



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 02:06 am BST

PDB ID : 7NWW / pdb_00007nww
EMDB ID : EMD-12636
Title : CspA-27 cotranslational folding intermediate 1
Authors : Agirrezabala, X.; Samatova, E.; Macher, M.; Liutkute, M.; Gil-Carton, D.;
Novacek, J.; Valle, M.; Rodnina, M.V.
Deposited on : 2021-03-17
Resolution : 3.05 Å(reported)
Based on initial model : 6ORE

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 : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

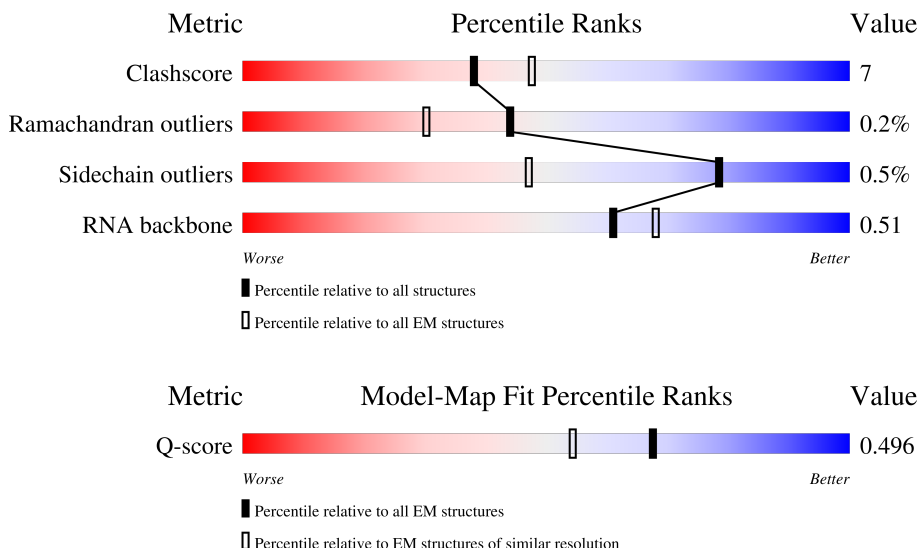
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 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	13971 (2.55 - 3.55)

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	1	2903	
2	2	1534	
3	3	120	

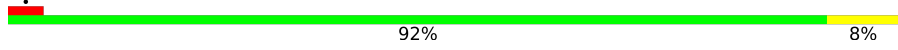
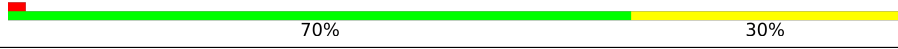
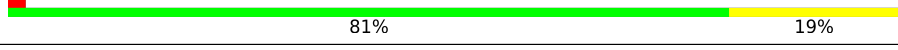
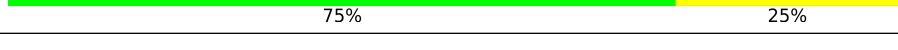
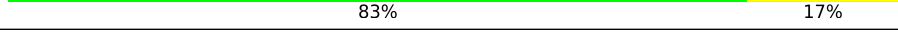
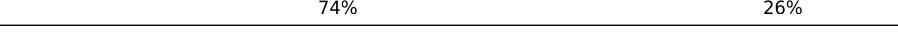
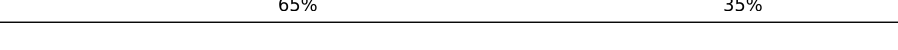
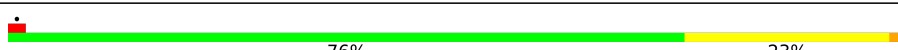
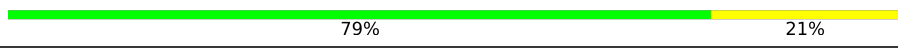
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Mol	Chain	Length	Quality of chain
4	4	6	
5	C	271	
6	D	209	
7	E	201	
8	F	177	
9	G	175	
10	H	149	
11	I	142	
12	J	123	
13	K	144	
14	L	136	
15	M	119	
16	N	116	
17	O	114	
18	P	117	
19	Q	103	
20	R	110	
21	S	94	
22	T	103	
23	U	94	
24	V	80	
25	W	77	
26	X	62	
27	Y	58	
28	Z	66	

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Mol	Chain	Length	Quality of chain
29	a	56	
30	b	52	
31	c	46	
32	d	64	
33	e	38	
34	f	225	
35	g	208	
36	h	205	
37	i	156	
38	j	104	
39	k	151	
40	l	129	
41	m	127	
42	n	99	
43	o	117	
44	p	123	
45	q	116	
46	r	100	
47	s	88	
48	t	82	
49	u	80	
50	v	66	
51	w	83	
52	x	86	
53	y	70	

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Mol	Chain	Length	Quality of chain
54	z	88	38% 40% 20%
55	B	27	19% 19% 52% 19% 11%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 145149 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	6	Total	C	N	O	P	0	0
			126	56	20	44	6		

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	G	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L13.

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

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

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

- Molecule 14 is a protein called 50S ribosomal protein L16.

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

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

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

- Molecule 17 is a protein called 50S ribosomal protein L19.

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

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	P	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 19 is a protein called 50S ribosomal protein L21.

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

- Molecule 20 is a protein called 50S ribosomal protein L22.

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

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 23 is a protein called 50S ribosomal protein L25.

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

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	80	Total	C	N	O	S	0	0
			601	370	121	109	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

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

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

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

- Molecule 29 is a protein called 50S ribosomal protein L32.

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

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	52	Total	C	N	O	S	0	0
			426	275	78	73			

- Molecule 31 is a protein called 50S ribosomal protein L34.

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

- Molecule 32 is a protein called 50S ribosomal protein L35.

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

- Molecule 33 is a protein called 50S ribosomal protein L36.

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

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

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

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

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

- Molecule 40 is a protein called 30S ribosomal protein S8.

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

- Molecule 41 is a protein called 30S ribosomal protein S9.

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

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

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

- Molecule 47 is a protein called 30S ribosomal protein S15.

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

- Molecule 48 is a protein called 30S ribosomal protein S16.

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

- Molecule 49 is a protein called 30S ribosomal protein S17.

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

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	w	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	x	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	y	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is a RNA chain called tRNA-Ser.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	z	88	Total	C	N	O	P	0	0
			1891	841	341	621	88		

- Molecule 55 is a protein called 7.4 kDa cold shock protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	B	27	Total	C	N	O	S	0	0
			205	132	32	39	2		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	278	Total 278	Mg 278	0
56	2	119	Total 119	Mg 119	0
56	3	8	Total 8	Mg 8	0
56	C	1	Total 1	Mg 1	0
56	D	1	Total 1	Mg 1	0
56	P	1	Total 1	Mg 1	0
56	a	1	Total 1	Mg 1	0
56	h	1	Total 1	Mg 1	0
56	q	1	Total 1	Mg 1	0
56	z	2	Total 2	Mg 2	0

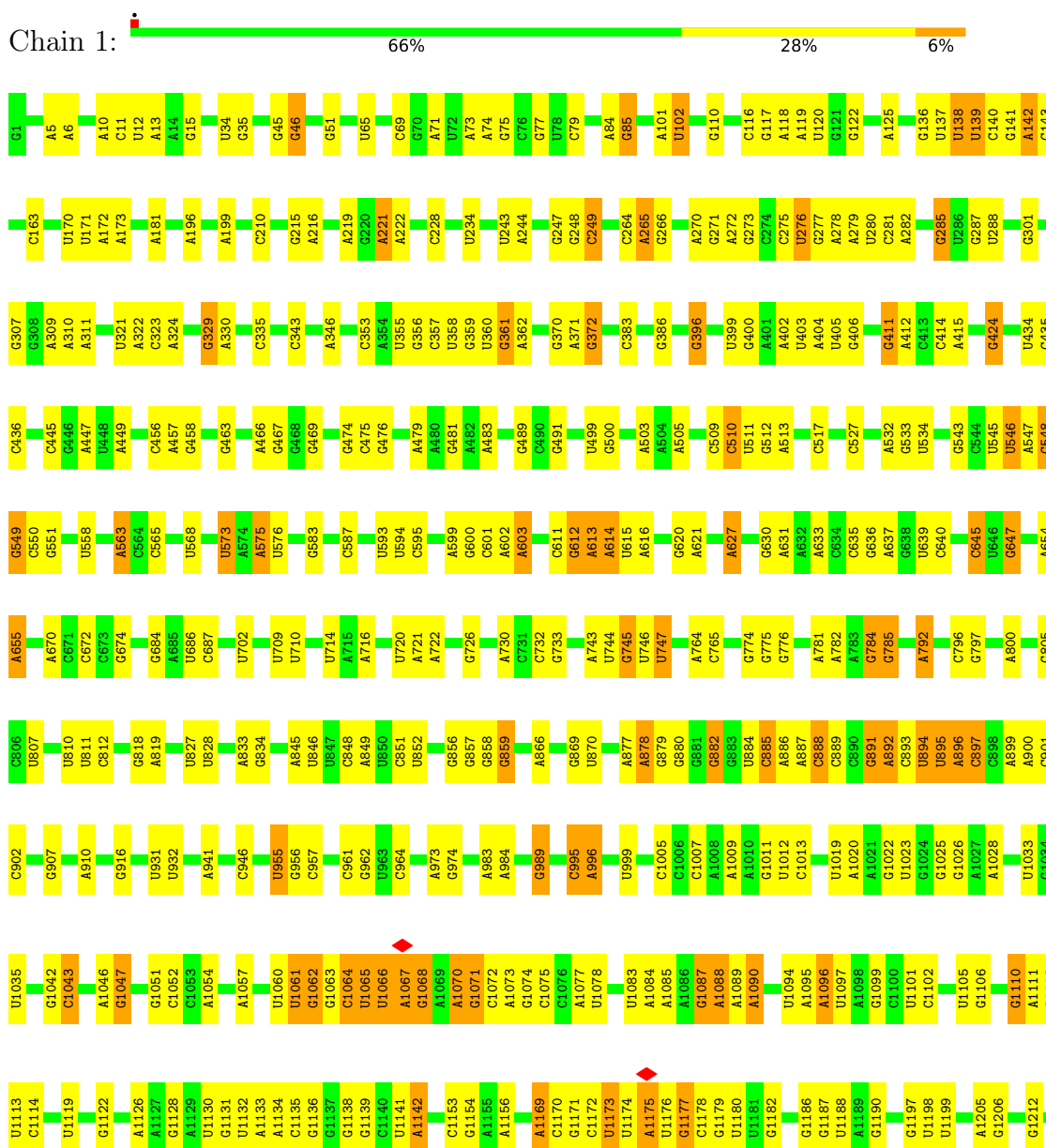
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	Z	1	Total 1	Zn 1	0
57	e	1	Total 1	Zn 1	0

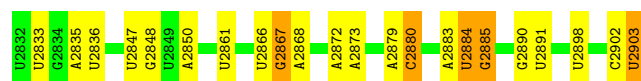
3 Residue-property plots

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

• Molecule 1: 23S rRNA

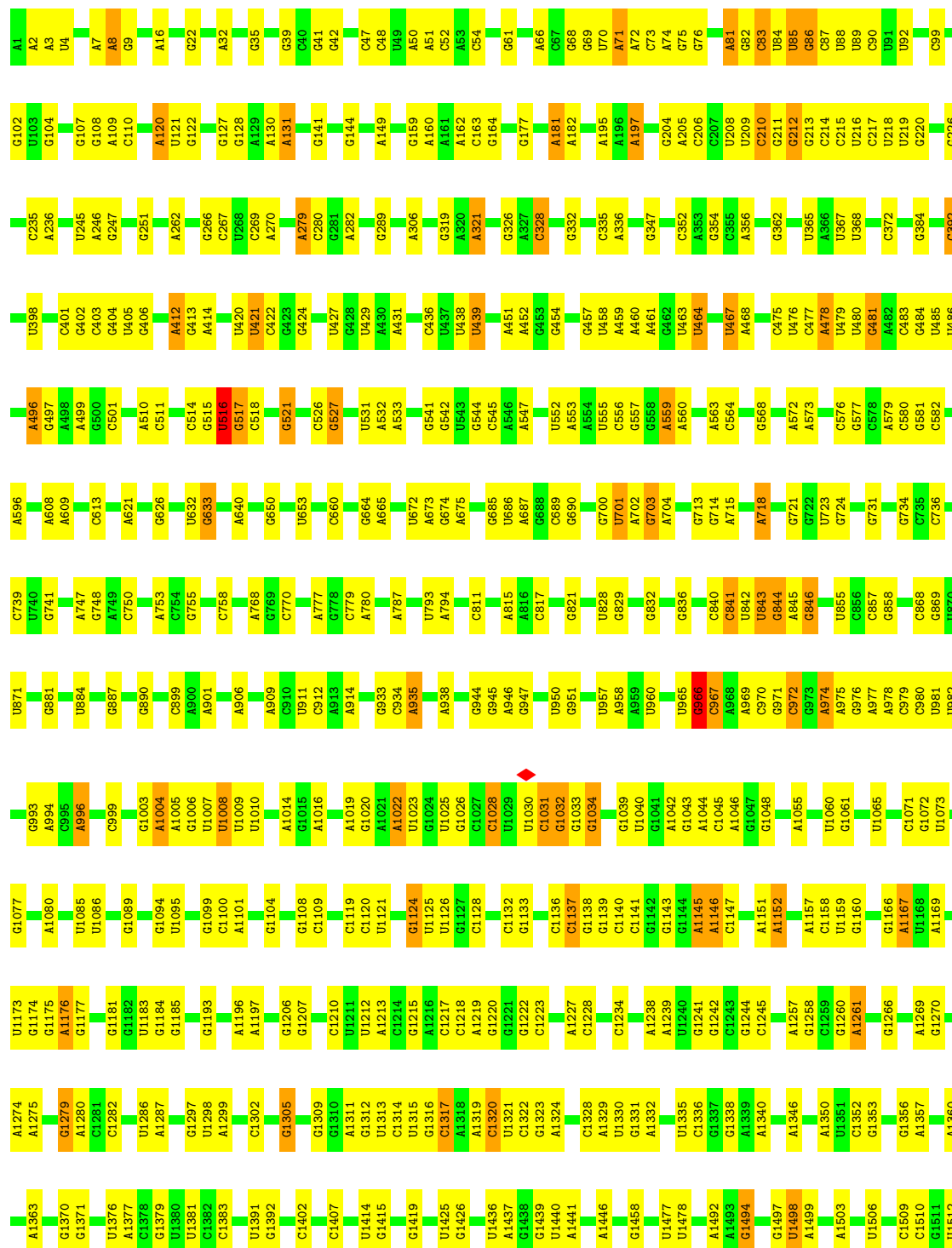


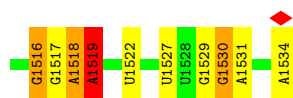
A2725	G2567	A2476	C2347	C2258	U2167	A2101	U1993	A1858	G1738	A1569	U1468	C1349	U1217
A2726	G2570	U2477	C2350	A2266	G2168	G2102	C1997	G1862	G1743	C1577	A1469	C1350	G1218
U2728	U2571	A2478	A2267	A2267	A2169	C2103	G2002	G1863	U1705	U1578	A1470	U1351	U1231
G2729	A2572	U2479	G2357	A2273	A2170	U2106	A2009	U1865	A1746	A1579	G1475	G1357	G1232
G2732	C2573	A2480	A2358	A2276	A2172	G2107	G2012	C1868	U1747	A1580	U1476	G1358	G1236
A2733	G2574	G2481	G2359	G2279	A2173	A2108	G2012	G1869	A1754	G1581	G1482	A1237	A1237
A2733	C2575	A2482	G2360	G2279	C2174	U2109	U2022	G1870	A1755	A1583	G1482	C1363	G1238
G2744	U2580	G2483	G2361	C2283	A2176	G2110	G2023	A1871	G1756	U1584	U1485	A1365	A1244
A2748	G2581	G2485	G2364	C2283	C2177	U2111	G2024	A1872	G1764	C1585	U1486	A1365	A1244
A2748	U2585	C2486	G2365	G2286	U2178	G2112	G2024	G1873	C1764	A1586	G1490	G1368	A1247
G2751	U2586	U2491	G2375	A2287	C2179	U2113	C2025	U1883	G1770	G1587	G1248	G1369	G1248
A2752	C2591	G2494	A2377	A2288	U2180	A2114	U2026	G1884	U1770	U1588	U1249	C1370	U1249
A2753	G2592	G2495	A2378	U2291	U2181	G2115	A2030	A1912	A1773	U1589	G1250	G1371	G1250
U2756	G2592	G2496	A2378	G2292	U2182	G2116	G2032	A1913	U1773	A1590	A1494	C1251	C1251
A2757	A2602	A2497	G2383	G2293	A2184	U2118	G2032	A1913	U1773	A1591	A1495	G1252	G1252
A2757	C2498	C2498	U2384	G2294	U2185	A2119	A2033	G1896	U1779	A1591	A1496	U1379	A1253
A2764	U2605	C2499	C2385	U2297	U2186	G2120	G2043	G1906	U1782	A1608	A1503	G1380	G1256
A2766	U2609	G2502	U2387	A2297	U2187	G2121	C2043	G1907	U1782	A1618	A1504	A1383	G1256
A2766	U2609	A2503	U2387	C2300	U2188	G2121	C2043	U1911	A1784	G1622	A1508	A1386	G1266
C2767	U2613	U2504	U2402	C2301	U2189	U2122	C2050	A1912	A1789	A1622	A1509	A1387	G1271
G2777	A2614	G2505	C2403	U2302	G2190	G2123	A2051	A1913	C1790	A1634	G1510	A1286	A1272
A2778	U2616	U2506	U2406	U2302	A2191	G2124	A2052	G1914	A1791	A1634	G1510	A1286	A1272
U2779	C2619	C2507	A2407	U2305	U2192	G2125	G2053	3TD1915	A1791	U1647	G1514	A1393	A1275
G2780	U2629	G2508	A2407	U2306	G2193	A2126	G2054	A1916	U1796	U1648	A1515	U1394	C1278
C2788	U2636	U2511	G2415	G2308	U2194	G2127	G2055	U1917	U1798	G1649	A1522	U1397	G1279
G2791	U2637	A2512	U2423	A2309	U2195	G2128	A2060	U1923	U1799	G1650	U1523	U1407	G1283
A2792	U2637	A2513	U2423	C2310	G2196	C2129	G2061	C1924	U1799	G1651	U1524	G1407	G1283
C2793	C2646	G2514	A2424	A2311	U2197	U2130	A1801	C1800	C1800	A1652	A1525	U1408	A1286
C2794	U2655	G2515	A2425	C2312	U2198	U2131	C2063	G1929	A1802	G1659	C1526	U1410	A1286
U2797	U2656	A2516	A2426	A2313	G2204	U2132	C2064	G1930	A1802	U1659	G1527	G1410	A1286
U2798	U2657	A2517	C2427	A2314	G2204	U2133	C2064	U1936	A1808	A1664	A1528	U1411	C1286
A2799	C2658	U2518	G2428	G2316	A2211	A2134	C2065	A1937	A1809	A1664	G1529	U1411	C1286
A2800	G2663	U2519	G2429	A2317	A2225	U2139	G2069	A1938	A1810	A1668	G1530	G1416	G1300
U2804	G2664	G2520	A2430	G2318	A2225	G2140	C2069	U1939	A1811	A1671	G1530	C1417	A1301
C2805	U2676	G2523	U2431	G2319	U2229	A2142	C2072	G1964	C1816	U1671	A1532	G1418	C1315
G2808	U2687	G2532	U2441	G2320	U2233	C2143	U2076	U1955	G1817	G1673	A1534	A1420	C1315
A2809	G2687	G2535	G2445	G2321	G2234	C2145	U2079	C1967	G1824	G1674	A1535	G1421	A1321
A2810	G2688	G2535	G2445	G2322	G2235	C2146	A2080	C1962	G1824	G1686	C1536	A1427	A1322
G2811	U2689	G2535	G2445	G2323	U2236	A2147	U2081	C1967	G1828	G1687	G1537	C1428	C1323
U2818	U2690	A2542	U2449	A2326	G2238	U2149	A2082	U1971	U1829	U1688	U1539	G1429	U1326
G2819	U2698	A2547	U2450	U2329	G2239	C2150	U2086	A1970	A1829	A1700	C1541	G1430	A1327
A2820	C2699	U2547	U2450	U2330	U2243	U2151	G2087	U1971	C1833	G1715	U1542	A1432	U1329
A2821	U2552	G2458	U2457	A2333	G2246	G2152	G2093	U1972	C1833	G1715	U1543	A1433	C1330
G2822	G2714	G2458	U2457	A2334	A2247	G2157	G2094	G1980	U1894	A1722	A1544	C1437	G1341
A2823	C2715	G2459	A2459	U2335	A2248	A2168	A2095	A1981	G1835	G1723	A1544	C1437	G1341
G2824	C2716	G2467	C2467	A2336	U2249	C2169	C2096	U1982	A1847	G1723	U1554	G1450	G1343
G2825	G2717	U2468	U2468	A2336	U2249	C2160	A2097	G1983	A1848	U1729	U1554	G1451	U1344
G2831	G2718	A2469	A2469	G2345	G2251	C2161	U2098	U1991	U1856	G1730	U1559	G1452	C1345
		G2470	G2470	A2346	G2252	C2164	G2100	G1992	G1857	C1732	A1566	U1460	C1348



• Molecule 2: 16S rRNA

Chain 2: 66% 30% .





• Molecule 3: 5S rRNA

Chain 3: 78% 17% 5%



• Molecule 4: mRNA

Chain 4: 67% 33%



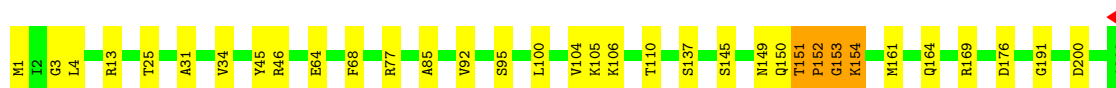
• Molecule 5: 50S ribosomal protein L2

Chain C: 78% 22%



• Molecule 6: 50S ribosomal protein L3

Chain D: 84% 14%



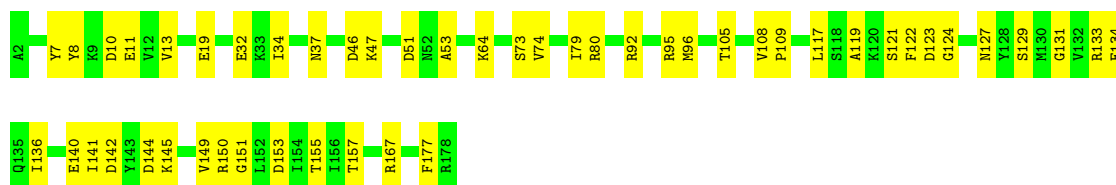
• Molecule 7: 50S ribosomal protein L4

Chain E: 79% 21%



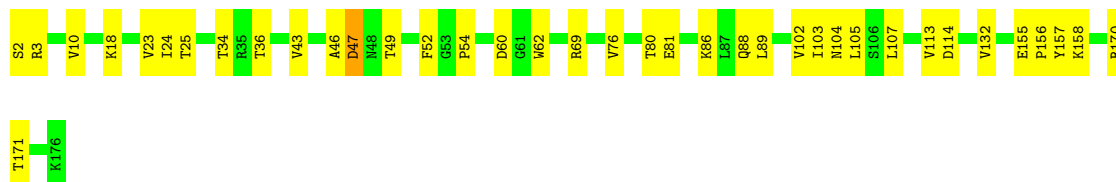
• Molecule 8: 50S ribosomal protein L5

Chain F: 72% 28%



• Molecule 9: 50S ribosomal protein L6

Chain G: 78% 21% .



• Molecule 10: 50S ribosomal protein L9

Chain H: 56% 50% 47% .



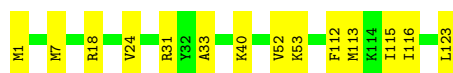
• Molecule 11: 50S ribosomal protein L13

Chain I: 85% 14% .



• Molecule 12: 50S ribosomal protein L14

Chain J: 89% 11%

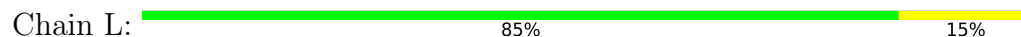


• Molecule 13: 50S ribosomal protein L15

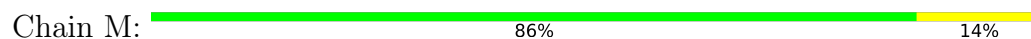
Chain K: 81% 19%



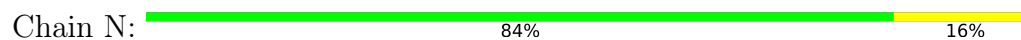
- Molecule 14: 50S ribosomal protein L16



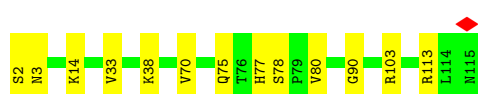
- Molecule 15: 50S ribosomal protein L17



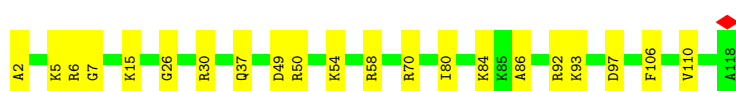
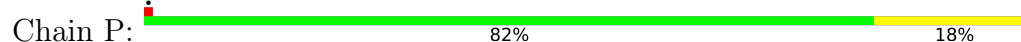
- Molecule 16: 50S ribosomal protein L18



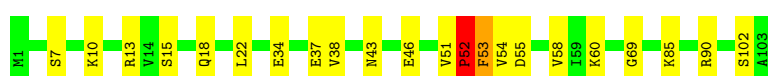
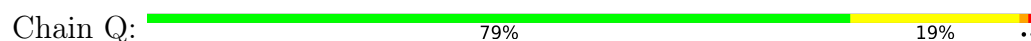
- Molecule 17: 50S ribosomal protein L19



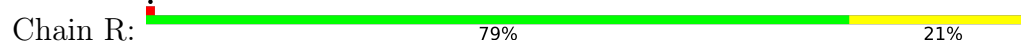
- Molecule 18: 50S ribosomal protein L20

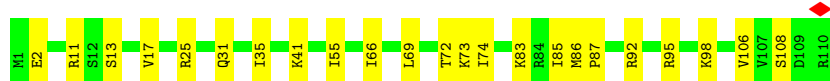


- Molecule 19: 50S ribosomal protein L21

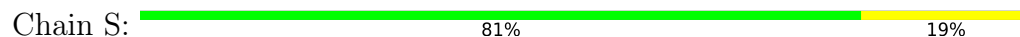


- Molecule 20: 50S ribosomal protein L22

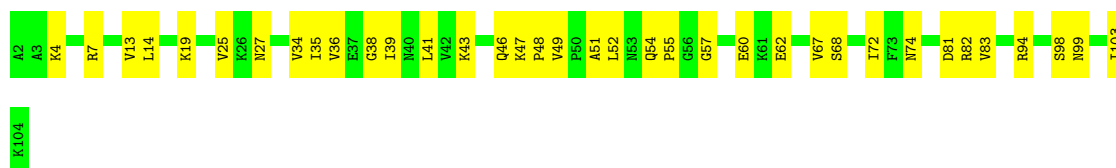




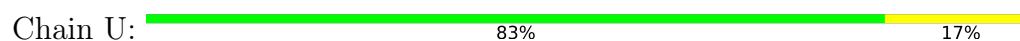
- Molecule 21: 50S ribosomal protein L23



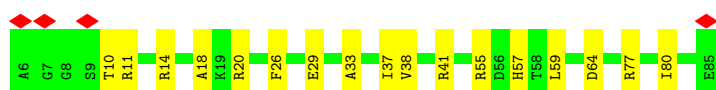
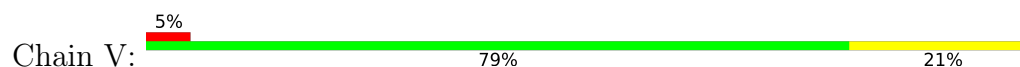
- Molecule 22: 50S ribosomal protein L24



- Molecule 23: 50S ribosomal protein L25



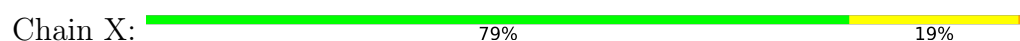
- Molecule 24: 50S ribosomal protein L27



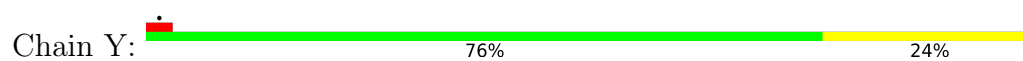
- Molecule 25: 50S ribosomal protein L28



- Molecule 26: 50S ribosomal protein L29



- Molecule 27: 50S ribosomal protein L30



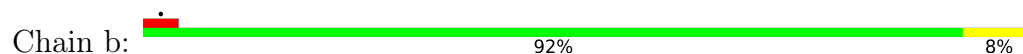
- Molecule 28: 50S ribosomal protein L31



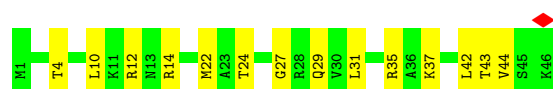
- Molecule 29: 50S ribosomal protein L32



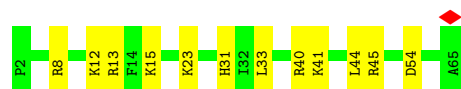
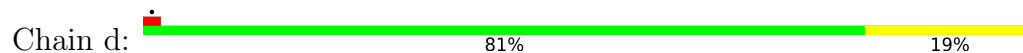
- Molecule 30: 50S ribosomal protein L33



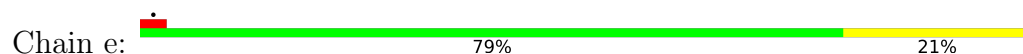
- Molecule 31: 50S ribosomal protein L34



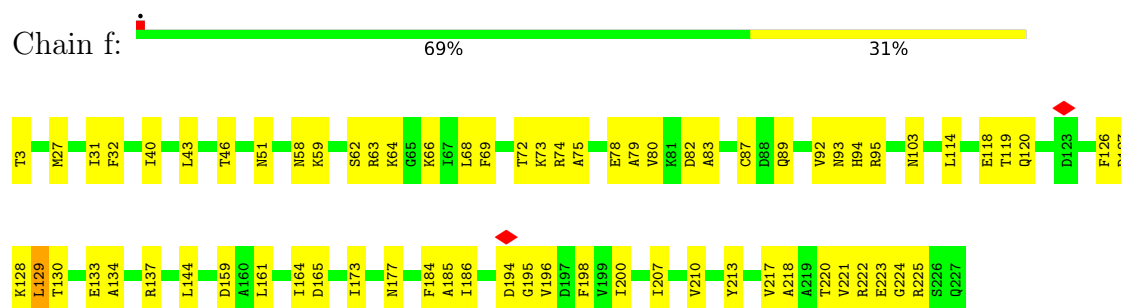
- Molecule 32: 50S ribosomal protein L35



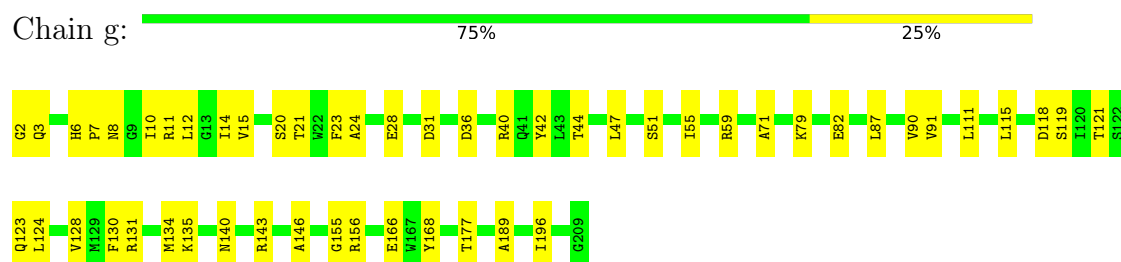
- Molecule 33: 50S ribosomal protein L36



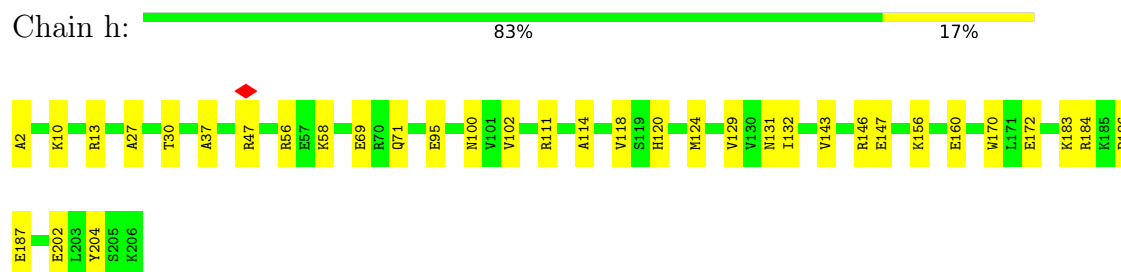
- Molecule 34: 30S ribosomal protein S2



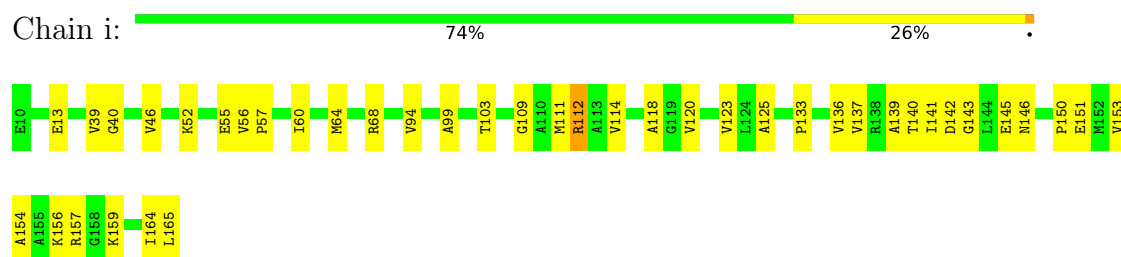
- Molecule 35: 30S ribosomal protein S3



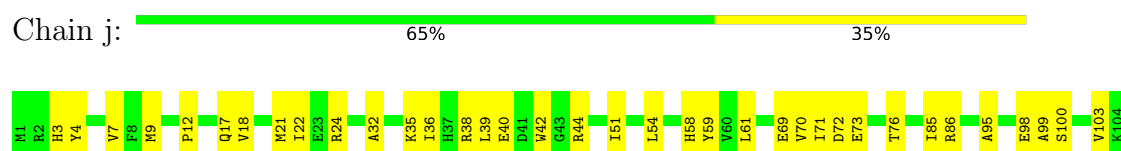
- Molecule 36: 30S ribosomal protein S4



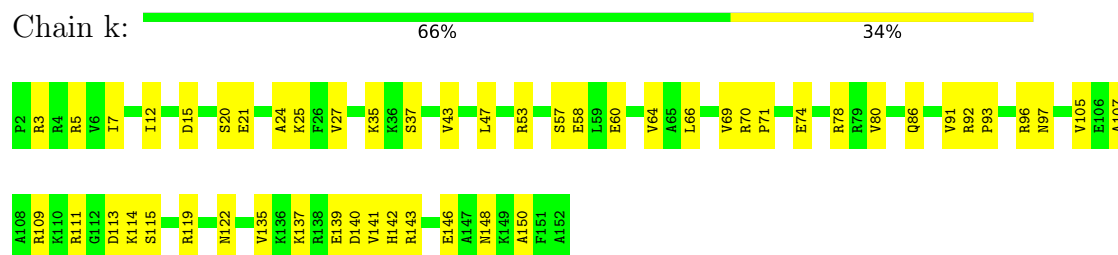
- Molecule 37: 30S ribosomal protein S5



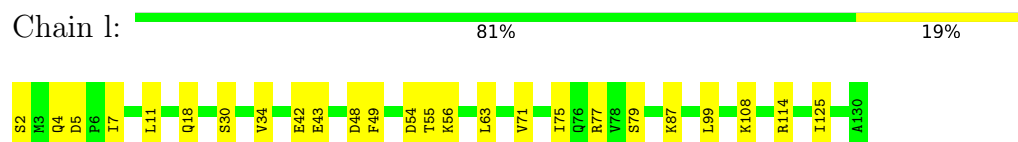
- Molecule 38: 30S ribosomal protein S6



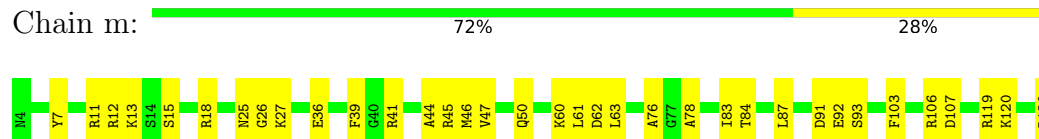
- Molecule 39: 30S ribosomal protein S7



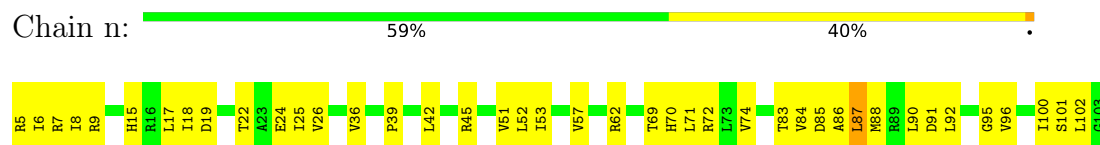
- Molecule 40: 30S ribosomal protein S8



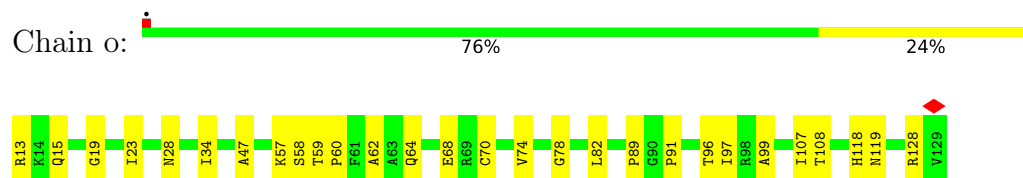
- Molecule 41: 30S ribosomal protein S9



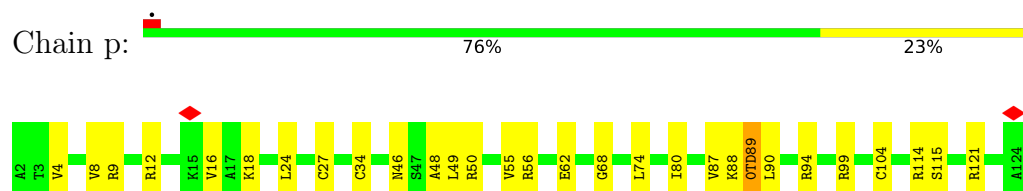
- Molecule 42: 30S ribosomal protein S10



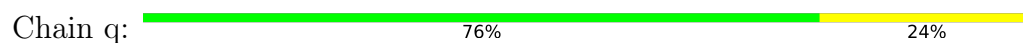
- Molecule 43: 30S ribosomal protein S11



- Molecule 44: 30S ribosomal protein S12

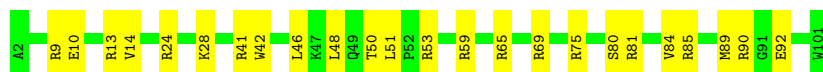


- Molecule 45: 30S ribosomal protein S13

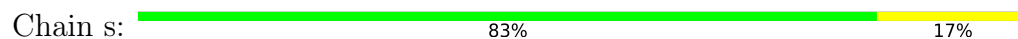




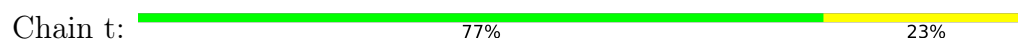
- Molecule 46: 30S ribosomal protein S14



- Molecule 47: 30S ribosomal protein S15



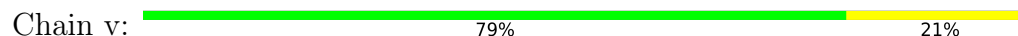
- Molecule 48: 30S ribosomal protein S16



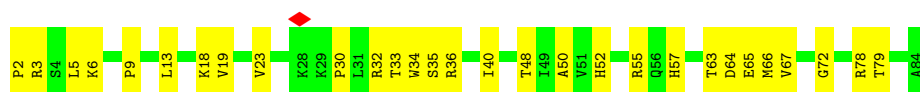
- Molecule 49: 30S ribosomal protein S17



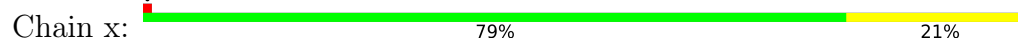
- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19

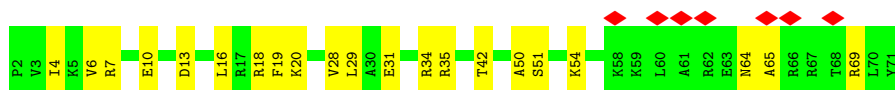


- Molecule 52: 30S ribosomal protein S20

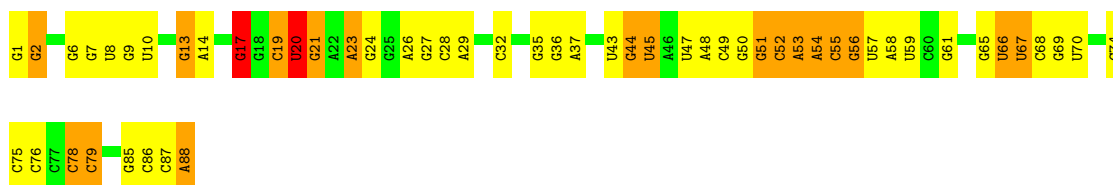




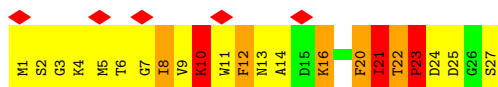
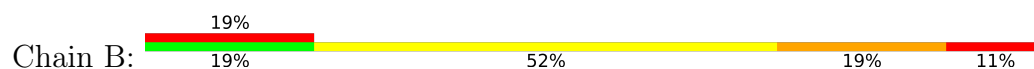
- Molecule 53: 30S ribosomal protein S21



- Molecule 54: tRNA-Ser



- Molecule 55: 7.4 kDa cold shock protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35573	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.2	Depositor
Minimum defocus (nm)	0.5	Depositor
Maximum defocus (nm)	2.2	Depositor
Magnification	75000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.136	Depositor
Minimum map value	-0.054	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.02	Depositor
Map size ($\text{\AA}$)	428.00003, 428.00003, 428.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 1MG, PSU, 2MA, OMG, ZN, 3TD, G7M, MA6, 0TD, 5MC, UR3, 2MG, 5MU, 4OC, OMC, 6MZ, OMU, FME

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	1	0.49	0/69286	0.47	2/108087 (0.0%)
2	2	0.44	0/36590	0.44	0/57074
3	3	0.42	0/2872	0.42	0/4478
4	4	0.35	0/139	0.31	0/214
5	C	0.65	0/2121	0.56	0/2852
6	D	0.65	0/1586	0.55	0/2134
7	E	0.59	0/1571	0.60	0/2113
8	F	0.48	0/1434	0.60	0/1926
9	G	0.44	0/1333	0.60	0/1805
10	H	0.40	0/1122	0.90	0/1515
11	I	0.64	0/1152	0.55	0/1551
12	J	0.62	0/955	0.56	0/1279
13	K	0.62	0/1062	0.59	0/1413
14	L	0.61	0/1093	0.57	0/1460
15	M	0.66	0/964	0.63	0/1289
16	N	0.53	0/902	0.61	0/1209
17	O	0.61	0/929	0.50	0/1242
18	P	0.71	0/960	0.66	0/1278
19	Q	0.57	0/829	0.57	2/1107 (0.2%)
20	R	0.67	0/864	0.64	0/1156
21	S	0.57	0/752	0.54	0/1005
22	T	0.48	0/796	0.52	0/1062
23	U	0.54	0/766	0.54	0/1025
24	V	0.64	0/608	0.53	0/804
25	W	0.61	0/635	0.58	0/848
26	X	0.52	0/502	0.70	1/667 (0.1%)
27	Y	0.61	0/452	0.53	0/605
28	Z	0.35	0/531	0.62	0/709
29	a	0.60	0/450	0.56	0/599
30	b	0.51	0/433	0.53	0/576
31	c	0.69	0/380	0.61	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	d	0.68	0/513	0.64	0/676
33	e	0.64	0/303	0.55	0/397
34	f	0.44	0/1791	0.71	0/2413
35	g	0.50	0/1663	0.59	0/2241
36	h	0.51	0/1665	0.58	0/2227
37	i	0.61	0/1165	0.68	0/1568
38	j	0.49	0/867	0.58	0/1171
39	k	0.46	0/1195	0.63	0/1602
40	l	0.57	0/989	0.55	0/1326
41	m	0.50	0/1034	0.61	0/1375
42	n	0.47	0/800	0.67	0/1082
43	o	0.48	0/893	0.55	0/1205
44	p	0.55	0/960	0.59	0/1286
45	q	0.50	0/909	0.67	0/1215
46	r	0.53	0/817	0.62	0/1088
47	s	0.54	0/722	0.60	0/964
48	t	0.55	0/659	0.58	0/884
49	u	0.47	0/657	0.51	0/881
50	v	0.52	0/553	0.62	0/743
51	w	0.45	0/680	0.58	0/915
52	x	0.55	0/675	0.67	0/895
53	y	0.42	0/597	0.68	0/792
54	z	0.46	2/2062 (0.1%)	0.55	4/3208 (0.1%)
55	B	0.74	0/200	1.52	4/267 (1.5%)
All	All	0.50	2/156438 (0.0%)	0.50	13/234001 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	z	20	U	C5-C6	6.83	1.47	1.34
54	z	20	U	C2-N3	5.56	1.48	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	B	22	THR	CA-C-N	8.44	130.39	119.84
55	B	22	THR	C-N-CA	8.44	130.39	119.84
55	B	23	PRO	CA-N-CD	-8.38	100.26	112.00
54	z	8	U	O5'-P-OP1	-7.61	85.19	108.00
54	z	67	U	O5'-P-OP1	-7.23	86.32	108.00
54	z	19	C	OP2-P-O3'	-7.14	86.57	108.00
1	1	2512	C	C5'-C4'-C3'	6.63	125.95	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	19	C	OP1-P-O3'	-5.68	90.94	108.00
55	B	23	PRO	N-CA-CB	-5.53	97.44	103.25
1	1	2149	U	N1-C1'-C2'	5.36	120.03	112.00
26	X	48	ARG	CA-CB-CG	5.26	124.62	114.10
19	Q	52	PRO	CA-C-N	5.01	131.11	121.54
19	Q	52	PRO	C-N-CA	5.01	131.11	121.54

There are no chirality outliers.

There are no planarity outliers.

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	1	62336	0	31368	535	0
2	2	32929	0	16585	274	0
3	3	2569	0	1301	13	0
4	4	126	0	65	2	0
5	C	2082	0	2154	39	0
6	D	1565	0	1616	24	0
7	E	1552	0	1619	32	0
8	F	1410	0	1444	38	0
9	G	1313	0	1358	26	0
10	H	1111	0	1148	84	0
11	I	1129	0	1162	17	0
12	J	946	0	1023	11	0
13	K	1053	0	1129	22	0
14	L	1074	0	1157	16	0
15	M	951	0	994	13	0
16	N	892	0	923	17	0
17	O	917	0	962	9	0
18	P	947	0	1019	21	0
19	Q	816	0	839	18	0
20	R	857	0	922	16	0
21	S	746	0	811	13	0
22	T	788	0	843	26	0
23	U	753	0	780	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	V	601	0	615	12	0
25	W	625	0	652	8	0
26	X	501	0	531	9	0
27	Y	448	0	488	8	0
28	Z	522	0	520	23	0
29	a	444	0	458	13	0
30	b	426	0	464	2	0
31	c	377	0	418	12	0
32	d	504	0	572	10	0
33	e	302	0	340	6	0
34	f	1760	0	1787	56	0
35	g	1636	0	1710	40	0
36	h	1643	0	1706	37	0
37	i	1152	0	1196	36	0
38	j	848	0	846	31	0
39	k	1181	0	1238	36	0
40	l	979	0	1031	18	0
41	m	1022	0	1070	29	0
42	n	790	0	831	31	0
43	o	877	0	887	22	0
44	p	957	0	1017	24	0
45	q	900	0	965	25	0
46	r	805	0	844	23	0
47	s	714	0	734	12	0
48	t	649	0	666	13	0
49	u	648	0	691	15	0
50	v	544	0	560	8	0
51	w	663	0	688	26	0
52	x	669	0	719	17	0
53	y	589	0	629	19	0
54	z	1891	0	956	58	0
55	B	205	0	195	40	0
56	1	278	0	0	0	0
56	2	119	0	0	0	0
56	3	8	0	0	0	0
56	C	1	0	0	0	0
56	D	1	0	0	0	0
56	P	1	0	0	0	0
56	a	1	0	0	0	0
56	h	1	0	0	0	0
56	q	1	0	0	0	0
56	z	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	Z	1	0	0	0	0
57	e	1	0	0	0	0
All	All	145149	0	97246	1718	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 7.

All (1718) 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)
6:D:151:THR:HG23	6:D:152:PRO:HD3	1.31	1.05
1:1:2147:A:H62	1:1:2148:G:H21	1.06	1.01
7:E:67:ARG:HD2	55:B:10:LYS:HE3	1.45	0.97
54:z:55:C:O2'	54:z:56:G:O4'	1.85	0.95
55:B:9:VAL:CG2	55:B:11:TRP:CD1	2.56	0.89
41:m:84:THR:HG21	41:m:103:PHE:HB3	1.55	0.89
55:B:21:ILE:H	55:B:21:ILE:HD12	1.35	0.88
1:1:2571:U:O2'	6:D:151:THR:HG21	1.72	0.88
2:2:102:G:OP2	52:x:5:LYS:NZ	2.07	0.88
1:1:2130:U:O3'	1:1:2158:A:N6	2.09	0.86
2:2:1028:C:O2	2:2:1034:G:N2	2.09	0.86
1:1:1450:G:N2	1:1:1452:G:O6	2.09	0.85
54:z:67:U:O2	54:z:67:U:H2'	1.77	0.85
3:3:43:C:O2	8:F:92:ARG:NH2	2.09	0.85
1:1:2753:A:O2'	33:e:15:LYS:NZ	2.08	0.85
1:1:1779:U:OP2	1:1:1784:A:N6	2.10	0.85
21:S:69:ARG:NH2	21:S:72:GLN:O	2.11	0.84
7:E:149:ILE:HD11	7:E:188:MET:HG2	1.60	0.84
41:m:36:GLU:OE1	41:m:45:ARG:NH1	2.11	0.84
1:1:2293:G:OP1	16:N:94:ARG:NH1	2.10	0.83
1:1:1072:C:N4	1:1:1099:G:O6	2.11	0.83
35:g:28:GLU:OE1	35:g:28:GLU:N	2.11	0.83
1:1:517:C:OP2	29:a:10:ARG:NH2	2.12	0.82
54:z:88:A:HO3'	55:B:27:SER:HG	1.13	0.82
2:2:1005:A:H3'	2:2:1006:G:C8	2.14	0.82
1:1:2101:A:N6	1:1:2188:U:O4	2.12	0.82
38:j:51:ILE:HD12	38:j:85:ILE:HG21	1.61	0.82
1:1:1754:A:N1	1:1:2716:C:O2'	2.12	0.81
2:2:104:G:N7	52:x:9:LYS:NZ	2.28	0.81
2:2:626:G:O3'	48:t:51:ARG:NH1	2.12	0.81
1:1:1047:G:HO2'	1:1:1110:G:H1	1.28	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:B:9:VAL:HG22	55:B:11:TRP:CD1	2.16	0.81
1:1:877:A:O2'	1:1:900:A:N6	2.13	0.81
1:1:445:C:OP1	18:P:2:ALA:N	2.15	0.80
5:C:271:ARG:O	5:C:272:SER:OG	1.98	0.80
2:2:951:G:OP2	45:q:101:ARG:NH2	2.15	0.80
2:2:1298:U:OP2	39:k:114:LYS:NZ	2.13	0.80
1:1:301:G:OP2	22:T:82:ARG:NH1	2.14	0.80
2:2:1311:A:OP1	28:Z:59:ARG:NH1	2.14	0.80
45:q:9:ILE:HG23	45:q:18:ALA:HB1	1.63	0.80
1:1:1668:A:O2'	1:1:1674:G:N7	2.15	0.80
2:2:1222:G:OP2	2:2:1322:C:N4	2.14	0.80
54:z:51:G:O2'	54:z:54:A:N6	2.14	0.80
9:G:170:ARG:NH2	33:e:29:ALA:O	2.15	0.80
12:J:113:MET:SD	12:J:116:ILE:HD11	2.20	0.79
1:1:1169:A:N6	1:1:1180:U:O4	2.16	0.79
14:L:47:GLU:OE2	14:L:51:ARG:NE	2.16	0.79
1:1:627:A:OP1	13:K:78:ARG:NH1	2.15	0.79
2:2:979:C:O2	46:r:59:ARG:NH2	2.16	0.79
1:1:1364:G:OP2	25:W:2:SER:N	2.15	0.78
10:H:55:GLU:OE1	10:H:55:GLU:N	2.15	0.78
46:r:41:ARG:NH2	51:w:6:LYS:O	2.15	0.78
1:1:276:U:O2'	1:1:277:G:N7	2.16	0.78
2:2:1317:C:OP2	46:r:28:LYS:NZ	2.17	0.78
2:2:1055:A:N3	35:g:156:ARG:NH1	2.31	0.78
39:k:140:ASP:OD1	39:k:143:ARG:NH1	2.17	0.78
55:B:12:PHE:HD1	55:B:12:PHE:H	1.29	0.77
39:k:66:LEU:HD21	39:k:97:ASN:OD1	1.84	0.77
36:h:124:MET:HE3	36:h:146:ARG:HE	1.48	0.77
1:1:2116:G:N1	1:1:2162:G:OP2	2.17	0.77
38:j:69:GLU:OE1	38:j:69:GLU:N	2.16	0.77
21:S:6:ARG:NH1	21:S:37:ASP:OD1	2.18	0.77
2:2:718:A:O5'	43:o:119:ASN:ND2	2.18	0.77
2:2:1006:G:H8	2:2:1006:G:O5'	1.66	0.76
53:y:4:ILE:HD12	53:y:19:PHE:HD1	1.51	0.76
2:2:974:A:OP1	46:r:69:ARG:NH1	2.18	0.76
2:2:1126:U:O4	42:n:9:ARG:NH1	2.19	0.76
2:2:1241:G:OP1	39:k:35:LYS:NZ	2.18	0.76
1:1:249:C:O2	32:d:12:LYS:NZ	2.19	0.76
41:m:106:ARG:NH1	41:m:107:ASP:O	2.19	0.76
2:2:1152:A:OP1	42:n:70:HIS:ND1	2.18	0.76
48:t:18:GLN:OE1	48:t:35:ARG:NE	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:z:44:G:O2'	54:z:45:U:OP1	2.04	0.75
9:G:24:ILE:HD11	9:G:43:VAL:HG11	1.68	0.75
34:f:129:LEU:HD11	34:f:134:ALA:N	2.01	0.75
10:H:84:ALA:HA	10:H:91:PHE:H	1.52	0.75
1:1:1266:G:OP1	29:a:16:ARG:NE	2.17	0.74
10:H:66:ASN:OD1	10:H:67:ALA:N	2.20	0.74
2:2:1376:U:OP2	39:k:25:LYS:NZ	2.19	0.74
54:z:51:G:HO2'	54:z:54:A:N6	1.85	0.74
34:f:58:ASN:ND2	34:f:223:GLU:OE1	2.20	0.74
39:k:15:ASP:OD1	39:k:20:SER:N	2.20	0.74
1:1:219:A:N3	1:1:234:U:O2'	2.21	0.74
1:1:1007:C:OP1	11:I:37:ARG:NH2	2.20	0.74
1:1:2167:U:O5'	1:1:2167:U:H6	1.71	0.74
53:y:64:ASN:OD1	53:y:65:ALA:N	2.21	0.74
24:V:33:ALA:N	24:V:64:ASP:OD1	2.21	0.73
44:p:87:VAL:HG11	44:p:90:LEU:HD12	1.70	0.73
29:a:45:ALA:O	29:a:57:LYS:NZ	2.21	0.73
10:H:81:ALA:HA	10:H:147:VAL:HG23	1.70	0.73
55:B:9:VAL:HG21	55:B:11:TRP:NE1	2.03	0.73
1:1:956:G:O6	14:L:14:LYS:NZ	2.22	0.73
2:2:1080:A:OP1	37:i:52:LYS:HE2	1.89	0.73
54:z:67:U:O2	54:z:67:U:C2'	2.36	0.72
1:1:563:A:N3	18:P:37:GLN:NE2	2.37	0.72
55:B:4:LYS:HG3	55:B:8:ILE:HD11	1.72	0.72
1:1:1251:C:OP2	18:P:6:ARG:NH2	2.22	0.72
2:2:85:U:H1'	2:2:86:G:N7	2.04	0.72
38:j:51:ILE:O	38:j:54:LEU:HD23	1.88	0.72
2:2:673:A:O3'	38:j:86:ARG:NH2	2.23	0.72
39:k:27:VAL:HG12	39:k:43:VAL:HG21	1.72	0.72
24:V:11:ARG:O	24:V:14:ARG:NH1	2.23	0.71
2:2:938:A:N3	2:2:1376:U:O2'	2.20	0.71
5:C:180:GLU:OE2	5:C:267:ILE:HD12	1.90	0.71
28:Z:35:ASP:OD2	45:q:57:ARG:NE	2.23	0.71
16:N:27:VAL:HG21	16:N:40:ILE:HD12	1.73	0.71
1:1:2279:G:N7	24:V:14:ARG:NH2	2.39	0.71
55:B:9:VAL:HG21	55:B:11:TRP:CE2	2.25	0.71
39:k:5:ARG:NH1	39:k:7:ILE:HG22	2.05	0.71
51:w:33:THR:HG22	51:w:35:SER:H	1.55	0.71
54:z:9:G:H2'	54:z:9:G:N3	2.05	0.71
1:1:335:C:O2	22:T:68:SER:OG	2.08	0.71
34:f:130:THR:HG23	34:f:133:GLU:HB3	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:110:C:O2'	48:t:25:ARG:O	2.08	0.71
2:2:1516:2MG:N2	2:2:1519:MA6:OP2	2.24	0.71
42:n:26:VAL:HG13	42:n:36:VAL:HG11	1.73	0.71
10:H:14:SER:N	10:H:17:ASP:OD2	2.24	0.70
10:H:76:GLU:O	10:H:143:ILE:HG12	1.91	0.70
1:1:1172:C:O2'	1:1:1173:U:O4'	2.05	0.70
9:G:25:THR:HG22	9:G:34:THR:HG23	1.73	0.70
1:1:2146:C:O2'	1:1:2147:A:O5'	2.09	0.70
7:E:67:ARG:CD	55:B:10:LYS:HE3	2.21	0.70
1:1:1083:U:O2'	1:1:1085:A:OP2	2.07	0.70
1:1:1801:A:OP2	5:C:150:LYS:NZ	2.23	0.70
1:1:714:U:OP2	47:s:88:ARG:NH1	2.22	0.70
8:F:121:SER:OG	8:F:129:SER:O	2.09	0.70
2:2:1261:A:N6	2:2:1274:A:O2'	2.21	0.70
14:L:14:LYS:O	14:L:71:LYS:NZ	2.24	0.70
50:v:73:ARG:O	50:v:75:GLN:NE2	2.25	0.70
54:z:13:G:O2'	54:z:23:A:N6	2.21	0.70
2:2:107:G:N7	52:x:10:ARG:NH2	2.40	0.69
2:2:61:G:N7	52:x:6:SER:OG	2.24	0.69
2:2:8:A:N6	36:h:202:GLU:O	2.25	0.69
2:2:35:G:N3	44:p:115:SER:OG	2.25	0.69
17:O:33:VAL:HG22	17:O:38:LYS:HG2	1.75	0.69
40:l:5:ASP:OD2	40:l:77:ARG:NH1	2.25	0.69
1:1:475:C:O2	1:1:479:A:N6	2.26	0.69
35:g:14:ILE:HG22	35:g:15:VAL:HG23	1.75	0.69
2:2:890:G:O2'	2:2:906:A:N6	2.26	0.69
2:2:1340:A:HO2'	54:z:32:C:HO2'	1.41	0.68
11:I:19:ASP:OD1	11:I:58:ASN:ND2	2.26	0.68
1:1:1067:A:O2'	1:1:1068:G:O4'	2.11	0.68
30:b:8:LYS:HG2	30:b:24:THR:HG22	1.74	0.68
34:f:3:THR:N	34:f:51:ASN:HD21	1.92	0.68
10:H:55:GLU:HA	10:H:58:LEU:HD23	1.74	0.68
55:B:21:ILE:HD12	55:B:21:ILE:N	2.07	0.68
1:1:2126:A:N6	1:1:2171:A:OP2	2.27	0.68
7:E:117:ARG:NH2	7:E:183:PHE:O	2.27	0.68
55:B:9:VAL:CG2	55:B:11:TRP:NE1	2.57	0.68
1:1:611:C:C2'	1:1:612:G:H5'	2.24	0.68
1:1:2249:U:N3	1:1:2253:G:OP2	2.27	0.68
38:j:38:ARG:NH1	38:j:98:GLU:O	2.26	0.68
43:o:23:ILE:HD13	43:o:96:THR:HG21	1.74	0.68
36:h:47:ARG:NE	36:h:47:ARG:HA	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1166:G:N1	2:2:1169:A:OP2	2.26	0.68
10:H:117:LEU:HD13	10:H:120:GLY:HA2	1.76	0.68
2:2:1315:U:O2'	2:2:1360:A:N3	2.21	0.68
20:R:25:ARG:NH1	20:R:74:ILE:O	2.27	0.68
1:1:1754:A:O2'	17:O:103:ARG:NH2	2.27	0.67
2:2:1060:U:OP1	46:r:85:ARG:NH1	2.26	0.67
17:O:90:GLY:O	17:O:113:ARG:NH1	2.27	0.67
2:2:970:C:N4	41:m:130:ARG:O	2.27	0.67
2:2:544:G:OP1	36:h:56:ARG:NH2	2.26	0.67
6:D:25:THR:OG1	6:D:191:GLY:O	2.12	0.67
1:1:65:U:O2'	1:1:456:C:N3	2.27	0.67
1:1:1094:U:N3	1:1:1097:U:OP2	2.27	0.67
10:H:58:LEU:O	10:H:62:LEU:HD23	1.95	0.67
1:1:210:C:OP1	31:c:29:GLN:NE2	2.26	0.67
2:2:1080:A:OP1	37:i:52:LYS:CE	2.43	0.67
1:1:483:A:OP1	22:T:47:LYS:NZ	2.26	0.66
1:1:545:U:O2'	1:1:546:U:O3'	2.12	0.66
22:T:72:ILE:HD12	22:T:83:VAL:HG21	1.78	0.66
5:C:258:ARG:NH1	5:C:264:ASP:OD1	2.29	0.66
19:Q:38:VAL:HG13	19:Q:54:VAL:HB	1.76	0.66
21:S:8:LEU:HD23	21:S:50:LEU:HD21	1.77	0.66
37:i:55:GLU:HG3	37:i:57:PRO:HD2	1.78	0.66
37:i:142:ASP:OD1	37:i:143:GLY:N	2.28	0.66
55:B:21:ILE:H	55:B:21:ILE:CD1	2.08	0.66
35:g:40:ARG:NH1	35:g:55:ILE:O	2.27	0.66
37:i:154:ALA:HA	37:i:164:ILE:HD11	1.78	0.66
2:2:545:C:OP1	36:h:58:LYS:NZ	2.29	0.66
2:2:1193:G:O6	35:g:3:GLN:NE2	2.29	0.66
29:a:52:ARG:NH2	29:a:54:VAL:HG12	2.10	0.66
1:1:1153:C:OP1	18:P:92:ARG:NH2	2.29	0.66
1:1:1475:G:O2'	1:1:1514:G:O6	2.14	0.66
10:H:114:GLU:O	10:H:133:GLN:N	2.27	0.66
54:z:17:OMG:N2	54:z:70:U:O4'	2.29	0.66
1:1:2128:G:O2'	1:1:2174:C:O2'	2.07	0.66
1:1:2147:A:H62	1:1:2148:G:N2	1.87	0.66
26:X:49:ASP:OD1	26:X:52:ARG:NH2	2.29	0.66
2:2:626:G:OP1	48:t:35:ARG:NH2	2.29	0.65
2:2:1031:C:O3'	2:2:1032:G:N2	2.29	0.65
2:2:1234:C:OP1	41:m:119:ARG:NH2	2.29	0.65
6:D:1:MET:HE2	6:D:100:LEU:HD21	1.77	0.65
10:H:125:THR:HA	10:H:146:VAL:HG23	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:140:GLU:OE2	28:Z:26:SER:OG	2.09	0.65
35:g:121:THR:HG23	35:g:189:ALA:HB2	1.78	0.65
10:H:80:ILE:HD11	10:H:102:ALA:CB	2.25	0.65
1:1:1652:A:OP1	15:M:8:ARG:NH2	2.30	0.65
10:H:114:GLU:OE1	10:H:114:GLU:N	2.29	0.65
2:2:1006:G:C8	2:2:1006:G:O5'	2.50	0.65
2:2:1266:G:N2	2:2:1269:A:OP2	2.25	0.65
2:2:1360:A:OP2	46:r:75:ARG:NH2	2.29	0.65
37:i:157:ARG:NH1	40:l:43:GLU:OE2	2.28	0.65
1:1:2161:C:O2'	1:1:2173:A:H4'	1.97	0.65
1:1:2258:C:O2'	1:1:2427:C:OP2	2.14	0.65
20:R:85:ILE:HD11	55:B:3:GLY:O	1.96	0.65
1:1:2445:2MG:OP1	7:E:69:ARG:NH1	2.25	0.65
24:V:18:ALA:O	24:V:20:ARG:NH1	2.29	0.65
10:H:4:ILE:HD12	10:H:17:ASP:C	2.23	0.64
28:Z:51:VAL:HG23	28:Z:52:ALA:H	1.61	0.64
38:j:17:GLN:OE1	38:j:17:GLN:N	2.30	0.64
36:h:184:ARG:NH1	36:h:187:GLU:OE1	2.29	0.64
37:i:156:LYS:HG2	40:l:71:VAL:HG13	1.79	0.64
1:1:1084:A:N3	1:1:1105:U:O2'	2.27	0.64
43:o:28:ASN:O	43:o:57:LYS:NZ	2.25	0.64
45:q:16:VAL:O	45:q:20:THR:HG23	1.97	0.64
54:z:55:C:O2'	54:z:56:G:O5'	2.15	0.64
1:1:2125:G:H2'	1:1:2173:A:H61	1.62	0.64
1:1:1419:A:O2'	1:1:1421:G:N7	2.29	0.64
1:1:1789:A:OP2	5:C:221:ARG:NH1	2.30	0.64
8:F:46:ASP:OD1	8:F:47:LYS:N	2.30	0.64
40:l:11:LEU:HD22	40:l:75:ILE:HD11	1.79	0.64
54:z:17:OMG:H1'	54:z:69:G:H22	1.63	0.64
1:1:2305:U:O2'	8:F:133:ARG:NH1	2.24	0.64
1:1:2585:U:O2	55:B:24:ASP:O	2.15	0.64
34:f:59:LYS:O	34:f:62:SER:OG	2.08	0.64
28:Z:44:PHE:CD2	28:Z:45:THR:HG23	2.32	0.64
1:1:1818:U:O2'	5:C:153:GLN:O	2.12	0.64
23:U:64:VAL:HG22	23:U:69:GLU:HG3	1.80	0.64
22:T:27:ASN:OD1	22:T:35:ILE:HD12	1.97	0.63
8:F:119:ALA:HB1	8:F:167:ARG:HE	1.62	0.63
35:g:36:ASP:OD1	35:g:59:ARG:NH2	2.32	0.63
1:1:309:A:N3	1:1:329:G:O2'	2.32	0.63
5:C:258:ARG:NH2	5:C:263:THR:OG1	2.31	0.63
10:H:54:LEU:O	10:H:57:LYS:HG3	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:5:GLU:OE1	21:S:5:GLU:N	2.31	0.63
49:u:15:ASP:OD1	49:u:55:ILE:HD11	1.98	0.63
39:k:12:ILE:HG23	39:k:21:GLU:OE1	1.98	0.63
1:1:1217:U:OP1	18:P:15:LYS:NZ	2.28	0.63
1:1:2186:G:H2'	1:1:2187:U:C2	2.33	0.63
1:1:1378:A:O2'	1:1:1380:G:N7	2.31	0.63
2:2:1305:G:H21	2:2:1332:A:H2	1.47	0.63
1:1:870:U:OP1	14:L:6:ARG:NH1	2.31	0.63
41:m:12:ARG:HG3	41:m:13:LYS:H	1.64	0.63
1:1:2376:A:N3	16:N:111:ARG:NH1	2.47	0.62
1:1:2788:C:O2'	1:1:2809:A:N3	2.32	0.62
1:1:2885:G:O6	29:a:40:ARG:NH2	2.31	0.62
3:3:66:A:O4'	3:3:108:A:N6	2.30	0.62
1:1:527:C:O2'	1:1:2779:U:O2'	2.17	0.62
1:1:1869:G:N2	1:1:1871:A:O2'	2.31	0.62
31:c:31:LEU:HD22	31:c:42:LEU:CD2	2.30	0.62
1:1:2483:C:N3	14:L:123:LYS:NZ	2.38	0.62
7:E:21:ARG:O	7:E:114:ARG:NH2	2.33	0.62
24:V:37:ILE:HG22	24:V:38:VAL:HG23	1.80	0.62
38:j:40:GLU:CD	38:j:103:VAL:HG21	2.23	0.62
40:l:54:ASP:OD1	40:l:55:THR:N	2.32	0.62
1:1:2141:G:H22	1:1:2151:U:C2'	2.13	0.62
1:1:2194:U:H2'	1:1:2195:U:C6	2.35	0.62
1:1:1064:C:H41	1:1:1070:A:P	2.22	0.62
1:1:1187:G:OP1	19:Q:85:LYS:NZ	2.21	0.62
2:2:1124:G:O2'	2:2:1145:A:N6	2.33	0.62
10:H:91:PHE:O	10:H:123:ARG:NH1	2.33	0.62
15:M:59:SER:OG	15:M:62:ASN:OD1	2.10	0.62
16:N:15:ARG:NH2	16:N:95:SER:OG	2.33	0.62
1:1:2808:G:O2'	1:1:2890:G:O6	2.15	0.61
10:H:7:ASP:OD1	10:H:8:LYS:N	2.33	0.61
37:i:151:GLU:OE1	37:i:151:GLU:N	2.31	0.61
1:1:77:G:O2'	26:X:7:ARG:NH2	2.33	0.61
2:2:1010:U:N3	2:2:1020:G:C6	2.69	0.61
42:n:85:ASP:OD1	42:n:86:ALA:N	2.32	0.61
45:q:16:VAL:HG23	45:q:17:ILE:HD12	1.82	0.61
51:w:36:ARG:NH2	51:w:72:GLY:O	2.33	0.61
1:1:611:C:H2'	1:1:612:G:H5'	1.80	0.61
2:2:1377:A:OP1	39:k:92:ARG:NH1	2.33	0.61
8:F:117:LEU:N	8:F:177:PHE:O	2.33	0.61
41:m:62:ASP:C	41:m:63:LEU:HD12	2.26	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:r:42:TRP:O	46:r:46:LEU:HD23	2.01	0.61
1:1:280:U:O4	1:1:361:G:N2	2.33	0.61
1:1:2128:G:H21	1:1:2174:C:H5'	1.64	0.61
2:2:89:U:H2'	2:2:90:C:C6	2.35	0.61
2:2:981:U:OP1	46:r:9:ARG:NH1	2.34	0.61
51:w:50:ALA:HB1	51:w:57:HIS:HB3	1.82	0.61
1:1:458:G:O2'	1:1:469:G:O6	2.15	0.61
42:n:6:ILE:HG12	42:n:102:LEU:HD23	1.81	0.61
55:B:20:PHE:O	55:B:22:THR:N	2.33	0.61
37:i:136:VAL:O	37:i:140:THR:HG23	2.01	0.61
10:H:54:LEU:HD12	10:H:57:LYS:HE2	1.81	0.61
34:f:72:THR:HG22	34:f:93:ASN:C	2.26	0.61
2:2:1080:A:OP1	37:i:52:LYS:NZ	2.34	0.61
19:Q:51:VAL:HB	19:Q:52:PRO:HD3	1.83	0.61
35:g:47:LEU:HD12	35:g:47:LEU:N	2.15	0.61
1:1:1870:C:O2'	1:1:1871:A:O4'	2.18	0.60
21:S:6:ARG:O	21:S:10:VAL:HG23	2.01	0.60
31:c:24:THR:HG23	31:c:27:GLY:H	1.64	0.60
2:2:542:G:OP1	36:h:10:LYS:NZ	2.24	0.60
7:E:118:LEU:HD11	7:E:188:MET:SD	2.40	0.60
1:1:2484:G:OP1	14:L:44:ARG:NH1	2.31	0.60
52:x:82:GLN:O	52:x:85:LYS:HG3	2.01	0.60
1:1:1798:U:OP2	5:C:271:ARG:NH2	2.34	0.60
1:1:2051:A:N6	1:1:2614:A:O2'	2.33	0.60
1:1:2311:A:O2'	1:1:2312:U:O4'	2.19	0.60
9:G:25:THR:HG22	9:G:34:THR:CG2	2.30	0.60
2:2:356:A:N3	2:2:368:U:O2'	2.25	0.60
10:H:6:LEU:O	10:H:15:LEU:HD12	2.02	0.60
48:t:6:LEU:HD23	48:t:17:TYR:CG	2.37	0.60
1:1:2316:G:H2'	1:1:2317:A:H8	1.67	0.60
2:2:1060:U:H5''	42:n:53:ILE:HD12	1.83	0.60
34:f:3:THR:N	34:f:51:ASN:ND2	2.48	0.60
53:y:50:ALA:O	53:y:54:LYS:HG2	2.01	0.60
37:i:57:PRO:HA	37:i:60:ILE:HG12	1.83	0.60
54:z:43:U:O2'	54:z:44:G:OP1	2.18	0.60
2:2:673:A:H2'	2:2:674:G:C8	2.36	0.60
36:h:47:ARG:HG2	36:h:47:ARG:HH11	1.66	0.60
42:n:42:LEU:HB2	42:n:71:LEU:HB3	1.84	0.60
15:M:54:LEU:HD11	15:M:62:ASN:HD22	1.66	0.60
17:O:14:LYS:HE2	17:O:77:HIS:HA	1.84	0.60
1:1:1042:G:O2'	1:1:1043:C:H5''	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:53:GLU:OE1	10:H:53:GLU:N	2.35	0.59
34:f:129:LEU:HD11	34:f:134:ALA:CA	2.31	0.59
43:o:70:CYS:O	43:o:74:VAL:HG22	2.02	0.59
9:G:2:SER:OG	9:G:3:ARG:N	2.35	0.59
44:p:56:ARG:NE	44:p:62:GLU:OE1	2.32	0.59
1:1:2162:G:H5''	1:1:2173:A:H5''	1.84	0.59
16:N:4:LYS:NZ	16:N:8:ILE:HD11	2.17	0.59
2:2:1119:C:OP2	41:m:11:ARG:NH1	2.35	0.59
1:1:402:A:H2'	1:1:403:U:H5'	1.84	0.59
45:q:9:ILE:CG2	45:q:18:ALA:HB1	2.33	0.59
50:v:14:THR:HG21	50:v:48:ARG:HG3	1.84	0.59
1:1:1094:U:O2'	1:1:1096:A:N7	2.35	0.59
31:c:10:LEU:HD11	31:c:14:ARG:NE	2.18	0.59
44:p:46:ASN:ND2	44:p:89:0TD:SB	2.76	0.59
46:r:46:LEU:O	46:r:50:THR:HG23	2.03	0.59
2:2:933:G:O6	39:k:3:ARG:NH2	2.33	0.59
22:T:36:VAL:HG11	22:T:39:ILE:HD12	1.85	0.59
38:j:32:ALA:HB2	38:j:70:VAL:HG11	1.85	0.59
44:p:48:ALA:C	44:p:49:LEU:HD12	2.27	0.59
53:y:16:LEU:HD23	53:y:20:LYS:HE2	1.83	0.59
1:1:2114:A:H62	1:1:2169:A:H61	1.51	0.59
1:1:2051:A:O2'	1:1:2614:A:N6	2.36	0.58
1:1:2585:U:H3	55:B:25:ASP:HA	1.66	0.58
5:C:142:HIS:ND1	5:C:193:GLY:O	2.36	0.58
16:N:28:VAL:HG12	16:N:93:ASP:O	2.02	0.58
1:1:247:G:O6	32:d:12:LYS:NZ	2.22	0.58
44:p:99:ARG:NE	44:p:104:CYS:SG	2.76	0.58
7:E:1:MET:HB3	7:E:14:VAL:HG23	1.84	0.58
43:o:23:ILE:HD13	43:o:96:THR:CG2	2.32	0.58
1:1:1064:C:O2'	1:1:1065:U:O5'	2.21	0.58
6:D:152:PRO:O	6:D:154:LYS:N	2.36	0.58
35:g:51:SER:HB2	35:g:71:ALA:HB3	1.86	0.58
1:1:2159:G:H2'	1:1:2160:C:C6	2.38	0.58
10:H:100:ALA:HB1	10:H:110:VAL:O	2.03	0.58
1:1:2168:G:N7	1:1:2169:A:N6	2.51	0.58
2:2:405:U:O4	36:h:2:ALA:N	2.37	0.58
2:2:770:C:O2'	2:2:899:C:N3	2.36	0.58
5:C:125:LYS:HG2	5:C:128:ASN:OD1	2.02	0.58
54:z:51:G:N2	54:z:53:A:O5'	2.37	0.58
13:K:70:LYS:O	13:K:74:THR:HG23	2.04	0.58
53:y:7:ARG:N	53:y:10:GLU:OE1	2.31	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:792:A:N3	1:1:2072:C:O2'	2.34	0.57
34:f:32:PHE:N	34:f:40:ILE:O	2.33	0.57
34:f:78:GLU:N	34:f:78:GLU:OE2	2.36	0.57
35:g:134:MET:HE2	35:g:168:TYR:HD2	1.69	0.57
42:n:87:LEU:HD12	42:n:88:MET:N	2.19	0.57
1:1:2350:C:OP2	32:d:45:ARG:NH2	2.38	0.57
2:2:996:A:N1	2:2:1045:C:O2'	2.34	0.57
2:2:1527:U:OP2	53:y:42:THR:HG22	2.04	0.57
16:N:4:LYS:HZ3	16:N:8:ILE:HD11	1.69	0.57
22:T:41:LEU:HB3	22:T:60:GLU:OE2	2.04	0.57
34:f:130:THR:HG23	34:f:133:GLU:CB	2.34	0.57
10:H:84:ALA:HB3	10:H:148:ALA:CB	2.34	0.57
36:h:146:ARG:HG2	36:h:147:GLU:N	2.20	0.57
47:s:78:TYR:OH	47:s:89:ARG:O	2.22	0.57
1:1:511:U:H2'	1:1:512:G:H5'	1.86	0.57
28:Z:16:CYS:SG	28:Z:17:SER:N	2.78	0.57
40:l:77:ARG:NE	40:l:79:SER:O	2.37	0.57
53:y:31:GLU:OE2	53:y:34:ARG:NH2	2.37	0.57
1:1:2104:C:H42	1:1:2185:U:H3	1.52	0.57
1:1:2831:G:N2	1:1:2884:U:OP2	2.38	0.57
5:C:29:PRO:HG2	5:C:34:LEU:HD11	1.86	0.57
28:Z:63:ARG:NH1	51:w:5:LEU:HD21	2.20	0.57
1:1:1062:G:N7	1:1:1088:A:O2'	2.35	0.57
2:2:911:U:OP2	44:p:94:ARG:NH2	2.38	0.57
37:i:157:ARG:NH2	40:l:99:LEU:O	2.38	0.57
1:1:500:G:N1	1:1:503:A:OP2	2.38	0.56
2:2:841:C:H2'	2:2:843:U:H5'	1.85	0.56
37:i:165:LEU:HD12	40:l:114:ARG:HD2	1.87	0.56
1:1:2175:C:H2'	1:1:2176:A:C8	2.40	0.56
9:G:18:LYS:CG	9:G:25:THR:OG1	2.53	0.56
2:2:438:U:H3	2:2:496:A:H62	1.52	0.56
2:2:464:U:N3	2:2:467:U:OP2	2.36	0.56
8:F:144:ASP:OD1	8:F:145:LYS:N	2.38	0.56
1:1:1054:A:H61	1:1:1105:U:H3	1.54	0.56
10:H:54:LEU:HD12	10:H:57:LYS:CE	2.35	0.56
24:V:26:PHE:N	24:V:29:GLU:OE1	2.36	0.56
39:k:113:ASP:OD2	39:k:122:ASN:ND2	2.37	0.56
1:1:1914:C:H2'	1:1:1915:3TD:O4	2.04	0.56
1:1:2171:A:O2'	1:1:2173:A:OP1	2.23	0.56
2:2:521:G:N7	44:p:50:ARG:NH2	2.52	0.56
55:B:11:TRP:HA	55:B:14:ALA:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:36:VAL:CG1	22:T:39:ILE:HD12	2.35	0.56
34:f:82:ASP:OD1	34:f:83:ALA:N	2.38	0.56
55:B:20:PHE:N	55:B:20:PHE:CD1	2.74	0.56
1:1:244:A:OP2	32:d:8:ARG:NH2	2.30	0.56
2:2:552:U:H2'	2:2:553:A:H8	1.70	0.56
21:S:11:LEU:O	26:X:29:ARG:NH1	2.38	0.56
1:1:882:G:O6	1:1:894:U:O2	2.24	0.56
2:2:362:G:N2	2:2:365:U:OP2	2.33	0.56
2:2:481:G:O2'	2:2:483:C:N4	2.39	0.56
21:S:93:LEU:HD23	21:S:94:ASP:N	2.20	0.56
1:1:2162:G:O2'	1:1:2163:A:N7	2.29	0.56
27:Y:6:LYS:HB2	27:Y:58:GLU:HB3	1.88	0.56
20:R:92:ARG:NH1	55:B:12:PHE:O	2.39	0.56
10:H:4:ILE:HD12	10:H:17:ASP:O	2.05	0.55
34:f:185:ALA:HB3	34:f:196:VAL:HG11	1.89	0.55
2:2:1005:A:H3'	2:2:1006:G:H8	1.67	0.55
19:Q:52:PRO:HD2	19:Q:53:PHE:H	1.70	0.55
35:g:24:ALA:HB1	35:g:28:GLU:HG2	1.87	0.55
55:B:12:PHE:N	55:B:12:PHE:CD1	2.74	0.55
1:1:85:G:OP2	22:T:7:ARG:HB2	2.06	0.55
1:1:811:U:H2'	13:K:21:ARG:HA	1.88	0.55
7:E:67:ARG:HD2	55:B:10:LYS:CE	2.28	0.55
38:j:51:ILE:CD1	38:j:85:ILE:HG21	2.35	0.55
1:1:1173:U:O2	1:1:1174:U:N3	2.38	0.55
2:2:1350:A:OP2	41:m:120:LYS:NZ	2.40	0.55
8:F:74:VAL:HG22	8:F:79:ILE:HD11	1.87	0.55
1:1:2079:U:O2'	25:W:23:ASN:OD1	2.23	0.55
10:H:80:ILE:HD11	10:H:102:ALA:HB1	1.87	0.55
14:L:49:ALA:HB1	14:L:120:ALA:HB1	1.87	0.55
1:1:102:U:O4	26:X:2:LYS:N	2.40	0.55
1:1:1266:G:OP2	29:a:17:ARG:NE	2.34	0.55
2:2:1014:A:OP2	51:w:18:LYS:NZ	2.39	0.55
1:1:396:G:OP2	25:W:10:LYS:NZ	2.40	0.55
1:1:2250:G:O2'	1:1:2496:C:OP1	2.24	0.55
19:Q:69:GLY:O	19:Q:90:ARG:NE	2.33	0.55
23:U:76:ASP:OD1	23:U:77:VAL:N	2.39	0.55
54:z:68:C:H2'	54:z:69:G:C8	2.42	0.55
39:k:71:PRO:O	39:k:96:ARG:HG2	2.07	0.55
43:o:108:THR:O	53:y:6:VAL:HG23	2.06	0.55
1:1:2387:U:O4'	24:V:41:ARG:NH1	2.40	0.55
3:3:79:G:N7	23:U:14:LYS:NZ	2.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:53:ALA:HB2	8:F:150:ARG:HE	1.72	0.55
10:H:55:GLU:HA	10:H:58:LEU:CD2	2.36	0.55
16:N:70:ALA:O	16:N:74:VAL:HG23	2.07	0.55
1:1:964:C:O2'	1:1:2273:A:N3	2.36	0.55
10:H:69:ALA:HA	10:H:72:ILE:HG12	1.87	0.55
54:z:65:G:C2	54:z:66:5MU:O2	2.59	0.55
1:1:324:A:OP2	1:1:1205:A:N6	2.40	0.54
1:1:599:A:O2'	1:1:600:G:H5'	2.08	0.54
1:1:894:U:O2'	1:1:895:U:O5'	2.14	0.54
49:u:22:VAL:HG22	49:u:45:HIS:CD2	2.42	0.54
1:1:672:C:OP2	13:K:42:SER:OG	2.20	0.54
1:1:1527:G:N1	1:1:1544:A:OP2	2.34	0.54
2:2:999:C:N3	2:2:1042:A:N6	2.55	0.54
19:Q:52:PRO:O	19:Q:53:PHE:CG	2.60	0.54
54:z:50:G:C6	54:z:51:G:C6	2.95	0.54
1:1:1244:A:O2'	7:E:29:HIS:NE2	2.33	0.54
2:2:1003:G:N2	2:2:1005:A:O5'	2.39	0.54
52:x:4:ILE:HG22	52:x:6:SER:H	1.71	0.54
1:1:573:U:O2'	1:1:575:A:OP1	2.22	0.54
11:I:114:LEU:HG	11:I:118:MET:HE3	1.89	0.54
19:Q:58:VAL:HG13	19:Q:102:SER:OG	2.07	0.54
2:2:127:G:O2'	49:u:6:ARG:NH1	2.40	0.54
1:1:1071:G:H21	1:1:1089:A:HO2'	1.55	0.54
1:1:2477:U:O2	33:e:4:ARG:NH2	2.40	0.54
6:D:151:THR:CG2	6:D:152:PRO:HD3	2.22	0.54
45:q:100:GLN:OE1	45:q:100:GLN:N	2.40	0.54
2:2:1137:C:O2	2:2:1138:G:N2	2.40	0.54
10:H:84:ALA:HB2	10:H:90:LEU:HD12	1.89	0.54
37:i:99:ALA:HB1	37:i:103:THR:HG21	1.89	0.54
43:o:15:GLN:NE2	43:o:78:GLY:O	2.40	0.54
54:z:1:G:O2'	54:z:2:G:O5'	2.26	0.54
1:1:797:G:OP1	7:E:55:SER:OG	2.25	0.54
30:b:13:SER:HA	30:b:49:TYR:CD1	2.42	0.54
37:i:39:VAL:HG12	37:i:40:GLY:N	2.23	0.54
1:1:1071:G:N2	1:1:1089:A:HO2'	2.06	0.54
1:1:1754:A:O3'	17:O:103:ARG:NH2	2.41	0.54
1:1:2457:PSU:HN3	1:1:2494:G:H1	1.56	0.54
23:U:75:GLN:HB2	23:U:92:VAL:HG23	1.90	0.54
39:k:137:LYS:O	39:k:141:VAL:HG23	2.08	0.54
54:z:55:C:O2'	54:z:56:G:P	2.65	0.54
1:1:1266:G:O2'	1:1:2012:G:O6	2.21	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2885:G:O6	29:a:29:SER:OG	2.24	0.54
2:2:842:U:C2'	2:2:844:G:H21	2.21	0.54
3:3:42:C:OP1	8:F:64:LYS:NZ	2.30	0.54
38:j:32:ALA:CB	38:j:70:VAL:HG11	2.38	0.54
45:q:29:ARG:O	45:q:33:ILE:HG12	2.08	0.54
1:1:1341:G:OP2	1:1:1394:U:O2'	2.20	0.53
9:G:18:LYS:HG2	9:G:25:THR:OG1	2.08	0.53
1:1:1871:A:H1'	1:1:1872:A:C8	2.44	0.53
2:2:501:C:OP1	44:p:114:ARG:NH2	2.35	0.53
14:L:110:GLU:O	14:L:114:ARG:HG2	2.08	0.53
20:R:2:GLU:N	20:R:2:GLU:OE1	2.41	0.53
31:c:31:LEU:HD22	31:c:42:LEU:HD21	1.90	0.53
38:j:51:ILE:HD12	38:j:85:ILE:CG2	2.37	0.53
55:B:20:PHE:N	55:B:20:PHE:HD1	2.06	0.53
1:1:1915:3TD:H2'	1:1:1916:A:O4'	2.08	0.53
1:1:2149:U:H2'	1:1:2150:C:O4'	2.08	0.53
10:H:63:ALA:O	10:H:66:ASN:OD1	2.25	0.53
18:P:97:ASP:OD2	19:Q:13:ARG:NH1	2.41	0.53
35:g:40:ARG:O	35:g:44:THR:HG23	2.08	0.53
44:p:16:VAL:O	44:p:16:VAL:HG13	2.05	0.53
51:w:30:PRO:HA	51:w:48:THR:O	2.08	0.53
55:B:5:MET:HA	55:B:8:ILE:HG13	1.89	0.53
55:B:13:ASN:O	55:B:16:LYS:N	2.40	0.53
10:H:70:GLU:HG2	10:H:140:ALA:HB2	1.91	0.53
19:Q:52:PRO:CD	19:Q:53:PHE:H	2.22	0.53
25:W:72:ARG:NH1	25:W:78:TYR:OH	2.40	0.53
49:u:25:ILE:HD11	49:u:61:ILE:HD11	1.90	0.53
1:1:1077:A:N6	1:1:1078:U:O2	2.42	0.53
2:2:401:C:O2'	2:2:621:A:N3	2.40	0.53
2:2:946:A:H2'	2:2:947:G:C8	2.43	0.53
2:2:1176:A:H2'	2:2:1177:G:C8	2.43	0.53
10:H:66:ASN:ND2	10:H:135:HIS:CG	2.76	0.53
36:h:27:ALA:O	36:h:30:THR:OG1	2.23	0.53
1:1:620:G:H4'	1:1:621:A:O5'	2.09	0.53
38:j:98:GLU:OE1	38:j:98:GLU:N	2.37	0.53
10:H:51:ARG:HA	10:H:54:LEU:HB3	1.91	0.53
34:f:173:ILE:HG22	34:f:177:ASN:OD1	2.08	0.53
38:j:22:ILE:HG21	38:j:39:LEU:HD21	1.90	0.53
40:l:30:SER:O	40:l:34:VAL:HG23	2.09	0.53
1:1:639:U:H2'	1:1:640:C:C6	2.44	0.53
1:1:1532:A:C6	1:1:1540:G:C6	2.96	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2108:A:H62	1:1:2178:C:N4	2.07	0.53
10:H:58:LEU:HA	10:H:61:VAL:HG22	1.90	0.53
35:g:131:ARG:O	35:g:135:LYS:HG2	2.09	0.53
35:g:155:GLY:O	35:g:196:ILE:HG12	2.09	0.53
45:q:3:ARG:HH11	45:q:3:ARG:HG3	1.72	0.53
1:1:989:G:OP2	27:Y:12:SER:OG	2.27	0.53
22:T:94:ARG:HB3	22:T:103:ILE:HD12	1.91	0.53
47:s:4:SER:O	47:s:8:THR:HG23	2.09	0.53
1:1:2469:A:N6	1:1:2481:G:O2'	2.42	0.52
36:h:124:MET:HE3	36:h:146:ARG:NE	2.21	0.52
54:z:21:G:N2	54:z:57:U:O4	2.42	0.52
1:1:621:A:OP2	13:K:99:ASN:ND2	2.42	0.52
1:1:1715:G:O2'	1:1:1743:G:O6	2.18	0.52
2:2:685:G:N1	2:2:704:A:OP2	2.33	0.52
2:2:1498:UR3:OP2	4:4:4:U:O2'	2.27	0.52
5:C:71:LYS:O	5:C:118:SER:OG	2.27	0.52
9:G:46:ALA:O	9:G:47:ASP:OD1	2.26	0.52
13:K:124:GLY:C	13:K:125:LEU:HD12	2.33	0.52
23:U:58:SER:O	23:U:73:LYS:NZ	2.42	0.52
28:Z:55:GLY:HA3	28:Z:58:ASP:OD2	2.09	0.52
35:g:131:ARG:NH2	35:g:166:GLU:OE1	2.42	0.52
38:j:3:HIS:CD2	38:j:95:ALA:HB2	2.44	0.52
39:k:53:ARG:NH2	39:k:122:ASN:OD1	2.42	0.52
48:t:19:VAL:HG22	48:t:37:GLY:C	2.34	0.52
53:y:4:ILE:HD12	53:y:19:PHE:CD1	2.38	0.52
54:z:55:C:C2	54:z:56:G:C8	2.97	0.52
1:1:243:U:OP2	32:d:8:ARG:NH1	2.42	0.52
34:f:207:ILE:HA	34:f:210:VAL:HG22	1.92	0.52
35:g:121:THR:HG23	35:g:189:ALA:CB	2.40	0.52
36:h:146:ARG:HG2	36:h:147:GLU:H	1.75	0.52
1:1:402:A:H2'	1:1:403:U:C5'	2.38	0.52
2:2:82:G:H1	2:2:86:G:H1	1.58	0.52
41:m:47:VAL:CG2	41:m:76:ALA:HB1	2.39	0.52
50:v:42:SER:OG	50:v:47:THR:O	2.27	0.52
1:1:1047:G:O2'	1:1:1110:G:N1	2.32	0.52
1:1:1363:C:O2'	1:1:1809:A:N3	2.39	0.52
1:1:1912:A:HO2'	2:2:1494:G:HO2'	1.57	0.52
10:H:67:ALA:O	10:H:71:LYS:HD3	2.09	0.52
1:1:2101:A:N6	1:1:2188:U:C4	2.77	0.52
1:1:2167:U:O5'	1:1:2167:U:C6	2.59	0.52
1:1:2658:C:OP1	9:G:158:LYS:NZ	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:80:ILE:HD11	10:H:102:ALA:HB2	1.91	0.52
16:N:27:VAL:CG2	16:N:40:ILE:HD12	2.38	0.52
37:i:133:PRO:HA	37:i:136:VAL:HG12	1.92	0.52
38:j:9:MET:HG2	38:j:59:TYR:CE1	2.45	0.52
53:y:13:ASP:N	53:y:13:ASP:OD1	2.41	0.52
1:1:996:A:OP2	18:P:93:LYS:NZ	2.29	0.52
1:1:1067:A:C3'	1:1:1068:G:H5''	2.40	0.52
20:R:13:SER:O	20:R:17:VAL:HG23	2.08	0.52
1:1:1173:U:H4'	1:1:1174:U:H5'	1.91	0.52
1:1:2359:C:O2'	32:d:54:ASP:OD2	2.27	0.52
1:1:2387:U:OP1	24:V:55:ARG:NH2	2.32	0.52
3:3:74:U:O2	23:U:29:ILE:HD13	2.10	0.52
34:f:128:LYS:HD2	34:f:128:LYS:O	2.10	0.52
49:u:48:ASP:CG	49:u:75:LEU:HD21	2.34	0.52
55:B:9:VAL:O	55:B:10:LYS:C	2.52	0.52
1:1:307:G:N1	1:1:310:A:OP2	2.38	0.52
1:1:355:U:H2'	1:1:356:G:H8	1.75	0.52
37:i:111:MET:SD	37:i:125:ALA:HB1	2.50	0.52
49:u:76:VAL:HG23	49:u:77:ARG:HG2	1.91	0.52
2:2:120:A:O2'	2:2:122:G:N7	2.27	0.51
22:T:7:ARG:O	22:T:25:VAL:HB	2.09	0.51
3:3:5:U:OP1	3:3:61:G:O2'	2.28	0.51
29:a:40:ARG:HG3	29:a:41:HIS:ND1	2.25	0.51
42:n:90:LEU:HD23	42:n:91:ASP:N	2.24	0.51
1:1:137:U:C2'	1:1:138:U:H5'	2.40	0.51
2:2:1458:G:OP1	52:x:30:THR:OG1	2.26	0.51
7:E:189:THR:HG22	7:E:191:ASP:H	1.74	0.51
10:H:51:ARG:HB3	10:H:55:GLU:CD	2.36	0.51
10:H:135:HIS:CB	10:H:138:VAL:HG22	2.40	0.51
46:r:90:ARG:HB2	46:r:92:GLU:OE1	2.10	0.51
1:1:1248:G:OP1	7:E:44:ARG:NH2	2.42	0.51
1:1:1534:U:O2	1:1:1538:G:C6	2.63	0.51
1:1:2128:G:C2	1:1:2173:A:O2'	2.64	0.51
1:1:2636:C:O2'	6:D:45:TYR:OH	2.26	0.51
1:1:2902:C:N4	1:1:2903:U:O4	2.44	0.51
10:H:135:HIS:HB3	10:H:138:VAL:HG22	1.91	0.51
1:1:323:C:H2'	7:E:163:ASN:OD1	2.10	0.51
1:1:856:G:H2'	1:1:857:G:C8	2.45	0.51
1:1:1028:A:OP2	1:1:1126:A:N6	2.31	0.51
2:2:392:C:OP1	48:t:8:ARG:NH2	2.44	0.51
9:G:104:ASN:ND2	9:G:114:ASP:OD1	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Z:51:VAL:HG23	28:Z:52:ALA:N	2.25	0.51
53:y:64:ASN:OD1	53:y:64:ASN:C	2.53	0.51
54:z:51:G:H2'	54:z:52:C:O4'	2.10	0.51
1:1:2183:A:H2'	1:1:2184:A:C8	2.46	0.51
2:2:811:C:O2'	2:2:901:A:N1	2.44	0.51
3:3:1:U:O2'	3:3:2:G:H8	1.93	0.51
7:E:77:ILE:HG22	7:E:77:ILE:O	2.09	0.51
20:R:55:ILE:HG23	20:R:66:ILE:HD12	1.92	0.51
27:Y:17:LEU:HD12	27:Y:20:HIS:CE1	2.46	0.51
41:m:25:ASN:OD1	41:m:27:LYS:HG3	2.11	0.51
1:1:400:G:N7	25:W:57:ARG:NH1	2.57	0.51
1:1:1278:C:O2'	15:M:27:SER:OG	2.24	0.51
1:1:2110:G:O2'	1:1:2120:G:O5'	2.29	0.51
1:1:2126:A:N1	1:1:2163:A:H5'	2.26	0.51
5:C:117:GLN:O	5:C:128:ASN:ND2	2.40	0.51
27:Y:24:LEU:HD11	27:Y:54:MET:CE	2.41	0.51
36:h:47:ARG:HA	36:h:47:ARG:CZ	2.41	0.51
1:1:1590:A:H2'	1:1:1591:A:C8	2.45	0.51
2:2:1319:A:O2'	2:2:1323:G:N7	2.30	0.51
9:G:105:LEU:HD13	9:G:107:LEU:HD11	1.93	0.51
10:H:51:ARG:HB3	10:H:55:GLU:OE2	2.11	0.51
1:1:2127:G:H21	1:1:2173:A:H1'	1.76	0.51
2:2:452:A:H62	2:2:480:U:H3	1.59	0.51
3:3:48:U:OP1	16:N:30:ARG:NH2	2.41	0.51
15:M:24:MET:SD	15:M:44:LEU:HD22	2.51	0.51
1:1:170:U:H2'	1:1:171:U:C6	2.46	0.51
1:1:1797:G:HO2'	5:C:257:THR:HG1	1.59	0.51
11:I:13:ARG:NH1	11:I:49:ASP:O	2.41	0.51
36:h:129:VAL:HB	36:h:146:ARG:HH21	1.75	0.51
44:p:4:VAL:O	44:p:8:VAL:HG23	2.10	0.51
46:r:46:LEU:HD12	51:w:13:LEU:HB3	1.92	0.51
1:1:228:C:N4	1:1:2407:A:N3	2.55	0.50
1:1:2523:G:HO2'	1:1:2764:A:HO2'	1.54	0.50
2:2:404:G:O6	36:h:2:ALA:N	2.44	0.50
2:2:496:A:H2'	2:2:496:A:N3	2.25	0.50
9:G:76:VAL:O	9:G:80:THR:HG22	2.11	0.50
13:K:132:ARG:HG3	13:K:142:ILE:HD12	1.92	0.50
21:S:93:LEU:HD23	21:S:94:ASP:C	2.36	0.50
27:Y:57:VAL:HG22	27:Y:59:GLU:OE2	2.11	0.50
1:1:882:G:N1	1:1:895:U:O4'	2.44	0.50
1:1:1664:A:H2	12:J:1:MET:HE1	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2141:G:H22	1:1:2151:U:H2'	1.77	0.50
6:D:3:GLY:C	6:D:4:LEU:HD12	2.36	0.50
27:Y:47:MET:O	27:Y:51:VAL:HG22	2.11	0.50
28:Z:59:ARG:O	28:Z:63:ARG:HG3	2.11	0.50
29:a:52:ARG:HH21	29:a:54:VAL:HG12	1.72	0.50
34:f:68:LEU:HD11	34:f:92:VAL:HG23	1.93	0.50
43:o:19:GLY:C	43:o:82:LEU:HD12	2.36	0.50
1:1:2532:G:O2'	1:1:2657:A:N1	2.45	0.50
44:p:48:ALA:O	44:p:49:LEU:HD12	2.11	0.50
1:1:645:C:H2'	1:1:647:G:C8	2.46	0.50
1:1:2192:U:H2'	1:1:2193:G:O4'	2.11	0.50
20:R:86:MET:SD	20:R:87:PRO:HD2	2.51	0.50
36:h:146:ARG:CG	36:h:147:GLU:H	2.25	0.50
39:k:69:VAL:HG12	39:k:135:VAL:HG12	1.92	0.50
41:m:36:GLU:O	41:m:45:ARG:NH2	2.45	0.50
42:n:15:HIS:HA	42:n:18:ILE:HG22	1.93	0.50
42:n:52:LEU:O	46:r:81:ARG:NH1	2.40	0.50
49:u:7:THR:C	49:u:8:LEU:HD12	2.36	0.50
54:z:44:G:C2'	54:z:45:U:OP1	2.59	0.50
54:z:49:C:H2'	54:z:50:G:C8	2.47	0.50
1:1:372:G:O2'	1:1:400:G:O6	2.19	0.50
1:1:2193:G:C6	1:1:2194:U:C4	2.99	0.50
24:V:59:LEU:CD1	24:V:80:ILE:HD12	2.41	0.50
28:Z:55:GLY:CA	28:Z:58:ASP:OD2	2.60	0.50
35:g:7:PRO:HA	35:g:10:ILE:HG22	1.92	0.50
37:i:139:ALA:O	37:i:142:ASP:OD1	2.29	0.50
41:m:47:VAL:HG12	41:m:50:GLN:OE1	2.11	0.50
1:1:1827:U:OP2	5:C:221:ARG:NE	2.43	0.50
2:2:855:U:OP2	2:2:871:U:N3	2.36	0.50
8:F:32:GLU:HG2	8:F:157:THR:O	2.12	0.50
9:G:54:PRO:HG2	9:G:62:TRP:CE2	2.46	0.50
45:q:3:ARG:HG3	45:q:3:ARG:NH1	2.25	0.50
47:s:21:ASP:O	47:s:22:THR:HG22	2.11	0.50
54:z:50:G:O6	54:z:56:G:C6	2.64	0.50
37:i:46:VAL:HG22	37:i:118:ALA:HA	1.94	0.50
38:j:9:MET:HE3	38:j:59:TYR:CE1	2.46	0.50
1:1:601:C:H2'	1:1:602:A:O4'	2.12	0.50
15:M:47:VAL:O	15:M:51:LEU:HD23	2.10	0.50
22:T:34:VAL:HG13	22:T:67:VAL:HG22	1.93	0.50
34:f:63:ARG:O	34:f:64:LYS:HG2	2.12	0.50
40:l:18:GLN:OE1	40:l:63:LEU:HD13	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2850:A:OP2	1:1:2866:U:N3	2.39	0.50
5:C:107:PRO:HD2	5:C:110:LEU:HD22	1.93	0.50
34:f:133:GLU:O	34:f:137:ARG:HG2	2.12	0.50
35:g:123:GLN:HB3	35:g:128:VAL:HG21	1.94	0.50
37:i:142:ASP:OD1	37:i:142:ASP:C	2.54	0.50
46:r:10:GLU:O	46:r:14:VAL:HG23	2.11	0.50
1:1:2148:G:H2'	1:1:2149:U:C6	2.47	0.49
1:1:2402:U:O2'	1:1:2403:C:H5''	2.12	0.49
1:1:2880:C:O3'	15:M:90:ARG:NH2	2.45	0.49
2:2:580:C:H2'	2:2:581:G:O4'	2.12	0.49
2:2:944:G:N1	2:2:1338:G:OP2	2.40	0.49
48:t:46:LYS:N	48:t:46:LYS:HD2	2.27	0.49
55:B:16:LYS:NZ	55:B:16:LYS:CB	2.75	0.49
1:1:69:C:O2	1:1:73:A:O2'	2.28	0.49
1:1:1105:U:H2'	1:1:1106:G:H8	1.77	0.49
9:G:102:VAL:HG12	9:G:103:ILE:N	2.26	0.49
37:i:153:VAL:HG23	37:i:164:ILE:HD13	1.92	0.49
46:r:80:SER:O	46:r:84:VAL:HG23	2.12	0.49
54:z:51:G:C2'	54:z:52:C:O5'	2.61	0.49
1:1:137:U:H2'	1:1:138:U:H5'	1.93	0.49
1:1:2655:G:O2'	1:1:2664:G:O6	2.26	0.49
2:2:459:A:H2'	2:2:460:A:C8	2.47	0.49
2:2:1167:A:O2'	2:2:1169:A:N7	2.43	0.49
24:V:18:ALA:O	24:V:20:ARG:HD2	2.12	0.49
34:f:27:MET:O	34:f:31:ILE:HG13	2.12	0.49
34:f:217:VAL:O	34:f:221:VAL:HG22	2.12	0.49
53:y:4:ILE:CD1	53:y:19:PHE:HA	2.42	0.49
1:1:818:G:N1	1:1:1188:U:OP2	2.35	0.49
1:1:2063:C:O2	1:1:2450:A:N1	2.46	0.49
1:1:2308:G:O6	1:1:2311:A:N7	2.45	0.49
2:2:501:C:OP2	44:p:121:ARG:NH1	2.45	0.49
2:2:1241:G:H2'	2:2:1242:G:H8	1.77	0.49
34:f:93:ASN:OD1	34:f:94:HIS:N	2.45	0.49
34:f:185:ALA:HB3	34:f:196:VAL:CG1	2.42	0.49
51:w:19:VAL:O	51:w:23:VAL:HG23	2.11	0.49
1:1:445:C:O2'	1:1:449:A:N3	2.37	0.49
1:1:2308:G:H2'	1:1:2310:C:H41	1.77	0.49
1:1:2512:C:H1'	6:D:145:SER:O	2.12	0.49
1:1:2822:G:OP1	6:D:164:GLN:NE2	2.44	0.49
2:2:552:U:H2'	2:2:553:A:C8	2.46	0.49
6:D:34:VAL:HB	6:D:92:VAL:O	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:47:GLU:OE2	14:L:50:ARG:NH1	2.45	0.49
19:Q:52:PRO:O	19:Q:53:PHE:CD2	2.65	0.49
44:p:24:LEU:HD23	44:p:27:CYS:O	2.12	0.49
54:z:26:A:H2'	54:z:27:G:O4'	2.12	0.49
1:1:2112:G:OP2	1:1:2119:A:H2'	2.12	0.49
2:2:1008:U:N3	2:2:1022:A:C2	2.80	0.49
8:F:53:ALA:CB	8:F:150:ARG:HE	2.24	0.49
16:N:94:ARG:HD2	16:N:97:PHE:O	2.13	0.49
28:Z:48:GLN:OE1	28:Z:48:GLN:N	2.43	0.49
38:j:7:VAL:HG22	38:j:61:LEU:CD1	2.43	0.49
1:1:321:U:O3'	7:E:162:ARG:NH1	2.40	0.49
1:1:1870:C:HO2'	1:1:1871:A:C1'	2.26	0.49
1:1:2125:G:N1	1:1:2171:A:OP2	2.39	0.49
1:1:2148:G:H2'	1:1:2149:U:H6	1.76	0.49
1:1:2561:U:O3'	12:J:40:LYS:NZ	2.42	0.49
2:2:427:U:OP1	36:h:13:ARG:NH1	2.45	0.49
2:2:842:U:O2	2:2:844:G:H5'	2.13	0.49
2:2:978:A:C2	2:2:1319:A:C4	3.00	0.49
5:C:262:ARG:O	5:C:265:LYS:NZ	2.45	0.49
41:m:60:LYS:HB3	41:m:61:LEU:HD12	1.95	0.49
42:n:39:PRO:HA	42:n:74:VAL:HG22	1.94	0.49
1:1:639:U:H2'	1:1:640:C:H6	1.77	0.49
1:1:2144:G:N2	1:1:2148:G:H1	2.11	0.49
2:2:1183:U:O2'	2:2:1185:G:OP2	2.30	0.49
2:2:1314:C:N4	51:w:2:PRO:O	2.45	0.49
1:1:721:A:H2'	1:1:722:A:C8	2.47	0.49
1:1:2425:A:H5''	1:1:2427:C:O4'	2.13	0.49
45:q:46:SER:C	45:q:47:GLU:HG3	2.37	0.49
54:z:44:G:O2'	54:z:45:U:P	2.71	0.49
2:2:108:G:H5'	2:2:109:A:H5''	1.94	0.49
2:2:269:C:H2'	2:2:270:A:C8	2.48	0.49
2:2:1039:G:H2'	2:2:1040:U:C6	2.48	0.49
2:2:1222:G:H5''	51:w:78:ARG:HD2	1.95	0.49
7:E:129:PRO:HB3	7:E:156:ASN:HA	1.95	0.49
11:I:57:LEU:HD23	11:I:125:TYR:HB2	1.95	0.49
14:L:1:MET:HE3	14:L:44:ARG:HG3	1.95	0.49
18:P:50:ARG:O	18:P:54:LYS:NZ	2.43	0.49
22:T:43:LYS:CG	22:T:60:GLU:OE1	2.61	0.49
49:u:20:SER:OG	49:u:71:LYS:NZ	2.46	0.49
55:B:6:THR:HG23	55:B:7:GLY:N	2.28	0.49
1:1:11:C:H2'	1:1:12:U:H5'	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:285:G:C6	1:1:356:G:C6	3.00	0.48
1:1:1087:G:H22	1:1:1102:C:H42	1.61	0.48
1:1:2305:U:H5''	8:F:131:GLY:HA3	1.95	0.48
2:2:496:A:O2'	2:2:497:G:C8	2.63	0.48
2:2:1010:U:C2	2:2:1020:G:C2	3.01	0.48
3:3:43:C:OP1	28:Z:2:LYS:N	2.40	0.48
8:F:32:GLU:OE2	8:F:157:THR:HG22	2.13	0.48
10:H:100:ALA:O	10:H:104:THR:HG22	2.13	0.48
13:K:74:THR:HG22	13:K:107:PHE:HB2	1.94	0.48
22:T:74:ASN:ND2	22:T:81:ASP:OD2	2.44	0.48
55:B:16:LYS:O	55:B:16:LYS:HG2	2.11	0.48
1:1:2591:C:H2'	1:1:2592:G:C8	2.48	0.48
37:i:13:GLU:OE2	37:i:68:ARG:NH1	2.45	0.48
52:x:35:VAL:HG11	52:x:79:LEU:HD13	1.94	0.48
1:1:2291:U:H2'	1:1:2292:U:C6	2.48	0.48
1:1:2512:C:O5'	1:1:2512:C:H6	1.96	0.48
2:2:1320:C:N3	51:w:36:ARG:NH1	2.60	0.48
3:3:13:G:N2	3:3:16:G:N3	2.61	0.48
34:f:72:THR:HG22	34:f:93:ASN:O	2.13	0.48
41:m:91:ASP:OD1	41:m:93:SER:OG	2.25	0.48
1:1:1432:G:H2'	1:1:1433:A:C8	2.49	0.48
1:1:1469:A:H2'	1:1:1470:A:C8	2.48	0.48
1:1:2030:6MZ:C2	1:1:2499:C:H5''	2.44	0.48
1:1:2050:C:H2'	1:1:2051:A:O4'	2.14	0.48
1:1:2141:G:N1	1:1:2151:U:O2	2.47	0.48
1:1:2728:U:O2'	1:1:2729:G:H8	1.97	0.48
10:H:75:LEU:HD21	10:H:106:ALA:O	2.13	0.48
38:j:72:ASP:OD1	38:j:73:GLU:N	2.47	0.48
2:2:516:PSU:H4'	2:2:517:G:OP1	2.12	0.48
2:2:672:U:H2'	2:2:673:A:C8	2.49	0.48
2:2:768:A:N3	2:2:1512:U:O2'	2.46	0.48
2:2:980:C:O2'	46:r:13:ARG:NH1	2.47	0.48
7:E:150:THR:HG22	7:E:152:GLU:H	1.78	0.48
10:H:87:GLU:OE1	38:j:17:GLN:HB3	2.12	0.48
22:T:13:VAL:HG21	22:T:39:ILE:HD13	1.95	0.48
35:g:20:SER:OG	35:g:40:ARG:NH2	2.46	0.48
35:g:87:LEU:O	35:g:91:VAL:HG23	2.13	0.48
36:h:47:ARG:HG2	36:h:47:ARG:NH1	2.29	0.48
39:k:115:SER:O	39:k:119:ARG:HG3	2.13	0.48
1:1:282:A:C6	1:1:359:G:C6	3.02	0.48
1:1:955:PSU:HN3	1:1:962:G:H1	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2121:G:OP1	1:1:2169:A:N3	2.47	0.48
1:1:2141:G:N1	1:1:2151:U:C2	2.79	0.48
39:k:24:ALA:HA	39:k:27:VAL:HG22	1.94	0.48
40:l:87:LYS:HG3	40:l:125:ILE:HD11	1.96	0.48
1:1:2134:A:N6	1:1:2157:G:H1'	2.28	0.48
1:1:2294:G:OP1	16:N:10:ARG:HD3	2.14	0.48
2:2:559:A:H4'	2:2:560:A:H3'	1.95	0.48
2:2:1033:G:H2'	2:2:1034:G:C8	2.49	0.48
2:2:1086:U:H3	2:2:1099:G:H22	1.62	0.48
15:M:87:PHE:HD1	15:M:90:ARG:HD3	1.79	0.48
42:n:84:VAL:HG13	42:n:85:ASP:N	2.29	0.48
47:s:21:ASP:O	47:s:23:GLY:N	2.47	0.48
49:u:7:THR:HG21	49:u:60:GLU:OE2	2.13	0.48
54:z:1:G:C6	54:z:85:G:C2	3.02	0.48
1:1:402:A:C2'	1:1:403:U:H5'	2.43	0.48
1:1:2190:G:H2'	1:1:2191:A:H8	1.79	0.48
2:2:958:A:OP1	51:w:55:ARG:NH1	2.46	0.48
7:E:152:GLU:CD	7:E:153:LEU:N	2.71	0.48
8:F:95:ARG:NE	28:Z:1:MET:SD	2.87	0.48
39:k:135:VAL:O	39:k:139:GLU:HG2	2.13	0.48
55:B:1:FME:O	55:B:2:SER:OG	2.27	0.48
1:1:889:C:P	54:z:52:C:H41	2.36	0.48
1:1:1217:U:P	18:P:15:LYS:HZ3	2.35	0.48
2:2:1071:C:H2'	2:2:1072:G:H8	1.78	0.48
10:H:15:LEU:C	10:H:15:LEU:HD23	2.39	0.48
14:L:136:MET:HE1	23:U:74:ALA:O	2.14	0.48
40:l:2:SER:OG	40:l:4:GLN:NE2	2.46	0.48
51:w:64:ASP:OD1	51:w:65:GLU:N	2.47	0.48
1:1:510:C:C2'	1:1:511:U:H5'	2.44	0.47
1:1:1028:A:N3	1:1:2486:C:O2'	2.24	0.47
2:2:844:G:N1	2:2:846:G:H1'	2.29	0.47
8:F:122:PHE:O	8:F:123:ASP:OD1	2.32	0.47
22:T:43:LYS:HG2	22:T:60:GLU:OE1	2.14	0.47
34:f:89:GLN:OE1	34:f:89:GLN:HA	2.14	0.47
38:j:35:LYS:O	38:j:36:ILE:HD13	2.13	0.47
38:j:100:SER:OG	38:j:103:VAL:HG23	2.14	0.47
1:1:534:U:O2'	18:P:49:ASP:OD2	2.27	0.47
1:1:548:G:H3'	1:1:549:G:O4'	2.14	0.47
1:1:636:G:N7	13:K:109:LYS:HE2	2.28	0.47
5:C:69:ARG:NH1	5:C:129:THR:OG1	2.47	0.47
9:G:86:LYS:HG2	9:G:132:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:46:PHE:CD1	10:H:50:ARG:NH1	2.82	0.47
10:H:49:ALA:HB3	10:H:50:ARG:HD3	1.96	0.47
10:H:93:SER:OG	10:H:94:ILE:N	2.46	0.47
20:R:72:THR:HG21	20:R:108:SER:OG	2.14	0.47
34:f:120:GLN:O	34:f:126:PHE:HB2	2.14	0.47
47:s:21:ASP:OD1	47:s:22:THR:N	2.43	0.47
1:1:1779:U:H5	1:1:1784:A:N7	2.12	0.47
1:1:2585:U:O2	55:B:24:ASP:C	2.58	0.47
2:2:713:G:H2'	2:2:714:G:C8	2.49	0.47
9:G:155:GLU:HG2	9:G:157:TYR:H	1.78	0.47
11:I:95:ARG:CZ	11:I:96:ARG:HB3	2.45	0.47
22:T:46:GLN:N	22:T:57:GLY:O	2.41	0.47
38:j:42:TRP:HB2	38:j:59:TYR:HB2	1.97	0.47
39:k:60:GLU:O	39:k:64:VAL:HG23	2.13	0.47
41:m:26:GLY:N	41:m:62:ASP:OD1	2.46	0.47
1:1:281:C:H2'	1:1:282:A:H8	1.80	0.47
1:1:357:C:C2	1:1:358:U:C5	3.02	0.47
1:1:743:A:O2'	1:1:1659:G:OP1	2.27	0.47
1:1:1322:A:C5	1:1:1323:C:C5	3.02	0.47
2:2:1439:G:OP2	52:x:33:LYS:NZ	2.46	0.47
5:C:51:THR:HG23	5:C:54:ILE:HD12	1.96	0.47
8:F:105:THR:HG21	28:Z:22:MET:SD	2.54	0.47
10:H:40:THR:OG1	10:H:43:ASN:HB3	2.14	0.47
38:j:18:VAL:HG21	38:j:58:HIS:CD2	2.49	0.47
42:n:8:ILE:HG12	42:n:100:ILE:HG22	1.97	0.47
2:2:972:C:O2'	42:n:57:VAL:HG23	2.14	0.47
8:F:19:GLU:O	8:F:19:GLU:HG2	2.14	0.47
8:F:142:ASP:OD2	8:F:144:ASP:OD1	2.32	0.47
10:H:101:ASP:C	10:H:104:THR:HG22	2.40	0.47
26:X:7:ARG:NH1	26:X:59:GLU:OE1	2.47	0.47
43:o:107:ILE:HG23	53:y:6:VAL:HG21	1.96	0.47
51:w:40:ILE:HD12	51:w:66:MET:O	2.14	0.47
54:z:49:C:C2	54:z:50:G:N7	2.83	0.47
1:1:287:G:H2'	1:1:288:U:C6	2.50	0.47
1:1:1250:G:H5'	18:P:6:ARG:HD3	1.96	0.47
1:1:1582:C:O2'	1:1:1585:C:N3	2.39	0.47
2:2:477:C:H2'	2:2:478:A:C8	2.50	0.47
2:2:1060:U:H2'	2:2:1061:G:H8	1.79	0.47
2:2:1279:G:O2'	2:2:1282:C:N4	2.47	0.47
2:2:1530:G:H2'	2:2:1531:A:C8	2.49	0.47
7:E:48:THR:O	7:E:52:VAL:HG23	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:c:42:LEU:HD23	31:c:43:THR:HG23	1.97	0.47
1:1:549:G:H2'	1:1:550:C:C6	2.49	0.47
1:1:859:G:O2'	1:1:916:G:O6	2.27	0.47
1:1:878:A:C6	1:1:900:A:C8	3.03	0.47
1:1:1074:G:H2'	1:1:1075:C:C6	2.50	0.47
1:1:2585:U:O2	55:B:25:ASP:HA	2.14	0.47
2:2:1220:G:P	46:r:53:ARG:HH12	2.38	0.47
34:f:184:PHE:HD1	34:f:198:PHE:HB2	1.79	0.47
45:q:20:THR:HG22	45:q:26:GLY:C	2.39	0.47
1:1:1485:U:H2'	1:1:1486:U:C6	2.50	0.47
1:1:2053:G:O6	1:1:2614:A:H2	1.98	0.47
1:1:2128:G:H2'	1:1:2129:C:O4'	2.15	0.47
2:2:16:A:N3	2:2:1080:A:O2'	2.45	0.47
2:2:675:A:H1'	43:o:118:HIS:CD2	2.50	0.47
2:2:857:C:H2'	2:2:858:G:O4'	2.15	0.47
41:m:15:SER:OG	41:m:78:ALA:HB2	2.15	0.47
44:p:87:VAL:HG11	44:p:90:LEU:CD1	2.40	0.47
1:1:784:G:O2'	1:1:785:G:O5'	2.26	0.47
1:1:1824:G:OP1	5:C:52:ARG:HG3	2.14	0.47
2:2:208:U:O2	2:2:212:G:C2	2.68	0.47
2:2:1145:A:O2'	2:2:1146:A:O4'	2.33	0.47
2:2:1522:U:H5''	43:o:128:ARG:NH2	2.30	0.47
10:H:82:SER:OG	10:H:90:LEU:HD11	2.15	0.47
14:L:53:MET:HG3	14:L:63:ILE:HD13	1.97	0.47
36:h:95:GLU:HA	36:h:100:ASN:HD22	1.80	0.47
48:t:5:ARG:NH2	48:t:27:ALA:O	2.47	0.47
1:1:1077:A:H61	1:1:1088:A:H2'	1.80	0.47
1:1:2113:U:N3	1:1:2114:A:N7	2.62	0.47
1:1:2313:C:H2'	1:1:2314:A:H8	1.78	0.47
1:1:2314:A:O4'	8:F:155:THR:HG21	2.14	0.47
6:D:13:ARG:NH1	17:O:75:GLN:OE1	2.30	0.47
10:H:51:ARG:HG3	10:H:54:LEU:HD23	1.97	0.47
19:Q:37:GLU:OE1	19:Q:37:GLU:HA	2.14	0.47
37:i:94:VAL:HG13	37:i:111:MET:HE1	1.96	0.47
39:k:69:VAL:CG1	39:k:135:VAL:HG12	2.44	0.47
44:p:55:VAL:HG21	44:p:80:ILE:HD11	1.96	0.47
52:x:32:ILE:HG12	52:x:54:MET:HE2	1.97	0.47
1:1:79:C:O2'	1:1:346:A:N3	2.39	0.46
1:1:635:C:H2'	1:1:636:G:O4'	2.16	0.46
1:1:1584:U:H5'	1:1:1585:C:C6	2.50	0.46
1:1:2190:G:H2'	1:1:2191:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2328:A:H2'	1:1:2329:U:C6	2.50	0.46
1:1:2519:U:O4'	1:1:2542:A:N6	2.47	0.46
2:2:41:G:H2'	2:2:42:G:H8	1.80	0.46
32:d:40:ARG:O	32:d:44:LEU:HG	2.16	0.46
35:g:140:ASN:OD1	35:g:143:ARG:NH2	2.41	0.46
1:1:279:A:N6	1:1:361:G:H1'	2.30	0.46
1:1:587:C:OP2	13:K:21:ARG:NH2	2.37	0.46
1:1:630:G:N2	1:1:633:A:OP2	2.37	0.46
1:1:2305:U:O2	8:F:151:GLY:HA3	2.15	0.46
2:2:246:A:C2	2:2:282:A:C5	3.03	0.46
2:2:412:A:H62	2:2:431:A:H61	1.64	0.46
2:2:945:G:C2	2:2:946:A:C8	3.02	0.46
37:i:111:MET:HA	37:i:114:VAL:HG12	1.96	0.46
54:z:52:C:H4'	54:z:53:A:OP1	2.14	0.46
1:1:1009:A:N3	1:1:1153:C:O2'	2.46	0.46
1:1:1141:U:H4'	1:1:1142:A:O4'	2.16	0.46
1:1:1954:G:O2'	1:1:1956:U:O4	2.29	0.46
1:1:2305:U:N3	8:F:151:GLY:O	2.48	0.46
1:1:2575:C:H5'	6:D:149:ASN:HB2	1.96	0.46
1:1:2793:C:H2'	1:1:2794:C:C6	2.50	0.46
2:2:750:C:O2'	47:s:21:ASP:O	2.22	0.46
2:2:1073:U:O2	34:f:103:ASN:ND2	2.48	0.46
2:2:1391:U:H2'	2:2:1392:G:C8	2.50	0.46
5:C:161:TYR:HB3	5:C:194:GLU:HG2	1.96	0.46
10:H:90:LEU:HB3	10:H:123:ARG:C	2.41	0.46
11:I:89:PHE:O	11:I:93:ILE:HG12	2.14	0.46
13:K:29:LYS:HG3	13:K:30:THR:HG23	1.96	0.46
14:L:114:ARG:HD2	14:L:130:PHE:CD2	2.50	0.46
22:T:99:ASN:C	22:T:99:ASN:OD1	2.58	0.46
34:f:58:ASN:ND2	34:f:220:THR:O	2.44	0.46
37:i:142:ASP:HA	37:i:145:GLU:HG2	1.98	0.46
42:n:57:VAL:O	42:n:57:VAL:HG13	2.15	0.46
1:1:1796:U:H2'	1:1:1797:G:H8	1.80	0.46
1:1:2585:U:N3	55:B:25:ASP:HA	2.31	0.46
2:2:454:G:H1	2:2:478:A:H61	1.63	0.46
2:2:632:U:H5''	2:2:633:G:C8	2.50	0.46
6:D:106:LYS:HE2	6:D:176:ASP:OD1	2.15	0.46
8:F:134:GLU:OE2	8:F:136:ILE:HD12	2.16	0.46
26:X:44:LYS:O	26:X:48:ARG:HD2	2.16	0.46
34:f:218:ALA:HA	34:f:221:VAL:HG22	1.97	0.46
36:h:143:VAL:O	36:h:143:VAL:HG23	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:i:142:ASP:O	37:i:145:GLU:HG2	2.15	0.46
47:s:26:GLU:HG3	47:s:81:LEU:HD22	1.97	0.46
1:1:447:A:OP1	18:P:5:LYS:NZ	2.48	0.46
1:1:2314:A:H1'	8:F:155:THR:HG21	1.97	0.46
1:1:2646:C:OP2	1:1:2732:G:O2'	2.34	0.46
1:1:2793:C:H2'	1:1:2794:C:H6	1.79	0.46
2:2:579:A:O2'	47:s:54:ARG:NH1	2.39	0.46
2:2:1128:C:H1'	2:2:1147:C:H42	1.80	0.46
2:2:1356:G:H2'	2:2:1357:A:C8	2.50	0.46
8:F:34:ILE:HD12	8:F:96:MET:HG3	1.97	0.46
32:d:15:LYS:HB2	32:d:23:LYS:HE2	1.98	0.46
34:f:130:THR:CG2	34:f:133:GLU:HB3	2.43	0.46
38:j:7:VAL:HG22	38:j:61:LEU:HD13	1.96	0.46
42:n:25:ILE:HD13	42:n:90:LEU:HD13	1.98	0.46
54:z:65:G:O2'	54:z:66:5MU:H5''	2.16	0.46
2:2:701:U:O2	2:2:703:G:N1	2.48	0.46
2:2:1330:U:O4	2:2:1331:G:N1	2.48	0.46
2:2:1518:MA6:O5'	2:2:1518:MA6:H8	2.16	0.46
6:D:31:ALA:HB1	6:D:95:SER:OG	2.15	0.46
9:G:80:THR:HG23	9:G:81:GLU:HG3	1.97	0.46
34:f:87:CYS:CB	34:f:221:VAL:HG21	2.45	0.46
39:k:66:LEU:O	39:k:70:ARG:HG3	2.16	0.46
42:n:52:LEU:HD23	42:n:62:ARG:HG2	1.96	0.46
45:q:22:ILE:HB	45:q:25:VAL:HG22	1.98	0.46
54:z:20:U:H5''	54:z:20:U:H6	1.81	0.46
2:2:579:A:H2'	2:2:580:C:C6	2.51	0.46
2:2:1323:G:H2'	2:2:1324:A:C8	2.51	0.46
5:C:232:HIS:CG	5:C:240:PHE:HE1	2.33	0.46
8:F:149:VAL:HG23	8:F:149:VAL:O	2.16	0.46
40:l:55:THR:HG23	40:l:56:LYS:H	1.79	0.46
42:n:17:LEU:CD2	42:n:96:VAL:HG23	2.45	0.46
1:1:2168:G:H8	1:1:2168:G:O5'	1.97	0.46
1:1:2170:A:C2	1:1:2171:A:C4	3.04	0.46
1:1:2676:C:OP1	12:J:31:ARG:NH2	2.48	0.46
1:1:2780:G:OP2	11:I:120:ARG:NE	2.37	0.46
2:2:131:A:O2'	2:2:262:A:N3	2.44	0.46
2:2:459:A:H2'	2:2:460:A:H8	1.81	0.46
2:2:881:G:OP2	44:p:9:ARG:NH1	2.49	0.46
7:E:176:ASP:OD1	7:E:176:ASP:N	2.48	0.46
23:U:21:ARG:HE	23:U:87:GLN:HA	1.81	0.46
54:z:50:G:C6	54:z:51:G:O6	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:z:58:A:H2'	54:z:59:U:O4'	2.16	0.46
1:1:563:A:C2'	18:P:37:GLN:HE21	2.28	0.46
1:1:2297:A:N1	1:1:2321:U:H5	2.13	0.46
19:Q:7:SER:OG	19:Q:22:LEU:HD22	2.16	0.46
39:k:105:VAL:O	39:k:109:ARG:HG3	2.16	0.46
54:z:26:A:C4	54:z:27:G:C8	3.04	0.46
1:1:2111:U:H1'	1:1:2119:A:OP1	2.16	0.46
2:2:235:C:H2'	2:2:236:A:C8	2.51	0.46
2:2:556:C:H2'	2:2:557:G:O4'	2.15	0.46
2:2:1321:U:OP2	2:2:1322:C:O2'	2.30	0.46
7:E:41:GLN:HG2	7:E:43:THR:HG23	1.98	0.46
9:G:23:VAL:HG22	9:G:36:THR:OG1	2.15	0.46
22:T:38:GLY:N	22:T:62:GLU:OE2	2.49	0.46
34:f:58:ASN:HB2	34:f:220:THR:OG1	2.16	0.46
34:f:127:ASP:O	34:f:128:LYS:HB3	2.16	0.46
45:q:4:ILE:CG1	45:q:9:ILE:HD12	2.45	0.46
50:v:23:TYR:HA	50:v:58:ALA:HB1	1.96	0.46
1:1:810:U:N3	13:K:29:LYS:O	2.50	0.45
1:1:2139:U:O2	1:1:2140:G:N7	2.49	0.45
1:1:2364:C:H2'	1:1:2365:G:O4'	2.16	0.45
8:F:47:LYS:HE2	8:F:47:LYS:HA	1.98	0.45
10:H:135:HIS:HB3	10:H:138:VAL:H	1.79	0.45
40:l:5:ASP:CG	40:l:77:ARG:HH12	2.25	0.45
51:w:34:TRP:CD1	51:w:52:HIS:CG	3.05	0.45
1:1:1051:G:C5	1:1:1052:C:C5	3.04	0.45
1:1:2102:G:C5	1:1:2188:U:C2	3.05	0.45
1:1:2314:A:C1'	8:F:155:THR:HG21	2.46	0.45
7:E:106:LYS:HG3	7:E:200:LEU:HD23	1.98	0.45
7:E:200:LEU:HD12	7:E:200:LEU:N	2.30	0.45
10:H:135:HIS:CG	10:H:136:SER:N	2.84	0.45
34:f:62:SER:HA	34:f:224:GLY:O	2.16	0.45
34:f:194:ASP:OD1	34:f:195:GLY:N	2.49	0.45
36:h:146:ARG:CG	36:h:147:GLU:N	2.78	0.45
42:n:7:ARG:HB2	42:n:101:SER:HB2	1.98	0.45
42:n:51:VAL:HB	46:r:81:ARG:HB2	1.98	0.45
49:u:17:MET:HG3	49:u:20:SER:HB2	1.97	0.45
1:1:613:A:H4'	1:1:614:A:OP1	2.17	0.45
1:1:882:G:O6	1:1:894:U:C2	2.69	0.45
1:1:1250:G:H4'	18:P:6:ARG:HD2	1.98	0.45
2:2:214:C:H2'	2:2:215:C:H6	1.80	0.45
3:3:48:U:P	16:N:30:ARG:HH22	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:Y:40:ASP:OD1	27:Y:45:ARG:NE	2.47	0.45
36:h:118:VAL:HG12	36:h:131:ASN:O	2.15	0.45
46:r:48:LEU:HD12	46:r:51:LEU:HD12	1.99	0.45
2:2:1309:G:P	45:q:87:ARG:HH11	2.38	0.45
15:M:38:LEU:HB3	15:M:39:PRO:HD3	1.99	0.45
17:O:2:SER:OG	17:O:3:ASN:N	2.50	0.45
18:P:106:PHE:O	18:P:110:VAL:HG23	2.16	0.45
37:i:150:PRO:HA	37:i:153:VAL:HG22	1.97	0.45
41:m:83:ILE:O	41:m:87:LEU:HD13	2.16	0.45
1:1:1020:A:N1	1:1:1141:U:O2'	2.41	0.45
1:1:1154:G:P	18:P:58:ARG:HE	2.39	0.45
1:1:2140:G:C6	1:1:2152:G:C8	3.04	0.45
2:2:451:A:H4'	2:2:452:A:O4'	2.15	0.45
2:2:1100:C:P	53:y:69:ARG:HH11	2.39	0.45
34:f:207:ILE:O	34:f:210:VAL:HG22	2.16	0.45
35:g:8:ASN:O	35:g:12:LEU:HG	2.17	0.45
35:g:118:ASP:OD1	35:g:119:SER:N	2.50	0.45
55:B:20:PHE:C	55:B:23:PRO:HD3	2.42	0.45
1:1:636:G:N1	13:K:76:GLU:OE1	2.42	0.45
1:1:2848:G:O2'	1:1:2867:G:N2	2.37	0.45
2:2:2:A:N3	2:2:613:C:O2'	2.49	0.45
2:2:1016:A:HO2'	2:2:1217:C:HO2'	1.63	0.45
5:C:271:ARG:O	5:C:272:SER:CB	2.64	0.45
34:f:68:LEU:HB3	34:f:161:LEU:HD12	1.99	0.45
38:j:40:GLU:OE2	38:j:99:ALA:HA	2.17	0.45
40:l:48:ASP:OD1	40:l:49:PHE:N	2.50	0.45
48:t:69:ASP:N	48:t:69:ASP:OD1	2.50	0.45
51:w:3:ARG:NH1	51:w:9:PRO:O	2.50	0.45
52:x:28:MET:HE1	52:x:67:ILE:HG21	1.97	0.45
54:z:27:G:C4	54:z:28:C:C5	3.04	0.45
1:1:138:U:H1'	1:1:141:G:O6	2.17	0.45
1:1:796:C:OP1	7:E:57:LYS:NZ	2.50	0.45
1:1:1090:A:N1	1:1:1102:C:C2	2.85	0.45
1:1:1275:A:N1	1:1:1295:C:O2'	2.48	0.45
1:1:1358:G:C8	1:1:1371:G:O6	2.70	0.45
1:1:2233:U:H2'	1:1:2234:G:C8	2.52	0.45
2:2:739:C:O2'	47:s:42:HIS:ND1	2.46	0.45
2:2:1223:C:OP1	51:w:78:ARG:NH1	2.49	0.45
19:Q:55:ASP:OD1	19:Q:55:ASP:N	2.49	0.45
21:S:33:LYS:HG3	21:S:80:TRP:CE3	2.51	0.45
22:T:98:SER:O	22:T:99:ASN:OD1	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:n:22:THR:O	42:n:26:VAL:HG23	2.16	0.45
54:z:48:A:H2'	54:z:49:C:C6	2.52	0.45
1:1:2751:G:H5'	1:1:2752:C:C5	2.52	0.45
2:2:109:A:C6	2:2:326:G:C6	3.05	0.45
2:2:1007:U:H2'	2:2:1008:U:C6	2.52	0.45
10:H:93:SER:CB	10:H:121:VAL:HG22	2.47	0.45
37:i:159:LYS:NZ	40:l:42:GLU:O	2.43	0.45
1:1:1722:A:O2'	1:1:1723:G:H5'	2.17	0.45
1:1:1980:G:O2'	1:1:1982:U:OP2	2.26	0.45
1:1:2086:U:H2'	1:1:2087:G:C8	2.51	0.45
1:1:2127:G:H21	1:1:2173:A:C1'	2.30	0.45
1:1:2580:PSU:OP1	6:D:137:SER:OG	2.19	0.45
2:2:1010:U:N3	2:2:1020:G:N1	2.65	0.45
8:F:142:ASP:OD2	8:F:145:LYS:HG2	2.17	0.45
35:g:11:ARG:NH2	35:g:177:THR:O	2.37	0.45
35:g:123:GLN:HB3	35:g:128:VAL:CG2	2.47	0.45
38:j:69:GLU:O	38:j:72:ASP:OD1	2.35	0.45
43:o:34:ILE:HG12	43:o:70:CYS:SG	2.57	0.45
1:1:414:C:H2'	1:1:415:A:H8	1.82	0.45
1:1:891:G:N1	1:1:892:A:C8	2.85	0.45
2:2:439:U:O2	36:h:120:HIS:CD2	2.70	0.45
2:2:664:G:H22	2:2:741:G:H1	1.65	0.45
2:2:1152:A:P	42:n:72:ARG:HH22	2.40	0.45
9:G:105:LEU:HB2	9:G:113:VAL:HB	1.99	0.45
31:c:10:LEU:HD11	31:c:14:ARG:CZ	2.47	0.45
40:l:7:ILE:O	40:l:11:LEU:HG	2.17	0.45
1:1:1172:C:H2'	1:1:1173:U:C2	2.52	0.44
1:1:2266:A:H4'	1:1:2267:A:N3	2.31	0.44
2:2:1004:A:H2'	2:2:1005:A:O4'	2.17	0.44
5:C:91:ILE:HD12	5:C:103:TYR:CD1	2.52	0.44
5:C:144:VAL:HB	5:C:154:LEU:HB2	1.98	0.44
10:H:130:VAL:HG13	10:H:130:VAL:O	2.17	0.44
19:Q:15:SER:OG	19:Q:18:GLN:OE1	2.09	0.44
37:i:109:GLY:O	37:i:112:ARG:HG2	2.18	0.44
39:k:93:PRO:HA	39:k:96:ARG:HD3	1.99	0.44
1:1:12:U:H2'	1:1:13:A:H5'	1.98	0.44
10:H:9:VAL:HB	10:H:12:LEU:HD21	1.99	0.44
10:H:101:ASP:O	10:H:104:THR:CG2	2.66	0.44
28:Z:46:GLY:O	28:Z:49:ARG:HG3	2.17	0.44
34:f:222:ARG:HG2	34:f:225:ARG:NH1	2.32	0.44
36:h:95:GLU:HA	36:h:100:ASN:ND2	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:i:120:VAL:HG11	37:i:123:VAL:HG13	1.99	0.44
38:j:21:MET:HG2	38:j:24:ARG:HH21	1.82	0.44
39:k:47:LEU:HB3	39:k:58:GLU:HB3	1.99	0.44
41:m:44:ALA:HA	41:m:47:VAL:HG22	1.98	0.44
41:m:46:MET:O	41:m:50:GLN:HG3	2.18	0.44
51:w:32:ARG:HA	51:w:50:ALA:HB3	2.00	0.44
1:1:848:C:H2'	1:1:849:A:C8	2.52	0.44
1:1:995:C:O2	11:I:3:THR:OG1	2.28	0.44
1:1:996:A:OP1	19:Q:10:LYS:HD2	2.17	0.44
1:1:2619:C:O2	6:D:161:MET:HE1	2.17	0.44
2:2:1218:C:H2'	2:2:1219:A:C8	2.53	0.44
7:E:52:VAL:O	7:E:74:LYS:HE2	2.17	0.44
10:H:117:LEU:HB3	10:H:120:GLY:HA2	1.99	0.44
22:T:48:PRO:HG3	22:T:55:PRO:O	2.18	0.44
39:k:113:ASP:HB2	39:k:119:ARG:HG2	2.00	0.44
42:n:5:ARG:HD3	42:n:5:ARG:N	2.31	0.44
45:q:54:ASP:OD1	45:q:57:ARG:NH1	2.50	0.44
51:w:63:THR:HG22	51:w:64:ASP:OD1	2.17	0.44
1:1:172:A:H2'	1:1:173:A:C8	2.52	0.44
1:1:2134:A:O2'	1:1:2159:G:N3	2.48	0.44
1:1:2508:G:H1	1:1:2580:PSU:HN3	1.64	0.44
1:1:2515:C:H2'	1:1:2516:A:H8	1.83	0.44
2:2:582:C:OP2	2:2:758:C:N4	2.41	0.44
10:H:83:LYS:O	10:H:90:LEU:HD12	2.18	0.44
10:H:94:ILE:HG23	10:H:94:ILE:O	2.16	0.44
34:f:164:ILE:O	34:f:186:ILE:HB	2.18	0.44
1:1:1357:C:H2'	1:1:1358:G:O4'	2.17	0.44
1:1:1469:A:OP2	1:1:1522:A:N6	2.44	0.44
1:1:2804:U:H2'	1:1:2805:C:C6	2.53	0.44
2:2:514:C:H2'	2:2:515:G:H8	1.82	0.44
2:2:840:C:HO2'	2:2:841:C:H5	1.60	0.44
2:2:911:U:H2'	2:2:912:C:C6	2.53	0.44
15:M:65:LEU:O	15:M:69:ARG:HG3	2.18	0.44
53:y:28:VAL:HG23	53:y:29:LEU:N	2.32	0.44
1:1:359:G:C6	1:1:360:U:C4	3.06	0.44
1:1:1138:G:H21	11:I:108:MET:HE2	1.83	0.44
1:1:1370:C:H2'	1:1:1371:G:O4'	2.18	0.44
1:1:2585:U:C2	55:B:25:ASP:HA	2.52	0.44
21:S:65:GLY:N	21:S:79:ASP:OD1	2.42	0.44
35:g:6:HIS:HB3	46:r:89:MET:SD	2.56	0.44
39:k:80:VAL:O	39:k:80:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:m:130:ARG:HD2	54:z:36:G:OP1	2.17	0.44
42:n:90:LEU:HD23	42:n:90:LEU:C	2.43	0.44
43:o:13:ARG:NE	43:o:13:ARG:HA	2.33	0.44
43:o:96:THR:HG23	43:o:97:ILE:N	2.32	0.44
48:t:76:LYS:O	48:t:80:LYS:HG2	2.17	0.44
54:z:53:A:H3'	54:z:54:A:H5'	2.00	0.44
1:1:558:U:OP1	11:I:113:PRO:HD2	2.17	0.44
1:1:1540:G:C6	1:1:1541:C:C4	3.06	0.44
1:1:2128:G:N3	1:1:2173:A:O2'	2.51	0.44
1:1:2375:G:N2	1:1:2378:A:OP2	2.41	0.44
2:2:335:C:H2'	2:2:336:A:H8	1.82	0.44
5:C:130:LEU:O	5:C:135:ILE:HD11	2.17	0.44
9:G:156:PRO:O	9:G:171:THR:HA	2.18	0.44
10:H:93:SER:OG	10:H:121:VAL:HG22	2.18	0.44
38:j:4:TYR:CD2	38:j:71:ILE:HG13	2.52	0.44
41:m:39:PHE:O	41:m:45:ARG:NE	2.47	0.44
1:1:1198:U:H2'	1:1:1199:U:C6	2.53	0.44
1:1:1410:G:C2'	1:1:1411:U:O5'	2.66	0.44
1:1:1746:A:H2'	1:1:1747:U:C6	2.53	0.44
2:2:515:G:H3'	2:2:516:PSU:O4	2.17	0.44
2:2:640:A:O2'	40:l:108:LYS:HE3	2.18	0.44
2:2:935:A:O2'	2:2:1383:C:N3	2.51	0.44
10:H:4:ILE:HA	10:H:17:ASP:O	2.18	0.44
12:J:24:VAL:HG13	12:J:33:ALA:HB2	1.99	0.44
27:Y:23:THR:HG23	27:Y:47:MET:HG2	1.99	0.44
39:k:107:ALA:O	39:k:111:ARG:HG3	2.17	0.44
54:z:51:G:H2'	54:z:52:C:C4'	2.48	0.44
54:z:53:A:H8	54:z:55:C:C5	2.36	0.44
1:1:2166:U:H3'	1:1:2167:U:C6	2.52	0.44
2:2:1270:G:HO2'	2:2:1313:U:HO2'	1.58	0.44
2:2:1439:G:P	52:x:33:LYS:HZ3	2.40	0.44
5:C:225:MET:SD	5:C:230:HIS:HB2	2.57	0.44
39:k:150:ALA:HB1	43:o:59:THR:HG21	2.00	0.44
43:o:58:SER:O	43:o:91:PRO:HG3	2.17	0.44
43:o:64:GLN:O	43:o:68:GLU:HG3	2.17	0.44
47:s:40:GLN:OE1	47:s:40:GLN:HA	2.18	0.44
1:1:593:U:H2'	1:1:594:U:C6	2.53	0.43
1:1:1722:A:H2'	1:1:1723:G:O4'	2.17	0.43
1:1:2184:A:H2'	1:1:2185:U:C6	2.53	0.43
2:2:1157:A:C2	2:2:1181:G:C4	3.06	0.43
2:2:1518:MA6:N6	2:2:1519:MA6:H93	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:10:VAL:HA	9:G:49:THR:HG22	2.01	0.43
10:H:67:ALA:O	10:H:71:LYS:CD	2.66	0.43
21:S:14:PRO:HD3	26:X:30:MET:SD	2.58	0.43
23:U:1:MET:HE2	23:U:3:THR:OG1	2.18	0.43
25:W:40:VAL:HG12	25:W:43:GLU:H	1.83	0.43
39:k:78:ARG:HG2	39:k:80:VAL:HG23	2.00	0.43
54:z:1:G:O2'	54:z:2:G:P	2.76	0.43
54:z:9:G:N3	54:z:9:G:C2'	2.78	0.43
54:z:56:G:C6	54:z:57:U:C4	3.06	0.43
1:1:896:A:C4'	1:1:897:C:OP1	2.65	0.43
1:1:2195:U:O2'	1:1:2196:C:H5'	2.18	0.43
2:2:868:C:H2'	2:2:869:G:O4'	2.18	0.43
2:2:1316:G:N1	2:2:1319:A:OP2	2.49	0.43
12:J:112:PHE:CD1	12:J:115:ILE:HD12	2.52	0.43
29:a:3:VAL:HG22	29:a:4:GLN:N	2.32	0.43
45:q:46:SER:O	45:q:47:GLU:HG3	2.18	0.43
45:q:49:SER:OG	45:q:52:GLN:HG3	2.18	0.43
51:w:63:THR:HG22	51:w:64:ASP:N	2.33	0.43
1:1:142:A:H2'	1:1:143:C:C6	2.53	0.43
1:1:278:A:C6	1:1:362:A:C8	3.06	0.43
1:1:357:C:H2'	1:1:358:U:H6	1.83	0.43
1:1:807:U:OP2	13:K:41:ARG:NH1	2.51	0.43
1:1:1827:U:H2'	1:1:1828:G:O4'	2.19	0.43
1:1:1936:A:OP2	1:1:1962:5MC:N4	2.42	0.43
2:2:714:G:H2'	2:2:715:A:C8	2.54	0.43
2:2:1061:G:OP2	35:g:2:GLY:O	2.36	0.43
5:C:210:ALA:HA	5:C:213:TRP:CE3	2.53	0.43
20:R:11:ARG:NH2	20:R:98:LYS:HE3	2.32	0.43
29:a:23:THR:O	29:a:23:THR:HG23	2.17	0.43
35:g:51:SER:HB3	35:g:115:LEU:HD22	2.00	0.43
42:n:45:ARG:HB3	42:n:69:THR:HB	2.00	0.43
52:x:35:VAL:HG22	52:x:50:ALA:CB	2.48	0.43
2:2:102:G:OP2	52:x:5:LYS:CE	2.67	0.43
2:2:541:G:H2'	2:2:542:G:O4'	2.18	0.43
2:2:1173:U:C2	2:2:1174:G:C8	3.06	0.43
6:D:104:VAL:HG12	6:D:105:LYS:N	2.33	0.43
9:G:52:PHE:CE2	9:G:69:ARG:HA	2.53	0.43
28:Z:47:LYS:O	28:Z:50:ASP:OD1	2.36	0.43
51:w:64:ASP:O	51:w:67:VAL:HG23	2.18	0.43
1:1:463:G:N2	1:1:466:A:OP2	2.43	0.43
1:1:1231:U:H2'	1:1:1232:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:24:G:N7	3:3:56:G:H2'	2.32	0.43
7:E:105:LEU:O	7:E:109:LEU:HD13	2.19	0.43
10:H:42:LYS:O	10:H:42:LYS:HD3	2.18	0.43
12:J:52:VAL:C	12:J:53:LYS:HG2	2.43	0.43
50:v:25:ASP:O	50:v:29:LEU:HD13	2.17	0.43
1:1:322:A:P	7:E:162:ARG:HH11	2.41	0.43
1:1:2164:C:OP2	1:1:2170:A:N7	2.52	0.43
2:2:1317:C:OP1	46:r:24:ARG:NH2	2.40	0.43
22:T:4:LYS:O	22:T:94:ARG:NH2	2.45	0.43
44:p:68:GLY:O	44:p:99:ARG:NH1	2.50	0.43
49:u:15:ASP:CG	49:u:55:ILE:HD11	2.43	0.43
49:u:19:LYS:HA	49:u:48:ASP:O	2.18	0.43
55:B:10:LYS:HB2	55:B:10:LYS:HE2	1.59	0.43
1:1:476:G:N1	1:1:479:A:OP2	2.50	0.43
1:1:877:A:C6	1:1:899:A:C6	3.06	0.43
1:1:878:A:H3'	1:1:879:G:H8	1.83	0.43
1:1:2301:C:H2'	1:1:2302:U:H6	1.84	0.43
1:1:2313:C:H2'	1:1:2314:A:C8	2.52	0.43
2:2:279:A:H5''	2:2:280:C:H3'	2.00	0.43
2:2:335:C:H2'	2:2:336:A:C8	2.54	0.43
9:G:43:VAL:HG23	9:G:52:PHE:CE1	2.54	0.43
10:H:140:ALA:C	10:H:141:LYS:HD3	2.44	0.43
16:N:41:ALA:HB3	16:N:43:ASN:OD1	2.18	0.43
35:g:47:LEU:HD11	35:g:87:LEU:HD11	2.00	0.43
36:h:100:ASN:OD1	36:h:111:ARG:NH1	2.50	0.43
36:h:156:LYS:O	36:h:160:GLU:HG2	2.19	0.43
39:k:142:HIS:O	39:k:146:GLU:OE1	2.36	0.43
1:1:411:G:OP2	1:1:2406:A:O2'	2.33	0.43
1:1:414:C:O2	1:1:1864:U:O2'	2.34	0.43
1:1:583:G:OP1	18:P:7:GLY:HA2	2.18	0.43
1:1:603:A:O5'	1:1:655:A:N6	2.47	0.43
1:1:781:A:OP1	5:C:217:ARG:NH2	2.41	0.43
1:1:1068:G:N2	1:1:1095:A:H1'	2.34	0.43
2:2:216:U:H2'	2:2:217:C:C6	2.54	0.43
7:E:83:VAL:HB	7:E:86:ALA:HB2	2.00	0.43
20:R:92:ARG:HE	55:B:12:PHE:HB3	1.84	0.43
34:f:73:LYS:HE2	34:f:165:ASP:HB2	2.01	0.43
48:t:61:VAL:HG21	48:t:67:ILE:HD11	2.00	0.43
1:1:2591:C:H2'	1:1:2592:G:H8	1.83	0.43
2:2:1006:G:H2'	2:2:1007:U:C6	2.53	0.43
8:F:10:ASP:OD1	8:F:11:GLU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:37:ASN:HB3	8:F:153:ASP:OD1	2.18	0.43
13:K:61:LEU:O	32:d:13:ARG:NE	2.33	0.43
14:L:27:SER:N	14:L:104:GLU:OE2	2.52	0.43
34:f:213:TYR:O	34:f:217:VAL:HG23	2.19	0.43
39:k:37:SER:HA	41:m:41:ARG:HH22	1.84	0.43
45:q:11:ASP:HA	45:q:45:ILE:HB	2.01	0.43
47:s:3:LEU:HB2	47:s:35:GLN:OE1	2.18	0.43
1:1:878:A:C8	1:1:879:G:C8	3.07	0.43
1:1:1283:G:N1	1:1:1286:A:OP2	2.52	0.43
1:1:2581:G:OP2	1:1:2581:G:N2	2.52	0.43
2:2:1128:C:O2'	2:2:1147:C:N3	2.42	0.43
10:H:122:LEU:O	10:H:124:THR:N	2.49	0.43
12:J:112:PHE:HD1	12:J:115:ILE:HD12	1.84	0.43
26:X:32:ALA:HB2	26:X:37:LEU:HD23	2.01	0.43
34:f:74:ARG:O	34:f:74:ARG:HG2	2.19	0.43
46:r:41:ARG:HH22	51:w:6:LYS:HB2	1.84	0.43
54:z:28:C:C2	54:z:29:A:C8	3.06	0.43
1:1:270:A:H5'	1:1:271:G:H5''	2.00	0.42
1:1:1138:G:N2	11:I:108:MET:HE2	2.33	0.42
1:1:2116:G:O6	1:1:2171:A:C6	2.72	0.42
2:2:197:A:N1	2:2:220:G:O2'	2.46	0.42
2:2:205:A:H2'	2:2:206:C:C6	2.54	0.42
2:2:209:U:H3'	2:2:210:C:O2	2.18	0.42
2:2:475:C:H2'	2:2:476:U:H6	1.84	0.42
5:C:108:LYS:HA	5:C:196:GLY:HA2	2.00	0.42
54:z:49:C:H2'	54:z:50:G:H8	1.84	0.42
1:1:116:C:H2'	1:1:117:G:O4'	2.19	0.42
1:1:414:C:H2'	1:1:415:A:C8	2.54	0.42
1:1:1087:G:N1	1:1:1089:A:C2	2.88	0.42
1:1:1323:C:OP1	20:R:98:LYS:HE2	2.18	0.42
1:1:2128:G:O2'	1:1:2174:C:H1'	2.19	0.42
2:2:842:U:H2'	2:2:844:G:H21	1.83	0.42
2:2:1010:U:C2	2:2:1020:G:N1	2.86	0.42
2:2:1077:G:N2	2:2:1080:A:OP2	2.33	0.42
10:H:84:ALA:HB3	10:H:148:ALA:HB1	2.00	0.42
10:H:101:ASP:O	10:H:104:THR:HG22	2.19	0.42
13:K:82:LEU:O	13:K:85:VAL:HG22	2.19	0.42
34:f:79:ALA:O	34:f:82:ASP:OD1	2.37	0.42
34:f:119:THR:O	34:f:120:GLN:C	2.63	0.42
36:h:100:ASN:CG	36:h:111:ARG:HH12	2.26	0.42
39:k:5:ARG:CZ	39:k:7:ILE:HG22	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:z:78:C:C2'	54:z:79:C:H5'	2.48	0.42
1:1:474:G:C6	1:1:510:C:N4	2.88	0.42
1:1:601:C:O5'	1:1:601:C:H6	2.02	0.42
1:1:1278:C:H2'	1:1:1279:G:H8	1.84	0.42
1:1:1590:A:H2'	1:1:1591:A:H8	1.83	0.42
1:1:1818:U:OP2	5:C:156:ARG:NE	2.53	0.42
2:2:736:C:OP1	50:v:61:ARG:NH2	2.52	0.42
2:2:1436:U:H2'	2:2:1437:A:H8	1.83	0.42
13:K:19:LEU:HD12	13:K:19:LEU:N	2.34	0.42
13:K:117:THR:HG23	13:K:118:THR:N	2.34	0.42
18:P:86:ALA:O	19:Q:51:VAL:HG13	2.19	0.42
1:1:370:G:O2'	1:1:424:G:OP1	2.38	0.42
1:1:1495:A:N3	1:1:1578:U:O2'	2.44	0.42
1:1:2698:U:H2'	1:1:2699:C:C6	2.54	0.42
2:2:208:U:H2'	2:2:210:C:N3	2.34	0.42
2:2:1425:U:H2'	2:2:1426:G:H8	1.83	0.42
34:f:186:ILE:HD13	34:f:200:ILE:HB	2.00	0.42
1:1:1072:C:OP2	1:1:1097:U:OP1	2.38	0.42
1:1:1429:G:H2'	1:1:1430:G:H8	1.85	0.42
1:1:2145:C:O2	1:1:2145:C:C2'	2.66	0.42
1:1:2185:U:H2'	1:1:2186:G:C8	2.54	0.42
1:1:2246:G:H2'	1:1:2247:A:C8	2.55	0.42
1:1:2322:A:H2'	1:1:2323:G:O4'	2.19	0.42
1:1:2333:A:OP2	24:V:77:ARG:NH2	2.39	0.42
2:2:159:G:N2	2:2:162:A:OP2	2.49	0.42
2:2:555:U:H2'	2:2:556:C:C6	2.55	0.42
2:2:779:C:H2'	2:2:780:A:O4'	2.19	0.42
2:2:1509:C:C2	2:2:1510:C:C5	3.08	0.42
12:J:7:MET:HE3	12:J:18:ARG:HG3	2.01	0.42
28:Z:44:PHE:HA	28:Z:48:GLN:HE22	1.84	0.42
38:j:72:ASP:O	38:j:76:THR:HG23	2.19	0.42
43:o:64:GLN:HB2	43:o:99:ALA:HB2	2.02	0.42
45:q:7:ILE:HD13	45:q:66:GLU:OE2	2.18	0.42
49:u:25:ILE:HD12	49:u:44:LEU:HD12	2.01	0.42
54:z:44:G:H2'	54:z:45:U:O4'	2.20	0.42
54:z:74:C:C2	54:z:75:C:C6	3.07	0.42
1:1:499:U:H5''	22:T:43:LYS:HE2	2.01	0.42
1:1:714:U:O2'	1:1:716:A:N7	2.42	0.42
1:1:781:A:P	5:C:217:ARG:HH22	2.43	0.42
1:1:2081:U:H2'	1:1:2082:A:H8	1.84	0.42
1:1:2195:U:H2'	1:1:2196:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:3:A:H5''	2:2:4:U:O4'	2.20	0.42
2:2:212:G:C4	2:2:213:G:C8	3.07	0.42
4:4:3:C:O2	4:4:3:C:O5'	2.38	0.42
5:C:2:ALA:N	5:C:199:GLU:OE2	2.53	0.42
5:C:133:ARG:NE	5:C:187:ASP:OD1	2.43	0.42
10:H:57:LYS:HD2	10:H:58:LEU:N	2.35	0.42
11:I:95:ARG:NH1	11:I:96:ARG:HB3	2.35	0.42
35:g:7:PRO:O	35:g:11:ARG:HD3	2.19	0.42
1:1:5:A:H2'	1:1:6:A:C8	2.55	0.42
1:1:674:G:H5''	7:E:71:GLY:N	2.35	0.42
1:1:1174:U:H1'	1:1:1177:G:C2	2.54	0.42
1:1:1190:G:H5''	13:K:32:GLY:HA2	2.01	0.42
1:1:2102:G:H3'	1:1:2103:C:C5	2.54	0.42
1:1:2104:C:H2'	1:1:2105:U:O4'	2.19	0.42
1:1:2798:U:H4'	1:1:2799:A:H5'	2.00	0.42
2:2:420:U:O2'	2:2:421:U:O2	2.31	0.42
2:2:1120:C:H2'	2:2:1121:U:C6	2.54	0.42
54:z:9:G:H1	54:z:13:G:N2	2.17	0.42
54:z:68:C:H2'	54:z:69:G:O4'	2.18	0.42
1:1:136:G:C6	1:1:137:U:C4	3.07	0.42
1:1:1066:U:H2'	1:1:1067:A:H2'	2.02	0.42
1:1:1790:C:H2'	1:1:1791:A:C5	2.53	0.42
1:1:1863:G:H2'	1:1:1864:U:H6	1.85	0.42
1:1:2847:U:H2'	1:1:2848:G:O4'	2.19	0.42
2:2:1352:C:N3	2:2:1371:G:C6	2.88	0.42
21:S:10:VAL:HG13	21:S:38:ALA:CB	2.49	0.42
34:f:74:ARG:O	34:f:74:ARG:CG	2.67	0.42
34:f:218:ALA:HA	34:f:221:VAL:CG2	2.49	0.42
36:h:172:GLU:HB2	36:h:183:LYS:HD2	2.02	0.42
48:t:4:ILE:HG12	48:t:21:VAL:HG22	2.01	0.42
52:x:32:ILE:HG12	52:x:54:MET:CE	2.49	0.42
1:1:221:A:N1	1:1:265:A:O2'	2.53	0.42
1:1:901:C:H2'	1:1:902:C:O4'	2.20	0.42
1:1:1019:U:OP1	1:1:1035:U:O2'	2.31	0.42
1:1:1061:U:O2'	1:1:1062:G:H5'	2.20	0.42
1:1:1067:A:H3'	1:1:1068:G:H5''	2.01	0.42
1:1:1534:U:O2'	1:1:1537:G:O6	2.37	0.42
1:1:1584:U:H5''	1:1:1585:C:O4'	2.20	0.42
1:1:1671:U:O2'	1:1:1673:G:N7	2.40	0.42
1:1:2125:G:H21	1:1:2174:C:N4	2.18	0.42
1:1:2178:C:H2'	1:1:2179:C:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:83:C:H2'	2:2:85:U:C4	2.55	0.42
2:2:181:A:N6	2:2:195:A:C8	2.88	0.42
2:2:269:C:H2'	2:2:270:A:H8	1.85	0.42
2:2:402:G:OP1	36:h:71:GLN:HG2	2.19	0.42
6:D:110:THR:HG21	6:D:169:ARG:CZ	2.50	0.42
6:D:153:GLY:O	6:D:154:LYS:HB3	2.18	0.42
12:J:123:LEU:HD21	17:O:70:VAL:HG11	2.02	0.42
13:K:124:GLY:H	13:K:144:GLU:HA	1.85	0.42
18:P:80:ILE:O	18:P:84:LYS:HG2	2.20	0.42
28:Z:37:CYS:SG	28:Z:39:LYS:HB3	2.59	0.42
36:h:102:VAL:HB	36:h:114:ALA:HB1	2.01	0.42
42:n:24:GLU:OE2	42:n:90:LEU:HD11	2.19	0.42
1:1:1068:G:C2	1:1:1095:A:H1'	2.55	0.42
1:1:1342:A:O2'	1:1:1344:U:OP2	2.29	0.42
1:1:1496:A:N3	1:1:1577:C:O2'	2.51	0.42
1:1:2025:C:H2'	1:1:2026:U:C6	2.55	0.42
2:2:81:A:N7	2:2:83:C:C4	2.87	0.42
2:2:403:C:OP2	36:h:71:GLN:NE2	2.49	0.42
2:2:1048:G:O6	2:2:1210:C:N4	2.53	0.42
19:Q:34:GLU:HG2	19:Q:60:LYS:HG2	2.02	0.42
36:h:13:ARG:NH2	36:h:37:ALA:O	2.53	0.42
42:n:19:ASP:HA	42:n:22:THR:HG22	2.02	0.42
42:n:83:THR:O	42:n:87:LEU:HG	2.19	0.42
54:z:6:G:H2'	54:z:7:G:C8	2.55	0.42
1:1:356:G:C6	1:1:357:C:C4	3.08	0.41
1:1:613:A:O4'	1:1:614:A:C8	2.73	0.41
1:1:807:U:OP1	13:K:36:LYS:HE2	2.20	0.41
1:1:2076:U:OP2	1:1:2238:G:N2	2.43	0.41
1:1:2236:U:H2'	1:1:2237:G:O4'	2.20	0.41
2:2:41:G:H2'	2:2:42:G:C8	2.55	0.41
2:2:214:C:H2'	2:2:215:C:C6	2.54	0.41
2:2:689:C:H2'	2:2:690:G:O4'	2.19	0.41
2:2:1147:C:H1'	41:m:18:ARG:HH21	1.86	0.41
6:D:46:ARG:NH1	6:D:85:ALA:O	2.49	0.41
7:E:97:ASN:ND2	7:E:100:MET:SD	2.91	0.41
10:H:47:PHE:O	10:H:51:ARG:N	2.53	0.41
10:H:121:VAL:HG13	10:H:122:LEU:N	2.35	0.41
34:f:73:LYS:C	34:f:75:ALA:H	2.28	0.41
43:o:47:ALA:HB1	43:o:62:ALA:HB1	2.02	0.41
45:q:4:ILE:HG13	45:q:9:ILE:HD12	2.01	0.41
54:z:56:G:C4	54:z:57:U:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:z:87:C:H5''	54:z:88:A:OP2	2.20	0.41
1:1:1416:G:C4	1:1:1417:C:C5	3.08	0.41
1:1:2108:A:H2	1:1:2181:U:O2	2.03	0.41
1:1:2140:G:H2'	1:1:2141:G:O4'	2.20	0.41
1:1:2167:U:HO2'	1:1:2169:A:H62	1.68	0.41
1:1:2636:C:H2'	1:1:2637:U:C6	2.55	0.41
1:1:2799:A:O2'	1:1:2800:A:H5''	2.20	0.41
2:2:71:A:H61	2:2:99:C:H1'	1.85	0.41
2:2:858:G:O6	2:2:869:G:C8	2.73	0.41
8:F:73:SER:OG	8:F:80:ARG:HA	2.20	0.41
31:c:12:ARG:HG2	31:c:44:VAL:HG11	2.01	0.41
31:c:35:ARG:HE	31:c:42:LEU:HD11	1.85	0.41
35:g:79:LYS:HB2	35:g:82:GLU:HB2	2.02	0.41
37:i:143:GLY:O	37:i:146:ASN:OD1	2.38	0.41
1:1:833:A:H2'	1:1:834:G:C8	2.54	0.41
1:1:1722:A:N6	1:1:1738:G:H1'	2.34	0.41
1:1:1883:U:H2'	1:1:1884:G:O4'	2.20	0.41
1:1:2102:G:N7	1:1:2188:U:N3	2.67	0.41
1:1:2314:A:H2'	1:1:2315:G:C8	2.55	0.41
1:1:2477:U:H2'	33:e:2:LYS:HE2	2.02	0.41
2:2:526:C:OP2	44:p:88:LYS:HE3	2.20	0.41
2:2:1145:A:O2'	2:2:1146:A:O5'	2.35	0.41
6:D:77:ARG:NH1	6:D:200:ASP:OD1	2.39	0.41
8:F:7:TYR:O	8:F:10:ASP:OD1	2.37	0.41
10:H:77:THR:HA	10:H:143:ILE:O	2.20	0.41
13:K:127:VAL:HG12	13:K:128:THR:O	2.20	0.41
17:O:78:SER:OG	17:O:80:VAL:HG12	2.20	0.41
29:a:30:VAL:HG22	29:a:37:LYS:HG2	2.03	0.41
35:g:10:ILE:HG23	35:g:11:ARG:HD2	2.02	0.41
52:x:31:PHE:O	52:x:35:VAL:HG23	2.19	0.41
53:y:31:GLU:OE2	53:y:35:ARG:NE	2.48	0.41
53:y:51:SER:HA	53:y:54:LYS:NZ	2.35	0.41
1:1:957:C:N4	1:1:2459:A:C8	2.89	0.41
1:1:1315:C:O2'	1:1:1392:A:N3	2.49	0.41
1:1:1328:A:H2'	1:1:1330:C:C5	2.55	0.41
1:1:1349:C:C2	1:1:1350:C:C5	3.09	0.41
1:1:2109:U:OP1	1:1:2150:C:O2	2.38	0.41
2:2:563:A:N3	44:p:12:ARG:NH1	2.68	0.41
2:2:1006:G:H8	2:2:1006:G:P	2.44	0.41
5:C:138:GLY:N	5:C:164:ILE:O	2.51	0.41
6:D:64:GLU:HG2	6:D:68:PHE:HE2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:8:ALA:HB3	7:E:122:GLU:OE2	2.21	0.41
8:F:123:ASP:OD2	8:F:127:ASN:HB2	2.20	0.41
10:H:54:LEU:O	10:H:58:LEU:HD23	2.19	0.41
11:I:37:ARG:HD2	11:I:118:MET:HE1	2.03	0.41
19:Q:43:ASN:HB3	19:Q:46:GLU:HB3	2.03	0.41
20:R:83:LYS:HD2	20:R:95:ARG:HH21	1.85	0.41
21:S:4:GLU:O	21:S:8:LEU:HG	2.20	0.41
24:V:41:ARG:O	24:V:57:HIS:ND1	2.52	0.41
28:Z:41:HIS:O	28:Z:44:PHE:CE1	2.74	0.41
1:1:434:U:O2	1:1:436:C:N4	2.53	0.41
1:1:568:U:H1'	1:1:2030:6MZ:H9C1	2.02	0.41
1:1:1686:C:H2'	1:1:1687:G:O4'	2.20	0.41
1:1:2100:G:C6	1:1:2190:G:C6	3.08	0.41
1:1:2140:G:C6	1:1:2141:G:C2	3.09	0.41
1:1:2687:U:H2'	1:1:2688:G:O4'	2.21	0.41
1:1:2850:A:N7	1:1:2868:A:O2'	2.44	0.41
2:2:1356:G:H2'	2:2:1357:A:H8	1.85	0.41
10:H:83:LYS:O	10:H:90:LEU:CD1	2.69	0.41
10:H:93:SER:HB2	10:H:121:VAL:HG22	2.03	0.41
10:H:123:ARG:HB3	10:H:123:ARG:CZ	2.50	0.41
11:I:95:ARG:HE	11:I:95:ARG:HB3	1.66	0.41
34:f:66:LYS:O	34:f:159:ASP:OD1	2.38	0.41
34:f:73:LYS:C	34:f:75:ALA:N	2.79	0.41
37:i:137:VAL:O	37:i:141:ILE:HG12	2.20	0.41
41:m:91:ASP:CG	41:m:93:SER:HG	2.22	0.41
50:v:74:HIS:O	50:v:75:GLN:OE1	2.39	0.41
1:1:12:U:H2'	1:1:12:U:O2	2.20	0.41
1:1:138:U:O2'	1:1:139:U:O2	2.26	0.41
1:1:687:C:H1'	31:c:4:THR:HG22	2.02	0.41
1:1:1326:U:H2'	1:1:1327:A:H8	1.86	0.41
1:1:1341:G:OP1	1:1:1397:U:N3	2.45	0.41
1:1:1688:U:O2'	1:1:1700:A:N7	2.48	0.41
1:1:2109:U:C5'	1:1:2142:A:H2	2.33	0.41
1:1:2503:2MA:O2'	1:1:2505:G:OP2	2.36	0.41
2:2:1048:G:C6	2:2:1210:C:N4	2.89	0.41
2:2:1414:U:H2'	2:2:1415:G:H8	1.84	0.41
8:F:8:TYR:O	8:F:13:VAL:HG23	2.20	0.41
10:H:42:LYS:HD3	10:H:42:LYS:C	2.45	0.41
16:N:53:THR:HG21	16:N:65:THR:O	2.20	0.41
20:R:69:LEU:HD23	20:R:69:LEU:HA	1.84	0.41
36:h:69:GLU:OE2	36:h:204:TYR:OH	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:u:29:VAL:HG22	49:u:30:LYS:N	2.36	0.41
1:1:45:G:H5''	1:1:46:G:H5'	2.02	0.41
1:1:1348:C:C5	1:1:1349:C:C5	3.08	0.41
1:1:1770:G:C6	1:1:1983:G:C6	3.08	0.41
1:1:2134:A:H1'	1:1:2159:G:N3	2.36	0.41
1:1:2148:G:C4	1:1:2149:U:H5	2.39	0.41
2:2:672:U:H2'	2:2:673:A:H8	1.85	0.41
2:2:966:2MG:HM22	54:z:35:G:C5'	2.51	0.41
10:H:84:ALA:HB3	10:H:148:ALA:HB2	2.01	0.41
32:d:33:LEU:O	32:d:41:LYS:NZ	2.46	0.41
38:j:9:MET:HG2	38:j:59:TYR:CD1	2.55	0.41
1:1:565:C:N3	1:1:576:U:O4	2.54	0.41
1:1:631:A:N3	1:1:2415:G:O2'	2.44	0.41
1:1:1197:G:H2'	1:1:1198:U:H6	1.85	0.41
1:1:2009:A:OP1	20:R:41:LYS:HE2	2.20	0.41
1:1:2119:A:C4	1:1:2170:A:C6	3.09	0.41
2:2:957:U:H4'	51:w:79:THR:HG23	2.03	0.41
2:2:1028:C:C2	2:2:1034:G:N2	2.79	0.41
2:2:1034:G:H8	2:2:1034:G:OP2	2.04	0.41
2:2:1080:A:P	37:i:52:LYS:NZ	2.94	0.41
5:C:145:GLU:HB2	5:C:188:CYS:HB3	2.03	0.41
14:L:36:VAL:HG13	23:U:82:TYR:CD2	2.56	0.41
31:c:22:MET:SD	31:c:31:LEU:HD12	2.61	0.41
34:f:87:CYS:HA	34:f:225:ARG:HH12	1.85	0.41
37:i:64:MET:O	37:i:68:ARG:HG3	2.21	0.41
46:r:46:LEU:HD12	51:w:13:LEU:CB	2.51	0.41
49:u:58:VAL:O	49:u:79:VAL:O	2.39	0.41
1:1:2053:G:O6	1:1:2614:A:C2	2.73	0.41
1:1:2117:A:O2'	1:1:2119:A:OP1	2.22	0.41
1:1:2169:A:H8	1:1:2169:A:O5'	2.04	0.41
1:1:2511:U:O4	1:1:2575:C:N3	2.53	0.41
2:2:718:A:C5'	43:o:119:ASN:ND2	2.84	0.41
2:2:1022:A:N6	2:2:1023:U:N3	2.69	0.41
2:2:1055:A:C6	2:2:1206:G:C5	3.09	0.41
2:2:1477:U:H2'	2:2:1478:U:C6	2.56	0.41
3:3:15:A:O4'	3:3:109:A:C8	2.73	0.41
9:G:60:ASP:OD1	9:G:60:ASP:N	2.54	0.41
10:H:3:VAL:HG22	10:H:36:ALA:HB1	2.03	0.41
10:H:47:PHE:HA	10:H:51:ARG:HB2	2.01	0.41
10:H:63:ALA:HA	10:H:66:ASN:ND2	2.35	0.41
25:W:17:ASN:CG	25:W:27:ARG:HD2	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:Z:11:GLU:HA	28:Z:25:ARG:HA	2.03	0.41
34:f:69:PHE:HB3	34:f:80:VAL:CG2	2.51	0.41
34:f:114:LEU:HD12	34:f:144:LEU:C	2.46	0.41
35:g:111:LEU:HD22	35:g:146:ALA:HB2	2.02	0.41
35:g:124:LEU:HD21	35:g:130:PHE:HB3	2.03	0.41
36:h:118:VAL:HG11	36:h:132:ILE:C	2.46	0.41
38:j:12:PRO:HB2	38:j:44:ARG:NH1	2.35	0.41
39:k:74:GLU:HG2	39:k:91:VAL:HG22	2.03	0.41
41:m:91:ASP:O	41:m:92:GLU:HB3	2.20	0.41
42:n:91:ASP:C	42:n:92:LEU:HD22	2.46	0.41
50:v:30:LYS:HA	50:v:33:ILE:HG12	2.02	0.41
55:B:4:LYS:O	55:B:5:MET:HB2	2.20	0.41
55:B:12:PHE:HD1	55:B:12:PHE:N	2.03	0.41
55:B:16:LYS:HB3	55:B:16:LYS:HZ3	1.85	0.41
1:1:851:C:H2'	1:1:852:U:C6	2.56	0.41
1:1:885:C:H2'	1:1:886:A:C8	2.56	0.41
1:1:888:C:H2'	1:1:889:C:O4'	2.21	0.41
1:1:891:G:H2'	1:1:892:A:H5''	2.03	0.41
1:1:1042:G:C4	1:1:1043:C:C5	3.09	0.41
1:1:1071:G:C6	1:1:1089:A:C2	3.09	0.41
1:1:1113:U:C2	1:1:1114:C:C5	3.09	0.41
1:1:1407:G:H3'	1:1:1408:G:H5''	2.02	0.41
1:1:1536:C:O2	1:1:1537:G:N2	2.54	0.41
1:1:1544:A:H2'	1:1:1545:A:C8	2.56	0.41
1:1:2134:A:H61	1:1:2157:G:H1'	1.86	0.41
1:1:2467:C:O2	14:L:123:LYS:NZ	2.50	0.41
1:1:2766:A:C5	1:1:2767:C:C5	3.09	0.41
1:1:2880:C:O2'	15:M:90:ARG:NH2	2.36	0.41
5:C:168:ASP:OD1	5:C:168:ASP:N	2.54	0.41
8:F:47:LYS:O	8:F:51:ASP:N	2.48	0.41
9:G:88:GLN:C	9:G:89:LEU:HD12	2.46	0.41
10:H:57:LYS:HA	10:H:60:GLU:HG2	2.03	0.41
10:H:132:PHE:O	10:H:139:PHE:CB	2.69	0.41
22:T:14:LEU:O	22:T:19:LYS:HG3	2.21	0.41
33:e:30:GLU:HG3	33:e:32:LYS:H	1.86	0.41
35:g:47:LEU:N	35:g:47:LEU:CD1	2.80	0.41
39:k:86:GLN:O	39:k:148:ASN:HB3	2.20	0.41
41:m:25:ASN:OD1	41:m:62:ASP:OD1	2.39	0.41
43:o:60:PRO:HD3	43:o:91:PRO:HB2	2.03	0.41
1:1:594:U:H2'	1:1:595:C:C6	2.56	0.40
1:1:720:U:H2'	1:1:721:A:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:744:U:H3'	1:1:745:1MG:H8	1.86	0.40
1:1:1386:C:H2'	1:1:1387:A:C8	2.56	0.40
1:1:1528:A:OP2	1:1:1543:G:N2	2.54	0.40
1:1:2102:G:C6	1:1:2188:U:C2	3.09	0.40
1:1:2162:G:H5''	1:1:2173:A:C5'	2.50	0.40
2:2:686:U:O4	2:2:703:G:O2'	2.26	0.40
2:2:909:A:OP1	44:p:18:LYS:HD2	2.20	0.40
2:2:1244:G:H2'	2:2:1245:C:C6	2.56	0.40
2:2:1328:C:H2'	2:2:1329:A:O4'	2.20	0.40
2:2:1530:G:H2'	2:2:1531:A:H8	1.85	0.40
8:F:108:VAL:HB	8:F:109:PRO:HD3	2.02	0.40
25:W:27:ARG:NH1	25:W:29:PHE:CZ	2.88	0.40
33:e:31:PRO:O	33:e:34:LYS:HG2	2.21	0.40
35:g:21:THR:O	35:g:21:THR:HG22	2.20	0.40
35:g:31:ASP:OD1	46:r:65:ARG:NH2	2.48	0.40
36:h:170:TRP:CD2	36:h:186:PRO:HB3	2.56	0.40
1:1:281:C:H2'	1:1:282:A:C8	2.56	0.40
1:1:732:C:H2'	1:1:733:G:O4'	2.20	0.40
1:1:1062:G:H2'	1:1:1063:G:C8	2.57	0.40
1:1:1071:G:N2	1:1:1089:A:O2'	2.47	0.40
1:1:1664:A:C2	12:J:1:MET:HE1	2.55	0.40
1:1:1856:U:H2'	1:1:1857:G:O4'	2.21	0.40
1:1:2064:C:H2'	1:1:2065:C:C6	2.56	0.40
1:1:2098:U:H2'	1:1:2099:U:O4'	2.21	0.40
1:1:2102:G:H3'	1:1:2103:C:C6	2.56	0.40
2:2:218:U:H2'	2:2:219:U:O4'	2.20	0.40
2:2:321:A:N7	2:2:328:C:O2'	2.48	0.40
2:2:1032:G:H3'	2:2:1032:G:N3	2.36	0.40
2:2:1033:G:C6	2:2:1034:G:C6	3.09	0.40
2:2:1147:C:O3'	41:m:7:TYR:OH	2.39	0.40
2:2:1439:G:OP1	52:x:33:LYS:HD3	2.21	0.40
5:C:205:LEU:N	5:C:205:LEU:HD12	2.36	0.40
11:I:77:HIS:CE1	11:I:80:HIS:O	2.75	0.40
16:N:53:THR:HB	16:N:65:THR:HB	2.02	0.40
20:R:31:GLN:O	20:R:35:ILE:HG13	2.21	0.40
22:T:51:ALA:O	22:T:52:LEU:HB2	2.20	0.40
35:g:23:PHE:HB2	42:n:95:GLY:O	2.21	0.40
36:h:118:VAL:HG12	36:h:131:ASN:C	2.46	0.40
44:p:34:CYS:SG	44:p:74:LEU:HD12	2.62	0.40
51:w:40:ILE:HB	51:w:66:MET:O	2.21	0.40
1:1:2570:G:H2'	1:1:2571:U:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1100:C:P	34:f:95:ARG:HD3	2.61	0.40
10:H:75:LEU:CD2	10:H:106:ALA:O	2.69	0.40
18:P:26:GLY:O	18:P:30:ARG:NH1	2.52	0.40
26:X:59:GLU:O	26:X:63:ALA:HB3	2.22	0.40
28:Z:51:VAL:CG2	28:Z:52:ALA:H	2.33	0.40
28:Z:56:ARG:O	28:Z:59:ARG:HG2	2.21	0.40
34:f:43:LEU:HA	34:f:46:THR:HB	2.03	0.40
35:g:118:ASP:OD1	35:g:118:ASP:C	2.64	0.40
37:i:56:VAL:HB	37:i:57:PRO:HD3	2.03	0.40
45:q:45:ILE:HA	45:q:48:LEU:HD12	2.03	0.40
1:1:1011:G:OP2	18:P:70:ARG:NH1	2.52	0.40
1:1:1913:A:N1	2:2:1492:A:H2'	2.36	0.40
2:2:460:A:H2'	2:2:461:A:C8	2.56	0.40
2:2:1039:G:H2'	2:2:1040:U:H6	1.85	0.40
2:2:1440:U:O2'	2:2:1441:A:O5'	2.19	0.40
9:G:25:THR:HG22	9:G:34:THR:OG1	2.22	0.40
11:I:73:VAL:HG11	11:I:75:TYR:CZ	2.57	0.40
22:T:49:VAL:HG22	22:T:54:GLN:HB2	2.04	0.40
35:g:42:TYR:CE2	35:g:90:VAL:HG21	2.56	0.40
37:i:46:VAL:HG21	37:i:118:ALA:HB2	2.03	0.40
41:m:60:LYS:CB	41:m:61:LEU:HD12	2.51	0.40
44:p:50:ARG:HG3	44:p:90:LEU:HD21	2.02	0.40
44:p:99:ARG:HE	44:p:104:CYS:HG	1.69	0.40
45:q:116:ILE:O	45:q:116:ILE:HG13	2.20	0.40
53:y:4:ILE:HG23	53:y:18:ARG:NH2	2.37	0.40
1:1:469:G:O6	31:c:37:LYS:HE2	2.21	0.40
1:1:684:G:C6	1:1:774:G:C4	3.10	0.40
1:1:888:C:C6	45:q:92:ARG:HD2	2.56	0.40
1:1:984:A:H2'	1:1:984:A:N3	2.37	0.40
1:1:1175:A:P	1:1:1177:G:H1'	2.61	0.40
1:1:1526:C:H2'	1:1:1527:G:O4'	2.22	0.40
1:1:2097:A:C6	1:1:2193:G:C6	3.09	0.40
1:1:2300:C:O2'	1:1:2301:C:H5'	2.22	0.40
1:1:2301:C:H2'	1:1:2302:U:C6	2.56	0.40
1:1:2329:U:H2'	1:1:2330:G:C8	2.56	0.40
1:1:2572:A:N6	6:D:150:GLN:OE1	2.51	0.40
2:2:88:U:C5	2:2:89:U:C5	3.10	0.40
2:2:608:A:H2'	2:2:609:A:O4'	2.22	0.40
2:2:687:A:C2	2:2:704:A:C5	3.10	0.40
2:2:950:U:H3'	45:q:101:ARG:HH22	1.86	0.40
5:C:43:ARG:HA	5:C:48:ARG:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:38:LEU:HD11	15:M:42:LYS:HE3	2.04	0.40
15:M:118:ARG:NH1	29:a:54:VAL:O	2.54	0.40
16:N:4:LYS:O	16:N:8:ILE:HG13	2.22	0.40
20:R:73:LYS:HB2	20:R:106:VAL:HB	2.02	0.40
39:k:57:SER:HB3	39:k:60:GLU:HB2	2.04	0.40
43:o:89:PRO:HB3	53:y:29:LEU:CD2	2.51	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	
5	C	269/271 (99%)	256 (95%)	13 (5%)	0	100	100
6	D	207/209 (99%)	201 (97%)	3 (1%)	3 (1%)	9	29
7	E	199/201 (99%)	198 (100%)	1 (0%)	0	100	100
8	F	175/177 (99%)	166 (95%)	8 (5%)	1 (1%)	21	48
9	G	173/175 (99%)	163 (94%)	10 (6%)	0	100	100
10	H	147/149 (99%)	137 (93%)	10 (7%)	0	100	100
11	I	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
12	J	121/123 (98%)	119 (98%)	2 (2%)	0	100	100
13	K	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
14	L	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	M	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
16	N	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
17	O	112/114 (98%)	111 (99%)	1 (1%)	0	100	100
18	P	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	Q	101/103 (98%)	94 (93%)	5 (5%)	2 (2%)	6	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	R	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
21	S	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
22	T	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
23	U	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
24	V	78/80 (98%)	74 (95%)	4 (5%)	0	100	100
25	W	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	X	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
27	Y	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
28	Z	64/66 (97%)	60 (94%)	4 (6%)	0	100	100
29	a	54/56 (96%)	52 (96%)	2 (4%)	0	100	100
30	b	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
31	c	44/46 (96%)	44 (100%)	0	0	100	100
32	d	62/64 (97%)	58 (94%)	4 (6%)	0	100	100
33	e	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
34	f	223/225 (99%)	206 (92%)	17 (8%)	0	100	100
35	g	206/208 (99%)	197 (96%)	9 (4%)	0	100	100
36	h	203/205 (99%)	200 (98%)	3 (2%)	0	100	100
37	i	154/156 (99%)	144 (94%)	10 (6%)	0	100	100
38	j	102/104 (98%)	98 (96%)	4 (4%)	0	100	100
39	k	149/151 (99%)	145 (97%)	4 (3%)	0	100	100
40	l	127/129 (98%)	125 (98%)	2 (2%)	0	100	100
41	m	125/127 (98%)	117 (94%)	8 (6%)	0	100	100
42	n	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
43	o	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
44	p	120/123 (98%)	112 (93%)	8 (7%)	0	100	100
45	q	114/116 (98%)	109 (96%)	5 (4%)	0	100	100
46	r	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
47	s	86/88 (98%)	84 (98%)	2 (2%)	0	100	100
48	t	80/82 (98%)	78 (98%)	2 (2%)	0	100	100
49	u	78/80 (98%)	75 (96%)	3 (4%)	0	100	100
50	v	64/66 (97%)	64 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	w	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
52	x	84/86 (98%)	84 (100%)	0	0	100	100
53	y	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
55	B	25/27 (93%)	17 (68%)	5 (20%)	3 (12%)	0	1
All	All	5637/5738 (98%)	5426 (96%)	202 (4%)	9 (0%)	44	70

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	D	152	PRO
55	B	21	ILE
55	B	23	PRO
6	D	153	GLY
6	D	154	LYS
55	B	10	LYS
19	Q	52	PRO
19	Q	53	PHE
8	F	124	GLY

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	
5	C	216/216 (100%)	216 (100%)	0	100	100
6	D	164/164 (100%)	163 (99%)	1 (1%)	78	81
7	E	165/165 (100%)	165 (100%)	0	100	100
8	F	148/148 (100%)	147 (99%)	1 (1%)	76	80
9	G	136/136 (100%)	135 (99%)	1 (1%)	76	80
10	H	114/114 (100%)	110 (96%)	4 (4%)	32	59
11	I	116/116 (100%)	115 (99%)	1 (1%)	70	78
12	J	104/104 (100%)	104 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	K	103/103 (100%)	103 (100%)	0	100	100
14	L	109/109 (100%)	109 (100%)	0	100	100
15	M	99/99 (100%)	99 (100%)	0	100	100
16	N	86/86 (100%)	86 (100%)	0	100	100
17	O	99/99 (100%)	99 (100%)	0	100	100
18	P	89/89 (100%)	89 (100%)	0	100	100
19	Q	84/84 (100%)	84 (100%)	0	100	100
20	R	93/93 (100%)	93 (100%)	0	100	100
21	S	81/81 (100%)	81 (100%)	0	100	100
22	T	84/84 (100%)	84 (100%)	0	100	100
23	U	78/78 (100%)	78 (100%)	0	100	100
24	V	59/59 (100%)	58 (98%)	1 (2%)	53	71
25	W	67/67 (100%)	67 (100%)	0	100	100
26	X	54/54 (100%)	53 (98%)	1 (2%)	50	69
27	Y	48/48 (100%)	48 (100%)	0	100	100
28	Z	59/59 (100%)	59 (100%)	0	100	100
29	a	47/47 (100%)	47 (100%)	0	100	100
30	b	47/47 (100%)	47 (100%)	0	100	100
31	c	38/38 (100%)	38 (100%)	0	100	100
32	d	51/51 (100%)	50 (98%)	1 (2%)	48	69
33	e	34/34 (100%)	34 (100%)	0	100	100
34	f	187/187 (100%)	185 (99%)	2 (1%)	65	76
35	g	171/171 (100%)	171 (100%)	0	100	100
36	h	172/172 (100%)	172 (100%)	0	100	100
37	i	119/119 (100%)	118 (99%)	1 (1%)	73	79
38	j	91/91 (100%)	91 (100%)	0	100	100
39	k	124/124 (100%)	124 (100%)	0	100	100
40	l	104/104 (100%)	104 (100%)	0	100	100
41	m	105/105 (100%)	105 (100%)	0	100	100
42	n	86/86 (100%)	85 (99%)	1 (1%)	63	75
43	o	90/90 (100%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	p	102/102 (100%)	102 (100%)	0	100	100
45	q	94/94 (100%)	94 (100%)	0	100	100
46	r	83/83 (100%)	83 (100%)	0	100	100
47	s	76/76 (100%)	76 (100%)	0	100	100
48	t	65/65 (100%)	65 (100%)	0	100	100
49	u	74/74 (100%)	74 (100%)	0	100	100
50	v	57/57 (100%)	57 (100%)	0	100	100
51	w	72/72 (100%)	72 (100%)	0	100	100
52	x	65/65 (100%)	64 (98%)	1 (2%)	57	73
53	y	60/60 (100%)	60 (100%)	0	100	100
55	B	20/20 (100%)	13 (65%)	7 (35%)	0	0
All	All	4689/4689 (100%)	4666 (100%)	23 (0%)	78	82

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	D	151	THR
8	F	141	ILE
9	G	47	ASP
10	H	43	ASN
10	H	55	GLU
10	H	82	SER
10	H	122	LEU
11	I	95	ARG
24	V	10	THR
26	X	58	ASN
32	d	31	HIS
34	f	118	GLU
34	f	129	LEU
37	i	112	ARG
42	n	87	LEU
52	x	57	ILE
55	B	8	ILE
55	B	10	LYS
55	B	12	PHE
55	B	16	LYS
55	B	20	PHE
55	B	21	ILE

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Mol	Chain	Res	Type
55	B	23	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
5	C	70	ASN
5	C	86	ASN
5	C	226	ASN
7	E	136	GLN
10	H	11	ASN
10	H	73	ASN
13	K	104	GLN
14	L	60	GLN
15	M	9	GLN
15	M	31	HIS
15	M	73	ASN
16	N	98	GLN
17	O	56	HIS
17	O	66	ASN
22	T	46	GLN
25	W	36	HIS
26	X	39	GLN
28	Z	33	ASN
32	d	31	HIS
34	f	51	ASN
36	h	40	GLN
37	i	97	GLN
37	i	121	HIS
38	j	58	HIS
38	j	68	GLN
41	m	4	ASN
41	m	110	GLN
44	p	5	ASN
45	q	14	HIS
46	r	66	GLN
47	s	50	HIS
51	w	69	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	492 (16%)	9 (0%)
2	2	1532/1534 (99%)	255 (16%)	5 (0%)
3	3	119/120 (99%)	15 (12%)	0
4	4	5/6 (83%)	0	0
54	z	87/88 (98%)	26 (29%)	0
All	All	4645/4651 (99%)	788 (16%)	14 (0%)

All (788) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	15	G
1	1	34	U
1	1	35	G
1	1	46	G
1	1	51	G
1	1	71	A
1	1	74	A
1	1	75	G
1	1	84	A
1	1	85	G
1	1	101	A
1	1	102	U
1	1	110	G
1	1	118	A
1	1	119	A
1	1	120	U
1	1	122	G
1	1	125	A
1	1	138	U
1	1	139	U
1	1	140	C
1	1	142	A
1	1	163	C
1	1	181	A
1	1	196	A
1	1	199	A
1	1	215	G
1	1	216	A
1	1	221	A
1	1	222	A
1	1	248	G
1	1	249	C

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Mol	Chain	Res	Type
1	1	264	C
1	1	265	A
1	1	266	G
1	1	272	A
1	1	273	G
1	1	275	C
1	1	276	U
1	1	285	G
1	1	311	A
1	1	329	G
1	1	330	A
1	1	343	C
1	1	353	C
1	1	361	G
1	1	371	A
1	1	372	G
1	1	383	C
1	1	386	G
1	1	396	G
1	1	399	U
1	1	405	U
1	1	406	G
1	1	411	G
1	1	412	A
1	1	424	G
1	1	435	C
1	1	457	A
1	1	467	G
1	1	481	G
1	1	489	G
1	1	491	G
1	1	505	A
1	1	509	C
1	1	510	C
1	1	513	A
1	1	532	A
1	1	533	G
1	1	543	G
1	1	546	U
1	1	547	A
1	1	548	G
1	1	549	G

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Mol	Chain	Res	Type
1	1	551	G
1	1	563	A
1	1	573	U
1	1	575	A
1	1	603	A
1	1	612	G
1	1	613	A
1	1	614	A
1	1	615	U
1	1	616	A
1	1	627	A
1	1	637	A
1	1	645	C
1	1	647	G
1	1	654	A
1	1	655	A
1	1	670	A
1	1	686	U
1	1	702	U
1	1	709	U
1	1	710	U
1	1	726	G
1	1	730	A
1	1	747	5MU
1	1	764	A
1	1	765	C
1	1	775	G
1	1	776	G
1	1	782	A
1	1	784	G
1	1	785	G
1	1	792	A
1	1	800	A
1	1	805	G
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	845	A
1	1	846	U
1	1	858	G
1	1	859	G

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Mol	Chain	Res	Type
1	1	866	A
1	1	869	G
1	1	878	A
1	1	880	G
1	1	882	G
1	1	884	U
1	1	885	C
1	1	887	A
1	1	888	C
1	1	891	G
1	1	892	A
1	1	893	C
1	1	895	U
1	1	896	A
1	1	897	C
1	1	907	G
1	1	910	A
1	1	931	U
1	1	932	U
1	1	941	A
1	1	946	C
1	1	961	C
1	1	973	A
1	1	974	G
1	1	983	A
1	1	989	G
1	1	995	C
1	1	996	A
1	1	999	U
1	1	1005	C
1	1	1012	U
1	1	1013	C
1	1	1022	G
1	1	1023	U
1	1	1025	G
1	1	1026	G
1	1	1033	U
1	1	1043	C
1	1	1046	A
1	1	1047	G
1	1	1057	A
1	1	1060	U

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Mol	Chain	Res	Type
1	1	1061	U
1	1	1062	G
1	1	1064	C
1	1	1065	U
1	1	1066	U
1	1	1067	A
1	1	1068	G
1	1	1070	A
1	1	1071	G
1	1	1073	A
1	1	1087	G
1	1	1088	A
1	1	1090	A
1	1	1096	A
1	1	1101	U
1	1	1110	G
1	1	1111	A
1	1	1112	G
1	1	1119	U
1	1	1122	G
1	1	1128	G
1	1	1130	U
1	1	1131	G
1	1	1132	U
1	1	1133	A
1	1	1134	A
1	1	1135	C
1	1	1136	G
1	1	1139	G
1	1	1142	A
1	1	1156	A
1	1	1169	A
1	1	1170	C
1	1	1171	G
1	1	1173	U
1	1	1175	A
1	1	1176	U
1	1	1177	G
1	1	1178	C
1	1	1179	G
1	1	1182	G
1	1	1186	G

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Mol	Chain	Res	Type
1	1	1206	G
1	1	1212	G
1	1	1218	G
1	1	1236	G
1	1	1238	G
1	1	1247	A
1	1	1250	G
1	1	1253	A
1	1	1256	G
1	1	1266	G
1	1	1271	G
1	1	1272	A
1	1	1300	G
1	1	1301	A
1	1	1321	A
1	1	1329	U
1	1	1341	G
1	1	1345	C
1	1	1352	U
1	1	1365	A
1	1	1368	G
1	1	1379	U
1	1	1380	G
1	1	1383	A
1	1	1386	C
1	1	1408	G
1	1	1411	U
1	1	1417	C
1	1	1419	A
1	1	1427	A
1	1	1428	C
1	1	1437	C
1	1	1460	U
1	1	1468	U
1	1	1476	U
1	1	1482	G
1	1	1490	A
1	1	1493	C
1	1	1494	A
1	1	1503	A
1	1	1504	A
1	1	1508	A

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Mol	Chain	Res	Type
1	1	1509	A
1	1	1510	G
1	1	1515	A
1	1	1524	G
1	1	1529	G
1	1	1530	G
1	1	1532	A
1	1	1535	A
1	1	1536	C
1	1	1537	G
1	1	1554	U
1	1	1559	U
1	1	1566	A
1	1	1569	A
1	1	1578	U
1	1	1580	A
1	1	1583	A
1	1	1587	G
1	1	1589	U
1	1	1590	A
1	1	1608	A
1	1	1618	6MZ
1	1	1622	G
1	1	1634	A
1	1	1647	U
1	1	1648	U
1	1	1649	G
1	1	1651	G
1	1	1674	G
1	1	1715	G
1	1	1729	U
1	1	1730	C
1	1	1732	C
1	1	1738	G
1	1	1756	G
1	1	1764	C
1	1	1773	A
1	1	1782	U
1	1	1791	A
1	1	1800	C
1	1	1801	A
1	1	1802	A

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Mol	Chain	Res	Type
1	1	1808	A
1	1	1811	G
1	1	1816	C
1	1	1829	A
1	1	1833	C
1	1	1835	2MG
1	1	1847	A
1	1	1848	A
1	1	1858	A
1	1	1862	G
1	1	1865	U
1	1	1868	C
1	1	1869	G
1	1	1870	C
1	1	1871	A
1	1	1872	A
1	1	1873	G
1	1	1896	G
1	1	1906	G
1	1	1907	G
1	1	1912	A
1	1	1914	C
1	1	1923	U
1	1	1924	C
1	1	1929	G
1	1	1930	G
1	1	1936	A
1	1	1937	A
1	1	1938	A
1	1	1955	U
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1991	U
1	1	1992	G
1	1	1993	U
1	1	1997	C
1	1	2002	G
1	1	2022	U
1	1	2023	C
1	1	2030	6MZ

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Mol	Chain	Res	Type
1	1	2031	A
1	1	2033	A
1	1	2043	C
1	1	2052	A
1	1	2055	C
1	1	2056	G
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	G7M
1	1	2093	G
1	1	2095	A
1	1	2100	G
1	1	2102	G
1	1	2107	G
1	1	2110	G
1	1	2112	G
1	1	2113	U
1	1	2115	G
1	1	2116	G
1	1	2117	A
1	1	2118	U
1	1	2119	A
1	1	2121	G
1	1	2122	U
1	1	2125	G
1	1	2131	U
1	1	2132	U
1	1	2133	G
1	1	2134	A
1	1	2139	U
1	1	2140	G
1	1	2145	C
1	1	2146	C
1	1	2147	A
1	1	2151	U
1	1	2152	G
1	1	2158	A
1	1	2159	G
1	1	2162	G
1	1	2163	A
1	1	2164	C

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Mol	Chain	Res	Type
1	1	2165	C
1	1	2169	A
1	1	2171	A
1	1	2172	U
1	1	2173	A
1	1	2178	C
1	1	2183	A
1	1	2189	U
1	1	2190	G
1	1	2191	A
1	1	2194	U
1	1	2198	A
1	1	2204	G
1	1	2211	A
1	1	2225	A
1	1	2229	U
1	1	2238	G
1	1	2239	G
1	1	2243	U
1	1	2250	G
1	1	2278	A
1	1	2283	C
1	1	2286	G
1	1	2287	A
1	1	2288	A
1	1	2305	U
1	1	2309	A
1	1	2319	G
1	1	2322	A
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2334	U
1	1	2336	A
1	1	2345	G
1	1	2347	C
1	1	2350	C
1	1	2357	G
1	1	2361	G
1	1	2376	A
1	1	2383	G
1	1	2385	C

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Mol	Chain	Res	Type
1	1	2402	U
1	1	2403	C
1	1	2406	A
1	1	2423	U
1	1	2424	C
1	1	2425	A
1	1	2429	G
1	1	2430	A
1	1	2431	U
1	1	2435	A
1	1	2441	U
1	1	2445	2MG
1	1	2448	A
1	1	2470	G
1	1	2476	A
1	1	2478	A
1	1	2480	C
1	1	2491	U
1	1	2498	OMC
1	1	2502	G
1	1	2504	PSU
1	1	2505	G
1	1	2506	U
1	1	2507	C
1	1	2513	A
1	1	2518	A
1	1	2520	C
1	1	2529	G
1	1	2535	G
1	1	2547	A
1	1	2554	U
1	1	2566	A
1	1	2567	G
1	1	2572	A
1	1	2573	C
1	1	2586	U
1	1	2602	A
1	1	2609	U
1	1	2613	U
1	1	2629	U
1	1	2646	C
1	1	2663	G

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Mol	Chain	Res	Type
1	1	2689	U
1	1	2690	U
1	1	2714	G
1	1	2716	C
1	1	2718	G
1	1	2725	A
1	1	2726	A
1	1	2733	A
1	1	2744	G
1	1	2748	A
1	1	2751	G
1	1	2757	A
1	1	2765	A
1	1	2777	G
1	1	2778	A
1	1	2791	G
1	1	2793	C
1	1	2797	U
1	1	2799	A
1	1	2811	G
1	1	2818	U
1	1	2820	A
1	1	2823	A
1	1	2825	G
1	1	2833	U
1	1	2835	A
1	1	2836	U
1	1	2861	U
1	1	2867	G
1	1	2872	A
1	1	2873	A
1	1	2879	A
1	1	2880	C
1	1	2883	A
1	1	2884	U
1	1	2885	G
1	1	2891	U
1	1	2898	U
1	1	2903	U
2	2	7	A
2	2	8	A
2	2	9	G

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Mol	Chain	Res	Type
2	2	22	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	50	A
2	2	51	A
2	2	52	C
2	2	54	C
2	2	66	A
2	2	68	G
2	2	69	G
2	2	70	U
2	2	71	A
2	2	72	A
2	2	73	C
2	2	74	A
2	2	75	G
2	2	76	G
2	2	81	A
2	2	83	C
2	2	84	U
2	2	85	U
2	2	86	G
2	2	87	C
2	2	92	U
2	2	120	A
2	2	121	U
2	2	128	G
2	2	130	A
2	2	131	A
2	2	141	G
2	2	144	G
2	2	149	A
2	2	160	A
2	2	163	C
2	2	164	G
2	2	177	G
2	2	181	A
2	2	182	A
2	2	197	A
2	2	204	G

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Mol	Chain	Res	Type
2	2	210	C
2	2	211	G
2	2	212	G
2	2	226	G
2	2	245	U
2	2	247	G
2	2	251	G
2	2	266	G
2	2	267	C
2	2	279	A
2	2	289	G
2	2	306	A
2	2	319	G
2	2	321	A
2	2	328	C
2	2	332	G
2	2	347	G
2	2	352	C
2	2	354	G
2	2	367	U
2	2	372	C
2	2	384	G
2	2	392	C
2	2	398	U
2	2	406	G
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	424	G
2	2	429	U
2	2	436	C
2	2	439	U
2	2	457	G
2	2	458	U
2	2	463	U
2	2	464	U
2	2	467	U
2	2	468	A
2	2	478	A
2	2	479	U

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Mol	Chain	Res	Type
2	2	481	G
2	2	484	G
2	2	485	U
2	2	486	U
2	2	496	A
2	2	499	A
2	2	510	A
2	2	511	C
2	2	517	G
2	2	518	C
2	2	521	G
2	2	527	G7M
2	2	531	U
2	2	532	A
2	2	533	A
2	2	547	A
2	2	559	A
2	2	564	C
2	2	568	G
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	596	A
2	2	633	G
2	2	650	G
2	2	653	U
2	2	660	C
2	2	665	A
2	2	700	G
2	2	701	U
2	2	702	A
2	2	703	G
2	2	718	A
2	2	721	G
2	2	723	U
2	2	724	G
2	2	731	G
2	2	734	G
2	2	747	A
2	2	748	G
2	2	753	A

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Mol	Chain	Res	Type
2	2	755	G
2	2	777	A
2	2	787	A
2	2	793	U
2	2	794	A
2	2	815	A
2	2	817	C
2	2	821	G
2	2	828	U
2	2	829	G
2	2	832	G
2	2	836	G
2	2	841	C
2	2	843	U
2	2	844	G
2	2	845	A
2	2	846	G
2	2	884	U
2	2	887	G
2	2	914	A
2	2	934	C
2	2	935	A
2	2	960	U
2	2	965	U
2	2	966	2MG
2	2	967	5MC
2	2	969	A
2	2	971	G
2	2	972	C
2	2	974	A
2	2	975	A
2	2	976	G
2	2	977	A
2	2	982	U
2	2	993	G
2	2	994	A
2	2	996	A
2	2	1004	A
2	2	1008	U
2	2	1009	U
2	2	1019	A
2	2	1022	A

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Mol	Chain	Res	Type
2	2	1025	U
2	2	1026	G
2	2	1028	C
2	2	1030	U
2	2	1031	C
2	2	1032	G
2	2	1034	G
2	2	1043	G
2	2	1044	A
2	2	1046	A
2	2	1065	U
2	2	1085	U
2	2	1089	G
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1104	G
2	2	1108	G
2	2	1124	G
2	2	1125	U
2	2	1132	C
2	2	1133	G
2	2	1136	C
2	2	1137	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1143	G
2	2	1145	A
2	2	1146	A
2	2	1151	A
2	2	1152	A
2	2	1158	C
2	2	1159	U
2	2	1160	G
2	2	1167	A
2	2	1175	G
2	2	1176	A
2	2	1184	G
2	2	1196	A
2	2	1197	A
2	2	1212	U

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Mol	Chain	Res	Type
2	2	1213	A
2	2	1215	G
2	2	1227	A
2	2	1228	C
2	2	1238	A
2	2	1239	A
2	2	1257	A
2	2	1258	G
2	2	1260	G
2	2	1261	A
2	2	1275	A
2	2	1279	G
2	2	1280	A
2	2	1286	U
2	2	1287	A
2	2	1297	G
2	2	1299	A
2	2	1302	C
2	2	1305	G
2	2	1312	G
2	2	1317	C
2	2	1320	C
2	2	1335	U
2	2	1336	C
2	2	1346	A
2	2	1353	G
2	2	1363	A
2	2	1370	G
2	2	1379	G
2	2	1381	U
2	2	1419	G
2	2	1446	A
2	2	1494	G
2	2	1497	G
2	2	1499	A
2	2	1503	A
2	2	1506	U
2	2	1517	G
2	2	1519	MA6
2	2	1529	G
2	2	1530	G
2	2	1534	A

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Mol	Chain	Res	Type
3	3	2	G
3	3	9	G
3	3	13	G
3	3	24	G
3	3	35	C
3	3	36	C
3	3	45	A
3	3	51	G
3	3	56	G
3	3	66	A
3	3	88	C
3	3	89	U
3	3	90	C
3	3	99	A
3	3	109	A
54	z	2	G
54	z	10	U
54	z	13	G
54	z	14	A
54	z	17	OMG
54	z	19	C
54	z	20	U
54	z	21	G
54	z	23	A
54	z	24	G
54	z	37	A
54	z	44	G
54	z	45	U
54	z	47	U
54	z	51	G
54	z	52	C
54	z	53	A
54	z	54	A
54	z	55	C
54	z	56	G
54	z	61	G
54	z	76	C
54	z	78	C
54	z	79	C
54	z	86	C
54	z	88	A

All (14) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	404	A
1	1	613	A
1	1	784	G
1	1	894	U
1	1	896	A
1	1	1379	U
1	1	2146	C
1	1	2189	U
1	1	2756	U
2	2	86	G
2	2	516	PSU
2	2	966	2MG
2	2	1109	C
2	2	1145	A

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

37 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
1	PSU	1	955	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.97	4 (18%)
1	OMU	1	2552	1	19,22,23	2.86	8 (42%)	26,31,34	1.63	4 (15%)
1	6MZ	1	2030	1	22,25,26	2.40	6 (27%)	30,36,39	3.35	11 (36%)
2	MA6	2	1518	2	23,26,27	1.46	4 (17%)	34,38,41	3.28	11 (32%)
2	UR3	2	1498	2	19,22,23	2.58	6 (31%)	26,32,35	1.08	1 (3%)
1	OMG	1	2251	1,54	23,26,27	2.20	7 (30%)	33,38,41	1.67	7 (21%)
1	5MU	1	1939	1,56	19,22,23	4.58	7 (36%)	28,32,35	3.66	9 (32%)
2	2MG	2	1516	2	23,26,27	2.66	8 (34%)	32,38,41	2.07	10 (31%)
2	G7M	2	527	2	23,26,27	2.67	8 (34%)	35,39,42	2.25	11 (31%)
1	2MA	1	2503	1,56	22,25,26	3.62	9 (40%)	33,37,40	2.27	9 (27%)
1	PSU	1	746	1,56	18,21,22	1.00	1 (5%)	22,30,33	1.70	3 (13%)
2	PSU	2	516	56,2	18,21,22	0.94	2 (11%)	22,30,33	1.86	5 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	5MC	2	1407	2	18,22,23	3.25	7 (38%)	26,32,35	1.07	1 (3%)
44	0TD	p	89	44	7,9,10	1.43	1 (14%)	6,11,13	1.86	2 (33%)
54	5MU	z	66	54	19,22,23	4.72	7 (36%)	28,32,35	3.94	9 (32%)
2	5MC	2	967	2	18,22,23	3.41	7 (38%)	26,32,35	0.98	2 (7%)
1	OMC	1	2498	1,56	19,22,23	2.68	7 (36%)	26,31,34	0.83	0
1	PSU	1	2457	1	18,21,22	1.00	2 (11%)	22,30,33	2.02	5 (22%)
1	PSU	1	2580	1	18,21,22	1.02	1 (5%)	22,30,33	2.02	6 (27%)
1	PSU	1	2605	1	18,21,22	0.98	2 (11%)	22,30,33	1.92	4 (18%)
2	2MG	2	1207	2	23,26,27	2.74	8 (34%)	32,38,41	1.99	8 (25%)
2	2MG	2	966	2	23,26,27	2.76	9 (39%)	32,38,41	2.08	9 (28%)
1	2MG	1	1835	1	23,26,27	2.69	8 (34%)	32,38,41	2.02	7 (21%)
2	MA6	2	1519	2	23,26,27	1.48	4 (17%)	34,38,41	3.38	11 (32%)
1	PSU	1	1911	1	18,21,22	0.99	1 (5%)	22,30,33	1.89	4 (18%)
2	4OC	2	1402	2	20,23,24	2.91	8 (40%)	26,32,35	0.91	0
1	2MG	1	2445	1	23,26,27	2.60	8 (34%)	32,38,41	1.95	9 (28%)
1	1MG	1	745	1	22,26,27	2.81	7 (31%)	33,39,42	2.08	7 (21%)
1	5MC	1	1962	1	18,22,23	3.31	7 (38%)	26,32,35	1.07	2 (7%)
1	5MU	1	747	1	19,22,23	4.60	7 (36%)	28,32,35	3.68	9 (32%)
1	6MZ	1	1618	1	22,25,26	2.37	6 (27%)	30,36,39	3.40	11 (36%)
55	FME	B	1	55	8,9,10	0.96	0	7,9,11	0.69	0
1	G7M	1	2069	1	23,26,27	2.63	9 (39%)	35,39,42	2.18	12 (34%)
54	OMG	z	17	54	27,27,27	3.47	9 (33%)	40,41,41	6.56	15 (37%)
1	PSU	1	2504	1	18,21,22	1.03	2 (11%)	22,30,33	1.81	4 (18%)
1	PSU	1	1917	1	18,21,22	1.02	2 (11%)	22,30,33	1.99	5 (22%)
1	3TD	1	1915	1	18,22,23	4.06	7 (38%)	22,32,35	1.56	2 (9%)

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
1	PSU	1	955	1,56	-	0/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	6MZ	1	2030	1	-	4/9/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	1	2251	1,54	-	0/9/27/28	0/3/3/3
1	5MU	1	1939	1,56	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	G7M	2	527	2	-	3/7/25/26	0/3/3/3
1	2MA	1	2503	1,56	-	2/7/25/26	0/3/3/3
1	PSU	1	746	1,56	-	1/7/25/26	0/2/2/2
2	PSU	2	516	56,2	-	2/7/25/26	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
44	0TD	p	89	44	-	2/7/12/14	-
54	5MU	z	66	54	-	4/7/25/26	0/2/2/2
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1,56	-	0/9/27/28	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1207	2	-	0/9/27/28	0/3/3/3
2	2MG	2	966	2	-	2/9/27/28	0/3/3/3
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
2	MA6	2	1519	2	-	2/11/29/30	0/3/3/3
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
55	FME	B	1	55	-	5/7/9/11	-
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
54	OMG	z	17	54	-	6/12/28/28	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	2/7/25/26	0/2/2/2

All (203) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	11.81	1.49	1.35
1	1	2503	2MA	C4-N3	11.06	1.48	1.34
54	z	66	5MU	C6-N1	10.76	1.56	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	747	5MU	C2-N1	10.70	1.55	1.38
1	1	1939	5MU	C2-N1	10.26	1.54	1.38
54	z	17	OMG	O6-C6	-10.18	1.04	1.23
1	1	1939	5MU	C6-N1	9.96	1.55	1.38
54	z	66	5MU	C4-C5	9.92	1.61	1.44
54	z	66	5MU	C2-N1	9.88	1.54	1.38
1	1	747	5MU	C6-N1	9.79	1.54	1.38
1	1	1939	5MU	C4-C5	9.16	1.60	1.44
1	1	2030	6MZ	C6-N6	9.09	1.44	1.34
1	1	1915	3TD	C2-N1	9.08	1.49	1.37
1	1	1618	6MZ	C6-N6	9.03	1.44	1.34
1	1	747	5MU	C4-C5	9.02	1.59	1.44
2	2	1407	5MC	C6-C5	8.68	1.48	1.34
2	2	967	5MC	C6-C5	8.52	1.48	1.34
54	z	17	OMG	C4-N3	8.52	1.54	1.34
1	1	745	1MG	C2-N2	8.14	1.49	1.34
1	1	1962	5MC	C6-C5	8.08	1.47	1.34
54	z	17	OMG	C2-N3	8.02	1.52	1.33
1	1	1939	5MU	C4-N3	-7.68	1.24	1.38
1	1	747	5MU	C4-N3	-7.67	1.24	1.38
2	2	966	2MG	C2-N3	7.47	1.46	1.31
54	z	66	5MU	C4-N3	-7.42	1.25	1.38
2	2	1207	2MG	C2-N3	7.33	1.45	1.31
1	1	1835	2MG	C2-N3	7.28	1.45	1.31
2	2	1516	2MG	C2-N3	6.99	1.45	1.31
1	1	2445	2MG	C2-N3	6.79	1.44	1.31
1	1	2069	G7M	C5-N7	-6.71	1.31	1.39
1	1	2552	OMU	C2-N1	6.52	1.48	1.38
2	2	1402	4OC	C4-N3	6.46	1.44	1.32
2	2	527	G7M	C5-N7	-6.37	1.31	1.39
1	1	1962	5MC	C4-N3	6.37	1.44	1.34
1	1	2552	OMU	C2-N3	6.34	1.49	1.38
2	2	1498	UR3	C6-C5	6.27	1.49	1.35
2	2	967	5MC	C4-N3	6.25	1.44	1.34
2	2	966	2MG	C4-N3	6.25	1.49	1.34
1	1	2503	2MA	C2-N3	6.17	1.45	1.34
2	2	1207	2MG	C4-N3	6.10	1.48	1.34
2	2	527	G7M	C4-N3	6.09	1.48	1.34
1	1	1835	2MG	C4-N3	6.04	1.48	1.34
2	2	967	5MC	C2-N3	5.89	1.48	1.36
1	1	2503	2MA	C6-N1	5.89	1.43	1.35
2	2	1516	2MG	C4-N3	5.88	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	z	66	5MU	C6-C5	5.86	1.44	1.34
1	1	1962	5MC	C2-N3	5.79	1.48	1.36
2	2	1407	5MC	C4-N3	5.77	1.43	1.34
2	2	1402	4OC	C6-C5	5.74	1.48	1.35
1	1	745	1MG	C4-N3	5.69	1.47	1.34
1	1	1915	3TD	C6-N1	5.65	1.45	1.36
2	2	1498	UR3	C2-N1	5.63	1.46	1.38
1	1	2445	2MG	C4-N3	5.59	1.47	1.34
1	1	1939	5MU	C6-C5	5.59	1.43	1.34
1	1	2251	OMG	C4-N3	5.58	1.47	1.34
1	1	747	5MU	C6-C5	5.56	1.43	1.34
2	2	1402	4OC	C2-N3	5.55	1.47	1.36
1	1	2498	OMC	C6-C5	5.54	1.47	1.35
1	1	2498	OMC	C2-N3	5.51	1.47	1.36
1	1	2069	G7M	C4-N3	5.45	1.47	1.34
54	z	17	OMG	C2-N1	5.43	1.51	1.37
1	1	2552	OMU	C6-C5	5.34	1.47	1.35
1	1	2503	2MA	C2-N1	5.32	1.43	1.34
2	2	527	G7M	C2-N3	5.25	1.45	1.33
2	2	1407	5MC	C2-N3	5.14	1.46	1.36
2	2	966	2MG	C2-N2	5.12	1.44	1.33
2	2	1207	2MG	C2-N2	5.07	1.44	1.33
2	2	1498	UR3	C2-N3	5.04	1.48	1.39
1	1	2251	OMG	C2-N3	4.97	1.45	1.33
1	1	745	1MG	C2-N3	4.88	1.43	1.34
1	1	1835	2MG	C2-N2	4.83	1.44	1.33
2	2	1516	2MG	C2-N2	4.80	1.44	1.33
1	1	2069	G7M	C2-N3	4.61	1.44	1.33
2	2	527	G7M	C2-N2	4.56	1.45	1.34
1	1	2445	2MG	C2-N2	4.56	1.43	1.33
1	1	1915	3TD	C2-N3	4.50	1.48	1.38
1	1	2498	OMC	C4-N3	4.47	1.43	1.34
2	2	1402	4OC	C4-N4	4.38	1.44	1.35
1	1	2498	OMC	C4-N4	4.37	1.44	1.33
2	2	1207	2MG	C2-N1	4.28	1.43	1.36
2	2	967	5MC	C6-N1	4.25	1.45	1.38
1	1	2503	2MA	C5-C6	4.25	1.52	1.41
2	2	967	5MC	C4-N4	4.18	1.45	1.34
1	1	1962	5MC	C4-N4	4.14	1.44	1.34
2	2	966	2MG	C2-N1	4.10	1.43	1.36
2	2	1516	2MG	C2-N1	4.05	1.43	1.36
1	1	2069	G7M	C2-N2	4.04	1.43	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1407	5MC	C4-N4	4.03	1.44	1.34
1	1	745	1MG	C5-N7	-4.01	1.31	1.39
2	2	967	5MC	C2-N1	3.99	1.48	1.40
1	1	1835	2MG	C2-N1	3.95	1.43	1.36
1	1	2445	2MG	C2-N1	3.92	1.43	1.36
2	2	1407	5MC	C6-N1	3.91	1.44	1.38
1	1	1962	5MC	C2-N1	3.91	1.48	1.40
1	1	2552	OMU	C4-N3	3.85	1.45	1.38
1	1	1962	5MC	C6-N1	3.84	1.44	1.38
1	1	2503	2MA	C6-N6	-3.78	1.24	1.34
1	1	745	1MG	O6-C6	-3.77	1.15	1.23
54	z	17	OMG	C2-N2	3.68	1.43	1.34
2	2	1402	4OC	C2-N1	3.67	1.48	1.40
1	1	2498	OMC	C2-N1	3.64	1.47	1.40
2	2	1519	MA6	C5-C4	-3.55	1.32	1.39
1	1	2445	2MG	C5-N7	-3.52	1.32	1.39
1	1	1835	2MG	C5-N7	-3.43	1.32	1.39
2	2	1402	4OC	C5-C4	3.40	1.48	1.40
2	2	1518	MA6	C5-C4	-3.35	1.32	1.39
1	1	747	5MU	O4-C4	-3.34	1.17	1.23
2	2	1407	5MC	C2-N1	3.33	1.47	1.40
2	2	1207	2MG	C5-N7	-3.29	1.32	1.39
54	z	66	5MU	O2-C2	-3.28	1.17	1.23
1	1	2251	OMG	C5-N7	-3.28	1.32	1.39
54	z	17	OMG	C6-N1	3.27	1.44	1.38
2	2	1516	2MG	C5-N7	-3.19	1.32	1.39
1	1	2030	6MZ	C5-N7	-3.19	1.33	1.39
2	2	966	2MG	C5-N7	-3.19	1.32	1.39
1	1	2030	6MZ	C5-C4	-3.17	1.33	1.39
1	1	2069	G7M	C5-C6	3.16	1.52	1.43
1	1	2251	OMG	C2-N2	3.14	1.41	1.34
2	2	527	G7M	C5-C6	3.14	1.52	1.43
1	1	1618	6MZ	C5-C4	-3.14	1.33	1.39
1	1	1939	5MU	O4-C4	-3.13	1.17	1.23
1	1	2503	2MA	C4-N9	-3.09	1.30	1.37
54	z	17	OMG	C5-N7	-3.06	1.33	1.39
1	1	1618	6MZ	C5-N7	-3.06	1.33	1.39
2	2	1518	MA6	C6-N6	3.02	1.45	1.36
2	2	1519	MA6	C6-N6	3.00	1.45	1.36
2	2	1402	4OC	O2-C2	-3.00	1.18	1.23
1	1	2498	OMC	O2-C2	-3.00	1.18	1.23
54	z	66	5MU	O4-C4	-2.99	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1962	5MC	O2-C2	-2.99	1.18	1.23
2	2	1407	5MC	O2-C2	-2.98	1.18	1.23
1	1	2251	OMG	O6-C6	-2.97	1.17	1.23
1	1	2552	OMU	O4-C4	-2.96	1.18	1.24
2	2	967	5MC	O2-C2	-2.86	1.18	1.23
1	1	2069	G7M	O6-C6	-2.85	1.18	1.23
1	1	2503	2MA	C5-N7	-2.84	1.33	1.39
1	1	745	1MG	C5-C6	2.81	1.52	1.45
1	1	1835	2MG	O6-C6	-2.77	1.18	1.23
1	1	2069	G7M	C4-N9	-2.72	1.31	1.38
2	2	1402	4OC	C6-N1	2.72	1.44	1.38
1	1	2445	2MG	O6-C6	-2.72	1.18	1.23
54	z	17	OMG	C5-C6	2.70	1.54	1.44
2	2	527	G7M	O6-C6	-2.69	1.18	1.23
1	1	745	1MG	C4-N9	-2.69	1.31	1.38
2	2	1498	UR3	C6-N1	2.68	1.44	1.38
1	1	1939	5MU	O2-C2	-2.68	1.18	1.23
2	2	1518	MA6	C5-N7	-2.67	1.34	1.39
1	1	2251	OMG	C4-N9	-2.66	1.31	1.38
2	2	1518	MA6	C8-N9	-2.62	1.32	1.37
1	1	2030	6MZ	C8-N9	-2.61	1.32	1.37
2	2	966	2MG	O6-C6	-2.59	1.18	1.23
2	2	1207	2MG	O6-C6	-2.59	1.18	1.23
1	1	746	PSU	C6-C5	2.58	1.38	1.35
1	1	1917	PSU	C6-C5	2.58	1.38	1.35
1	1	2504	PSU	C6-C5	2.57	1.38	1.35
1	1	2030	6MZ	C6-N1	-2.57	1.30	1.35
2	2	1519	MA6	C8-N9	-2.57	1.32	1.37
1	1	2552	OMU	O2-C2	-2.55	1.18	1.23
1	1	1915	3TD	O2-C2	-2.54	1.18	1.23
2	2	1516	2MG	O6-C6	-2.54	1.18	1.23
1	1	2445	2MG	C4-N9	-2.54	1.31	1.38
1	1	747	5MU	O2-C2	-2.53	1.18	1.23
1	1	1618	6MZ	C6-N1	-2.53	1.31	1.35
2	2	1519	MA6	C5-N7	-2.52	1.34	1.39
1	1	1911	PSU	C6-C5	2.51	1.38	1.35
2	2	1516	2MG	C4-N9	-2.50	1.31	1.38
1	1	1618	6MZ	C8-N9	-2.46	1.33	1.37
2	2	527	G7M	C2-N1	2.46	1.43	1.37
54	z	17	OMG	C4-N9	-2.45	1.31	1.38
1	1	1915	3TD	O4-C4	-2.43	1.18	1.23
2	2	516	PSU	C6-C5	2.43	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2498	OMC	C6-N1	2.40	1.43	1.38
2	2	1516	2MG	C5-C6	2.38	1.53	1.44
1	1	2069	G7M	C2-N1	2.38	1.43	1.37
2	2	1498	UR3	C3U-N3	-2.37	1.42	1.47
1	1	2069	G7M	CN7-N7	-2.34	1.42	1.46
2	2	1207	2MG	C5-C6	2.33	1.53	1.44
2	2	966	2MG	C5-C6	2.32	1.53	1.44
1	1	2552	OMU	C6-N1	2.29	1.43	1.38
1	1	2457	PSU	C6-C5	2.22	1.37	1.35
1	1	955	PSU	C4-C5	-2.22	1.37	1.44
1	1	1835	2MG	C5-C6	2.22	1.52	1.44
1	1	2605	PSU	C6-C5	2.21	1.37	1.35
2	2	1207	2MG	C4-N9	-2.18	1.32	1.38
1	1	1915	3TD	C4-N3	2.17	1.45	1.40
1	1	2552	OMU	C5-C4	2.16	1.48	1.43
1	1	2504	PSU	C4-C5	-2.13	1.38	1.44
2	2	527	G7M	C4-N9	-2.13	1.32	1.38
2	2	1498	UR3	O2-C2	-2.13	1.18	1.22
1	1	2580	PSU	C4-C5	-2.12	1.38	1.44
1	1	2605	PSU	C4-C5	-2.11	1.38	1.44
1	1	2457	PSU	C4-C5	-2.11	1.38	1.44
1	1	2503	2MA	C5-C4	-2.10	1.35	1.39
2	2	966	2MG	C4-N9	-2.10	1.32	1.38
2	2	966	2MG	C6-N1	2.10	1.42	1.38
44	p	89	0TD	CSB-SB	-2.09	1.75	1.79
1	1	2445	2MG	C5-C6	2.08	1.52	1.44
1	1	2251	OMG	C5-C6	2.06	1.52	1.44
1	1	1835	2MG	C4-N9	-2.05	1.32	1.38
1	1	1917	PSU	C4-C5	-2.05	1.38	1.44
2	2	516	PSU	C4-C5	-2.05	1.38	1.44
1	1	2030	6MZ	C5-C6	-2.04	1.36	1.41
1	1	1618	6MZ	C5-C6	-2.01	1.36	1.41

All (229) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	17	OMG	O6-C6-N1	-29.89	62.83	120.12
54	z	17	OMG	O6-C6-C5	-23.73	63.64	126.60
2	2	1519	MA6	N1-C6-N6	-14.09	101.67	117.08
2	2	1518	MA6	N1-C6-N6	-13.31	102.53	117.08
1	1	747	5MU	C5-C4-N3	12.34	125.85	115.31
1	1	1939	5MU	C5-C4-N3	12.12	125.66	115.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	z	66	5MU	C5-C4-N3	11.97	125.53	115.31
54	z	66	5MU	C5-C6-N1	-9.90	113.16	123.34
1	1	1939	5MU	C5-C6-N1	-9.89	113.17	123.34
1	1	747	5MU	C5-C6-N1	-9.62	113.44	123.34
1	1	1618	6MZ	C4-N9-C1'	-8.95	105.27	126.59
1	1	2030	6MZ	C1'-N9-C8	8.92	147.26	127.14
1	1	1618	6MZ	C1'-N9-C8	8.90	147.24	127.14
1	1	2030	6MZ	C4-N9-C1'	-8.81	105.60	126.59
2	2	1519	MA6	C5-C6-N6	6.94	137.38	125.30
1	1	2030	6MZ	C5-C4-N3	-6.63	118.09	126.75
2	2	1518	MA6	C5-C6-N6	6.50	136.62	125.30
1	1	1618	6MZ	C5-C4-N3	-6.37	118.44	126.75
1	1	745	1MG	C1'-N9-C4	-6.32	107.72	126.50
54	z	17	OMG	OP3-P-OP1	-6.22	86.33	110.68
1	1	2503	2MA	C1'-N9-C8	-6.07	113.42	127.14
2	2	966	2MG	C2-N3-C4	5.90	119.36	112.04
1	1	747	5MU	O4-C4-C5	-5.89	118.07	124.90
1	1	1835	2MG	C2-N3-C4	5.87	119.31	112.04
1	1	745	1MG	C1'-N9-C8	5.85	143.36	126.70
54	z	66	5MU	C5M-C5-C4	5.80	125.15	118.77
2	2	1207	2MG	C2-N3-C4	5.77	119.19	112.04
2	2	1516	2MG	C2-N3-C4	5.76	119.18	112.04
54	z	17	OMG	OP3-P-O5'	-5.69	91.60	106.73
54	z	66	5MU	C5M-C5-C6	-5.65	115.31	122.85
2	2	527	G7M	CN7-N7-C5	5.64	133.78	126.77
1	1	2503	2MA	N9-C8-N7	-5.55	106.33	113.91
54	z	17	OMG	C2-N1-C6	-5.54	115.00	125.10
54	z	66	5MU	C4-N3-C2	-5.50	120.23	127.35
2	2	1519	MA6	N1-C2-N3	-5.47	120.04	128.60
1	1	1939	5MU	O4-C4-C5	-5.46	118.57	124.90
54	z	66	5MU	N3-C2-N1	5.43	122.10	114.89
1	1	2457	PSU	C4-N3-C2	-5.39	118.57	126.34
1	1	2030	6MZ	N1-C2-N3	-5.37	120.21	128.60
1	1	747	5MU	C4-N3-C2	-5.34	120.43	127.35
1	1	2445	2MG	C2-N3-C4	5.34	118.66	112.04
2	2	1518	MA6	N1-C2-N3	-5.30	120.30	128.60
1	1	1835	2MG	C5-C4-N3	-5.28	119.89	128.46
1	1	1618	6MZ	N1-C2-N3	-5.28	120.35	128.60
1	1	2069	G7M	CN7-N7-C5	5.26	133.30	126.77
54	z	17	OMG	C5-C6-N1	5.23	126.46	113.19
54	z	17	OMG	OP2-P-OP1	5.19	131.01	110.68
1	1	2605	PSU	C4-N3-C2	-5.17	118.89	126.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1939	5MU	C4-N3-C2	-5.16	120.68	127.35
54	z	17	OMG	OP3-P-OP2	-5.12	88.06	107.64
2	2	1518	MA6	C5-C4-N3	-5.09	120.10	126.75
1	1	2580	PSU	C4-N3-C2	-5.08	119.02	126.34
2	2	966	2MG	C5-C4-N3	-5.07	120.23	128.46
1	1	1917	PSU	C4-N3-C2	-5.04	119.08	126.34
1	1	955	PSU	C4-N3-C2	-5.04	119.08	126.34
1	1	2552	OMU	C4-N3-C2	-5.01	119.97	126.58
1	1	2457	PSU	N1-C2-N3	4.98	120.78	115.13
1	1	2580	PSU	N1-C2-N3	4.97	120.76	115.13
1	1	1911	PSU	C4-N3-C2	-4.97	119.18	126.34
1	1	1917	PSU	N1-C2-N3	4.94	120.72	115.13
2	2	1207	2MG	C5-C4-N3	-4.93	120.46	128.46
54	z	66	5MU	O2-C2-N1	-4.90	116.27	122.79
1	1	1618	6MZ	C9-N6-C6	-4.90	118.66	122.87
2	2	1519	MA6	C5-C4-N3	-4.87	120.39	126.75
1	1	2069	G7M	CN7-N7-C8	-4.85	117.35	124.84
2	2	516	PSU	C4-N3-C2	-4.83	119.38	126.34
1	1	2504	PSU	C4-N3-C2	-4.80	119.42	126.34
1	1	1911	PSU	N1-C2-N3	4.79	120.56	115.13
1	1	1915	3TD	N1-C2-N3	4.78	119.91	116.14
1	1	746	PSU	C4-N3-C2	-4.78	119.45	126.34
2	2	1516	2MG	C5-C4-N3	-4.77	120.72	128.46
2	2	527	G7M	CN7-N7-C8	-4.73	117.53	124.84
54	z	66	5MU	O4-C4-C5	-4.67	119.48	124.90
1	1	2445	2MG	C5-C4-N3	-4.66	120.90	128.46
1	1	955	PSU	N1-C2-N3	4.65	120.40	115.13
1	1	1939	5MU	N3-C2-N1	4.61	121.00	114.89
1	1	745	1MG	C5-C4-N3	-4.54	121.09	128.46
1	1	2251	OMG	C5-C4-N3	-4.51	121.14	128.46
2	2	1519	MA6	N9-C8-N7	-4.47	107.80	113.91
1	1	747	5MU	N3-C2-N1	4.46	120.81	114.89
1	1	2605	PSU	N1-C2-N3	4.46	120.18	115.13
1	1	2504	PSU	N1-C2-N3	4.43	120.15	115.13
1	1	2030	6MZ	N3-C4-N9	4.33	134.22	127.08
2	2	1518	MA6	N9-C8-N7	-4.33	107.99	113.91
2	2	1516	2MG	C2-N1-C6	-4.33	119.50	124.48
1	1	2503	2MA	C5-C4-N3	-4.32	122.33	127.19
2	2	516	PSU	N1-C2-N3	4.29	119.99	115.13
1	1	1835	2MG	C2-N1-C6	-4.28	119.55	124.48
1	1	2503	2MA	C4-N9-C8	4.26	110.35	105.73
2	2	966	2MG	C2-N1-C6	-4.25	119.59	124.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2445	2MG	C2-N1-C6	-4.23	119.61	124.48
2	2	527	G7M	C1'-N9-C8	-4.23	112.47	126.74
1	1	746	PSU	N1-C2-N3	4.20	119.89	115.13
1	1	1618	6MZ	N3-C4-N9	4.19	133.98	127.08
2	2	1207	2MG	C2-N1-C6	-4.12	119.74	124.48
1	1	2030	6MZ	C2-N3-C4	4.11	121.46	111.75
2	2	1407	5MC	C5-C6-N1	-4.07	119.15	123.34
2	2	527	G7M	C1'-N9-C4	4.06	138.56	126.50
1	1	2503	2MA	C4-N9-C1'	4.04	136.22	126.59
2	2	527	G7M	C5-C4-N3	-4.01	120.45	128.15
1	1	1939	5MU	C5M-C5-C6	-3.95	117.58	122.85
1	1	1618	6MZ	C2-N3-C4	3.92	121.02	111.75
1	1	1618	6MZ	C4-C5-C6	3.90	119.83	116.81
2	2	527	G7M	C2-N3-C4	3.86	119.18	112.30
1	1	1915	3TD	C4-N3-C2	-3.83	120.45	124.61
1	1	2030	6MZ	C4-C5-C6	3.80	119.75	116.81
1	1	2030	6MZ	C9-N6-C6	-3.80	119.60	122.87
1	1	2069	G7M	C2-N3-C4	3.79	119.06	112.30
1	1	1939	5MU	C5M-C5-C4	3.74	122.88	118.77
2	2	1498	UR3	C4-N3-C2	-3.71	121.07	124.56
2	2	1518	MA6	N3-C4-N9	3.66	133.12	127.08
1	1	1618	6MZ	C5-C6-N1	3.64	122.08	118.20
1	1	2030	6MZ	C5-C6-N1	3.62	122.05	118.20
1	1	2069	G7M	C5-C4-N3	-3.61	121.22	128.15
1	1	2552	OMU	N3-C2-N1	3.60	119.67	114.89
1	1	747	5MU	C5M-C5-C6	-3.60	118.04	122.85
44	p	89	0TD	OD2-CG-CB	3.59	120.90	113.15
1	1	1618	6MZ	N9-C8-N7	-3.57	109.03	113.91
1	1	2251	OMG	C2-N3-C4	3.54	118.61	112.30
1	1	2069	G7M	C5-C6-N1	3.53	119.16	111.79
2	2	527	G7M	C5-C6-N1	3.52	119.15	111.79
2	2	527	G7M	O6-C6-C5	-3.52	120.11	128.06
2	2	1519	MA6	C2-N3-C4	3.50	120.01	111.75
1	1	2069	G7M	O6-C6-C5	-3.49	120.19	128.06
1	1	1835	2MG	N9-C4-N3	3.41	132.79	125.94
2	2	1518	MA6	C4-C5-C6	3.40	119.69	115.88
1	1	2030	6MZ	N9-C8-N7	-3.37	109.30	113.91
2	2	1518	MA6	C2-N3-C4	3.35	119.67	111.75
1	1	2069	G7M	C1'-N9-C8	-3.34	115.47	126.74
2	2	1519	MA6	C2-N1-C6	3.24	119.41	111.75
2	2	1518	MA6	C2-N1-C6	3.24	119.39	111.75
2	2	527	G7M	N9-C4-N3	3.22	132.41	125.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	955	PSU	C6-C5-C4	3.22	120.45	118.20
1	1	747	5MU	C5M-C5-C4	3.21	122.30	118.77
2	2	966	2MG	N9-C4-N3	3.19	132.35	125.94
54	z	17	OMG	C6-C5-N7	3.17	136.13	130.25
1	1	2580	PSU	O2-C2-N1	-3.16	119.31	122.79
1	1	2069	G7M	C2-N1-C6	-3.08	119.48	125.10
1	1	2503	2MA	CM2-C2-N1	3.08	121.96	117.15
54	z	17	OMG	O5'-P-OP1	3.08	115.11	106.47
1	1	2503	2MA	C5-N7-C8	3.07	107.87	103.51
1	1	1917	PSU	O2-C2-N1	-3.05	119.43	122.79
1	1	2251	OMG	C2-N1-C6	-3.05	119.54	125.10
2	2	1207	2MG	N9-C4-N3	3.03	132.02	125.94
1	1	2251	OMG	N9-C8-N7	-3.01	107.72	113.39
1	1	2552	OMU	C5-C4-N3	3.01	119.35	114.84
1	1	2069	G7M	C1'-N9-C4	3.00	135.41	126.50
1	1	745	1MG	N9-C4-N3	2.99	131.94	125.94
2	2	1518	MA6	C4-N9-C8	2.98	108.96	105.73
2	2	1519	MA6	C4-C5-C6	2.97	119.21	115.88
1	1	745	1MG	C2-N3-C4	2.95	118.62	111.98
2	2	1519	MA6	N3-C4-N9	2.95	131.95	127.08
1	1	747	5MU	O2-C2-N1	-2.94	118.88	122.79
1	1	1939	5MU	O2-C2-N1	-2.90	118.94	122.79
1	1	2503	2MA	N3-C2-N1	-2.88	120.43	125.72
1	1	1911	PSU	O2-C2-N1	-2.87	119.63	122.79
1	1	746	PSU	O2-C2-N1	-2.87	119.63	122.79
1	1	2457	PSU	O2-C2-N1	-2.86	119.64	122.79
2	2	967	5MC	C5-C6-N1	-2.86	120.40	123.34
2	2	1516	2MG	N9-C8-N7	-2.86	108.01	113.39
54	z	17	OMG	C5-C4-N3	-2.85	123.84	128.46
1	1	745	1MG	N9-C8-N7	-2.82	108.08	113.39
1	1	1962	5MC	C5-C6-N1	-2.79	120.47	123.34
1	1	2552	OMU	O4-C4-C5	-2.77	120.29	125.16
2	2	966	2MG	N9-C8-N7	-2.76	108.19	113.39
1	1	1917	PSU	C6-C5-C4	2.75	120.12	118.20
2	2	1519	MA6	C4-N9-C8	2.72	108.68	105.73
1	1	2445	2MG	N9-C8-N7	-2.72	108.27	113.39
54	z	66	5MU	O4-C4-N3	-2.68	114.98	120.12
2	2	1516	2MG	C1'-N9-C4	-2.68	118.55	126.50
1	1	2605	PSU	C6-C5-C4	2.67	120.07	118.20
1	1	2605	PSU	O2-C2-N1	-2.67	119.85	122.79
2	2	527	G7M	C2-N1-C6	-2.67	120.23	125.10
1	1	2445	2MG	N9-C4-N3	2.66	131.28	125.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1519	MA6	C5-N7-C8	2.64	107.27	103.51
2	2	1207	2MG	N9-C8-N7	-2.64	108.43	113.39
1	1	2251	OMG	N9-C4-N3	2.63	131.22	125.94
1	1	2580	PSU	C6-C5-C4	2.63	120.04	118.20
2	2	1516	2MG	N9-C4-N3	2.63	131.21	125.94
54	z	17	OMG	OP2-P-O5'	2.61	113.67	106.73
1	1	1618	6MZ	C5-N7-C8	2.59	107.19	103.51
2	2	966	2MG	C5-C6-N1	2.59	119.77	113.19
2	2	516	PSU	O2-C2-N1	-2.59	119.94	122.79
1	1	2030	6MZ	C5-N7-C8	2.58	107.17	103.51
1	1	2504	PSU	O2-C2-N1	-2.56	119.97	122.79
1	1	1835	2MG	C5-C6-N1	2.54	119.63	113.19
2	2	966	2MG	O6-C6-C5	-2.53	119.88	126.60
2	2	1516	2MG	C5-C6-N1	2.50	119.55	113.19
1	1	2069	G7M	N2-C2-N1	2.50	122.03	116.71
1	1	2503	2MA	N3-C4-N9	2.48	130.44	126.99
1	1	955	PSU	O2-C2-N1	-2.48	120.06	122.79
54	z	17	OMG	N9-C8-N7	-2.48	108.72	113.39
2	2	1207	2MG	C5-C6-N1	2.48	119.48	113.19
1	1	1835	2MG	N9-C8-N7	-2.47	108.74	113.39
1	1	2445	2MG	O6-C6-C5	-2.45	120.10	126.60
2	2	1518	MA6	C5-N7-C8	2.45	106.99	103.51
1	1	2251	OMG	C5-C6-N1	2.44	119.39	113.19
1	1	2251	OMG	O6-C6-C5	-2.42	120.18	126.60
2	2	1207	2MG	O6-C6-C5	-2.41	120.20	126.60
1	1	2445	2MG	C5-C6-N1	2.37	119.22	113.19
1	1	2069	G7M	N9-C8-N7	-2.36	106.38	112.21
1	1	2580	PSU	C6-N1-C2	-2.35	120.28	122.68
1	1	1835	2MG	O6-C6-C5	-2.35	120.36	126.60
2	2	1516	2MG	O6-C6-C5	-2.33	120.42	126.60
2	2	967	5MC	CM5-C5-C6	-2.33	119.74	122.85
1	1	2504	PSU	C6-C5-C4	2.31	119.81	118.20
1	1	2069	G7M	N9-C4-N3	2.30	130.56	125.94
1	1	2580	PSU	O4'-C1'-C2'	2.30	108.38	105.14
1	1	1939	5MU	O4-C4-N3	-2.27	115.77	120.12
1	1	1917	PSU	C6-N1-C2	-2.27	120.37	122.68
1	1	1911	PSU	C6-N1-C2	-2.25	120.39	122.68
1	1	2457	PSU	O4'-C1'-C2'	2.24	108.31	105.14
2	2	1516	2MG	C1'-N9-C8	2.24	133.08	126.70
54	z	17	OMG	O2'-C2'-C1'	2.23	113.44	109.08
1	1	2445	2MG	C1'-N9-C4	-2.21	119.93	126.50
44	p	89	0TD	OD1-CG-CB	-2.20	117.84	122.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2445	2MG	CM2-N2-C2	-2.19	119.02	123.86
2	2	1516	2MG	CM2-N2-C2	-2.18	119.04	123.86
1	1	747	5MU	O4-C4-N3	-2.11	116.08	120.12
1	1	2457	PSU	C6-N1-C2	-2.10	120.54	122.68
2	2	516	PSU	O4'-C1'-C2'	2.09	108.09	105.14
1	1	745	1MG	C5-C6-N1	2.07	118.91	114.91
54	z	17	OMG	N9-C4-N3	2.07	130.09	125.94
2	2	966	2MG	N1-C2-N3	-2.07	120.76	123.95
2	2	966	2MG	CM2-N2-C2	-2.06	119.31	123.86
2	2	527	G7M	N9-C8-N7	-2.06	107.12	112.21
2	2	1207	2MG	N1-C2-N3	-2.04	120.79	123.95
1	1	1962	5MC	CM5-C5-C6	-2.03	120.14	122.85
2	2	516	PSU	C6-N1-C2	-2.03	120.61	122.68

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
55	B	1	FME	O1-CN-N-CA
55	B	1	FME	N-CA-CB-CG
55	B	1	FME	C-CA-CB-CG
55	B	1	FME	O-C-CA-CB
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1618	6MZ	O4'-C4'-C5'-O5'
1	1	1618	6MZ	C3'-C4'-C5'-O5'
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6
1	1	2030	6MZ	N1-C6-N6-C9
1	1	2445	2MG	C3'-C4'-C5'-O5'
1	1	2504	PSU	O4'-C4'-C5'-O5'
54	z	17	OMG	C1'-C2'-O2'-CM2
54	z	66	5MU	C2'-C1'-N1-C2
54	z	66	5MU	C2'-C1'-N1-C6
55	B	1	FME	CA-CB-CG-SD
2	2	1519	MA6	C3'-C4'-C5'-O5'
1	1	2030	6MZ	O4'-C4'-C5'-O5'
1	1	2030	6MZ	C3'-C4'-C5'-O5'
1	1	2504	PSU	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
2	2	527	G7M	O4'-C4'-C5'-O5'
2	2	1402	4OC	O4'-C4'-C5'-O5'
54	z	66	5MU	O4'-C1'-N1-C2
1	1	1835	2MG	C3'-C4'-C5'-O5'
1	1	1835	2MG	O4'-C4'-C5'-O5'
1	1	2445	2MG	O4'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C4'-C5'-O5'
2	2	966	2MG	C3'-C4'-C5'-O5'
54	z	66	5MU	O4'-C1'-N1-C6
54	z	17	OMG	C5'-O5'-P-OP1
2	2	966	2MG	O4'-C4'-C5'-O5'
2	2	1402	4OC	C3'-C4'-C5'-O5'
1	1	1618	6MZ	C5-C6-N6-C9
44	p	89	0TD	CG-CB-SB-CSB
2	2	527	G7M	C4'-C5'-O5'-P
44	p	89	0TD	SB-CB-CG-OD1
1	1	2552	OMU	C3'-C2'-O2'-CM2
1	1	2503	2MA	C3'-C4'-C5'-O5'
54	z	17	OMG	O4'-C1'-N9-C4
1	1	2030	6MZ	C5-C6-N6-C9
54	z	17	OMG	O4'-C1'-N9-C8
54	z	17	OMG	C5'-O5'-P-OP2
1	1	746	PSU	O4'-C1'-C5-C6
1	1	2069	G7M	O4'-C4'-C5'-O5'
54	z	17	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

19 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	955	PSU	1	0
1	1	2030	6MZ	2	0
2	2	1518	MA6	2	0
2	2	1498	UR3	1	0
2	2	1516	2MG	1	0
1	1	2503	2MA	1	0
2	2	516	PSU	2	0
44	p	89	0TD	1	0
54	z	66	5MU	2	0
1	1	2457	PSU	1	0
1	1	2580	PSU	2	0
2	2	966	2MG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	1519	MA6	2	0
1	1	2445	2MG	1	0
1	1	745	1MG	1	0
1	1	1962	5MC	1	0
55	B	1	FME	1	0
54	z	17	OMG	2	0
1	1	1915	3TD	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 415 ligands modelled in this entry, 415 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](#)

There are no chain breaks in this entry.

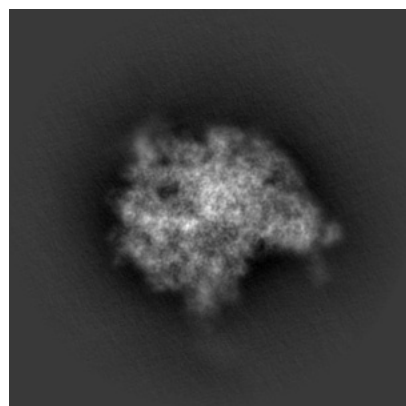
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-12636. These allow visual inspection of the internal detail of the map and identification of artifacts.

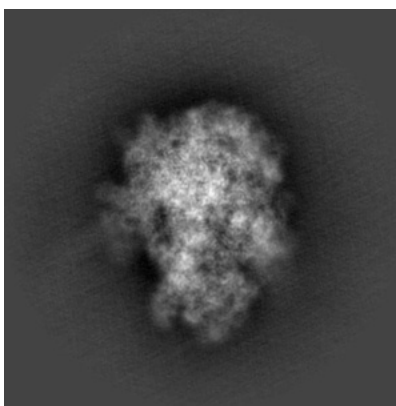
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

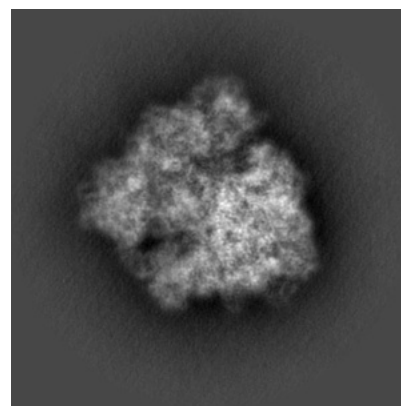
6.1.1 Primary map



X

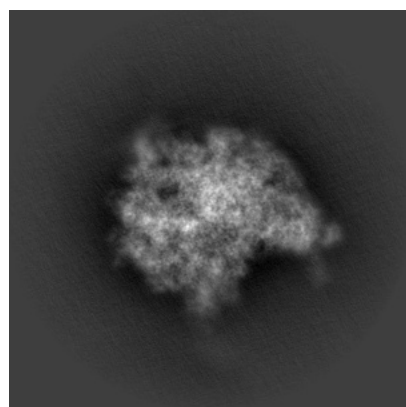


Y

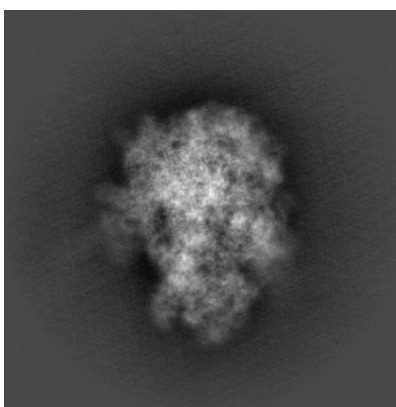


Z

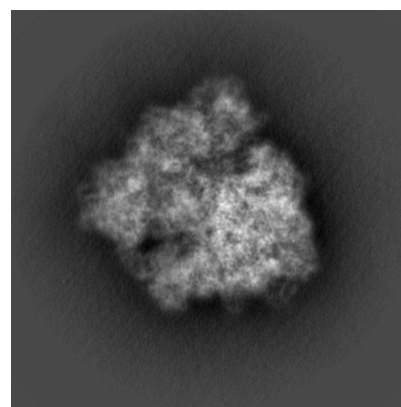
6.1.2 Raw map



X



Y

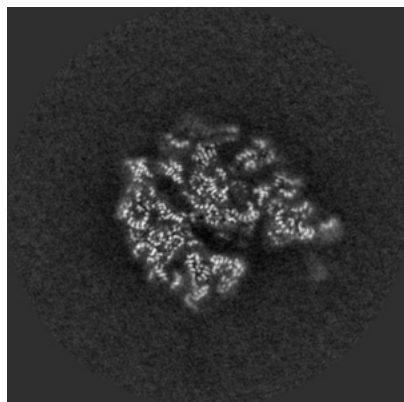


Z

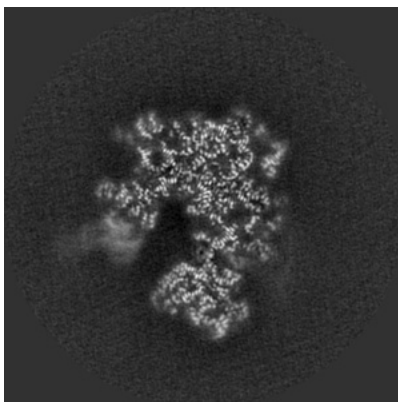
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

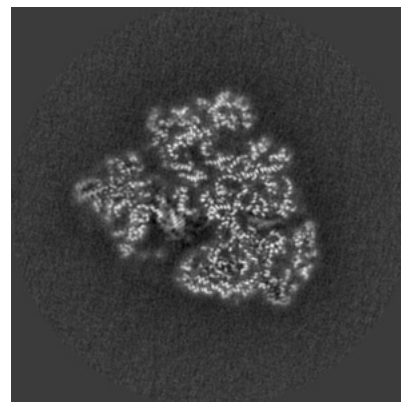
6.2.1 Primary map



X Index: 200

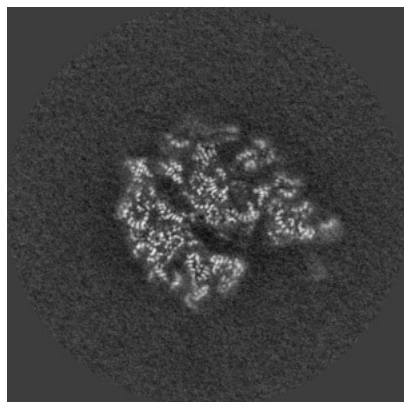


Y Index: 200

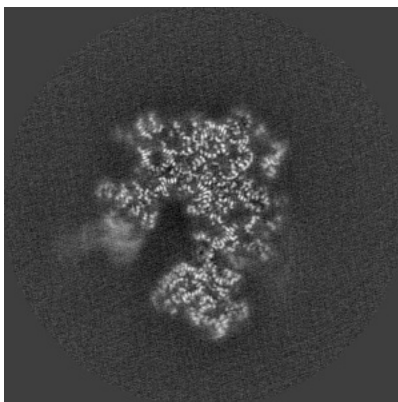


Z Index: 200

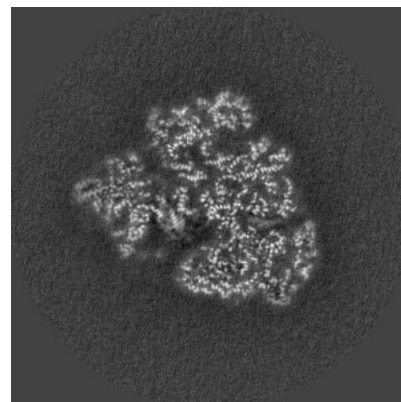
6.2.2 Raw map



X Index: 200



Y Index: 200

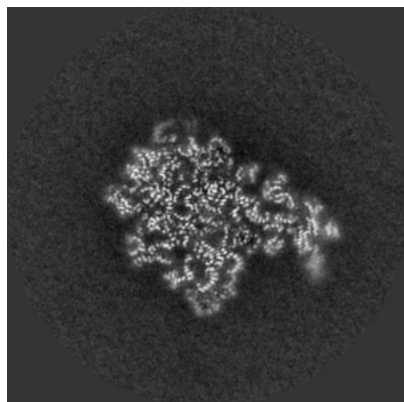


Z Index: 200

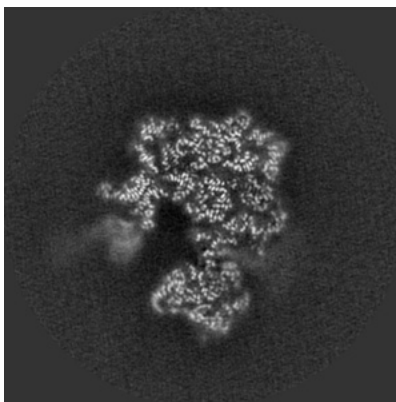
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

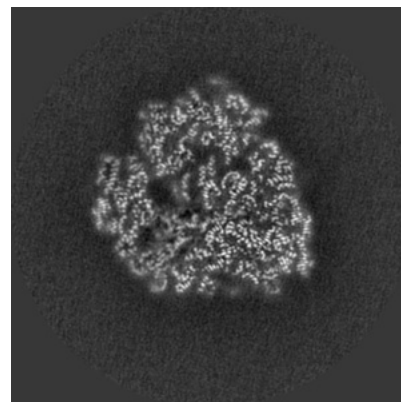
6.3.1 Primary map



X Index: 216

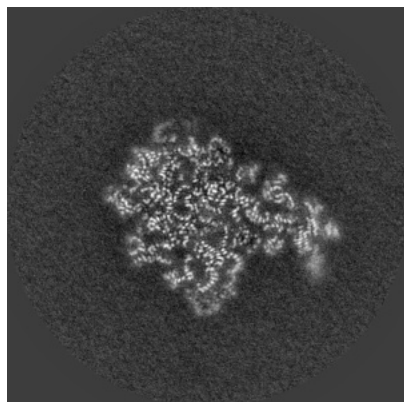


Y Index: 205

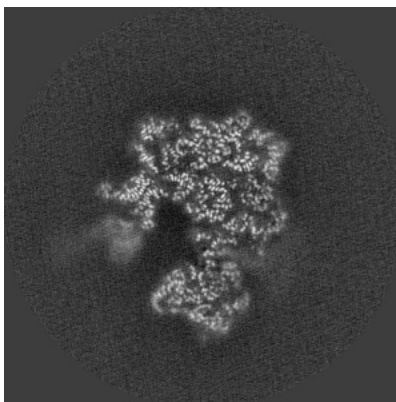


Z Index: 188

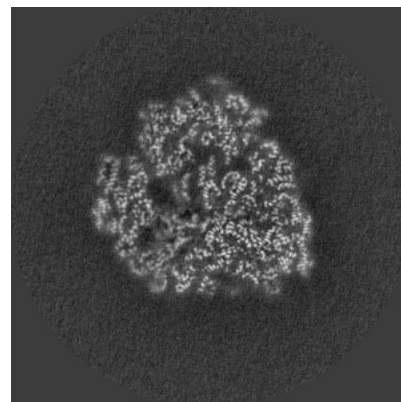
6.3.2 Raw map



X Index: 216



Y Index: 205

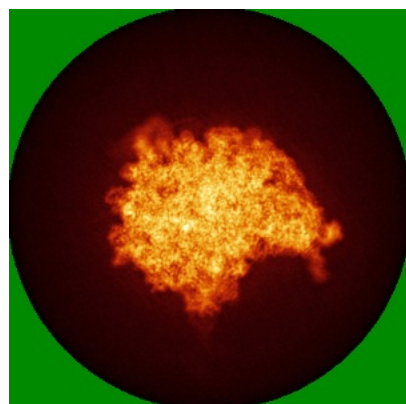


Z Index: 188

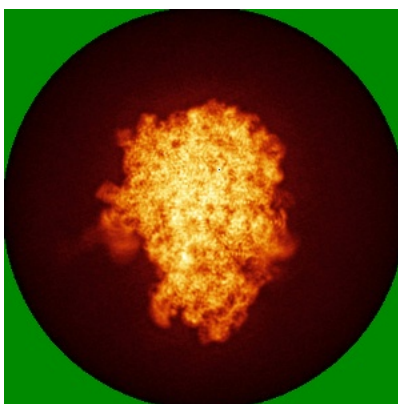
The images above show the largest variance slices of the map in three orthogonal directions.

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

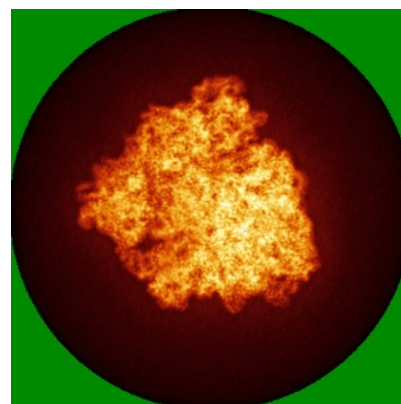
6.4.1 Primary map



X

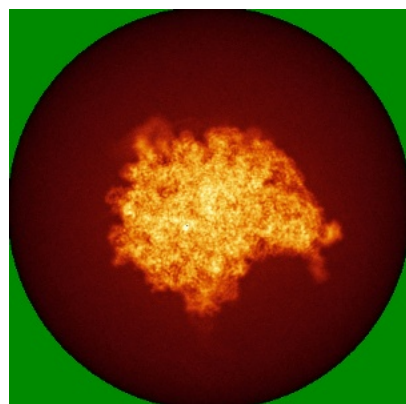


Y

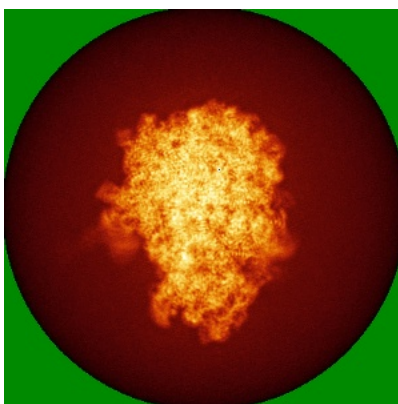


Z

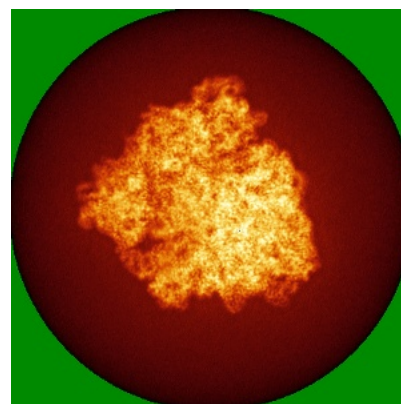
6.4.2 Raw map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. 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



X



Y



Z

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.

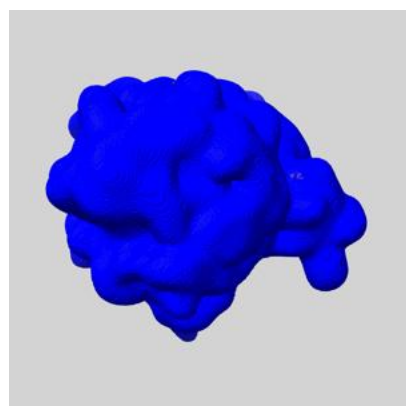
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

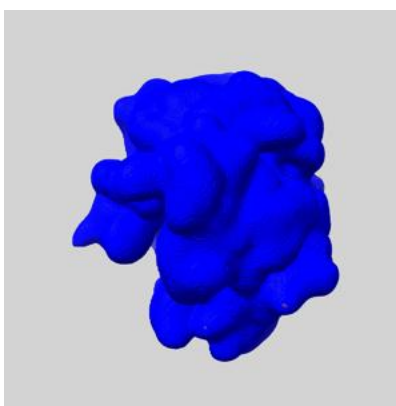
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

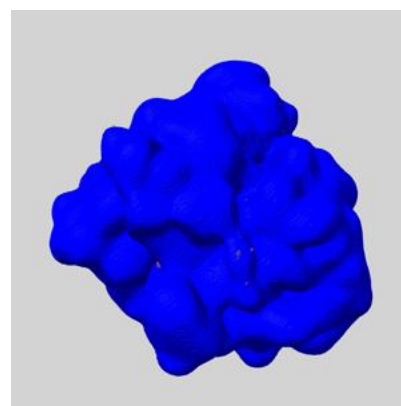
6.6.1 emd_12636_msk_1.map [i](#)



X



Y

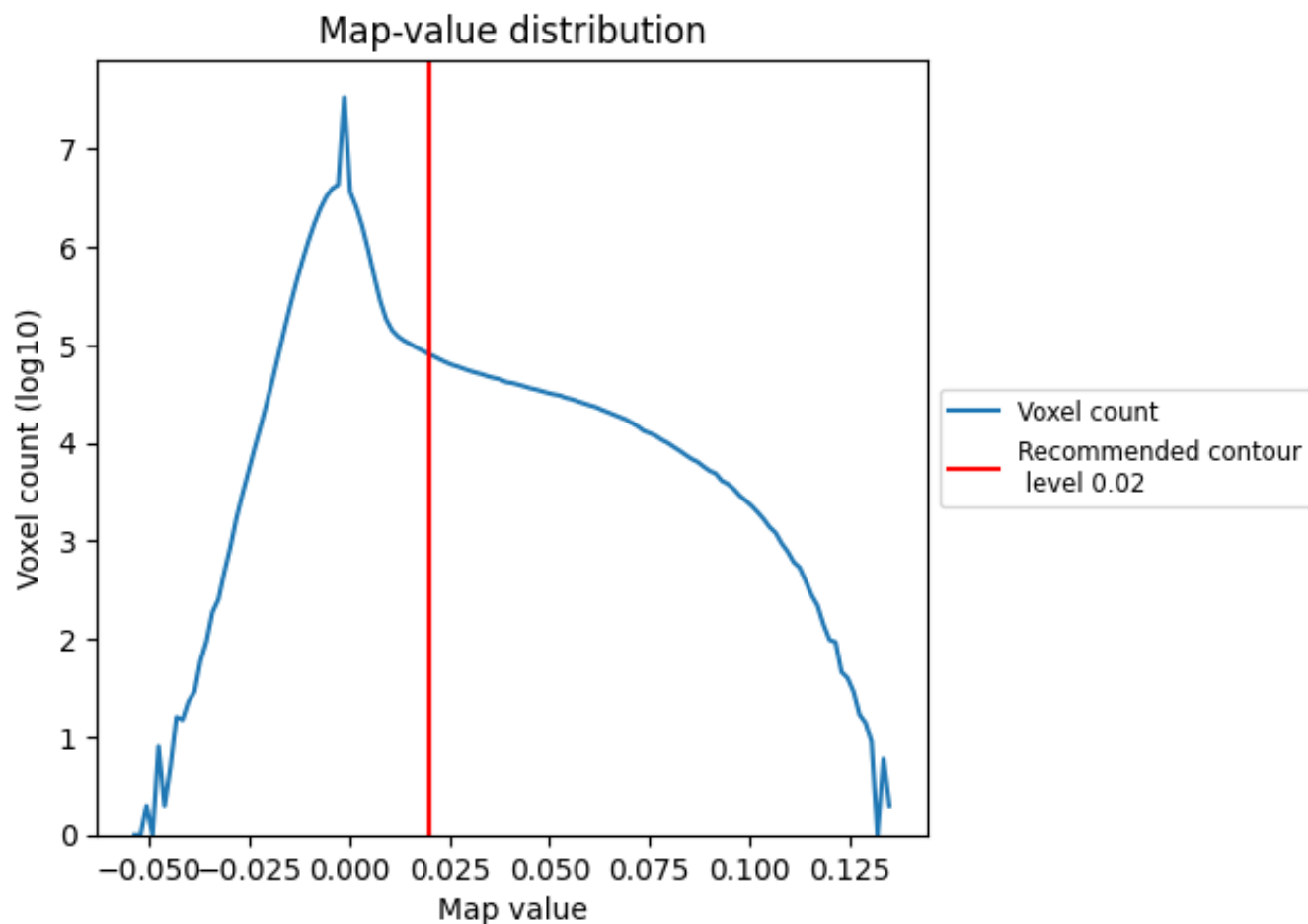


Z

7 Map analysis [i](#)

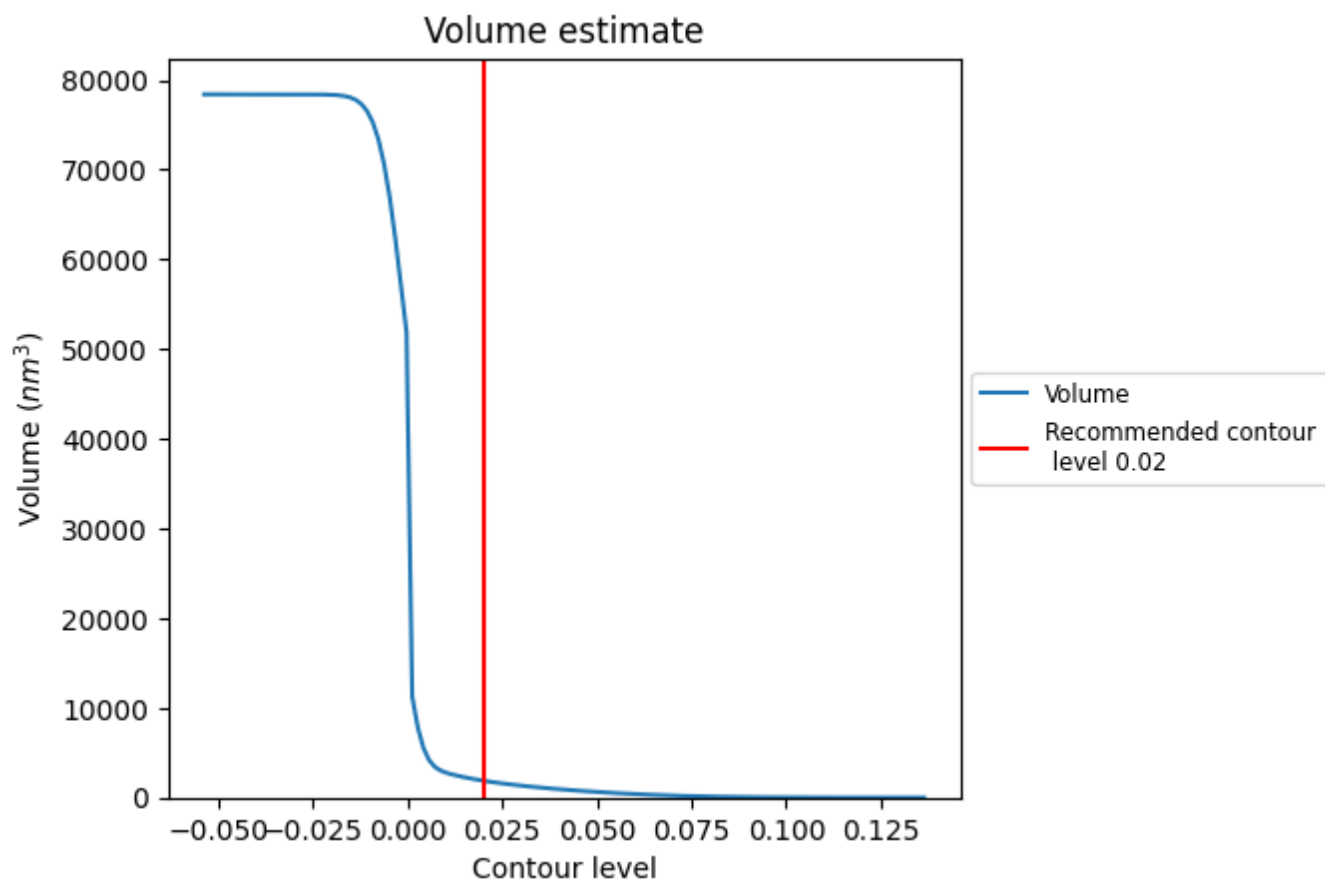
This section contains the results of statistical analysis of the map.

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.

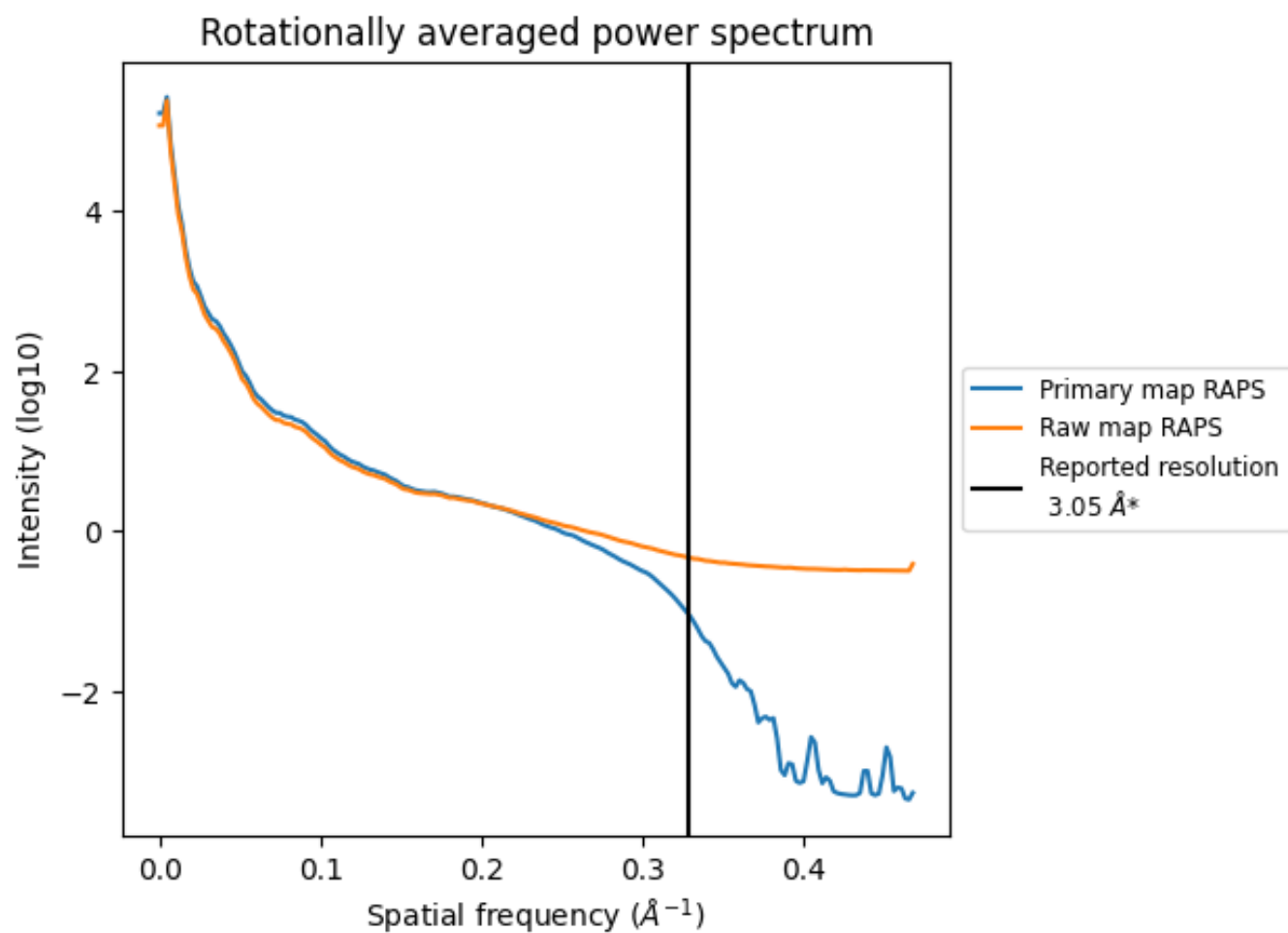
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1881 nm^3 ; this corresponds to an approximate mass of 1699 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 ⓘ

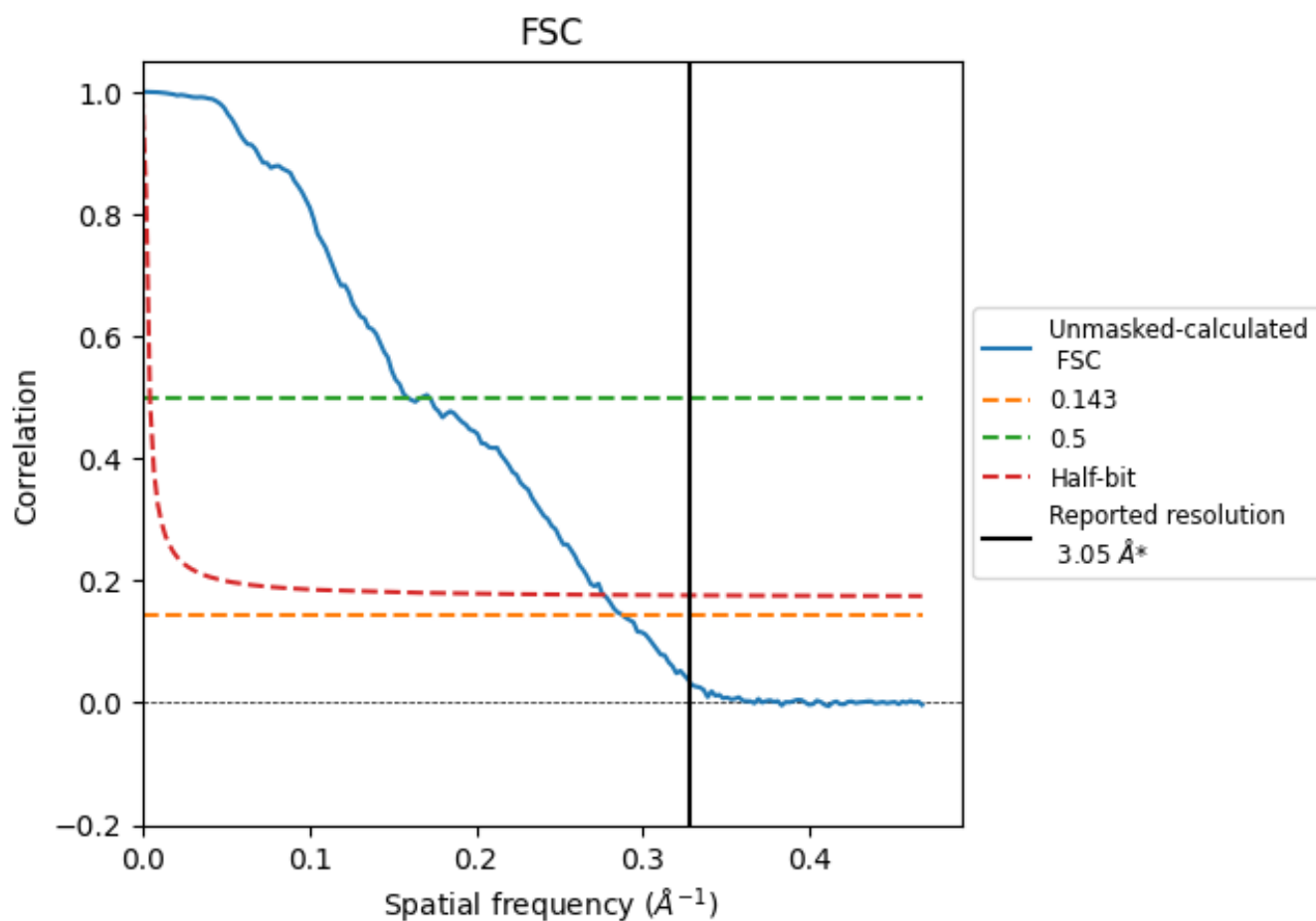


*Reported resolution corresponds to spatial frequency of 0.328 Å⁻¹

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 0.328 Å⁻¹

8.2 Resolution estimates [i](#)

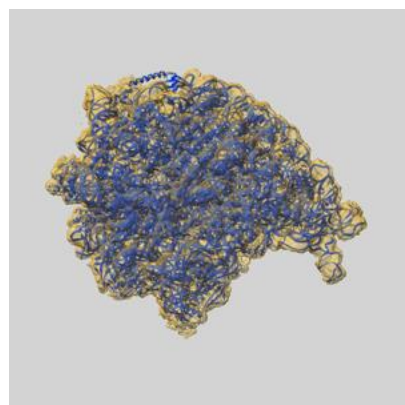
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.05	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.47	6.31	3.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.47 differs from the reported value 3.05 by more than 10 %

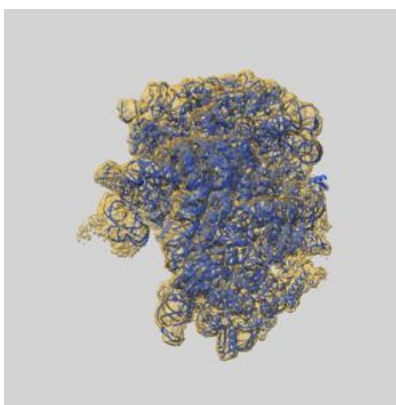
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-12636 and PDB model 7NWW. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

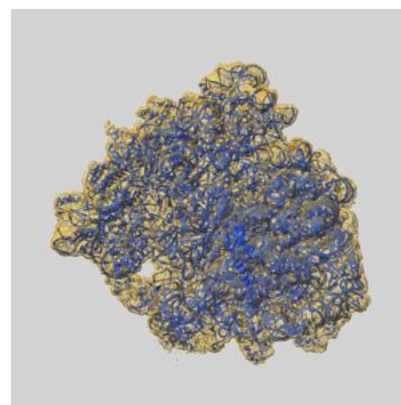
9.1 Map-model overlay [i](#)



X



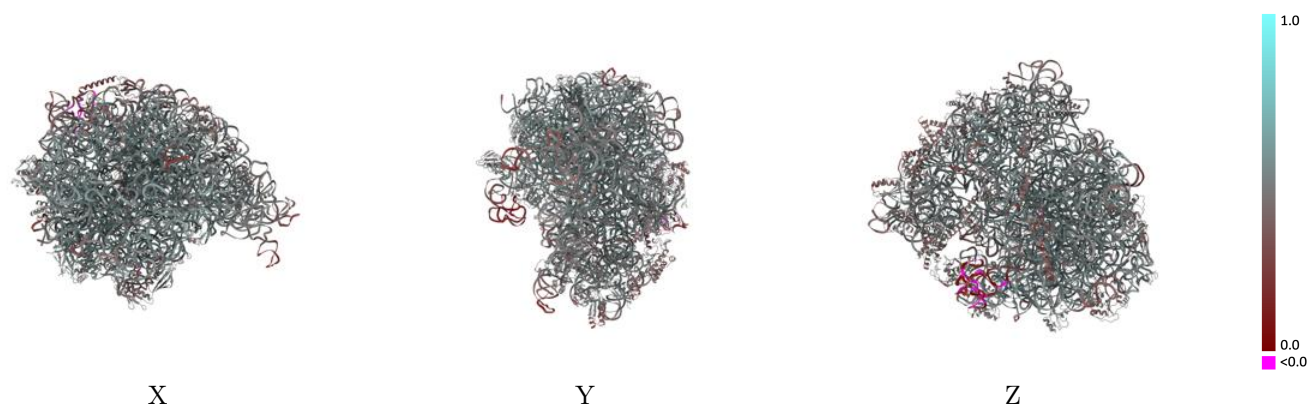
Y



Z

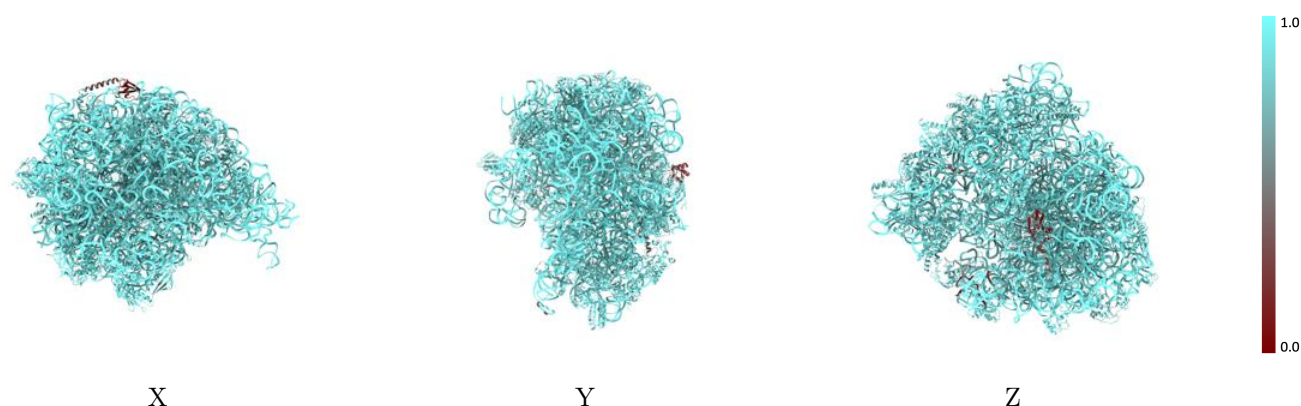
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



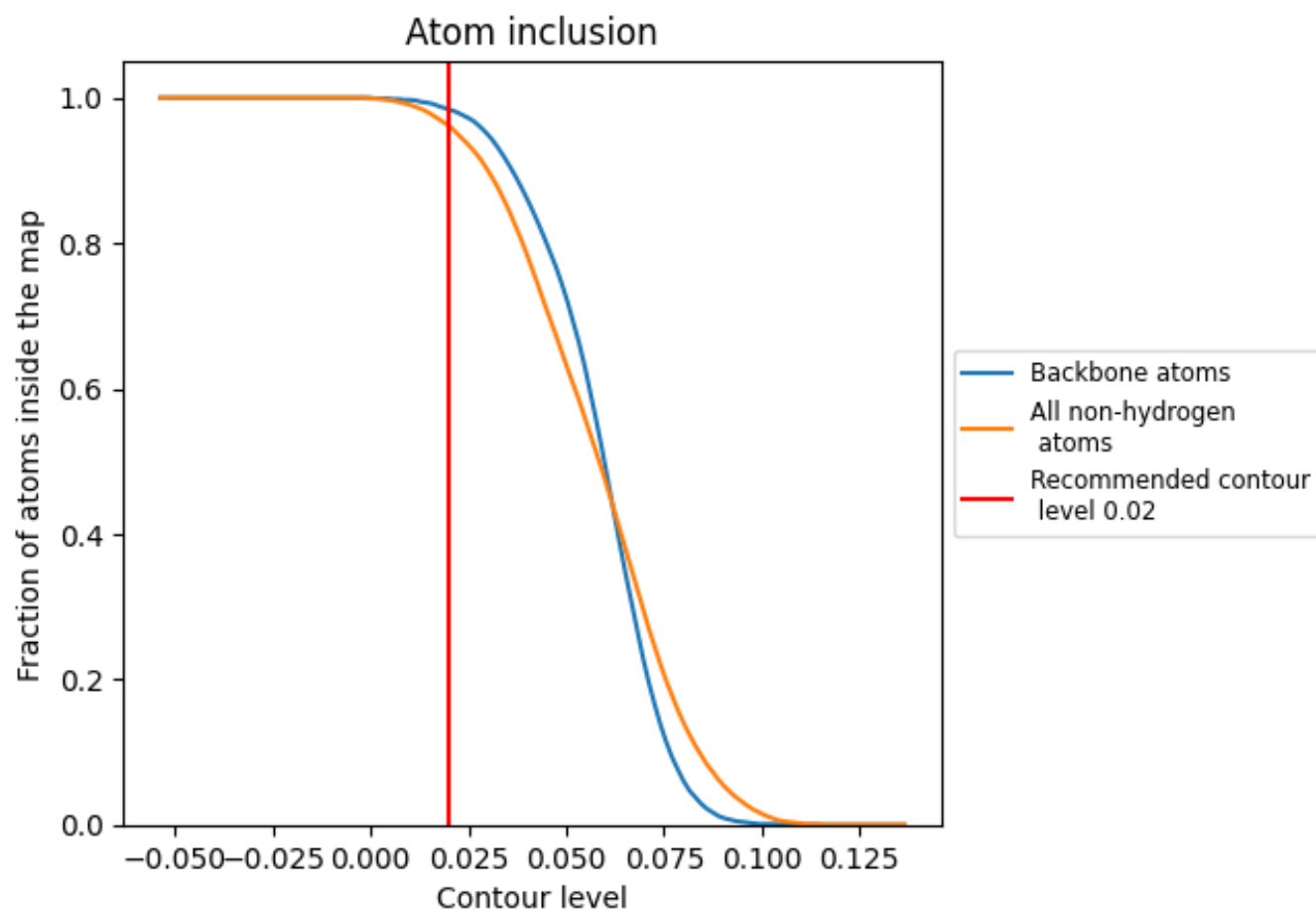
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.4960
1	 0.9870	 0.5060
2	 0.9950	 0.5000
3	 0.9970	 0.5020
4	 0.9760	 0.4690
B	 0.5780	 0.2920
C	 0.9170	 0.5390
D	 0.9280	 0.5320
E	 0.9100	 0.4950
F	 0.9060	 0.4440
G	 0.9250	 0.4540
H	 0.4140	 0.3480
I	 0.9240	 0.5180
J	 0.8690	 0.5220
K	 0.9320	 0.5170
L	 0.9080	 0.5180
M	 0.9540	 0.5300
N	 0.9440	 0.4750
O	 0.9080	 0.5250
P	 0.9480	 0.5200
Q	 0.9370	 0.5140
R	 0.8890	 0.5150
S	 0.9080	 0.4890
T	 0.9120	 0.4820
U	 0.9040	 0.4910
V	 0.9060	 0.5380
W	 0.9180	 0.5130
X	 0.9000	 0.4340
Y	 0.9110	 0.5020
Z	 0.8810	 0.3970
a	 0.9230	 0.5150
b	 0.8540	 0.5010
c	 0.9270	 0.5390
d	 0.9230	 0.5500
e	 0.9280	 0.5300



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Chain	Atom inclusion	Q-score
f	 0.8690	 0.4140
g	 0.9050	 0.4620
h	 0.9040	 0.4580
i	 0.9180	 0.4910
j	 0.9060	 0.4500
k	 0.8810	 0.4250
l	 0.9170	 0.4930
m	 0.9200	 0.4560
n	 0.8810	 0.4370
o	 0.9110	 0.4710
p	 0.8810	 0.5070
q	 0.9080	 0.4460
r	 0.9350	 0.4710
s	 0.9260	 0.4570
t	 0.9470	 0.4950
u	 0.8910	 0.4700
v	 0.9230	 0.4760
w	 0.9400	 0.4700
x	 0.9270	 0.4650
y	 0.7640	 0.4020
z	 0.9710	 0.4330