43
32:R3:778:G:H2'	32:R3:779:C:H6	1.83	0.43
52:su:16:ARG:O	52:su:16:ARG:NE	2.43	0.43
6:18:30:ARG:HH22	31:R2:48:U:P	2.42	0.43
6:18:34:HIS:ND1	6:18:53:THR:OG1	2.50	0.43
6:18:43:ASN:OD1	6:18:43:ASN:N	2.39	0.43
7:19:26:GLU:OE2	7:19:43:GLU:HG3	2.18	0.43
12:23:64:LYS:HA	12:23:79:ASP:HB3	2.00	0.43
26:5:47:LYS:HE3	26:5:47:LYS:HB3	1.69	0.43
27:6:36:LEU:HD12	27:6:36:LEU:HA	1.81	0.43
30:R1:520:G:H2'	30:R1:521:U:H6	1.82	0.43
30:R1:1385:A:O2'	30:R1:1396:U:O2	2.31	0.43
30:R1:1505:A:H2'	30:R1:1506:U:C6	2.53	0.43
30:R1:2547:A:H2'	30:R1:2548:U:C6	2.54	0.43
31:R2:5:U:OP1	31:R2:61:G:O2'	2.31	0.43
32:R3:17:U:H2'	32:R3:18:C:C6	2.53	0.43
32:R3:68:G:N7	32:R3:69:G:C8	2.87	0.43
32:R3:425:G:H2'	32:R3:426:U:C6	2.53	0.43
32:R3:1355:G:H2'	32:R3:1356:G:C8	2.53	0.43
35:sd:10:LEU:HD13	35:sd:62:ARG:HD2	2.01	0.43
36:se:146:MET:HE2	36:se:146:MET:HB3	1.84	0.43
8:2:126:GLY:N	8:2:191:LEU:O	2.40	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:35:32:LEU:HD13	30:R1:2419:U:OP2	2.17	0.43
30:R1:285:G:C6	30:R1:356:G:C5	3.06	0.43
30:R1:947:A:C6	30:R1:971:G:C6	3.06	0.43
30:R1:1091:G:H2'	30:R1:1092:C:H6	1.80	0.43
30:R1:2186:G:H2'	30:R1:2187:U:C6	2.52	0.43
30:R1:2718:G:H2'	30:R1:2719:G:O4'	2.18	0.43
32:R3:301:G:O2'	32:R3:302:G:OP1	2.31	0.43
32:R3:354:G:N7	32:R3:355:C:C4	2.87	0.43
32:R3:562:U:H5	43:sl:14:LYS:HE2	1.82	0.43
33:sb:13:VAL:HB	33:sb:207:ARG:HD2	1.99	0.43
34:sc:8:GLY:HA2	45:sn:88:MET:O	2.19	0.43
35:sd:27:ILE:CG1	35:sd:28:ASP:H	2.24	0.43
35:sd:144:ILE:HD11	35:sd:177:MET:HG3	2.00	0.43
35:sd:177:MET:HE2	35:sd:177:MET:HB3	1.94	0.43
51:st:2:ASN:ND2	51:st:3:ILE:HG23	2.33	0.43
51:st:30:PHE:O	51:st:34:VAL:HG23	2.17	0.43
54:33:41:VAL:HG12	54:33:42:VAL:HG13	2.01	0.43
2:14:9:ASN:OD1	2:14:18:ARG:NH1	2.51	0.43
2:14:10:VAL:HG11	2:14:16:ALA:O	2.19	0.43
3:15:36:LYS:NZ	30:R1:567:U:O3'	2.38	0.43
3:15:141:LYS:HB3	3:15:141:LYS:HE2	1.57	0.43
5:17:55:ALA:HA	5:17:80:PHE:CE2	2.53	0.43
12:23:18:GLU:O	12:23:22:THR:HG23	2.17	0.43
13:24:85:ARG:HH12	13:24:101:THR:HB	1.84	0.43
15:27:75:LYS:HE2	15:27:75:LYS:HB2	1.77	0.43
18:3:11:MET:HE2	30:R1:2682:A:C8	2.53	0.43
19:30:18:LYS:HB3	19:30:18:LYS:HE2	1.76	0.43
23:35:63:TYR:HH	30:R1:592:A:HO2'	1.65	0.43
26:5:36:ASN:OD1	26:5:36:ASN:C	2.62	0.43
27:6:136:ASP:C	27:6:136:ASP:OD1	2.60	0.43
30:R1:1529:G:C4	30:R1:1530:G:C8	3.07	0.43
32:R3:312:C:H2'	32:R3:313:A:H8	1.84	0.43
32:R3:360:G:H2'	32:R3:361:G:C8	2.53	0.43
32:R3:369:G:HO2'	32:R3:370:C:H6	1.66	0.43
32:R3:497:G:H4'	32:R3:498:A:OP1	2.18	0.43
32:R3:550:G:H2'	32:R3:551:U:C6	2.52	0.43
32:R3:709:U:H2'	32:R3:710:G:H8	1.84	0.43
32:R3:1102:A:C6	32:R3:1103:C:N4	2.86	0.43
32:R3:1496:C:C4	32:R3:1497:G:N7	2.87	0.43
34:sc:171:ARG:HD2	34:sc:173:PRO:HD3	2.00	0.43
38:sg:71:THR:O	38:sg:90:VAL:HG12	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:si:29:ILE:HD13	40:si:29:ILE:HA	1.85	0.43
45:sn:65:GLN:HG2	45:sn:82:LYS:HG2	2.01	0.43
50:ss:13:HIS:O	50:ss:17:LYS:HG3	2.19	0.43
14:25:65:VAL:O	14:25:68:LYS:HG2	2.18	0.43
15:27:41:ARG:NH2	30:R1:2387:U:H4'	2.34	0.43
26:5:51:ASN:OD1	26:5:51:ASN:N	2.51	0.43
30:R1:118:A:C8	30:R1:119:A:C8	3.06	0.43
30:R1:217:A:C4	30:R1:218:A:C8	3.07	0.43
30:R1:285:G:N7	30:R1:356:G:N1	2.66	0.43
30:R1:329:G:C2	30:R1:477:A:C2	3.07	0.43
30:R1:634:C:H2'	30:R1:635:C:C6	2.54	0.43
30:R1:1108:U:H2'	30:R1:1109:C:N3	2.33	0.43
30:R1:2154:A:C8	30:R1:2155:U:H5	2.37	0.43
30:R1:2750:A:O2'	30:R1:2752:C:N4	2.42	0.43
30:R1:2861:U:H2'	30:R1:2862:G:C8	2.54	0.43
32:R3:593:U:H2'	32:R3:594:U:H6	1.83	0.43
32:R3:704:A:C4	32:R3:705:G:C8	3.07	0.43
32:R3:1002:G:N3	32:R3:1040:U:N3	2.67	0.43
32:R3:1015:G:H2'	32:R3:1016:A:C8	2.54	0.43
32:R3:1103:C:O2'	32:R3:1104:G:H8	2.02	0.43
32:R3:1163:A:H2'	32:R3:1164:G:H8	1.82	0.43
32:R3:1251:A:H2'	32:R3:1252:A:C8	2.54	0.43
32:R3:1368:A:OP2	40:si:113:LYS:HB3	2.19	0.43
33:sb:15:PHE:HE1	33:sb:42:LEU:HD11	1.83	0.43
33:sb:118:THR:HA	33:sb:121:GLN:HB3	2.00	0.43
33:sb:165:ALA:HB3	33:sb:190:SER:OG	2.19	0.43
38:sg:24:LYS:HB3	38:sg:100:MET:HE1	2.01	0.43
40:si:79:ARG:NH2	40:si:102:PHE:HD1	2.16	0.43
40:si:113:LYS:O	40:si:113:LYS:HD3	2.19	0.43
41:sj:39:PRO:O	41:sj:40:ILE:HD13	2.18	0.43
44:sm:18:LEU:O	44:sm:21:ILE:HG13	2.18	0.43
1:13:96:ARG:HH21	30:R1:2640:G:P	2.39	0.43
12:23:35:ALA:C	12:23:37:ASP:H	2.27	0.43
26:5:3:LEU:CD1	26:5:100:GLU:HB2	2.43	0.43
30:R1:776:G:N2	30:R1:2241:A:OP1	2.45	0.43
30:R1:838:C:C2	30:R1:941:A:C6	3.07	0.43
30:R1:1198:U:H2'	30:R1:1199:U:C6	2.54	0.43
30:R1:1550:C:OP1	30:R1:1720:U:O2'	2.33	0.43
30:R1:2233:U:H2'	30:R1:2234:G:H8	1.82	0.43
31:R2:33:G:C2	31:R2:50:A:C2	3.07	0.43
32:R3:373:A:C2	32:R3:374:A:C8	3.07	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:459:A:N7	32:R3:460:A:N6	2.66	0.43
42:sk:126:ARG:HD2	42:sk:126:ARG:HA	1.70	0.43
6:18:31:THR:HG21	31:R2:28:C:OP1	2.19	0.43
17:29:2:LYS:HE2	30:R1:77:G:H5'	2.01	0.43
26:5:132:ARG:CZ	30:R1:2305:U:H1'	2.47	0.43
30:R1:319:G:H1	30:R1:323:C:H41	1.66	0.43
30:R1:1493:C:H5'	30:R1:1494:A:OP2	2.19	0.43
30:R1:1796:U:H2'	30:R1:1797:G:H8	1.83	0.43
30:R1:2027:G:H2'	30:R1:2028:U:C6	2.53	0.43
30:R1:2513:A:C2	30:R1:2574:G:C2	3.07	0.43
30:R1:2651:C:H2'	30:R1:2652:C:C6	2.54	0.43
30:R1:2660:A:H2'	30:R1:2661:G:C8	2.54	0.43
31:R2:7:G:H22	31:R2:113:C:H5	1.67	0.43
32:R3:131:A:H2'	32:R3:132:C:C6	2.53	0.43
32:R3:505:G:H2'	32:R3:506:G:C8	2.54	0.43
32:R3:1130:A:O2'	32:R3:1131:G:O5'	2.37	0.43
32:R3:1235:U:H2'	32:R3:1236:A:O4'	2.19	0.43
33:sb:17:HIS:HE2	33:sb:39:ILE:HG12	1.83	0.43
39:sh:76:ARG:NH1	39:sh:78:SER:O	2.52	0.43
44:sm:70:ARG:O	44:sm:74:MET:HB2	2.19	0.43
53:T:66:C:H2'	53:T:67:C:C6	2.53	0.43
1:13:13:ARG:HD3	1:13:51:GLY:O	2.19	0.43
4:16:12:MET:HE3	4:16:12:MET:HB2	1.93	0.43
10:21:21:ARG:HE	10:21:21:ARG:HB2	1.62	0.43
15:27:32:LEU:HD23	15:27:64:ASP:HB3	2.00	0.43
21:32:30:ASP:OD1	21:32:31:LYS:N	2.51	0.43
30:R1:141:G:H2'	30:R1:142:A:O4'	2.18	0.43
30:R1:1720:U:H2'	30:R1:1721:G:O4'	2.18	0.43
30:R1:1864:U:OP1	30:R1:2410:G:O2'	2.36	0.43
30:R1:2230:G:H2'	30:R1:2231:U:H6	1.84	0.43
32:R3:79:G:H3'	32:R3:79:G:OP2	2.19	0.43
32:R3:260:G:H2'	32:R3:261:U:C6	2.53	0.43
32:R3:728:A:H2'	32:R3:729:A:C8	2.54	0.43
32:R3:736:C:O2'	37:sf:89:VAL:O	2.29	0.43
32:R3:784:A:N6	32:R3:799:G:C6	2.87	0.43
32:R3:1241:G:H2'	32:R3:1242:G:H8	1.83	0.43
36:se:37:VAL:HG12	36:se:47:PHE:HB3	2.01	0.43
37:sf:93:LYS:HE2	37:sf:93:LYS:HA	2.00	0.43
7:19:1:SER:HA	7:19:4:ILE:HB	2.01	0.42
8:2:74:PRO:HB2	8:2:96:LYS:HE2	2.00	0.42
9:20:48:ASP:OD2	30:R1:559:G:N2	2.51	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:22:88:ARG:HD2	11:22:88:ARG:HA	1.79	0.42
16:28:51:SER:OG	16:28:52:ALA:N	2.52	0.42
18:3:25:THR:HG21	18:3:193:VAL:CG2	2.49	0.42
30:R1:156:A:H2	30:R1:169:G:N2	2.17	0.42
30:R1:1295:C:C2	30:R1:1296:G:C8	3.08	0.42
30:R1:1853:A:H2'	30:R1:1854:A:H8	1.82	0.42
30:R1:2154:A:H2'	30:R1:2155:U:C6	2.50	0.42
32:R3:555:U:H2'	32:R3:556:C:H6	1.84	0.42
32:R3:1437:A:H2'	32:R3:1438:G:H8	1.84	0.42
33:sb:65:LYS:HD2	33:sb:89:PHE:CZ	2.53	0.42
34:sc:146:LYS:HB2	34:sc:202:PHE:CD2	2.54	0.42
13:24:73:ASN:C	13:24:75:ALA:H	2.25	0.42
20:31:56:ARG:HG2	20:31:59:ARG:NE	2.29	0.42
30:R1:152:A:N1	30:R1:173:A:N1	2.67	0.42
30:R1:297:G:H2'	30:R1:298:G:O4'	2.19	0.42
30:R1:359:G:C5	30:R1:360:U:C4	3.07	0.42
30:R1:1310:G:N2	30:R1:1313:U:C4	2.87	0.42
30:R1:1416:G:H2'	30:R1:1417:C:C6	2.54	0.42
30:R1:2591:C:C2	30:R1:2592:G:N7	2.87	0.42
33:sb:202:ASN:OD1	33:sb:203:ASP:N	2.52	0.42
35:sd:14:GLU:OE1	35:sd:14:GLU:N	2.53	0.42
37:sf:4:TYR:HE2	37:sf:91:ARG:HD3	1.83	0.42
53:T:62:C:H2'	53:T:63:G:H8	1.84	0.42
5:17:1:MET:HG2	5:17:3:HIS:CD2	2.54	0.42
8:2:65:ASP:C	8:2:65:ASP:OD1	2.62	0.42
20:31:12:ILE:HD11	20:31:31:ASP:HA	2.01	0.42
20:31:38:SER:OG	26:5:104:THR:HA	2.20	0.42
30:R1:1046:A:H5'	30:R1:1047:G:H5''	2.01	0.42
30:R1:1296:G:OP1	30:R1:2709:G:O2'	2.34	0.42
30:R1:1383:A:C2	30:R1:1406:U:H1'	2.54	0.42
30:R1:2494:G:C2	30:R1:2495:G:C8	3.07	0.42
32:R3:735:C:H2'	32:R3:736:C:H6	1.84	0.42
32:R3:917:G:H2'	32:R3:918:A:C8	2.54	0.42
32:R3:1149:C:H4'	32:R3:1150:A:OP1	2.19	0.42
32:R3:1349:A:OP2	40:si:119:LYS:NZ	2.51	0.42
33:sb:8:MET:HG2	33:sb:10:LYS:HE3	2.02	0.42
33:sb:63:LYS:HG3	33:sb:224:ARG:HD2	2.01	0.42
33:sb:203:ASP:N	33:sb:203:ASP:OD1	2.50	0.42
35:sd:25:ARG:NH1	35:sd:29:THR:OG1	2.51	0.42
36:se:159:SER:OG	36:se:162:GLU:OE2	2.36	0.42
44:sm:22:TYR:HB3	44:sm:65:GLU:HG2	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:13:65:THR:OG1	1:13:66:GLY:N	2.53	0.42
3:15:132:ARG:O	3:15:136:GLU:HG3	2.19	0.42
6:18:50:ALA:O	6:18:81:ARG:NH1	2.52	0.42
21:32:52:LYS:HB2	21:32:52:LYS:HE2	1.81	0.42
25:4:131:THR:HG23	30:R1:321:U:OP2	2.19	0.42
26:5:33:ILE:CG2	26:5:90:LEU:HB2	2.49	0.42
26:5:35:LEU:HD13	26:5:151:LEU:HD13	2.01	0.42
30:R1:532:A:N1	30:R1:2020:A:H1'	2.34	0.42
30:R1:1275:A:N1	30:R1:1295:C:O2'	2.47	0.42
30:R1:1797:G:C6	30:R1:1823:G:C6	3.08	0.42
30:R1:2262:U:H2'	30:R1:2263:C:H6	1.84	0.42
31:R2:45:A:C4	31:R2:46:A:C8	3.07	0.42
32:R3:209:U:H5	32:R3:211:G:C8	2.38	0.42
32:R3:636:U:H2'	32:R3:637:C:H6	1.83	0.42
35:sd:149:LYS:C	35:sd:150:LYS:HG2	2.44	0.42
2:14:73:ASP:OD2	2:14:75:SER:OG	2.29	0.42
8:2:153:LEU:HD13	8:2:175:LEU:HD21	2.00	0.42
8:2:199:HIS:HB3	30:R1:1820:U:O2	2.19	0.42
20:31:12:ILE:HD12	20:31:12:ILE:HA	1.87	0.42
22:34:46:LYS:HB3	22:34:46:LYS:HE3	1.84	0.42
24:36:34:LYS:NZ	30:R1:2743:U:OP1	2.51	0.42
27:6:3:VAL:HG21	30:R1:2748:A:H4'	2.02	0.42
27:6:120:ILE:HD11	27:6:139:VAL:HG13	2.02	0.42
30:R1:543:G:C6	30:R1:551:G:C6	3.07	0.42
30:R1:1110:G:O2'	30:R1:1111:A:O4'	2.30	0.42
30:R1:1178:C:H2'	30:R1:1179:G:H4'	2.00	0.42
30:R1:1587:G:H2'	30:R1:1588:G:H8	1.83	0.42
30:R1:2148:G:H2'	30:R1:2149:U:C6	2.55	0.42
30:R1:2641:G:O6	30:R1:2774:C:N4	2.52	0.42
32:R3:235:C:H2'	32:R3:236:A:C8	2.55	0.42
32:R3:980:C:O2'	45:sn:12:ARG:NH2	2.52	0.42
32:R3:1423:G:H2'	32:R3:1424:U:C6	2.55	0.42
32:R3:1423:G:H2'	32:R3:1424:U:H6	1.84	0.42
33:sb:104:LYS:H	33:sb:104:LYS:HG3	1.69	0.42
35:sd:46:ARG:HA	35:sd:46:ARG:HE	1.85	0.42
35:sd:104:MET:SD	35:sd:170:LEU:HD22	2.58	0.42
3:15:4:ASN:O	3:15:4:ASN:ND2	2.52	0.42
17:29:7:ARG:HB2	17:29:7:ARG:HH11	1.84	0.42
28:9:96:THR:O	28:9:112:LYS:HD3	2.19	0.42
30:R1:395:U:H2'	30:R1:396:G:N7	2.35	0.42
30:R1:960:A:C8	30:R1:962:G:C8	3.08	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:1100:C:H2'	30:R1:1101:U:C6	2.55	0.42
30:R1:1197:G:H2'	30:R1:1198:U:H6	1.84	0.42
30:R1:1374:G:H2'	30:R1:1375:U:O4'	2.19	0.42
30:R1:1495:A:H2'	30:R1:1496:A:C8	2.54	0.42
30:R1:2159:G:O2'	30:R1:2160:C:O4'	2.33	0.42
32:R3:118:U:O4	32:R3:289:G:H4'	2.19	0.42
32:R3:504:C:C2	32:R3:542:G:N2	2.88	0.42
32:R3:1160:G:C2	32:R3:1161:C:C6	3.07	0.42
34:sc:36:PHE:CE1	45:sn:65:GLN:NE2	2.87	0.42
37:sf:2:ARG:H	37:sf:2:ARG:HG2	1.68	0.42
2:14:107:LEU:HB2	2:14:116:ILE:HD11	2.02	0.42
3:15:30:THR:HG23	30:R1:810:U:C4	2.55	0.42
3:15:91:ASP:N	3:15:94:THR:OG1	2.43	0.42
3:15:109:LYS:HG3	3:15:126:ARG:O	2.19	0.42
8:2:34:GLU:CD	8:2:63:ILE:HD11	2.44	0.42
26:5:70:ARG:HH12	26:5:71:LYS:HB2	1.85	0.42
30:R1:135:U:H2'	30:R1:136:G:C8	2.54	0.42
30:R1:974:G:O2'	30:R1:989:G:N2	2.49	0.42
30:R1:1047:G:H22	30:R1:1110:G:H5''	1.84	0.42
30:R1:1071:G:H4'	30:R1:1088:A:O2'	2.19	0.42
30:R1:1319:C:O2'	30:R1:1320:C:H5'	2.19	0.42
30:R1:1549:A:H2'	30:R1:1550:C:C6	2.55	0.42
30:R1:2349:G:C6	30:R1:2369:A:C6	3.07	0.42
30:R1:2497:A:OP2	30:R1:2497:A:H8	2.03	0.42
30:R1:2591:C:H2'	30:R1:2592:G:C8	2.54	0.42
30:R1:2869:G:H2'	30:R1:2870:C:O4'	2.20	0.42
32:R3:526:C:OP2	43:sl:87:LYS:NZ	2.51	0.42
32:R3:1245:C:H2'	32:R3:1246:A:C8	2.55	0.42
40:si:5:TYR:CZ	40:si:88:GLU:HB3	2.54	0.42
41:sj:15:HIS:O	41:sj:18:ILE:HG22	2.20	0.42
51:st:56:ILE:O	51:st:60:GLN:HG2	2.20	0.42
52:su:61:ARG:O	52:su:61:ARG:HG2	2.20	0.42
54:33:34:GLU:C	54:33:35:LEU:HD22	2.45	0.42
8:2:140:VAL:HG23	8:2:191:LEU:HA	2.02	0.42
17:29:30:MET:HE3	17:29:30:MET:HB3	1.83	0.42
22:34:34:ARG:NH2	22:34:42:LEU:O	2.45	0.42
30:R1:564:C:H2'	30:R1:565:C:C6	2.55	0.42
30:R1:879:G:H2'	30:R1:880:G:O4'	2.19	0.42
30:R1:1059:G:H21	30:R1:1079:C:H2'	1.84	0.42
30:R1:1425:G:O5'	30:R1:1425:G:H8	2.03	0.42
30:R1:1755:A:N6	30:R1:2694:G:O2'	2.52	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2100:G:N2	30:R1:2191:A:C8	2.88	0.42
30:R1:2249:U:O2'	30:R1:2250:G:H5'	2.20	0.42
30:R1:2898:U:H2'	30:R1:2899:A:H8	1.84	0.42
32:R3:745:G:C2	32:R3:746:A:C5	3.07	0.42
32:R3:773:G:C6	32:R3:807:A:C6	3.08	0.42
32:R3:948:C:H2'	32:R3:949:A:H8	1.85	0.42
32:R3:1102:A:C2'	32:R3:1103:C:H5'	2.49	0.42
32:R3:1118:U:H2'	32:R3:1119:C:H6	1.85	0.42
33:sb:47:PRO:O	33:sb:51:GLU:HG3	2.19	0.42
35:sd:81:LEU:HD12	35:sd:81:LEU:HA	1.88	0.42
36:se:158:LYS:HD2	36:se:158:LYS:N	2.35	0.42
47:sp:16:PHE:CD2	47:sp:40:ASN:HB3	2.55	0.42
3:15:77:ILE:O	3:15:110:VAL:HA	2.19	0.42
13:24:4:ILE:HD13	13:24:4:ILE:HA	1.87	0.42
27:6:84:LYS:HA	27:6:84:LYS:HD2	1.87	0.42
30:R1:133:U:H2'	30:R1:134:G:O4'	2.20	0.42
30:R1:320:A:H4'	30:R1:322:A:N7	2.35	0.42
30:R1:948:C:O2	30:R1:984:A:O2'	2.23	0.42
30:R1:1223:G:C6	30:R1:1227:G:C6	3.08	0.42
30:R1:1288:G:OP1	30:R1:1289:C:N4	2.49	0.42
30:R1:2838:G:C4	30:R1:2839:G:C8	3.08	0.42
30:R1:2900:A:H8	30:R1:2900:A:OP2	2.03	0.42
32:R3:399:G:H2'	32:R3:400:C:C6	2.55	0.42
32:R3:424:G:N1	32:R3:425:G:C6	2.88	0.42
32:R3:863:U:O2'	32:R3:864:A:O5'	2.36	0.42
32:R3:990:C:H41	32:R3:1215:G:H1	1.67	0.42
32:R3:1312:G:H5'	50:ss:5:LYS:CE	2.50	0.42
32:R3:1413:A:H2	32:R3:1487:G:H22	1.66	0.42
32:R3:1430:A:C2	32:R3:1471:U:C2	3.07	0.42
32:R3:1464:U:H2'	32:R3:1465:A:H8	1.83	0.42
36:se:106:ALA:HB2	36:se:124:ALA:HB3	2.02	0.42
41:sj:86:ALA:C	41:sj:87:LEU:HD12	2.45	0.42
42:sk:22:ILE:H	42:sk:22:ILE:HG12	1.71	0.42
45:sn:30:ILE:HG21	45:sn:40:ARG:HA	2.02	0.42
52:su:11:PHE:C	52:su:13:VAL:H	2.28	0.42
17:29:13:GLU:HA	17:29:16:THR:HG22	2.02	0.42
18:3:133:THR:CG2	18:3:134:HIS:H	2.32	0.42
25:4:127:GLU:H	25:4:127:GLU:CD	2.25	0.42
27:6:36:LEU:HG	27:6:40:VAL:HG11	2.01	0.42
30:R1:142:A:H2'	30:R1:143:C:H5''	2.02	0.42
30:R1:859:G:H4'	30:R1:860:U:O5'	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2105:U:HO2'	30:R1:2106:U:P	2.40	0.42
30:R1:2429:G:H5''	30:R1:2430:A:OP2	2.20	0.42
30:R1:2530:A:OP2	30:R1:2535:G:N2	2.53	0.42
30:R1:2663:G:O2'	30:R1:2664:G:OP1	2.38	0.42
32:R3:160:A:H2'	32:R3:161:A:H8	1.83	0.42
32:R3:763:G:H2'	32:R3:764:C:C6	2.54	0.42
32:R3:851:G:C2	32:R3:852:G:C8	3.08	0.42
32:R3:1074:G:O4'	33:sb:102:ASN:ND2	2.53	0.42
34:sc:63:ILE:HG22	34:sc:98:ALA:HA	2.00	0.42
36:se:93:VAL:HG23	36:se:126:ALA:HB2	2.02	0.42
40:si:79:ARG:HG2	40:si:79:ARG:NH1	2.32	0.42
51:st:60:GLN:HG2	51:st:60:GLN:H	1.68	0.42
4:16:111:GLU:HA	4:16:111:GLU:OE2	2.20	0.41
10:21:37:GLU:HG2	10:21:53:PHE:CE2	2.54	0.41
10:21:71:LYS:HE3	10:21:71:LYS:HB2	1.82	0.41
13:24:17:ASP:HB3	13:24:20:LYS:HD3	2.02	0.41
18:3:83:ARG:NH1	30:R1:2637:U:H5''	2.35	0.41
18:3:124:ARG:NH1	18:3:161:MET:O	2.52	0.41
24:36:36:ARG:HG2	24:36:37:GLN:N	2.35	0.41
30:R1:668:A:H2'	30:R1:670:A:H62	1.85	0.41
30:R1:912:C:O2'	30:R1:913:U:H5'	2.20	0.41
30:R1:1186:G:H8	30:R1:1186:G:O5'	2.03	0.41
30:R1:1619:G:C2	30:R1:1620:G:C8	3.08	0.41
30:R1:2067:G:O2'	30:R1:2069:G:H5''	2.21	0.41
30:R1:2679:A:H2'	30:R1:2680:U:H6	1.83	0.41
32:R3:502:A:H2'	32:R3:503:C:C6	2.55	0.41
32:R3:705:G:C4	32:R3:706:A:C8	3.08	0.41
32:R3:735:C:C2	32:R3:736:C:C5	3.08	0.41
32:R3:1034:G:C2	32:R3:1035:A:C5	3.07	0.41
32:R3:1250:A:H2'	32:R3:1251:A:H8	1.84	0.41
32:R3:1270:G:HO2'	32:R3:1271:A:P	2.42	0.41
32:R3:1527:U:H2'	32:R3:1528:U:C6	2.55	0.41
34:sc:22:PHE:C	34:sc:22:PHE:CD2	2.98	0.41
44:sm:69:ARG:H	44:sm:69:ARG:HG2	1.47	0.41
50:ss:31:ARG:HD2	50:ss:56:HIS:CD2	2.54	0.41
50:ss:49:ALA:HA	50:ss:57:VAL:O	2.20	0.41
52:su:61:ARG:O	52:su:63:ASN:N	2.50	0.41
5:17:35:LYS:HB2	5:17:112:TYR:CE2	2.55	0.41
6:18:18:LEU:HD23	6:18:18:LEU:HA	1.91	0.41
13:24:46:LYS:HG2	13:24:47:PRO:HD2	2.02	0.41
30:R1:170:U:H2'	30:R1:171:U:C6	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:839:U:H2'	30:R1:840:C:C6	2.55	0.41
30:R1:949:G:C2	30:R1:969:G:C2	3.07	0.41
30:R1:2033:A:O2'	30:R1:2035:G:OP2	2.34	0.41
30:R1:2601:C:N4	30:R1:2603:G:O6	2.53	0.41
32:R3:513:C:H2'	32:R3:514:C:H6	1.85	0.41
32:R3:602:A:H2'	32:R3:603:U:H6	1.85	0.41
32:R3:678:U:H2'	32:R3:679:C:C6	2.54	0.41
32:R3:780:A:H5''	42:sk:124:LYS:HE3	2.03	0.41
32:R3:837:U:O2	32:R3:849:G:O6	2.38	0.41
32:R3:932:C:OP1	38:sg:3:ARG:HG3	2.20	0.41
32:R3:1094:G:O2'	32:R3:1095:U:OP1	2.37	0.41
37:sf:53:LYS:C	37:sf:54:LEU:HD12	2.45	0.41
40:si:50:PRO:HG2	40:si:82:ILE:HD13	2.02	0.41
41:sj:35:GLN:HB3	41:sj:78:GLU:OE1	2.20	0.41
50:ss:11:ASP:OD1	50:ss:11:ASP:N	2.52	0.41
3:15:78:ARG:NH2	30:R1:626:A:N3	2.64	0.41
13:24:39:ASN:O	13:24:61:GLU:HA	2.19	0.41
16:28:22:ASN:OD1	16:28:22:ASN:N	2.53	0.41
23:35:53:ASP:O	23:35:57:VAL:HG23	2.21	0.41
25:4:165:HIS:ND1	30:R1:1205:A:C4	2.88	0.41
26:5:139:GLU:OE1	26:5:139:GLU:N	2.52	0.41
27:6:138:GLN:NE2	30:R1:2759:G:N2	2.69	0.41
30:R1:396:G:C6	30:R1:397:U:C4	3.07	0.41
30:R1:1016:G:O6	30:R1:1147:A:N6	2.53	0.41
30:R1:1534:U:O2'	30:R1:1537:G:O6	2.34	0.41
30:R1:2090:A:N6	30:R1:2230:G:O6	2.52	0.41
32:R3:958:A:N3	50:ss:54:ARG:NH2	2.69	0.41
33:sb:14:HIS:HD1	33:sb:14:HIS:C	2.28	0.41
36:se:105:ILE:HD11	36:se:123:LEU:HD13	2.00	0.41
41:sj:59:LYS:O	41:sj:62:ARG:HD3	2.20	0.41
52:su:3:ILE:HB	52:su:4:LYS:H	1.72	0.41
10:21:69:GLY:O	10:21:90:ARG:NH1	2.53	0.41
27:6:109:SER:HB3	30:R1:2667:C:N3	2.36	0.41
30:R1:412:A:H2'	30:R1:412:A:N3	2.34	0.41
30:R1:1062:G:P	30:R1:1062:G:H8	2.43	0.41
30:R1:1356:G:C6	30:R1:1357:C:C4	3.08	0.41
30:R1:2108:A:C2	30:R1:2109:U:H1'	2.56	0.41
30:R1:2329:U:H2'	30:R1:2330:G:C8	2.55	0.41
30:R1:2487:G:H2'	30:R1:2488:G:C8	2.50	0.41
30:R1:2522:U:O2'	30:R1:2647:U:OP1	2.23	0.41
32:R3:106:C:H2'	32:R3:107:G:O4'	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R3:438:U:H3'	32:R3:439:U:C5'	2.50	0.41
32:R3:570:G:H2'	32:R3:571:U:C6	2.56	0.41
32:R3:1130:A:C5	32:R3:1146:A:C6	3.09	0.41
32:R3:1515:G:N1	32:R3:1521:C:N3	2.68	0.41
35:sd:84:ASN:HB3	35:sd:87:GLU:HB3	2.02	0.41
41:sj:39:PRO:HA	41:sj:73:LEU:O	2.20	0.41
41:sj:85:ASP:C	41:sj:88:MET:HE1	2.46	0.41
46:so:69:LEU:HB3	46:so:77:TYR:HB2	2.03	0.41
46:so:78:THR:O	46:so:82:GLU:HG2	2.21	0.41
50:ss:11:ASP:OD2	50:ss:36:ARG:NH1	2.53	0.41
51:st:36:ALA:O	51:st:40:ALA:N	2.54	0.41
52:su:11:PHE:CG	52:su:12:ASP:N	2.88	0.41
3:15:43:GLY:N	30:R1:671:C:OP1	2.51	0.41
4:16:30:SER:N	4:16:106:ASP:OD2	2.54	0.41
4:16:60:GLN:N	4:16:60:GLN:CD	2.79	0.41
6:18:15:ARG:HG3	6:18:25:ARG:NH1	2.36	0.41
8:2:164:VAL:HG21	8:2:180:MET:HE2	2.02	0.41
8:2:227:VAL:HG11	30:R1:784:G:N1	2.36	0.41
10:21:73:LYS:HB2	10:21:73:LYS:HE2	1.77	0.41
20:31:39:LYS:HB2	20:31:39:LYS:HE3	1.91	0.41
23:35:29:ARG:HA	23:35:29:ARG:HD2	1.96	0.41
26:5:37:MET:HG2	26:5:150:GLY:O	2.20	0.41
30:R1:148:U:H2'	30:R1:149:A:C8	2.54	0.41
30:R1:284:U:O2	30:R1:356:G:C2	2.73	0.41
30:R1:581:C:H2'	30:R1:582:A:C8	2.55	0.41
30:R1:684:G:C2	30:R1:794:A:C2	3.08	0.41
30:R1:741:U:H2'	30:R1:742:A:C8	2.55	0.41
30:R1:1294:U:C4	30:R1:1295:C:C5	3.09	0.41
32:R3:306:A:C5	32:R3:307:C:C5	3.08	0.41
32:R3:402:G:O2'	32:R3:403:C:P	2.79	0.41
32:R3:634:C:H2'	32:R3:635:A:H8	1.85	0.41
32:R3:713:G:H2'	32:R3:714:G:C8	2.55	0.41
32:R3:945:G:C2	32:R3:946:A:C8	3.09	0.41
49:sr:41:SER:HA	49:sr:44:THR:HG22	2.03	0.41
50:ss:5:LYS:HD3	50:ss:5:LYS:HA	1.76	0.41
50:ss:44:ILE:HG23	50:ss:62:THR:HA	2.02	0.41
8:2:152:GLN:HB3	30:R1:1818:U:N3	2.36	0.41
12:23:34:VAL:HG11	12:23:43:ILE:HD13	2.01	0.41
14:25:76:ASP:OD1	14:25:77:VAL:N	2.54	0.41
17:29:9:LYS:HG2	17:29:12:GLU:HB3	2.03	0.41
25:4:99:LYS:HB3	25:4:99:LYS:HE3	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:40:U:H2'	30:R1:41:C:C6	2.55	0.41
30:R1:445:C:O2'	30:R1:446:G:H5'	2.21	0.41
30:R1:480:A:H2	30:R1:499:U:O2	2.04	0.41
30:R1:594:U:H2'	30:R1:595:C:H6	1.86	0.41
30:R1:1654:A:N7	30:R1:2005:A:H2	2.18	0.41
30:R1:1715:G:HO2'	30:R1:1716:U:H6	1.67	0.41
30:R1:2037:A:C6	30:R1:2038:G:C6	3.08	0.41
30:R1:2557:G:H2'	30:R1:2558:C:C6	2.55	0.41
30:R1:2699:C:HO2'	30:R1:2700:A:P	2.42	0.41
32:R3:88:U:H2'	32:R3:89:U:O4'	2.21	0.41
32:R3:198:G:H2'	32:R3:199:A:H8	1.86	0.41
32:R3:442:G:H2'	32:R3:443:C:C6	2.56	0.41
32:R3:841:C:O2	32:R3:843:U:H5''	2.21	0.41
32:R3:1036:A:H2'	32:R3:1037:C:C5	2.55	0.41
32:R3:1477:U:H2'	32:R3:1478:U:C6	2.56	0.41
33:sb:35:ASN:HB2	33:sb:37:VAL:HG22	2.03	0.41
46:so:86:LEU:O	46:so:87:ARG:HB2	2.20	0.41
51:st:43:LYS:HZ1	51:st:85:LEU:HG	1.85	0.41
5:17:1:MET:N	30:R1:1654:A:OP2	2.36	0.41
7:19:48:ALA:HB1	7:19:95:LYS:HD3	2.03	0.41
9:20:46:TYR:O	9:20:50:ARG:NH1	2.54	0.41
10:21:6:GLN:HE22	10:21:37:GLU:HB3	1.85	0.41
19:30:31:ILE:H	19:30:31:ILE:HG13	1.73	0.41
30:R1:827:U:O2'	30:R1:2068:U:C2	2.73	0.41
30:R1:2074:U:O2'	30:R1:2597:G:H1'	2.20	0.41
30:R1:2194:U:H2'	30:R1:2195:U:C5	2.56	0.41
32:R3:45:G:H2'	32:R3:46:G:H8	1.85	0.41
32:R3:360:G:O2'	32:R3:361:G:H5'	2.21	0.41
32:R3:500:G:HO2'	32:R3:501:C:P	2.43	0.41
32:R3:962:C:H5	32:R3:973:G:N1	2.16	0.41
32:R3:1315:U:H2'	32:R3:1316:G:O4'	2.21	0.41
32:R3:1337:G:H5''	32:R3:1338:G:OP1	2.20	0.41
37:sf:52:ASN:ND2	37:sf:52:ASN:C	2.78	0.41
49:sr:68:PRO:HB2	49:sr:70:THR:O	2.20	0.41
51:st:43:LYS:NZ	51:st:85:LEU:HG	2.36	0.41
8:2:132:ARG:HG2	8:2:132:ARG:HH11	1.85	0.41
13:24:44:HIS:HB3	30:R1:483:A:O4'	2.20	0.41
16:28:36:ARG:HA	16:28:47:THR:HA	2.03	0.41
18:3:133:THR:CG2	18:3:134:HIS:N	2.83	0.41
23:35:58:ILE:HD13	23:35:58:ILE:HA	1.90	0.41
30:R1:508:A:H2'	30:R1:508:A:N3	2.36	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:629:G:H1'	30:R1:639:U:O2'	2.21	0.41
30:R1:878:A:N6	30:R1:899:A:O2'	2.51	0.41
30:R1:1532:A:N1	30:R1:1540:G:C6	2.89	0.41
30:R1:1539:U:H2'	30:R1:1540:G:H8	1.86	0.41
30:R1:1809:A:H2'	30:R1:1810:A:C8	2.56	0.41
32:R3:363:A:C6	43:sl:27:PRO:HD2	2.55	0.41
32:R3:756:C:H2'	32:R3:757:U:C6	2.56	0.41
32:R3:1118:U:P	40:si:105:ARG:HE	2.44	0.41
32:R3:1312:G:H5'	50:ss:5:LYS:HE2	2.02	0.41
32:R3:1320:C:N3	50:ss:71:GLY:HA3	2.35	0.41
34:sc:67:ILE:HB	34:sc:102:ILE:HD13	2.03	0.41
37:sf:43:GLY:O	37:sf:58:HIS:ND1	2.53	0.41
40:si:18:VAL:HG21	40:si:81:GLY:C	2.46	0.41
40:si:91:GLU:H	40:si:91:GLU:HG2	1.70	0.41
52:su:9:GLU:C	52:su:9:GLU:OE1	2.63	0.41
52:su:35:GLU:HG2	52:su:36:PHE:N	2.24	0.41
52:su:36:PHE:CG	52:su:39:LYS:HE3	2.56	0.41
54:33:25:ASN:ND2	54:33:28:THR:HG22	2.36	0.41
2:14:73:ASP:OD2	2:14:73:ASP:C	2.64	0.41
4:16:36:VAL:HG22	14:25:82:TYR:HB2	2.03	0.41
9:20:24:TYR:CG	9:20:25:GLY:N	2.89	0.41
18:3:130:GLN:OE1	30:R1:2578:G:N2	2.53	0.41
20:31:50:ASP:OD1	20:31:50:ASP:C	2.63	0.41
21:32:2:VAL:HG13	30:R1:2015:A:N1	2.36	0.41
25:4:27:LEU:HD13	25:4:100:MET:HG2	2.03	0.41
26:5:15:LEU:HD23	26:5:15:LEU:HA	1.86	0.41
26:5:97:GLU:O	26:5:101:ARG:HG3	2.21	0.41
26:5:146:ASP:HB2	26:5:149:ARG:HH21	1.85	0.41
27:6:136:ASP:OD1	27:6:138:GLN:N	2.53	0.41
30:R1:17:G:H2'	30:R1:18:U:C6	2.55	0.41
30:R1:181:A:H2'	30:R1:182:A:H8	1.85	0.41
30:R1:721:A:H2'	30:R1:722:A:C8	2.56	0.41
30:R1:756:A:H2'	30:R1:757:G:O4'	2.21	0.41
30:R1:953:G:C2	30:R1:954:G:C8	3.08	0.41
30:R1:1020:A:H1'	30:R1:1021:A:OP2	2.21	0.41
30:R1:1039:A:H2'	30:R1:1040:A:O4'	2.20	0.41
30:R1:1086:A:H5'	30:R1:1104:C:H1'	2.03	0.41
30:R1:1195:G:C2	30:R1:1196:C:C5	3.09	0.41
30:R1:1282:U:H2'	30:R1:1283:G:O4'	2.20	0.41
30:R1:1310:G:N2	30:R1:1313:U:O4	2.54	0.41
30:R1:2148:G:C4	30:R1:2149:U:H5	2.39	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2345:G:N3	30:R1:2381:A:H2'	2.36	0.41
30:R1:2899:A:H2'	30:R1:2900:A:C8	2.56	0.41
32:R3:184:G:H2'	32:R3:185:U:H6	1.86	0.41
32:R3:223:A:H2'	32:R3:224:U:C6	2.56	0.41
32:R3:408:A:N6	32:R3:435:A:H62	2.19	0.41
32:R3:499:A:O4'	32:R3:547:A:N6	2.53	0.41
32:R3:505:G:C2	32:R3:506:G:C5	3.09	0.41
32:R3:521:G:N7	43:sl:49:ARG:NH1	2.69	0.41
32:R3:562:U:O2'	43:sl:12:ALA:O	2.31	0.41
32:R3:966:G:O2'	40:si:128:LYS:O	2.39	0.41
32:R3:1150:A:O2'	32:R3:1151:A:O5'	2.34	0.41
32:R3:1204:A:H2'	32:R3:1205:U:O4'	2.20	0.41
33:sb:34:ARG:HE	33:sb:34:ARG:HB3	1.76	0.41
34:sc:44:LYS:HB3	34:sc:44:LYS:HE2	1.95	0.41
34:sc:102:ILE:HD13	34:sc:102:ILE:HA	1.87	0.41
37:sf:52:ASN:C	37:sf:52:ASN:HD22	2.17	0.41
38:sg:137:ARG:O	38:sg:140:VAL:HG12	2.21	0.41
46:so:31:LEU:HD12	46:so:62:ARG:HB2	2.02	0.41
50:ss:41:PRO:O	50:ss:44:ILE:HG12	2.21	0.41
53:T:19:G:C2	53:T:57:A:C2	3.09	0.41
54:33:29:LYS:HA	54:33:29:LYS:HD2	1.97	0.41
2:14:32:TYR:OH	30:R1:2726:A:H5'	2.21	0.41
3:15:4:ASN:HB3	30:R1:1203:U:H1'	2.03	0.41
4:16:40:ARG:H	4:16:40:ARG:HG2	1.69	0.41
6:18:94:ARG:HG2	6:18:97:PHE:O	2.21	0.41
13:24:40:LEU:HD13	13:24:40:LEU:HA	1.82	0.41
13:24:43:LYS:HG2	13:24:45:GLN:HG3	2.01	0.41
18:3:149:ASN:CG	18:3:150:GLN:H	2.28	0.41
25:4:45:ALA:HB2	25:4:89:PRO:HD3	2.03	0.41
30:R1:319:G:H22	30:R1:323:C:H5	1.69	0.41
30:R1:628:G:C6	30:R1:636:G:C2	3.09	0.41
30:R1:666:A:H2'	30:R1:667:U:C6	2.56	0.41
30:R1:1727:C:H2'	30:R1:1728:C:O4'	2.21	0.41
30:R1:2306:C:OP2	30:R1:2307:G:O2'	2.35	0.41
32:R3:53:A:C6	32:R3:359:G:C6	3.09	0.41
32:R3:355:C:HO2'	32:R3:388:G:H8	1.66	0.41
32:R3:575:G:O2'	32:R3:821:G:OP2	2.36	0.41
32:R3:602:A:H2'	32:R3:603:U:C6	2.56	0.41
1:13:39:LYS:HG2	1:13:44:TYR:CE2	2.56	0.40
16:28:7:THR:OG1	16:28:8:GLY:N	2.54	0.40
27:6:17:LYS:HD3	27:6:17:LYS:HA	1.68	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:340:A:H2'	30:R1:341:C:O4'	2.20	0.40
30:R1:402:A:N1	30:R1:403:U:H1'	2.36	0.40
30:R1:857:G:N2	30:R1:2269:G:O4'	2.53	0.40
30:R1:2455:G:H2'	30:R1:2456:C:C6	2.57	0.40
32:R3:4:U:C5	32:R3:613:C:H1'	2.56	0.40
32:R3:256:U:H2'	32:R3:257:G:C8	2.55	0.40
32:R3:258:G:C4	32:R3:259:G:C8	3.09	0.40
43:sl:74:GLN:C	43:sl:76:HIS:H	2.29	0.40
43:sl:98:ARG:NE	43:sl:103:CYS:SG	2.85	0.40
45:sn:88:MET:HE3	45:sn:88:MET:HB2	1.84	0.40
48:sq:57:VAL:HG13	48:sq:78:VAL:CG2	2.51	0.40
2:14:70:ARG:NH2	30:R1:2683:C:O2	2.54	0.40
18:3:1:MET:HB3	18:3:2:ILE:H	1.56	0.40
20:31:13:THR:O	20:31:13:THR:OG1	2.35	0.40
30:R1:135:U:H2'	30:R1:136:G:H8	1.87	0.40
30:R1:500:G:N2	30:R1:503:A:H5'	2.31	0.40
30:R1:521:U:H2'	30:R1:522:A:C8	2.55	0.40
30:R1:1361:G:H2'	30:R1:1362:C:H6	1.86	0.40
30:R1:1539:U:H2'	30:R1:1540:G:C8	2.57	0.40
30:R1:1593:A:H2'	30:R1:1594:U:H6	1.85	0.40
31:R2:34:A:H5''	31:R2:35:C:OP1	2.21	0.40
31:R2:39:A:C4	31:R2:44:G:N2	2.89	0.40
32:R3:28:A:O2'	32:R3:296:U:OP1	2.34	0.40
32:R3:45:G:H2'	32:R3:46:G:C8	2.56	0.40
32:R3:109:A:C4	32:R3:327:A:C2	3.10	0.40
32:R3:312:C:H2'	32:R3:313:A:C8	2.56	0.40
32:R3:552:U:C6	32:R3:553:A:C8	3.10	0.40
32:R3:990:C:H5	32:R3:1215:G:H1	1.69	0.40
2:14:24:VAL:HG13	2:14:33:ALA:HB2	2.03	0.40
3:15:123:ARG:NE	3:15:143:GLU:OE2	2.52	0.40
5:17:75:ILE:HD13	5:17:75:ILE:HA	1.89	0.40
15:27:19:LYS:HA	15:27:19:LYS:HD3	1.90	0.40
23:35:8:GLY:O	23:35:12:ARG:NH1	2.55	0.40
30:R1:271:G:C2	30:R1:367:G:C2	3.09	0.40
30:R1:296:U:H2'	30:R1:297:G:C8	2.57	0.40
30:R1:548:G:H2'	30:R1:549:G:O4'	2.22	0.40
30:R1:671:C:H2'	30:R1:672:C:C6	2.56	0.40
30:R1:1011:G:C6	30:R1:1151:A:C6	3.10	0.40
30:R1:1645:G:H5''	30:R1:1646:C:H5'	2.03	0.40
30:R1:1796:U:H2'	30:R1:1797:G:C8	2.57	0.40
30:R1:2117:A:N1	30:R1:2170:A:N1	2.70	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:2888:C:H2'	30:R1:2889:C:H6	1.86	0.40
32:R3:75:G:H3'	32:R3:76:G:H8	1.86	0.40
32:R3:1171:A:H2'	32:R3:1172:C:C6	2.57	0.40
33:sb:22:TRP:HB3	33:sb:38:HIS:ND1	2.36	0.40
36:se:63:MET:C	36:se:67:ARG:HH21	2.29	0.40
41:sj:23:ALA:O	41:sj:27:GLU:HG2	2.21	0.40
41:sj:52:LEU:O	45:sn:80:ARG:NH1	2.54	0.40
52:su:36:PHE:C	52:su:38:GLU:H	2.29	0.40
1:13:47:HIS:ND1	1:13:48:VAL:HG13	2.36	0.40
5:17:79:LEU:C	5:17:81:ASN:H	2.30	0.40
8:2:219:VAL:HG21	30:R1:782:A:N7	2.36	0.40
14:25:34:LYS:HB2	14:25:34:LYS:HE2	1.93	0.40
30:R1:1056:G:C2	30:R1:1102:C:H5	2.38	0.40
30:R1:1113:U:H2'	30:R1:1114:C:H6	1.86	0.40
30:R1:1218:G:N1	30:R1:1232:G:C5	2.89	0.40
30:R1:1224:U:H2'	30:R1:1225:G:C8	2.56	0.40
30:R1:1232:G:C5	30:R1:1233:C:C5	3.09	0.40
30:R1:1506:U:H2'	30:R1:1507:C:C6	2.56	0.40
30:R1:1542:U:H2'	30:R1:1543:G:O4'	2.22	0.40
30:R1:2553:G:N2	30:R1:2583:G:H1'	2.36	0.40
30:R1:2590:A:H2'	30:R1:2591:C:H6	1.87	0.40
31:R2:20:G:C6	31:R2:64:G:C6	3.10	0.40
31:R2:32:U:C4	31:R2:33:G:N7	2.89	0.40
32:R3:390:U:H4'	47:sp:28:ARG:NH2	2.37	0.40
32:R3:561:U:HO2'	32:R3:562:U:P	2.43	0.40
32:R3:604:G:C6	32:R3:635:A:C6	3.10	0.40
32:R3:654:G:C6	32:R3:655:A:C5	3.09	0.40
32:R3:1297:G:H4'	32:R3:1298:U:O5'	2.21	0.40
33:sb:13:VAL:HB	33:sb:207:ARG:NH1	2.34	0.40
33:sb:26:MET:HG3	33:sb:192:PRO:HD3	2.04	0.40
33:sb:183:PHE:CD1	33:sb:197:PHE:HB2	2.57	0.40
34:sc:11:LEU:HD11	45:sn:88:MET:O	2.21	0.40
38:sg:46:LEU:HB3	38:sg:57:GLU:OE1	2.21	0.40
3:15:30:THR:HG23	30:R1:810:U:O4	2.22	0.40
4:16:60:GLN:N	4:16:60:GLN:OE1	2.54	0.40
8:2:220:ARG:NE	30:R1:1827:U:OP2	2.54	0.40
11:22:1:MET:O	11:22:3:THR:HG23	2.21	0.40
25:4:112:LEU:HD22	25:4:117:ARG:HB2	2.04	0.40
26:5:33:ILE:HG22	26:5:95:MET:HG2	2.04	0.40
26:5:91:ARG:HD2	31:R2:43:C:O2	2.22	0.40
27:6:35:THR:OG1	27:6:36:LEU:N	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:R1:100:U:H1'	30:R1:101:A:C4	2.57	0.40
30:R1:196:A:O2'	30:R1:805:G:O6	2.30	0.40
30:R1:714:U:N3	30:R1:717:C:OP2	2.52	0.40
30:R1:1771:C:H2'	30:R1:1772:A:H8	1.87	0.40
30:R1:1831:G:H2'	30:R1:1832:C:C6	2.56	0.40
30:R1:1843:C:H2'	30:R1:1844:C:H6	1.87	0.40
30:R1:1844:C:C2	30:R1:1845:G:C8	3.09	0.40
30:R1:2233:U:H2'	30:R1:2234:G:C8	2.57	0.40
30:R1:2302:U:N3	30:R1:2303:G:N7	2.69	0.40
30:R1:2547:A:C8	30:R1:2566:A:C8	3.10	0.40
30:R1:2570:G:H2'	30:R1:2571:U:O4'	2.21	0.40
30:R1:2809:A:H2'	30:R1:2810:A:C8	2.57	0.40
32:R3:119:A:H4'	32:R3:120:A:H5'	2.04	0.40
32:R3:454:G:C2	32:R3:455:G:C8	3.10	0.40
32:R3:978:A:C6	32:R3:1318:A:C6	3.10	0.40
32:R3:1071:C:H2'	32:R3:1072:G:C8	2.57	0.40
32:R3:1130:A:O2'	32:R3:1131:G:C8	2.72	0.40
32:R3:1250:A:N3	32:R3:1370:G:O2'	2.51	0.40
32:R3:1305:G:H22	32:R3:1331:G:H1'	1.87	0.40
34:sc:176:THR:HG22	34:sc:178:ARG:HG2	2.03	0.40
36:se:51:LYS:O	36:se:61:LYS:NZ	2.27	0.40
36:se:90:GLY:O	36:se:129:SER:N	2.46	0.40
38:sg:47:GLU:OE2	38:sg:51:GLN:NE2	2.53	0.40
43:sl:11:ARG:HD3	43:sl:11:ARG:HA	1.93	0.40
44:sm:64:VAL:CG2	44:sm:65:GLU:N	2.84	0.40
52:su:53:LYS:O	52:su:57:LYS:HD2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	13	140/142 (99%)	133 (95%)	7 (5%)	0	100	100
2	14	120/122 (98%)	101 (84%)	19 (16%)	0	100	100
3	15	142/144 (99%)	127 (89%)	15 (11%)	0	100	100
4	16	134/136 (98%)	124 (92%)	10 (8%)	0	100	100
5	17	118/120 (98%)	104 (88%)	14 (12%)	0	100	100
6	18	114/116 (98%)	107 (94%)	7 (6%)	0	100	100
7	19	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
8	2	269/271 (99%)	239 (89%)	30 (11%)	0	100	100
9	20	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
10	21	101/103 (98%)	90 (89%)	11 (11%)	0	100	100
11	22	108/110 (98%)	99 (92%)	8 (7%)	1 (1%)	14	43
12	23	91/93 (98%)	77 (85%)	14 (15%)	0	100	100
13	24	100/102 (98%)	88 (88%)	12 (12%)	0	100	100
14	25	92/94 (98%)	85 (92%)	7 (8%)	0	100	100
15	27	74/76 (97%)	69 (93%)	5 (7%)	0	100	100
16	28	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
17	29	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
18	3	207/209 (99%)	187 (90%)	20 (10%)	0	100	100
19	30	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
20	31	64/66 (97%)	54 (84%)	10 (16%)	0	100	100
21	32	54/56 (96%)	47 (87%)	7 (13%)	0	100	100
22	34	44/46 (96%)	38 (86%)	5 (11%)	1 (2%)	5	25
23	35	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
24	36	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
25	4	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
26	5	175/177 (99%)	166 (95%)	9 (5%)	0	100	100
27	6	174/176 (99%)	156 (90%)	18 (10%)	0	100	100
28	9	147/149 (99%)	130 (88%)	17 (12%)	0	100	100
33	sb	216/218 (99%)	194 (90%)	21 (10%)	1 (0%)	24	55
34	sc	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
35	sd	203/205 (99%)	179 (88%)	24 (12%)	0	100	100
36	se	155/157 (99%)	127 (82%)	27 (17%)	1 (1%)	21	52

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	sf	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
38	sg	149/151 (99%)	138 (93%)	11 (7%)	0	100	100
39	sh	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
40	si	125/127 (98%)	101 (81%)	23 (18%)	1 (1%)	16	45
41	sj	96/98 (98%)	85 (88%)	10 (10%)	1 (1%)	12	40
42	sk	114/116 (98%)	102 (90%)	12 (10%)	0	100	100
43	sl	121/123 (98%)	90 (74%)	31 (26%)	0	100	100
44	sm	112/114 (98%)	96 (86%)	16 (14%)	0	100	100
45	sn	98/100 (98%)	80 (82%)	18 (18%)	0	100	100
46	so	86/88 (98%)	80 (93%)	6 (7%)	0	100	100
47	sp	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
48	sq	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
49	sr	63/65 (97%)	58 (92%)	5 (8%)	0	100	100
50	ss	77/79 (98%)	69 (90%)	8 (10%)	0	100	100
51	st	83/85 (98%)	82 (99%)	1 (1%)	0	100	100
52	su	63/65 (97%)	41 (65%)	22 (35%)	0	100	100
54	33	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
All	All	5580/5678 (98%)	5009 (90%)	565 (10%)	6 (0%)	49	75

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	sb	18	GLN
36	se	122	VAL
11	22	2	GLU
40	si	91	GLU
41	sj	57	VAL
22	34	44	VAL

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	13	116/116 (100%)	113 (97%)	3 (3%)	40	64
2	14	103/103 (100%)	101 (98%)	2 (2%)	50	68
3	15	103/103 (100%)	103 (100%)	0	100	100
4	16	109/109 (100%)	109 (100%)	0	100	100
5	17	100/100 (100%)	100 (100%)	0	100	100
6	18	86/86 (100%)	86 (100%)	0	100	100
7	19	99/99 (100%)	99 (100%)	0	100	100
8	2	216/216 (100%)	216 (100%)	0	100	100
9	20	89/89 (100%)	88 (99%)	1 (1%)	65	76
10	21	84/84 (100%)	84 (100%)	0	100	100
11	22	93/93 (100%)	92 (99%)	1 (1%)	65	76
12	23	80/80 (100%)	80 (100%)	0	100	100
13	24	83/83 (100%)	83 (100%)	0	100	100
14	25	78/78 (100%)	76 (97%)	2 (3%)	40	64
15	27	58/58 (100%)	56 (97%)	2 (3%)	32	59
16	28	67/67 (100%)	67 (100%)	0	100	100
17	29	55/55 (100%)	55 (100%)	0	100	100
18	3	164/164 (100%)	164 (100%)	0	100	100
19	30	48/48 (100%)	48 (100%)	0	100	100
20	31	59/59 (100%)	59 (100%)	0	100	100
21	32	47/47 (100%)	47 (100%)	0	100	100
22	34	38/38 (100%)	37 (97%)	1 (3%)	40	64
23	35	51/51 (100%)	51 (100%)	0	100	100
24	36	34/34 (100%)	34 (100%)	0	100	100
25	4	165/165 (100%)	164 (99%)	1 (1%)	78	81
26	5	148/148 (100%)	148 (100%)	0	100	100
27	6	137/137 (100%)	137 (100%)	0	100	100
28	9	114/114 (100%)	113 (99%)	1 (1%)	70	78
33	sb	180/180 (100%)	180 (100%)	0	100	100
34	sc	170/170 (100%)	170 (100%)	0	100	100
35	sd	172/172 (100%)	172 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	se	119/119 (100%)	118 (99%)	1 (1%)	73	79
37	sf	87/87 (100%)	87 (100%)	0	100	100
38	sg	124/124 (100%)	123 (99%)	1 (1%)	73	79
39	sh	104/104 (100%)	103 (99%)	1 (1%)	68	76
40	si	105/105 (100%)	105 (100%)	0	100	100
41	sj	86/86 (100%)	84 (98%)	2 (2%)	44	66
42	sk	89/89 (100%)	88 (99%)	1 (1%)	65	76
43	sl	103/103 (100%)	103 (100%)	0	100	100
44	sm	92/92 (100%)	92 (100%)	0	100	100
45	sn	83/83 (100%)	82 (99%)	1 (1%)	63	75
46	so	76/76 (100%)	76 (100%)	0	100	100
47	sp	65/65 (100%)	64 (98%)	1 (2%)	57	72
48	sq	74/74 (100%)	73 (99%)	1 (1%)	59	73
49	sr	56/56 (100%)	56 (100%)	0	100	100
50	ss	70/70 (100%)	69 (99%)	1 (1%)	59	73
51	st	65/65 (100%)	65 (100%)	0	100	100
52	su	55/55 (100%)	55 (100%)	0	100	100
54	33	45/45 (100%)	45 (100%)	0	100	100
All	All	4644/4644 (100%)	4620 (100%)	24 (0%)	78	83

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	13	52	ASP
1	13	84	ILE
1	13	138	GLN
2	14	32	TYR
2	14	95	ILE
9	20	8	ILE
11	22	85	ILE
14	25	49	ASN
14	25	66	ASP
15	27	64	ASP
15	27	82	ILE
22	34	22	MET
25	4	80	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
28	9	98	ASP
36	se	18	ASN
38	sg	22	LEU
39	sh	84	ILE
41	sj	63	ASP
41	sj	71	LEU
42	sk	35	ASP
45	sn	61	ASN
47	sp	52	LEU
48	sq	7	LEU
50	ss	61	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
3	15	4	ASN
4	16	13	HIS
5	17	11	ASN
5	17	13	ASN
6	18	38	GLN
7	19	11	GLN
7	19	55	HIS
8	2	14	HIS
8	2	85	ASN
9	20	71	ASN
11	22	40	ASN
13	24	44	HIS
15	27	46	HIS
16	28	15	ASN
17	29	36	GLN
17	29	39	GLN
17	29	41	HIS
18	3	32	ASN
18	3	49	GLN
18	3	185	ASN
20	31	48	GLN
22	34	16	HIS
24	36	37	GLN
28	9	2	GLN
33	sb	145	ASN
34	sc	5	HIS
35	sd	99	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
35	sd	130	ASN
36	se	121	ASN
36	se	147	ASN
38	sg	67	ASN
39	sh	3	GLN
42	sk	63	GLN
42	sk	100	ASN
43	sl	58	ASN
45	sn	65	GLN
46	so	36	ASN
46	so	37	HIS
47	sp	26	ASN
47	sp	29	ASN
51	st	2	ASN
51	st	54	GLN
51	st	69	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
29	M	8/9 (88%)	0	0
30	R1	2899/2903 (99%)	566 (19%)	14 (0%)
31	R2	118/119 (99%)	23 (19%)	0
32	R3	1530/1531 (99%)	405 (26%)	24 (1%)
53	T	76/78 (97%)	16 (21%)	2 (2%)
All	All	4631/4640 (99%)	1010 (21%)	40 (0%)

All (1010) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
30	R1	3	U
30	R1	10	A
30	R1	12	U
30	R1	14	A
30	R1	15	G
30	R1	34	U
30	R1	35	G
30	R1	36	G
30	R1	46	G
30	R1	51	G
30	R1	60	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	71	A
30	R1	74	A
30	R1	75	G
30	R1	78	U
30	R1	79	C
30	R1	80	G
30	R1	83	A
30	R1	84	A
30	R1	85	G
30	R1	88	G
30	R1	100	U
30	R1	101	A
30	R1	102	U
30	R1	118	A
30	R1	120	U
30	R1	125	A
30	R1	134	G
30	R1	137	U
30	R1	138	U
30	R1	139	U
30	R1	140	C
30	R1	143	C
30	R1	144	A
30	R1	146	A
30	R1	148	U
30	R1	152	A
30	R1	154	U
30	R1	156	A
30	R1	159	G
30	R1	160	A
30	R1	162	U
30	R1	164	C
30	R1	165	A
30	R1	178	G
30	R1	181	A
30	R1	196	A
30	R1	199	A
30	R1	215	G
30	R1	216	A
30	R1	219	A
30	R1	220	G
30	R1	221	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	222	A
30	R1	228	C
30	R1	230	G
30	R1	248	G
30	R1	249	C
30	R1	256	A
30	R1	264	C
30	R1	265	A
30	R1	266	G
30	R1	267	C
30	R1	274	C
30	R1	275	C
30	R1	276	U
30	R1	277	G
30	R1	282	A
30	R1	283	G
30	R1	291	G
30	R1	302	C
30	R1	311	A
30	R1	329	G
30	R1	330	A
30	R1	342	A
30	R1	343	C
30	R1	352	A
30	R1	353	C
30	R1	354	A
30	R1	361	G
30	R1	362	A
30	R1	364	C
30	R1	371	A
30	R1	372	G
30	R1	373	U
30	R1	386	G
30	R1	387	U
30	R1	388	G
30	R1	389	G
30	R1	401	A
30	R1	404	A
30	R1	405	U
30	R1	406	G
30	R1	411	G
30	R1	412	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	413	C
30	R1	414	C
30	R1	416	U
30	R1	424	G
30	R1	428	A
30	R1	443	A
30	R1	473	G
30	R1	481	G
30	R1	491	G
30	R1	505	A
30	R1	509	C
30	R1	510	C
30	R1	512	G
30	R1	518	G
30	R1	527	C
30	R1	529	A
30	R1	530	G
30	R1	531	C
30	R1	532	A
30	R1	533	G
30	R1	543	G
30	R1	545	U
30	R1	546	U
30	R1	548	G
30	R1	549	G
30	R1	550	C
30	R1	555	G
30	R1	563	A
30	R1	573	U
30	R1	575	A
30	R1	603	A
30	R1	614	A
30	R1	615	U
30	R1	627	A
30	R1	634	C
30	R1	637	A
30	R1	645	C
30	R1	647	G
30	R1	653	U
30	R1	654	A
30	R1	655	A
30	R1	656	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	685	A
30	R1	686	U
30	R1	689	A
30	R1	691	C
30	R1	711	G
30	R1	713	G
30	R1	730	A
30	R1	738	G
30	R1	746	U
30	R1	747	U
30	R1	752	A
30	R1	764	A
30	R1	765	C
30	R1	775	G
30	R1	776	G
30	R1	782	A
30	R1	784	G
30	R1	785	G
30	R1	792	A
30	R1	805	G
30	R1	812	C
30	R1	819	A
30	R1	827	U
30	R1	828	U
30	R1	829	A
30	R1	845	A
30	R1	846	U
30	R1	847	U
30	R1	860	U
30	R1	872	U
30	R1	878	A
30	R1	886	A
30	R1	887	U
30	R1	888	C
30	R1	891	G
30	R1	892	A
30	R1	893	C
30	R1	894	U
30	R1	895	U
30	R1	896	A
30	R1	898	C
30	R1	910	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	914	G
30	R1	927	A
30	R1	931	U
30	R1	932	U
30	R1	941	A
30	R1	945	A
30	R1	946	C
30	R1	953	G
30	R1	961	C
30	R1	973	A
30	R1	974	G
30	R1	979	A
30	R1	983	A
30	R1	984	A
30	R1	989	G
30	R1	990	A
30	R1	995	C
30	R1	996	A
30	R1	997	G
30	R1	999	U
30	R1	1005	C
30	R1	1009	A
30	R1	1012	U
30	R1	1013	C
30	R1	1021	A
30	R1	1022	G
30	R1	1026	G
30	R1	1033	U
30	R1	1046	A
30	R1	1047	G
30	R1	1051	G
30	R1	1055	G
30	R1	1056	G
30	R1	1060	U
30	R1	1061	U
30	R1	1062	G
30	R1	1063	G
30	R1	1064	C
30	R1	1066	U
30	R1	1067	A
30	R1	1070	A
30	R1	1071	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	1072	C
30	R1	1073	A
30	R1	1074	G
30	R1	1075	C
30	R1	1076	C
30	R1	1078	U
30	R1	1084	A
30	R1	1085	A
30	R1	1087	G
30	R1	1088	A
30	R1	1090	A
30	R1	1091	G
30	R1	1095	A
30	R1	1096	A
30	R1	1101	U
30	R1	1103	A
30	R1	1104	C
30	R1	1106	G
30	R1	1109	C
30	R1	1110	G
30	R1	1111	A
30	R1	1112	G
30	R1	1116	G
30	R1	1125	G
30	R1	1132	U
30	R1	1133	A
30	R1	1135	C
30	R1	1136	G
30	R1	1142	A
30	R1	1166	G
30	R1	1171	G
30	R1	1173	U
30	R1	1174	U
30	R1	1175	A
30	R1	1176	U
30	R1	1177	G
30	R1	1179	G
30	R1	1180	U
30	R1	1181	U
30	R1	1195	G
30	R1	1204	A
30	R1	1250	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	1253	A
30	R1	1255	U
30	R1	1256	G
30	R1	1271	G
30	R1	1272	A
30	R1	1273	U
30	R1	1300	G
30	R1	1301	A
30	R1	1316	U
30	R1	1341	G
30	R1	1345	C
30	R1	1352	U
30	R1	1365	A
30	R1	1368	G
30	R1	1376	C
30	R1	1379	U
30	R1	1383	A
30	R1	1386	C
30	R1	1395	A
30	R1	1412	U
30	R1	1416	G
30	R1	1420	A
30	R1	1428	C
30	R1	1431	A
30	R1	1434	A
30	R1	1452	G
30	R1	1453	A
30	R1	1459	G
30	R1	1475	G
30	R1	1478	G
30	R1	1481	U
30	R1	1482	G
30	R1	1490	A
30	R1	1493	C
30	R1	1494	A
30	R1	1508	A
30	R1	1509	A
30	R1	1515	A
30	R1	1519	G
30	R1	1523	U
30	R1	1533	C
30	R1	1534	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	1535	A
30	R1	1536	C
30	R1	1537	G
30	R1	1558	C
30	R1	1560	G
30	R1	1566	A
30	R1	1569	A
30	R1	1578	U
30	R1	1583	A
30	R1	1584	U
30	R1	1610	A
30	R1	1616	A
30	R1	1647	U
30	R1	1648	U
30	R1	1649	G
30	R1	1674	G
30	R1	1677	A
30	R1	1698	A
30	R1	1715	G
30	R1	1729	U
30	R1	1732	C
30	R1	1733	G
30	R1	1738	G
30	R1	1756	G
30	R1	1758	U
30	R1	1764	C
30	R1	1769	U
30	R1	1773	A
30	R1	1776	G
30	R1	1781	U
30	R1	1785	A
30	R1	1800	C
30	R1	1801	A
30	R1	1808	A
30	R1	1811	G
30	R1	1816	C
30	R1	1829	A
30	R1	1848	A
30	R1	1869	G
30	R1	1870	C
30	R1	1871	A
30	R1	1873	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	1884	G
30	R1	1901	A
30	R1	1906	G
30	R1	1913	A
30	R1	1914	C
30	R1	1915	U
30	R1	1919	A
30	R1	1929	G
30	R1	1930	G
30	R1	1937	A
30	R1	1938	A
30	R1	1943	U
30	R1	1955	U
30	R1	1966	A
30	R1	1967	C
30	R1	1970	A
30	R1	1971	U
30	R1	1972	G
30	R1	1991	U
30	R1	1992	G
30	R1	1993	U
30	R1	1997	C
30	R1	2013	A
30	R1	2022	U
30	R1	2023	C
30	R1	2030	A
30	R1	2031	A
30	R1	2033	A
30	R1	2043	C
30	R1	2052	A
30	R1	2055	C
30	R1	2056	G
30	R1	2059	A
30	R1	2060	A
30	R1	2061	G
30	R1	2062	A
30	R1	2069	G
30	R1	2076	U
30	R1	2080	A
30	R1	2095	A
30	R1	2097	A
30	R1	2099	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	2104	C
30	R1	2106	U
30	R1	2109	U
30	R1	2111	U
30	R1	2113	U
30	R1	2114	A
30	R1	2115	G
30	R1	2116	G
30	R1	2117	A
30	R1	2119	A
30	R1	2123	G
30	R1	2124	G
30	R1	2126	A
30	R1	2127	G
30	R1	2128	G
30	R1	2130	U
30	R1	2131	U
30	R1	2132	U
30	R1	2133	G
30	R1	2135	A
30	R1	2136	G
30	R1	2138	G
30	R1	2140	G
30	R1	2141	G
30	R1	2146	C
30	R1	2147	A
30	R1	2148	G
30	R1	2150	C
30	R1	2153	C
30	R1	2154	A
30	R1	2156	G
30	R1	2157	G
30	R1	2158	A
30	R1	2159	G
30	R1	2161	C
30	R1	2163	A
30	R1	2165	C
30	R1	2167	U
30	R1	2168	G
30	R1	2169	A
30	R1	2171	A
30	R1	2172	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	2173	A
30	R1	2174	C
30	R1	2175	C
30	R1	2176	A
30	R1	2177	C
30	R1	2178	C
30	R1	2179	C
30	R1	2182	U
30	R1	2184	A
30	R1	2186	G
30	R1	2188	U
30	R1	2189	U
30	R1	2190	G
30	R1	2204	G
30	R1	2211	A
30	R1	2214	C
30	R1	2225	A
30	R1	2226	C
30	R1	2238	G
30	R1	2239	G
30	R1	2250	G
30	R1	2266	A
30	R1	2279	G
30	R1	2283	C
30	R1	2286	G
30	R1	2287	A
30	R1	2291	U
30	R1	2297	A
30	R1	2305	U
30	R1	2316	G
30	R1	2319	G
30	R1	2322	A
30	R1	2325	G
30	R1	2327	A
30	R1	2333	A
30	R1	2334	U
30	R1	2335	A
30	R1	2345	G
30	R1	2347	C
30	R1	2359	C
30	R1	2361	G
30	R1	2371	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	2383	G
30	R1	2385	C
30	R1	2402	U
30	R1	2403	C
30	R1	2423	U
30	R1	2428	G
30	R1	2429	G
30	R1	2430	A
30	R1	2434	A
30	R1	2435	A
30	R1	2439	A
30	R1	2441	U
30	R1	2447	G
30	R1	2448	A
30	R1	2470	G
30	R1	2474	U
30	R1	2476	A
30	R1	2498	C
30	R1	2500	U
30	R1	2502	G
30	R1	2503	A
30	R1	2504	U
30	R1	2505	G
30	R1	2506	U
30	R1	2507	C
30	R1	2513	A
30	R1	2518	A
30	R1	2520	C
30	R1	2535	G
30	R1	2547	A
30	R1	2554	U
30	R1	2562	U
30	R1	2563	U
30	R1	2564	A
30	R1	2566	A
30	R1	2567	G
30	R1	2572	A
30	R1	2573	C
30	R1	2585	U
30	R1	2586	U
30	R1	2602	A
30	R1	2609	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	2613	U
30	R1	2629	U
30	R1	2662	A
30	R1	2663	G
30	R1	2664	G
30	R1	2666	C
30	R1	2669	G
30	R1	2671	G
30	R1	2682	A
30	R1	2689	U
30	R1	2690	U
30	R1	2700	A
30	R1	2706	A
30	R1	2713	U
30	R1	2714	G
30	R1	2716	C
30	R1	2726	A
30	R1	2732	G
30	R1	2733	A
30	R1	2738	A
30	R1	2744	G
30	R1	2748	A
30	R1	2751	G
30	R1	2761	A
30	R1	2765	A
30	R1	2774	C
30	R1	2775	G
30	R1	2778	A
30	R1	2779	U
30	R1	2796	U
30	R1	2797	U
30	R1	2798	U
30	R1	2799	A
30	R1	2800	A
30	R1	2808	G
30	R1	2815	C
30	R1	2816	G
30	R1	2818	U
30	R1	2820	A
30	R1	2835	A
30	R1	2840	C
30	R1	2849	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	2859	G
30	R1	2861	U
30	R1	2867	G
30	R1	2873	A
30	R1	2879	A
30	R1	2880	C
30	R1	2883	A
30	R1	2897	U
30	R1	2900	A
31	R2	12	C
31	R2	13	G
31	R2	25	U
31	R2	35	C
31	R2	41	G
31	R2	42	C
31	R2	44	G
31	R2	52	A
31	R2	62	C
31	R2	66	A
31	R2	67	G
31	R2	87	U
31	R2	88	C
31	R2	89	U
31	R2	90	C
31	R2	107	G
31	R2	108	A
31	R2	109	A
31	R2	111	U
31	R2	113	C
31	R2	114	C
31	R2	118	C
31	R2	119	A
32	R3	3	A
32	R3	4	U
32	R3	5	U
32	R3	6	G
32	R3	9	G
32	R3	22	G
32	R3	30	U
32	R3	31	G
32	R3	32	A
32	R3	39	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	47	C
32	R3	48	C
32	R3	49	U
32	R3	50	A
32	R3	51	A
32	R3	53	A
32	R3	54	C
32	R3	60	A
32	R3	61	G
32	R3	62	U
32	R3	66	A
32	R3	70	U
32	R3	77	A
32	R3	78	A
32	R3	79	G
32	R3	80	A
32	R3	81	A
32	R3	82	G
32	R3	83	C
32	R3	84	U
32	R3	85	U
32	R3	87	C
32	R3	90	C
32	R3	91	U
32	R3	92	U
32	R3	94	G
32	R3	95	C
32	R3	96	U
32	R3	115	G
32	R3	118	U
32	R3	120	A
32	R3	121	U
32	R3	122	G
32	R3	130	A
32	R3	131	A
32	R3	133	U
32	R3	142	G
32	R3	149	A
32	R3	161	A
32	R3	170	U
32	R3	171	A
32	R3	172	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	173	U
32	R3	177	G
32	R3	181	A
32	R3	183	C
32	R3	184	G
32	R3	190	A
32	R3	197	A
32	R3	202	G
32	R3	204	G
32	R3	205	A
32	R3	206	C
32	R3	207	C
32	R3	208	U
32	R3	209	U
32	R3	210	C
32	R3	215	C
32	R3	216	U
32	R3	217	C
32	R3	220	G
32	R3	224	U
32	R3	226	G
32	R3	240	G
32	R3	243	A
32	R3	245	U
32	R3	246	A
32	R3	247	G
32	R3	250	A
32	R3	251	G
32	R3	255	G
32	R3	262	A
32	R3	266	G
32	R3	267	C
32	R3	270	A
32	R3	272	C
32	R3	274	A
32	R3	283	U
32	R3	287	U
32	R3	289	G
32	R3	290	C
32	R3	293	G
32	R3	302	G
32	R3	306	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	313	A
32	R3	316	C
32	R3	319	G
32	R3	322	C
32	R3	323	U
32	R3	324	G
32	R3	328	C
32	R3	329	A
32	R3	330	C
32	R3	331	G
32	R3	332	G
32	R3	333	U
32	R3	338	A
32	R3	339	C
32	R3	344	A
32	R3	345	C
32	R3	347	G
32	R3	352	C
32	R3	353	A
32	R3	354	G
32	R3	360	G
32	R3	363	A
32	R3	364	A
32	R3	367	U
32	R3	369	G
32	R3	370	C
32	R3	372	C
32	R3	376	G
32	R3	377	G
32	R3	378	G
32	R3	379	C
32	R3	381	C
32	R3	384	G
32	R3	388	G
32	R3	389	A
32	R3	390	U
32	R3	391	G
32	R3	392	C
32	R3	394	G
32	R3	401	C
32	R3	403	C
32	R3	406	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	412	A
32	R3	413	G
32	R3	415	A
32	R3	416	G
32	R3	418	C
32	R3	419	C
32	R3	421	U
32	R3	422	C
32	R3	425	G
32	R3	426	U
32	R3	429	U
32	R3	437	U
32	R3	438	U
32	R3	439	U
32	R3	451	A
32	R3	454	G
32	R3	457	G
32	R3	458	U
32	R3	460	A
32	R3	461	A
32	R3	462	G
32	R3	463	U
32	R3	464	U
32	R3	465	A
32	R3	466	A
32	R3	467	U
32	R3	468	A
32	R3	469	C
32	R3	470	C
32	R3	472	U
32	R3	473	U
32	R3	475	C
32	R3	476	U
32	R3	481	G
32	R3	482	A
32	R3	484	G
32	R3	494	G
32	R3	495	A
32	R3	496	A
32	R3	497	G
32	R3	498	A
32	R3	501	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	509	A
32	R3	511	C
32	R3	514	C
32	R3	518	C
32	R3	521	G
32	R3	524	G
32	R3	527	G
32	R3	529	G
32	R3	530	G
32	R3	531	U
32	R3	532	A
32	R3	540	G
32	R3	541	G
32	R3	545	C
32	R3	547	A
32	R3	549	C
32	R3	562	U
32	R3	564	C
32	R3	573	A
32	R3	576	C
32	R3	577	G
32	R3	579	A
32	R3	589	U
32	R3	596	A
32	R3	607	A
32	R3	610	U
32	R3	613	C
32	R3	618	C
32	R3	624	C
32	R3	632	U
32	R3	640	A
32	R3	650	G
32	R3	653	U
32	R3	665	A
32	R3	673	A
32	R3	682	G
32	R3	684	U
32	R3	686	U
32	R3	688	G
32	R3	694	A
32	R3	703	G
32	R3	713	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	721	G
32	R3	723	U
32	R3	724	G
32	R3	731	G
32	R3	738	C
32	R3	739	C
32	R3	747	A
32	R3	749	A
32	R3	754	C
32	R3	755	G
32	R3	774	G
32	R3	777	A
32	R3	779	C
32	R3	781	A
32	R3	791	G
32	R3	792	A
32	R3	793	U
32	R3	794	A
32	R3	815	A
32	R3	817	C
32	R3	821	G
32	R3	829	G
32	R3	832	G
32	R3	836	G
32	R3	838	G
32	R3	839	C
32	R3	842	U
32	R3	843	U
32	R3	844	G
32	R3	846	G
32	R3	847	G
32	R3	849	G
32	R3	853	C
32	R3	858	G
32	R3	863	U
32	R3	864	A
32	R3	870	U
32	R3	871	U
32	R3	872	A
32	R3	876	C
32	R3	878	A
32	R3	889	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	902	G
32	R3	914	A
32	R3	926	G
32	R3	933	G
32	R3	935	A
32	R3	956	U
32	R3	958	A
32	R3	959	A
32	R3	960	U
32	R3	961	U
32	R3	966	G
32	R3	968	A
32	R3	969	A
32	R3	974	A
32	R3	975	A
32	R3	976	G
32	R3	977	A
32	R3	981	U
32	R3	982	U
32	R3	989	U
32	R3	991	U
32	R3	992	U
32	R3	993	G
32	R3	994	A
32	R3	1000	A
32	R3	1002	G
32	R3	1003	G
32	R3	1004	A
32	R3	1006	G
32	R3	1007	U
32	R3	1017	U
32	R3	1022	A
32	R3	1026	G
32	R3	1028	C
32	R3	1029	U
32	R3	1031	C
32	R3	1033	G
32	R3	1035	A
32	R3	1036	A
32	R3	1038	C
32	R3	1039	G
32	R3	1040	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	1041	G
32	R3	1042	A
32	R3	1044	A
32	R3	1045	C
32	R3	1049	U
32	R3	1050	G
32	R3	1052	U
32	R3	1056	U
32	R3	1084	G
32	R3	1085	U
32	R3	1086	U
32	R3	1094	G
32	R3	1095	U
32	R3	1101	A
32	R3	1103	C
32	R3	1104	G
32	R3	1108	G
32	R3	1113	C
32	R3	1121	U
32	R3	1123	U
32	R3	1124	G
32	R3	1125	U
32	R3	1126	U
32	R3	1130	A
32	R3	1131	G
32	R3	1133	G
32	R3	1136	C
32	R3	1137	C
32	R3	1138	G
32	R3	1139	G
32	R3	1142	G
32	R3	1150	A
32	R3	1151	A
32	R3	1158	C
32	R3	1159	U
32	R3	1169	A
32	R3	1182	G
32	R3	1187	G
32	R3	1196	A
32	R3	1199	U
32	R3	1208	C
32	R3	1212	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	1213	A
32	R3	1214	C
32	R3	1226	C
32	R3	1227	A
32	R3	1228	C
32	R3	1236	A
32	R3	1238	A
32	R3	1256	A
32	R3	1257	A
32	R3	1258	G
32	R3	1261	A
32	R3	1268	G
32	R3	1271	A
32	R3	1275	A
32	R3	1280	A
32	R3	1285	A
32	R3	1286	U
32	R3	1287	A
32	R3	1297	G
32	R3	1298	U
32	R3	1300	G
32	R3	1302	C
32	R3	1305	G
32	R3	1306	A
32	R3	1310	G
32	R3	1314	C
32	R3	1320	C
32	R3	1323	G
32	R3	1332	A
32	R3	1333	A
32	R3	1336	C
32	R3	1338	G
32	R3	1346	A
32	R3	1353	G
32	R3	1363	A
32	R3	1364	U
32	R3	1370	G
32	R3	1376	U
32	R3	1378	C
32	R3	1419	G
32	R3	1432	G
32	R3	1434	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R3	1441	A
32	R3	1442	G
32	R3	1446	A
32	R3	1451	U
32	R3	1452	C
32	R3	1453	G
32	R3	1472	U
32	R3	1493	A
32	R3	1497	G
32	R3	1499	A
32	R3	1502	A
32	R3	1503	A
32	R3	1505	G
32	R3	1506	U
32	R3	1517	G
32	R3	1529	G
32	R3	1530	G
53	T	8	4SU
53	T	9	G
53	T	15	C
53	T	16	C
53	T	17	U
53	T	18	G
53	T	19	G
53	T	21	A
53	T	22	G
53	T	32	4OC
53	T	42	G
53	T	47	U
53	T	55	PSU
53	T	57	A
53	T	61	C
53	T	76	A

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
30	R1	70	G
30	R1	100	U
30	R1	360	U
30	R1	784	G
30	R1	859	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
30	R1	1020	A
30	R1	1050	A
30	R1	1847	G
30	R1	2105	U
30	R1	2189	U
30	R1	2663	G
30	R1	2665	A
30	R1	2839	G
30	R1	2896	C
32	R3	2	A
32	R3	120	A
32	R3	288	A
32	R3	301	G
32	R3	312	C
32	R3	363	A
32	R3	375	U
32	R3	453	G
32	R3	461	A
32	R3	497	G
32	R3	500	G
32	R3	561	U
32	R3	588	G
32	R3	612	C
32	R3	672	U
32	R3	753	A
32	R3	837	U
32	R3	870	U
32	R3	1125	U
32	R3	1132	C
32	R3	1149	C
32	R3	1270	G
32	R3	1297	G
32	R3	1305	G
53	T	8	4SU
53	T	17	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
53	PSU	T	55	53	18,21,22	2.28	8 (44%)	21,30,33	2.07	4 (19%)
53	4OC	T	32	53	20,23,24	2.86	4 (20%)	25,32,35	2.11	6 (24%)
53	MUM	T	54	53	18,22,22	2.84	3 (16%)	19,32,32	2.14	5 (26%)
53	H2U	T	20	53	18,21,22	4.42	5 (27%)	19,30,33	4.09	6 (31%)
53	FME	T	101	53	8,9,10	0.99	0	8,9,11	0.96	0
53	4SU	T	8	53	18,21,22	3.37	7 (38%)	25,30,33	2.31	6 (24%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	PSU	T	55	53	-	1/7/25/26	0/2/2/2
53	4OC	T	32	53	1/1/5/6	4/9/29/30	0/2/2/2
53	MUM	T	54	53	1/1/9/10	0/7/41/41	0/2/2/2
53	H2U	T	20	53	2/2/8/9	4/7/38/39	0/2/2/2
53	FME	T	101	53	-	1/7/9/11	-
53	4SU	T	8	53	2/2/5/5	4/7/25/26	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	T	54	MUM	C6-N1	-10.45	1.34	1.46
53	T	20	H2U	O4-C4	10.42	1.43	1.23
53	T	32	4OC	O2-C2	9.48	1.41	1.23
53	T	20	H2U	C2-N1	9.32	1.48	1.35
53	T	8	4SU	C4-S4	8.73	1.84	1.68
53	T	20	H2U	O2-C2	8.44	1.38	1.23
53	T	8	4SU	O2-C2	7.33	1.36	1.23
53	T	20	H2U	C2-N3	7.00	1.50	1.38
53	T	32	4OC	C4-N4	5.91	1.48	1.36
53	T	20	H2U	C4-N3	5.70	1.47	1.37
53	T	8	4SU	C4-N3	-5.31	1.32	1.37
53	T	55	PSU	C1'-C5	-4.61	1.39	1.50
53	T	32	4OC	C2-N1	-4.55	1.30	1.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
53	T	8	4SU	C2-N1	-4.45	1.31	1.38
53	T	54	MUM	C6-C5	-3.82	1.40	1.51
53	T	55	PSU	C2-N1	-3.80	1.31	1.36
53	T	55	PSU	C6-C5	3.47	1.39	1.35
53	T	55	PSU	C4-N3	-3.44	1.32	1.38
53	T	55	PSU	C2-N3	-3.23	1.32	1.37
53	T	8	4SU	C5-C4	-3.22	1.38	1.42
53	T	54	MUM	C2-N3	-3.18	1.32	1.38
53	T	8	4SU	C2-N3	-2.78	1.33	1.38
53	T	55	PSU	C6-N1	-2.54	1.32	1.36
53	T	32	4OC	C6-N1	-2.43	1.32	1.38
53	T	55	PSU	O4-C4	-2.40	1.19	1.23
53	T	55	PSU	O2-C2	-2.16	1.18	1.23
53	T	8	4SU	C6-N1	-2.08	1.33	1.38

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	T	20	H2U	O2-C2-N1	-12.11	108.54	123.10
53	T	20	H2U	O4-C4-N3	-7.30	109.04	120.30
53	T	20	H2U	O2-C2-N3	-6.81	108.92	121.49
53	T	20	H2U	O4-C4-C5	-6.64	108.61	122.20
53	T	8	4SU	C4-N3-C2	-6.18	121.39	127.31
53	T	55	PSU	N1-C2-N3	6.15	121.66	115.17
53	T	32	4OC	C1'-N1-C2	5.96	131.62	118.44
53	T	54	MUM	C4-N3-C2	-5.27	120.41	126.83
53	T	8	4SU	C5-C4-N3	5.17	119.56	114.75
53	T	54	MUM	N3-C2-N1	4.94	121.61	116.65
53	T	32	4OC	O2-C2-N3	-4.70	114.92	122.33
53	T	8	4SU	N3-C2-N1	4.64	120.93	114.89
53	T	32	4OC	C1'-N1-C6	-4.18	111.84	120.78
53	T	55	PSU	C4-N3-C2	-4.11	120.71	126.37
53	T	20	H2U	N3-C2-N1	-4.04	112.58	116.65
53	T	55	PSU	O2-C2-N1	-3.81	118.86	122.79
53	T	8	4SU	C5-C4-S4	-3.77	120.00	124.31
53	T	54	MUM	C5M-C5-C6	3.63	120.43	112.05
53	T	54	MUM	O2-C2-N1	-3.24	119.21	123.10
53	T	8	4SU	C6-C5-C4	-2.98	117.37	119.95
53	T	55	PSU	C5-C6-N1	-2.85	118.19	122.14
53	T	32	4OC	C5-C4-N3	-2.83	118.17	122.60
53	T	8	4SU	C1'-N1-C2	2.83	122.68	117.59
53	T	20	H2U	C5-C4-N3	-2.76	113.76	116.69

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	T	32	4OC	N1-C2-N3	2.62	123.34	118.80
53	T	54	MUM	C6-C5-C4	2.53	118.79	111.53
53	T	32	4OC	C6-N1-C2	-2.33	116.53	120.46

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
53	T	8	4SU	C2'
53	T	8	4SU	C3'
53	T	20	H2U	C2'
53	T	20	H2U	C1'
53	T	32	4OC	C2'
53	T	54	MUM	C5

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
53	T	8	4SU	C3'-C4'-C5'-O5'
53	T	20	H2U	O4'-C1'-N1-C6
53	T	32	4OC	O4'-C4'-C5'-O5'
53	T	20	H2U	C2'-C1'-N1-C2
53	T	101	FME	CA-CB-CG-SD
53	T	32	4OC	C2'-C1'-N1-C2
53	T	8	4SU	O4'-C4'-C5'-O5'
53	T	32	4OC	C3'-C4'-C5'-O5'
53	T	32	4OC	C2'-C1'-N1-C6
53	T	8	4SU	O4'-C1'-N1-C2
53	T	8	4SU	O4'-C1'-N1-C6
53	T	20	H2U	C2'-C1'-N1-C6
53	T	55	PSU	C4'-C5'-O5'-P
53	T	20	H2U	O4'-C1'-N1-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
53	T	32	4OC	2	0
53	T	101	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 161 ligands modelled in this entry, 161 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
30	R1	5
32	R3	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R3	210:C	O3'	211:G	P	6.13
1	R1	2101:A	O3'	2102:G	P	3.78
1	R1	2194:U	O3'	2195:U	P	3.78
1	R1	2186:G	O3'	2187:U	P	3.51
1	R1	2097:A	O3'	2098:U	P	3.46
1	R3	460:A	O3'	461:A	P	3.20
1	R1	2188:U	O3'	2189:U	P	3.09

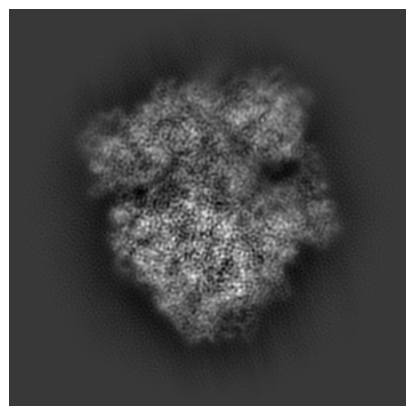
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40932. These allow visual inspection of the internal detail of the map and identification of artifacts.

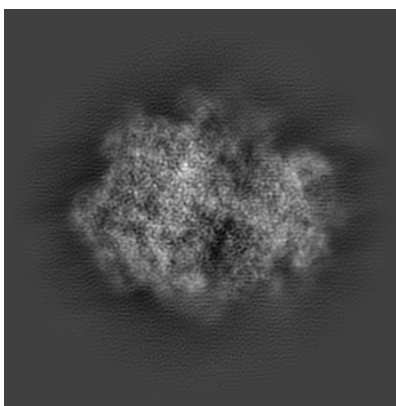
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

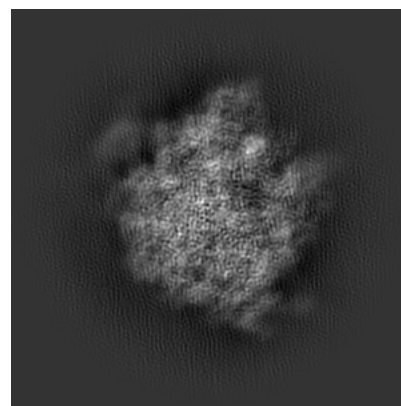
6.1.1 Primary map



X

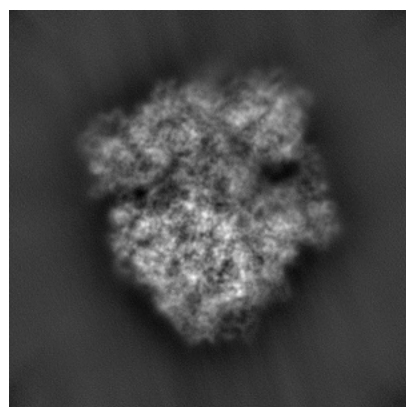


Y

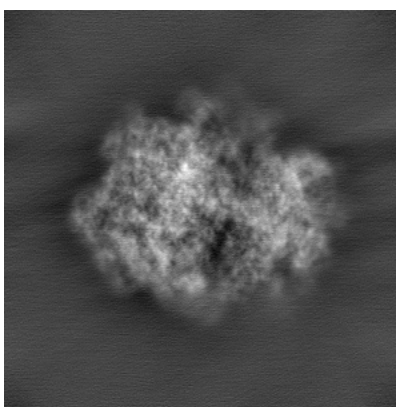


Z

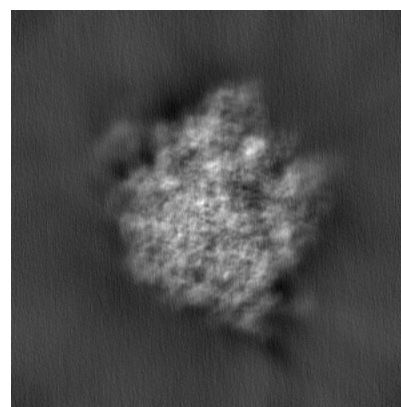
6.1.2 Raw map



X



Y

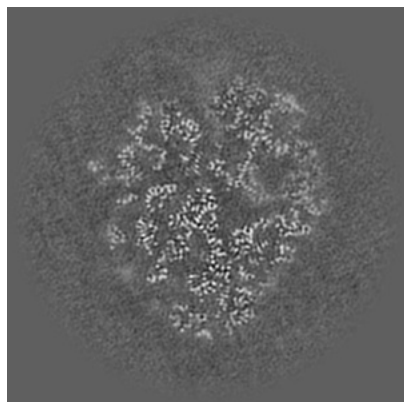


Z

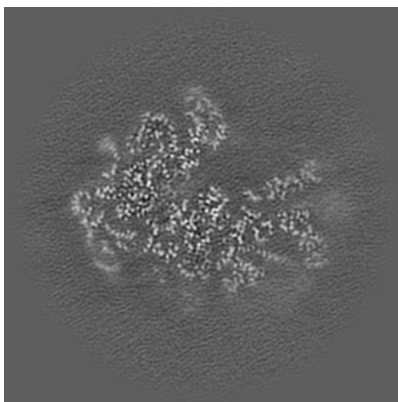
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

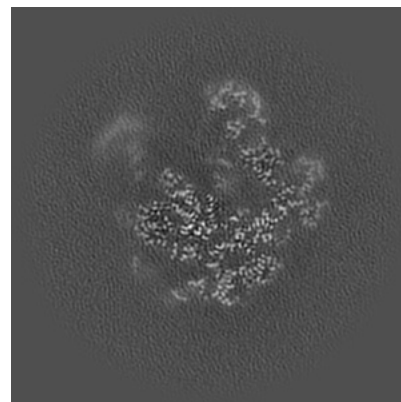
6.2.1 Primary map



X Index: 200

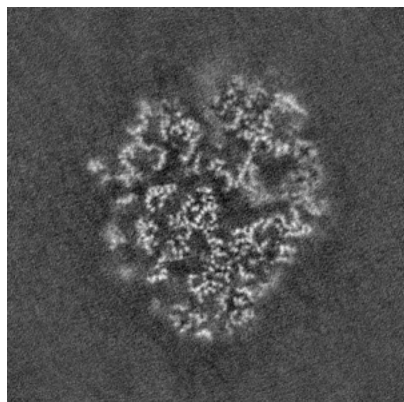


Y Index: 200

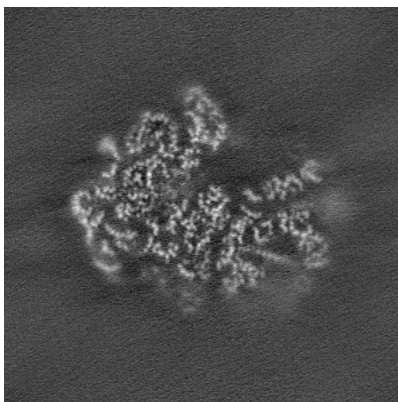


Z Index: 200

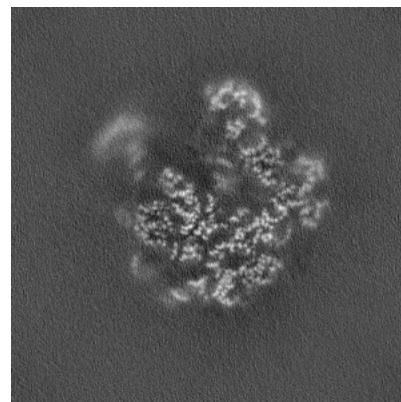
6.2.2 Raw map



X Index: 200



Y Index: 200

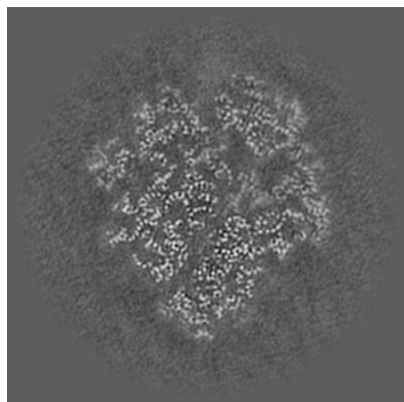


Z Index: 200

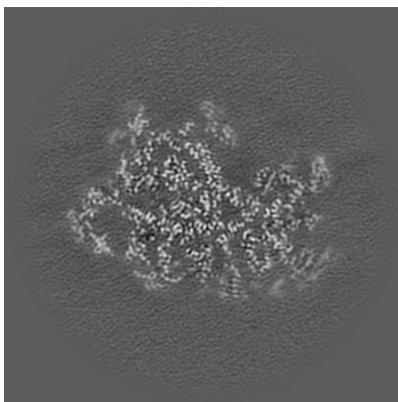
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

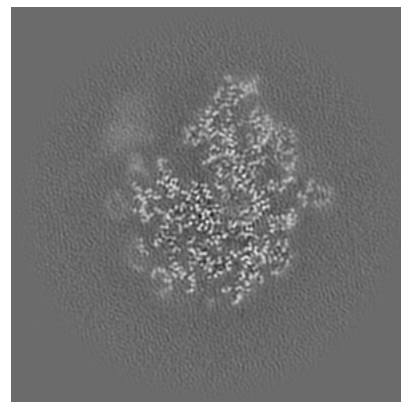
6.3.1 Primary map



X Index: 208

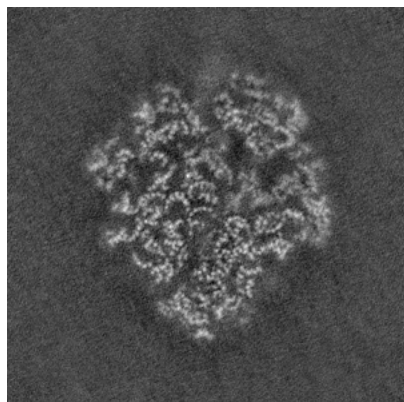


Y Index: 181

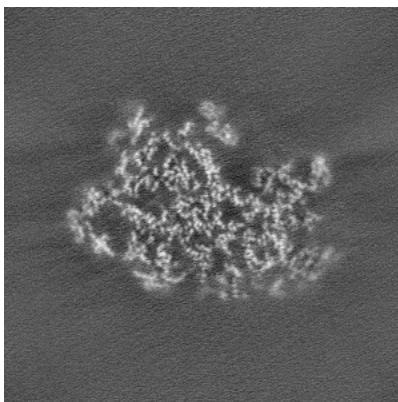


Z Index: 182

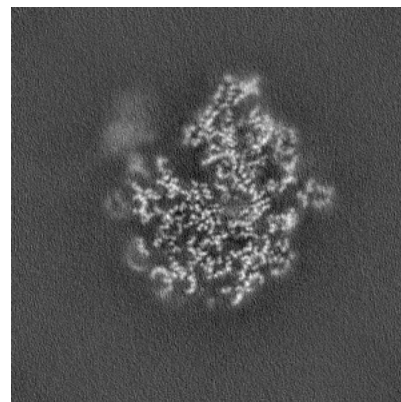
6.3.2 Raw map



X Index: 208



Y Index: 182

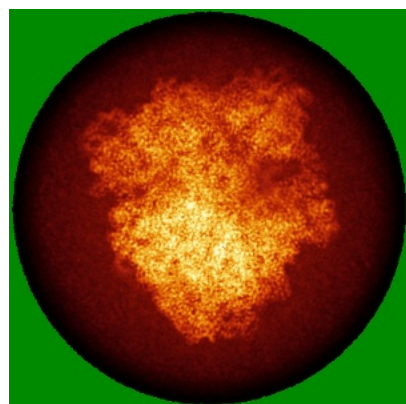


Z Index: 182

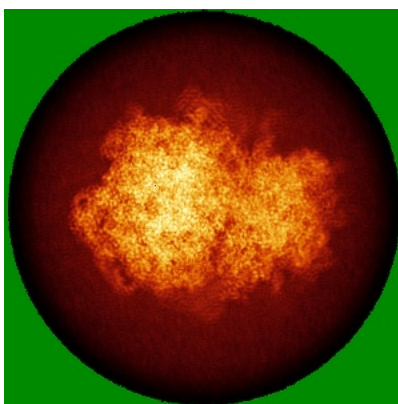
The images above show the largest variance slices of the map in three orthogonal directions.

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

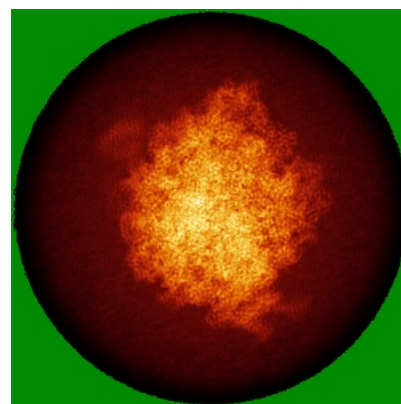
6.4.1 Primary map



X

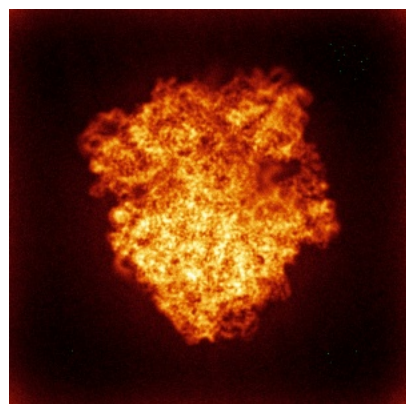


Y

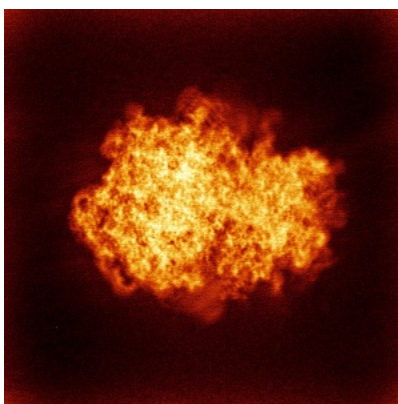


Z

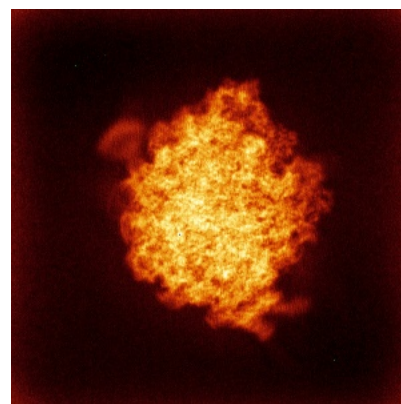
6.4.2 Raw map



X



Y

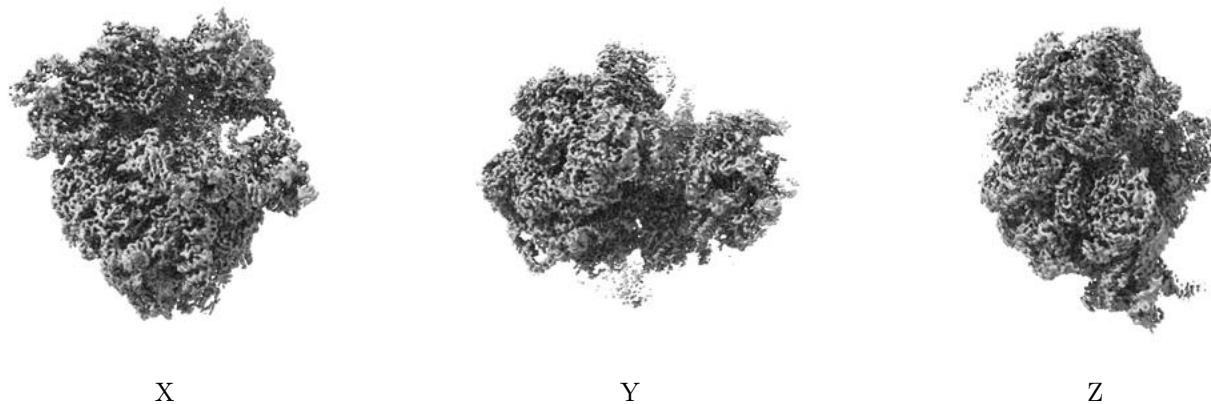


Z

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.

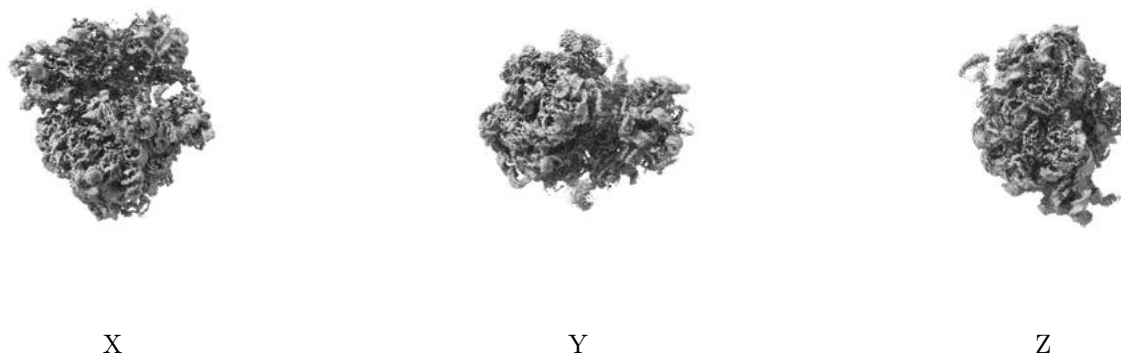
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.55. 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.

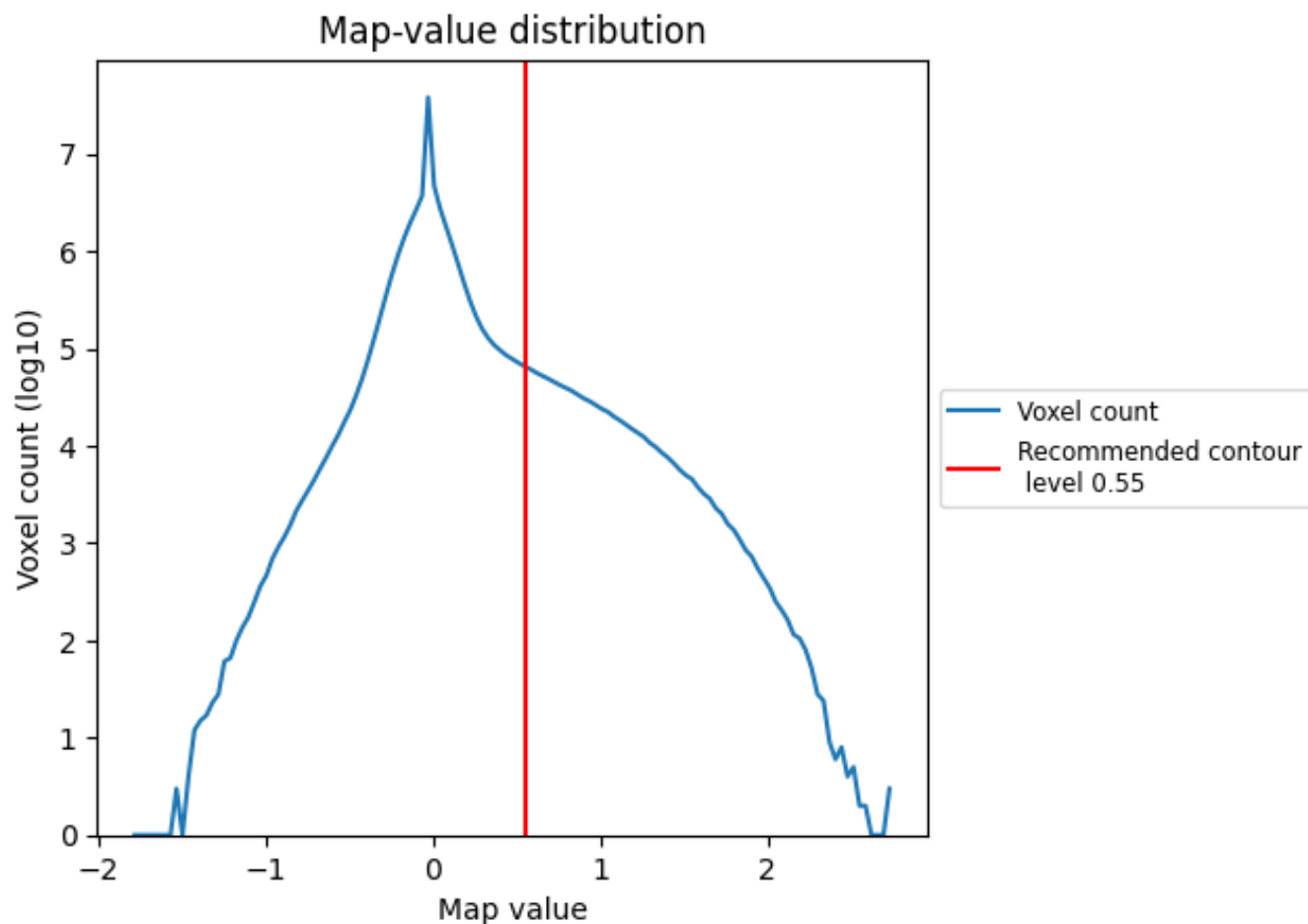
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

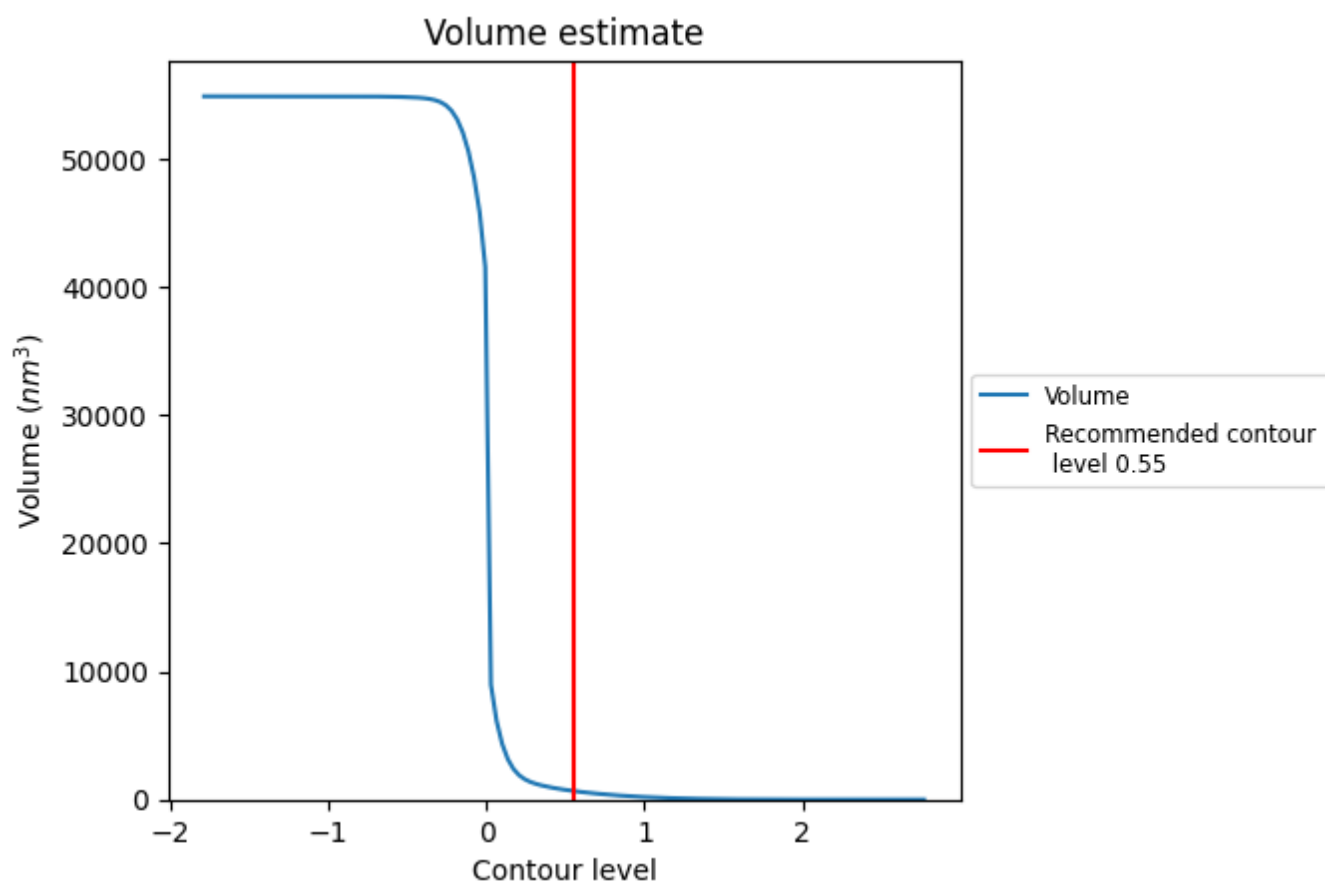
This section contains the results of statistical analysis of the map.

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.

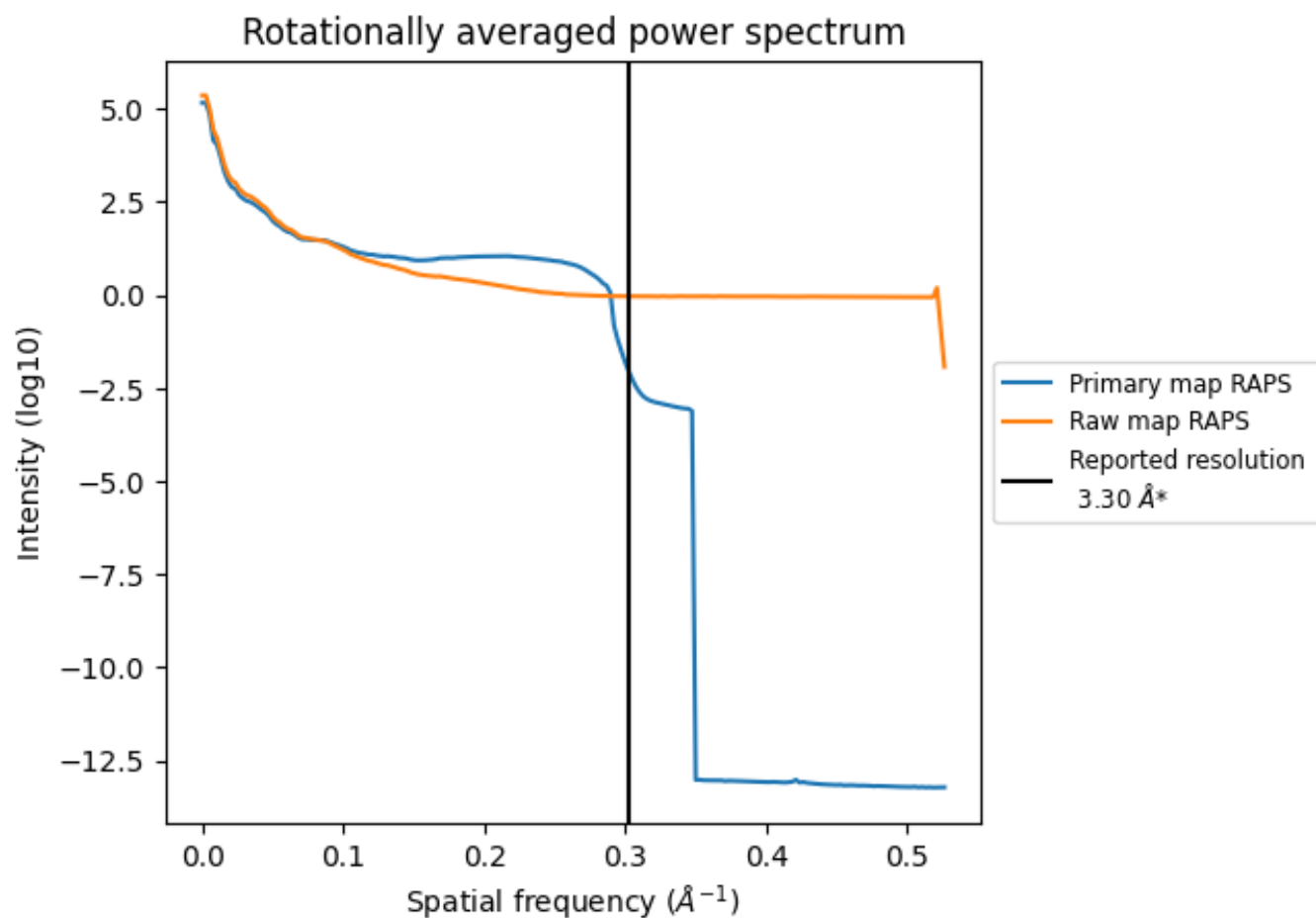
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 671 nm³; this corresponds to an approximate mass of 606 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 ⓘ

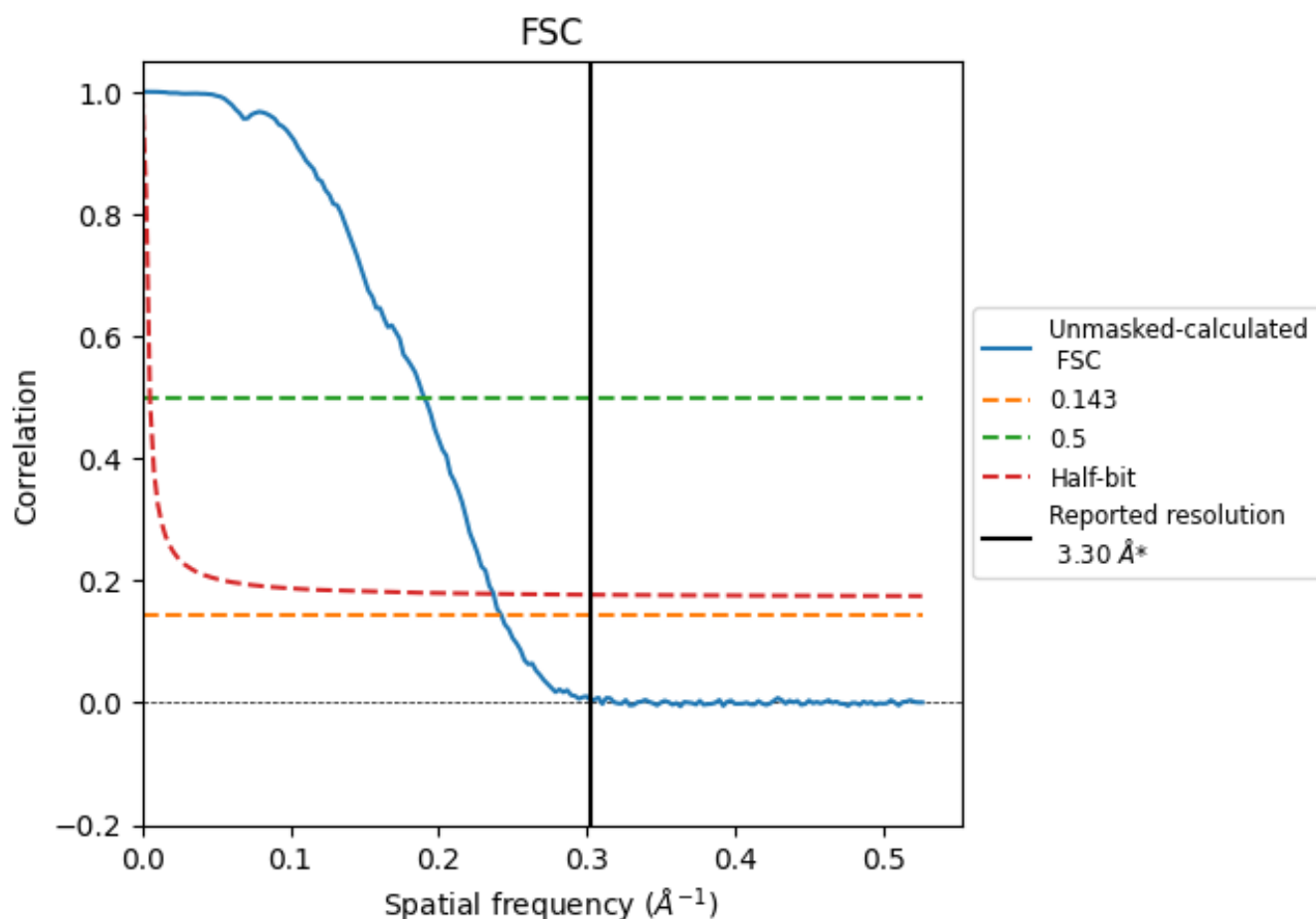


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 0.303 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

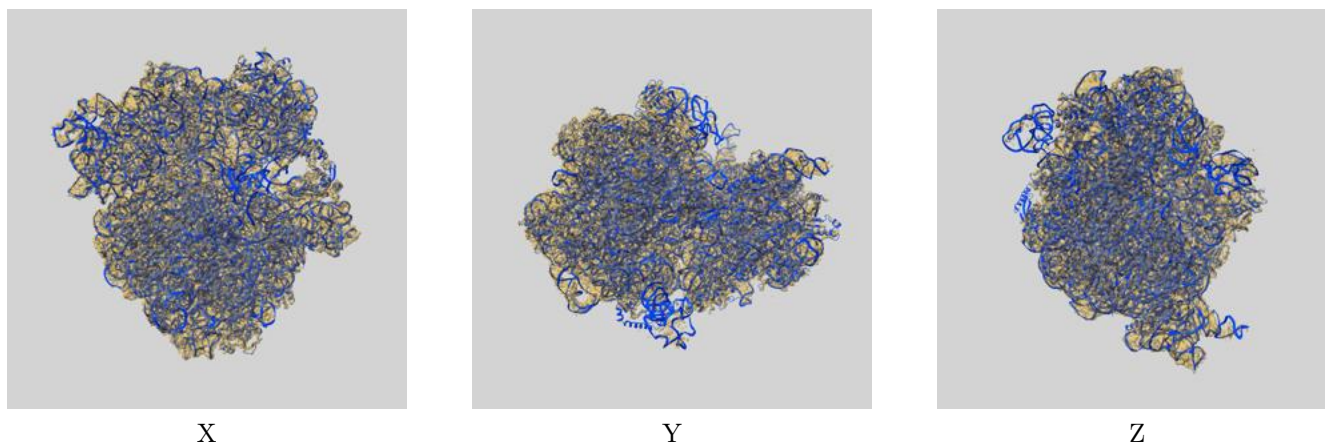
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.13	5.26	4.22

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.13 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

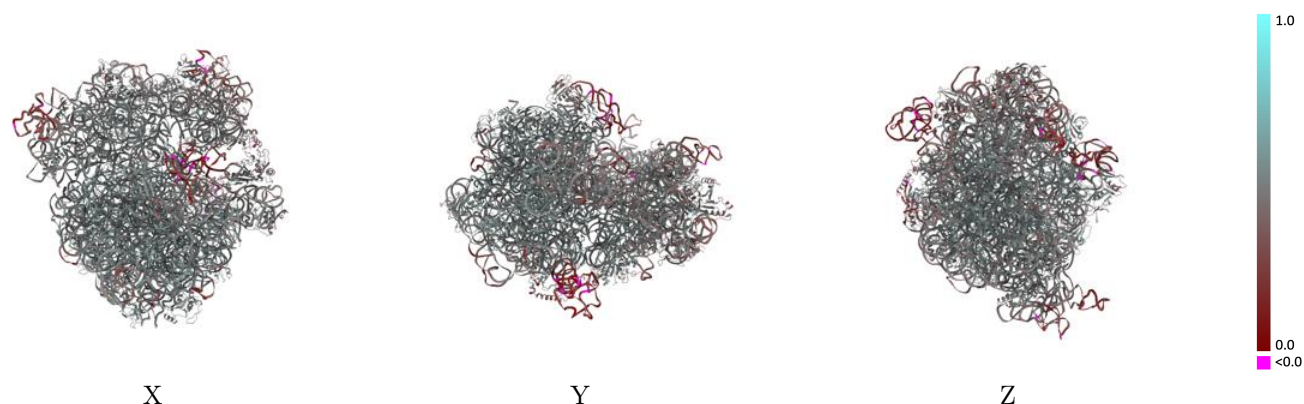
This section contains information regarding the fit between EMDB map EMD-40932 and PDB model 9NKL. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



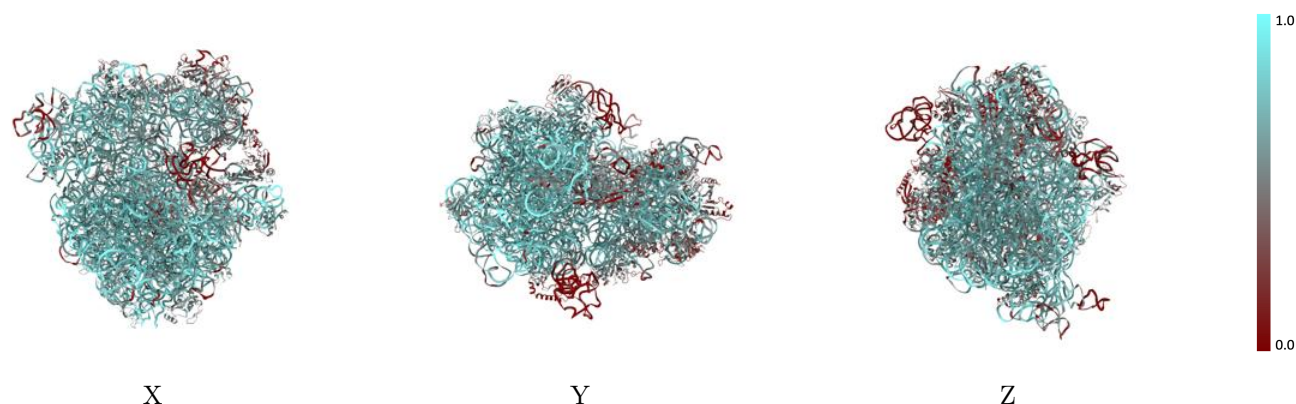
The images above show the 3D surface view of the map at the recommended contour level 0.55 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



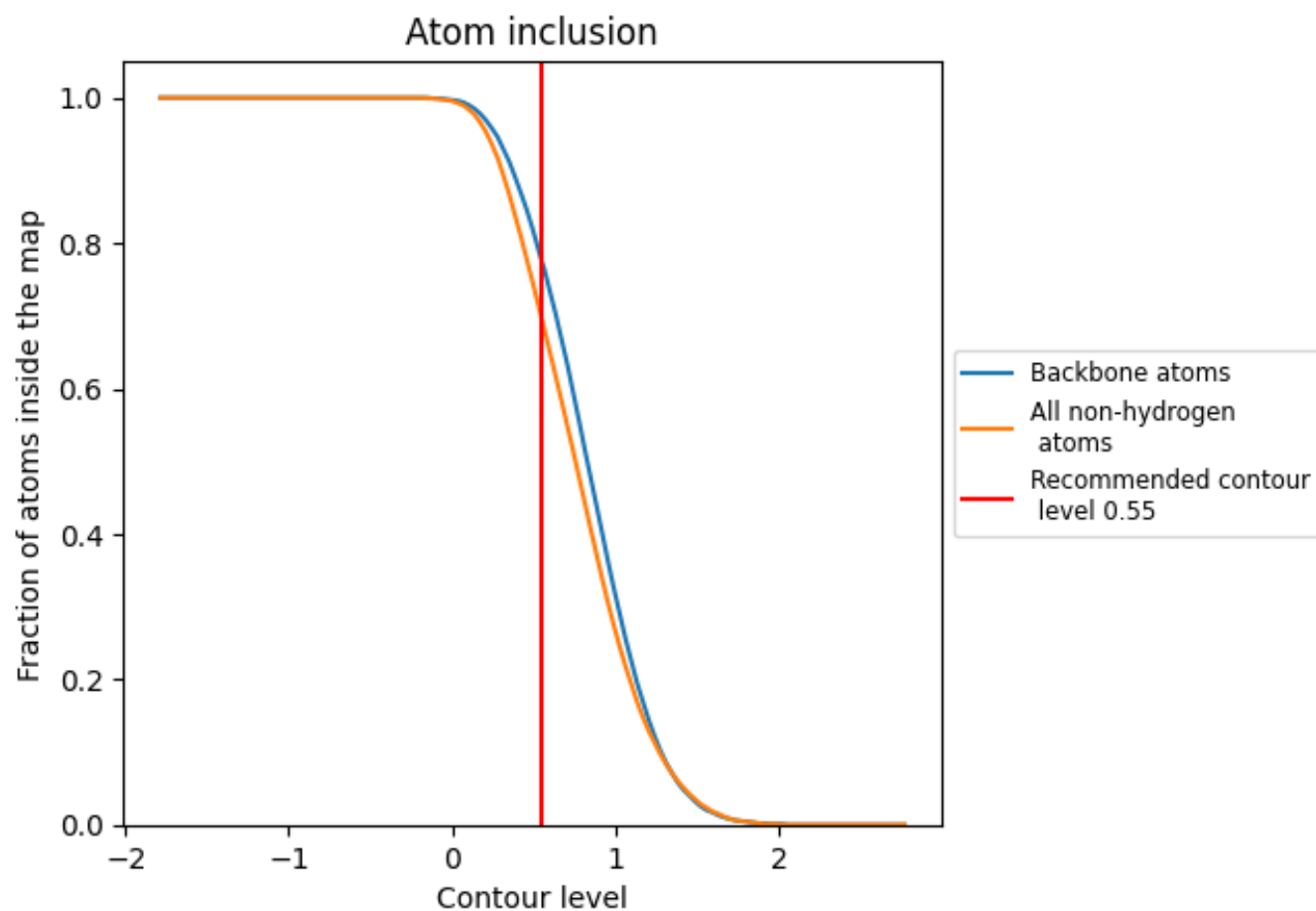
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.55).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 69% 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 (0.55) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6940	 0.4760
13	 0.6750	 0.5350
14	 0.6360	 0.5480
15	 0.6740	 0.5340
16	 0.6370	 0.5370
17	 0.7200	 0.5360
18	 0.5630	 0.4810
19	 0.6430	 0.5350
2	 0.6680	 0.5530
20	 0.7270	 0.5450
21	 0.6370	 0.5190
22	 0.6590	 0.5360
23	 0.5750	 0.5030
24	 0.5980	 0.5090
25	 0.5790	 0.5130
27	 0.6750	 0.5500
28	 0.6700	 0.5390
29	 0.5880	 0.4790
3	 0.6810	 0.5400
30	 0.6250	 0.5290
31	 0.1120	 0.3770
32	 0.6900	 0.5330
33	 0.6910	 0.5080
34	 0.7100	 0.5550
35	 0.7090	 0.5550
36	 0.6270	 0.5280
4	 0.5710	 0.5120
5	 0.4250	 0.4530
6	 0.4550	 0.4610
9	 0.1120	 0.3380
M	 0.6100	 0.4960
R1	 0.7750	 0.4740
R2	 0.7880	 0.4580
R3	 0.7430	 0.4590
T	 0.4990	 0.4240



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
sb	 0.3150	 0.4310
sc	 0.5050	 0.4900
sd	 0.4770	 0.4800
se	 0.5800	 0.5050
sf	 0.4950	 0.4730
sg	 0.4000	 0.4560
sh	 0.6070	 0.5170
si	 0.4210	 0.4500
sj	 0.3440	 0.4340
sk	 0.5420	 0.4980
sl	 0.5370	 0.5170
sm	 0.4410	 0.4670
sn	 0.4730	 0.4450
so	 0.5970	 0.5110
sp	 0.5530	 0.4960
sq	 0.5210	 0.4970
sr	 0.4590	 0.4590
ss	 0.4350	 0.4500
st	 0.5230	 0.4930
su	 0.3370	 0.3910