



## Full wwPDB EM Validation Report ⓘ

Nov 2, 2022 – 10:59 PM EDT

PDB ID : 5U9G  
EMDB ID : EMD-8522  
Title : 3.2 Å cryo-EM ArfA-RF2 ribosome rescue complex (Structure I)  
Authors : Demo, G.; Svidritskiy, E.; Madireddy, R.; Diaz-Avalos, R.; Grant, T.; Grigorieff, N.; Sousa, D.; Korostelev, A.A.  
Deposited on : 2016-12-16  
Resolution : 3.20 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](mailto: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>.

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

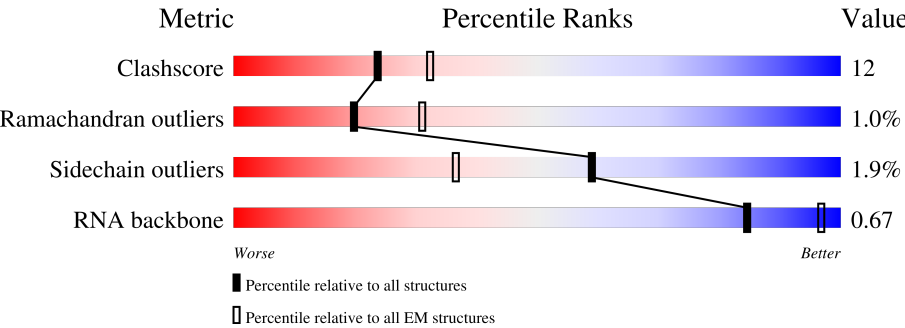
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 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.









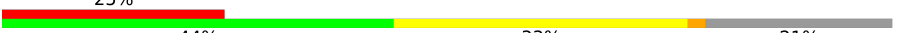


















Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	1539	
2	01	2903	
3	02	119	
4	Y	72	
5	W	77	
5	X	77	
6	03	234	


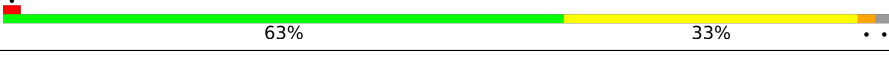
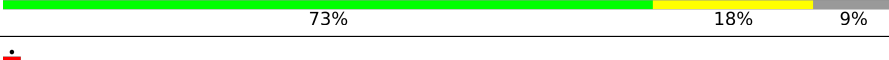
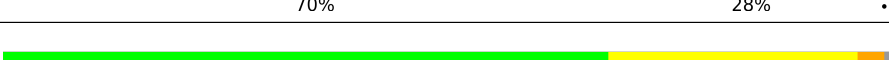
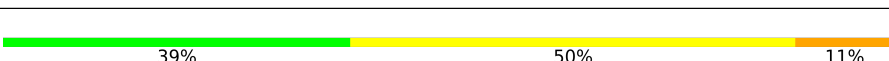


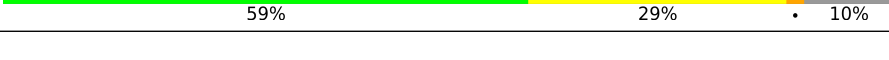
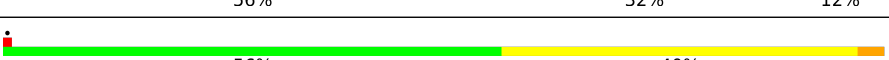
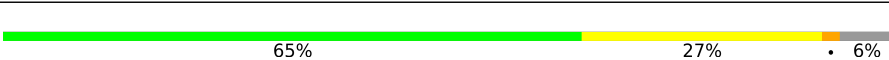
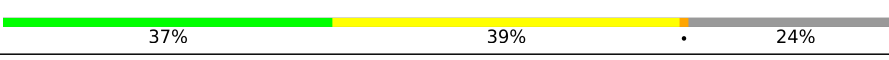













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Mol	Chain	Length	Quality of chain
7	04	273	
8	05	209	
9	06	201	
10	07	179	
11	08	177	
12	09	149	
13	10	165	
14	11	142	
15	12	142	
16	13	123	
17	14	144	
18	15	136	
19	16	127	
20	17	117	
21	18	115	
22	19	118	
23	20	103	
24	21	110	
25	22	100	
26	23	104	
27	24	94	
28	25	85	
29	26	78	
30	27	63	
31	28	59	

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Mol	Chain	Length	Quality of chain
32	29	70	
33	30	57	
34	31	55	
35	32	46	
36	33	65	
37	34	38	
38	V	14	
39	Z	365	
40	B	241	
41	C	233	
42	D	206	
43	E	167	
44	F	131	
45	G	156	
46	H	130	
47	I	130	
48	J	103	
49	K	129	
50	L	124	
51	M	118	
52	N	101	
53	O	89	
54	P	82	
55	Q	84	
56	R	75	

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Mol	Chain	Length	Quality of chain
57	S	92	<div><div></div><div>50%</div><div>36%</div><div>14%</div></div>
58	T	87	<div><div></div><div>60%</div><div>37%</div><div>..</div></div>
59	U	71	<div><div></div><div>51%</div><div>35%</div><div>6%</div><div>8%</div></div>

## 2 Entry composition [i](#)

There are 61 unique types of molecules in this entry. The entry contains 152649 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	01	2903	Total	C	N	O	P	0	0
			62318	27801	11467	20148	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
01	1847	G	A	conflict	GB 42756

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	02	119	Total	C	N	O	P	0	0
			2546	1135	466	827	118		

- Molecule 4 is a protein called Alternative ribosome-rescue factor A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Y	32	Total	C	N	O	S	0	0
			249	155	53	40	1		

- Molecule 5 is a RNA chain called fMet-tRNA (P- and E-site).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	X	77	Total	C	N	O	P	0	0
			1622	723	289	534	76		
5	W	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	03	220	Total	C	N	O	S	0	0
			1353	804	270	277	2		

- Molecule 7 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	04	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 8 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	05	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 9 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	06	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 10 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	07	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	08	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	09	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 13 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	10	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 14 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	11	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 15 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	12	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 16 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	13	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	14	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 18 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	15	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	16	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.



Mol	Chain	Residues	Atoms				AltConf	Trace
20	17	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 21 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	18	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 22 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	19	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 23 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	20	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 24 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	21	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	22	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	23	102	Total	C	N	O	0	0
			779	492	146	141		

- Molecule 27 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	24	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 28 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	25	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 29 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	26	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 30 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	27	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 31 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	28	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 32 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	29	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 33 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	30	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 34 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	31	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 35 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	32	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 36 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	33	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 37 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	34	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 38 is a RNA chain called truncated mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	V	14	Total	C	N	O	P	0	0
			306	138	64	91	13		

- Molecule 39 is a protein called Peptide chain release factor RF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	361	Total	C	N	O	S	0	0
			2814	1728	499	578	9		

- Molecule 40 is a protein called 30S ribosomal protein S2.

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

- Molecule 41 is a protein called 30S ribosomal protein S3.

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

- Molecule 42 is a protein called 30S ribosomal protein S4.

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

- Molecule 43 is a protein called 30S ribosomal protein S5.

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

- Molecule 44 is a protein called 30S ribosomal protein S6.

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

- Molecule 45 is a protein called 30S ribosomal protein S7.

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

- Molecule 46 is a protein called 30S ribosomal protein S8.

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

- Molecule 47 is a protein called 30S ribosomal protein S9.

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

- Molecule 48 is a protein called 30S ribosomal protein S10.

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

- Molecule 49 is a protein called 30S ribosomal protein S11.

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

- Molecule 50 is a protein called 30S ribosomal protein S12.

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

- Molecule 51 is a protein called 30S ribosomal protein S13.

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

- Molecule 52 is a protein called 30S ribosomal protein S14.

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

- Molecule 53 is a protein called 30S ribosomal protein S15.

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

- Molecule 54 is a protein called 30S ribosomal protein S16.

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

- Molecule 55 is a protein called 30S ribosomal protein S17.

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

- Molecule 56 is a protein called 30S ribosomal protein S18.

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

- Molecule 57 is a protein called 30S ribosomal protein S19.

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

- Molecule 58 is a protein called 30S ribosomal protein S20.

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

- Molecule 59 is a protein called 30S ribosomal protein S21.

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

- Molecule 60 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
60	A	97	Total	Mg	0
			97	97	
60	01	239	Total	Mg	0
			239	239	
60	02	4	Total	Mg	0
			4	4	
60	X	2	Total	Mg	0
			2	2	
60	14	1	Total	Mg	0
			1	1	
60	25	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
60	30	1	Total 1	Mg 1	0
60	W	2	Total 2	Mg 2	0
60	H	1	Total 1	Mg 1	0

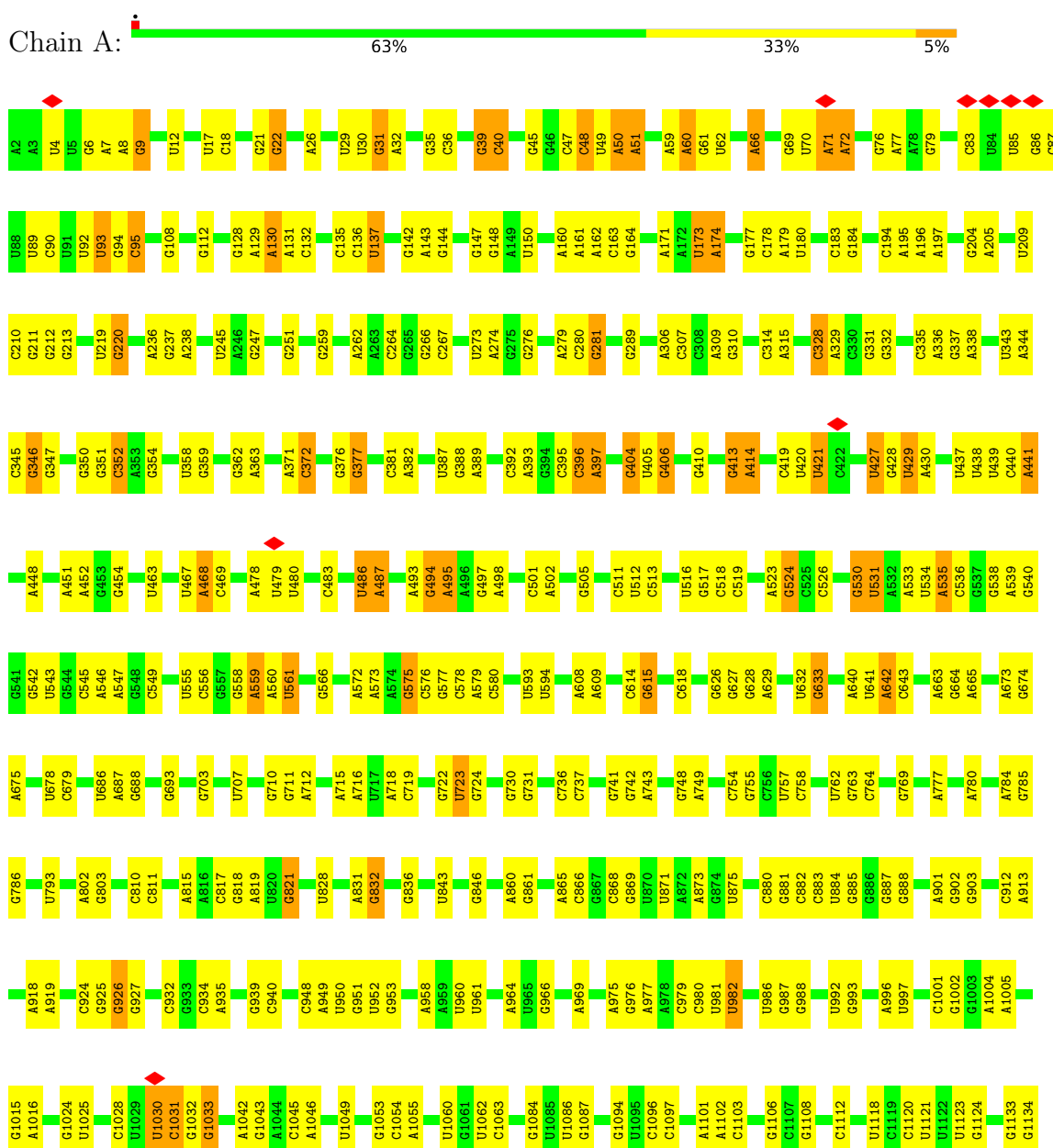
- Molecule 61 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	34	1	Total 1	Zn 1	0

### 3 Residue-property plots

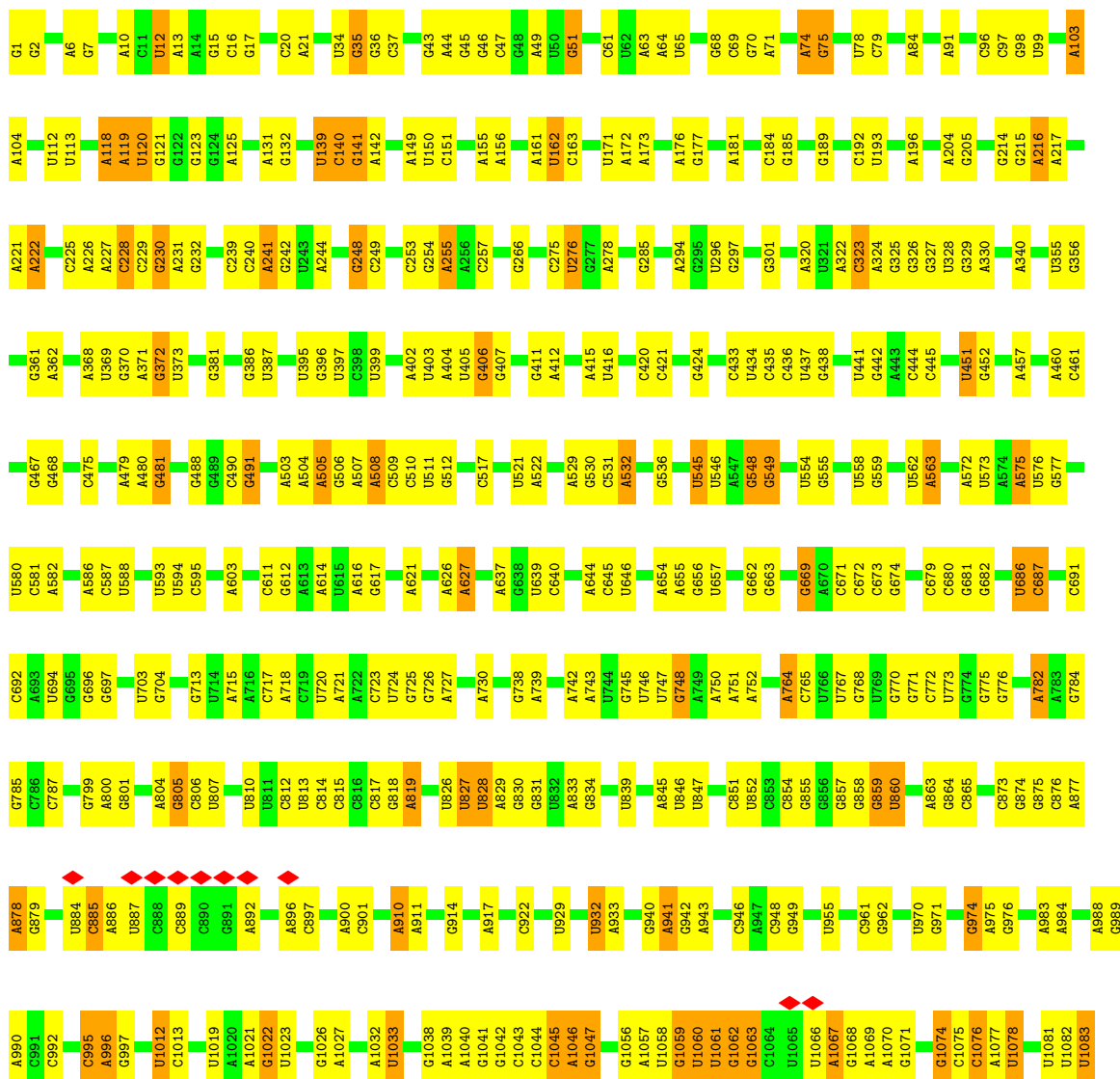
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

#### • Molecule 1: 16S ribosomal RNA

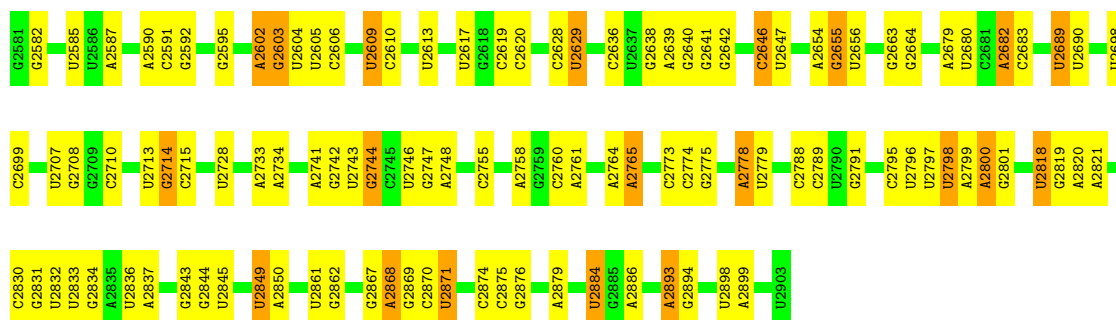




- Molecule 2: 23S ribosomal RNA



G2484	G2370	C2283	A2184	U2092	A2005	G1906	A1794	G1681	U1563	A1434	U1318	G1186	A1084
G2485	G2371	A2284	U2185	G2093	G2010	C1909	C1796	A1690	C1564	G1441	C1319	G1187	A1085
G2486	G2372	C2285	G2188	A2094	U2011	G1910	U1796	C1691	A1566	U1442	C1320	U1188	A1086
		A2287	U2189	A2101	G2012	U1912	G1797	G1695	G1567	U1443	U1326	G1190	G1087
	C2380	U2292	U2194	C2103	A2013	A1913	U1798	G1696	G1568	G1444	G1332	U1198	A1088
	A2381	G2293	U2195	G2107	A2020	C1914	G1799	G1697	A1569			U1199	A1089
	G2382	G2294	C2196	A2108	C2021	U1915	C1800	A1698	U1578	G1450	A1336	C1209	A1090
	G2383	G2295	U2197	U2022	U1916	A1801	U1799	G1698		C1451	G1337	U1201	A1095
	C2385	U2296	A2198	G2109	U1917	G1807	A1700	C1700	A1563	A1453	G1338	U1202	A1096
		A2297	U2203	G2110	G2024	A1808	A1701	A1718	U1584	C1454	G1339	U1203	U1097
	A2303	A2298	G2204	U2111	G2029	A1809		G1710	C1585		U1344		A1098
	U2390	U2299		C2112	G2030	A1810	G1711	A1711	A1586	G1459	C1345	G1212	G1099
	U2402	U2302	A2212	U2113	A2030	G1920	G1811		G1587	U1460			C1104
	G2403	G2303	U2213	G2115	A2031	U1923	C1816	G1715	A1593	G1463	C1357	U1219	A1111
	U2404	G2304	C2214	G2118	A2032	C1924	U1817	U1716	U1594	G1464	G1358	G1220	G1112
	G2405	U2305	C2215	U2118	U2034	A1928	U1818	A1717	C1595		A1359	G1225	U1113
	A2406		G2216	A2119	G2035	G1929		G1718	U1599	U1468	G1360	G1239	C1114
			G2217	G2120	G2036	U1931	A1821		C1600	U1476	G1361	U1240	G1115
			G2218	G2121	A2037	G1935	C1822	C1726	G1601		A1365		G1122
			G2219	U2122	G2038	U1936	G1826	C1727	U1602	G1482		G1250	U1130
			G2220	G2123	U2039	A1936	U1827	U1728	A1603		A1373	G1251	G1131
			G2221	G2124	G2040	A1937	G1828	C1730	C1604		C1376	G1252	U1132
			G2222	G2125		U1938	A1829		C1605		G1377	A1254	A1133
			G2223	A2126	C2043			G1738	U1609	U1506	U1379	U1255	C1135
			G2224	C2044	C2045	U1943	C1838	A1746	A1614	A1508	G1380	C1257	G1138
			C2225	G2046		U1944	G1839	U1747	C1615	A1509		U1258	G1139
			C2226	G2055	G2056	G1945		C1748	A1616	G1510		C1263	C1140
			G2230	C2060	A2062	U1955	G1842	U1749				U1264	U1141
			G2233	A2061	A2062	U1963	C1843	U1750	A1637	A1515	C1386	A1265	A1142
			G2234	A2154		G1964	G1845	G1751			U1394		U1148
			G2238	C2153		G1965	G1846	G1752	G1645	G1521		A1268	G1149
			G2239	A2158		A1966	G1847	G1753	U1647	U1522		A1269	A1156
			G2240	C2161		C1967		A1754	U1648	G1524	U1409	G1270	
			U2241	U2162	G2068	G1968	U1855	G1756	G1649		G1410	G1271	
			G2242	A2163	G2069	A1969	U1856	A1757	A1650	A1535	U1415	A1272	G1167
			U2243	C2164	A2070	U1970	G1857	U1758	G1651	C1536	G1416	G1277	G1168
			U2244	C2165	C2071	U1971		A1759	A1652	G1537	C1417		A1169
				U2166	G2072	G1972	G1869	C1760			G1418	U1287	C1170
			A2247	U2166	C2073		C1870		U1657	C1541	A1419	G1297	G1171
			C2248	A2170	U2074	A1978	A1871	G1764	C1658	U1542	A1420		U1172
			U2249	A2171	U2075	U1979	G1872				G1421		U1174
			G2250	C2172	U2079	G1980	C1873	A1773	A1664	A1548		G1300	G1177
				U2172	A2080	U1981	C1874	G1774	A1665	A1549	G1424	A1301	C1178
			U2257	A2173	U2081	U1982	G1875	U1775	G1666	A1551	G1425	A1308	G1179
			C2258	C2174	G2082			G1776	G1667		A1427	G1309	U1181
			C2263	C2175	G2083	U1991	U1882	U1779	A1668	G1555		G1310	U1182
				A2176	G2084	G1992	G1884	A1780	A1669			G1311	G1183
				C2177	U2086	U1993	U1885					U1316	U1184
			A2266	C2178	G2087	G1994	A1885	A1783	A1672	C1558		G1317	G1185
			A2267	C2179	A2088	U1996	G1888	A1784	G1673	U1559			
			A2268	U2180	C2089	C1997		C1790	G1674	G1560			
				U2181			A1901	A1791	U1690				
			A2281	U2182	C2091	G2004							
			G2282	A2183									



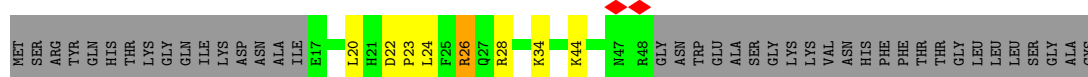
• Molecule 3: 5S ribosomal RNA

Chain 02: 66% 32% .



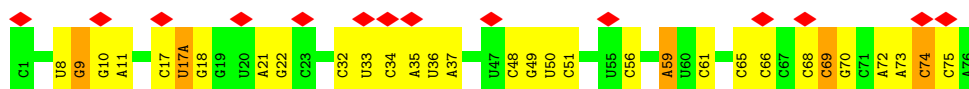
• Molecule 4: Alternative ribosome-rescue factor A

Chain Y: 33% 10% 56% .



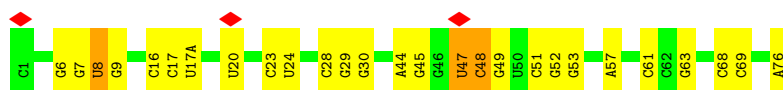
• Molecule 5: fMet-tRNA (P- and E-site)

Chain X: 18% 60% 34% 6%



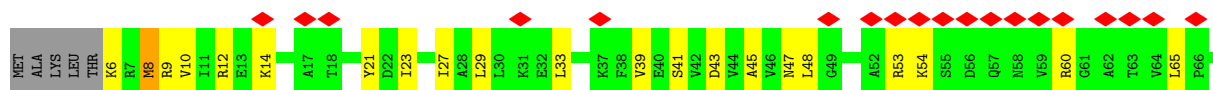
• Molecule 5: fMet-tRNA (P- and E-site)

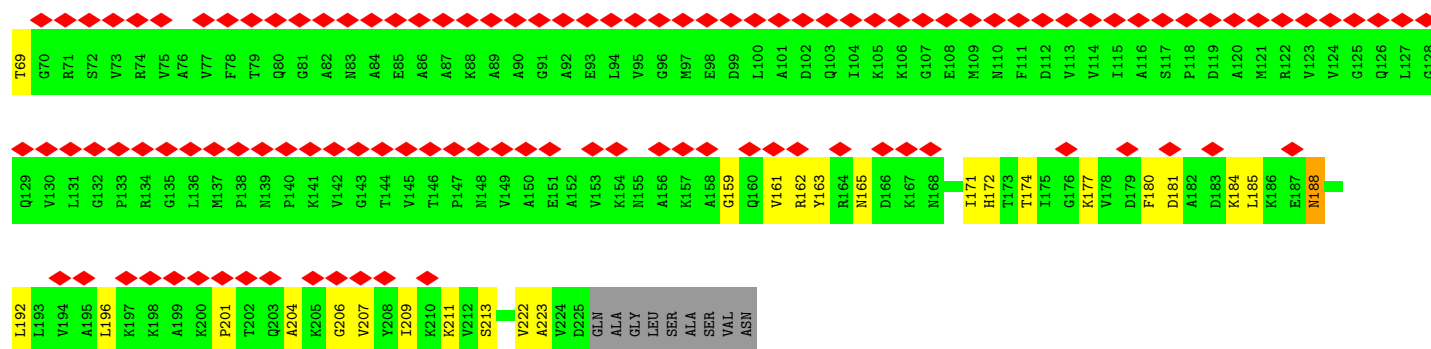
Chain W: 65% 31% .



• Molecule 6: 50S ribosomal protein L1

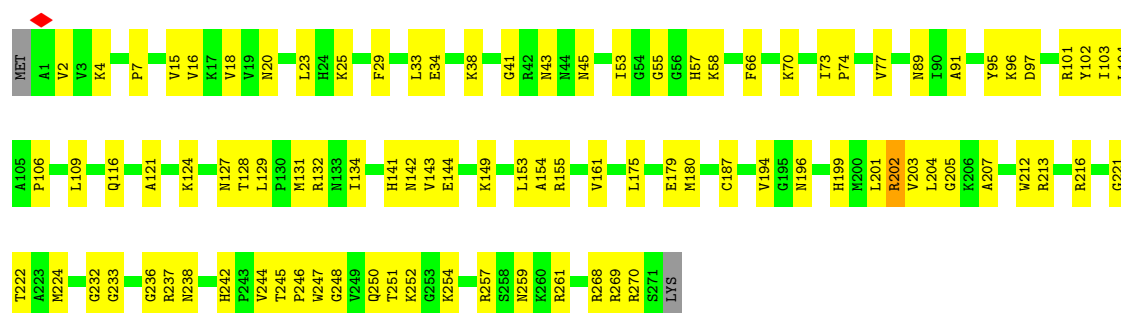
Chain 03: 56% 74% 19% 6%





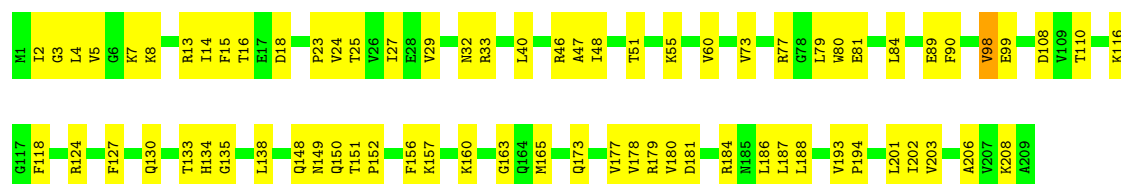
• Molecule 7: 50S ribosomal protein L2

Chain 04: 65% 34%



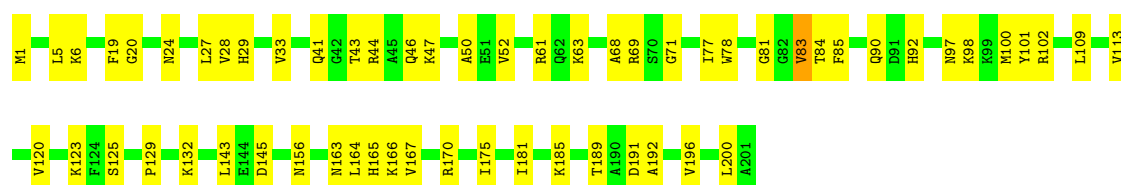
• Molecule 8: 50S ribosomal protein L3

Chain 05: 65% 34%



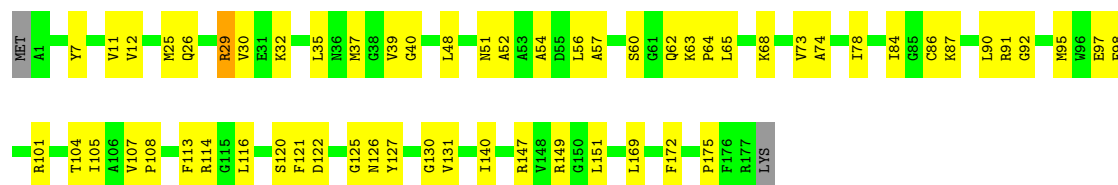
• Molecule 9: 50S ribosomal protein L4

Chain 06: 71% 29%

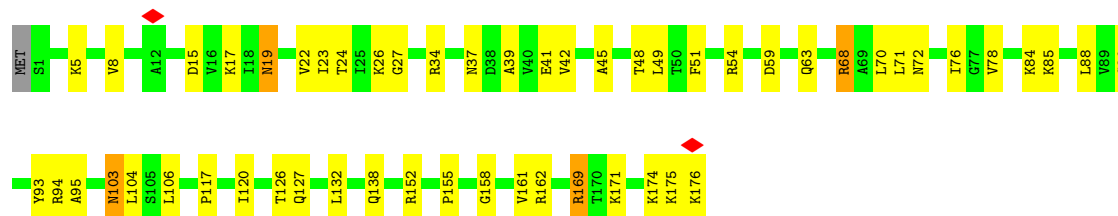


• Molecule 10: 50S ribosomal protein L5

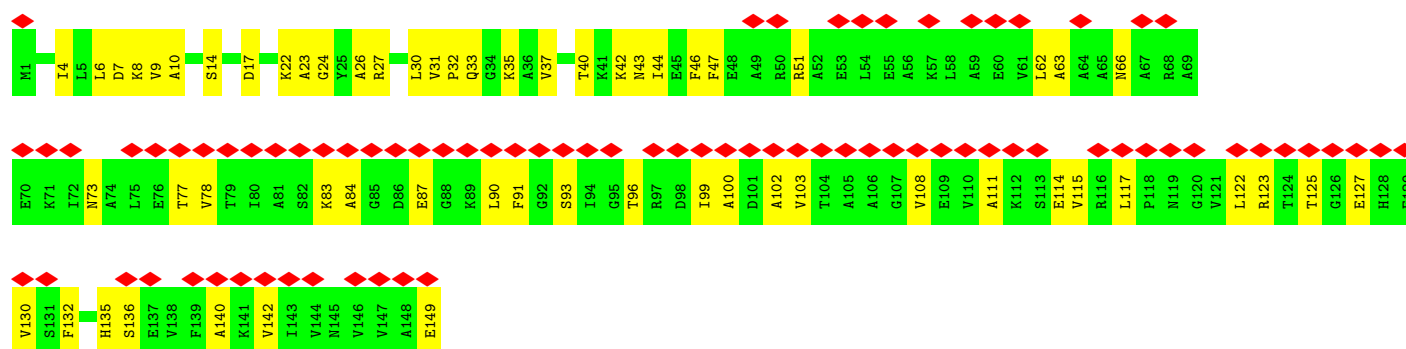
Chain 07: 66% 32%



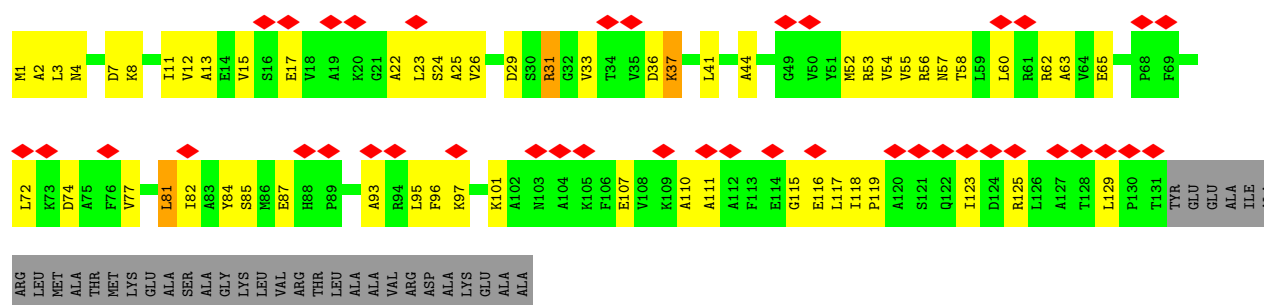
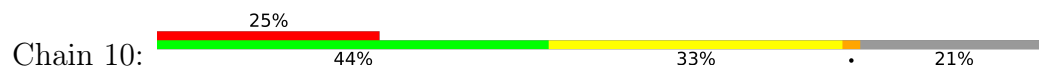
• Molecule 11: 50S ribosomal protein L6



• Molecule 12: 50S ribosomal protein L9

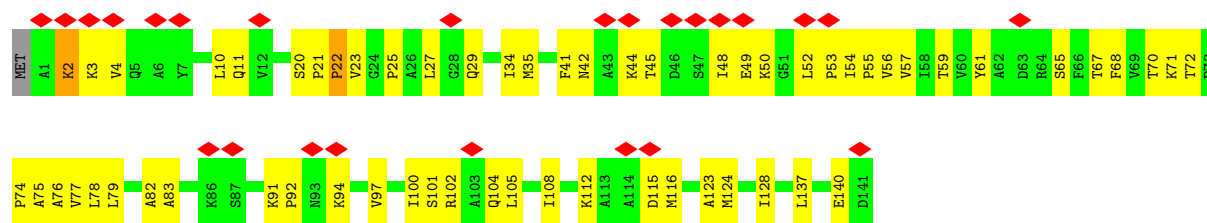


• Molecule 13: 50S ribosomal protein L10



• Molecule 14: 50S ribosomal protein L11





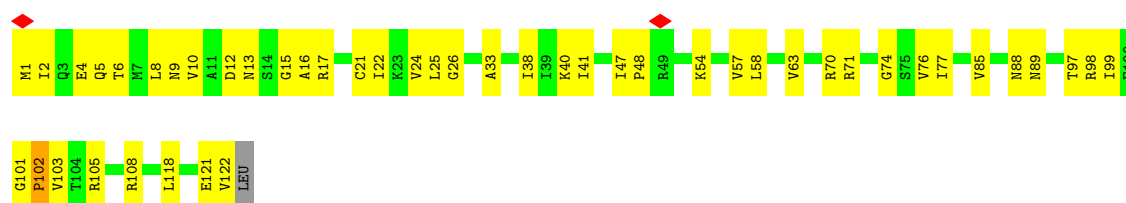
- Molecule 15: 50S ribosomal protein L13

Chain 12: 68% 30% .



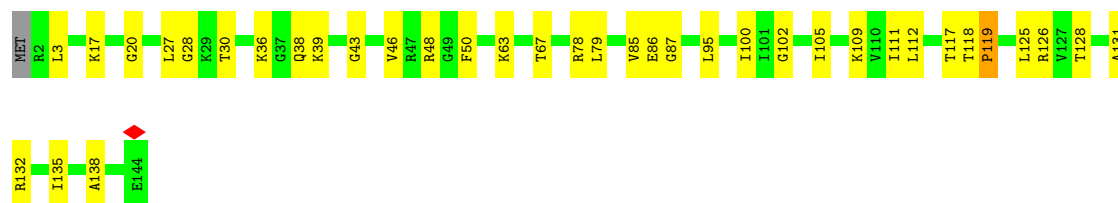
- Molecule 16: 50S ribosomal protein L14

Chain 13: 61% 37% ..



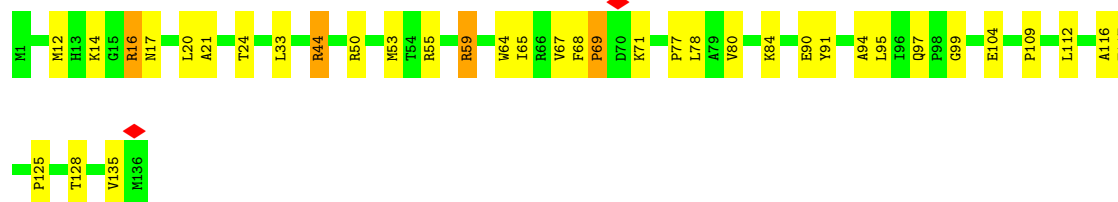
- Molecule 17: 50S ribosomal protein L15

Chain 14: 74% 25% ..

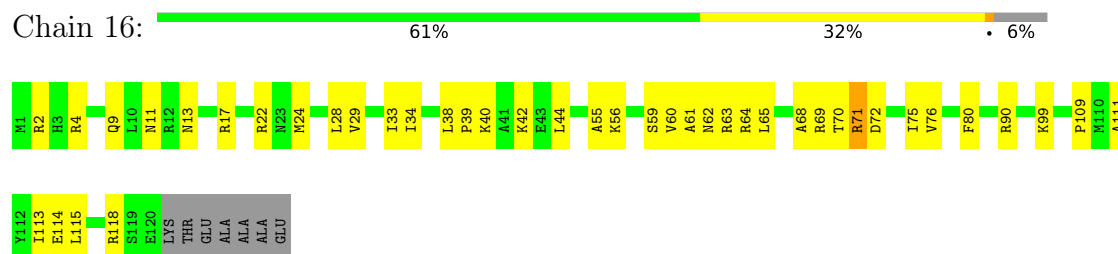


- Molecule 18: 50S ribosomal protein L16

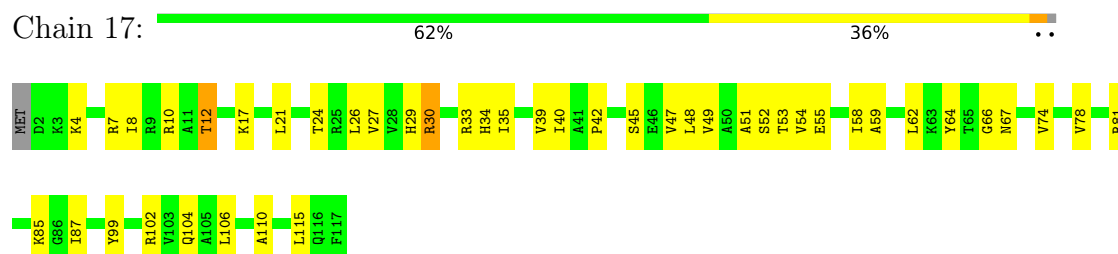
Chain 15: 73% 24% .



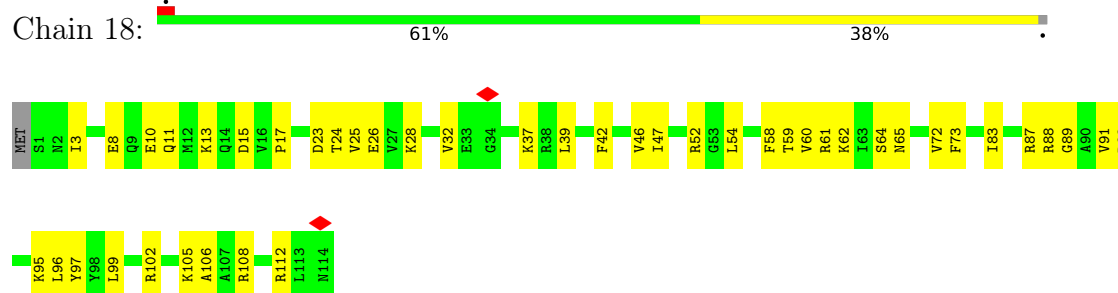
- Molecule 19: 50S ribosomal protein L17



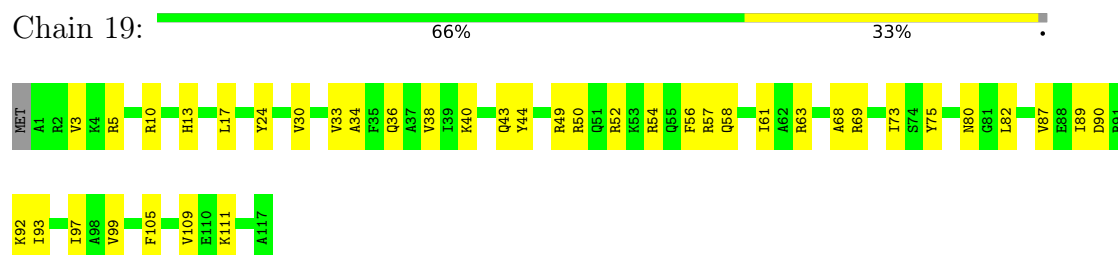
- Molecule 20: 50S ribosomal protein L18



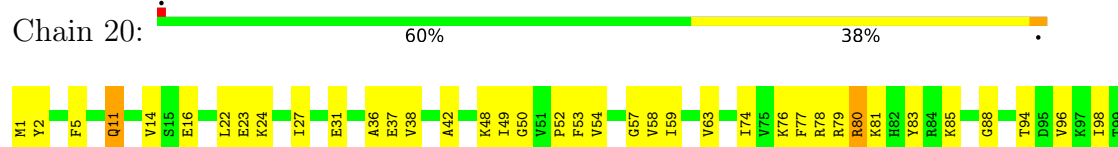
- Molecule 21: 50S ribosomal protein L19



- Molecule 22: 50S ribosomal protein L20



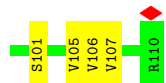
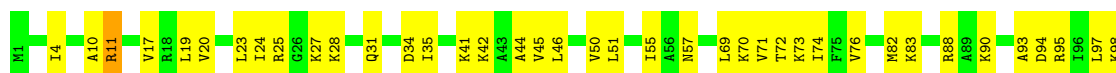
- Molecule 23: 50S ribosomal protein L21





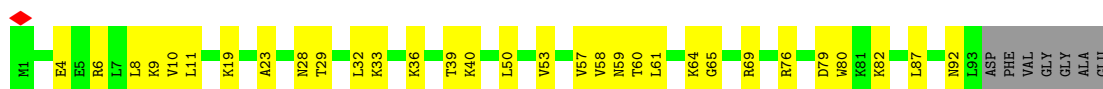
- Molecule 24: 50S ribosomal protein L22

Chain 21: 61% 38%



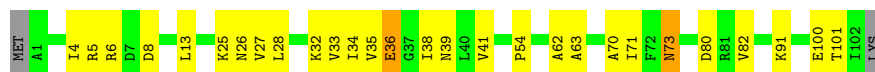
- Molecule 25: 50S ribosomal protein L23

Chain 22: 62% 31% 7%



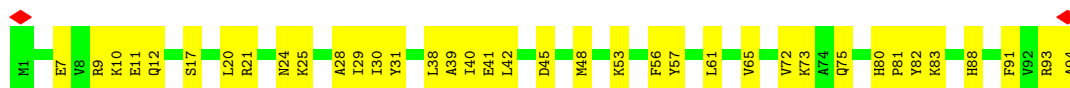
- Molecule 26: 50S ribosomal protein L24

Chain 23: 71% 25%



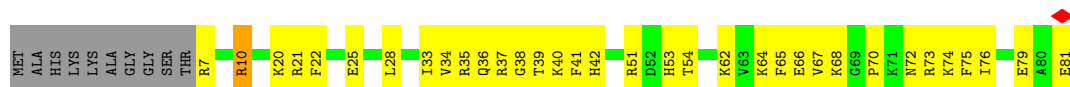
- Molecule 27: 50S ribosomal protein L25

Chain 24: 61% 39%



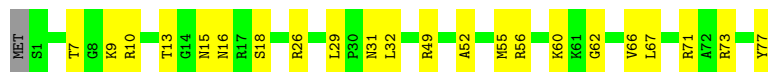
- Molecule 28: 50S ribosomal protein L27

Chain 25: 48% 39% 12%



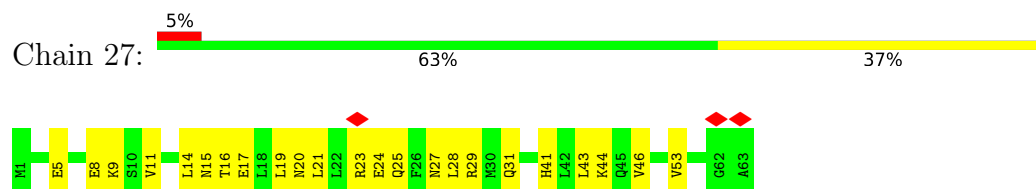
- Molecule 29: 50S ribosomal protein L28

Chain 26: 71% 28%

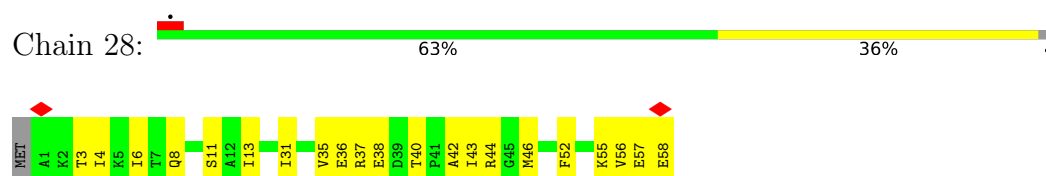




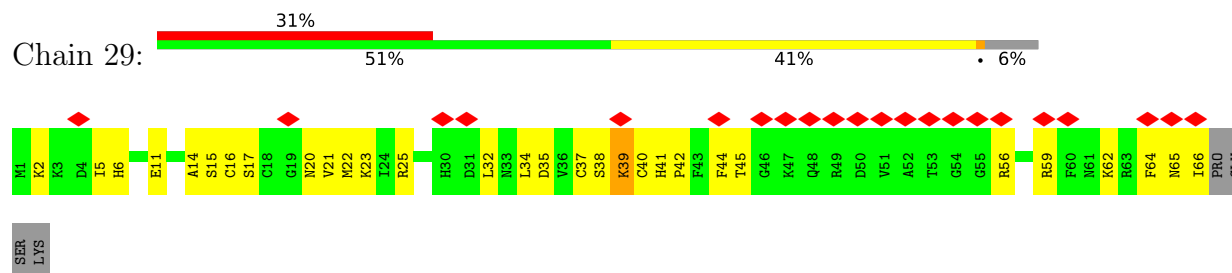
- Molecule 30: 50S ribosomal protein L29



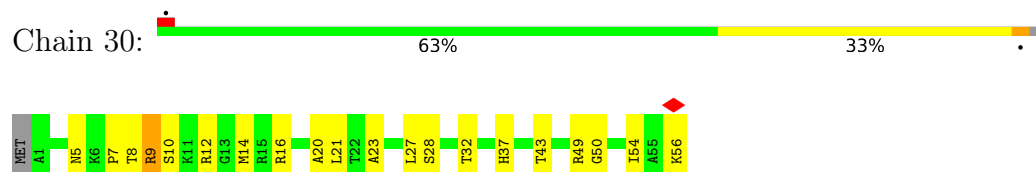
- Molecule 31: 50S ribosomal protein L30



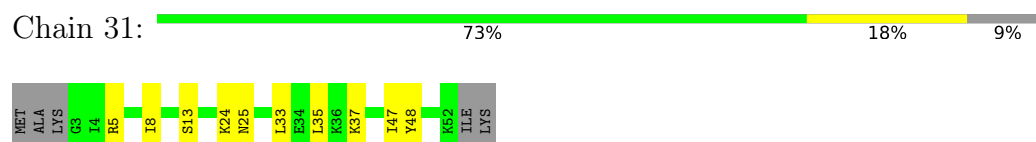
- Molecule 32: 50S ribosomal protein L31



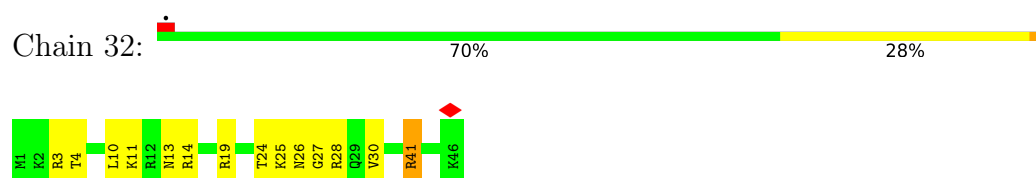
- Molecule 33: 50S ribosomal protein L32



- Molecule 34: 50S ribosomal protein L33



- Molecule 35: 50S ribosomal protein L34



- Molecule 36: 50S ribosomal protein L35

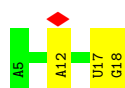
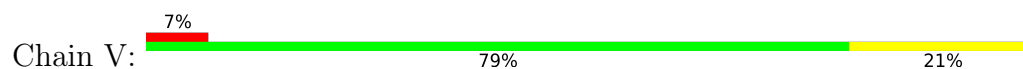




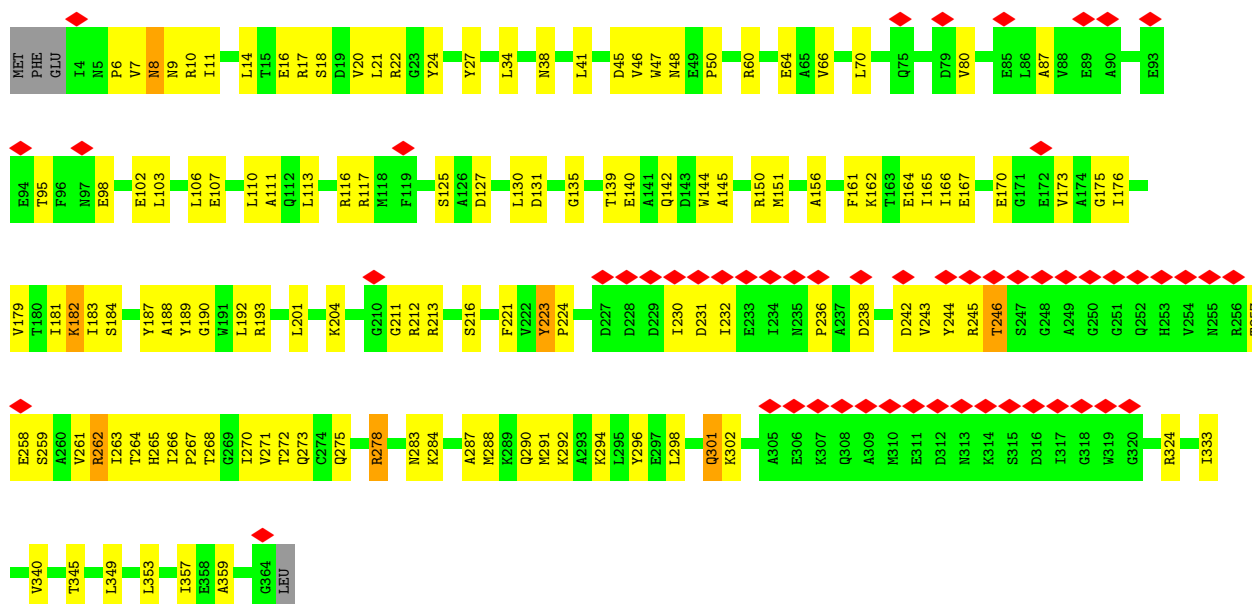
- Molecule 37: 50S ribosomal protein L36



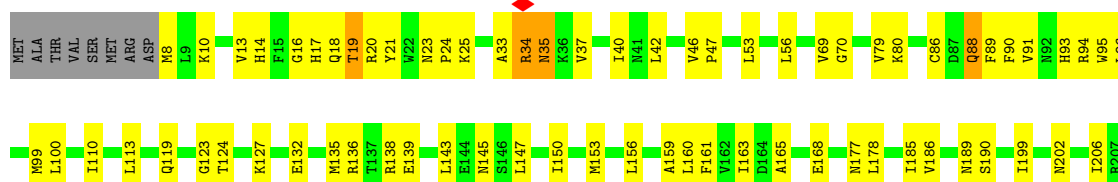
- Molecule 38: truncated mRNA



- Molecule 39: Peptide chain release factor RF2



- Molecule 40: 30S ribosomal protein S2



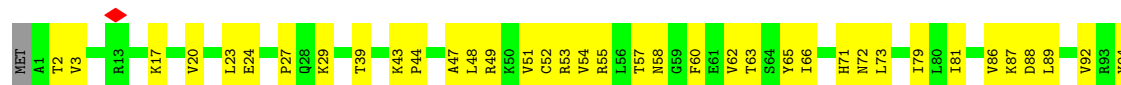


- Chain G:  67% 29% ..

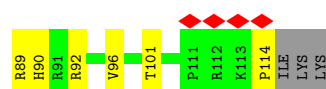
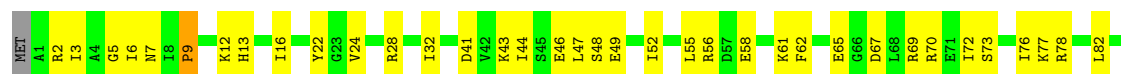




- Molecule 50: 30S ribosomal protein S12



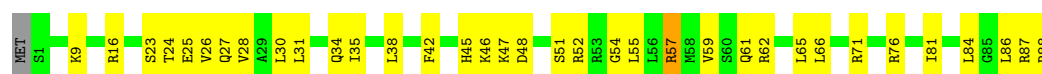
- Molecule 51: 30S ribosomal protein S13



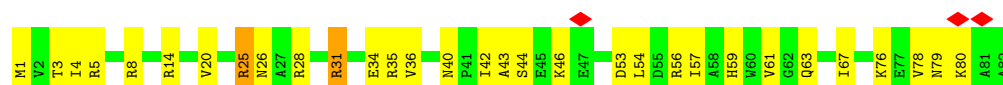
- Molecule 52: 30S ribosomal protein S14



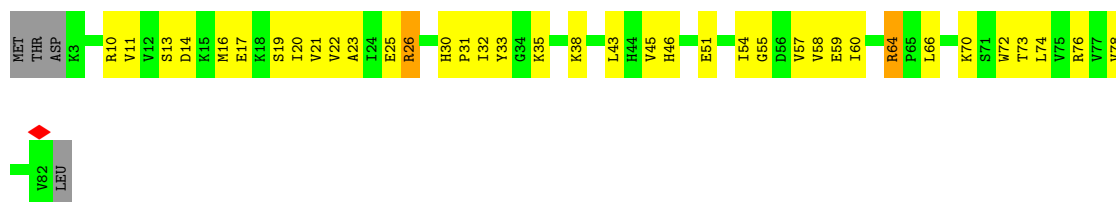
- Molecule 53: 30S ribosomal protein S15



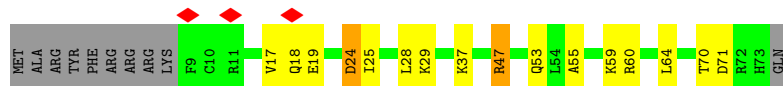
- Molecule 54: 30S ribosomal protein S16



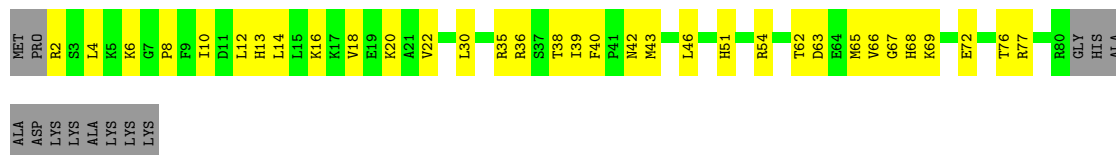
## • Molecule 55: 30S ribosomal protein S17

Chain Q:  51% 42% 5%

## • Molecule 56: 30S ribosomal protein S18

Chain R:  65% 19% 13%

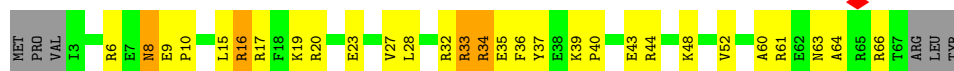
## • Molecule 57: 30S ribosomal protein S19

Chain S:  50% 36% 14%

## • Molecule 58: 30S ribosomal protein S20

Chain T:  60% 37% 2%

## • Molecule 59: 30S ribosomal protein S21

Chain U:  51% 35% 6% 8%

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	139861	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 ( $e^-/\text{\AA}^2$ )	1.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	29000	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	17.734	Depositor
Minimum map value	-5.902	Depositor
Average map value	-1.160	Depositor
Map value standard deviation	1.507	Depositor
Recommended contour level	2.5	Depositor
Map size ( $\text{\AA}$ )	388.80002, 388.80002, 388.80002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.215, 1.215, 1.215	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	0.25	0/36963	0.65	0/57662
2	01	0.24	0/69797	0.65	1/108890 (0.0%)
3	02	0.25	0/2847	0.65	0/4440
4	Y	0.31	0/253	0.54	0/330
5	W	0.25	0/1832	0.64	0/2855
5	X	0.29	0/1811	0.67	1/2822 (0.0%)
6	03	0.28	0/1361	0.58	1/1796 (0.1%)
7	04	0.29	0/2121	0.59	0/2852
8	05	0.33	0/1586	0.57	0/2134
9	06	0.30	0/1571	0.58	1/2113 (0.0%)
10	07	0.32	0/1434	0.54	0/1926
11	08	0.29	0/1343	0.55	0/1816
12	09	0.31	0/1122	0.57	0/1515
13	10	0.35	0/1001	0.64	0/1350
14	11	0.31	0/1046	0.58	0/1410
15	12	0.30	0/1152	0.56	0/1551
16	13	0.30	0/947	0.60	0/1268
17	14	0.32	0/1054	0.59	0/1403
18	15	0.32	0/1093	0.59	0/1460
19	16	0.30	0/973	0.55	0/1301
20	17	0.28	0/902	0.55	0/1209
21	18	0.31	0/929	0.54	0/1242
22	19	0.29	0/960	0.46	0/1278
23	20	0.33	0/829	0.63	1/1107 (0.1%)
24	21	0.28	0/864	0.56	0/1156
25	22	0.30	0/744	0.54	0/994
26	23	0.33	0/787	0.61	0/1051
27	24	0.30	0/766	0.55	0/1025
28	25	0.34	0/582	0.58	0/769
29	26	0.30	0/635	0.52	0/848
30	27	0.28	0/510	0.47	0/677
31	28	0.27	0/453	0.51	0/605



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
32	29	0.31	0/531	0.52	0/709
33	30	0.31	0/450	0.58	0/599
34	31	0.30	0/416	0.52	0/554
35	32	0.30	0/380	0.51	0/498
36	33	0.31	0/513	0.61	0/676
37	34	0.23	0/303	0.40	0/397
38	V	0.21	0/345	0.60	0/538
39	Z	0.31	0/2854	0.56	0/3842
40	B	0.31	0/1735	0.57	0/2338
41	C	0.30	0/1651	0.54	0/2225
42	D	0.29	0/1665	0.59	0/2227
43	E	0.31	0/1169	0.59	0/1573
44	F	0.32	0/835	0.62	0/1128
45	G	0.29	0/1195	0.55	0/1602
46	H	0.30	0/989	0.57	0/1326
47	I	0.31	0/1034	0.59	0/1375
48	J	0.30	0/796	0.64	0/1077
49	K	0.31	0/885	0.60	0/1195
50	L	0.31	0/969	0.67	1/1300 (0.1%)
51	M	0.28	0/892	0.57	0/1193
52	N	0.34	0/817	0.64	3/1088 (0.3%)
53	O	0.28	0/722	0.52	0/964
54	P	0.32	0/659	0.57	0/884
55	Q	0.30	0/657	0.58	0/881
56	R	0.30	0/544	0.57	0/731
57	S	0.32	0/652	0.56	0/877
58	T	0.28	0/671	0.44	0/888
59	U	0.37	0/550	0.67	0/728
All	All	0.27	0/165147	0.63	9/246268 (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
39	Z	0	2
52	N	0	1
All	All	0	3

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	06	81	GLY	N-CA-C	-7.61	94.08	113.10
52	N	55	SER	C-N-CD	-7.29	104.56	120.60
6	03	206	GLY	N-CA-C	-6.01	98.08	113.10
2	01	1178	C	N1-C1'-C2'	5.90	121.67	114.00
5	X	17(A)	U	N1-C1'-C2'	5.89	121.66	114.00
23	20	50	GLY	N-CA-C	-5.73	98.78	113.10
50	L	117	GLY	N-CA-C	5.68	127.30	113.10
52	N	56	PRO	N-CA-C	-5.53	97.71	112.10
52	N	55	SER	C-N-CA	5.34	144.45	122.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
52	N	55	SER	Mainchain
39	Z	236	PRO	Peptide
39	Z	246	THR	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	33012	0	16618	430	0
2	01	62318	0	31345	807	0
3	02	2546	0	1292	41	0
4	Y	249	0	255	13	0
5	W	1640	0	837	15	0
5	X	1622	0	827	17	0
6	03	1353	0	1159	38	0
7	04	2082	0	2157	79	0
8	05	1565	0	1616	69	0
9	06	1552	0	1619	47	0
10	07	1410	0	1447	56	0
11	08	1323	0	1374	54	0
12	09	1111	0	1148	51	0
13	10	988	0	1025	57	0
14	11	1032	0	1088	49	0
15	12	1129	0	1162	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
16	13	938	0	1012	38	0
17	14	1045	0	1117	30	0
18	15	1074	0	1157	31	0
19	16	960	0	1000	54	0
20	17	892	0	923	35	0
21	18	917	0	965	45	0
22	19	947	0	1022	35	0
23	20	816	0	839	36	0
24	21	857	0	922	38	0
25	22	738	0	807	30	0
26	23	779	0	834	17	0
27	24	753	0	780	34	0
28	25	575	0	592	30	0
29	26	625	0	655	22	0
30	27	509	0	543	19	0
31	28	449	0	491	18	0
32	29	522	0	524	28	0
33	30	444	0	461	26	0
34	31	409	0	440	8	0
35	32	377	0	418	22	0
36	33	504	0	574	16	0
37	34	302	0	340	30	0
38	V	306	0	154	1	0
39	Z	2814	0	2682	105	0
40	B	1704	0	1732	66	0
41	C	1624	0	1699	64	0
42	D	1643	0	1710	78	0
43	E	1156	0	1199	42	0
44	F	817	0	808	51	0
45	G	1181	0	1240	43	0
46	H	979	0	1034	28	0
47	I	1022	0	1070	59	0
48	J	786	0	828	52	0
49	K	869	0	878	42	0
50	L	955	0	1019	36	0
51	M	883	0	944	48	0
52	N	805	0	847	55	0
53	O	714	0	737	31	0
54	P	649	0	666	28	0
55	Q	648	0	691	36	0
56	R	535	0	552	18	0
57	S	637	0	665	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	T	665	0	714	29	0
59	U	544	0	579	32	0
60	01	239	0	0	0	0
60	02	4	0	0	0	0
60	14	1	0	0	0	0
60	25	1	0	0	0	0
60	30	1	0	0	0	0
60	A	97	0	0	0	0
60	H	1	0	0	0	0
60	W	2	0	0	0	0
60	X	2	0	0	0	0
61	34	1	0	0	0	0
All	All	152649	0	103833	3103	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 12.

All (3103) 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)
2:01:45:G:H5''	2:01:46:G:H5'	1.26	1.16
1:A:376:G:H2'	1:A:377:G:H5''	1.33	1.08
2:01:1173:U:H2'	2:01:1174:U:H4'	1.36	1.04
1:A:9:G:H5'	43:E:107:GLY:HA3	1.44	1.00
18:15:50:ARG:HD3	18:15:65:ILE:HD11	1.41	1.00
48:J:42:LEU:HD11	48:J:73:LEU:HG	1.43	0.99
2:01:2870:C:H2'	2:01:2871:U:H5''	1.44	0.99
2:01:548:G:H2'	2:01:549:G:H4'	1.46	0.98
2:01:1058:U:H2'	2:01:1059:G:H4'	1.44	0.97
16:13:13:ASN:HD21	16:13:98:ARG:HB2	1.29	0.97
39:Z:21:LEU:HD21	39:Z:110:LEU:HG	1.48	0.96
53:O:84:LEU:HD23	53:O:86:LEU:HD23	1.47	0.95
1:A:516:U:H5	1:A:533:A:H62	1.12	0.95
1:A:440:C:H2'	1:A:441:A:H5''	1.46	0.94
1:A:136:C:H2'	1:A:137:U:H5''	1.48	0.94
33:30:8:THR:HG22	33:30:9:ARG:HD2	1.50	0.94
2:01:1697:G:H3'	2:01:1698:A:H5''	1.48	0.94
37:34:11:CYS:HB2	37:34:14:CYS:SG	2.08	0.93
40:B:124:THR:HG22	40:B:127:LYS:HD2	1.50	0.93
1:A:718:A:H5'	49:K:118:ASN:HB2	1.50	0.93
28:25:36:GLN:HE22	28:25:41:PHE:H	1.16	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:C:69:THR:HG21	41:C:75:VAL:HG21	1.52	0.92
52:N:52:ARG:HG3	52:N:58:ARG:HH12	1.33	0.91
39:Z:130:LEU:HD21	39:Z:192:LEU:HD21	1.49	0.91
1:A:179:A:H61	1:A:196:A:H62	1.19	0.90
54:P:5:ARG:HH22	54:P:26:ASN:HB2	1.34	0.90
16:13:13:ASN:ND2	16:13:98:ARG:HB2	1.85	0.89
2:01:275:C:H2'	2:01:276:U:H4'	1.54	0.89
39:Z:6:PRO:HA	39:Z:9:ASN:HD22	1.38	0.88
1:A:376:G:C2'	1:A:377:G:H5''	2.04	0.88
27:24:17:SER:HB3	27:24:21:ARG:HH12	1.39	0.87
46:H:10:LEU:HD22	46:H:74:ILE:HD11	1.54	0.87
15:12:58:ASN:HD21	15:12:128:ASN:ND2	1.73	0.86
7:04:77:VAL:HG21	7:04:109:LEU:HD11	1.54	0.86
2:01:1652:A:H62	19:16:11:ASN:HD21	1.22	0.86
39:Z:24:TYR:HB3	39:Z:117:ARG:HE	1.41	0.86
52:N:73:LEU:HD12	52:N:83:VAL:HG21	1.56	0.86
1:A:92:U:H2'	1:A:93:U:H4'	1.58	0.86
2:01:2188:U:H3'	2:01:2189:U:H5''	1.58	0.86
1:A:1259:C:H3'	1:A:1260:G:H5''	1.56	0.85
2:01:74:A:H4'	2:01:75:G:H5''	1.57	0.85
1:A:39:G:H2'	1:A:40:C:H5''	1.56	0.85
47:I:114:LYS:HE3	47:I:117:LEU:HD12	1.57	0.85
1:A:981:U:H3'	1:A:982:U:H5''	1.57	0.84
37:34:19:ARG:HD2	37:34:24:ARG:HD2	1.60	0.84
44:F:36:ILE:HD11	44:F:39:LEU:HB2	1.59	0.84
1:A:1108:G:H5'	41:C:175:HIS:CD2	2.12	0.83
13:10:54:VAL:HG21	13:10:56:ARG:HH21	1.40	0.83
2:01:1082:U:H3'	2:01:1083:U:H5''	1.59	0.83
10:07:35:LEU:HD21	10:07:151:LEU:HD22	1.60	0.83
1:A:420:U:H4'	1:A:421:U:H5	1.43	0.83
57:S:4:LEU:HD23	57:S:4:LEU:H	1.44	0.82
2:01:2508:G:H1	2:01:2580:U:H5	1.25	0.82
11:08:15:ASP:HB2	11:08:26:LYS:HB2	1.60	0.82
2:01:1807:G:H2'	2:01:1808:A:H5'	1.61	0.82
45:G:78:ARG:HD2	45:G:78:ARG:H	1.44	0.82
18:15:77:PRO:HG2	18:15:80:VAL:HG21	1.60	0.82
21:18:88:ARG:HE	21:18:112:ARG:HH21	1.22	0.82
24:21:82:MET:HB2	24:21:98:LYS:HB2	1.62	0.82
57:S:40:PHE:H	57:S:43:MET:HE3	1.45	0.82
1:A:614:C:H2'	1:A:615:G:H5''	1.62	0.82
11:08:117:PRO:HD2	11:08:120:ILE:HG13	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:G:H5''	54:P:5:ARG:HB2	1.62	0.81
1:A:1306:A:N6	1:A:1331:G:H1'	1.95	0.81
22:19:111:LYS:HD2	23:20:48:LYS:HE2	1.61	0.81
59:U:16:ARG:HB2	59:U:19:LYS:HD2	1.60	0.81
2:01:884:U:H3'	2:01:885:C:H5''	1.61	0.81
21:18:88:ARG:HE	21:18:112:ARG:NH2	1.78	0.80
2:01:1521:G:H3'	2:01:1522:A:H5''	1.64	0.80
52:N:52:ARG:HG3	52:N:58:ARG:NH1	1.95	0.80
56:R:47:ARG:H	56:R:47:ARG:HD2	1.46	0.80
2:01:955:U:H5	2:01:962:G:H1	1.29	0.80
2:01:1061:U:H3'	2:01:1062:G:H5'	1.62	0.80
43:E:96:GLN:HB3	43:E:123:LEU:HB2	1.62	0.79
2:01:2107:G:H2'	2:01:2108:A:H4'	1.65	0.79
1:A:1187:G:H4'	47:I:112:ARG:HH21	1.46	0.79
1:A:1228:C:H5''	51:M:114:PRO:HG3	1.64	0.79
2:01:2870:C:C2'	2:01:2871:U:H5''	2.11	0.79
3:02:45:A:H5'	10:07:91:ARG:HH11	1.47	0.79
40:B:19:THR:HG23	40:B:21:TYR:H	1.48	0.79
41:C:9:ILE:HA	52:N:97:LYS:HD3	1.65	0.79
19:16:63:ARG:HH11	19:16:76:VAL:HG12	1.48	0.78
13:10:1:MET:HG2	13:10:2:ALA:H	1.48	0.78
44:F:66:ALA:HB3	44:F:71:ILE:HD11	1.66	0.78
11:08:132:LEU:HD23	11:08:132:LEU:H	1.48	0.78
2:01:1558:C:H4'	2:01:1559:U:H5''	1.65	0.78
58:T:80:ALA:HA	58:T:83:ASN:HD22	1.49	0.78
2:01:1651:G:H4'	19:16:39:PRO:HG2	1.66	0.78
1:A:136:C:C2'	1:A:137:U:H5''	2.14	0.77
19:16:38:LEU:HD21	19:16:99:LYS:HG2	1.66	0.77
2:01:2553:G:H3'	2:01:2554:U:H5''	1.64	0.77
40:B:165:ALA:HB3	40:B:190:SER:HB3	1.67	0.77
28:25:39:THR:HG23	28:25:53:HIS:HD2	1.49	0.77
25:22:76:ARG:HB3	25:22:76:ARG:NH1	1.99	0.77
13:10:3:LEU:HD23	13:10:3:LEU:H	1.49	0.77
45:G:49:LEU:HB2	45:G:123:LEU:HD23	1.65	0.76
2:01:2502:G:H5'	2:01:2503:A:H5''	1.67	0.76
8:05:16:THR:HG22	8:05:18:ASP:H	1.51	0.76
14:11:21:PRO:HB2	14:11:22:PRO:HD3	1.66	0.76
51:M:28:ARG:HH21	51:M:62:PHE:HB2	1.50	0.76
42:D:158:LEU:HD21	42:D:174:ALA:HB1	1.65	0.76
13:10:23:LEU:HD21	13:10:96:PHE:HB2	1.67	0.76
2:01:1664:A:H61	2:01:1996:C:H42	1.32	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:73:A:H3'	5:X:74:C:C5'	2.15	0.76
1:A:769:G:H4'	1:A:1513:A:H4'	1.68	0.76
2:01:1141:U:H4'	2:01:1142:A:O4'	1.86	0.76
1:A:440:C:C2'	1:A:441:A:H5''	2.15	0.75
1:A:723:U:H5'	59:U:48:LYS:HG3	1.68	0.75
40:B:8:MET:HG2	40:B:10:LYS:H	1.50	0.75
47:I:83:THR:HG23	47:I:97:LEU:HD21	1.69	0.75
2:01:2297:A:N6	2:01:2319:G:H1'	2.02	0.75
13:10:23:LEU:HD12	13:10:119:PRO:HG3	1.67	0.75
2:01:704:G:H2'	2:01:726:G:H22	1.49	0.75
44:F:47:LEU:HD12	44:F:55:HIS:HA	1.67	0.75
8:05:108:ASP:OD2	8:05:206:ALA:HA	1.86	0.74
14:11:55:PRO:HG2	14:11:71:LYS:HB2	1.69	0.74
17:14:3:LEU:HD23	17:14:3:LEU:H	1.51	0.74
2:01:517:C:H5''	33:30:12:ARG:HH12	1.52	0.74
10:07:48:LEU:HA	10:07:51:ASN:HD22	1.53	0.74
21:18:47:ILE:HB	21:18:59:THR:HG23	1.67	0.74
2:01:215:G:H4'	2:01:216:A:H4'	1.68	0.74
47:I:24:ASN:HD22	47:I:26:LYS:CE	2.00	0.74
53:O:48:ASP:HB3	53:O:51:SER:HB2	1.70	0.74
2:01:2109:U:H3	2:01:2180:U:H3	1.34	0.74
49:K:126:ARG:HA	49:K:126:ARG:HE	1.52	0.74
8:05:181:ASP:HB2	8:05:186:LEU:HB2	1.69	0.74
25:22:40:LYS:HZ3	25:22:60:THR:HG22	1.52	0.74
9:06:5:LEU:HD23	9:06:6:LYS:N	2.03	0.74
27:24:56:PHE:CE1	27:24:61:LEU:HD21	2.23	0.74
46:H:77:VAL:HG12	46:H:84:ILE:HD12	1.70	0.74
41:C:16:PRO:HG2	41:C:53:ARG:HH22	1.51	0.73
2:01:2092:U:H4'	2:01:2093:G:H5''	1.70	0.73
25:22:76:ARG:HB3	25:22:76:ARG:HH11	1.53	0.73
45:G:49:LEU:HD22	45:G:123:LEU:HD22	1.70	0.73
45:G:113:LYS:HB2	45:G:117:LEU:HD23	1.70	0.73
1:A:328:C:H4'	1:A:329:A:H5'	1.69	0.73
2:01:775:G:H4'	2:01:776:G:H5'	1.69	0.73
42:D:10:LEU:HD13	42:D:62:ARG:HD2	1.71	0.73
42:D:25:ARG:HH21	42:D:29:THR:HB	1.53	0.73
1:A:1219:A:H5''	52:N:52:ARG:NH1	2.04	0.73
5:X:68:C:H2'	5:X:69:C:O4'	1.89	0.73
40:B:33:ALA:HB3	40:B:37:VAL:HG23	1.70	0.73
1:A:530:G:H3'	1:A:531:U:C5'	2.19	0.72
13:10:77:VAL:HG12	13:10:82:ILE:HG13	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1187:G:H4'	47:I:112:ARG:NH2	2.04	0.72
44:F:51:ILE:HD12	44:F:86:ARG:HE	1.54	0.72
40:B:86:CYS:HB2	40:B:88:GLN:HE22	1.53	0.72
30:27:17:GLU:HA	30:27:20:ASN:HD22	1.53	0.72
7:04:124:LYS:HB3	7:04:127:ASN:ND2	2.04	0.72
55:Q:46:HIS:HB2	55:Q:70:LYS:HZ3	1.54	0.72
1:A:1432:G:H1'	1:A:1468:A:H62	1.55	0.72
25:22:61:LEU:HD11	25:22:82:LYS:HE2	1.71	0.72
7:04:16:VAL:HB	7:04:203:VAL:HG22	1.71	0.71
46:H:11:THR:HA	46:H:14:ARG:HH12	1.54	0.71
54:P:14:ARG:HE	54:P:42:ILE:HD12	1.55	0.71
39:Z:87:ALA:HB2	39:Z:95:THR:HG22	1.71	0.71
2:01:1019:U:H3	2:01:1142:A:H62	1.38	0.71
47:I:29:ILE:HD11	47:I:66:VAL:HG12	1.71	0.71
2:01:929:U:H4'	31:28:37:ARG:HH21	1.53	0.71
2:01:2353:G:H2'	2:01:2354:C:H5''	1.72	0.71
2:01:992:C:H4'	23:20:74:ILE:HD13	1.72	0.71
2:01:1993:U:H4'	8:05:133:THR:HG21	1.71	0.71
59:U:15:LEU:HA	59:U:17:ARG:HH11	1.56	0.71
39:Z:41:LEU:HD23	39:Z:41:LEU:O	1.91	0.71
43:E:163:ILE:HD12	43:E:164:LEU:N	2.06	0.71
28:25:20:LYS:HE2	28:25:20:LYS:HA	1.73	0.70
1:A:1060:U:H5	41:C:1:GLY:HA3	1.56	0.70
1:A:1432:G:H1'	1:A:1468:A:N6	2.06	0.70
41:C:35:ASP:HB2	41:C:56:ILE:HD13	1.72	0.70
52:N:63:CYS:HB3	52:N:67:GLY:H	1.56	0.70
2:01:240:C:H3'	2:01:241:A:H5''	1.74	0.70
2:01:1901:A:H4'	7:04:252:LYS:HD3	1.74	0.70
45:G:39:GLU:OE1	47:I:42:THR:HB	1.90	0.70
49:K:22:ILE:HG21	49:K:95:THR:HG21	1.74	0.70
3:02:43:C:H4'	10:07:62:GLN:HE22	1.57	0.70
10:07:74:ALA:HB2	5:W:57:A:H5'	1.73	0.70
28:25:36:GLN:NE2	28:25:41:PHE:H	1.90	0.70
53:O:61:GLN:O	53:O:65:LEU:HD13	1.92	0.70
2:01:2305:U:H5''	10:07:130:GLY:HA3	1.74	0.69
51:M:55:LEU:HD12	51:M:56:ARG:N	2.06	0.69
1:A:1028:C:H42	1:A:1033:G:H1	1.41	0.69
2:01:885:C:H2'	2:01:886:A:C8	2.28	0.69
42:D:13:ARG:HD2	42:D:37:PRO:HB2	1.74	0.69
51:M:48:SER:O	51:M:52:ILE:HG13	1.93	0.69
47:I:104:THR:HG22	47:I:106:ASP:H	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:11:61:TYR:HD2	14:11:65:SER:HB3	1.57	0.69
1:A:310:G:H5''	54:P:31:ARG:HB2	1.73	0.69
42:D:57:LYS:HD3	42:D:202:LEU:HD23	1.74	0.69
53:O:31:LEU:O	53:O:35:ILE:HG12	1.93	0.69
1:A:1330:U:H4'	51:M:22:TYR:CE1	2.28	0.69
55:Q:19:SER:C	55:Q:20:ILE:HD12	2.13	0.69
48:J:59:LYS:HE2	48:J:62:ARG:HH21	1.58	0.69
1:A:614:C:C2'	1:A:615:G:H5''	2.23	0.69
2:01:663:G:H5''	17:14:17:LYS:HG2	1.75	0.69
12:09:78:VAL:HG11	12:09:102:ALA:HB1	1.73	0.69
49:K:72:ALA:HA	49:K:74:LYS:HZ3	1.58	0.69
50:L:109:ARG:HH12	50:L:112:ALA:H	1.39	0.69
17:14:119:PRO:HG3	17:14:138:ALA:O	1.93	0.69
28:25:67:VAL:HG22	28:25:74:LYS:HE2	1.75	0.69
2:01:1075:C:H3'	2:01:1076:C:H5''	1.74	0.69
7:04:250:GLN:HB3	7:04:254:LYS:HD2	1.74	0.69
24:21:11:ARG:H	24:21:11:ARG:HD2	1.57	0.69
51:M:24:VAL:HG23	51:M:28:ARG:HB3	1.75	0.69
2:01:74:A:H4'	2:01:75:G:C5'	2.23	0.68
59:U:40:PRO:HA	59:U:43:GLU:HG2	1.75	0.68
1:A:112:G:H21	1:A:354:G:H5'	1.58	0.68
1:A:1150:A:H4'	48:J:43:PRO:HG3	1.76	0.68
2:01:244:A:H5''	17:14:67:THR:HG21	1.74	0.68
10:07:97:GLU:HB2	32:29:25:ARG:HH21	1.57	0.68
1:A:1054:C:N4	39:Z:212:ARG:H	1.90	0.68
2:01:884:U:H3'	2:01:885:C:C5'	2.23	0.68
2:01:45:G:C5'	2:01:46:G:H5'	2.16	0.68
3:02:3:C:H3'	3:02:4:C:H5''	1.74	0.68
44:F:76:THR:HA	44:F:79:ARG:HH12	1.59	0.68
8:05:179:ARG:HB2	8:05:188:LEU:HD12	1.75	0.68
21:18:88:ARG:NE	21:18:112:ARG:HH21	1.91	0.68
46:H:11:THR:HA	46:H:14:ARG:NH1	2.09	0.68
2:01:1203:U:H4'	17:14:3:LEU:HD21	1.75	0.68
11:08:90:GLY:HA3	11:08:93:TYR:CD2	2.29	0.68
43:E:96:GLN:NE2	43:E:97:PRO:HD2	2.08	0.68
16:13:58:LEU:HD23	16:13:58:LEU:H	1.58	0.68
42:D:56:GLU:HG2	42:D:198:LEU:HB2	1.76	0.68
44:F:53:LYS:HG2	44:F:54:LEU:H	1.57	0.68
26:23:39:ASN:HB2	26:23:62:ALA:H	1.59	0.68
2:01:674:G:H5''	9:06:71:GLY:N	2.09	0.68
41:C:19:SER:OG	52:N:91:GLU:O	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:G:C2'	1:A:40:C:H5''	2.24	0.67
11:08:169:ARG:H	11:08:169:ARG:HD2	1.59	0.67
1:A:538:G:H5'	50:L:110:LYS:HB2	1.75	0.67
6:03:181:ASP:HB3	6:03:184:LYS:HG2	1.76	0.67
44:F:81:ASN:HD21	44:F:83:ALA:HB3	1.60	0.67
1:A:59:A:H3'	1:A:331:G:H22	1.59	0.67
1:A:1054:C:H41	39:Z:211:GLY:HA3	1.59	0.67
21:18:32:VAL:HG12	21:18:37:LYS:HA	1.76	0.67
54:P:36:VAL:HG23	54:P:53:ASP:HB2	1.74	0.67
1:A:1422:G:H5'	16:13:48:PRO:HG3	1.76	0.67
6:03:180:PHE:HB2	6:03:185:LEU:HD21	1.76	0.67
50:L:58:ASN:HD21	50:L:60:PHE:HD2	1.43	0.67
2:01:1173:U:C2'	2:01:1174:U:H4'	2.17	0.67
3:02:3:C:C3'	3:02:4:C:H5''	2.25	0.67
35:32:3:ARG:HA	35:32:3:ARG:NE	2.10	0.67
36:33:32:LEU:HD23	36:33:35:LYS:HD2	1.77	0.67
2:01:751:A:H5'	24:21:90:LYS:HA	1.76	0.67
32:29:64:PHE:O	32:29:66:ILE:HG13	1.95	0.67
2:01:2529:G:H4'	11:08:174:LYS:HE2	1.77	0.67
2:01:2800:A:H3'	2:01:2801:G:H5'	1.75	0.67
15:12:32:LEU:HD22	15:12:54:ILE:HD12	1.76	0.67
19:16:28:LEU:HD23	19:16:28:LEU:O	1.95	0.67
25:22:40:LYS:NZ	25:22:60:THR:HG22	2.10	0.67
34:31:13:SER:HB3	34:31:47:ILE:HG13	1.76	0.67
2:01:704:G:H2'	2:01:726:G:N2	2.10	0.67
2:01:1459:G:H2'	2:01:1460:U:H5''	1.76	0.67
10:07:73:VAL:H	10:07:78:ILE:HG13	1.60	0.67
14:11:72:THR:HB	14:11:115:ASP:HB2	1.77	0.67
2:01:1012:U:H3	15:12:27:ARG:HD2	1.60	0.66
24:21:74:ILE:HD13	24:21:105:VAL:HG22	1.76	0.66
2:01:955:U:H5	2:01:962:G:N1	1.92	0.66
1:A:1103:C:H5''	40:B:96:LEU:HD22	1.78	0.66
8:05:7:LYS:HD3	8:05:77:ARG:HH22	1.60	0.66
15:12:17:VAL:HG23	15:12:137:PRO:HB2	1.78	0.66
21:18:28:LYS:HB3	21:18:39:LEU:HD11	1.78	0.66
43:E:98:ALA:HB2	43:E:123:LEU:HG	1.77	0.66
8:05:46:ARG:HG2	8:05:84:LEU:HB2	1.78	0.66
13:10:26:VAL:HG12	13:10:84:TYR:HA	1.76	0.66
43:E:96:GLN:HE21	43:E:97:PRO:HD2	1.61	0.66
2:01:2297:A:N1	2:01:2321:U:H5	1.93	0.66
43:E:44:ARG:HE	43:E:70:MET:HB3	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:B:42:LEU:HD23	40:B:42:LEU:H	1.61	0.66
51:M:89:ARG:HB2	51:M:96:VAL:HG12	1.76	0.66
2:01:1645:G:H5''	2:01:1646:C:H5'	1.78	0.66
37:34:24:ARG:HH22	37:34:36:ARG:HH11	1.43	0.66
43:E:98:ALA:HB1	43:E:101:GLY:HA3	1.78	0.66
55:Q:46:HIS:HB2	55:Q:70:LYS:NZ	2.10	0.66
2:01:1084:A:H5''	13:10:54:VAL:HG13	1.77	0.66
7:04:104:LEU:HD12	7:04:142:ASN:HD22	1.61	0.66
9:06:46:GLN:HB3	9:06:83:VAL:HG21	1.78	0.66
2:01:1838:C:H4'	2:01:1839:G:H5'	1.78	0.66
47:I:24:ASN:HD22	47:I:26:LYS:HE2	1.59	0.66
52:N:8:ARG:HB3	52:N:12:ARG:HH12	1.60	0.66
13:10:44:ALA:HA	13:10:52:MET:SD	2.36	0.66
56:R:17:VAL:HG22	56:R:18:GLN:H	1.61	0.66
16:13:71:ARG:HE	16:13:77:ILE:HD11	1.60	0.65
42:D:45:PRO:HB2	42:D:47:LEU:HD12	1.77	0.65
48:J:80:THR:HG22	48:J:81:GLU:H	1.60	0.65
2:01:974:G:H1'	2:01:975:A:C8	2.31	0.65
2:01:2457:U:H5	2:01:2494:G:H1	1.44	0.65
3:02:118:C:H2'	3:02:119:A:H8	1.60	0.65
5:X:36:U:H2'	5:X:37:A:H5'	1.77	0.65
15:12:99:ARG:O	15:12:103:ILE:HG13	1.96	0.65
54:P:25:ARG:HD3	54:P:25:ARG:H	1.61	0.65
47:I:60:LEU:HD12	47:I:60:LEU:O	1.97	0.65
21:18:3:ILE:H	21:18:3:ILE:HD12	1.61	0.65
2:01:2188:U:H2'	2:01:2189:U:H4'	1.78	0.65
2:01:2884:U:C1'	33:30:49:ARG:HH12	2.10	0.65
31:28:4:ILE:HG23	31:28:58:GLU:HG2	1.79	0.65
44:F:81:ASN:ND2	44:F:83:ALA:HB3	2.12	0.65
1:A:719:C:N4	56:R:59:LYS:HE2	2.11	0.65
2:01:548:G:H2'	2:01:549:G:C4'	2.24	0.65
3:02:3:C:H2'	3:02:4:C:H5''	1.78	0.65
2:01:322:A:H5'	2:01:340:A:H1'	1.79	0.65
2:01:361:G:O2'	2:01:362:A:H5'	1.97	0.65
2:01:805:G:H5''	17:14:38:GLN:HG3	1.79	0.65
2:01:1857:G:H1'	2:01:1885:A:N6	2.11	0.65
2:01:2107:G:H3'	2:01:2108:A:H5''	1.78	0.65
7:04:144:GLU:HB2	7:04:187:CYS:HB3	1.79	0.65
39:Z:162:LYS:HB3	39:Z:184:SER:HB3	1.79	0.65
1:A:1506:U:O2'	1:A:1507:A:H5'	1.96	0.65
8:05:2:ILE:HG13	8:05:3:GLY:H	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:704:G:H1'	2:01:727:A:N6	2.12	0.65
33:30:9:ARG:HD2	33:30:9:ARG:H	1.62	0.65
2:01:1114:C:H2'	2:01:1115:G:O4'	1.96	0.64
2:01:1476:U:H3	2:01:1515:A:H62	1.44	0.64
5:X:73:A:H3'	5:X:74:C:H5''	1.77	0.64
1:A:454:G:H22	1:A:478:A:H2	1.43	0.64
1:A:501:C:H2'	1:A:502:A:C8	2.32	0.64
2:01:1177:G:H2'	2:01:1178:C:H4'	1.80	0.64
8:05:151:THR:HB	8:05:152:PRO:HD3	1.79	0.64
51:M:77:LYS:HB3	51:M:77:LYS:NZ	2.12	0.64
1:A:71:A:H3'	1:A:72:A:H5''	1.80	0.64
2:01:503:A:H4'	2:01:505:A:H5''	1.78	0.64
19:16:38:LEU:HB2	19:16:39:PRO:HD3	1.79	0.64
14:11:3:LYS:HG3	14:11:4:VAL:HG13	1.80	0.64
41:C:149:LYS:HE2	41:C:168:ARG:HD3	1.78	0.64
45:G:105:GLU:OE2	45:G:136:LYS:HE3	1.97	0.64
9:06:143:LEU:HD22	9:06:185:LYS:HG3	1.80	0.64
40:B:88:GLN:NE2	40:B:220:VAL:HG11	2.12	0.64
10:07:73:VAL:HB	10:07:78:ILE:HD11	1.78	0.64
37:34:14:CYS:HB3	37:34:27:CYS:SG	2.37	0.64
39:Z:113:LEU:HD23	39:Z:113:LEU:O	1.98	0.64
39:Z:265:HIS:HB3	39:Z:270:ILE:HB	1.79	0.64
41:C:107:LYS:HB3	41:C:143:LEU:HD21	1.78	0.64
59:U:16:ARG:HE	59:U:20:ARG:HH22	1.46	0.64
5:X:65:C:H2'	5:X:66:C:C6	2.32	0.64
50:L:3:VAL:HG13	55:Q:35:LYS:HD2	1.79	0.64
2:01:435:C:H2'	2:01:436:C:H5'	1.80	0.64
2:01:940:G:H2'	2:01:941:A:H5''	1.80	0.64
7:04:245:THR:HB	7:04:246:PRO:HD2	1.78	0.64
23:20:80:ARG:HG2	23:20:80:ARG:HH11	1.62	0.64
33:30:54:ILE:HG23	33:30:56:LYS:H	1.61	0.64
6:03:192:LEU:O	6:03:192:LEU:HD13	1.98	0.64
10:07:107:VAL:HG23	10:07:108:PRO:HD3	1.80	0.64
2:01:2389:G:H5''	2:01:2390:U:O4'	1.98	0.64
15:12:6:ALA:H	15:12:45:THR:HG21	1.62	0.64
2:01:1131:G:OP2	15:12:82:GLY:HA2	1.98	0.63
2:01:2297:A:H62	2:01:2319:G:H1'	1.62	0.63
10:07:40:GLY:HA2	10:07:84:ILE:HD11	1.78	0.63
18:15:53:MET:HG3	18:15:116:ALA:HB1	1.80	0.63
54:P:5:ARG:NH2	54:P:26:ASN:HB2	2.08	0.63
41:C:156:LEU:HD12	41:C:156:LEU:O	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:H:28:SER:HB3	46:H:56:PRO:HB2	1.80	0.63
51:M:28:ARG:NH2	51:M:62:PHE:HB2	2.13	0.63
52:N:65:GLN:HE21	52:N:82:LYS:HE2	1.62	0.63
2:01:1142:A:H4'	15:12:27:ARG:HH22	1.63	0.63
13:10:87:GLU:HG2	13:10:93:ALA:HB3	1.80	0.63
49:K:80:ASN:ND2	49:K:105:ARG:HD2	2.13	0.63
1:A:427:U:H5''	1:A:428:G:H2'	1.80	0.63
1:A:575:G:HO2'	1:A:821:G:H5'	1.63	0.63
2:01:2743:U:H2'	2:01:2744:G:H5''	1.81	0.63
42:D:31:CYS:HB3	42:D:32:LYS:HD3	1.81	0.63
1:A:673:A:H4'	44:F:86:ARG:HH12	1.63	0.63
12:09:6:LEU:O	12:09:6:LEU:HD23	1.98	0.63
59:U:8:ASN:HD22	59:U:8:ASN:H	1.47	0.63
32:29:11:GLU:HB2	32:29:23:LYS:HE3	1.81	0.63
2:01:713:G:H21	2:01:718:A:H62	1.45	0.63
14:11:25:PRO:O	14:11:29:GLN:HG2	1.98	0.63
53:O:55:LEU:O	53:O:55:LEU:HD23	1.99	0.63
1:A:614:C:C3'	1:A:615:G:H5''	2.28	0.63
10:07:32:LYS:HB3	10:07:91:ARG:NH2	2.13	0.63
41:C:35:ASP:HA	41:C:38:VAL:HG22	1.81	0.63
2:01:226:A:H2'	2:01:227:A:C8	2.34	0.63
2:01:674:G:H5''	9:06:71:GLY:H	1.64	0.62
2:01:1082:U:H3'	2:01:1083:U:C5'	2.29	0.62
40:B:14:HIS:CD2	40:B:42:LEU:HB3	2.34	0.62
44:F:42:TRP:HE1	44:F:61:LEU:HD22	1.64	0.62
47:I:20:ILE:HG21	47:I:60:LEU:HD22	1.81	0.62
1:A:136:C:C3'	1:A:137:U:H5''	2.29	0.62
1:A:1305:G:H22	1:A:1331:G:H2'	1.63	0.62
10:07:60:SER:HB2	10:07:90:LEU:HD21	1.81	0.62
42:D:117:VAL:HG22	42:D:122:ILE:HD12	1.81	0.62
2:01:644:A:H2'	2:01:645:C:C4'	2.29	0.62
2:01:770:G:H5''	35:32:10:LEU:HD23	1.80	0.62
2:01:1140:C:H5'	15:12:26:GLY:HA3	1.81	0.62
16:13:63:VAL:HG21	16:13:85:VAL:HG23	1.80	0.62
44:F:4:TYR:CE2	44:F:71:ILE:HG13	2.34	0.62
48:J:57:VAL:HG22	48:J:58:ASN:H	1.63	0.62
1:A:262:A:H4'	58:T:67:HIS:CD2	2.34	0.62
1:A:352:C:H4'	1:A:354:G:OP1	1.99	0.62
2:01:2020:A:H62	33:30:5:ASN:ND2	1.98	0.62
6:03:48:LEU:HD22	6:03:165:ASN:ND2	2.13	0.62
14:11:21:PRO:HB2	14:11:22:PRO:CD	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:06:24:ASN:ND2	9:06:27:LEU:HB2	2.13	0.62
20:17:48:LEU:HD21	20:17:87:ILE:HG13	1.81	0.62
55:Q:58:VAL:HG23	55:Q:76:ARG:O	2.00	0.62
1:A:405:U:H1'	1:A:498:A:H2'	1.81	0.62
2:01:644:A:H2'	2:01:645:C:H4'	1.82	0.62
2:01:1225:G:H5'	23:20:88:GLY:H	1.65	0.62
14:11:91:LYS:HB2	14:11:94:LYS:HB2	1.80	0.62
2:01:1697:G:C3'	2:01:1698:A:H5''	2.28	0.62
4:Y:20:LEU:O	4:Y:20:LEU:HD23	1.98	0.62
9:06:175:ILE:O	9:06:175:ILE:HD12	1.99	0.62
31:28:55:LYS:HG2	31:28:57:GLU:HG2	1.82	0.62
55:Q:10:ARG:HD3	55:Q:55:GLY:HA2	1.81	0.62
1:A:1226:C:H2'	51:M:101:THR:HG22	1.81	0.62
2:01:45:G:H5''	2:01:46:G:C5'	2.16	0.62
2:01:511:U:H2'	2:01:512:G:H5'	1.80	0.62
2:01:1084:A:H5''	13:10:54:VAL:CG1	2.29	0.62
19:16:90:ARG:HB2	19:16:90:ARG:NH1	2.14	0.62
55:Q:59:GLU:HG3	55:Q:76:ARG:NH2	2.15	0.62
2:01:2884:U:H1'	33:30:49:ARG:HH12	1.65	0.62
20:17:21:LEU:O	20:17:21:LEU:HD23	1.99	0.62
39:Z:21:LEU:HD23	39:Z:113:LEU:HD13	1.81	0.62
1:A:1196:A:H1'	4:Y:34:LYS:HD3	1.81	0.62
49:K:124:LYS:HA	59:U:34:ARG:HB3	1.80	0.62
2:01:1084:A:N3	13:10:56:ARG:HD2	2.15	0.61
14:11:53:PRO:HG2	14:11:77:VAL:HG11	1.80	0.61
2:01:1061:U:H3'	2:01:1062:G:C5'	2.30	0.61
11:08:171:LYS:HB2	11:08:171:LYS:NZ	2.15	0.61
24:21:83:LYS:HB2	24:21:83:LYS:NZ	2.14	0.61
45:G:24:LYS:HB2	45:G:24:LYS:NZ	2.16	0.61
1:A:875:U:O2'	46:H:14:ARG:HD2	2.00	0.61
2:01:1651:G:H5'	19:16:39:PRO:HB2	1.81	0.61
2:01:1810:A:H2'	2:01:1811:G:O4'	2.00	0.61
2:01:2071:A:H2'	2:01:2072:C:C6	2.35	0.61
19:16:38:LEU:HD22	19:16:42:LYS:NZ	2.14	0.61
42:D:200:VAL:HG11	43:E:102:THR:HG22	1.82	0.61
50:L:98:ARG:HB2	50:L:116:TYR:HA	1.82	0.61
54:P:78:VAL:HG13	54:P:80:LYS:H	1.64	0.61
1:A:1241:G:H2'	1:A:1242:G:H8	1.65	0.61
34:31:37:LYS:HB2	34:31:48:TYR:CE2	2.35	0.61
1:A:1318:A:H2'	1:A:1319:A:H5'	1.81	0.61
2:01:481:G:H1'	2:01:506:G:N2	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1081:U:H4'	14:11:123:ALA:HB1	1.82	0.61
2:01:1535:A:H3'	2:01:1536:C:H5'	1.83	0.61
2:01:2537:U:H2'	2:01:2538:C:C6	2.36	0.61
8:05:184:ARG:HD2	8:05:186:LEU:HD11	1.82	0.61
10:07:113:PHE:HB3	32:29:41:HIS:HE1	1.65	0.61
16:13:13:ASN:HD21	16:13:98:ARG:CB	2.08	0.61
20:17:110:ALA:HB1	20:17:115:LEU:HD23	1.81	0.61
12:09:96:THR:HG22	12:09:117:LEU:HG	1.83	0.61
32:29:32:LEU:HD22	32:29:34:LEU:HD23	1.82	0.61
57:S:35:ARG:HD3	57:S:51:HIS:O	1.99	0.61
1:A:1306:A:H61	1:A:1331:G:H1'	1.64	0.61
12:09:132:PHE:HB2	12:09:140:ALA:HB3	1.83	0.61
14:11:83:ALA:HB2	14:11:100:ILE:HD11	1.82	0.61
40:B:23:ASN:ND2	40:B:25:LYS:HB2	2.15	0.61
3:02:2:G:H2'	3:02:3:C:C6	2.35	0.61
23:20:2:TYR:CE1	23:20:42:ALA:HB3	2.35	0.61
40:B:19:THR:HG23	40:B:21:TYR:N	2.15	0.61
43:E:81:GLN:HE21	43:E:81:GLN:HA	1.65	0.61
1:A:12:U:H4'	1:A:526:C:H4'	1.83	0.61
11:08:103:ASN:HD22	11:08:104:LEU:N	1.99	0.61
15:12:93:ILE:HD13	15:12:100:VAL:HG21	1.83	0.61
16:13:76:VAL:HG12	21:18:72:VAL:HG22	1.82	0.61
1:A:707:U:H4'	49:K:21:HIS:ND1	2.16	0.61
1:A:1477:U:H2'	1:A:1478:U:C6	2.36	0.61
32:29:16:CYS:HA	32:29:34:LEU:HB2	1.83	0.61
45:G:38:ALA:O	45:G:42:VAL:HG23	2.01	0.61
9:06:98:LYS:HB3	9:06:102:ARG:HH22	1.66	0.60
38:V:17:U:H2'	38:V:18:G:C8	2.36	0.60
48:J:32:THR:HG23	48:J:33:GLY:H	1.65	0.60
1:A:1162:C:H2'	1:A:1163:A:H8	1.66	0.60
2:01:215:G:C4'	2:01:216:A:H4'	2.31	0.60
24:21:25:ARG:HE	24:21:74:ILE:HG23	1.66	0.60
46:H:73:SER:HB2	46:H:129:ALA:HB3	1.83	0.60
2:01:876:C:H2'	2:01:877:A:H5'	1.83	0.60
2:01:1801:A:H5''	2:01:2203:U:H2'	1.82	0.60
3:02:3:C:C2'	3:02:4:C:H5''	2.32	0.60
49:K:34:THR:HG22	49:K:40:ALA:HA	1.83	0.60
2:01:810:U:O4	17:14:30:THR:HG22	2.01	0.60
47:I:24:ASN:HB3	47:I:26:LYS:HE2	1.84	0.60
53:O:25:GLU:OE1	53:O:76:ARG:HD3	2.00	0.60
59:U:40:PRO:O	59:U:44:ARG:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:257:THR:HG22	39:Z:259:SER:H	1.67	0.60
39:Z:272:THR:HG21	39:Z:291:MET:HA	1.84	0.60
1:A:1226:C:H5''	51:M:101:THR:HG21	1.83	0.60
2:01:2328:A:H2'	2:01:2329:U:C6	2.36	0.60
19:16:56:LYS:NZ	19:16:56:LYS:HB3	2.17	0.60
49:K:88:PRO:HA	49:K:92:ARG:HH11	1.66	0.60
6:03:65:LEU:HB2	6:03:188:ASN:HD21	1.67	0.60
7:04:33:LEU:HD23	7:04:34:GLU:N	2.17	0.60
27:24:30:ILE:HB	27:24:38:LEU:HB2	1.84	0.60
30:27:23:ARG:HA	30:27:23:ARG:HE	1.66	0.60
47:I:98:ARG:HG2	47:I:103:VAL:HG21	1.84	0.60
1:A:730:G:H2'	1:A:731:G:H5'	1.83	0.60
2:01:402:A:H2'	2:01:403:U:H5'	1.82	0.60
8:05:178:VAL:HG12	8:05:179:ARG:HG3	1.83	0.60
13:10:11:ILE:HG13	13:10:65:GLU:OE1	2.02	0.60
21:18:3:ILE:HD12	21:18:3:ILE:N	2.17	0.60
24:21:19:LEU:HD23	24:21:41:LYS:NZ	2.17	0.60
2:01:929:U:H4'	31:28:37:ARG:NH2	2.16	0.60
7:04:20:ASN:HB3	7:04:23:LEU:HG	1.83	0.60
42:D:59:LYS:O	42:D:63:ILE:HG13	2.02	0.60
46:H:6:ILE:HD11	46:H:31:LEU:HD23	1.84	0.60
14:11:25:PRO:HB2	39:Z:47:TRP:HE1	1.67	0.60
19:16:59:SER:HB2	19:16:62:ASN:HD22	1.67	0.60
45:G:138:GLU:HB3	45:G:142:ARG:HH12	1.66	0.60
1:A:219:U:H2'	1:A:220:G:C4'	2.32	0.59
12:09:84:ALA:HA	12:09:91:PHE:H	1.67	0.59
5:W:47:U:H3'	5:W:48:C:H5'	1.85	0.59
2:01:69:C:O2'	2:01:70:G:H5'	2.02	0.59
11:08:45:ALA:HB3	11:08:48:THR:O	2.02	0.59
26:23:27:VAL:HG12	26:23:33:VAL:HG12	1.84	0.59
41:C:9:ILE:HG23	41:C:10:ARG:HG3	1.83	0.59
1:A:1319:A:HO2'	57:S:2:ARG:N	1.99	0.59
16:13:10:VAL:HG21	16:13:16:ALA:HB3	1.84	0.59
58:T:59:ARG:HG2	58:T:63:LYS:HE2	1.84	0.59
2:01:161:A:H3'	2:01:162:U:H5''	1.83	0.59
2:01:1148:U:C3'	2:01:1149:G:H5''	2.32	0.59
3:02:118:C:H2'	3:02:119:A:C8	2.37	0.59
12:09:27:ARG:HH12	29:26:55:MET:HB3	1.66	0.59
14:11:50:LYS:HB3	14:11:50:LYS:HZ3	1.67	0.59
27:24:53:LYS:HB2	27:24:53:LYS:NZ	2.17	0.59
39:Z:181:ILE:N	39:Z:181:ILE:HD12	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2313:C:H5''	10:07:87:LYS:HD3	1.85	0.59
24:21:83:LYS:HD2	24:21:95:ARG:NH1	2.17	0.59
37:34:34:LYS:NZ	37:34:34:LYS:HB3	2.18	0.59
39:Z:156:ALA:HB1	39:Z:161:PHE:HB2	1.85	0.59
39:Z:193:ARG:NH1	39:Z:193:ARG:HB3	2.18	0.59
41:C:19:SER:HB2	41:C:21:TRP:HE1	1.67	0.59
47:I:105:ARG:O	47:I:105:ARG:HD3	2.01	0.59
1:A:1227:A:H2'	1:A:1228:C:H5'	1.84	0.59
1:A:1399:C:H1'	1:A:1400:C:OP2	2.02	0.59
2:01:1082:U:H2'	2:01:1083:U:H4'	1.84	0.59
14:11:124:MET:O	14:11:128:ILE:HG13	2.03	0.59
17:14:95:LEU:HD11	17:14:125:LEU:HD21	1.83	0.59
17:14:95:LEU:HD22	17:14:100:ILE:HD11	1.84	0.59
48:J:91:ASP:O	48:J:92:LEU:HB2	2.02	0.59
1:A:31:G:N2	1:A:47:C:H5''	2.17	0.59
1:A:501:C:H2'	1:A:502:A:H8	1.68	0.59
2:01:1178:C:H2'	2:01:1178:C:O2	2.02	0.59
2:01:1652:A:H62	19:16:11:ASN:ND2	1.96	0.59
8:05:55:LYS:HD3	8:05:77:ARG:HA	1.83	0.59
40:B:17:HIS:HB3	40:B:37:VAL:HB	1.85	0.59
44:F:81:ASN:HD22	44:F:84:VAL:H	1.50	0.59
1:A:211:G:H2'	1:A:212:G:H5'	1.85	0.59
2:01:372:G:O4'	29:26:60:LYS:HD3	2.03	0.59
2:01:1026:G:H2'	2:01:1027:A:H8	1.67	0.59
2:01:2836:U:H2'	2:01:2837:A:C8	2.37	0.59
46:H:9:MET:HG3	46:H:26:MET:SD	2.43	0.59
59:U:23:GLU:OE2	59:U:27:VAL:HG11	2.03	0.59
1:A:194:C:H5'	58:T:55:PRO:HA	1.85	0.59
11:08:19:ASN:HB3	11:08:22:VAL:HB	1.84	0.59
43:E:110:MET:O	43:E:114:LEU:HD13	2.02	0.59
1:A:1171:A:H2'	1:A:1172:C:C6	2.38	0.59
2:01:1468:U:H2'	2:01:1522:A:N6	2.18	0.59
10:07:151:LEU:HD12	10:07:151:LEU:O	2.03	0.59
15:12:47:HIS:ND1	15:12:48:VAL:HG23	2.17	0.59
18:15:14:LYS:NZ	18:15:14:LYS:HB2	2.17	0.59
40:B:13:VAL:HG23	40:B:208:ALA:HB2	1.85	0.59
40:B:139:GLU:O	40:B:143:LEU:HD23	2.02	0.59
1:A:715:A:H2'	1:A:716:A:C8	2.38	0.58
2:01:1344:U:H3'	2:01:1345:C:H5'	1.85	0.58
14:11:21:PRO:HG3	39:Z:38:ASN:OD1	2.03	0.58
22:19:89:ILE:HD12	22:19:89:ILE:H	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:19:89:ILE:HD12	22:19:89:ILE:N	2.18	0.58
28:25:34:VAL:HG11	28:25:41:PHE:HD2	1.68	0.58
39:Z:131:ASP:HB3	39:Z:221:PHE:HB3	1.85	0.58
1:A:986:U:H2'	1:A:987:G:C8	2.38	0.58
2:01:2845:U:H4'	21:18:52:ARG:NH1	2.18	0.58
14:11:42:ASN:HA	14:11:45:THR:HG22	1.85	0.58
20:17:24:THR:HG22	20:17:42:PRO:HD3	1.83	0.58
31:28:8:GLN:HE21	31:28:31:ILE:HG22	1.67	0.58
34:31:8:ILE:HD13	34:31:24:LYS:HB2	1.85	0.58
39:Z:127:ASP:HA	39:Z:188:ALA:HB3	1.85	0.58
1:A:1492:A:H1'	4:Y:26:ARG:CB	2.33	0.58
2:01:1060:U:O2'	14:11:74:PRO:HB3	2.01	0.58
15:12:58:ASN:HD21	15:12:128:ASN:HD22	1.51	0.58
29:26:32:LEU:HD21	29:26:49:ARG:HB3	1.86	0.58
44:F:93:LYS:HB3	44:F:93:LYS:NZ	2.18	0.58
50:L:54:VAL:HG21	50:L:81:ILE:HD11	1.86	0.58
50:L:71:HIS:HB2	50:L:73:LEU:HD13	1.84	0.58
2:01:381:G:H5''	29:26:15:ASN:HD22	1.68	0.58
2:01:1450:G:H21	2:01:1452:G:H1	1.50	0.58
2:01:2074:U:H2'	2:01:2075:U:C6	2.38	0.58
51:M:3:ILE:O	51:M:3:ILE:HD12	2.03	0.58
2:01:639:U:H2'	2:01:640:C:C6	2.39	0.58
2:01:1075:C:C3'	2:01:1076:C:H5''	2.33	0.58
2:01:1287:A:C2	2:01:1649:G:H4'	2.37	0.58
2:01:2870:C:C3'	2:01:2871:U:H5''	2.32	0.58
12:09:40:THR:HB	12:09:43:ASN:HD22	1.68	0.58
44:F:1:MET:HG3	44:F:67:PRO:HG3	1.85	0.58
46:H:29:SER:HB3	46:H:32:LYS:HG3	1.86	0.58
55:Q:32:ILE:HD12	55:Q:32:ILE:N	2.18	0.58
1:A:130:A:O2'	1:A:264:C:H5'	2.03	0.58
2:01:192:C:H2'	2:01:193:U:H5'	1.84	0.58
41:C:71:ARG:O	41:C:75:VAL:HG23	2.04	0.58
8:05:46:ARG:HH22	8:05:89:GLU:HB2	1.69	0.58
41:C:185:THR:HG23	41:C:197:VAL:O	2.03	0.58
43:E:104:ILE:HG23	43:E:111:ARG:NH1	2.19	0.58
46:H:45:ILE:HG13	46:H:46:GLU:H	1.68	0.58
2:01:1076:C:H2'	2:01:1077:A:O4'	2.04	0.58
2:01:1142:A:H4'	15:12:27:ARG:NH2	2.18	0.58
2:01:1373:A:H5'	2:01:2212:A:H1'	1.85	0.58
8:05:27:ILE:HB	8:05:187:LEU:HB3	1.86	0.58
12:09:62:LEU:HD23	12:09:66:ASN:ND2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:22:4:GLU:O	25:22:8:LEU:HD13	2.03	0.58
52:N:50:LEU:HD12	52:N:51:PRO:HD2	1.84	0.58
1:A:1259:C:C3'	1:A:1260:G:H5''	2.32	0.58
2:01:563:A:H4'	22:19:40:LYS:NZ	2.19	0.58
2:01:782:A:C2	7:04:224:MET:HG2	2.38	0.58
2:01:1454:C:H5'	19:16:63:ARG:NH2	2.18	0.58
2:01:2122:U:H2'	2:01:2123:G:O4'	2.04	0.58
2:01:2642:G:H5'	15:12:80:HIS:CD2	2.39	0.58
25:22:53:VAL:HG22	25:22:92:ASN:HB2	1.86	0.58
28:25:34:VAL:HG11	28:25:41:PHE:CD2	2.39	0.58
46:H:91:LEU:HD12	46:H:92:PRO:HD2	1.85	0.58
1:A:362:G:H5''	50:L:57:THR:HG21	1.85	0.58
2:01:2682:A:C2	8:05:23:PRO:HB3	2.39	0.58
9:06:97:ASN:HB2	9:06:100:MET:HG3	1.86	0.58
24:21:34:ASP:HB3	33:30:27:LEU:HD11	1.86	0.58
2:01:121:G:H4'	2:01:149:A:H5'	1.86	0.57
7:04:74:PRO:HG2	7:04:96:LYS:HG3	1.85	0.57
8:05:4:LEU:HD22	8:05:32:ASN:HD22	1.68	0.57
39:Z:264:THR:HG22	39:Z:271:VAL:HG22	1.84	0.57
40:B:91:VAL:HG21	40:B:95:TRP:HD1	1.68	0.57
48:J:80:THR:HG22	48:J:81:GLU:N	2.18	0.57
49:K:88:PRO:HB2	59:U:28:LEU:HD22	1.86	0.57
1:A:505:G:H5'	1:A:534:U:O2'	2.05	0.57
13:10:8:LYS:O	13:10:12:VAL:HG23	2.03	0.57
18:15:71:LYS:HZ3	18:15:95:LEU:HD11	1.69	0.57
26:23:25:LYS:HD3	26:23:36:GLU:HB3	1.86	0.57
43:E:106:ALA:HB1	43:E:110:MET:HE3	1.85	0.57
44:F:75:GLU:HA	44:F:78:PHE:HD2	1.69	0.57
48:J:40:ILE:HB	48:J:73:LEU:HB2	1.85	0.57
52:N:36:SER:HB2	52:N:40:ARG:NH1	2.19	0.57
3:02:43:C:H4'	10:07:62:GLN:NE2	2.19	0.57
5:X:49:G:H2'	5:X:50:U:C6	2.39	0.57
21:18:105:LYS:HB3	21:18:108:ARG:HH22	1.69	0.57
26:23:35:VAL:HB	26:23:38:ILE:HG13	1.86	0.57
1:A:511:C:H2'	1:A:512:U:O2	2.05	0.57
1:A:1240:U:H4'	45:G:37:THR:CG2	2.34	0.57
2:01:942:G:H2'	2:01:943:A:O4'	2.03	0.57
2:01:1857:G:H1'	2:01:1885:A:H61	1.69	0.57
2:01:2066:C:O2'	2:01:2067:G:H5'	2.04	0.57
2:01:2297:A:N1	2:01:2321:U:C5	2.72	0.57
9:06:181:ILE:HD13	17:14:3:LEU:HB3	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:09:31:VAL:HB	12:09:32:PRO:HD3	1.86	0.57
13:10:3:LEU:H	13:10:3:LEU:CD2	2.17	0.57
19:16:55:ALA:HA	19:16:80:PHE:CE1	2.39	0.57
23:20:11:GLN:HE21	23:20:11:GLN:H	1.53	0.57
40:B:46:VAL:HB	40:B:47:PRO:HD3	1.85	0.57
40:B:132:GLU:O	40:B:136:ARG:HG2	2.04	0.57
52:N:31:SER:HA	57:S:6:LYS:NZ	2.19	0.57
1:A:1422:G:H5'	16:13:48:PRO:CG	2.35	0.57
7:04:131:MET:HE2	7:04:187:CYS:HB2	1.86	0.57
37:34:36:ARG:HG2	37:34:37:GLN:N	2.20	0.57
50:L:79:ILE:HG22	50:L:103:CYS:HB2	1.86	0.57
2:01:1068:G:N2	2:01:1095:A:H1'	2.19	0.57
2:01:1148:U:H2'	2:01:1149:G:H5''	1.85	0.57
12:09:23:ALA:O	12:09:27:ARG:HG2	2.04	0.57
19:16:59:SER:O	19:16:63:ARG:HG3	2.05	0.57
35:32:41:ARG:H	35:32:41:ARG:HD2	1.69	0.57
39:Z:11:ILE:HG12	39:Z:103:LEU:HD13	1.86	0.57
55:Q:31:PRO:HB2	55:Q:32:ILE:HD12	1.85	0.57
1:A:9:G:H4'	43:E:108:GLY:H	1.69	0.57
27:24:42:LEU:HD11	27:24:91:PHE:HE2	1.70	0.57
49:K:80:ASN:HD21	49:K:105:ARG:HD2	1.70	0.57
50:L:43:LYS:HG3	50:L:44:PRO:HD3	1.85	0.57
52:N:42:ASN:N	52:N:42:ASN:HD22	2.01	0.57
1:A:419:C:H2'	1:A:420:U:O4'	2.05	0.57
2:01:2353:G:C2'	2:01:2354:C:H5''	2.35	0.57
30:27:24:GLU:O	30:27:28:LEU:HD12	2.05	0.57
2:01:738:G:O2'	2:01:739:A:H5'	2.04	0.57
2:01:1433:A:H2'	2:01:1434:A:O4'	2.05	0.57
2:01:2029:G:O6	2:01:2032:G:H5''	2.05	0.57
2:01:2526:G:H1'	37:34:1:MET:H1	1.70	0.57
6:03:23:ILE:O	6:03:27:ILE:HG13	2.04	0.57
11:08:8:VAL:HB	11:08:49:LEU:HB2	1.86	0.57
14:11:75:ALA:O	14:11:79:LEU:HD23	2.05	0.57
49:K:63:GLN:HG3	49:K:98:ALA:HB2	1.87	0.57
1:A:1379:G:O2'	1:A:1380:U:H5'	2.05	0.57
2:01:704:G:H1'	2:01:727:A:H61	1.69	0.56
2:01:1846:G:H2'	2:01:1847:G:O4'	2.05	0.56
2:01:2164:C:H2'	2:01:2165:C:H5'	1.87	0.56
2:01:2834:G:H2'	2:01:2879:A:H61	1.70	0.56
19:16:44:LEU:HD23	19:16:113:ILE:HD13	1.87	0.56
24:21:51:LEU:O	24:21:55:ILE:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:I:61:ASP:C	47:I:62:LEU:HD12	2.26	0.56
2:O1:242:G:H5''	36:33:63:TYR:CE2	2.40	0.56
10:07:63:LYS:HD2	32:29:5:ILE:HB	1.87	0.56
43:E:132:PRO:O	43:E:136:VAL:HG23	2.05	0.56
54:P:61:VAL:HG22	54:P:67:ILE:HD11	1.86	0.56
1:A:9:G:H5'	43:E:107:GLY:CA	2.29	0.56
1:A:686:U:H1'	49:K:43:TRP:HE1	1.70	0.56
2:O1:1451:C:H4'	2:O1:1452:G:O4'	2.05	0.56
2:O1:1979:U:O2'	2:O1:1980:G:H5'	2.05	0.56
2:O1:2092:U:C4'	2:O1:2093:G:H5''	2.35	0.56
23:20:16:GLU:OE1	23:20:100:GLY:HA2	2.05	0.56
23:20:76:LYS:HD2	23:20:85:LYS:HD2	1.86	0.56
31:28:40:THR:HG22	31:28:42:ALA:H	1.70	0.56
35:32:10:LEU:HD11	35:32:14:ARG:HH11	1.71	0.56
39:Z:130:LEU:CD2	39:Z:192:LEU:HD21	2.29	0.56
40:B:185:ILE:HA	40:B:199:ILE:HB	1.87	0.56
41:C:120:THR:HG23	41:C:188:ALA:HA	1.88	0.56
44:F:51:ILE:HD12	44:F:86:ARG:HH21	1.70	0.56
44:F:51:ILE:CD1	44:F:86:ARG:HE	2.18	0.56
47:I:118:ARG:HG2	47:I:119:LYS:HG3	1.87	0.56
50:L:86:VAL:HG23	50:L:88:ASP:H	1.68	0.56
52:N:40:ARG:HD2	52:N:40:ARG:O	2.05	0.56
55:Q:25:GLU:OE1	55:Q:38:LYS:HE2	2.05	0.56
1:A:673:A:H2'	1:A:674:G:C8	2.41	0.56
1:A:884:U:H4'	1:A:885:G:H5''	1.86	0.56
10:07:147:ARG:HG2	10:07:149:ARG:NH1	2.19	0.56
11:08:49:LEU:HD13	11:08:71:LEU:HD21	1.87	0.56
30:27:17:GLU:HB2	30:27:53:VAL:HG11	1.87	0.56
40:B:53:LEU:HB3	40:B:219:THR:HG21	1.87	0.56
50:L:113:ARG:HB2	50:L:118:VAL:HB	1.87	0.56
1:A:511:C:O2'	1:A:512:U:H5'	2.06	0.56
2:O1:2530:A:N6	11:08:155:PRO:HG3	2.21	0.56
27:24:20:LEU:HG	27:24:25:LYS:O	2.06	0.56
37:34:22:VAL:HG11	37:34:36:ARG:NH1	2.20	0.56
44:F:76:THR:HA	44:F:79:ARG:NH1	2.20	0.56
51:M:7:ASN:CG	51:M:9:PRO:HD3	2.25	0.56
51:M:16:ILE:H	51:M:16:ILE:HD12	1.71	0.56
53:O:34:GLN:HE22	53:O:38:LEU:HB2	1.69	0.56
53:O:87:ARG:HG3	53:O:88:ARG:HG2	1.87	0.56
1:A:128:G:O2'	1:A:129:A:H5'	2.05	0.56
1:A:437:U:O2'	1:A:438:U:H5'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2249:U:H3'	2:01:2250:G:H5'	1.88	0.56
2:01:2849:U:H4'	2:01:2868:A:C2	2.41	0.56
27:24:29:ILE:HG22	27:24:88:HIS:HE1	1.70	0.56
56:R:60:ARG:O	56:R:64:LEU:HD13	2.05	0.56
1:A:440:C:C3'	1:A:441:A:H5''	2.35	0.56
2:01:828:U:H2'	2:01:829:A:C8	2.40	0.56
2:01:1182:G:H2'	2:01:1183:U:O4'	2.04	0.56
2:01:1319:C:O2'	2:01:1320:C:H5'	2.04	0.56
26:23:4:ILE:HD12	26:23:4:ILE:N	2.21	0.56
40:B:86:CYS:HB2	40:B:88:GLN:NE2	2.21	0.56
42:D:113:ALA:O	42:D:117:VAL:HG23	2.06	0.56
1:A:1436:U:H2'	1:A:1437:A:H8	1.71	0.56
2:01:297:G:OP1	26:23:91:LYS:HD3	2.06	0.56
21:18:59:THR:HB	21:18:72:VAL:HG12	1.86	0.56
37:34:14:CYS:CB	37:34:27:CYS:SG	2.94	0.56
39:Z:151:MET:CE	39:Z:353:LEU:HD11	2.35	0.56
40:B:18:GLN:HB3	40:B:189:ASN:HD22	1.71	0.56
44:F:29:ILE:HG21	44:F:64:VAL:HG21	1.88	0.56
45:G:94:ARG:HG2	45:G:98:LEU:HD23	1.87	0.56
1:A:530:G:H3'	1:A:531:U:H5'	1.88	0.56
1:A:664:G:H22	1:A:741:G:H1	1.54	0.56
2:01:2175:C:O2'	2:01:2176:A:H5'	2.06	0.56
2:01:2298:A:H2'	2:01:2299:U:O4'	2.06	0.56
2:01:2514:U:H4'	15:12:81:ILE:HG21	1.88	0.56
10:07:40:GLY:HA2	10:07:84:ILE:CD1	2.36	0.56
10:07:65:LEU:HD23	10:07:87:LYS:HE2	1.88	0.56
17:14:48:ARG:HD2	36:33:59:ALA:O	2.05	0.56
19:16:90:ARG:HB2	19:16:90:ARG:HH11	1.71	0.56
21:18:17:PRO:HD2	21:18:83:ILE:HD11	1.86	0.56
23:20:11:GLN:H	23:20:11:GLN:NE2	2.04	0.56
7:04:128:THR:C	7:04:129:LEU:HD12	2.25	0.56
40:B:135:MET:HA	40:B:138:ARG:HG2	1.87	0.56
52:N:3:GLN:OE1	52:N:6:LYS:HD3	2.06	0.56
53:O:9:LYS:NZ	53:O:9:LYS:HB3	2.21	0.56
54:P:34:GLU:OE2	54:P:56:ARG:HD3	2.05	0.56
1:A:560:A:H5'	1:A:566:G:N2	2.22	0.55
13:10:96:PHE:CD2	13:10:129:LEU:HD21	2.41	0.55
17:14:39:LYS:HB2	17:14:39:LYS:NZ	2.21	0.55
21:18:62:LYS:NZ	21:18:62:LYS:HB3	2.21	0.55
26:23:28:LEU:HD12	26:23:32:LYS:HB2	1.87	0.55
35:32:41:ARG:HD2	35:32:41:ARG:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1594:U:H2'	2:01:1595:C:C6	2.41	0.55
7:04:257:ARG:HH11	7:04:257:ARG:HG3	1.70	0.55
12:09:62:LEU:HD23	12:09:66:ASN:HD21	1.69	0.55
14:11:54:ILE:HD11	14:11:70:THR:OG1	2.06	0.55
19:16:38:LEU:HD22	19:16:42:LYS:HZ3	1.71	0.55
30:27:16:THR:HG22	30:27:20:ASN:HD21	1.70	0.55
33:30:49:ARG:O	33:30:49:ARG:HG2	2.04	0.55
2:01:141:G:H3'	2:01:142:A:O4'	2.06	0.55
2:01:593:U:H2'	2:01:594:U:C6	2.41	0.55
2:01:1874:C:H2'	2:01:1875:G:O4'	2.05	0.55
11:08:90:GLY:HA3	11:08:93:TYR:HD2	1.71	0.55
32:29:16:CYS:HB3	32:29:20:ASN:H	1.70	0.55
40:B:177:ASN:N	40:B:177:ASN:HD22	2.03	0.55
49:K:86:LYS:HG2	49:K:112:VAL:HG23	1.87	0.55
1:A:60:A:H3'	58:T:4:LYS:HE3	1.87	0.55
1:A:211:G:C2'	1:A:212:G:H5'	2.36	0.55
2:01:813:U:H2'	2:01:814:C:C6	2.40	0.55
2:01:1443:U:H2'	2:01:1444:G:H8	1.71	0.55
3:02:87:U:H5''	3:02:88:C:OP2	2.04	0.55
10:07:107:VAL:CG2	10:07:108:PRO:HD3	2.37	0.55
13:10:24:SER:H	13:10:118:ILE:HD12	1.71	0.55
20:17:30:ARG:HD2	20:17:102:ARG:NH1	2.22	0.55
39:Z:18:SER:O	39:Z:22:ARG:HG3	2.07	0.55
55:Q:16:MET:HG2	55:Q:19:SER:HB2	1.88	0.55
1:A:831:A:H2'	1:A:832:G:H5''	1.88	0.55
2:01:878:A:H3'	2:01:879:G:H8	1.71	0.55
7:04:153:LEU:HD13	7:04:175:LEU:HD21	1.87	0.55
12:09:47:PHE:HD1	12:09:51:ARG:HD2	1.71	0.55
24:21:23:LEU:HD11	33:30:23:ALA:HB2	1.88	0.55
49:K:109:ILE:N	49:K:109:ILE:HD12	2.21	0.55
57:S:12:LEU:HD12	57:S:13:HIS:N	2.21	0.55
1:A:1151:A:H5'	48:J:43:PRO:HA	1.88	0.55
1:A:1240:U:H4'	45:G:37:THR:HG22	1.89	0.55
2:01:402:A:C2'	2:01:403:U:H5'	2.37	0.55
2:01:2350:C:H2'	2:01:2351:G:O4'	2.07	0.55
2:01:2836:U:H2'	2:01:2837:A:H8	1.71	0.55
11:08:34:ARG:HE	11:08:70:LEU:HD13	1.71	0.55
39:Z:353:LEU:O	39:Z:357:ILE:HG13	2.05	0.55
1:A:150:U:H3	1:A:171:A:H62	1.55	0.55
2:01:548:G:H3'	2:01:549:G:H5''	1.89	0.55
2:01:1148:U:H3'	2:01:1149:G:H5''	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1917:U:O2'	2:01:1918:A:H5'	2.06	0.55
5:X:72:A:H2'	5:X:73:A:H4'	1.88	0.55
8:05:25:THR:HG21	8:05:193:VAL:HG22	1.88	0.55
11:08:68:ARG:HH11	11:08:68:ARG:HG3	1.72	0.55
35:32:11:LYS:HB2	35:32:11:LYS:NZ	2.22	0.55
43:E:40:ASP:OD2	43:E:42:ASN:HB2	2.07	0.55
43:E:133:ILE:HD12	43:E:133:ILE:N	2.22	0.55
46:H:46:GLU:O	46:H:61:THR:HB	2.06	0.55
58:T:82:ILE:O	58:T:86:ALA:HB3	2.07	0.55
1:A:1216:A:H5''	52:N:4:SER:OG	2.06	0.55
2:01:475:C:H4'	2:01:510:C:H5'	1.89	0.55
6:03:21:TYR:HB2	6:03:222:VAL:HG11	1.87	0.55
19:16:9:GLN:HA	19:16:17:ARG:HH21	1.71	0.55
25:22:11:LEU:HD11	25:22:32:LEU:HD22	1.88	0.55
25:22:61:LEU:HD11	25:22:82:LYS:HB3	1.88	0.55
40:B:91:VAL:HG21	40:B:95:TRP:CD1	2.42	0.55
52:N:31:SER:HA	57:S:6:LYS:HZ2	1.71	0.55
58:T:34:VAL:HG11	58:T:78:LEU:HD21	1.89	0.55
1:A:414:A:H2'	1:A:414:A:N3	2.22	0.55
1:A:1347:G:O2'	1:A:1348:U:H5	1.90	0.55
1:A:1356:G:H2'	1:A:1357:A:C8	2.42	0.55
2:01:488:G:H22	2:01:491:G:H5''	1.72	0.55
2:01:799:G:H5''	2:01:800:A:H2'	1.89	0.55
2:01:2010:G:H5''	24:21:42:LYS:HB2	1.89	0.55
8:05:33:ARG:HD3	8:05:73:VAL:HB	1.89	0.55
8:05:46:ARG:HG2	8:05:84:LEU:HD12	1.89	0.55
11:08:126:THR:HG22	11:08:127:GLN:N	2.21	0.55
20:17:81:ARG:O	20:17:85:LYS:HD3	2.07	0.55
21:18:24:THR:HB	21:18:87:ARG:HG2	1.89	0.55
22:19:40:LYS:HG3	22:19:44:TYR:CE2	2.41	0.55
25:22:9:LYS:NZ	25:22:9:LYS:HB3	2.22	0.55
42:D:61:ARG:HH21	42:D:67:LEU:HA	1.71	0.55
59:U:60:ALA:HA	59:U:63:ASN:ND2	2.22	0.55
1:A:543:U:OP1	42:D:13:ARG:HG3	2.07	0.55
1:A:1230:C:H5'	5:W:30:G:H5''	1.88	0.55
2:01:2432:A:H1'	5:X:75:C:H5'	1.89	0.55
39:Z:34:LEU:O	39:Z:34:LEU:HD13	2.07	0.55
42:D:184:LYS:HD3	42:D:185:PRO:HD2	1.88	0.55
48:J:15:HIS:HA	48:J:18:ILE:HG22	1.89	0.55
50:L:47:ALA:HB3	50:L:49:ARG:HE	1.71	0.55
50:L:109:ARG:HB3	50:L:118:VAL:HG21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
57:S:43:MET:HA	57:S:46:LEU:HD12	1.89	0.55
1:A:1031:C:H4'	1:A:1033:G:H21	1.71	0.54
1:A:1120:C:H2'	1:A:1121:U:C6	2.43	0.54
2:01:118:A:H5'	2:01:119:A:H8	1.72	0.54
2:01:1360:G:H2'	2:01:1361:G:H5'	1.89	0.54
18:15:71:LYS:NZ	18:15:95:LEU:HD11	2.22	0.54
55:Q:35:LYS:NZ	55:Q:35:LYS:HB3	2.21	0.54
2:01:575:A:O2'	2:01:576:U:H5'	2.07	0.54
2:01:1394:U:H4'	2:01:1603:A:H4'	1.89	0.54
2:01:2087:G:H2'	2:01:2088:A:H8	1.73	0.54
2:01:2183:A:H2'	2:01:2184:A:H8	1.71	0.54
6:03:47:ASN:C	6:03:48:LEU:HD12	2.27	0.54
9:06:41:GLN:HG2	9:06:43:THR:HG23	1.88	0.54
16:13:71:ARG:HE	16:13:77:ILE:CD1	2.20	0.54
39:Z:7:VAL:O	39:Z:11:ILE:HG13	2.07	0.54
58:T:2:ASN:CG	58:T:3:ILE:H	2.11	0.54
58:T:34:VAL:O	58:T:38:ILE:HG13	2.07	0.54
1:A:575:G:O2'	1:A:821:G:H5'	2.06	0.54
2:01:433:C:O2'	2:01:434:U:H5'	2.07	0.54
2:01:1779:U:H5	2:01:1784:A:N7	2.05	0.54
2:01:2590:A:H61	2:01:2604:U:H3	1.53	0.54
6:03:41:SER:HA	6:03:177:LYS:HD3	1.88	0.54
13:10:22:ALA:HA	13:10:118:ILE:HG21	1.89	0.54
36:33:22:LYS:HA	36:33:48:MET:HA	1.89	0.54
37:34:36:ARG:HH11	37:34:36:ARG:HG3	1.72	0.54
41:C:13:ILE:N	41:C:13:ILE:HD12	2.23	0.54
41:C:55:VAL:CG2	41:C:66:THR:HB	2.36	0.54
45:G:137:ARG:O	45:G:137:ARG:HD2	2.07	0.54
47:I:80:HIS:O	47:I:84:ARG:HG2	2.07	0.54
54:P:67:ILE:N	54:P:67:ILE:HD12	2.23	0.54
1:A:1412:C:H2'	1:A:1413:A:C8	2.43	0.54
2:01:745:G:H21	2:01:750:A:H61	1.53	0.54
2:01:1041:G:H2'	2:01:1042:G:H8	1.73	0.54
2:01:1443:U:H2'	2:01:1444:G:C8	2.42	0.54
8:05:2:ILE:HG13	8:05:3:GLY:N	2.21	0.54
8:05:4:LEU:HD22	8:05:32:ASN:ND2	2.22	0.54
11:08:17:LYS:HB2	11:08:24:THR:HB	1.88	0.54
23:20:11:GLN:NE2	23:20:11:GLN:N	2.56	0.54
30:27:14:LEU:O	30:27:14:LEU:HD23	2.06	0.54
30:27:23:ARG:HA	30:27:23:ARG:NE	2.21	0.54
42:D:45:PRO:HB2	42:D:47:LEU:CD1	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:395:U:H2'	2:01:396:G:C8	2.42	0.54
2:01:1076:C:O2'	14:11:92:PRO:HG3	2.06	0.54
2:01:1084:A:P	13:10:53:ARG:HG3	2.48	0.54
2:01:2039:U:H2'	2:01:2040:G:C8	2.42	0.54
7:04:246:PRO:HG2	7:04:247:TRP:CE3	2.43	0.54
20:17:40:ILE:HG12	20:17:47:VAL:HG12	1.90	0.54
42:D:149:LYS:HG3	42:D:177:MET:CE	2.38	0.54
1:A:259:G:P	58:T:77:ASN:HD22	2.30	0.54
2:01:140:C:H2'	2:01:141:G:H4'	1.89	0.54
2:01:558:U:P	15:12:113:PRO:HD2	2.48	0.54
2:01:2238:G:N3	2:01:2238:G:H2'	2.22	0.54
2:01:2353:G:C3'	2:01:2354:C:H5''	2.38	0.54
6:03:8:MET:O	6:03:12:ARG:HG3	2.07	0.54
18:15:69:PRO:HA	18:15:94:ALA:HB2	1.89	0.54
20:17:35:ILE:HD11	20:17:106:LEU:HD12	1.89	0.54
41:C:180:ASP:HB3	41:C:204:GLY:H	1.72	0.54
48:J:59:LYS:CE	48:J:62:ARG:HH21	2.21	0.54
1:A:276:G:H5'	55:Q:16:MET:CE	2.38	0.54
1:A:358:U:H2'	1:A:359:G:H8	1.73	0.54
1:A:1001:C:H2'	1:A:1002:G:C8	2.43	0.54
1:A:1219:A:H5''	52:N:52:ARG:HH12	1.73	0.54
2:01:184:C:H4'	2:01:217:A:C2	2.42	0.54
2:01:1794:A:H2'	2:01:1795:C:C6	2.43	0.54
2:01:2475:C:H2'	2:01:2476:A:H5'	1.90	0.54
2:01:2834:G:H2'	2:01:2879:A:N6	2.23	0.54
7:04:131:MET:CE	7:04:187:CYS:HB2	2.38	0.54
11:08:88:LEU:HD22	11:08:95:ALA:HB2	1.89	0.54
24:21:74:ILE:CD1	24:21:105:VAL:HG22	2.37	0.54
39:Z:345:THR:O	39:Z:349:LEU:HG	2.07	0.54
47:I:41:GLU:HG3	47:I:42:THR:N	2.22	0.54
49:K:111:ASP:OD2	59:U:19:LYS:HD3	2.07	0.54
1:A:39:G:C3'	1:A:40:C:H5''	2.38	0.54
1:A:219:U:H3'	1:A:220:G:H5''	1.90	0.54
2:01:1252:G:OP2	22:19:13:HIS:HE1	1.90	0.54
2:01:2257:U:O2'	2:01:2258:C:H5'	2.08	0.54
2:01:2360:G:H2'	2:01:2361:G:H5'	1.90	0.54
23:20:58:VAL:O	23:20:58:VAL:HG13	2.08	0.54
36:33:39:ARG:O	36:33:43:LEU:HG	2.08	0.54
48:J:42:LEU:HD11	48:J:73:LEU:CG	2.29	0.54
1:A:711:G:O2'	1:A:712:A:H5'	2.08	0.54
2:01:1077:A:H2'	2:01:1078:U:H5'	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:08:27:GLY:HA3	11:08:78:VAL:HB	1.89	0.54
16:13:97:THR:O	16:13:118:LEU:HD13	2.08	0.54
46:H:95:MET:O	46:H:98:LEU:HD13	2.08	0.54
47:I:76:GLY:HA2	47:I:79:ARG:HG2	1.90	0.54
55:Q:22:VAL:HG22	55:Q:23:ALA:N	2.22	0.54
1:A:376:G:C3'	1:A:377:G:H5''	2.38	0.54
1:A:526:C:OP2	50:L:87:LYS:HE2	2.07	0.54
2:01:508:A:O2'	2:01:509:C:H5'	2.08	0.54
2:01:2746:U:H1'	11:08:138:GLN:HE22	1.73	0.54
3:02:57:A:C2	10:07:25:MET:HB3	2.43	0.54
32:29:2:LYS:HE2	32:29:5:ILE:HD13	1.90	0.54
39:Z:110:LEU:HD23	39:Z:110:LEU:O	2.07	0.54
48:J:7:ARG:O	48:J:101:SER:N	2.40	0.54
48:J:57:VAL:O	48:J:58:ASN:HB2	2.08	0.54
49:K:72:ALA:H	49:K:74:LYS:HZ2	1.57	0.54
1:A:437:U:C4'	42:D:153:ARG:HH12	2.21	0.53
1:A:958:A:C2	57:S:54:ARG:HB3	2.43	0.53
1:A:1123:U:O2'	1:A:1124:G:H5'	2.08	0.53
2:01:2322:A:H2'	2:01:2323:G:O4'	2.07	0.53
2:01:2578:G:H21	8:05:130:GLN:HE22	1.56	0.53
2:01:2698:U:H2'	2:01:2699:C:C6	2.43	0.53
8:05:4:LEU:HD13	8:05:29:VAL:HG11	1.89	0.53
11:08:84:LYS:C	11:08:85:LYS:HD3	2.28	0.53
14:11:22:PRO:HB3	39:Z:60:ARG:HH22	1.73	0.53
29:26:31:ASN:HD22	29:26:52:ALA:HB2	1.73	0.53
39:Z:189:TYR:CZ	39:Z:224:PRO:HD3	2.43	0.53
42:D:109:THR:HG22	42:D:111:ALA:H	1.73	0.53
52:N:11:LYS:O	52:N:15:LEU:HD13	2.08	0.53
1:A:332:G:OP1	58:T:4:LYS:HG3	2.09	0.53
1:A:92:U:H3'	1:A:93:U:H5''	1.89	0.53
1:A:831:A:C3'	1:A:832:G:H5''	2.38	0.53
2:01:1040:A:O2'	2:01:1041:G:H5'	2.07	0.53
7:04:41:GLY:CA	7:04:53:ILE:HD11	2.39	0.53
11:08:88:LEU:CD2	11:08:95:ALA:HB2	2.39	0.53
11:08:169:ARG:H	11:08:169:ARG:CD	2.22	0.53
21:18:88:ARG:HH11	21:18:112:ARG:HE	1.54	0.53
45:G:125:ASP:OD1	45:G:130:LYS:HE2	2.08	0.53
1:A:194:C:O2'	1:A:195:A:H5'	2.08	0.53
2:01:2334:U:C4'	20:17:12:THR:HB	2.38	0.53
40:B:156:LEU:HD12	40:B:156:LEU:O	2.08	0.53
50:L:39:THR:O	50:L:49:ARG:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M:49:GLU:HA	51:M:52:ILE:HD12	1.89	0.53
1:A:8:A:N7	42:D:205:LYS:HA	2.23	0.53
1:A:17:U:H2'	1:A:18:C:C6	2.44	0.53
1:A:626:G:H2'	1:A:627:G:C8	2.43	0.53
2:01:1255:U:C6	9:06:68:ALA:HA	2.43	0.53
12:09:90:LEU:HD23	12:09:93:SER:HA	1.90	0.53
13:10:58:THR:HA	13:10:63:ALA:HB2	1.89	0.53
32:29:17:SER:HB2	51:M:56:ARG:HH22	1.74	0.53
42:D:2:ARG:HB2	42:D:4:LEU:HD23	1.90	0.53
45:G:35:LYS:O	45:G:39:GLU:HG3	2.07	0.53
47:I:79:ARG:HH11	47:I:79:ARG:HG3	1.74	0.53
56:R:53:GLN:HA	56:R:53:GLN:HE21	1.74	0.53
1:A:219:U:C3'	1:A:220:G:H5''	2.39	0.53
2:01:1043:C:H2'	2:01:1044:C:O4'	2.08	0.53
14:11:11:GLN:HE22	14:11:41:PHE:HB2	1.73	0.53
18:15:16:ARG:HD2	18:15:16:ARG:N	2.23	0.53
36:33:28:LEU:HD21	36:33:43:LEU:HB2	1.90	0.53
1:A:1513:A:H2'	1:A:1514:G:C8	2.44	0.53
2:01:2636:C:H4'	8:05:81:GLU:HG3	1.90	0.53
7:04:66:PHE:HD1	7:04:142:ASN:HD21	1.57	0.53
12:09:4:ILE:HG23	12:09:37:VAL:HG23	1.91	0.53
19:16:34:ILE:HD11	19:16:44:LEU:CD2	2.39	0.53
22:19:90:ASP:OD2	22:19:92:LYS:HB3	2.08	0.53
29:26:62:GLY:O	29:26:66:VAL:HG23	2.09	0.53
33:30:37:HIS:CD2	33:30:43:THR:HG22	2.43	0.53
56:R:17:VAL:HG22	56:R:18:GLN:N	2.21	0.53
58:T:24:ARG:HB3	58:T:28:ARG:HH12	1.73	0.53
2:01:932:U:H5'	2:01:933:A:N7	2.24	0.53
2:01:2086:U:H2'	2:01:2087:G:C8	2.44	0.53
7:04:89:ASN:N	7:04:89:ASN:HD22	2.06	0.53
20:17:4:LYS:O	20:17:8:ILE:HG13	2.08	0.53
31:28:40:THR:HB	31:28:43:ILE:HG12	1.90	0.53
41:C:150:VAL:HG22	41:C:199:VAL:HG23	1.90	0.53
48:J:11:LYS:HG2	48:J:71:LEU:CD2	2.39	0.53
2:01:2641:G:H5'	15:12:78:THR:CG2	2.39	0.53
6:03:180:PHE:HB2	6:03:185:LEU:CD2	2.39	0.53
25:22:69:ARG:NH1	25:22:69:ARG:HB3	2.24	0.53
40:B:16:GLY:HA2	40:B:202:ASN:ND2	2.24	0.53
40:B:40:ILE:HD12	40:B:40:ILE:N	2.24	0.53
42:D:100:VAL:O	42:D:104:MET:HG2	2.09	0.53
54:P:28:ARG:HD2	54:P:28:ARG:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:493:A:H2'	1:A:494:G:C8	2.44	0.53
9:06:196:VAL:O	9:06:200:LEU:HD13	2.08	0.53
13:10:23:LEU:N	13:10:118:ILE:HD12	2.23	0.53
39:Z:238:ASP:OD2	39:Z:266:ILE:HG13	2.07	0.53
42:D:71:PHE:HE1	42:D:93:LEU:HD11	1.73	0.53
1:A:39:G:H2'	1:A:40:C:C5'	2.34	0.52
1:A:406:G:H5'	42:D:4:LEU:CD1	2.39	0.52
2:01:1882:U:H2'	2:01:1883:U:C6	2.44	0.52
13:10:25:ALA:HA	13:10:115:GLY:HA2	1.91	0.52
15:12:53:TYR:CE1	15:12:121:LYS:HG3	2.44	0.52
19:16:33:ILE:HG21	19:16:118:ARG:NH1	2.23	0.52
19:16:63:ARG:NH1	19:16:76:VAL:HG12	2.22	0.52
27:24:17:SER:HB3	27:24:21:ARG:NH1	2.17	0.52
35:32:26:ASN:HD22	35:32:26:ASN:N	2.06	0.52
39:Z:333:ILE:HD12	39:Z:333:ILE:N	2.23	0.52
53:O:81:ILE:HG22	53:O:86:LEU:HD11	1.89	0.52
58:T:2:ASN:ND2	58:T:3:ILE:H	2.07	0.52
2:01:61:C:OP1	30:27:44:LYS:HB2	2.09	0.52
2:01:253:C:OP2	36:33:4:LYS:HE3	2.08	0.52
2:01:1139:G:O2'	2:01:1140:C:H5'	2.09	0.52
2:01:1181:U:H2'	2:01:1182:G:C8	2.45	0.52
2:01:1609:A:H1'	2:01:1616:A:O4'	2.09	0.52
2:01:1826:G:OP1	7:04:222:THR:HG23	2.09	0.52
3:02:75:G:H5''	27:24:12:GLN:NE2	2.24	0.52
17:14:102:GLY:O	17:14:105:ILE:HD13	2.08	0.52
39:Z:278:ARG:O	39:Z:278:ARG:HD3	2.09	0.52
1:A:663:A:H5'	1:A:836:G:OP1	2.09	0.52
1:A:1280:A:O2'	1:A:1281:C:H5'	2.08	0.52
2:01:572:A:H61	2:01:2029:G:H21	1.56	0.52
4:Y:44:LYS:NZ	4:Y:44:LYS:HB3	2.24	0.52
10:07:122:ASP:OD1	10:07:126:ASN:HB2	2.09	0.52
21:18:102:ARG:HD2	21:18:106:ALA:HB1	1.92	0.52
32:29:59:ARG:HH21	32:29:62:LYS:HB2	1.75	0.52
47:I:90:ASP:C	47:I:94:ARG:HG2	2.30	0.52
49:K:74:LYS:HD3	49:K:74:LYS:H	1.74	0.52
58:T:66:ILE:HG23	58:T:70:LYS:HD3	1.91	0.52
1:A:558:G:H3'	1:A:559:A:H5'	1.90	0.52
1:A:736:C:H2'	1:A:737:C:C6	2.45	0.52
1:A:865:A:H2'	1:A:866:C:C6	2.45	0.52
1:A:1292:G:H5'	47:I:40:ARG:HE	1.74	0.52
2:01:662:G:O2'	2:01:663:G:H5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:703:U:H2'	2:01:704:G:O4'	2.09	0.52
2:01:2295:C:O2'	2:01:2296:U:H5'	2.08	0.52
6:03:29:LEU:O	6:03:33:LEU:HG	2.10	0.52
16:13:21:CYS:HA	16:13:41:ILE:HG22	1.90	0.52
16:13:102:PRO:HB3	16:13:121:GLU:HB2	1.91	0.52
22:19:54:ARG:O	22:19:58:GLN:HG3	2.09	0.52
45:G:29:LEU:HD23	45:G:29:LEU:O	2.10	0.52
48:J:7:ARG:N	48:J:101:SER:O	2.43	0.52
48:J:82:LYS:O	48:J:86:ALA:N	2.43	0.52
49:K:72:ALA:HA	49:K:74:LYS:NZ	2.24	0.52
51:M:16:ILE:HD12	51:M:16:ILE:N	2.25	0.52
51:M:77:LYS:HB3	51:M:77:LYS:HZ3	1.72	0.52
1:A:463:U:H3	1:A:469:C:H42	1.56	0.52
1:A:1005:A:H62	1:A:1024:G:H1'	1.74	0.52
11:08:23:ILE:HD12	11:08:23:ILE:N	2.24	0.52
14:11:108:ILE:O	14:11:112:LYS:HG2	2.09	0.52
16:13:58:LEU:HD23	16:13:58:LEU:N	2.24	0.52
18:15:78:LEU:N	18:15:78:LEU:HD12	2.25	0.52
18:15:109:PRO:HD2	18:15:112:LEU:HD12	1.90	0.52
21:18:13:LYS:HG2	21:18:15:ASP:OD1	2.09	0.52
41:C:56:ILE:HG23	41:C:63:ILE:HD11	1.92	0.52
42:D:116:LEU:HD23	42:D:153:ARG:HH21	1.75	0.52
42:D:149:LYS:NZ	42:D:149:LYS:HB3	2.25	0.52
59:U:16:ARG:HE	59:U:20:ARG:NH2	2.07	0.52
2:01:948:C:H2'	2:01:949:G:H8	1.75	0.52
2:01:948:C:H2'	2:01:949:G:C8	2.45	0.52
2:01:1300:G:H4'	2:01:1301:A:H5'	1.91	0.52
2:01:2638:G:H1'	2:01:2778:A:H61	1.75	0.52
8:05:149:ASN:O	8:05:152:PRO:HD2	2.10	0.52
10:07:39:VAL:HG13	10:07:40:GLY:N	2.24	0.52
15:12:74:TYR:CD2	15:12:92:MET:HG3	2.44	0.52
16:13:99:ILE:HD12	16:13:99:ILE:N	2.25	0.52
19:16:2:ARG:O	19:16:2:ARG:HD3	2.09	0.52
22:19:34:ALA:O	22:19:38:VAL:HG23	2.10	0.52
24:21:4:ILE:HG22	24:21:106:VAL:HG22	1.91	0.52
48:J:52:LEU:N	48:J:52:LEU:HD12	2.24	0.52
57:S:63:ASP:O	57:S:66:VAL:HG13	2.10	0.52
1:A:1060:U:C5	41:C:1:GLY:HA3	2.42	0.52
2:01:155:A:H2'	2:01:156:A:C8	2.45	0.52
2:01:910:A:H62	18:15:12:MET:HA	1.74	0.52
2:01:1255:U:C5	9:06:68:ALA:HA	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2120:G:H2'	2:01:2121:G:C8	2.44	0.52
47:I:119:LYS:HB2	47:I:119:LYS:NZ	2.25	0.52
57:S:66:VAL:HG23	57:S:67:GLY:N	2.25	0.52
1:A:108:G:N1	58:T:9:ARG:HG2	2.24	0.52
1:A:1273:C:H2'	1:A:1274:A:O4'	2.10	0.52
2:01:1965:C:H5''	2:01:1966:A:H2'	1.92	0.52
2:01:2039:U:H2'	2:01:2040:G:H8	1.74	0.52
3:02:52:A:H61	20:17:33:ARG:HB2	1.75	0.52
6:03:163:TYR:HB2	6:03:171:ILE:HD11	1.92	0.52
8:05:40:LEU:N	8:05:40:LEU:HD12	2.25	0.52
11:08:103:ASN:HD22	11:08:104:LEU:H	1.56	0.52
13:10:129:LEU:O	13:10:129:LEU:HD12	2.10	0.52
25:22:61:LEU:CD1	25:22:82:LYS:HB3	2.40	0.52
41:C:72:PRO:O	41:C:76:ILE:HG12	2.09	0.52
46:H:88:LYS:HE2	46:H:119:GLY:HA2	1.92	0.52
47:I:94:ARG:O	47:I:98:ARG:N	2.39	0.52
52:N:59:GLN:HA	52:N:59:GLN:HE21	1.74	0.52
1:A:618:C:H1'	54:P:14:ARG:HH12	1.74	0.52
2:01:686:U:H3'	2:01:687:C:H5'	1.91	0.52
2:01:2444:G:OP2	9:06:63:LYS:HD2	2.10	0.52
7:04:202:ARG:HD2	7:04:202:ARG:O	2.09	0.52
9:06:123:LYS:HE3	9:06:125:SER:HB3	1.91	0.52
17:14:105:ILE:N	17:14:105:ILE:HD12	2.25	0.52
20:17:53:THR:HG23	20:17:74:VAL:HG11	1.91	0.52
24:21:83:LYS:HD2	24:21:95:ARG:HH11	1.74	0.52
47:I:24:ASN:HD22	47:I:26:LYS:NZ	2.07	0.52
2:01:581:C:H2'	2:01:582:A:C8	2.45	0.52
2:01:1023:U:O2'	2:01:1122:G:H5'	2.09	0.52
2:01:2243:U:H2'	2:01:2244:U:C6	2.45	0.52
15:12:4:PHE:CD2	22:19:99:VAL:HG11	2.45	0.52
18:15:33:LEU:HD21	18:15:128:THR:HB	1.91	0.52
23:20:27:ILE:HG23	23:20:31:GLU:OE1	2.10	0.52
52:N:22:LYS:O	52:N:22:LYS:HD3	2.10	0.52
1:A:1241:G:H2'	1:A:1242:G:C8	2.44	0.51
2:01:671:C:H2'	2:01:672:C:C6	2.45	0.51
2:01:989:G:OP2	31:28:11:SER:HB2	2.10	0.51
2:01:2639:A:H2'	2:01:2640:G:O4'	2.11	0.51
14:11:41:PHE:O	14:11:45:THR:HG22	2.09	0.51
39:Z:80:VAL:HG21	39:Z:106:LEU:HD11	1.93	0.51
44:F:76:THR:HG23	44:F:79:ARG:NH2	2.25	0.51
48:J:24:GLU:O	48:J:28:THR:N	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:J:32:THR:HG23	48:J:33:GLY:N	2.24	0.51
56:R:37:LYS:HB2	56:R:37:LYS:NZ	2.25	0.51
59:U:8:ASN:H	59:U:8:ASN:ND2	2.06	0.51
2:01:96:C:H4'	30:27:41:HIS:CD2	2.45	0.51
2:01:2092:U:H4'	2:01:2093:G:C5'	2.38	0.51
5:X:36:U:C2'	5:X:37:A:H5'	2.40	0.51
8:05:124:ARG:HA	8:05:165:MET:CE	2.40	0.51
13:10:95:LEU:HD22	13:10:95:LEU:N	2.25	0.51
27:24:56:PHE:HE1	27:24:61:LEU:HD21	1.73	0.51
47:I:78:ILE:O	47:I:82:ILE:HG13	2.11	0.51
58:T:24:ARG:HB3	58:T:28:ARG:NH1	2.26	0.51
1:A:395:C:N4	1:A:396:C:H41	2.07	0.51
1:A:1049:U:O2'	52:N:2:LYS:HD3	2.10	0.51
2:01:717:C:H2'	2:01:718:A:H5'	1.92	0.51
2:01:1186:G:H2'	2:01:1187:G:O4'	2.10	0.51
2:01:1827:U:O2'	2:01:1828:G:H5'	2.09	0.51
12:09:27:ARG:NH1	29:26:55:MET:HE2	2.26	0.51
40:B:161:PHE:CZ	40:B:216:VAL:HG21	2.45	0.51
42:D:88:ASN:HD22	42:D:88:ASN:N	2.08	0.51
46:H:50:VAL:HG22	46:H:50:VAL:O	2.11	0.51
48:J:89:ARG:C	48:J:90:LEU:HD12	2.30	0.51
1:A:396:C:O2'	1:A:397:A:H5''	2.10	0.51
1:A:413:G:H1'	1:A:428:G:H22	1.76	0.51
1:A:1162:C:H2'	1:A:1163:A:C8	2.45	0.51
6:03:47:ASN:HD22	6:03:211:LYS:HB3	1.76	0.51
9:06:77:ILE:HG13	9:06:78:TRP:HD1	1.74	0.51
11:08:93:TYR:CD1	11:08:106:LEU:HA	2.46	0.51
12:09:99:ILE:HD12	12:09:117:LEU:HD21	1.93	0.51
25:22:64:LYS:NZ	25:22:64:LYS:HB3	2.25	0.51
39:Z:284:LYS:O	39:Z:288:MET:HG3	2.10	0.51
1:A:952:U:H4'	1:A:964:A:H61	1.74	0.51
2:01:488:G:N2	2:01:491:G:H5''	2.25	0.51
2:01:1424:G:H2'	2:01:1425:G:O4'	2.10	0.51
2:01:2011:U:H2'	2:01:2012:G:O4'	2.10	0.51
2:01:2380:C:H5'	20:17:17:LYS:HE3	1.91	0.51
9:06:132:LYS:O	9:06:132:LYS:HD3	2.11	0.51
32:29:5:ILE:HG13	32:29:6:HIS:CD2	2.46	0.51
33:30:12:ARG:HD2	33:30:16:ARG:NH2	2.25	0.51
41:C:111:ASP:HB3	41:C:114:LEU:HD12	1.93	0.51
43:E:40:ASP:OD1	43:E:44:ARG:HB3	2.11	0.51
46:H:45:ILE:HG13	46:H:46:GLU:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:Q:20:ILE:O	55:Q:45:VAL:N	2.43	0.51
1:A:29:U:O2'	1:A:30:U:H5'	2.11	0.51
2:01:545:U:H2'	2:01:546:U:O4'	2.11	0.51
2:01:1565:C:O2'	2:01:1566:A:H2'	2.10	0.51
2:01:2022:U:O2'	2:01:2617:U:H5'	2.11	0.51
2:01:2114:A:N3	2:01:2114:A:H2'	2.25	0.51
3:02:83:G:H4'	31:28:52:PHE:CD2	2.46	0.51
26:23:26:ASN:ND2	26:23:34:ILE:HD11	2.25	0.51
1:A:1024:G:O2'	1:A:1025:U:H5'	2.10	0.51
2:01:49:A:H5'	2:01:51:G:O4'	2.10	0.51
2:01:1637:A:H5'	2:01:1760:C:O2'	2.11	0.51
2:01:1923:U:H2'	2:01:1924:C:C6	2.46	0.51
22:19:13:HIS:O	22:19:17:LEU:HD13	2.11	0.51
49:K:88:PRO:HA	49:K:92:ARG:HD2	1.93	0.51
1:A:1278:G:H5'	1:A:1279:G:H5'	1.91	0.51
2:01:2520:C:O2'	2:01:2521:C:H5'	2.11	0.51
6:03:163:TYR:HD2	6:03:171:ILE:HG12	1.76	0.51
55:Q:32:ILE:HD12	55:Q:32:ILE:H	1.74	0.51
59:U:36:PHE:HB3	59:U:39:LYS:HB3	1.91	0.51
2:01:851:C:H2'	2:01:852:U:C6	2.46	0.51
3:02:12:C:H42	28:25:70:PRO:HG3	1.75	0.51
3:02:55:U:O2'	3:02:56:G:H5'	2.10	0.51
10:07:140:ILE:HD12	10:07:140:ILE:N	2.26	0.51
17:14:117:THR:HG22	17:14:118:THR:N	2.26	0.51
43:E:73:VAL:HG11	43:E:143:LEU:HB3	1.93	0.51
43:E:104:ILE:HG23	43:E:104:ILE:O	2.11	0.51
44:F:47:LEU:HD13	44:F:51:ILE:HG12	1.93	0.51
48:J:57:VAL:HG22	48:J:58:ASN:N	2.24	0.51
55:Q:26:ARG:O	55:Q:26:ARG:HD3	2.11	0.51
2:01:2788:C:H2'	2:01:2789:C:C6	2.46	0.51
2:01:2799:A:H2'	2:01:2800:A:H5'	1.92	0.51
12:09:8:LYS:HG2	12:09:8:LYS:O	2.10	0.51
13:10:33:VAL:HG22	13:10:36:ASP:OD2	2.10	0.51
21:18:62:LYS:HB3	21:18:62:LYS:HZ3	1.74	0.51
24:21:11:ARG:HD2	24:21:11:ARG:N	2.24	0.51
27:24:81:PRO:HG2	27:24:82:TYR:CD1	2.46	0.51
40:B:79:VAL:HA	40:B:213:LEU:HD21	1.93	0.51
40:B:91:VAL:HG23	40:B:91:VAL:O	2.11	0.51
42:D:183:ARG:HG2	42:D:183:ARG:HH11	1.76	0.51
52:N:63:CYS:HB2	52:N:79:SER:OG	2.11	0.51
57:S:36:ARG:O	57:S:69:LYS:HD2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1317:C:H4'	52:N:47:LEU:HD21	1.92	0.50
2:01:826:U:H2'	2:01:828:U:O4'	2.11	0.50
7:04:213:ARG:HH11	7:04:213:ARG:HG3	1.76	0.50
11:08:5:LYS:HB2	11:08:5:LYS:NZ	2.25	0.50
5:W:6:G:O2'	5:W:7:G:H5'	2.11	0.50
40:B:23:ASN:HD21	40:B:25:LYS:HB2	1.75	0.50
1:A:162:A:H2'	1:A:163:C:O4'	2.12	0.50
1:A:538:G:OP1	50:L:109:ARG:HD2	2.11	0.50
2:01:189:G:P	29:26:13:THR:HG21	2.51	0.50
2:01:1336:A:H2'	2:01:1337:G:C8	2.46	0.50
13:10:97:LYS:O	13:10:101:LYS:HG3	2.10	0.50
25:22:61:LEU:HD12	25:22:61:LEU:O	2.12	0.50
28:25:66:GLU:N	28:25:75:PHE:O	2.42	0.50
36:33:36:ALA:HB3	36:33:39:ARG:HG2	1.93	0.50
39:Z:144:TRP:CE2	39:Z:201:LEU:HB2	2.47	0.50
40:B:42:LEU:H	40:B:42:LEU:CD2	2.24	0.50
42:D:31:CYS:HB3	42:D:32:LYS:CD	2.40	0.50
48:J:40:ILE:HG22	48:J:42:LEU:HG	1.93	0.50
54:P:20:VAL:HA	54:P:35:ARG:HA	1.93	0.50
1:A:1497:G:O2'	1:A:1498:U:H5'	2.11	0.50
2:01:767:U:H2'	2:01:768:G:H8	1.77	0.50
2:01:1909:C:H2'	2:01:1910:G:H8	1.77	0.50
2:01:2178:C:H2'	2:01:2179:C:C5	2.46	0.50
2:01:2469:A:H1'	18:15:55:ARG:NH2	2.26	0.50
12:09:14:SER:HB3	12:09:17:ASP:OD2	2.11	0.50
21:18:23:ASP:O	21:18:46:VAL:HG23	2.11	0.50
24:21:69:LEU:HG	24:21:107:VAL:HG22	1.94	0.50
33:30:8:THR:HG22	33:30:9:ARG:H	1.75	0.50
39:Z:16:GLU:O	39:Z:20:VAL:HG23	2.12	0.50
40:B:99:MET:C	40:B:100:LEU:HD12	2.31	0.50
43:E:107:GLY:H	43:E:110:MET:HE2	1.76	0.50
1:A:381:C:H2'	1:A:382:A:O4'	2.11	0.50
1:A:632:U:H3'	1:A:633:G:H5'	1.93	0.50
2:01:854:C:O2'	2:01:855:G:H5'	2.12	0.50
2:01:1339:G:H5''	25:22:19:LYS:HD3	1.93	0.50
2:01:1665:A:H1'	16:13:1:MET:HB2	1.93	0.50
15:12:134:ALA:HB3	15:12:135:GLN:HE22	1.77	0.50
24:21:19:LEU:HG	33:30:21:LEU:HG	1.93	0.50
39:Z:270:ILE:HG23	39:Z:294:LYS:HD3	1.94	0.50
40:B:80:LYS:HA	40:B:90:PHE:CE2	2.47	0.50
2:01:900:A:H2'	2:01:901:C:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:948:C:H1'	2:01:984:A:O2'	2.12	0.50
2:01:1564:C:H2'	2:01:1565:C:O4'	2.12	0.50
2:01:1799:G:C8	7:04:179:GLU:HG3	2.46	0.50
2:01:2747:G:O6	2:01:2755:C:H5''	2.12	0.50
8:05:7:LYS:HD3	8:05:77:ARG:HH12	1.76	0.50
22:19:68:ALA:HB1	22:19:73:ILE:HG23	1.93	0.50
24:21:24:ILE:HG13	24:21:24:ILE:O	2.12	0.50
35:32:19:ARG:HG2	35:32:19:ARG:HH21	1.76	0.50
41:C:178:ARG:HD2	41:C:206:ILE:HB	1.92	0.50
43:E:15:ILE:HD12	43:E:15:ILE:N	2.25	0.50
48:J:44:THR:HG23	48:J:69:THR:O	2.12	0.50
1:A:741:G:H4'	53:O:54:GLY:HA3	1.94	0.50
6:03:209:ILE:HG13	6:03:209:ILE:O	2.12	0.50
9:06:5:LEU:HD23	9:06:6:LYS:H	1.76	0.50
12:09:40:THR:HB	12:09:43:ASN:ND2	2.26	0.50
12:09:40:THR:O	12:09:44:ILE:HG12	2.11	0.50
27:24:7:GLU:O	27:24:41:GLU:HG2	2.11	0.50
27:24:83:LYS:HB2	27:24:83:LYS:NZ	2.27	0.50
29:26:31:ASN:ND2	29:26:52:ALA:HB2	2.26	0.50
40:B:94:ARG:HD2	40:B:94:ARG:N	2.26	0.50
40:B:159:ALA:C	40:B:160:LEU:HD12	2.32	0.50
42:D:60:VAL:HG21	42:D:199:ILE:HD11	1.93	0.50
59:U:32:ARG:HG3	59:U:33:ARG:HG3	1.93	0.50
2:01:680:C:H2'	2:01:681:G:C8	2.46	0.50
2:01:873:C:H2'	2:01:874:G:C8	2.47	0.50
2:01:1783:A:N1	2:01:2587:A:H2'	2.27	0.50
2:01:2125:G:H1	2:01:2170:A:H5'	1.76	0.50
7:04:244:VAL:HA	7:04:251:THR:HG22	1.93	0.50
8:05:179:ARG:H	8:05:188:LEU:HB2	1.76	0.50
12:09:103:VAL:HG12	12:09:108:VAL:HB	1.93	0.50
17:14:131:ALA:O	17:14:135:ILE:HG13	2.12	0.50
20:17:49:VAL:HG21	20:17:81:ARG:HB3	1.94	0.50
30:27:21:LEU:HA	30:27:25:GLN:HB3	1.92	0.50
36:33:35:LYS:O	36:33:40:LYS:HE3	2.12	0.50
58:T:56:ILE:HD12	58:T:56:ILE:N	2.26	0.50
1:A:420:U:H4'	1:A:421:U:C5	2.33	0.50
2:01:322:A:OP2	9:06:163:ASN:HB2	2.12	0.50
2:01:420:C:O2'	2:01:421:C:H5'	2.10	0.50
2:01:827:U:H4'	2:01:828:U:C5	2.46	0.50
2:01:962:G:H21	2:01:2250:G:H1	1.59	0.50
2:01:1148:U:C2'	2:01:1149:G:H5''	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1378:A:H1'	2:01:1379:U:C5	2.47	0.50
2:01:1509:A:H2'	2:01:1510:G:C8	2.47	0.50
2:01:1657:U:H2'	2:01:1658:C:C6	2.46	0.50
2:01:1909:C:H2'	2:01:1910:G:C8	2.47	0.50
2:01:1936:A:H3'	2:01:1937:A:H5'	1.94	0.50
2:01:2162:G:H2'	2:01:2163:A:H5'	1.94	0.50
2:01:2267:A:H5''	2:01:2268:A:H5'	1.92	0.50
2:01:2553:G:C3'	2:01:2554:U:H5''	2.40	0.50
4:Y:22:ASP:OD1	4:Y:23:PRO:HD2	2.11	0.50
10:07:56:LEU:HD13	10:07:86:CYS:HB2	1.94	0.50
25:22:28:ASN:OD1	25:22:87:LEU:HB2	2.12	0.50
26:23:5:ARG:HB2	26:23:8:ASP:OD2	2.11	0.50
44:F:90:MET:HE1	56:R:60:ARG:HD3	1.93	0.50
49:K:33:ILE:HG23	49:K:69:CYS:SG	2.52	0.50
2:01:813:U:H2'	2:01:814:C:H6	1.77	0.50
2:01:941:A:H2'	2:01:942:G:O4'	2.12	0.50
2:01:1170:C:H2'	2:01:1171:G:C8	2.46	0.50
2:01:2087:G:H2'	2:01:2088:A:C8	2.47	0.50
2:01:2465:C:O2'	2:01:2466:C:H5'	2.11	0.50
3:02:53:A:H2'	3:02:53:A:N3	2.26	0.50
7:04:41:GLY:HA2	7:04:53:ILE:HD11	1.94	0.50
13:10:8:LYS:NZ	13:10:8:LYS:HB3	2.27	0.50
15:12:7:LYS:N	15:12:7:LYS:HD2	2.27	0.50
21:18:88:ARG:NH1	21:18:112:ARG:HE	2.08	0.50
27:24:9:ARG:HH21	27:24:39:ALA:HB1	1.77	0.50
48:J:5:ARG:HD3	48:J:79:PRO:HD3	1.93	0.50
50:L:49:ARG:HG3	50:L:89:LEU:HD11	1.93	0.50
1:A:1329:A:H5''	51:M:24:VAL:HA	1.94	0.49
2:01:2282:G:H4'	2:01:2389:G:O2'	2.12	0.49
2:01:2547:A:H2'	2:01:2548:U:C6	2.47	0.49
2:01:2655:G:O2'	2:01:2656:U:H5	1.95	0.49
21:18:105:LYS:HB3	21:18:108:ARG:NH2	2.26	0.49
53:O:45:HIS:O	53:O:47:LYS:N	2.44	0.49
56:R:47:ARG:H	56:R:47:ARG:CD	2.19	0.49
2:01:691:C:O2'	2:01:692:C:H5'	2.12	0.49
2:01:2452:C:N4	2:01:2504:U:C4	2.79	0.49
5:X:72:A:H2'	5:X:73:A:C4'	2.42	0.49
13:10:24:SER:N	13:10:118:ILE:HD12	2.27	0.49
14:11:56:VAL:HG22	14:11:57:VAL:N	2.26	0.49
36:33:31:ILE:O	36:33:35:LYS:HE3	2.12	0.49
39:Z:340:VAL:HG21	39:Z:359:ALA:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
48:J:65:TYR:HA	52:N:97:LYS:O	2.12	0.49
1:A:1210:C:H2'	1:A:1211:U:H5'	1.93	0.49
1:A:1414:U:H2'	1:A:1415:G:H8	1.77	0.49
1:A:1436:U:H2'	1:A:1437:A:C8	2.47	0.49
2:01:586:A:H5'	9:06:84:THR:HG21	1.93	0.49
2:01:1666:G:O2'	2:01:1667:G:H5'	2.13	0.49
2:01:2194:U:H2'	2:01:2195:U:C6	2.47	0.49
2:01:2239:G:H5'	7:04:248:GLY:HA3	1.92	0.49
2:01:2281:A:O2'	2:01:2282:G:H5'	2.12	0.49
2:01:2683:C:C4'	8:05:13:ARG:HH11	2.24	0.49
45:G:28:ILE:HG22	45:G:28:ILE:O	2.12	0.49
45:G:46:LEU:HD11	45:G:57:GLU:HB3	1.93	0.49
45:G:78:ARG:H	45:G:78:ARG:CD	2.22	0.49
46:H:34:ALA:O	46:H:38:VAL:HG23	2.12	0.49
52:N:79:SER:O	52:N:83:VAL:HG23	2.11	0.49
1:A:762:U:H2'	1:A:763:G:C8	2.47	0.49
2:01:2884:U:H1'	33:30:49:ARG:NH1	2.28	0.49
3:02:12:C:N4	28:25:70:PRO:HG3	2.27	0.49
13:10:117:LEU:N	13:10:117:LEU:HD12	2.27	0.49
25:22:33:LYS:HG2	25:22:80:TRP:CZ3	2.48	0.49
27:24:80:HIS:ND1	27:24:81:PRO:HD2	2.28	0.49
31:28:6:ILE:HD12	31:28:6:ILE:N	2.28	0.49
37:34:5:ALA:O	37:34:38:GLY:HA2	2.11	0.49
39:Z:45:ASP:HA	39:Z:48:ASN:HD22	1.77	0.49
42:D:58:GLN:O	42:D:62:ARG:HG2	2.13	0.49
43:E:96:GLN:HG2	43:E:123:LEU:HD12	1.95	0.49
52:N:65:GLN:HE21	52:N:82:LYS:CE	2.25	0.49
1:A:31:G:H1	1:A:48:C:H5''	1.78	0.49
1:A:675:A:H1'	49:K:117:HIS:CD2	2.47	0.49
2:01:687:C:H42	2:01:787:C:H4'	1.77	0.49
2:01:1454:C:O2'	19:16:60:VAL:HG22	2.13	0.49
2:01:2529:G:OP2	2:01:2530:A:H5''	2.11	0.49
19:16:13:ASN:O	19:16:17:ARG:HG3	2.12	0.49
41:C:179:ALA:HB1	41:C:202:PHE:HE1	1.77	0.49
41:C:203:LYS:HB2	41:C:203:LYS:NZ	2.27	0.49
42:D:1:ALA:HA	42:D:67:LEU:HD11	1.94	0.49
48:J:9:ARG:HB3	48:J:99:GLN:HB3	1.94	0.49
2:01:189:G:H2'	2:01:205:G:N2	2.27	0.49
2:01:1225:G:OP1	23:20:88:GLY:HA3	2.12	0.49
2:01:1386:C:H2'	2:01:1387:A:C8	2.47	0.49
7:04:57:HIS:CD2	7:04:58:LYS:H	2.30	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:202:ILE:N	8:05:202:ILE:HD12	2.28	0.49
10:07:125:GLY:C	10:07:126:ASN:HD22	2.16	0.49
23:20:79:ARG:HG3	23:20:80:ARG:HE	1.77	0.49
35:32:26:ASN:N	35:32:26:ASN:ND2	2.60	0.49
39:Z:87:ALA:HB2	39:Z:95:THR:CG2	2.40	0.49
40:B:93:HIS:CD2	40:B:145:ASN:HB2	2.48	0.49
41:C:21:TRP:HB3	41:C:58:ARG:HB3	1.94	0.49
44:F:54:LEU:HD12	44:F:54:LEU:O	2.13	0.49
55:Q:46:HIS:HB3	55:Q:73:THR:HG22	1.95	0.49
1:A:132:C:H5'	1:A:262:A:O2'	2.13	0.49
1:A:1062:U:H2'	1:A:1063:C:C6	2.48	0.49
2:01:460:A:H2'	2:01:461:C:O4'	2.13	0.49
2:01:1277:G:H5''	19:16:40:LYS:NZ	2.28	0.49
2:01:1386:C:H2'	2:01:1387:A:H8	1.78	0.49
2:01:1417:C:H4'	2:01:1587:G:H21	1.77	0.49
2:01:1700:A:H2'	2:01:1701:A:H5'	1.95	0.49
12:09:62:LEU:CD2	12:09:66:ASN:HD21	2.26	0.49
14:11:50:LYS:HZ3	14:11:50:LYS:CB	2.25	0.49
17:14:17:LYS:HD2	17:14:27:LEU:HD21	1.95	0.49
41:C:107:LYS:HD3	41:C:143:LEU:HG	1.94	0.49
46:H:31:LEU:O	46:H:35:ILE:HG13	2.13	0.49
48:J:40:ILE:HG23	48:J:41:PRO:HD2	1.93	0.49
50:L:109:ARG:NH1	50:L:112:ALA:H	2.06	0.49
1:A:517:G:H4'	1:A:519:C:C2	2.48	0.49
1:A:754:C:H5'	53:O:71:ARG:NH2	2.27	0.49
1:A:784:A:H2'	1:A:785:G:C8	2.47	0.49
1:A:996:A:H2'	1:A:997:U:C6	2.48	0.49
2:01:669:G:H2'	2:01:669:G:N3	2.28	0.49
2:01:2224:G:H4'	2:01:2226:C:C2	2.48	0.49
12:09:62:LEU:HD23	12:09:62:LEU:O	2.13	0.49
15:12:74:TYR:HD2	15:12:92:MET:HG3	1.78	0.49
17:14:128:THR:O	17:14:132:ARG:HG3	2.13	0.49
21:18:10:GLU:HG3	21:18:11:GLN:HG3	1.94	0.49
39:Z:150:ARG:HG2	39:Z:150:ARG:HH11	1.76	0.49
40:B:70:GLY:HA2	40:B:163:ILE:CG2	2.43	0.49
41:C:119:ILE:HG23	41:C:132:ALA:HB1	1.95	0.49
42:D:123:MET:HG3	42:D:145:ARG:HB2	1.95	0.49
49:K:86:LYS:CG	49:K:112:VAL:HG23	2.43	0.49
1:A:219:U:H2'	1:A:220:G:C5'	2.43	0.49
1:A:950:U:H2'	1:A:951:G:H8	1.78	0.49
1:A:1147:C:H4'	47:I:6:TYR:CE2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1930:G:N2	2:01:1968:G:H2'	2.27	0.49
2:01:2543:G:H21	2:01:2646:C:H5''	1.77	0.49
7:04:4:LYS:HB2	7:04:4:LYS:NZ	2.27	0.49
7:04:131:MET:HG2	7:04:134:ILE:HD12	1.95	0.49
26:23:26:ASN:O	26:23:34:ILE:HG12	2.13	0.49
28:25:67:VAL:O	28:25:67:VAL:HG12	2.13	0.49
37:34:24:ARG:HG2	37:34:24:ARG:HH21	1.78	0.49
39:Z:164:GLU:HB2	39:Z:182:LYS:HB3	1.94	0.49
41:C:81:GLU:O	41:C:85:LYS:HG3	2.12	0.49
47:I:14:SER:HA	47:I:68:GLY:HA3	1.95	0.49
47:I:89:TYR:HB3	47:I:93:LEU:HB2	1.94	0.49
47:I:118:ARG:HH11	47:I:118:ARG:HG3	1.78	0.49
48:J:49:PHE:N	48:J:65:TYR:O	2.44	0.49
53:O:28:VAL:HG11	53:O:66:LEU:HD21	1.95	0.49
2:01:1263:U:O2'	33:30:7:PRO:HD2	2.12	0.49
2:01:1521:G:H3'	2:01:1522:A:C5'	2.39	0.49
2:01:1796:U:H2'	2:01:1797:G:H8	1.76	0.49
15:12:69:ARG:HA	15:12:89:PHE:HD2	1.77	0.49
24:21:88:ARG:HG3	24:21:94:ASP:OD2	2.13	0.49
42:D:100:VAL:HG21	42:D:136:VAL:HG21	1.93	0.49
42:D:149:LYS:HG3	42:D:177:MET:HE3	1.95	0.49
47:I:115:VAL:HG11	48:J:62:ARG:HB2	1.95	0.49
50:L:109:ARG:HH11	50:L:109:ARG:HG3	1.78	0.49
1:A:831:A:H3'	1:A:832:G:H5''	1.95	0.48
1:A:868:C:H2'	1:A:869:G:O4'	2.12	0.48
1:A:1148:U:H2'	1:A:1149:C:O4'	2.13	0.48
1:A:1236:A:H4'	1:A:1304:G:H4'	1.94	0.48
2:01:239:C:HO2'	2:01:621:A:H2	1.61	0.48
7:04:116:GLN:HG3	7:04:121:ALA:HB2	1.95	0.48
24:21:72:THR:HG22	24:21:73:LYS:HG3	1.95	0.48
39:Z:166:ILE:HD11	39:Z:182:LYS:HB2	1.95	0.48
53:O:34:GLN:NE2	53:O:38:LEU:HB2	2.28	0.48
1:A:371:A:H2'	1:A:372:C:O4'	2.13	0.48
1:A:413:G:H1'	1:A:428:G:N2	2.27	0.48
1:A:516:U:O4	1:A:533:A:N7	2.46	0.48
2:01:112:U:H2'	2:01:113:U:H5'	1.94	0.48
2:01:771:G:OP1	35:32:14:ARG:HD2	2.14	0.48
2:01:2578:G:H21	8:05:130:GLN:NE2	2.11	0.48
2:01:2743:U:C3'	2:01:2744:G:H5''	2.43	0.48
25:22:11:LEU:HD23	25:22:50:LEU:HD23	1.94	0.48
25:22:76:ARG:HH11	25:22:76:ARG:CB	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:I:114:LYS:CE	47:I:117:LEU:HD12	2.38	0.48
50:L:86:VAL:HG21	50:L:89:LEU:HD13	1.95	0.48
52:N:55:SER:HB2	52:N:56:PRO:HA	1.95	0.48
53:O:28:VAL:HG13	53:O:62:ARG:HG3	1.95	0.48
57:S:4:LEU:H	57:S:4:LEU:CD2	2.22	0.48
58:T:84:LYS:HB2	58:T:84:LYS:NZ	2.27	0.48
1:A:939:G:H2'	1:A:940:C:C6	2.48	0.48
2:01:225:C:H2'	2:01:226:A:O4'	2.13	0.48
2:01:594:U:H2'	2:01:595:C:C6	2.48	0.48
2:01:974:G:H2'	2:01:974:G:N3	2.29	0.48
2:01:2153:C:H2'	2:01:2154:A:H5'	1.94	0.48
2:01:2679:A:O2'	2:01:2680:U:H5'	2.12	0.48
7:04:18:VAL:HG23	7:04:202:ARG:HB3	1.95	0.48
10:07:98:PHE:HA	10:07:101:ARG:CZ	2.44	0.48
13:10:72:LEU:HD12	13:10:72:LEU:N	2.28	0.48
43:E:68:ARG:O	43:E:68:ARG:HD2	2.13	0.48
44:F:18:VAL:O	44:F:22:ILE:HG13	2.13	0.48
1:A:50:A:H4'	1:A:51:A:H5'	1.96	0.48
1:A:1060:U:H4'	48:J:53:ILE:HG23	1.94	0.48
2:01:17:G:H4'	22:19:24:TYR:HE1	1.78	0.48
2:01:1697:G:H4'	2:01:1978:A:H5''	1.94	0.48
2:01:2094:A:P	12:09:22:LYS:HD2	2.53	0.48
2:01:2477:U:O4	37:34:10:LEU:HD22	2.13	0.48
7:04:124:LYS:HB3	7:04:127:ASN:HD22	1.76	0.48
27:24:40:ILE:HD12	27:24:40:ILE:O	2.14	0.48
29:26:67:LEU:HG	29:26:71:ARG:NH1	2.28	0.48
35:32:10:LEU:HD11	35:32:14:ARG:NH1	2.28	0.48
39:Z:80:VAL:HG22	39:Z:102:GLU:HB3	1.96	0.48
41:C:72:PRO:HG3	41:C:104:GLU:OE2	2.13	0.48
43:E:131:ASN:HD22	43:E:134:ASN:ND2	2.11	0.48
1:A:901:A:H2'	1:A:902:G:H5'	1.95	0.48
2:01:715:A:H4'	53:O:62:ARG:HH22	1.77	0.48
2:01:995:C:H6	2:01:995:C:H5'	1.78	0.48
2:01:2184:A:C2'	2:01:2185:U:H5'	2.44	0.48
2:01:2345:G:H21	2:01:2381:A:H3'	1.78	0.48
2:01:2743:U:C2'	2:01:2744:G:H5''	2.43	0.48
3:02:48:U:H2'	3:02:49:C:C6	2.48	0.48
8:05:2:ILE:HD13	8:05:90:PHE:HE2	1.77	0.48
8:05:156:PHE:HB3	15:12:81:ILE:HG12	1.95	0.48
10:07:62:GLN:OE1	10:07:90:LEU:HD23	2.13	0.48
15:12:84:ILE:HG23	15:12:84:ILE:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:204:LYS:HA	39:Z:213:ARG:HA	1.94	0.48
42:D:32:LYS:HD3	42:D:32:LYS:N	2.29	0.48
44:F:81:ASN:HD22	44:F:84:VAL:HG23	1.76	0.48
44:F:97:THR:HG23	44:F:98:GLU:HG3	1.95	0.48
45:G:144:ALA:O	45:G:148:LYS:HG3	2.14	0.48
55:Q:13:SER:HB2	55:Q:21:VAL:CG1	2.42	0.48
1:A:641:U:H4'	1:A:642:A:H8	1.79	0.48
1:A:710:G:O2'	1:A:711:G:H5'	2.13	0.48
1:A:1084:G:H5'	1:A:1102:A:OP2	2.13	0.48
2:01:139:U:H2'	2:01:140:C:C5	2.49	0.48
2:01:172:A:H2'	2:01:173:A:C8	2.49	0.48
2:01:1038:G:H2'	2:01:1039:A:C8	2.49	0.48
2:01:1067:A:H2'	2:01:1068:G:C8	2.48	0.48
2:01:1077:A:N6	2:01:1088:A:H2'	2.28	0.48
2:01:1138:G:H2'	2:01:1139:G:O4'	2.13	0.48
2:01:1565:C:O2'	2:01:1566:A:C8	2.67	0.48
2:01:2161:C:O2	2:01:2161:C:H3'	2.13	0.48
2:01:2795:C:H2'	2:01:2796:U:O4'	2.14	0.48
15:12:99:ARG:HA	15:12:102:GLU:HB2	1.96	0.48
27:24:31:TYR:OH	27:24:75:GLN:HG2	2.13	0.48
36:33:54:LEU:O	36:33:58:ILE:HG13	2.14	0.48
44:F:3:HIS:HB2	44:F:92:THR:HA	1.95	0.48
44:F:42:TRP:CD1	44:F:61:LEU:HD13	2.49	0.48
44:F:90:MET:CE	56:R:60:ARG:HD3	2.44	0.48
1:A:430:A:OP1	42:D:8:LEU:HG	2.14	0.48
1:A:950:U:H2'	1:A:951:G:C8	2.49	0.48
2:01:78:U:H2'	2:01:79:C:C6	2.48	0.48
6:03:41:SER:HB3	6:03:177:LYS:NZ	2.29	0.48
7:04:196:ASN:ND2	7:04:199:HIS:HB2	2.28	0.48
9:06:29:HIS:O	9:06:33:VAL:HG23	2.14	0.48
16:13:15:GLY:O	16:13:47:ILE:HG12	2.14	0.48
18:15:44:ARG:N	18:15:44:ARG:HD2	2.29	0.48
26:23:25:LYS:HB2	26:23:34:ILE:HG13	1.95	0.48
27:24:81:PRO:HG2	27:24:82:TYR:HD1	1.79	0.48
39:Z:14:LEU:O	39:Z:14:LEU:HD23	2.14	0.48
40:B:33:ALA:HB3	40:B:37:VAL:CG2	2.41	0.48
1:A:26:A:H61	1:A:558:G:H1'	1.78	0.48
2:01:1201:U:H2'	2:01:1202:G:H8	1.79	0.48
2:01:2334:U:H4'	20:17:12:THR:HB	1.95	0.48
2:01:2462:C:H1'	2:01:2491:U:O4	2.13	0.48
2:01:2799:A:C2'	2:01:2800:A:H5'	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:02:106:G:H2'	3:02:107:G:O4'	2.14	0.48
5:X:32:C:H2'	5:X:33:U:O4'	2.14	0.48
10:07:54:ALA:HA	10:07:57:ALA:HB3	1.95	0.48
11:08:41:GLU:HG2	11:08:54:ARG:CG	2.44	0.48
12:09:111:ALA:HB3	12:09:114:GLU:HG3	1.95	0.48
18:15:17:ASN:OD1	18:15:95:LEU:HB3	2.14	0.48
28:25:33:ILE:HG22	28:25:34:VAL:HG23	1.96	0.48
32:29:14:ALA:N	32:29:22:MET:O	2.45	0.48
35:32:41:ARG:HG3	35:32:41:ARG:HH21	1.78	0.48
39:Z:113:LEU:HD23	39:Z:117:ARG:HB2	1.96	0.48
40:B:18:GLN:HB3	40:B:189:ASN:ND2	2.28	0.48
42:D:46:ARG:HG2	42:D:46:ARG:HH11	1.79	0.48
51:M:13:HIS:CD2	51:M:41:ASP:HA	2.49	0.48
52:N:50:LEU:CD1	52:N:51:PRO:HD2	2.43	0.48
52:N:66:THR:HG21	52:N:82:LYS:HD3	1.95	0.48
1:A:346:G:H2'	1:A:347:G:H5'	1.96	0.48
1:A:420:U:HO2'	1:A:421:U:H6	1.58	0.48
1:A:593:U:H2'	1:A:594:U:C6	2.49	0.48
2:01:397:U:OP2	29:26:9:LYS:HD3	2.14	0.48
2:01:932:U:H5'	2:01:933:A:C8	2.49	0.48
2:01:2563:U:H5''	16:13:26:GLY:O	2.13	0.48
2:01:2845:U:H3	2:01:2871:U:H3	1.61	0.48
3:02:112:G:H21	20:17:45:SER:HB2	1.78	0.48
7:04:106:PRO:HD2	7:04:109:LEU:HB2	1.95	0.48
11:08:49:LEU:CD1	11:08:71:LEU:HD21	2.44	0.48
12:09:47:PHE:CD1	12:09:51:ARG:HD2	2.48	0.48
15:12:116:ARG:O	15:12:120:ARG:HG3	2.13	0.48
25:22:59:ASN:HD22	25:22:59:ASN:N	2.11	0.48
27:24:48:MET:O	27:24:48:MET:HE3	2.14	0.48
37:34:17:VAL:CG1	37:34:19:ARG:HG3	2.44	0.48
5:W:52:G:H2'	5:W:53:G:H8	1.79	0.48
39:Z:262:ARG:HE	39:Z:264:THR:CG2	2.27	0.48
40:B:160:LEU:HD12	40:B:160:LEU:N	2.28	0.48
42:D:3:TYR:CZ	42:D:10:LEU:HD21	2.49	0.48
47:I:89:TYR:CG	47:I:93:LEU:HD12	2.49	0.48
55:Q:64:ARG:O	55:Q:66:LEU:HD12	2.13	0.48
58:T:27:MET:O	58:T:31:ILE:HG13	2.14	0.48
59:U:8:ASN:HD22	59:U:8:ASN:N	2.08	0.48
59:U:61:ARG:HH11	59:U:61:ARG:HG3	1.79	0.48
1:A:377:G:OP1	54:P:3:THR:HG21	2.14	0.48
1:A:545:C:O2'	1:A:549:C:H5''	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:C:H2'	1:A:949:A:H8	1.79	0.48
1:A:1292:G:C5'	47:I:40:ARG:HE	2.26	0.48
2:01:1336:A:H2'	2:01:1337:G:H8	1.77	0.48
2:01:1463:C:H2'	2:01:1464:G:C8	2.48	0.48
2:01:2093:G:N7	2:01:2225:A:H2'	2.29	0.48
2:01:2170:A:O2'	2:01:2171:A:H4'	2.14	0.48
2:01:2217:G:O2'	2:01:2218:G:H5'	2.12	0.48
2:01:2514:U:H2'	2:01:2515:C:C6	2.49	0.48
8:05:173:GLN:NE2	8:05:208:LYS:HD2	2.28	0.48
13:10:31:ARG:O	13:10:31:ARG:HD3	2.14	0.48
13:10:72:LEU:HD12	13:10:72:LEU:H	1.79	0.48
14:11:97:VAL:HB	14:11:137:LEU:HD12	1.95	0.48
16:13:70:ARG:HH21	16:13:74:GLY:HA2	1.78	0.48
19:16:75:ILE:N	19:16:75:ILE:HD12	2.29	0.48
21:18:95:LYS:HD3	21:18:97:TYR:CE2	2.49	0.48
22:19:10:ARG:HA	22:19:10:ARG:HE	1.78	0.48
23:20:5:PHE:HB3	23:20:59:ILE:HD12	1.96	0.48
39:Z:190:GLY:HA2	39:Z:193:ARG:HH12	1.79	0.48
39:Z:223:TYR:HE2	39:Z:290:GLN:HB2	1.79	0.48
42:D:33:ILE:HG13	42:D:34:GLU:N	2.29	0.48
43:E:82:HIS:CE1	43:E:146:MET:HG3	2.49	0.48
47:I:74:GLN:O	47:I:78:ILE:HG13	2.13	0.48
1:A:219:U:H2'	1:A:220:G:H5''	1.95	0.47
1:A:346:G:C2'	1:A:347:G:H5'	2.43	0.47
1:A:1527:U:O2'	1:A:1528:U:H5'	2.14	0.47
2:01:172:A:H2'	2:01:173:A:H8	1.78	0.47
2:01:204:A:O3'	2:01:205:G:H4'	2.14	0.47
2:01:2314:A:H2'	2:01:2315:G:C8	2.49	0.47
2:01:2317:A:H2'	2:01:2318:G:O4'	2.14	0.47
14:11:34:ILE:HG13	14:11:35:MET:N	2.28	0.47
15:12:93:ILE:O	15:12:97:PRO:HG3	2.14	0.47
16:13:63:VAL:HG11	16:13:103:VAL:HG12	1.96	0.47
33:30:10:SER:O	33:30:14:MET:HG3	2.13	0.47
39:Z:24:TYR:HB3	39:Z:117:ARG:NE	2.20	0.47
39:Z:324:ARG:HG3	39:Z:324:ARG:HH11	1.79	0.47
51:M:89:ARG:HH21	51:M:92:ARG:HD2	1.78	0.47
59:U:16:ARG:HD2	59:U:20:ARG:NH1	2.29	0.47
2:01:395:U:H2'	2:01:396:G:H8	1.77	0.47
2:01:723:C:H2'	2:01:724:U:O4'	2.14	0.47
2:01:1669:A:O4'	16:13:5:GLN:HG3	2.14	0.47
2:01:1672:A:C2	2:01:2582:G:H5'	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2466:C:OP1	37:34:4:ARG:HB3	2.13	0.47
2:01:2641:G:H5'	15:12:78:THR:HG22	1.95	0.47
3:02:7:G:H5''	20:17:29:HIS:CD2	2.50	0.47
8:05:184:ARG:HH21	8:05:184:ARG:HG3	1.78	0.47
10:07:7:TYR:O	10:07:12:VAL:HG23	2.15	0.47
17:14:79:LEU:HD12	17:14:112:LEU:HD12	1.96	0.47
18:15:24:THR:HG22	18:15:99:GLY:O	2.14	0.47
23:20:57:GLY:HA2	23:20:102:SER:HB2	1.96	0.47
29:26:31:ASN:HD22	29:26:52:ALA:CB	2.26	0.47
39:Z:10:ARG:HH21	39:Z:103:LEU:HD23	1.78	0.47
45:G:68:VAL:HA	45:G:137:ARG:HG3	1.95	0.47
46:H:124:ILE:O	46:H:124:ILE:HG13	2.14	0.47
52:N:92:ILE:HG21	52:N:95:LEU:HD22	1.96	0.47
1:A:1370:G:O2'	1:A:1371:G:H5'	2.14	0.47
2:01:6:A:H5''	15:12:131:ASN:HD22	1.79	0.47
2:01:254:G:C2'	2:01:255:A:H5''	2.44	0.47
2:01:940:G:C2'	2:01:941:A:H5''	2.44	0.47
2:01:1032:A:O2'	2:01:1033:U:H5'	2.14	0.47
2:01:1651:G:H5'	19:16:39:PRO:CB	2.44	0.47
2:01:1930:G:O2'	2:01:1931:U:C5	2.67	0.47
2:01:2680:U:H5'	8:05:194:PRO:HA	1.96	0.47
7:04:143:VAL:HB	7:04:153:LEU:HB2	1.97	0.47
9:06:189:THR:HG22	9:06:191:ASP:H	1.79	0.47
11:08:8:VAL:HG21	11:08:71:LEU:HD23	1.95	0.47
16:13:76:VAL:HG12	21:18:72:VAL:CG2	2.44	0.47
23:20:22:LEU:HD12	23:20:23:GLU:O	2.13	0.47
28:25:35:ARG:NH1	28:25:54:THR:HG21	2.29	0.47
39:Z:139:THR:HG22	39:Z:173:VAL:HB	1.96	0.47
39:Z:243:VAL:HG22	39:Z:261:VAL:HG13	1.96	0.47
41:C:19:SER:HB2	41:C:21:TRP:NE1	2.29	0.47
51:M:22:TYR:HD2	51:M:65:GLU:HA	1.80	0.47
1:A:1429:A:H2'	1:A:1430:A:H8	1.79	0.47
2:01:679:C:H2'	2:01:680:C:C6	2.49	0.47
2:01:1697:G:H3'	2:01:1698:A:C5'	2.34	0.47
2:01:2266:A:H4'	2:01:2267:A:N3	2.30	0.47
2:01:2292:U:H2'	2:01:2293:G:C8	2.49	0.47
2:01:2605:U:H2'	2:01:2606:C:C6	2.49	0.47
14:11:2:LYS:H	14:11:2:LYS:HD2	1.79	0.47
19:16:29:VAL:O	19:16:29:VAL:HG12	2.14	0.47
39:Z:170:GLU:HA	39:Z:176:ILE:HA	1.96	0.47
40:B:34:ARG:HD3	40:B:35:ASN:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:K:30:ILE:HA	49:K:45:THR:HG22	1.97	0.47
51:M:2:ARG:N	51:M:7:ASN:O	2.47	0.47
1:A:174:A:H2'	1:A:174:A:N3	2.29	0.47
2:01:46:G:H2'	2:01:47:C:C6	2.49	0.47
2:01:680:C:H2'	2:01:681:G:H8	1.78	0.47
7:04:154:ALA:HB2	7:04:161:VAL:HG23	1.95	0.47
16:13:2:ILE:HD12	16:13:2:ILE:N	2.29	0.47
20:17:26:LEU:HD23	20:17:27:VAL:N	2.29	0.47
41:C:68:HIS:HA	41:C:103:ALA:HB3	1.96	0.47
49:K:81:LEU:N	49:K:81:LEU:HD23	2.29	0.47
50:L:65:TYR:HB2	50:L:92:VAL:HG11	1.96	0.47
51:M:44:ILE:HA	51:M:47:LEU:HG	1.96	0.47
54:P:40:ASN:HD22	54:P:43:ALA:CA	2.28	0.47
58:T:73:ARG:HB3	58:T:73:ARG:HH11	1.78	0.47
1:A:77:A:H61	1:A:92:U:H3	1.61	0.47
1:A:404:G:N7	42:D:1:ALA:HB3	2.30	0.47
1:A:981:U:C3'	1:A:982:U:H5''	2.38	0.47
1:A:1316:G:H2'	1:A:1317:C:H5''	1.96	0.47
2:01:1427:A:H4'	2:01:1428:C:O4'	2.14	0.47
2:01:1746:A:H2'	2:01:1747:U:C6	2.50	0.47
2:01:2869:G:H2'	2:01:2870:C:O4'	2.15	0.47
9:06:129:PRO:HG3	9:06:156:ASN:HA	1.97	0.47
11:08:158:GLY:HA3	11:08:162:ARG:NH1	2.29	0.47
18:15:64:TRP:HB2	18:15:104:GLU:HB2	1.97	0.47
41:C:46:LEU:HB3	41:C:49:ALA:HB3	1.96	0.47
45:G:121:ASN:HD22	45:G:121:ASN:N	2.11	0.47
49:K:83:VAL:HG23	49:K:106:ILE:HG23	1.96	0.47
1:A:177:G:H2'	1:A:178:C:H6	1.79	0.47
1:A:707:U:OP1	49:K:86:LYS:HD3	2.14	0.47
1:A:802:A:H2'	1:A:803:G:O4'	2.14	0.47
1:A:1144:G:O2'	1:A:1145:A:H5'	2.15	0.47
1:A:1225:A:H4'	57:S:77:ARG:HD3	1.97	0.47
1:A:1347:G:O2'	1:A:1348:U:C5	2.68	0.47
1:A:1369:C:OP2	47:I:112:ARG:HG3	2.14	0.47
1:A:1513:A:H2'	1:A:1514:G:H8	1.79	0.47
2:01:325:G:H2'	2:01:326:G:H8	1.80	0.47
2:01:1250:G:H5''	22:19:5:ARG:CD	2.45	0.47
2:01:2045:C:H5''	33:30:14:MET:CE	2.45	0.47
2:01:2743:U:H2'	2:01:2744:G:C5'	2.45	0.47
3:02:30:C:H2'	3:02:31:C:H5'	1.96	0.47
3:02:116:G:H4'	20:17:54:VAL:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:03:60:ARG:HG2	6:03:60:ARG:HH11	1.80	0.47
10:07:97:GLU:HG3	10:07:101:ARG:NH2	2.29	0.47
12:09:99:ILE:HD13	12:09:130:VAL:HG21	1.96	0.47
24:21:11:ARG:H	24:21:11:ARG:CD	2.24	0.47
24:21:17:VAL:HG12	24:21:76:VAL:HG21	1.96	0.47
25:22:6:ARG:O	25:22:10:VAL:HG23	2.15	0.47
30:27:5:GLU:HA	30:27:8:GLU:OE2	2.15	0.47
49:K:19:VAL:HG23	49:K:36:ARG:HA	1.97	0.47
53:O:42:PHE:HE1	53:O:48:ASP:HB2	1.78	0.47
54:P:59:HIS:O	54:P:63:GLN:HG2	2.14	0.47
59:U:64:ALA:HB1	59:U:66:ARG:HG3	1.96	0.47
1:A:451:A:H4'	1:A:452:A:O4'	2.15	0.47
2:01:452:G:OP1	9:06:52:VAL:HG13	2.14	0.47
2:01:546:U:H1'	2:01:548:G:O6	2.14	0.47
2:01:1601:G:C2'	2:01:1602:U:H5'	2.44	0.47
2:01:2572:A:N7	8:05:150:GLN:HG3	2.29	0.47
2:01:2628:C:H3'	2:01:2629:U:H5'	1.96	0.47
3:02:2:G:H2'	3:02:3:C:H6	1.78	0.47
3:02:3:C:H3'	3:02:4:C:C5'	2.43	0.47
3:02:42:C:C4	10:07:65:LEU:HD22	2.50	0.47
6:03:48:LEU:HD22	6:03:165:ASN:HD21	1.78	0.47
8:05:5:VAL:HG11	8:05:80:TRP:CZ3	2.49	0.47
8:05:60:VAL:O	8:05:60:VAL:HG13	2.15	0.47
28:25:7:ARG:HH22	5:W:63:G:H5''	1.80	0.47
42:D:167:PRO:HB3	42:D:169:TRP:CZ3	2.50	0.47
47:I:62:LEU:HD12	47:I:62:LEU:N	2.30	0.47
56:R:53:GLN:HA	56:R:53:GLN:NE2	2.30	0.47
1:A:59:A:H1'	1:A:354:G:N2	2.29	0.47
1:A:179:A:H2'	1:A:179:A:N3	2.30	0.47
1:A:1225:A:H5'	1:A:1226:C:OP2	2.14	0.47
2:01:325:G:H2'	2:01:326:G:C8	2.50	0.47
2:01:1083:U:H2'	2:01:1085:A:OP2	2.15	0.47
2:01:1563:U:H2'	2:01:1564:C:C6	2.50	0.47
2:01:2024:G:OP2	2:01:2034:U:H4'	2.15	0.47
2:01:2124:G:H3'	2:01:2125:G:C5'	2.45	0.47
6:03:9:ARG:HA	6:03:12:ARG:HE	1.80	0.47
7:04:179:GLU:OE2	7:04:270:ARG:N	2.48	0.47
9:06:109:LEU:O	9:06:113:VAL:HG23	2.15	0.47
12:09:42:LYS:HE2	12:09:46:PHE:HE2	1.80	0.47
13:10:29:ASP:H	13:10:81:LEU:HD22	1.79	0.47
17:14:46:VAL:HB	17:14:50:PHE:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:29:11:GLU:HA	32:29:25:ARG:HA	1.96	0.47
33:30:32:THR:OG1	33:30:50:GLY:HA2	2.15	0.47
39:Z:278:ARG:HD3	39:Z:278:ARG:C	2.35	0.47
45:G:3:ARG:HH11	45:G:3:ARG:HG3	1.79	0.47
53:O:24:THR:O	53:O:28:VAL:HG23	2.15	0.47
54:P:40:ASN:HD22	54:P:43:ALA:HA	1.80	0.47
1:A:429:U:P	42:D:8:LEU:HD11	2.55	0.47
1:A:831:A:C2'	1:A:832:G:H5''	2.45	0.47
1:A:1372:U:H2'	1:A:1373:G:O4'	2.15	0.47
2:01:682:G:H5'	35:32:26:ASN:OD1	2.15	0.47
2:01:692:C:P	7:04:55:GLY:H	2.37	0.47
7:04:38:LYS:NZ	7:04:58:LYS:HA	2.30	0.47
8:05:48:ILE:HG23	8:05:84:LEU:HD21	1.97	0.47
10:07:114:ARG:NH2	51:M:67:ASP:OD1	2.46	0.47
19:16:22:ARG:HG3	19:16:70:THR:HA	1.97	0.47
20:17:7:ARG:HH11	20:17:7:ARG:HG3	1.80	0.47
21:18:95:LYS:HD3	21:18:97:TYR:HE2	1.79	0.47
22:19:43:GLN:NE2	23:20:77:PHE:HB3	2.29	0.47
39:Z:232:ILE:O	39:Z:232:ILE:HG13	2.15	0.47
48:J:82:LYS:HD2	48:J:85:ASP:HB3	1.97	0.47
57:S:8:PRO:HB2	57:S:38:THR:HG21	1.97	0.47
1:A:1346:A:H2'	1:A:1346:A:N3	2.31	0.46
1:A:1354:U:H2'	1:A:1355:G:H8	1.80	0.46
2:01:1690:A:H2'	2:01:1691:C:O4'	2.15	0.46
2:01:2249:U:O2'	2:01:2250:G:H5''	2.15	0.46
5:X:68:C:H2'	5:X:69:C:C4'	2.44	0.46
14:11:59:THR:CG2	14:11:67:THR:HB	2.45	0.46
28:25:51:ARG:HH11	28:25:51:ARG:HG3	1.79	0.46
39:Z:20:VAL:HG12	39:Z:24:TYR:CE2	2.51	0.46
39:Z:242:ASP:HB3	39:Z:262:ARG:HB3	1.97	0.46
42:D:94:GLU:HA	42:D:99:ASN:OD1	2.15	0.46
45:G:37:THR:O	45:G:41:ILE:HG13	2.16	0.46
55:Q:57:VAL:HG23	55:Q:78:VAL:O	2.15	0.46
56:R:25:ILE:O	56:R:29:LYS:HG3	2.15	0.46
57:S:30:LEU:HD12	57:S:30:LEU:N	2.30	0.46
1:A:335:C:H2'	1:A:336:A:C8	2.49	0.46
1:A:1463:U:OP1	21:18:108:ARG:HD2	2.16	0.46
2:01:2343:U:O2'	2:01:2344:U:H5'	2.15	0.46
3:02:111:U:H2'	3:02:112:G:H8	1.80	0.46
19:16:72:ASP:O	19:16:76:VAL:HG23	2.14	0.46
22:19:105:PHE:O	22:19:109:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:24:45:ASP:HA	27:24:48:MET:HB3	1.97	0.46
34:31:5:ARG:HH11	34:31:25:ASN:HB2	1.80	0.46
40:B:42:LEU:HD23	40:B:42:LEU:N	2.28	0.46
1:A:337:G:H2'	1:A:338:A:C8	2.50	0.46
1:A:1504:G:H4'	1:A:1505:G:O4'	2.15	0.46
2:01:1:G:H2'	2:01:2:G:C8	2.50	0.46
2:01:467:G:O2'	2:01:468:G:H5'	2.15	0.46
2:01:1087:G:C3'	2:01:1088:A:H5''	2.46	0.46
2:01:1981:A:H5''	2:01:1982:U:OP2	2.15	0.46
2:01:2363:G:O2'	2:01:2364:C:H5'	2.15	0.46
2:01:2591:C:H2'	2:01:2592:G:H8	1.80	0.46
2:01:2646:C:H2'	2:01:2647:U:O4'	2.15	0.46
2:01:2746:U:H1'	11:08:138:GLN:NE2	2.30	0.46
10:07:7:TYR:OH	10:07:29:ARG:HG3	2.15	0.46
29:26:67:LEU:HG	29:26:71:ARG:HH12	1.80	0.46
39:Z:298:LEU:O	39:Z:302:LYS:HG2	2.16	0.46
40:B:165:ALA:HB2	40:B:186:VAL:HG12	1.96	0.46
42:D:23:GLY:HA2	42:D:160:LEU:HD21	1.96	0.46
50:L:17:LYS:HB2	50:L:17:LYS:NZ	2.30	0.46
1:A:309:A:H2'	1:A:310:G:H8	1.79	0.46
1:A:780:A:OP1	49:K:124:LYS:HG3	2.15	0.46
1:A:1410:A:H2'	1:A:1411:C:C6	2.50	0.46
2:01:864:G:O2'	2:01:865:C:H5'	2.16	0.46
2:01:2485:G:O2'	2:01:2486:C:H5'	2.15	0.46
11:08:175:LYS:HG3	11:08:176:LYS:HG3	1.96	0.46
12:09:125:THR:HG22	12:09:125:THR:O	2.15	0.46
27:24:28:ALA:HB3	27:24:40:ILE:HD12	1.98	0.46
30:27:9:LYS:HG2	30:27:11:VAL:H	1.80	0.46
36:33:14:LYS:HD3	36:33:22:LYS:HE3	1.97	0.46
43:E:75:LEU:O	43:E:75:LEU:HD12	2.15	0.46
48:J:21:ALA:O	48:J:25:ILE:HG12	2.16	0.46
1:A:748:G:H2'	1:A:749:A:H8	1.80	0.46
1:A:1170:A:H2'	1:A:1171:A:O4'	2.15	0.46
1:A:1173:U:H2'	1:A:1174:G:H8	1.80	0.46
1:A:1218:C:H2'	1:A:1219:A:C8	2.50	0.46
1:A:1305:G:N2	1:A:1331:G:H2'	2.30	0.46
2:01:123:G:H4'	2:01:1376:C:O5'	2.15	0.46
2:01:125:A:H4'	35:32:13:ASN:O	2.15	0.46
2:01:970:U:H2'	2:01:971:G:H8	1.80	0.46
2:01:1063:G:H4'	14:11:76:ALA:HB1	1.98	0.46
2:01:1156:A:C8	22:19:50:ARG:HD3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1506:U:H2'	2:01:1507:C:C6	2.51	0.46
2:01:2874:C:OP1	19:16:4:ARG:HD2	2.15	0.46
8:05:148:GLN:OE1	8:05:148:GLN:N	2.49	0.46
11:08:88:LEU:HG	11:08:161:VAL:HG22	1.97	0.46
39:Z:176:ILE:C	39:Z:176:ILE:HD12	2.36	0.46
40:B:56:LEU:HD13	40:B:216:VAL:HG13	1.97	0.46
41:C:38:VAL:O	41:C:42:LEU:HD13	2.15	0.46
50:L:54:VAL:N	50:L:62:VAL:O	2.48	0.46
52:N:92:ILE:N	52:N:92:ILE:HD12	2.30	0.46
1:A:21:G:H2'	1:A:22:G:C8	2.51	0.46
1:A:1251:A:O2'	1:A:1370:G:H5'	2.16	0.46
1:A:1384:C:H2'	1:A:1385:G:C8	2.50	0.46
2:01:176:A:O2'	2:01:177:G:H5'	2.15	0.46
2:01:644:A:H2'	2:01:645:C:C5'	2.45	0.46
2:01:1912:A:N7	2:01:1917:U:O4	2.48	0.46
2:01:2124:G:H2'	2:01:2125:G:H4'	1.96	0.46
3:02:23:G:H2'	3:02:24:G:C8	2.50	0.46
9:06:192:ALA:O	9:06:196:VAL:HG23	2.15	0.46
10:07:131:VAL:HG22	10:07:151:LEU:O	2.15	0.46
13:10:37:LYS:HD3	13:10:41:LEU:HD12	1.97	0.46
13:10:60:LEU:HD12	13:10:60:LEU:N	2.30	0.46
14:11:101:SER:HA	14:11:140:GLU:HG3	1.98	0.46
26:23:71:ILE:CD1	26:23:82:VAL:HG22	2.45	0.46
32:29:35:ASP:HA	51:M:56:ARG:NH1	2.31	0.46
39:Z:98:GLU:O	39:Z:102:GLU:HG2	2.16	0.46
48:J:49:PHE:HZ	52:N:75:LYS:HG2	1.81	0.46
59:U:17:ARG:HA	59:U:20:ARG:HH11	1.80	0.46
1:A:76:G:H2'	1:A:77:A:O4'	2.16	0.46
1:A:142:G:H2'	1:A:143:A:O4'	2.15	0.46
1:A:614:C:H3'	1:A:615:G:H5''	1.97	0.46
2:01:694:U:OP1	2:01:1569:A:H1'	2.16	0.46
8:05:24:VAL:HG22	8:05:178:VAL:HG21	1.97	0.46
18:15:20:LEU:HD13	27:24:81:PRO:HG3	1.97	0.46
25:22:69:ARG:CB	25:22:69:ARG:HH11	2.29	0.46
31:28:35:VAL:HG22	31:28:36:GLU:N	2.31	0.46
35:32:26:ASN:O	35:32:30:VAL:HG23	2.15	0.46
40:B:119:GLN:HA	40:B:123:GLY:HA3	1.98	0.46
42:D:97:LEU:HB2	42:D:134:TYR:HB3	1.97	0.46
42:D:104:MET:CE	42:D:170:LEU:HD13	2.45	0.46
44:F:46:GLN:HA	44:F:56:LYS:HG2	1.98	0.46
52:N:64:ARG:HG3	52:N:77:GLY:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:U:H5	1:A:533:A:N6	1.96	0.46
2:01:15:G:O2'	2:01:16:C:H5'	2.16	0.46
2:01:2091:C:H5''	12:09:27:ARG:HH22	1.81	0.46
2:01:2543:G:H2'	2:01:2544:G:C8	2.49	0.46
8:05:116:LYS:HD2	8:05:165:MET:HG2	1.98	0.46
10:07:121:PHE:CE1	10:07:127:TYR:HB2	2.50	0.46
14:11:44:LYS:HB2	14:11:68:PHE:HE2	1.81	0.46
17:14:63:LYS:HB3	17:14:63:LYS:NZ	2.30	0.46
18:15:33:LEU:HD23	18:15:33:LEU:C	2.36	0.46
28:25:7:ARG:O	28:25:10:ARG:NH1	2.49	0.46
28:25:37:ARG:HG2	28:25:37:ARG:HH11	1.80	0.46
42:D:27:ILE:HB	42:D:33:ILE:HG21	1.97	0.46
44:F:76:THR:HG23	44:F:79:ARG:HH22	1.81	0.46
47:I:109:GLN:NE2	47:I:110:VAL:HB	2.30	0.46
58:T:43:LYS:HG2	58:T:86:ALA:HA	1.97	0.46
1:A:350:G:H2'	1:A:351:G:C8	2.51	0.46
1:A:363:A:C2	50:L:27:PRO:HD2	2.51	0.46
1:A:392:C:H2'	1:A:393:A:H8	1.80	0.46
1:A:730:G:C2'	1:A:731:G:H5'	2.46	0.46
1:A:748:G:H2'	1:A:749:A:C8	2.51	0.46
1:A:1045:C:O2'	1:A:1046:A:H5'	2.16	0.46
1:A:1221:G:O3'	57:S:76:THR:HG21	2.16	0.46
2:01:435:C:C2'	2:01:436:C:H5'	2.45	0.46
2:01:2247:A:H2'	2:01:2248:C:C6	2.51	0.46
2:01:2360:G:C2'	2:01:2361:G:H5'	2.46	0.46
11:08:169:ARG:HD2	11:08:169:ARG:N	2.26	0.46
15:12:17:VAL:HG13	15:12:57:LEU:HD13	1.98	0.46
16:13:63:VAL:CG1	16:13:103:VAL:HG12	2.46	0.46
40:B:177:ASN:C	40:B:178:LEU:HD12	2.36	0.46
42:D:8:LEU:O	42:D:12:ARG:HG3	2.16	0.46
42:D:99:ASN:HD21	42:D:103:ARG:HE	1.64	0.46
48:J:102:LEU:O	48:J:102:LEU:HD12	2.15	0.46
54:P:76:LYS:O	54:P:79:ASN:ND2	2.48	0.46
1:A:932:C:H5''	45:G:3:ARG:NH2	2.31	0.46
1:A:1254:A:H2'	1:A:1255:G:H8	1.80	0.46
2:01:103:A:H2'	2:01:104:A:O4'	2.15	0.46
2:01:558:U:OP1	15:12:113:PRO:HD2	2.16	0.46
2:01:563:A:H4'	22:19:40:LYS:HZ3	1.80	0.46
2:01:1131:G:H21	2:01:1132:U:H5	1.63	0.46
2:01:1666:G:C2'	2:01:1667:G:H5'	2.46	0.46
2:01:1869:G:H3'	2:01:1870:C:C5'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2572:A:H5'	2:01:2574:G:H4'	1.98	0.46
2:01:2765:A:H3'	2:01:2765:A:N3	2.31	0.46
7:04:43:ASN:HD21	7:04:45:ASN:HD22	1.63	0.46
8:05:13:ARG:HD3	8:05:15:PHE:CZ	2.51	0.46
8:05:180:VAL:O	8:05:180:VAL:HG23	2.16	0.46
10:07:121:PHE:HZ	10:07:169:LEU:HD12	1.81	0.46
39:Z:167:GLU:HG2	39:Z:275:GLN:HB2	1.98	0.46
39:Z:244:TYR:HE1	39:Z:262:ARG:HB2	1.79	0.46
45:G:58:LEU:C	45:G:58:LEU:HD23	2.37	0.46
51:M:89:ARG:NE	51:M:89:ARG:HA	2.30	0.46
54:P:8:ARG:HH11	54:P:8:ARG:HG3	1.80	0.46
55:Q:10:ARG:HD2	55:Q:11:VAL:N	2.30	0.46
1:A:530:G:H3'	1:A:531:U:H5''	1.95	0.45
1:A:539:A:H2'	1:A:540:G:C8	2.51	0.45
2:01:415:A:H2'	2:01:416:U:C6	2.52	0.45
2:01:611:C:H2'	2:01:612:G:O4'	2.15	0.45
2:01:1059:G:H5'	2:01:1061:U:OP2	2.15	0.45
2:01:1454:C:O2'	19:16:60:VAL:HG13	2.16	0.45
2:01:2082:A:H2'	2:01:2083:G:O4'	2.16	0.45
2:01:2263:C:H4'	2:01:2329:U:H4'	1.98	0.45
2:01:2898:U:H2'	2:01:2899:A:C8	2.51	0.45
3:02:57:A:H4'	10:07:26:GLN:HE21	1.81	0.45
3:02:111:U:H2'	3:02:112:G:C8	2.51	0.45
8:05:133:THR:HG23	8:05:134:HIS:CD2	2.51	0.45
11:08:88:LEU:HD12	11:08:88:LEU:N	2.31	0.45
11:08:132:LEU:H	11:08:132:LEU:CD2	2.25	0.45
15:12:14:ASP:CG	15:12:15:TRP:H	2.18	0.45
20:17:59:ALA:HA	20:17:62:LEU:HD12	1.98	0.45
20:17:64:TYR:HB3	20:17:67:ASN:HD21	1.81	0.45
23:20:24:LYS:HA	23:20:94:THR:OG1	2.16	0.45
37:34:36:ARG:CG	37:34:37:GLN:N	2.78	0.45
39:Z:145:ALA:HB1	39:Z:176:ILE:CD1	2.46	0.45
40:B:216:VAL:O	40:B:220:VAL:HG23	2.16	0.45
43:E:104:ILE:HD11	43:E:114:LEU:HB2	1.97	0.45
48:J:59:LYS:HE2	48:J:62:ARG:NH2	2.28	0.45
49:K:24:ALA:HB1	49:K:29:THR:HG22	1.97	0.45
1:A:1308:U:H5''	51:M:96:VAL:HG22	1.98	0.45
2:01:240:C:C3'	2:01:241:A:H5''	2.44	0.45
2:01:1060:U:O2	2:01:1060:U:H3'	2.15	0.45
2:01:2055:C:H5'	2:01:2056:G:O5'	2.17	0.45
7:04:74:PRO:HA	7:04:116:GLN:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:05:8:LYS:HB2	8:05:201:LEU:HD11	1.98	0.45
10:07:30:VAL:HG13	10:07:30:VAL:O	2.16	0.45
12:09:135:HIS:ND1	12:09:136:SER:N	2.65	0.45
13:10:57:ASN:HB3	13:10:62:ARG:HG2	1.99	0.45
17:14:109:LYS:NZ	17:14:126:ARG:HG2	2.31	0.45
20:17:58:ILE:O	20:17:62:LEU:HG	2.16	0.45
24:21:19:LEU:HD11	33:30:20:ALA:HA	1.97	0.45
41:C:28:PHE:HE2	52:N:76:PHE:HD1	1.62	0.45
52:N:9:GLU:OE2	52:N:62:ARG:HG2	2.16	0.45
1:A:579:A:H2'	1:A:580:C:C6	2.52	0.45
1:A:1150:A:N3	48:J:41:PRO:HG3	2.31	0.45
2:01:451:U:H4'	9:06:47:LYS:NZ	2.32	0.45
2:01:858:G:H5'	28:25:40:LYS:HE2	1.98	0.45
2:01:1919:A:H2'	2:01:1920:C:H5'	1.97	0.45
2:01:2123:G:H4'	6:03:172:HIS:HB2	1.98	0.45
12:09:122:LEU:HD12	12:09:122:LEU:N	2.32	0.45
20:17:52:SER:OG	20:17:53:THR:N	2.48	0.45
22:19:82:LEU:HD22	22:19:87:VAL:HG21	1.97	0.45
36:33:36:ALA:O	36:33:40:LYS:HG3	2.16	0.45
41:C:79:LYS:HB2	41:C:81:GLU:OE1	2.16	0.45
49:K:126:ARG:HE	49:K:126:ARG:CA	2.24	0.45
50:L:58:ASN:ND2	50:L:60:PHE:CD2	2.84	0.45
1:A:912:C:O2'	1:A:913:A:H5'	2.16	0.45
1:A:1422:G:H4'	16:13:48:PRO:HB3	1.98	0.45
2:01:112:U:C2'	2:01:113:U:H5'	2.47	0.45
2:01:441:U:O2'	2:01:442:G:H5'	2.16	0.45
2:01:1258:U:H2'	2:01:1259:G:C8	2.50	0.45
2:01:1666:G:H4'	16:13:6:THR:HG23	1.99	0.45
2:01:1856:U:H2'	2:01:1857:G:O4'	2.16	0.45
2:01:2404:U:H2'	2:01:2405:G:O4'	2.16	0.45
2:01:2412:A:H2'	2:01:2413:G:O4'	2.16	0.45
4:Y:28:ARG:HH11	4:Y:28:ARG:HG2	1.82	0.45
12:09:100:ALA:HB2	12:09:115:VAL:HG21	1.98	0.45
14:11:49:GLU:H	14:11:49:GLU:CD	2.20	0.45
19:16:64:ARG:HH21	19:16:64:ARG:HG3	1.82	0.45
32:29:20:ASN:HB2	32:29:39:LYS:HE3	1.98	0.45
40:B:95:TRP:HZ2	40:B:100:LEU:HD13	1.82	0.45
44:F:51:ILE:HD12	44:F:86:ARG:NE	2.27	0.45
51:M:58:GLU:OE2	51:M:61:LYS:HD3	2.16	0.45
55:Q:16:MET:HG3	55:Q:17:GLU:H	1.81	0.45
1:A:763:G:H2'	1:A:764:C:H6	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1380:U:C4	45:G:2:ARG:HG3	2.52	0.45
2:01:1463:C:H2'	2:01:1464:G:H8	1.81	0.45
2:01:1541:C:H2'	2:01:1542:U:O4'	2.17	0.45
2:01:1914:C:H5'	2:01:1915:U:OP2	2.16	0.45
2:01:2070:A:H2'	2:01:2071:A:O4'	2.16	0.45
14:11:48:ILE:HG22	14:11:49:GLU:N	2.32	0.45
19:16:72:ASP:HB3	19:16:75:ILE:HD13	1.97	0.45
22:19:30:VAL:HG12	22:19:33:VAL:H	1.82	0.45
23:20:14:VAL:HG21	23:20:98:ILE:HG13	1.99	0.45
30:27:20:ASN:O	30:27:25:GLN:N	2.50	0.45
32:29:66:ILE:HG21	52:N:38:GLU:OE2	2.16	0.45
39:Z:21:LEU:CD2	39:Z:110:LEU:HG	2.34	0.45
40:B:150:ILE:HD11	40:B:153:MET:HE1	1.99	0.45
47:I:76:GLY:O	47:I:79:ARG:HG2	2.16	0.45
48:J:9:ARG:O	48:J:99:GLN:N	2.49	0.45
54:P:54:LEU:HD23	54:P:57:ILE:HD12	1.97	0.45
58:T:79:THR:HA	58:T:82:ILE:HG12	1.97	0.45
1:A:77:A:N6	1:A:92:U:H3	2.15	0.45
1:A:160:A:H2'	1:A:161:A:O4'	2.17	0.45
1:A:785:G:O2'	1:A:786:G:H5'	2.17	0.45
2:01:68:G:H2'	2:01:69:C:O4'	2.17	0.45
2:01:1753:G:OP1	21:18:92:ARG:HD3	2.16	0.45
2:01:2294:G:OP1	20:17:10:ARG:HD2	2.17	0.45
8:05:7:LYS:HB2	8:05:77:ARG:HH12	1.82	0.45
8:05:14:ILE:HG23	21:18:11:GLN:HE22	1.82	0.45
8:05:148:GLN:HB2	8:05:152:PRO:HG2	1.99	0.45
11:08:68:ARG:C	11:08:68:ARG:HD3	2.37	0.45
14:11:23:VAL:HG12	14:11:27:LEU:HG	1.99	0.45
37:34:33:HIS:O	37:34:35:GLN:HG3	2.17	0.45
44:F:42:TRP:NE1	44:F:61:LEU:HD13	2.30	0.45
45:G:49:LEU:HD12	45:G:50:ALA:N	2.32	0.45
50:L:23:LEU:HD23	50:L:29:LYS:NZ	2.32	0.45
51:M:70:ARG:HH11	51:M:70:ARG:HG3	1.81	0.45
52:N:55:SER:CB	52:N:56:PRO:CA	2.94	0.45
57:S:66:VAL:HG23	57:S:67:GLY:H	1.82	0.45
1:A:1096:C:H2'	1:A:1097:C:C6	2.52	0.45
2:01:863:A:H2'	2:01:864:G:C8	2.51	0.45
2:01:873:C:H2'	2:01:874:G:H8	1.80	0.45
2:01:910:A:H2'	2:01:911:A:C8	2.52	0.45
2:01:2124:G:H4'	6:03:43:ASP:HB3	1.98	0.45
2:01:2457:U:O4	2:01:2494:G:O6	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2682:A:O2'	2:01:2683:C:H5'	2.16	0.45
7:04:70:LYS:HE2	7:04:73:ILE:HD12	1.99	0.45
8:05:187:LEU:HD21	8:05:203:VAL:HG11	1.98	0.45
10:07:57:ALA:HB2	10:07:64:PRO:HD3	1.98	0.45
13:10:11:ILE:O	13:10:15:VAL:HG23	2.17	0.45
16:13:22:ILE:HG12	16:13:40:LYS:O	2.17	0.45
17:14:17:LYS:HD2	17:14:27:LEU:CD2	2.46	0.45
39:Z:125:SER:HA	39:Z:187:TYR:CD1	2.51	0.45
39:Z:230:ILE:O	39:Z:231:ASP:HB2	2.16	0.45
40:B:100:LEU:HD12	40:B:100:LEU:N	2.32	0.45
43:E:38:VAL:HG22	43:E:66:ALA:HB1	1.99	0.45
44:F:18:VAL:CG1	44:F:19:PRO:HD3	2.46	0.45
51:M:69:ARG:HA	51:M:72:ILE:HG12	1.97	0.45
1:A:135:C:H2'	1:A:136:C:H5'	1.99	0.45
1:A:204:G:H2'	1:A:205:A:C8	2.52	0.45
1:A:236:A:H5''	55:Q:43:LEU:HD21	1.97	0.45
1:A:880:C:H2'	1:A:881:G:H8	1.82	0.45
1:A:1312:G:N7	57:S:2:ARG:HD2	2.31	0.45
2:01:521:U:H2'	2:01:522:A:C8	2.52	0.45
2:01:720:U:H2'	2:01:721:A:C8	2.52	0.45
2:01:940:G:C3'	2:01:941:A:H5''	2.47	0.45
2:01:2578:G:O2'	2:01:2579:C:H5'	2.17	0.45
2:01:2580:U:O2	2:01:2580:U:O4'	2.34	0.45
2:01:2609:U:H5'	2:01:2610:C:OP2	2.16	0.45
9:06:84:THR:HG23	9:06:85:PHE:N	2.31	0.45
12:09:4:ILE:HD11	12:09:47:PHE:CD2	2.52	0.45
19:16:24:MET:HG2	19:16:44:LEU:HD22	1.99	0.45
42:D:120:LYS:HG2	42:D:130:ASN:HB3	1.98	0.45
53:O:23:SER:O	53:O:27:GLN:HG3	2.16	0.45
1:A:1210:C:C2'	1:A:1211:U:H5'	2.47	0.45
2:01:1790:C:O2'	7:04:207:ALA:HB2	2.16	0.45
2:01:1827:U:H5'	2:01:1971:U:OP2	2.17	0.45
2:01:2248:C:H2'	2:01:2249:U:H5'	1.99	0.45
5:X:50:U:H2'	5:X:51:C:C6	2.52	0.45
8:05:127:PHE:HZ	8:05:160:LYS:HB2	1.82	0.45
14:11:10:LEU:HD13	14:11:23:VAL:HG13	1.99	0.45
19:16:59:SER:CB	19:16:62:ASN:HD22	2.29	0.45
20:17:106:LEU:HD23	20:17:106:LEU:C	2.36	0.45
21:18:91:VAL:HG21	21:18:96:LEU:HD21	1.99	0.45
24:21:28:LYS:HG2	24:21:70:LYS:HE2	1.99	0.45
29:26:10:ARG:HG2	29:26:10:ARG:HH11	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:34:17:VAL:HG12	37:34:19:ARG:HG3	1.97	0.45
37:34:30:GLU:H	37:34:30:GLU:CD	2.19	0.45
39:Z:107:GLU:O	39:Z:111:ALA:N	2.50	0.45
48:J:11:LYS:HG2	48:J:71:LEU:HD23	1.98	0.45
1:A:66:A:H4'	1:A:173:U:N3	2.32	0.45
1:A:641:U:H4'	1:A:642:A:C8	2.52	0.45
1:A:1158:C:H3'	1:A:1158:C:O2	2.16	0.45
1:A:1202:U:H2'	1:A:1203:C:O4'	2.16	0.45
1:A:1317:C:H4'	52:N:47:LEU:CD2	2.46	0.45
2:01:1187:G:H5''	23:20:83:TYR:CZ	2.52	0.45
2:01:1568:G:H5'	7:04:58:LYS:O	2.17	0.45
2:01:1799:G:H8	7:04:179:GLU:HG3	1.81	0.45
2:01:2188:U:H2'	2:01:2189:U:C4'	2.46	0.45
10:07:37:MET:CE	10:07:52:ALA:HB1	2.47	0.45
22:19:50:ARG:HH11	22:19:50:ARG:HG3	1.82	0.45
24:21:74:ILE:HG23	24:21:74:ILE:O	2.17	0.45
47:I:15:ALA:N	47:I:67:LYS:O	2.49	0.45
48:J:80:THR:CG2	48:J:81:GLU:H	2.30	0.45
53:O:55:LEU:HD23	53:O:55:LEU:C	2.37	0.45
1:A:742:G:O2'	1:A:743:A:H5'	2.17	0.44
1:A:1282:C:H6	1:A:1282:C:O5'	1.99	0.44
1:A:1352:C:H2'	1:A:1353:G:C8	2.52	0.44
2:01:20:C:H2'	2:01:21:A:H8	1.82	0.44
2:01:296:U:H2'	2:01:297:G:H8	1.82	0.44
2:01:687:C:H5''	35:32:4:THR:O	2.16	0.44
2:01:1748:C:O2'	2:01:1749:A:H5'	2.16	0.44
2:01:2898:U:H2'	2:01:2899:A:H8	1.82	0.44
13:10:4:ASN:HA	13:10:7:ASP:HB2	1.99	0.44
16:13:4:GLU:OE2	16:13:24:VAL:HG23	2.18	0.44
16:13:57:VAL:HG23	16:13:57:VAL:O	2.17	0.44
35:32:24:THR:HG23	35:32:27:GLY:H	1.81	0.44
41:C:5:HIS:CG	52:N:88:MET:HB3	2.53	0.44
41:C:129:PHE:HD1	41:C:129:PHE:H	1.65	0.44
55:Q:43:LEU:HD13	55:Q:72:TRP:CE2	2.51	0.44
56:R:55:ALA:O	56:R:59:LYS:HG2	2.17	0.44
1:A:988:G:H1'	1:A:1015:G:H22	1.82	0.44
2:01:296:U:H2'	2:01:297:G:C8	2.52	0.44
2:01:859:G:HO2'	2:01:860:U:H6	1.59	0.44
2:01:1380:G:H1'	2:01:1569:A:H61	1.81	0.44
2:01:1826:G:H2'	2:01:1827:U:C6	2.52	0.44
2:01:2188:U:C3'	2:01:2189:U:H5''	2.40	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2285:C:O2'	2:01:2287:A:H1'	2.16	0.44
2:01:2286:G:H4'	2:01:2287:A:O4'	2.17	0.44
2:01:2466:C:H5''	37:34:6:SER:OG	2.17	0.44
2:01:2467:C:H2'	2:01:2468:A:O4'	2.18	0.44
10:07:35:LEU:HD23	10:07:35:LEU:O	2.17	0.44
13:10:37:LYS:HD2	13:10:37:LYS:C	2.37	0.44
14:11:20:SER:OG	14:11:21:PRO:HD3	2.17	0.44
20:17:106:LEU:HD23	20:17:106:LEU:O	2.17	0.44
25:22:65:GLY:H	25:22:79:ASP:HB3	1.82	0.44
28:25:39:THR:HG23	28:25:53:HIS:CD2	2.40	0.44
37:34:25:VAL:O	37:34:25:VAL:HG12	2.18	0.44
39:Z:165:ILE:HG13	39:Z:165:ILE:O	2.18	0.44
39:Z:182:LYS:HD3	39:Z:183:ILE:N	2.32	0.44
40:B:34:ARG:HG2	40:B:34:ARG:HH11	1.83	0.44
51:M:89:ARG:HA	51:M:89:ARG:HE	1.82	0.44
52:N:31:SER:C	57:S:6:LYS:HZ1	2.21	0.44
1:A:31:G:N1	1:A:48:C:H5''	2.31	0.44
1:A:608:A:H2'	1:A:609:A:O4'	2.17	0.44
1:A:1133:G:H2'	1:A:1134:G:C8	2.52	0.44
2:01:98:G:O2'	2:01:99:U:H5'	2.17	0.44
2:01:254:G:H2'	2:01:255:A:H5''	1.98	0.44
2:01:368:A:C2'	2:01:369:U:H5'	2.47	0.44
2:01:368:A:H2'	2:01:369:U:H5'	1.99	0.44
2:01:372:G:N7	29:26:56:ARG:HB3	2.32	0.44
2:01:1420:A:H5'	2:01:1421:G:OP2	2.17	0.44
2:01:1599:U:OP1	25:22:39:THR:HA	2.17	0.44
2:01:2595:G:H1	7:04:238:ASN:HD21	1.63	0.44
2:01:2603:G:O2'	2:01:2604:U:H5'	2.18	0.44
10:07:11:VAL:HG21	10:07:172:PHE:CE1	2.52	0.44
16:13:17:ARG:HE	16:13:47:ILE:HG22	1.82	0.44
18:15:90:GLU:HB2	18:15:91:TYR:HD1	1.82	0.44
24:21:31:GLN:O	24:21:35:ILE:HG13	2.17	0.44
31:28:4:ILE:N	31:28:37:ARG:O	2.42	0.44
42:D:13:ARG:HD2	42:D:37:PRO:CB	2.46	0.44
42:D:29:THR:O	42:D:29:THR:HG22	2.17	0.44
51:M:43:LYS:HB2	51:M:46:GLU:HG3	1.99	0.44
53:O:48:ASP:O	53:O:52:ARG:N	2.50	0.44
54:P:40:ASN:ND2	54:P:43:ALA:HA	2.33	0.44
59:U:40:PRO:O	59:U:44:ARG:N	2.50	0.44
1:A:45:G:H5''	1:A:307:C:O2'	2.18	0.44
1:A:131:A:H2'	1:A:132:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:924:C:H2'	1:A:925:G:C8	2.53	0.44
1:A:986:U:H2'	1:A:987:G:H8	1.78	0.44
2:01:361:G:C2'	2:01:362:A:H5'	2.47	0.44
2:01:828:U:H4'	2:01:831:G:N1	2.32	0.44
2:01:1045:C:H5'	2:01:1046:A:H5''	2.00	0.44
2:01:1268:A:H2'	2:01:1269:A:O4'	2.17	0.44
2:01:1415:U:O2'	2:01:1416:G:H4'	2.17	0.44
2:01:1710:G:H2'	2:01:1711:A:C8	2.52	0.44
2:01:2526:G:H1'	37:34:1:MET:N	2.32	0.44
2:01:2654:A:O3'	2:01:2655:G:H4'	2.17	0.44
6:03:69:THR:OG1	6:03:177:LYS:HE2	2.16	0.44
12:09:26:ALA:HA	12:09:30:LEU:HD12	1.99	0.44
14:11:52:LEU:HD12	14:11:52:LEU:N	2.32	0.44
14:11:91:LYS:CB	14:11:94:LYS:HB2	2.45	0.44
19:16:33:ILE:HG22	19:16:114:GLU:CB	2.48	0.44
27:24:24:ASN:C	27:24:25:LYS:HD2	2.38	0.44
28:25:64:LYS:HB2	28:25:79:GLU:OE1	2.18	0.44
39:Z:189:TYR:CG	39:Z:224:PRO:HB3	2.52	0.44
40:B:13:VAL:HG23	40:B:13:VAL:O	2.17	0.44
43:E:59:ILE:O	43:E:63:MET:HG2	2.17	0.44
44:F:15:SER:O	44:F:18:VAL:HG12	2.18	0.44
44:F:45:ARG:HG2	44:F:45:ARG:HH11	1.83	0.44
45:G:113:LYS:HB2	45:G:117:LEU:CD2	2.44	0.44
53:O:55:LEU:HD23	53:O:59:VAL:HG23	1.99	0.44
1:A:628:G:H2'	1:A:629:A:C8	2.53	0.44
1:A:828:U:H2'	40:B:24:PRO:HB2	1.98	0.44
1:A:1492:A:C1'	4:Y:26:ARG:HD3	2.47	0.44
2:01:876:C:C2'	2:01:877:A:H5'	2.46	0.44
2:01:2170:A:H2'	2:01:2171:A:C4'	2.47	0.44
2:01:2220:U:H2'	2:01:2221:G:H8	1.83	0.44
9:06:19:PHE:HB3	9:06:113:VAL:HG21	1.99	0.44
12:09:27:ARG:NH1	29:26:55:MET:HB3	2.31	0.44
14:11:102:ARG:HA	14:11:105:LEU:HD12	2.00	0.44
28:25:62:LYS:HE3	28:25:81:GLU:HG2	2.00	0.44
39:Z:273:GLN:OE1	39:Z:273:GLN:N	2.51	0.44
41:C:82:ASP:O	41:C:86:LEU:HG	2.16	0.44
42:D:117:VAL:CG2	42:D:122:ILE:HD12	2.46	0.44
44:F:98:GLU:HB3	44:F:99:ALA:H	1.61	0.44
51:M:101:THR:HG22	51:M:101:THR:O	2.16	0.44
52:N:34:ASN:O	52:N:36:SER:N	2.51	0.44
1:A:686:U:H2'	1:A:687:A:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:757:U:H2'	1:A:758:C:O4'	2.18	0.44
1:A:1348:U:H4'	47:I:121:ARG:HG3	2.00	0.44
1:A:1514:G:O2'	1:A:1515:G:H5'	2.18	0.44
2:01:20:C:H2'	2:01:21:A:C8	2.53	0.44
2:01:320:A:H4'	2:01:322:A:N7	2.32	0.44
2:01:886:A:H1'	2:01:889:C:H41	1.83	0.44
2:01:1219:U:H2'	2:01:1220:G:C8	2.53	0.44
2:01:1265:A:N1	2:01:2013:A:H5''	2.33	0.44
2:01:1357:C:H2'	2:01:1358:G:O4'	2.17	0.44
2:01:1548:A:H2'	2:01:1549:A:C8	2.52	0.44
2:01:1566:A:H5'	7:04:213:ARG:HH22	1.82	0.44
2:01:1827:U:H2'	2:01:1828:G:O4'	2.18	0.44
2:01:2184:A:H2'	2:01:2185:U:H5'	1.99	0.44
2:01:2233:U:H2'	2:01:2234:G:C8	2.53	0.44
2:01:2353:G:H2'	2:01:2354:C:C5'	2.44	0.44
2:01:2619:C:OP1	8:05:157:LYS:HE3	2.18	0.44
9:06:24:ASN:O	9:06:28:VAL:HG23	2.18	0.44
17:14:78:ARG:HH21	17:14:78:ARG:HG2	1.81	0.44
21:18:105:LYS:O	21:18:108:ARG:NH2	2.50	0.44
27:24:73:LYS:HG3	27:24:94:ALA:HB3	2.00	0.44
28:25:66:GLU:HB2	28:25:75:PHE:HB2	2.00	0.44
29:26:7:THR:HG21	29:26:9:LYS:NZ	2.32	0.44
29:26:56:ARG:HG2	29:26:56:ARG:HH11	1.83	0.44
32:29:44:PHE:H	32:29:44:PHE:HD1	1.63	0.44
41:C:126:ARG:HD3	41:C:126:ARG:N	2.33	0.44
42:D:110:ARG:O	42:D:114:ARG:HG3	2.17	0.44
53:O:52:ARG:HG2	53:O:52:ARG:HH11	1.83	0.44
54:P:14:ARG:HH11	54:P:14:ARG:HG3	1.83	0.44
57:S:14:LEU:O	57:S:18:VAL:HG23	2.18	0.44
2:01:6:A:C5'	15:12:131:ASN:HD22	2.31	0.44
2:01:437:U:H2'	2:01:438:G:C8	2.52	0.44
2:01:554:U:H2'	2:01:555:G:O4'	2.17	0.44
2:01:562:U:O4'	2:01:2036:C:H5'	2.18	0.44
2:01:1056:G:H5''	2:01:1057:A:O4'	2.16	0.44
2:01:2183:A:H2'	2:01:2184:A:C8	2.50	0.44
2:01:2196:C:O2'	2:01:2197:U:H5'	2.18	0.44
2:01:2619:C:O2'	2:01:2620:C:H5'	2.18	0.44
7:04:244:VAL:CA	7:04:251:THR:HG22	2.48	0.44
13:10:33:VAL:HG23	13:10:36:ASP:H	1.82	0.44
13:10:81:LEU:HD23	13:10:81:LEU:C	2.38	0.44
16:13:2:ILE:O	16:13:33:ALA:N	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:18:61:ARG:NH2	21:18:99:LEU:O	2.51	0.44
21:18:87:ARG:HH11	21:18:87:ARG:HG3	1.83	0.44
27:24:53:LYS:HB2	27:24:53:LYS:HZ3	1.82	0.44
39:Z:14:LEU:HD23	39:Z:14:LEU:C	2.38	0.44
39:Z:333:ILE:HD11	39:Z:345:THR:HG22	2.00	0.44
40:B:17:HIS:CG	40:B:37:VAL:HB	2.53	0.44
41:C:139:ASN:HD22	41:C:139:ASN:N	2.14	0.44
41:C:152:VAL:O	41:C:152:VAL:HG23	2.18	0.44
47:I:20:ILE:CG2	47:I:60:LEU:HD22	2.47	0.44
47:I:89:TYR:HB3	47:I:93:LEU:HD12	1.99	0.44
49:K:26:PHE:HZ	59:U:28:LEU:HD11	1.82	0.44
54:P:67:ILE:HD12	54:P:67:ILE:H	1.81	0.44
55:Q:10:ARG:HH11	55:Q:10:ARG:HG3	1.83	0.44
1:A:763:G:H2'	1:A:764:C:C6	2.52	0.44
2:01:64:A:H2'	2:01:65:U:C6	2.52	0.44
2:01:227:A:O2'	2:01:228:C:H4'	2.17	0.44
2:01:627:A:N7	17:14:111:ILE:HD12	2.33	0.44
2:01:696:G:O2'	2:01:697:G:H5'	2.18	0.44
2:01:941:A:O2'	2:01:1190:G:H4'	2.17	0.44
2:01:1326:U:C2	2:01:1648:U:H1'	2.52	0.44
2:01:1790:C:H2'	2:01:1791:A:C5	2.53	0.44
3:02:116:G:P	20:17:55:GLU:HG2	2.58	0.44
6:03:161:VAL:HG21	6:03:174:THR:H	1.83	0.44
7:04:25:LYS:HB3	7:04:25:LYS:NZ	2.33	0.44
7:04:141:HIS:CD2	7:04:194:VAL:HG22	2.52	0.44
9:06:165:HIS:ND1	9:06:166:LYS:HD3	2.33	0.44
12:09:99:ILE:O	12:09:103:VAL:HG23	2.18	0.44
14:11:72:THR:HG22	14:11:116:MET:HE3	2.00	0.44
28:25:65:PHE:CD1	28:25:76:ILE:HG12	2.53	0.44
39:Z:27:TYR:HB2	39:Z:70:LEU:HD21	1.99	0.44
39:Z:66:VAL:HG13	39:Z:116:ARG:HH12	1.83	0.44
40:B:150:ILE:O	40:B:150:ILE:HG12	2.18	0.44
41:C:28:PHE:HE2	52:N:76:PHE:CD1	2.36	0.44
41:C:155:ARG:HD3	41:C:192:TYR:O	2.18	0.44
57:S:68:HIS:HB3	57:S:72:GLU:OE2	2.17	0.44
1:A:494:G:H2'	1:A:495:A:H4'	2.00	0.44
1:A:560:A:H4'	1:A:561:U:H5'	2.00	0.44
1:A:948:C:H2'	1:A:949:A:C8	2.53	0.44
1:A:1016:A:H4'	1:A:1218:C:H4'	2.00	0.44
1:A:1190:G:H5'	41:C:175:HIS:HE1	1.83	0.44
2:01:672:C:O2'	2:01:673:C:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2372:U:H2'	2:01:2373:G:H8	1.83	0.44
2:01:2591:C:H2'	2:01:2592:G:C8	2.53	0.44
2:01:2655:G:H2'	2:01:2664:G:C6	2.53	0.44
11:08:37:ASN:ND2	11:08:39:ALA:H	2.16	0.44
14:11:101:SER:O	14:11:105:LEU:HG	2.17	0.44
21:18:64:SER:OG	21:18:65:ASN:N	2.50	0.44
31:28:3:THR:HA	31:28:38:GLU:HA	1.99	0.44
41:C:163:ARG:HG3	41:C:163:ARG:HH11	1.82	0.44
42:D:158:LEU:HD23	42:D:158:LEU:O	2.18	0.44
45:G:4:ARG:HD2	45:G:6:ILE:HD13	2.00	0.44
49:K:124:LYS:C	49:K:124:LYS:HD2	2.38	0.44
1:A:393:A:H5'	1:A:483:C:O2'	2.18	0.43
1:A:1227:A:C2'	1:A:1228:C:H5'	2.48	0.43
2:01:746:U:H5'	2:01:748:G:H1'	1.99	0.43
2:01:1842:G:H1'	7:04:242:HIS:CD2	2.53	0.43
4:Y:24:LEU:HD23	4:Y:24:LEU:C	2.38	0.43
6:03:10:VAL:O	6:03:14:LYS:HG3	2.18	0.43
7:04:237:ARG:HH11	7:04:237:ARG:HG3	1.82	0.43
13:10:25:ALA:O	13:10:85:SER:OG	2.34	0.43
19:16:65:LEU:O	19:16:69:ARG:HG2	2.17	0.43
24:21:97:LEU:HD12	24:21:97:LEU:N	2.33	0.43
40:B:69:VAL:HG12	40:B:168:GLU:OE2	2.18	0.43
40:B:178:LEU:HD12	40:B:178:LEU:N	2.33	0.43
41:C:122:GLN:HB3	41:C:127:VAL:HG11	1.98	0.43
43:E:102:THR:H	43:E:121:ASN:HD22	1.65	0.43
48:J:57:VAL:O	48:J:58:ASN:CB	2.66	0.43
53:O:86:LEU:HD12	53:O:87:ARG:N	2.33	0.43
1:A:71:A:H3'	1:A:72:A:C5'	2.46	0.43
1:A:132:C:H5'	1:A:262:A:HO2'	1.83	0.43
1:A:410:G:H2'	1:A:429:U:C4	2.54	0.43
1:A:486:U:O2'	1:A:487:A:H8	2.01	0.43
1:A:535:A:H5'	1:A:536:C:H5	1.82	0.43
1:A:887:G:H2'	1:A:888:G:H5'	2.01	0.43
1:A:1042:A:H2'	1:A:1043:G:O4'	2.18	0.43
1:A:1369:C:P	47:I:112:ARG:HG3	2.58	0.43
2:01:807:U:OP2	17:14:36:LYS:HD2	2.18	0.43
2:01:940:G:H2'	2:01:941:A:C5'	2.48	0.43
2:01:1936:A:H2	2:01:1943:U:H3	1.66	0.43
2:01:2221:G:O2'	2:01:2222:C:H5'	2.18	0.43
2:01:2758:A:C2	11:08:70:LEU:HD11	2.52	0.43
2:01:2760:C:O2'	2:01:2761:A:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:04:15:VAL:HG22	7:04:205:GLY:HA3	2.00	0.43
7:04:103:ILE:C	7:04:103:ILE:HD12	2.38	0.43
9:06:90:GLN:HG3	9:06:92:HIS:CE1	2.53	0.43
12:09:63:ALA:HA	12:09:66:ASN:HD22	1.82	0.43
15:12:128:ASN:O	15:12:128:ASN:OD1	2.37	0.43
16:13:12:ASP:HB3	16:13:99:ILE:HG13	2.00	0.43
19:16:29:VAL:HG11	19:16:75:ILE:HG23	1.99	0.43
23:20:49:ILE:HG22	23:20:54:VAL:HB	2.01	0.43
26:23:73:ASN:HB2	26:23:80:ASP:OD2	2.18	0.43
27:24:65:VAL:O	27:24:65:VAL:HG13	2.17	0.43
39:Z:245:ARG:NH1	39:Z:259:SER:OG	2.50	0.43
47:I:122:ARG:HG3	47:I:122:ARG:HH11	1.82	0.43
53:O:26:VAL:O	53:O:30:LEU:HD13	2.17	0.43
59:U:36:PHE:HB3	59:U:40:PRO:HD3	1.99	0.43
1:A:314:C:O2'	1:A:315:A:H5'	2.17	0.43
1:A:372:C:H41	1:A:387:U:H2'	1.82	0.43
1:A:1086:U:H2'	1:A:1087:G:H5'	2.00	0.43
2:01:230:G:O2'	2:01:231:A:H5'	2.18	0.43
2:01:491:G:N3	2:01:491:G:H2'	2.33	0.43
2:01:922:C:H1'	28:25:22:PHE:HD2	1.84	0.43
2:01:2180:U:H2'	2:01:2181:U:O4'	2.18	0.43
2:01:2204:G:H4'	7:04:149:LYS:CD	2.49	0.43
7:04:124:LYS:HB3	7:04:127:ASN:HD21	1.80	0.43
10:07:105:ILE:C	10:07:108:PRO:HD2	2.39	0.43
12:09:46:PHE:HB3	12:09:51:ARG:HH12	1.84	0.43
14:11:50:LYS:HB3	14:11:50:LYS:NZ	2.32	0.43
23:20:1:MET:CE	23:20:101:ILE:HD12	2.48	0.43
24:21:57:ASN:HD22	24:21:57:ASN:N	2.15	0.43
26:23:100:GLU:CD	26:23:101:THR:H	2.21	0.43
27:24:80:HIS:HE1	27:24:82:TYR:CE1	2.36	0.43
30:27:43:LEU:O	30:27:43:LEU:HD13	2.17	0.43
37:34:16:ILE:HD13	37:34:25:VAL:HG22	2.00	0.43
44:F:9:MET:HG3	44:F:85:ILE:HG13	1.99	0.43
47:I:122:ARG:C	47:I:122:ARG:HD3	2.38	0.43
55:Q:30:HIS:HD2	55:Q:33:TYR:H	1.65	0.43
57:S:16:LYS:O	57:S:20:LYS:HG3	2.17	0.43
1:A:523:A:C2'	1:A:524:G:H5''	2.48	0.43
1:A:546:A:H5''	42:D:69:ARG:NH2	2.33	0.43
2:01:1604:C:O2'	2:01:1605:C:H5'	2.18	0.43
2:01:2353:G:O3'	28:25:28:LEU:HD12	2.18	0.43
3:02:30:C:C2'	3:02:31:C:H5'	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:X:9:G:H5'	5:X:11:A:OP2	2.18	0.43
8:05:51:THR:HB	8:05:79:LEU:HD23	2.00	0.43
8:05:124:ARG:NH1	8:05:163:GLY:HA3	2.33	0.43
9:06:120:VAL:HG23	9:06:120:VAL:O	2.19	0.43
21:18:89:GLY:O	21:18:112:ARG:NH1	2.51	0.43
36:33:28:LEU:HD11	36:33:43:LEU:O	2.19	0.43
5:W:51:C:H2'	5:W:52:G:H8	1.83	0.43
42:D:2:ARG:HG2	42:D:2:ARG:HH11	1.82	0.43
50:L:52:CYS:SG	50:L:66:ILE:HD11	2.58	0.43
51:M:69:ARG:HG2	51:M:69:ARG:HH11	1.84	0.43
1:A:762:U:H2'	1:A:763:G:H8	1.83	0.43
2:01:521:U:H2'	2:01:522:A:H8	1.82	0.43
2:01:818:G:C2'	2:01:819:A:H5''	2.49	0.43
2:01:1454:C:H5'	19:16:63:ARG:HH21	1.84	0.43
2:01:1775:U:H2'	2:01:1776:G:O4'	2.18	0.43
2:01:1917:U:C2'	2:01:1918:A:H5'	2.48	0.43
7:04:23:LEU:HD21	7:04:89:ASN:OD1	2.18	0.43
7:04:132:ARG:HD2	12:09:123:ARG:NH1	2.34	0.43
7:04:221:GLY:HA2	7:04:224:MET:SD	2.59	0.43
9:06:44:ARG:HH12	9:06:90:GLN:NE2	2.17	0.43
18:15:50:ARG:HH21	18:15:50:ARG:HG2	1.84	0.43
27:24:28:ALA:HB3	27:24:40:ILE:CD1	2.48	0.43
31:28:44:ARG:HH21	31:28:44:ARG:HG2	1.82	0.43
31:28:56:VAL:O	31:28:56:VAL:HG13	2.19	0.43
5:W:52:G:H2'	5:W:53:G:C8	2.54	0.43
41:C:12:GLY:C	41:C:13:ILE:HD12	2.39	0.43
42:D:176:LYS:O	42:D:177:MET:HG2	2.18	0.43
43:E:131:ASN:HD22	43:E:134:ASN:HD22	1.67	0.43
44:F:42:TRP:NE1	44:F:61:LEU:HD22	2.30	0.43
1:A:26:A:N6	1:A:558:G:H1'	2.34	0.43
1:A:95:C:O2	1:A:95:C:H2'	2.18	0.43
1:A:437:U:H5'	42:D:153:ARG:HH12	1.84	0.43
1:A:1492:A:N3	4:Y:26:ARG:HB3	2.33	0.43
2:01:671:C:OP1	17:14:43:GLY:N	2.51	0.43
2:01:917:A:H5''	2:01:2268:A:H61	1.83	0.43
2:01:1695:G:H1'	7:04:7:PRO:O	2.19	0.43
2:01:1726:C:H2'	2:01:1727:C:C6	2.54	0.43
2:01:2602:A:H5'	2:01:2603:G:OP1	2.18	0.43
2:01:2830:C:O2'	2:01:2831:G:H5'	2.18	0.43
3:02:12:C:H1'	3:02:15:A:C2	2.54	0.43
4:Y:24:LEU:HD12	50:L:48:LEU:HD21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:11:54:ILE:HG23	14:11:54:ILE:O	2.19	0.43
22:19:57:ARG:HG2	22:19:57:ARG:HH11	1.84	0.43
39:Z:21:LEU:HA	39:Z:24:TYR:HD2	1.83	0.43
45:G:77:ARG:HH11	45:G:77:ARG:HG2	1.84	0.43
49:K:60:PHE:O	49:K:64:VAL:HG23	2.18	0.43
1:A:279:A:H5'	1:A:281:G:O4'	2.19	0.43
2:01:119:A:H4'	2:01:120:U:H5'	2.01	0.43
2:01:801:G:C8	9:06:50:ALA:HB2	2.54	0.43
2:01:1583:A:H4'	2:01:1585:C:N4	2.34	0.43
2:01:2188:U:H3'	2:01:2189:U:C5'	2.38	0.43
2:01:2345:G:N3	2:01:2381:A:H2'	2.34	0.43
2:01:2370:G:H2'	2:01:2371:G:C8	2.53	0.43
2:01:2508:G:N1	2:01:2580:U:H5	2.04	0.43
3:02:13:G:O2'	3:02:15:A:H2'	2.19	0.43
4:Y:44:LYS:HB3	4:Y:44:LYS:HZ3	1.82	0.43
6:03:201:PRO:HD2	6:03:204:ALA:HB2	2.01	0.43
7:04:2:VAL:HG21	7:04:201:LEU:HD22	2.01	0.43
9:06:145:ASP:HA	9:06:166:LYS:HB3	2.01	0.43
9:06:170:ARG:HG2	9:06:170:ARG:HH21	1.84	0.43
14:11:22:PRO:HG2	14:11:23:VAL:HG23	2.01	0.43
20:17:39:VAL:HG11	20:17:48:LEU:HD23	2.00	0.43
23:20:85:LYS:HB2	23:20:85:LYS:NZ	2.34	0.43
24:21:25:ARG:HH11	24:21:25:ARG:HG3	1.83	0.43
34:31:5:ARG:NH1	34:31:25:ASN:HB2	2.33	0.43
34:31:35:LEU:HD13	34:31:37:LYS:HE3	1.99	0.43
42:D:58:GLN:OE1	42:D:58:GLN:HA	2.18	0.43
44:F:47:LEU:HD21	44:F:57:ALA:HB3	2.00	0.43
1:A:784:A:H2'	1:A:785:G:H8	1.84	0.43
1:A:1520:C:H2'	1:A:1521:C:C6	2.53	0.43
1:A:1522:U:H2'	1:A:1523:G:H8	1.83	0.43
2:01:587:C:H5'	9:06:85:PHE:CE2	2.53	0.43
2:01:616:A:H4'	9:06:101:TYR:CE2	2.54	0.43
2:01:1550:C:H2'	2:01:1551:A:H8	1.83	0.43
2:01:2079:U:H4'	2:01:2433:A:C2	2.54	0.43
5:X:10:G:H2'	5:X:11:A:C8	2.54	0.43
20:17:51:ALA:HB3	20:17:78:VAL:HG22	2.01	0.43
25:22:69:ARG:NH1	25:22:69:ARG:CB	2.82	0.43
37:34:34:LYS:HB3	37:34:34:LYS:HZ2	1.84	0.43
42:D:55:ARG:HG2	42:D:55:ARG:HH11	1.83	0.43
52:N:45:LEU:HD23	52:N:45:LEU:C	2.39	0.43
53:O:27:GLN:O	53:O:31:LEU:HG	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:817:C:O2'	2:01:839:U:H5''	2.19	0.43
2:01:1111:A:H2'	2:01:1112:G:H4'	2.00	0.43
2:01:1178:C:O2	2:01:1178:C:C2'	2.67	0.43
2:01:2818:U:H2'	2:01:2819:G:H8	1.83	0.43
2:01:2834:G:O6	2:01:2879:A:H2'	2.19	0.43
3:02:30:C:H2'	3:02:31:C:O4'	2.19	0.43
9:06:164:LEU:HD13	9:06:167:VAL:HG21	2.01	0.43
10:07:92:GLY:O	10:07:95:MET:HG2	2.18	0.43
13:10:8:LYS:HG2	13:10:12:VAL:HG23	2.01	0.43
19:16:38:LEU:HG	19:16:109:PRO:O	2.19	0.43
24:21:42:LYS:O	24:21:45:VAL:HG12	2.18	0.43
43:E:132:PRO:HA	43:E:135:VAL:HG22	1.99	0.43
1:A:1133:G:H2'	1:A:1134:G:H8	1.84	0.43
1:A:1216:A:H2'	1:A:1217:C:C6	2.54	0.43
2:01:976:G:H4'	2:01:1156:A:N7	2.34	0.43
2:01:1669:A:O3'	2:01:2549:G:H5'	2.18	0.43
2:01:2045:C:H5''	33:30:14:MET:HE1	2.01	0.43
2:01:2126:A:H2	2:01:2163:A:H5''	1.84	0.43
2:01:2170:A:C2'	2:01:2171:A:H4'	2.49	0.43
2:01:2285:C:OP2	34:31:5:ARG:HD3	2.19	0.43
2:01:2832:U:H1'	2:01:2834:G:C2	2.54	0.43
7:04:38:LYS:HZ3	7:04:58:LYS:HA	1.84	0.43
7:04:180:MET:HB2	7:04:268:ARG:HB3	2.01	0.43
9:06:97:ASN:HB2	9:06:100:MET:CG	2.47	0.43
10:07:140:ILE:HD12	10:07:140:ILE:H	1.83	0.43
21:18:17:PRO:HD2	21:18:83:ILE:CD1	2.49	0.43
25:22:23:ALA:HB1	25:22:29:THR:HG23	2.01	0.43
27:24:21:ARG:HG2	27:24:21:ARG:HH11	1.84	0.43
30:27:25:GLN:O	30:27:29:ARG:HG3	2.18	0.43
32:29:56:ARG:CB	51:M:78:ARG:HH22	2.32	0.43
36:33:15:LYS:NZ	36:33:19:GLY:HA2	2.33	0.43
47:I:44:ARG:HG2	47:I:44:ARG:HH11	1.84	0.43
55:Q:22:VAL:HG21	55:Q:60:ILE:HD11	2.01	0.43
57:S:18:VAL:O	57:S:22:VAL:HG23	2.19	0.43
57:S:39:ILE:HA	57:S:43:MET:CE	2.49	0.43
58:T:16:ALA:O	58:T:20:ASN:ND2	2.51	0.43
1:A:558:G:H3'	1:A:559:A:C5'	2.49	0.42
1:A:952:U:H2'	1:A:953:G:H8	1.84	0.42
1:A:1143:G:H2'	1:A:1144:G:C8	2.54	0.42
1:A:1219:A:H2'	1:A:1220:G:C8	2.54	0.42
1:A:1405:G:O2'	1:A:1406:U:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:1074:G:H2'	2:01:1075:C:C6	2.54	0.42
2:01:1239:G:H2'	2:01:1240:U:O4'	2.18	0.42
2:01:1409:U:H2'	2:01:1410:G:C8	2.54	0.42
2:01:1429:G:H2'	2:01:1430:G:H8	1.84	0.42
2:01:2134:A:H3'	2:01:2134:A:N3	2.34	0.42
7:04:95:TYR:CE2	7:04:101:ARG:HD2	2.54	0.42
8:05:177:VAL:O	8:05:177:VAL:HG13	2.19	0.42
9:06:84:THR:HG23	9:06:85:PHE:H	1.84	0.42
12:09:33:GLN:CG	12:09:35:LYS:HE2	2.49	0.42
12:09:77:THR:O	12:09:77:THR:HG23	2.19	0.42
17:14:117:THR:HG22	17:14:118:THR:H	1.83	0.42
19:16:59:SER:HB2	19:16:62:ASN:HB2	2.01	0.42
24:21:83:LYS:HB2	24:21:83:LYS:HZ2	1.82	0.42
28:25:66:GLU:O	28:25:74:LYS:HD3	2.19	0.42
39:Z:301:GLN:OE1	39:Z:301:GLN:O	2.37	0.42
43:E:68:ARG:HH11	43:E:68:ARG:HG3	1.84	0.42
45:G:149:ALA:HB1	49:K:58:THR:HG21	2.01	0.42
46:H:76:ARG:HH12	46:H:125:ILE:HG23	1.84	0.42
53:O:81:ILE:HG22	53:O:86:LEU:CD1	2.49	0.42
58:T:2:ASN:ND2	58:T:3:ILE:N	2.66	0.42
1:A:61:G:H2'	1:A:62:U:O4'	2.20	0.42
1:A:555:U:H2'	1:A:556:C:C6	2.53	0.42
1:A:1251:A:H2'	1:A:1252:A:C8	2.54	0.42
2:01:184:C:H2'	2:01:185:G:C8	2.54	0.42
2:01:372:G:O2'	2:01:373:U:H5	2.02	0.42
2:01:580:U:O3'	22:19:30:VAL:HG13	2.19	0.42
2:01:1045:C:H4'	2:01:1047:G:H1'	2.00	0.42
2:01:1854:A:N6	2:01:1888:G:H1'	2.34	0.42
2:01:2663:G:H2'	2:01:2664:G:O4'	2.20	0.42
6:03:39:VAL:O	6:03:39:VAL:HG13	2.19	0.42
6:03:211:LYS:HD2	6:03:223:ALA:HB1	2.01	0.42
10:07:116:LEU:HD12	10:07:175:PRO:O	2.18	0.42
11:08:126:THR:HG22	11:08:127:GLN:H	1.82	0.42
20:17:64:TYR:HB3	20:17:67:ASN:ND2	2.33	0.42
23:20:1:MET:HE2	23:20:101:ILE:HD12	2.01	0.42
32:29:17:SER:CB	51:M:56:ARG:HH22	2.32	0.42
32:29:42:PRO:HB2	32:29:45:THR:OG1	2.19	0.42
32:29:56:ARG:HB2	51:M:78:ARG:HH22	1.84	0.42
37:34:1:MET:HE1	37:34:36:ARG:HB2	2.00	0.42
39:Z:267:PRO:O	39:Z:268:THR:OG1	2.33	0.42
40:B:113:LEU:HD13	40:B:143:LEU:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
51:M:28:ARG:O	51:M:32:ILE:HG12	2.18	0.42
1:A:674:G:H21	49:K:117:HIS:HB2	1.85	0.42
1:A:810:C:O2'	1:A:811:C:H5'	2.19	0.42
1:A:918:A:H2'	1:A:919:A:O4'	2.18	0.42
1:A:1030:U:H3'	1:A:1031:C:H5'	2.00	0.42
1:A:1240:U:OP1	45:G:115:MET:HG2	2.19	0.42
1:A:1324:A:H4'	1:A:1362:A:O3'	2.19	0.42
2:01:192:C:C2'	2:01:193:U:H5'	2.49	0.42
2:01:226:A:H5''	2:01:257:C:O2'	2.18	0.42
2:01:833:A:H2'	2:01:834:G:H8	1.85	0.42
2:01:990:A:H61	23:20:78:ARG:HH11	1.67	0.42
2:01:996:A:H2'	2:01:997:G:H8	1.83	0.42
2:01:1021:A:H2'	2:01:1022:G:H4'	2.00	0.42
2:01:1167:C:H2'	2:01:1168:G:H8	1.83	0.42
2:01:1651:G:C4'	19:16:39:PRO:HG2	2.45	0.42
7:04:179:GLU:OE2	7:04:270:ARG:HB2	2.18	0.42
11:08:34:ARG:HH11	11:08:34:ARG:HG3	1.84	0.42
12:09:4:ILE:CG2	12:09:37:VAL:HG23	2.48	0.42
13:10:3:LEU:HD23	13:10:3:LEU:N	2.25	0.42
13:10:107:GLU:HG2	13:10:110:ALA:HB2	2.01	0.42
18:15:135:VAL:HG11	27:24:57:TYR:CD2	2.54	0.42
23:20:78:ARG:HB2	23:20:83:TYR:HB3	2.00	0.42
35:32:25:LYS:HG3	35:32:28:ARG:HH21	1.83	0.42
43:E:79:THR:OG1	43:E:80:LEU:N	2.52	0.42
46:H:120:LEU:HD12	46:H:120:LEU:O	2.19	0.42
47:I:89:TYR:CD1	47:I:93:LEU:HD12	2.55	0.42
48:J:89:ARG:HH11	48:J:89:ARG:HG2	1.83	0.42
53:O:38:LEU:HD23	53:O:55:LEU:HD12	2.01	0.42
55:Q:10:ARG:HD2	55:Q:11:VAL:O	2.19	0.42
55:Q:16:MET:CG	55:Q:19:SER:HB2	2.49	0.42
1:A:1173:U:H2'	1:A:1174:G:C8	2.54	0.42
1:A:1228:C:H5''	51:M:114:PRO:CG	2.44	0.42
2:01:131:A:H2'	2:01:132:G:H8	1.84	0.42
2:01:1431:A:H2'	2:01:1432:G:C8	2.55	0.42
2:01:1658:C:H5'	8:05:138:LEU:HD23	2.01	0.42
2:01:1935:G:H1'	2:01:1964:G:N2	2.34	0.42
2:01:2861:U:H2'	2:01:2862:G:C8	2.54	0.42
2:01:2886:A:H2	33:30:28:SER:HA	1.84	0.42
13:10:31:ARG:HH11	13:10:31:ARG:HG3	1.84	0.42
23:20:80:ARG:HG2	23:20:80:ARG:NH1	2.31	0.42
41:C:56:ILE:CG2	41:C:63:ILE:HD11	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:C:149:LYS:HD2	41:C:200:TRP:CE3	2.54	0.42
44:F:35:LYS:HD3	44:F:37:HIS:CE1	2.55	0.42
48:J:57:VAL:CG2	48:J:58:ASN:H	2.32	0.42
48:J:89:ARG:HB2	48:J:90:LEU:HD12	2.00	0.42
51:M:65:GLU:O	51:M:69:ARG:HG3	2.19	0.42
51:M:82:LEU:HD11	57:S:65:MET:HG3	2.01	0.42
59:U:35:GLU:O	59:U:36:PHE:HB2	2.19	0.42
1:A:108:G:C6	58:T:9:ARG:HG2	2.55	0.42
1:A:427:U:H4'	1:A:542:G:OP1	2.20	0.42
1:A:1384:C:H2'	1:A:1385:G:H8	1.85	0.42
2:01:150:U:H2'	2:01:151:C:C6	2.55	0.42
2:01:171:U:H2'	2:01:172:A:C8	2.53	0.42
2:01:1183:U:H2'	2:01:1184:U:C6	2.55	0.42
10:07:56:LEU:HD13	10:07:86:CYS:CB	2.50	0.42
11:08:59:ASP:O	11:08:63:GLN:N	2.47	0.42
12:09:62:LEU:O	12:09:66:ASN:ND2	2.52	0.42
20:17:35:ILE:CD1	20:17:106:LEU:HD12	2.49	0.42
21:18:52:ARG:HH11	21:18:52:ARG:HG3	1.85	0.42
27:24:10:LYS:HG3	27:24:11:GLU:HG2	2.01	0.42
29:26:73:ARG:NH1	29:26:73:ARG:HB2	2.35	0.42
30:27:27:ASN:O	30:27:31:GLN:HG2	2.18	0.42
31:28:42:ALA:O	31:28:46:MET:HG3	2.19	0.42
32:29:15:SER:HA	32:29:21:VAL:HA	2.01	0.42
37:34:25:VAL:HB	37:34:35:GLN:HB2	2.00	0.42
41:C:135:ARG:HH11	41:C:135:ARG:HG3	1.85	0.42
42:D:79:ALA:HA	42:D:85:THR:CG2	2.49	0.42
42:D:190:LEU:C	42:D:190:LEU:HD12	2.39	0.42
44:F:64:VAL:HG22	44:F:65:GLU:N	2.34	0.42
48:J:5:ARG:HD3	48:J:79:PRO:CD	2.50	0.42
48:J:6:ILE:O	48:J:76:ILE:N	2.52	0.42
48:J:80:THR:HB	48:J:83:THR:OG1	2.18	0.42
50:L:49:ARG:NH1	50:L:88:ASP:OD2	2.52	0.42
59:U:36:PHE:CD1	59:U:39:LYS:HD3	2.53	0.42
59:U:60:ALA:HA	59:U:63:ASN:HD21	1.84	0.42
2:01:804:A:H2'	2:01:806:C:C4	2.55	0.42
2:01:992:C:H4'	23:20:74:ILE:CD1	2.46	0.42
2:01:1993:U:H2'	2:01:1994:C:O4'	2.19	0.42
2:01:2004:G:H2'	2:01:2005:A:O4'	2.19	0.42
2:01:2164:C:C2'	2:01:2165:C:H5'	2.48	0.42
2:01:2240:U:O2'	2:01:2241:A:H5'	2.19	0.42
2:01:2773:C:H2'	2:01:2774:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:03:65:LEU:HD21	6:03:159:GLY:O	2.19	0.42
8:05:98:VAL:HG12	8:05:99:GLU:OE2	2.20	0.42
10:07:56:LEU:HD23	10:07:56:LEU:C	2.40	0.42
15:12:75:TYR:HB3	15:12:84:ILE:HD11	2.01	0.42
17:14:20:GLY:HA2	17:14:28:GLY:HA2	2.00	0.42
22:19:49:ARG:HG2	22:19:52:ARG:NH2	2.34	0.42
22:19:93:ILE:O	22:19:97:ILE:HG13	2.18	0.42
32:29:59:ARG:HH21	32:29:62:LYS:CB	2.33	0.42
42:D:7:LYS:HB3	42:D:20:LEU:HD13	2.01	0.42
50:L:20:VAL:HB	50:L:94:TYR:CE1	2.54	0.42
55:Q:22:VAL:HG22	55:Q:23:ALA:H	1.84	0.42
55:Q:26:ARG:HG2	55:Q:26:ARG:HH11	1.85	0.42
1:A:179:A:H61	1:A:196:A:N6	2.01	0.42
1:A:372:C:N4	1:A:387:U:H2'	2.35	0.42
1:A:1254:A:H2'	1:A:1255:G:C8	2.54	0.42
1:A:1432:G:H3'	21:18:105:LYS:HD2	2.02	0.42
2:01:2080:A:H5'	29:26:18:SER:HB2	2.00	0.42
2:01:2297:A:H2'	2:01:2297:A:N3	2.34	0.42
6:03:48:LEU:HD21	6:03:196:LEU:HD11	2.02	0.42
18:15:77:PRO:HG2	18:15:80:VAL:CG2	2.40	0.42
42:D:10:LEU:HD22	42:D:62:ARG:HE	1.84	0.42
44:F:38:ARG:HB3	44:F:63:ASN:HB2	2.02	0.42
44:F:81:ASN:ND2	44:F:84:VAL:HG23	2.34	0.42
45:G:49:LEU:HD22	45:G:123:LEU:CD2	2.46	0.42
47:I:129:ARG:HG2	47:I:129:ARG:HH11	1.85	0.42
49:K:24:ALA:CB	49:K:29:THR:HG22	2.50	0.42
52:N:84:ARG:O	52:N:84:ARG:HD3	2.19	0.42
55:Q:14:ASP:OD2	55:Q:54:ILE:HB	2.19	0.42
56:R:70:THR:OG1	56:R:71:ASP:N	2.53	0.42
1:A:212:G:H2'	1:A:213:G:H8	1.84	0.42
1:A:926:G:OP2	1:A:927:G:H5''	2.19	0.42
1:A:1144:G:N2	1:A:1146:A:H62	2.17	0.42
2:01:420:C:H2'	2:01:421:C:O4'	2.20	0.42
2:01:1087:G:H3'	2:01:1088:A:H5''	2.01	0.42
2:01:1177:G:C8	2:01:1178:C:H1'	2.55	0.42
2:01:2092:U:H5''	12:09:24:GLY:HA3	2.02	0.42
2:01:2372:U:H2'	2:01:2373:G:C8	2.55	0.42
2:01:2578:G:N2	8:05:130:GLN:NE2	2.67	0.42
6:03:53:ARG:HH11	6:03:53:ARG:HG2	1.85	0.42
6:03:54:LYS:HD2	6:03:54:LYS:N	2.35	0.42
7:04:29:PHE:HB3	7:04:102:TYR:OH	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:04:57:HIS:HD2	7:04:58:LYS:H	1.68	0.42
8:05:99:GLU:CD	8:05:99:GLU:H	2.23	0.42
12:09:87:GLU:HG2	44:F:21:MET:SD	2.60	0.42
33:30:8:THR:HG22	33:30:9:ARG:N	2.34	0.42
33:30:9:ARG:HD2	33:30:9:ARG:N	2.34	0.42
36:33:46:LYS:HD2	36:33:46:LYS:N	2.34	0.42
5:W:51:C:H2'	5:W:52:G:C8	2.53	0.42
40:B:110:ILE:HD13	40:B:147:LEU:HD13	2.02	0.42
50:L:43:LYS:CG	50:L:44:PRO:HD3	2.49	0.42
56:R:70:THR:HG23	56:R:71:ASP:O	2.19	0.42
1:A:545:C:H5'	42:D:68:GLU:CB	2.50	0.42
1:A:1106:G:H4'	41:C:170:GLY:O	2.20	0.42
1:A:1312:G:O2'	1:A:1313:U:H5'	2.20	0.42
2:01:184:C:H4'	2:01:217:A:H2	1.84	0.42
2:01:656:G:O2'	2:01:657:U:H5'	2.20	0.42
2:01:1133:A:H4'	2:01:1134:A:H5''	2.01	0.42
2:01:1250:G:H5''	22:19:5:ARG:HD3	2.02	0.42
2:01:1308:A:H2'	2:01:1309:G:O4'	2.20	0.42
2:01:2875:C:H2'	2:01:2876:G:C8	2.55	0.42
19:16:28:LEU:HD21	19:16:115:LEU:HG	2.01	0.42
21:18:3:ILE:H	21:18:3:ILE:CD1	2.30	0.42
21:18:105:LYS:O	21:18:108:ARG:HG2	2.20	0.42
22:19:63:ARG:HH11	22:19:63:ARG:HG3	1.84	0.42
39:Z:17:ARG:O	39:Z:21:LEU:HD13	2.20	0.42
41:C:166:TRP:HZ3	41:C:168:ARG:HG2	1.85	0.42
47:I:113:LYS:HE2	47:I:118:ARG:O	2.19	0.42
48:J:10:LEU:HB2	48:J:72:ARG:HB2	2.01	0.42
1:A:860:A:H2'	1:A:861:G:O4'	2.19	0.42
1:A:1346:A:H2	47:I:108:ARG:NH2	2.18	0.42
1:A:1402:C:H2'	1:A:1403:C:O4'	2.20	0.42
2:01:355:U:H2'	2:01:356:G:C8	2.55	0.42
2:01:1199:U:H1'	22:19:3:VAL:HG22	2.02	0.42
2:01:2102:G:H2'	2:01:2103:C:O4'	2.20	0.42
2:01:2557:G:H2'	2:01:2558:C:C6	2.54	0.42
7:04:269:ARG:HG2	7:04:269:ARG:HH11	1.85	0.42
10:07:73:VAL:CB	10:07:78:ILE:HD11	2.50	0.42
12:09:115:VAL:HA	12:09:132:PHE:HD1	1.85	0.42
34:31:24:LYS:HD3	34:31:33:LEU:HD11	2.00	0.42
37:34:13:ASN:OD1	37:34:13:ASN:N	2.53	0.42
39:Z:193:ARG:HH11	39:Z:193:ARG:CB	2.33	0.42
40:B:13:VAL:CG2	40:B:208:ALA:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:L:51:VAL:HG12	50:L:65:TYR:HD1	1.85	0.42
53:O:57:ARG:HH11	53:O:57:ARG:HG3	1.85	0.42
1:A:439:U:H5''	42:D:120:LYS:NZ	2.35	0.41
1:A:493:A:H2'	1:A:494:G:N7	2.34	0.41
1:A:719:C:O2'	56:R:37:LYS:HB3	2.20	0.41
1:A:1112:C:H1'	41:C:178:ARG:HH11	1.85	0.41
2:01:815:C:OP2	23:20:85:LYS:HE3	2.20	0.41
2:01:1058:U:H3'	2:01:1059:G:H5''	2.02	0.41
2:01:1680:U:C2'	2:01:1681:G:H5'	2.49	0.41
2:01:1717:A:H2'	2:01:1718:G:O4'	2.20	0.41
6:03:9:ARG:HG2	6:03:9:ARG:HH11	1.85	0.41
8:05:47:ALA:HA	8:05:84:LEU:HG	2.02	0.41
10:07:104:THR:HA	32:29:38:SER:HB3	2.01	0.41
11:08:171:LYS:HB2	11:08:171:LYS:HZ2	1.84	0.41
15:12:72:LYS:HB3	15:12:89:PHE:HB2	2.02	0.41
15:12:134:ALA:HB3	15:12:135:GLN:NE2	2.35	0.41
18:15:21:ALA:HB2	18:15:97:GLN:HB2	2.02	0.41
22:19:82:LEU:HB3	22:19:87:VAL:CG2	2.50	0.41
24:21:20:VAL:HG11	24:21:44:ALA:HA	2.01	0.41
24:21:27:LYS:O	24:21:71:VAL:HG23	2.20	0.41
27:24:61:LEU:HD12	27:24:61:LEU:N	2.35	0.41
27:24:72:VAL:HG12	27:24:93:ARG:HA	2.01	0.41
30:27:28:LEU:HD12	30:27:46:VAL:HG21	2.02	0.41
35:32:11:LYS:HB2	35:32:11:LYS:HZ2	1.85	0.41
5:W:8:U:H5'	5:W:49:G:OP2	2.19	0.41
39:Z:261:VAL:HG21	39:Z:283:ASN:HB2	2.02	0.41
39:Z:292:LYS:O	39:Z:296:TYR:N	2.53	0.41
43:E:17:VAL:O	43:E:17:VAL:HG13	2.20	0.41
43:E:156:ARG:HD3	46:H:42:GLU:O	2.19	0.41
50:L:89:LEU:HD12	50:L:89:LEU:N	2.34	0.41
52:N:45:LEU:HD23	52:N:45:LEU:O	2.20	0.41
57:S:12:LEU:HD12	57:S:12:LEU:C	2.40	0.41
57:S:62:THR:H	57:S:65:MET:HE3	1.85	0.41
1:A:35:G:H2'	1:A:36:C:C6	2.55	0.41
1:A:59:A:H2'	1:A:59:A:N3	2.35	0.41
1:A:674:G:H2'	1:A:675:A:C8	2.56	0.41
1:A:1258:G:H2'	1:A:1259:C:C6	2.55	0.41
2:01:131:A:H2'	2:01:132:G:C8	2.54	0.41
2:01:327:G:O2'	2:01:328:U:H5'	2.21	0.41
2:01:479:A:H4'	2:01:480:A:H5'	2.02	0.41
2:01:532:A:H2'	2:01:532:A:N3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2135:A:H1'	2:01:2158:A:H5'	2.01	0.41
2:01:2485:G:O3'	18:15:125:PRO:HB3	2.20	0.41
2:01:2590:A:OP2	7:04:236:GLY:HA2	2.20	0.41
2:01:2638:G:H22	2:01:2775:G:H2'	1.84	0.41
2:01:2655:G:HO2'	2:01:2656:U:H5	1.68	0.41
2:01:2689:U:O2	2:01:2713:U:H5''	2.20	0.41
2:01:2708:G:H1'	19:16:71:ARG:NH2	2.35	0.41
2:01:2789:C:H2'	2:01:2893:A:N7	2.36	0.41
2:01:2845:U:H4'	21:18:52:ARG:HH12	1.82	0.41
2:01:2861:U:H2'	2:01:2862:G:H8	1.85	0.41
7:04:74:PRO:HG2	7:04:96:LYS:CG	2.50	0.41
11:08:59:ASP:O	11:08:63:GLN:HG2	2.19	0.41
28:25:21:ARG:HD2	28:25:25:GLU:OE2	2.20	0.41
32:29:37:CYS:HB3	32:29:40:CYS:HB3	2.02	0.41
33:30:54:ILE:HD11	33:30:56:LYS:HE3	2.02	0.41
41:C:163:ARG:HG3	41:C:163:ARG:NH1	2.34	0.41
44:F:2:ARG:HG2	44:F:2:ARG:HH11	1.86	0.41
44:F:38:ARG:NE	44:F:38:ARG:HA	2.35	0.41
58:T:73:ARG:HH11	58:T:73:ARG:CB	2.33	0.41
1:A:108:G:H1	58:T:9:ARG:HG2	1.85	0.41
1:A:640:A:H2'	1:A:641:U:H5'	2.01	0.41
1:A:1302:C:H5	51:M:12:LYS:HE3	1.85	0.41
1:A:1413:A:H2	1:A:1487:G:H22	1.66	0.41
2:01:96:C:H4'	30:27:41:HIS:NE2	2.36	0.41
2:01:222:A:N6	2:01:232:G:H1'	2.35	0.41
2:01:616:A:H2'	2:01:617:G:O4'	2.20	0.41
2:01:687:C:H1'	35:32:4:THR:HG22	2.03	0.41
2:01:751:A:C5'	24:21:90:LYS:HA	2.47	0.41
2:01:989:G:C8	31:28:13:ILE:HD12	2.55	0.41
2:01:1971:U:H5'	2:01:1972:G:H5''	2.02	0.41
2:01:2124:G:H3'	2:01:2125:G:H5''	2.02	0.41
5:X:69:C:H2'	5:X:70:G:H8	1.85	0.41
12:09:33:GLN:HG3	12:09:35:LYS:HE2	2.02	0.41
13:10:52:MET:O	13:10:52:MET:HG2	2.20	0.41
18:15:59:ARG:C	18:15:59:ARG:HD3	2.41	0.41
18:15:67:VAL:HG22	18:15:68:PHE:N	2.35	0.41
19:16:33:ILE:HG22	19:16:114:GLU:HB2	2.01	0.41
19:16:38:LEU:HD23	19:16:111:ALA:HB2	2.02	0.41
21:18:42:PHE:HE2	21:18:60:VAL:HG23	1.85	0.41
23:20:37:GLU:OE1	23:20:37:GLU:N	2.53	0.41
5:W:44:A:O2'	5:W:45:G:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:Z:46:VAL:HG13	39:Z:47:TRP:N	2.36	0.41
41:C:35:ASP:HB2	41:C:56:ILE:CD1	2.46	0.41
42:D:106:PHE:CD1	42:D:144:ILE:HD11	2.56	0.41
52:N:42:ASN:N	52:N:42:ASN:ND2	2.67	0.41
1:A:212:G:O2'	1:A:213:G:H5'	2.19	0.41
1:A:1203:C:H2'	1:A:1204:A:H8	1.85	0.41
1:A:1325:C:O2'	1:A:1326:U:H5'	2.20	0.41
2:01:955:U:C5	2:01:962:G:N1	2.68	0.41
2:01:1188:U:H4'	23:20:81:LYS:O	2.20	0.41
2:01:1535:A:H3'	2:01:1536:C:C5'	2.50	0.41
2:01:2553:G:H2'	2:01:2554:U:H4'	2.01	0.41
4:Y:20:LEU:HD21	39:Z:135:GLY:HA2	2.02	0.41
8:05:24:VAL:HG11	8:05:188:LEU:HB3	2.02	0.41
11:08:152:ARG:HH21	11:08:152:ARG:HG3	1.85	0.41
13:10:23:LEU:H	13:10:118:ILE:HG21	1.84	0.41
13:10:54:VAL:HG13	13:10:54:VAL:O	2.20	0.41
18:15:78:LEU:HD12	18:15:78:LEU:H	1.84	0.41
35:32:19:ARG:HG2	35:32:19:ARG:NH2	2.35	0.41
5:W:16:C:O2'	5:W:17:C:H5'	2.20	0.41
46:H:4:ASP:HB2	46:H:80:PRO:HG3	2.02	0.41
51:M:7:ASN:HD21	51:M:9:PRO:HG3	1.86	0.41
56:R:53:GLN:HE21	56:R:53:GLN:CA	2.31	0.41
1:A:219:U:C2'	1:A:220:G:H5''	2.50	0.41
2:01:12:U:O2'	2:01:13:A:H5'	2.20	0.41
2:01:536:G:H4'	22:19:56:PHE:CZ	2.55	0.41
2:01:626:A:H3'	2:01:627:A:C5'	2.51	0.41
2:01:1198:U:H2'	2:01:1199:U:C6	2.55	0.41
2:01:1310:G:H2'	2:01:1311:G:H5'	2.02	0.41
2:01:2020:A:H5'	33:30:8:THR:OG1	2.20	0.41
2:01:2843:G:O2'	2:01:2844:G:H5'	2.21	0.41
3:02:7:G:H5''	20:17:29:HIS:NE2	2.35	0.41
3:02:76:G:O2'	3:02:77:U:H5'	2.21	0.41
11:08:23:ILE:HD11	11:08:42:VAL:HG11	2.02	0.41
13:10:74:ASP:OD1	13:10:116:GLU:HB3	2.20	0.41
22:19:69:ARG:HH21	22:19:69:ARG:HG3	1.85	0.41
24:21:46:LEU:O	24:21:50:VAL:HG23	2.21	0.41
25:22:9:LYS:HB3	25:22:9:LYS:HZ3	1.85	0.41
25:22:32:LEU:HD12	25:22:32:LEU:O	2.21	0.41
39:Z:179:VAL:HG22	39:Z:181:ILE:HD11	2.01	0.41
44:F:3:HIS:N	44:F:92:THR:HG22	2.35	0.41
49:K:20:ALA:HA	49:K:33:ILE:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:K:23:HIS:HB3	49:K:30:ILE:CG2	2.51	0.41
51:M:76:ILE:HG23	51:M:90:HIS:CD2	2.55	0.41
52:N:59:GLN:HA	52:N:59:GLN:NE2	2.34	0.41
54:P:44:SER:H	54:P:46:LYS:NZ	2.18	0.41
1:A:112:G:N2	1:A:354:G:H5'	2.32	0.41
1:A:237:G:H2'	1:A:238:A:O4'	2.20	0.41
1:A:626:G:H2'	1:A:627:G:H8	1.84	0.41
1:A:643:C:OP1	46:H:30:LYS:HE3	2.21	0.41
1:A:952:U:C4'	1:A:964:A:H61	2.33	0.41
1:A:1112:C:H1'	41:C:178:ARG:NH1	2.35	0.41
2:01:35:G:H2'	2:01:36:G:O4'	2.21	0.41
2:01:248:G:N3	2:01:2431:U:H4'	2.35	0.41
2:01:399:U:OP1	2:01:2090:A:H5''	2.20	0.41
2:01:742:A:H2'	2:01:743:A:C8	2.56	0.41
2:01:970:U:H2'	2:01:971:G:C8	2.54	0.41
2:01:1045:C:H4'	2:01:1047:G:C1'	2.50	0.41
2:01:1441:G:H2'	2:01:1442:U:C6	2.55	0.41
2:01:1821:A:H2'	2:01:1822:C:C6	2.54	0.41
3:02:15:A:H5'	3:02:16:G:C8	2.55	0.41
5:X:48:C:H2'	5:X:59:A:H4'	2.03	0.41
8:05:110:THR:HB	8:05:202:ILE:HB	2.01	0.41
11:08:51:PHE:CE2	11:08:68:ARG:HA	2.55	0.41
11:08:94:ARG:HH11	11:08:94:ARG:HG3	1.86	0.41
12:09:7:ASP:CG	12:09:8:LYS:H	2.24	0.41
13:10:13:ALA:O	13:10:17:GLU:HG3	2.21	0.41
13:10:23:LEU:H	13:10:118:ILE:HB	1.85	0.41
15:12:39:LYS:O	15:12:39:LYS:HG2	2.20	0.41
15:12:121:LYS:N	15:12:121:LYS:HD2	2.35	0.41
18:15:16:ARG:HG3	18:15:16:ARG:HH11	1.86	0.41
18:15:33:LEU:HB2	18:15:117:PHE:CD1	2.56	0.41
21:18:58:PHE:O	21:18:73:PHE:N	2.49	0.41
23:20:38:VAL:HG13	23:20:54:VAL:HG12	2.02	0.41
37:34:1:MET:CE	37:34:36:ARG:HB2	2.50	0.41
39:Z:150:ARG:HG2	39:Z:150:ARG:NH1	2.35	0.41
43:E:14:LEU:C	43:E:15:ILE:HD12	2.40	0.41
47:I:109:GLN:NE2	47:I:110:VAL:N	2.69	0.41
52:N:84:ARG:HD3	52:N:84:ARG:C	2.41	0.41
54:P:4:ILE:HD12	54:P:67:ILE:HG13	2.01	0.41
1:A:392:C:H2'	1:A:393:A:C8	2.56	0.41
1:A:754:C:H5'	53:O:71:ARG:HH22	1.85	0.41
1:A:1471:U:O2'	1:A:1472:U:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1496:C:H2'	1:A:1497:G:O4'	2.21	0.41
2:01:96:C:H2'	2:01:97:C:C6	2.56	0.41
2:01:764:A:O2'	2:01:765:C:H5'	2.21	0.41
2:01:859:G:O2'	2:01:860:U:C6	2.69	0.41
2:01:1300:G:H4'	2:01:1301:A:C5'	2.51	0.41
2:01:1843:C:H2'	2:01:1844:C:C6	2.55	0.41
2:01:2107:G:H3'	2:01:2108:A:C5'	2.47	0.41
6:03:48:LEU:HD12	6:03:48:LEU:N	2.35	0.41
6:03:60:ARG:NH2	6:03:162:ARG:HB2	2.36	0.41
6:03:181:ASP:HB3	6:03:184:LYS:CG	2.48	0.41
9:06:1:MET:CE	9:06:20:GLY:HA3	2.50	0.41
10:07:98:PHE:HD1	10:07:101:ARG:NH1	2.19	0.41
14:11:23:VAL:C	14:11:25:PRO:HD2	2.41	0.41
14:11:78:LEU:O	14:11:82:ALA:N	2.50	0.41
15:12:111:LYS:O	15:12:111:LYS:HD2	2.20	0.41
16:13:8:LEU:O	16:13:9:ASN:ND2	2.48	0.41
19:16:63:ARG:HG2	19:16:80:PHE:CE2	2.55	0.41
21:18:8:GLU:HG3	21:18:54:LEU:HB2	2.03	0.41
21:18:25:VAL:HG22	21:18:26:GLU:N	2.36	0.41
22:19:10:ARG:HA	22:19:10:ARG:NE	2.36	0.41
23:20:36:ALA:N	23:20:37:GLU:OE1	2.54	0.41
26:23:13:LEU:HD11	26:23:70:ALA:HB2	2.03	0.41
28:25:42:HIS:CD2	28:25:73:ARG:HD3	2.56	0.41
35:32:3:ARG:NE	35:32:3:ARG:CA	2.81	0.41
40:B:89:PHE:CE2	40:B:153:MET:HG3	2.55	0.41
43:E:63:MET:HB3	43:E:67:ARG:HH12	1.86	0.41
48:J:6:ILE:CD1	48:J:79:PRO:HB3	2.50	0.41
51:M:73:SER:O	51:M:77:LYS:HG3	2.20	0.41
56:R:24:ASP:O	56:R:28:LEU:HD23	2.20	0.41
1:A:715:A:H2'	1:A:716:A:H8	1.84	0.41
1:A:1196:A:C1'	4:Y:34:LYS:HD3	2.50	0.41
2:01:7:G:H4'	15:12:15:TRP:HH2	1.85	0.41
2:01:43:G:H2'	2:01:44:A:O4'	2.20	0.41
2:01:189:G:H2'	2:01:205:G:H22	1.85	0.41
2:01:724:U:O2'	2:01:725:G:H5'	2.20	0.41
2:01:845:A:H3'	2:01:845:A:N3	2.36	0.41
2:01:1140:C:H2'	2:01:1141:U:H5'	2.03	0.41
2:01:1297:C:OP1	2:01:2710:C:H4'	2.20	0.41
2:01:1755:A:H2'	2:01:1756:G:H5'	2.02	0.41
2:01:2318:G:H2'	2:01:2319:G:O4'	2.21	0.41
2:01:2714:G:O2'	2:01:2715:C:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:08:85:LYS:HD3	11:08:85:LYS:N	2.35	0.41
13:10:33:VAL:N	13:10:36:ASP:HB2	2.36	0.41
19:16:33:ILE:HG21	19:16:118:ARG:HH12	1.85	0.41
26:23:39:ASN:O	26:23:41:VAL:HG23	2.21	0.41
32:29:2:LYS:HB2	32:29:5:ILE:HD11	2.02	0.41
32:29:32:LEU:HD22	32:29:34:LEU:CD2	2.50	0.41
5:W:23:C:H2'	5:W:24:U:C6	2.56	0.41
39:Z:8:ASN:ND2	39:Z:8:ASN:O	2.54	0.41
40:B:40:ILE:HD12	40:B:40:ILE:H	1.86	0.41
40:B:70:GLY:HA2	40:B:163:ILE:HG21	2.02	0.41
41:C:52:SER:HB3	41:C:111:ASP:OD2	2.21	0.41
42:D:27:ILE:C	42:D:29:THR:H	2.22	0.41
43:E:89:THR:O	43:E:89:THR:HG22	2.20	0.41
44:F:29:ILE:HG22	44:F:34:GLY:HA3	2.02	0.41
45:G:14:ASP:OD1	45:G:15:PRO:HD2	2.21	0.41
45:G:91:ARG:HH11	45:G:91:ARG:HG2	1.85	0.41
46:H:37:ASN:O	46:H:37:ASN:ND2	2.54	0.41
47:I:112:ARG:HD2	52:N:100:TRP:NE1	2.35	0.41
58:T:47:GLN:O	58:T:51:ASN:ND2	2.54	0.41
59:U:61:ARG:HG3	59:U:61:ARG:NH1	2.36	0.41
1:A:17:U:H2'	1:A:18:C:H6	1.86	0.41
1:A:35:G:H21	50:L:114:SER:HB2	1.86	0.41
1:A:112:G:H4'	1:A:389:A:H5''	2.03	0.41
1:A:147:G:H2'	1:A:148:G:C8	2.56	0.41
1:A:273:U:O2'	1:A:274:A:H5'	2.21	0.41
1:A:578:C:H2'	1:A:579:A:C8	2.55	0.41
1:A:618:C:H1'	54:P:14:ARG:NH1	2.36	0.41
1:A:722:G:H3'	1:A:722:G:N3	2.36	0.41
1:A:758:C:H4'	1:A:880:C:H4'	2.02	0.41
1:A:902:G:O2'	1:A:903:G:H5'	2.21	0.41
1:A:932:C:H5''	45:G:3:ARG:HH22	1.86	0.41
1:A:1195:C:H5''	1:A:1196:A:OP2	2.20	0.41
1:A:1487:G:O2'	1:A:1488:G:H5'	2.20	0.41
2:01:155:A:H2'	2:01:156:A:H8	1.83	0.41
2:01:214:G:O2'	2:01:215:G:H5'	2.21	0.41
2:01:372:G:O2'	2:01:373:U:C5	2.73	0.41
2:01:674:G:H1'	9:06:69:ARG:HD3	2.02	0.41
2:01:817:C:H2'	2:01:818:G:O4'	2.20	0.41
2:01:875:G:H2'	2:01:876:C:C6	2.56	0.41
2:01:988:A:C8	31:28:13:ILE:HG13	2.55	0.41
2:01:1019:U:H3	2:01:1142:A:N6	2.11	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2197:U:H1'	2:01:2198:A:C8	2.55	0.41
2:01:2330:G:H21	28:25:38:GLY:HA3	1.86	0.41
2:01:2508:G:O6	2:01:2580:U:O4	2.39	0.41
2:01:2707:U:H2'	2:01:2708:G:C8	2.55	0.41
2:01:2733:A:O2'	2:01:2734:A:H5'	2.21	0.41
3:02:42:C:C5	10:07:65:LEU:HD22	2.56	0.41
6:03:65:LEU:HD23	6:03:65:LEU:N	2.36	0.41
7:04:73:ILE:HG21	7:04:97:ASP:OD2	2.20	0.41
7:04:216:ARG:HH11	7:04:216:ARG:HG2	1.85	0.41
8:05:118:PHE:CE1	8:05:163:GLY:HA2	2.56	0.41
8:05:184:ARG:HD2	8:05:186:LEU:CD1	2.47	0.41
10:07:68:LYS:HB3	10:07:68:LYS:HZ3	1.86	0.41
12:09:130:VAL:O	12:09:142:VAL:HG12	2.21	0.41
13:10:53:ARG:HG2	13:10:55:VAL:HG13	2.03	0.41
14:11:104:GLN:O	14:11:108:ILE:HG13	2.21	0.41
16:13:103:VAL:O	16:13:122:VAL:HB	2.20	0.41
16:13:105:ARG:HH21	16:13:108:ARG:NH1	2.19	0.41
18:15:84:LYS:N	18:15:84:LYS:HD2	2.36	0.41
19:16:61:ALA:O	19:16:65:LEU:HD13	2.21	0.41
19:16:64:ARG:O	19:16:68:ALA:N	2.51	0.41
19:16:72:ASP:CB	19:16:75:ILE:HD13	2.51	0.41
23:20:63:VAL:HA	23:20:96:VAL:HG12	2.01	0.41
28:25:66:GLU:HB3	28:25:68:LYS:HG2	2.02	0.41
5:W:28:C:H2'	5:W:29:G:H8	1.85	0.41
39:Z:17:ARG:HD2	39:Z:110:LEU:HD11	2.03	0.41
39:Z:110:LEU:HD23	39:Z:110:LEU:C	2.41	0.41
39:Z:246:THR:N	39:Z:258:GLU:O	2.52	0.41
39:Z:263:ILE:HD12	39:Z:287:ALA:HB3	2.03	0.41
41:C:131:ARG:HH11	41:C:131:ARG:HG3	1.86	0.41
41:C:174:LEU:HD12	41:C:174:LEU:N	2.36	0.41
42:D:158:LEU:HD11	42:D:174:ALA:HA	2.03	0.41
42:D:171:GLU:HB2	42:D:180:THR:HB	2.02	0.41
42:D:196:GLU:H	42:D:196:GLU:CD	2.23	0.41
44:F:9:MET:HB3	44:F:59:TYR:HD1	1.85	0.41
44:F:36:ILE:HA	44:F:64:VAL:HG23	2.01	0.41
45:G:4:ARG:HD2	45:G:6:ILE:CD1	2.51	0.41
47:I:32:ARG:HG2	47:I:32:ARG:HH11	1.86	0.41
47:I:79:ARG:HG3	47:I:79:ARG:NH1	2.35	0.41
51:M:22:TYR:HB3	51:M:65:GLU:HG2	2.02	0.41
51:M:69:ARG:HG2	51:M:69:ARG:NH1	2.36	0.41
55:Q:16:MET:HB3	55:Q:19:SER:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
59:U:16:ARG:HD2	59:U:20:ARG:HH12	1.86	0.41
1:A:1368:A:OP2	47:I:113:LYS:HG2	2.20	0.41
1:A:1486:G:H2'	1:A:1487:G:O4'	2.21	0.41
2:01:558:U:H2'	2:01:559:G:H8	1.86	0.41
2:01:1130:U:C2	8:05:152:PRO:HA	2.56	0.41
2:01:2475:C:C2'	2:01:2476:A:H5'	2.49	0.41
11:08:103:ASN:ND2	11:08:104:LEU:N	2.66	0.41
13:10:26:VAL:HG11	13:10:82:ILE:CG2	2.50	0.41
16:13:25:LEU:HD12	16:13:38:ILE:HG22	2.03	0.41
16:13:54:LYS:NZ	16:13:54:LYS:HB3	2.36	0.41
19:16:90:ARG:HH11	19:16:90:ARG:CB	2.34	0.41
22:19:61:ILE:HG23	22:19:75:TYR:CE2	2.56	0.41
25:22:87:LEU:HD12	25:22:87:LEU:N	2.36	0.41
42:D:48:SER:O	42:D:52:VAL:HG23	2.21	0.41
47:I:109:GLN:NE2	47:I:110:VAL:H	2.19	0.41
49:K:107:THR:HG23	49:K:108:ASN:OD1	2.21	0.41
1:A:1412:C:H2'	1:A:1413:A:H8	1.85	0.40
2:01:576:U:H2'	2:01:577:G:C8	2.56	0.40
2:01:1316:U:H2'	2:01:1317:G:H8	1.86	0.40
2:01:1593:A:H2'	2:01:1594:U:O4'	2.20	0.40
2:01:1614:A:C2	24:21:93:ALA:HB2	2.56	0.40
2:01:1664:A:H61	2:01:1996:C:N4	2.09	0.40
9:06:44:ARG:NH1	9:06:90:GLN:NE2	2.69	0.40
12:09:83:LYS:HA	12:09:149:GLU:HB3	2.01	0.40
17:14:85:VAL:HG12	17:14:86:GLU:N	2.36	0.40
20:17:99:TYR:CE1	20:17:104:GLN:HA	2.56	0.40
23:20:52:PRO:O	23:20:53:PHE:HB2	2.21	0.40
30:27:15:ASN:O	30:27:19:LEU:HG	2.21	0.40
37:34:11:CYS:CB	37:34:14:CYS:SG	2.97	0.40
39:Z:46:VAL:HG13	39:Z:47:TRP:HD1	1.86	0.40
41:C:118:SER:O	41:C:122:GLN:HG2	2.20	0.40
45:G:82:SER:OG	45:G:83:THR:N	2.52	0.40
47:I:119:LYS:HB2	47:I:119:LYS:HZ2	1.84	0.40
54:P:40:ASN:HD22	54:P:43:ALA:HB2	1.86	0.40
58:T:52:GLU:O	58:T:56:ILE:HD13	2.21	0.40
59:U:48:LYS:O	59:U:52:VAL:HG23	2.21	0.40
1:A:1279:G:H5''	48:J:9:ARG:NH1	2.36	0.40
2:01:323:C:H5'	9:06:163:ASN:HD21	1.87	0.40
2:01:444:C:O2'	2:01:445:C:H5'	2.20	0.40
2:01:1252:G:H22	22:19:36:GLN:NE2	2.19	0.40
2:01:2038:G:H2'	2:01:2039:U:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:01:2101:A:H2'	2:01:2102:G:C8	2.55	0.40
2:01:2484:G:O2'	2:01:2485:G:H5'	2.20	0.40
2:01:2741:A:H2'	2:01:2742:G:O4'	2.20	0.40
6:03:45:ALA:N	6:03:213:SER:O	2.54	0.40
7:04:91:ALA:HB3	7:04:103:ILE:HD11	2.04	0.40
11:08:174:LYS:HE3	11:08:174:LYS:HB3	1.96	0.40
26:23:39:ASN:OD1	26:23:63:ALA:O	2.39	0.40
5:W:68:C:H2'	5:W:69:C:C6	2.57	0.40
39:Z:60:ARG:HG2	39:Z:64:GLU:OE1	2.21	0.40
39:Z:142:GLN:HB3	39:Z:175:GLY:HA3	2.02	0.40
42:D:190:LEU:HD12	42:D:192:ALA:H	1.86	0.40
48:J:7:ARG:HG3	48:J:7:ARG:HH11	1.86	0.40
49:K:126:ARG:HA	49:K:126:ARG:NE	2.28	0.40
52:N:92:ILE:HG22	52:N:95:LEU:HB2	2.03	0.40
55:Q:51:GLU:OE1	55:Q:74:LEU:HD11	2.21	0.40
1:A:468:A:H2'	1:A:468:A:N3	2.36	0.40
1:A:678:U:H2'	1:A:679:C:C6	2.56	0.40
2:01:37:C:H4'	2:01:451:U:OP1	2.21	0.40
2:01:772:C:O2'	2:01:773:U:H5'	2.21	0.40
2:01:1096:A:H3'	2:01:1097:U:C5'	2.52	0.40
2:01:1750:G:O2'	2:01:1751:U:H5'	2.21	0.40
2:01:1818:U:H5	7:04:155:ARG:CZ	2.34	0.40
2:01:2215:C:H2'	2:01:2216:G:C8	2.56	0.40
2:01:2230:G:O3'	29:26:29:LEU:HB2	2.22	0.40
2:01:2469:A:H2'	2:01:2470:G:O4'	2.22	0.40
2:01:2515:C:H2'	2:01:2516:A:H8	1.86	0.40
2:01:2683:C:H4'	8:05:13:ARG:HH11	1.87	0.40
7:04:261:ARG:HH11	7:04:261:ARG:HG2	1.86	0.40
20:17:66:GLY:HA2	20:17:102:ARG:HH21	1.87	0.40
25:22:57:VAL:HG22	25:22:58:VAL:N	2.36	0.40
27:24:17:SER:O	27:24:21:ARG:HG2	2.20	0.40
39:Z:131:ASP:O	39:Z:221:PHE:N	2.48	0.40
39:Z:140:GLU:HG3	39:Z:216:SER:HB2	2.03	0.40
40:B:88:GLN:OE1	40:B:88:GLN:N	2.54	0.40
41:C:142:ARG:HG3	41:C:142:ARG:HH11	1.86	0.40
46:H:9:MET:O	46:H:13:ILE:HG13	2.20	0.40
52:N:2:LYS:O	52:N:5:MET:N	2.54	0.40
52:N:48:GLN:NE2	57:S:10:ILE:O	2.42	0.40
55:Q:19:SER:OG	55:Q:70:LYS:HE3	2.21	0.40
1:A:1219:A:H2'	1:A:1220:G:H8	1.86	0.40
1:A:1219:A:OP1	52:N:52:ARG:HG2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1344:C:O2'	1:A:1345:U:H5'	2.21	0.40
2:01:406:G:H2'	2:01:407:G:C8	2.57	0.40
2:01:833:A:H2'	2:01:834:G:C8	2.56	0.40
2:01:1148:U:H2'	2:01:1149:G:O4'	2.22	0.40
2:01:2170:A:H2'	2:01:2171:A:H4'	2.01	0.40
2:01:2371:G:O2'	2:01:2372:U:H5'	2.22	0.40
2:01:2443:C:O2'	2:01:2444:G:H5'	2.21	0.40
2:01:2553:G:H2'	2:01:2554:U:C4'	2.52	0.40
2:01:2733:A:C6	8:05:208:LYS:HG3	2.57	0.40
15:12:34:ARG:HH11	15:12:34:ARG:HG2	1.85	0.40
42:D:127:ARG:HG3	42:D:127:ARG:HH11	1.87	0.40
42:D:183:ARG:HG2	42:D:183:ARG:NH1	2.37	0.40
45:G:4:ARG:HG2	45:G:4:ARG:HH11	1.86	0.40
45:G:31:VAL:HG22	45:G:32:ASP:CG	2.41	0.40
45:G:36:SER:HA	45:G:39:GLU:OE1	2.20	0.40
47:I:118:ARG:HG3	47:I:118:ARG:NH1	2.36	0.40
50:L:53:ARG:HA	50:L:63:THR:HA	2.04	0.40
57:S:18:VAL:CG1	57:S:42:ASN:HD21	2.34	0.40
1:A:177:G:H2'	1:A:178:C:C6	2.56	0.40
1:A:693:G:P	49:K:126:ARG:HH12	2.44	0.40
1:A:882:C:O2'	1:A:883:C:H5'	2.21	0.40
1:A:979:C:H2'	1:A:980:C:H5'	2.02	0.40
1:A:1351:U:H2'	1:A:1352:C:C6	2.56	0.40
2:01:176:A:C2'	2:01:177:G:H5'	2.52	0.40
2:01:782:A:N3	7:04:224:MET:HG2	2.36	0.40
2:01:857:G:H2'	2:01:858:G:O4'	2.21	0.40
2:01:1727:C:H2'	2:01:1728:C:O4'	2.22	0.40
2:01:1928:A:H2'	2:01:1929:G:O4'	2.21	0.40
2:01:1982:U:H6	2:01:1982:U:H5'	1.86	0.40
2:01:2302:U:H2'	2:01:2303:G:H8	1.87	0.40
2:01:2470:G:O2'	2:01:2471:A:H5'	2.21	0.40
2:01:2682:A:H61	2:01:2728:U:H1'	1.86	0.40
2:01:2798:U:H4'	2:01:2799:A:C4	2.56	0.40
7:04:89:ASN:N	7:04:89:ASN:ND2	2.68	0.40
11:08:72:ASN:O	11:08:76:ILE:HG12	2.21	0.40
13:10:37:LYS:HD3	13:10:41:LEU:CD1	2.52	0.40
13:10:125:ARG:HH11	13:10:125:ARG:HG2	1.86	0.40
24:21:10:ALA:HB3	24:21:101:SER:HB2	2.03	0.40
29:26:67:LEU:HD11	29:26:77:TYR:CD2	2.57	0.40
37:34:20:ASP:C	37:34:22:VAL:H	2.24	0.40
39:Z:48:ASN:C	39:Z:50:PRO:HD3	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:D:62:ARG:HG2	42:D:62:ARG:HH11	1.86	0.40
43:E:114:LEU:HD12	43:E:114:LEU:N	2.36	0.40
45:G:110:ARG:HG3	45:G:110:ARG:HH11	1.86	0.40
46:H:95:MET:SD	46:H:129:ALA:HB1	2.61	0.40
52:N:50:LEU:CG	52:N:51:PRO:HD2	2.51	0.40
59:U:6:ARG:HH11	59:U:6:ARG:HB2	1.87	0.40
59:U:6:ARG:NH1	59:U:6:ARG:CB	2.85	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Y	30/72 (42%)	26 (87%)	4 (13%)	0	100	100
6	03	218/234 (93%)	192 (88%)	25 (12%)	1 (0%)	29	67
7	04	269/273 (98%)	244 (91%)	22 (8%)	3 (1%)	14	51
8	05	207/209 (99%)	181 (87%)	24 (12%)	2 (1%)	15	54
9	06	199/201 (99%)	179 (90%)	18 (9%)	2 (1%)	15	54
10	07	175/179 (98%)	148 (85%)	26 (15%)	1 (1%)	25	64
11	08	174/177 (98%)	164 (94%)	10 (6%)	0	100	100
12	09	147/149 (99%)	136 (92%)	9 (6%)	2 (1%)	11	46
13	10	129/165 (78%)	94 (73%)	32 (25%)	3 (2%)	6	34
14	11	139/142 (98%)	121 (87%)	17 (12%)	1 (1%)	22	61
15	12	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
16	13	120/123 (98%)	102 (85%)	15 (12%)	3 (2%)	5	32
17	14	141/144 (98%)	126 (89%)	13 (9%)	2 (1%)	11	46
18	15	134/136 (98%)	122 (91%)	11 (8%)	1 (1%)	22	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	16	118/127 (93%)	102 (86%)	15 (13%)	1 (1%)	19	58
20	17	114/117 (97%)	106 (93%)	7 (6%)	1 (1%)	17	56
21	18	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
22	19	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
23	20	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
24	21	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
25	22	91/100 (91%)	84 (92%)	6 (7%)	1 (1%)	14	51
26	23	100/104 (96%)	87 (87%)	12 (12%)	1 (1%)	15	54
27	24	92/94 (98%)	86 (94%)	6 (6%)	0	100	100
28	25	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
29	26	75/78 (96%)	66 (88%)	9 (12%)	0	100	100
30	27	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
31	28	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
32	29	64/70 (91%)	54 (84%)	9 (14%)	1 (2%)	9	43
33	30	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
34	31	48/55 (87%)	45 (94%)	3 (6%)	0	100	100
35	32	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
36	33	62/65 (95%)	57 (92%)	4 (6%)	1 (2%)	9	43
37	34	36/38 (95%)	29 (81%)	6 (17%)	1 (3%)	5	29
39	Z	359/365 (98%)	310 (86%)	49 (14%)	0	100	100
40	B	216/241 (90%)	188 (87%)	26 (12%)	2 (1%)	17	56
41	C	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
42	D	203/206 (98%)	176 (87%)	24 (12%)	3 (2%)	10	44
43	E	155/167 (93%)	137 (88%)	18 (12%)	0	100	100
44	F	98/131 (75%)	83 (85%)	14 (14%)	1 (1%)	15	54
45	G	149/156 (96%)	133 (89%)	16 (11%)	0	100	100
46	H	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
47	I	125/130 (96%)	107 (86%)	17 (14%)	1 (1%)	19	58
48	J	96/103 (93%)	78 (81%)	11 (12%)	7 (7%)	1	7
49	K	114/129 (88%)	96 (84%)	16 (14%)	2 (2%)	8	41
50	L	121/124 (98%)	99 (82%)	19 (16%)	3 (2%)	5	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	M	112/118 (95%)	100 (89%)	9 (8%)	3 (3%)	5	30
52	N	98/101 (97%)	80 (82%)	13 (13%)	5 (5%)	2	15
53	O	86/89 (97%)	82 (95%)	3 (4%)	1 (1%)	13	49
54	P	80/82 (98%)	67 (84%)	13 (16%)	0	100	100
55	Q	78/84 (93%)	61 (78%)	17 (22%)	0	100	100
56	R	63/75 (84%)	52 (82%)	10 (16%)	1 (2%)	9	43
57	S	77/92 (84%)	67 (87%)	10 (13%)	0	100	100
58	T	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
59	U	63/71 (89%)	46 (73%)	12 (19%)	5 (8%)	1	6
All	All	6453/6864 (94%)	5709 (88%)	682 (11%)	62 (1%)	20	54

All (62) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	03	207	VAL
9	06	61	ARG
9	06	83	VAL
13	10	123	ILE
16	13	89	ASN
17	14	119	PRO
32	29	65	ASN
36	33	31	ILE
40	B	19	THR
40	B	206	ILE
42	D	31	CYS
47	I	91	GLU
48	J	58	ASN
48	J	92	LEU
52	N	55	SER
52	N	97	LYS
52	N	98	ALA
53	O	46	LYS
59	U	8	ASN
12	09	9	VAL
12	09	10	ALA
13	10	81	LEU
13	10	111	ALA
20	17	34	HIS
48	J	93	ALA

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Mol	Chain	Res	Type
48	J	94	ALA
49	K	25	SER
52	N	35	ALA
8	05	135	GLY
25	22	36	LYS
42	D	28	ASP
50	L	2	THR
50	L	24	GLU
51	M	5	GLY
59	U	10	PRO
59	U	34	ARG
59	U	37	TYR
16	13	102	PRO
26	23	54	PRO
44	F	94	HIS
10	07	120	SER
16	13	101	GLY
17	14	87	GLY
42	D	26	ALA
48	J	42	LEU
50	L	119	LYS
52	N	53	ASP
56	R	19	GLU
59	U	9	GLU
7	04	204	LEU
18	15	69	PRO
19	16	71	ARG
7	04	233	GLY
48	J	43	PRO
37	34	25	VAL
51	M	6	ILE
8	05	98	VAL
7	04	232	GLY
14	11	22	PRO
48	J	79	PRO
49	K	87	GLY
51	M	9	PRO

### 5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	Y	24/59 (41%)	23 (96%)	1 (4%)	30	65
6	03	106/181 (59%)	103 (97%)	3 (3%)	43	74
7	04	216/218 (99%)	213 (99%)	3 (1%)	67	86
8	05	164/164 (100%)	164 (100%)	0	100	100
9	06	165/165 (100%)	165 (100%)	0	100	100
10	07	148/150 (99%)	147 (99%)	1 (1%)	84	94
11	08	137/138 (99%)	133 (97%)	4 (3%)	42	74
12	09	114/114 (100%)	112 (98%)	2 (2%)	59	82
13	10	100/123 (81%)	98 (98%)	2 (2%)	55	80
14	11	109/110 (99%)	108 (99%)	1 (1%)	78	91
15	12	116/116 (100%)	113 (97%)	3 (3%)	46	76
16	13	103/104 (99%)	102 (99%)	1 (1%)	76	90
17	14	102/103 (99%)	102 (100%)	0	100	100
18	15	109/109 (100%)	106 (97%)	3 (3%)	43	74
19	16	100/104 (96%)	100 (100%)	0	100	100
20	17	86/87 (99%)	84 (98%)	2 (2%)	50	78
21	18	99/100 (99%)	99 (100%)	0	100	100
22	19	89/90 (99%)	88 (99%)	1 (1%)	73	88
23	20	84/84 (100%)	82 (98%)	2 (2%)	49	77
24	21	93/93 (100%)	92 (99%)	1 (1%)	73	88
25	22	80/84 (95%)	80 (100%)	0	100	100
26	23	83/85 (98%)	80 (96%)	3 (4%)	35	69
27	24	78/78 (100%)	78 (100%)	0	100	100
28	25	57/63 (90%)	55 (96%)	2 (4%)	36	69
29	26	67/68 (98%)	65 (97%)	2 (3%)	41	73
30	27	55/55 (100%)	55 (100%)	0	100	100
31	28	48/49 (98%)	48 (100%)	0	100	100
32	29	59/62 (95%)	58 (98%)	1 (2%)	60	83
33	30	47/48 (98%)	46 (98%)	1 (2%)	53	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	31	45/49 (92%)	45 (100%)	0	100	100
35	32	38/38 (100%)	37 (97%)	1 (3%)	46	76
36	33	51/52 (98%)	49 (96%)	2 (4%)	32	67
37	34	34/34 (100%)	31 (91%)	3 (9%)	10	36
39	Z	296/311 (95%)	290 (98%)	6 (2%)	55	80
40	B	180/199 (90%)	176 (98%)	4 (2%)	52	79
41	C	170/190 (90%)	168 (99%)	2 (1%)	71	88
42	D	172/173 (99%)	164 (95%)	8 (5%)	26	62
43	E	119/126 (94%)	113 (95%)	6 (5%)	24	60
44	F	87/112 (78%)	85 (98%)	2 (2%)	50	78
45	G	124/129 (96%)	123 (99%)	1 (1%)	81	93
46	H	104/105 (99%)	101 (97%)	3 (3%)	42	74
47	I	105/107 (98%)	104 (99%)	1 (1%)	76	90
48	J	86/90 (96%)	85 (99%)	1 (1%)	71	88
49	K	89/99 (90%)	84 (94%)	5 (6%)	21	57
50	L	103/104 (99%)	101 (98%)	2 (2%)	57	81
51	M	92/96 (96%)	92 (100%)	0	100	100
52	N	83/84 (99%)	83 (100%)	0	100	100
53	O	76/77 (99%)	74 (97%)	2 (3%)	46	76
54	P	65/65 (100%)	62 (95%)	3 (5%)	27	63
55	Q	74/78 (95%)	72 (97%)	2 (3%)	44	75
56	R	56/65 (86%)	54 (96%)	2 (4%)	35	69
57	S	70/79 (89%)	70 (100%)	0	100	100
58	T	65/66 (98%)	63 (97%)	2 (3%)	40	72
59	U	55/61 (90%)	53 (96%)	2 (4%)	35	69
All	All	5277/5593 (94%)	5178 (98%)	99 (2%)	59	81

All (99) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	Y	26	ARG
6	03	6	LYS
6	03	8	MET

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Mol	Chain	Res	Type
6	03	188	ASN
7	04	202	ARG
7	04	212	TRP
7	04	259	ASN
10	07	29	ARG
11	08	19	ASN
11	08	68	ARG
11	08	103	ASN
11	08	169	ARG
12	09	73	ASN
12	09	127	GLU
13	10	31	ARG
13	10	37	LYS
14	11	2	LYS
15	12	7	LYS
15	12	111	LYS
15	12	121	LYS
16	13	88	ASN
18	15	16	ARG
18	15	44	ARG
18	15	59	ARG
20	17	12	THR
20	17	30	ARG
22	19	80	ASN
23	20	11	GLN
23	20	80	ARG
24	21	11	ARG
26	23	6	ARG
26	23	36	GLU
26	23	73	ASN
28	25	10	ARG
28	25	72	ASN
29	26	16	ASN
29	26	26	ARG
32	29	39	LYS
33	30	9	ARG
35	32	41	ARG
36	33	48	MET
36	33	61	LEU
37	34	13	ASN
37	34	14	CYS
37	34	27	CYS

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Mol	Chain	Res	Type
39	Z	8	ASN
39	Z	182	LYS
39	Z	223	TYR
39	Z	262	ARG
39	Z	278	ARG
39	Z	301	GLN
40	B	20	ARG
40	B	34	ARG
40	B	35	ASN
40	B	88	GLN
41	C	24	ASN
41	C	163	ARG
42	D	20	LEU
42	D	27	ILE
42	D	31	CYS
42	D	32	LYS
42	D	33	ILE
42	D	80	ARG
42	D	99	ASN
42	D	196	GLU
43	E	9	GLU
43	E	75	LEU
43	E	79	THR
43	E	81	GLN
43	E	145	ASN
43	E	161	GLU
44	F	14	GLN
44	F	94	HIS
45	G	78	ARG
46	H	37	ASN
46	H	113	ARG
46	H	120	LEU
47	I	122	ARG
48	J	91	ASP
49	K	14	GLN
49	K	74	LYS
49	K	100	ASN
49	K	124	LYS
49	K	126	ARG
50	L	55	ARG
50	L	72	ASN
53	O	16	ARG

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Mol	Chain	Res	Type
53	O	57	ARG
54	P	1	MET
54	P	25	ARG
54	P	31	ARG
55	Q	26	ARG
55	Q	64	ARG
56	R	24	ASP
56	R	47	ARG
58	T	2	ASN
58	T	7	LYS
59	U	16	ARG
59	U	33	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (142) such sidechains are listed below:

Mol	Chain	Res	Type
4	Y	27	GLN
6	03	165	ASN
6	03	188	ASN
7	04	44	ASN
7	04	45	ASN
7	04	52	HIS
7	04	85	ASN
7	04	89	ASN
7	04	133	ASN
7	04	142	ASN
7	04	196	ASN
8	05	32	ASN
8	05	130	GLN
8	05	173	GLN
9	06	90	GLN
9	06	156	ASN
9	06	163	ASN
10	07	26	GLN
10	07	51	ASN
10	07	62	GLN
10	07	126	ASN
11	08	19	ASN
11	08	37	ASN
11	08	103	ASN
11	08	138	GLN
12	09	43	ASN

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Mol	Chain	Res	Type
12	09	66	ASN
12	09	73	ASN
14	11	106	GLN
15	12	128	ASN
15	12	132	HIS
15	12	135	GLN
16	13	3	GLN
16	13	5	GLN
16	13	9	ASN
16	13	82	ASN
16	13	88	ASN
17	14	54	GLN
18	15	3	GLN
18	15	45	GLN
19	16	11	ASN
19	16	62	ASN
21	18	6	GLN
21	18	51	ASN
21	18	76	HIS
22	19	13	HIS
22	19	36	GLN
22	19	43	GLN
22	19	80	ASN
23	20	11	GLN
23	20	18	GLN
23	20	89	HIS
24	21	15	GLN
24	21	40	ASN
24	21	57	ASN
26	23	39	ASN
26	23	68	ASN
26	23	73	ASN
26	23	98	ASN
27	24	12	GLN
28	25	36	GLN
28	25	53	HIS
28	25	72	ASN
29	26	15	ASN
29	26	16	ASN
29	26	31	ASN
30	27	15	ASN
30	27	20	ASN

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Mol	Chain	Res	Type
30	27	36	GLN
30	27	58	ASN
31	28	8	GLN
32	29	6	HIS
32	29	20	ASN
32	29	41	HIS
32	29	61	ASN
33	30	5	ASN
33	30	40	HIS
35	32	13	ASN
35	32	26	ASN
35	32	29	GLN
37	34	37	GLN
39	Z	8	ASN
39	Z	9	ASN
39	Z	48	ASN
39	Z	286	GLN
40	B	18	GLN
40	B	23	ASN
40	B	35	ASN
40	B	50	ASN
40	B	167	HIS
40	B	176	ASN
40	B	177	ASN
40	B	189	ASN
41	C	2	GLN
41	C	24	ASN
41	C	31	ASN
41	C	139	ASN
41	C	175	HIS
42	D	40	HIS
42	D	73	ASN
42	D	88	ASN
42	D	115	GLN
43	E	76	ASN
43	E	81	GLN
43	E	96	GLN
43	E	131	ASN
43	E	145	ASN
44	F	17	GLN
44	F	52	ASN
44	F	81	ASN

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Mol	Chain	Res	Type
44	F	94	HIS
45	G	27	ASN
45	G	96	ASN
45	G	121	ASN
46	H	37	ASN
47	I	24	ASN
47	I	74	GLN
47	I	80	HIS
47	I	109	GLN
48	J	58	ASN
49	K	80	ASN
49	K	100	ASN
50	L	4	ASN
50	L	45	ASN
50	L	72	ASN
51	M	7	ASN
51	M	13	HIS
52	N	42	ASN
52	N	59	GLN
52	N	65	GLN
53	O	27	GLN
53	O	34	GLN
54	P	40	ASN
54	P	79	ASN
55	Q	30	HIS
56	R	30	ASN
56	R	53	GLN
58	T	2	ASN
58	T	81	GLN
58	T	83	ASN
59	U	8	ASN
59	U	63	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1538/1539 (99%)	176 (11%)	3 (0%)
2	01	2902/2903 (99%)	332 (11%)	3 (0%)
3	02	118/119 (99%)	9 (7%)	0
38	V	13/14 (92%)	1 (7%)	0
5	W	76/77 (98%)	8 (10%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	X	76/77 (98%)	14 (18%)	0
All	All	4723/4729 (99%)	540 (11%)	6 (0%)

All (540) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	6	G
1	A	7	A
1	A	9	G
1	A	22	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	40	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	60	A
1	A	66	A
1	A	70	U
1	A	71	A
1	A	72	A
1	A	79	G
1	A	83	C
1	A	85	U
1	A	86	G
1	A	87	C
1	A	89	U
1	A	90	C
1	A	93	U
1	A	94	G
1	A	95	C
1	A	130	A
1	A	137	U
1	A	144	G
1	A	164	G
1	A	173	U
1	A	174	A
1	A	180	U
1	A	183	C

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Mol	Chain	Res	Type
1	A	184	G
1	A	197	A
1	A	209	U
1	A	210	C
1	A	220	G
1	A	245	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	281	G
1	A	289	G
1	A	306	A
1	A	328	C
1	A	344	A
1	A	345	C
1	A	346	G
1	A	352	C
1	A	372	C
1	A	377	G
1	A	388	G
1	A	396	C
1	A	397	A
1	A	404	G
1	A	406	G
1	A	413	G
1	A	414	A
1	A	421	U
1	A	427	U
1	A	429	U
1	A	441	A
1	A	448	A
1	A	467	U
1	A	468	A
1	A	479	U
1	A	480	U
1	A	486	U
1	A	487	A
1	A	494	G
1	A	495	A
1	A	497	G

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Mol	Chain	Res	Type
1	A	513	C
1	A	518	C
1	A	524	G
1	A	530	G
1	A	531	U
1	A	535	A
1	A	547	A
1	A	559	A
1	A	561	U
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	C
1	A	577	G
1	A	615	G
1	A	633	G
1	A	642	A
1	A	665	A
1	A	688	G
1	A	703	G
1	A	723	U
1	A	724	G
1	A	755	G
1	A	777	A
1	A	793	U
1	A	815	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	832	G
1	A	843	U
1	A	846	G
1	A	871	U
1	A	873	A
1	A	926	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A

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Mol	Chain	Res	Type
1	A	975	A
1	A	976	G
1	A	977	A
1	A	982	U
1	A	992	U
1	A	993	G
1	A	1004	A
1	A	1030	U
1	A	1031	C
1	A	1032	G
1	A	1033	G
1	A	1053	G
1	A	1055	A
1	A	1094	G
1	A	1101	A
1	A	1118	U
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1159	U
1	A	1168	U
1	A	1182	G
1	A	1184	G
1	A	1196	A
1	A	1197	A
1	A	1201	A
1	A	1212	U
1	A	1213	A
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1238	A
1	A	1240	U
1	A	1258	G
1	A	1260	G
1	A	1261	A
1	A	1280	A
1	A	1286	U
1	A	1287	A
1	A	1300	G
1	A	1317	C
1	A	1346	A

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Mol	Chain	Res	Type
1	A	1347	G
1	A	1381	U
1	A	1395	C
1	A	1398	A
1	A	1400	C
1	A	1446	A
1	A	1451	U
1	A	1452	C
1	A	1492	A
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1529	G
1	A	1530	G
2	01	10	A
2	01	12	U
2	01	34	U
2	01	35	G
2	01	51	G
2	01	63	A
2	01	71	A
2	01	74	A
2	01	75	G
2	01	84	A
2	01	91	A
2	01	103	A
2	01	118	A
2	01	119	A
2	01	120	U
2	01	139	U
2	01	140	C
2	01	141	G
2	01	162	U
2	01	163	C
2	01	181	A
2	01	196	A
2	01	216	A
2	01	221	A
2	01	222	A
2	01	228	C
2	01	229	C
2	01	230	G

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Mol	Chain	Res	Type
2	01	241	A
2	01	248	G
2	01	249	C
2	01	255	A
2	01	266	G
2	01	276	U
2	01	278	A
2	01	285	G
2	01	294	A
2	01	301	G
2	01	323	C
2	01	324	A
2	01	329	G
2	01	330	A
2	01	370	G
2	01	371	A
2	01	372	G
2	01	386	G
2	01	387	U
2	01	404	A
2	01	405	U
2	01	406	G
2	01	411	G
2	01	412	A
2	01	424	G
2	01	451	U
2	01	457	A
2	01	481	G
2	01	491	G
2	01	504	A
2	01	505	A
2	01	507	A
2	01	508	A
2	01	529	A
2	01	530	G
2	01	531	C
2	01	532	A
2	01	545	U
2	01	548	G
2	01	549	G
2	01	563	A
2	01	573	U

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Mol	Chain	Res	Type
2	01	575	A
2	01	588	U
2	01	603	A
2	01	614	A
2	01	627	A
2	01	637	A
2	01	646	U
2	01	654	A
2	01	655	A
2	01	669	G
2	01	686	U
2	01	687	C
2	01	730	A
2	01	747	U
2	01	748	G
2	01	752	A
2	01	764	A
2	01	782	A
2	01	784	G
2	01	785	G
2	01	805	G
2	01	812	C
2	01	819	A
2	01	827	U
2	01	828	U
2	01	830	G
2	01	846	U
2	01	847	U
2	01	860	U
2	01	878	A
2	01	885	C
2	01	887	U
2	01	892	A
2	01	896	A
2	01	897	C
2	01	910	A
2	01	914	G
2	01	932	U
2	01	941	A
2	01	946	C
2	01	961	C
2	01	974	G

*Continued on next page...*

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Mol	Chain	Res	Type
2	01	983	A
2	01	995	C
2	01	996	A
2	01	1012	U
2	01	1013	C
2	01	1022	G
2	01	1033	U
2	01	1045	C
2	01	1046	A
2	01	1047	G
2	01	1059	G
2	01	1060	U
2	01	1061	U
2	01	1062	G
2	01	1063	G
2	01	1066	U
2	01	1067	A
2	01	1069	A
2	01	1070	A
2	01	1071	G
2	01	1074	G
2	01	1076	C
2	01	1078	U
2	01	1083	U
2	01	1084	A
2	01	1088	A
2	01	1089	A
2	01	1090	A
2	01	1095	A
2	01	1096	A
2	01	1097	U
2	01	1099	G
2	01	1104	C
2	01	1111	A
2	01	1130	U
2	01	1132	U
2	01	1133	A
2	01	1135	C
2	01	1149	G
2	01	1174	U
2	01	1178	C
2	01	1179	G

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Mol	Chain	Res	Type
2	01	1180	U
2	01	1212	G
2	01	1250	G
2	01	1253	A
2	01	1256	G
2	01	1271	G
2	01	1272	A
2	01	1301	A
2	01	1332	G
2	01	1345	C
2	01	1365	A
2	01	1378	A
2	01	1379	U
2	01	1383	A
2	01	1416	G
2	01	1419	A
2	01	1420	A
2	01	1428	C
2	01	1454	C
2	01	1482	G
2	01	1490	A
2	01	1498	C
2	01	1515	A
2	01	1524	G
2	01	1535	A
2	01	1536	C
2	01	1537	G
2	01	1555	G
2	01	1559	U
2	01	1560	G
2	01	1569	A
2	01	1578	U
2	01	1616	A
2	01	1647	U
2	01	1648	U
2	01	1674	G
2	01	1698	A
2	01	1715	G
2	01	1729	U
2	01	1730	C
2	01	1738	G
2	01	1758	U

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Mol	Chain	Res	Type
2	01	1764	C
2	01	1773	A
2	01	1780	A
2	01	1800	C
2	01	1801	A
2	01	1808	A
2	01	1816	C
2	01	1829	A
2	01	1871	A
2	01	1873	G
2	01	1901	A
2	01	1906	G
2	01	1914	C
2	01	1929	G
2	01	1930	G
2	01	1937	A
2	01	1938	A
2	01	1944	U
2	01	1945	G
2	01	1955	U
2	01	1963	U
2	01	1967	C
2	01	1970	A
2	01	1972	G
2	01	1981	A
2	01	1982	U
2	01	1991	U
2	01	1992	G
2	01	1993	U
2	01	1997	C
2	01	2022	U
2	01	2023	C
2	01	2030	A
2	01	2031	A
2	01	2036	C
2	01	2043	C
2	01	2055	C
2	01	2056	G
2	01	2060	A
2	01	2061	G
2	01	2062	A
2	01	2069	G

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Mol	Chain	Res	Type
2	01	2072	C
2	01	2093	G
2	01	2108	A
2	01	2111	U
2	01	2112	G
2	01	2115	G
2	01	2118	U
2	01	2121	G
2	01	2125	G
2	01	2127	G
2	01	2132	U
2	01	2166	U
2	01	2172	U
2	01	2173	A
2	01	2179	C
2	01	2189	U
2	01	2198	A
2	01	2203	U
2	01	2204	G
2	01	2213	U
2	01	2214	C
2	01	2225	A
2	01	2239	G
2	01	2250	G
2	01	2283	C
2	01	2287	A
2	01	2305	U
2	01	2309	A
2	01	2325	G
2	01	2327	A
2	01	2334	U
2	01	2335	A
2	01	2350	C
2	01	2354	C
2	01	2383	G
2	01	2385	C
2	01	2402	U
2	01	2406	A
2	01	2423	U
2	01	2424	C
2	01	2425	A
2	01	2429	G

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Mol	Chain	Res	Type
2	01	2430	A
2	01	2435	A
2	01	2441	U
2	01	2448	A
2	01	2476	A
2	01	2498	C
2	01	2502	G
2	01	2504	U
2	01	2505	G
2	01	2518	A
2	01	2520	C
2	01	2529	G
2	01	2547	A
2	01	2554	U
2	01	2566	A
2	01	2567	G
2	01	2572	A
2	01	2573	C
2	01	2585	U
2	01	2602	A
2	01	2603	G
2	01	2609	U
2	01	2613	U
2	01	2629	U
2	01	2646	C
2	01	2655	G
2	01	2682	A
2	01	2689	U
2	01	2690	U
2	01	2714	G
2	01	2744	G
2	01	2748	A
2	01	2764	A
2	01	2765	A
2	01	2778	A
2	01	2779	U
2	01	2791	G
2	01	2797	U
2	01	2798	U
2	01	2800	A
2	01	2818	U
2	01	2820	A

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Mol	Chain	Res	Type
2	01	2821	A
2	01	2833	U
2	01	2849	U
2	01	2850	A
2	01	2867	G
2	01	2868	A
2	01	2871	U
2	01	2884	U
2	01	2893	A
2	01	2894	G
3	02	4	C
3	02	13	G
3	02	15	A
3	02	35	C
3	02	44	G
3	02	67	G
3	02	89	U
3	02	90	C
3	02	109	A
5	X	8	U
5	X	9	G
5	X	17	C
5	X	17(A)	U
5	X	18	G
5	X	21	A
5	X	22	G
5	X	34	C
5	X	35	A
5	X	56	C
5	X	59	A
5	X	61	C
5	X	69	C
5	X	74	C
38	V	12	A
5	W	8	U
5	W	9	G
5	W	17(A)	U
5	W	20	U
5	W	47	U
5	W	48	C
5	W	61	C
5	W	76	A



All (6) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	69	G
1	A	343	U
1	A	1399	C
2	01	490	C
2	01	859	G
2	01	2326	C

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 349 ligands modelled in this entry, 349 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

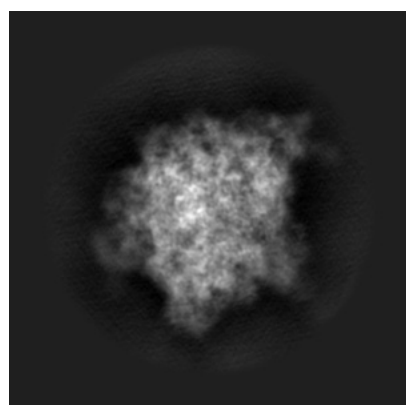
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8522. These allow visual inspection of the internal detail of the map and identification of artifacts.

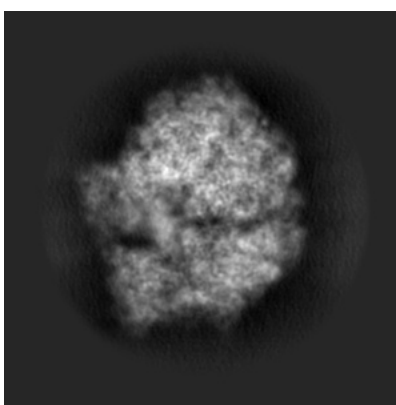
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

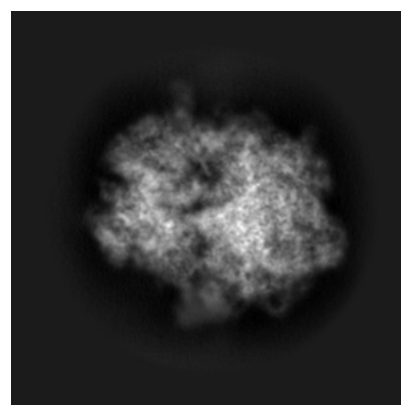
#### 6.1.1 Primary map



X



Y

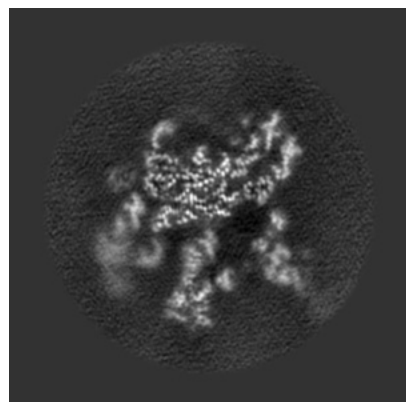


Z

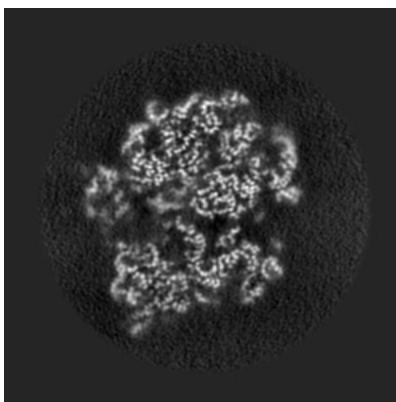
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

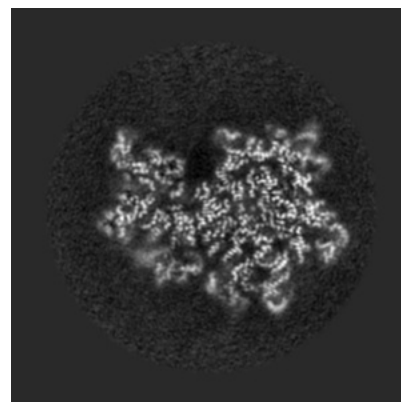
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

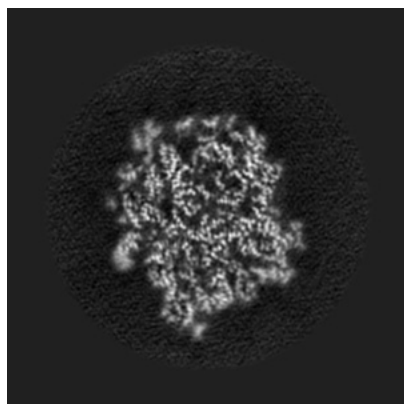


Z Index: 160

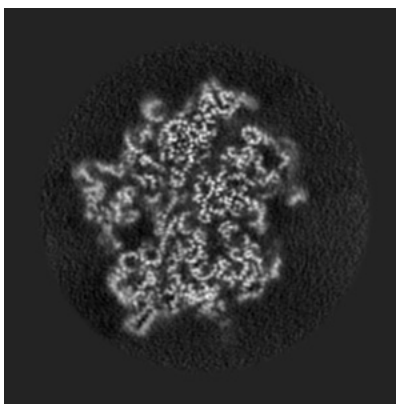
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

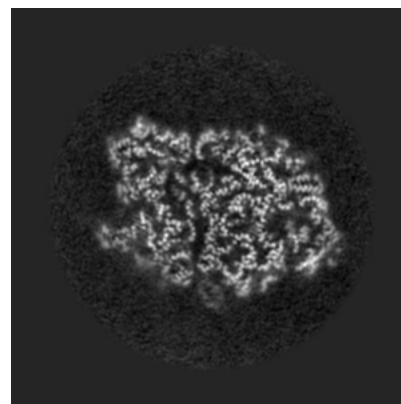
### 6.3.1 Primary map



X Index: 188



Y Index: 154



Z Index: 185

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

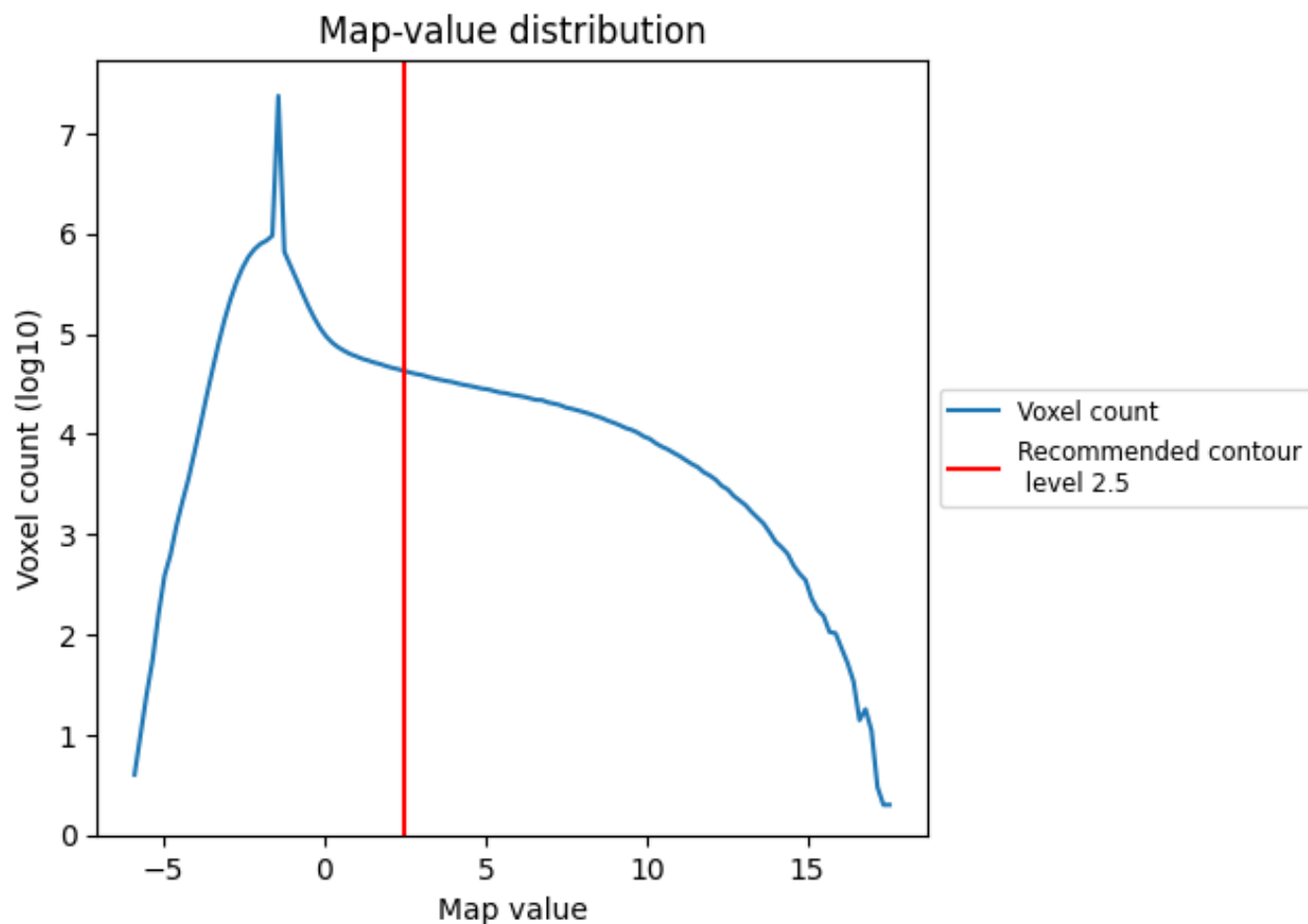
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

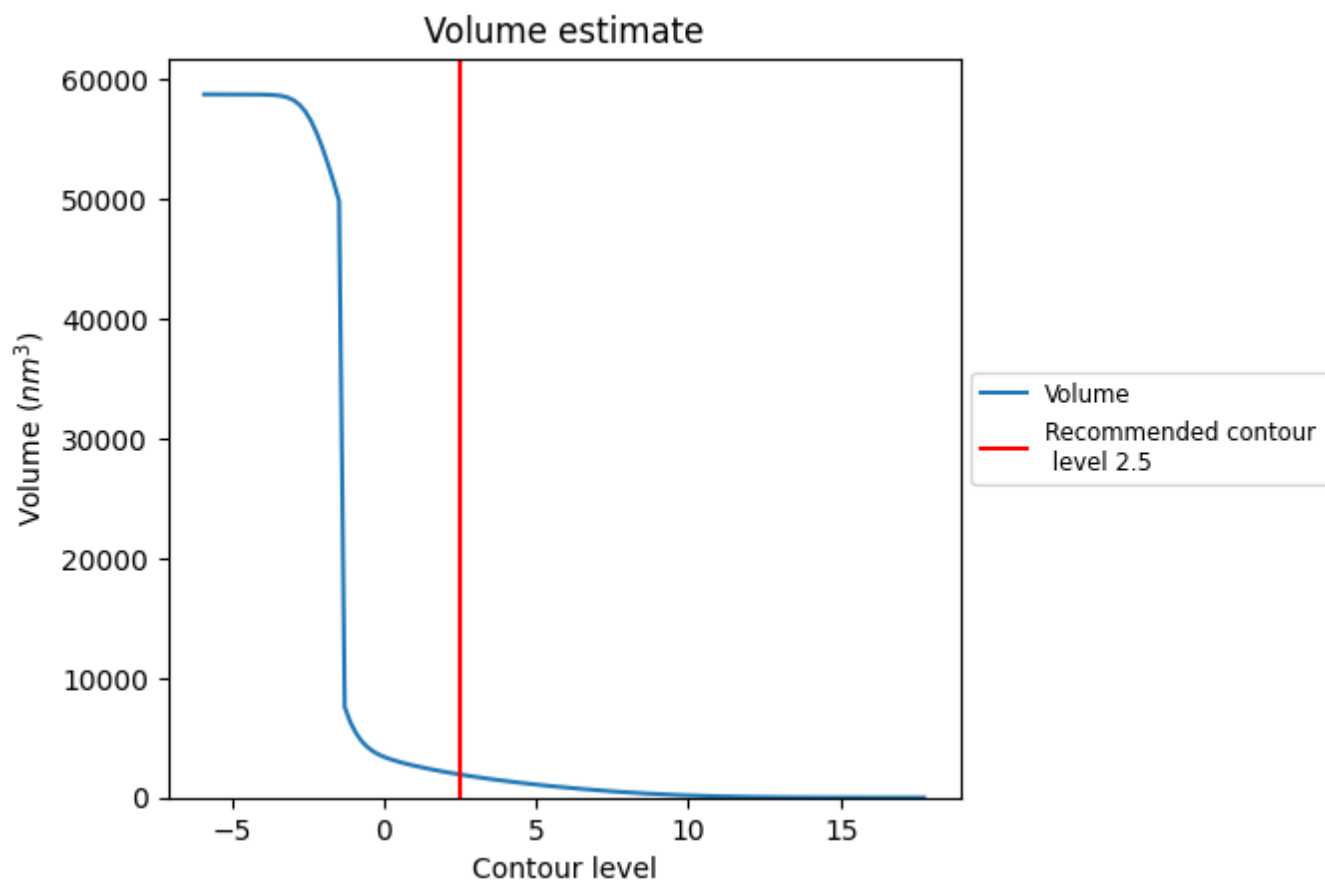
This section contains the results of statistical analysis of the map.

### 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.

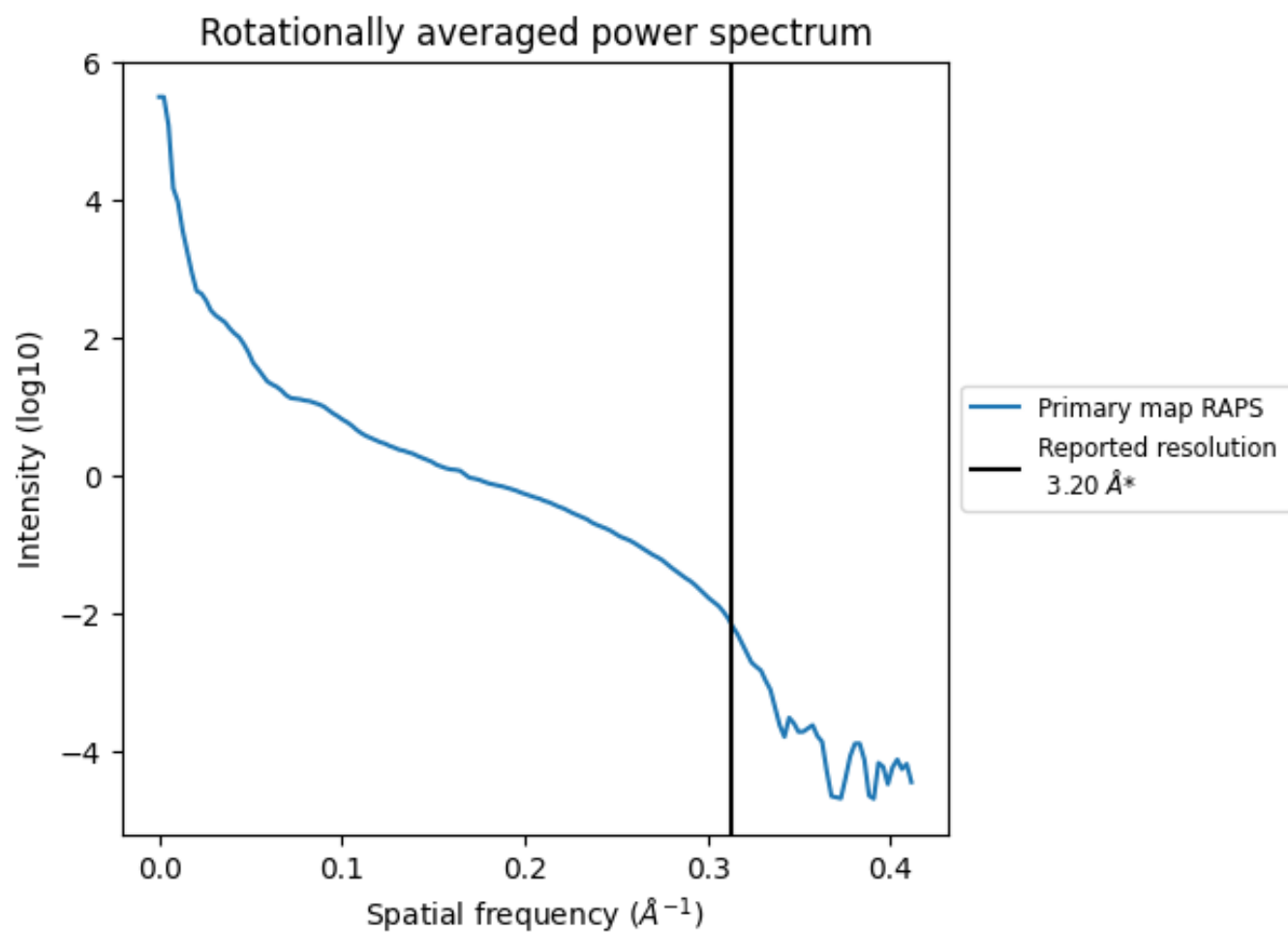
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1927 nm<sup>3</sup>; this corresponds to an approximate mass of 1740 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 0.312  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation

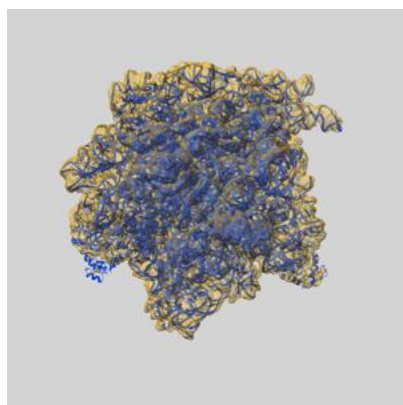
This section was not generated. No FSC curve or half-maps provided.



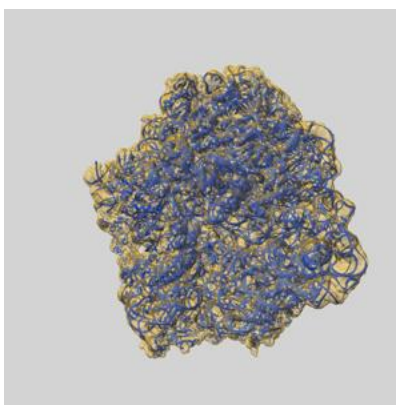
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8522 and PDB model 5U9G. Per-residue inclusion information can be found in section 3 on page 16.

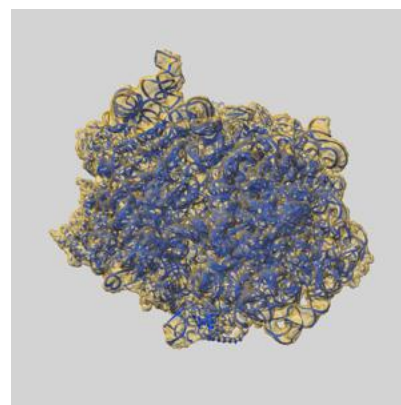
### 9.1 Map-model overlay [i](#)



X



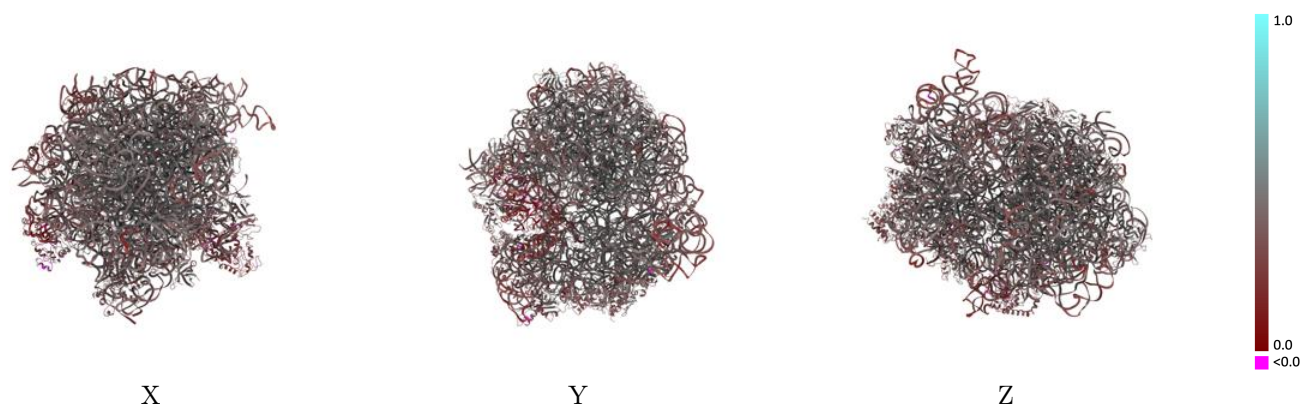
Y



Z

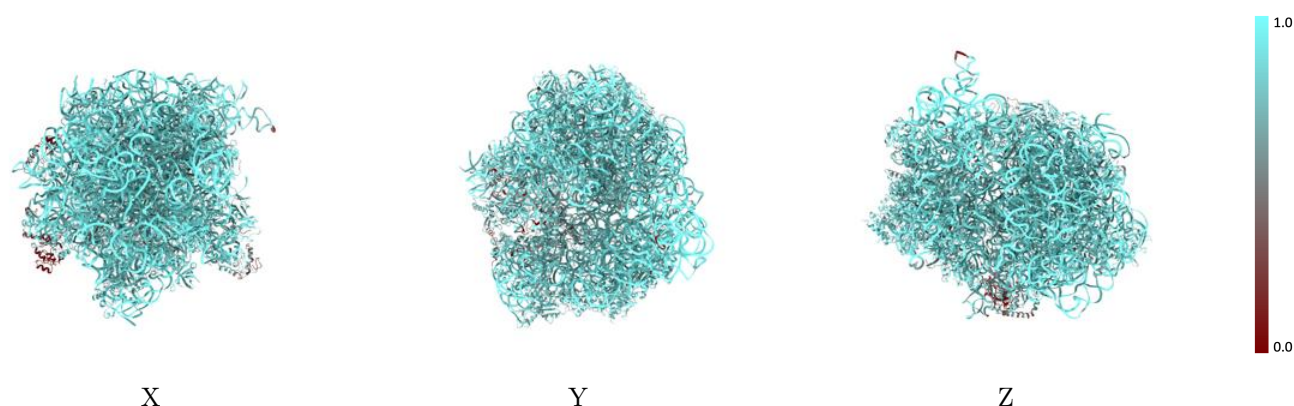
The images above show the 3D surface view of the map at the recommended contour level 2.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



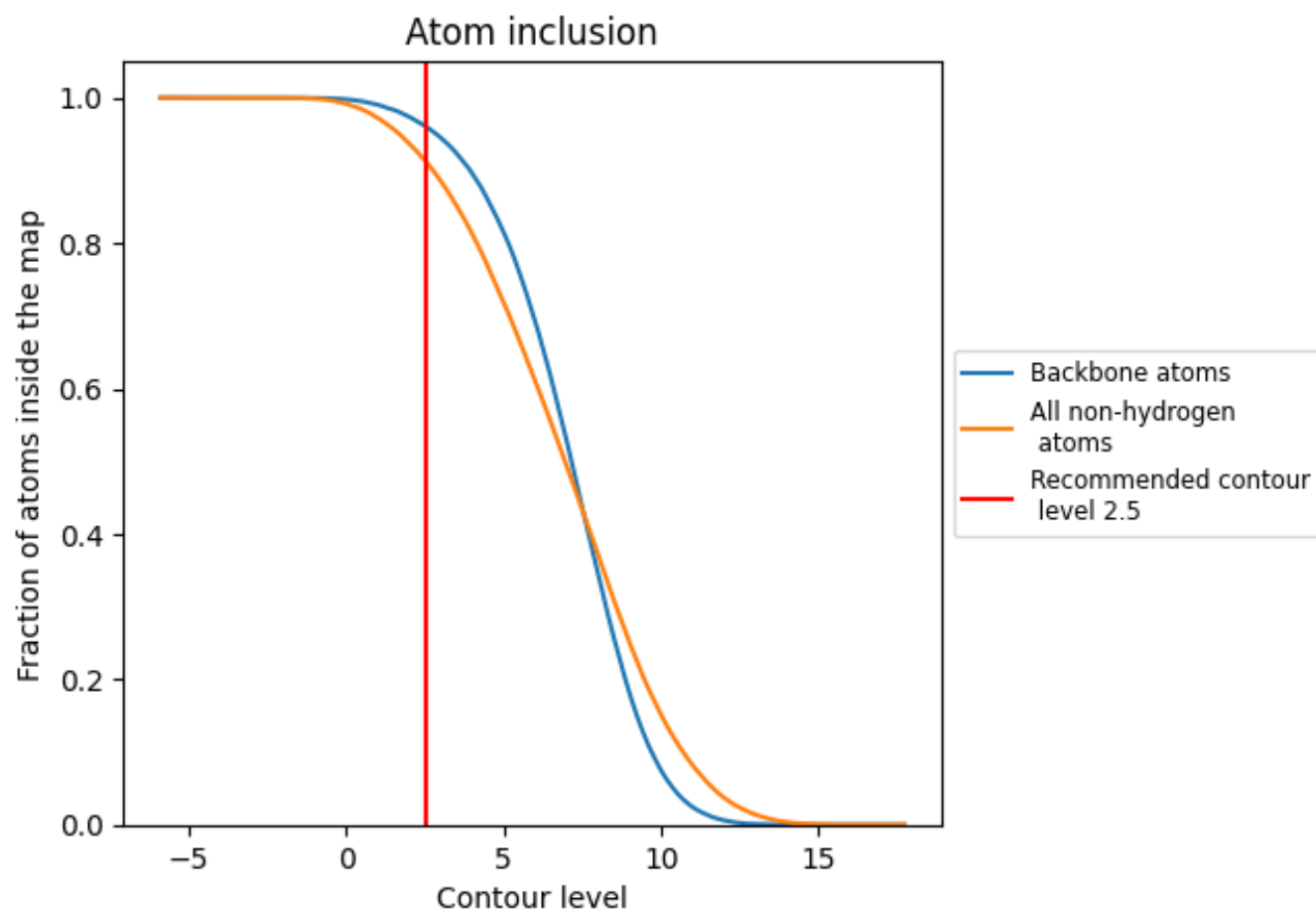
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (2.5).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































The table lists the average atom inclusion at the recommended contour level (2.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9136	 0.3870
01	 0.9762	 0.4080
02	 0.9839	 0.3710
03	 0.4326	 0.2010
04	 0.8393	 0.4400
05	 0.8687	 0.4320
06	 0.8592	 0.3960
07	 0.8602	 0.3290
08	 0.8458	 0.3660
09	 0.3896	 0.3110
10	 0.5424	 0.2010
11	 0.6898	 0.2190
12	 0.8755	 0.4110
13	 0.7853	 0.4230
14	 0.8682	 0.4130
15	 0.8244	 0.4150
16	 0.8807	 0.3950
17	 0.8934	 0.3600
18	 0.8367	 0.4100
19	 0.8943	 0.4060
20	 0.8783	 0.4170
21	 0.8254	 0.4100
22	 0.7950	 0.3750
23	 0.8475	 0.3900
24	 0.8686	 0.3900
25	 0.9125	 0.4380
26	 0.8469	 0.4180
27	 0.8089	 0.3180
28	 0.8604	 0.4030
29	 0.5225	 0.2850
30	 0.8671	 0.4190
31	 0.7855	 0.4030
32	 0.8620	 0.4390
33	 0.8798	 0.4370
34	 0.8396	 0.4150



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Chain	Atom inclusion	Q-score
A	 0.9760	 0.3940
B	 0.8078	 0.3340
C	 0.8169	 0.3840
D	 0.8340	 0.3630
E	 0.8580	 0.4040
F	 0.8128	 0.3560
G	 0.8024	 0.3250
H	 0.8678	 0.3970
I	 0.8621	 0.3430
J	 0.8187	 0.3360
K	 0.8568	 0.3880
L	 0.8100	 0.4200
M	 0.7861	 0.3240
N	 0.8475	 0.3470
O	 0.8623	 0.3550
P	 0.8852	 0.3970
Q	 0.8544	 0.3840
R	 0.8268	 0.3740
S	 0.8647	 0.3550
T	 0.8385	 0.3400
U	 0.7408	 0.2680
V	 0.8856	 0.3090
W	 0.9111	 0.3830
X	 0.6201	 0.2200
Y	 0.7934	 0.3870
Z	 0.6488	 0.2770