



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 10:01 AM UTC

PDB ID : 5ND8 / pdb_00005nd8
EMDB ID : EMD-3624
Title : Hibernating ribosome from Staphylococcus aureus (Unrotated state)
Authors : Khusainov, I.; Vicens, Q.; Ayupov, R.; Usachev, K.; Myasnikov, A.; Simonetti, A.; Validov, S.; Kieffer, B.; Yusupova, G.; Yusupov, M.; Hashem, Y.
Deposited on : 2017-03-07
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

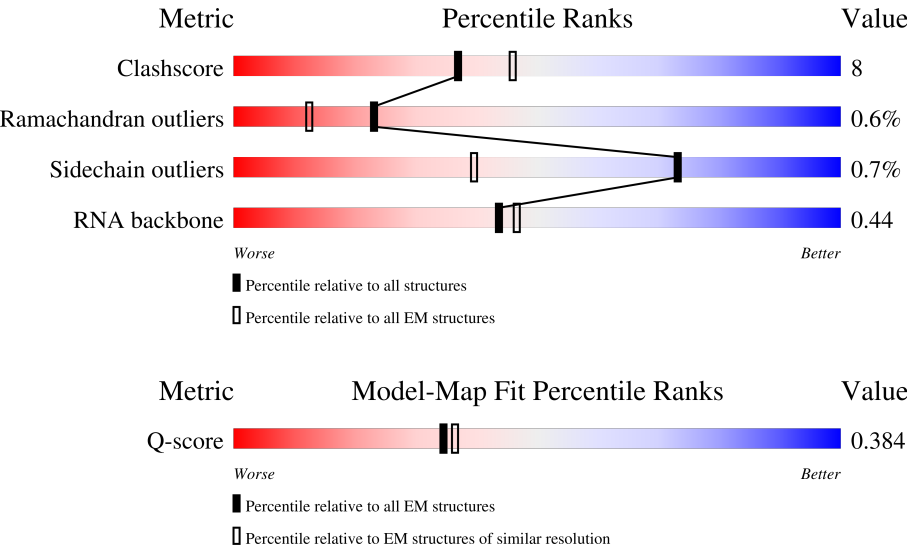
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	a	1547	62% 31% 6%
2	b	255	58% 68% 18% 13%
3	c	217	71% 73% 21% 6%

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Mol	Chain	Length	Quality of chain
4	d	200	
5	e	166	
6	f	98	
7	g	156	
8	h	132	
9	i	132	
10	j	102	
11	k	129	
12	l	137	
13	m	121	
14	n	61	
15	o	89	
16	p	91	
17	q	87	
18	r	80	
19	s	92	
20	t	83	
21	u	58	
22	v	190	
23	A	2918	
24	B	114	
25	D	277	
26	E	220	
27	F	207	
28	G	179	

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Mol	Chain	Length	Quality of chain
29	H	178	
30	M	145	
31	N	122	
32	O	146	
33	P	144	
34	Q	122	
35	R	119	
36	S	116	
37	T	118	
38	U	102	
39	V	117	
40	W	91	
41	X	105	
42	Y	217	
43	Z	94	
44	0	62	
45	1	69	
46	2	59	
47	3	84	
48	4	58	
49	5	49	
50	6	45	
51	7	66	
52	8	37	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 141043 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1542	Total	C	N	O	P	0	0
			33026	14745	6024	10715	1542		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	222	Total	C	N	O	S	0	0
			1789	1139	313	330	7		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	204	Total	C	N	O	S	0	0
			1609	1012	302	293	2		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	197	Total	C	N	O	S	0	0
			1600	1009	300	289	2		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	159	Total	C	N	O	S	0	0
			1185	745	217	221	2		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	f	94	Total	C	N	O	S	0	0
			781	494	137	147	3		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	143	Total	C	N	O	S	0	0
			1142	712	216	210	4		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	131	Total	C	N	O	S	0	0
			1032	652	183	193	4		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	i	128	Total	C	N	O	S	0	0
			1017	629	203	184	1		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	j	99	Total	C	N	O	S	0	0
			791	498	144	147	2		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	k	118	Total	C	N	O	S	0	0
			880	543	169	165	3		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	l	135	Total	C	N	O	S	0	0
			1058	658	214	184	2		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	m	110	Total	C	N	O	S	0	0
			877	537	175	164	1		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	n	60	Total	C	N	O	S	0	0
			502	317	100	80	5		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	o	88	Total	C	N	O	S	0	0
			738	454	153	130	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	p	90	Total	C	N	O	S	0	0
			712	448	132	131	1		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	q	85	Total	C	N	O	S	0	0
			698	441	125	131	1		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	r	58	Total	C	N	O	S	0	0
			478	303	90	83	2		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	s	82	Total	C	N	O	S	0	0
			661	426	118	115	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	t	80	Total	C	N	O	S	0	0
			606	367	119	118	2		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	u	47	Total	C	N	O	0	0
			396	243	82	71		

- Molecule 22 is a protein called Ribosome hibernation promotion factor.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	v	98	Total	C	N	O	0	0
			808	506	150	152		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A	2912	Total	C	N	O	P	0	0
			62440	27876	11422	20230	2912		

- Molecule 24 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	114	Total	C	N	O	P	0	0
			2430	1086	436	794	114		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	275	Total	C	N	O	S	0	0
			2103	1309	417	372	5		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	218	Total	C	N	O	S	0	0
			1649	1030	304	310	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	199	Total	C	N	O	S	0	0
			1524	955	281	286	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	G	166	Total	C	N	O	S	0	0
			1311	832	223	250	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	H	164	Total	C	N	O	S	0	0
			1284	799	232	250	3		

- Molecule 30 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	145	Total	C	N	O	S	0	0
			1151	717	211	220	3		

- Molecule 31 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	N	122	Total	C	N	O	S	0	0
			920	572	174	170	4		

- Molecule 32 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	O	131	Total	C	N	O	S	0	0
			997	618	197	181	1		

- Molecule 33 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	P	132	Total	C	N	O	S	0	0
			1056	676	202	175	3		

- Molecule 34 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Q	117	Total	C	N	O	S	0	0
			924	564	179	180	1		

- Molecule 35 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	R	119	Total	C	N	O	S	0	0
			922	574	174	173	1		

- Molecule 36 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	S	107	Total	C	N	O	S	0	0
			862	544	173	145			

- Molecule 37 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	T	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 38 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	U	102	Total	C	N	O	S	0	0
			799	506	142	150	1		

- Molecule 39 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	V	112	Total	C	N	O	S	0	0
			862	537	164	158	3		

- Molecule 40 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	W	89	Total	C	N	O	S	0	0
			725	457	130	134	4		

- Molecule 41 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	X	87	Total	C	N	O	S	0	0
			668	423	122	122	1		

- Molecule 42 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Y	94	Total	C	N	O	S	0	0
			738	471	131	134	2		

- Molecule 43 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Z	76	Total	C	N	O		0	0
			585	361	114	110			

- Molecule 44 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	0	46	Total	C	N	O		0	0
			373	231	83	59			

- Molecule 45 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1	65	Total	C	N	O		0	0
			536	330	101	105			

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	2	57	Total	C	N	O		0	0
			441	274	83	84			

- Molecule 47 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3	83	Total	C	N	O	S	0	0
			677	430	116	128	3		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	4	43	Total	C	N	O	S	0	0
			351	214	76	57	4		

- Molecule 49 is a protein called 50S ribosomal protein L33 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	5	28	Total	C	N	O	S	0	0
			229	137	45	43	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	6	44	Total	C	N	O	S	0	0
			373	228	90	54	1		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	7	60	Total	C	N	O	S	0	0
			487	300	108	77	2		

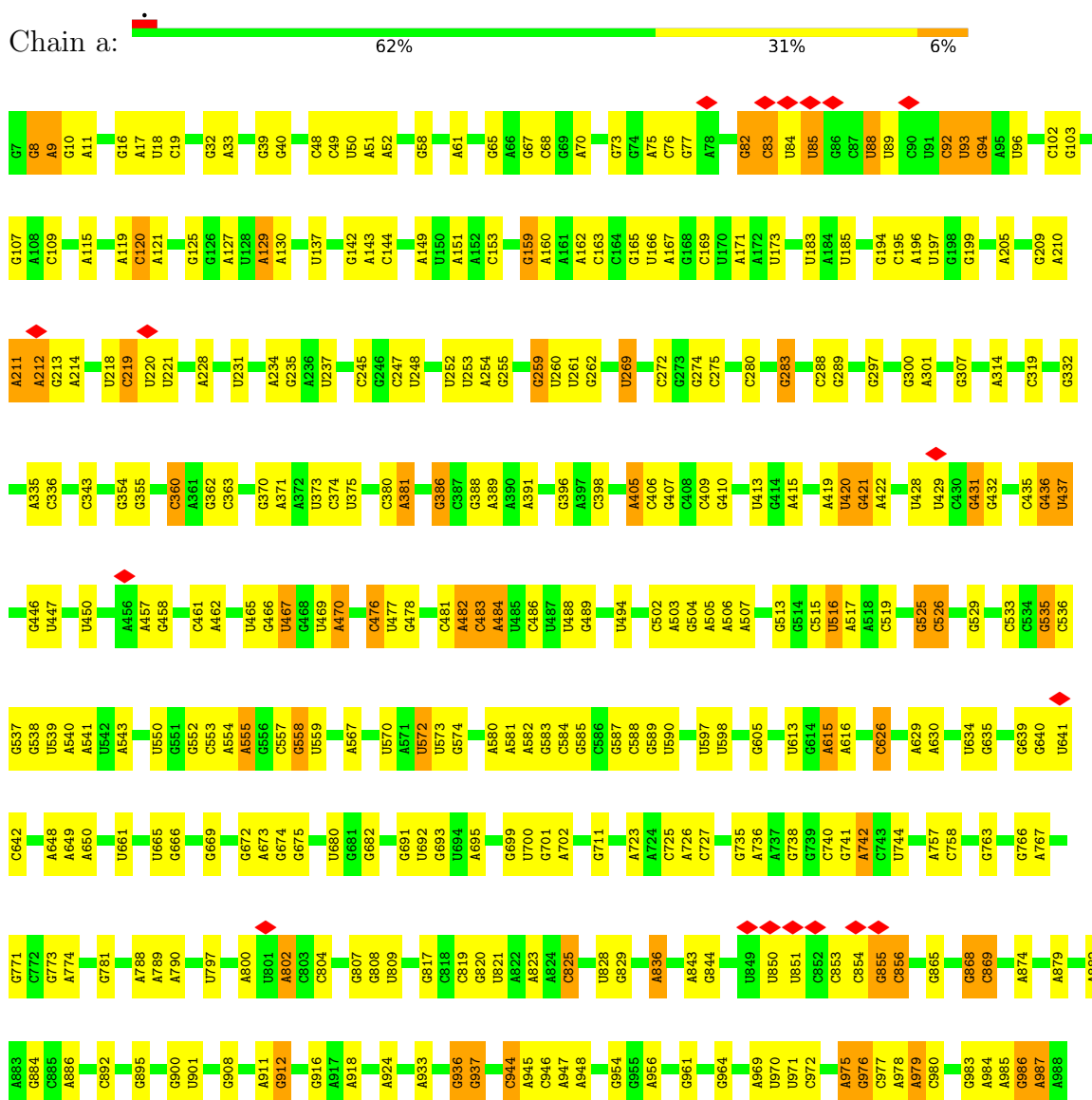
- Molecule 52 is a protein called 50S ribosomal protein L36.

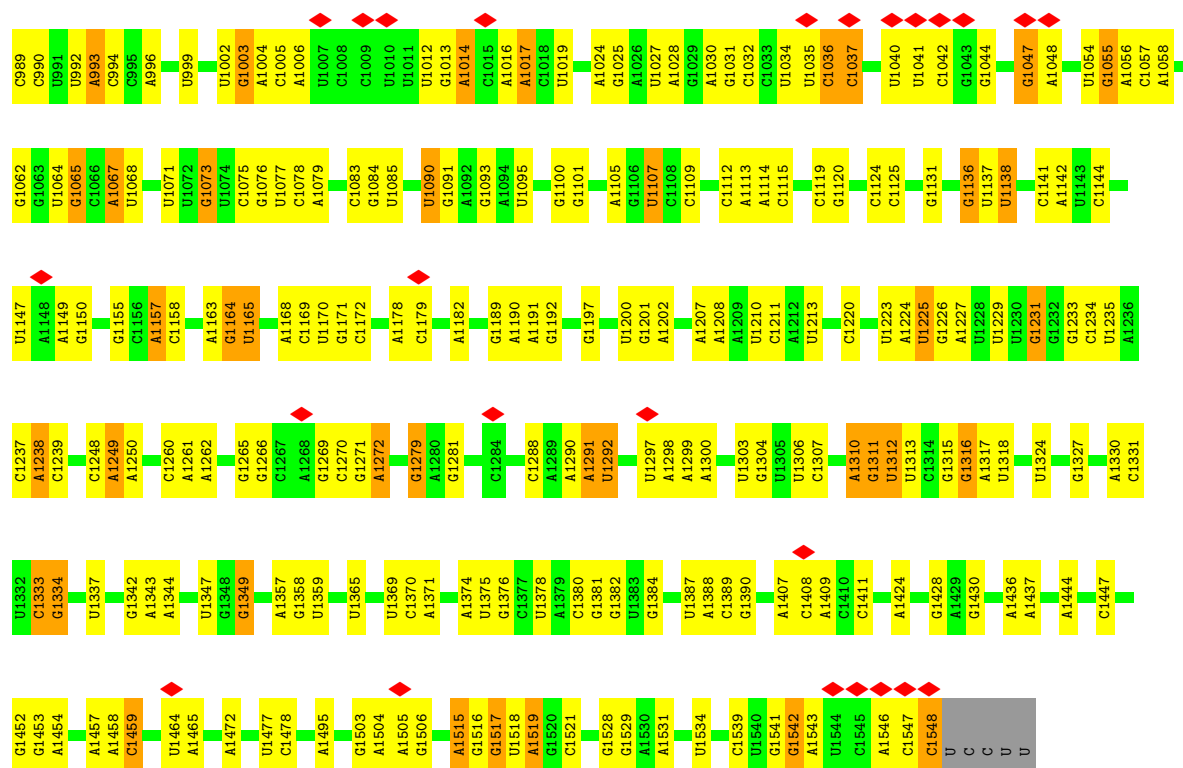
Mol	Chain	Residues	Atoms					AltConf	Trace
52	8	37	Total	C	N	O	S	0	0
			297	186	60	46	5		

3 Residue-property plots [i](#)

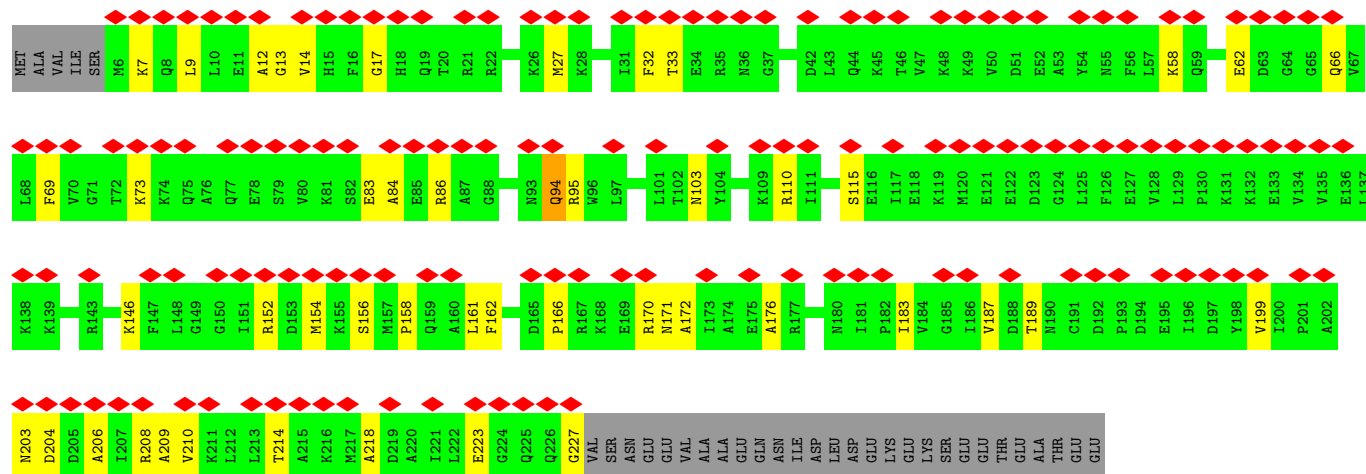
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

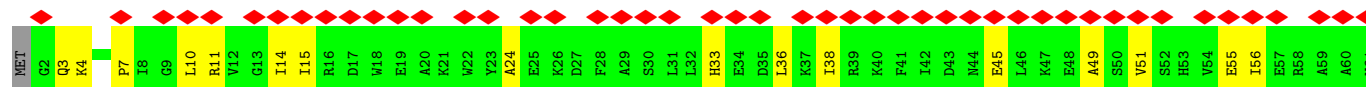


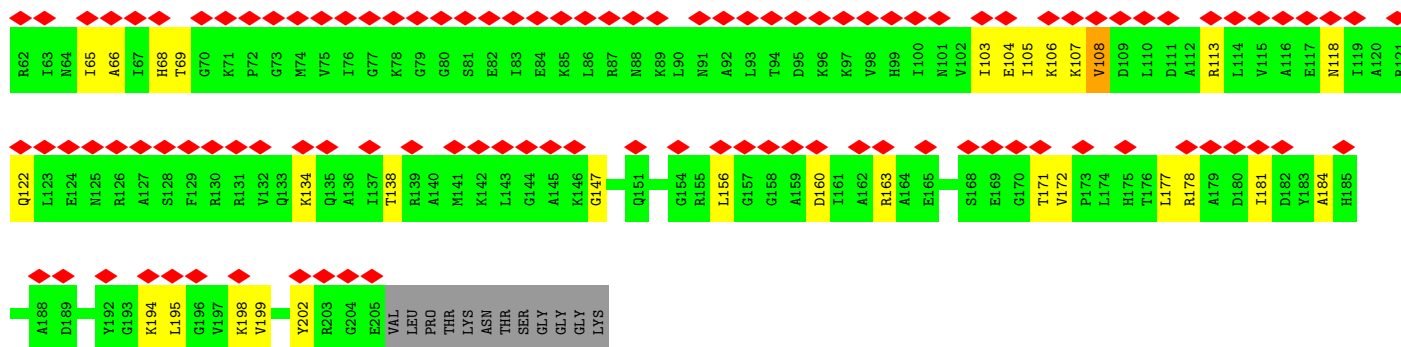


• Molecule 2: 30S ribosomal protein S2

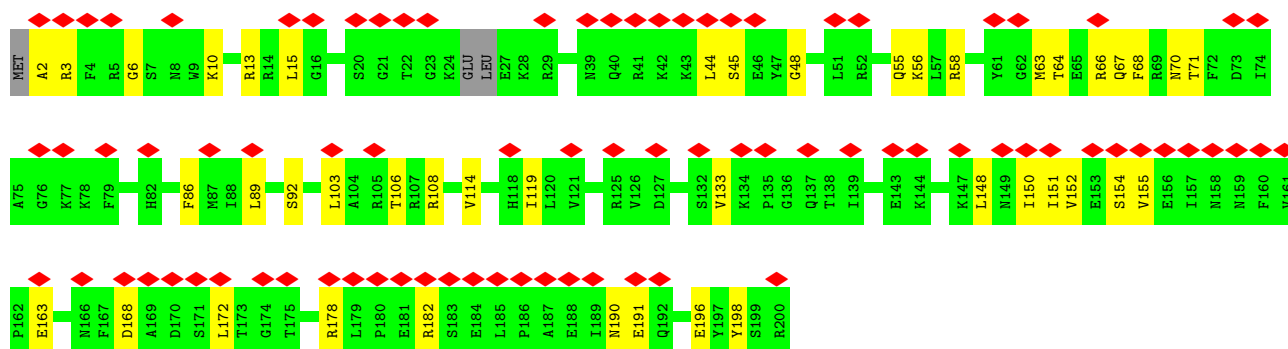
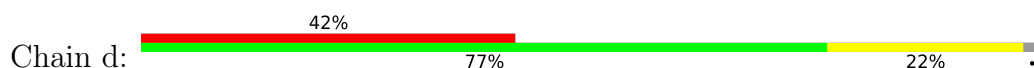


• Molecule 3: 30S ribosomal protein S3

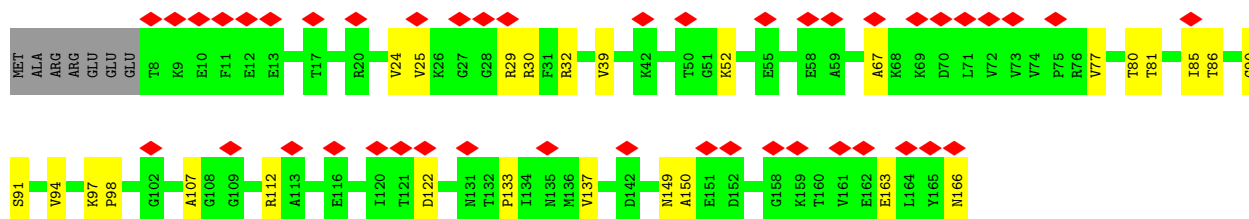
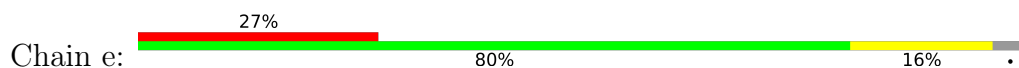




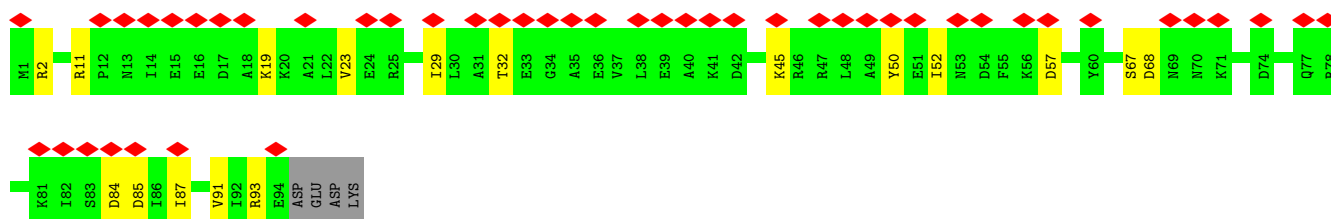
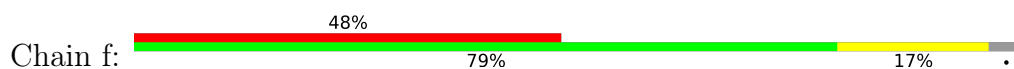
• Molecule 4: 30S ribosomal protein S4



• Molecule 5: 30S ribosomal protein S5

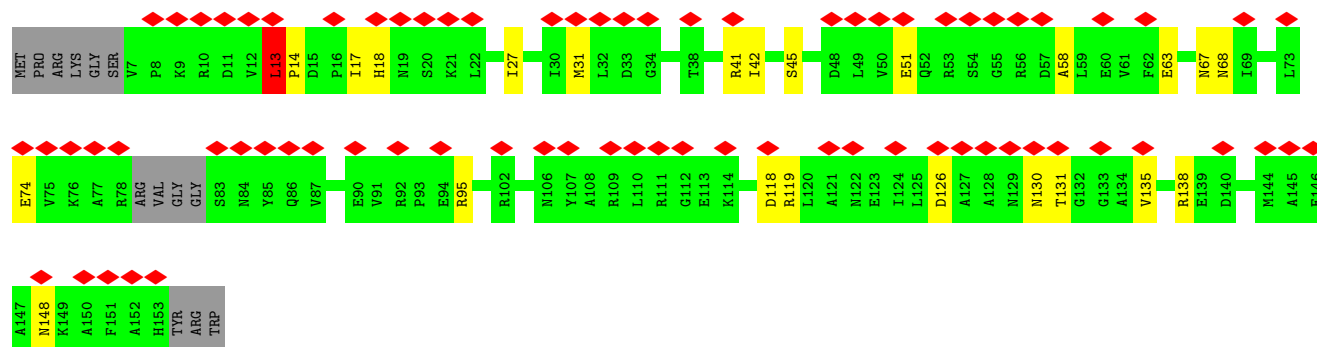


• Molecule 6: 30S ribosomal protein S6



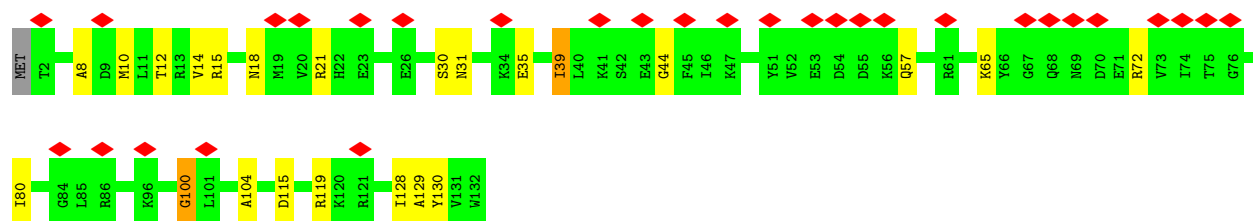
• Molecule 7: 30S ribosomal protein S7

Chain g: 



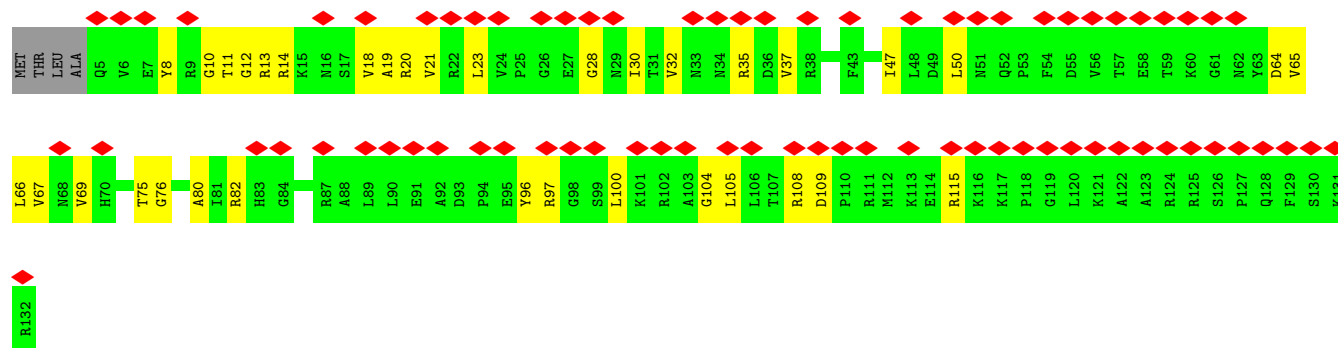
• Molecule 8: 30S ribosomal protein S8

Chain h: 



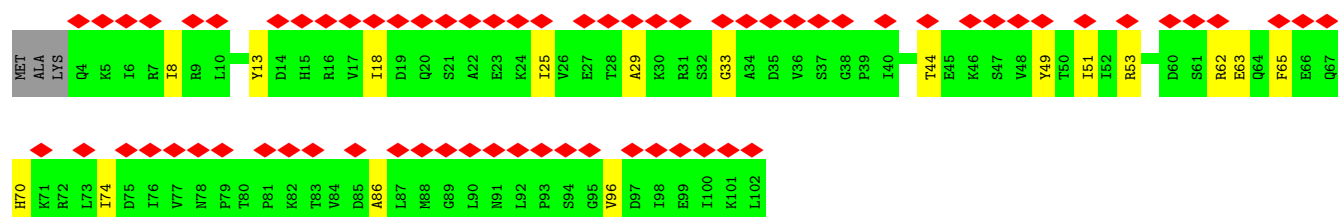
• Molecule 9: 30S ribosomal protein S9

Chain i: 

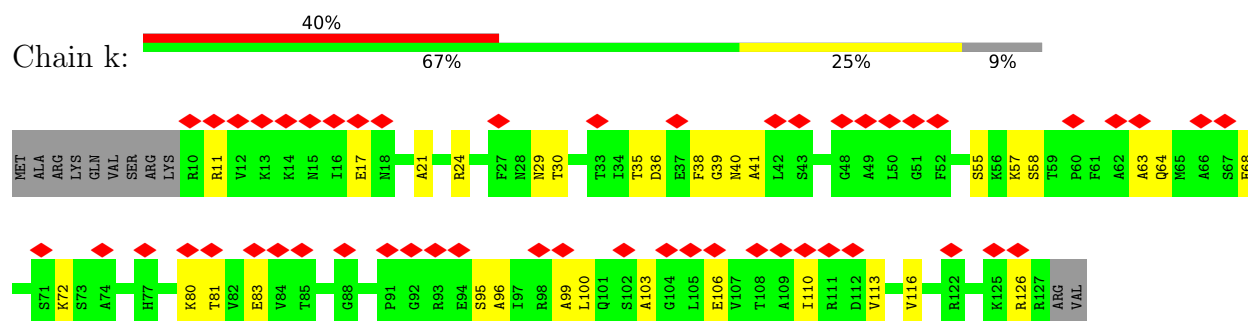


• Molecule 10: 30S ribosomal protein S10

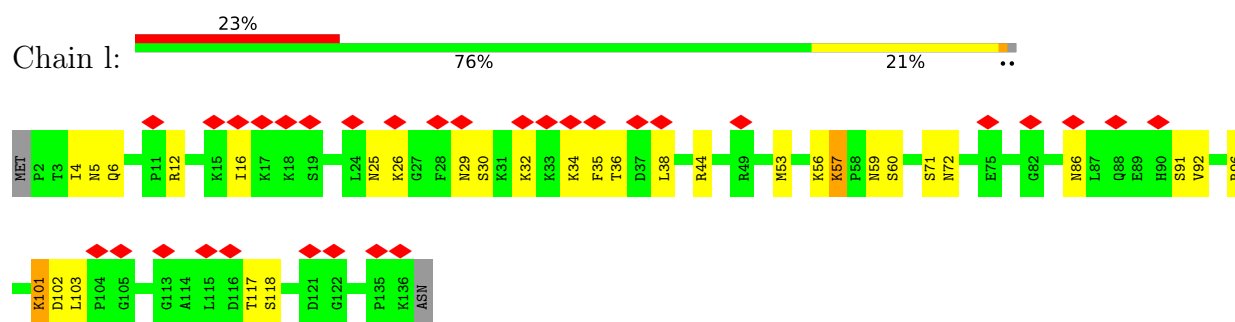
Chain j: 



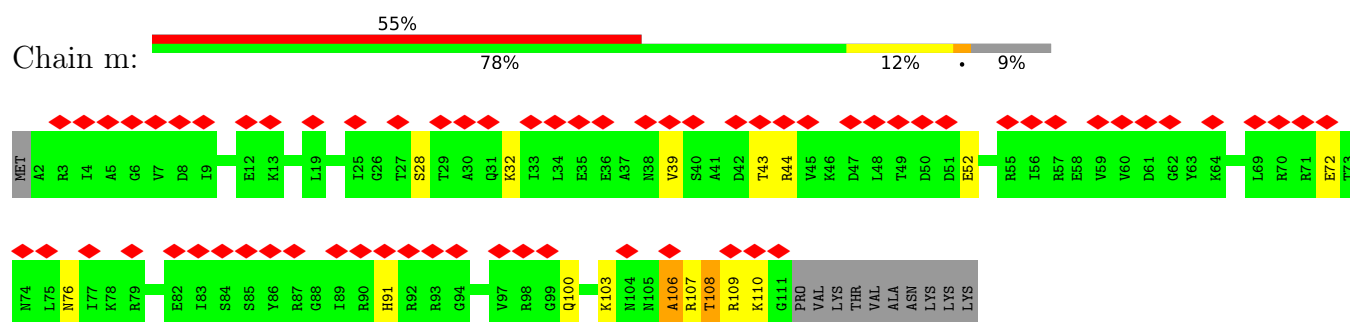
- Molecule 11: 30S ribosomal protein S11



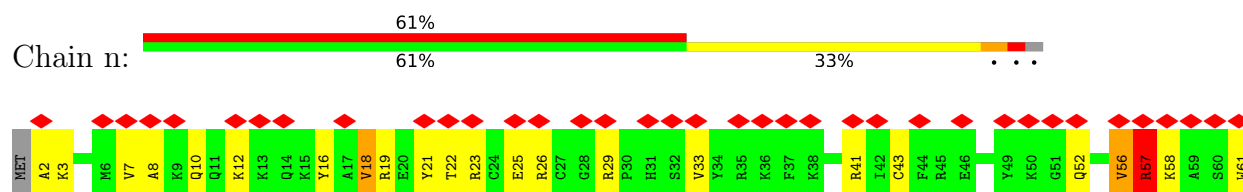
- Molecule 12: 30S ribosomal protein S12



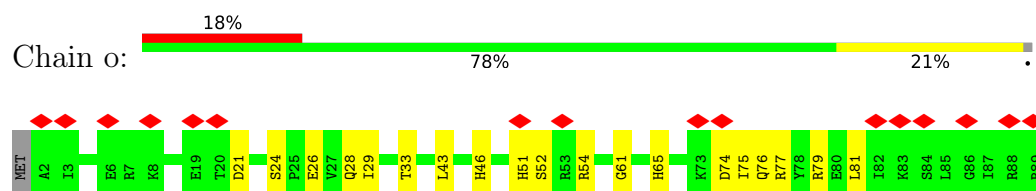
- Molecule 13: 30S ribosomal protein S13



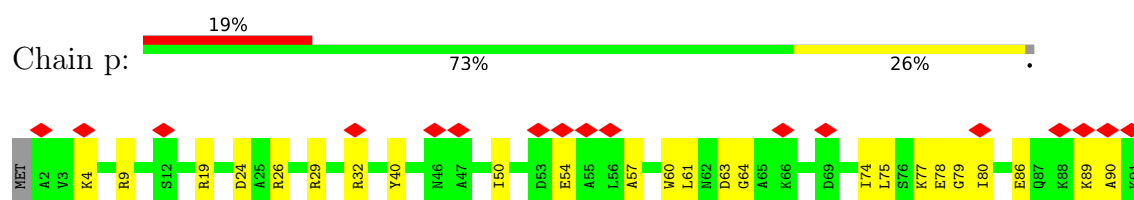
- Molecule 14: 30S ribosomal protein S14 type Z



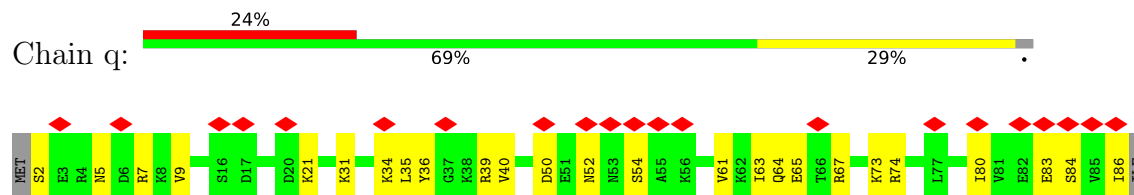
- Molecule 15: 30S ribosomal protein S15



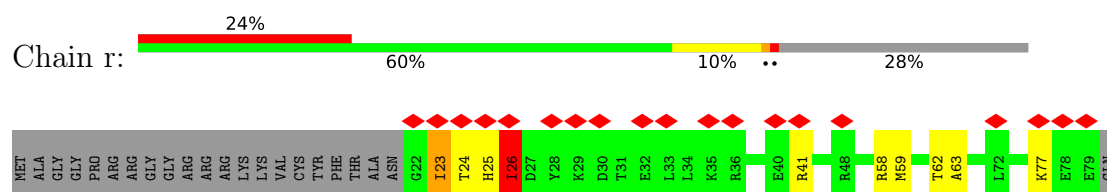
- Molecule 16: 30S ribosomal protein S16



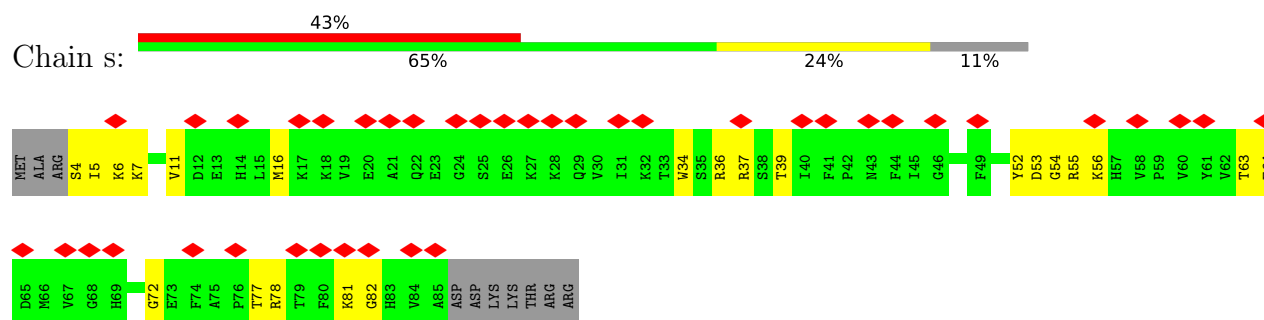
- Molecule 17: 30S ribosomal protein S17



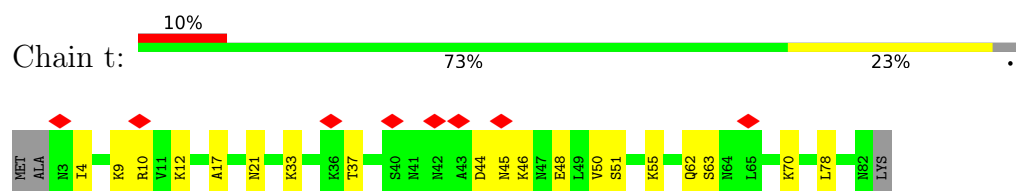
- Molecule 18: 30S ribosomal protein S18



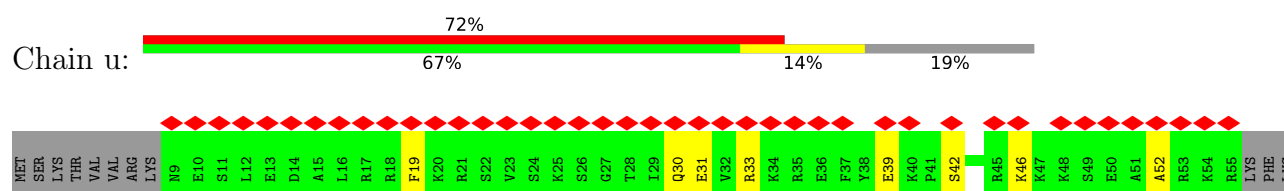
- Molecule 19: 30S ribosomal protein S19



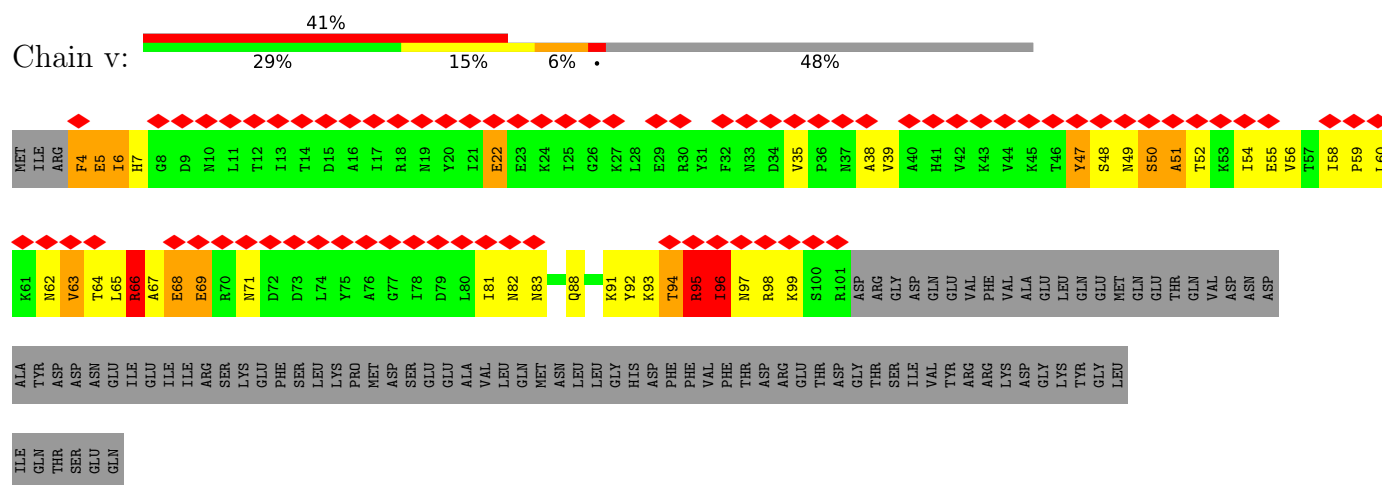
- Molecule 20: 30S ribosomal protein S20



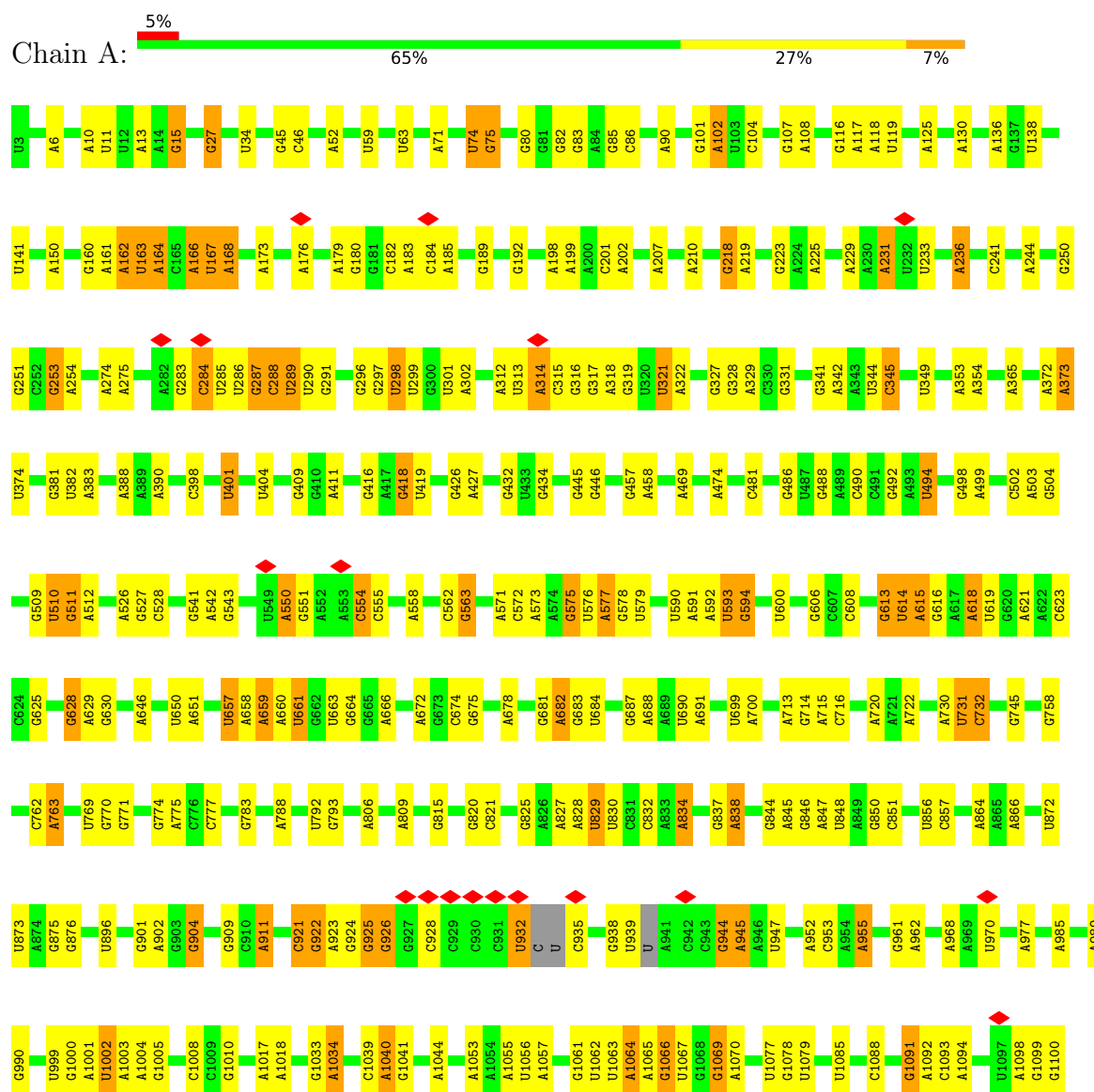
- Molecule 21: 30S ribosomal protein S21



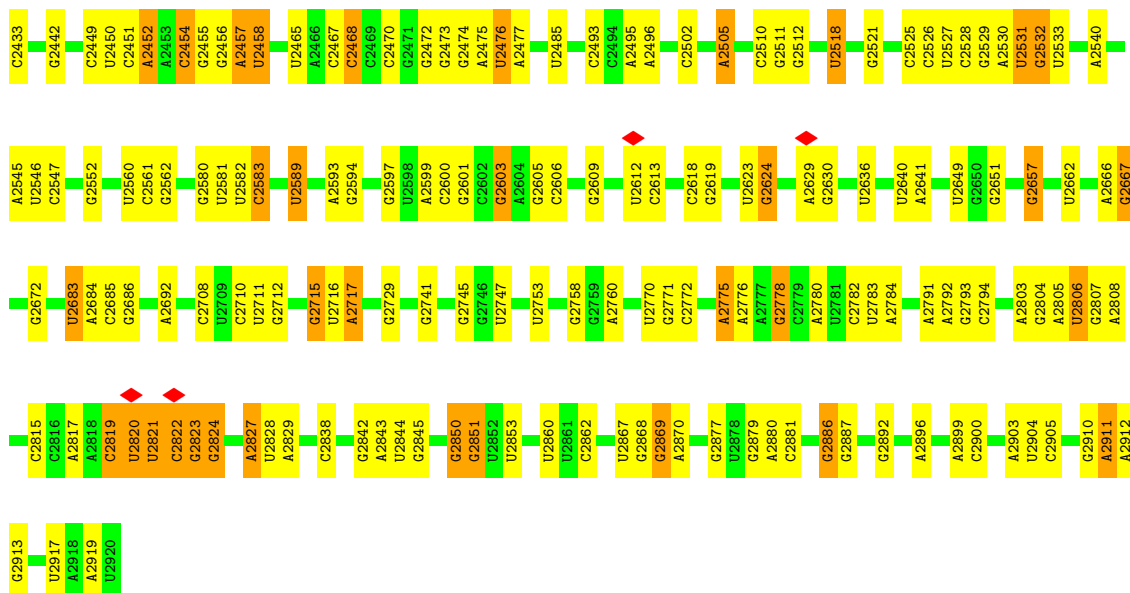
- Molecule 22: Ribosome hibernation promotion factor



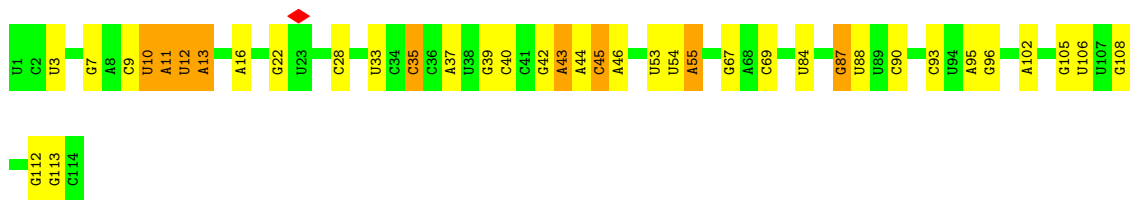
• Molecule 23: 23S ribosomal RNA



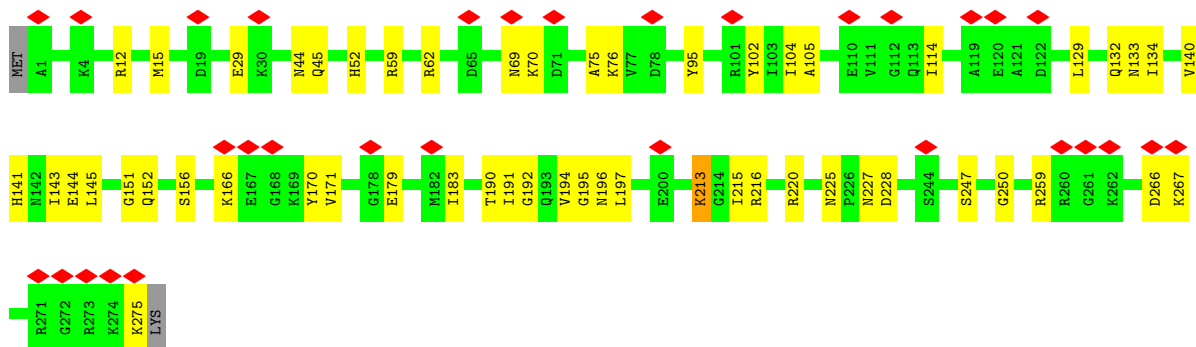
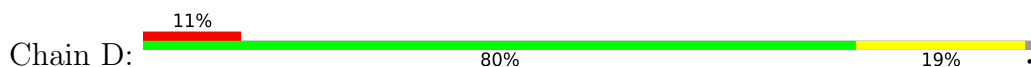
G2335	A2336	A2337	A2338	U2339	A2345	U2346	A2347	G2352	G2357	G2358	C2359	A2360	U2361	A2362	A2363	G2366	U2370	U2371	G2372	A2373	C2374	U2375	G2376	G2377	G2378	C2383	C2386	A2387	A2393	A2396	G2397	A2398	A2399	A2403	A2404	G2410	A2411	C2412	A2415	G2416	U2417	G2418	A2419	U2429	G2432											
C2231	C2236	U2237	U2238	A2239	U2240	G2244	A2250	G2251	A2252	C2253	A2260	G2261	G2265	G2266	G2273	U2276	G2277	G2278	G2279	G2280	G2285	U2289	C2290	C2291	U2292	A2293	A2294	A2295	G2298	U2299	A2300	A2301	C2302	G2303	G2304	A2305	C2310	A2314	G2315	G2316	A2325	G2331	U2332	U2333	G2334											
A2161	A2162	A2163	C2164	G2165	U2166	G2167	A2168	C2169	C2170	G2171	C2172	A2173	U2174	G2175	C2176	U2177	U2178	A2179	A2180	G2181	U2182	G2183	G2184	A2185	C2186	G2187	C2188	G2189	C2190	U2191	C2192	G2193	U2194	G2195	G2196	G2197	A2198	U2199	A2200	C2201	U2202	A2203	C2204	C2205	C2206	U2207	A2208	U2216	G2217	G2218	G2219	U2220	U2221	A2226	C2229	G2230
U1953	A1954	A1955	G1956	U1957	U1958	G1962	A1963	A1964	A1965	U1966	U1967	C1968	C1969	U1970	U1978	A1979	A1980	A1981	U1982	C1989	G1990	G1991	C1992	A1993	C1994	G1995	A1996	A1997	A1998	G1999	U2009	U2018	U2019	U2020	C2023	A2024	C2033	A2040	U2046	A2047	G2048	G2056	A2057	A2058	G2059	A2060	U2061	G2062								
A1836	A1842	U1843	G1844	U1845	A1846	G1851	A1856	C1857	G1862	C1865	G1866	U1879	G1884	A1885	A1886	U1891	U1897	C1898	G1902	A1903	A1904	G1905	G1910	A1911	U1912	U1913	A1916	A1927	A1928	C1929	G1930	G1933	U1938	A1939	A1943	U1944	A1945	A1946	C1947	C1952																
U1504	G1505	C1506	A1507	G1508	C1509	U1510	G1511	G1518	A1519	U1520	A1521	G1522	U1525	A1533	G1534	G1550	U1552	A1553	A1554	G1555	G1559	A1560	G1561	C1562	G1566	A1567	U1568	G1569	G1570	G1571	G1574	A1575	G1577	A1578	U1579	U1580	U1581	G1582	G1583	A1584	G1585	U1586	U1587	U1588	C1589	G1591	A1592	G1593								
U1594	C1595	G1596	U1597	U1598	C1604	A1605	C1606	G1613	A1614	U1615	A1616	A1617	A1618	U1625	A1628	U1629	G1630	A1631	A1632	A1635	U1636	C1643	G1651	A1652	A1653	C1654	C1655	G1656	G1657	A1658	C1659	A1660	C1661	A1662	G1663	A1666	A1676	G1677	U1683	A1690	G1691	C1692	G1693	G1697	A1698	U1703										
A1708	A1709	G1718	A1721	A1726	G1731	U1732	U1737	C1738	G1739	G1740	U1741	A1742	G1743	G1759	G1760	U1762	U1763	A1764	A1765	C1766	G1767	C1768	G1772	G1783	U1784	G1790	G1791	A1800	U1806	A1807	U1808	C1809	A1810	A1811	A1812	A1816	C1817	A1818	G1826	U1827	U1828	A1829	U1835													
A1836	A1842	U1843	G1844	U1845	A1846	G1851	A1856	C1857	G1862	C1865	G1866	U1879	G1884	A1885	A1886	U1891	U1897	C1898	G1902	A1903	A1904	G1905	G1910	A1911	U1912	U1913	A1916	A1927	A1928	C1929	G1930	G1933	U1938	A1939	A1943	U1944	A1945	A1946	C1947	C1952																
U1953	A1954	A1955	G1956	U1957	U1958	G1962	A1963	A1964	A1965	U1966	U1967	C1968	C1969	U1970	U1978	A1979	A1980	A1981	U1982	C1989	G1990	G1991	C1992	A1993	C1994	G1995	A1996	A1997	A1998	G1999	U2009	U2018	U2019	U2020	C2023	A2024	C2033	A2040	U2046	A2047	G2048	G2056	A2057	A2058	G2059	A2060	U2061	G2062								
C2070	G2073	A2078	C2082	G2083	A2087	G2088	A2089	G2096	G2097	G2098	G2099	U2102	U2103	G2107	A2117	U2118	U2119	G2120	U2124	G2127	C2131	A2132	G2133	C2134	U2135	U2136	U2137	U2138	A2139	C2140	A2141	G2142	G2143	A2144	U2145	A2146	G2147	G2151	G2152	A2153	G2154	C2155	C2156	U2157	U2158	U2159	U2160									
A2161	A2162	A2163	C2164	G2165	U2166	G2167	A2168	C2169	C2170	G2171	C2172	A2173	U2174	G2175	C2176	U2177	U2178	A2179	A2180	G2181	U2182	G2183	G2184	A2185	C2186	G2187	C2188	G2189	C2190	U2191	C2192	G2193	U2194	G2195	G2196	G2197	A2198	U2199	A2200	C2201	U2202	A2203	C2204	C2205	C2206	U2207	A2208	U2216	G2217	G2218	G2219	U2220	U2221	A2226	C2229	G2230
C2231	C2236	U2237	U2238	A2239	U2240	G2244	A2250	G2251	A2252	C2253	A2260	G2261	G2265	G2266	G2273	U2276	G2277	G2278	G2279	G2280	G2285	U2289	C2290	C2291	U2292	A2293	A2294	A2295	G2298	U2299	A2300	A2301	C2302	G2303	G2304	A2305	C2310	A2314	G2315	G2316	A2325	G2331	U2332	U2333	G2334											
A2335	A2336	A2337	A2338	U2339	A2345	U2346	A2347	G2352	G2357	G2358	C2359	A2360	U2361	A2362	A2363	G2366	U2370	U2371	G2372	A2373	C2374	U2375	G2376	G2377	G2378	C2383	C2386	A2387	A2393	A2396	G2397	A2398	A2399	A2403	A2404	G2410	A2411	C2412	A2415	G2416	U2417	G2418	A2419	U2429	G2432											



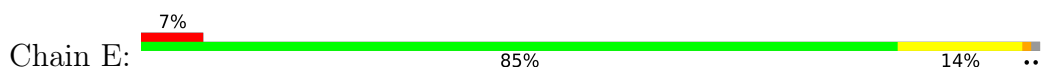
• Molecule 24: 5S ribosomal RNA

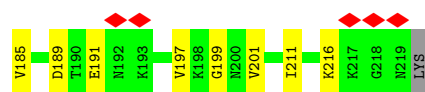


• Molecule 25: 50S ribosomal protein L2

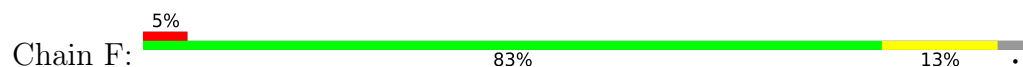


• Molecule 26: 50S ribosomal protein L3

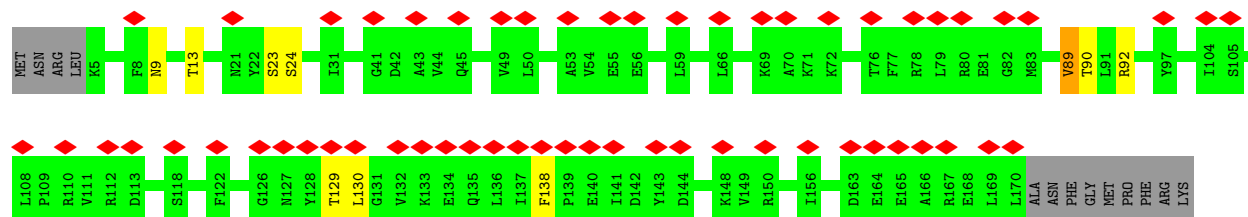
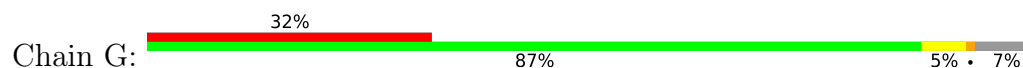




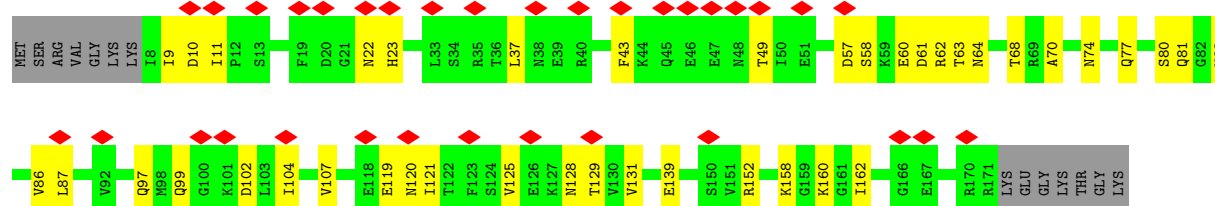
- Molecule 27: 50S ribosomal protein L4



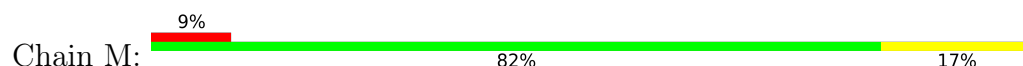
- Molecule 28: 50S ribosomal protein L5



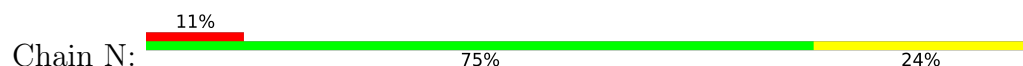
- Molecule 29: 50S ribosomal protein L6

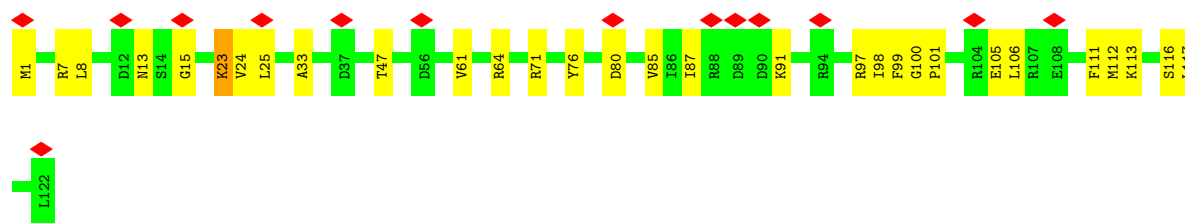


- Molecule 30: 50S ribosomal protein L13

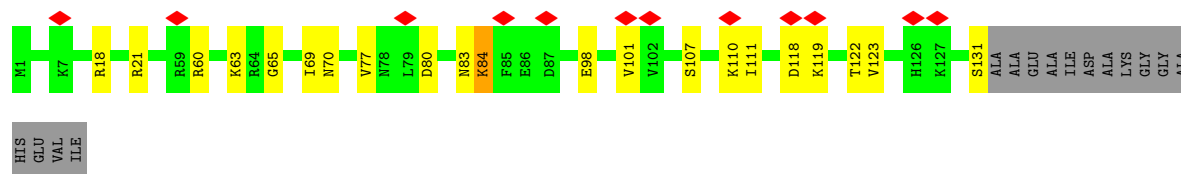
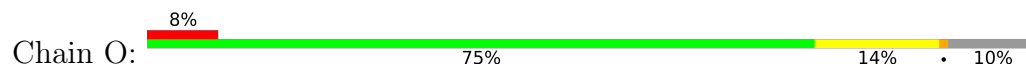


- Molecule 31: 50S ribosomal protein L14

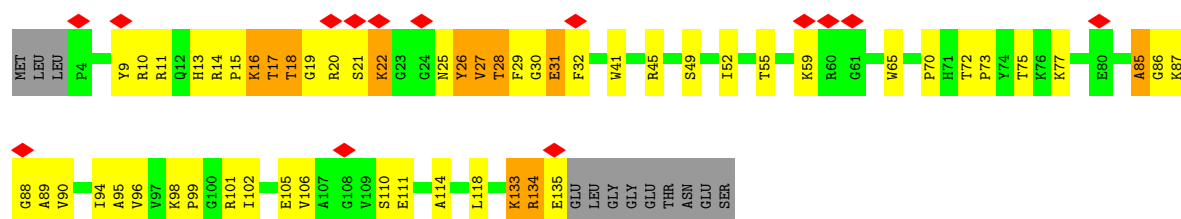




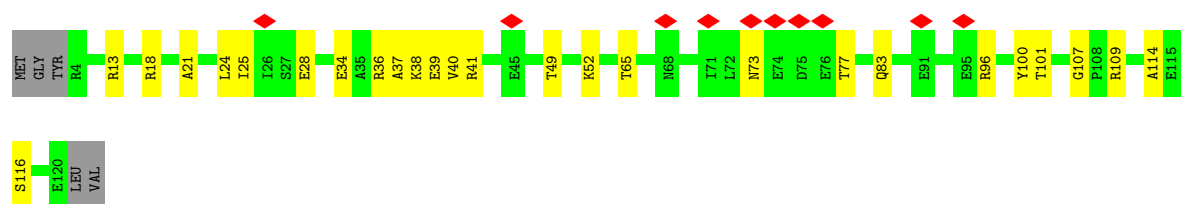
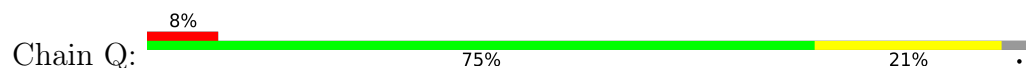
• Molecule 32: 50S ribosomal protein L15



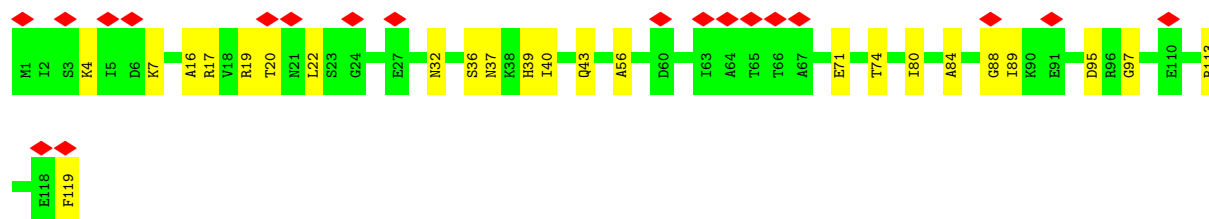
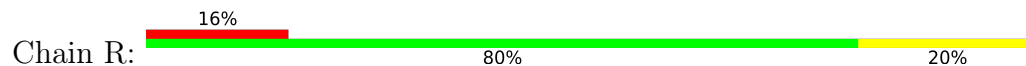
• Molecule 33: 50S ribosomal protein L16



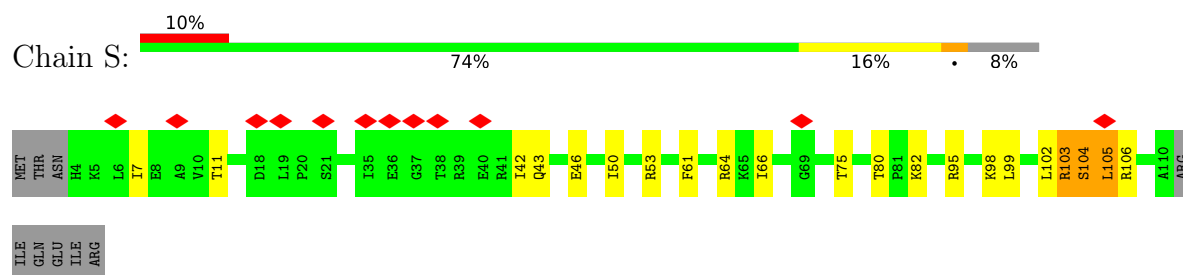
• Molecule 34: 50S ribosomal protein L17



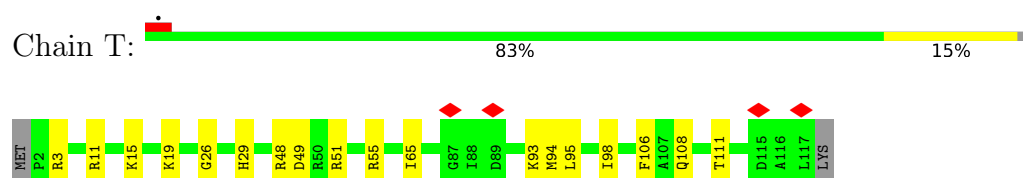
• Molecule 35: 50S ribosomal protein L18



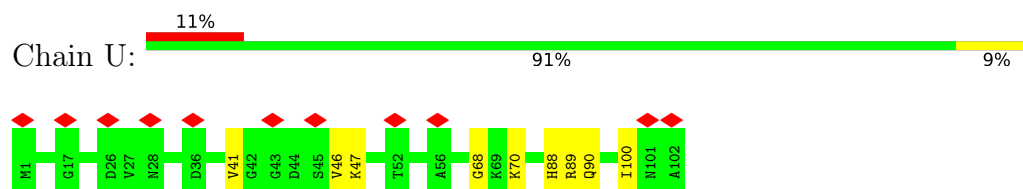
- Molecule 36: 50S ribosomal protein L19



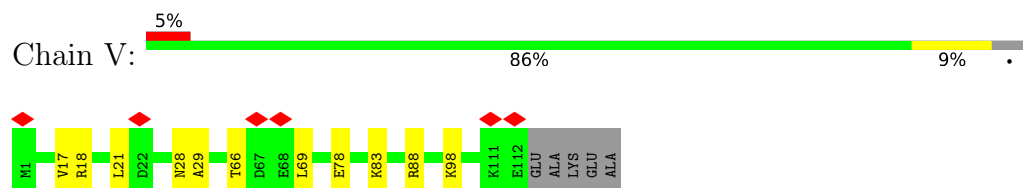
- Molecule 37: 50S ribosomal protein L20



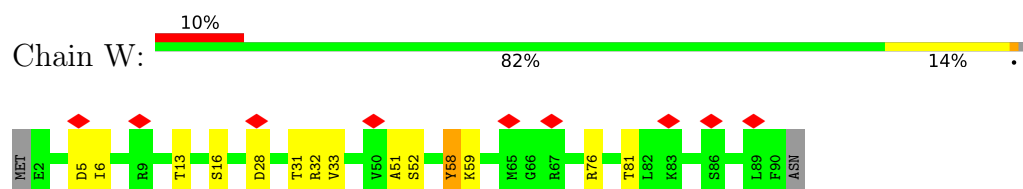
- Molecule 38: 50S ribosomal protein L21



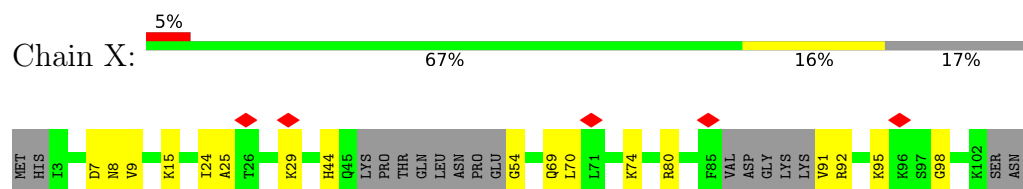
- Molecule 39: 50S ribosomal protein L22



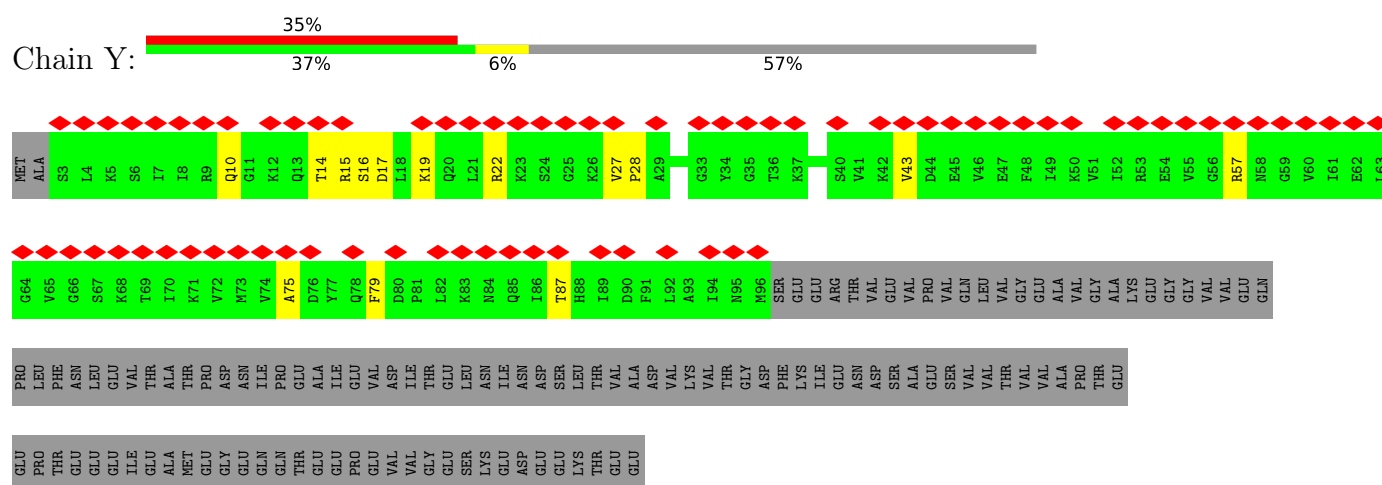
- Molecule 40: 50S ribosomal protein L23



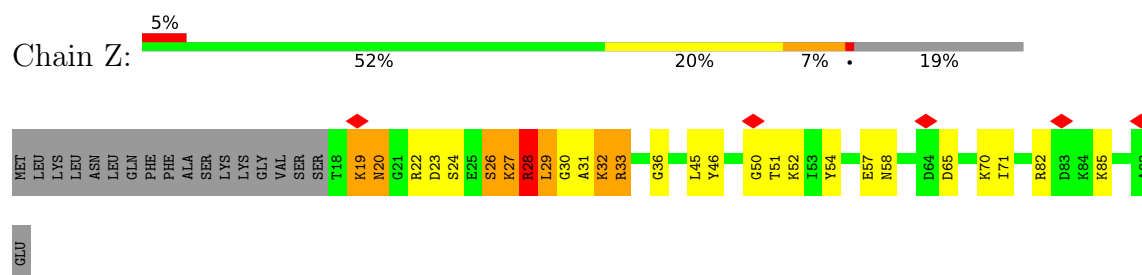
- Molecule 41: 50S ribosomal protein L24



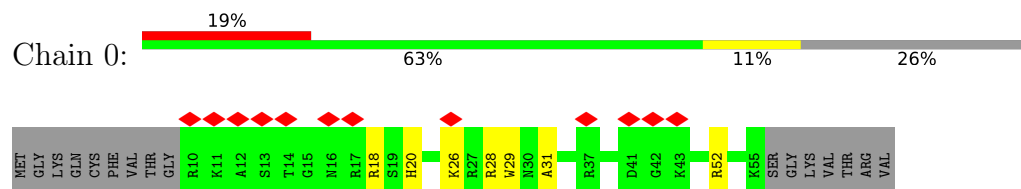
- Molecule 42: 50S ribosomal protein L25



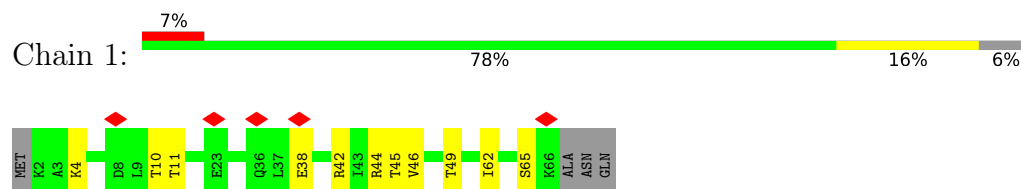
- Molecule 43: 50S ribosomal protein L27



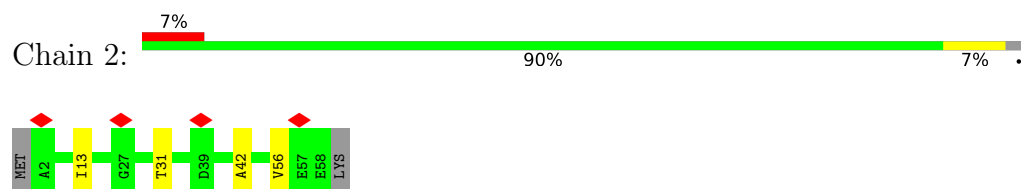
- Molecule 44: 50S ribosomal protein L28



- Molecule 45: 50S ribosomal protein L29

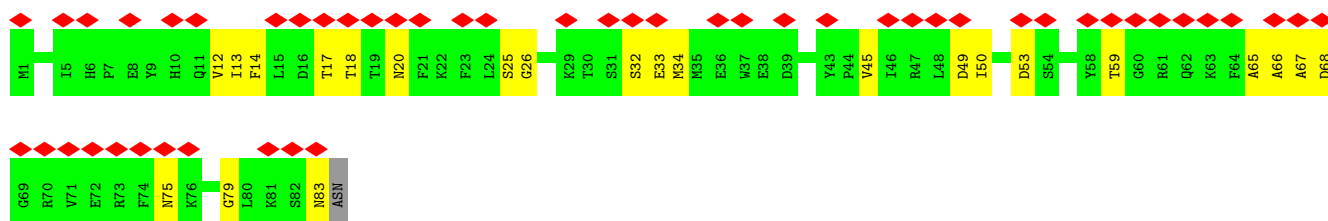


- Molecule 46: 50S ribosomal protein L30

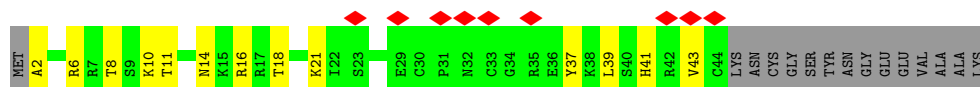


- Molecule 47: 50S ribosomal protein L31 type B

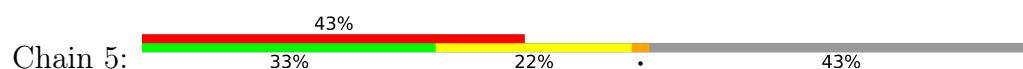




• Molecule 48: 50S ribosomal protein L32



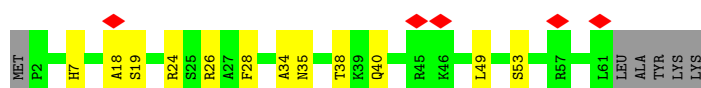
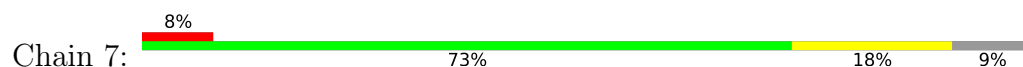
• Molecule 49: 50S ribosomal protein L33 2



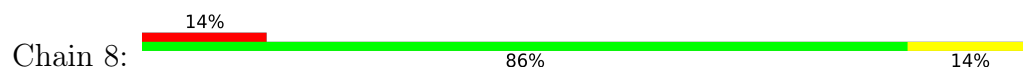
• Molecule 50: 50S ribosomal protein L34



• Molecule 51: 50S ribosomal protein L35



• Molecule 52: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	83000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.253	Depositor
Minimum map value	-0.114	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.045	Depositor
Map size (Å)	374.0, 374.0, 374.0	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	a	0.38	0/36976	0.43	0/57663
2	b	0.34	0/1816	0.58	0/2436
3	c	0.35	0/1631	0.62	3/2190 (0.1%)
4	d	0.35	0/1629	0.58	0/2185
5	e	0.40	0/1199	0.55	0/1616
6	f	0.41	0/792	0.58	0/1062
7	g	0.34	0/1157	0.64	0/1557
8	h	0.45	0/1044	0.65	0/1401
9	i	0.33	0/1033	0.61	0/1386
10	j	0.34	0/803	0.56	0/1082
11	k	0.35	0/895	0.57	0/1207
12	l	0.45	0/1075	0.71	0/1439
13	m	0.35	0/883	0.72	0/1182
14	n	0.41	0/512	0.84	3/678 (0.4%)
15	o	0.46	0/747	0.65	0/996
16	p	0.43	0/723	0.59	0/971
17	q	0.40	0/706	0.61	0/944
18	r	0.42	0/485	0.64	0/648
19	s	0.34	0/679	0.71	0/912
20	t	0.39	0/606	0.69	2/810 (0.2%)
21	u	0.35	0/399	0.63	0/523
22	v	0.38	0/818	1.08	9/1101 (0.8%)
23	A	0.51	0/69927	0.49	0/109056
24	B	0.38	0/2717	0.44	0/4232
25	D	0.64	0/2138	0.67	1/2869 (0.0%)
26	E	0.58	0/1673	0.65	0/2243
27	F	0.55	0/1547	0.64	0/2088
28	G	0.38	0/1326	0.70	0/1780
29	H	0.36	0/1302	0.53	0/1757
30	M	0.54	0/1173	0.64	0/1578
31	N	0.58	0/927	0.65	0/1243
32	O	0.54	0/1010	0.78	0/1344
33	P	0.55	0/1080	0.73	1/1448 (0.1%)
34	Q	0.56	0/927	0.66	0/1238

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	R	0.39	0/931	0.64	0/1244
36	S	0.56	0/874	0.69	0/1168
37	T	0.67	0/955	0.66	0/1265
38	U	0.54	0/809	0.58	0/1080
39	V	0.62	0/870	0.65	0/1171
40	W	0.60	1/733 (0.1%)	0.61	0/978
41	X	0.46	0/672	0.68	0/893
42	Y	0.31	0/746	0.60	0/1000
43	Z	0.58	0/591	0.58	0/785
44	0	0.45	0/378	0.68	0/504
45	1	0.45	0/537	0.63	0/714
46	2	0.52	0/443	0.62	0/597
47	3	0.39	0/694	0.77	0/930
48	4	0.58	0/357	0.60	0/474
49	5	0.35	0/230	0.69	0/303
50	6	0.76	0/377	0.74	0/491
51	7	0.64	0/491	0.85	0/643
52	8	0.47	0/300	0.57	0/393
All	All	0.47	1/153343 (0.0%)	0.53	19/229498 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	b	0	1
3	c	0	1
4	d	0	2
6	f	0	1
7	g	0	1
12	l	0	1
13	m	0	1
14	n	0	2
17	q	0	1
18	r	0	1
19	s	0	1
22	v	0	8
25	D	0	1
26	E	0	3
28	G	0	1
31	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
32	O	0	4
33	P	0	3
35	R	0	1
36	S	0	3
38	U	0	2
40	W	0	1
41	X	0	1
45	1	0	1
50	6	0	1
51	7	0	2
52	8	0	1
All	All	0	47

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	W	58	TYR	C-N	-8.91	1.20	1.33

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	v	95	ARG	CA-C-N	7.39	135.28	121.97
22	v	95	ARG	C-N-CA	7.39	135.28	121.97
22	v	96	ILE	N-CA-C	-7.07	94.63	109.34
22	v	50	SER	N-CA-C	6.85	125.38	110.80
14	n	56	VAL	CA-C-N	6.50	133.40	121.70
14	n	56	VAL	C-N-CA	6.50	133.40	121.70
25	D	213	LYS	N-CA-C	6.49	118.23	111.03
22	v	47	TYR	CA-C-N	6.18	132.82	121.70
22	v	47	TYR	C-N-CA	6.18	132.82	121.70
14	n	57	ARG	CA-CB-CG	6.18	126.46	114.10
20	t	44	ASP	CA-C-N	5.56	131.71	121.70
20	t	44	ASP	C-N-CA	5.56	131.71	121.70
33	P	14	ARG	N-CA-C	5.54	113.21	108.22
22	v	94	THR	N-CA-C	5.47	117.31	110.91
22	v	95	ARG	N-CA-C	5.30	125.83	111.00
22	v	35	VAL	CG1-CB-CG2	5.15	122.13	110.80
3	c	108	VAL	CG1-CB-CG2	5.04	121.88	110.80
3	c	107	LYS	CA-C-N	5.01	130.72	121.70
3	c	107	LYS	C-N-CA	5.01	130.72	121.70

There are no chirality outliers.

All (47) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
45	1	4	LYS	Peptide
50	6	15	LYS	Peptide
51	7	24	ARG	Peptide
51	7	28	PHE	Peptide
52	8	27	CYS	Peptide
25	D	166	LYS	Peptide
26	E	140	PRO	Peptide
26	E	142	SER	Peptide
26	E	9	LYS	Peptide
28	G	138	PHE	Peptide
31	N	23	LYS	Peptide
32	O	101	VAL	Peptide
32	O	110	LYS	Peptide
32	O	65	GLY	Peptide
32	O	84	LYS	Peptide
33	P	59	LYS	Peptide
33	P	85	ALA	Peptide
33	P	90	VAL	Peptide
35	R	89	ILE	Peptide
36	S	103	ARG	Peptide
36	S	104	SER	Peptide
36	S	105	LEU	Peptide
38	U	100	ILE	Peptide
38	U	47	LYS	Peptide
40	W	28	ASP	Peptide
41	X	91	VAL	Peptide
2	b	94	GLN	Peptide
3	c	160	ASP	Peptide
4	d	198	TYR	Peptide
4	d	44	LEU	Peptide
6	f	68	ASP	Peptide
7	g	13	LEU	Peptide
12	l	32	LYS	Peptide
13	m	106	ALA	Peptide
14	n	18	VAL	Peptide
14	n	57	ARG	Peptide
17	q	5	ASN	Peptide
18	r	26	ILE	Peptide
19	s	34	TRP	Peptide
22	v	49	ASN	Peptide
22	v	50	SER	Peptide
22	v	51	ALA	Peptide

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Mol	Chain	Res	Type	Group
22	v	66	ARG	Sidechain
22	v	91	LYS	Peptide
22	v	92	TYR	Peptide
22	v	95	ARG	Peptide
22	v	96	ILE	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	33026	0	16627	337	0
2	b	1789	0	1847	31	0
3	c	1609	0	1668	36	0
4	d	1600	0	1628	33	0
5	e	1185	0	1249	20	0
6	f	781	0	784	11	0
7	g	1142	0	1173	17	0
8	h	1032	0	1082	17	0
9	i	1017	0	1039	22	0
10	j	791	0	829	11	0
11	k	880	0	899	23	0
12	l	1058	0	1130	37	0
13	m	877	0	919	13	0
14	n	502	0	527	18	0
15	o	738	0	769	13	0
16	p	712	0	744	17	0
17	q	698	0	738	24	0
18	r	478	0	510	15	0
19	s	661	0	664	17	0
20	t	606	0	650	13	0
21	u	396	0	423	7	0
22	v	808	0	829	97	0
23	A	62440	0	31385	492	0
24	B	2430	0	1229	29	0
25	D	2103	0	2221	36	0
26	E	1649	0	1689	19	0
27	F	1524	0	1570	16	0
28	G	1311	0	1366	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	H	1284	0	1301	28	0
30	M	1151	0	1145	18	0
31	N	920	0	981	17	0
32	O	997	0	1044	12	0
33	P	1056	0	1116	120	0
34	Q	924	0	970	17	0
35	R	922	0	968	17	0
36	S	862	0	932	15	0
37	T	943	0	1014	14	0
38	U	799	0	836	4	0
39	V	862	0	920	8	0
40	W	725	0	761	8	0
41	X	668	0	725	11	0
42	Y	738	0	787	9	0
43	Z	585	0	597	69	0
44	0	373	0	407	6	0
45	1	536	0	567	7	0
46	2	441	0	478	4	0
47	3	677	0	655	16	0
48	4	351	0	372	13	0
49	5	229	0	224	16	0
50	6	373	0	420	10	0
51	7	487	0	548	6	0
52	8	297	0	342	3	0
All	All	141043	0	94298	1586	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 8.

All (1586) 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)
49:5:35:PHE:CE1	49:5:37:SER:HB2	1.41	1.55
33:P:22:LYS:CB	33:P:98:LYS:HB3	1.33	1.53
33:P:22:LYS:HB3	33:P:98:LYS:CB	1.41	1.48
33:P:29:PHE:CD2	33:P:105:GLU:OE2	1.68	1.43
22:v:68:GLU:O	22:v:81:ILE:CD1	1.65	1.43
33:P:22:LYS:HG2	33:P:99:PRO:CD	1.48	1.41
1:a:975:A:C2	22:v:5:GLU:OE2	1.70	1.40
22:v:65:LEU:HD11	22:v:88:GLN:CB	1.50	1.39
49:5:35:PHE:HE1	49:5:37:SER:CB	1.34	1.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:v:65:LEU:CD1	22:v:88:GLN:HB3	1.53	1.37
33:P:17:THR:HG21	33:P:96:VAL:CG1	1.51	1.37
1:a:975:A:N1	22:v:5:GLU:OE2	1.59	1.36
18:r:26:ILE:HG13	18:r:63:ALA:CB	1.54	1.36
33:P:32:PHE:CE2	33:P:111:GLU:CA	1.81	1.36
33:P:22:LYS:CB	33:P:98:LYS:CB	2.01	1.32
1:a:975:A:C2	22:v:5:GLU:CD	2.08	1.32
33:P:22:LYS:HA	33:P:98:LYS:CB	1.60	1.30
33:P:22:LYS:CG	33:P:99:PRO:HD2	1.62	1.29
33:P:21:SER:C	33:P:98:LYS:HD2	1.58	1.28
22:v:4:PHE:CE2	22:v:22:GLU:OE2	1.85	1.28
1:a:533:C:P	12:l:101:LYS:NZ	2.07	1.27
33:P:31:GLU:O	33:P:133:LYS:HA	1.25	1.27
33:P:17:THR:CG2	33:P:96:VAL:HG11	1.63	1.27
33:P:22:LYS:HD2	33:P:99:PRO:O	1.33	1.25
33:P:22:LYS:CA	33:P:98:LYS:CB	2.13	1.24
22:v:58:ILE:O	22:v:64:THR:OG1	1.55	1.22
22:v:68:GLU:CG	22:v:69:GLU:H	1.49	1.21
23:A:2383:C:H4'	43:Z:28:ARG:HG2	1.21	1.20
33:P:22:LYS:CA	33:P:98:LYS:HB3	1.71	1.20
43:Z:30:GLY:O	43:Z:32:LYS:HE3	1.43	1.19
33:P:32:PHE:CE2	33:P:111:GLU:HA	0.91	1.19
33:P:29:PHE:HD2	33:P:105:GLU:OE2	0.87	1.18
1:a:533:C:OP2	12:l:101:LYS:NZ	1.74	1.16
22:v:4:PHE:CZ	22:v:22:GLU:OE2	1.98	1.16
33:P:32:PHE:HE2	33:P:111:GLU:CA	1.27	1.15
22:v:68:GLU:HG2	22:v:69:GLU:N	1.49	1.13
22:v:4:PHE:CB	22:v:39:VAL:HA	1.75	1.13
33:P:28:THR:HA	33:P:134:ARG:NH1	1.64	1.13
1:a:533:C:P	12:l:101:LYS:HZ1	1.69	1.13
22:v:59:PRO:HA	22:v:64:THR:OG1	1.49	1.12
33:P:22:LYS:CA	33:P:98:LYS:HD2	1.79	1.11
33:P:22:LYS:N	33:P:98:LYS:HD2	1.65	1.11
22:v:68:GLU:C	22:v:81:ILE:HD13	1.75	1.11
33:P:27:VAL:HG23	33:P:105:GLU:OE1	1.51	1.10
18:r:26:ILE:HG13	18:r:63:ALA:HB3	1.34	1.09
22:v:4:PHE:HB2	22:v:39:VAL:HA	1.26	1.09
1:a:975:A:O2'	1:a:976:G:H5''	1.54	1.08
33:P:22:LYS:HB3	33:P:98:LYS:C	1.79	1.07
33:P:22:LYS:HA	33:P:98:LYS:HB2	1.30	1.07
33:P:25:ASN:O	33:P:26:TYR:CG	2.08	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:P:21:SER:O	33:P:98:LYS:CD	2.03	1.07
33:P:22:LYS:HA	33:P:98:LYS:CD	1.85	1.06
33:P:22:LYS:HD3	33:P:99:PRO:HG2	1.12	1.06
33:P:22:LYS:HB3	33:P:98:LYS:CA	1.87	1.05
33:P:21:SER:O	33:P:98:LYS:HD2	1.56	1.04
23:A:2383:C:H4'	43:Z:28:ARG:CG	1.87	1.04
33:P:27:VAL:CG2	33:P:105:GLU:OE1	2.04	1.04
22:v:65:LEU:HD21	22:v:88:GLN:OE1	1.58	1.04
23:A:1581:U:O5'	23:A:1584:A:C2	2.11	1.03
33:P:21:SER:C	33:P:98:LYS:CD	2.33	1.01
22:v:68:GLU:O	22:v:81:ILE:HD13	0.83	1.01
23:A:2304:G:P	43:Z:19:LYS:HE2	2.01	1.01
49:5:35:PHE:C	49:5:35:PHE:HD1	1.66	1.01
23:A:2304:G:OP2	43:Z:19:LYS:HD3	1.61	1.00
33:P:25:ASN:O	33:P:26:TYR:CD2	2.14	1.00
23:A:1002:U:C5	24:B:87:G:N1	2.29	0.99
23:A:615:A:H61	23:A:2056:G:H21	0.99	0.98
1:a:975:A:O2'	1:a:976:G:C5'	2.11	0.98
22:v:4:PHE:HE2	22:v:22:GLU:OE2	1.38	0.98
1:a:836:A:H62	1:a:868:G:H21	1.01	0.97
33:P:86:GLY:HA3	43:Z:19:LYS:HE3	1.41	0.97
33:P:22:LYS:CD	33:P:99:PRO:O	2.11	0.97
1:a:1249:A:N6	1:a:1312:U:O2	1.99	0.95
23:A:2289:U:OP2	43:Z:24:SER:OG	1.84	0.95
33:P:22:LYS:CA	33:P:98:LYS:HB2	1.87	0.94
23:A:2127:G:N1	23:A:2216:U:O2	1.99	0.94
33:P:22:LYS:HA	33:P:98:LYS:HD2	1.35	0.93
33:P:22:LYS:CD	33:P:99:PRO:HG2	1.98	0.93
43:Z:33:ARG:HG2	43:Z:45:LEU:HD23	1.51	0.92
1:a:533:C:OP1	12:l:101:LYS:NZ	2.01	0.92
23:A:2298:G:C5'	43:Z:28:ARG:NH2	2.33	0.92
18:r:26:ILE:CG1	18:r:63:ALA:CB	2.46	0.92
12:l:101:LYS:H	12:l:101:LYS:HD2	1.35	0.91
33:P:22:LYS:CG	33:P:98:LYS:HB3	2.00	0.91
49:5:35:PHE:CE1	49:5:37:SER:CB	2.24	0.91
49:5:35:PHE:C	49:5:35:PHE:CD1	2.42	0.91
33:P:31:GLU:O	33:P:133:LYS:CA	2.17	0.90
33:P:21:SER:O	33:P:98:LYS:CE	2.20	0.90
23:A:1584:A:O5'	23:A:1585:G:H8	1.52	0.90
1:a:533:C:P	12:l:101:LYS:HZ3	1.81	0.90
1:a:1168:A:N6	1:a:1189:G:N3	2.19	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:v:59:PRO:CA	22:v:64:THR:OG1	2.19	0.89
1:a:626:C:N3	1:a:630:A:N6	2.20	0.89
33:P:22:LYS:HA	33:P:98:LYS:CG	2.02	0.89
22:v:4:PHE:CB	22:v:39:VAL:CA	2.39	0.88
33:P:29:PHE:HD2	33:P:105:GLU:CD	1.82	0.88
33:P:22:LYS:HD3	33:P:99:PRO:CG	2.01	0.88
1:a:420:U:O2'	1:a:421:G:O4'	1.92	0.88
23:A:2289:U:OP2	43:Z:24:SER:CB	2.22	0.88
23:A:1581:U:H3'	23:A:1584:A:H2	1.37	0.87
1:a:836:A:H62	1:a:868:G:N2	1.72	0.87
1:a:587:G:O2'	15:o:54:ARG:NH1	2.08	0.87
43:Z:27:LYS:O	43:Z:29:LEU:N	2.09	0.85
23:A:1002:U:C5	24:B:87:G:N2	2.43	0.85
33:P:32:PHE:CD2	33:P:111:GLU:HA	2.02	0.85
23:A:1002:U:C4	24:B:87:G:N2	2.43	0.85
22:v:68:GLU:HG2	22:v:69:GLU:H	0.70	0.85
18:r:26:ILE:HG13	18:r:63:ALA:HB2	1.59	0.85
1:a:961:G:N7	13:m:103:LYS:NZ	2.25	0.84
33:P:22:LYS:CG	33:P:99:PRO:CD	2.36	0.84
1:a:969:A:HO2'	1:a:994:C:HO2'	1.20	0.84
23:A:615:A:H61	23:A:2056:G:N2	1.74	0.84
1:a:398:C:O3'	16:p:9:ARG:NH2	2.10	0.84
23:A:1708:A:H61	23:A:2023:C:N4	1.75	0.84
23:A:1002:U:H5	24:B:87:G:H1	1.19	0.84
22:v:58:ILE:C	22:v:64:THR:OG1	2.21	0.84
23:A:1302:G:OP1	48:4:16:ARG:NH1	2.11	0.83
22:v:4:PHE:HB2	22:v:39:VAL:CA	2.03	0.83
23:A:1078:G:O4'	52:8:18:LYS:NZ	2.12	0.83
33:P:9:TYR:CD1	33:P:10:ARG:N	2.47	0.83
23:A:615:A:N6	23:A:2056:G:H21	1.75	0.83
33:P:32:PHE:HB3	33:P:114:ALA:HB1	1.60	0.83
23:A:575:G:O2'	23:A:577:A:N7	2.10	0.83
23:A:1257:G:OP2	37:T:19:LYS:NZ	2.11	0.83
25:D:247:SER:OG	25:D:250:GLY:O	1.96	0.83
23:A:955:A:N3	23:A:2291:C:O2'	2.12	0.83
22:v:56:VAL:HG12	22:v:67:ALA:O	1.77	0.82
22:v:66:ARG:HB2	22:v:66:ARG:CZ	2.09	0.82
43:Z:31:ALA:HA	43:Z:46:TYR:HD1	1.44	0.81
1:a:435:C:OP1	4:d:13:ARG:NH1	2.15	0.81
1:a:1265:G:N2	1:a:1270:C:O2'	2.14	0.80
22:v:68:GLU:CG	22:v:69:GLU:N	2.22	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:975:A:H2	22:v:5:GLU:CD	1.90	0.80
22:v:60:LEU:HB2	22:v:63:VAL:O	1.81	0.80
23:A:2822:C:O2'	23:A:2823:G:O4'	2.00	0.80
23:A:1449:A:N7	23:A:1635:A:C6	2.49	0.80
23:A:2530:A:O2'	23:A:2532:G:OP2	1.99	0.80
18:r:26:ILE:HG13	18:r:63:ALA:HB1	1.64	0.80
23:A:2143:G:N2	23:A:2188:C:OP1	2.14	0.80
22:v:4:PHE:HZ	22:v:22:GLU:CD	1.90	0.79
1:a:1079:A:N1	1:a:1120:G:O2'	2.16	0.79
23:A:1584:A:O5'	23:A:1585:G:C8	2.35	0.79
23:A:1938:U:O2'	23:A:1945:A:N1	2.15	0.79
33:P:32:PHE:O	33:P:118:LEU:HD11	1.81	0.79
22:v:66:ARG:CZ	22:v:66:ARG:CB	2.60	0.79
23:A:418:G:O2'	23:A:446:G:O6	2.00	0.79
23:A:608:C:N4	23:A:619:U:O4	2.14	0.79
23:A:2060:A:O2'	23:A:2062:G:OP2	1.99	0.79
1:a:550:U:OP1	4:d:10:LYS:NZ	2.16	0.79
23:A:731:U:O5'	50:6:12:LYS:NZ	2.16	0.79
23:A:1652:A:O2'	23:A:1654:A:OP2	2.00	0.79
23:A:2649:U:O2'	23:A:2845:G:N2	2.15	0.79
1:a:533:C:OP1	12:l:101:LYS:CE	2.30	0.79
1:a:552:G:OP1	4:d:55:GLN:NE2	2.15	0.79
1:a:1504:A:OP1	12:l:57:LYS:NZ	2.15	0.79
23:A:52:A:OP2	23:A:118:A:N6	2.16	0.78
23:A:192:G:OP2	44:0:28:ARG:NH2	2.16	0.78
23:A:2124:U:O4	23:A:2219:C:N4	2.14	0.78
1:a:194:G:N2	1:a:197:U:OP2	2.17	0.78
1:a:1017:A:N6	1:a:1032:C:O2	2.17	0.78
1:a:415:A:OP1	4:d:108:ARG:NH2	2.15	0.78
34:Q:24:LEU:O	34:Q:28:GLU:HA	1.81	0.78
1:a:1164:G:O2'	1:a:1165:U:O5'	2.02	0.78
23:A:1288:G:OP1	32:O:21:ARG:NH2	2.17	0.78
1:a:73:G:N2	1:a:96:U:O4	2.16	0.78
23:A:1250:G:HO2'	23:A:1274:G:H1	1.28	0.78
23:A:2372:G:O6	23:A:2398:G:N2	2.17	0.78
25:D:29:GLU:OE1	25:D:102:TYR:OH	2.00	0.77
1:a:1388:A:OP1	7:g:95:ARG:NH2	2.16	0.77
23:A:1708:A:H61	23:A:2023:C:H42	1.29	0.77
26:E:133:ARG:NH1	26:E:169:MET:O	2.17	0.77
11:k:68:GLU:OE1	11:k:72:LYS:NZ	2.18	0.77
22:v:4:PHE:CD1	22:v:38:ALA:HB3	2.19	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1581:U:O5'	23:A:1584:A:N1	2.15	0.77
5:e:86:THR:OG1	5:e:94:VAL:O	2.00	0.77
23:A:864:A:OP2	23:A:1226:G:N2	2.16	0.77
1:a:975:A:O4'	1:a:979:A:C8	2.38	0.77
23:A:2821:U:OP2	23:A:2824:G:N2	2.17	0.77
1:a:1333:C:OP1	19:s:78:ARG:NH2	2.17	0.77
22:v:4:PHE:HZ	22:v:22:GLU:OE2	1.67	0.77
1:a:1281:G:HO2'	1:a:1324:U:HO2'	1.27	0.77
1:a:615:A:OP1	1:a:639:G:N2	2.17	0.77
1:a:961:G:N3	1:a:980:C:O2'	2.18	0.77
1:a:989:C:OP1	1:a:1234:C:N4	2.18	0.77
1:a:437:U:OP2	4:d:13:ARG:NH2	2.17	0.76
1:a:836:A:N6	1:a:868:G:H21	1.82	0.76
23:A:1806:U:OP2	23:A:1811:A:N6	2.18	0.76
43:Z:27:LYS:C	43:Z:29:LEU:H	1.92	0.76
23:A:1306:C:O2'	23:A:1307:G:H5'	1.84	0.76
23:A:1584:A:P	23:A:1585:G:H8	2.07	0.76
23:A:2362:A:OP1	35:R:17:ARG:NH1	2.18	0.76
49:5:40:ASN:OD1	49:5:41:LYS:NZ	2.19	0.76
1:a:692:U:O2'	11:k:41:ALA:N	2.19	0.76
9:i:11:THR:O	9:i:108:ARG:NH2	2.19	0.76
23:A:2304:G:OP2	43:Z:19:LYS:CD	2.33	0.76
1:a:1266:G:O2'	1:a:1269:G:N3	2.19	0.76
23:A:373:A:N6	23:A:1248:U:O4	2.19	0.76
23:A:928:C:N4	23:A:939:U:O2	2.18	0.76
30:M:42:LYS:NZ	30:M:51:THR:O	2.16	0.76
12:l:86:ASN:ND2	12:l:118:SER:O	2.19	0.76
15:o:76:GLN:OE1	15:o:79:ARG:NH2	2.18	0.76
23:A:672:A:O4'	23:A:682:A:N6	2.19	0.76
23:A:1111:A:N6	23:A:1140:A:OP1	2.19	0.76
23:A:1651:C:N4	23:A:1666:A:OP2	2.18	0.76
1:a:476:C:O2'	1:a:478:G:OP2	2.02	0.76
23:A:650:U:O2	23:A:666:A:N6	2.19	0.76
22:v:4:PHE:CZ	22:v:22:GLU:CD	2.64	0.75
23:A:1708:A:N6	23:A:2023:C:H42	1.84	0.75
23:A:2136:U:OP1	23:A:2169:G:N2	2.19	0.75
23:A:2842:G:O2'	23:A:2844:U:OP2	2.02	0.75
1:a:1137:U:O2'	1:a:1138:U:O5'	2.04	0.75
1:a:936:G:O6	1:a:1516:G:N2	2.19	0.75
29:H:107:VAL:O	29:H:152:ARG:NH1	2.19	0.75
33:P:9:TYR:HD1	33:P:10:ARG:C	1.94	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:116:G:OP2	23:A:118:A:O2'	2.03	0.75
23:A:1991:G:O2'	23:A:1994:C:OP2	2.04	0.75
23:A:59:U:O2'	23:A:74:U:OP2	2.04	0.75
1:a:421:G:N2	1:a:436:G:O3'	2.20	0.75
49:5:35:PHE:CE1	49:5:37:SER:CA	2.69	0.75
1:a:65:G:N2	1:a:70:A:N1	2.35	0.74
13:m:107:ARG:O	13:m:110:LYS:N	2.20	0.74
23:A:628:G:N7	23:A:1294:G:N2	2.35	0.74
18:r:25:HIS:HB3	18:r:26:ILE:HG12	1.69	0.74
23:A:2418:G:N2	23:A:2449:C:N3	2.34	0.74
33:P:22:LYS:HB3	33:P:98:LYS:HB2	1.57	0.74
22:v:22:GLU:OE1	22:v:22:GLU:HA	1.87	0.74
23:A:614:U:O2'	23:A:616:G:OP2	2.05	0.74
1:a:1071:U:OP2	3:c:198:LYS:NZ	2.18	0.74
33:P:21:SER:O	33:P:98:LYS:HE2	1.85	0.74
22:v:65:LEU:HD23	22:v:65:LEU:O	1.86	0.74
23:A:2298:G:H5''	43:Z:28:ARG:NH2	2.02	0.74
34:Q:52:LYS:NZ	34:Q:96:ARG:O	2.21	0.74
1:a:1107:U:OP1	1:a:1120:G:N2	2.18	0.74
23:A:925:G:N2	23:A:926:G:N7	2.35	0.74
37:T:48:ARG:NH2	37:T:49:ASP:OD1	2.21	0.74
43:Z:19:LYS:H	43:Z:19:LYS:HD2	1.53	0.74
1:a:693:G:OP2	11:k:11:ARG:NH1	2.21	0.74
1:a:1303:U:OP1	7:g:41:ARG:NH2	2.21	0.74
1:a:9:A:N6	4:d:196:GLU:O	2.21	0.73
1:a:526:C:OP2	1:a:538:G:O2'	2.05	0.73
1:a:1220:C:O2'	1:a:1225:U:O4	2.05	0.73
12:l:101:LYS:HD2	12:l:101:LYS:N	2.03	0.73
23:A:419:U:OP2	44:0:52:ARG:NH1	2.21	0.73
1:a:691:G:N2	11:k:40:ASN:OD1	2.15	0.73
1:a:948:A:N3	1:a:1387:U:O2'	2.16	0.73
23:A:1288:G:O2'	23:A:1289:A:OP2	2.06	0.73
23:A:1884:G:N2	23:A:1913:U:O4	2.20	0.73
23:A:1581:U:H3'	23:A:1584:A:C2	2.22	0.73
24:B:45:C:OP2	35:R:7:LYS:NZ	2.18	0.73
33:P:32:PHE:CE2	33:P:111:GLU:C	2.65	0.73
22:v:59:PRO:HA	22:v:64:THR:CB	2.17	0.73
33:P:22:LYS:HB3	33:P:98:LYS:HB3	1.09	0.73
1:a:467:U:O4	1:a:483:C:N4	2.17	0.73
23:A:1101:A:N6	23:A:1131:G:OP2	2.22	0.73
23:A:2684:A:O2'	29:H:160:LYS:NZ	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:533:C:OP1	12:l:101:LYS:HE2	1.88	0.73
33:P:28:THR:HA	33:P:134:ARG:HH12	1.52	0.73
17:q:52:ASN:OD1	17:q:54:SER:OG	2.05	0.72
23:A:1002:U:C6	24:B:87:G:N2	2.56	0.72
23:A:2383:C:H5'	43:Z:28:ARG:HG3	1.69	0.72
48:4:18:THR:O	48:4:21:LYS:NZ	2.21	0.72
1:a:360:C:O2	1:a:363:C:N4	2.22	0.72
32:O:80:ASP:O	32:O:83:ASN:ND2	2.22	0.72
23:A:1255:A:OP2	37:T:11:ARG:NH1	2.21	0.72
1:a:699:G:O6	11:k:57:LYS:NZ	2.22	0.72
23:A:318:A:N6	23:A:401:U:O4	2.21	0.72
23:A:902:A:OP1	43:Z:85:LYS:NZ	2.17	0.72
23:A:1135:G:O2'	23:A:1146:C:N3	2.21	0.72
23:A:2229:C:O2'	23:A:2231:C:OP1	2.03	0.72
1:a:804:C:OP2	11:k:126:ARG:NH1	2.23	0.72
23:A:1379:A:O2'	23:A:1381:U:OP2	2.08	0.72
23:A:2304:G:P	43:Z:19:LYS:CE	2.78	0.72
27:F:117:LYS:O	27:F:121:ASN:N	2.22	0.72
1:a:68:C:HO2'	1:a:171:A:HO2'	1.34	0.72
40:W:13:THR:O	40:W:16:SER:OG	2.04	0.72
17:q:65:GLU:OE1	17:q:74:ARG:NH2	2.22	0.71
23:A:2298:G:C5'	43:Z:28:ARG:HH22	2.01	0.71
23:A:2869:G:OP1	36:S:95:ARG:NH2	2.23	0.71
20:t:62:GLN:NE2	20:t:63:SER:OG	2.23	0.71
1:a:1014:A:OP1	1:a:1035:U:O2'	2.07	0.71
23:A:1121:A:O2'	23:A:1122:U:O4'	2.08	0.71
33:P:31:GLU:O	33:P:31:GLU:HG2	1.89	0.71
4:d:182:ARG:NH2	4:d:191:GLU:OE1	2.23	0.71
1:a:1025:G:N2	1:a:1229:U:O2	2.24	0.71
1:a:1047:G:OP2	1:a:1048:A:N6	2.23	0.71
23:A:1851:G:OP2	25:D:52:HIS:NE2	2.21	0.71
23:A:2717:A:OP2	34:Q:13:ARG:NH2	2.24	0.71
38:U:88:HIS:NE2	38:U:90:GLN:OE1	2.19	0.71
5:e:80:THR:OG1	5:e:122:ASP:OD1	2.07	0.71
9:i:14:ARG:NH1	9:i:109:ASP:OD2	2.24	0.71
23:A:904:G:N2	23:A:962:A:OP2	2.20	0.71
23:A:1301:U:O2'	48:4:8:THR:OG1	2.06	0.71
33:P:22:LYS:CB	33:P:98:LYS:C	2.63	0.70
41:X:44:HIS:O	41:X:54:GLY:N	2.24	0.70
49:5:32:MET:SD	49:5:46:ARG:NH1	2.64	0.70
1:a:559:U:O2'	12:l:96:ARG:NH2	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1076:G:N2	1:a:1202:A:OP2	2.22	0.70
6:f:52:ILE:HG21	6:f:87:ILE:CG2	2.22	0.70
15:o:61:GLY:O	15:o:65:HIS:ND1	2.23	0.70
23:A:1361:G:O2'	23:A:1363:U:OP2	2.07	0.70
23:A:1553:A:O2'	23:A:1555:G:N7	2.22	0.70
22:v:66:ARG:HB2	22:v:66:ARG:NH1	2.07	0.70
23:A:922:G:N2	23:A:945:A:N7	2.37	0.70
23:A:2142:G:N2	23:A:2189:G:OP1	2.24	0.70
37:T:26:GLY:O	37:T:29:HIS:ND1	2.23	0.70
1:a:1539:C:OP2	21:u:42:SER:OG	2.08	0.70
33:P:17:THR:HG21	33:P:96:VAL:HG11	0.76	0.70
1:a:261:U:O4'	1:a:283:G:N2	2.20	0.70
23:A:720:A:N3	23:A:2470:C:O2'	2.25	0.70
23:A:2404:A:O2'	35:R:119:PHE:OXT	2.10	0.70
29:H:119:GLU:OE2	29:H:120:ASN:ND2	2.25	0.70
33:P:32:PHE:CG	33:P:114:ALA:HB3	2.27	0.70
1:a:195:C:O2'	17:q:64:GLN:OE1	2.10	0.70
23:A:1591:G:O2'	23:A:1592:A:O4'	2.09	0.70
23:A:1449:A:N7	23:A:1635:A:N1	2.40	0.70
23:A:1349:U:O4	40:W:59:LYS:NZ	2.25	0.70
23:A:2505:A:OP1	52:8:31:LYS:NZ	2.17	0.70
1:a:235:G:N2	16:p:63:ASP:O	2.24	0.69
23:A:1002:U:C5	24:B:87:G:C2	2.80	0.69
33:P:28:THR:CA	33:P:134:ARG:NH1	2.51	0.69
7:g:63:GLU:OE2	7:g:67:ASN:ND2	2.24	0.69
11:k:55:SER:O	11:k:58:SER:OG	2.10	0.69
23:A:1169:G:OP2	23:A:1170:A:O2'	2.09	0.69
47:3:53:ASP:OD1	47:3:59:THR:OG1	2.11	0.69
1:a:109:C:O2'	16:p:26:ARG:O	2.10	0.69
1:a:446:G:N2	1:a:504:G:N7	2.38	0.69
23:A:2473:G:N2	23:A:2476:U:O2	2.22	0.69
24:B:35:C:N3	24:B:46:A:O2'	2.22	0.69
33:P:30:GLY:HA3	33:P:106:VAL:O	1.92	0.69
36:S:102:LEU:O	36:S:103:ARG:NE	2.26	0.69
23:A:714:G:N2	23:A:846:G:O6	2.26	0.69
28:G:89:VAL:O	28:G:92:ARG:N	2.24	0.69
23:A:621:A:O2'	23:A:623:C:OP2	2.10	0.69
23:A:1091:G:N2	23:A:1154:G:O2'	2.26	0.69
22:v:56:VAL:N	22:v:67:ALA:O	2.24	0.69
26:E:26:THR:OG1	26:E:199:GLY:O	2.09	0.69
1:a:102:C:OP1	20:t:12:LYS:NZ	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:307:G:N2	1:a:574:G:O6	2.26	0.69
1:a:682:G:O3'	6:f:50:TYR:OH	2.11	0.69
22:v:68:GLU:O	22:v:69:GLU:HB2	1.92	0.69
31:N:71:ARG:NE	31:N:105:GLU:OE2	2.26	0.69
51:7:26:ARG:O	51:7:40:GLN:NE2	2.26	0.69
43:Z:31:ALA:CA	43:Z:46:TYR:HD1	2.06	0.69
1:a:1384:G:OP2	9:i:75:THR:OG1	2.08	0.69
1:a:1411:C:O4'	22:v:88:GLN:NE2	2.25	0.69
1:a:82:G:O6	1:a:88:U:O2'	2.07	0.68
22:v:56:VAL:CG1	22:v:67:ALA:HB3	2.23	0.68
23:A:1323:A:O2'	23:A:1325:U:OP2	2.10	0.68
1:a:675:G:OP1	1:a:740:C:O2'	2.11	0.68
1:a:1528:G:N2	1:a:1531:A:OP2	2.26	0.68
23:A:2056:G:O2'	23:A:2057:A:OP1	2.11	0.68
33:P:32:PHE:CG	33:P:114:ALA:CB	2.76	0.68
1:a:409:C:O2'	1:a:629:A:N3	2.20	0.68
8:h:44:GLY:O	8:h:65:LYS:NZ	2.20	0.68
23:A:1360:G:O2'	23:A:1361:G:O5'	2.11	0.68
23:A:1891:U:O2	23:A:1905:G:O6	2.11	0.68
23:A:2403:A:N3	35:R:113:ARG:NH2	2.42	0.68
36:S:80:THR:HG22	36:S:82:LYS:H	1.57	0.68
23:A:1306:C:N4	23:A:2040:A:C8	2.62	0.68
23:A:1578:A:N6	23:A:1591:G:N7	2.42	0.68
38:U:68:GLY:O	38:U:89:ARG:NH2	2.27	0.68
44:O:29:TRP:CZ3	44:O:31:ALA:HB2	2.28	0.68
1:a:975:A:O4'	1:a:979:A:N9	2.27	0.68
1:a:1131:G:OP2	9:i:13:ARG:NH1	2.27	0.68
23:A:494:U:O4	23:A:625:G:N2	2.26	0.68
23:A:1449:A:C8	23:A:1635:A:N6	2.62	0.68
1:a:1262:A:N3	1:a:1380:C:O2'	2.23	0.68
8:h:80:ILE:HD11	8:h:130:TYR:CD2	2.28	0.68
23:A:2298:G:H5'	43:Z:28:ARG:HH21	1.58	0.68
33:P:9:TYR:CG	33:P:10:ARG:N	2.61	0.68
23:A:2304:G:OP1	43:Z:19:LYS:HG2	1.93	0.67
1:a:900:G:O2'	1:a:916:G:O6	2.13	0.67
1:a:1093:G:OP2	5:e:32:ARG:NH2	2.27	0.67
13:m:91:HIS:O	13:m:109:ARG:NH2	2.27	0.67
18:r:59:MET:O	18:r:62:THR:OG1	2.11	0.67
23:A:1400:C:O2'	23:A:1836:A:N3	2.26	0.67
23:A:1583:G:H3'	23:A:1584:A:H5''	1.76	0.67
23:A:1582:U:OP2	23:A:1584:A:C2	2.47	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2298:G:H5'	43:Z:28:ARG:HH22	1.57	0.67
33:P:9:TYR:CD1	33:P:10:ARG:CA	2.77	0.67
12:l:56:LYS:O	12:l:57:LYS:O	2.13	0.67
1:a:1065:G:O2'	1:a:1210:U:OP2	2.06	0.67
1:a:1115:C:O2'	2:b:110:ARG:NH2	2.28	0.67
23:A:1306:C:O2'	23:A:1307:G:C5'	2.42	0.67
36:S:61:PHE:O	36:S:75:THR:OG1	2.08	0.67
1:a:1124:C:O2'	3:c:178:ARG:NE	2.27	0.67
23:A:2298:G:H4'	43:Z:28:ARG:NH2	2.09	0.67
3:c:156:LEU:O	3:c:163:ARG:NH2	2.27	0.67
24:B:108:G:OP2	24:B:108:G:N2	2.24	0.67
33:P:22:LYS:CB	33:P:98:LYS:HB2	2.03	0.67
23:A:27:G:N2	23:A:558:A:OP2	2.28	0.66
1:a:1227:A:OP1	14:n:2:ALA:N	2.28	0.66
23:A:1576:A:H61	23:A:1587:C:H41	1.42	0.66
23:A:2298:G:H5'	43:Z:28:ARG:NH2	2.10	0.66
23:A:2827:A:H61	23:A:2912:A:H62	1.43	0.66
1:a:1330:A:O2'	1:a:1334:G:N7	2.28	0.66
23:A:2334:G:O2'	23:A:2337:A:OP2	2.14	0.66
23:A:2657:G:O2'	23:A:2911:A:O2'	2.11	0.66
1:a:725:C:O2'	1:a:742:A:O4'	2.05	0.66
1:a:1189:G:OP1	9:i:97:ARG:NH1	2.27	0.66
33:P:9:TYR:CD1	33:P:10:ARG:C	2.74	0.66
1:a:977:C:OP2	1:a:978:A:O2'	2.12	0.66
23:A:1581:U:O5'	23:A:1584:A:H2	1.74	0.66
23:A:2162:A:N6	23:A:2183:G:O2'	2.25	0.66
23:A:2293:A:N6	23:A:2300:A:OP2	2.28	0.66
1:a:1073:G:N7	3:c:3:GLN:NE2	2.43	0.66
1:a:1290:A:O2'	1:a:1292:U:OP2	2.10	0.66
22:v:4:PHE:HD1	22:v:38:ALA:N	1.94	0.66
49:5:35:PHE:HE1	49:5:37:SER:HB2	0.52	0.66
23:A:2127:G:C6	23:A:2216:U:O2	2.48	0.66
24:B:90:C:OP1	42:Y:19:LYS:NZ	2.24	0.66
1:a:605:G:O3'	17:q:39:ARG:NH2	2.28	0.66
23:A:1491:C:O2	23:A:1574:G:N2	2.29	0.66
23:A:1518:G:O2'	23:A:1519:U:O5'	2.13	0.66
33:P:27:VAL:HG22	33:P:105:GLU:OE1	1.95	0.66
1:a:428:U:O2'	1:a:431:G:O6	2.07	0.66
1:a:1233:G:OP2	1:a:1333:C:N4	2.29	0.66
33:P:32:PHE:CD2	33:P:114:ALA:HB3	2.30	0.66
33:P:86:GLY:HA3	43:Z:19:LYS:CE	2.22	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:410:G:OP2	4:d:66:ARG:NH1	2.29	0.65
1:a:823:A:O4'	1:a:825:C:N4	2.28	0.65
22:v:68:GLU:O	22:v:69:GLU:CB	2.43	0.65
23:A:1000:G:N7	33:P:16:LYS:NZ	2.44	0.65
33:P:75:THR:OG1	33:P:89:ALA:O	2.07	0.65
18:r:41:ARG:O	18:r:77:LYS:N	2.29	0.65
23:A:1357:G:OP2	23:A:1357:G:N2	2.26	0.65
23:A:2877:G:N2	23:A:2880:A:OP2	2.26	0.65
23:A:1250:G:N2	23:A:1274:G:O2'	2.30	0.65
43:Z:19:LYS:HD2	43:Z:19:LYS:N	2.11	0.65
49:5:35:PHE:HD1	49:5:35:PHE:O	1.79	0.65
20:t:17:ALA:O	20:t:21:ASN:ND2	2.29	0.65
23:A:922:G:N1	23:A:944:G:O6	2.29	0.65
23:A:1452:C:N3	23:A:1632:A:N6	2.43	0.65
47:3:17:THR:HG23	47:3:18:THR:HG23	1.78	0.65
1:a:465:U:C4	1:a:486:C:N4	2.65	0.65
1:a:976:G:C6	1:a:977:C:N4	2.64	0.65
22:v:4:PHE:CD1	22:v:38:ALA:CA	2.79	0.65
5:e:107:ALA:O	5:e:112:ARG:NH2	2.30	0.65
22:v:4:PHE:HD1	22:v:38:ALA:H	1.43	0.65
23:A:342:A:OP1	41:X:80:ARG:NH1	2.29	0.65
31:N:13:ASN:OD1	31:N:97:ARG:N	2.30	0.65
1:a:125:G:OP1	1:a:613:U:O2'	2.06	0.65
1:a:218:U:OP2	1:a:219:C:N4	2.29	0.65
1:a:1093:G:N7	5:e:52:LYS:NZ	2.45	0.65
23:A:1255:A:OP1	37:T:15:LYS:NZ	2.28	0.65
23:A:2710:C:O2	31:N:76:TYR:OH	2.15	0.65
6:f:45:LYS:NZ	6:f:57:ASP:OD2	2.23	0.65
33:P:31:GLU:HG2	33:P:133:LYS:HB3	1.78	0.65
22:v:56:VAL:HG13	22:v:67:ALA:HB3	1.78	0.65
1:a:975:A:H2	22:v:5:GLU:CG	2.10	0.64
26:E:185:VAL:HG22	26:E:197:VAL:HG12	1.78	0.64
1:a:975:A:H1'	1:a:979:A:C5	2.32	0.64
7:g:118:ASP:OD1	7:g:119:ARG:N	2.31	0.64
9:i:115:ARG:NH1	14:n:61:TRP:OXT	2.29	0.64
23:A:1067:U:OP2	23:A:1069:G:O2'	2.15	0.64
1:a:1085:U:O2'	2:b:103:ASN:OD1	2.10	0.64
43:Z:28:ARG:O	43:Z:32:LYS:NZ	2.19	0.64
45:1:42:ARG:O	45:1:45:THR:OG1	2.16	0.64
1:a:1327:G:OP2	19:s:6:LYS:NZ	2.29	0.64
14:n:3:LYS:O	14:n:7:VAL:HG23	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:O:83:ASN:OD1	32:O:84:LYS:N	2.31	0.64
45:1:62:ILE:O	45:1:65:SER:OG	2.09	0.64
50:6:31:VAL:HG22	50:6:34:ARG:HH21	1.63	0.64
1:a:103:G:OP2	20:t:9:LYS:NZ	2.24	0.64
1:a:790:A:H62	1:a:808:G:H21	1.45	0.64
19:s:36:ARG:NH1	19:s:72:GLY:O	2.30	0.64
23:A:1584:A:OP1	23:A:1585:G:C8	2.50	0.64
22:v:97:ASN:O	22:v:98:ARG:NE	2.27	0.64
23:A:1583:G:H3'	23:A:1584:A:C5'	2.27	0.64
1:a:541:A:O2'	1:a:543:A:OP2	2.14	0.64
1:a:975:A:O2'	1:a:976:G:O5'	2.10	0.64
23:A:528:C:N4	23:A:551:G:O2'	2.31	0.64
23:A:2141:A:O2'	23:A:2193:G:O2'	2.15	0.64
23:A:138:U:N3	23:A:141:U:OP2	2.30	0.64
23:A:312:A:O2'	23:A:315:C:O2	2.16	0.64
23:A:1591:G:OP2	23:A:1592:A:N6	2.31	0.64
25:D:171:VAL:N	25:D:183:ILE:O	2.31	0.64
1:a:975:A:C2	22:v:5:GLU:CG	2.80	0.64
23:A:2383:C:C4'	43:Z:28:ARG:CG	2.72	0.64
29:H:9:ILE:O	29:H:49:THR:OG1	2.09	0.64
1:a:504:G:N2	1:a:506:A:OP2	2.30	0.63
9:i:12:GLY:N	9:i:19:ALA:O	2.31	0.63
12:l:86:ASN:ND2	12:l:118:SER:OG	2.32	0.63
22:v:4:PHE:CE1	22:v:38:ALA:HB3	2.32	0.63
22:v:5:GLU:O	22:v:7:HIS:N	2.31	0.63
23:A:1631:G:OP1	23:A:1631:G:N2	2.32	0.63
7:g:68:ASN:O	7:g:138:ARG:NE	2.29	0.63
9:i:66:LEU:HD13	9:i:67:VAL:N	2.13	0.63
23:A:1298:G:OP1	39:V:83:LYS:NZ	2.31	0.63
23:A:2024:A:OP2	26:E:138:ARG:NH1	2.31	0.63
1:a:332:G:N1	1:a:335:A:OP2	2.31	0.63
1:a:1458:A:OP1	1:a:1459:C:N4	2.32	0.63
22:v:65:LEU:CD1	22:v:88:GLN:CB	2.36	0.63
23:A:672:A:N7	32:O:70:ASN:ND2	2.41	0.63
23:A:1064:A:N1	23:A:1185:U:O2'	2.29	0.63
1:a:975:A:C5'	1:a:975:A:H8	2.11	0.63
27:F:144:SER:HA	27:F:186:ILE:HG21	1.80	0.63
22:v:60:LEU:CA	22:v:63:VAL:O	2.47	0.63
23:A:2869:G:N2	23:A:2886:G:O3'	2.30	0.63
1:a:515:C:OP2	1:a:516:U:O2'	2.13	0.63
1:a:976:G:N1	1:a:977:C:C4	2.66	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:142:G:O2'	1:a:210:A:N1	2.31	0.63
1:a:195:C:O2	17:q:7:ARG:NE	2.32	0.63
23:A:2683:U:N3	23:A:2692:A:C8	2.66	0.63
2:b:94:GLN:NE2	2:b:146:LYS:O	2.28	0.62
3:c:56:ILE:HG22	3:c:65:ILE:HG22	1.81	0.62
43:Z:33:ARG:HG2	43:Z:45:LEU:CD2	2.28	0.62
23:A:2375:U:OP2	51:7:35:ASN:ND2	2.32	0.62
1:a:370:G:OP2	12:l:44:ARG:NH2	2.32	0.62
43:Z:27:LYS:HD3	43:Z:27:LYS:H	1.64	0.62
22:v:60:LEU:N	22:v:63:VAL:O	2.30	0.62
23:A:488:G:N2	27:F:48:THR:O	2.31	0.62
23:A:1891:U:C2	23:A:1905:G:O6	2.52	0.62
23:A:2250:A:OP1	25:D:170:TYR:OH	2.10	0.62
1:a:1542:G:O6	21:u:46:LYS:NZ	2.22	0.62
3:c:134:LYS:O	3:c:138:THR:OG1	2.15	0.62
15:o:29:ILE:O	15:o:33:THR:OG1	2.14	0.62
29:H:64:ASN:O	29:H:68:THR:OG1	2.10	0.62
9:i:76:GLY:O	9:i:80:ALA:N	2.31	0.62
23:A:1002:U:C4	24:B:87:G:N1	2.67	0.62
23:A:1306:C:C2	23:A:2040:A:C6	2.88	0.62
41:X:7:ASP:OD2	41:X:69:GLN:NE2	2.32	0.62
1:a:1158:C:O2	9:i:20:ARG:NH1	2.32	0.62
6:f:2:ARG:N	6:f:67:SER:O	2.33	0.62
22:v:60:LEU:CB	22:v:63:VAL:O	2.48	0.62
23:A:254:A:OP1	51:7:7:HIS:NE2	2.32	0.62
23:A:2347:A:O2'	23:A:2360:A:N7	2.30	0.62
1:a:1200:U:OP1	10:j:53:ARG:NH2	2.32	0.62
17:q:31:LYS:O	17:q:40:VAL:N	2.32	0.62
1:a:247:C:OP1	17:q:34:LYS:NZ	2.32	0.62
1:a:987:A:N6	1:a:1235:U:OP1	2.26	0.62
33:P:32:PHE:CB	33:P:114:ALA:HB1	2.30	0.62
1:a:1428:G:O2'	1:a:1495:A:N6	2.31	0.62
23:A:2560:U:OP1	23:A:2692:A:O2'	2.17	0.62
33:P:28:THR:HA	33:P:134:ARG:CZ	2.29	0.62
40:W:51:ALA:HB1	40:W:81:THR:HG23	1.82	0.61
1:a:129:A:OP1	17:q:2:SER:OG	2.13	0.61
31:N:64:ARG:NH1	31:N:100:GLY:O	2.32	0.61
2:b:66:GLN:NE2	2:b:156:SER:O	2.34	0.61
23:A:86:C:OP1	41:X:29:LYS:NZ	2.21	0.61
1:a:388:G:N2	1:a:391:A:OP2	2.21	0.61
1:a:405:A:O2'	1:a:407:G:OP2	2.10	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:e:166:ASN:OD1	8:h:100:GLY:N	2.34	0.61
23:A:2589:U:O2'	31:N:23:LYS:NZ	2.33	0.61
1:a:533:C:P	12:l:101:LYS:CE	2.88	0.61
2:b:9:LEU:O	2:b:13:GLY:N	2.32	0.61
22:v:65:LEU:HD11	22:v:88:GLN:HB3	0.69	0.61
23:A:1306:C:C4	23:A:2040:A:C5	2.88	0.61
41:X:95:LYS:N	41:X:98:GLY:O	2.33	0.61
14:n:8:ALA:O	14:n:12:LYS:N	2.34	0.61
23:A:2383:C:C5'	43:Z:28:ARG:HG3	2.30	0.61
23:A:528:C:O2'	23:A:542:A:N1	2.33	0.61
3:c:14:ILE:HG22	3:c:15:ILE:HG23	1.82	0.61
21:u:39:GLU:OE1	21:u:39:GLU:N	2.34	0.61
23:A:1309:G:O2'	23:A:1662:A:OP1	2.15	0.61
23:A:2305:A:OP1	33:P:13:HIS:ND1	2.33	0.61
1:a:984:A:N1	1:a:993:A:N6	2.41	0.61
9:i:32:VAL:HG23	9:i:67:VAL:HG13	1.81	0.61
45:l:46:VAL:O	45:l:49:THR:OG1	2.17	0.61
1:a:143:A:O2'	1:a:212:A:OP1	2.13	0.61
1:a:1262:A:H61	1:a:1365:U:HO2'	1.48	0.61
1:a:1327:G:N1	1:a:1330:A:OP2	2.34	0.61
23:A:1957:G:O2'	23:A:1995:G:O6	2.18	0.61
29:H:60:GLU:O	29:H:63:THR:OG1	2.15	0.60
34:Q:21:ALA:O	34:Q:25:ILE:HD12	2.00	0.60
1:a:1516:G:O4'	1:a:1517:G:N2	2.34	0.60
23:A:1963:A:OP2	23:A:1989:C:N4	2.35	0.60
33:P:32:PHE:CD2	33:P:114:ALA:CB	2.84	0.60
1:a:1318:U:OP1	13:m:100:GLN:NE2	2.33	0.60
1:a:1213:U:O4'	14:n:29:ARG:NH2	2.35	0.60
2:b:166:PRO:O	2:b:170:ARG:N	2.34	0.60
22:v:54:ILE:O	22:v:68:GLU:HG2	2.01	0.60
23:A:287:G:N2	23:A:289:U:O4'	2.33	0.60
47:3:66:ALA:HB1	47:3:68:ASP:OD1	2.01	0.60
1:a:370:G:N2	1:a:373:U:OP2	2.35	0.60
1:a:1279:G:N3	1:a:1337:U:O2'	2.28	0.60
23:A:1826:G:N2	23:A:1846:A:OP2	2.30	0.60
1:a:209:G:N2	1:a:231:U:O4'	2.34	0.60
1:a:976:G:C6	22:v:66:ARG:NH2	2.70	0.60
1:a:773:G:H1	1:a:820:G:HO2'	1.47	0.60
12:l:102:ASP:OD1	12:l:103:LEU:N	2.34	0.60
23:A:1306:C:C4	23:A:2040:A:N7	2.69	0.60
1:a:1316:G:O2'	1:a:1317:A:OP2	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:d:67:GLN:O	4:d:71:THR:OG1	2.14	0.60
23:A:659:A:O2'	27:F:43:SER:OG	2.20	0.60
23:A:1579:C:N4	23:A:1582:U:O4	2.35	0.60
33:P:28:THR:CA	33:P:134:ARG:HH12	2.14	0.60
1:a:555:A:OP2	4:d:3:ARG:NH1	2.35	0.60
3:c:7:PRO:O	3:c:11:ARG:N	2.34	0.60
17:q:7:ARG:O	17:q:9:VAL:HG13	2.01	0.60
23:A:125:A:C2	50:6:23:MET:HE1	2.37	0.60
23:A:2298:G:H4'	43:Z:28:ARG:HH22	1.65	0.60
1:a:800:A:O2'	1:a:802:A:N7	2.27	0.60
1:a:790:A:H62	1:a:808:G:N2	2.00	0.59
7:g:74:GLU:OE1	7:g:74:GLU:N	2.35	0.59
23:A:616:G:N2	23:A:2058:A:OP1	2.35	0.59
37:T:108:GLN:O	37:T:111:THR:OG1	2.19	0.59
1:a:1231:G:N2	19:s:54:GLY:O	2.35	0.59
2:b:83:GLU:OE2	2:b:218:ALA:HB2	2.03	0.59
23:A:1584:A:P	23:A:1585:G:C8	2.95	0.59
35:R:84:ALA:O	35:R:88:GLY:N	2.34	0.59
51:7:34:ALA:O	51:7:38:THR:OG1	2.06	0.59
1:a:557:C:N4	1:a:558:G:O6	2.35	0.59
1:a:976:G:C5	22:v:66:ARG:CZ	2.84	0.59
1:a:1374:A:O2'	1:a:1376:G:N7	2.34	0.59
14:n:10:GLN:OE1	14:n:21:TYR:N	2.34	0.59
22:v:60:LEU:HD13	22:v:64:THR:HA	1.84	0.59
25:D:132:GLN:OE1	25:D:133:ASN:ND2	2.35	0.59
31:N:80:ASP:OD2	36:S:64:ARG:NH2	2.36	0.59
23:A:166:A:O2'	23:A:167:U:OP2	2.19	0.59
23:A:1581:U:P	23:A:1584:A:C2	2.95	0.59
23:A:2770:U:OP2	23:A:2782:C:N4	2.35	0.59
23:A:427:A:OP1	44:0:20:HIS:NE2	2.29	0.59
23:A:1306:C:H2'	23:A:1307:G:C8	2.38	0.59
1:a:481:C:O4'	16:p:89:LYS:NZ	2.29	0.59
4:d:150:ILE:O	4:d:154:SER:OG	2.10	0.59
23:A:2276:U:N3	23:A:2280:G:OP2	2.35	0.59
23:A:2860:U:H5''	34:Q:49:THR:HG21	1.85	0.59
3:c:45:GLU:O	3:c:49:ALA:N	2.34	0.59
1:a:211:A:N1	1:a:228:A:O2'	2.32	0.59
22:v:65:LEU:HD11	22:v:88:GLN:HB2	1.73	0.59
23:A:1378:U:OP1	23:A:1434:U:N3	2.36	0.59
4:d:45:SER:O	4:d:48:GLY:N	2.35	0.59
12:l:56:LYS:O	12:l:57:LYS:C	2.46	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2745:G:O2'	23:A:2867:U:OP1	2.20	0.59
1:a:626:C:C2	1:a:630:A:N6	2.71	0.59
23:A:2078:A:N6	23:A:2641:A:O2'	2.36	0.59
23:A:2806:U:OP1	23:A:2807:G:N2	2.35	0.59
24:B:28:C:OP2	35:R:37:ASN:ND2	2.35	0.59
1:a:572:U:OP1	12:l:12:ARG:NH2	2.36	0.58
23:A:2667:G:OP1	30:M:100:ARG:NH1	2.35	0.58
1:a:1262:A:N6	1:a:1365:U:O2'	2.33	0.58
23:A:618:A:OP2	23:A:2526:C:O2'	2.22	0.58
35:R:56:ALA:HB3	35:R:80:ILE:HD11	1.85	0.58
14:n:26:ARG:NH1	14:n:43:CYS:SG	2.76	0.58
18:r:26:ILE:HB	18:r:63:ALA:HB1	1.85	0.58
23:A:688:A:N1	23:A:2396:A:O2'	2.29	0.58
23:A:1137:G:N2	23:A:1143:G:N7	2.51	0.58
30:M:72:ASP:OD1	30:M:73:LYS:N	2.37	0.58
43:Z:29:LEU:HD23	43:Z:29:LEU:O	2.02	0.58
22:v:65:LEU:HD23	22:v:65:LEU:C	2.28	0.58
19:s:39:THR:OG1	47:3:83:ASN:O	2.15	0.58
22:v:98:ARG:HB3	22:v:99:LYS:HA	1.86	0.58
23:A:1885:G:H2'	23:A:1910:G:H22	1.68	0.58
23:A:2804:G:OP2	23:A:2808:A:O2'	2.21	0.58
1:a:1306:U:O3'	13:m:43:THR:OG1	2.22	0.58
15:o:43:LEU:O	15:o:46:HIS:O	2.21	0.58
1:a:597:U:O2'	8:h:57:GLN:OE1	2.14	0.58
1:a:975:A:H8	1:a:975:A:O5'	1.86	0.58
1:a:1378:U:O3'	10:j:62:ARG:NH2	2.37	0.58
23:A:1306:C:H2'	23:A:1307:G:H8	1.69	0.58
23:A:1360:G:HO2'	23:A:1361:G:P	2.26	0.58
41:X:24:ILE:HG22	41:X:25:ALA:H	1.69	0.58
1:a:421:G:N2	1:a:436:G:O2'	2.37	0.58
1:a:976:G:C6	22:v:66:ARG:CZ	2.87	0.58
23:A:1002:U:C4	24:B:87:G:C2	2.92	0.58
23:A:1396:A:OP2	23:A:1408:G:N1	2.35	0.58
23:A:1581:U:H5	23:A:1584:A:H1'	1.69	0.58
23:A:2672:G:N2	23:A:2794:C:OP2	2.37	0.58
1:a:8:G:O6	5:e:97:LYS:NZ	2.24	0.58
13:m:72:GLU:O	13:m:76:ASN:ND2	2.37	0.58
23:A:1063:U:O2'	23:A:1065:A:N7	2.36	0.58
22:v:6:ILE:O	22:v:6:ILE:HG22	2.03	0.57
25:D:141:HIS:ND1	25:D:192:GLY:O	2.34	0.57
43:Z:30:GLY:O	43:Z:32:LYS:CE	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:3:65:ALA:O	47:3:67:ALA:HB3	2.04	0.57
1:a:819:C:O2'	1:a:911:A:N1	2.37	0.57
1:a:1083:C:OP1	5:e:30:ARG:NH2	2.36	0.57
23:A:1002:U:C2	24:B:87:G:N2	2.72	0.57
23:A:1093:C:N4	23:A:2778:G:O6	2.34	0.57
25:D:29:GLU:OE1	25:D:29:GLU:N	2.36	0.57
22:v:68:GLU:N	22:v:81:ILE:HD11	2.19	0.57
31:N:112:MET:O	31:N:116:SER:N	2.38	0.57
49:5:35:PHE:CD1	49:5:35:PHE:O	2.56	0.57
1:a:83:C:O2'	1:a:85:U:OP2	2.20	0.57
7:g:68:ASN:ND2	7:g:130:ASN:OD1	2.37	0.57
23:A:2277:G:OP1	23:A:2302:C:O2'	2.19	0.57
23:A:2298:G:OP1	43:Z:26:SER:OG	2.18	0.57
1:a:127:A:O2'	17:q:7:ARG:NH1	2.37	0.57
1:a:371:A:H62	12:l:38:LEU:HD11	1.69	0.57
23:A:2851:G:N2	23:A:2904:U:OP2	2.35	0.57
33:P:32:PHE:CB	33:P:114:ALA:CB	2.83	0.57
1:a:75:A:N6	1:a:94:G:O2'	2.38	0.57
1:a:554:A:OP2	4:d:58:ARG:NH2	2.36	0.57
17:q:31:LYS:N	17:q:40:VAL:O	2.37	0.57
23:A:1000:G:N2	23:A:1004:A:OP2	2.35	0.57
8:h:128:ILE:HG22	8:h:129:ALA:HB2	1.87	0.57
23:A:2161:A:H61	23:A:2184:G:C2'	2.18	0.57
30:M:65:PHE:O	30:M:66:THR:OG1	2.16	0.57
33:P:26:TYR:OH	42:Y:79:PHE:O	2.23	0.57
33:P:29:PHE:HB3	33:P:65:TRP:CZ3	2.40	0.57
1:a:971:U:O2	1:a:993:A:O2'	2.22	0.57
1:a:1324:U:OP1	19:s:7:LYS:NZ	2.24	0.57
22:v:4:PHE:CD1	22:v:38:ALA:CB	2.86	0.57
1:a:16:G:O4'	1:a:1407:A:O2'	2.22	0.57
1:a:483:C:O2'	1:a:484:A:O5'	2.23	0.57
1:a:525:G:N2	1:a:538:G:OP1	2.38	0.57
1:a:151:A:OP2	1:a:169:C:N4	2.37	0.56
1:a:975:A:C1'	1:a:979:A:C8	2.88	0.56
4:d:66:ARG:O	4:d:70:ASN:ND2	2.38	0.56
23:A:1002:U:N3	24:B:87:G:N2	2.52	0.56
23:A:1094:A:N3	23:A:2778:G:N2	2.50	0.56
23:A:1450:A:O2'	23:A:1451:U:O4'	2.12	0.56
23:A:1827:C:OP1	25:D:259:ARG:NH1	2.35	0.56
23:A:2304:G:OP2	43:Z:19:LYS:HE2	2.04	0.56
33:P:70:PRO:HA	33:P:95:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Z:27:LYS:H	43:Z:27:LYS:CD	2.18	0.56
8:h:8:ALA:O	8:h:12:THR:OG1	2.16	0.56
23:A:192:G:O2'	23:A:210:A:N6	2.37	0.56
35:R:71:GLU:O	35:R:74:THR:OG1	2.12	0.56
6:f:84:ASP:OD1	6:f:85:ASP:N	2.38	0.56
23:A:1237:U:HO2'	23:A:1288:G:H1	1.52	0.56
29:H:10:ASP:OD1	29:H:11:ILE:N	2.38	0.56
8:h:104:ALA:HB2	8:h:130:TYR:CD1	2.41	0.56
33:P:22:LYS:HG2	33:P:99:PRO:HD2	0.65	0.56
33:P:28:THR:HG22	33:P:134:ARG:NH1	2.21	0.56
1:a:237:U:O2'	16:p:24:ASP:OD1	2.24	0.56
1:a:797:U:N3	1:a:800:A:OP2	2.38	0.56
23:A:932:U:N3	23:A:935:C:N3	2.53	0.56
30:M:58:ILE:HD11	30:M:129:ALA:C	2.31	0.56
23:A:2195:G:N1	23:A:2197:G:N7	2.53	0.56
24:B:7:G:OP1	35:R:19:ARG:NH1	2.39	0.56
3:c:55:GLU:OE1	3:c:55:GLU:N	2.38	0.56
23:A:83:G:N1	23:A:101:G:O2'	2.33	0.56
23:A:2298:G:C4'	43:Z:28:ARG:NH2	2.68	0.56
23:A:2298:G:C4'	43:Z:28:ARG:HH22	2.19	0.56
23:A:1377:U:OP2	40:W:58:TYR:OH	2.23	0.56
47:3:12:VAL:HG13	47:3:13:ILE:HG13	1.87	0.56
7:g:148:ASN:O	7:g:148:ASN:ND2	2.38	0.56
20:t:33:LYS:O	20:t:37:THR:OG1	2.09	0.56
42:Y:27:VAL:HG12	42:Y:28:PRO:O	2.06	0.56
1:a:1076:G:O3'	1:a:1201:G:N2	2.34	0.55
3:c:194:LYS:C	3:c:195:LEU:HD12	2.32	0.55
31:N:7:ARG:C	31:N:8:LEU:HD12	2.31	0.55
1:a:107:G:O6	20:t:10:ARG:NE	2.38	0.55
1:a:319:C:OP1	16:p:32:ARG:NH1	2.39	0.55
12:l:29:ASN:ND2	12:l:71:SER:O	2.40	0.55
23:A:562:C:O2'	39:V:78:GLU:OE2	2.22	0.55
23:A:600:U:OP1	30:M:114:ARG:NH1	2.39	0.55
7:g:42:ILE:O	7:g:45:SER:OG	2.23	0.55
9:i:32:VAL:N	9:i:35:ARG:O	2.39	0.55
20:t:45:ASN:N	20:t:48:GLU:OE2	2.38	0.55
23:A:650:U:C2	23:A:666:A:N6	2.74	0.55
23:A:1301:U:O3'	48:4:8:THR:OG1	2.25	0.55
23:A:2118:U:OP2	23:A:2119:U:O2'	2.15	0.55
12:l:26:LYS:O	12:l:72:ASN:ND2	2.33	0.55
33:P:22:LYS:HG2	33:P:99:PRO:CG	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:Q:100:TYR:O	34:Q:101:THR:OG1	2.18	0.55
1:a:1408:C:OP2	5:e:29:ARG:NH2	2.37	0.55
43:Z:70:LYS:HB2	43:Z:71:ILE:HD12	1.88	0.55
1:a:1279:G:H21	1:a:1337:U:H2'	1.72	0.55
22:v:47:TYR:N	22:v:48:SER:HA	2.22	0.55
23:A:1520:A:OP2	23:A:1521:A:N6	2.39	0.55
23:A:2686:G:OP1	29:H:158:LYS:NZ	2.32	0.55
25:D:194:VAL:HG12	25:D:195:GLY:H	1.71	0.55
1:a:1055:G:O2'	1:a:1056:A:O5'	2.24	0.55
1:a:1310:A:HO2'	1:a:1312:U:H6	1.55	0.55
23:A:2512:G:OP1	33:P:45:ARG:NH2	2.39	0.55
42:Y:57:ARG:NH2	42:Y:75:ALA:O	2.40	0.55
1:a:1534:U:O3'	11:k:126:ARG:NH2	2.38	0.55
33:P:9:TYR:HD1	33:P:11:ARG:N	2.05	0.55
23:A:909:G:N2	23:A:911:A:H61	2.05	0.55
23:A:2618:C:N4	23:A:2619:G:O6	2.39	0.55
2:b:115:SER:OG	2:b:152:ARG:NH2	2.40	0.54
23:A:955:A:H62	33:P:15:PRO:HD3	1.71	0.54
23:A:2851:G:H21	23:A:2904:U:P	2.30	0.54
29:H:57:ASP:OD1	29:H:62:ARG:NH1	2.40	0.54
1:a:937:G:O2'	1:a:1515:A:N6	2.39	0.54
22:v:55:GLU:HG3	22:v:68:GLU:HB2	1.89	0.54
23:A:1615:G:OP1	25:D:62:ARG:NH2	2.39	0.54
43:Z:57:GLU:N	43:Z:57:GLU:OE1	2.40	0.54
23:A:321:U:O2'	23:A:322:A:OP1	2.22	0.54
23:A:2046:U:OP2	48:4:6:ARG:NH2	2.39	0.54
29:H:61:ASP:OD1	29:H:62:ARG:N	2.40	0.54
1:a:975:A:HO2'	1:a:976:G:P	2.30	0.54
23:A:2236:C:OP2	23:A:2237:U:O2'	2.22	0.54
44:0:29:TRP:CH2	44:0:31:ALA:HB2	2.42	0.54
33:P:22:LYS:HD2	33:P:99:PRO:C	2.23	0.54
47:3:12:VAL:HG13	47:3:13:ILE:CG1	2.38	0.54
1:a:195:C:N4	17:q:2:SER:O	2.36	0.54
1:a:790:A:N6	1:a:808:G:H21	2.05	0.54
23:A:592:A:O2'	23:A:593:U:O5'	2.25	0.54
23:A:2261:G:H8	23:A:2261:G:O5'	1.91	0.54
23:A:2776:A:H1'	29:H:63:THR:HG22	1.90	0.54
11:k:17:GLU:O	11:k:81:THR:OG1	2.22	0.54
15:o:74:ASP:OD1	15:o:75:ILE:N	2.40	0.54
11:k:64:GLN:HE21	11:k:95:SER:HB3	1.73	0.54
22:v:59:PRO:N	22:v:64:THR:OG1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:77:GLN:OE1	29:H:83:TYR:OH	2.15	0.54
43:Z:27:LYS:HD3	43:Z:27:LYS:N	2.23	0.54
25:D:76:LYS:HG2	25:D:114:ILE:HG22	1.90	0.54
23:A:2119:U:N3	23:A:2253:C:OP2	2.41	0.54
25:D:196:ASN:HD22	25:D:197:LEU:N	2.05	0.54
1:a:990:C:O2'	14:n:19:ARG:O	2.15	0.53
23:A:1550:G:O2'	23:A:1551:U:O4'	2.25	0.53
26:E:156:MET:SD	26:E:156:MET:N	2.81	0.53
33:P:25:ASN:O	33:P:26:TYR:CD1	2.59	0.53
45:1:45:THR:O	45:1:49:THR:HG23	2.08	0.53
1:a:1548:C:N4	21:u:52:ALA:O	2.41	0.53
23:A:921:C:N4	23:A:922:G:O6	2.41	0.53
1:a:648:A:N6	1:a:649:A:N1	2.56	0.53
22:v:62:ASN:O	22:v:62:ASN:ND2	2.40	0.53
34:Q:107:GLY:O	34:Q:116:SER:OG	2.19	0.53
42:Y:22:ARG:HE	42:Y:87:THR:HG23	1.73	0.53
1:a:598:U:OP1	8:h:31:ASN:ND2	2.42	0.53
3:c:118:ASN:OD1	3:c:122:GLN:NE2	2.38	0.53
23:A:419:U:OP2	23:A:446:G:N1	2.40	0.53
26:E:38:LYS:NZ	26:E:96:VAL:O	2.37	0.53
29:H:70:ALA:O	29:H:74:ASN:ND2	2.41	0.53
1:a:735:G:N1	1:a:738:G:OP2	2.40	0.53
10:j:44:THR:HG23	10:j:70:HIS:HA	1.91	0.53
23:A:579:U:O2'	37:T:49:ASP:OD2	2.19	0.53
23:A:1581:U:C6	23:A:1584:A:N3	2.76	0.53
33:P:22:LYS:CD	33:P:99:PRO:CG	2.73	0.53
2:b:83:GLU:CD	2:b:218:ALA:HB2	2.33	0.53
25:D:171:VAL:O	25:D:183:ILE:N	2.37	0.53
27:F:177:THR:OG1	27:F:180:GLY:N	2.39	0.53
29:H:22:ASN:OD1	29:H:23:HIS:N	2.42	0.53
23:A:1360:G:OP1	39:V:98:LYS:NZ	2.34	0.53
34:Q:39:GLU:OE1	34:Q:39:GLU:N	2.42	0.53
1:a:598:U:OP1	8:h:30:SER:OG	2.27	0.53
4:d:114:VAL:HG23	4:d:119:ILE:HD11	1.91	0.53
23:A:416:G:OP2	23:A:469:A:N6	2.42	0.53
17:q:86:ILE:HD12	17:q:86:ILE:O	2.09	0.53
23:A:275:A:H62	23:A:296:G:N2	2.06	0.53
39:V:28:ASN:OD1	39:V:29:ALA:N	2.42	0.53
1:a:996:A:N3	19:s:52:TYR:OH	2.38	0.52
16:p:9:ARG:O	16:p:29:ARG:NH1	2.42	0.52
23:A:10:A:O2'	23:A:11:U:O4'	2.16	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:659:A:HO2'	27:F:43:SER:HG	1.49	0.52
23:A:788:A:O2'	23:A:1703:U:OP1	2.27	0.52
47:3:75:ASN:O	47:3:79:GLY:N	2.41	0.52
1:a:269:U:OP2	20:t:70:LYS:NZ	2.23	0.52
1:a:1262:A:N6	1:a:1365:U:HO2'	2.06	0.52
23:A:388:A:N3	23:A:390:A:N6	2.57	0.52
23:A:1008:C:O2'	23:A:2300:A:N3	2.36	0.52
23:A:2772:C:O2'	29:H:139:GLU:O	2.26	0.52
1:a:18:U:O2'	1:a:1091:G:O2'	2.25	0.52
23:A:1521:A:O4'	23:A:1561:G:N2	2.42	0.52
23:A:2518:U:O2'	23:A:2597:G:OP1	2.26	0.52
1:a:975:A:C5'	1:a:975:A:C8	2.92	0.52
1:a:1458:A:P	1:a:1459:C:H41	2.32	0.52
23:A:953:C:OP1	33:P:101:ARG:NH2	2.39	0.52
4:d:103:LEU:HD23	4:d:155:VAL:HG22	1.92	0.52
5:e:163:GLU:N	5:e:163:GLU:OE1	2.43	0.52
19:s:4:SER:OG	19:s:5:ILE:N	2.41	0.52
23:A:509:G:N2	23:A:512:A:OP2	2.37	0.52
23:A:526:A:H61	23:A:550:A:H61	1.58	0.52
23:A:968:A:O2'	43:Z:36:GLY:O	2.26	0.52
23:A:2304:G:OP2	43:Z:19:LYS:CE	2.58	0.52
34:Q:73:ASN:ND2	34:Q:77:THR:O	2.42	0.52
40:W:33:VAL:O	40:W:76:ARG:NH1	2.42	0.52
47:3:66:ALA:HA	47:3:67:ALA:HB3	1.91	0.52
23:A:2860:U:C5'	34:Q:49:THR:HG21	2.39	0.52
1:a:1101:G:O6	1:a:1109:C:N4	2.42	0.52
8:h:115:ASP:OD2	8:h:119:ARG:NH1	2.42	0.52
23:A:1306:C:N3	23:A:2040:A:C5	2.78	0.52
23:A:2048:G:OP1	48:4:11:THR:OG1	2.28	0.52
23:A:2332:U:OP2	23:A:2334:G:N1	2.42	0.52
23:A:2581:U:O2'	23:A:2582:U:O4'	2.28	0.52
9:i:96:TYR:O	9:i:100:LEU:N	2.42	0.52
23:A:1763:U:O2'	23:A:1766:C:N4	2.43	0.52
24:B:9:C:HO2'	24:B:13:A:H61	1.50	0.52
1:a:1095:U:O2'	1:a:1114:A:OP2	2.28	0.52
4:d:151:ILE:O	4:d:155:VAL:HG23	2.09	0.52
16:p:86:GLU:O	16:p:90:ALA:HB2	2.09	0.52
32:O:69:ILE:O	32:O:98:GLU:N	2.43	0.52
1:a:343:C:O2'	1:a:1444:A:N3	2.42	0.52
1:a:435:C:OP2	1:a:436:G:O2'	2.23	0.52
1:a:1037:C:O2	1:a:1047:G:N1	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1079:A:O2'	1:a:1105:A:O2'	2.18	0.52
4:d:168:ASP:O	4:d:172:LEU:N	2.40	0.52
23:A:283:G:N2	23:A:289:U:O2	2.43	0.52
30:M:140:ASN:OD1	30:M:141:TYR:N	2.43	0.52
2:b:171:ASN:OD1	2:b:172:ALA:N	2.42	0.51
23:A:2775:A:N7	23:A:2780:A:N6	2.57	0.51
45:1:10:THR:O	45:1:11:THR:OG1	2.17	0.51
1:a:1516:G:OP1	1:a:1519:A:O2'	2.20	0.51
3:c:7:PRO:O	3:c:10:LEU:N	2.43	0.51
11:k:110:ILE:HG22	21:u:19:PHE:CE1	2.46	0.51
12:l:53:MET:SD	12:l:103:LEU:HD12	2.50	0.51
16:p:75:LEU:O	16:p:79:GLY:N	2.40	0.51
20:t:45:ASN:O	20:t:45:ASN:ND2	2.39	0.51
23:A:2171:G:N2	23:A:2173:U:O4'	2.43	0.51
25:D:12:ARG:NE	25:D:15:MET:SD	2.77	0.51
1:a:262:G:O3'	17:q:73:LYS:NZ	2.36	0.51
3:c:51:VAL:HG12	3:c:69:THR:HB	1.92	0.51
23:A:758:G:H21	23:A:763:A:H2	1.58	0.51
29:H:128:ASN:OD1	29:H:129:THR:N	2.42	0.51
1:a:1085:U:O2	2:b:103:ASN:ND2	2.43	0.51
23:A:1635:A:O2'	23:A:1636:U:O5'	2.28	0.51
23:A:2467:C:O2'	23:A:2468:C:O4'	2.23	0.51
30:M:58:ILE:HD11	30:M:129:ALA:O	2.10	0.51
7:g:130:ASN:HA	7:g:135:VAL:HG21	1.93	0.51
25:D:44:ASN:OD1	25:D:45:GLN:N	2.44	0.51
33:P:25:ASN:C	33:P:26:TYR:CG	2.82	0.51
42:Y:15:ARG:O	42:Y:17:ASP:N	2.44	0.51
1:a:536:C:H41	12:l:59:ASN:CG	2.19	0.51
1:a:969:A:N6	19:s:77:THR:O	2.44	0.51
2:b:154:MET:HE3	2:b:158:PRO:HG3	1.92	0.51
22:v:4:PHE:CD1	22:v:4:PHE:N	2.78	0.51
23:A:160:G:O2'	23:A:168:A:N1	2.43	0.51
23:A:1112:G:H22	23:A:1140:A:C4'	2.24	0.51
43:Z:27:LYS:CD	43:Z:27:LYS:N	2.73	0.51
5:e:149:ASN:HD22	5:e:150:ALA:H	1.57	0.51
47:3:49:ASP:OD1	47:3:50:ILE:N	2.43	0.51
13:m:107:ARG:HG3	13:m:108:THR:H	1.76	0.51
24:B:9:C:O2'	24:B:13:A:N6	2.23	0.51
32:O:119:LYS:O	32:O:123:VAL:HG12	2.10	0.51
1:a:843:A:OP1	18:r:58:ARG:NH2	2.44	0.51
1:a:1234:C:OP2	19:s:78:ARG:NH2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:198:A:N6	23:A:201:C:OP2	2.43	0.51
23:A:2540:A:OP1	26:E:168:LYS:NZ	2.42	0.51
15:o:43:LEU:O	15:o:46:HIS:C	2.54	0.50
23:A:2432:G:OP1	32:O:63:LYS:NZ	2.34	0.50
31:N:15:GLY:O	31:N:47:THR:N	2.45	0.50
1:a:446:G:O2'	1:a:502:C:N4	2.43	0.50
1:a:1155:G:N2	1:a:1157:A:H62	2.09	0.50
23:A:562:C:OP2	48:4:10:LYS:NZ	2.26	0.50
1:a:413:U:O4	4:d:2:ALA:N	2.44	0.50
23:A:2474:G:N2	23:A:2477:A:OP2	2.34	0.50
23:A:2662:U:OP1	26:E:89:ARG:NH1	2.42	0.50
25:D:227:ASN:OD1	25:D:228:ASP:N	2.44	0.50
26:E:9:LYS:O	26:E:11:GLY:N	2.45	0.50
1:a:947:A:O2'	1:a:1389:C:N4	2.44	0.50
3:c:51:VAL:HG12	3:c:69:THR:CB	2.41	0.50
23:A:1033:G:C8	46:2:13:ILE:HD11	2.47	0.50
25:D:69:ASN:OD1	25:D:70:LYS:N	2.44	0.50
23:A:86:C:P	41:X:29:LYS:HZ1	2.33	0.50
23:A:1092:A:P	23:A:1154:G:H22	2.34	0.50
23:A:1488:A:N6	23:A:1490:G:O6	2.45	0.50
23:A:1505:G:N7	23:A:1506:C:N4	2.59	0.50
15:o:75:ILE:HD13	17:q:86:ILE:HD11	1.92	0.50
19:s:53:ASP:OD1	19:s:54:GLY:N	2.44	0.50
23:A:1508:C:N4	23:A:1509:G:O6	2.43	0.50
23:A:1520:A:H61	23:A:1562:C:H1'	1.77	0.50
23:A:2359:C:OP1	43:Z:54:TYR:OH	2.27	0.50
33:P:29:PHE:CE2	33:P:105:GLU:OE2	2.49	0.50
23:A:1099:G:H1	23:A:1148:C:H42	1.58	0.50
23:A:1105:U:O2'	23:A:1109:U:O4	2.29	0.50
33:P:31:GLU:HG2	33:P:133:LYS:CB	2.42	0.50
36:S:7:ILE:O	36:S:11:THR:OG1	2.17	0.50
1:a:975:A:O4'	1:a:979:A:C1'	2.60	0.50
11:k:29:ASN:OD1	11:k:30:THR:N	2.45	0.50
23:A:2870:A:OP2	23:A:2886:G:N2	2.31	0.50
26:E:131:ILE:HD11	26:E:149:ARG:CZ	2.41	0.50
27:F:196:GLU:O	27:F:200:LYS:N	2.44	0.50
1:a:1288:C:O2'	1:a:1290:A:N7	2.45	0.50
2:b:187:VAL:HG21	2:b:199:VAL:HG13	1.94	0.50
18:r:23:ILE:O	18:r:23:ILE:HG22	2.11	0.50
23:A:1510:U:H3	23:A:1571:G:H22	1.59	0.50
28:G:129:THR:C	28:G:130:LEU:HD22	2.36	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:b:203:ASN:OD1	2:b:204:ASP:N	2.45	0.49
23:A:657:U:N3	23:A:659:A:N1	2.60	0.49
23:A:1968:C:N4	23:A:1992:C:O4'	2.44	0.49
23:A:1982:U:O4	23:A:2583:C:N4	2.44	0.49
23:A:2207:U:O4	23:A:2208:A:N6	2.44	0.49
1:a:744:U:O2'	6:f:91:VAL:O	2.30	0.49
1:a:1447:C:H42	1:a:1477:U:H3	1.60	0.49
12:l:101:LYS:H	12:l:101:LYS:CD	2.16	0.49
22:v:66:ARG:HG3	22:v:67:ALA:N	2.27	0.49
27:F:112:SER:O	27:F:115:SER:OG	2.27	0.49
2:b:176:ALA:HB1	2:b:183:ILE:HD11	1.94	0.49
5:e:81:THR:HG23	5:e:98:PRO:HG3	1.94	0.49
23:A:313:U:O2'	23:A:314:A:O4'	2.29	0.49
23:A:1215:U:O2'	23:A:1217:U:O2	2.29	0.49
24:B:95:A:O2'	24:B:96:G:O4'	2.30	0.49
33:P:32:PHE:CZ	33:P:111:GLU:C	2.78	0.49
1:a:1025:G:N3	1:a:1229:U:O2'	2.35	0.49
23:A:275:A:N6	23:A:296:G:H21	2.11	0.49
23:A:1359:A:N1	23:A:1370:C:O2'	2.40	0.49
23:A:1579:C:O2	23:A:1580:A:N6	2.45	0.49
23:A:83:G:N2	23:A:101:G:O3'	2.36	0.49
23:A:1487:G:N2	23:A:1597:U:O2	2.44	0.49
23:A:2641:A:O4'	48:4:2:ALA:N	2.46	0.49
27:F:197:ALA:O	27:F:201:LYS:N	2.41	0.49
22:v:68:GLU:CD	22:v:69:GLU:H	2.16	0.49
23:A:341:G:N1	23:A:382:U:OP2	2.42	0.49
23:A:1040:A:OP2	37:T:93:LYS:NZ	2.46	0.49
23:A:1584:A:OP1	23:A:1585:G:H8	1.91	0.49
27:F:21:ASP:O	27:F:25:GLY:N	2.46	0.49
1:a:986:G:OP2	1:a:1369:U:O2'	2.30	0.49
23:A:1410:A:O2'	23:A:2238:U:O4	2.27	0.49
23:A:1582:U:O3'	23:A:1583:G:N2	2.38	0.49
33:P:22:LYS:N	33:P:98:LYS:CD	2.57	0.49
1:a:465:U:N3	1:a:486:C:N4	2.61	0.49
4:d:163:GLU:OE2	4:d:178:ARG:NH2	2.46	0.49
7:g:126:ASP:OD1	7:g:131:THR:OG1	2.27	0.49
8:h:104:ALA:HB2	8:h:130:TYR:CE1	2.46	0.49
23:A:672:A:N3	23:A:681:G:N2	2.56	0.49
12:l:5:ASN:OD1	12:l:6:GLN:N	2.46	0.49
17:q:83:GLU:O	17:q:84:SER:OG	2.20	0.49
23:A:1127:U:O2'	23:A:1129:A:N7	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:2260:A:H2'	23:A:2261:G:C8	2.48	0.49
23:A:2867:U:OP1	36:S:98:LYS:NZ	2.44	0.49
26:E:9:LYS:HZ3	26:E:201:VAL:HG23	1.78	0.49
2:b:58:LYS:O	2:b:62:GLU:N	2.44	0.49
17:q:21:LYS:O	17:q:50:ASP:N	2.46	0.49
23:A:909:G:H21	23:A:911:A:H61	1.60	0.49
23:A:1581:U:P	23:A:1584:A:N1	2.86	0.49
23:A:1978:U:N3	23:A:1981:G:OP2	2.41	0.49
23:A:2711:U:OP2	36:S:53:ARG:NH1	2.45	0.49
25:D:266:ASP:OD1	25:D:267:LYS:N	2.45	0.49
1:a:589:G:N1	1:a:767:A:OP2	2.42	0.48
4:d:64:THR:O	4:d:68:PHE:N	2.46	0.48
22:v:56:VAL:CG1	22:v:67:ALA:O	2.55	0.48
29:H:22:ASN:O	29:H:37:LEU:N	2.43	0.48
35:R:36:SER:N	35:R:39:HIS:O	2.46	0.48
6:f:19:LYS:O	6:f:23:VAL:HG23	2.12	0.48
29:H:152:ARG:O	29:H:162:ILE:N	2.44	0.48
31:N:113:LYS:O	31:N:117:LEU:HD13	2.13	0.48
43:Z:27:LYS:C	43:Z:29:LEU:N	2.58	0.48
20:t:50:VAL:HG23	20:t:78:LEU:HD22	1.94	0.48
23:A:674:C:O2	23:A:684:U:O2'	2.31	0.48
1:a:1141:C:N4	1:a:1155:G:O6	2.46	0.48
2:b:161:LEU:HD22	2:b:183:ILE:HG23	1.94	0.48
3:c:69:THR:O	3:c:105:ILE:HG22	2.13	0.48
23:A:342:A:N1	23:A:365:A:O2'	2.37	0.48
23:A:372:A:H61	41:X:15:LYS:HB2	1.77	0.48
33:P:22:LYS:CD	33:P:99:PRO:CD	2.91	0.48
5:e:149:ASN:HD22	5:e:150:ALA:N	2.10	0.48
23:A:675:G:N2	23:A:678:A:OP2	2.40	0.48
23:A:1806:U:O2	23:A:1810:A:N6	2.46	0.48
23:A:2189:G:O2'	23:A:2190:C:O4'	2.19	0.48
7:g:13:LEU:H	7:g:13:LEU:HD23	1.78	0.48
11:k:36:ASP:OD1	11:k:40:ASN:N	2.43	0.48
23:A:1395:G:N1	23:A:1408:G:N7	2.61	0.48
28:G:23:SER:O	28:G:24:SER:OG	2.27	0.48
40:W:52:SER:O	40:W:81:THR:HG22	2.13	0.48
1:a:371:A:H62	12:l:38:LEU:CD1	2.27	0.48
5:e:90:GLY:O	5:e:91:SER:OG	2.23	0.48
9:i:100:LEU:O	9:i:104:GLY:N	2.47	0.48
22:v:54:ILE:O	22:v:68:GLU:CG	2.62	0.48
23:A:909:G:H21	23:A:911:A:N6	2.11	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:1885:G:O2'	23:A:1911:A:N6	2.47	0.48
33:P:22:LYS:CG	33:P:99:PRO:CG	2.91	0.48
23:A:1518:G:HO2'	23:A:1519:U:P	2.37	0.48
23:A:2465:U:O2'	23:A:2467:C:OP1	2.31	0.48
35:R:56:ALA:CB	35:R:80:ILE:HD11	2.43	0.48
1:a:976:G:C2	1:a:977:C:C4	3.01	0.48
1:a:976:G:N1	1:a:977:C:N4	2.62	0.48
3:c:181:ILE:HG22	3:c:202:TYR:HA	1.96	0.48
10:j:51:ILE:HD12	14:n:41:ARG:HG3	1.95	0.48
23:A:510:U:O2'	23:A:511:G:O5'	2.32	0.48
23:A:1100:G:N2	23:A:1148:C:O2	2.47	0.48
23:A:2776:A:C1'	29:H:63:THR:HG22	2.43	0.48
24:B:16:A:N1	24:B:105:G:N2	2.62	0.48
42:Y:27:VAL:N	42:Y:43:VAL:O	2.46	0.48
1:a:261:U:C1'	1:a:283:G:H21	2.24	0.47
1:a:972:C:H42	1:a:983:G:H1	1.62	0.47
1:a:1003:G:H2'	1:a:1005:C:H41	1.79	0.47
1:a:1248:C:H4'	1:a:1311:G:H22	1.79	0.47
12:l:56:LYS:C	12:l:57:LYS:O	2.56	0.47
16:p:78:GLU:OE1	16:p:80:ILE:HG23	2.14	0.47
1:a:573:U:OP2	1:a:574:G:O2'	2.32	0.47
1:a:1112:C:OP1	2:b:95:ARG:NH1	2.46	0.47
2:b:32:PHE:O	2:b:33:THR:OG1	2.26	0.47
23:A:1099:G:H21	23:A:1128:A:H2	1.62	0.47
23:A:1488:A:H61	23:A:1595:C:H42	1.61	0.47
23:A:1498:U:OP2	34:Q:83:GLN:NE2	2.43	0.47
23:A:1927:A:O2'	23:A:1928:A:OP1	2.27	0.47
3:c:56:ILE:HG22	3:c:65:ILE:CG2	2.45	0.47
23:A:1726:A:OP1	23:A:1743:G:N1	2.45	0.47
3:c:172:VAL:O	3:c:172:VAL:HG13	2.15	0.47
10:j:49:TYR:O	10:j:65:PHE:N	2.47	0.47
18:r:25:HIS:HA	18:r:26:ILE:HA	1.60	0.47
23:A:2285:C:O2'	23:A:2454:C:OP2	2.31	0.47
23:A:2827:A:N6	23:A:2912:A:H62	2.10	0.47
1:a:535:G:O2'	1:a:543:A:N1	2.44	0.47
1:a:1004:A:O4'	1:a:1227:A:O2'	2.32	0.47
1:a:1136:G:N2	1:a:1137:U:O4	2.45	0.47
22:v:60:LEU:C	22:v:63:VAL:O	2.57	0.47
23:A:1129:A:O2'	23:A:1148:C:O2'	2.26	0.47
33:P:70:PRO:CA	33:P:95:ALA:HB2	2.45	0.47
50:6:43:LEU:O	50:6:44:SER:OG	2.24	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1315:G:O2'	1:a:1344:A:N6	2.41	0.47
1:a:1371:A:C8	14:n:18:VAL:HG11	2.50	0.47
5:e:39:VAL:HG12	5:e:67:ALA:HB1	1.95	0.47
23:A:1845:U:O2'	25:D:152:GLN:O	2.21	0.47
23:A:2383:C:C5'	43:Z:28:ARG:CG	2.91	0.47
1:a:874:A:O2'	1:a:1090:U:O4	2.19	0.47
1:a:1147:U:O2'	1:a:1149:A:N7	2.45	0.47
4:d:86:PHE:O	4:d:89:LEU:N	2.47	0.47
7:g:51:GLU:OE2	7:g:58:ALA:HB2	2.15	0.47
23:A:999:U:OP1	33:P:87:LYS:NZ	2.44	0.47
23:A:1112:G:H3'	23:A:1113:A:H5''	1.97	0.47
23:A:1962:G:N2	23:A:1991:G:O4'	2.48	0.47
23:A:2304:G:P	43:Z:19:LYS:CD	3.03	0.47
24:B:22:G:N7	24:B:54:U:O2'	2.44	0.47
49:5:11:GLU:O	49:5:38:ARG:NH2	2.42	0.47
1:a:1005:C:N3	1:a:1058:A:O2'	2.47	0.47
1:a:1231:G:OP1	19:s:37:ARG:NH1	2.47	0.47
1:a:1369:U:OP2	1:a:1370:C:N4	2.47	0.47
2:b:17:GLY:O	2:b:203:ASN:ND2	2.47	0.47
20:t:46:LYS:O	20:t:50:VAL:HG12	2.15	0.47
23:A:82:G:N2	23:A:104:C:N3	2.63	0.47
23:A:1737:U:OP2	23:A:1738:C:N4	2.45	0.47
31:N:87:ILE:HD11	31:N:91:LYS:C	2.40	0.47
1:a:634:U:OP1	16:p:19:ARG:NH2	2.46	0.47
1:a:1271:G:O2'	1:a:1272:A:OP2	2.25	0.47
10:j:25:ILE:HG23	10:j:86:ALA:O	2.14	0.47
11:k:35:THR:HG22	11:k:41:ALA:HA	1.97	0.47
22:v:56:VAL:HG12	22:v:67:ALA:C	2.39	0.47
23:A:511:G:OP1	50:6:13:HIS:NE2	2.38	0.47
25:D:215:ILE:HG22	25:D:216:ARG:N	2.30	0.47
37:T:65:ILE:HD11	37:T:95:LEU:HB2	1.97	0.47
47:3:32:SER:OG	47:3:33:GLU:OE1	2.32	0.47
1:a:788:A:N6	1:a:809:U:OP2	2.46	0.46
1:a:975:A:H1'	1:a:979:A:N7	2.30	0.46
1:a:1006:A:N1	1:a:1057:C:O2'	2.36	0.46
12:l:91:SER:OG	12:l:92:VAL:N	2.48	0.46
17:q:9:VAL:HG12	17:q:63:ILE:O	2.16	0.46
22:v:94:THR:N	22:v:95:ARG:HB2	2.30	0.46
23:A:2510:C:O2	33:P:49:SER:OG	2.33	0.46
29:H:58:SER:O	29:H:62:ARG:NH1	2.48	0.46
37:T:94:MET:O	37:T:98:ILE:N	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:Z:58:ASN:HD22	43:Z:71:ILE:HD13	1.80	0.46
50:6:35:ARG:NH2	50:6:42:VAL:O	2.45	0.46
1:a:976:G:C6	1:a:977:C:C4	3.03	0.46
1:a:1019:U:O2	1:a:1031:G:N2	2.48	0.46
2:b:223:GLU:O	2:b:227:GLY:N	2.46	0.46
3:c:11:ARG:HD2	3:c:15:ILE:HD11	1.97	0.46
15:o:51:HIS:CD2	15:o:52:SER:HG	2.34	0.46
22:v:60:LEU:CD1	22:v:64:THR:HA	2.44	0.46
23:A:1584:A:H3'	23:A:1585:G:H5'	1.97	0.46
52:8:17:ILE:HD11	52:8:24:MET:HB3	1.97	0.46
1:a:19:C:H1'	1:a:1091:G:H21	1.80	0.46
1:a:1164:G:O2'	1:a:1165:U:O4'	2.34	0.46
1:a:1307:C:OP1	13:m:44:ARG:NE	2.48	0.46
3:c:113:ARG:HD2	3:c:184:ALA:HB1	1.97	0.46
11:k:80:LYS:O	11:k:106:GLU:N	2.49	0.46
23:A:614:U:O5'	23:A:2057:A:N6	2.44	0.46
23:A:1835:U:O2'	23:A:1836:A:O4'	2.33	0.46
33:P:41:TRP:CD1	33:P:41:TRP:O	2.68	0.46
39:V:17:VAL:HG12	39:V:21:LEU:HD13	1.97	0.46
9:i:28:GLY:N	9:i:64:ASP:OD1	2.49	0.46
17:q:83:GLU:N	17:q:83:GLU:OE1	2.48	0.46
23:A:1709:A:O2'	31:N:1:MET:N	2.44	0.46
24:B:37:A:O2'	24:B:44:A:N1	2.40	0.46
43:Z:31:ALA:HB2	43:Z:46:TYR:CD1	2.50	0.46
1:a:39:G:H22	1:a:405:A:H5'	1.80	0.46
11:k:24:ARG:O	11:k:30:THR:OG1	2.20	0.46
19:s:11:VAL:HG21	19:s:16:MET:HB2	1.97	0.46
23:A:1199:A:O3'	37:T:55:ARG:NH2	2.43	0.46
25:D:215:ILE:HG22	25:D:216:ARG:H	1.81	0.46
32:O:118:ASP:O	32:O:122:THR:HG22	2.16	0.46
1:a:665:U:H1'	15:o:28:GLN:HE21	1.81	0.46
4:d:103:LEU:CD2	4:d:155:VAL:HG22	2.45	0.46
9:i:47:ILE:HA	9:i:50:LEU:HD13	1.98	0.46
1:a:774:A:N7	1:a:821:U:O4	2.49	0.46
9:i:30:ILE:HD13	9:i:65:VAL:HB	1.97	0.46
14:n:22:THR:O	14:n:33:VAL:HG11	2.16	0.46
23:A:2099:G:N3	23:A:2467:C:N4	2.64	0.46
29:H:99:GLN:N	29:H:102:ASP:O	2.49	0.46
8:h:35:GLU:O	8:h:39:ILE:HD12	2.16	0.46
23:A:1184:C:O2'	23:A:1187:A:O2'	2.21	0.46
23:A:2383:C:C4'	43:Z:28:ARG:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:M:59:ASN:N	30:M:128:GLY:O	2.46	0.46
1:a:159:G:O2'	1:a:162:A:N6	2.48	0.46
3:c:33:HIS:ND1	14:n:25:GLU:OE1	2.49	0.46
23:A:83:G:H21	23:A:102:A:H2	1.63	0.46
23:A:1033:G:O2'	23:A:1034:A:OP2	2.27	0.46
23:A:1053:A:OP2	30:M:40:LYS:NZ	2.47	0.46
23:A:2715:G:N1	23:A:2747:U:OP2	2.43	0.46
27:F:29:ASN:OD1	27:F:30:ASN:N	2.47	0.46
29:H:125:VAL:HG13	29:H:131:VAL:HG12	1.97	0.46
38:U:41:VAL:HG13	38:U:46:VAL:HA	1.97	0.46
48:4:37:TYR:CE1	48:4:43:VAL:HG22	2.51	0.46
1:a:300:G:H21	1:a:616:A:H61	1.64	0.46
3:c:36:LEU:HD23	14:n:52:GLN:HE22	1.80	0.46
14:n:56:VAL:HA	14:n:57:ARG:HG3	1.97	0.46
23:A:1135:G:N3	23:A:1146:C:N4	2.64	0.46
23:A:1306:C:C2'	23:A:1307:G:O5'	2.64	0.46
33:P:22:LYS:CG	33:P:99:PRO:N	2.77	0.46
33:P:32:PHE:O	33:P:118:LEU:CD1	2.59	0.46
23:A:829:U:O4'	25:D:225:ASN:ND2	2.49	0.45
23:A:2442:G:O2'	32:O:60:ARG:NH1	2.49	0.45
23:A:2819:C:H3'	23:A:2820:U:H5''	1.97	0.45
23:A:2917:U:O2'	30:M:135:ALA:O	2.27	0.45
27:F:155:VAL:HG22	27:F:156:THR:O	2.15	0.45
1:a:76:C:N3	1:a:93:U:O4	2.50	0.45
1:a:77:G:H22	1:a:92:C:C2'	2.29	0.45
8:h:80:ILE:HD11	8:h:130:TYR:HD2	1.79	0.45
23:A:1066:G:O6	30:M:69:LYS:NZ	2.48	0.45
24:B:53:U:O2'	24:B:55:A:N7	2.46	0.45
36:S:42:ILE:HD12	36:S:43:GLN:CA	2.46	0.45
1:a:853:C:O4'	1:a:855:G:N2	2.49	0.45
15:o:21:ASP:OD1	15:o:24:SER:OG	2.33	0.45
23:A:2357:G:O3'	43:Z:52:LYS:NZ	2.45	0.45
43:Z:51:THR:HG21	43:Z:54:TYR:CD1	2.52	0.45
51:7:49:LEU:O	51:7:53:SER:N	2.47	0.45
1:a:976:G:C2	1:a:977:C:N3	2.85	0.45
1:a:1300:A:N1	1:a:1382:G:O2'	2.30	0.45
9:i:8:TYR:N	9:i:23:LEU:O	2.49	0.45
23:A:250:G:N2	23:A:254:A:OP2	2.49	0.45
32:O:111:ILE:O	32:O:131:SER:N	2.49	0.45
33:P:110:SER:OG	33:P:111:GLU:N	2.49	0.45
43:Z:30:GLY:O	43:Z:31:ALA:C	2.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:482:A:O2'	1:a:483:C:OP2	2.18	0.45
5:e:77:VAL:HG13	5:e:77:VAL:O	2.17	0.45
8:h:12:THR:HG22	8:h:15:ARG:HH21	1.82	0.45
12:l:29:ASN:OD1	12:l:30:SER:N	2.49	0.45
13:m:28:SER:OG	13:m:32:LYS:NZ	2.50	0.45
25:D:129:LEU:HD11	25:D:134:ILE:HD11	1.99	0.45
42:Y:10:GLN:HE21	42:Y:14:THR:HG21	1.81	0.45
22:v:52:THR:N	22:v:71:ASN:O	2.50	0.45
1:a:1250:A:H62	1:a:1310:A:N6	2.14	0.45
1:a:1316:G:N2	1:a:1342:G:O2'	2.30	0.45
11:k:116:VAL:O	11:k:116:VAL:HG23	2.17	0.45
16:p:60:TRP:NE1	16:p:64:GLY:O	2.50	0.45
23:A:1039:C:O2'	23:A:1040:A:OP2	2.29	0.45
23:A:2378:G:H1'	23:A:2393:A:H61	1.82	0.45
40:W:31:THR:HG22	40:W:32:ARG:N	2.32	0.45
1:a:166:U:O4	1:a:167:A:N6	2.50	0.45
1:a:701:G:O2'	22:v:97:ASN:ND2	2.47	0.45
5:e:85:ILE:HD12	5:e:86:THR:N	2.32	0.45
23:A:1835:U:O2'	23:A:1836:A:O5'	2.34	0.45
36:S:66:ILE:HG22	36:S:66:ILE:O	2.16	0.45
43:Z:70:LYS:C	43:Z:71:ILE:HD12	2.42	0.45
1:a:1013:G:OP2	1:a:1036:C:N4	2.46	0.45
16:p:40:TYR:HD1	16:p:50:ILE:HG22	1.82	0.45
22:v:4:PHE:HD1	22:v:38:ALA:CA	2.27	0.45
23:A:1731:G:N2	23:A:1732:U:O2	2.49	0.45
23:A:1886:A:C8	23:A:1910:G:N2	2.84	0.45
1:a:300:G:N2	1:a:616:A:H61	2.15	0.45
1:a:537:G:N1	12:l:60:SER:O	2.47	0.45
1:a:1452:G:O2'	1:a:1472:A:N6	2.49	0.45
7:g:17:ILE:HG22	7:g:18:HIS:ND1	2.31	0.45
13:m:106:ALA:N	13:m:107:ARG:HB2	2.32	0.45
22:v:66:ARG:CZ	22:v:66:ARG:HB3	2.46	0.45
23:A:590:U:OP1	23:A:1257:G:O2'	2.35	0.45
51:7:18:ALA:O	51:7:19:SER:OG	2.33	0.45
1:a:820:G:OP1	1:a:912:G:N2	2.41	0.44
1:a:1168:A:N7	1:a:1191:A:N6	2.65	0.44
1:a:1281:G:O2'	1:a:1324:U:O2'	2.09	0.44
2:b:7:LYS:HE3	2:b:12:ALA:HB2	1.99	0.44
25:D:144:GLU:OE2	25:D:151:GLY:N	2.49	0.44
27:F:144:SER:O	27:F:145:THR:OG1	2.34	0.44
33:P:29:PHE:CD2	33:P:105:GLU:CD	2.72	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:r:26:ILE:CG1	18:r:63:ALA:HB1	2.36	0.44
23:A:167:U:H3'	23:A:168:A:H5''	1.98	0.44
23:A:1010:G:O4'	23:A:2294:A:N6	2.50	0.44
23:A:1390:A:OP2	23:A:1414:G:N1	2.47	0.44
34:Q:18:ARG:NE	34:Q:65:THR:O	2.43	0.44
1:a:272:C:O2'	17:q:67:ARG:NH1	2.51	0.44
2:b:206:ALA:HB3	2:b:209:ALA:HB3	1.99	0.44
23:A:896:U:O2	46:2:42:ALA:HB1	2.16	0.44
23:A:1033:G:OP1	46:2:31:THR:OG1	2.27	0.44
23:A:2127:G:O6	23:A:2216:U:O2	2.36	0.44
34:Q:34:GLU:O	34:Q:37:ALA:HB3	2.17	0.44
43:Z:19:LYS:HB2	43:Z:20:ASN:H	1.50	0.44
1:a:1119:C:OP1	3:c:171:THR:OG1	2.35	0.44
3:c:103:ILE:HG23	3:c:103:ILE:O	2.18	0.44
12:l:16:ILE:H	12:l:16:ILE:HD12	1.81	0.44
17:q:35:LEU:HD22	17:q:36:TYR:CE2	2.53	0.44
32:O:77:VAL:O	32:O:107:SER:OG	2.26	0.44
33:P:41:TRP:CD1	33:P:41:TRP:H	2.36	0.44
1:a:976:G:C5	22:v:66:ARG:NH1	2.85	0.44
43:Z:28:ARG:HD3	43:Z:28:ARG:HA	1.48	0.44
16:p:74:ILE:O	16:p:77:LYS:N	2.50	0.44
23:A:901:G:H2'	23:A:902:A:C8	2.53	0.44
31:N:61:VAL:N	31:N:85:VAL:O	2.49	0.44
33:P:52:ILE:HA	33:P:55:THR:HG22	1.99	0.44
47:3:12:VAL:HG13	47:3:13:ILE:HD12	2.00	0.44
49:5:35:PHE:HD1	49:5:36:CYS:N	2.12	0.44
1:a:129:A:O5'	17:q:2:SER:N	2.51	0.44
2:b:69:PHE:CD2	2:b:84:ALA:HB2	2.52	0.44
23:A:6:A:O2'	30:M:133:HIS:ND1	2.37	0.44
23:A:732:C:H42	23:A:832:C:H4'	1.83	0.44
23:A:2452:A:N3	23:A:2454:C:N4	2.66	0.44
34:Q:109:ARG:N	34:Q:114:ALA:O	2.51	0.44
1:a:470:A:N7	1:a:476:C:N4	2.66	0.44
1:a:1055:G:O2'	1:a:1056:A:O4'	2.22	0.44
2:b:14:VAL:HG13	2:b:208:ARG:NE	2.32	0.44
23:A:231:A:O2'	23:A:233:U:OP2	2.36	0.44
23:A:2304:G:OP1	43:Z:19:LYS:CE	2.66	0.44
26:E:56:LYS:NZ	26:E:66:ASN:O	2.46	0.44
1:a:944:C:N3	1:a:947:A:N6	2.65	0.44
3:c:147:GLY:O	3:c:202:TYR:N	2.51	0.44
23:A:815:G:OP1	50:6:9:ASN:ND2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:H:97:GLN:HB3	29:H:104:ILE:HD11	1.99	0.44
47:3:12:VAL:HG12	47:3:45:VAL:HG21	1.98	0.44
1:a:68:C:O2'	1:a:171:A:O2'	2.08	0.43
1:a:1077:U:P	1:a:1201:G:H22	2.39	0.43
3:c:106:LYS:C	3:c:108:VAL:HA	2.43	0.43
19:s:63:THR:OG1	19:s:64:GLU:OE1	2.36	0.43
22:v:94:THR:H	22:v:95:ARG:HB2	1.84	0.43
23:A:1512:U:OP2	23:A:1567:A:N6	2.51	0.43
30:M:43:VAL:HG23	30:M:44:THR:HG23	1.99	0.43
1:a:869:C:OP2	1:a:879:A:N6	2.47	0.43
20:t:51:SER:OG	20:t:55:LYS:NZ	2.46	0.43
22:v:60:LEU:HB2	22:v:63:VAL:C	2.41	0.43
23:A:1698:A:N6	23:A:2033:C:O4'	2.51	0.43
23:A:2869:G:OP2	36:S:95:ARG:NH1	2.51	0.43
1:a:954:G:N1	1:a:1349:G:OP2	2.46	0.43
2:b:161:LEU:HD23	2:b:162:PHE:N	2.33	0.43
5:e:133:PRO:O	5:e:137:VAL:HG23	2.17	0.43
23:A:745:G:O2'	23:A:1676:A:N3	2.45	0.43
23:A:2160:G:O2'	23:A:2183:G:O6	2.23	0.43
23:A:2457:A:O2'	23:A:2458:U:OP2	2.33	0.43
28:G:9:ASN:O	28:G:13:THR:CB	2.65	0.43
2:b:73:LYS:NZ	2:b:204:ASP:OD2	2.52	0.43
22:v:5:GLU:OE2	22:v:7:HIS:ND1	2.52	0.43
23:A:250:G:O2'	23:A:253:G:O6	2.35	0.43
23:A:2495:A:O2'	23:A:2496:A:O4'	2.37	0.43
1:a:129:A:N3	17:q:2:SER:N	2.66	0.43
1:a:1054:U:N3	1:a:1055:G:O6	2.51	0.43
4:d:106:THR:HG22	4:d:108:ARG:N	2.34	0.43
13:m:39:VAL:HG12	13:m:52:GLU:CD	2.43	0.43
15:o:24:SER:O	15:o:26:GLU:N	2.51	0.43
22:v:4:PHE:CD1	22:v:38:ALA:N	2.79	0.43
23:A:83:G:O2'	23:A:101:G:N2	2.51	0.43
23:A:283:G:N7	23:A:284:C:O2'	2.44	0.43
23:A:838:A:OP2	23:A:2098:A:O2'	2.35	0.43
23:A:1044:A:OP2	23:A:1198:G:N1	2.45	0.43
23:A:1457:U:H2'	23:A:1458:A:O4'	2.19	0.43
31:N:98:ILE:HG22	31:N:99:PHE:O	2.17	0.43
35:R:16:ALA:O	35:R:20:THR:OG1	2.21	0.43
36:S:42:ILE:HD12	36:S:43:GLN:N	2.34	0.43
1:a:386:G:OP2	16:p:4:LYS:NZ	2.51	0.43
13:m:107:ARG:O	13:m:109:ARG:N	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:13:A:N6	23:A:571:A:OP2	2.51	0.43
23:A:298:U:O2'	23:A:299:U:OP2	2.33	0.43
23:A:1718:G:H21	23:A:1721:A:H61	1.66	0.43
33:P:32:PHE:HE2	33:P:111:GLU:N	2.03	0.43
50:6:15:LYS:O	50:6:17:HIS:N	2.52	0.43
50:6:35:ARG:HE	50:6:43:LEU:HD23	1.83	0.43
2:b:210:VAL:O	2:b:214:THR:HG23	2.19	0.43
7:g:126:ASP:O	7:g:131:THR:OG1	2.37	0.43
22:v:96:ILE:HD13	22:v:96:ILE:HA	1.99	0.43
1:a:120:C:N4	1:a:245:C:H41	2.17	0.43
1:a:209:G:O2'	1:a:210:A:O5'	2.35	0.43
1:a:726:A:O2'	21:u:31:GLU:OE2	2.37	0.43
4:d:106:THR:HG22	4:d:108:ARG:H	1.83	0.43
23:A:45:G:N7	23:A:218:G:O2'	2.50	0.43
23:A:1062:U:O2'	23:A:1164:G:N2	2.50	0.43
31:N:24:VAL:O	31:N:24:VAL:HG12	2.19	0.43
33:P:26:TYR:O	33:P:102:ILE:HG13	2.19	0.43
1:a:975:A:HO2'	1:a:976:G:C5'	2.14	0.43
23:A:1816:A:OP2	25:D:220:ARG:NH2	2.52	0.43
25:D:59:ARG:NH2	25:D:213:LYS:O	2.52	0.43
25:D:190:THR:OG1	25:D:191:ILE:N	2.49	0.43
37:T:98:ILE:HG22	37:T:106:PHE:HB2	2.01	0.43
23:A:223:G:N1	23:A:474:A:OP2	2.42	0.43
23:A:1969:C:O2'	23:A:1970:U:OP1	2.34	0.43
24:B:69:C:H42	24:B:102:A:H61	1.67	0.43
1:a:129:A:N1	1:a:199:G:O2'	2.50	0.42
1:a:1260:C:N4	1:a:1299:A:OP2	2.52	0.42
7:g:27:ILE:O	7:g:31:MET:N	2.52	0.42
10:j:63:GLU:OE2	14:n:58:LYS:NZ	2.52	0.42
11:k:38:PHE:HB2	11:k:39:GLY:HA2	2.00	0.42
14:n:10:GLN:HG3	14:n:23:ARG:HE	1.84	0.42
23:A:329:A:N1	23:A:398:C:N4	2.66	0.42
24:B:3:U:H3	24:B:112:G:H22	1.65	0.42
1:a:976:G:N2	1:a:977:C:C2	2.87	0.42
1:a:1137:U:HO2'	1:a:1138:U:P	2.41	0.42
23:A:660:A:C3'	23:A:661:U:H5'	2.49	0.42
23:A:1135:G:N2	23:A:1145:U:O2	2.52	0.42
23:A:2870:A:P	23:A:2886:G:H22	2.38	0.42
33:P:13:HIS:NE2	33:P:88:GLY:O	2.52	0.42
43:Z:20:ASN:N	43:Z:20:ASN:OD1	2.50	0.42
47:3:14:PHE:HE2	47:3:20:ASN:HD22	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:f:29:ILE:O	6:f:32:THR:HG22	2.18	0.42
23:A:660:A:H2'	23:A:661:U:H5'	2.01	0.42
23:A:769:U:H2'	23:A:770:G:O4'	2.18	0.42
23:A:1458:A:N1	23:A:1459:A:N6	2.67	0.42
23:A:2905:C:H42	48:4:39:LEU:HD22	1.84	0.42
24:B:13:A:OP2	24:B:67:G:N2	2.50	0.42
25:D:144:GLU:C	25:D:145:LEU:HD12	2.44	0.42
29:H:80:SER:OG	29:H:81:GLN:NE2	2.52	0.42
33:P:77:LYS:NZ	33:P:85:ALA:O	2.53	0.42
35:R:95:ASP:OD1	35:R:97:GLY:N	2.52	0.42
1:a:964:G:H21	1:a:1238:A:H62	1.66	0.42
1:a:1224:A:O2'	1:a:1226:G:N7	2.41	0.42
4:d:148:LEU:O	4:d:152:VAL:HG12	2.19	0.42
19:s:53:ASP:OD1	19:s:55:ARG:N	2.47	0.42
23:A:1200:A:O4'	37:T:51:ARG:NE	2.51	0.42
23:A:1582:U:OP2	23:A:1584:A:N1	2.52	0.42
23:A:2685:C:H5'	29:H:160:LYS:HZ3	1.83	0.42
25:D:143:ILE:O	25:D:152:GLN:N	2.47	0.42
30:M:117:GLU:O	30:M:120:GLY:N	2.53	0.42
33:P:32:PHE:HB3	33:P:114:ALA:CB	2.37	0.42
1:a:381:A:H1'	1:a:489:G:H21	1.84	0.42
8:h:10:MET:O	8:h:14:VAL:HG23	2.19	0.42
12:l:25:ASN:O	12:l:36:THR:HG22	2.20	0.42
22:v:5:GLU:OE1	22:v:7:HIS:CE1	2.73	0.42
22:v:55:GLU:HA	22:v:68:GLU:HA	2.02	0.42
23:A:283:G:H3'	23:A:284:C:C5'	2.49	0.42
23:A:687:G:H21	23:A:691:A:H62	1.66	0.42
23:A:1324:A:N1	23:A:1692:C:O2'	2.43	0.42
43:Z:31:ALA:CA	43:Z:46:TYR:CD1	2.94	0.42
4:d:63:MET:HE2	4:d:68:PHE:HD1	1.84	0.42
4:d:151:ILE:O	4:d:154:SER:N	2.53	0.42
6:f:11:ARG:NH2	6:f:85:ASP:OD1	2.52	0.42
23:A:563:G:O5'	39:V:18:ARG:NH1	2.53	0.42
23:A:594:G:O2'	23:A:1258:A:N3	2.47	0.42
23:A:857:C:H42	32:O:18:ARG:HH22	1.67	0.42
23:A:1576:A:H61	23:A:1587:C:N4	2.12	0.42
26:E:114:ASP:OD1	26:E:115:VAL:N	2.53	0.42
1:a:989:C:N3	14:n:16:TYR:OH	2.53	0.42
1:a:1083:C:H2'	1:a:1084:G:C8	2.54	0.42
1:a:1115:C:O3'	2:b:110:ARG:NH2	2.49	0.42
1:a:1125:C:H1'	3:c:177:LEU:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:p:54:GLU:HG3	16:p:80:ILE:HG22	2.00	0.42
18:r:26:ILE:CB	18:r:63:ALA:HB1	2.47	0.42
20:t:4:ILE:H	20:t:4:ILE:HD12	1.84	0.42
23:A:162:A:O2'	23:A:163:U:OP1	2.26	0.42
23:A:241:C:O2'	23:A:651:A:N3	2.43	0.42
23:A:288:C:O2'	23:A:289:U:OP2	2.27	0.42
23:A:2399:G:H1'	49:5:42:GLN:HE22	1.83	0.42
24:B:43:A:O3'	35:R:4:LYS:NZ	2.46	0.42
25:D:75:ALA:HB2	25:D:95:TYR:CD1	2.54	0.42
27:F:125:VAL:HG22	27:F:126:VAL:H	1.84	0.42
30:M:143:LEU:HD23	30:M:143:LEU:H	1.84	0.42
41:X:70:LEU:HD13	41:X:74:LYS:HA	2.01	0.42
23:A:1658:A:N6	39:V:88:ARG:O	2.47	0.42
23:A:2527:U:O2'	23:A:2531:U:OP1	2.33	0.42
1:a:672:G:O2'	1:a:674:G:OP2	2.28	0.42
3:c:184:ALA:HB3	3:c:199:VAL:CG1	2.50	0.42
8:h:21:ARG:HE	8:h:72:ARG:NH2	2.17	0.42
9:i:30:ILE:HG21	9:i:37:VAL:HB	2.02	0.42
11:k:96:ALA:O	11:k:99:ALA:HB3	2.20	0.42
23:A:1261:G:N7	38:U:70:LYS:NZ	2.68	0.42
40:W:5:ASP:OD1	40:W:6:ILE:HD12	2.20	0.42
43:Z:31:ALA:HB2	43:Z:46:TYR:CE1	2.54	0.42
3:c:38:ILE:HD12	3:c:38:ILE:H	1.85	0.42
22:v:68:GLU:CD	22:v:69:GLU:N	2.77	0.42
23:A:163:U:O2'	23:A:164:A:OP2	2.30	0.42
23:A:1039:C:H42	30:M:4:THR:HG22	1.84	0.42
23:A:1944:U:O4	23:A:1945:A:N6	2.52	0.42
33:P:25:ASN:O	33:P:26:TYR:CE2	2.71	0.42
43:Z:50:GLY:N	43:Z:65:ASP:OD2	2.53	0.42
1:a:823:A:N6	1:a:1521:C:O2'	2.49	0.41
1:a:850:U:N3	1:a:853:C:OP2	2.48	0.41
3:c:36:LEU:CD2	14:n:52:GLN:HE22	2.33	0.41
4:d:151:ILE:O	4:d:155:VAL:N	2.48	0.41
23:A:13:A:O2'	23:A:15:G:O6	2.38	0.41
23:A:2850:G:OP1	26:E:67:LYS:NZ	2.49	0.41
26:E:189:ASP:OD1	26:E:191:GLU:N	2.51	0.41
29:H:86:VAL:C	29:H:87:LEU:HD12	2.45	0.41
41:X:70:LEU:HD12	41:X:70:LEU:O	2.19	0.41
46:2:56:VAL:HG23	46:2:56:VAL:O	2.20	0.41
48:4:37:TYR:CD1	48:4:43:VAL:HG22	2.55	0.41
3:c:69:THR:HG23	3:c:104:GLU:OE1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:i:10:GLY:O	9:i:21:VAL:N	2.54	0.41
23:A:1593:G:O2'	23:A:1594:U:O4'	2.23	0.41
23:A:1726:A:P	23:A:1743:G:H22	2.43	0.41
24:B:11:A:OP1	43:Z:82:ARG:NE	2.53	0.41
27:F:6:VAL:HG12	27:F:7:LEU:O	2.20	0.41
31:N:24:VAL:CG1	31:N:33:ALA:HB2	2.50	0.41
33:P:111:GLU:O	33:P:114:ALA:HB3	2.20	0.41
34:Q:36:ARG:O	34:Q:40:VAL:HG12	2.20	0.41
47:3:12:VAL:HG13	47:3:13:ILE:CD1	2.50	0.41
47:3:25:SER:OG	47:3:26:GLY:N	2.48	0.41
49:5:8:ALA:N	49:5:16:ASN:OD1	2.53	0.41
4:d:190:ASN:OD1	4:d:191:GLU:N	2.54	0.41
8:h:18:ASN:O	8:h:72:ARG:NH2	2.43	0.41
12:l:4:ILE:N	12:l:4:ILE:HD12	2.36	0.41
12:l:56:LYS:O	12:l:56:LYS:HG3	2.19	0.41
23:A:1306:C:N4	23:A:2040:A:N7	2.68	0.41
23:A:1767:G:HO2'	23:A:1768:C:P	2.43	0.41
23:A:2386:C:H2'	23:A:2387:A:O4'	2.19	0.41
23:A:2829:A:OP2	23:A:2910:G:N1	2.47	0.41
36:S:50:ILE:HG23	36:S:99:LEU:O	2.19	0.41
1:a:700:U:O2'	1:a:702:A:N7	2.40	0.41
3:c:49:ALA:HB1	3:c:51:VAL:HG13	2.02	0.41
5:e:24:VAL:HG22	5:e:25:VAL:O	2.19	0.41
23:A:2102:U:H1'	23:A:2624:G:H21	1.84	0.41
25:D:104:ILE:HG22	25:D:105:ALA:N	2.35	0.41
25:D:156:SER:O	25:D:194:VAL:HG11	2.20	0.41
33:P:22:LYS:CA	33:P:98:LYS:CD	2.57	0.41
41:X:8:ASN:OD1	41:X:9:VAL:N	2.53	0.41
43:Z:70:LYS:CB	43:Z:71:ILE:HD12	2.50	0.41
1:a:582:A:HO2'	1:a:892:C:HO2'	1.66	0.41
3:c:66:ALA:C	3:c:103:ILE:HG22	2.45	0.41
11:k:30:THR:HG21	11:k:63:ALA:HB2	2.03	0.41
22:v:60:LEU:HD13	22:v:64:THR:CA	2.50	0.41
23:A:344:U:O2'	23:A:345:C:OP2	2.31	0.41
23:A:1581:U:C3'	23:A:1584:A:H2	2.21	0.41
23:A:2477:A:N7	23:A:2528:C:N4	2.68	0.41
23:A:2710:C:OP1	36:S:53:ARG:NH1	2.47	0.41
26:E:5:ILE:O	26:E:211:ILE:N	2.54	0.41
34:Q:107:GLY:O	34:Q:116:SER:N	2.53	0.41
35:R:40:ILE:HD12	35:R:40:ILE:C	2.45	0.41
1:a:1003:G:N7	1:a:1224:A:N6	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:A:834:A:N6	23:A:1658:A:OP2	2.50	0.41
23:A:1598:U:OP1	23:A:1762:U:O2'	2.34	0.41
23:A:1663:G:H21	50:6:2:VAL:HG23	1.85	0.41
26:E:23:ILE:HG22	26:E:24:PRO:O	2.21	0.41
29:H:43:PHE:HE1	29:H:68:THR:HG21	1.85	0.41
36:S:46:GLU:OE1	36:S:46:GLU:N	2.53	0.41
1:a:1315:G:N1	1:a:1343:A:OP2	2.47	0.41
23:A:274:A:H61	23:A:297:G:H1'	1.85	0.41
23:A:341:G:O2'	23:A:383:A:N6	2.53	0.41
23:A:1290:G:O2'	23:A:1291:A:O4'	2.39	0.41
23:A:1385:G:O6	23:A:1643:C:N4	2.54	0.41
25:D:179:GLU:OE1	25:D:275:LYS:NZ	2.51	0.41
39:V:66:THR:HA	39:V:69:LEU:HD12	2.02	0.41
42:Y:27:VAL:O	42:Y:43:VAL:N	2.53	0.41
49:5:35:PHE:CE1	49:5:37:SER:N	2.89	0.41
1:a:461:C:H41	1:a:488:U:H3	1.69	0.41
1:a:908:G:N2	1:a:911:A:OP2	2.46	0.41
1:a:975:A:N3	22:v:5:GLU:CD	2.69	0.41
4:d:92:SER:OG	4:d:133:VAL:O	2.37	0.41
6:f:52:ILE:HG21	6:f:87:ILE:HG23	2.03	0.41
10:j:8:ILE:HD11	10:j:74:ILE:HB	2.03	0.41
17:q:61:VAL:HG12	17:q:80:ILE:HG22	2.02	0.41
23:A:1104:U:N3	23:A:1132:A:C8	2.87	0.41
23:A:1521:A:H2'	23:A:1559:G:H22	1.86	0.41
23:A:2132:A:H2'	23:A:2133:G:O4'	2.20	0.41
23:A:2325:A:N6	23:A:2345:A:O2'	2.54	0.41
24:B:10:U:O2'	24:B:12:U:OP1	2.39	0.41
34:Q:38:LYS:O	34:Q:41:ARG:HB3	2.20	0.41
1:a:259:G:O6	1:a:280:C:N4	2.54	0.41
1:a:1077:U:O2'	1:a:1078:C:OP2	2.38	0.41
3:c:68:HIS:CE1	3:c:103:ILE:HG21	2.56	0.41
4:d:6:GLY:O	4:d:108:ARG:NH1	2.54	0.41
9:i:18:VAL:O	9:i:69:VAL:HG23	2.21	0.41
9:i:82:ARG:HD3	9:i:105:LEU:HD22	2.02	0.41
10:j:29:ALA:O	10:j:33:GLY:N	2.54	0.41
13:m:106:ALA:HB3	13:m:107:ARG:HA	2.02	0.41
19:s:53:ASP:OD1	19:s:56:LYS:N	2.52	0.41
21:u:30:GLN:HA	21:u:33:ARG:HB3	2.03	0.41
23:A:492:G:OP1	37:T:3:ARG:NH2	2.54	0.41
23:A:1130:A:H1'	23:A:1147:A:H62	1.85	0.41
23:A:2418:G:O6	23:A:2451:C:H2'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:E:9:LYS:O	26:E:9:LYS:HG2	2.21	0.41
1:a:1138:U:N3	1:a:1291:A:OP1	2.43	0.41
7:g:148:ASN:HD22	7:g:148:ASN:C	2.29	0.41
18:r:26:ILE:CG1	18:r:63:ALA:HB2	2.33	0.41
23:A:613:G:H2'	23:A:2057:A:N1	2.35	0.41
23:A:829:U:O2'	23:A:830:U:OP2	2.38	0.41
23:A:904:G:O2'	23:A:961:G:O6	2.36	0.41
33:P:72:THR:HG22	33:P:73:PRO:O	2.21	0.41
33:P:86:GLY:CA	43:Z:19:LYS:CE	2.96	0.41
44:0:18:ARG:HE	44:0:26:LYS:HA	1.86	0.41
23:A:1828:U:O3'	23:A:2230:G:N2	2.53	0.40
23:A:2603:G:O2'	23:A:2606:C:OP2	2.37	0.40
35:R:32:ASN:OD1	35:R:43:GLN:N	2.55	0.40
48:4:39:LEU:O	48:4:41:HIS:ND1	2.52	0.40
1:a:975:A:O2'	1:a:976:G:P	2.77	0.40
1:a:1064:U:O2'	1:a:1067:A:OP2	2.38	0.40
2:b:27:MET:HE1	2:b:189:THR:HA	2.02	0.40
6:f:2:ARG:HE	6:f:93:ARG:HE	1.70	0.40
11:k:100:LEU:O	11:k:103:ALA:HB3	2.21	0.40
12:l:117:THR:HG23	12:l:117:THR:O	2.20	0.40
16:p:57:ALA:O	16:p:61:LEU:HD23	2.21	0.40
19:s:81:LYS:H	19:s:82:GLY:HA2	1.86	0.40
33:P:86:GLY:CA	43:Z:19:LYS:HE3	2.29	0.40
35:R:22:LEU:HD12	35:R:22:LEU:O	2.21	0.40
45:1:38:GLU:N	45:1:38:GLU:OE1	2.55	0.40
1:a:701:G:H1'	22:v:97:ASN:HD22	1.86	0.40
1:a:1017:A:H61	1:a:1032:C:C2'	2.35	0.40
2:b:86:ARG:NH2	2:b:218:ALA:HB3	2.36	0.40
3:c:24:ALA:HB1	10:j:13:TYR:CZ	2.56	0.40
11:k:21:ALA:N	11:k:83:GLU:O	2.44	0.40
23:A:75:G:OP1	45:1:44:ARG:NH2	2.50	0.40
23:A:236:A:N6	23:A:474:A:H61	2.19	0.40
23:A:550:A:O2'	23:A:554:C:O2'	2.31	0.40
23:A:2758:G:O3'	26:E:216:LYS:NZ	2.53	0.40
23:A:2869:G:N7	23:A:2887:G:N2	2.69	0.40
25:D:247:SER:O	25:D:250:GLY:N	2.54	0.40
29:H:120:ASN:O	29:H:121:ILE:HD13	2.21	0.40
33:P:72:THR:O	33:P:94:ILE:N	2.49	0.40
1:a:209:G:HO2'	1:a:210:A:C5'	2.34	0.40
1:a:590:U:OP2	1:a:766:G:N1	2.48	0.40
1:a:853:C:O2'	1:a:856:C:N4	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:a:1503:G:H2'	1:a:1504:A:O4'	2.21	0.40
4:d:15:LEU:HD13	4:d:56:LYS:CB	2.52	0.40
5:e:24:VAL:HG23	5:e:29:ARG:HG2	2.03	0.40
10:j:18:ILE:HD11	10:j:96:VAL:HG23	2.03	0.40
11:k:113:VAL:O	11:k:113:VAL:HG13	2.21	0.40
12:l:34:LYS:H	12:l:35:PHE:HA	1.87	0.40
15:o:77:ARG:O	15:o:81:LEU:HD23	2.22	0.40
22:v:82:ASN:OD1	22:v:83:ASN:N	2.53	0.40
23:A:349:U:H3	23:A:353:A:H62	1.70	0.40
23:A:651:A:OP2	23:A:664:G:N1	2.44	0.40
23:A:1615:G:O2'	23:A:1616:A:OP2	2.32	0.40
25:D:140:VAL:HG12	25:D:191:ILE:HA	2.02	0.40
27:F:80:ALA:HB1	27:F:81:PRO:HD2	2.02	0.40
31:N:106:LEU:HD13	31:N:111:PHE:HB2	2.04	0.40
48:4:11:THR:O	48:4:14:ASN:N	2.54	0.40
1:a:421:G:H1'	1:a:436:G:H21	1.86	0.40
23:A:275:A:N6	23:A:296:G:N2	2.67	0.40
23:A:1879:U:O2	23:A:1916:A:N7	2.55	0.40
30:M:74:VAL:HG11	30:M:76:TYR:CE1	2.55	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	
2	b	220/255 (86%)	186 (84%)	34 (16%)	0	100	100
3	c	202/217 (93%)	173 (86%)	29 (14%)	0	100	100
4	d	193/200 (96%)	169 (88%)	24 (12%)	0	100	100
5	e	157/166 (95%)	134 (85%)	23 (15%)	0	100	100
6	f	92/98 (94%)	77 (84%)	15 (16%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	g	139/156 (89%)	115 (83%)	22 (16%)	2 (1%)	9	37
8	h	129/132 (98%)	107 (83%)	21 (16%)	1 (1%)	16	48
9	i	126/132 (96%)	115 (91%)	11 (9%)	0	100	100
10	j	97/102 (95%)	81 (84%)	16 (16%)	0	100	100
11	k	116/129 (90%)	100 (86%)	16 (14%)	0	100	100
12	l	133/137 (97%)	109 (82%)	23 (17%)	1 (1%)	16	48
13	m	108/121 (89%)	94 (87%)	13 (12%)	1 (1%)	14	45
14	n	58/61 (95%)	45 (78%)	13 (22%)	0	100	100
15	o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
16	p	88/91 (97%)	70 (80%)	18 (20%)	0	100	100
17	q	83/87 (95%)	63 (76%)	20 (24%)	0	100	100
18	r	56/80 (70%)	53 (95%)	3 (5%)	0	100	100
19	s	80/92 (87%)	60 (75%)	20 (25%)	0	100	100
20	t	78/83 (94%)	68 (87%)	10 (13%)	0	100	100
21	u	45/58 (78%)	45 (100%)	0	0	100	100
22	v	96/190 (50%)	74 (77%)	16 (17%)	6 (6%)	1	14
25	D	273/277 (99%)	228 (84%)	45 (16%)	0	100	100
26	E	216/220 (98%)	171 (79%)	43 (20%)	2 (1%)	14	45
27	F	197/207 (95%)	150 (76%)	47 (24%)	0	100	100
28	G	164/179 (92%)	121 (74%)	42 (26%)	1 (1%)	21	52
29	H	162/178 (91%)	138 (85%)	24 (15%)	0	100	100
30	M	143/145 (99%)	119 (83%)	23 (16%)	1 (1%)	18	50
31	N	120/122 (98%)	95 (79%)	23 (19%)	2 (2%)	7	34
32	O	129/146 (88%)	93 (72%)	36 (28%)	0	100	100
33	P	130/144 (90%)	96 (74%)	31 (24%)	3 (2%)	5	30
34	Q	115/122 (94%)	94 (82%)	21 (18%)	0	100	100
35	R	117/119 (98%)	95 (81%)	22 (19%)	0	100	100
36	S	105/116 (90%)	86 (82%)	16 (15%)	3 (3%)	3	26
37	T	114/118 (97%)	100 (88%)	14 (12%)	0	100	100
38	U	100/102 (98%)	86 (86%)	14 (14%)	0	100	100
39	V	110/117 (94%)	100 (91%)	10 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	W	87/91 (96%)	64 (74%)	23 (26%)	0	100	100
41	X	81/105 (77%)	59 (73%)	21 (26%)	1 (1%)	10	40
42	Y	92/217 (42%)	65 (71%)	26 (28%)	1 (1%)	11	42
43	Z	74/94 (79%)	53 (72%)	19 (26%)	2 (3%)	4	27
44	0	44/62 (71%)	32 (73%)	12 (27%)	0	100	100
45	1	63/69 (91%)	60 (95%)	3 (5%)	0	100	100
46	2	55/59 (93%)	49 (89%)	6 (11%)	0	100	100
47	3	81/84 (96%)	62 (76%)	18 (22%)	1 (1%)	10	40
48	4	41/58 (71%)	36 (88%)	5 (12%)	0	100	100
49	5	24/49 (49%)	16 (67%)	8 (33%)	0	100	100
50	6	42/45 (93%)	35 (83%)	5 (12%)	2 (5%)	2	17
51	7	58/66 (88%)	44 (76%)	14 (24%)	0	100	100
52	8	35/37 (95%)	32 (91%)	3 (9%)	0	100	100
All	All	5354/6024 (89%)	4397 (82%)	927 (17%)	30 (1%)	23	52

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	v	6	ILE
22	v	51	ALA
22	v	69	GLU
22	v	93	LYS
26	E	10	ILE
26	E	142	SER
36	S	105	LEU
43	Z	28	ARG
50	6	15	LYS
7	g	13	LEU
13	m	108	THR
33	P	18	THR
36	S	104	SER
41	X	92	ARG
42	Y	16	SER
43	Z	26	SER
50	6	16	VAL
12	l	57	LYS
28	G	90	THR

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Mol	Chain	Res	Type
30	M	66	THR
33	P	26	TYR
31	N	25	LEU
36	S	106	ARG
47	3	34	MET
7	g	14	PRO
22	v	63	VAL
8	h	100	GLY
31	N	101	PRO
22	v	96	ILE
33	P	19	GLY

5.3.2 Protein sidechains [i](#)

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	
2	b	192/221 (87%)	192 (100%)	0	100	100
3	c	165/175 (94%)	164 (99%)	1 (1%)	78	79
4	d	172/175 (98%)	172 (100%)	0	100	100
5	e	125/131 (95%)	125 (100%)	0	100	100
6	f	82/86 (95%)	82 (100%)	0	100	100
7	g	122/132 (92%)	122 (100%)	0	100	100
8	h	112/113 (99%)	111 (99%)	1 (1%)	70	75
9	i	106/109 (97%)	106 (100%)	0	100	100
10	j	89/91 (98%)	89 (100%)	0	100	100
11	k	94/104 (90%)	94 (100%)	0	100	100
12	l	117/119 (98%)	116 (99%)	1 (1%)	70	75
13	m	94/104 (90%)	94 (100%)	0	100	100
14	n	52/53 (98%)	52 (100%)	0	100	100
15	o	80/81 (99%)	80 (100%)	0	100	100
16	p	76/77 (99%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	q	80/82 (98%)	80 (100%)	0	100	100
18	r	52/68 (76%)	49 (94%)	3 (6%)	18	45
19	s	71/80 (89%)	71 (100%)	0	100	100
20	t	67/69 (97%)	67 (100%)	0	100	100
21	u	43/54 (80%)	43 (100%)	0	100	100
22	v	89/173 (51%)	83 (93%)	6 (7%)	15	42
25	D	222/224 (99%)	222 (100%)	0	100	100
26	E	175/177 (99%)	175 (100%)	0	100	100
27	F	163/169 (96%)	163 (100%)	0	100	100
28	G	147/158 (93%)	146 (99%)	1 (1%)	76	77
29	H	144/155 (93%)	144 (100%)	0	100	100
30	M	123/123 (100%)	123 (100%)	0	100	100
31	N	100/100 (100%)	100 (100%)	0	100	100
32	O	104/112 (93%)	104 (100%)	0	100	100
33	P	109/119 (92%)	98 (90%)	11 (10%)	7	29
34	Q	98/102 (96%)	98 (100%)	0	100	100
35	R	95/95 (100%)	95 (100%)	0	100	100
36	S	93/102 (91%)	93 (100%)	0	100	100
37	T	96/98 (98%)	96 (100%)	0	100	100
38	U	86/86 (100%)	86 (100%)	0	100	100
39	V	91/94 (97%)	91 (100%)	0	100	100
40	W	80/82 (98%)	80 (100%)	0	100	100
41	X	73/90 (81%)	73 (100%)	0	100	100
42	Y	83/190 (44%)	83 (100%)	0	100	100
43	Z	59/75 (79%)	50 (85%)	9 (15%)	3	16
44	0	39/52 (75%)	39 (100%)	0	100	100
45	1	59/62 (95%)	59 (100%)	0	100	100
46	2	51/53 (96%)	51 (100%)	0	100	100
47	3	74/75 (99%)	74 (100%)	0	100	100
48	4	40/51 (78%)	40 (100%)	0	100	100
49	5	26/47 (55%)	25 (96%)	1 (4%)	29	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	6	39/40 (98%)	39 (100%)	0	100	100
51	7	52/57 (91%)	52 (100%)	0	100	100
52	8	35/35 (100%)	35 (100%)	0	100	100
All	All	4636/5120 (90%)	4602 (99%)	34 (1%)	73	77

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	c	4	LYS
8	h	39	ILE
12	l	101	LYS
18	r	23	ILE
18	r	24	THR
18	r	26	ILE
22	v	4	PHE
22	v	5	GLU
22	v	22	GLU
22	v	66	ARG
22	v	68	GLU
22	v	96	ILE
28	G	89	VAL
33	P	16	LYS
33	P	17	THR
33	P	18	THR
33	P	20	ARG
33	P	22	LYS
33	P	27	VAL
33	P	28	THR
33	P	31	GLU
33	P	133	LYS
33	P	134	ARG
33	P	135	GLU
43	Z	19	LYS
43	Z	20	ASN
43	Z	22	ARG
43	Z	23	ASP
43	Z	27	LYS
43	Z	28	ARG
43	Z	29	LEU
43	Z	32	LYS
43	Z	33	ARG

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Mol	Chain	Res	Type
49	5	35	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
2	b	24	ASN
2	b	44	GLN
2	b	75	GLN
3	c	61	ASN
3	c	68	HIS
3	c	125	ASN
4	d	85	ASN
5	e	149	ASN
6	f	13	ASN
6	f	53	ASN
7	g	19	ASN
8	h	18	ASN
8	h	31	ASN
9	i	68	ASN
10	j	15	HIS
10	j	78	ASN
11	k	22	HIS
11	k	64	GLN
12	l	73	ASN
12	l	86	ASN
12	l	109	HIS
14	n	11	GLN
14	n	14	GLN
14	n	52	GLN
16	p	15	ASN
17	q	49	HIS
19	s	14	HIS
20	t	34	ASN
20	t	62	GLN
22	v	33	ASN
22	v	83	ASN
22	v	97	ASN
25	D	113	GLN
25	D	133	ASN
25	D	196	ASN
25	D	198	GLN
25	D	203	ASN

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Mol	Chain	Res	Type
27	F	82	GLN
27	F	179	GLN
27	F	182	ASN
29	H	74	ASN
29	H	81	GLN
29	H	120	ASN
31	N	45	ASN
34	Q	73	ASN
35	R	55	GLN
39	V	40	ASN
39	V	102	HIS
42	Y	10	GLN
43	Z	58	ASN
44	0	32	ASN
46	2	32	ASN
47	3	6	HIS
47	3	10	HIS
47	3	20	ASN
49	5	16	ASN
49	5	42	GLN
50	6	17	HIS
52	8	29	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1541/1547 (99%)	303 (19%)	0
23	A	2907/2918 (99%)	625 (21%)	8 (0%)
24	B	113/114 (99%)	18 (15%)	0
All	All	4561/4579 (99%)	946 (20%)	8 (0%)

All (946) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	8	G
1	a	9	A
1	a	10	G
1	a	11	A
1	a	17	A
1	a	32	G
1	a	33	A

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Mol	Chain	Res	Type
1	a	40	G
1	a	48	C
1	a	49	C
1	a	50	U
1	a	51	A
1	a	52	A
1	a	58	G
1	a	61	A
1	a	67	G
1	a	82	G
1	a	83	C
1	a	84	U
1	a	85	U
1	a	88	U
1	a	89	U
1	a	92	C
1	a	93	U
1	a	94	G
1	a	115	A
1	a	119	A
1	a	120	C
1	a	121	A
1	a	129	A
1	a	130	A
1	a	137	U
1	a	144	C
1	a	149	A
1	a	153	C
1	a	159	G
1	a	160	A
1	a	163	C
1	a	165	G
1	a	173	U
1	a	183	U
1	a	185	U
1	a	196	A
1	a	205	A
1	a	211	A
1	a	212	A
1	a	213	G
1	a	214	A
1	a	219	C

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Mol	Chain	Res	Type
1	a	220	U
1	a	221	U
1	a	234	A
1	a	248	U
1	a	252	U
1	a	253	U
1	a	254	A
1	a	255	G
1	a	259	G
1	a	260	U
1	a	269	U
1	a	274	G
1	a	275	C
1	a	283	G
1	a	288	C
1	a	289	G
1	a	297	G
1	a	301	A
1	a	314	A
1	a	336	C
1	a	354	G
1	a	355	G
1	a	360	C
1	a	362	G
1	a	374	C
1	a	375	U
1	a	380	C
1	a	381	A
1	a	386	G
1	a	389	A
1	a	396	G
1	a	405	A
1	a	406	C
1	a	419	A
1	a	420	U
1	a	421	G
1	a	422	A
1	a	429	U
1	a	431	G
1	a	432	G
1	a	436	G
1	a	437	U

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Mol	Chain	Res	Type
1	a	447	U
1	a	450	U
1	a	457	A
1	a	458	G
1	a	462	A
1	a	466	G
1	a	467	U
1	a	469	U
1	a	470	A
1	a	476	C
1	a	477	U
1	a	482	A
1	a	483	C
1	a	484	A
1	a	494	U
1	a	503	A
1	a	505	A
1	a	507	A
1	a	513	G
1	a	516	U
1	a	517	A
1	a	519	C
1	a	525	G
1	a	526	C
1	a	529	G
1	a	535	G
1	a	539	U
1	a	540	A
1	a	553	C
1	a	555	A
1	a	558	G
1	a	567	A
1	a	570	U
1	a	572	U
1	a	580	A
1	a	581	A
1	a	583	G
1	a	584	C
1	a	585	G
1	a	588	C
1	a	615	A
1	a	626	C

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Mol	Chain	Res	Type
1	a	635	G
1	a	640	G
1	a	641	U
1	a	642	C
1	a	650	A
1	a	661	U
1	a	666	G
1	a	669	G
1	a	673	A
1	a	680	U
1	a	695	A
1	a	711	G
1	a	723	A
1	a	727	C
1	a	736	A
1	a	741	G
1	a	742	A
1	a	757	A
1	a	758	C
1	a	763	G
1	a	771	G
1	a	781	G
1	a	789	A
1	a	802	A
1	a	807	G
1	a	817	G
1	a	825	C
1	a	828	U
1	a	829	G
1	a	836	A
1	a	844	G
1	a	851	U
1	a	854	C
1	a	855	G
1	a	856	C
1	a	865	G
1	a	868	G
1	a	869	C
1	a	882	A
1	a	884	G
1	a	886	A
1	a	895	G

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Mol	Chain	Res	Type
1	a	901	U
1	a	912	G
1	a	918	A
1	a	924	A
1	a	933	A
1	a	936	G
1	a	937	G
1	a	944	C
1	a	945	A
1	a	946	C
1	a	956	A
1	a	970	U
1	a	975	A
1	a	976	G
1	a	979	A
1	a	985	A
1	a	986	G
1	a	987	A
1	a	992	U
1	a	993	A
1	a	999	U
1	a	1002	U
1	a	1003	G
1	a	1012	U
1	a	1014	A
1	a	1016	A
1	a	1017	A
1	a	1024	A
1	a	1027	U
1	a	1028	A
1	a	1030	A
1	a	1034	U
1	a	1036	C
1	a	1037	C
1	a	1040	U
1	a	1041	U
1	a	1042	C
1	a	1044	G
1	a	1047	G
1	a	1055	G
1	a	1062	G
1	a	1065	G

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Mol	Chain	Res	Type
1	a	1067	A
1	a	1068	U
1	a	1073	G
1	a	1075	C
1	a	1090	U
1	a	1100	G
1	a	1107	U
1	a	1113	A
1	a	1136	G
1	a	1138	U
1	a	1142	A
1	a	1144	C
1	a	1150	G
1	a	1157	A
1	a	1163	A
1	a	1164	G
1	a	1165	U
1	a	1169	C
1	a	1170	U
1	a	1171	G
1	a	1172	C
1	a	1178	A
1	a	1179	C
1	a	1182	A
1	a	1190	A
1	a	1192	G
1	a	1197	G
1	a	1207	A
1	a	1208	A
1	a	1211	C
1	a	1223	U
1	a	1225	U
1	a	1231	G
1	a	1237	C
1	a	1238	A
1	a	1239	C
1	a	1249	A
1	a	1261	A
1	a	1272	A
1	a	1279	G
1	a	1291	A
1	a	1292	U

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Mol	Chain	Res	Type
1	a	1297	U
1	a	1298	A
1	a	1304	G
1	a	1310	A
1	a	1311	G
1	a	1312	U
1	a	1313	U
1	a	1316	G
1	a	1331	C
1	a	1333	C
1	a	1334	G
1	a	1347	U
1	a	1349	G
1	a	1357	A
1	a	1358	G
1	a	1359	U
1	a	1375	U
1	a	1381	G
1	a	1390	G
1	a	1409	A
1	a	1424	A
1	a	1430	G
1	a	1436	A
1	a	1437	A
1	a	1453	G
1	a	1454	A
1	a	1457	A
1	a	1459	C
1	a	1464	U
1	a	1465	A
1	a	1478	C
1	a	1505	A
1	a	1506	G
1	a	1515	A
1	a	1517	G
1	a	1518	U
1	a	1519	A
1	a	1529	G
1	a	1541	G
1	a	1542	G
1	a	1543	A
1	a	1546	A

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Mol	Chain	Res	Type
1	a	1547	C
1	a	1548	C
23	A	15	G
23	A	27	G
23	A	34	U
23	A	46	C
23	A	63	U
23	A	71	A
23	A	74	U
23	A	75	G
23	A	80	G
23	A	85	G
23	A	90	A
23	A	102	A
23	A	107	G
23	A	108	A
23	A	117	A
23	A	119	U
23	A	130	A
23	A	136	A
23	A	150	A
23	A	161	A
23	A	162	A
23	A	163	U
23	A	164	A
23	A	166	A
23	A	167	U
23	A	168	A
23	A	173	A
23	A	176	A
23	A	180	G
23	A	182	C
23	A	183	A
23	A	184	C
23	A	185	A
23	A	189	G
23	A	199	A
23	A	202	A
23	A	207	A
23	A	218	G
23	A	219	A
23	A	225	A

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Mol	Chain	Res	Type
23	A	229	A
23	A	231	A
23	A	236	A
23	A	244	A
23	A	251	G
23	A	253	G
23	A	284	C
23	A	285	U
23	A	286	U
23	A	287	G
23	A	288	C
23	A	289	U
23	A	290	U
23	A	291	G
23	A	298	U
23	A	301	U
23	A	302	A
23	A	314	A
23	A	316	G
23	A	317	G
23	A	319	G
23	A	321	U
23	A	327	G
23	A	328	G
23	A	331	G
23	A	345	C
23	A	354	A
23	A	373	A
23	A	374	U
23	A	381	G
23	A	401	U
23	A	404	U
23	A	409	G
23	A	411	A
23	A	418	G
23	A	426	G
23	A	432	G
23	A	434	G
23	A	445	G
23	A	457	G
23	A	458	A
23	A	481	C

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Mol	Chain	Res	Type
23	A	486	G
23	A	490	C
23	A	494	U
23	A	498	G
23	A	499	A
23	A	502	C
23	A	503	A
23	A	504	G
23	A	510	U
23	A	511	G
23	A	527	G
23	A	541	G
23	A	543	G
23	A	550	A
23	A	554	C
23	A	555	C
23	A	563	G
23	A	572	C
23	A	573	A
23	A	575	G
23	A	576	U
23	A	577	A
23	A	578	G
23	A	591	A
23	A	593	U
23	A	594	G
23	A	606	G
23	A	613	G
23	A	614	U
23	A	615	A
23	A	618	A
23	A	628	G
23	A	629	A
23	A	630	G
23	A	646	A
23	A	657	U
23	A	658	A
23	A	659	A
23	A	661	U
23	A	663	U
23	A	682	A
23	A	683	G

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Mol	Chain	Res	Type
23	A	690	U
23	A	699	U
23	A	700	A
23	A	713	A
23	A	715	A
23	A	716	C
23	A	722	A
23	A	730	A
23	A	731	U
23	A	732	C
23	A	762	C
23	A	763	A
23	A	771	G
23	A	774	G
23	A	775	A
23	A	777	C
23	A	783	G
23	A	792	U
23	A	793	G
23	A	806	A
23	A	809	A
23	A	820	G
23	A	821	C
23	A	825	G
23	A	827	A
23	A	828	A
23	A	829	U
23	A	834	A
23	A	837	G
23	A	838	A
23	A	844	G
23	A	845	A
23	A	847	A
23	A	848	U
23	A	850	G
23	A	851	C
23	A	856	U
23	A	866	A
23	A	872	U
23	A	873	U
23	A	875	G
23	A	876	G

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Mol	Chain	Res	Type
23	A	904	G
23	A	911	A
23	A	921	C
23	A	922	G
23	A	923	A
23	A	924	G
23	A	925	G
23	A	926	G
23	A	932	U
23	A	938	G
23	A	944	G
23	A	945	A
23	A	947	U
23	A	952	A
23	A	955	A
23	A	970	U
23	A	977	A
23	A	985	A
23	A	989	A
23	A	990	G
23	A	1001	A
23	A	1002	U
23	A	1003	A
23	A	1005	G
23	A	1017	A
23	A	1018	A
23	A	1034	A
23	A	1040	A
23	A	1041	G
23	A	1055	A
23	A	1056	U
23	A	1057	A
23	A	1061	G
23	A	1064	A
23	A	1066	G
23	A	1069	G
23	A	1070	A
23	A	1077	U
23	A	1079	U
23	A	1085	U
23	A	1088	C
23	A	1091	G

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Mol	Chain	Res	Type
23	A	1098	A
23	A	1101	A
23	A	1102	U
23	A	1105	U
23	A	1109	U
23	A	1111	A
23	A	1113	A
23	A	1114	A
23	A	1115	G
23	A	1117	A
23	A	1121	A
23	A	1122	U
23	A	1123	C
23	A	1125	U
23	A	1126	U
23	A	1128	A
23	A	1131	G
23	A	1132	A
23	A	1133	G
23	A	1138	U
23	A	1139	A
23	A	1140	A
23	A	1143	G
23	A	1145	U
23	A	1146	C
23	A	1149	U
23	A	1150	A
23	A	1154	G
23	A	1155	A
23	A	1156	G
23	A	1158	G
23	A	1160	C
23	A	1163	U
23	A	1172	A
23	A	1177	A
23	A	1178	C
23	A	1179	C
23	A	1183	G
23	A	1185	U
23	A	1187	A
23	A	1188	A
23	A	1195	A

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Mol	Chain	Res	Type
23	A	1205	U
23	A	1217	U
23	A	1218	G
23	A	1245	G
23	A	1248	U
23	A	1249	U
23	A	1250	G
23	A	1258	A
23	A	1265	G
23	A	1274	G
23	A	1276	G
23	A	1278	G
23	A	1286	G
23	A	1287	U
23	A	1288	G
23	A	1289	A
23	A	1290	G
23	A	1291	A
23	A	1293	U
23	A	1294	G
23	A	1300	G
23	A	1303	A
23	A	1309	G
23	A	1310	A
23	A	1312	A
23	A	1313	G
23	A	1323	A
23	A	1324	A
23	A	1337	A
23	A	1338	U
23	A	1339	U
23	A	1343	U
23	A	1361	G
23	A	1377	U
23	A	1378	U
23	A	1397	G
23	A	1402	A
23	A	1405	G
23	A	1415	A
23	A	1416	U
23	A	1421	A
23	A	1423	C

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Mol	Chain	Res	Type
23	A	1429	G
23	A	1432	A
23	A	1440	A
23	A	1451	U
23	A	1454	U
23	A	1455	U
23	A	1459	A
23	A	1463	A
23	A	1464	U
23	A	1471	A
23	A	1472	C
23	A	1479	G
23	A	1480	G
23	A	1481	A
23	A	1489	A
23	A	1490	G
23	A	1491	C
23	A	1494	G
23	A	1495	C
23	A	1496	G
23	A	1498	U
23	A	1499	U
23	A	1503	U
23	A	1504	U
23	A	1505	G
23	A	1510	U
23	A	1519	U
23	A	1520	A
23	A	1522	G
23	A	1533	A
23	A	1534	G
23	A	1551	U
23	A	1552	U
23	A	1553	A
23	A	1555	G
23	A	1559	G
23	A	1561	G
23	A	1566	G
23	A	1567	A
23	A	1568	U
23	A	1569	G
23	A	1577	G

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Mol	Chain	Res	Type
23	A	1578	A
23	A	1579	C
23	A	1580	A
23	A	1581	U
23	A	1582	U
23	A	1583	G
23	A	1584	A
23	A	1585	G
23	A	1590	C
23	A	1595	C
23	A	1604	C
23	A	1605	A
23	A	1606	C
23	A	1613	G
23	A	1614	A
23	A	1616	A
23	A	1618	A
23	A	1625	U
23	A	1628	A
23	A	1630	A
23	A	1631	G
23	A	1632	A
23	A	1635	A
23	A	1636	U
23	A	1651	C
23	A	1652	A
23	A	1655	C
23	A	1657	G
23	A	1659	C
23	A	1660	A
23	A	1661	C
23	A	1662	A
23	A	1676	A
23	A	1677	G
23	A	1683	U
23	A	1690	A
23	A	1692	C
23	A	1693	G
23	A	1697	G
23	A	1698	A
23	A	1718	G
23	A	1738	C

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Mol	Chain	Res	Type
23	A	1739	G
23	A	1740	G
23	A	1742	A
23	A	1743	G
23	A	1759	G
23	A	1761	G
23	A	1763	U
23	A	1765	A
23	A	1768	C
23	A	1772	G
23	A	1783	G
23	A	1784	U
23	A	1790	G
23	A	1791	G
23	A	1800	A
23	A	1808	U
23	A	1812	A
23	A	1818	A
23	A	1827	C
23	A	1828	U
23	A	1829	A
23	A	1835	U
23	A	1842	A
23	A	1843	U
23	A	1844	G
23	A	1846	A
23	A	1856	A
23	A	1857	C
23	A	1862	G
23	A	1865	C
23	A	1866	G
23	A	1897	U
23	A	1898	C
23	A	1902	G
23	A	1903	A
23	A	1930	G
23	A	1933	G
23	A	1939	A
23	A	1952	C
23	A	1954	A
23	A	1956	G
23	A	1957	G

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Mol	Chain	Res	Type
23	A	1958	U
23	A	1963	A
23	A	1964	A
23	A	1965	A
23	A	1967	U
23	A	1969	C
23	A	1970	U
23	A	1979	A
23	A	1981	G
23	A	1982	U
23	A	1991	G
23	A	1992	C
23	A	1993	A
23	A	1994	C
23	A	1997	A
23	A	1998	A
23	A	1999	G
23	A	2009	U
23	A	2018	U
23	A	2020	U
23	A	2047	A
23	A	2057	A
23	A	2058	A
23	A	2059	G
23	A	2061	U
23	A	2070	C
23	A	2073	G
23	A	2082	C
23	A	2083	G
23	A	2087	A
23	A	2088	G
23	A	2089	A
23	A	2096	G
23	A	2103	U
23	A	2107	G
23	A	2117	A
23	A	2120	G
23	A	2138	U
23	A	2139	A
23	A	2140	C
23	A	2143	G
23	A	2145	U

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Mol	Chain	Res	Type
23	A	2146	A
23	A	2147	G
23	A	2153	A
23	A	2155	C
23	A	2159	U
23	A	2160	G
23	A	2161	A
23	A	2163	A
23	A	2172	C
23	A	2173	U
23	A	2175	G
23	A	2176	C
23	A	2184	G
23	A	2188	C
23	A	2189	G
23	A	2193	G
23	A	2194	U
23	A	2195	G
23	A	2198	A
23	A	2200	A
23	A	2203	A
23	A	2217	G
23	A	2218	G
23	A	2221	U
23	A	2226	A
23	A	2230	G
23	A	2231	C
23	A	2239	A
23	A	2240	U
23	A	2244	G
23	A	2252	A
23	A	2265	G
23	A	2266	G
23	A	2273	G
23	A	2278	G
23	A	2290	C
23	A	2293	A
23	A	2295	A
23	A	2310	C
23	A	2314	A
23	A	2316	G
23	A	2331	G

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Mol	Chain	Res	Type
23	A	2332	U
23	A	2334	G
23	A	2335	G
23	A	2337	A
23	A	2339	U
23	A	2347	A
23	A	2352	G
23	A	2360	A
23	A	2361	U
23	A	2362	A
23	A	2363	A
23	A	2366	G
23	A	2370	U
23	A	2372	G
23	A	2374	C
23	A	2377	C
23	A	2410	G
23	A	2412	C
23	A	2415	A
23	A	2417	U
23	A	2419	A
23	A	2433	C
23	A	2450	U
23	A	2452	A
23	A	2454	C
23	A	2455	G
23	A	2456	G
23	A	2457	A
23	A	2458	U
23	A	2468	C
23	A	2472	G
23	A	2475	A
23	A	2476	U
23	A	2485	U
23	A	2493	C
23	A	2502	C
23	A	2505	A
23	A	2511	G
23	A	2518	U
23	A	2521	G
23	A	2525	C
23	A	2529	G

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Mol	Chain	Res	Type
23	A	2531	U
23	A	2532	G
23	A	2533	U
23	A	2545	A
23	A	2546	U
23	A	2547	C
23	A	2552	G
23	A	2561	C
23	A	2562	G
23	A	2580	G
23	A	2583	C
23	A	2589	U
23	A	2593	A
23	A	2594	G
23	A	2599	A
23	A	2600	C
23	A	2601	G
23	A	2603	G
23	A	2605	G
23	A	2609	G
23	A	2612	U
23	A	2613	C
23	A	2623	U
23	A	2624	G
23	A	2629	A
23	A	2630	G
23	A	2636	U
23	A	2640	U
23	A	2651	G
23	A	2657	G
23	A	2666	A
23	A	2667	G
23	A	2683	U
23	A	2708	C
23	A	2712	G
23	A	2716	U
23	A	2717	A
23	A	2729	G
23	A	2741	G
23	A	2753	U
23	A	2760	A
23	A	2771	G

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Mol	Chain	Res	Type
23	A	2775	A
23	A	2778	G
23	A	2783	U
23	A	2784	A
23	A	2791	A
23	A	2792	A
23	A	2793	G
23	A	2803	A
23	A	2805	A
23	A	2806	U
23	A	2815	C
23	A	2817	A
23	A	2819	C
23	A	2820	U
23	A	2821	U
23	A	2822	C
23	A	2823	G
23	A	2824	G
23	A	2827	A
23	A	2828	U
23	A	2838	C
23	A	2843	A
23	A	2850	G
23	A	2851	G
23	A	2853	U
23	A	2862	C
23	A	2868	G
23	A	2869	G
23	A	2879	G
23	A	2881	C
23	A	2886	G
23	A	2892	G
23	A	2896	A
23	A	2899	A
23	A	2900	C
23	A	2903	A
23	A	2911	A
23	A	2913	G
23	A	2919	A
24	B	10	U
24	B	11	A
24	B	12	U

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Mol	Chain	Res	Type
24	B	13	A
24	B	33	U
24	B	35	C
24	B	39	G
24	B	40	C
24	B	42	G
24	B	43	A
24	B	45	C
24	B	55	A
24	B	84	U
24	B	87	G
24	B	88	U
24	B	93	C
24	B	106	U
24	B	113	G

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
23	A	179	A
23	A	593	U
23	A	1104	U
23	A	1288	G
23	A	1478	A
23	A	1982	U
23	A	2056	G
23	A	2715	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	A	1
40	W	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1569:G	O3'	1570:G	P	3.93
1	W	58:TYR	C	59:LYS	N	1.20

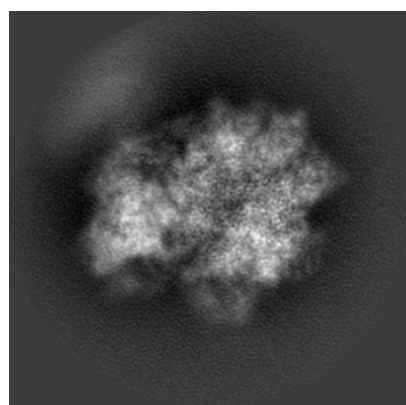
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3624. These allow visual inspection of the internal detail of the map and identification of artifacts.

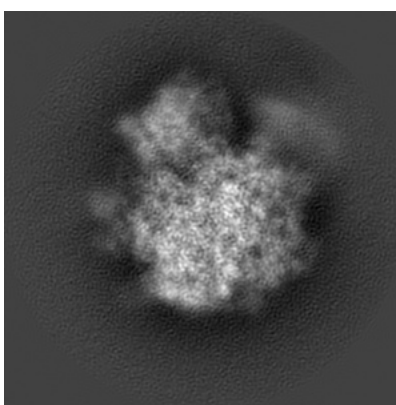
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

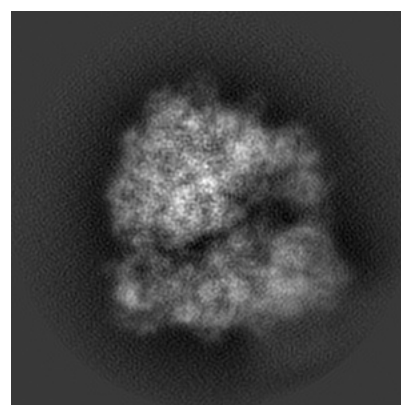
6.1.1 Primary map



X



Y

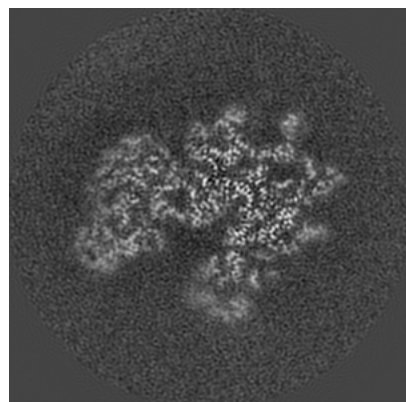


Z

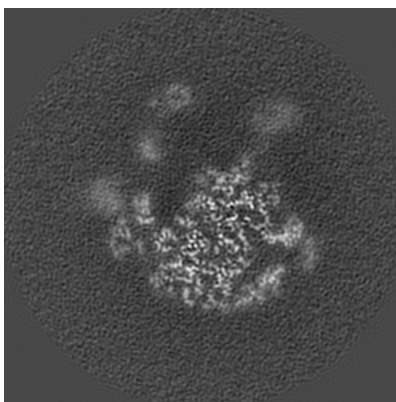
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

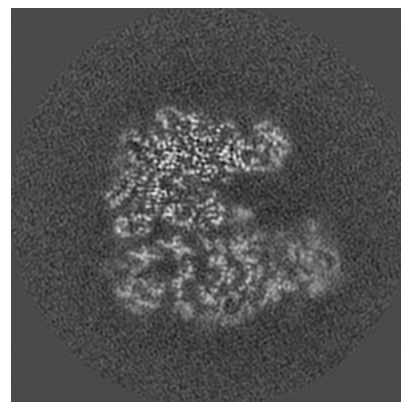
6.2.1 Primary map



X Index: 170



Y Index: 170

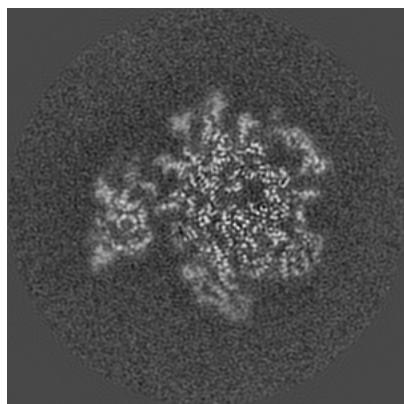


Z Index: 170

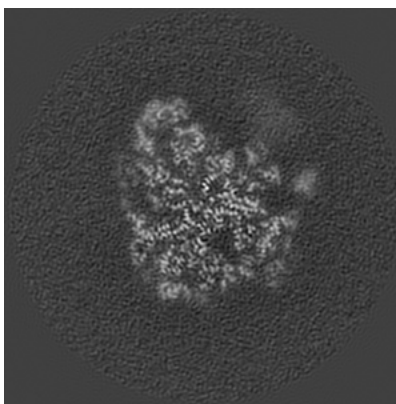
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

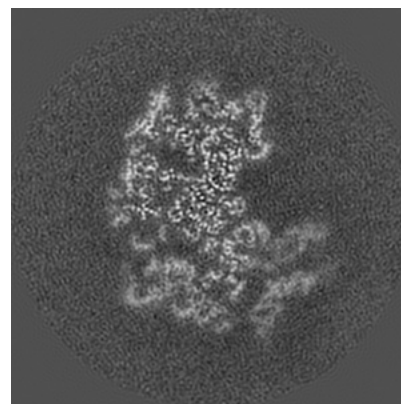
6.3.1 Primary map



X Index: 142



Y Index: 213

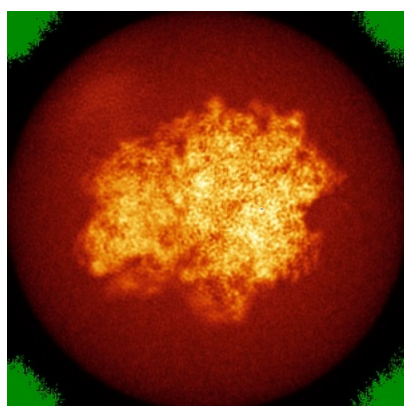


Z Index: 189

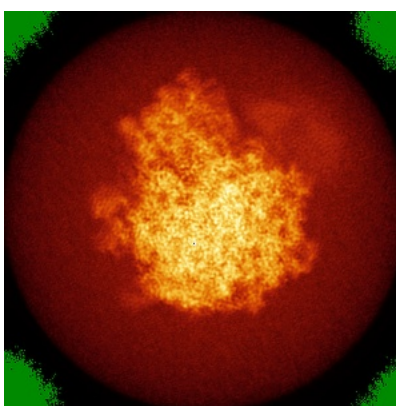
The images above show the largest variance slices of the map in three orthogonal directions.

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

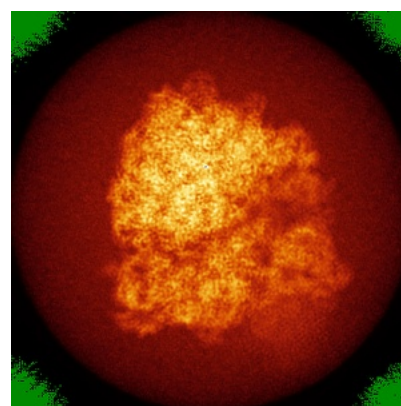
6.4.1 Primary map



X



Y

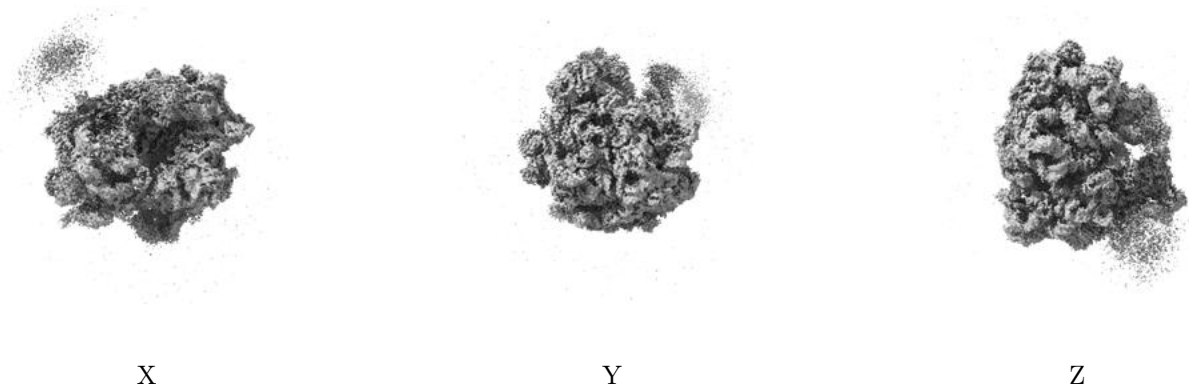


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

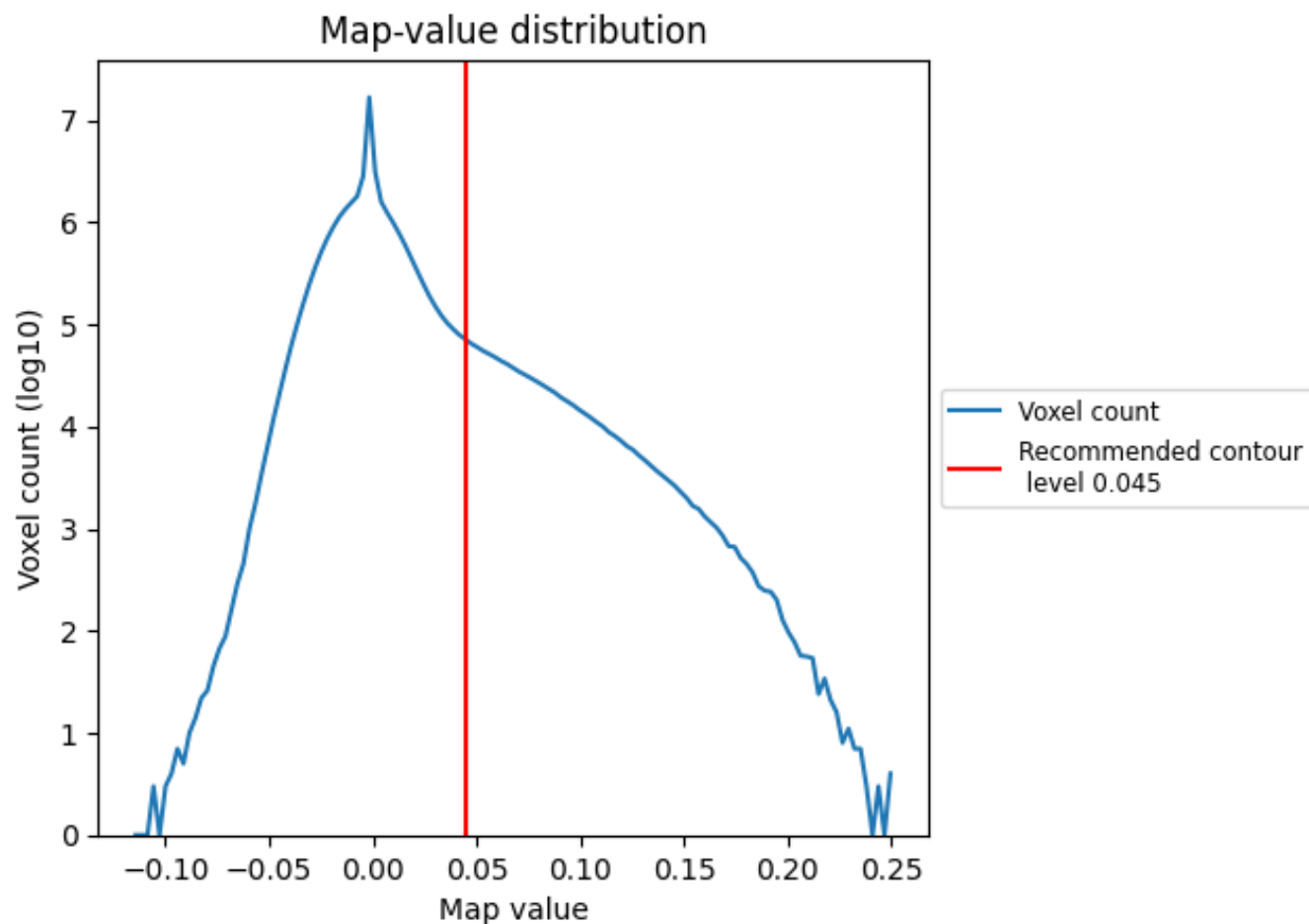
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

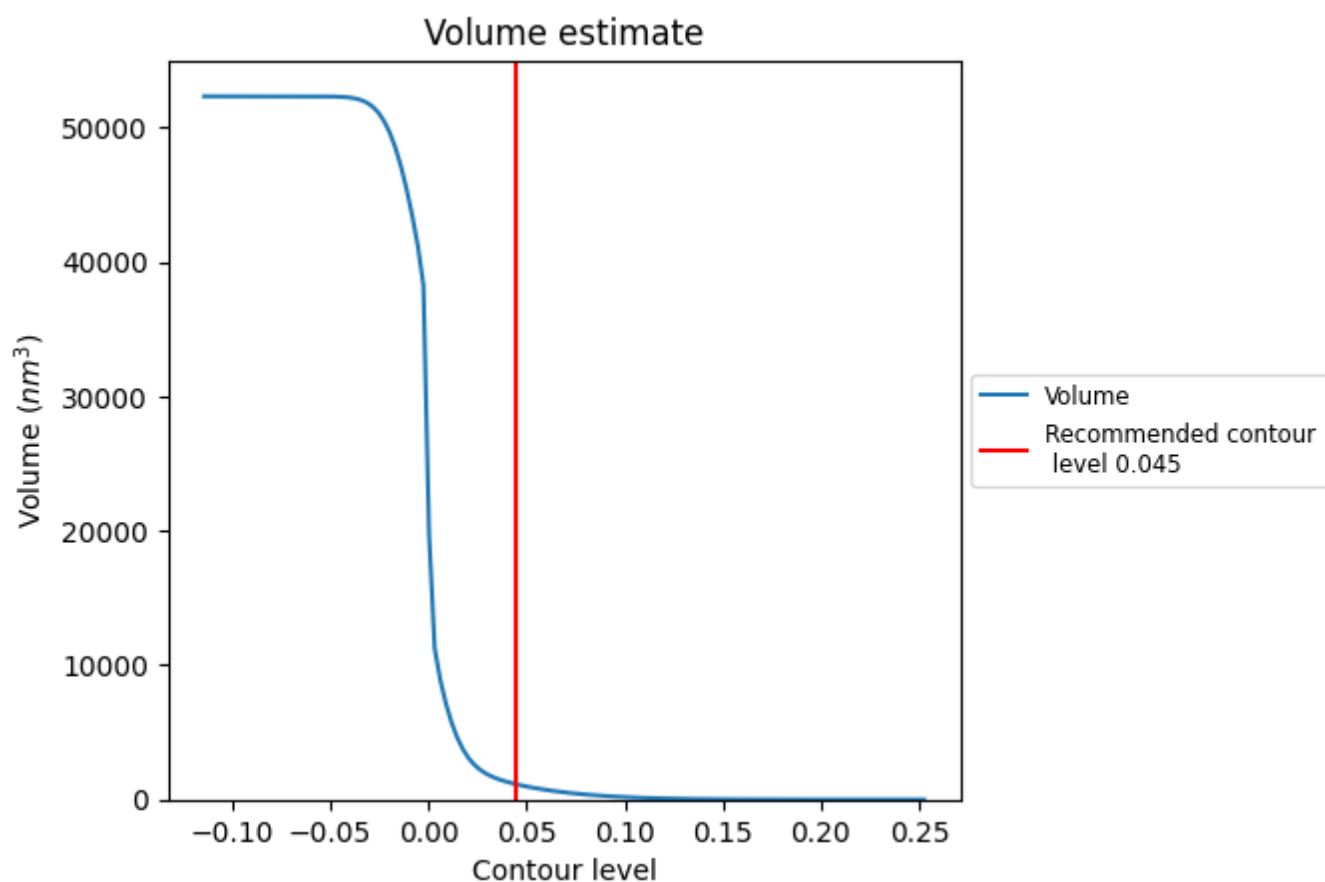
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

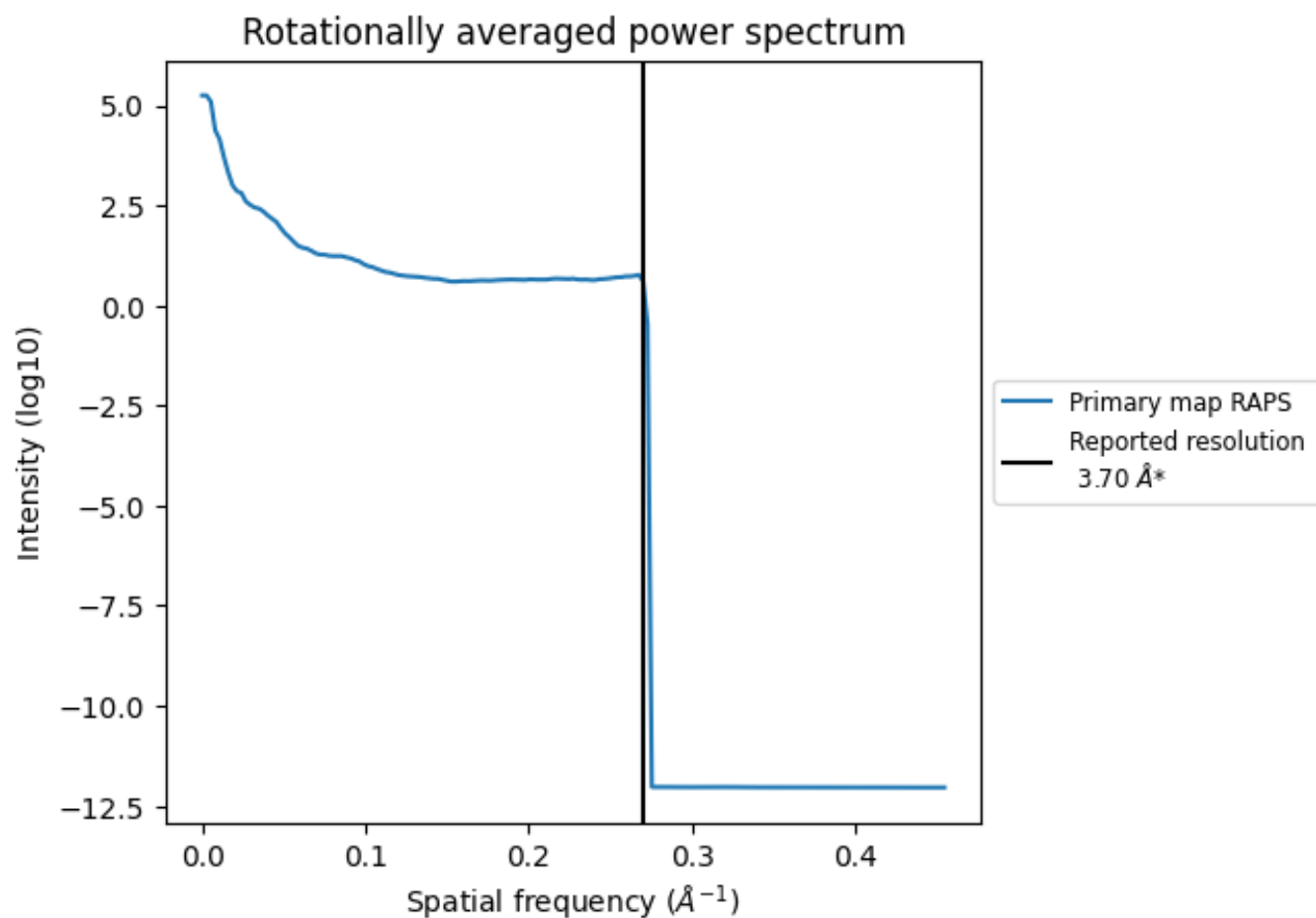
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1129 nm³; this corresponds to an approximate mass of 1020 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 0.270 Å⁻¹

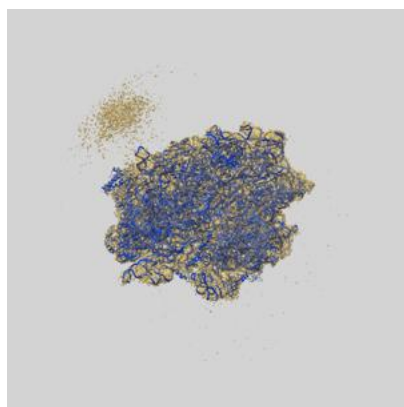
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

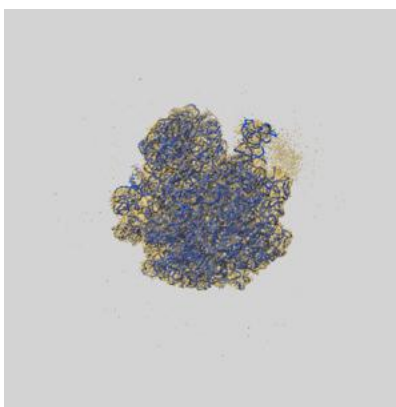
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3624 and PDB model 5ND8. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

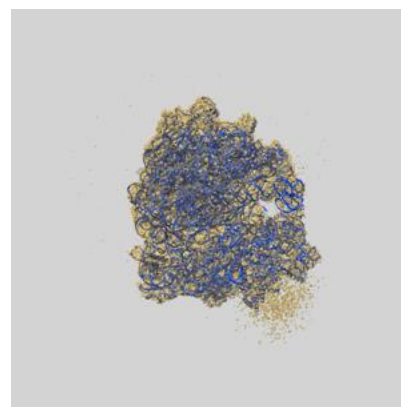
9.1 Map-model overlay [i](#)



X



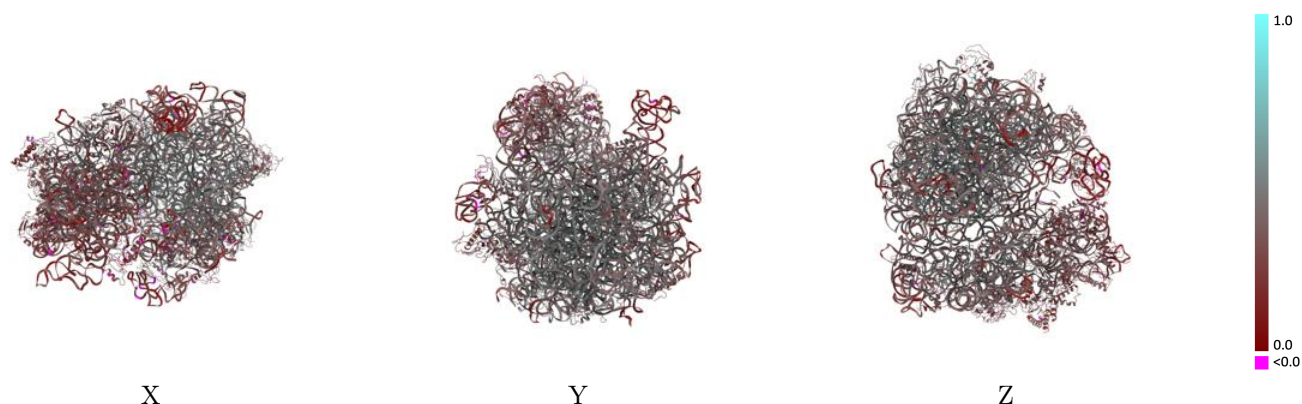
Y



Z

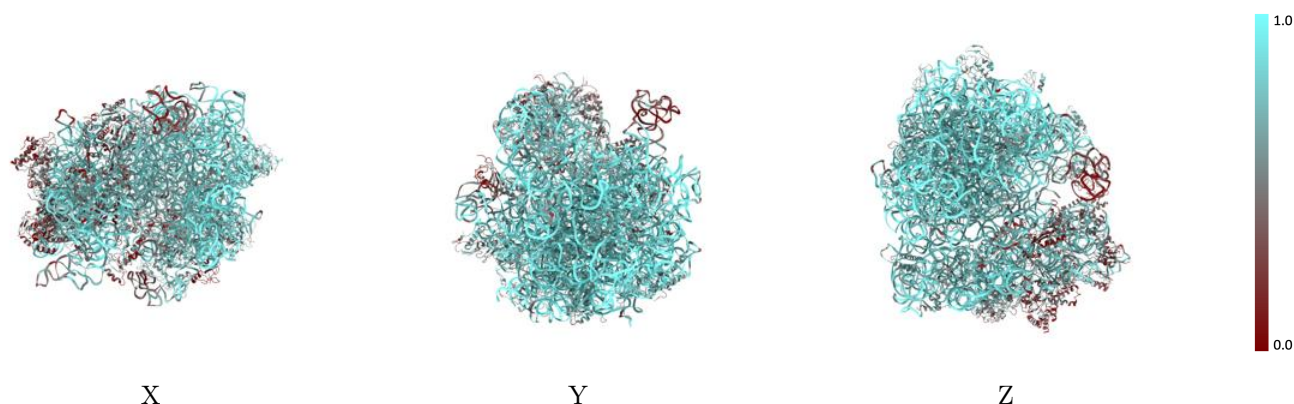
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



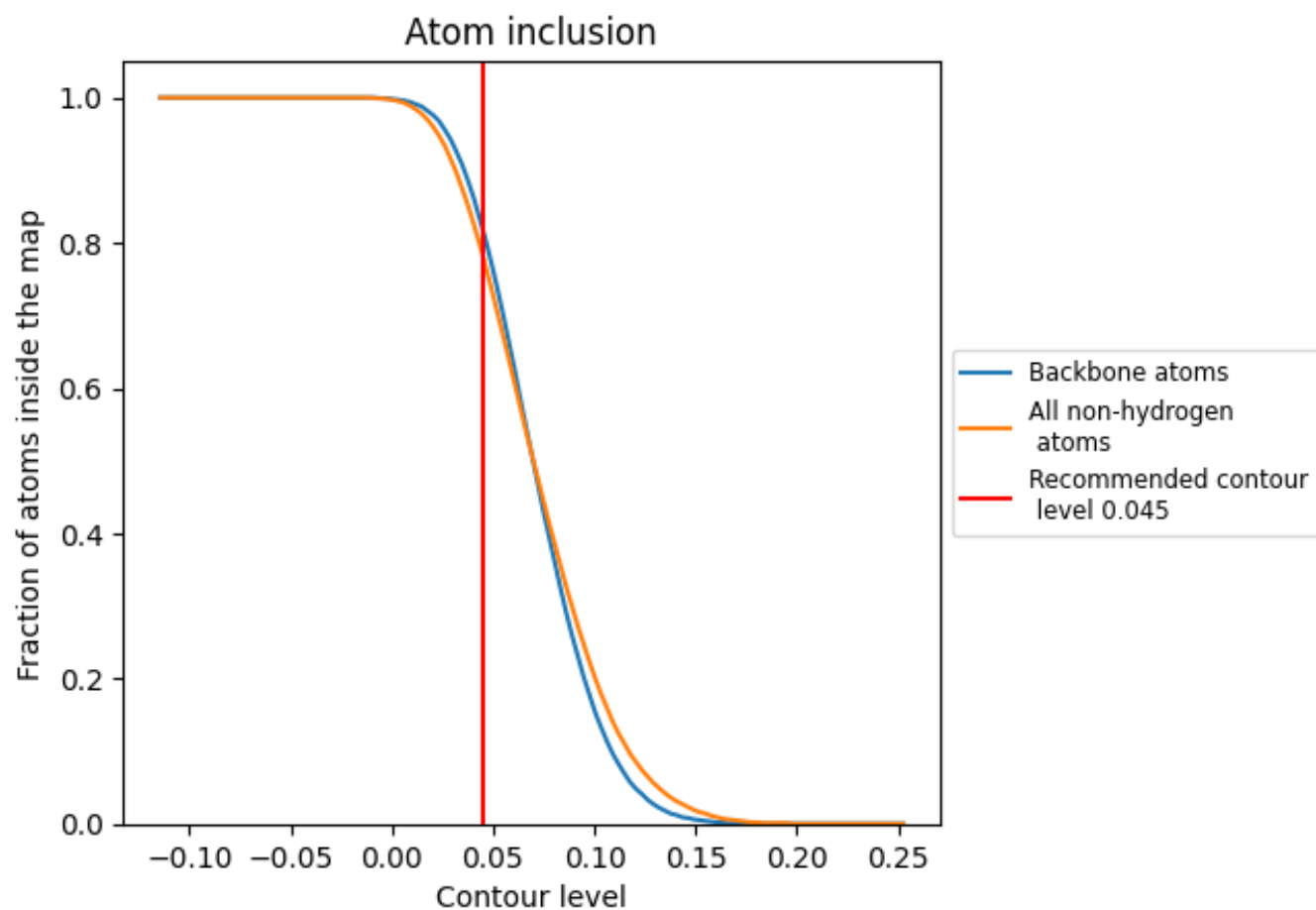
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7820	 0.3840
0	 0.5940	 0.3890
1	 0.6560	 0.3660
2	 0.6910	 0.4250
3	 0.3340	 0.1880
4	 0.6220	 0.4270
5	 0.2700	 0.2780
6	 0.7500	 0.4580
7	 0.7160	 0.4150
8	 0.6560	 0.4350
A	 0.8910	 0.4180
B	 0.9160	 0.3550
D	 0.6900	 0.4560
E	 0.7080	 0.4370
F	 0.6970	 0.4010
G	 0.5130	 0.2740
H	 0.5880	 0.3120
M	 0.7180	 0.4260
N	 0.6310	 0.4420
O	 0.7120	 0.3960
P	 0.6810	 0.3890
Q	 0.6930	 0.4180
R	 0.6300	 0.3130
S	 0.6610	 0.4230
T	 0.7460	 0.4280
U	 0.6930	 0.4290
V	 0.7160	 0.4610
W	 0.6630	 0.4070
X	 0.6370	 0.3690
Y	 0.2150	 0.3000
Z	 0.7420	 0.4350
a	 0.8630	 0.3590
b	 0.3210	 0.2990
c	 0.2730	 0.2950
d	 0.4840	 0.2820



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Chain	Atom inclusion	Q-score
e	 0.5060	 0.3720
f	 0.4370	 0.3500
g	 0.4080	 0.2700
h	 0.5670	 0.3590
i	 0.3430	 0.2470
j	 0.2900	 0.2630
k	 0.4610	 0.3280
l	 0.5970	 0.3860
m	 0.3720	 0.2240
n	 0.3830	 0.2700
o	 0.6110	 0.3480
p	 0.5990	 0.3520
q	 0.5650	 0.3710
r	 0.4990	 0.3840
s	 0.3950	 0.2130
t	 0.6390	 0.3320
u	 0.1560	 0.2810
v	 0.2260	 0.2870