



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 01:52 AM UTC

PDB ID : 6HTQ / pdb_00006htq
EMDB ID : EMD-0270
Title : Stringent response control by a bifunctional RelA enzyme in the presence and absence of the ribosome
Authors : Wilson, D.N.; Abdelshahid, M.
Deposited on : 2018-10-04
Resolution : 4.50 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:

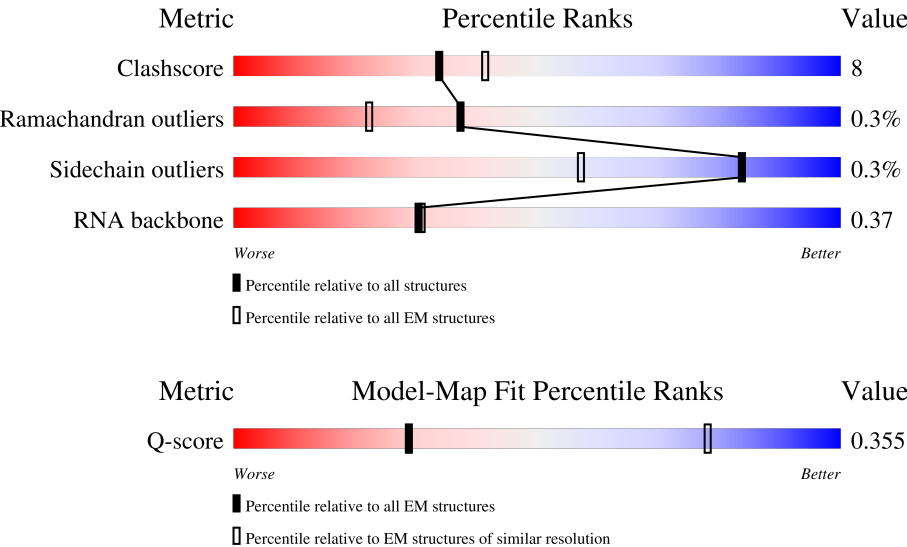
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



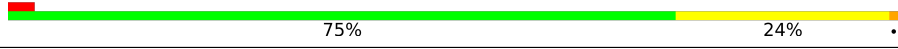
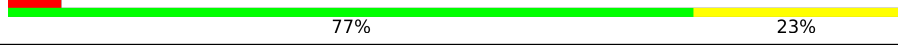
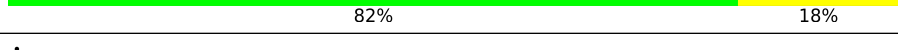
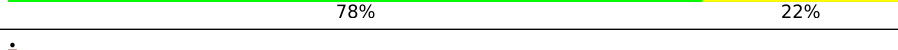
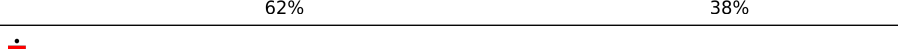
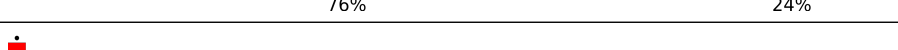
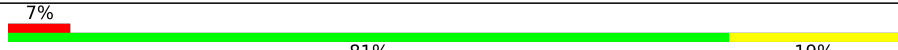
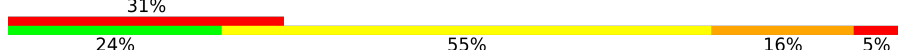
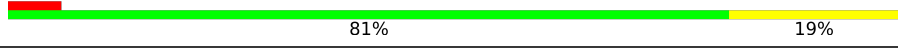
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2937 (4.00 - 5.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2925	
2	B	112	
3	C	272	

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Mol	Chain	Length	Quality of chain
4	D	206	
5	E	205	
6	F	176	
7	G	175	
8	J	142	
9	K	122	
10	L	146	
11	M	135	
12	N	119	
13	O	120	
14	P	115	
15	Q	117	
16	R	101	
17	S	109	
18	T	90	
19	U	101	
20	V	82	
21	W	58	
22	X	65	
23	Y	58	
24	1	54	
25	2	48	
26	3	44	
27	4	64	
28	5	37	

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Mol	Chain	Length	Quality of chain
29	Z	63	
30	a	1533	
31	b	218	
32	c	206	
33	d	195	
34	e	164	
35	f	92	
36	g	149	
37	h	131	
38	i	125	
39	j	95	
40	k	114	
41	l	136	
42	m	108	
43	n	60	
44	o	85	
45	p	88	
46	q	84	
47	r	64	
48	s	78	
49	t	83	
50	v	87	
51	x	341	
52	u	76	
53	w	75	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 146680 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2887	Total	C	N	O	P	0	0
			61997	27661	11460	19992	2884		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2392	1068	435	778	111		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	272	Total	C	N	O	S	0	0
			2083	1296	408	373	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	176	Total	C	N	O	S	0	0
			1386	882	241	256	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	135	Total	C	N	O	S	0	0
			1076	690	205	176	5		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	O	120	Total	C	N	O	S	0	0
			912	564	176	171	1		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	P	115	Total	C	N	O	S	0	0
			944	600	185	158	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	90	Total	C	N	O	S	0	0
			725	452	134	136	3		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	101	Total	C	N	O	S	0	0
			762	478	142	138	4		

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	82	Total	C	N	O		0	0
			630	390	123	117			

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	58	Total	C	N	O	S	0	0
			444	275	92	75	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	1	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 25 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	2	48	Total	C	N	O	S	0	0
			401	244	80	73	4		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	3	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	4	64	Total	C	N	O	S	0	0
			512	321	107	82	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	5	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 29 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	63	Total	C	N	O	S	0	0
			499	312	91	91	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	1533	Total	C	N	O	P	0	0
			32891	14667	6034	10657	1533		

- Molecule 31 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	218	Total	C	N	O	S	0	0
			1757	1119	309	323	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	206	Total	C	N	O	S	0	0
			1619	1011	304	301	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	195	Total	C	N	O	S	0	0
			1568	991	291	284	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	e	164	Total	C	N	O	S	0	0
			1218	767	225	224	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	f	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	149	Total	C	N	O	S	0	0
			1181	740	220	215	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	131	Total	C	N	O	S	0	0
			1036	655	191	187	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	125	Total	C	N	O	S	0	0
			966	599	191	175	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	95	Total	C	N	O	S	0	0
			761	479	139	141	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	114	Total	C	N	O	S	0	0
			838	516	164	156	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	136	Total	C	N	O	S	0	0
			1052	653	211	186	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
42	m	108	Total	C	N	O	0	0
			868	534	176	158		

- Molecule 43 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	60	Total	C	N	O	S	0	0
			497	317	98	77	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	85	Total	C	N	O	S	0	0
			710	436	144	129	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	88	Total	C	N	O	S	0	0
			695	441	128	124	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 47 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	78	Total	C	N	O	S	0	0
			633	409	112	110	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 50 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	v	87	Total	C	N	O	P	0	0
			1861	829	333	612	87		

- Molecule 51 is a protein called GTP pyrophosphokinase.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	341	Total	C	N	O	S	0	0
			2752	1717	504	524	7		

- Molecule 52 is a RNA chain called A/R-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	76	Total	C	N	O	P	0	0
			1623	723	289	535	76		

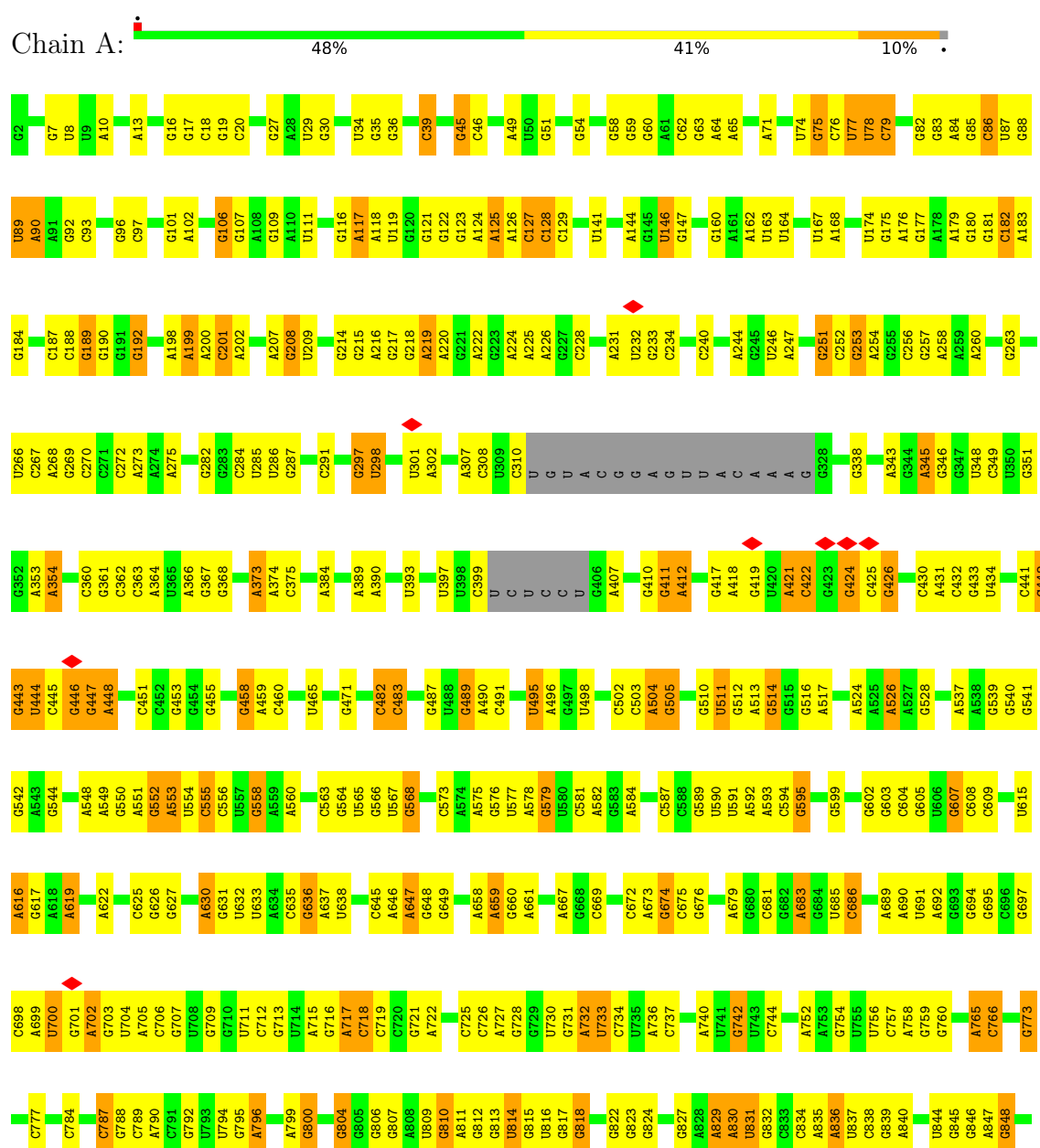
- Molecule 53 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	w	75	Total	C	N	O	P	0	0
			1599	713	285	526	75		

3 Residue-property plots

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

• Molecule 1: 23S ribosomal RNA

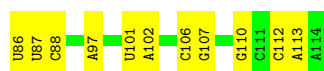


G1898	U1899	G1902	A1905	A1913	A1914	A1928	A1929	A1930	G1931	G1932	G1935	C1938	C1939	U1940	A1941	A1942	C1943	U1944	A1945	A1946	A1947	A1948	A1949	G1950	G1951	U1952	C1953	A1956	A1957	G1958	G1959	G1962	C1963	G1964	A1965	A1966	A1967	U1968	U1969	U1972	U1973	G1977	G1978	A1981	A1982	G1983	U1984	U1985								
U1825	C1826	U1827	G1828	C1829	G1830	A1831	A1832	C1833	C1834	A1835	A1836	U1837	A1838	A1839	G1840	G1841	C1842	A1843	A1844	A1845	G1846	U1847	A1848	U1849	A1850	G1851	G1852	G1853	G1854	C1855	U1856	G1857	A1858	C1859	C1866	C1867	G1868	C1869	U1870	G1871	G1872	U1873	A1877	A1878	A1882	A1883	G1884	A1885	G1886	G1887	A1888	C1889	G1890	A1891	G1892	U1893
U1756	G1757	U1758	U1759	A1760	U1764	G1765	G1766	A1767	A1768	C1771	A1774	G1775	U1776	G1777	A1778	G1779	C1780	C1781	G1782	C1783	A1784	G1785	U1786	G1787	A1788	A1789	U1790	A1791	U1792	G1793	A1797	G1798	G1799	C1800	G1801	A1802	C1803	U1804	G1805	U1806	U1807	U1808	A1809	G1810	C1811	A1812	A1813	A1814	A1815	A1816	C1817	A1820	G1821			
U1666	G1671	A1672	G1673	G1674	A1675	A1676	A1677	A1678	A1679	A1680	C1683	A1686	G1687	A1691	U1692	C1693	G1696	A1697	G1698	A1699	A1700	U1704	U1708	A1709	G1712	A1713	A1714	G1715	U1716	G1719	C1720	A1721	C1722	A1723	A1724	A1734	U1738	C1739	G1740	G1741	G1742	A1743	G1744	A1745	A1746	G1747	G1748									
U1505	A1506	U1507	C1508	U1513	C1514	C1515	A1516	G1521	G1525	A1526	C1527	U1528	U1529	G1530	G1531	A1532	A1533	G1537	G1538	C1539	A1540	A1541	A1542	A1543	C1544	U1547	C1550	C1551	C1552	A1553	U	A1555	A1556	G1557	G1558	C1559	U1560	G1561	U1565	A1566	U1567	G1568	A1569	U1570	G1571	C1572	A1573	G1574	A1575	G1576	C1577	G				
A	A	A	U	U	A	A	G	U	A	A1592	A1593	G1594	U1595	U1596	C1597	C1598	C1604	A1608	A1614	A1615	G1616	A1617	A1618	A1619	A1620	G1621	U1626	A1627	G1628	A1631	G1632	G1633	U1634	G1639	G1640	U1641	C1644	C1645	C1649	C1652	A1653	A1654	A1655	G1658	A1661											
U1417	U1418	U1419	G1422	A1423	A1424	A1425	A1426	G1427	G1431	A1432	U1433	A1434	U1435	U1436	C1437	A1442	U1448	C1449	A1453	U1457	U1458	U1459	G1460	C1463	A1464	A1465	U1466	G1467	G1472	A1473	C1474	G1475	C1476	A1477	G1478	G1479	G1482	U1489	A1490	A1491	U1498	A1499	U1500	U1501	G1502	A1504										
G1338	A1339	U1340	U1341	G1349	U1350	U1351	U1352	C1353	G1359	A1360	A1361	G1362	G1363	C1364	U1365	C1366	C1367	U1368	C1369	G1370	G1371	C1372	A1375	G1376	G1377	G1378	U1379	A1380	A1381	G1382	U1383	C1384	G1385	G1386	G1387	A1388	C1389	G1394	G1397	A1398	G1399	C1400	C1402	A1403	A1404	A1405	A1406	G1407	G1408	G1410	U1411	A1412				
A1260	C1261	G1262	G1263	A1266	G1267	G1268	A1269	C1270	G1275	G1276	A1277	G1278	U1282	A1287	U1288	U1289	G1292	A1293	A1294	U1295	G1296	C1297	G1298	G1299	G1300	U1301	A1302	U1303	G1304	A1305	G1306	U1307	A1308	G1311	A1312	A1313	A1314	G1315	G1319	U1320	U1321	G1322	A1323	G1324	A1325	A1326	U1327	C1328	C1333	C1337						
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A1006	G1007	C1011	G1012	U1013	A1014	G1015	U1016	C1017	G1018	A1019	A1020	A1026	A1027	C1028	A1029	G1030	C1031	C1032	C1033	A1034	G1035	A1036	C1037	G1038	G1039	C1040	C1041	U1042	G1043	A1054	A1055	A1056	G1057	U1058	A1059	U1065	A1066	A1067	G1068	U1069	G1070	G1071	G1072	A1073	U1076	U1079	U1090	U1091	A1092	G1093	A1094	U1004	A1005			
A851	G852	C853	U854	G855	U858	C859	U860	C864	G865	A866	A867	A868	U869	A870	U874	U875	A876	G877	G878	U881	U886	U891	U892	G895	U901	G902	G903	A904	G905	G906	U907	A908	G909	A910	G911	C912	A913	C914	U915	G916	G920	G921	A925	G926	G927	G928	G929	C930	C931							
C932	C933	U934	A935	C936	C937	G938	G939	G940	U941	U942	A943	C944	G945	G946	A947	U954	A957	A958	C959	U960	C961	G962	G963	A964	G965	U966	G967	A970	G973	U977	A978	U979	C981	G984	G985	A987	G988	C990	A991	G992	A993	G998	A999	G1000	U1001	G1002	A1003	U1004	A1005							



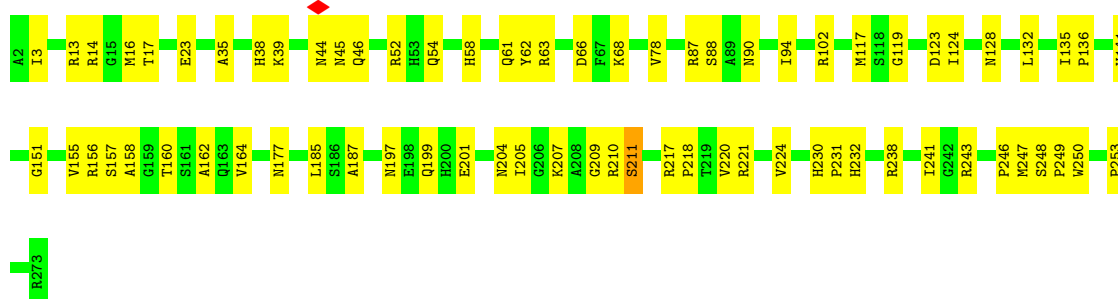
Response	Percentage
Used	53%
Not used	40%
Don't know	7%





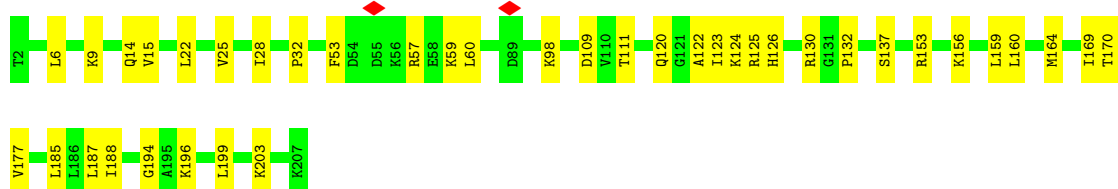
• Molecule 3: 50S ribosomal protein L2

Chain C: 74% 26%



• Molecule 4: 50S ribosomal protein L3

Chain D: 81% 19%



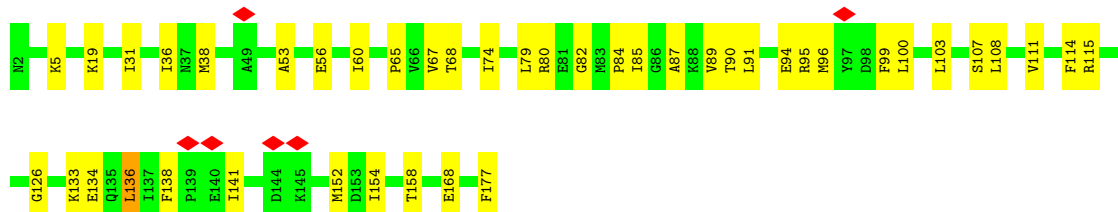
• Molecule 5: 50S ribosomal protein L4

Chain E: 80% 20%

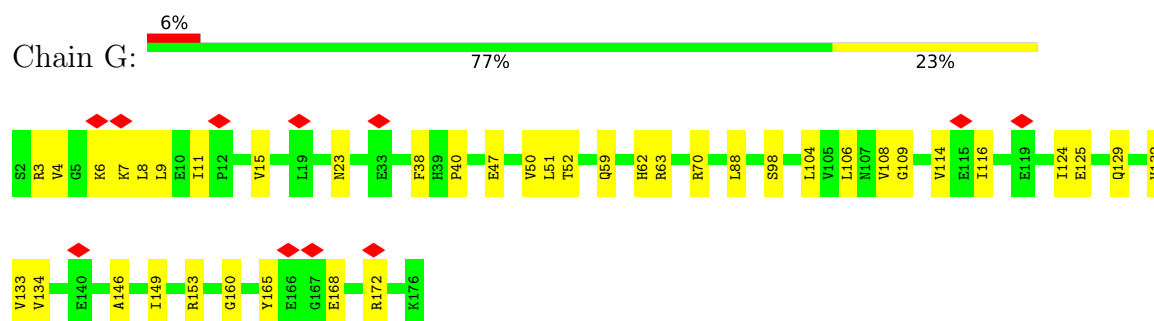


• Molecule 6: 50S ribosomal protein L5

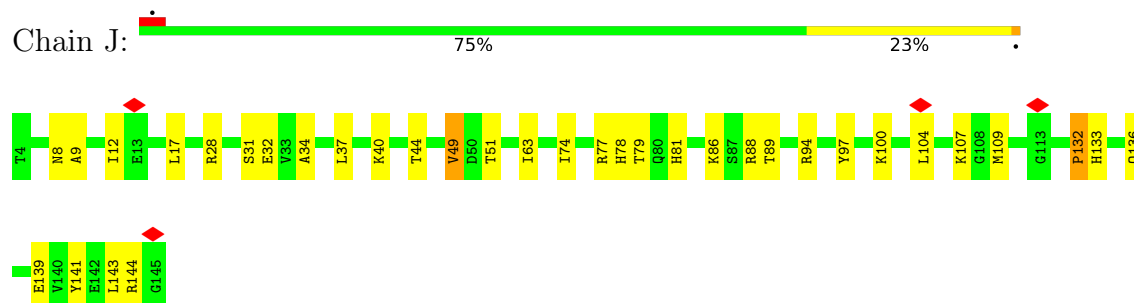
Chain F: 75% 24%



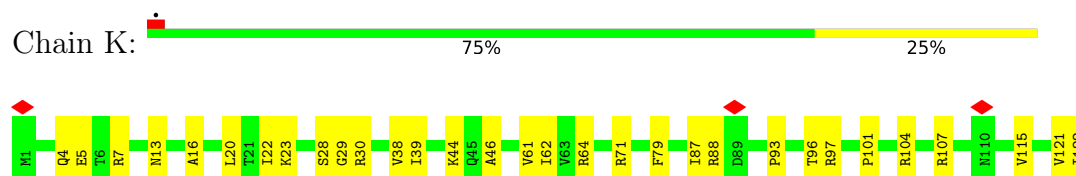
• Molecule 7: 50S ribosomal protein L6



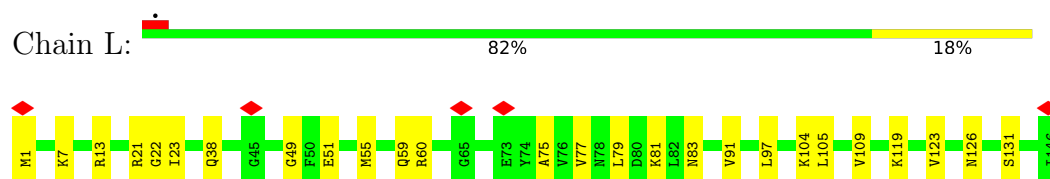
• Molecule 8: 50S ribosomal protein L13



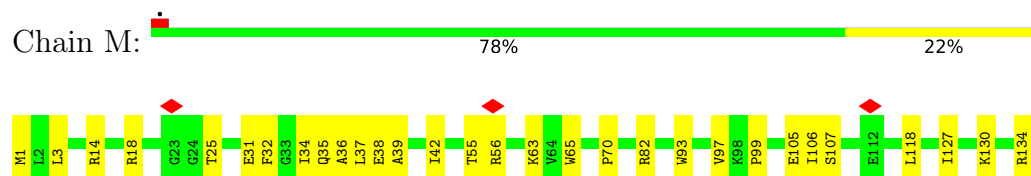
• Molecule 9: 50S ribosomal protein L14



• Molecule 10: 50S ribosomal protein L15

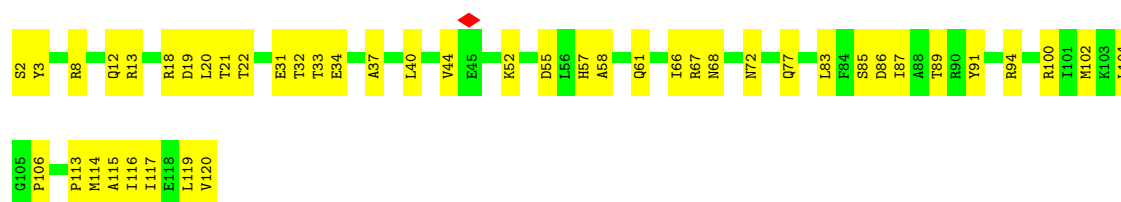


• Molecule 11: 50S ribosomal protein L16

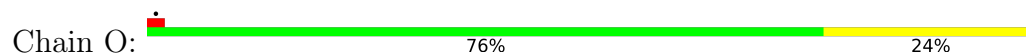


• Molecule 12: 50S ribosomal protein L17





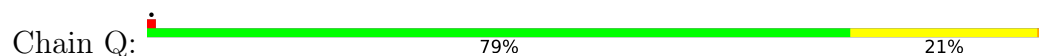
- Molecule 13: 50S ribosomal protein L18



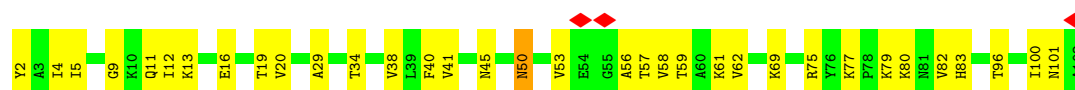
- Molecule 14: 50S ribosomal protein L19



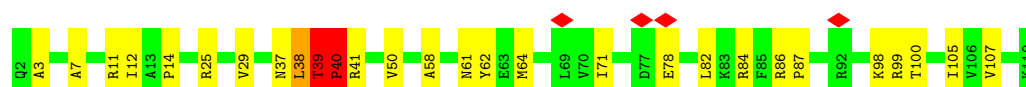
- Molecule 15: 50S ribosomal protein L20



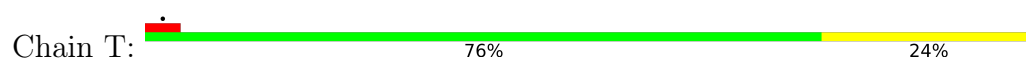
- Molecule 16: 50S ribosomal protein L21



- Molecule 17: 50S ribosomal protein L22

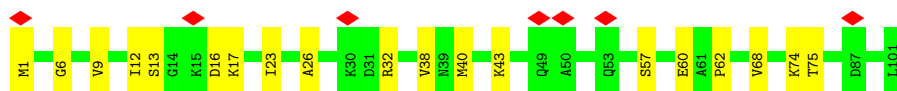
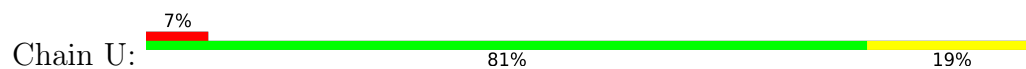


- Molecule 18: 50S ribosomal protein L23





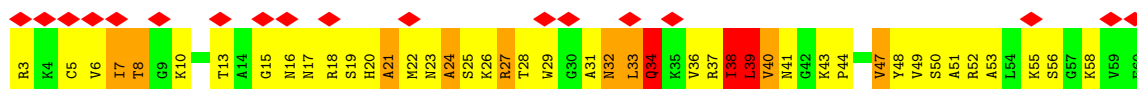
- Molecule 19: 50S ribosomal protein L24



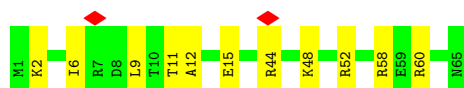
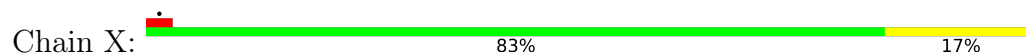
- Molecule 20: 50S ribosomal protein L27



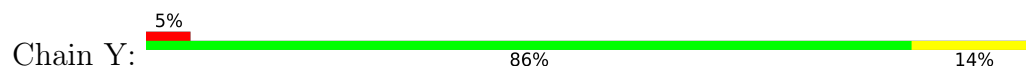
- Molecule 21: 50S ribosomal protein L28



- Molecule 22: 50S ribosomal protein L29



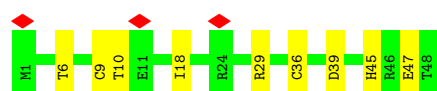
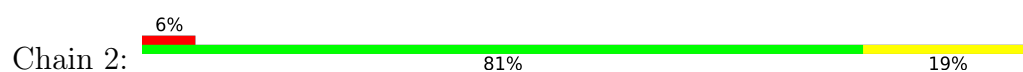
- Molecule 23: 50S ribosomal protein L30



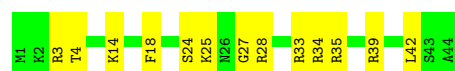
- Molecule 24: 50S ribosomal protein L32



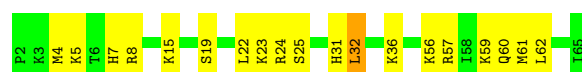
- Molecule 25: 50S ribosomal protein L33 1



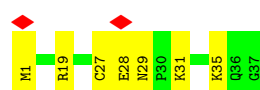
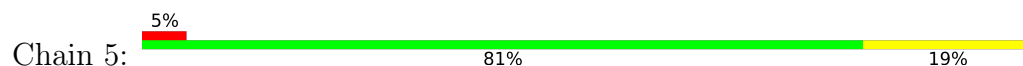
- Molecule 26: 50S ribosomal protein L34



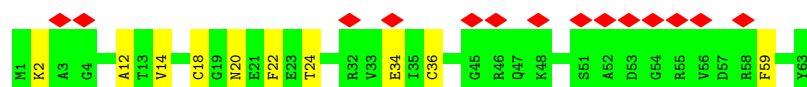
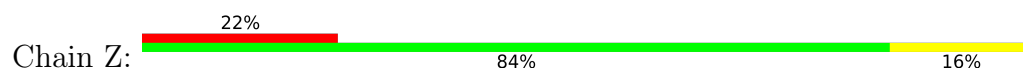
- Molecule 27: 50S ribosomal protein L35



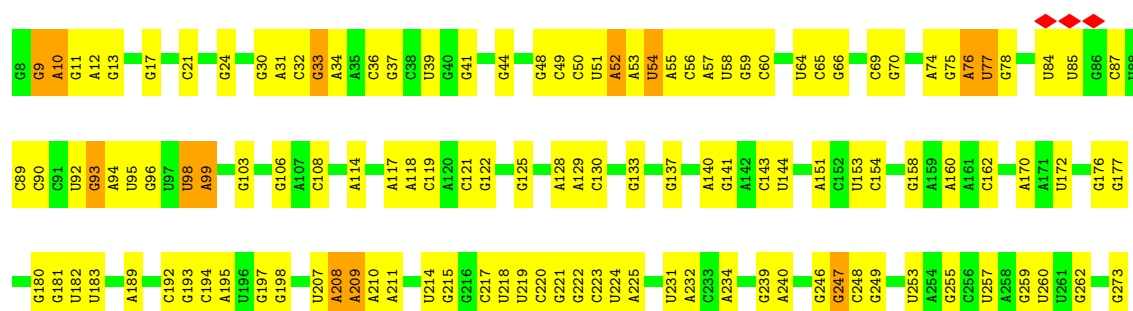
- Molecule 28: 50S ribosomal protein L36



- Molecule 29: 50S ribosomal protein L31

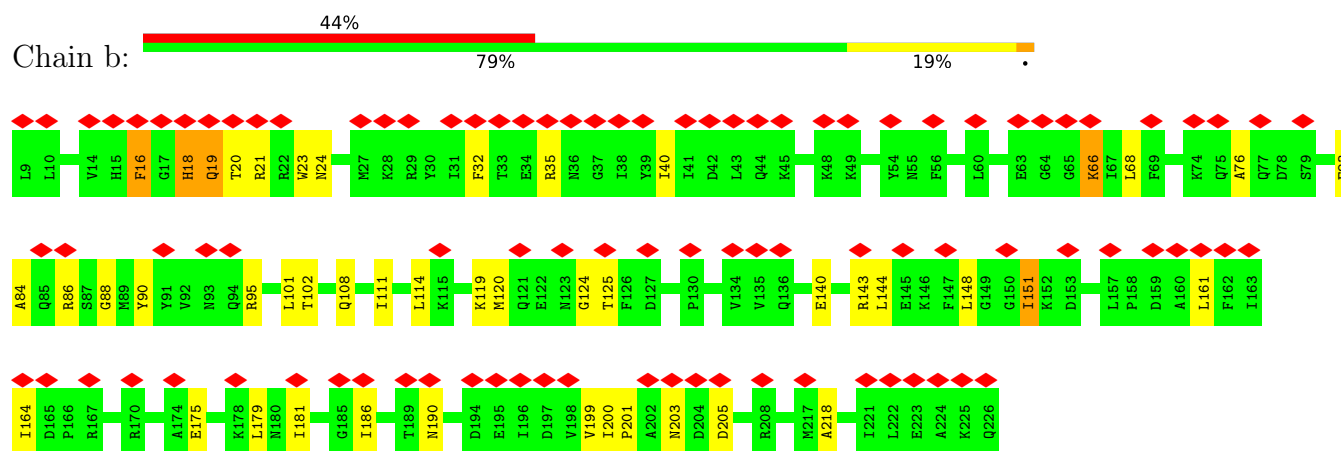


- Molecule 30: 16S rRNA

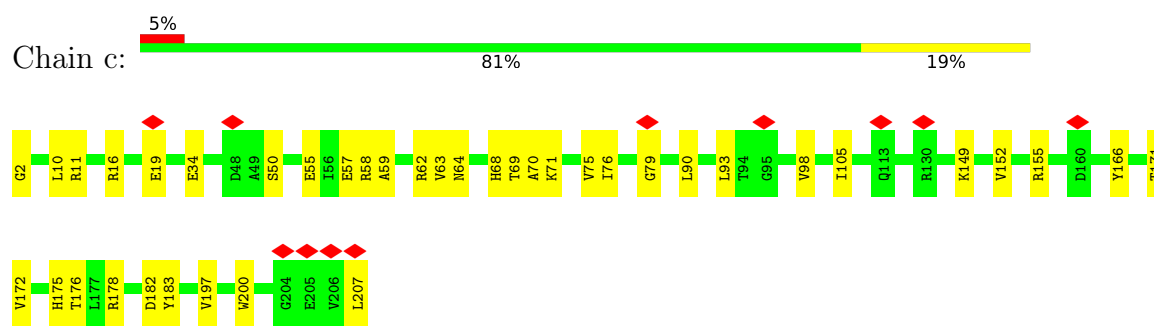


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C1487	G1394	G1318	G1229	A1140	C1055	A985	A912	C826	U732	A361	G530	G446	U276
A1488	G1395		G1230	G1141		G986	A913		G733	U447	G533	U448	A277
	G1396	G1321	G1231	C1142	G1058	A987	G914	G834	G734	G362	G533	G449	A278
	C1397	U1322	U1232	A1143	U1059	A988	U915		C735	U366	G536	G455	G283
	C1398	C1323	U1233	U1144	C1060	C989		A838	G736	A367	G536	G455	G284
	U1400	U1324	A1234	U1145	C1064	C990	A918	G839	A737	U373	C537	A456	C285
	G1409	G1325	C1235	C1146	U1065	A993	A919	U840	A738	U373	G538	A457	G286
	G1401	C1326	A1236	A1147	A1065	A994	G920	G841	G739	C374	G539	G458	A287
	U1402	A1327		G1148	U1066	C995	U921		G740	U375	U540	A459	
	A1403	A1328	G1240	U1149	G1067	C996	U922	G845	G741		A541	A460	G289
		U1329	U1241	U1150	U1070	A996	A923	G846	G742	C378	A542	C461	
	C1406	U1330	G1242	G1151	G1071	U999	A924	G847	A743	G379	U543	G466	C293
	A1407	C1331	C1243	G1152		U999	A925	G848	G750	A381	A544	C467	G294
	C1408	G1332		G1153	C1000	U1001	U930	G849		A382	C545	G466	
	U1335		C1246	A1154	G1074	U1001	U931	U850	U754	U383	G546	C472	G297
	A1336	U1247	A1247	A1155	U1075	U1002	U931	U851	G755	U383	U551	C472	C298
	G1336	A1248	A1248	C1156	C1076	G1003	G932	U852	U756	G384	G552	G473	C299
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	G1340			U1159	C1079	C1008	G938	C855	C759	G388	A556	U476	U304
		G1343	C1258			C1009		C856		A389		A477	G305
		C1344	A1259	A1166	G1082	U1010	C942		G764	A390	G559	G478	A306
	U1345	U1345	A1260	G1169	U1085	C1011	G943	C859	C765	A391	U560	C481	G307
	G1346				C1086	G1013	A945	U860	U766	G392	U561	G482	A308
		U1354	C1264	G1175	G1087	A1014		U861				G483	
		A1355	G1265	A1176	U1088	C1015	G949	A862	G767	U395	C564	G483	G313
	G1356	G1356	G1267	C1177	G1089	C1015		G863	A768	G396		U484	U315
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	A1435		G1269	U1179	G1091	A1017	U953	G865		C486	A569	C487	C316
	U1359	A1360	A1270	A1180	U1018	C1019	G954	C866	G774	G399			G317
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	G1362	C1362		A1278	G1094	G957	A956	A874	G782	C406	U574	A901	U325
	C1363	C1363	A1283	A1188	U1095	A1024	C958	A875	G783	G407	G575	G326	
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	A1442	A1443		G1190	U1100	G1026	A959	C877	A786	C411	G577	U495	
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	G1460	C1368	A1288	U1192	A1102	A1028	G961	C878		G412	U413	A329	
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		U1380	A1308	U1211	G1117	G1042	A975	G900	C815	G432	U599	A346	
	C1469	G1381	G1309	U1221	G1117	G1118		U901	A816	A433	U434	C347	
	A1470		U1310	U1221	G1118		A978	A901	C817	U335	U434		
	G1471	U1385	U1311	A1222		G1046		A902	A818	A435	U517	A352	
		A1386	C1312	U1223	C1122	A1047	A979	C903	G818	G436	A518	C353	
		C1387	G1313	G1224	C1123	A1048	G980	A903		U737	G354	G355	
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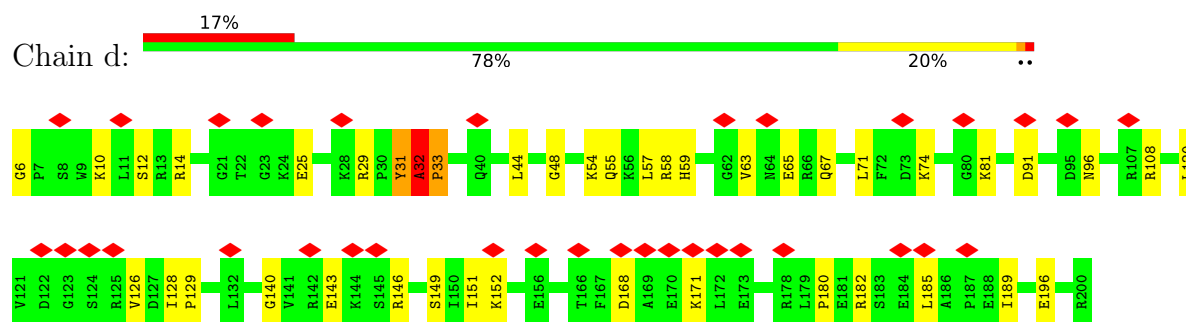
- Molecule 31: 30S ribosomal protein S2



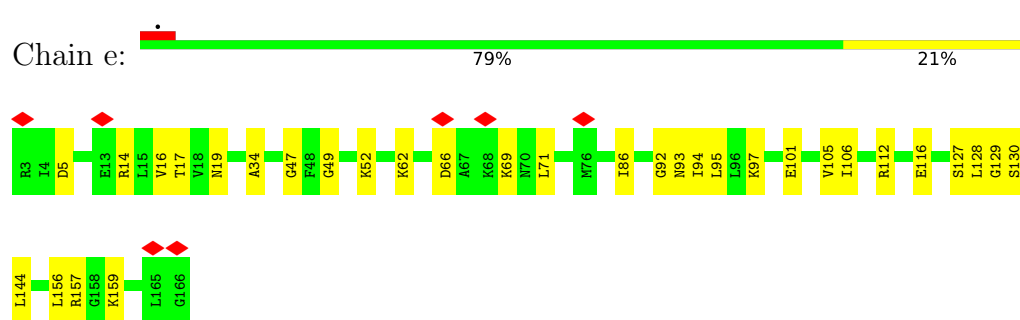
- Molecule 32: 30S ribosomal protein S3



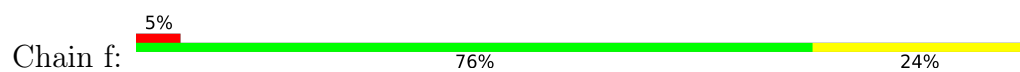
- Molecule 33: 30S ribosomal protein S4



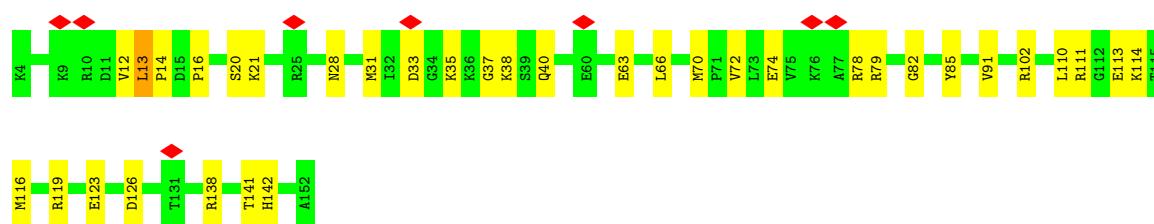
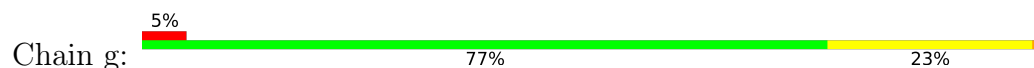
- Molecule 34: 30S ribosomal protein S5



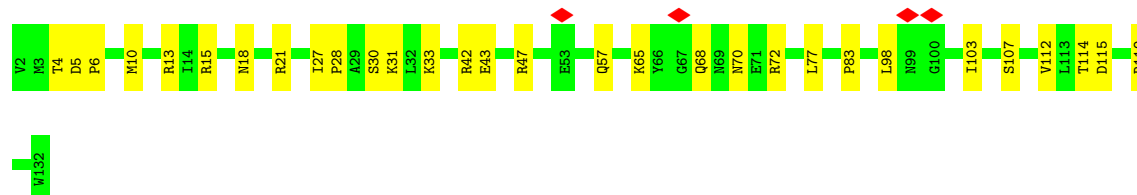
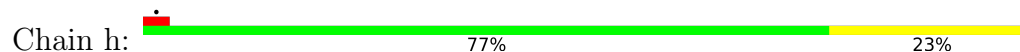
- Molecule 35: 30S ribosomal protein S6



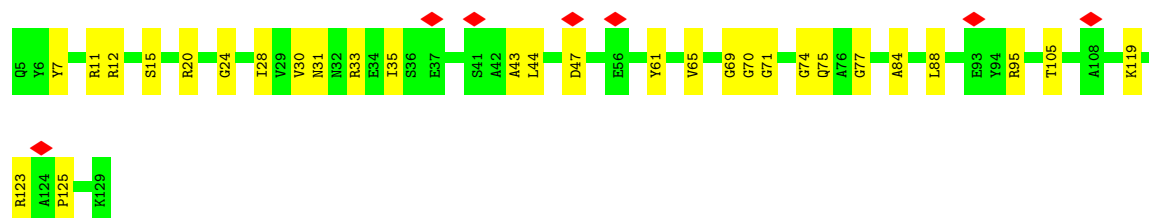
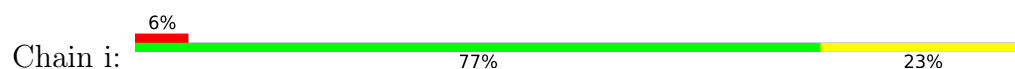
- Molecule 36: 30S ribosomal protein S7



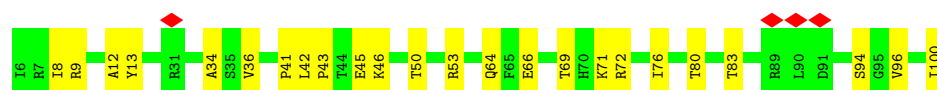
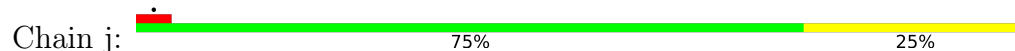
- Molecule 37: 30S ribosomal protein S8



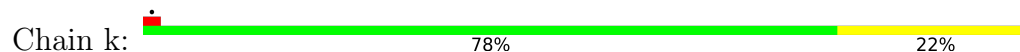
- Molecule 38: 30S ribosomal protein S9



- Molecule 39: 30S ribosomal protein S10

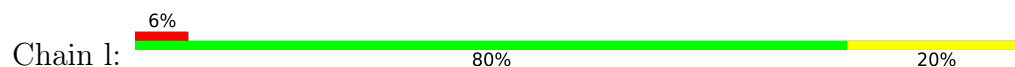


- Molecule 40: 30S ribosomal protein S11

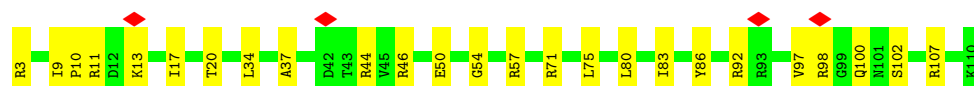
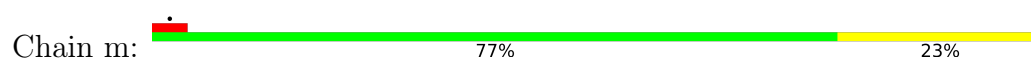




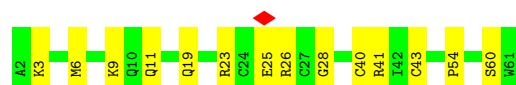
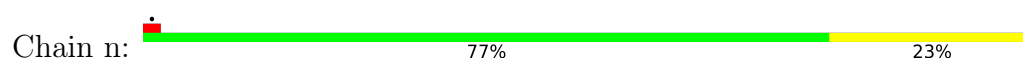
- Molecule 41: 30S ribosomal protein S12



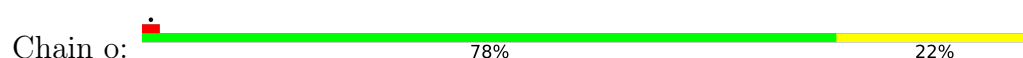
- Molecule 42: 30S ribosomal protein S13



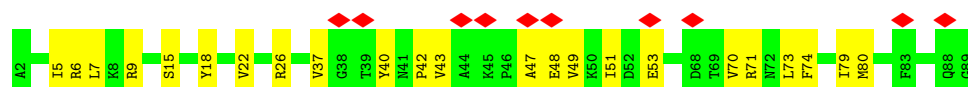
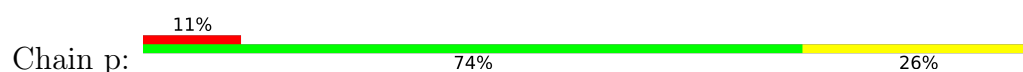
- Molecule 43: 30S ribosomal protein S14



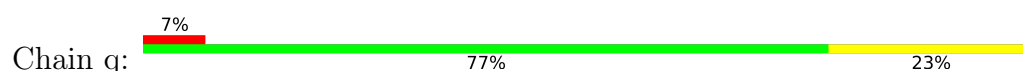
- Molecule 44: 30S ribosomal protein S15

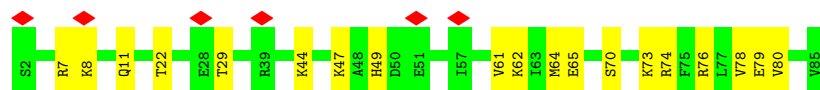


- Molecule 45: 30S ribosomal protein S16

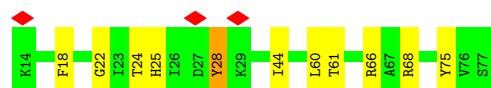
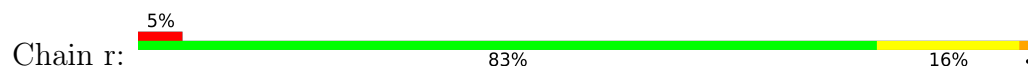


- Molecule 46: 30S ribosomal protein S17





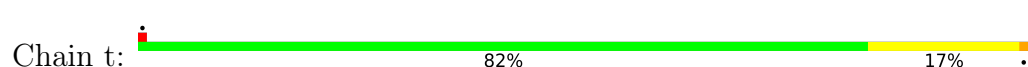
- Molecule 47: 30S ribosomal protein S18



- Molecule 48: 30S ribosomal protein S19



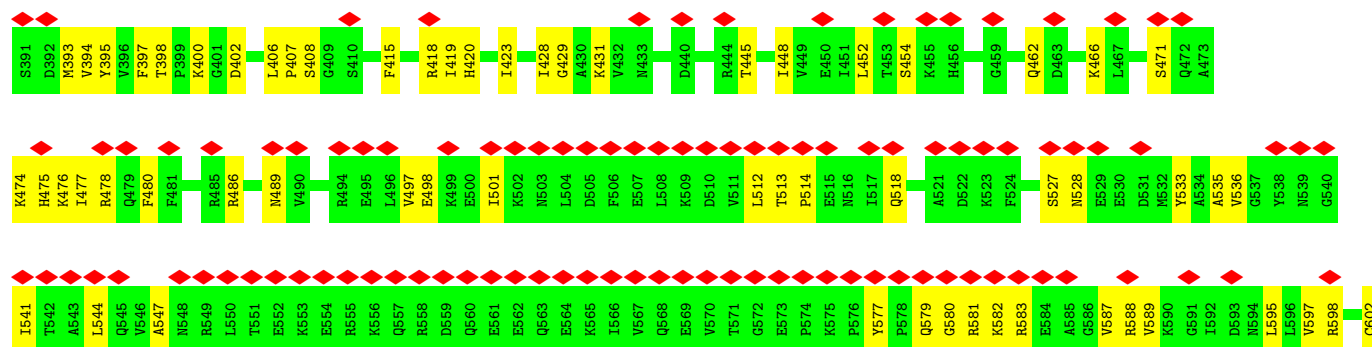
- Molecule 49: 30S ribosomal protein S20

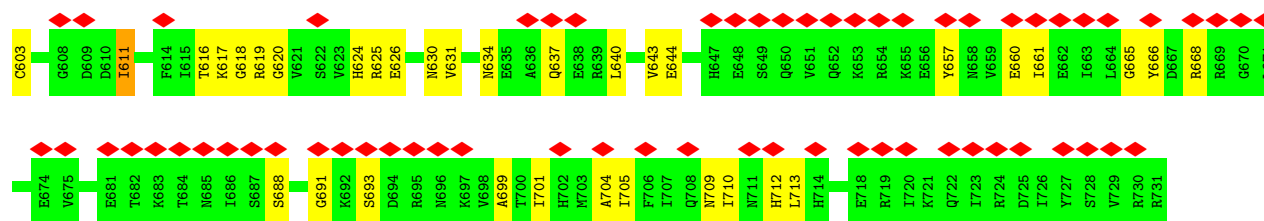


- Molecule 50: P-tRNA

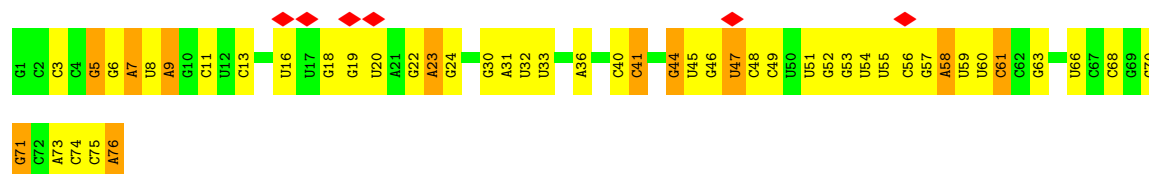


- Molecule 51: GTP pyrophosphokinase

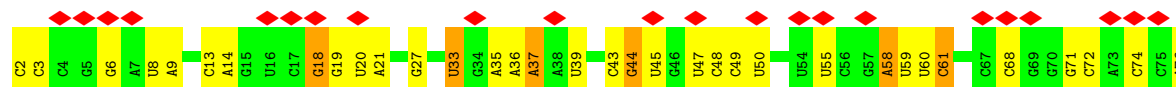




• Molecule 52: A/R-tRNA



• Molecule 53: E-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	650054	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 ($e^-/\text{\AA}^2$)	2.4	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	0.465	Depositor
Minimum map value	-0.311	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.0471	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	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	0.45	6/69438 (0.0%)	0.43	3/108311 (0.0%)
2	B	0.20	0/2675	0.34	0/4170
3	C	0.38	0/2120	0.70	1/2845 (0.0%)
4	D	0.35	0/1591	0.64	0/2132
5	E	0.28	0/1580	0.58	0/2132
6	F	0.22	0/1405	0.59	1/1887 (0.1%)
7	G	0.17	0/1360	0.42	0/1832
8	J	0.30	0/1146	0.61	0/1542
9	K	0.36	0/927	0.65	2/1245 (0.2%)
10	L	0.28	0/1093	0.57	0/1457
11	M	0.27	0/1099	0.53	0/1468
12	N	0.30	0/960	0.60	0/1284
13	O	0.20	0/921	0.55	0/1236
14	P	0.30	0/957	0.59	0/1279
15	Q	0.36	0/952	0.67	0/1266
16	R	0.25	0/797	0.59	0/1070
17	S	0.32	0/851	0.75	3/1146 (0.3%)
18	T	0.23	0/731	0.49	0/974
19	U	0.21	0/772	0.55	0/1032
20	V	0.30	0/638	0.73	2/847 (0.2%)
21	W	4.07	2/448 (0.4%)	1.58	7/596 (1.2%)
22	X	0.17	0/531	0.47	0/707
23	Y	0.26	0/457	0.58	0/613
24	1	0.33	0/433	0.68	0/574
25	2	0.22	0/406	0.56	0/540
26	3	0.36	0/370	0.56	0/483
27	4	0.31	0/519	0.61	0/680
28	5	0.23	0/299	0.46	0/393
29	Z	0.21	0/509	0.50	0/678
30	a	0.26	0/36826	0.37	2/57450 (0.0%)
31	b	0.19	0/1782	0.62	5/2392 (0.2%)
32	c	0.23	0/1641	0.52	0/2208
33	d	0.26	0/1598	0.63	0/2147
34	e	0.28	0/1230	0.60	0/1655

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	f	0.19	0/766	0.43	0/1031
36	g	0.22	0/1196	0.56	0/1604
37	h	0.28	0/1048	0.61	0/1407
38	i	0.24	0/979	0.64	0/1315
39	j	0.25	0/773	0.55	0/1044
40	k	0.22	0/852	0.50	0/1153
41	l	0.28	0/1069	0.64	0/1435
42	m	0.26	0/873	0.66	0/1166
43	n	0.29	0/507	0.71	0/672
44	o	0.22	0/718	0.56	0/960
45	p	0.22	0/708	0.60	0/950
46	q	0.22	0/699	0.57	0/933
47	r	0.21	0/526	0.61	0/705
48	s	0.22	0/649	0.51	0/872
49	t	0.20	0/639	0.56	0/852
50	v	0.21	0/2080	0.33	0/3242
51	x	0.21	0/2794	0.58	2/3757 (0.1%)
52	u	0.15	0/1813	0.31	0/2823
53	w	0.16	0/1786	0.33	0/2782
All	All	0.41	8/159537 (0.0%)	0.46	28/238974 (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
3	C	0	1
4	D	0	2
8	J	0	1
15	Q	0	2
16	R	0	1
17	S	0	1
21	W	0	9
29	Z	0	1
31	b	0	3
32	c	0	1
33	d	0	3
36	g	0	1
37	h	0	1
41	l	0	2
45	p	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
51	x	0	1
All	All	0	31

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	W	34	GLN	CD-NE2	85.13	3.12	1.33
1	A	2120	U	C2-N3	37.51	2.12	1.37
1	A	2120	U	N3-C4	36.41	2.11	1.38
1	A	2120	U	N1-C2	35.30	2.09	1.38
1	A	2120	U	N1-C6	33.53	2.05	1.38
1	A	2120	U	C4-C5	31.52	2.06	1.43
1	A	2120	U	C5-C6	30.56	1.95	1.34
21	W	34	GLN	CG-CD	5.62	1.66	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	W	34	GLN	CG-CD-NE2	10.47	132.10	116.40
21	W	34	GLN	CG-CD-OE1	-9.23	102.35	120.80
17	S	38	LEU	CA-C-N	6.06	136.58	121.80
17	S	38	LEU	C-N-CA	6.06	136.58	121.80
1	A	2260	U	O4'-C1'-N1	6.03	117.54	108.50
21	W	36	VAL	CA-C-N	5.90	129.49	120.82
21	W	36	VAL	C-N-CA	5.90	129.49	120.82
21	W	39	LEU	CA-CB-CG	5.71	136.29	116.30
31	b	66	LYS	CA-C-N	5.66	132.16	121.97
31	b	66	LYS	C-N-CA	5.66	132.16	121.97
21	W	7	ILE	O-C-N	-5.64	115.52	122.57
3	C	218	PRO	N-CA-C	5.43	119.10	111.33
31	b	151	ILE	N-CA-C	-5.42	107.19	112.29
1	A	2155	A	P-O3'-C3'	5.32	128.18	120.20
21	W	40	VAL	N-CA-C	-5.23	105.36	113.16
1	A	1305	A	P-O3'-C3'	5.19	127.98	120.20
17	S	40	PRO	N-CA-C	5.19	123.15	112.47
20	V	64	ASP	CA-C-N	5.19	131.45	121.54
20	V	64	ASP	C-N-CA	5.19	131.45	121.54
9	K	88	ARG	CA-C-N	5.10	131.28	121.54
9	K	88	ARG	C-N-CA	5.10	131.28	121.54
51	x	527	SER	CA-C-N	5.09	131.26	121.54
51	x	527	SER	C-N-CA	5.09	131.26	121.54
6	F	82	GLY	N-CA-C	-5.08	105.21	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	756	U	C2'-C3'-O3'	5.05	117.07	109.50
30	a	92	U	P-O3'-C3'	5.02	127.72	120.20
31	b	148	LEU	CA-C-N	5.01	131.24	121.41
31	b	148	LEU	C-N-CA	5.01	131.24	121.41

There are no chirality outliers.

All (31) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	211	SER	Peptide
4	D	122	ALA	Peptide
4	D	53	PHE	Peptide
8	J	132	PRO	Peptide
15	Q	91	ASN	Peptide
15	Q	92	ARG	Peptide
16	R	50	ASN	Peptide
17	S	39	THR	Peptide
21	W	21	ALA	Peptide
21	W	24	ALA	Peptide
21	W	27	ARG	Peptide
21	W	28	THR	Peptide
21	W	32	ASN	Peptide
21	W	34	GLN	Peptide
21	W	38	ILE	Peptide
21	W	39	LEU	Peptide
21	W	44	PRO	Peptide
29	Z	59	PHE	Peptide
31	b	16	PHE	Peptide
31	b	18	HIS	Peptide
31	b	66	LYS	Peptide
32	c	166	TYR	Peptide
33	d	31	TYR	Peptide
33	d	32	ALA	Peptide
33	d	33	PRO	Peptide
36	g	13	LEU	Peptide
37	h	98	LEU	Peptide
41	l	34	GLU	Peptide
41	l	57	LYS	Peptide
45	p	37	VAL	Peptide
51	x	577	TYR	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	61997	0	31214	577	0
2	B	2392	0	1213	17	0
3	C	2083	0	2168	52	0
4	D	1569	0	1637	25	0
5	E	1561	0	1647	30	0
6	F	1386	0	1446	27	0
7	G	1342	0	1388	25	0
8	J	1123	0	1162	22	0
9	K	920	0	977	20	0
10	L	1081	0	1132	19	0
11	M	1076	0	1145	18	0
12	N	953	0	983	34	0
13	O	912	0	947	20	0
14	P	944	0	1020	24	0
15	Q	940	0	1005	20	0
16	R	786	0	826	24	0
17	S	842	0	899	20	0
18	T	725	0	770	15	0
19	U	762	0	821	10	0
20	V	630	0	644	20	0
21	W	444	0	487	64	0
22	X	530	0	568	8	0
23	Y	455	0	491	8	0
24	1	426	0	441	14	0
25	2	401	0	413	6	0
26	3	367	0	410	12	0
27	4	512	0	564	14	0
28	5	296	0	342	5	0
29	Z	499	0	491	7	0
30	a	32891	0	16559	315	0
31	b	1757	0	1830	29	0
32	c	1619	0	1658	25	0
33	d	1568	0	1604	30	0
34	e	1218	0	1300	26	0
35	f	755	0	746	14	0
36	g	1181	0	1235	25	0
37	h	1036	0	1095	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	i	966	0	1005	21	0
39	j	761	0	795	15	0
40	k	838	0	854	18	0
41	l	1052	0	1112	20	0
42	m	868	0	925	17	0
43	n	497	0	531	12	0
44	o	710	0	735	13	0
45	p	695	0	721	15	0
46	q	691	0	728	13	0
47	r	518	0	555	7	0
48	s	633	0	649	13	0
49	t	637	0	696	12	0
50	v	1861	0	938	14	0
51	x	2752	0	2789	64	0
52	u	1623	0	820	22	0
53	w	1599	0	810	8	0
All	All	146680	0	97941	1573	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 (1573) 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)
1:A:2120:U:C5	1:A:2120:U:C6	1.95	1.53
1:A:2120:U:C5	1:A:2120:U:C4	2.06	1.41
1:A:2120:U:C6	1:A:2120:U:N1	2.05	1.25
1:A:2120:U:N1	1:A:2120:U:C2	2.09	1.20
1:A:2120:U:C4	1:A:2120:U:N3	2.11	1.19
1:A:2120:U:C2	1:A:2120:U:N3	2.12	1.18
1:A:2120:U:C2	21:W:34:GLN:NE2	2.41	0.89
1:A:2120:U:C4	21:W:34:GLN:NE2	2.48	0.81
1:A:2120:U:N3	21:W:34:GLN:NE2	2.32	0.76
1:A:425:C:H42	21:W:58:LYS:HA	1.51	0.75
1:A:1410:G:H5''	21:W:23:ASN:HB3	1.68	0.75
30:a:1246:C:H42	30:a:1346:G:H1	1.35	0.74
1:A:818:G:HO2'	1:A:1394:G:HO2'	1.34	0.72
30:a:774:G:H1	30:a:821:G:HO2'	1.37	0.72
1:A:2120:U:C6	21:W:34:GLN:NE2	2.58	0.72
1:A:1983:G:H21	1:A:1985:U:H3	1.38	0.71
1:A:2120:U:N1	21:W:34:GLN:NE2	2.38	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2120:U:C5	21:W:34:GLN:NE2	2.60	0.70
1:A:2655:C:H42	1:A:2806:G:H1	1.40	0.70
1:A:2120:U:C2	21:W:34:GLN:CD	2.70	0.69
1:A:579:G:H1	1:A:604:C:H42	1.39	0.69
1:A:2880:U:H3	1:A:2887:A:H61	1.39	0.69
1:A:446:G:H3'	21:W:37:ARG:HD2	1.75	0.68
1:A:447:G:N2	21:W:41:ASN:O	2.26	0.68
1:A:852:G:H22	1:A:875:U:H5'	1.58	0.68
1:A:2130:G:H1	1:A:2217:U:H3	1.41	0.68
1:A:2120:U:C4	21:W:34:GLN:CD	2.72	0.68
4:D:57:ARG:H	4:D:60:LEU:HD12	1.59	0.67
7:G:23:ASN:HB3	7:G:38:PHE:H	1.59	0.67
30:a:1288:A:H5''	39:j:9:ARG:HH22	1.59	0.67
1:A:2493:C:H42	1:A:2515:G:H1	1.44	0.66
1:A:1304:G:OP1	24:l:16:ARG:NH2	2.28	0.66
30:a:895:G:H1	30:a:922:C:H42	1.43	0.66
1:A:1847:U:H5''	3:C:157:SER:HB3	1.78	0.66
1:A:2590:A:N3	9:K:23:LYS:NZ	2.43	0.66
30:a:1079:C:H42	30:a:1116:G:H1	1.44	0.66
7:G:165:TYR:HB2	7:G:168:GLU:HB2	1.78	0.65
30:a:1091:G:N7	34:e:52:LYS:NZ	2.43	0.65
1:A:256:C:OP2	27:4:5:LYS:NZ	2.30	0.65
36:g:79:ARG:NH2	53:w:33:U:O2'	2.29	0.65
1:A:2120:U:N3	1:A:2257:G:O6	2.29	0.65
32:c:57:GLU:HB2	32:c:64:ASN:HB2	1.77	0.65
13:O:34:PHE:HB3	13:O:41:TYR:HB2	1.78	0.65
30:a:1116:G:H5''	32:c:171:THR:HG22	1.78	0.65
1:A:2749:U:H3	1:A:2898:A:H62	1.45	0.65
11:M:39:ALA:HB2	11:M:99:PRO:HD3	1.79	0.65
25:2:36:CYS:SG	25:2:45:HIS:NE2	2.70	0.65
7:G:4:VAL:O	7:G:70:ARG:NH1	2.30	0.65
3:C:45:ASN:ND2	21:W:23:ASN:OD1	2.29	0.64
11:M:42:ILE:HD12	11:M:97:VAL:HG21	1.79	0.64
30:a:1071:G:N7	32:c:2:GLY:N	2.45	0.64
52:u:51:U:H3	52:u:63:G:H1	1.45	0.64
52:u:53:G:H1	52:u:61:C:H42	1.46	0.64
1:A:2120:U:H5'	1:A:2121:U:H2'	1.79	0.64
1:A:1941:A:H8	30:a:1505:U:H1'	1.62	0.64
30:a:1503:A:H62	52:u:36:A:H61	1.43	0.64
51:x:588:ARG:HB3	51:x:644:GLU:HB2	1.78	0.64
6:F:96:MET:N	6:F:96:MET:SD	2.71	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:88:ARG:NH1	8:J:97:TYR:OH	2.31	0.64
30:a:1264:G:H3'	30:a:1288:A:H61	1.61	0.63
1:A:2171:G:H1	1:A:2178:C:H42	1.47	0.63
1:A:1019:A:H5'	16:R:80:LYS:HG2	1.80	0.63
1:A:1042:A:H2'	1:A:1043:G:H8	1.63	0.63
1:A:1759:U:H3	1:A:1774:A:H62	1.46	0.63
6:F:80:ARG:NH2	50:v:19:G:N7	2.47	0.63
1:A:2882:G:N2	1:A:2885:A:OP2	2.32	0.63
48:s:24:GLU:HG3	48:s:25:THR:HG23	1.80	0.63
1:A:121:G:H1	1:A:128:C:H42	1.47	0.62
1:A:1841:G:H1'	21:W:21:ALA:HB1	1.81	0.62
1:A:1292:G:H1	15:Q:37:GLN:HE21	1.47	0.62
1:A:1820:A:N6	1:A:1857:G:O2'	2.32	0.62
30:a:133:G:H1	45:p:26:ARG:HH22	1.47	0.62
1:A:1460:G:O2'	1:A:1631:A:N6	2.32	0.62
1:A:2125:U:H3	1:A:2222:C:H42	1.45	0.62
33:d:14:ARG:HA	33:d:32:ALA:HB1	1.81	0.62
3:C:16:MET:SD	3:C:210:ARG:NH2	2.72	0.62
30:a:1441:G:HO2'	30:a:1477:G:H1	1.45	0.62
1:A:2120:U:N3	21:W:34:GLN:CD	2.58	0.62
32:c:70:ALA:HA	32:c:105:ILE:H	1.65	0.62
1:A:444:U:H4'	21:W:49:VAL:HG13	1.81	0.62
3:C:185:LEU:HD23	3:C:187:ALA:H	1.65	0.62
1:A:2128:U:H3	1:A:2219:G:H1	1.48	0.61
7:G:47:GLU:HB2	7:G:50:VAL:HB	1.82	0.61
1:A:246:U:OP2	27:4:8:ARG:NH2	2.30	0.61
25:2:9:CYS:SG	25:2:10:THR:N	2.74	0.61
46:q:29:THR:O	46:q:44:LYS:NZ	2.34	0.61
1:A:1457:U:H5'	1:A:1458:U:H5'	1.83	0.61
10:L:77:VAL:HG12	10:L:79:LEU:H	1.66	0.61
30:a:1159:U:H4'	39:j:43:PRO:HG3	1.83	0.61
1:A:737:C:O2'	3:C:217:ARG:NH2	2.34	0.61
1:A:784:C:N4	1:A:806:G:O6	2.34	0.61
16:R:5:ILE:HG22	16:R:38:VAL:HG22	1.83	0.61
30:a:1235:C:H2'	42:m:102:SER:HB3	1.82	0.61
1:A:2746:G:N2	1:A:2873:G:OP1	2.34	0.61
42:m:11:ARG:HB3	42:m:46:ARG:HB3	1.82	0.61
7:G:9:LEU:HB2	7:G:51:LEU:HB2	1.82	0.61
13:O:44:ILE:HD12	13:O:54:ALA:HB3	1.83	0.61
1:A:1408:G:N2	21:W:17:ASN:O	2.33	0.60
30:a:421:G:N2	30:a:436:G:O2'	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:f:43:TRP:HB2	35:f:60:TYR:HB2	1.82	0.60
1:A:1026:A:N6	1:A:2056:G:O2'	2.34	0.60
1:A:1242:U:H2'	1:A:1243:A:H8	1.66	0.60
1:A:1036:A:N3	16:R:75:ARG:NH1	2.50	0.60
2:B:47:C:OP2	13:O:35:ARG:NH2	2.35	0.60
30:a:958:C:H2'	30:a:959:A:H8	1.66	0.60
1:A:1965:A:OP2	1:A:1991:C:N4	2.35	0.60
6:F:38:MET:HB3	6:F:87:ALA:H	1.66	0.60
1:A:39:C:H42	1:A:487:G:H1	1.50	0.60
10:L:55:MET:O	10:L:60:ARG:NH2	2.34	0.60
30:a:560:U:O2'	41:l:96:ARG:NH2	2.34	0.60
1:A:2076:C:H2'	1:A:2077:G:H8	1.66	0.60
6:F:115:ARG:HH12	42:m:71:ARG:HD2	1.67	0.60
13:O:113:ALA:HB1	13:O:118:LEU:HD12	1.84	0.60
1:A:2116:G:O6	1:A:2261:C:N4	2.34	0.60
1:A:2259:G:H1'	21:W:32:ASN:HB3	1.83	0.60
6:F:36:ILE:HB	6:F:89:VAL:HB	1.84	0.60
19:U:6:GLY:H	19:U:23:ILE:HB	1.66	0.60
1:A:127:C:OP2	18:T:33:ARG:NH2	2.35	0.60
1:A:967:G:N2	1:A:2298:A:OP2	2.34	0.60
1:A:1002:G:N2	1:A:1006:A:OP2	2.35	0.60
3:C:117:MET:HG3	3:C:119:GLY:H	1.67	0.60
4:D:6:LEU:HD12	4:D:199:LEU:HD21	1.84	0.60
4:D:14:GLN:HG2	4:D:22:LEU:HD22	1.83	0.60
1:A:1614:A:OP1	3:C:210:ARG:NH1	2.34	0.60
1:A:1835:C:C2	21:W:20:HIS:HB3	2.37	0.60
8:J:74:ILE:HG12	8:J:89:THR:HG22	1.84	0.60
37:h:30:SER:H	37:h:33:LYS:HD2	1.65	0.60
15:Q:92:ARG:HD2	16:R:11:GLN:HB2	1.84	0.59
35:f:41:LYS:HB3	35:f:62:ILE:HB	1.84	0.59
1:A:1201:A:H5''	15:Q:55:ARG:HD3	1.83	0.59
7:G:106:LEU:HB2	7:G:114:VAL:HB	1.83	0.59
24:l:32:SER:OG	24:l:46:CYS:SG	2.60	0.59
33:d:55:GLN:HA	33:d:58:ARG:HG2	1.83	0.59
1:A:1176:U:OP2	1:A:2599:G:N2	2.35	0.59
24:l:38:LEU:HD12	24:l:41:ARG:HD2	1.83	0.59
30:a:458:G:H4'	45:p:42:PRO:HB2	1.84	0.59
30:a:444:C:H5'	33:d:149:SER:HB2	1.84	0.59
39:j:42:LEU:HD22	39:j:71:LYS:HD2	1.85	0.59
50:v:15:A:H2'	50:v:70:G:H1	1.68	0.59
1:A:984:G:H2'	1:A:985:G:H8	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:A:H62	1:A:298:U:H3	1.49	0.59
1:A:353:A:N3	1:A:373:A:O2'	2.34	0.59
15:Q:86:SER:HA	15:Q:116:GLN:HG3	1.84	0.59
1:A:2152:A:H61	1:A:2203:C:H42	1.50	0.59
6:F:100:LEU:HD23	6:F:103:LEU:HD12	1.84	0.59
30:a:1230:G:OP1	48:s:36:ARG:NH1	2.36	0.59
1:A:129:C:OP1	1:A:1387:G:N2	2.36	0.59
36:g:82:GLY:O	53:w:37:A:N6	2.36	0.59
6:F:65:PRO:HB2	6:F:87:ALA:HB1	1.84	0.58
29:Z:18:CYS:SG	29:Z:20:ASN:ND2	2.75	0.58
1:A:1403:G:O2'	1:A:1838:A:N1	2.35	0.58
28:5:27:CYS:SG	28:5:28:GLU:N	2.76	0.58
30:a:1074:G:O2'	30:a:1199:G:N2	2.36	0.58
30:a:1187:G:N2	30:a:1190:G:OP2	2.37	0.58
38:i:30:VAL:HA	38:i:65:VAL:HB	1.85	0.58
1:A:2865:U:H3	1:A:2902:A:H61	1.50	0.58
1:A:565:U:H5''	17:S:25:ARG:HH12	1.66	0.58
1:A:1806:U:H3	1:A:1816:A:H61	1.50	0.58
1:A:2386:U:H5'	20:V:28:ARG:HH22	1.68	0.58
3:C:44:ASN:HB3	21:W:22:MET:HB2	1.83	0.58
1:A:201:C:H4'	1:A:2272:U:H4'	1.84	0.58
1:A:2145:G:N7	1:A:2195:G:N2	2.52	0.58
30:a:10:A:N6	33:d:196:GLU:O	2.37	0.58
30:a:692:G:N2	40:k:41:GLY:O	2.37	0.58
30:a:665:G:O2'	44:o:28:GLN:NE2	2.36	0.58
30:a:1140:A:O2'	38:i:20:ARG:NH2	2.36	0.58
32:c:149:LYS:HB2	32:c:172:VAL:HG21	1.86	0.58
1:A:737:C:O2'	1:A:827:G:OP1	2.22	0.58
30:a:331:U:OP1	49:t:21:ASN:ND2	2.37	0.58
30:a:1316:U:OP1	42:m:100:GLN:NE2	2.37	0.58
30:a:70:G:N2	30:a:151:A:N3	2.49	0.58
30:a:176:G:H5'	49:t:60:LYS:HZ3	1.69	0.58
30:a:530:G:N7	41:l:63:ARG:NH1	2.51	0.58
34:e:156:LEU:HD23	37:h:68:GLN:HE21	1.69	0.58
4:D:123:ILE:HD11	4:D:130:ARG:HB3	1.85	0.58
30:a:1104:G:O2'	30:a:1118:G:N2	2.36	0.58
1:A:74:U:H3'	22:X:44:ARG:HH22	1.68	0.57
1:A:384:A:O2'	5:E:168:ARG:NH1	2.37	0.57
1:A:854:U:H2'	1:A:855:G:H8	1.69	0.57
1:A:2307:A:OP2	20:V:20:ASN:ND2	2.37	0.57
1:A:1938:C:H2'	1:A:1939:G:H8	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:h:103:ILE:HD11	37:h:114:THR:HB	1.86	0.57
1:A:1839:A:N6	21:W:17:ASN:O	2.37	0.57
1:A:2555:G:H1'	28:5:1:MET:HG2	1.86	0.57
30:a:846:G:H1	30:a:859:C:H42	1.53	0.57
37:h:42:ARG:HG3	37:h:43:GLU:HG3	1.86	0.57
1:A:214:G:OP1	26:3:25:LYS:NZ	2.38	0.57
1:A:1741:G:N2	1:A:2006:A:O2'	2.36	0.57
6:F:119:LYS:NZ	6:F:177:PHE:O	2.38	0.57
13:O:45:ILE:HG12	13:O:52:THR:HG22	1.85	0.57
51:x:486:ARG:HA	51:x:489:ASN:HB2	1.86	0.57
1:A:364:A:N3	5:E:169:ASN:ND2	2.53	0.57
1:A:421:A:N6	1:A:448:A:N7	2.52	0.57
30:a:1198:U:H4'	32:c:10:LEU:HD11	1.87	0.57
4:D:156:LYS:O	8:J:81:HIS:ND1	2.37	0.57
8:J:104:LEU:HD23	8:J:107:LYS:HD2	1.87	0.57
36:g:74:GLU:HG3	36:g:91:VAL:HG22	1.87	0.57
36:g:111:ARG:NH1	36:g:123:GLU:OE1	2.38	0.57
1:A:1738:U:O2	3:C:14:ARG:NH1	2.38	0.57
12:N:102:MET:HB2	12:N:116:ILE:HB	1.86	0.57
30:a:850:U:H3	30:a:855:G:H22	1.53	0.57
43:n:40:CYS:SG	43:n:41:ARG:N	2.77	0.57
1:A:1188:A:H4'	8:J:28:ARG:HH12	1.70	0.57
3:C:155:VAL:HG21	3:C:162:ALA:HB2	1.87	0.57
30:a:381:A:N1	30:a:399:G:O2'	2.37	0.57
30:a:1108:C:OP2	31:b:143:ARG:NH1	2.38	0.57
36:g:13:LEU:HD13	36:g:21:LYS:HD3	1.87	0.57
1:A:719:C:N4	1:A:855:G:O6	2.38	0.57
46:q:22:THR:HG22	46:q:49:HIS:HA	1.86	0.57
7:G:104:LEU:HB3	7:G:116:ILE:HB	1.86	0.56
15:Q:68:ALA:O	15:Q:72:ASN:ND2	2.38	0.56
33:d:149:SER:HA	33:d:152:LYS:HB3	1.87	0.56
34:e:92:GLY:HA2	34:e:129:GLY:HA3	1.87	0.56
1:A:2721:C:H2'	1:A:2722:A:H8	1.70	0.56
6:F:60:ILE:HG12	6:F:138:PHE:HZ	1.70	0.56
21:W:33:LEU:HA	21:W:49:VAL:HB	1.86	0.56
30:a:224:U:O2'	30:a:477:A:N6	2.37	0.56
33:d:54:LYS:NZ	33:d:65:GLU:OE2	2.32	0.56
1:A:636:G:H2'	1:A:637:A:H8	1.69	0.56
1:A:906:G:OP1	20:V:52:LYS:NZ	2.38	0.56
1:A:1649:C:O2'	1:A:1655:A:N6	2.32	0.56
1:A:1734:A:OP2	1:A:1743:A:N6	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2518:G:N2	1:A:2520:U:O4	2.37	0.56
14:P:21:ARG:HD3	14:P:22:PRO:HD2	1.86	0.56
1:A:930:C:H42	1:A:940:G:H1	1.54	0.56
1:A:1940:U:O2	1:A:1948:A:N6	2.38	0.56
2:B:44:A:H5''	13:O:7:LYS:HE3	1.88	0.56
6:F:5:LYS:NZ	6:F:94:GLU:O	2.37	0.56
30:a:378:C:H2'	30:a:379:G:H8	1.69	0.56
30:a:1070:U:H4'	39:j:53:ARG:HG2	1.87	0.56
30:a:1315:A:N6	30:a:1340:G:O2'	2.38	0.56
30:a:69:C:HO2'	30:a:170:A:HO2'	1.53	0.56
1:A:1851:G:H2'	1:A:1852:G:H8	1.70	0.56
1:A:2382:G:N2	1:A:2393:C:O2	2.39	0.56
30:a:839:G:H1	30:a:866:C:H42	1.52	0.56
30:a:1158:C:OP2	38:i:11:ARG:NH2	2.39	0.56
32:c:16:ARG:NH2	32:c:182:ASP:OD1	2.39	0.56
40:k:90:GLY:H	40:k:116:THR:HG22	1.70	0.56
52:u:30:G:N2	52:u:40:C:O2	2.38	0.56
1:A:1474:C:N4	1:A:1618:A:OP2	2.38	0.56
1:A:1831:A:OP1	1:A:1843:G:N1	2.38	0.56
3:C:88:SER:O	3:C:197:ASN:ND2	2.38	0.56
5:E:151:LYS:HE3	5:E:189:HIS:HA	1.88	0.56
39:j:50:THR:HG22	39:j:64:GLN:HG2	1.87	0.56
48:s:31:VAL:HB	48:s:49:ILE:HG22	1.87	0.56
1:A:2674:G:N2	1:A:2795:G:OP1	2.39	0.56
3:C:66:ASP:OD2	3:C:102:ARG:NH1	2.33	0.56
3:C:158:ALA:HB1	3:C:197:ASN:HB2	1.87	0.56
39:j:8:ILE:HG12	39:j:100:ILE:HG12	1.88	0.56
52:u:58:A:N6	52:u:61:C:N3	2.53	0.56
1:A:442:C:H2'	21:W:8:THR:HA	1.88	0.56
1:A:1055:A:OP2	8:J:40:LYS:NZ	2.38	0.56
33:d:57:LEU:HD12	33:d:189:ILE:HG21	1.88	0.56
36:g:116:MET:HA	36:g:119:ARG:HB2	1.86	0.56
39:j:34:ALA:HB2	39:j:83:THR:HG21	1.87	0.56
1:A:75:G:OP1	22:X:44:ARG:NH2	2.39	0.56
1:A:1859:C:H42	1:A:2004:G:H1	1.53	0.56
17:S:29:VAL:HG22	17:S:71:ILE:HG13	1.87	0.56
30:a:738:A:H2'	30:a:739:G:H8	1.71	0.56
30:a:1105:U:OP1	30:a:1118:G:N2	2.38	0.56
33:d:143:GLU:HA	33:d:146:ARG:HB2	1.86	0.56
41:l:100:VAL:HG12	41:l:103:LEU:H	1.71	0.56
1:A:2120:U:N1	21:W:34:GLN:CD	2.64	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2880:U:H2'	1:A:2881:G:H8	1.70	0.55
6:F:133:LYS:HG2	6:F:134:GLU:HG3	1.87	0.55
4:D:125:ARG:NH2	4:D:160:LEU:O	2.40	0.55
12:N:22:THR:HG21	12:N:67:ARG:H	1.71	0.55
16:R:34:THR:HG22	16:R:59:THR:HG22	1.89	0.55
30:a:411:C:H5'	33:d:129:PRO:HD2	1.87	0.55
30:a:1423:C:H2'	30:a:1424:G:H8	1.70	0.55
31:b:32:PHE:HB2	31:b:40:ILE:HB	1.87	0.55
51:x:626:GLU:HA	51:x:631:VAL:HG11	1.87	0.55
1:A:443:G:H21	21:W:51:ALA:HA	1.71	0.55
1:A:1941:A:N6	30:a:1416:C:O2'	2.38	0.55
1:A:1296:G:N2	5:E:82:GLN:O	2.39	0.55
1:A:2874:G:N7	1:A:2892:G:N2	2.55	0.55
7:G:3:ARG:HG2	7:G:6:LYS:HG2	1.88	0.55
30:a:180:G:H1	30:a:208:A:H2'	1.71	0.55
30:a:223:C:O2	30:a:474:A:N6	2.39	0.55
1:A:609:C:H5	16:R:79:LYS:HE3	1.72	0.55
1:A:615:U:O2'	1:A:617:G:OP2	2.24	0.55
1:A:1105:G:H1	1:A:1125:C:H42	1.55	0.55
1:A:1482:G:N2	1:A:1604:C:O2	2.34	0.55
1:A:2062:A:N6	1:A:2065:C:N3	2.54	0.55
29:Z:34:GLU:HG2	42:m:57:ARG:HH21	1.70	0.55
30:a:834:G:O2'	37:h:13:ARG:NH2	2.40	0.55
31:b:86:ARG:HH21	31:b:218:ALA:HB3	1.72	0.55
1:A:1432:A:N7	18:T:16:ARG:NH2	2.49	0.55
30:a:699:G:H1'	30:a:707:G:H22	1.72	0.55
1:A:160:G:O2'	1:A:168:A:N6	2.40	0.55
1:A:645:C:O2'	5:E:104:LYS:NZ	2.39	0.55
1:A:787:C:H42	1:A:804:G:H1	1.54	0.55
1:A:1652:C:N4	1:A:1666:U:OP2	2.39	0.55
7:G:160:GLY:H	7:G:172:ARG:HH22	1.53	0.55
20:V:79:ARG:HD3	20:V:81:GLY:H	1.72	0.55
30:a:885:C:O2'	37:h:15:ARG:NH1	2.37	0.55
32:c:11:ARG:NH2	32:c:176:THR:O	2.39	0.55
1:A:814:U:H2'	1:A:815:G:H8	1.72	0.55
1:A:1449:C:N4	1:A:1639:G:N3	2.54	0.55
1:A:2120:U:C6	21:W:34:GLN:CD	2.84	0.55
30:a:1065:A:N3	32:c:155:ARG:NH1	2.54	0.55
30:a:1329:C:O2	48:s:36:ARG:NH2	2.40	0.55
46:q:8:LYS:HB3	46:q:65:GLU:HG2	1.88	0.55
51:x:395:TYR:H	51:x:445:THR:HG23	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2572:G:H2'	1:A:2573:G:H8	1.72	0.55
4:D:25:VAL:HG22	4:D:177:VAL:HG21	1.88	0.55
1:A:254:A:OP1	27:4:7:HIS:NE2	2.34	0.55
1:A:2778:A:H4'	7:G:63:ARG:HB3	1.89	0.55
2:B:82:G:OP2	23:Y:15:ARG:NH1	2.40	0.55
36:g:63:GLU:HG3	36:g:66:LEU:HD12	1.89	0.55
46:q:7:ARG:HB2	46:q:64:MET:HE3	1.87	0.55
1:A:247:A:H62	1:A:257:G:H21	1.54	0.54
1:A:726:C:H2'	1:A:727:A:H8	1.72	0.54
1:A:998:G:OP1	11:M:18:ARG:NH1	2.39	0.54
1:A:1011:C:H2'	1:A:1012:G:H8	1.72	0.54
1:A:1106:U:H1'	1:A:1108:G:H5'	1.88	0.54
38:i:24:GLY:H	38:i:61:TYR:HA	1.72	0.54
44:o:5:GLN:O	44:o:9:ASN:ND2	2.40	0.54
51:x:420:HIS:HB3	51:x:423:ILE:HG12	1.89	0.54
1:A:721:G:H5''	5:E:76:GLY:H	1.71	0.54
1:A:840:A:OP2	1:A:2100:A:O2'	2.25	0.54
1:A:1401:C:O2'	21:W:27:ARG:NH1	2.40	0.54
11:M:32:PHE:HB2	11:M:106:ILE:HB	1.89	0.54
30:a:305:G:N2	30:a:308:A:OP2	2.37	0.54
30:a:1260:A:N3	30:a:1378:C:O2'	2.40	0.54
38:i:28:ILE:HB	38:i:35:ILE:HD11	1.89	0.54
44:o:33:THR:HG22	44:o:63:ARG:HH11	1.72	0.54
3:C:35:ALA:HB3	3:C:62:TYR:HB3	1.89	0.54
39:j:46:LYS:NZ	39:j:66:GLU:OE2	2.35	0.54
1:A:343:A:HO2'	1:A:362:C:HO2'	1.54	0.54
1:A:715:A:N6	1:A:717:A:O2'	2.41	0.54
1:A:1038:C:H2'	1:A:1039:G:H8	1.72	0.54
1:A:1945:A:N6	30:a:1417:A:O2'	2.40	0.54
1:A:2385:C:O3'	20:V:28:ARG:NH2	2.40	0.54
30:a:52:A:OP1	41:l:29:ASN:ND2	2.37	0.54
30:a:1325:G:N1	30:a:1328:A:OP2	2.39	0.54
44:o:68:THR:HG22	44:o:71:ARG:HH12	1.71	0.54
1:A:345:A:H8	19:U:12:ILE:HA	1.72	0.54
1:A:1102:G:H22	1:A:1147:U:H3'	1.72	0.54
1:A:2162:G:H1'	1:A:2187:A:H61	1.72	0.54
1:A:2670:A:OP1	8:J:77:ARG:NH2	2.41	0.54
6:F:136:LEU:HA	6:F:141:ILE:HG13	1.89	0.54
16:R:19:THR:HG22	16:R:96:THR:HG22	1.90	0.54
16:R:58:VAL:HG22	16:R:101:ASN:H	1.73	0.54
29:Z:20:ASN:ND2	29:Z:36:CYS:SG	2.80	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:388:G:N2	30:a:391:A:OP2	2.37	0.54
30:a:1395:G:H2'	30:a:1396:G:H8	1.73	0.54
47:r:28:TYR:OH	47:r:66:ARG:NH1	2.41	0.54
1:A:1833:G:H1	1:A:1842:C:H42	1.55	0.54
30:a:689:C:H2'	30:a:690:A:H8	1.72	0.54
33:d:81:LYS:NZ	34:e:101:GLU:O	2.41	0.54
37:h:28:PRO:O	37:h:57:GLN:NE2	2.41	0.54
1:A:1789:A:N6	1:A:1790:U:O4	2.40	0.54
14:P:37:ARG:HH22	30:a:352:A:H4'	1.72	0.54
50:v:8:U:H5'	50:v:60:A:H5'	1.87	0.54
1:A:144:A:HO2'	18:T:2:LYS:N	2.06	0.54
1:A:1067:A:H2'	1:A:1068:G:H4'	1.89	0.54
1:A:1138:C:O2	1:A:1145:G:N2	2.41	0.54
1:A:2170:A:H61	1:A:2179:U:H3	1.56	0.54
1:A:2380:G:O2'	1:A:2395:A:N6	2.41	0.54
5:E:152:ALA:HB3	5:E:173:VAL:HG22	1.90	0.54
18:T:27:THR:HG22	18:T:80:ILE:HG13	1.90	0.54
31:b:83:GLU:OE1	31:b:86:ARG:NH2	2.40	0.54
34:e:157:ARG:O	37:h:65:LYS:NZ	2.41	0.54
1:A:504:A:H61	1:A:517:A:H5''	1.73	0.54
1:A:2364:A:OP2	13:O:17:ARG:NH2	2.41	0.54
12:N:31:GLU:HG2	12:N:116:ILE:HG12	1.90	0.54
30:a:530:G:OP1	41:l:84:GLY:N	2.40	0.54
30:a:698:C:OP1	40:k:48:SER:OG	2.26	0.54
1:A:124:A:OP1	26:3:14:LYS:NZ	2.41	0.54
1:A:541:G:N3	17:S:61:ASN:ND2	2.55	0.54
6:F:53:ALA:HA	6:F:56:GLU:HB3	1.90	0.54
10:L:91:VAL:HB	10:L:123:VAL:HA	1.90	0.54
33:d:182:ARG:NH2	33:d:189:ILE:O	2.41	0.54
1:A:422:C:N4	21:W:41:ASN:HA	2.24	0.53
1:A:881:U:OP1	27:4:56:LYS:NZ	2.39	0.53
1:A:1854:G:N2	1:A:1930:A:OP1	2.42	0.53
9:K:71:ARG:HH22	9:K:104:ARG:HD3	1.73	0.53
1:A:125:A:H5'	26:3:18:PHE:HB3	1.90	0.53
12:N:52:LYS:NZ	12:N:94:ARG:O	2.38	0.53
1:A:511:U:H1'	1:A:733:U:H5	1.74	0.53
1:A:526:A:N1	1:A:552:G:N2	2.57	0.53
15:Q:46:ALA:O	15:Q:50:ARG:NH1	2.41	0.53
17:S:82:LEU:HB2	17:S:98:LYS:HB2	1.90	0.53
21:W:5:CYS:SG	21:W:6:VAL:N	2.82	0.53
36:g:78:ARG:HB3	36:g:85:TYR:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:8:ARG:HB3	12:N:12:GLN:HB2	1.90	0.53
17:S:14:PRO:HG3	17:S:78:GLU:HB3	1.91	0.53
52:u:9:A:H2'	52:u:11:C:H41	1.73	0.53
1:A:2817:C:O2'	1:A:2834:A:N3	2.39	0.53
5:E:205:VAL:HG13	5:E:206:LEU:HG	1.90	0.53
1:A:2715:G:H1	1:A:2752:C:H42	1.57	0.53
6:F:68:THR:OG1	6:F:85:ILE:O	2.26	0.53
12:N:72:ASN:HB2	12:N:77:GLN:HB3	1.90	0.53
30:a:215:G:H1	30:a:224:U:H3	1.57	0.53
41:l:67:ARG:HA	41:l:77:THR:HA	1.91	0.53
1:A:752:A:OP2	1:A:773:G:N2	2.41	0.53
1:A:1816:A:OP1	3:C:238:ARG:NH2	2.41	0.53
22:X:6:ILE:O	22:X:60:ARG:NH2	2.41	0.53
30:a:425:G:H1	30:a:434:U:H3	1.56	0.53
30:a:505:G:H1	30:a:507:A:H62	1.56	0.53
30:a:726:C:O3'	40:k:121:ASN:ND2	2.42	0.53
32:c:16:ARG:HH22	32:c:182:ASP:HA	1.73	0.53
33:d:168:ASP:HB3	33:d:171:LYS:HB3	1.90	0.53
1:A:444:U:H5	21:W:7:ILE:HD13	1.73	0.53
1:A:669:C:OP2	10:L:104:LYS:NZ	2.38	0.53
1:A:1094:A:OP2	1:A:1156:G:N2	2.41	0.53
2:B:30:C:H42	2:B:48:G:H1	1.56	0.53
11:M:65:TRP:HB2	11:M:105:GLU:HB2	1.91	0.53
20:V:46:TYR:HB3	20:V:67:LEU:HD12	1.90	0.53
30:a:277:C:H2'	30:a:278:A:H8	1.73	0.53
1:A:1056:A:OP1	15:Q:66:ASN:ND2	2.42	0.53
8:J:34:ALA:HA	8:J:37:LEU:HD12	1.91	0.53
30:a:57:A:OP2	30:a:360:C:N4	2.37	0.53
30:a:967:U:OP2	51:x:579:GLN:NE2	2.42	0.53
30:a:1375:C:OP1	38:i:119:LYS:NZ	2.41	0.53
32:c:69:THR:HG21	32:c:75:VAL:HG21	1.91	0.53
51:x:634:ASN:O	51:x:637:GLN:NE2	2.40	0.53
1:A:351:G:N1	1:A:354:A:OP2	2.42	0.53
1:A:1002:G:O2'	1:A:1005:A:N7	2.39	0.53
1:A:1382:G:N2	1:A:1383:U:O2	2.42	0.53
1:A:1403:G:H5'	21:W:29:TRP:H	1.74	0.53
1:A:1616:G:OP2	3:C:63:ARG:NH2	2.40	0.53
1:A:2120:U:C5	21:W:34:GLN:CD	2.87	0.53
1:A:2361:C:OP1	20:V:84:ARG:NH1	2.41	0.53
30:a:1329:C:N3	48:s:36:ARG:NH1	2.56	0.53
30:a:1441:G:O2'	30:a:1477:G:N1	2.31	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:i:31:ASN:O	38:i:33:ARG:NH1	2.43	0.53
46:q:22:THR:HG21	46:q:73:LYS:HD3	1.90	0.53
1:A:674:G:HO2'	1:A:697:G:HO2'	1.56	0.52
1:A:1962:G:N2	1:A:2002:G:O2'	2.41	0.52
1:A:2703:G:H4'	9:K:30:ARG:HE	1.73	0.52
2:B:11:A:N6	2:B:67:G:O2'	2.32	0.52
30:a:989:C:OP1	30:a:1232:C:N4	2.42	0.52
31:b:16:PHE:HB2	31:b:40:ILE:HA	1.90	0.52
45:p:71:ARG:HE	45:p:80:MET:HE2	1.72	0.52
12:N:94:ARG:NH1	12:N:120:VAL:O	2.42	0.52
41:l:70:LEU:HD21	41:l:95:ILE:HD12	1.91	0.52
1:A:932:C:H4'	51:x:624:HIS:HE1	1.73	0.52
1:A:1093:G:O2'	1:A:1157:A:N6	2.41	0.52
1:A:2738:G:H5'	12:N:18:ARG:HH12	1.74	0.52
4:D:177:VAL:N	4:D:187:LEU:O	2.39	0.52
30:a:783:G:O6	30:a:814:C:N4	2.42	0.52
1:A:111:U:OP1	22:X:58:ARG:NH2	2.43	0.52
1:A:425:C:H2'	21:W:56:SER:HB2	1.92	0.52
1:A:1315:G:N2	12:N:19:ASP:OD2	2.43	0.52
1:A:1574:G:N1	1:A:1592:A:OP2	2.41	0.52
9:K:104:ARG:HH22	14:P:34:GLU:HG2	1.74	0.52
20:V:19:LYS:O	20:V:22:ARG:NH1	2.43	0.52
23:Y:5:GLU:HG3	23:Y:36:VAL:HG22	1.91	0.52
30:a:921:U:OP2	41:l:107:ARG:NH2	2.42	0.52
33:d:6:GLY:O	33:d:108:ARG:NH1	2.38	0.52
36:g:20:SER:OG	36:g:21:LYS:N	2.42	0.52
1:A:2653:G:H2'	1:A:2654:G:H8	1.75	0.52
5:E:164:ALA:HA	5:E:175:VAL:HG11	1.91	0.52
14:P:20:PHE:H	14:P:50:ARG:HH22	1.57	0.52
15:Q:63:THR:HA	15:Q:66:ASN:HD22	1.73	0.52
30:a:710:U:H5''	30:a:711:A:H2'	1.91	0.52
30:a:959:A:H61	30:a:1241:U:H3	1.57	0.52
1:A:744:C:O2	1:A:813:G:N2	2.42	0.52
1:A:1059:A:H61	1:A:1195:U:H3	1.58	0.52
5:E:161:GLU:HA	5:E:164:ALA:HB3	1.92	0.52
30:a:183:U:O2	49:t:76:LYS:NZ	2.42	0.52
41:l:87:LEU:HD21	41:l:117:THR:HG22	1.91	0.52
51:x:512:LEU:HD12	51:x:514:PRO:HD3	1.90	0.52
1:A:51:G:H21	1:A:117:A:H62	1.57	0.52
1:A:217:G:N3	1:A:219:A:O2'	2.43	0.52
1:A:2535:U:OP2	1:A:2605:G:N1	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:Q:108:GLN:OE1	16:R:45:ASN:ND2	2.43	0.52
30:a:537:C:N4	30:a:538:G:O6	2.43	0.52
30:a:1156:C:O2'	38:i:7:TYR:OH	2.25	0.52
35:f:4:TYR:OH	35:f:92:LYS:NZ	2.43	0.52
43:n:6:MET:HB3	43:n:23:ARG:HH22	1.75	0.52
52:u:30:G:N2	52:u:41:C:O2	2.43	0.52
1:A:1817:C:OP1	3:C:221:ARG:NH1	2.43	0.52
1:A:2009:G:O2'	1:A:2011:U:OP2	2.27	0.52
1:A:2332:G:H1	1:A:2342:C:H42	1.56	0.52
2:B:41:C:N3	6:F:90:THR:OG1	2.43	0.52
7:G:7:LYS:HB2	7:G:70:ARG:HH12	1.74	0.52
9:K:20:LEU:HD13	9:K:44:LYS:HE3	1.91	0.52
12:N:83:LEU:HA	12:N:87:ILE:HD12	1.91	0.52
30:a:800:G:N2	30:a:1507:G:O3'	2.42	0.52
30:a:1082:G:OP1	34:e:62:LYS:NZ	2.42	0.52
31:b:199:VAL:HG22	31:b:201:PRO:HD3	1.92	0.52
50:v:19:G:N2	50:v:68:A:O2'	2.43	0.52
1:A:902:G:O2'	20:V:76:LYS:NZ	2.43	0.52
1:A:1262:C:H2'	1:A:1263:G:H8	1.75	0.52
1:A:1337:C:H42	1:A:1687:G:H1	1.58	0.52
15:Q:8:THR:HB	15:Q:12:LYS:HE3	1.91	0.52
30:a:756:U:O2'	30:a:757:A:O4'	2.28	0.52
30:a:1226:C:OP1	43:n:9:LYS:NZ	2.42	0.52
39:j:12:ALA:HB2	39:j:96:VAL:HA	1.90	0.52
50:v:4:G:H1	50:v:80:C:H42	1.56	0.52
1:A:1365:U:O2'	1:A:2039:G:O2'	2.26	0.52
1:A:2681:U:H3	1:A:2697:G:H1	1.57	0.52
1:A:2737:G:O2'	12:N:18:ARG:NH1	2.43	0.52
7:G:8:LEU:O	7:G:70:ARG:NH2	2.42	0.52
15:Q:92:ARG:NH1	16:R:9:GLY:O	2.43	0.52
30:a:1522:U:H2'	30:a:1523:A:H8	1.75	0.52
30:a:1526:G:N1	30:a:1529:A:OP2	2.40	0.52
36:g:35:LYS:HB3	36:g:38:LYS:HB2	1.92	0.52
51:x:709:ASN:O	51:x:713:LEU:N	2.43	0.52
53:w:18:G:H1	53:w:55:U:H1'	1.75	0.52
1:A:1853:G:OP1	3:C:52:ARG:NH1	2.42	0.51
1:A:1996:C:H5'	1:A:2621:G:H4'	1.92	0.51
5:E:8:ASN:HD22	5:E:12:SER:HB3	1.74	0.51
14:P:71:GLU:OE2	14:P:101:ARG:NH2	2.43	0.51
30:a:1314:G:O2'	30:a:1315:A:O4'	2.28	0.51
37:h:47:ARG:HG3	37:h:65:LYS:HA	1.90	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2823:C:H2'	1:A:2824:G:C8	2.45	0.51
11:M:34:ILE:HB	11:M:118:LEU:HD13	1.92	0.51
30:a:546:G:H5''	41:l:123:ARG:HH22	1.74	0.51
36:g:66:LEU:HB3	36:g:70:MET:HE3	1.92	0.51
45:p:5:ILE:HG12	45:p:22:VAL:HG22	1.92	0.51
50:v:6:G:H1	50:v:78:C:H42	1.58	0.51
1:A:182:C:O3'	1:A:183:A:O2'	2.28	0.51
1:A:675:C:H2'	1:A:676:G:H8	1.75	0.51
1:A:891:G:N2	1:A:981:C:O2	2.44	0.51
6:F:36:ILE:HG12	6:F:154:ILE:HG12	1.92	0.51
9:K:104:ARG:HG2	9:K:121:VAL:HG12	1.92	0.51
9:K:122:ILE:HG21	14:P:70:VAL:HG11	1.92	0.51
30:a:1088:U:O2'	34:e:138:ARG:NH1	2.43	0.51
1:A:16:G:H2'	1:A:17:G:H8	1.74	0.51
1:A:411:G:N2	1:A:412:A:N1	2.55	0.51
1:A:925:A:N6	1:A:946:G:O2'	2.44	0.51
14:P:39:ARG:NH2	30:a:353:C:OP1	2.44	0.51
41:l:98:GLY:HA3	41:l:109:HIS:HD2	1.75	0.51
1:A:869:U:H2'	1:A:870:A:H8	1.76	0.51
1:A:1499:A:N6	1:A:1508:C:O2	2.43	0.51
1:A:1989:A:O2'	30:a:1494:U:O2'	2.28	0.51
6:F:152:MET:HE3	6:F:154:ILE:HD11	1.92	0.51
43:n:40:CYS:HB3	43:n:43:CYS:HB2	1.91	0.51
51:x:398:THR:HG22	51:x:402:ASP:H	1.76	0.51
51:x:634:ASN:HD22	51:x:640:LEU:HD11	1.74	0.51
1:A:699:A:H5'	1:A:700:U:H5''	1.91	0.51
1:A:1478:G:H2'	1:A:1479:G:C8	2.46	0.51
5:E:3:LYS:HG2	5:E:18:GLU:HG2	1.92	0.51
16:R:53:VAL:HG13	16:R:56:ALA:HB3	1.93	0.51
36:g:79:ARG:HH22	53:w:36:A:H62	1.58	0.51
50:v:74:C:H2'	50:v:75:G:H8	1.75	0.51
51:x:581:ARG:HH11	51:x:657:TYR:HE1	1.59	0.51
12:N:33:THR:HA	12:N:114:MET:HA	1.93	0.51
30:a:1258:C:O2'	38:i:75:GLN:NE2	2.43	0.51
42:m:3:ARG:HD3	42:m:9:ILE:HG12	1.92	0.51
46:q:61:VAL:HG23	46:q:80:VAL:HA	1.91	0.51
51:x:665:GLY:O	51:x:699:ALA:N	2.43	0.51
1:A:834:C:OP1	1:A:1809:A:N6	2.44	0.51
1:A:2074:C:H5''	24:l:15:LEU:HD13	1.93	0.51
6:F:31:ILE:HA	6:F:158:THR:HA	1.92	0.51
7:G:116:ILE:HD13	7:G:149:ILE:HG12	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:P:92:VAL:HG11	14:P:97:LEU:HD21	1.92	0.51
21:W:32:ASN:HB2	21:W:50:SER:HA	1.92	0.51
30:a:1026:A:HO2'	30:a:1226:C:HO2'	1.54	0.51
51:x:709:ASN:H	51:x:712:HIS:HB2	1.76	0.51
26:3:24:SER:OG	26:3:27:GLY:N	2.39	0.51
30:a:262:G:O3'	46:q:73:LYS:NZ	2.37	0.51
30:a:673:G:H22	30:a:750:G:H1	1.59	0.51
42:m:71:ARG:O	42:m:75:LEU:N	2.39	0.51
49:t:33:LYS:O	49:t:37:ALA:N	2.40	0.51
49:t:62:VAL:HG11	49:t:69:LYS:HG3	1.93	0.51
1:A:659:A:H3'	1:A:660:G:H8	1.76	0.51
1:A:2383:A:O3'	20:V:33:ARG:NH2	2.43	0.51
14:P:26:LEU:HD21	14:P:84:ILE:HG23	1.93	0.51
1:A:443:G:N2	21:W:53:ALA:H	2.09	0.50
19:U:32:ARG:HB3	19:U:62:PRO:HB2	1.93	0.50
19:U:40:MET:HA	19:U:60:GLU:HA	1.93	0.50
30:a:217:C:O2'	30:a:475:A:N1	2.42	0.50
31:b:20:THR:OG1	31:b:21:ARG:N	2.43	0.50
47:r:18:PHE:O	47:r:22:GLY:N	2.44	0.50
1:A:7:G:O2'	8:J:136:GLN:NE2	2.43	0.50
1:A:1033:C:H5'	23:Y:10:ARG:HH22	1.76	0.50
1:A:1338:G:H21	1:A:1686:A:H62	1.59	0.50
1:A:1377:G:H5''	18:T:14:THR:HG22	1.93	0.50
1:A:2190:C:H2'	1:A:2191:A:H8	1.75	0.50
5:E:117:LYS:HA	5:E:120:ASP:HB2	1.92	0.50
18:T:20:LEU:HD22	18:T:25:LYS:HD2	1.92	0.50
30:a:75:G:O2'	30:a:94:A:N6	2.44	0.50
30:a:792:C:OP1	30:a:1525:C:O2'	2.27	0.50
1:A:1036:A:O2'	1:A:1038:C:OP2	2.29	0.50
1:A:2668:A:H3'	1:A:2669:G:H8	1.77	0.50
3:C:141:VAL:HG21	3:C:164:VAL:HG23	1.94	0.50
12:N:102:MET:HE1	24:1:49:TYR:HB3	1.93	0.50
50:v:68:A:N6	50:v:69:A:N1	2.59	0.50
51:x:406:LEU:HD21	51:x:418:ARG:HB2	1.92	0.50
6:F:111:VAL:HB	6:F:114:PHE:HB2	1.92	0.50
8:J:12:ILE:HD13	8:J:51:THR:HA	1.93	0.50
12:N:20:LEU:HB3	12:N:40:LEU:HD11	1.92	0.50
30:a:193:G:H2'	30:a:194:C:H2'	1.94	0.50
1:A:2554:G:O2'	1:A:2771:G:O2'	2.28	0.50
1:A:2824:G:N2	1:A:2827:A:OP2	2.44	0.50
8:J:31:SER:HA	8:J:109:MET:HE1	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:C:O2'	1:A:390:A:N3	2.41	0.50
1:A:1090:U:H4'	1:A:1157:A:H61	1.76	0.50
1:A:2144:G:N2	1:A:2148:A:OP1	2.45	0.50
1:A:2384:C:O2	20:V:47:ARG:NH2	2.44	0.50
9:K:22:ILE:HG22	9:K:23:LYS:HG3	1.94	0.50
11:M:36:ALA:HB1	11:M:127:ILE:HG21	1.92	0.50
14:P:48:ILE:HD11	14:P:62:ARG:HD2	1.93	0.50
16:R:2:TYR:N	16:R:41:VAL:O	2.45	0.50
26:3:24:SER:O	26:3:28:ARG:NE	2.45	0.50
30:a:1147:A:N6	30:a:1149:U:O2'	2.44	0.50
1:A:683:A:OP1	10:L:131:SER:OG	2.29	0.50
1:A:935:A:H5'	42:m:92:ARG:HD2	1.93	0.50
1:A:1406:A:N6	21:W:16:ASN:OD1	2.41	0.50
1:A:1652:C:H4'	1:A:1653:A:H5'	1.93	0.50
1:A:2108:U:O2	1:A:2271:G:N2	2.43	0.50
1:A:2243:C:N4	1:A:2244:G:O6	2.45	0.50
1:A:2325:U:H3	1:A:2364:A:H62	1.59	0.50
6:F:91:LEU:HB3	6:F:96:MET:HG3	1.94	0.50
9:K:87:ILE:HA	9:K:93:PRO:HA	1.94	0.50
12:N:37:ALA:HA	12:N:117:ILE:HD11	1.93	0.50
32:c:152:VAL:HG22	32:c:197:VAL:HG22	1.93	0.50
1:A:198:A:H3'	1:A:199:A:H4'	1.93	0.50
1:A:617:G:O2'	1:A:619:A:OP1	2.30	0.50
1:A:1527:C:N4	1:A:1557:G:O6	2.44	0.50
1:A:1837:U:H3'	21:W:17:ASN:HD21	1.77	0.50
30:a:904:G:H1	30:a:915:U:H3	1.58	0.50
1:A:1184:G:H21	8:J:109:MET:HE3	1.77	0.50
1:A:1886:G:H8	1:A:1914:A:H62	1.60	0.50
1:A:2806:G:OP2	1:A:2810:A:O2'	2.26	0.50
3:C:68:LYS:HA	3:C:151:GLY:HA2	1.94	0.50
10:L:109:VAL:H	10:L:126:ASN:HD22	1.59	0.50
12:N:77:GLN:NE2	12:N:85:SER:OG	2.44	0.50
30:a:794:G:H2'	30:a:795:G:H8	1.76	0.50
30:a:1175:G:N1	30:a:1178:A:OP2	2.36	0.50
30:a:1196:G:N3	43:n:60:SER:OG	2.41	0.50
34:e:16:VAL:HG12	34:e:17:THR:HG23	1.94	0.50
39:j:41:PRO:HA	39:j:72:ARG:HG2	1.94	0.50
51:x:691:GLY:HA2	51:x:701:ILE:HA	1.94	0.50
1:A:905:G:N2	1:A:2298:A:OP2	2.40	0.49
23:Y:39:ASP:OD1	23:Y:44:ARG:NH2	2.45	0.49
27:4:56:LYS:HA	27:4:59:LYS:HE3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:563:C:OP1	24:l:13:LYS:NZ	2.43	0.49
1:A:867:A:N3	1:A:989:U:O2'	2.44	0.49
1:A:1013:U:H2'	1:A:1014:A:H8	1.75	0.49
1:A:1208:G:H2'	1:A:1209:G:H8	1.76	0.49
22:X:9:LEU:HD13	22:X:11:THR:H	1.76	0.49
30:a:400:G:OP1	45:p:9:ARG:NH1	2.45	0.49
30:a:1110:C:OP2	31:b:95:ARG:NH1	2.45	0.49
34:e:93:ASN:HB2	34:e:128:LEU:HB2	1.92	0.49
37:h:10:MET:HE3	37:h:27:ILE:HD13	1.93	0.49
42:m:44:ARG:HB3	42:m:46:ARG:HG2	1.94	0.49
1:A:935:A:N6	1:A:937:C:O2'	2.46	0.49
1:A:1950:G:H2'	1:A:1951:G:H8	1.77	0.49
13:O:19:ARG:HH12	13:O:23:SER:HA	1.77	0.49
30:a:1518:G:H1	30:a:1538:U:H3	1.60	0.49
34:e:105:VAL:O	34:e:112:ARG:NH2	2.45	0.49
1:A:568:G:O2'	1:A:587:C:O2'	2.29	0.49
1:A:2003:C:N4	1:A:2004:G:O6	2.45	0.49
1:A:2708:A:H5'	4:D:169:ILE:HD13	1.93	0.49
7:G:11:ILE:HG23	7:G:15:VAL:HB	1.94	0.49
14:P:49:LYS:HB3	14:P:60:THR:HG22	1.95	0.49
30:a:614:U:H2'	30:a:615:G:H8	1.77	0.49
39:j:36:VAL:HG22	39:j:76:ILE:HG12	1.93	0.49
1:A:2670:A:H5''	8:J:79:THR:HG22	1.95	0.49
1:A:2888:C:OP1	14:P:91:LYS:NZ	2.38	0.49
4:D:32:PRO:HB3	4:D:98:LYS:HG2	1.95	0.49
23:Y:5:GLU:HB2	23:Y:57:LYS:HB3	1.94	0.49
30:a:957:G:H5''	42:m:107:ARG:HB2	1.93	0.49
30:a:962:U:H4'	30:a:974:A:H61	1.77	0.49
30:a:996:A:N3	48:s:52:TYR:OH	2.37	0.49
31:b:186:ILE:HA	31:b:200:ILE:HB	1.95	0.49
1:A:1514:C:O2	1:A:1572:G:N2	2.45	0.49
3:C:248:SER:OG	3:C:250:TRP:O	2.30	0.49
1:A:426:G:H4'	21:W:55:LYS:HE2	1.94	0.49
1:A:848:G:O6	5:E:53:ASN:ND2	2.43	0.49
1:A:1001:U:OP2	11:M:14:ARG:NH1	2.46	0.49
1:A:1700:A:H5'	4:D:120:GLN:HG2	1.94	0.49
1:A:2259:G:O2'	21:W:32:ASN:ND2	2.45	0.49
30:a:12:A:H2'	30:a:13:G:C8	2.47	0.49
34:e:86:ILE:HG12	34:e:95:LEU:HB2	1.95	0.49
45:p:15:SER:HB2	45:p:43:VAL:HG11	1.93	0.49
51:x:544:LEU:HA	51:x:547:ALA:HB3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:977:U:O4	1:A:978:A:N6	2.46	0.49
3:C:23:GLU:OE1	3:C:90:ASN:ND2	2.45	0.49
10:L:83:ASN:O	10:L:119:LYS:NZ	2.45	0.49
12:N:104:LEU:HB2	12:N:114:MET:HB2	1.95	0.49
30:a:12:A:H2'	30:a:13:G:H8	1.76	0.49
1:A:86:C:H42	1:A:97:C:H42	1.61	0.49
1:A:217:G:H21	1:A:219:A:H1'	1.78	0.49
1:A:1017:C:O2'	1:A:1029:A:N3	2.44	0.49
1:A:1715:C:H42	1:A:1719:G:H5''	1.77	0.49
30:a:434:U:OP1	33:d:29:ARG:NE	2.46	0.49
36:g:37:GLY:HA2	36:g:40:GLN:HB2	1.94	0.49
1:A:752:A:N6	1:A:773:G:O2'	2.44	0.49
5:E:131:LEU:HB2	5:E:162:ALA:HB1	1.95	0.49
20:V:75:VAL:HG22	20:V:89:VAL:HG22	1.95	0.49
30:a:873:U:H1'	30:a:877:G:H22	1.78	0.49
30:a:1449:U:O2	30:a:1471:G:N2	2.45	0.49
32:c:178:ARG:NH2	32:c:207:LEU:O	2.46	0.49
37:h:21:ARG:HH22	37:h:70:ASN:HB3	1.78	0.49
46:q:78:VAL:HG12	46:q:79:GLU:HG2	1.93	0.49
1:A:759:G:H1	1:A:766:C:H42	1.60	0.48
1:A:2909:U:O4	24:l:37:LYS:NZ	2.35	0.48
3:C:123:ASP:O	3:C:128:ASN:ND2	2.46	0.48
7:G:146:ALA:HA	7:G:149:ILE:HD12	1.95	0.48
13:O:24:GLY:O	13:O:47:ASP:N	2.41	0.48
14:P:58:THR:HA	14:P:75:PRO:HA	1.95	0.48
16:R:57:THR:O	16:R:101:ASN:ND2	2.38	0.48
17:S:38:LEU:HD22	24:l:38:LEU:HB2	1.95	0.48
30:a:473:G:N1	30:a:476:U:OP2	2.46	0.48
30:a:625:G:N2	30:a:633:C:O2	2.39	0.48
51:x:476:LYS:O	51:x:480:PHE:N	2.46	0.48
51:x:518:GLN:NE2	51:x:533:TYR:OH	2.46	0.48
51:x:709:ASN:HB3	51:x:712:HIS:H	1.77	0.48
52:u:5:G:H2'	52:u:6:G:H8	1.78	0.48
1:A:363:C:OP2	5:E:137:LYS:NZ	2.42	0.48
1:A:1756:U:H5''	1:A:1757:G:H5''	1.95	0.48
21:W:38:ILE:HD13	21:W:40:VAL:HG12	1.94	0.48
30:a:121:C:H2'	30:a:122:G:H8	1.77	0.48
30:a:1122:C:N4	32:c:175:HIS:O	2.45	0.48
1:A:2537:G:H2'	1:A:2538:G:H8	1.77	0.48
3:C:46:GLN:NE2	21:W:19:SER:O	2.46	0.48
6:F:95:ARG:O	6:F:99:PHE:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:x:693:SER:HA	51:x:699:ALA:HA	1.95	0.48
1:A:706:C:H2'	1:A:707:G:H8	1.79	0.48
1:A:2163:A:O2'	1:A:2188:G:N3	2.46	0.48
13:O:35:ARG:HE	13:O:105:ARG:HH21	1.62	0.48
17:S:62:TYR:HB3	17:S:64:MET:HG3	1.94	0.48
18:T:84:THR:OG1	18:T:87:SER:OG	2.31	0.48
30:a:561:U:H4'	41:l:96:ARG:HB2	1.95	0.48
30:a:888:U:H5'	37:h:83:PRO:HG2	1.95	0.48
30:a:1153:G:H21	30:a:1155:A:H62	1.61	0.48
30:a:1270:A:N6	30:a:1283:A:O2'	2.47	0.48
30:a:1368:C:O2'	30:a:1370:G:N7	2.40	0.48
31:b:32:PHE:N	31:b:40:ILE:O	2.44	0.48
39:j:45:GLU:O	39:j:69:THR:OG1	2.27	0.48
45:p:51:ILE:HG22	45:p:53:GLU:H	1.79	0.48
1:A:141:U:H3	1:A:1641:U:H1'	1.77	0.48
30:a:231:U:H2'	30:a:232:A:H8	1.78	0.48
32:c:183:TYR:HD1	32:c:200:TRP:HB3	1.78	0.48
40:k:49:ALA:HB1	40:k:54:PHE:HB2	1.95	0.48
43:n:11:GLN:NE2	43:n:25:GLU:OE1	2.47	0.48
49:t:28:MET:HE3	49:t:58:ILE:HG12	1.95	0.48
51:x:431:LYS:HE3	51:x:452:LEU:HD21	1.95	0.48
1:A:27:G:N2	1:A:558:G:O2'	2.47	0.48
1:A:676:G:N2	1:A:679:A:OP2	2.41	0.48
1:A:1799:G:H22	1:A:2012:C:H1'	1.79	0.48
1:A:2028:C:OP1	4:D:124:LYS:NZ	2.41	0.48
1:A:2573:G:H4'	1:A:2674:G:H5''	1.96	0.48
1:A:2593:A:N6	1:A:2594:A:N1	2.62	0.48
2:B:10:G:OP1	20:V:79:ARG:NH2	2.47	0.48
2:B:63:C:O2'	2:B:106:C:N4	2.36	0.48
4:D:111:THR:HA	4:D:170:THR:HA	1.96	0.48
34:e:94:ILE:HG12	34:e:127:SER:HA	1.95	0.48
51:x:581:ARG:HD3	51:x:583:ARG:HB2	1.96	0.48
1:A:796:A:H61	1:A:800:G:H21	1.60	0.48
1:A:1205:U:H2'	1:A:1206:G:H8	1.78	0.48
19:U:74:LYS:HD3	19:U:75:THR:HG23	1.95	0.48
27:4:32:LEU:O	27:4:36:LYS:NZ	2.44	0.48
29:Z:14:VAL:HB	29:Z:22:PHE:HB3	1.94	0.48
30:a:324:C:OP2	30:a:359:G:O2'	2.31	0.48
31:b:203:ASN:ND2	31:b:205:ASP:OD1	2.47	0.48
34:e:157:ARG:HH11	34:e:159:LYS:HZ2	1.62	0.48
51:x:398:THR:HG23	51:x:400:LYS:H	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:A:H61	1:A:201:C:H3'	1.78	0.48
1:A:595:G:O5'	16:R:69:LYS:NZ	2.44	0.48
1:A:1002:G:H2'	1:A:1003:A:H2'	1.96	0.48
1:A:2054:C:OP1	4:D:153:ARG:NE	2.42	0.48
1:A:2695:C:N4	7:G:109:GLY:O	2.46	0.48
1:A:2712:C:H41	1:A:2756:G:H21	1.61	0.48
1:A:2859:G:OP1	4:D:59:LYS:NZ	2.39	0.48
18:T:20:LEU:HB3	18:T:25:LYS:HG3	1.94	0.48
27:4:15:LYS:HB3	27:4:23:LYS:HE3	1.94	0.48
35:f:7:MET:HE2	35:f:89:ILE:HD11	1.96	0.48
52:u:9:A:O2'	52:u:44:G:N2	2.47	0.48
1:A:625:C:H2'	1:A:626:G:H8	1.79	0.48
1:A:1365:U:H2'	1:A:1366:C:H6	1.78	0.48
1:A:1847:U:OP2	3:C:87:ARG:NH1	2.46	0.48
5:E:154:ILE:HG12	5:E:193:LEU:HD22	1.96	0.48
12:N:100:ARG:HG3	12:N:120:VAL:HB	1.95	0.48
30:a:495:U:H2'	30:a:496:A:H8	1.79	0.48
30:a:500:A:H2'	30:a:501:A:H8	1.78	0.48
30:a:683:G:H21	40:k:120:HIS:CD2	2.32	0.48
30:a:704:A:H2'	30:a:705:A:C8	2.48	0.48
30:a:1469:C:H2'	30:a:1470:A:H8	1.79	0.48
34:e:5:ASP:HB2	34:e:71:LEU:HB2	1.94	0.48
46:q:47:LYS:HB2	46:q:73:LYS:HA	1.96	0.48
1:A:681:C:O2'	1:A:685:U:OP1	2.31	0.48
1:A:1504:A:H2	1:A:2731:G:H22	1.61	0.48
1:A:2100:A:H2'	1:A:2101:G:H8	1.79	0.48
12:N:91:TYR:OH	12:N:119:LEU:O	2.31	0.48
30:a:21:C:OP1	34:e:130:SER:OG	2.28	0.48
30:a:754:U:OP1	30:a:861:U:O2'	2.32	0.48
30:a:1317:C:H5''	42:m:97:VAL:HB	1.96	0.48
1:A:927:G:N2	1:A:944:C:O2	2.38	0.47
1:A:1847:U:OP2	3:C:156:ARG:NE	2.43	0.47
2:B:11:A:H8	2:B:67:G:H21	1.61	0.47
30:a:277:C:H2'	30:a:278:A:C8	2.49	0.47
34:e:14:ARG:NH2	34:e:116:GLU:OE1	2.42	0.47
1:A:721:G:H2'	1:A:851:A:H61	1.80	0.47
1:A:1672:A:H2'	1:A:1673:G:H8	1.79	0.47
1:A:1673:G:O6	1:A:1683:C:N4	2.46	0.47
1:A:1987:C:H2'	1:A:1988:G:H8	1.79	0.47
2:B:3:U:H2'	2:B:4:G:H8	1.79	0.47
16:R:16:GLU:HB2	16:R:100:ILE:HG12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:434:U:OP1	33:d:31:TYR:OH	2.29	0.47
7:G:124:ILE:HG12	7:G:134:VAL:HG22	1.96	0.47
12:N:22:THR:HG22	12:N:66:ILE:HG23	1.95	0.47
12:N:106:PRO:HG3	17:S:40:PRO:HG3	1.95	0.47
30:a:413:U:OP1	30:a:414:G:O2'	2.32	0.47
30:a:1487:C:H2'	30:a:1488:A:C8	2.49	0.47
37:h:21:ARG:NH1	37:h:70:ASN:OD1	2.45	0.47
51:x:688:SER:HB3	51:x:704:ALA:HB3	1.95	0.47
1:A:560:A:N3	1:A:625:C:O2'	2.46	0.47
1:A:1422:C:OP1	1:A:1621:G:N2	2.48	0.47
1:A:2281:G:O6	50:v:85:C:N4	2.47	0.47
8:J:32:GLU:HB2	8:J:143:LEU:HD22	1.95	0.47
14:P:14:ARG:HH11	14:P:17:LEU:HD11	1.80	0.47
24:l:43:CYS:O	24:l:47:GLY:N	2.44	0.47
26:3:35:ARG:HE	26:3:42:LEU:HD21	1.80	0.47
30:a:505:G:N2	30:a:507:A:OP2	2.42	0.47
1:A:2146:A:N6	1:A:2200:A:N1	2.62	0.47
1:A:2394:G:O2'	1:A:2395:A:O4'	2.32	0.47
7:G:88:LEU:N	7:G:132:VAL:O	2.46	0.47
21:W:33:LEU:H	21:W:33:LEU:HG	1.46	0.47
30:a:699:G:OP2	40:k:31:ASN:ND2	2.31	0.47
36:g:113:GLU:H	36:g:119:ARG:HD2	1.80	0.47
37:h:115:ASP:OD1	37:h:119:ARG:NH1	2.48	0.47
1:A:608:C:O2	15:Q:37:GLN:NE2	2.47	0.47
1:A:1289:U:O2'	10:L:21:ARG:NH1	2.48	0.47
3:C:136:PRO:HG3	35:f:81:ILE:HG23	1.96	0.47
8:J:63:ILE:O	8:J:94:ARG:NH1	2.42	0.47
11:M:63:LYS:N	11:M:107:SER:OG	2.46	0.47
17:S:86:ARG:HD3	17:S:87:PRO:HD2	1.96	0.47
21:W:47:VAL:HG12	21:W:48:TYR:H	1.80	0.47
29:Z:12:ALA:N	29:Z:24:THR:O	2.48	0.47
34:e:141:LEU:HD23	34:e:144:LEU:HD12	1.97	0.47
1:A:886:U:O2'	1:A:1232:G:N3	2.47	0.47
1:A:1598:C:OP1	1:A:1764:U:O2'	2.32	0.47
1:A:2038:G:H5'	17:S:41:ARG:HG2	1.95	0.47
1:A:2086:G:H1'	24:l:3:VAL:HG21	1.95	0.47
6:F:19:LYS:NZ	6:F:168:GLU:OE1	2.45	0.47
11:M:38:GLU:HB2	11:M:127:ILE:HG23	1.96	0.47
30:a:313:G:H4'	30:a:314:A:H5''	1.96	0.47
30:a:455:G:H21	30:a:496:A:H62	1.61	0.47
30:a:777:A:N3	30:a:1522:U:O2'	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:815:C:H2'	30:a:816:A:C8	2.50	0.47
32:c:19:GLU:HA	32:c:55:GLU:HG2	1.95	0.47
35:f:37:ILE:HA	35:f:65:VAL:HG22	1.96	0.47
45:p:7:LEU:HG	45:p:70:VAL:HG22	1.97	0.47
50:v:46:G:H1	50:v:58:U:H3	1.63	0.47
1:A:505:G:N2	1:A:517:A:OP2	2.48	0.47
1:A:2014:G:H2'	1:A:2015:G:H8	1.80	0.47
4:D:132:PRO:O	4:D:137:SER:OG	2.32	0.47
11:M:37:LEU:HD11	11:M:130:LYS:HB3	1.97	0.47
12:N:57:HIS:CE1	12:N:61:GLN:HE21	2.33	0.47
30:a:553:G:OP1	33:d:55:GLN:NE2	2.37	0.47
51:x:660:GLU:HA	51:x:704:ALA:HA	1.96	0.47
1:A:712:C:H2'	1:A:713:G:H8	1.78	0.47
1:A:1408:G:H2'	21:W:24:ALA:HB3	1.97	0.47
1:A:2197:G:N2	1:A:2200:A:OP2	2.47	0.47
30:a:949:G:OP1	36:g:102:ARG:NH1	2.48	0.47
35:f:71:ALA:O	35:f:75:PHE:N	2.45	0.47
35:f:76:ASP:O	35:f:80:LYS:NZ	2.47	0.47
36:g:12:VAL:HG12	36:g:14:PRO:HD2	1.97	0.47
1:A:514:G:OP1	26:3:33:ARG:NE	2.35	0.47
1:A:1409:C:O2	21:W:25:SER:OG	2.33	0.47
1:A:2730:U:O2'	12:N:68:ASN:ND2	2.48	0.47
30:a:64:U:H3	30:a:103:G:H1	1.63	0.47
1:A:251:G:O2'	1:A:2461:A:OP1	2.31	0.46
1:A:992:G:O6	1:A:1018:G:N2	2.48	0.46
1:A:999:A:H2'	1:A:1000:G:H8	1.80	0.46
1:A:2120:U:H3	1:A:2258:U:H3	1.63	0.46
1:A:2721:C:O2	1:A:2872:U:O2'	2.33	0.46
30:a:160:A:N1	30:a:355:G:O2'	2.48	0.46
30:a:817:C:H2'	30:a:818:G:H8	1.79	0.46
38:i:7:TYR:HD1	38:i:20:ARG:HB3	1.80	0.46
52:u:47:U:O4	52:u:49:C:O2'	2.32	0.46
1:A:539:G:O2'	17:S:7:ALA:O	2.32	0.46
1:A:1321:U:H3	1:A:1325:A:H62	1.63	0.46
9:K:28:SER:OG	9:K:29:GLY:N	2.49	0.46
9:K:38:VAL:HG22	9:K:61:VAL:HG22	1.98	0.46
12:N:2:SER:OG	12:N:3:TYR:N	2.45	0.46
33:d:91:ASP:HA	33:d:96:ASN:HD22	1.80	0.46
38:i:44:LEU:HA	38:i:47:ASP:HB2	1.96	0.46
51:x:478:ARG:NH2	52:u:68:C:OP1	2.46	0.46
1:A:228:C:HO2'	1:A:260:A:HO2'	1.61	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:A:OP2	21:W:41:ASN:ND2	2.47	0.46
1:A:1165:U:H2'	1:A:1166:G:H8	1.81	0.46
1:A:2601:A:OP1	1:A:2603:G:O2'	2.33	0.46
10:L:23:ILE:HD11	16:R:83:HIS:CD2	2.51	0.46
12:N:55:ASP:H	12:N:58:ALA:HB3	1.80	0.46
27:4:22:LEU:HD21	27:4:62:LEU:HD11	1.96	0.46
30:a:299:C:O2	30:a:317:G:N2	2.37	0.46
30:a:724:A:H2'	30:a:725:A:H8	1.79	0.46
30:a:919:A:N3	30:a:1422:A:O2'	2.48	0.46
51:x:535:ALA:HA	51:x:541:ILE:HD12	1.96	0.46
1:A:447:G:H21	21:W:43:LYS:H	1.63	0.46
1:A:675:C:N4	1:A:676:G:O6	2.48	0.46
1:A:790:A:O2'	1:A:1704:U:OP1	2.33	0.46
1:A:1067:A:H61	1:A:1188:A:H61	1.63	0.46
1:A:1453:A:N6	1:A:1633:G:O6	2.48	0.46
1:A:2725:U:H2'	1:A:2726:G:H8	1.80	0.46
7:G:125:GLU:N	7:G:133:VAL:O	2.43	0.46
11:M:70:PRO:HB2	11:M:93:TRP:HB3	1.97	0.46
30:a:968:A:N7	48:s:55:ARG:NH1	2.63	0.46
33:d:44:LEU:HB3	33:d:48:GLY:HA3	1.98	0.46
33:d:180:PRO:HB2	33:d:185:LEU:HD11	1.98	0.46
51:x:616:THR:OG1	51:x:618:GLY:O	2.28	0.46
1:A:1070:G:H21	1:A:1190:A:H4'	1.79	0.46
1:A:2718:U:OP2	1:A:2897:G:N1	2.43	0.46
10:L:75:ALA:HB3	10:L:109:VAL:HA	1.98	0.46
17:S:50:VAL:HG12	17:S:105:ILE:HD12	1.98	0.46
31:b:68:LEU:HB2	31:b:161:LEU:HA	1.96	0.46
44:o:13:ASN:HA	44:o:16:LYS:HE3	1.97	0.46
48:s:50:ALA:HB1	48:s:57:HIS:HB3	1.98	0.46
1:A:1825:U:H2'	1:A:1826:C:C6	2.51	0.46
19:U:9:VAL:HG13	19:U:68:VAL:HG13	1.98	0.46
28:5:29:ASN:HD21	28:5:31:LYS:HE3	1.81	0.46
30:a:890:C:H2'	30:a:891:G:H8	1.80	0.46
35:f:42:ASP:OD1	35:f:61:GLN:NE2	2.49	0.46
40:k:38:ASP:N	40:k:42:ASN:O	2.46	0.46
47:r:68:ARG:HB3	47:r:75:TYR:CZ	2.50	0.46
1:A:987:A:N3	1:A:1231:G:O2'	2.48	0.46
1:A:1394:G:OP1	3:C:38:HIS:NE2	2.49	0.46
1:A:2065:C:H2'	1:A:2066:A:H8	1.80	0.46
1:A:2334:U:O2'	1:A:2335:U:O4'	2.31	0.46
3:C:132:LEU:HD23	3:C:135:ILE:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:136:THR:HG22	5:E:167:ALA:H	1.80	0.46
20:V:17:SER:OG	50:v:3:C:OP1	2.34	0.46
21:W:10:LYS:HZ3	21:W:52:ARG:HD2	1.81	0.46
26:3:25:LYS:HA	26:3:28:ARG:HH21	1.80	0.46
30:a:674:A:H62	30:a:733:G:H1	1.64	0.46
1:A:106:G:H2'	1:A:107:G:H8	1.81	0.46
1:A:228:C:O2'	1:A:260:A:O2'	2.29	0.46
1:A:878:G:O2'	10:L:38:GLN:OE1	2.30	0.46
1:A:2472:C:H2'	1:A:2473:G:C8	2.50	0.46
3:C:241:ILE:HD13	3:C:246:PRO:HG3	1.98	0.46
11:M:31:GLU:HA	11:M:134:ARG:HB2	1.98	0.46
18:T:9:LYS:HE3	18:T:31:ASP:HB3	1.96	0.46
30:a:993:A:O2'	30:a:994:C:O4'	2.33	0.46
30:a:995:C:H2'	30:a:996:A:C8	2.51	0.46
51:x:474:LYS:O	51:x:478:ARG:N	2.45	0.46
1:A:721:G:H5''	5:E:76:GLY:N	2.30	0.46
1:A:1528:U:H3	1:A:1557:G:H1	1.64	0.46
1:A:2421:A:OP1	27:4:31:HIS:NE2	2.49	0.46
5:E:34:PHE:HE2	10:L:13:ARG:HE	1.63	0.46
16:R:12:ILE:HG21	16:R:20:VAL:HG11	1.97	0.46
30:a:972:C:H2'	30:a:973:G:H8	1.81	0.46
30:a:1188:A:OP2	38:i:95:ARG:NH2	2.48	0.46
32:c:90:LEU:HD23	32:c:93:LEU:HD12	1.98	0.46
1:A:89:U:H5''	1:A:90:A:H2'	1.98	0.46
1:A:443:G:O5'	21:W:8:THR:N	2.49	0.46
1:A:1249:U:H2'	1:A:1250:G:H21	1.81	0.46
1:A:1676:G:N2	1:A:1679:A:OP2	2.49	0.46
3:C:13:ARG:NH1	3:C:16:MET:SD	2.88	0.46
3:C:124:ILE:HG21	35:f:81:ILE:HG21	1.97	0.46
3:C:230:HIS:HD2	3:C:232:HIS:H	1.64	0.46
30:a:54:U:H2'	30:a:55:A:H8	1.81	0.46
30:a:56:C:OP1	30:a:359:G:N2	2.49	0.46
30:a:75:G:O2'	30:a:93:G:O6	2.31	0.46
30:a:326:G:H2'	30:a:327:G:H8	1.81	0.46
30:a:720:G:H2'	30:a:721:A:H8	1.80	0.46
30:a:912:G:H2'	30:a:913:A:H8	1.81	0.46
30:a:990:C:H1'	43:n:19:GLN:HG2	1.97	0.46
44:o:9:ASN:O	44:o:13:ASN:ND2	2.49	0.46
1:A:731:G:N2	1:A:835:A:OP2	2.42	0.45
1:A:2207:C:N4	1:A:2209:U:O4	2.48	0.45
10:L:49:GLY:H	27:4:61:MET:HE3	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:T:32:VAL:O	18:T:77:ARG:NH1	2.48	0.45
22:X:48:LYS:HG2	22:X:52:ARG:HH21	1.81	0.45
30:a:9:G:N7	34:e:97:LYS:NZ	2.55	0.45
30:a:445:U:H3	30:a:504:A:H62	1.64	0.45
32:c:63:VAL:HB	32:c:98:VAL:HA	1.96	0.45
40:k:25:ILE:HG23	40:k:88:VAL:HA	1.98	0.45
51:x:419:ILE:HD12	52:u:76:A:H8	1.81	0.45
1:A:443:G:H5''	21:W:7:ILE:H	1.80	0.45
1:A:1852:G:OP1	3:C:54:GLN:NE2	2.49	0.45
1:A:2415:U:O2'	20:V:64:ASP:OD1	2.31	0.45
1:A:2835:A:H62	1:A:2915:G:H21	1.62	0.45
2:B:36:C:H2'	2:B:37:A:H8	1.80	0.45
39:j:34:ALA:HA	39:j:80:THR:HG21	1.97	0.45
46:q:64:MET:N	46:q:76:ARG:O	2.49	0.45
51:x:611:ILE:HG22	51:x:625:ARG:HA	1.98	0.45
51:x:617:LYS:HE2	51:x:619:ARG:HH12	1.81	0.45
1:A:189:G:H2'	1:A:190:G:H8	1.81	0.45
1:A:424:G:O6	21:W:58:LYS:NZ	2.44	0.45
1:A:647:A:O5'	1:A:702:A:N6	2.50	0.45
1:A:789:C:H2'	1:A:790:A:H8	1.81	0.45
1:A:858:U:H5''	10:L:22:GLY:HA2	1.99	0.45
1:A:1056:A:H5''	15:Q:66:ASN:HD21	1.80	0.45
1:A:1475:G:O2'	1:A:1476:C:O4'	2.35	0.45
1:A:1618:A:OP1	3:C:61:GLN:NE2	2.49	0.45
1:A:2017:C:OP1	9:K:7:ARG:NH1	2.44	0.45
1:A:2318:G:N2	1:A:2375:A:OP1	2.36	0.45
9:K:107:ARG:HE	9:K:115:VAL:HG11	1.80	0.45
11:M:1:MET:HE3	11:M:3:LEU:HD21	1.98	0.45
30:a:209:A:O5'	49:t:63:LYS:NZ	2.49	0.45
30:a:260:U:O2	30:a:283:G:N2	2.49	0.45
30:a:329:A:H2	30:a:340:G:H22	1.65	0.45
35:f:9:ILE:HD12	35:f:87:ARG:HB2	1.98	0.45
42:m:50:GLU:O	42:m:54:GLY:N	2.45	0.45
43:n:3:LYS:NZ	43:n:28:GLY:O	2.38	0.45
45:p:18:TYR:HB2	45:p:40:TYR:HB3	1.98	0.45
48:s:11:VAL:HB	48:s:41:PHE:HE2	1.82	0.45
1:A:45:G:H21	1:A:183:A:H61	1.64	0.45
1:A:727:A:H2'	1:A:728:G:H8	1.82	0.45
1:A:796:A:N6	1:A:800:G:H21	2.15	0.45
1:A:1007:G:N2	1:A:2059:A:OP1	2.48	0.45
1:A:2262:A:H2'	1:A:2263:G:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2900:A:H4'	14:P:1:MET:HB2	1.99	0.45
27:4:4:MET:HE1	27:4:60:GLN:HE21	1.81	0.45
30:a:1385:U:H2'	30:a:1386:A:C8	2.52	0.45
30:a:1400:U:H2'	30:a:1401:G:H8	1.82	0.45
30:a:1463:A:H2'	30:a:1464:G:C8	2.52	0.45
32:c:68:HIS:HB3	32:c:105:ILE:HD11	1.99	0.45
36:g:72:VAL:HB	36:g:142:HIS:HE1	1.81	0.45
52:u:60:U:H5''	52:u:61:C:H5	1.80	0.45
1:A:602:G:H2'	1:A:603:G:H8	1.82	0.45
1:A:854:U:H2'	1:A:855:G:C8	2.51	0.45
1:A:933:C:OP1	51:x:598:ARG:NH1	2.49	0.45
1:A:934:U:OP2	51:x:619:ARG:NH1	2.50	0.45
1:A:2719:A:OP2	12:N:13:ARG:NH1	2.50	0.45
14:P:14:ARG:HH12	14:P:81:ILE:HB	1.81	0.45
30:a:957:G:HO2'	30:a:1315:A:HO2'	1.64	0.45
1:A:1463:C:H42	1:A:1628:G:H1	1.65	0.45
1:A:1817:C:H4'	3:C:224:VAL:HG11	1.98	0.45
8:J:8:ASN:HD22	8:J:44:THR:HB	1.82	0.45
19:U:43:LYS:O	19:U:57:SER:N	2.50	0.45
30:a:177:G:OP1	49:t:56:LYS:NZ	2.34	0.45
45:p:74:PHE:HB3	45:p:79:ILE:HB	1.98	0.45
51:x:497:VAL:HG23	51:x:536:VAL:HG22	1.99	0.45
1:A:630:A:O2'	1:A:718:C:O2	2.34	0.45
1:A:1893:U:OP1	1:A:2439:G:O2'	2.34	0.45
30:a:214:U:H3	30:a:225:A:H61	1.65	0.45
30:a:700:G:O6	40:k:59:LYS:NZ	2.38	0.45
32:c:59:ALA:HB3	32:c:62:ARG:HB2	1.98	0.45
38:i:69:GLY:O	38:i:75:GLN:NE2	2.39	0.45
45:p:6:ARG:HA	45:p:70:VAL:HG21	1.97	0.45
45:p:70:VAL:HG12	45:p:74:PHE:HE2	1.82	0.45
1:A:482:C:O2'	1:A:483:C:O4'	2.33	0.45
1:A:1386:G:H1	1:A:1644:C:H42	1.63	0.45
1:A:2751:G:OP1	4:D:196:LYS:NZ	2.40	0.45
1:A:2821:U:H3	1:A:2830:A:H61	1.65	0.45
3:C:205:ILE:HD13	3:C:211:SER:HB3	1.97	0.45
6:F:74:ILE:N	6:F:79:LEU:O	2.46	0.45
6:F:107:SER:OG	6:F:108:LEU:N	2.49	0.45
30:a:1322:U:H3'	48:s:5:LEU:HD13	1.98	0.45
36:g:28:ASN:HA	36:g:31:MET:HE3	1.98	0.45
1:A:627:G:OP2	15:Q:14:ARG:NH1	2.49	0.45
1:A:939:G:O2'	1:A:940:G:O5'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1417:A:O2'	1:A:1419:G:OP2	2.35	0.45
1:A:1866:C:O2'	1:A:1956:A:N3	2.44	0.45
25:2:29:ARG:HG3	25:2:47:GLU:HB3	1.99	0.45
30:a:1359:A:OP1	38:i:123:ARG:NH1	2.50	0.45
31:b:18:HIS:CD2	31:b:19:GLN:HG2	2.52	0.45
31:b:23:TRP:HA	31:b:190:ASN:HB3	1.99	0.45
48:s:32:LYS:HA	48:s:50:ALA:HB3	1.98	0.45
1:A:704:U:H2'	1:A:705:A:C8	2.52	0.45
1:A:742:G:OP1	1:A:1419:G:O2'	2.27	0.45
8:J:78:HIS:ND1	8:J:79:THR:O	2.32	0.45
30:a:76:A:H1'	30:a:77:U:H5	1.82	0.45
30:a:299:C:H2'	30:a:300:G:C8	2.51	0.45
30:a:590:G:N1	30:a:768:A:OP2	2.35	0.45
30:a:849:G:H21	31:b:35:ARG:HH22	1.65	0.45
30:a:956:A:H2'	30:a:957:G:C8	2.52	0.45
30:a:1318:G:N7	42:m:98:ARG:NH2	2.65	0.45
30:a:1416:C:H42	30:a:1504:G:H1	1.64	0.45
33:d:55:GLN:HB3	33:d:59:HIS:HD2	1.82	0.45
41:l:116:ASP:HB2	51:x:466:LYS:HZ1	1.82	0.45
47:r:44:ILE:HD13	47:r:61:THR:HG22	1.99	0.45
51:x:587:VAL:HB	51:x:597:VAL:HG21	1.98	0.45
1:A:686:C:N4	1:A:694:G:O6	2.50	0.44
1:A:2671:G:OP2	8:J:86:LYS:NZ	2.49	0.44
10:L:97:LEU:HD21	10:L:105:LEU:HB2	1.98	0.44
11:M:56:ARG:HG2	51:x:668:ARG:HH11	1.82	0.44
15:Q:88:ILE:O	16:R:50:ASN:ND2	2.44	0.44
15:Q:98:LEU:HB3	16:R:13:LYS:HD2	1.98	0.44
31:b:114:LEU:HD22	31:b:144:LEU:HB3	1.98	0.44
49:t:61:ALA:HB1	49:t:67:VAL:HG21	1.99	0.44
51:x:661:ILE:HD12	51:x:705:ILE:HD11	1.99	0.44
1:A:58:G:H2'	1:A:59:G:H8	1.83	0.44
1:A:1103:A:N6	1:A:1133:G:OP2	2.50	0.44
1:A:2717:G:O2'	1:A:2750:A:N6	2.51	0.44
4:D:124:LYS:HG2	4:D:164:MET:HE1	2.00	0.44
14:P:60:THR:HB	14:P:73:THR:HG22	2.00	0.44
15:Q:78:ARG:HB3	15:Q:117:LEU:HD11	1.99	0.44
19:U:16:ASP:HB3	19:U:38:VAL:HG13	2.00	0.44
30:a:511:C:H2'	30:a:512:A:H8	1.81	0.44
30:a:825:A:OP2	30:a:1536:G:O2'	2.33	0.44
30:a:901:U:H2'	30:a:902:A:H8	1.81	0.44
1:A:516:G:O6	26:3:39:ARG:NE	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1815:A:OP1	1:A:2009:G:N2	2.50	0.44
8:J:17:LEU:HD23	8:J:139:GLU:HB2	1.99	0.44
17:S:11:ARG:HA	17:S:100:THR:HG23	1.98	0.44
30:a:510:C:H5''	41:l:127:ARG:HB3	1.99	0.44
30:a:701:U:H5''	40:k:129:ARG:HH22	1.80	0.44
31:b:24:ASN:H	31:b:190:ASN:HA	1.82	0.44
32:c:34:GLU:HB3	32:c:58:ARG:HH22	1.82	0.44
1:A:697:G:OP1	27:4:19:SER:OG	2.35	0.44
13:O:29:PRO:HD2	13:O:93:VAL:HA	1.99	0.44
30:a:1046:G:O2'	30:a:1047:C:O4'	2.27	0.44
53:w:58:A:H3'	53:w:61:C:H41	1.83	0.44
1:A:192:G:H2'	1:A:208:G:H22	1.82	0.44
1:A:901:U:H2'	1:A:902:G:H8	1.83	0.44
1:A:1709:A:N1	1:A:2755:U:N3	2.65	0.44
30:a:30:G:O2'	30:a:304:U:OP1	2.26	0.44
30:a:247:G:N2	30:a:298:C:O3'	2.50	0.44
30:a:542:A:O2'	30:a:544:A:OP2	2.32	0.44
30:a:1017:A:H61	30:a:1032:C:H42	1.65	0.44
30:a:1278:A:H1'	30:a:1335:U:H1'	1.98	0.44
30:a:1363:C:H2'	30:a:1364:G:H8	1.81	0.44
33:d:12:SER:OG	33:d:25:GLU:OE1	2.35	0.44
51:x:398:THR:HA	51:x:415:PHE:HZ	1.83	0.44
1:A:661:A:H2	5:E:180:GLY:HA2	1.83	0.44
1:A:1305:A:H61	1:A:2042:A:H5''	1.82	0.44
1:A:1821:G:O2'	1:A:1859:C:OP1	2.25	0.44
1:A:1977:G:H21	30:a:1427:A:H2	1.64	0.44
1:A:2778:A:H3'	1:A:2779:A:H2'	2.00	0.44
9:K:64:ARG:NH1	9:K:101:PRO:O	2.44	0.44
15:Q:92:ARG:O	15:Q:94:MET:N	2.50	0.44
16:R:61:LYS:O	16:R:96:THR:OG1	2.33	0.44
30:a:133:G:H1	45:p:26:ARG:NH2	2.13	0.44
30:a:220:C:O2	30:a:221:G:N2	2.50	0.44
30:a:285:C:N4	30:a:286:G:O6	2.49	0.44
30:a:1487:C:H2'	30:a:1488:A:H8	1.83	0.44
32:c:70:ALA:HB2	32:c:105:ILE:HB	1.99	0.44
45:p:49:VAL:HG11	45:p:73:LEU:HD22	1.99	0.44
50:v:66:U:C2	50:v:68:A:H5''	2.53	0.44
51:x:478:ARG:HH12	52:u:68:C:H5''	1.82	0.44
1:A:2028:C:H2'	1:A:2029:G:H8	1.82	0.44
1:A:2042:A:H61	1:A:2642:U:H3	1.64	0.44
1:A:2083:A:OP1	1:A:2084:C:O2'	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2268:G:N2	1:A:2269:C:O2	2.51	0.44
1:A:2622:U:H2'	1:A:2623:C:H6	1.82	0.44
6:F:126:GLY:O	6:F:158:THR:OG1	2.31	0.44
30:a:58:U:H2'	30:a:59:G:C8	2.53	0.44
30:a:484:U:H2'	30:a:485:A:H8	1.82	0.44
30:a:953:U:H2'	30:a:954:G:H8	1.82	0.44
44:o:39:LEU:HD22	44:o:56:LEU:HD12	1.99	0.44
1:A:217:G:H1'	1:A:220:A:H5'	1.99	0.44
1:A:836:A:H5'	26:3:4:THR:HG21	1.99	0.44
1:A:1231:G:H2'	1:A:1232:G:C8	2.53	0.44
1:A:1363:G:H3'	1:A:1364:C:H4'	1.99	0.44
46:q:70:SER:O	46:q:74:ARG:NH1	2.47	0.44
51:x:581:ARG:NH2	51:x:582:LYS:O	2.51	0.44
51:x:602:CYS:SG	51:x:603:CYS:N	2.91	0.44
53:w:8:U:H5'	53:w:49:C:H5'	2.00	0.44
1:A:78:U:H3	1:A:107:G:H1	1.66	0.44
1:A:89:U:H3'	1:A:90:A:H8	1.83	0.44
1:A:732:A:O2'	1:A:736:A:N6	2.51	0.44
1:A:2245:G:H1'	1:A:2246:G:H5'	2.00	0.44
15:Q:28:LYS:HG2	15:Q:34:VAL:HG12	2.00	0.44
30:a:36:C:H2'	30:a:37:G:H8	1.83	0.44
30:a:192:C:H2'	30:a:193:G:H8	1.83	0.44
30:a:599:U:OP1	37:h:31:LYS:N	2.51	0.44
30:a:724:A:H2'	30:a:725:A:C8	2.52	0.44
30:a:968:A:OP2	51:x:580:GLY:N	2.51	0.44
30:a:1087:G:N2	30:a:1090:A:OP2	2.44	0.44
30:a:1190:G:O2'	30:a:1191:G:N7	2.48	0.44
51:x:616:THR:OG1	51:x:620:GLY:O	2.36	0.44
1:A:460:C:H42	1:A:2439:G:H1	1.66	0.43
1:A:553:A:N3	1:A:555:C:N4	2.66	0.43
1:A:1093:G:H22	1:A:1156:G:H2'	1.83	0.43
1:A:1231:G:H2'	1:A:1232:G:H8	1.82	0.43
1:A:1404:A:O3'	21:W:13:THR:HB	2.17	0.43
1:A:2432:C:N3	1:A:2444:G:N1	2.66	0.43
1:A:2551:U:O2'	1:A:2676:U:OP1	2.27	0.43
18:T:3:ASP:HA	18:T:4:PRO:HD3	1.85	0.43
25:2:6:THR:HA	25:2:18:ILE:HG12	2.00	0.43
30:a:1059:U:H5	43:n:3:LYS:HD3	1.82	0.43
30:a:1248:A:O2'	36:g:114:LYS:O	2.33	0.43
51:x:393:MET:HA	51:x:407:PRO:HA	1.99	0.43
1:A:675:C:O2	1:A:685:U:O2'	2.31	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:760:G:H21	1:A:765:A:H2	1.65	0.43
1:A:920:G:H2'	1:A:921:G:H8	1.82	0.43
1:A:984:G:H2'	1:A:985:G:C8	2.51	0.43
1:A:1191:C:H2'	1:A:1192:G:H8	1.83	0.43
1:A:2093:C:O2	1:A:2479:A:N6	2.51	0.43
9:K:4:GLN:HG2	9:K:5:GLU:HG2	2.00	0.43
13:O:40:ILE:HG22	13:O:58:THR:HG23	1.99	0.43
30:a:683:G:H21	40:k:120:HIS:HD2	1.66	0.43
52:u:53:G:N2	52:u:54:U:O4	2.51	0.43
1:A:510:G:N2	1:A:513:A:OP2	2.50	0.43
1:A:992:G:H2'	1:A:993:A:H8	1.84	0.43
1:A:1513:U:HO2'	1:A:1594:G:HO2'	1.67	0.43
1:A:2162:G:O2'	1:A:2187:A:N1	2.42	0.43
1:A:2372:U:H2'	1:A:2373:U:H6	1.84	0.43
25:2:36:CYS:HG	25:2:45:HIS:CE1	2.36	0.43
30:a:293:C:H2'	30:a:294:G:C8	2.53	0.43
30:a:1085:U:OP2	34:e:69:LYS:NZ	2.50	0.43
32:c:57:GLU:OE1	39:j:94:SER:OG	2.33	0.43
36:g:138:ARG:O	36:g:141:THR:OG1	2.36	0.43
51:x:589:VAL:HB	51:x:595:LEU:HD12	1.99	0.43
52:u:7:A:O2'	52:u:49:C:O4'	2.33	0.43
1:A:2155:A:N1	1:A:2191:A:O2'	2.48	0.43
1:A:2876:A:H1'	12:N:57:HIS:HD2	1.84	0.43
3:C:17:THR:HG1	3:C:204:ASN:N	2.14	0.43
4:D:9:LYS:NZ	4:D:194:GLY:O	2.49	0.43
30:a:98:U:H1'	30:a:99:A:H2	1.82	0.43
31:b:18:HIS:HD2	31:b:19:GLN:HG2	1.81	0.43
33:d:58:ARG:NH2	33:d:63:VAL:O	2.47	0.43
37:h:18:ASN:O	37:h:72:ARG:NE	2.46	0.43
51:x:611:ILE:HD12	51:x:643:VAL:HG23	2.01	0.43
1:A:431:A:N6	1:A:458:G:O6	2.52	0.43
1:A:1322:G:N2	1:A:1325:A:OP2	2.50	0.43
1:A:1951:G:O2'	50:v:26:C:O2'	2.37	0.43
2:B:6:U:O2'	13:O:30:ARG:NH2	2.51	0.43
16:R:4:ILE:HD12	16:R:40:PHE:HB3	2.00	0.43
17:S:58:ALA:HA	17:S:62:TYR:HB2	2.01	0.43
20:V:41:GLY:N	20:V:72:ASP:OD1	2.51	0.43
30:a:435:C:H5''	33:d:10:LYS:HE3	2.01	0.43
33:d:71:LEU:HD23	33:d:74:LYS:HD2	2.01	0.43
38:i:71:GLY:O	38:i:75:GLN:N	2.46	0.43
1:A:625:C:H2'	1:A:626:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:160:THR:HB	3:C:177:ASN:HD21	1.83	0.43
14:P:106:LYS:NZ	30:a:1442:A:OP1	2.45	0.43
30:a:968:A:N6	48:s:77:THR:O	2.52	0.43
30:a:1381:U:OP1	38:i:74:GLY:N	2.48	0.43
51:x:428:ILE:HD11	51:x:454:SER:HB3	2.01	0.43
1:A:694:G:H2'	1:A:695:G:H8	1.84	0.43
1:A:1078:A:H2	1:A:1168:G:H22	1.67	0.43
1:A:1403:G:H2'	21:W:15:GLY:H	1.83	0.43
1:A:1828:G:N2	1:A:1847:U:O2'	2.51	0.43
3:C:247:MET:HA	3:C:253:PRO:HA	2.00	0.43
4:D:126:HIS:CD2	4:D:159:LEU:HB3	2.53	0.43
4:D:185:LEU:HD13	14:P:8:ILE:HD11	2.01	0.43
12:N:102:MET:O	12:N:116:ILE:N	2.49	0.43
30:a:54:U:H2'	30:a:55:A:C8	2.54	0.43
30:a:95:U:H2'	30:a:96:G:H8	1.84	0.43
30:a:352:A:H5''	30:a:353:C:H5	1.84	0.43
1:A:179:A:O2'	1:A:180:G:O4'	2.35	0.43
1:A:1349:G:H21	1:A:1655:A:H8	1.65	0.43
1:A:2469:C:H5''	1:A:2616:A:H4'	2.01	0.43
1:A:2719:A:OP1	12:N:3:TYR:OH	2.36	0.43
2:B:112:C:H2'	2:B:113:A:H8	1.84	0.43
8:J:9:ALA:HA	8:J:49:VAL:HG11	2.01	0.43
30:a:239:G:H2'	30:a:240:A:H8	1.83	0.43
30:a:1026:A:O2'	30:a:1226:C:O2'	2.30	0.43
30:a:1400:U:H2'	30:a:1401:G:C8	2.54	0.43
34:e:49:GLY:HA3	34:e:66:ASP:HB3	2.01	0.43
38:i:84:ALA:O	38:i:88:LEU:N	2.51	0.43
1:A:77:U:H1'	1:A:78:U:H5'	2.01	0.43
1:A:859:C:H2'	1:A:860:U:H6	1.84	0.43
12:N:34:GLU:N	12:N:113:PRO:O	2.50	0.43
30:a:560:U:HO2'	41:l:96:ARG:NH2	2.15	0.43
30:a:759:C:H1'	44:o:23:GLY:H	1.83	0.43
30:a:958:C:H2'	30:a:959:A:C8	2.51	0.43
30:a:1188:A:O2'	38:i:105:THR:O	2.33	0.43
31:b:108:GLN:HA	31:b:111:ILE:HG22	2.01	0.43
33:d:196:GLU:OE1	34:e:112:ARG:NH1	2.37	0.43
41:l:44:ARG:NH2	51:x:462:GLN:OE1	2.46	0.43
1:A:116:G:OP2	1:A:118:A:O2'	2.30	0.43
1:A:1033:C:H5'	23:Y:10:ARG:HH12	1.84	0.43
1:A:1123:A:H2'	1:A:1125:C:H5''	2.01	0.43
1:A:1408:G:N3	21:W:18:ARG:NH2	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2853:C:H2'	1:A:2854:A:C8	2.54	0.43
30:a:667:G:H1'	44:o:22:THR:HB	2.00	0.43
30:a:671:A:H2'	30:a:672:A:H8	1.83	0.43
32:c:76:ILE:HB	32:c:79:GLY:HA2	2.01	0.43
34:e:47:GLY:HA3	34:e:71:LEU:HD23	2.01	0.43
43:n:26:ARG:NH2	43:n:43:CYS:SG	2.91	0.43
1:A:581:C:O2	1:A:602:G:N2	2.41	0.42
1:A:672:C:O2	10:L:81:LYS:NZ	2.48	0.42
1:A:1465:A:O2'	1:A:1467:G:N7	2.45	0.42
1:A:2784:C:OP1	28:5:19:ARG:NH2	2.52	0.42
2:B:46:A:H5''	13:O:35:ARG:HH22	1.84	0.42
13:O:69:GLY:O	13:O:105:ARG:NH1	2.52	0.42
21:W:3:ARG:NE	21:W:31:ALA:H	2.16	0.42
24:1:28:THR:O	24:1:37:LYS:N	2.40	0.42
30:a:449:G:N2	30:a:503:C:N3	2.66	0.42
30:a:505:G:N2	30:a:507:A:N7	2.57	0.42
30:a:938:G:O6	30:a:1398:C:N4	2.51	0.42
30:a:1229:G:H2'	30:a:1230:G:H8	1.84	0.42
30:a:1299:U:OP1	36:g:38:LYS:NZ	2.45	0.42
42:m:34:LEU:HA	42:m:37:ALA:HB3	2.00	0.42
53:w:2:C:N3	53:w:72:C:N4	2.67	0.42
1:A:1242:U:H2'	1:A:1243:A:C8	2.51	0.42
1:A:2234:C:H42	1:A:2248:G:H1	1.67	0.42
1:A:2477:A:H3'	1:A:2478:U:H2'	2.01	0.42
3:C:3:ILE:HD11	3:C:199:GLN:HB2	2.02	0.42
7:G:104:LEU:HD23	7:G:116:ILE:HD12	2.00	0.42
31:b:101:LEU:N	31:b:175:GLU:OE2	2.50	0.42
52:u:30:G:H2'	52:u:31:A:H8	1.84	0.42
1:A:715:A:H2'	1:A:717:A:H62	1.84	0.42
1:A:1941:A:H2	1:A:1946:U:H3	1.67	0.42
1:A:2017:C:H2'	1:A:2018:A:H8	1.84	0.42
3:C:78:VAL:HA	3:C:94:ILE:HG22	2.01	0.42
7:G:23:ASN:HD21	7:G:40:PRO:HA	1.84	0.42
20:V:80:PHE:HB2	20:V:84:ARG:HB3	2.01	0.42
1:A:616:A:H61	1:A:2058:G:H21	1.66	0.42
1:A:868:A:H2'	1:A:992:G:H8	1.84	0.42
1:A:2159:U:O2'	1:A:2162:G:O2'	2.35	0.42
1:A:2213:U:H2'	1:A:2214:G:C8	2.54	0.42
1:A:2259:G:H21	21:W:51:ALA:HB2	1.84	0.42
4:D:109:ASP:HB3	4:D:203:LYS:HB2	2.02	0.42
9:K:16:ALA:HA	9:K:46:ALA:HA	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:N:86:ASP:O	12:N:89:THR:OG1	2.34	0.42
30:a:634:G:H2'	30:a:635:G:H8	1.83	0.42
30:a:720:G:H2'	30:a:721:A:C8	2.54	0.42
30:a:1009:C:N4	30:a:1010:U:O4	2.52	0.42
30:a:1469:C:H2'	30:a:1470:A:C8	2.54	0.42
40:k:22:ILE:HG23	40:k:39:THR:HA	2.00	0.42
51:x:474:LYS:HA	51:x:477:ILE:HB	2.00	0.42
1:A:602:G:H2'	1:A:603:G:C8	2.54	0.42
1:A:2284:G:H21	20:V:16:GLY:HA2	1.84	0.42
1:A:2403:C:N4	1:A:2404:G:O6	2.52	0.42
1:A:2542:A:H2'	1:A:2543:U:C6	2.55	0.42
14:P:91:LYS:HB2	14:P:113:ILE:HG21	2.01	0.42
24:l:37:LYS:HG3	24:l:43:CYS:HB2	2.00	0.42
30:a:436:G:H5'	33:d:10:LYS:HD2	2.01	0.42
30:a:716:U:H4'	40:k:24:HIS:CD2	2.55	0.42
30:a:735:C:H2'	30:a:736:G:C8	2.55	0.42
30:a:1522:U:H2'	30:a:1523:A:C8	2.55	0.42
35:f:30:LEU:HD13	35:f:65:VAL:HG21	2.01	0.42
38:i:12:ARG:HD2	38:i:77:GLY:HA3	2.01	0.42
44:o:42:HIS:O	44:o:45:THR:OG1	2.31	0.42
1:A:444:U:OP2	21:W:5:CYS:HB2	2.19	0.42
1:A:660:G:N2	5:E:182:ASN:OD1	2.52	0.42
1:A:876:A:N7	1:A:2276:A:O2'	2.52	0.42
1:A:2759:C:H2'	1:A:2760:G:H8	1.84	0.42
3:C:39:LYS:HZ1	3:C:58:HIS:C	2.27	0.42
3:C:205:ILE:HG23	3:C:210:ARG:HD2	2.01	0.42
5:E:127:GLU:HB3	5:E:196:LYS:HE2	2.00	0.42
7:G:59:GLN:HB2	7:G:62:HIS:HD2	1.85	0.42
9:K:64:ARG:HB2	9:K:79:PHE:CG	2.54	0.42
23:Y:9:LYS:HE3	23:Y:10:ARG:HB2	2.01	0.42
30:a:955:G:N2	30:a:1343:G:O2'	2.53	0.42
30:a:1473:C:H2'	30:a:1474:G:C8	2.55	0.42
33:d:120:LEU:N	33:d:140:GLY:O	2.42	0.42
41:l:28:TYR:HB2	41:l:72:ASN:HA	2.00	0.42
1:A:273:A:OP2	1:A:297:G:N2	2.40	0.42
1:A:366:A:OP1	5:E:168:ARG:NE	2.53	0.42
1:A:607:G:H1	1:A:622:A:H61	1.68	0.42
1:A:2146:A:H2'	1:A:2147:U:H3'	2.02	0.42
2:B:38:U:H5	29:Z:2:LYS:HE3	1.84	0.42
11:M:55:THR:OG1	51:x:666:TYR:OH	2.31	0.42
12:N:102:MET:HE2	24:l:54:ILE:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:653:U:H2'	30:a:654:G:H8	1.84	0.42
30:a:983:G:O6	30:a:984:A:N6	2.52	0.42
30:a:1088:U:H4'	34:e:138:ARG:HH12	1.85	0.42
33:d:126:VAL:HG12	33:d:128:ILE:H	1.84	0.42
35:f:63:VAL:HG12	35:f:65:VAL:HG23	2.02	0.42
38:i:15:SER:HB3	38:i:70:GLY:HA3	2.02	0.42
40:k:83:THR:HA	40:k:108:GLU:HB3	2.02	0.42
44:o:25:PRO:HB3	44:o:66:LEU:HD22	2.00	0.42
44:o:74:ASP:OD2	44:o:77:ARG:NH1	2.52	0.42
1:A:910:A:H2'	1:A:911:G:H8	1.83	0.42
1:A:1409:C:O2'	21:W:24:ALA:O	2.30	0.42
1:A:1868:G:H2'	1:A:1869:G:H8	1.84	0.42
1:A:2028:C:H2'	1:A:2029:G:C8	2.55	0.42
1:A:2070:U:H2'	1:A:2071:A:H8	1.83	0.42
1:A:2446:C:H2'	1:A:2447:A:C8	2.55	0.42
13:O:14:ARG:HG3	13:O:17:ARG:HH12	1.84	0.42
14:P:9:THR:HB	14:P:55:ILE:HD12	2.02	0.42
21:W:32:ASN:N	21:W:49:VAL:O	2.53	0.42
30:a:406:C:H2'	30:a:407:G:C8	2.54	0.42
30:a:411:C:OP2	33:d:67:GLN:NE2	2.42	0.42
30:a:473:G:H21	30:a:477:A:H2	1.68	0.42
30:a:500:A:H2'	30:a:501:A:C8	2.55	0.42
30:a:890:C:H5''	41:l:9:ARG:HH12	1.85	0.42
30:a:1227:C:H2'	30:a:1228:U:C6	2.55	0.42
31:b:90:TYR:HB3	31:b:151:ILE:HG22	2.02	0.42
31:b:120:MET:SD	31:b:125:THR:OG1	2.76	0.42
39:j:13:TYR:HE2	43:n:54:PRO:HB2	1.85	0.42
52:u:9:A:OP2	52:u:13:C:N4	2.52	0.42
1:A:2644:U:C2	24:l:4:PRO:HA	2.54	0.42
1:A:2725:U:H2'	1:A:2726:G:C8	2.54	0.42
3:C:207:LYS:HB3	3:C:209:GLY:H	1.83	0.42
9:K:13:ASN:OD1	9:K:96:THR:OG1	2.36	0.42
18:T:19:ASP:O	18:T:22:THR:OG1	2.31	0.42
30:a:224:U:H2'	30:a:225:A:C8	2.55	0.42
30:a:316:C:H2'	30:a:317:G:H8	1.84	0.42
30:a:1361:C:H2'	30:a:1362:G:C8	2.55	0.42
36:g:111:ARG:HH12	36:g:123:GLU:HA	1.85	0.42
41:l:113:GLY:H	41:l:117:THR:HG1	1.67	0.42
52:u:7:A:H61	52:u:66:U:H3	1.66	0.42
1:A:2273:U:H1'	1:A:2463:A:C5	2.54	0.42
1:A:2695:C:H41	7:G:153:ARG:HH22	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:40:GLN:OE1	5:E:184:LEU:N	2.53	0.42
8:J:141:TYR:OH	8:J:144:ARG:NH2	2.53	0.42
22:X:12:ALA:HA	22:X:15:GLU:HB3	2.02	0.42
31:b:140:GLU:HG2	31:b:144:LEU:HD13	2.02	0.42
51:x:397:PHE:HB2	51:x:448:ILE:HA	2.01	0.42
1:A:240:C:H42	1:A:263:G:H1	1.67	0.41
1:A:816:U:H2'	1:A:817:G:H8	1.85	0.41
1:A:1198:C:H2'	1:A:1199:C:H6	1.85	0.41
1:A:1362:G:OP1	17:S:84:ARG:NE	2.49	0.41
1:A:1674:G:O2'	1:A:2727:U:OP1	2.36	0.41
1:A:2296:A:H61	1:A:2301:U:H3	1.68	0.41
3:C:46:GLN:HE21	21:W:18:ARG:NH1	2.18	0.41
3:C:243:ARG:NE	3:C:247:MET:SD	2.78	0.41
30:a:208:A:H5''	49:t:60:LYS:HG3	2.02	0.41
30:a:366:U:H2'	30:a:367:A:H8	1.84	0.41
30:a:503:C:H2'	30:a:505:G:H8	1.85	0.41
30:a:1134:G:N2	30:a:1135:U:O4	2.52	0.41
36:g:111:ARG:NH1	36:g:126:ASP:OD2	2.53	0.41
37:h:107:SER:HA	37:h:112:VAL:HA	2.01	0.41
41:l:43:LYS:HD2	41:l:70:LEU:HD13	2.02	0.41
52:u:23:A:H2'	52:u:24:G:H8	1.84	0.41
1:A:490:A:C8	5:E:45:ARG:HD3	2.55	0.41
1:A:2537:G:H2'	1:A:2538:G:C8	2.54	0.41
3:C:157:SER:O	3:C:160:THR:OG1	2.36	0.41
7:G:8:LEU:HD22	7:G:52:THR:HG22	2.01	0.41
10:L:51:GLU:OE2	27:4:57:ARG:NH2	2.53	0.41
13:O:79:GLU:O	13:O:83:LYS:N	2.51	0.41
26:3:34:ARG:HG3	26:3:42:LEU:HD12	2.02	0.41
30:a:846:G:H2'	30:a:847:G:H8	1.85	0.41
30:a:1416:C:H2'	30:a:1417:A:H8	1.85	0.41
1:A:2187:A:H4'	1:A:2188:G:H5'	2.02	0.41
15:Q:75:SER:HG	15:Q:78:ARG:H	1.68	0.41
17:S:12:ILE:HD12	17:S:12:ILE:HA	1.88	0.41
30:a:10:A:C8	34:e:106:ILE:HG23	2.55	0.41
30:a:231:U:H2'	30:a:232:A:C8	2.56	0.41
30:a:343:C:O2'	30:a:1442:A:N3	2.48	0.41
30:a:728:C:N3	47:r:68:ARG:NH1	2.56	0.41
30:a:1047:C:H2'	30:a:1048:A:C8	2.54	0.41
30:a:1473:C:H2'	30:a:1474:G:H8	1.84	0.41
47:r:24:THR:OG1	47:r:25:HIS:N	2.53	0.41
1:A:1029:A:H62	1:A:1030:G:N2	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1404:A:H5'	21:W:15:GLY:HA3	2.01	0.41
1:A:1408:G:H1	1:A:1838:A:N6	2.18	0.41
1:A:2771:G:OP1	28:5:35:LYS:NZ	2.43	0.41
5:E:135:LYS:HG2	5:E:137:LYS:H	1.85	0.41
10:L:1:MET:HE1	10:L:7:LYS:H	1.85	0.41
11:M:25:THR:O	11:M:35:GLN:NE2	2.53	0.41
30:a:21:C:OP1	34:e:132:THR:OG1	2.36	0.41
30:a:33:G:H21	30:a:48:G:H5''	1.85	0.41
42:m:80:LEU:HA	42:m:83:ILE:HG12	2.02	0.41
51:x:429:GLY:H	51:x:452:LEU:HB2	1.85	0.41
51:x:709:ASN:HD22	51:x:710:ILE:H	1.68	0.41
1:A:246:U:H2'	1:A:247:A:H8	1.86	0.41
1:A:2113:C:H42	1:A:2264:G:H1	1.69	0.41
12:N:32:THR:O	12:N:115:ALA:N	2.52	0.41
29:Z:14:VAL:O	29:Z:22:PHE:N	2.46	0.41
30:a:390:A:H2'	30:a:391:A:C8	2.56	0.41
30:a:918:A:H2'	30:a:919:A:C8	2.56	0.41
30:a:960:U:H2'	30:a:961:G:H8	1.84	0.41
31:b:84:ALA:O	31:b:88:GLY:N	2.53	0.41
31:b:102:THR:HG23	31:b:175:GLU:HB2	2.03	0.41
40:k:18:ILE:N	40:k:79:HIS:O	2.54	0.41
51:x:471:SER:O	51:x:475:HIS:N	2.53	0.41
1:A:77:U:O5'	22:X:2:LYS:NZ	2.53	0.41
1:A:1339:A:H4'	1:A:1340:A:H5'	2.02	0.41
1:A:1537:G:H2'	1:A:1538:G:H8	1.85	0.41
1:A:2122:G:H1'	1:A:2123:A:H5'	2.03	0.41
1:A:2875:A:P	1:A:2891:G:H22	2.44	0.41
5:E:122:ASN:HB3	5:E:191:LYS:HA	2.03	0.41
30:a:95:U:H2'	30:a:96:G:C8	2.55	0.41
30:a:643:C:H2'	30:a:644:A:C8	2.55	0.41
30:a:766:U:O2'	30:a:889:C:O2	2.29	0.41
46:q:11:GLN:HA	46:q:62:LYS:HA	2.03	0.41
48:s:28:LYS:HG2	48:s:29:GLN:H	1.85	0.41
51:x:602:CYS:HB2	51:x:630:ASN:HD22	1.86	0.41
1:A:82:G:N1	1:A:102:A:OP2	2.47	0.41
1:A:1837:U:N3	21:W:16:ASN:O	2.47	0.41
16:R:29:ALA:HA	16:R:62:VAL:HG12	2.02	0.41
16:R:77:LYS:HB2	16:R:82:VAL:HB	2.03	0.41
26:3:3:ARG:HA	26:3:3:ARG:HD3	1.80	0.41
30:a:1265:C:O2'	30:a:1287:C:N4	2.53	0.41
40:k:76:SER:O	40:k:80:GLY:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:m:17:ILE:O	42:m:20:THR:OG1	2.32	0.41
51:x:498:GLU:HA	51:x:501:ILE:HD12	2.03	0.41
52:u:23:A:H2'	52:u:24:G:C8	2.56	0.41
1:A:722:A:N3	1:A:2472:C:O2'	2.47	0.41
1:A:1196:C:H2'	1:A:1197:A:C8	2.56	0.41
1:A:1808:U:O2'	1:A:1812:A:N6	2.54	0.41
1:A:2099:G:H2'	1:A:2100:A:C8	2.55	0.41
2:B:70:G:H21	2:B:102:A:H62	1.69	0.41
5:E:75:GLN:OE1	5:E:82:GLN:NE2	2.54	0.41
8:J:97:TYR:HE2	8:J:100:LYS:HD2	1.86	0.41
9:K:39:ILE:HD11	9:K:62:ILE:HD11	2.02	0.41
13:O:8:ASN:OD1	13:O:11:ARG:NH2	2.53	0.41
17:S:37:ASN:HB3	17:S:38:LEU:HD12	2.02	0.41
30:a:1100:U:HO2'	30:a:1180:A:HO2'	1.65	0.41
30:a:1141:G:O6	30:a:1142:C:N4	2.53	0.41
30:a:1266:A:H4'	30:a:1267:G:H8	1.86	0.41
31:b:119:LYS:O	31:b:124:GLY:N	2.47	0.41
51:x:528:ASN:HB2	52:u:71:G:H4'	2.03	0.41
1:A:18:C:H2'	1:A:19:G:C8	2.56	0.41
1:A:86:C:H42	1:A:97:C:N4	2.18	0.41
1:A:146:U:H2'	1:A:147:G:C8	2.56	0.41
1:A:512:G:O2'	1:A:730:U:O2'	2.22	0.41
1:A:853:C:O2	1:A:2473:G:O2'	2.34	0.41
1:A:1379:U:H2'	18:T:57:MET:HE3	2.03	0.41
1:A:1849:U:O2	3:C:201:GLU:N	2.53	0.41
1:A:2247:C:H2'	1:A:2248:G:H8	1.86	0.41
3:C:231:PRO:HD2	3:C:249:PRO:HA	2.02	0.41
14:P:39:ARG:HH12	30:a:353:C:H5''	1.85	0.41
18:T:56:ILE:HG21	18:T:77:ARG:HE	1.86	0.41
30:a:108:C:O2'	45:p:26:ARG:O	2.34	0.41
30:a:984:A:OP2	43:n:41:ARG:NH2	2.54	0.41
30:a:1066:U:H2'	30:a:1067:G:H8	1.84	0.41
30:a:1395:G:H2'	30:a:1396:G:C8	2.55	0.41
30:a:1535:G:H2'	30:a:1536:G:H8	1.85	0.41
37:h:5:ASP:OD1	37:h:5:ASP:N	2.54	0.41
40:k:18:ILE:HG13	40:k:81:LEU:HB3	2.03	0.41
44:o:74:ASP:HB3	44:o:77:ARG:HB3	2.03	0.41
51:x:394:VAL:HG13	51:x:408:SER:HA	2.01	0.41
16:R:61:LYS:N	16:R:96:THR:O	2.44	0.41
17:S:39:THR:O	17:S:41:ARG:N	2.53	0.41
19:U:1:MET:HE1	19:U:26:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:a:1363:C:H2'	30:a:1364:G:C8	2.56	0.41
31:b:76:ALA:HB2	31:b:164:ILE:HD13	2.03	0.41
31:b:164:ILE:HA	31:b:186:ILE:HG23	2.01	0.41
33:d:91:ASP:OD1	33:d:96:ASN:ND2	2.53	0.41
51:x:513:THR:HA	51:x:514:PRO:HD3	1.86	0.41
1:A:253:G:H4'	10:L:59:GLN:HE21	1.86	0.40
1:A:757:C:H2'	1:A:758:A:H8	1.86	0.40
1:A:1327:U:H5	1:A:1365:U:H3	1.69	0.40
1:A:2287:C:O2'	1:A:2456:C:OP2	2.39	0.40
1:A:2318:G:H1'	1:A:2412:G:H21	1.86	0.40
1:A:2446:C:H2'	1:A:2447:A:H8	1.86	0.40
4:D:15:VAL:HB	4:D:25:VAL:HG21	2.03	0.40
13:O:11:ARG:HG3	13:O:100:TYR:CZ	2.56	0.40
14:P:17:LEU:HD22	14:P:84:ILE:HD12	2.03	0.40
20:V:83:ASP:OD1	20:V:83:ASP:N	2.53	0.40
30:a:391:A:C5	30:a:392:G:H1'	2.56	0.40
30:a:890:C:H2'	30:a:891:G:C8	2.56	0.40
30:a:969:A:O2'	30:a:994:C:O2'	2.33	0.40
36:g:16:PRO:HG3	38:i:43:ALA:HA	2.02	0.40
51:x:477:ILE:HA	51:x:480:PHE:HB3	2.03	0.40
1:A:495:U:O4	1:A:626:G:N2	2.52	0.40
1:A:635:C:N4	1:A:636:G:O6	2.54	0.40
1:A:830:A:H2'	1:A:831:U:H4'	2.03	0.40
1:A:906:G:N2	1:A:964:A:OP2	2.54	0.40
1:A:1565:U:H2'	1:A:1566:G:H8	1.86	0.40
1:A:1619:A:H2'	1:A:1620:A:H8	1.86	0.40
1:A:1645:C:H5'	18:T:58:ASN:HD21	1.86	0.40
4:D:28:ILE:HD12	4:D:188:ILE:HD12	2.04	0.40
4:D:124:LYS:HE3	4:D:124:LYS:HB2	1.84	0.40
7:G:98:SER:HB3	7:G:129:GLN:HE22	1.85	0.40
23:Y:15:ARG:HD3	23:Y:15:ARG:HA	1.89	0.40
30:a:345:G:H2'	30:a:346:A:C8	2.55	0.40
30:a:995:C:H2'	30:a:996:A:H8	1.86	0.40
30:a:1359:A:O2'	36:g:33:ASP:OD1	2.36	0.40
47:r:18:PHE:HZ	47:r:60:LEU:HD21	1.86	0.40
1:A:809:U:H4'	1:A:810:G:H5''	2.02	0.40
1:A:999:A:H2'	1:A:1000:G:C8	2.56	0.40
1:A:1302:A:OP2	17:S:99:ARG:NH2	2.51	0.40
1:A:1490:A:H61	1:A:1596:U:H3	1.68	0.40
1:A:2318:G:H22	1:A:2373:U:H1'	1.86	0.40
6:F:67:VAL:HG13	6:F:84:PRO:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:K:97:ARG:NE	30:a:347:C:OP2	2.53	0.40
14:P:39:ARG:HH22	30:a:353:C:H5''	1.87	0.40
17:S:3:ALA:HB3	17:S:107:VAL:HB	2.04	0.40
19:U:13:SER:HA	19:U:17:LYS:HG2	2.03	0.40
27:4:24:ARG:NH1	27:4:25:SER:O	2.52	0.40
30:a:327:G:H2'	30:a:328:G:H8	1.85	0.40
30:a:960:U:H2'	30:a:961:G:C8	2.57	0.40
30:a:1251:G:H1	30:a:1304:U:H3	1.69	0.40
31:b:179:LEU:HD22	31:b:181:ILE:HD11	2.03	0.40
37:h:6:PRO:HB2	37:h:33:LYS:HE3	2.04	0.40
42:m:10:PRO:HB2	42:m:13:LYS:HD3	2.03	0.40
46:q:47:LYS:HB3	46:q:73:LYS:HG2	2.04	0.40
1:A:829:A:C8	3:C:220:VAL:HG21	2.56	0.40
1:A:1401:C:C4	21:W:26:LYS:HB3	2.57	0.40
1:A:1833:G:O6	1:A:1843:G:N2	2.55	0.40
1:A:1998:A:O2'	1:A:2001:G:N3	2.45	0.40
11:M:82:ARG:HE	20:V:12:LYS:HG3	1.86	0.40
13:O:83:LYS:O	13:O:87:GLU:N	2.49	0.40
25:2:36:CYS:HB2	25:2:39:ASP:HB2	2.03	0.40
30:a:511:C:H2'	30:a:512:A:C8	2.56	0.40
34:e:19:ASN:HB3	34:e:34:ALA:HB3	2.03	0.40
50:v:74:C:H2'	50:v:75:G:C8	2.56	0.40
1:A:489:G:O4'	5:E:46:GLN:NE2	2.50	0.40
1:A:567:U:H2'	1:A:568:G:C8	2.57	0.40
1:A:1252:G:O2'	1:A:1275:G:O6	2.40	0.40
1:A:1616:G:OP1	3:C:61:GLN:N	2.50	0.40
1:A:1839:A:H4'	21:W:27:ARG:HG2	2.04	0.40
1:A:1877:A:H3'	1:A:1878:G:H8	1.86	0.40
1:A:2035:C:O2'	1:A:2848:A:N3	2.55	0.40
2:B:40:C:O2	6:F:90:THR:OG1	2.28	0.40
12:N:21:THR:HG22	12:N:44:VAL:HG22	2.03	0.40
30:a:1003:G:O2'	30:a:1004:A:N7	2.55	0.40
30:a:1087:G:N2	30:a:1089:G:H3'	2.36	0.40
32:c:50:SER:OG	32:c:71:LYS:NZ	2.44	0.40
35:f:46:ARG:HB2	35:f:60:TYR:HE2	1.86	0.40
37:h:15:ARG:NH2	37:h:77:LEU:O	2.44	0.40
49:t:28:MET:HE1	49:t:67:VAL:HG11	2.03	0.40
49:t:32:ILE:HG23	49:t:79:LEU:HD21	2.03	0.40
53:w:27:G:N2	53:w:44:G:N3	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	270/272 (99%)	239 (88%)	31 (12%)	0	100	100
4	D	204/206 (99%)	180 (88%)	24 (12%)	0	100	100
5	E	203/205 (99%)	180 (89%)	23 (11%)	0	100	100
6	F	174/176 (99%)	164 (94%)	10 (6%)	0	100	100
7	G	173/175 (99%)	157 (91%)	16 (9%)	0	100	100
8	J	140/142 (99%)	119 (85%)	19 (14%)	2 (1%)	9	39
9	K	120/122 (98%)	103 (86%)	17 (14%)	0	100	100
10	L	144/146 (99%)	134 (93%)	10 (7%)	0	100	100
11	M	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
12	N	117/119 (98%)	103 (88%)	14 (12%)	0	100	100
13	O	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
14	P	113/115 (98%)	104 (92%)	9 (8%)	0	100	100
15	Q	115/117 (98%)	107 (93%)	7 (6%)	1 (1%)	14	49
16	R	99/101 (98%)	84 (85%)	15 (15%)	0	100	100
17	S	107/109 (98%)	91 (85%)	14 (13%)	2 (2%)	6	32
18	T	88/90 (98%)	86 (98%)	2 (2%)	0	100	100
19	U	99/101 (98%)	87 (88%)	12 (12%)	0	100	100
20	V	80/82 (98%)	66 (82%)	14 (18%)	0	100	100
21	W	56/58 (97%)	34 (61%)	22 (39%)	0	100	100
22	X	63/65 (97%)	60 (95%)	3 (5%)	0	100	100
23	Y	56/58 (97%)	54 (96%)	2 (4%)	0	100	100
24	1	52/54 (96%)	43 (83%)	8 (15%)	1 (2%)	6	32
25	2	46/48 (96%)	41 (89%)	5 (11%)	0	100	100
26	3	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
27	4	62/64 (97%)	58 (94%)	4 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	5	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
29	Z	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
31	b	216/218 (99%)	191 (88%)	24 (11%)	1 (0%)	24	63
32	c	204/206 (99%)	183 (90%)	21 (10%)	0	100	100
33	d	193/195 (99%)	179 (93%)	12 (6%)	2 (1%)	12	47
34	e	162/164 (99%)	150 (93%)	12 (7%)	0	100	100
35	f	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
36	g	147/149 (99%)	132 (90%)	15 (10%)	0	100	100
37	h	129/131 (98%)	109 (84%)	19 (15%)	1 (1%)	16	53
38	i	123/125 (98%)	111 (90%)	11 (9%)	1 (1%)	16	53
39	j	93/95 (98%)	85 (91%)	8 (9%)	0	100	100
40	k	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
41	l	134/136 (98%)	115 (86%)	18 (13%)	1 (1%)	18	55
42	m	106/108 (98%)	95 (90%)	10 (9%)	1 (1%)	14	49
43	n	58/60 (97%)	50 (86%)	8 (14%)	0	100	100
44	o	83/85 (98%)	76 (92%)	7 (8%)	0	100	100
45	p	86/88 (98%)	77 (90%)	7 (8%)	2 (2%)	5	28
46	q	82/84 (98%)	73 (89%)	9 (11%)	0	100	100
47	r	62/64 (97%)	55 (89%)	6 (10%)	1 (2%)	7	37
48	s	76/78 (97%)	67 (88%)	9 (12%)	0	100	100
49	t	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	10	43
51	x	339/341 (99%)	292 (86%)	47 (14%)	0	100	100
All	All	5546/5640 (98%)	4959 (89%)	570 (10%)	17 (0%)	37	71

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	S	40	PRO
8	J	133	HIS
15	Q	93	LYS
45	p	47	ALA
49	t	69	LYS
37	h	4	THR
42	m	86	TYR

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Mol	Chain	Res	Type
8	J	132	PRO
45	p	48	GLU
31	b	19	GLN
47	r	28	TYR
24	l	51	GLY
33	d	32	ALA
33	d	33	PRO
17	S	39	THR
38	i	125	PRO
41	l	58	PRO

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	
3	C	220/220 (100%)	220 (100%)	0	100	100
4	D	167/167 (100%)	167 (100%)	0	100	100
5	E	169/169 (100%)	169 (100%)	0	100	100
6	F	151/151 (100%)	150 (99%)	1 (1%)	76	79
7	G	148/148 (100%)	147 (99%)	1 (1%)	76	79
8	J	120/120 (100%)	119 (99%)	1 (1%)	73	77
9	K	101/101 (100%)	101 (100%)	0	100	100
10	L	110/110 (100%)	110 (100%)	0	100	100
11	M	109/109 (100%)	109 (100%)	0	100	100
12	N	99/99 (100%)	99 (100%)	0	100	100
13	O	93/93 (100%)	93 (100%)	0	100	100
14	P	100/100 (100%)	100 (100%)	0	100	100
15	Q	96/96 (100%)	96 (100%)	0	100	100
16	R	83/83 (100%)	83 (100%)	0	100	100
17	S	90/90 (100%)	90 (100%)	0	100	100
18	T	81/81 (100%)	80 (99%)	1 (1%)	63	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	U	85/85 (100%)	85 (100%)	0	100	100
20	V	64/64 (100%)	64 (100%)	0	100	100
21	W	47/47 (100%)	42 (89%)	5 (11%)	6	22
22	X	56/56 (100%)	56 (100%)	0	100	100
23	Y	52/52 (100%)	52 (100%)	0	100	100
24	1	48/48 (100%)	47 (98%)	1 (2%)	47	65
25	2	46/46 (100%)	46 (100%)	0	100	100
26	3	39/39 (100%)	39 (100%)	0	100	100
27	4	54/54 (100%)	53 (98%)	1 (2%)	50	66
28	5	35/35 (100%)	35 (100%)	0	100	100
29	Z	53/53 (100%)	53 (100%)	0	100	100
31	b	189/189 (100%)	189 (100%)	0	100	100
32	c	168/168 (100%)	168 (100%)	0	100	100
33	d	169/169 (100%)	168 (99%)	1 (1%)	78	80
34	e	128/128 (100%)	128 (100%)	0	100	100
35	f	81/81 (100%)	81 (100%)	0	100	100
36	g	125/125 (100%)	124 (99%)	1 (1%)	73	77
37	h	111/111 (100%)	111 (100%)	0	100	100
38	i	98/98 (100%)	98 (100%)	0	100	100
39	j	86/86 (100%)	86 (100%)	0	100	100
40	k	86/86 (100%)	86 (100%)	0	100	100
41	l	114/114 (100%)	114 (100%)	0	100	100
42	m	94/94 (100%)	94 (100%)	0	100	100
43	n	53/53 (100%)	53 (100%)	0	100	100
44	o	80/80 (100%)	80 (100%)	0	100	100
45	p	74/74 (100%)	74 (100%)	0	100	100
46	q	77/77 (100%)	77 (100%)	0	100	100
47	r	56/56 (100%)	56 (100%)	0	100	100
48	s	70/70 (100%)	69 (99%)	1 (1%)	59	71
49	t	66/66 (100%)	66 (100%)	0	100	100
51	x	307/307 (100%)	306 (100%)	1 (0%)	86	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4748/4748 (100%)	4733 (100%)	15 (0%)	84 84

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	F	136	LEU
7	G	108	VAL
8	J	49	VAL
18	T	30	VAL
21	W	8	THR
21	W	33	LEU
21	W	38	ILE
21	W	39	LEU
21	W	47	VAL
24	1	38	LEU
27	4	32	LEU
33	d	151	ILE
36	g	110	LEU
48	s	49	ILE
51	x	611	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (74) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	45	ASN
3	C	142	HIS
3	C	226	ASN
3	C	232	HIS
4	D	14	GLN
4	D	33	ASN
5	E	8	ASN
5	E	10	ASN
5	E	29	ASN
5	E	188	ASN
8	J	8	ASN
8	J	136	GLN
10	L	27	ASN
10	L	59	GLN
10	L	126	ASN
11	M	46	GLN
12	N	57	HIS

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Mol	Chain	Res	Type
12	N	61	GLN
12	N	68	ASN
14	P	36	ASN
15	Q	38	GLN
15	Q	66	ASN
15	Q	72	ASN
16	R	45	ASN
16	R	83	HIS
20	V	37	GLN
21	W	17	ASN
21	W	32	ASN
21	W	34	GLN
22	X	27	ASN
23	Y	37	HIS
23	Y	52	HIS
24	1	40	HIS
24	1	50	ASN
25	2	26	ASN
27	4	40	GLN
27	4	60	GLN
29	Z	20	ASN
31	b	24	ASN
31	b	36	ASN
31	b	77	GLN
31	b	123	ASN
31	b	136	GLN
31	b	203	ASN
33	d	59	HIS
33	d	96	ASN
34	e	45	HIS
36	g	19	ASN
36	g	142	HIS
37	h	68	GLN
38	i	50	GLN
38	i	75	GLN
38	i	126	GLN
39	j	15	HIS
39	j	82	GLN
40	k	24	HIS
40	k	66	GLN
40	k	121	ASN
41	l	109	HIS

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Mol	Chain	Res	Type
42	m	100	GLN
44	o	9	ASN
44	o	42	HIS
44	o	46	HIS
44	o	83	ASN
46	q	33	HIS
47	r	69	GLN
48	s	47	HIS
49	t	84	ASN
51	x	425	ASN
51	x	469	GLN
51	x	503	ASN
51	x	518	GLN
51	x	634	ASN
51	x	709	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2878/2925 (98%)	977 (33%)	54 (1%)
2	B	111/112 (99%)	37 (33%)	3 (2%)
30	a	1532/1533 (99%)	420 (27%)	0
50	v	86/87 (98%)	20 (23%)	0
52	u	75/76 (98%)	32 (42%)	0
53	w	74/75 (98%)	27 (36%)	0
All	All	4756/4808 (98%)	1513 (31%)	57 (1%)

All (1513) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	U
1	A	10	A
1	A	13	A
1	A	20	C
1	A	29	U
1	A	30	G
1	A	34	U
1	A	35	G
1	A	36	G
1	A	39	C
1	A	45	G

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Mol	Chain	Res	Type
1	A	46	C
1	A	49	A
1	A	54	G
1	A	60	G
1	A	62	C
1	A	63	G
1	A	64	A
1	A	65	A
1	A	71	A
1	A	75	G
1	A	76	C
1	A	77	U
1	A	78	U
1	A	79	C
1	A	83	G
1	A	84	A
1	A	85	G
1	A	86	C
1	A	87	U
1	A	89	U
1	A	90	A
1	A	92	G
1	A	93	C
1	A	96	G
1	A	101	G
1	A	106	G
1	A	109	G
1	A	117	A
1	A	119	U
1	A	122	G
1	A	123	G
1	A	125	A
1	A	126	A
1	A	127	C
1	A	128	C
1	A	146	U
1	A	162	A
1	A	163	U
1	A	164	U
1	A	167	U
1	A	174	U
1	A	175	G

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Mol	Chain	Res	Type
1	A	176	A
1	A	177	G
1	A	182	C
1	A	184	G
1	A	187	C
1	A	188	C
1	A	189	G
1	A	192	G
1	A	199	A
1	A	200	A
1	A	201	C
1	A	202	A
1	A	207	A
1	A	208	G
1	A	209	U
1	A	215	G
1	A	216	A
1	A	218	G
1	A	219	A
1	A	222	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	231	A
1	A	232	U
1	A	233	G
1	A	234	C
1	A	244	A
1	A	251	G
1	A	252	C
1	A	253	G
1	A	258	A
1	A	266	U
1	A	267	C
1	A	268	A
1	A	269	G
1	A	270	C
1	A	272	C
1	A	275	A
1	A	282	G
1	A	284	C
1	A	285	U

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Mol	Chain	Res	Type
1	A	286	U
1	A	287	G
1	A	291	C
1	A	297	G
1	A	298	U
1	A	301	U
1	A	302	A
1	A	307	A
1	A	308	C
1	A	310	C
1	A	338	G
1	A	345	A
1	A	346	G
1	A	348	U
1	A	349	C
1	A	354	A
1	A	360	C
1	A	361	G
1	A	367	G
1	A	368	G
1	A	373	A
1	A	374	A
1	A	375	C
1	A	389	A
1	A	393	U
1	A	397	U
1	A	399	C
1	A	407	A
1	A	410	G
1	A	411	G
1	A	412	A
1	A	417	G
1	A	418	A
1	A	419	G
1	A	421	A
1	A	422	C
1	A	424	G
1	A	426	G
1	A	430	C
1	A	432	C
1	A	433	G
1	A	434	U

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Mol	Chain	Res	Type
1	A	441	C
1	A	442	C
1	A	443	G
1	A	444	U
1	A	445	C
1	A	446	G
1	A	447	G
1	A	448	A
1	A	451	C
1	A	453	G
1	A	458	G
1	A	459	A
1	A	465	U
1	A	471	G
1	A	482	C
1	A	483	C
1	A	489	G
1	A	491	C
1	A	495	U
1	A	496	A
1	A	498	U
1	A	502	C
1	A	503	C
1	A	504	A
1	A	505	G
1	A	511	U
1	A	514	G
1	A	524	A
1	A	526	A
1	A	528	G
1	A	537	A
1	A	540	G
1	A	542	G
1	A	544	G
1	A	548	A
1	A	550	G
1	A	551	A
1	A	552	G
1	A	553	A
1	A	554	U
1	A	555	C
1	A	556	C

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Mol	Chain	Res	Type
1	A	558	G
1	A	564	G
1	A	566	G
1	A	568	G
1	A	573	C
1	A	575	A
1	A	576	G
1	A	577	U
1	A	578	A
1	A	579	G
1	A	582	A
1	A	584	A
1	A	589	G
1	A	590	U
1	A	591	U
1	A	592	A
1	A	593	A
1	A	595	G
1	A	599	G
1	A	605	G
1	A	607	G
1	A	616	A
1	A	619	A
1	A	630	A
1	A	631	G
1	A	632	U
1	A	633	U
1	A	636	G
1	A	638	U
1	A	646	A
1	A	647	A
1	A	648	G
1	A	649	G
1	A	658	A
1	A	659	A
1	A	667	A
1	A	673	A
1	A	674	G
1	A	683	A
1	A	686	C
1	A	689	A
1	A	690	A

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Mol	Chain	Res	Type
1	A	691	U
1	A	692	A
1	A	698	C
1	A	700	U
1	A	701	G
1	A	702	A
1	A	703	G
1	A	709	G
1	A	711	U
1	A	716	G
1	A	717	A
1	A	718	C
1	A	725	C
1	A	732	A
1	A	733	U
1	A	734	C
1	A	740	A
1	A	742	G
1	A	754	G
1	A	765	A
1	A	766	C
1	A	773	G
1	A	777	C
1	A	787	C
1	A	788	G
1	A	792	G
1	A	794	U
1	A	795	G
1	A	796	A
1	A	799	A
1	A	800	G
1	A	804	G
1	A	807	G
1	A	810	G
1	A	811	A
1	A	812	G
1	A	814	U
1	A	818	G
1	A	822	G
1	A	823	G
1	A	824	G
1	A	829	A

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Mol	Chain	Res	Type
1	A	830	A
1	A	831	U
1	A	832	G
1	A	836	A
1	A	837	U
1	A	838	C
1	A	839	G
1	A	844	U
1	A	845	G
1	A	846	G
1	A	847	A
1	A	852	G
1	A	858	U
1	A	859	C
1	A	864	C
1	A	866	A
1	A	869	U
1	A	874	U
1	A	875	U
1	A	892	U
1	A	895	G
1	A	903	G
1	A	905	G
1	A	906	G
1	A	907	U
1	A	908	A
1	A	913	A
1	A	914	C
1	A	916	G
1	A	928	G
1	A	929	G
1	A	931	C
1	A	934	U
1	A	935	A
1	A	936	C
1	A	937	C
1	A	939	G
1	A	940	G
1	A	942	U
1	A	943	A
1	A	944	C
1	A	947	A

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Mol	Chain	Res	Type
1	A	954	U
1	A	957	A
1	A	958	A
1	A	959	C
1	A	960	U
1	A	961	C
1	A	962	C
1	A	964	A
1	A	966	U
1	A	970	A
1	A	973	G
1	A	977	U
1	A	979	U
1	A	987	A
1	A	990	C
1	A	991	A
1	A	992	G
1	A	1003	A
1	A	1004	U
1	A	1007	G
1	A	1016	U
1	A	1019	A
1	A	1020	A
1	A	1027	A
1	A	1028	C
1	A	1029	A
1	A	1031	C
1	A	1034	A
1	A	1035	G
1	A	1036	A
1	A	1037	C
1	A	1041	C
1	A	1042	A
1	A	1054	A
1	A	1058	U
1	A	1059	A
1	A	1065	U
1	A	1066	A
1	A	1068	G
1	A	1072	A
1	A	1073	A
1	A	1079	U

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Mol	Chain	Res	Type
1	A	1091	U
1	A	1101	G
1	A	1102	G
1	A	1103	A
1	A	1106	U
1	A	1107	U
1	A	1108	G
1	A	1109	G
1	A	1110	C
1	A	1111	U
1	A	1114	G
1	A	1116	A
1	A	1117	G
1	A	1118	C
1	A	1119	A
1	A	1120	G
1	A	1121	C
1	A	1123	A
1	A	1124	C
1	A	1125	C
1	A	1126	A
1	A	1127	U
1	A	1128	U
1	A	1134	A
1	A	1137	G
1	A	1143	U
1	A	1146	C
1	A	1158	G
1	A	1159	U
1	A	1160	G
1	A	1161	A
1	A	1173	A
1	A	1174	A
1	A	1177	G
1	A	1178	U
1	A	1179	A
1	A	1180	C
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1188	A
1	A	1189	A

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Mol	Chain	Res	Type
1	A	1203	G
1	A	1227	G
1	A	1229	U
1	A	1236	G
1	A	1244	A
1	A	1245	G
1	A	1248	C
1	A	1251	U
1	A	1252	G
1	A	1258	A
1	A	1259	G
1	A	1260	A
1	A	1261	C
1	A	1267	G
1	A	1270	C
1	A	1275	G
1	A	1276	G
1	A	1278	G
1	A	1282	U
1	A	1287	A
1	A	1288	G
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1297	C
1	A	1299	G
1	A	1301	U
1	A	1302	A
1	A	1305	A
1	A	1306	G
1	A	1307	U
1	A	1308	A
1	A	1311	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1319	G
1	A	1323	A
1	A	1325	A
1	A	1326	A
1	A	1328	C

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Mol	Chain	Res	Type
1	A	1333	C
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1351	U
1	A	1352	U
1	A	1353	C
1	A	1359	G
1	A	1360	A
1	A	1361	A
1	A	1364	C
1	A	1365	U
1	A	1367	G
1	A	1368	U
1	A	1369	C
1	A	1370	C
1	A	1371	G
1	A	1372	C
1	A	1375	A
1	A	1379	U
1	A	1380	U
1	A	1381	A
1	A	1382	G
1	A	1384	C
1	A	1385	G
1	A	1388	A
1	A	1389	C
1	A	1397	G
1	A	1398	A
1	A	1399	G
1	A	1402	C
1	A	1403	G
1	A	1404	A
1	A	1405	A
1	A	1406	A
1	A	1408	G
1	A	1409	C
1	A	1410	G
1	A	1411	U
1	A	1412	A
1	A	1417	A
1	A	1418	U

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Mol	Chain	Res	Type
1	A	1419	G
1	A	1422	C
1	A	1423	A
1	A	1424	A
1	A	1425	C
1	A	1426	A
1	A	1427	G
1	A	1431	G
1	A	1432	A
1	A	1434	A
1	A	1435	U
1	A	1436	U
1	A	1437	C
1	A	1442	A
1	A	1449	C
1	A	1458	U
1	A	1459	U
1	A	1460	G
1	A	1464	A
1	A	1465	A
1	A	1466	U
1	A	1472	G
1	A	1473	A
1	A	1474	C
1	A	1475	G
1	A	1476	C
1	A	1489	U
1	A	1490	A
1	A	1491	A
1	A	1498	U
1	A	1499	A
1	A	1500	U
1	A	1502	G
1	A	1505	U
1	A	1506	A
1	A	1507	U
1	A	1508	C
1	A	1516	A
1	A	1521	G
1	A	1525	G
1	A	1526	G
1	A	1527	C

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Mol	Chain	Res	Type
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1531	G
1	A	1533	A
1	A	1539	C
1	A	1540	A
1	A	1542	A
1	A	1543	U
1	A	1544	C
1	A	1547	U
1	A	1550	C
1	A	1551	C
1	A	1552	C
1	A	1553	A
1	A	1558	G
1	A	1559	C
1	A	1560	U
1	A	1561	G
1	A	1566	G
1	A	1567	U
1	A	1568	G
1	A	1569	A
1	A	1570	U
1	A	1571	G
1	A	1576	G
1	A	1594	G
1	A	1608	A
1	A	1614	A
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1631	A
1	A	1632	G
1	A	1634	U
1	A	1645	C
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1658	G
1	A	1661	A
1	A	1672	A

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Mol	Chain	Res	Type
1	A	1678	G
1	A	1679	A
1	A	1680	A
1	A	1683	C
1	A	1691	A
1	A	1692	U
1	A	1693	C
1	A	1696	G
1	A	1697	A
1	A	1699	A
1	A	1700	A
1	A	1708	U
1	A	1712	G
1	A	1713	A
1	A	1714	A
1	A	1716	U
1	A	1719	G
1	A	1720	C
1	A	1722	A
1	A	1724	A
1	A	1734	A
1	A	1738	U
1	A	1739	C
1	A	1740	G
1	A	1741	G
1	A	1744	G
1	A	1745	A
1	A	1746	A
1	A	1748	G
1	A	1756	U
1	A	1757	G
1	A	1758	U
1	A	1759	U
1	A	1760	A
1	A	1766	C
1	A	1768	A
1	A	1771	C
1	A	1774	A
1	A	1776	A
1	A	1777	G
1	A	1778	A
1	A	1779	G

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Mol	Chain	Res	Type
1	A	1781	C
1	A	1782	G
1	A	1785	G
1	A	1786	U
1	A	1787	G
1	A	1789	A
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1797	A
1	A	1799	G
1	A	1801	G
1	A	1802	A
1	A	1804	U
1	A	1809	A
1	A	1810	G
1	A	1811	C
1	A	1813	A
1	A	1814	A
1	A	1817	C
1	A	1829	C
1	A	1830	G
1	A	1831	A
1	A	1836	G
1	A	1837	U
1	A	1840	G
1	A	1841	G
1	A	1843	G
1	A	1845	A
1	A	1846	G
1	A	1848	A
1	A	1856	U
1	A	1858	A
1	A	1871	G
1	A	1872	C
1	A	1877	A
1	A	1878	G
1	A	1882	A
1	A	1883	A
1	A	1884	G
1	A	1885	A
1	A	1887	G

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Mol	Chain	Res	Type
1	A	1889	G
1	A	1891	G
1	A	1898	G
1	A	1899	U
1	A	1902	G
1	A	1905	A
1	A	1913	A
1	A	1928	A
1	A	1930	A
1	A	1932	G
1	A	1935	G
1	A	1943	C
1	A	1944	U
1	A	1945	A
1	A	1953	C
1	A	1956	A
1	A	1958	G
1	A	1959	G
1	A	1963	C
1	A	1965	A
1	A	1966	A
1	A	1967	A
1	A	1968	U
1	A	1969	U
1	A	1972	U
1	A	1973	U
1	A	1977	G
1	A	1978	G
1	A	1981	A
1	A	1984	U
1	A	1989	A
1	A	1991	C
1	A	1992	C
1	A	1993	G
1	A	1995	A
1	A	1996	C
1	A	1999	A
1	A	2000	A
1	A	2001	G
1	A	2003	C
1	A	2010	A
1	A	2021	G

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Mol	Chain	Res	Type
1	A	2022	U
1	A	2024	U
1	A	2026	A
1	A	2033	G
1	A	2038	G
1	A	2047	A
1	A	2051	U
1	A	2052	A
1	A	2053	C
1	A	2055	U
1	A	2059	A
1	A	2062	A
1	A	2063	U
1	A	2064	G
1	A	2065	C
1	A	2068	G
1	A	2070	U
1	A	2072	C
1	A	2075	G
1	A	2079	C
1	A	2080	A
1	A	2081	G
1	A	2084	C
1	A	2085	G
1	A	2086	G
1	A	2089	A
1	A	2090	G
1	A	2091	A
1	A	2095	C
1	A	2098	G
1	A	2105	U
1	A	2109	G
1	A	2113	C
1	A	2114	C
1	A	2119	A
1	A	2120	U
1	A	2121	U
1	A	2122	G
1	A	2123	A
1	A	2126	G
1	A	2127	U
1	A	2128	U

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Mol	Chain	Res	Type
1	A	2131	U
1	A	2133	C
1	A	2134	A
1	A	2135	G
1	A	2140	U
1	A	2141	A
1	A	2145	G
1	A	2146	A
1	A	2147	U
1	A	2148	A
1	A	2152	A
1	A	2155	A
1	A	2156	G
1	A	2159	U
1	A	2160	U
1	A	2161	G
1	A	2162	G
1	A	2175	C
1	A	2176	A
1	A	2177	G
1	A	2185	G
1	A	2192	U
1	A	2200	A
1	A	2201	U
1	A	2203	C
1	A	2205	A
1	A	2206	C
1	A	2209	U
1	A	2210	G
1	A	2212	C
1	A	2213	U
1	A	2219	G
1	A	2222	C
1	A	2227	A
1	A	2231	C
1	A	2232	G
1	A	2233	C
1	A	2240	U
1	A	2241	A
1	A	2245	G
1	A	2246	G
1	A	2249	G

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Mol	Chain	Res	Type
1	A	2254	A
1	A	2255	C
1	A	2256	A
1	A	2259	G
1	A	2260	U
1	A	2262	A
1	A	2268	G
1	A	2277	C
1	A	2278	U
1	A	2281	G
1	A	2288	G
1	A	2296	A
1	A	2297	A
1	A	2308	G
1	A	2312	C
1	A	2316	A
1	A	2317	A
1	A	2318	G
1	A	2324	C
1	A	2325	U
1	A	2326	C
1	A	2331	U
1	A	2333	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2338	A
1	A	2340	A
1	A	2341	U
1	A	2342	C
1	A	2343	A
1	A	2344	U
1	A	2345	U
1	A	2348	C
1	A	2349	A
1	A	2350	G
1	A	2351	A
1	A	2353	U
1	A	2354	G
1	A	2355	U
1	A	2356	A
1	A	2360	G

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Mol	Chain	Res	Type
1	A	2363	C
1	A	2364	A
1	A	2373	U
1	A	2375	A
1	A	2376	C
1	A	2379	C
1	A	2383	A
1	A	2387	A
1	A	2390	A
1	A	2401	G
1	A	2412	G
1	A	2414	C
1	A	2415	U
1	A	2420	G
1	A	2425	G
1	A	2431	U
1	A	2432	C
1	A	2435	C
1	A	2439	G
1	A	2452	U
1	A	2453	C
1	A	2454	A
1	A	2455	A
1	A	2457	G
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2464	A
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2471	C
1	A	2474	G
1	A	2477	A
1	A	2478	U
1	A	2479	A
1	A	2480	A
1	A	2481	C
1	A	2491	U
1	A	2494	C
1	A	2497	A
1	A	2504	C

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Mol	Chain	Res	Type
1	A	2505	A
1	A	2507	A
1	A	2510	G
1	A	2514	G
1	A	2516	G
1	A	2520	U
1	A	2523	G
1	A	2527	C
1	A	2531	G
1	A	2532	A
1	A	2533	U
1	A	2534	G
1	A	2542	A
1	A	2547	A
1	A	2549	C
1	A	2554	G
1	A	2558	G
1	A	2563	C
1	A	2564	G
1	A	2567	C
1	A	2571	A
1	A	2579	G
1	A	2583	U
1	A	2593	A
1	A	2595	A
1	A	2596	G
1	A	2598	G
1	A	2601	A
1	A	2602	C
1	A	2603	G
1	A	2607	G
1	A	2611	G
1	A	2613	U
1	A	2614	U
1	A	2615	C
1	A	2625	U
1	A	2629	A
1	A	2630	C
1	A	2631	A
1	A	2632	G
1	A	2638	U
1	A	2642	U

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Mol	Chain	Res	Type
1	A	2643	A
1	A	2644	U
1	A	2648	U
1	A	2649	C
1	A	2650	G
1	A	2651	C
1	A	2652	G
1	A	2654	G
1	A	2658	A
1	A	2659	G
1	A	2660	G
1	A	2661	A
1	A	2674	G
1	A	2676	U
1	A	2689	A
1	A	2692	G
1	A	2695	C
1	A	2696	C
1	A	2709	C
1	A	2714	G
1	A	2718	U
1	A	2719	A
1	A	2720	C
1	A	2728	U
1	A	2742	C
1	A	2743	G
1	A	2747	G
1	A	2752	C
1	A	2753	U
1	A	2754	A
1	A	2755	U
1	A	2756	G
1	A	2758	G
1	A	2762	A
1	A	2763	C
1	A	2764	G
1	A	2768	U
1	A	2770	A
1	A	2771	G
1	A	2773	G
1	A	2774	C
1	A	2777	A

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Mol	Chain	Res	Type
1	A	2781	C
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2794	A
1	A	2806	G
1	A	2807	A
1	A	2808	U
1	A	2813	U
1	A	2818	C
1	A	2820	U
1	A	2821	U
1	A	2823	C
1	A	2824	G
1	A	2825	C
1	A	2831	A
1	A	2843	G
1	A	2844	A
1	A	2845	A
1	A	2848	A
1	A	2859	G
1	A	2860	A
1	A	2862	A
1	A	2868	G
1	A	2886	C
1	A	2887	A
1	A	2892	G
1	A	2893	A
1	A	2897	G
1	A	2898	A
1	A	2899	C
1	A	2900	A
1	A	2901	G
1	A	2904	A
1	A	2905	C
1	A	2907	A
1	A	2908	A
1	A	2909	U
1	A	2911	G
1	A	2916	A
1	A	2917	G
1	A	2925	C

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Mol	Chain	Res	Type
2	B	10	G
2	B	11	A
2	B	12	U
2	B	13	A
2	B	15	C
2	B	19	G
2	B	22	G
2	B	23	U
2	B	28	C
2	B	32	U
2	B	33	U
2	B	38	U
2	B	39	A
2	B	40	C
2	B	42	G
2	B	48	G
2	B	49	G
2	B	50	A
2	B	51	A
2	B	52	G
2	B	53	U
2	B	54	U
2	B	55	A
2	B	59	U
2	B	60	C
2	B	62	U
2	B	63	C
2	B	66	C
2	B	80	G
2	B	82	G
2	B	86	U
2	B	87	U
2	B	88	C
2	B	97	A
2	B	101	U
2	B	107	G
2	B	110	G
30	a	9	G
30	a	10	A
30	a	11	G
30	a	17	G
30	a	24	G

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Mol	Chain	Res	Type
30	a	31	A
30	a	32	C
30	a	33	G
30	a	34	A
30	a	39	U
30	a	41	G
30	a	44	G
30	a	49	C
30	a	50	C
30	a	51	U
30	a	52	A
30	a	53	A
30	a	54	U
30	a	60	C
30	a	65	C
30	a	66	G
30	a	74	A
30	a	76	A
30	a	77	U
30	a	78	G
30	a	84	U
30	a	85	U
30	a	87	C
30	a	89	C
30	a	90	C
30	a	93	G
30	a	98	U
30	a	99	A
30	a	106	G
30	a	114	A
30	a	117	A
30	a	118	A
30	a	119	C
30	a	125	G
30	a	128	A
30	a	129	A
30	a	130	C
30	a	137	G
30	a	140	A
30	a	141	G
30	a	143	C
30	a	144	U

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Mol	Chain	Res	Type
30	a	153	U
30	a	154	C
30	a	158	G
30	a	162	C
30	a	172	U
30	a	181	G
30	a	182	U
30	a	189	A
30	a	195	A
30	a	197	G
30	a	198	G
30	a	207	U
30	a	208	A
30	a	209	A
30	a	210	A
30	a	211	A
30	a	218	U
30	a	219	U
30	a	222	G
30	a	234	A
30	a	246	G
30	a	247	G
30	a	248	C
30	a	249	G
30	a	253	U
30	a	255	G
30	a	257	U
30	a	259	G
30	a	273	G
30	a	274	G
30	a	275	C
30	a	287	A
30	a	289	G
30	a	297	G
30	a	306	A
30	a	307	G
30	a	314	A
30	a	336	C
30	a	337	A
30	a	338	C
30	a	340	G
30	a	344	A

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Mol	Chain	Res	Type
30	a	352	A
30	a	353	C
30	a	355	G
30	a	356	G
30	a	359	G
30	a	360	C
30	a	361	A
30	a	362	G
30	a	373	U
30	a	374	C
30	a	375	U
30	a	380	C
30	a	383	U
30	a	384	G
30	a	385	G
30	a	392	G
30	a	395	U
30	a	396	G
30	a	400	G
30	a	405	A
30	a	406	C
30	a	414	G
30	a	419	A
30	a	420	U
30	a	421	G
30	a	429	U
30	a	430	C
30	a	431	G
30	a	432	G
30	a	436	G
30	a	437	U
30	a	438	A
30	a	447	U
30	a	456	A
30	a	457	A
30	a	459	A
30	a	460	A
30	a	461	C
30	a	466	G
30	a	467	C
30	a	472	C
30	a	474	A

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Mol	Chain	Res	Type
30	a	475	A
30	a	476	U
30	a	477	A
30	a	478	G
30	a	481	C
30	a	482	G
30	a	483	G
30	a	485	A
30	a	487	C
30	a	490	G
30	a	491	A
30	a	494	G
30	a	495	U
30	a	504	A
30	a	506	A
30	a	508	A
30	a	517	U
30	a	518	A
30	a	519	A
30	a	520	C
30	a	526	G
30	a	527	C
30	a	533	G
30	a	536	G
30	a	540	U
30	a	541	A
30	a	542	A
30	a	551	U
30	a	556	A
30	a	559	G
30	a	564	C
30	a	568	A
30	a	569	A
30	a	573	U
30	a	575	G
30	a	576	G
30	a	577	G
30	a	581	A
30	a	582	A
30	a	584	G
30	a	585	G
30	a	586	G

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Mol	Chain	Res	Type
30	a	588	U
30	a	593	G
30	a	597	G
30	a	627	C
30	a	641	G
30	a	642	U
30	a	643	C
30	a	662	U
30	a	674	A
30	a	675	G
30	a	682	G
30	a	683	G
30	a	696	A
30	a	711	A
30	a	723	G
30	a	726	C
30	a	727	A
30	a	732	U
30	a	733	G
30	a	737	A
30	a	740	G
30	a	742	G
30	a	743	A
30	a	756	U
30	a	757	A
30	a	758	A
30	a	764	G
30	a	769	G
30	a	782	G
30	a	786	A
30	a	802	U
30	a	803	A
30	a	812	G
30	a	824	A
30	a	826	C
30	a	838	A
30	a	841	G
30	a	845	G
30	a	849	G
30	a	850	U
30	a	853	C
30	a	855	G

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Mol	Chain	Res	Type
30	a	856	C
30	a	861	U
30	a	863	G
30	a	865	G
30	a	875	A
30	a	879	A
30	a	883	A
30	a	889	C
30	a	899	A
30	a	909	C
30	a	910	A
30	a	924	A
30	a	925	A
30	a	930	U
30	a	932	G
30	a	934	C
30	a	942	C
30	a	944	C
30	a	945	A
30	a	963	G
30	a	964	G
30	a	966	U
30	a	967	U
30	a	970	U
30	a	975	A
30	a	978	A
30	a	979	A
30	a	981	G
30	a	982	C
30	a	984	A
30	a	985	A
30	a	986	G
30	a	987	A
30	a	990	C
30	a	993	A
30	a	999	U
30	a	1000	C
30	a	1002	U
30	a	1003	G
30	a	1008	C
30	a	1009	C
30	a	1010	U

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Mol	Chain	Res	Type
30	a	1011	C
30	a	1012	U
30	a	1013	G
30	a	1014	A
30	a	1015	C
30	a	1017	A
30	a	1019	C
30	a	1023	G
30	a	1024	A
30	a	1028	A
30	a	1030	G
30	a	1033	G
30	a	1035	C
30	a	1036	C
30	a	1039	U
30	a	1041	C
30	a	1042	G
30	a	1046	G
30	a	1047	C
30	a	1051	G
30	a	1052	U
30	a	1053	G
30	a	1055	C
30	a	1058	G
30	a	1060	G
30	a	1064	C
30	a	1065	A
30	a	1070	U
30	a	1071	G
30	a	1074	G
30	a	1075	U
30	a	1077	A
30	a	1085	U
30	a	1088	U
30	a	1093	U
30	a	1094	G
30	a	1095	U
30	a	1100	U
30	a	1102	A
30	a	1103	A
30	a	1104	G
30	a	1105	U

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Mol	Chain	Res	Type
30	a	1111	A
30	a	1112	A
30	a	1114	G
30	a	1123	C
30	a	1134	G
30	a	1140	A
30	a	1142	C
30	a	1143	A
30	a	1144	U
30	a	1145	U
30	a	1146	C
30	a	1148	G
30	a	1149	U
30	a	1151	G
30	a	1154	C
30	a	1166	A
30	a	1169	G
30	a	1176	A
30	a	1177	C
30	a	1190	G
30	a	1192	U
30	a	1193	G
30	a	1199	G
30	a	1200	A
30	a	1205	A
30	a	1206	A
30	a	1210	A
30	a	1211	U
30	a	1221	U
30	a	1222	A
30	a	1223	U
30	a	1224	G
30	a	1234	A
30	a	1236	A
30	a	1240	G
30	a	1243	C
30	a	1259	A
30	a	1266	A
30	a	1267	G
30	a	1269	G
30	a	1288	A
30	a	1289	A

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Mol	Chain	Res	Type
30	a	1294	A
30	a	1295	C
30	a	1296	A
30	a	1306	U
30	a	1307	C
30	a	1308	A
30	a	1309	G
30	a	1311	U
30	a	1312	C
30	a	1313	G
30	a	1314	G
30	a	1315	A
30	a	1321	G
30	a	1323	C
30	a	1324	U
30	a	1326	C
30	a	1331	C
30	a	1332	G
30	a	1335	U
30	a	1336	G
30	a	1340	G
30	a	1345	U
30	a	1354	U
30	a	1355	A
30	a	1356	G
30	a	1366	A
30	a	1368	C
30	a	1371	C
30	a	1372	A
30	a	1373	U
30	a	1376	C
30	a	1379	G
30	a	1388	G
30	a	1390	U
30	a	1394	G
30	a	1398	C
30	a	1402	U
30	a	1403	A
30	a	1406	C
30	a	1407	A
30	a	1408	C
30	a	1409	C

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Mol	Chain	Res	Type
30	a	1410	G
30	a	1411	C
30	a	1434	A
30	a	1435	A
30	a	1438	C
30	a	1439	C
30	a	1443	A
30	a	1451	A
30	a	1452	G
30	a	1455	A
30	a	1460	U
30	a	1461	U
30	a	1462	U
30	a	1463	A
30	a	1464	G
30	a	1486	A
30	a	1488	A
30	a	1494	U
30	a	1497	G
30	a	1499	G
30	a	1500	U
30	a	1501	G
30	a	1502	A
30	a	1503	A
30	a	1507	G
30	a	1509	A
30	a	1513	A
30	a	1516	U
30	a	1517	A
30	a	1518	G
30	a	1520	C
30	a	1526	G
30	a	1527	G
30	a	1529	A
30	a	1530	G
30	a	1539	G
30	a	1540	G
50	v	3	C
50	v	8	U
50	v	9	G
50	v	14	A
50	v	16	U

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Mol	Chain	Res	Type
50	v	17	U
50	v	19	G
50	v	20	U
50	v	21	A
50	v	22	G
50	v	23	A
50	v	24	C
50	v	36	A
50	v	44	G
50	v	50	A
50	v	51	A
50	v	58	U
50	v	67	C
50	v	68	A
50	v	87	A
52	u	3	C
52	u	5	G
52	u	7	A
52	u	8	U
52	u	9	A
52	u	16	U
52	u	18	G
52	u	19	G
52	u	20	U
52	u	22	G
52	u	23	A
52	u	32	U
52	u	33	U
52	u	41	C
52	u	44	G
52	u	45	U
52	u	46	G
52	u	47	U
52	u	48	C
52	u	52	G
52	u	55	U
52	u	56	C
52	u	57	G
52	u	58	A
52	u	59	U
52	u	61	C
52	u	70	G

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Mol	Chain	Res	Type
52	u	71	G
52	u	73	A
52	u	74	C
52	u	75	C
52	u	76	A
53	w	3	C
53	w	6	G
53	w	9	A
53	w	13	C
53	w	14	A
53	w	18	G
53	w	19	G
53	w	20	U
53	w	21	A
53	w	33	U
53	w	35	A
53	w	37	A
53	w	39	U
53	w	43	C
53	w	44	G
53	w	45	U
53	w	47	U
53	w	48	C
53	w	50	U
53	w	58	A
53	w	59	U
53	w	60	U
53	w	61	C
53	w	68	C
53	w	71	G
53	w	74	C
53	w	76	A

All (57) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	88	G
1	A	92	G
1	A	181	G
1	A	252	C
1	A	411	G
1	A	441	C

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Mol	Chain	Res	Type
1	A	447	G
1	A	455	G
1	A	459	A
1	A	549	A
1	A	575	A
1	A	576	G
1	A	594	C
1	A	689	A
1	A	756	U
1	A	810	G
1	A	848	G
1	A	855	G
1	A	1032	C
1	A	1036	A
1	A	1041	C
1	A	1172	A
1	A	1210	A
1	A	1243	A
1	A	1250	G
1	A	1266	A
1	A	1269	A
1	A	1305	A
1	A	1339	A
1	A	1351	U
1	A	1448	U
1	A	1525	G
1	A	1529	G
1	A	1530	G
1	A	1565	U
1	A	1631	A
1	A	1671	G
1	A	1784	A
1	A	1813	A
1	A	1828	G
1	A	1840	G
1	A	1882	A
1	A	2119	A
1	A	2127	U
1	A	2155	A
1	A	2254	A
1	A	2295	A
1	A	2316	A

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Mol	Chain	Res	Type
1	A	2452	U
1	A	2454	A
1	A	2468	A
1	A	2631	A
1	A	2805	A
1	A	2904	A
2	B	37	A
2	B	48	G
2	B	49	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
1	A	5

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	182:C	O3'	183:A	P	6.24
1	A	1449:C	O3'	1450:C	P	4.30
1	A	1452:C	O3'	1453:A	P	4.27

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	183:A	O3'	184:G	P	3.36
1	A	1451:U	O3'	1452:C	P	3.33

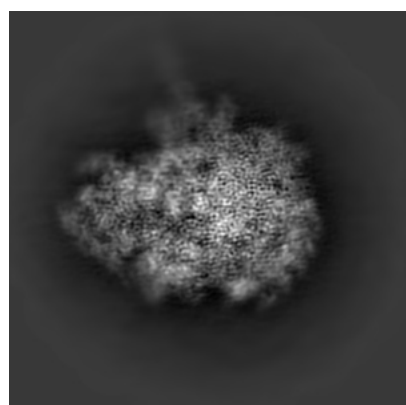
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0270. These allow visual inspection of the internal detail of the map and identification of artifacts.

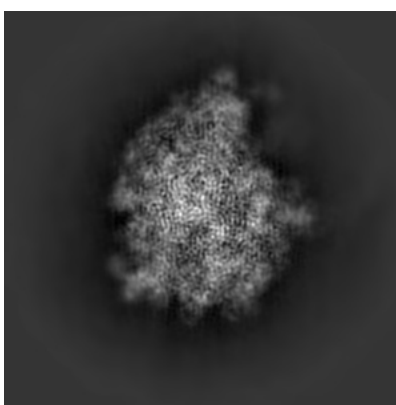
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

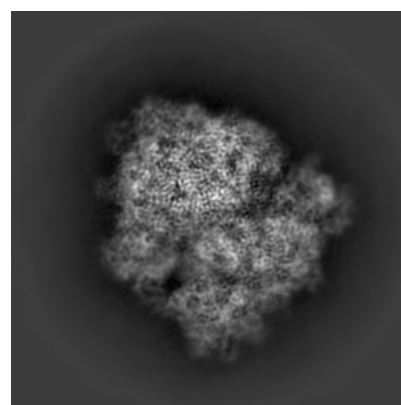
6.1.1 Primary map



X



Y

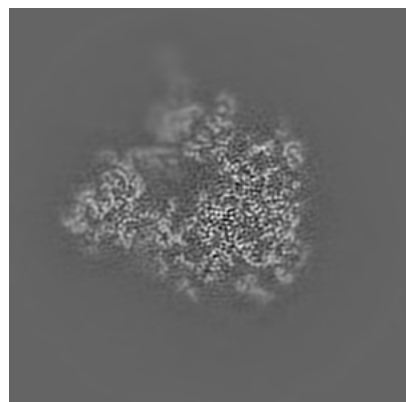


Z

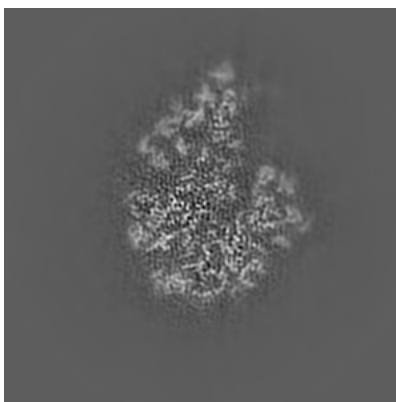
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

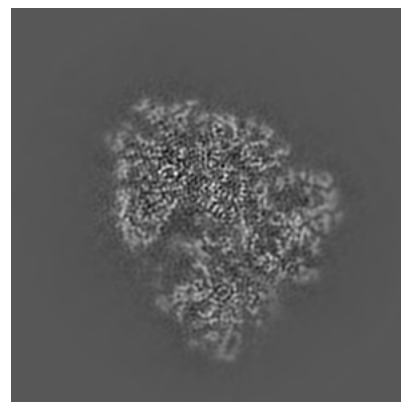
6.2.1 Primary map



X Index: 180



Y Index: 180

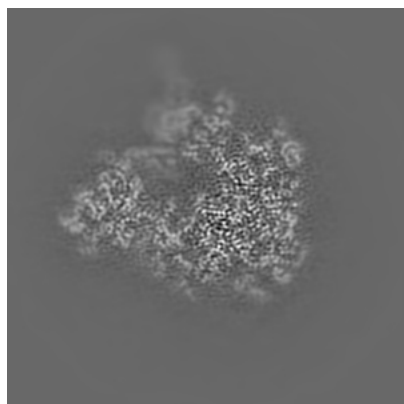


Z Index: 180

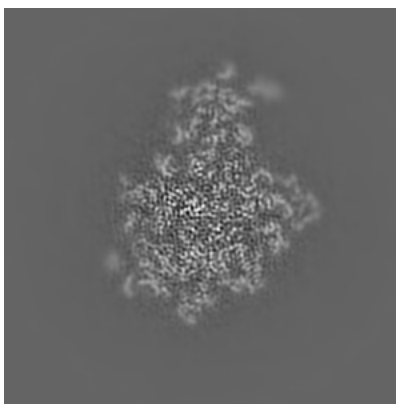
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

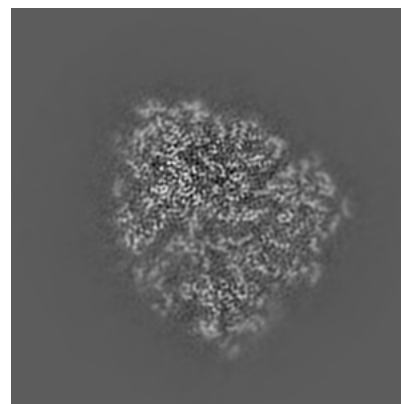
6.3.1 Primary map



X Index: 179



Y Index: 195

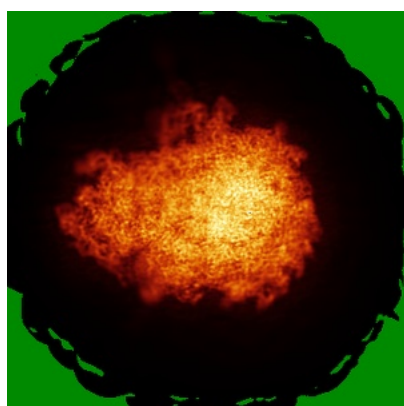


Z Index: 186

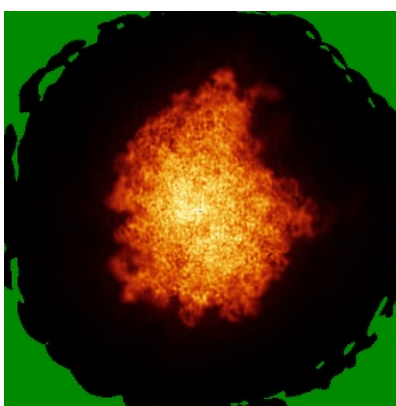
The images above show the largest variance slices of the map in three orthogonal directions.

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

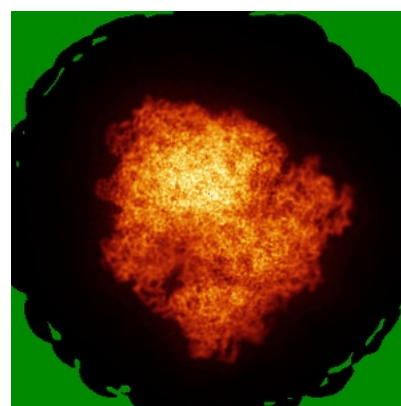
6.4.1 Primary map



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

This section was not generated.

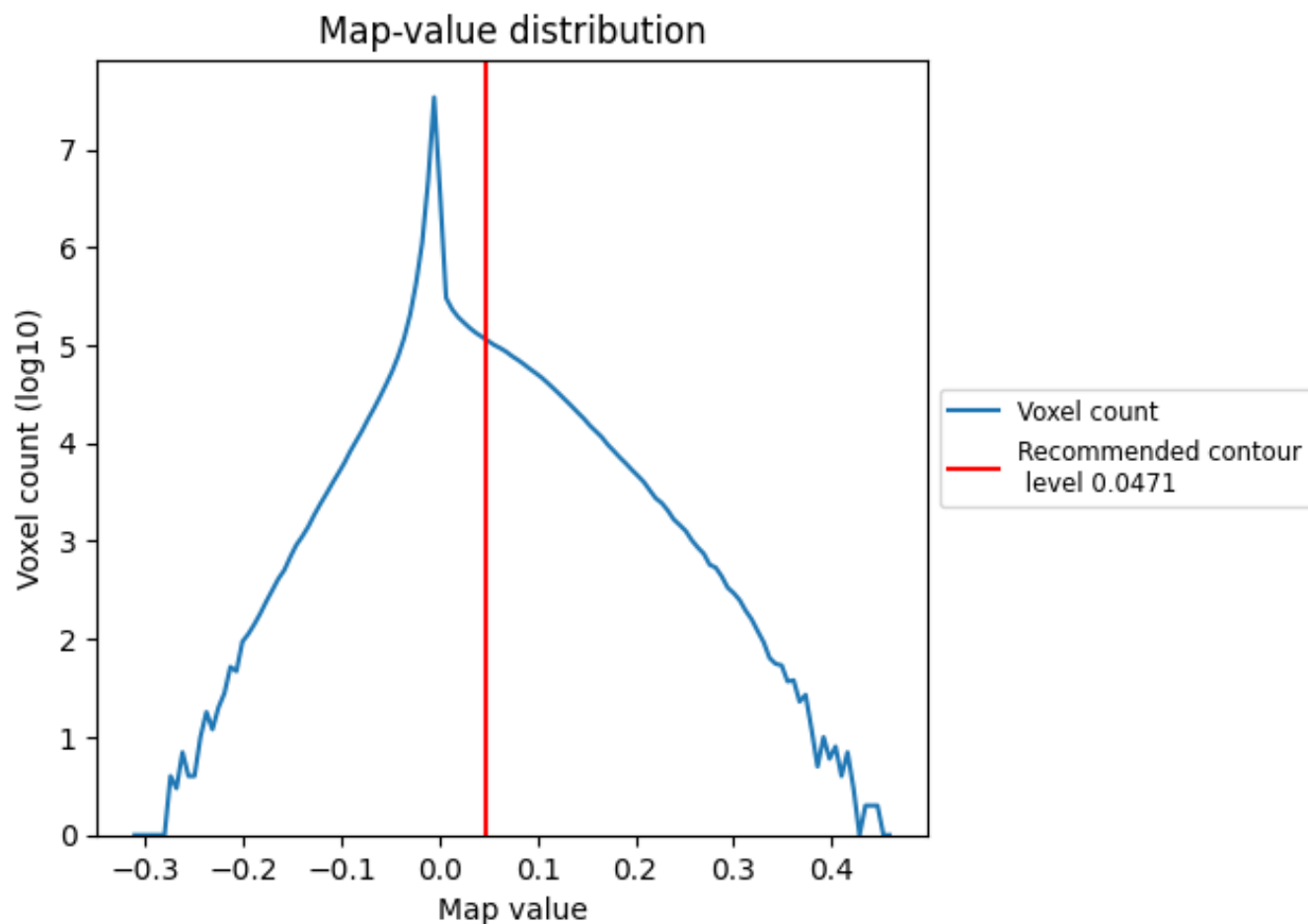
6.6 Mask visualisation

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

7 Map analysis [i](#)

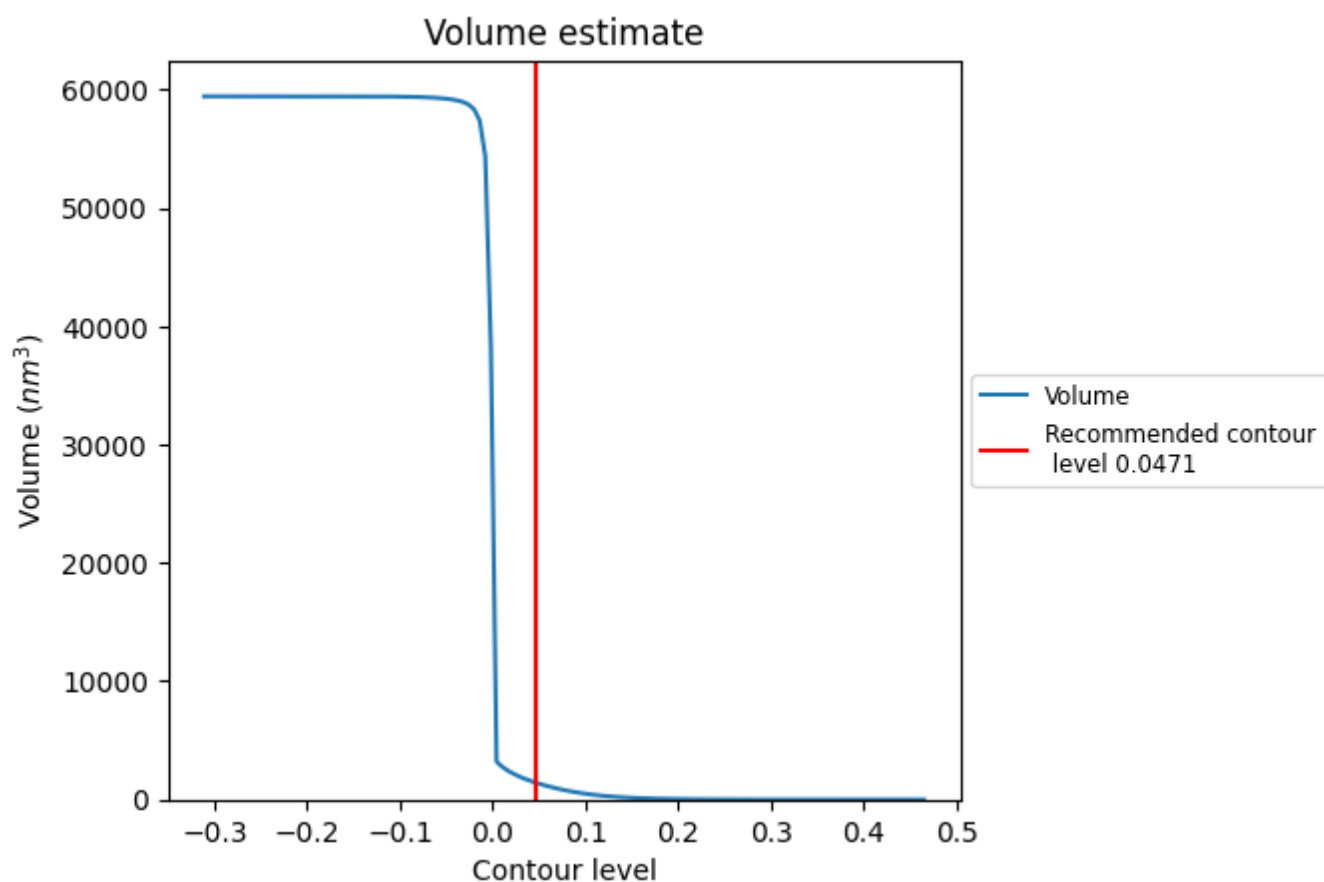
This section contains the results of statistical analysis of the map.

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.

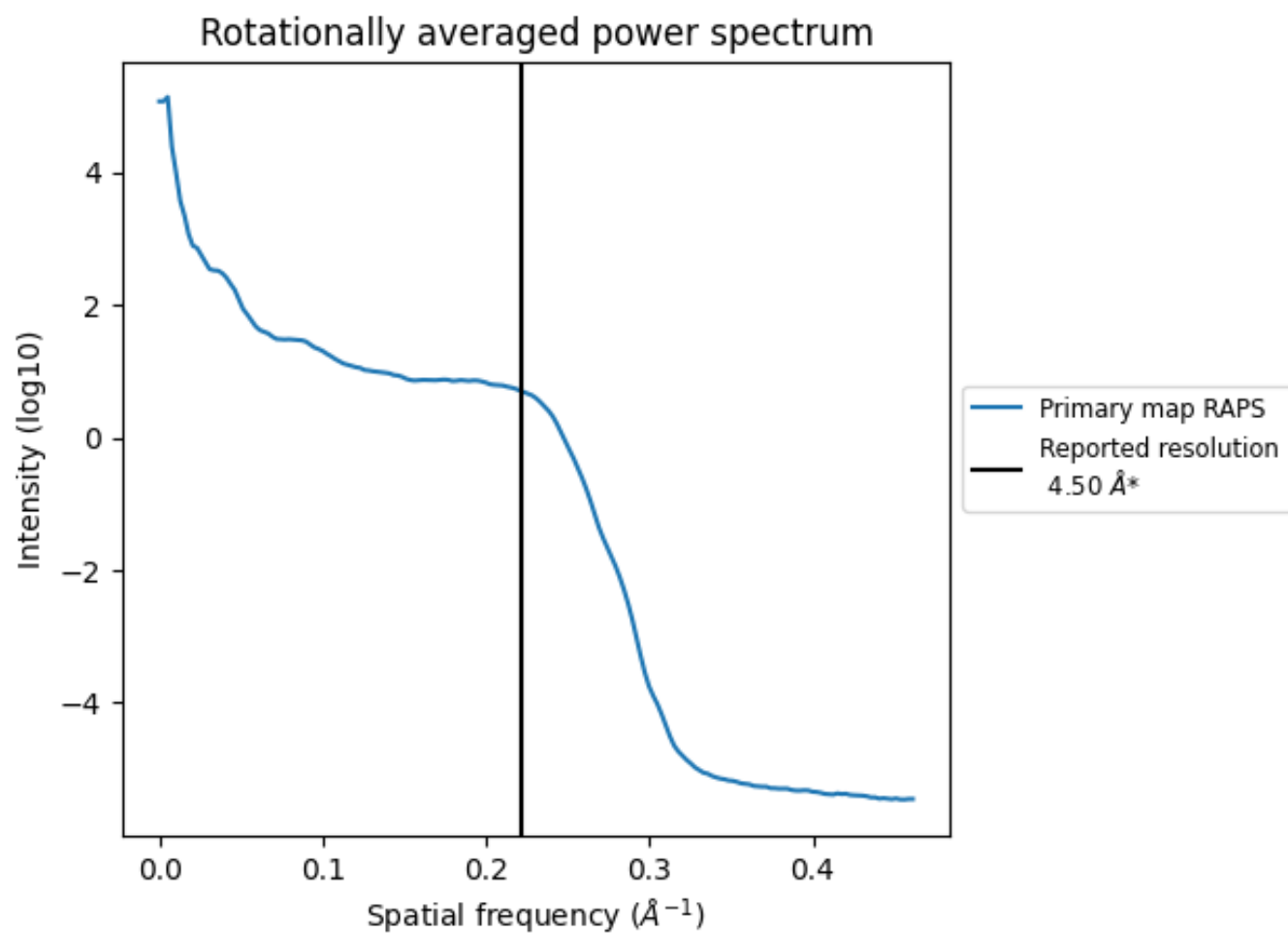
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1411 nm^3 ; this corresponds to an approximate mass of 1274 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 0.222 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

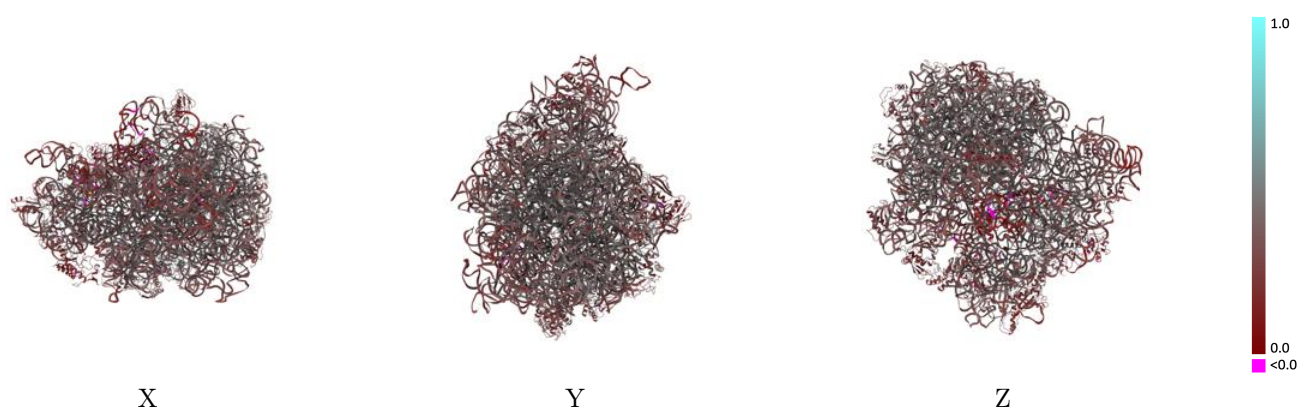
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0270 and PDB model 6HTQ. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)

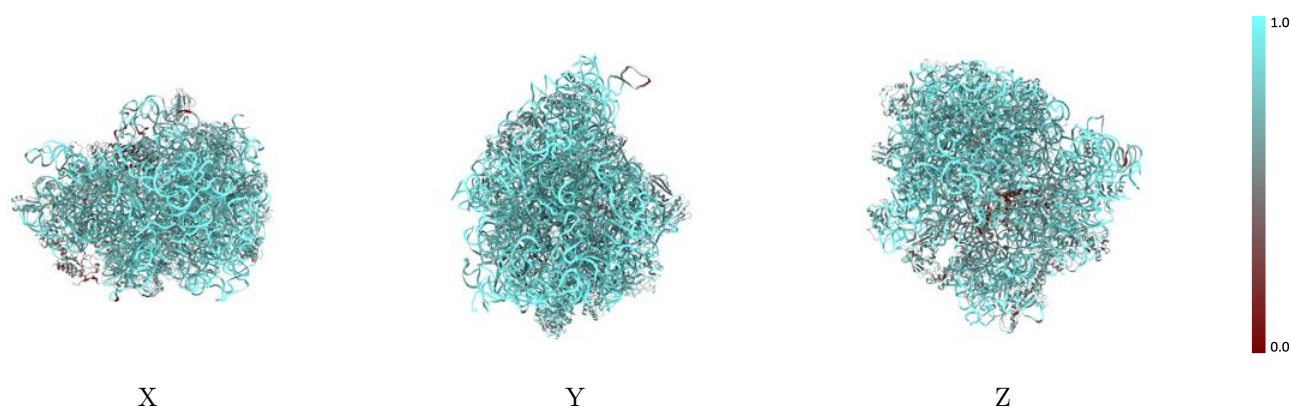
This section was not generated.

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



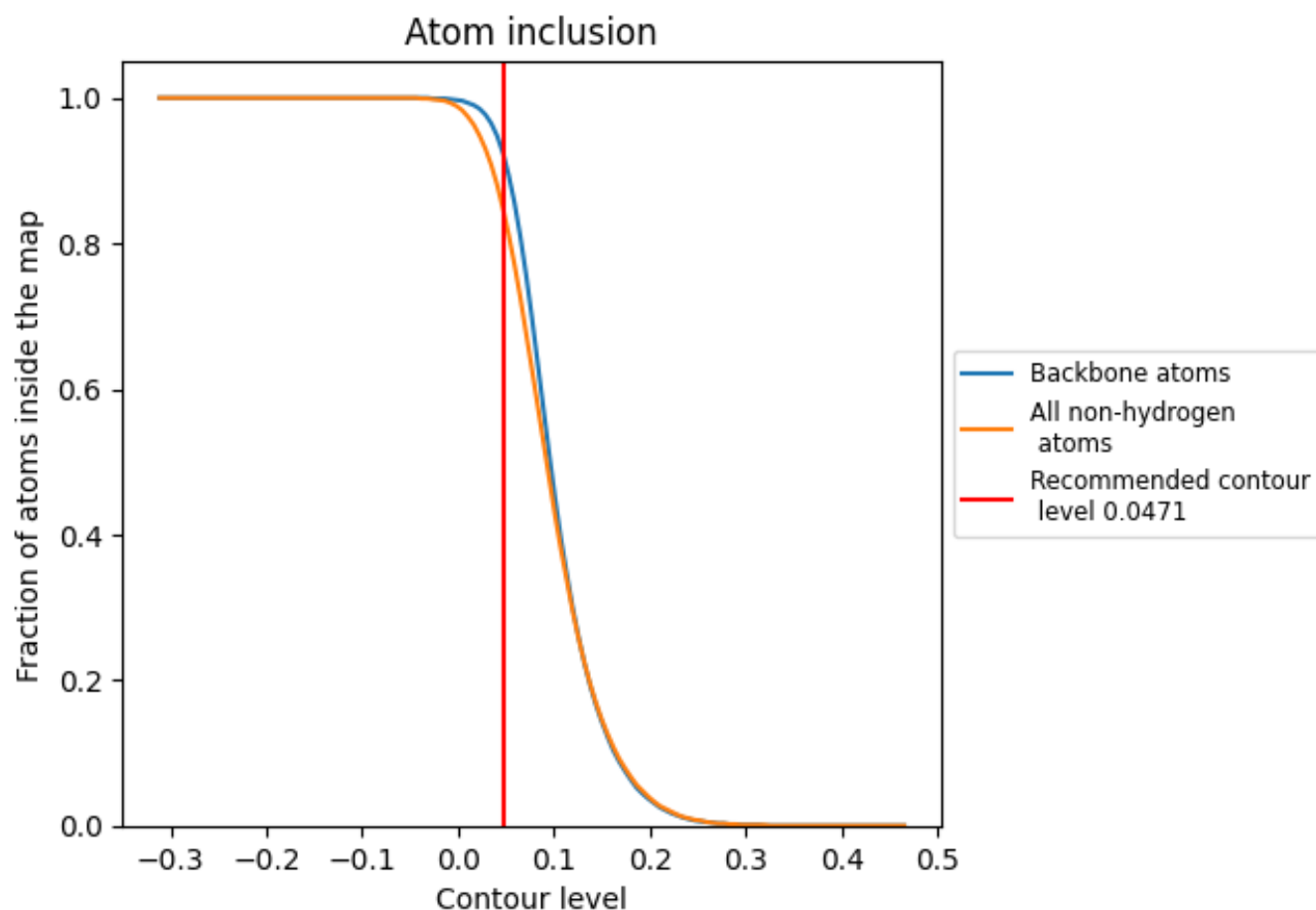
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0471).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (0.0471) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8460	 0.3550
1	 0.8450	 0.4240
2	 0.7490	 0.3660
3	 0.8550	 0.4380
4	 0.8000	 0.4360
5	 0.7170	 0.3800
A	 0.9220	 0.3790
B	 0.9570	 0.3490
C	 0.7940	 0.4330
D	 0.7780	 0.4050
E	 0.7340	 0.3460
F	 0.6590	 0.2610
G	 0.6590	 0.2660
J	 0.7800	 0.3980
K	 0.7590	 0.4160
L	 0.7550	 0.3880
M	 0.7440	 0.3800
N	 0.7630	 0.3790
O	 0.7040	 0.2730
P	 0.7540	 0.4020
Q	 0.7940	 0.3940
R	 0.6920	 0.3380
S	 0.7660	 0.3940
T	 0.7190	 0.3430
U	 0.7050	 0.3110
V	 0.7630	 0.3870
W	 0.5950	 0.1450
X	 0.6690	 0.2590
Y	 0.7170	 0.3590
Z	 0.5830	 0.2530
a	 0.9300	 0.3620
b	 0.4160	 0.2330
c	 0.6800	 0.3170
d	 0.6220	 0.2600
e	 0.7210	 0.3720



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Chain	Atom inclusion	Q-score
f	 0.7070	 0.3340
g	 0.6800	 0.2890
h	 0.7300	 0.3540
i	 0.7180	 0.3110
j	 0.6730	 0.3070
k	 0.7060	 0.3240
l	 0.7120	 0.3800
m	 0.6850	 0.2850
n	 0.7310	 0.3650
o	 0.7210	 0.3140
p	 0.6960	 0.2910
q	 0.6450	 0.3110
r	 0.6790	 0.3250
s	 0.6740	 0.2810
t	 0.6830	 0.2700
u	 0.6990	 0.2190
v	 0.8400	 0.3330
w	 0.5290	 0.1910
x	 0.3800	 0.1860