



Full wwPDB EM Validation Report ⓘ

Jun 30, 2026 – 01:19 PM JST

PDB ID : 9UZL / pdb_00009uzl
EMDB ID : EMD-64645
Title : EMCV IRES captured on mammalian 40S ribosome with initiator tRNA and eIF2
Authors : Das, D.; Hussain, T.
Deposited on : 2025-05-16
Resolution : 5.01 Å (reported)
Based on initial models : 6YAN, ., 8OZ0

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

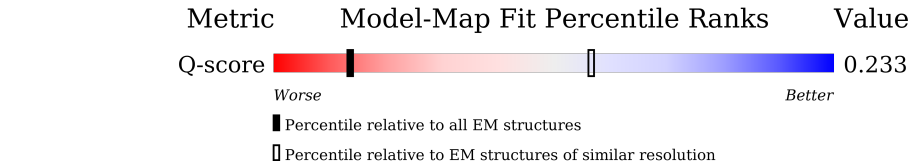
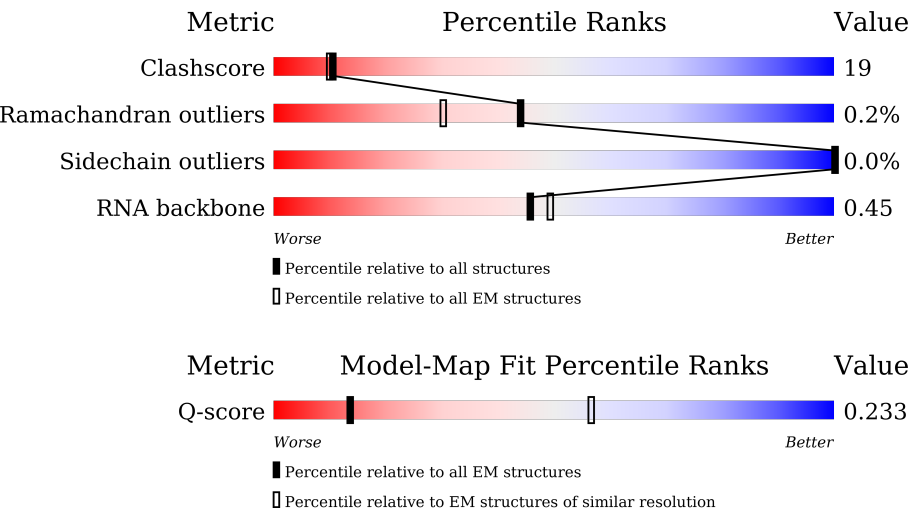
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.01 Å.

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



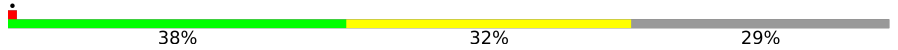
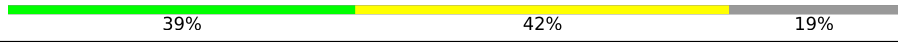
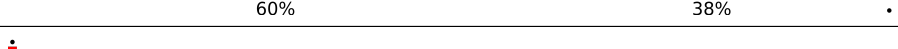
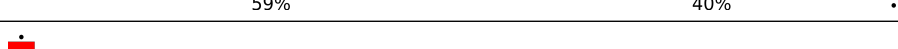
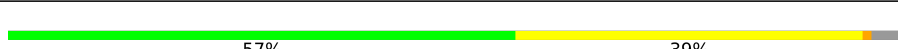
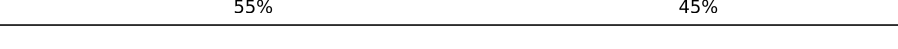
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	859 (4.51 - 5.51)

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

Mol	Chain	Length	Quality of chain
1	2	1863	29% 53% 11% 6%
2	A	315	14% 88% 12%
3	B	485	27% 92% . .

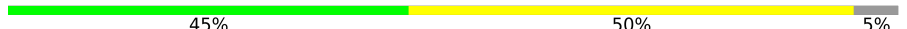
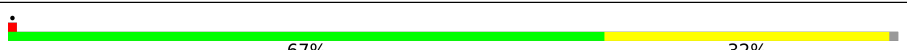
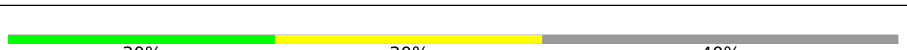
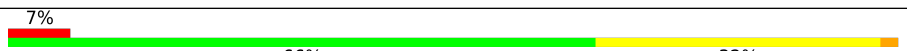
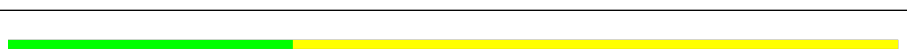
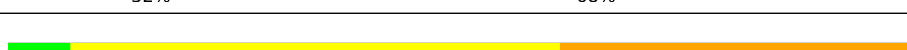
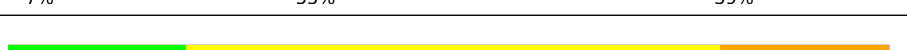
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Mol	Chain	Length	Quality of chain
4	C	295	
5	D	264	
6	E	226	
7	F	243	
8	G	263	
9	H	204	
10	I	249	
11	J	194	
12	K	206	
13	L	194	
14	M	225	
15	N	158	
16	O	132	
17	P	151	
18	Q	168	
19	R	145	
20	S	146	
21	T	135	
22	U	152	
23	V	141	
24	W	119	
25	X	82	
26	Y	130	
27	Z	143	
28	a	126	

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Mol	Chain	Length	Quality of chain
29	b	115	
30	c	84	
31	d	64	
32	e	56	
33	f	156	
34	g	317	
35	h	125	
36	i	59	
37	l	25	
38	y	75	
39	z	93	

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 83705 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1744	Total	C	N	O	P	0	0
			37195	16608	6662	12185	1740		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	A	278	Total	C	N	O	0	0
			1378	822	278	278		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	B	464	Total	C	N	O	0	0
			2281	1352	464	465		

- Molecule 4 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	215	Total	C	N	O	S	0	0
			1741	1107	309	310	15		

- Molecule 6 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	222	Total	C	N	O	S	0	0
			1721	1114	295	303	9		

- Molecule 7 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	227	Total	C	N	O	S	0	0
			1764	1124	317	315	8		

- Molecule 8 is a protein called Small ribosomal subunit protein eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	263	Total	C	N	O	S	0	0
			2083	1329	385	359	10		

- Molecule 9 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 10 is a protein called Small ribosomal subunit protein eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 11 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	190	Total	C	N	O	S	0	0
			1530	975	281	273	1		

- Molecule 12 is a protein called Small ribosomal subunit protein eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	206	Total	C	N	O	S	0	0
			1680	1054	329	292	5		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	182	Total	C	N	O	S	0	0
			1498	952	300	244	2		

- Molecule 14 is a protein called Small ribosomal subunit protein eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-30	THR	ALA	conflict	UNP A0AAG1W9A6

- Molecule 15 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	158	Total	C	N	O	S	0	0
			1296	827	241	221	7		

- Molecule 16 is a protein called Small ribosomal subunit protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	124	Total	C	N	O	S	0	0
			958	600	170	179	9		

- Molecule 17 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 18 is a protein called Ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 19 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	135	Total	C	N	O	S	0	0
			1111	704	211	189	7		

- Molecule 20 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	141	Total	C	N	O	S	0	0
			1123	715	212	193	3		

- Molecule 21 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	126	Total	C	N	O	S	0	0
			1019	639	188	187	5		

- Molecule 22 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	142	Total	C	N	O	S	0	0
			1172	733	239	199	1		

- Molecule 23 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	141	Total	C	N	O	S	0	0
			1113	701	213	196	3		

- Molecule 24 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 25 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	82	Total	C	N	O	S	0	0
			620	378	117	120	5		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	3	SER	ASN	conflict	UNP G1TM82
X	4	ASN	ASP	conflict	UNP G1TM82
X	33	PRO	GLN	conflict	UNP G1TM82
X	50	SER	PHE	conflict	UNP G1TM82
X	76	HIS	ASP	conflict	UNP G1TM82

- Molecule 26 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 27 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	142	Total	C	N	O	S	0	0
			1106	698	220	184	4		

- Molecule 28 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	126	Total	C	N	O	S	0	0
			1022	645	198	174	5		

- Molecule 29 is a protein called Small ribosomal subunit protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	99	Total	C	N	O	S	0	0
			789	491	162	130	6		

- Molecule 30 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	84	Total	C	N	O	S	0	0
			659	413	122	116	8		

- Molecule 31 is a protein called Small ribosomal subunit protein eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	64	Total	C	N	O	S	0	0
			507	308	102	95	2		

- Molecule 32 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 33 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 34 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 35 is a protein called Small ribosomal subunit protein eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 36 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	59	Total	C	N	O	S	0	0
			473	293	104	75	1		

- Molecule 37 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 38 is a RNA chain called Initiator tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	y	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 39 is a RNA chain called Encephalomyocarditis viral IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	z	93	Total	C	N	O	P	0	0
			1981	885	361	642	93		

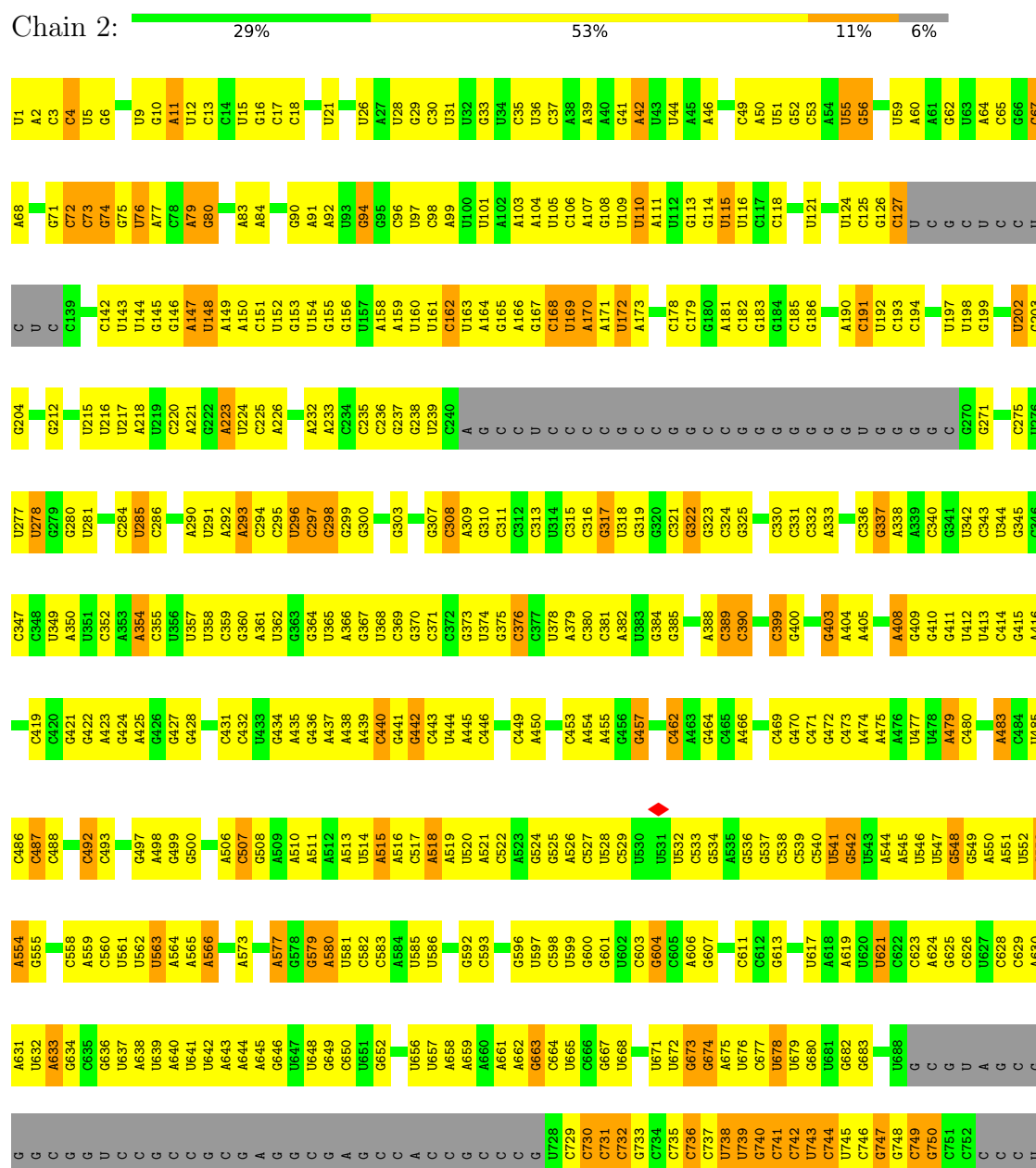
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	831	A	-	expression tag	GB 485965777
z	832	A	-	expression tag	GB 485965777
z	833	U	-	expression tag	GB 485965777
z	834	A	-	expression tag	GB 485965777
z	835	U	-	expression tag	GB 485965777
z	836	G	-	expression tag	GB 485965777
z	837	G	-	expression tag	GB 485965777
z	838	C	-	expression tag	GB 485965777

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.

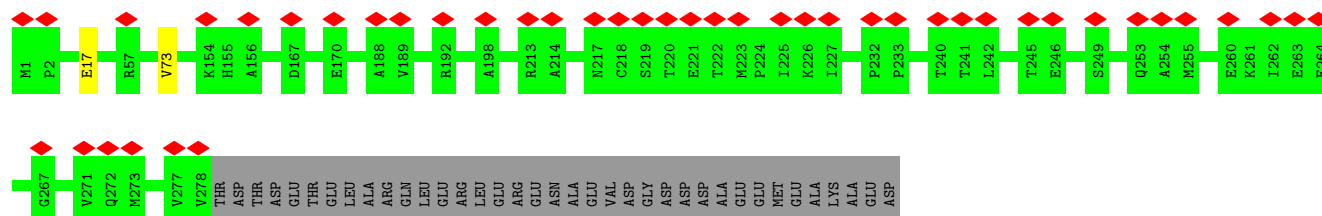
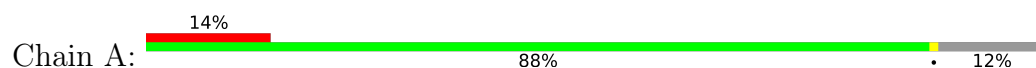
• Molecule 1: 18S ribosomal RNA



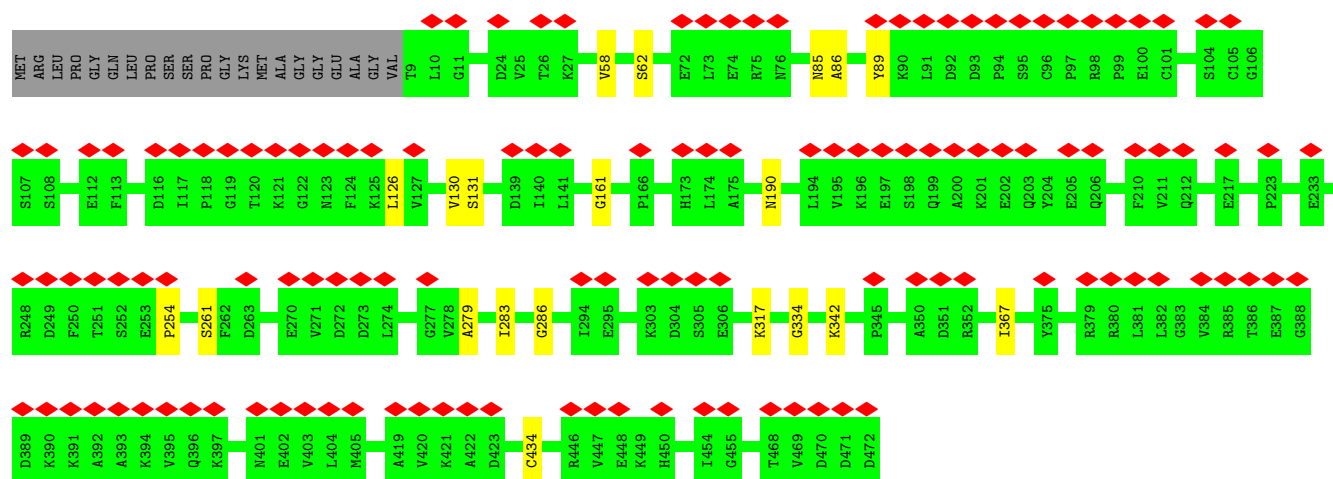
G1714	C1650	G1586	U1386	U1244	G1101	A1031	G955	U894	G827	C
U1715	G1651	C1587	C1367	C1245	C1102	A1032	U956	U895	G828	G
U1716	G1652	C1526	U1388	A1246	U1107	G1033	G957	U896	C829	A
G1717	G1653	C1527	A1451	A1247	U1108	C1034	A958	U897	C830	U
G1718	U1654	G1452	C1391	C1248	A1109	C1035	A959	G897	G831	G
C1655	G1655	U1453	A1392	A1249	U1110	U1041	A960	G898	C832	C
A1656	A1656	G1454	U1393	G1252	U1111	U1042	U961	A899	A833	U
U1720	G1593	G1455	G1394	G1253	U1112	U1043	U962	A900	G834	C
G1721	U1594	C1532	C1395	U1254	C1112	C1044	U963	C901	C835	U
U1724	A1596	U1534	U1396	A1254	C1113	A1045	U964	G902	G836	U
C1661	G1597	G1535	A1397	A1255	U1117	C1049	U965	G903	G837	A
U1728	G1598	U1536	A1398	G1259	G1118	U1057	G966	A904	C838	G
U1663	G1663	C1537	C1399	U1259	A1118	C1050	G967	G905	C839	C
G1664	G1600	U1538	U1400	A1261	C1119	A1051	U968	U840	U840	U
C1665	G1601	A1539	A1401	A1262	U1123	U1052	A976	G906	G841	G
G1732	A1602	A1540	G1402	C1262	C1123	C1053	A977	C907	G842	A
C1733	U1603	G1541	U1403	C1332	C1124	A1054	A978	A909	A843	G
C1734	U1604	C1542	U1404	C1333	G1125	U1055	A979	U910	U844	U
U1668	G1605	G1543	A1405	C1339	G1126	A1056	C980	G911	A845	G
G1669	G1606	U1544	C1406	U1339	A1129	U1057	U987	A912	C846	U
A1670	G1607	G1545	G1407	C1344	U1130	C1058	A986	U913	C847	C
U1671	U1607	U1546	A1408	G1345	C1131	C1059	G987	U914	C848	C
G1739	A1608	G1547	U1409	G1271	U1197	A1059	C987	A915	C849	C
U1740	A1673	U1472	A1473	A1272	G1199	C1060	A988	A916	A850	G
U1741	G1674	U1474	C1411	C1273	U1200	U1133	G989	G917	G	
C1742	G1675	G1475	C1412	A1274	C1201	C1063	A992	A918	U853	G
G1743	U1611	U1550	C1413	G1275	G1202	U1064	A854	G919	A854	U
U1676	C1612	A1551	G1414	C1281	G1203	G1065	A993	G920	G855	G
G1748	G1613	C1552	C1415	G1282	A1204	A1066	A994	G921	G856	C
C1677	A1614	U1553	C1416	U1283	C1137	G1067	G995	A922	A858	U
C1749	G1615	C1554	C1417	U1285	G1138	U1068	C996	G923	A860	U
C1679	U1616	C1555	C1418	G1286	A1139	U1069	U1000	G924	G861	U
U1616	U1617	U1556	G1419	A1287	A1140	G1072	G1001	G925	U862	G
G1681	U1617	A1556	C1420	G1288	C1135	A1073	G1002	G926	G863	U
C1682	A1618	U1557	C1421	A1289	C1136	C1074	C1003	G927	G864	U
C1683	C1623	C1558	G1422	G1290	G1137	C1075	A1004	G928	G794	U
G1684	G1624	C1559	U1423	A1291	A1141	C1076	A1005	G929	A865	U
C1685	A1625	G1560	C1424	G1292	C1142	U1079	G1006	G930	U796	U
U1686	U1626	U1561	G1425	A1293	C1143	A1080	A1007	G931	U797	U
U1687	G1627	G1562	C1426	G1294	C1144	C1081	G1008	G932	A798	U
G1688	C1628	C1563	G1427	A1295	G1154	G1082	G869	G933	C799	U
U1755	A1629	A1564	U1428	A1296	U1155	C1083	A871	U801	U801	U
C1689	C1630	C1567	C1429	G1297	U1156	G1084	C872	A807	A807	U
A1692	G1631	U1568	C1430	U1298	G1160	G1085	C873	C873	C873	U
C1693	C1632	C1569	C1431	A1299	G1161	C1086	C874	C874	C874	U
C1695	G1633	G1570	C1432	G1299	G1162	C1087	C875	C875	C875	U
C1696	G1634	U1571	C1433	U1300	G1163	C1088	C876	C876	C876	U
G1697	A1635	G1572	A1434	C1301	G1164	G1089	C877	C877	C877	U
C1698	U1637	U1573	C1435	C1302	U1234	A1091	C878	C878	C878	U
C1700	U1638	C1574	U1436	U1303	U1235	G1092	C879	C879	C879	U
G1701	U1639	A1575	U1437	A1294	G1165	C1093	C880	C880	C880	U
U1702	C1640	U1576	U1438	A1295	U1236	C1094	C881	C881	C881	U
G1703	C1641	C1577	C1439	A1296	A1166	G1095	C882	C882	C882	U
G1704	U1642	U1578	U1440	A1297	A1167	C1096	C883	C883	C883	U
U1707	G1643	G1579	C1441	U1298	U1237	G1097	C884	C884	C884	U
A1707	U1644	U1580	A1442	U1306	U1238	A1098	C885	C885	C885	U
C1708	U1645	U1581	G1443	C1307	U1239	C1099	C886	C886	C886	U
U1709	A1645	G1582	A1444	C1308	U1240	G1100	C887	C887	C887	U
A1710	U1646	C1583	U1445	A1382	U1241	C1101	C888	C888	C888	U
C1711	G1647	A1584	G1446	G1383	U1242	U1098	C889	C889	C889	U
U1784	A1784	C1712	G1447	A1384	G1170	C1099	C890	C890	C890	U
U1775	G1775	U1780	C1585	C1385	G1172	U1099	C891	C891	C891	U
G1776	C1766	G1766	C1586	U1310	U1310	G1100	C892	C892	C892	U
G1777	C1767	C1587	C1587	U1311	U1311	U1099	C893	C893	C893	U
G1778	C1768	G1768	C1588	U1312	U1312	U1099	C894	C894	C894	U
G1779	U1769	C1589	C1589	U1313	U1313	U1099	C895	C895	C895	U
U1780	C1770	C1590	C1590	U1314	U1314	U1099	C896	C896	C896	U
G1773	G1773	C1591	C1591	U1315	U1315	U1099	C897	C897	C897	U
G1774	C1774	C1592	C1592	U1316	U1316	U1099	C898	C898	C898	U
G1775	C1775	C1593	C1593	U1317	U1317	U1099	C899	C899	C899	U
G1776	C1776	C1594	C1594	U1318	U1318	U1099	C900	C900	C900	U
G1777	C1777	C1595	C1595	U1319	U1319	U1099	C901	C901	C901	U
G1778	C1778	C1596	C1596	U1320	U1320	U1099	C902	C902	C902	U
G1779	C1779	C1597	C1597	U1321	U1321	U1099	C903	C903	C903	U
U1780	C1780	C1598	C1598	U1322	U1322	U1099	C904	C904	C904	U
G1781	C1781	C1599	C1599	U1323	U1323	U1099	C905	C905	C905	U
G1782	C1782	C1600	C1600	U1324	U1324	U1099	C906	C906	C906	U
G1783	C1783	C1601	C1601	U1325	U1325	U1099	C907	C907	C907	U
G1784	C1784	C1602	C1602	U1326	U1326	U1099	C908	C908	C908	U
G1785	C1785	C1603	C1603	U1327	U1327	U1099	C909	C909	C909	U
G1786	C1786	C1604	C1604	U1328	U1328	U1099	C910	C910	C910	U
G1787	C1787	C1605	C1605	U1329	U1329	U1099	C911	C911	C911	U
G1788	C1788	C1606	C1606	U1330	U1330	U1099	C912	C912	C912	U
G1789	C1789	C1607	C1607	U1331	U1331	U1099	C913	C913	C913	U
G1790	C1790	C1608	C1608	U1332	U1332	U1099	C914	C914	C914	U
G1791	C1791	C1609	C1609	U1333	U1333	U1099	C915	C915	C915	U
G1792	C1792	C1610	C1610	U1334	U1334	U1099	C916	C916	C916	U
G1793	C1793	C1611	C1611	U1335	U1335	U1099	C917	C917	C917	U
G1794	C1794	C1612	C1612	U1336	U1336	U1099	C918	C918	C918	U
G1795	C1795	C1613	C1613	U1337	U1337	U1099	C919	C919	C919	U
G1796	C1796	C1614	C1614	U1338	U1338	U1099	C920	C920	C920	U
G1797	C1797	C1615	C1615	U1339	U1339	U1099	C921	C921	C921	U
G1798	C1798	C1616	C1616	U1340	U1340	U1099	C922	C922	C922	U
G1799	C1799	C1617	C1617	U1341	U1341	U1099	C923	C923	C923	U
G1800	C1800	C1618	C1618	U1342	U1342	U1099	C924	C924	C924	U
G1801	C1801	C1619	C1619	U1343	U1343	U1099	C925	C925	C925	U
G1802	C1802	C1620	C1620	U1344	U1344	U1099	C926	C926	C926	U
G1803	C1803	C1621	C1621	U1345	U1345	U1099	C927	C927	C927	U
G1804	C1804	C1622	C1622	U1346	U1346	U1099	C928	C928	C928	U
G1805	C1805	C1623	C1623	U1347	U1347	U1099	C929	C929	C929	U
G1806	C1806	C1624	C1624	U1348	U1348	U1099	C930	C930	C930	U
G1807	C1807	C1625	C1625	U1349	U1349	U1099	C931	C931	C931	U
G1808	C1808	C1626	C1626	U1350	U1350	U1099	C932	C932	C932	U
G1809	C1809	C1627	C1627	U1351	U1351	U1099	C933	C933	C933	U
G1810	C1810	C1628	C1628	U1352	U1352	U1099	C934	C934	C934	U
G1811	C1811	C1629	C1629	U1353	U1353	U1099	C935	C935	C935	U
G1812	C1812	C1630	C1630	U1354	U1354	U1099	C936	C936	C936	U
G1813	C1813	C1631	C1631	U1355	U1355	U1099	C937	C937	C937	U
G1814	C1814	C1632	C1632	U1356	U1356	U1099	C938	C938	C938	U
G1815	C1815	C1633	C1633	U1357	U1357	U1099	C939	C939	C939	U
G1816	C1816	C1634	C1634	U1358	U1358	U1099	C940	C940	C940	U
G1817	C1817	C1635	C1635	U1359	U1359	U1099	C941	C941	C941	U
G1818	C1818	C1636	C1636	U1360	U1360	U1099	C942	C942	C942	U
G1819	C1819	C1637	C1637	U1361	U1361	U1099	C943	C943	C943	U
G1820	C1820	C1638	C1638	U1362	U1362	U1099	C944	C944	C944	U
G1821	C1821	C1639	C1639	U1363	U1363	U1099	C945	C945	C945	U
G1822	C1822	C1640	C1640	U1364	U1364	U1099	C946	C946	C946	U
G1823	C1823	C1641	C1641	U1365	U1365	U1099	C947	C947	C947	U
G1824	C1824	C1642	C1642	U1366	U1366	U1099	C948	C948	C948	U
G1825	C1825	C1643	C1643	U1367	U1367	U1099	C949	C949	C949	U
G1826	C1826	C1644	C1644	U1368	U1368	U1099	C950	C950	C950	U
G1827	C1827	C1645	C1645	U1369	U1369	U1099	C951	C951	C951	U
G1828	C1828	C1646	C1646	U1370	U1370	U1099	C952	C952	C952	U
G1829</										



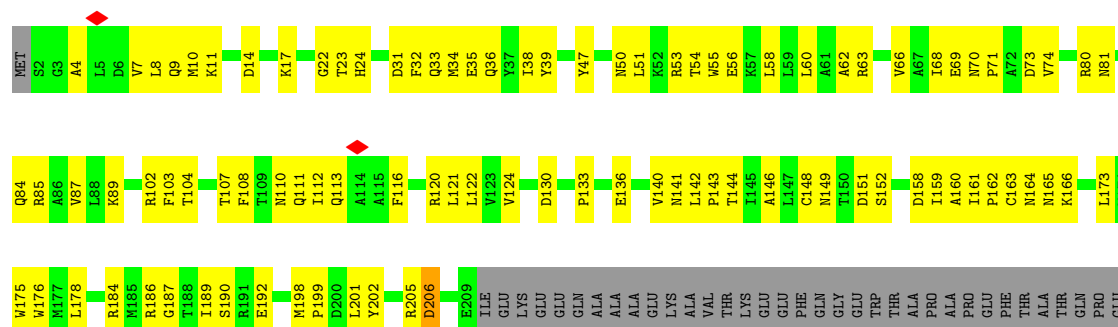
• Molecule 2: Eukaryotic translation initiation factor 2 subunit 1



• Molecule 3: Eukaryotic translation initiation factor 2 subunit 3



• Molecule 4: Small ribosomal subunit protein uS2



VAL
ALA
ASP
VAL
TRP
SER
GLU
GLY
VAL
GLN
VAL
VAL
PRO
SER
GLY
VAL
PRO
ILE
GLY
PHE
GLN
PHE
PRO
THR
GLU
ASP
TRP
SER
SER
ALA
GLN
PRO
ALA
ALA
THR
GLU
ASP
TRP
ASP
TRP
SER
SER
ALA
ALA
ALA
THR
GLU
THR
VAL
VAL
GLY
THR
THR
GLU
TRP
SER

• Molecule 5: Small ribosomal subunit protein eS1

Chain D: 39% 42% 19%

MET
ALA
VAL
GLY
TRP
LYS
ASN
LYS
VAL
GLN
THR
LYS
PRO
GLY
GLY
LYS
LYS
GLY
ALA
LYS
K19
V22
D23
S26
K27
K28
A35
P36
A37
GLU
ASP
M38
F39
M40
I41
R42
R43
PRO
THR
I44
G45
K46
GLN
T47
L48
THR
GLU
TRP
T50
R51
T52
Q53
D50
G61
L62
K63
G64
R65
L71
A72
Q75
N76
D77
E78
V79
F81
R82
K83
L86
I87
Q92
L97
T98
H101
M102
D104
L105
T106
R107
D108
K109
M110
C111
S112
M113
V114
I121
K128
T129
T130
D131
G132
Y133
L134
L135
H136
L137
F138
C139
F142
T143
K144
K145
C146
N147
N148
Q149
I150
R151
K152
V161
R162
R165
K166
K167
M168
M169
E170
I171
M172
T173
R174
M179
E183
V184
L185
L188
D191
S192
I193
D196
I197
E198
K199
A200
C201
Q202
S203
I204
Y205
P206
L207
H208
D209
V210
F211
R212
K213
R214
V215
K216
M217
L218
K219
K220
P221
K222
F223
E224
G226
K227
L228
M229
E230
L231
H232
G233
GLU
SER
SER
SER
GLY
LYS
ALA
THR
GLY
ASP
GLU
THR
GLY
VAL
GLU
ARG
ALA
ASP
GLY
TYR
GLU
PRO
PRO
VAL
GLN
SER
VAL

• Molecule 6: Small ribosomal subunit protein uS5

Chain E: 60% 38% .

GLY
LYS
ALA
GLY
D42
K43
E44
W45
D57
S62
L63
E64
E65
F69
S70
L71
P72
I73
K74
E77
I78
I79
F82
L83
Q84
L87
L92
K93
T94
M95
P96
V97
Q98
K99
Q100
T101
Q102
A103
R106
T107
A108
F109
K110
A111
F112
Y118
V122
G123
L124
C128
S129
K130
A133
I136
R137
I147
R151
R152
G153
Y154
W155
K158
K161
P162
H163
T164
V165
R166
T170
G171
R172
C173
G174
S175
R179
L180
R185
G186
T187
G188
I189
S191
A192
P195
K196
K197
L198
L199
L200
M201
D206
C207
L218
G219
N220
F221
A222
K223
F226
I229
K230
K231
Y232
S233
S234
Y235
L236
T237
P238
D239
L240
W241
F246
S249
P250
Y251
Q252
T255
H257
L258
V259
T263

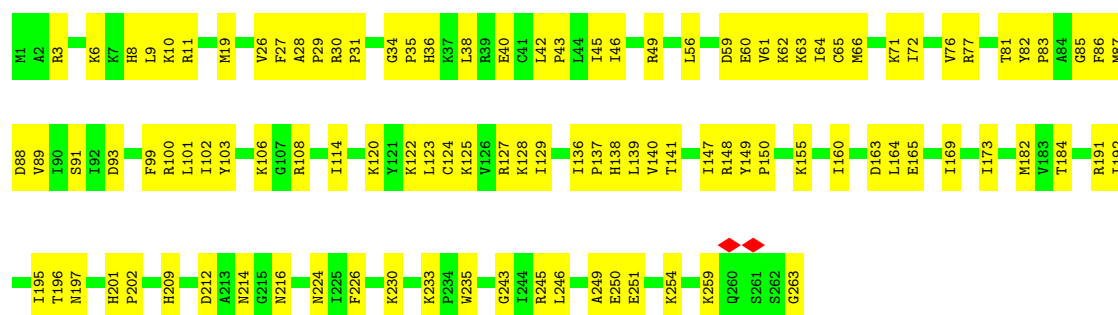
• Molecule 7: Small ribosomal subunit protein uS3

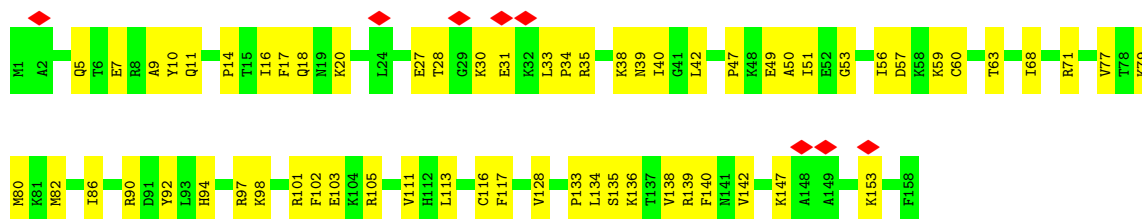
Chain F: 58% 35% 7%

M1
Q4
I5
S6
K7
K8
R9
K10
V11
V12
I16
A19
N22
E23
F24
L25
T26
L29
Y34
S35
G36
V37
T44
T50
L51
A52
T53
R54
T55
V58
K62
G63
R64
R65
I66
R67
E68
L69
I70
K75
R76
L86
Y87
A88
E89
K90
R94
I99
A100
Q101
S104
Y107
V115
G121
V122
L123
R124
F125
I126
K132
E135
V136
V137
V138
S139
G140
K141
L142
Q145
S149
M150
K151
F152
M157
I158
H159
S160
V164
N165
Y166
Y167
V168
R173
H174
V175
G180
V181
L182
K185
M189
D193
P194
S195
G196
K197
I198
K201
K202
P203
L204
P205
D206
H207
V208
S209
K214
D215
E216
L217
L218
P219
T220
K227
GLY
GLY
LYS
PRO
GLU
PRO
PRO
PRO
PRO
MET
MET
GLN
VAL
PRO
THR
ALA

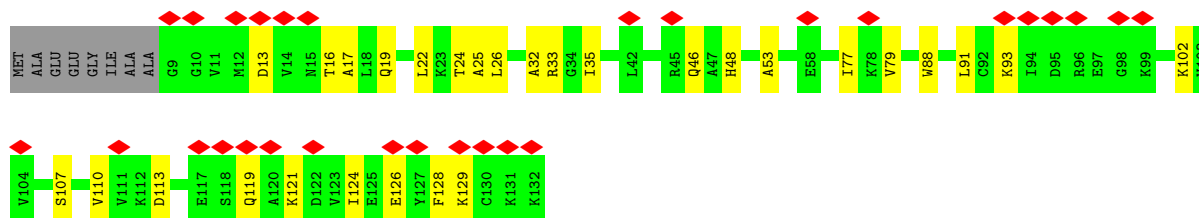
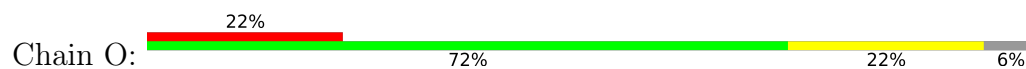
• Molecule 8: Small ribosomal subunit protein eS4

Chain G: 60% 40%

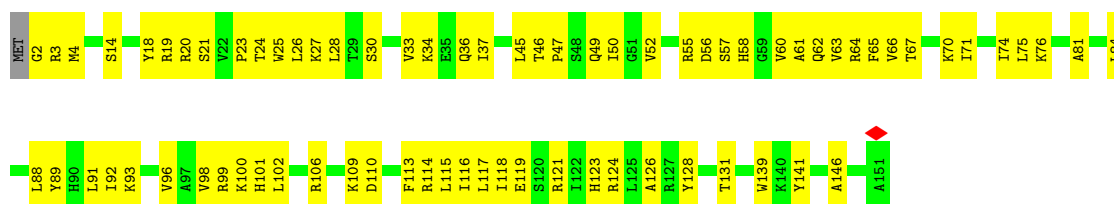




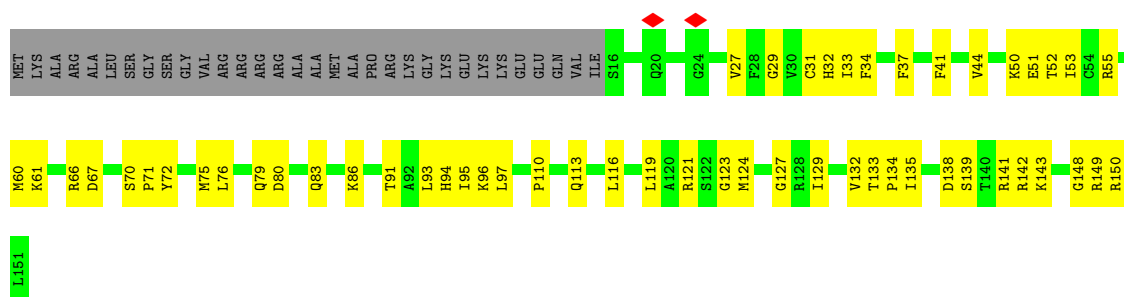
• Molecule 16: Small ribosomal subunit protein eS12



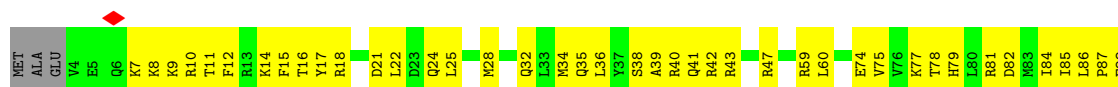
• Molecule 17: Small ribosomal subunit protein uS15



• Molecule 18: Ribosomal protein S14



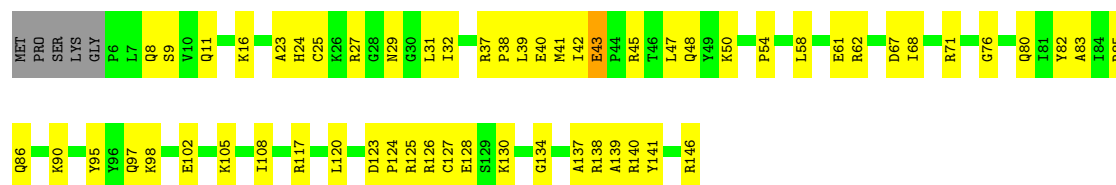
• Molecule 19: Small ribosomal subunit protein uS19





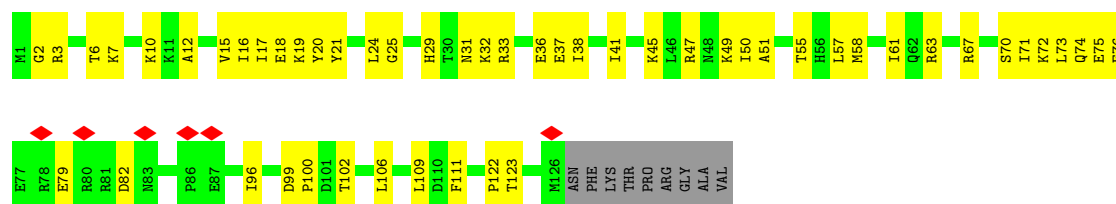
- Molecule 20: Small ribosomal subunit protein uS9

Chain S: 57% 39%



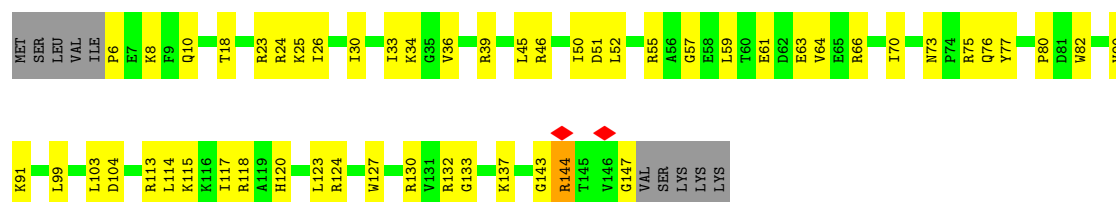
- Molecule 21: Small ribosomal subunit protein eS17

Chain T: 55% 39% 7%



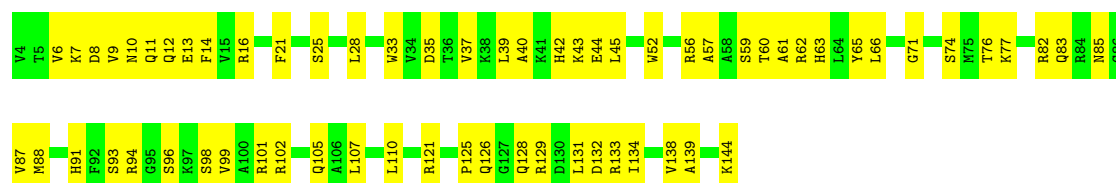
- Molecule 22: Small ribosomal subunit protein uS13

Chain U: 59% 34% 7%



- Molecule 23: Small ribosomal subunit protein eS19

Chain V: 55% 45%



- Molecule 24: Small ribosomal subunit protein uS10

Chain W: 53% 34% 13%



- Molecule 25: Small ribosomal subunit protein eS21



- Molecule 26: Small ribosomal subunit protein uS8



- Molecule 27: Small ribosomal subunit protein uS12

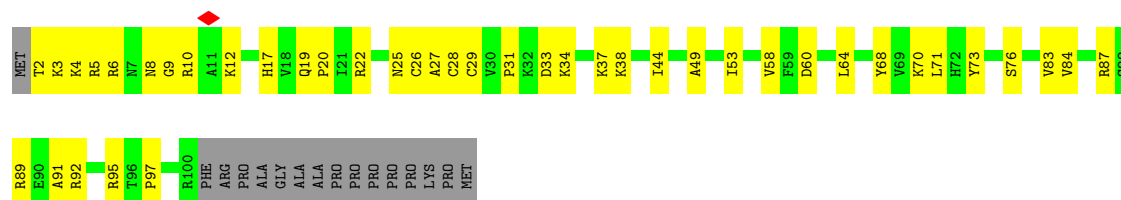


- Molecule 28: 40S ribosomal protein S24



- Molecule 29: Small ribosomal subunit protein eS26





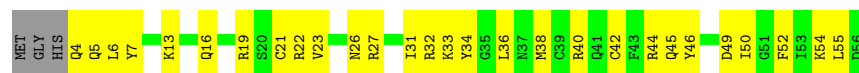
- Molecule 30: Small ribosomal subunit protein eS27



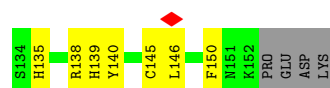
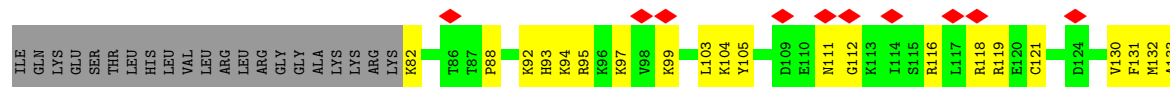
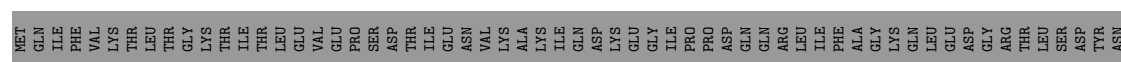
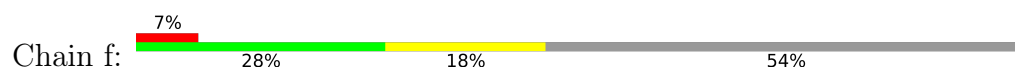
- Molecule 31: Small ribosomal subunit protein eS28



- Molecule 32: Small ribosomal subunit protein uS14

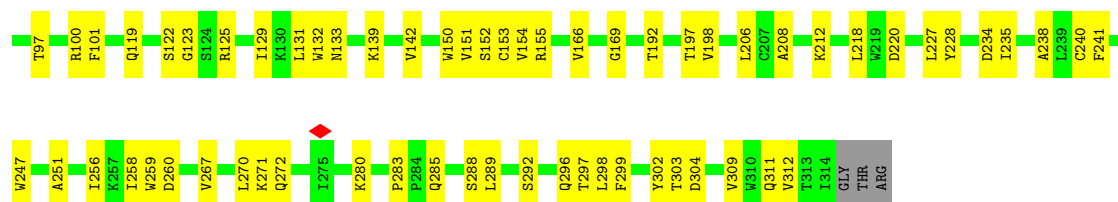


- Molecule 33: Ubiquitin-ribosomal protein eS31 fusion protein



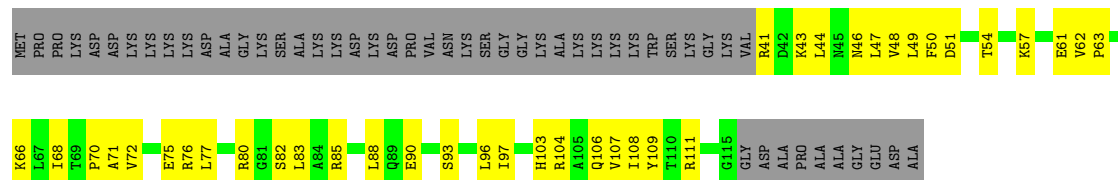
- Molecule 34: Small ribosomal subunit protein RACK1





• Molecule 35: Small ribosomal subunit protein eS25

Chain h: 30% 30% 40%



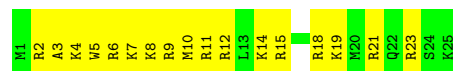
• Molecule 36: Small ribosomal subunit protein eS30

Chain i: 7% 66% 32%



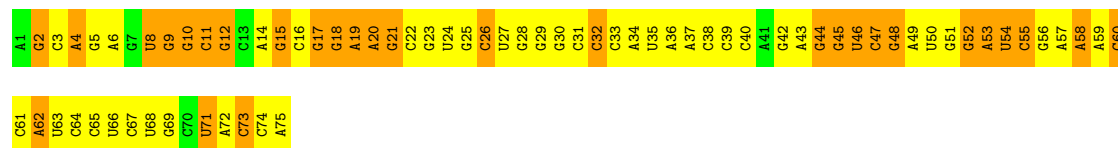
• Molecule 37: Small ribosomal subunit protein eS32

Chain l: 32% 68%



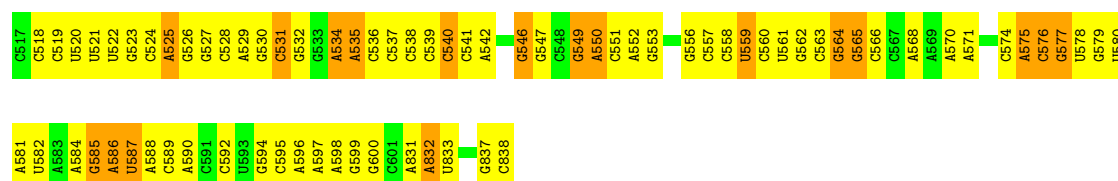
• Molecule 38: Initiator tRNA

Chain y: 7% 55% 39%



• Molecule 39: Encephalomyocarditis viral IRES

Chain z: 20% 60% 19%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	28439	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	36000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.554	Depositor
Minimum map value	-0.216	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.0618	Depositor
Map size ($\text{\AA}$)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.17, 1.17, 1.17	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.11	0/41588	0.28	0/64818
2	A	0.13	0/1377	0.36	0/1919
3	B	0.10	0/2280	0.31	0/3165
4	C	0.15	0/1679	0.42	0/2283
5	D	0.16	0/1769	0.48	0/2367
6	E	0.21	0/1757	0.50	0/2371
7	F	0.17	0/1792	0.48	2/2412 (0.1%)
8	G	0.14	0/2125	0.37	0/2856
9	H	0.16	0/1531	0.44	0/2059
10	I	0.16	0/1946	0.43	0/2590
11	J	0.16	0/1553	0.44	0/2079
12	K	0.14	0/1709	0.53	2/2278 (0.1%)
13	L	0.13	0/1522	0.38	0/2031
14	M	0.16	0/851	0.60	2/1147 (0.2%)
15	N	0.14	0/1319	0.42	0/1761
16	O	0.11	0/968	0.34	0/1296
17	P	0.17	0/1232	0.41	0/1656
18	Q	0.14	0/1029	0.40	0/1380
19	R	0.16	0/1132	0.52	0/1510
20	S	0.14	0/1141	0.46	0/1528
21	T	0.13	0/1031	0.45	0/1383
22	U	0.15	0/1190	0.49	0/1592
23	V	0.16	0/1133	0.41	0/1517
24	W	0.13	0/832	0.38	0/1117
25	X	0.12	0/627	0.41	0/839
26	Y	0.18	0/1051	0.50	0/1406
27	Z	0.16	0/1124	0.42	0/1500
28	a	0.15	0/1039	0.54	2/1380 (0.1%)
29	b	0.20	0/802	0.45	0/1076
30	c	0.19	0/673	0.63	4/902 (0.4%)
31	d	0.16	0/509	0.45	0/680
32	e	0.18	0/455	0.46	0/603
33	f	0.13	0/593	0.36	0/786
34	g	0.12	0/2493	0.38	0/3394

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	h	0.15	0/604	0.36	0/810
36	i	0.19	0/478	0.62	2/628 (0.3%)
37	l	0.17	0/241	0.49	0/305
38	y	0.13	0/1795	0.29	0/2798
39	z	0.11	0/2213	0.25	0/3442
All	All	0.13	0/89183	0.36	14/129664 (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
11	J	0	1
20	S	0	1
All	All	0	2

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	K	142	SER	CA-C-N	11.15	141.77	121.70
12	K	142	SER	C-N-CA	11.15	141.77	121.70
14	M	1	MET	CA-C-N	8.95	137.81	121.70
14	M	1	MET	C-N-CA	8.95	137.81	121.70
28	a	102	THR	CA-C-N	8.60	137.18	121.70
28	a	102	THR	C-N-CA	8.60	137.18	121.70
7	F	197	LYS	CA-C-N	6.86	134.04	121.70
7	F	197	LYS	C-N-CA	6.86	134.04	121.70
36	i	118	ASN	CA-C-N	6.65	133.66	121.70
36	i	118	ASN	C-N-CA	6.65	133.66	121.70
30	c	81	ARG	CA-C-N	6.41	133.25	121.70
30	c	81	ARG	C-N-CA	6.41	133.25	121.70
30	c	20	LYS	CA-C-N	6.27	128.68	120.28
30	c	20	LYS	C-N-CA	6.27	128.68	120.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	J	66	VAL	Peptide

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Mol	Chain	Res	Type	Group
20	S	43	GLU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37195	0	18794	1205	0
2	A	1378	0	611	1	0
3	B	2281	0	1035	10	0
4	C	1642	0	1646	88	0
5	D	1741	0	1815	84	0
6	E	1721	0	1812	84	0
7	F	1764	0	1863	67	0
8	G	2083	0	2189	99	0
9	H	1509	0	1563	72	0
10	I	1923	0	2089	74	0
11	J	1530	0	1627	61	0
12	K	1680	0	1762	87	0
13	L	1498	0	1608	58	0
14	M	827	0	854	46	0
15	N	1296	0	1374	60	0
16	O	958	0	993	22	0
17	P	1208	0	1294	69	0
18	Q	1016	0	1039	53	0
19	R	1111	0	1168	68	0
20	S	1123	0	1193	51	0
21	T	1019	0	1075	48	0
22	U	1172	0	1226	55	0
23	V	1113	0	1149	53	0
24	W	822	0	887	40	0
25	X	620	0	622	34	0
26	Y	1034	0	1080	57	0
27	Z	1106	0	1179	56	0
28	a	1022	0	1085	50	0
29	b	789	0	839	46	0
30	c	659	0	683	24	0
31	d	507	0	536	26	0
32	e	445	0	442	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	f	581	0	599	35	0
34	g	2436	0	2393	77	0
35	h	598	0	656	37	0
36	i	473	0	524	20	0
37	l	240	0	289	18	0
38	y	1604	0	816	79	0
39	z	1981	0	1011	71	0
All	All	83705	0	63420	2712	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 19.

All (2712) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1284:U:H3	1:2:1307:C:N4	1.45	1.14
1:2:432:C:N4	1:2:439:A:H62	1.51	1.08
1:2:957:G:C2	39:z:831:A:N1	2.24	1.05
1:2:432:C:H42	1:2:439:A:N6	1.53	1.04
1:2:149:A:N6	1:2:169:U:C2	2.26	1.03
1:2:124:U:H3	1:2:330:C:N4	1.58	1.00
1:2:957:G:N3	39:z:831:A:C6	2.29	1.00
1:2:1743:G:H1	1:2:1780:U:H3	1.06	1.00
1:2:800:U:H3	1:2:855:G:H1	1.08	0.99
32:e:36:LEU:HD12	32:e:38:MET:HE1	1.41	0.98
10:I:208:GLU:OE1	10:I:211:LYS:NZ	1.97	0.96
1:2:957:G:C2	39:z:831:A:C6	2.54	0.95
1:2:1704:G:H1	1:2:1818:A:N6	1.64	0.94
1:2:192:U:H3	1:2:203:G:H1	1.05	0.94
1:2:1751:G:H1	1:2:1769:U:H3	1.13	0.94
1:2:1223:G:H1	1:2:1526:A:H61	1.10	0.91
1:2:1647:G:H1	1:2:1667:U:H3	0.93	0.90
1:2:1652:G:H1	1:2:1662:U:H3	1.18	0.89
1:2:116:U:H3	1:2:337:G:H1	0.89	0.89
1:2:1266:G:H1	1:2:1507:U:H3	0.90	0.89
1:2:1704:G:H1	1:2:1818:A:H61	0.88	0.87
32:e:16:GLN:HG2	32:e:27:ARG:HH21	1.40	0.87
34:g:87:LEU:HB2	34:g:101:PHE:HB2	1.55	0.87
1:2:1320:G:H1	1:2:1500:U:H3	1.16	0.86
8:G:182:MET:HE1	8:G:192:ILE:HG12	1.57	0.86
1:2:1029:G:H1	1:2:1076:A:HO2'	1.19	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:483:A:H61	1:2:500:G:H1'	1.41	0.85
18:Q:71:PRO:HB2	31:d:63:ARG:HH12	1.42	0.85
1:2:1815:U:H2'	1:2:1816:A:H8	1.42	0.84
1:2:957:G:H21	39:z:831:A:H61	1.21	0.84
1:2:419:C:H5''	8:G:10:LYS:HE3	1.60	0.83
17:P:62:GLN:HG3	17:P:65:PHE:HD2	1.41	0.83
1:2:843:A:O2'	8:G:106:LYS:NZ	2.11	0.83
1:2:1223:G:H1	1:2:1526:A:N6	1.76	0.83
38:y:25:G:N1	38:y:43:A:C2	2.47	0.83
1:2:1648:U:H3	1:2:1666:G:H1	1.26	0.82
1:2:1717:G:H1	1:2:1806:U:H3	1.25	0.82
1:2:957:G:N2	39:z:831:A:H61	1.76	0.82
1:2:164:A:H3'	1:2:165:G:H21	1.45	0.81
4:C:51:LEU:HD21	21:T:109:LEU:HD12	1.61	0.81
34:g:59:LEU:HB3	34:g:90:TRP:HZ3	1.46	0.81
1:2:953:A:H3'	1:2:954:G:H21	1.44	0.81
1:2:668:U:H3	1:2:1023:A:H62	1.30	0.80
9:H:156:THR:HA	9:H:159:ARG:HH21	1.45	0.80
1:2:1139:A:O3'	1:2:1351:C:N4	2.15	0.80
1:2:313:C:N3	1:2:318:U:O4	2.16	0.79
1:2:683:G:O6	1:2:731:C:N4	2.16	0.79
25:X:14:PRO:HB2	25:X:23:ILE:HD11	1.64	0.79
1:2:1472:A:N7	21:T:3:ARG:NH2	2.28	0.79
27:Z:101:LEU:HB2	27:Z:124:LYS:HB2	1.64	0.78
14:M:7:ASN:ND2	14:M:39:ASN:O	2.17	0.78
24:W:81:GLN:HB2	32:e:55:LEU:HD21	1.64	0.78
1:2:1320:G:N2	1:2:1500:U:O2	2.16	0.77
12:K:42:ARG:HB3	12:K:58:LEU:O	1.84	0.77
8:G:45:ILE:HG22	8:G:61:VAL:HG11	1.65	0.77
6:E:151:ARG:HD3	6:E:166:ARG:HE	1.49	0.77
20:S:85:ARG:HH12	20:S:117:ARG:HD3	1.48	0.77
1:2:940:A:H61	1:2:978:G:H1	1.31	0.77
1:2:1268:C:OP1	33:f:94:LYS:NZ	2.17	0.77
1:2:1672:U:OP1	9:H:71:ARG:NH2	2.19	0.76
1:2:1414:C:N4	1:2:1421:G:OP2	2.18	0.76
30:c:1:MET:HE1	30:c:5:LYS:HB2	1.66	0.76
1:2:1408:C:H2'	1:2:1409:G:C8	2.19	0.76
15:N:16:ILE:HD11	15:N:34:PRO:HG2	1.68	0.76
1:2:924:G:H1	1:2:1009:U:H3	1.34	0.76
28:a:102:THR:OG1	28:a:106:GLN:NE2	2.18	0.75
13:L:134:HIS:HE1	13:L:164:PRO:HD2	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:7:GLU:HG2	15:N:9:ALA:H	1.50	0.75
24:W:63:ILE:HB	24:W:80:PHE:HB2	1.67	0.75
27:Z:107:ARG:NH1	27:Z:111:ALA:O	2.19	0.75
9:H:85:LYS:HB3	9:H:88:MET:HG2	1.69	0.75
12:K:36:THR:HG23	12:K:96:LEU:HB2	1.68	0.75
34:g:88:ARG:HB3	34:g:90:TRP:HE1	1.52	0.75
38:y:10:G:N7	38:y:45:G:C2	2.53	0.75
27:Z:1:MET:HE3	27:Z:3:LYS:HG3	1.67	0.75
1:2:551:A:O2'	13:L:132:GLN:NE2	2.20	0.75
1:2:309:A:H2	1:2:322:G:H22	1.35	0.75
12:K:190:LEU:HD21	12:K:198:TYR:CD2	2.22	0.75
1:2:236:C:N4	1:2:237:G:O6	2.20	0.74
1:2:4:C:H1'	13:L:18:ARG:HH22	1.53	0.74
4:C:38:ILE:HD11	4:C:47:TYR:HB3	1.67	0.74
27:Z:1:MET:SD	27:Z:5:ARG:NH2	2.61	0.74
15:N:97:ARG:O	15:N:97:ARG:NH1	2.20	0.74
1:2:826:A:OP2	1:2:842:G:N2	2.20	0.74
1:2:1350:G:N2	1:2:1353:A:OP2	2.21	0.74
14:M:27:VAL:HG12	14:M:43:LEU:HD21	1.70	0.73
11:J:77:VAL:HG23	11:J:78:ARG:HD2	1.69	0.73
1:2:434:G:H1	12:K:26:LYS:HE3	1.50	0.73
18:Q:142:ARG:O	29:b:22:ARG:NH2	2.21	0.73
27:Z:95:GLU:OE2	27:Z:140:ARG:NH2	2.22	0.73
14:M:65:ARG:NH2	32:e:21:CYS:O	2.22	0.73
1:2:1262:C:OP1	33:f:82:LYS:NZ	2.16	0.73
12:K:190:LEU:HD21	12:K:198:TYR:HD2	1.53	0.73
15:N:103:GLU:OE2	27:Z:10:ALA:N	2.22	0.73
4:C:122:LEU:HD13	4:C:124:VAL:HG23	1.71	0.73
1:2:1802:U:H2'	1:2:1803:A:H8	1.53	0.73
4:C:122:LEU:HD21	4:C:144:THR:HG22	1.69	0.73
5:D:143:THR:HA	5:D:207:LEU:HD23	1.70	0.73
10:I:52:ILE:HD11	10:I:109:LEU:HD12	1.71	0.73
1:2:409:G:O3'	26:Y:88:LYS:NZ	2.22	0.72
1:2:1651:G:H1	1:2:1663:U:H3	0.83	0.72
24:W:55:ARG:HA	24:W:87:ARG:HG3	1.71	0.72
1:2:53:C:OP1	28:a:112:ASN:ND2	2.22	0.72
34:g:59:LEU:HB3	34:g:90:TRP:CZ3	2.24	0.72
1:2:1732:G:O6	1:2:1791:U:O2	2.08	0.72
22:U:23:ARG:NH2	35:h:46:ASN:O	2.22	0.72
1:2:1072:G:O6	1:2:1073:A:N6	2.22	0.72
11:J:138:GLU:HG2	17:P:19:ARG:HH12	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:32:MET:HE3	10:I:33:ALA:H	1.54	0.72
21:T:31:ASN:ND2	21:T:51:ALA:O	2.22	0.72
4:C:81:ASN:HA	4:C:84:GLN:HE22	1.55	0.71
38:y:53:A:N6	38:y:61:C:O2	2.20	0.71
1:2:381:C:H2'	1:2:382:A:H8	1.55	0.71
1:2:1198:U:H2'	1:2:1199:G:C8	2.25	0.71
13:L:172:ARG:HD2	13:L:176:LYS:HZ3	1.55	0.71
1:2:1460:C:OP2	21:T:63:ARG:NH2	2.22	0.71
6:E:161:LYS:O	6:E:185:ARG:NH2	2.23	0.71
19:R:74:GLU:HG2	19:R:75:VAL:H	1.56	0.71
38:y:24:U:H2'	38:y:25:G:H8	1.56	0.71
1:2:668:U:O4	1:2:1023:A:N7	2.23	0.71
1:2:1226:C:HO2'	1:2:1660:G:H1	1.36	0.71
1:2:1418:G:H2'	1:2:1419:C:H2'	1.73	0.71
18:Q:142:ARG:HH21	29:b:22:ARG:HB3	1.56	0.71
22:U:46:ARG:HD2	23:V:35:ASP:HB3	1.71	0.71
1:2:1034:U:H1'	1:2:1176:C:H42	1.56	0.71
6:E:110:LYS:HD3	6:E:128:CYS:HB2	1.72	0.71
1:2:739:U:O2'	1:2:794:G:N2	2.24	0.70
1:2:1575:A:H5'	24:W:56:MET:HE3	1.73	0.70
19:R:18:ARG:H	22:U:91:LYS:HA	1.56	0.70
1:2:671:U:H4'	27:Z:9:THR:HG22	1.73	0.70
1:2:876:G:N2	1:2:876:G:OP2	2.24	0.70
7:F:214:LYS:NZ	21:T:19:LYS:O	2.24	0.70
29:b:87:ARG:NH1	29:b:91:ALA:O	2.20	0.70
1:2:957:G:N2	39:z:831:A:N6	2.38	0.70
34:g:206:LEU:HD11	34:g:218:LEU:HB3	1.72	0.70
1:2:1281:G:H22	33:f:104:LYS:HG2	1.57	0.70
7:F:204:LEU:HB2	7:F:208:VAL:HA	1.74	0.70
6:E:108:ARG:NH1	6:E:128:CYS:SG	2.64	0.70
19:R:15:PHE:HB3	22:U:91:LYS:HB3	1.74	0.70
10:I:121:ILE:HD12	10:I:122:PRO:HD2	1.74	0.69
12:K:113:TYR:HB3	12:K:121:LEU:HD21	1.74	0.69
14:M:61:GLN:HB2	14:M:68:TYR:HB2	1.73	0.69
29:b:38:LYS:HB3	29:b:71:LEU:HD11	1.74	0.69
1:2:1094:C:H2'	1:2:1095:G:C8	2.26	0.69
12:K:194:GLU:OE1	15:N:18:GLN:NE2	2.25	0.69
18:Q:79:GLN:O	18:Q:83:GLN:NE2	2.25	0.69
1:2:148:U:H2'	1:2:149:A:H8	1.55	0.69
26:Y:53:ILE:HB	26:Y:60:LYS:HB3	1.74	0.69
1:2:915:A:H62	1:2:1016:A:H2'	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:142:SER:H	12:K:143:LYS:HB2	1.58	0.69
34:g:6:THR:HG23	34:g:8:ARG:HH12	1.55	0.69
9:H:59:LYS:HB2	9:H:62:ARG:HB2	1.74	0.69
38:y:23:G:H2'	38:y:24:U:O4'	1.93	0.69
1:2:2:A:H5'	1:2:408:A:H5'	1.75	0.69
1:2:487:C:H4'	8:G:8:HIS:CD2	2.28	0.69
1:2:738:U:O2'	1:2:740:G:OP2	2.11	0.69
1:2:1643:G:N2	1:2:1670:A:OP2	2.25	0.69
1:2:1645:A:H5''	20:S:139:ALA:HB2	1.75	0.69
1:2:1709:U:H2'	1:2:1710:A:C8	2.28	0.69
15:N:86:ILE:HB	15:N:113:LEU:HD23	1.73	0.69
20:S:146:ARG:NH2	38:y:32:C:OP2	2.24	0.69
39:z:551:C:H2'	39:z:552:A:H8	1.58	0.69
1:2:947:C:H2'	1:2:948:G:H8	1.57	0.69
1:2:1584:A:H5''	23:V:82:ARG:HD2	1.75	0.69
1:2:1138:G:N2	1:2:1141:A:OP2	2.22	0.69
33:f:121:CYS:HB3	33:f:132:MET:HB2	1.75	0.69
29:b:83:VAL:HG23	29:b:84:VAL:HG23	1.75	0.68
1:2:1279:C:H42	16:O:102:LYS:HA	1.58	0.68
1:2:1491:G:N2	32:e:42:CYS:SG	2.65	0.68
5:D:83:LYS:HD3	5:D:106:THR:HG23	1.75	0.68
1:2:814:A:OP1	13:L:80:ARG:NH2	2.26	0.68
26:Y:94:LEU:HD11	26:Y:100:GLY:HA3	1.75	0.68
30:c:18:LYS:HD2	30:c:22:LYS:HD2	1.75	0.68
38:y:48:G:N2	39:z:550:A:O2'	2.26	0.68
1:2:275:C:N3	1:2:887:G:O2'	2.26	0.68
1:2:1060:C:OP1	18:Q:149:ARG:NH2	2.27	0.68
38:y:25:G:O6	38:y:43:A:N1	2.26	0.68
1:2:957:G:N3	39:z:831:A:N6	2.42	0.68
4:C:148:CYS:SG	4:C:152:SER:OG	2.49	0.68
7:F:137:VAL:HB	7:F:185:LYS:HB3	1.76	0.68
15:N:31:GLU:HG2	15:N:33:LEU:H	1.59	0.68
34:g:13:GLY:HA3	34:g:43:TRP:HH2	1.58	0.68
9:H:22:LYS:NZ	9:H:98:GLU:OE1	2.27	0.68
1:2:106:C:H2'	1:2:107:A:H8	1.59	0.68
12:K:199:LEU:HD13	12:K:202:ILE:HD11	1.75	0.68
1:2:1370:C:OP2	21:T:7:LYS:NZ	2.27	0.68
8:G:192:ILE:HG13	8:G:243:GLY:HA3	1.74	0.68
38:y:29:G:H2'	38:y:30:G:C8	2.28	0.68
39:z:518:C:H2'	39:z:519:C:C6	2.29	0.68
1:2:800:U:O2	1:2:855:G:N2	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:865:A:C6	11:J:114:GLN:HB3	2.29	0.67
1:2:842:G:C4	8:G:19:MET:HE1	2.29	0.67
1:2:1450:A:H5''	21:T:3:ARG:HH12	1.59	0.67
6:E:151:ARG:NH2	6:E:233:TYR:O	2.27	0.67
11:J:23:ILE:HG13	11:J:87:PHE:HE2	1.56	0.67
1:2:511:A:OP1	13:L:45:ARG:NH1	2.27	0.67
1:2:1536:G:N3	23:V:12:GLN:NE2	2.40	0.67
12:K:151:GLU:O	12:K:155:ASN:ND2	2.28	0.67
20:S:23:ALA:HB1	20:S:68:ILE:HD11	1.76	0.67
39:z:551:C:H2'	39:z:552:A:C8	2.29	0.67
1:2:923:C:O2	30:c:51:GLN:NE2	2.28	0.67
11:J:75:ILE:HG23	11:J:76:GLN:H	1.59	0.67
1:2:492:C:N3	28:a:84:LYS:NZ	2.42	0.67
1:2:995:G:H3'	29:b:17:HIS:CE1	2.29	0.67
1:2:1490:U:H4'	1:2:1491:G:H5''	1.75	0.67
1:2:1857:A:OP2	29:b:4:LYS:NZ	2.26	0.67
26:Y:11:LEU:HD21	26:Y:74:VAL:HB	1.77	0.67
19:R:41:GLN:HG3	19:R:84:ILE:HD12	1.77	0.67
1:2:1117:G:O2'	5:D:204:ILE:O	2.12	0.67
13:L:84:ILE:HD11	13:L:148:ILE:HG22	1.77	0.67
15:N:11:GLN:HB2	15:N:56:ILE:HG21	1.76	0.67
1:2:526:A:H62	1:2:537:G:H21	1.39	0.67
8:G:72:ILE:HD11	8:G:88:ASP:HB3	1.77	0.67
1:2:73:C:O2	1:2:74:G:H1'	1.95	0.67
1:2:1474:U:H2'	1:2:1475:G:C8	2.30	0.67
4:C:10:MET:HG2	21:T:111:PHE:HE2	1.60	0.67
8:G:11:ARG:HA	8:G:28:ALA:HB2	1.76	0.67
20:S:130:LYS:HA	20:S:137:ALA:HA	1.76	0.67
1:2:915:A:OP1	26:Y:57:ARG:NH1	2.28	0.66
11:J:65:PRO:O	11:J:98:ARG:NH2	2.28	0.66
34:g:155:ARG:HG2	34:g:198:VAL:HG23	1.77	0.66
1:2:1155:G:OP2	27:Z:5:ARG:NH1	2.28	0.66
35:h:62:VAL:HG11	35:h:96:LEU:HB3	1.77	0.66
38:y:11:C:N4	38:y:24:U:H3	1.93	0.66
1:2:411:G:H5'	15:N:98:LYS:HG3	1.77	0.66
1:2:835:C:H1'	1:2:837:G:H1'	1.78	0.66
6:E:93:LYS:HG3	6:E:218:LEU:HD21	1.77	0.66
38:y:3:C:H2'	38:y:4:A:C8	2.30	0.66
1:2:668:U:H3	1:2:1023:A:N6	1.93	0.66
1:2:957:G:C2	39:z:831:A:N6	2.62	0.66
9:H:55:ARG:NH2	20:S:123:ASP:OD1	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1451:A:H61	1:2:1467:C:H42	1.42	0.66
1:2:1555:U:HO2'	1:2:1578:C:HO2'	1.42	0.66
1:2:1773:G:H2'	1:2:1774:G:C8	2.31	0.66
1:2:124:U:H3	1:2:330:C:H42	0.76	0.66
20:S:31:LEU:HD22	20:S:67:ASP:HB3	1.78	0.66
1:2:1091:U:O3'	26:Y:20:ARG:NH1	2.29	0.66
12:K:37:LYS:NZ	12:K:93:THR:O	2.29	0.66
13:L:38:ARG:HA	36:i:105:ARG:HB3	1.78	0.66
1:2:1245:C:H5''	1:2:1246:A:H2'	1.78	0.66
36:i:118:ASN:H	36:i:119:VAL:HA	1.61	0.66
39:z:595:C:H2'	39:z:596:A:H8	1.61	0.66
1:2:77:A:H4'	10:I:176:ILE:HD12	1.76	0.66
1:2:166:A:H2'	1:2:167:G:H8	1.61	0.66
1:2:841:G:H2'	1:2:842:G:C8	2.30	0.66
10:I:51:ARG:NH1	10:I:52:ILE:O	2.29	0.66
11:J:139:ILE:O	17:P:19:ARG:NH1	2.27	0.66
14:M:3:MET:O	14:M:8:ARG:NH1	2.28	0.66
1:2:67:C:N4	1:2:151:C:O2'	2.29	0.65
1:2:1700:C:O2'	37:l:2:ARG:NH2	2.29	0.65
1:2:1717:G:N2	1:2:1806:U:O2	2.27	0.65
12:K:73:THR:O	12:K:74:ARG:NH1	2.26	0.65
15:N:60:CYS:SG	15:N:63:THR:OG1	2.54	0.65
1:2:492:C:O3'	8:G:62:LYS:NZ	2.29	0.65
1:2:526:A:H62	1:2:537:G:N2	1.93	0.65
26:Y:47:ILE:HD11	26:Y:63:VAL:HG11	1.78	0.65
1:2:940:A:N6	1:2:978:G:H1	1.94	0.65
1:2:1309:A:OP2	16:O:33:ARG:NH2	2.29	0.65
5:D:46:LYS:HE3	18:Q:27:VAL:HB	1.78	0.65
26:Y:94:LEU:HD12	26:Y:95:PRO:HD2	1.76	0.65
1:2:59:U:H5'	1:2:493:C:H41	1.61	0.65
8:G:230:LYS:HB3	8:G:233:LYS:HB2	1.77	0.65
22:U:23:ARG:O	22:U:55:ARG:NH1	2.29	0.65
1:2:940:A:H5''	18:Q:134:PRO:HB2	1.79	0.65
14:M:64:TRP:O	32:e:22:ARG:NH2	2.30	0.65
20:S:138:ARG:NH1	20:S:138:ARG:O	2.28	0.65
14:M:49:MET:HE3	14:M:69:TRP:CD1	2.31	0.65
1:2:667:G:N1	1:2:1023:A:OP2	2.25	0.65
1:2:957:G:H21	39:z:831:A:N6	1.94	0.65
8:G:64:ILE:HD11	28:a:18:LEU:HG	1.79	0.65
19:R:15:PHE:HB3	22:U:91:LYS:HD3	1.77	0.65
22:U:99:LEU:O	22:U:103:LEU:N	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1709:U:H2'	1:2:1710:A:H8	1.61	0.65
4:C:85:ARG:NH1	4:C:201:LEU:O	2.30	0.65
29:b:37:LYS:NZ	29:b:71:LEU:O	2.29	0.65
1:2:487:C:H4'	8:G:8:HIS:HD2	1.60	0.65
1:2:1457:G:H3'	1:2:1459:U:H3	1.62	0.65
4:C:56:GLU:OE2	25:X:82:ASN:ND2	2.29	0.65
1:2:745:U:H2'	1:2:746:C:C6	2.31	0.65
1:2:1099:C:H2'	1:2:1100:G:C8	2.31	0.65
1:2:1211:C:H42	1:2:1216:A:H61	1.44	0.65
1:2:365:U:H2'	1:2:366:A:C8	2.32	0.64
7:F:104:SER:HA	7:F:107:TYR:CE1	2.32	0.64
8:G:31:PRO:HG3	8:G:43:PRO:HG3	1.77	0.64
10:I:8:PRO:HD2	10:I:113:ILE:HG22	1.79	0.64
15:N:101:ARG:HB2	27:Z:10:ALA:HB2	1.79	0.64
17:P:119:GLU:OE2	17:P:123:HIS:NE2	2.29	0.64
1:2:941:U:H2'	1:2:942:U:C6	2.32	0.64
1:2:1152:U:O4	6:E:179:ARG:NH1	2.30	0.64
20:S:32:ILE:HB	20:S:39:LEU:HD21	1.79	0.64
1:2:1198:U:H2'	1:2:1199:G:H8	1.61	0.64
18:Q:34:PHE:HB3	18:Q:41:PHE:HB2	1.78	0.64
1:2:166:A:H2'	1:2:167:G:C8	2.33	0.64
1:2:815:G:OP2	13:L:80:ARG:NH1	2.30	0.64
1:2:847:C:H5''	1:2:848:G:H5'	1.79	0.64
4:C:141:ASN:ND2	25:X:31:SER:O	2.30	0.64
1:2:903:G:H2'	1:2:904:A:C8	2.32	0.64
14:M:5:LYS:HA	14:M:8:ARG:HD2	1.79	0.64
15:N:80:MET:SD	15:N:86:ILE:HD12	2.38	0.64
39:z:575:A:H8	39:z:576:C:H4'	1.63	0.64
1:2:922:A:H61	1:2:1011:U:H5	1.45	0.64
1:2:1240:U:H2'	1:2:1241:G:H8	1.62	0.64
16:O:126:GLU:HA	16:O:129:LYS:HG2	1.80	0.64
19:R:10:ARG:NH1	19:R:10:ARG:O	2.27	0.64
34:g:39:THR:HG22	34:g:60:ARG:HG2	1.79	0.64
1:2:1276:G:H1	1:2:1313:U:H3	1.45	0.64
24:W:61:LEU:HD23	24:W:82:MET:HG2	1.79	0.64
1:2:1519:G:O2'	38:y:29:G:OP1	2.14	0.64
8:G:43:PRO:HD2	8:G:46:ILE:HD12	1.80	0.64
19:R:17:TYR:HA	22:U:91:LYS:HG2	1.80	0.64
1:2:1333:C:HO2'	24:W:68:THR:HG1	1.44	0.63
1:2:1588:C:OP2	35:h:104:ARG:NH1	2.31	0.63
1:2:1007:A:H5''	17:P:3:ARG:HH22	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:102:PHE:CE1	27:Z:7:LEU:HB3	2.33	0.63
28:a:11:LYS:HB2	28:a:24:VAL:HG12	1.80	0.63
39:z:595:C:H2'	39:z:596:A:C8	2.33	0.63
1:2:1491:G:N2	32:e:45:GLN:OE1	2.31	0.63
5:D:136:HIS:HB3	5:D:216:LYS:HB2	1.79	0.63
16:O:35:ILE:HG13	33:f:103:LEU:HD13	1.80	0.63
18:Q:44:VAL:HG13	18:Q:53:ILE:HG13	1.81	0.63
1:2:606:A:H5''	27:Z:68:LYS:HZ1	1.63	0.63
1:2:1282:G:N2	1:2:1308:G:O2'	2.26	0.63
4:C:113:GLN:HB2	4:C:116:PHE:HB2	1.81	0.63
30:c:19:HIS:ND1	30:c:21:LYS:HB3	2.13	0.63
1:2:948:G:H21	18:Q:52:THR:HG21	1.63	0.63
1:2:980:C:O2'	18:Q:138:ASP:O	2.11	0.63
1:2:1054:A:OP1	38:y:37:A:O2'	2.17	0.63
1:2:1560:C:N4	1:2:1561:G:O6	2.31	0.63
1:2:1655:C:O5'	32:e:32:ARG:NH2	2.32	0.63
6:E:187:THR:N	6:E:206:ASP:OD2	2.32	0.63
7:F:1:MET:HG2	7:F:4:GLN:HB2	1.78	0.63
13:L:93:LYS:HB2	13:L:96:TYR:HD2	1.64	0.63
17:P:62:GLN:HG3	17:P:65:PHE:CD2	2.30	0.63
38:y:11:C:N4	38:y:24:U:N3	2.46	0.63
38:y:52:G:H21	38:y:53:A:H62	1.47	0.63
1:2:370:G:H5''	12:K:31:ARG:HH21	1.64	0.63
1:2:874:G:H22	1:2:904:A:H2	1.44	0.63
1:2:1139:A:H2'	1:2:1140:A:C8	2.34	0.63
1:2:1558:G:OP1	23:V:121:ARG:NH1	2.32	0.63
10:I:85:ARG:O	10:I:87:ARG:NH1	2.32	0.63
7:F:204:LEU:HD13	7:F:209:SER:H	1.63	0.63
18:Q:142:ARG:NH1	29:b:27:ALA:HB1	2.14	0.63
1:2:1198:U:O2	6:E:100:GLN:NE2	2.21	0.62
5:D:179:ASN:HB3	5:D:183:GLU:HG3	1.80	0.62
12:K:191:GLU:O	15:N:18:GLN:NE2	2.32	0.62
1:2:483:A:H62	1:2:499:G:H21	1.47	0.62
5:D:103:MET:HG3	5:D:215:VAL:HB	1.81	0.62
6:E:79:ILE:HG12	6:E:147:ILE:HD12	1.81	0.62
1:2:1802:U:H2'	1:2:1803:A:C8	2.34	0.62
1:2:1508:C:H4'	32:e:7:TYR:HE2	1.64	0.62
31:d:20:ARG:NH2	31:d:25:GLY:O	2.31	0.62
5:D:72:ALA:O	5:D:76:ASN:ND2	2.32	0.62
5:D:107:ARG:HA	5:D:110:MET:HE2	1.80	0.62
14:M:48:ALA:O	14:M:51:SER:OG	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:645:A:H4'	1:2:646:G:H3'	1.80	0.62
9:H:175:ASP:OD1	9:H:179:ASN:ND2	2.33	0.62
18:Q:32:HIS:HA	18:Q:96:LYS:HB3	1.80	0.62
19:R:8:LYS:HE2	19:R:14:LYS:HD2	1.82	0.62
22:U:26:ILE:HG12	22:U:59:LEU:HD11	1.80	0.62
1:2:155:G:H2'	1:2:156:G:H8	1.65	0.62
1:2:162:C:O2'	10:I:95:LYS:NZ	2.31	0.62
8:G:128:LYS:H	8:G:140:VAL:HB	1.62	0.62
11:J:46:THR:HG21	11:J:97:GLN:HG2	1.80	0.62
21:T:31:ASN:ND2	21:T:55:THR:OG1	2.27	0.62
1:2:109:U:O2'	15:N:71:ARG:NH2	2.33	0.62
1:2:1409:G:H2'	1:2:1410:A:H8	1.64	0.62
1:2:1736:U:OP1	12:K:42:ARG:NH1	2.33	0.62
5:D:23:ASP:O	5:D:27:LYS:NZ	2.33	0.62
8:G:10:LYS:HA	8:G:27:PHE:HA	1.79	0.62
30:c:18:LYS:O	30:c:23:ARG:NH1	2.28	0.62
1:2:965:U:H3'	1:2:966:G:H21	1.63	0.62
1:2:1090:C:O2	26:Y:16:ASN:ND2	2.32	0.62
1:2:1534:U:H2'	1:2:1535:G:C8	2.35	0.62
5:D:51:ARG:O	5:D:53:GLN:NE2	2.31	0.62
7:F:135:GLU:N	7:F:135:GLU:OE1	2.32	0.62
28:a:114:MET:HE2	28:a:124:ASN:HD21	1.65	0.62
34:g:258:ILE:HG23	34:g:267:VAL:HB	1.81	0.62
38:y:57:A:O2'	38:y:59:A:OP2	2.18	0.62
1:2:76:U:H4'	10:I:154:ARG:HA	1.82	0.61
1:2:640:A:OP2	27:Z:108:LYS:NZ	2.28	0.61
5:D:28:LYS:NZ	18:Q:51:GLU:OE2	2.33	0.61
15:N:136:LYS:O	15:N:139:ARG:NH1	2.33	0.61
21:T:106:LEU:HD13	21:T:109:LEU:HD13	1.80	0.61
1:2:951:A:H4'	1:2:952:G:H4'	1.81	0.61
7:F:12:VAL:HG11	32:e:36:LEU:HD21	1.82	0.61
8:G:88:ASP:OD1	8:G:122:LYS:NZ	2.33	0.61
11:J:19:PHE:O	11:J:23:ILE:HD12	2.00	0.61
1:2:1013:U:OP2	17:P:55:ARG:NH1	2.33	0.61
1:2:1531:G:H2'	1:2:1532:A:H8	1.65	0.61
1:2:1755:U:O2	1:2:1765:G:N2	2.33	0.61
19:R:34:MET:SD	19:R:35:GLN:NE2	2.73	0.61
7:F:62:LYS:HA	14:M:96:ARG:HG3	1.82	0.61
15:N:102:PHE:O	27:Z:8:ARG:HA	2.00	0.61
1:2:1300:U:H2'	1:2:1301:C:C6	2.36	0.61
39:z:525:A:H3'	39:z:526:G:H21	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:185:C:H2'	1:2:186:G:H8	1.65	0.61
12:K:31:ARG:HD2	12:K:56:ARG:HH21	1.66	0.61
1:2:914:U:O2'	26:Y:57:ARG:NH1	2.34	0.61
1:2:1139:A:OP1	6:E:175:SER:OG	2.18	0.61
1:2:1382:A:OP2	7:F:160:SER:OG	2.16	0.61
17:P:118:ILE:HG22	17:P:121:ARG:HH12	1.66	0.61
30:c:11:SER:HB2	30:c:15:GLU:HB2	1.83	0.61
35:h:57:LYS:HE3	35:h:61:GLU:HB3	1.82	0.61
1:2:124:U:OP1	8:G:148:ARG:NH2	2.33	0.61
1:2:202:U:H2'	1:2:203:G:C8	2.34	0.61
1:2:378:U:H2'	1:2:379:A:H8	1.66	0.61
6:E:153:GLY:N	6:E:164:THR:O	2.30	0.61
10:I:1:MET:N	10:I:18:VAL:O	2.34	0.61
1:2:1284:U:H3	1:2:1307:C:H42	0.72	0.61
9:H:77:MET:O	9:H:83:ASN:ND2	2.34	0.61
21:T:15:VAL:O	21:T:19:LYS:HG2	2.01	0.61
23:V:28:LEU:HD22	23:V:110:LEU:HD11	1.83	0.61
1:2:629:C:H2'	1:2:630:A:H8	1.66	0.61
1:2:1295:A:OP1	19:R:59:ARG:NH1	2.34	0.61
7:F:175:VAL:HG23	7:F:182:LEU:HB2	1.83	0.61
12:K:10:LYS:HD2	15:N:136:LYS:HE2	1.82	0.61
19:R:10:ARG:CZ	19:R:17:TYR:HB3	2.31	0.61
19:R:86:LEU:H	19:R:89:MET:HE2	1.65	0.61
1:2:832:G:N2	1:2:834:G:OP2	2.33	0.60
1:2:1179:A:OP2	37:l:18:ARG:NH1	2.33	0.60
1:2:1427:G:H2'	1:2:1428:U:C5	2.35	0.60
28:a:12:PHE:HE1	28:a:21:LYS:HB3	1.65	0.60
30:c:20:LYS:HD2	30:c:28:PRO:HA	1.81	0.60
5:D:80:ALA:O	5:D:83:LYS:NZ	2.26	0.60
8:G:26:VAL:HG13	8:G:27:PHE:HD1	1.65	0.60
39:z:599:G:H2'	39:z:600:G:C8	2.37	0.60
1:2:106:C:H2'	1:2:107:A:C8	2.36	0.60
1:2:866:A:N6	1:2:912:A:O5'	2.33	0.60
1:2:1546:U:H2'	1:2:1547:G:C4	2.37	0.60
4:C:4:ALA:HB3	4:C:8:LEU:HB2	1.84	0.60
24:W:70:CYS:H	32:e:40:ARG:HH22	1.48	0.60
1:2:1659:A:O2'	1:2:1660:G:H5'	2.02	0.60
12:K:45:THR:HG22	12:K:53:LYS:HD2	1.82	0.60
1:2:345:G:OP1	15:N:105:ARG:NH1	2.34	0.60
1:2:599:U:H2'	1:2:600:G:C8	2.37	0.60
1:2:1344:G:H22	1:2:1377:G:H1	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1371:G:H2'	1:2:1372:A:C8	2.35	0.60
1:2:1724:U:O2	1:2:1799:G:N2	2.33	0.60
6:E:189:ILE:HB	6:E:196:LYS:HD3	1.83	0.60
15:N:40:ILE:HG23	15:N:68:ILE:HD13	1.83	0.60
18:Q:27:VAL:H	18:Q:91:THR:HG1	1.48	0.60
20:S:37:ARG:HG2	23:V:7:LYS:HB3	1.84	0.60
28:a:106:GLN:HE21	28:a:107:ARG:HG3	1.65	0.60
39:z:589:C:H2'	39:z:590:A:C8	2.37	0.60
1:2:378:U:H2'	1:2:379:A:C8	2.36	0.60
1:2:444:U:H2'	1:2:445:A:H8	1.66	0.60
9:H:54:GLY:O	20:S:125:ARG:NH1	2.33	0.60
12:K:165:GLN:HG3	12:K:170:LYS:O	2.01	0.60
15:N:101:ARG:NH1	27:Z:6:GLY:O	2.34	0.60
20:S:146:ARG:NH1	38:y:34:A:OP2	2.34	0.60
34:g:5:MET:HE1	34:g:312:VAL:HG22	1.83	0.60
1:2:1300:U:H5''	33:f:92:LYS:HD2	1.82	0.60
4:C:58:LEU:HD11	4:C:178:LEU:HB3	1.82	0.60
19:R:17:TYR:HA	22:U:91:LYS:HA	1.83	0.60
1:2:1224:A:H2'	1:2:1225:G:C8	2.37	0.60
4:C:68:ILE:HD11	4:C:121:LEU:HG	1.84	0.60
4:C:122:LEU:HD23	4:C:142:LEU:HG	1.83	0.60
13:L:170:PRO:HB3	13:L:174:LYS:HD2	1.84	0.60
9:H:71:ARG:NH2	9:H:148:ASN:OD1	2.34	0.60
11:J:46:THR:HB	11:J:65:PRO:HG3	1.84	0.60
1:2:668:U:OP2	1:2:1022:C:N4	2.35	0.59
1:2:1626:U:O3'	22:U:34:LYS:NZ	2.35	0.59
14:M:32:HIS:HB2	14:M:40:VAL:HB	1.84	0.59
24:W:25:THR:O	24:W:111:GLU:HB2	2.01	0.59
24:W:82:MET:HE1	32:e:52:PHE:HB2	1.84	0.59
30:c:34:ASP:HB3	30:c:80:ARG:HG3	1.84	0.59
32:e:31:ILE:HG23	32:e:33:LYS:HZ3	1.66	0.59
1:2:360:G:N2	1:2:362:U:O4	2.35	0.59
22:U:115:LYS:NZ	39:z:566:C:OP1	2.35	0.59
23:V:10:ASN:H	23:V:144:LYS:HE2	1.66	0.59
24:W:51:LYS:HD2	24:W:90:ASP:HB3	1.84	0.59
39:z:564:G:H2'	39:z:565:G:H8	1.68	0.59
1:2:483:A:N6	1:2:500:G:H1'	2.14	0.59
1:2:1571:G:H2'	1:2:1572:G:C8	2.37	0.59
1:2:220:C:H2'	1:2:221:A:C8	2.37	0.59
1:2:1259:U:O2	32:e:16:GLN:NE2	2.36	0.59
1:2:1587:C:H5''	9:H:91:ARG:HH12	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:42:GLY:O	10:I:46:LYS:NZ	2.35	0.59
15:N:94:HIS:HB2	15:N:105:ARG:HD2	1.83	0.59
1:2:1281:G:N1	33:f:103:LEU:O	2.35	0.59
7:F:193:ASP:HB3	7:F:194:PRO:HD3	1.83	0.59
19:R:85:ILE:HD13	19:R:111:MET:HB3	1.83	0.59
28:a:87:PRO:HD2	28:a:90:ARG:HD2	1.83	0.59
1:2:1199:G:H4'	6:E:101:THR:HA	1.85	0.59
1:2:1540:A:H2'	1:2:1541:G:C8	2.37	0.59
1:2:1775:A:H2'	1:2:1776:G:C8	2.37	0.59
29:b:19:GLN:NE2	29:b:20:PRO:O	2.34	0.59
1:2:537:G:H2'	1:2:538:C:C6	2.38	0.59
1:2:784:G:H4'	10:I:237:LEU:HB2	1.83	0.59
1:2:800:U:OP1	26:Y:82:GLN:NE2	2.35	0.59
1:2:1493:G:N7	14:M:25:LYS:NZ	2.51	0.59
4:C:140:VAL:HA	6:E:72:PRO:HG2	1.84	0.59
13:L:152:ASP:OD1	13:L:153:SER:N	2.36	0.59
30:c:1:MET:HG3	30:c:3:LEU:H	1.68	0.59
1:2:155:G:H2'	1:2:156:G:C8	2.37	0.59
1:2:538:C:H2'	1:2:539:C:H6	1.68	0.59
17:P:58:HIS:HB2	17:P:60:VAL:HG12	1.84	0.59
19:R:38:SER:HB2	19:R:41:GLN:HB2	1.85	0.59
27:Z:71:ARG:HG2	27:Z:82:THR:HG22	1.84	0.59
34:g:31:ILE:HG22	34:g:43:TRP:HB2	1.84	0.59
1:2:1259:U:H1'	32:e:16:GLN:HE21	1.66	0.59
19:R:32:GLN:OE1	19:R:32:GLN:N	2.35	0.59
1:2:1161:G:OP2	1:2:1161:G:N2	2.30	0.58
1:2:1648:U:O2	1:2:1666:G:N2	2.22	0.58
33:f:105:TYR:HB2	33:f:131:PHE:HE2	1.68	0.58
1:2:16:G:H2'	1:2:17:C:C6	2.37	0.58
1:2:918:A:OP1	26:Y:28:ARG:NH1	2.29	0.58
1:2:1083:A:OP1	29:b:3:LYS:NZ	2.23	0.58
1:2:1623:C:H2'	1:2:1624:C:C6	2.38	0.58
4:C:54:THR:HG22	4:C:162:PRO:HB2	1.85	0.58
5:D:121:ILE:HD12	5:D:161:VAL:HG13	1.85	0.58
8:G:63:LYS:HA	8:G:66:MET:HE2	1.85	0.58
16:O:13:ASP:HB3	16:O:16:THR:HG22	1.85	0.58
35:h:82:SER:O	35:h:85:ARG:HG2	2.03	0.58
17:P:45:LEU:HB3	17:P:49:GLN:HB2	1.85	0.58
23:V:87:VAL:HG13	23:V:88:MET:HE2	1.85	0.58
39:z:564:G:H2'	39:z:565:G:C8	2.38	0.58
1:2:671:U:H5''	27:Z:8:ARG:HG3	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:65:C:N4	1:2:169:U:O2'	2.37	0.58
1:2:1534:U:H2'	1:2:1535:G:H8	1.67	0.58
4:C:89:LYS:HE3	4:C:201:LEU:HG	1.86	0.58
4:C:130:ASP:HB3	4:C:133:PRO:HG2	1.85	0.58
21:T:12:ALA:O	21:T:16:ILE:HG12	2.04	0.58
24:W:66:ARG:HA	24:W:77:TRP:CD1	2.39	0.58
1:2:1193:G:H2'	1:2:1194:G:H8	1.66	0.58
6:E:101:THR:HG23	6:E:103:ALA:H	1.69	0.58
10:I:18:VAL:HB	10:I:23:LYS:HZ1	1.68	0.58
33:f:139:HIS:HB2	33:f:150:PHE:HB2	1.85	0.58
38:y:11:C:N3	38:y:24:U:O2	2.37	0.58
1:2:644:A:OP2	1:2:645:A:O2'	2.18	0.58
1:2:1647:G:N2	1:2:1667:U:O2	2.24	0.58
1:2:1847:C:H2'	1:2:1848:U:C6	2.39	0.58
11:J:63:PHE:HB3	11:J:97:GLN:HB3	1.85	0.58
11:J:157:HIS:HB3	11:J:190:PRO:HG3	1.85	0.58
1:2:158:A:H2'	1:2:159:A:C8	2.39	0.58
1:2:165:G:H2'	1:2:166:A:C8	2.38	0.58
1:2:427:G:H3'	1:2:428:G:H21	1.67	0.58
12:K:3:ILE:HB	12:K:30:GLY:HA3	1.84	0.58
17:P:23:PRO:HB2	17:P:25:TRP:CZ3	2.38	0.58
19:R:18:ARG:HE	19:R:36:LEU:HB3	1.68	0.58
7:F:115:VAL:HG11	7:F:142:LEU:HD21	1.86	0.58
7:F:140:GLY:HA3	7:F:182:LEU:HD23	1.85	0.58
8:G:197:ASN:HB3	8:G:209:HIS:HB2	1.83	0.58
11:J:129:ILE:HD11	11:J:180:LEU:HD13	1.86	0.58
12:K:23:LYS:O	12:K:25:ARG:NH1	2.37	0.58
17:P:106:ARG:NH1	17:P:106:ARG:O	2.36	0.58
22:U:63:GLU:OE1	22:U:66:ARG:NH2	2.36	0.58
23:V:57:ALA:O	23:V:60:THR:OG1	2.15	0.58
1:2:633:A:OP2	13:L:38:ARG:NH1	2.36	0.58
11:J:41:ARG:HH11	11:J:42:GLU:H	1.52	0.58
14:M:17:LYS:HA	14:M:89:ILE:HD11	1.85	0.58
23:V:44:GLU:OE1	23:V:44:GLU:N	2.37	0.58
28:a:20:ARG:HD2	28:a:74:MET:HE2	1.86	0.58
29:b:10:ARG:HB3	29:b:33:ASP:O	2.04	0.58
1:2:116:U:O4	1:2:337:G:O6	2.21	0.57
1:2:332:C:H2'	1:2:333:A:H8	1.68	0.57
1:2:403:G:N2	1:2:415:G:H1'	2.19	0.57
1:2:1255:A:N6	1:2:1514:U:O5'	2.37	0.57
1:2:1562:G:H21	1:2:1562:G:P	2.26	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1598:G:N7	22:U:24:ARG:NH1	2.51	0.57
9:H:20:PHE:HA	9:H:48:TYR:HA	1.87	0.57
19:R:17:TYR:OH	19:R:18:ARG:NH2	2.37	0.57
22:U:61:GLU:HA	22:U:64:VAL:HG12	1.86	0.57
27:Z:100:VAL:HG12	27:Z:125:VAL:HG12	1.85	0.57
28:a:5:VAL:O	28:a:43:LYS:NZ	2.37	0.57
1:2:538:C:H2'	1:2:539:C:C6	2.38	0.57
1:2:1328:A:O2'	7:F:145:GLN:O	2.21	0.57
1:2:1574:A:O2'	1:2:1576:C:OP2	2.20	0.57
5:D:139:CYS:HA	5:D:212:VAL:HA	1.86	0.57
11:J:97:GLN:O	11:J:98:ARG:NE	2.37	0.57
14:M:8:ARG:HG2	14:M:12:TYR:HE2	1.69	0.57
17:P:96:VAL:HG23	17:P:99:ARG:HE	1.69	0.57
23:V:76:THR:HG22	23:V:94:ARG:HB3	1.85	0.57
38:y:3:C:H2'	38:y:4:A:H8	1.66	0.57
1:2:1388:U:H3	1:2:1474:U:H3	1.51	0.57
1:2:1716:U:H4'	1:2:1717:G:H5''	1.86	0.57
20:S:124:PRO:O	20:S:126:ARG:NH1	2.37	0.57
23:V:33:TRP:HZ2	23:V:102:ARG:HG3	1.68	0.57
1:2:125:C:OP2	10:I:198:ARG:NH2	2.37	0.57
1:2:921:G:H5''	17:P:91:LEU:HD21	1.86	0.57
1:2:1140:A:H2'	1:2:1141:A:C8	2.39	0.57
3:B:261:SER:HA	3:B:279:ALA:HA	1.86	0.57
29:b:44:ILE:HB	29:b:64:LEU:HD11	1.86	0.57
1:2:431:C:H2'	1:2:432:C:C6	2.40	0.57
1:2:1019:A:H2'	1:2:1020:A:C8	2.40	0.57
1:2:1160:G:H2'	1:2:1161:G:N3	2.19	0.57
1:2:1213:A:H2'	1:2:1214:C:C6	2.39	0.57
15:N:133:PRO:HG3	15:N:139:ARG:HG3	1.86	0.57
26:Y:53:ILE:N	26:Y:60:LYS:O	2.21	0.57
1:2:168:C:O2'	10:I:133:LEU:O	2.21	0.57
1:2:291:U:H2'	1:2:292:A:H8	1.68	0.57
6:E:191:SER:CB	6:E:196:LYS:HE3	2.35	0.57
7:F:8:LYS:HE2	24:W:59:LYS:HG2	1.86	0.57
24:W:50:VAL:HG23	24:W:91:LEU:HG	1.86	0.57
26:Y:11:LEU:O	26:Y:15:ASN:ND2	2.37	0.57
28:a:15:ASN:ND2	28:a:20:ARG:HE	2.02	0.57
1:2:788:C:HO2'	1:2:789:G:H8	1.51	0.57
1:2:842:G:OP2	8:G:108:ARG:NH2	2.38	0.57
1:2:1409:G:H2'	1:2:1410:A:C8	2.39	0.57
17:P:61:ALA:HB2	30:c:32:PHE:HZ	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:40:GLU:O	20:S:41:MET:HE2	2.05	0.57
25:X:21:ASN:HD21	26:Y:66:THR:HB	1.70	0.57
1:2:1211:C:H42	1:2:1216:A:N6	2.02	0.57
5:D:168:MET:O	5:D:172:MET:HG3	2.05	0.57
12:K:48:VAL:HG22	12:K:49:ARG:H	1.68	0.57
14:M:59:LYS:HE2	14:M:72:THR:HG22	1.86	0.57
34:g:88:ARG:HB3	34:g:90:TRP:NE1	2.18	0.57
1:2:732:C:N4	1:2:733:G:O6	2.37	0.57
1:2:1375:A:H2'	1:2:1376:C:C6	2.40	0.57
19:R:78:THR:N	19:R:95:GLY:O	2.36	0.57
20:S:11:GLN:HA	20:S:24:HIS:HA	1.86	0.57
28:a:7:ILE:HG23	28:a:25:ILE:HD11	1.86	0.57
36:i:89:GLN:N	36:i:89:GLN:OE1	2.38	0.57
1:2:149:A:N7	1:2:169:U:C4	2.73	0.56
1:2:833:A:H5''	28:a:47:MET:HE1	1.85	0.56
1:2:957:G:H4'	9:H:131:ALA:HB1	1.87	0.56
1:2:1320:G:H2'	1:2:1321:G:C8	2.40	0.56
1:2:1664:G:H5'	24:W:79:ARG:HH22	1.69	0.56
1:2:1712:C:O2'	37:l:21:ARG:NH2	2.38	0.56
6:E:83:LEU:HB3	6:E:87:LEU:HD21	1.86	0.56
22:U:123:LEU:HB3	22:U:127:TRP:CZ3	2.40	0.56
38:y:18:G:O5'	38:y:59:A:N6	2.38	0.56
1:2:515:A:N6	1:2:579:G:O6	2.39	0.56
1:2:1732:G:O6	1:2:1791:U:C2	2.58	0.56
1:2:1863:A:N6	5:D:114:VAL:O	2.38	0.56
4:C:187:GLY:O	25:X:45:ARG:NH2	2.34	0.56
24:W:86:LYS:O	24:W:87:ARG:NH1	2.35	0.56
25:X:31:SER:OG	25:X:57:GLY:N	2.36	0.56
38:y:56:G:O2'	38:y:57:A:O4'	2.23	0.56
1:2:28:U:H2'	1:2:29:G:C8	2.40	0.56
1:2:74:G:N7	10:I:170:ARG:NH2	2.49	0.56
1:2:1088:G:H2'	1:2:1089:A:H8	1.70	0.56
1:2:1751:G:O6	1:2:1769:U:O4	2.23	0.56
10:I:5:ILE:HG22	10:I:111:LEU:HD21	1.87	0.56
20:S:90:LYS:HE2	20:S:120:LEU:HA	1.87	0.56
34:g:283:PRO:O	34:g:285:GLN:NE2	2.37	0.56
37:l:8:LYS:HG3	37:l:12:ARG:NH1	2.20	0.56
38:y:54:U:N3	38:y:57:A:OP2	2.38	0.56
1:2:978:G:H2'	1:2:979:A:H8	1.70	0.56
1:2:1545:G:H3'	1:2:1574:A:H61	1.71	0.56
4:C:31:ASP:HB2	4:C:151:ASP:HA	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:149:ASN:OD1	4:C:166:LYS:NZ	2.39	0.56
19:R:94:VAL:HG12	19:R:107:ILE:HD11	1.86	0.56
24:W:94:PRO:HD2	24:W:97:ILE:HD11	1.86	0.56
25:X:40:ASP:OD2	25:X:43:THR:OG1	2.21	0.56
1:2:514:U:H5''	1:2:515:A:H5'	1.88	0.56
1:2:796:U:H2'	1:2:797:U:O4'	2.06	0.56
22:U:45:LEU:HD22	22:U:50:ILE:HD11	1.86	0.56
1:2:62:G:O2'	1:2:172:U:OP1	2.23	0.56
1:2:1537:C:OP1	23:V:62:ARG:NH2	2.32	0.56
1:2:1595:G:O3'	35:h:43:LYS:NZ	2.39	0.56
5:D:137:LEU:HB2	5:D:172:MET:HE1	1.88	0.56
13:L:176:LYS:O	13:L:180:LYS:HG2	2.06	0.56
26:Y:14:ILE:HD13	26:Y:25:VAL:HG21	1.86	0.56
26:Y:53:ILE:HD12	26:Y:60:LYS:HD2	1.87	0.56
33:f:92:LYS:NZ	33:f:94:LYS:HA	2.21	0.56
1:2:202:U:H2'	1:2:203:G:H8	1.71	0.56
1:2:518:A:H2'	1:2:519:A:H8	1.69	0.56
1:2:604:G:H5'	36:i:76:VAL:HG22	1.88	0.56
1:2:1246:A:H4'	24:W:73:GLY:HA2	1.87	0.56
1:2:1611:U:OP2	19:R:43:ARG:NH1	2.36	0.56
1:2:1717:G:H2'	1:2:1718:G:C8	2.41	0.56
9:H:35:LEU:HD21	9:H:146:ARG:HD2	1.87	0.56
10:I:93:LYS:NZ	10:I:94:ARG:O	2.36	0.56
15:N:57:ASP:OD2	15:N:60:CYS:N	2.37	0.56
17:P:52:VAL:HA	17:P:55:ARG:HG2	1.88	0.56
1:2:1199:G:H2'	1:2:1200:A:C8	2.41	0.56
39:z:522:U:H2'	39:z:523:G:H8	1.70	0.56
1:2:53:C:O2'	1:2:497:G:N7	2.39	0.56
1:2:886:U:H5'	1:2:887:G:H5''	1.88	0.56
1:2:1855:G:OP1	29:b:8:ASN:ND2	2.37	0.56
8:G:137:PRO:HG2	8:G:149:TYR:HA	1.88	0.56
10:I:188:LYS:HG3	10:I:191:ARG:HH12	1.70	0.56
16:O:119:GLN:HG2	16:O:121:LYS:HZ3	1.71	0.56
17:P:113:PHE:O	17:P:116:ILE:HG22	2.06	0.56
18:Q:33:ILE:N	18:Q:96:LYS:O	2.38	0.56
19:R:74:GLU:OE1	19:R:74:GLU:N	2.35	0.56
34:g:22:ALA:HB3	34:g:32:LEU:HB2	1.88	0.56
34:g:88:ARG:CB	34:g:90:TRP:HE1	2.17	0.56
10:I:44:GLU:HB3	10:I:48:TYR:HE2	1.71	0.56
13:L:48:PHE:O	13:L:52:LYS:HG2	2.06	0.56
23:V:57:ALA:HB1	23:V:107:LEU:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:126:GLN:NE2	23:V:126:GLN:O	2.38	0.56
34:g:129:ILE:HB	34:g:142:VAL:HB	1.88	0.56
1:2:149:A:N6	1:2:169:U:N3	2.53	0.55
1:2:1304:U:H4'	33:f:133:ALA:HB1	1.87	0.55
26:Y:10:ALA:O	26:Y:14:ILE:HG12	2.05	0.55
1:2:72:C:O4'	1:2:74:G:N2	2.39	0.55
1:2:1232:G:H21	1:2:1517:A:N6	2.03	0.55
1:2:1347:G:H2'	1:2:1348:G:H8	1.70	0.55
6:E:238:PRO:HA	6:E:241:TRP:CE2	2.41	0.55
7:F:6:SER:O	7:F:10:LYS:N	2.38	0.55
8:G:71:LYS:HB2	8:G:91:SER:HB2	1.88	0.55
14:M:2:LEU:HG	14:M:3:MET:HG3	1.88	0.55
28:a:88:LYS:HB2	28:a:97:TYR:HE2	1.71	0.55
39:z:597:A:H2'	39:z:598:A:C8	2.41	0.55
1:2:192:U:O2	1:2:203:G:N2	2.28	0.55
1:2:1170:U:H2'	1:2:1171:G:C8	2.41	0.55
6:E:151:ARG:HD3	6:E:166:ARG:NE	2.21	0.55
10:I:130:PRO:O	10:I:132:ARG:NH1	2.40	0.55
19:R:60:LEU:HD13	19:R:89:MET:HG3	1.88	0.55
20:S:8:GLN:HB2	20:S:27:ARG:HB2	1.87	0.55
1:2:1276:G:H22	1:2:1313:U:H3	1.54	0.55
1:2:1405:A:H2'	1:2:1406:C:O4'	2.07	0.55
1:2:1640:C:O3'	20:S:138:ARG:NE	2.40	0.55
2:A:17:GLU:N	2:A:73:VAL:O	2.32	0.55
4:C:7:VAL:HG11	25:X:43:THR:HA	1.87	0.55
9:H:27:ASP:O	9:H:29:GLN:NE2	2.39	0.55
12:K:100:CYS:SG	12:K:101:ILE:N	2.79	0.55
1:2:367:G:OP1	12:K:99:ASN:ND2	2.39	0.55
7:F:141:LYS:HE2	7:F:180:GLY:HA3	1.89	0.55
8:G:49:ARG:NH1	8:G:56:LEU:O	2.39	0.55
8:G:60:GLU:O	8:G:64:ILE:HG12	2.07	0.55
9:H:75:SER:O	9:H:76:MET:HE2	2.07	0.55
11:J:84:GLU:HG3	11:J:92:VAL:HG12	1.87	0.55
24:W:38:ASP:OD1	24:W:41:ARG:NH1	2.39	0.55
33:f:92:LYS:HZ1	33:f:94:LYS:HA	1.72	0.55
38:y:9:G:N1	38:y:15:G:O6	2.39	0.55
1:2:792:G:H2'	1:2:793:C:O4'	2.07	0.55
1:2:1743:G:O6	1:2:1780:U:O4	2.25	0.55
8:G:87:MET:HG3	8:G:87:MET:O	2.06	0.55
8:G:100:ARG:HB2	8:G:114:ILE:HD13	1.87	0.55
16:O:17:ALA:HA	16:O:124:ILE:HD12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:52:TRP:O	23:V:56:ARG:HG2	2.07	0.55
1:2:624:A:OP1	27:Z:134:TYR:OH	2.21	0.55
21:T:47:ARG:HA	21:T:50:ILE:HG12	1.88	0.55
26:Y:83:LEU:HD12	26:Y:117:ARG:HH21	1.71	0.55
1:2:1266:G:O6	1:2:1507:U:O4	2.23	0.55
1:2:1398:A:N6	1:2:1437:U:O2'	2.40	0.55
1:2:1448:A:N6	1:2:1469:G:O2'	2.39	0.55
1:2:1601:G:N2	1:2:1627:G:O2'	2.36	0.55
38:y:25:G:N1	38:y:43:A:H2	2.02	0.55
1:2:9:U:N3	1:2:12:U:OP2	2.37	0.55
1:2:98:C:OP2	1:2:416:A:O2'	2.23	0.55
1:2:1188:U:OP2	27:Z:119:ARG:NH2	2.33	0.55
1:2:1361:G:H2'	1:2:1362:G:C8	2.42	0.55
1:2:1675:G:H4'	31:d:20:ARG:HD3	1.88	0.55
4:C:31:ASP:HB3	4:C:34:MET:HB2	1.89	0.55
38:y:21:G:H2'	38:y:22:C:C6	2.42	0.55
1:2:370:G:OP1	12:K:56:ARG:NH2	2.40	0.55
1:2:1043:C:H2'	1:2:1044:G:C8	2.41	0.55
1:2:1294:G:N3	19:R:79:HIS:ND1	2.54	0.55
1:2:1688:G:H21	1:2:1828:A:H8	1.54	0.55
1:2:1700:C:H2'	1:2:1701:G:C8	2.41	0.55
17:P:33:VAL:O	17:P:37:ILE:HG12	2.07	0.55
1:2:950:U:H3	1:2:967:G:H1'	1.72	0.54
1:2:1142:C:H2'	1:2:1143:C:C6	2.42	0.54
1:2:1279:C:H4'	33:f:99:LYS:NZ	2.21	0.54
1:2:1571:G:H2'	1:2:1572:G:H8	1.72	0.54
1:2:1586:C:O3'	9:H:88:MET:HE1	2.07	0.54
5:D:218:LEU:O	5:D:219:LYS:HE2	2.07	0.54
7:F:22:ASN:O	7:F:26:THR:HG23	2.06	0.54
10:I:116:LYS:NZ	10:I:125:THR:OG1	2.35	0.54
20:S:29:ASN:N	20:S:67:ASP:OD1	2.37	0.54
25:X:34:MET:HE2	25:X:69:ILE:HD12	1.89	0.54
34:g:238:ALA:H	34:g:251:ALA:HB3	1.72	0.54
1:2:75:G:OP2	1:2:75:G:N2	2.35	0.54
1:2:492:C:O2	8:G:63:LYS:NZ	2.41	0.54
1:2:673:G:N1	1:2:1018:U:OP2	2.37	0.54
1:2:678:U:H5	1:2:736:C:H42	1.55	0.54
1:2:840:U:H2'	1:2:841:G:C8	2.42	0.54
1:2:937:C:H2'	1:2:938:G:C8	2.43	0.54
1:2:949:C:OP2	5:D:19:LYS:NZ	2.39	0.54
1:2:1503:G:C8	33:f:88:PRO:HD2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:70:LYS:O	17:P:74:ILE:HD12	2.06	0.54
22:U:147:GLY:HA2	38:y:27:U:H5''	1.90	0.54
26:Y:78:ARG:NH1	26:Y:126:LEU:HD13	2.23	0.54
27:Z:48:LYS:HE2	27:Z:101:LEU:HD21	1.89	0.54
28:a:100:LYS:NZ	28:a:101:LYS:O	2.36	0.54
1:2:5:U:H2'	1:2:6:G:C8	2.43	0.54
1:2:142:C:N4	1:2:319:G:OP2	2.40	0.54
1:2:900:A:H2'	1:2:901:C:C6	2.42	0.54
1:2:980:C:O2'	18:Q:138:ASP:OD2	2.24	0.54
6:E:106:ARG:HH22	6:E:108:ARG:HH21	1.54	0.54
9:H:21:GLY:H	9:H:48:TYR:HD1	1.53	0.54
23:V:11:GLN:OE1	23:V:62:ARG:NH1	2.40	0.54
24:W:48:LEU:HD23	24:W:91:LEU:HD23	1.89	0.54
28:a:22:GLN:HB2	28:a:72:PHE:HZ	1.73	0.54
29:b:28:CYS:SG	29:b:29:CYS:N	2.80	0.54
33:f:95:ARG:HG3	33:f:97:LYS:H	1.72	0.54
38:y:10:G:C8	38:y:45:G:N2	2.74	0.54
1:2:853:U:H4'	8:G:201:HIS:NE2	2.22	0.54
4:C:205:ARG:HD2	4:C:206:ASP:N	2.23	0.54
6:E:69:PHE:HD2	6:E:71:LEU:HB2	1.70	0.54
6:E:249:SER:HB2	6:E:252:GLN:HE22	1.72	0.54
23:V:13:GLU:OE2	23:V:16:ARG:NH1	2.40	0.54
27:Z:68:LYS:HZ2	36:i:83:VAL:HA	1.73	0.54
28:a:22:GLN:HB2	28:a:72:PHE:CZ	2.42	0.54
29:b:37:LYS:NZ	29:b:70:LYS:HG2	2.22	0.54
34:g:153:CYS:HB3	34:g:198:VAL:HG22	1.89	0.54
39:z:570:A:H3'	39:z:571:A:H8	1.71	0.54
1:2:94:G:OP1	8:G:8:HIS:ND1	2.40	0.54
1:2:921:G:H22	1:2:1013:U:H3	1.55	0.54
1:2:1173:U:H2'	1:2:1174:U:C6	2.42	0.54
1:2:1663:U:OP2	20:S:141:TYR:OH	2.24	0.54
5:D:23:ASP:O	5:D:26:SER:OG	2.24	0.54
5:D:40:ASN:OD1	5:D:75:GLN:NE2	2.40	0.54
5:D:205:TYR:CD1	5:D:206:PRO:HD2	2.42	0.54
6:E:241:TRP:CG	26:Y:68:ARG:HE	2.24	0.54
1:2:579:G:H5''	1:2:580:A:C8	2.43	0.54
1:2:1280:A:H4'	1:2:1281:G:H5''	1.89	0.54
5:D:217:MET:HE3	5:D:220:LYS:HG2	1.88	0.54
6:E:72:PRO:HG3	25:X:29:HIS:CG	2.43	0.54
10:I:64:LYS:HG2	10:I:97:VAL:HG21	1.89	0.54
38:y:9:G:N2	38:y:20:A:O4'	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:73:C:C2	1:2:74:G:H1'	2.43	0.54
1:2:389:C:H5''	1:2:390:C:H5	1.72	0.54
1:2:632:U:H4'	1:2:634:G:H4'	1.90	0.54
4:C:36:GLN:OE1	4:C:36:GLN:N	2.40	0.54
8:G:60:GLU:OE1	28:a:20:ARG:NH2	2.40	0.54
11:J:159:ASP:OD1	11:J:160:LYS:N	2.40	0.54
35:h:106:GLN:HE22	35:h:108:ILE:CD1	2.21	0.54
39:z:582:U:N3	39:z:585:G:OP2	2.30	0.54
1:2:159:A:H2	1:2:457:G:H21	1.54	0.54
1:2:1167:G:O2'	1:2:1183:G:O6	2.24	0.54
1:2:1376:C:H2'	1:2:1377:G:C8	2.43	0.54
1:2:1426:C:H2'	1:2:1427:G:C8	2.42	0.54
1:2:1643:G:H5''	20:S:125:ARG:HB3	1.90	0.54
1:2:1818:A:O2'	1:2:1819:A:H5''	2.07	0.54
7:F:19:ALA:HA	7:F:22:ASN:HD21	1.73	0.54
9:H:122:ARG:HH21	31:d:9:ILE:HD11	1.72	0.54
12:K:8:TRP:CD1	12:K:22:HIS:HE2	2.26	0.54
17:P:141:TYR:HE2	17:P:146:ALA:HB2	1.71	0.54
19:R:39:ALA:HA	19:R:42:ARG:HE	1.72	0.54
34:g:292:SER:OG	34:g:297:THR:OG1	2.25	0.54
1:2:64:A:N6	1:2:83:A:OP2	2.36	0.54
1:2:1043:C:H5''	18:Q:143:LYS:HD3	1.89	0.54
1:2:1563:C:H2'	1:2:1564:A:C4	2.42	0.54
6:E:133:ALA:O	6:E:137:ARG:HG2	2.07	0.54
8:G:195:ILE:HG23	8:G:196:THR:H	1.72	0.54
9:H:89:THR:HA	9:H:92:ILE:HG12	1.89	0.54
10:I:7:PHE:O	10:I:11:GLY:N	2.41	0.54
13:L:170:PRO:O	13:L:175:ARG:NH2	2.38	0.54
34:g:296:GLN:HG2	34:g:297:THR:HG23	1.90	0.54
36:i:107:LYS:O	36:i:110:MET:HG3	2.07	0.54
1:2:165:G:H2'	1:2:166:A:H8	1.73	0.54
1:2:600:G:H2'	1:2:601:G:C8	2.43	0.54
1:2:741:C:H2'	1:2:742:C:O4'	2.08	0.54
1:2:898:G:H2'	1:2:899:A:H8	1.72	0.54
1:2:937:C:H2'	1:2:938:G:H8	1.73	0.54
1:2:987:G:C6	1:2:1130:G:H4'	2.43	0.54
1:2:1289:A:H2'	1:2:1290:G:C8	2.42	0.54
3:B:161:GLY:N	3:B:190:ASN:O	2.35	0.54
5:D:185:VAL:HA	5:D:188:LEU:HG	1.89	0.54
12:K:142:SER:N	12:K:143:LYS:HB2	2.23	0.54
18:Q:142:ARG:HD2	18:Q:143:LYS:O	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:d:30:VAL:HG21	31:d:50:VAL:HG21	1.89	0.54
36:i:85:LYS:O	36:i:89:GLN:NE2	2.41	0.54
1:2:633:A:OP1	13:L:38:ARG:NH2	2.41	0.53
1:2:1574:A:O2'	1:2:1577:C:N4	2.40	0.53
1:2:1624:C:H2'	1:2:1625:A:H8	1.72	0.53
5:D:49:VAL:HG11	5:D:62:LEU:HB2	1.90	0.53
5:D:92:GLN:HG2	5:D:97:LEU:HD11	1.90	0.53
7:F:66:ILE:HD11	7:F:86:LEU:HB3	1.90	0.53
1:2:648:U:O3'	27:Z:17:ARG:NH2	2.41	0.53
1:2:1244:U:H2'	1:2:1245:C:C6	2.44	0.53
1:2:1428:U:H2'	1:2:1429:C:C6	2.43	0.53
1:2:1593:G:H3'	35:h:80:ARG:HD2	1.90	0.53
4:C:11:LYS:HZ2	4:C:184:ARG:HH12	1.55	0.53
7:F:101:GLN:HG3	7:F:126:ILE:HD11	1.89	0.53
10:I:224:ARG:O	10:I:227:GLN:HG3	2.08	0.53
13:L:50:LEU:HD12	13:L:53:ILE:HD11	1.89	0.53
22:U:113:ARG:O	22:U:117:ILE:HG12	2.08	0.53
37:l:7:LYS:HE2	37:l:11:ARG:HD2	1.88	0.53
1:2:649:G:O2'	1:2:652:G:O2'	2.23	0.53
1:2:1019:A:H2'	1:2:1020:A:H8	1.73	0.53
1:2:1531:G:H2'	1:2:1532:A:C8	2.43	0.53
1:2:1804:U:H2'	1:2:1805:C:C6	2.43	0.53
5:D:35:ALA:HB2	5:D:44:ILE:HD11	1.88	0.53
5:D:71:LEU:HB3	5:D:78:GLU:OE2	2.07	0.53
17:P:56:ASP:OD1	17:P:57:SER:N	2.40	0.53
32:e:19:ARG:NH2	32:e:32:ARG:HH21	2.07	0.53
1:2:480:C:O2'	1:2:564:A:N1	2.40	0.53
1:2:1108:U:H3	1:2:1109:A:N6	2.07	0.53
1:2:1163:G:H2'	1:2:1164:G:O4'	2.08	0.53
4:C:104:THR:O	4:C:107:THR:OG1	2.27	0.53
9:H:88:MET:N	9:H:88:MET:HE2	2.24	0.53
13:L:81:LEU:HB3	13:L:87:LEU:HD23	1.91	0.53
13:L:122:SER:H	13:L:125:HIS:HB3	1.73	0.53
28:a:54:VAL:HB	28:a:76:TYR:H	1.73	0.53
1:2:1196:A:H2'	1:2:1197:U:C6	2.44	0.53
11:J:99:ARG:HH21	11:J:100:ILE:HG12	1.73	0.53
12:K:142:SER:HA	12:K:145:ILE:HG13	1.90	0.53
19:R:8:LYS:O	19:R:14:LYS:HB3	2.07	0.53
21:T:99:ASP:OD1	21:T:102:THR:OG1	2.21	0.53
36:i:120:VAL:O	36:i:125:LYS:NZ	2.33	0.53
1:2:411:G:OP1	15:N:97:ARG:NH1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:110:GLN:OE1	9:H:110:GLN:N	2.35	0.53
10:I:7:PHE:CD1	10:I:113:ILE:HG21	2.44	0.53
18:Q:95:ILE:HG21	18:Q:116:LEU:HD11	1.90	0.53
18:Q:148:GLY:O	18:Q:150:ARG:NH1	2.42	0.53
21:T:99:ASP:HB2	21:T:100:PRO:HD2	1.90	0.53
26:Y:15:ASN:ND2	26:Y:72:CYS:SG	2.82	0.53
1:2:412:U:H2'	1:2:413:U:C6	2.44	0.53
1:2:440:C:OP1	8:G:3:ARG:NH2	2.41	0.53
1:2:1211:C:N4	1:2:1216:A:H61	2.07	0.53
1:2:1517:A:O2'	22:U:143:GLY:O	2.19	0.53
7:F:37:VAL:HG12	7:F:50:ILE:HD12	1.90	0.53
19:R:98:ASN:HB3	19:R:120:SER:HB2	1.91	0.53
24:W:20:ILE:HD13	24:W:98:VAL:HG11	1.90	0.53
34:g:5:MET:HA	34:g:5:MET:HE3	1.89	0.53
34:g:220:ASP:HB2	34:g:227:LEU:HD21	1.91	0.53
1:2:36:U:H2'	1:2:37:C:H6	1.73	0.53
1:2:1443:G:H4'	24:W:33:GLU:OE2	2.09	0.53
1:2:1668:U:O2'	9:H:84:GLY:O	2.20	0.53
11:J:64:VAL:HG22	11:J:96:ALA:HA	1.91	0.53
13:L:78:LEU:HD13	13:L:92:MET:HE1	1.91	0.53
24:W:66:ARG:HE	24:W:77:TRP:CD1	2.26	0.53
26:Y:15:ASN:HA	26:Y:18:GLU:HG2	1.90	0.53
35:h:82:SER:HA	35:h:85:ARG:HE	1.73	0.53
1:2:291:U:H2'	1:2:292:A:C8	2.44	0.53
1:2:526:A:N6	1:2:537:G:H21	2.07	0.53
1:2:663:G:H2'	1:2:664:C:C6	2.44	0.53
1:2:1344:G:N2	1:2:1377:G:H22	2.06	0.53
1:2:1412:C:H2'	1:2:1413:C:C6	2.44	0.53
4:C:69:GLU:HG3	6:E:255:THR:HG21	1.91	0.53
4:C:121:LEU:HD13	4:C:143:PRO:HG2	1.90	0.53
20:S:76:GLY:O	20:S:80:GLN:N	2.36	0.53
1:2:71:G:H22	10:I:170:ARG:HG3	1.73	0.53
1:2:914:U:H3'	17:P:64:ARG:HH22	1.73	0.53
1:2:993:A:H2'	1:2:994:A:C8	2.44	0.53
1:2:1006:G:H2'	1:2:1007:A:H8	1.73	0.53
1:2:1284:U:O2	1:2:1307:C:N3	2.42	0.53
1:2:1728:U:H2'	1:2:1729:G:O4'	2.08	0.53
3:B:89:TYR:HA	3:B:126:LEU:HA	1.91	0.53
6:E:196:LYS:HE2	6:E:196:LYS:HA	1.89	0.53
35:h:66:LYS:HA	35:h:111:ARG:HB2	1.91	0.53
39:z:831:A:H5''	39:z:832:A:C4	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:295:C:O2	12:K:184:ARG:NH2	2.30	0.52
1:2:1196:A:H2'	1:2:1197:U:H6	1.73	0.52
1:2:1294:G:H2'	1:2:1295:A:O4'	2.08	0.52
13:L:111:GLN:OE1	13:L:111:GLN:N	2.39	0.52
34:g:197:THR:HG21	34:g:238:ALA:HA	1.90	0.52
1:2:1245:C:OP2	1:2:1246:A:O2'	2.23	0.52
1:2:1451:A:H61	1:2:1467:C:N4	2.06	0.52
10:I:74:ARG:NH1	10:I:96:SER:OG	2.42	0.52
15:N:101:ARG:HH22	27:Z:5:ARG:HG3	1.73	0.52
39:z:532:G:O6	39:z:559:U:N3	2.42	0.52
1:2:551:A:OP2	13:L:174:LYS:N	2.39	0.52
1:2:864:G:N7	11:J:115:LYS:HG3	2.25	0.52
1:2:1199:G:H2'	1:2:1200:A:H8	1.74	0.52
5:D:27:LYS:HA	5:D:51:ARG:HE	1.75	0.52
5:D:151:ARG:HD3	5:D:152:LYS:H	1.75	0.52
7:F:196:GLY:H	7:F:198:ILE:HG13	1.75	0.52
8:G:184:THR:HG22	8:G:224:ASN:HA	1.91	0.52
17:P:26:LEU:HD21	17:P:66:VAL:HG11	1.92	0.52
35:h:106:GLN:NE2	35:h:107:VAL:O	2.42	0.52
38:y:18:G:N2	38:y:56:G:O2'	2.43	0.52
38:y:26:C:H2'	38:y:27:U:C6	2.44	0.52
38:y:34:A:H2'	38:y:35:U:C6	2.45	0.52
1:2:190:A:H3'	1:2:191:C:H5''	1.90	0.52
1:2:946:C:H2'	1:2:947:C:H6	1.74	0.52
1:2:947:C:H2'	1:2:948:G:C8	2.40	0.52
7:F:151:LYS:HG2	7:F:152:PHE:N	2.24	0.52
9:H:153:LEU:HG	9:H:189:ALA:HA	1.92	0.52
28:a:6:THR:HB	28:a:28:LEU:HB2	1.91	0.52
1:2:794:G:C5	11:J:106:ARG:HA	2.45	0.52
1:2:868:A:O2'	1:2:869:G:H8	1.93	0.52
1:2:958:A:H2'	1:2:959:A:O4'	2.09	0.52
1:2:1588:C:O2'	20:S:45:ARG:NH2	2.42	0.52
1:2:1648:U:H2'	1:2:1649:G:C8	2.45	0.52
6:E:71:LEU:HD12	6:E:72:PRO:HD2	1.91	0.52
6:E:84:GLY:H	6:E:87:LEU:HD23	1.74	0.52
6:E:233:TYR:OH	25:X:12:TYR:O	2.26	0.52
14:M:16:PHE:CE2	14:M:89:ILE:HG21	2.44	0.52
16:O:77:ILE:HG12	16:O:128:PHE:HE2	1.74	0.52
38:y:9:G:N7	38:y:19:A:O2'	2.42	0.52
1:2:293:A:H1'	12:K:73:THR:HG23	1.92	0.52
1:2:562:U:H2'	1:2:563:U:C2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1443:G:H2'	1:2:1444:A:C8	2.45	0.52
1:2:1640:C:H5''	20:S:138:ARG:CZ	2.40	0.52
4:C:17:LYS:HD3	4:C:173:LEU:HD11	1.91	0.52
17:P:27:LYS:HG3	17:P:28:LEU:HG	1.90	0.52
22:U:143:GLY:O	22:U:144:ARG:HD3	2.10	0.52
1:2:524:G:H2'	1:2:525:G:C8	2.45	0.52
1:2:1044:G:N1	1:2:1065:U:OP2	2.37	0.52
1:2:1382:A:H2'	1:2:1383:G:O4'	2.09	0.52
1:2:1404:U:OP1	20:S:71:ARG:NH1	2.43	0.52
10:I:7:PHE:CE2	10:I:9:ALA:HB3	2.45	0.52
10:I:204:GLU:O	10:I:208:GLU:HG2	2.10	0.52
23:V:61:ALA:O	23:V:65:TYR:N	2.43	0.52
28:a:106:GLN:H	28:a:106:GLN:CD	2.18	0.52
34:g:20:GLN:NE2	34:g:69:VAL:O	2.39	0.52
36:i:86:VAL:HG12	36:i:86:VAL:O	2.10	0.52
1:2:115:U:O2'	1:2:371:C:O2	2.22	0.52
1:2:191:C:H5'	12:K:143:LYS:HE3	1.90	0.52
1:2:858:A:N7	26:Y:107:SER:HA	2.25	0.52
1:2:869:G:O6	1:2:910:U:O2	2.28	0.52
1:2:1634:G:O2'	1:2:1635:A:O4'	2.27	0.52
4:C:11:LYS:NZ	4:C:192:GLU:OE1	2.35	0.52
8:G:35:PRO:HG2	8:G:36:HIS:HD1	1.75	0.52
35:h:62:VAL:HB	35:h:63:PRO:HD3	1.92	0.52
1:2:185:C:H2'	1:2:186:G:C8	2.44	0.52
1:2:903:G:H2'	1:2:904:A:H8	1.72	0.52
1:2:1013:U:H2'	1:2:1014:U:H6	1.75	0.52
1:2:1391:C:H2'	1:2:1392:A:N3	2.23	0.52
5:D:40:ASN:H	5:D:75:GLN:HE22	1.58	0.52
11:J:194:LEU:HD22	30:c:27:SER:HB2	1.92	0.52
14:M:65:ARG:NH1	32:e:22:ARG:O	2.40	0.52
19:R:10:ARG:HH12	19:R:21:ASP:HA	1.75	0.52
19:R:15:PHE:O	22:U:91:LYS:NZ	2.37	0.52
19:R:81:ARG:HB2	19:R:117:GLY:HA3	1.91	0.52
1:2:454:A:H3'	1:2:455:A:H8	1.75	0.52
1:2:600:G:H2'	1:2:601:G:H8	1.74	0.52
1:2:924:G:H2'	1:2:925:G:C8	2.45	0.52
1:2:1050:G:O6	1:2:1051:A:N6	2.42	0.52
1:2:1236:A:C4	19:R:100:LYS:HE2	2.45	0.52
1:2:1383:G:N1	7:F:206:ASP:O	2.25	0.52
5:D:144:LYS:HA	5:D:208:HIS:ND1	2.25	0.52
5:D:196:ASP:HA	5:D:199:LYS:HG2	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:191:SER:HB2	6:E:196:LYS:HE3	1.90	0.52
7:F:19:ALA:HA	7:F:22:ASN:ND2	2.25	0.52
9:H:144:LEU:O	9:H:148:ASN:ND2	2.43	0.52
9:H:162:ALA:HA	9:H:165:ASN:HB2	1.90	0.52
10:I:18:VAL:HB	10:I:23:LYS:NZ	2.24	0.52
1:2:104:A:OP1	12:K:12:ARG:NE	2.43	0.51
1:2:920:G:H1	1:2:1014:U:H3	1.58	0.51
1:2:1451:A:H2'	1:2:1452:G:C8	2.45	0.51
1:2:1615:A:H2'	19:R:40:ARG:NH2	2.24	0.51
1:2:1659:A:H2'	1:2:1661:C:H41	1.75	0.51
6:E:92:LEU:HB3	6:E:112:PHE:HB2	1.92	0.51
10:I:97:VAL:HG22	10:I:98:ARG:H	1.75	0.51
12:K:6:ASP:OD1	12:K:9:HIS:ND1	2.43	0.51
22:U:75:ARG:HH12	22:U:80:PRO:HA	1.74	0.51
34:g:17:TRP:CD1	34:g:303:THR:HG1	2.28	0.51
1:2:151:C:H2'	1:2:152:U:H6	1.76	0.51
1:2:507:C:H2'	1:2:508:G:O4'	2.10	0.51
1:2:932:G:H2'	1:2:933:C:C6	2.45	0.51
1:2:1789:G:H2'	1:2:1790:G:H8	1.75	0.51
10:I:32:MET:SD	10:I:63:MET:HE1	2.50	0.51
20:S:83:ALA:HA	20:S:86:GLN:HE21	1.75	0.51
30:c:37:CYS:SG	30:c:60:SER:OG	2.57	0.51
34:g:131:LEU:O	34:g:139:LYS:N	2.43	0.51
35:h:80:ARG:HB3	35:h:83:LEU:HB2	1.92	0.51
1:2:444:U:H2'	1:2:445:A:C8	2.45	0.51
1:2:577:A:H5'	1:2:582:C:C5	2.45	0.51
1:2:1093:G:H2'	1:2:1094:C:C6	2.46	0.51
1:2:1283:A:H5'	33:f:99:LYS:NZ	2.25	0.51
1:2:1861:U:P	29:b:10:ARG:HH22	2.33	0.51
4:C:60:LEU:HD11	4:C:159:ILE:HG12	1.93	0.51
19:R:8:LYS:HA	19:R:12:PHE:HD2	1.75	0.51
19:R:92:SER:O	19:R:93:MET:HE2	2.10	0.51
34:g:122:SER:HG	34:g:132:TRP:HE1	1.58	0.51
1:2:550:A:OP2	13:L:177:ASN:ND2	2.44	0.51
1:2:917:G:C4	30:c:21:LYS:HE2	2.45	0.51
1:2:1043:C:O3'	18:Q:141:ARG:NH1	2.42	0.51
1:2:1123:C:H4'	30:c:17:ARG:HH22	1.76	0.51
8:G:202:PRO:HB2	15:N:42:LEU:HD13	1.92	0.51
10:I:199:THR:HA	10:I:202:ASN:ND2	2.26	0.51
18:Q:61:LYS:HZ1	18:Q:80:ASP:HB2	1.76	0.51
24:W:40:ILE:O	24:W:44:LYS:HG2	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:81:VAL:HG13	26:Y:85:ASP:HB2	1.92	0.51
1:2:28:U:H2'	1:2:29:G:H8	1.75	0.51
1:2:606:A:H5''	27:Z:68:LYS:NZ	2.26	0.51
1:2:898:G:H2'	1:2:899:A:C8	2.45	0.51
1:2:1537:C:H2'	1:2:1538:U:C2	2.46	0.51
1:2:1651:G:O6	1:2:1663:U:O4	2.28	0.51
6:E:236:LEU:H	6:E:236:LEU:HD23	1.76	0.51
7:F:203:PRO:HA	7:F:208:VAL:HG13	1.92	0.51
14:M:43:LEU:H	14:M:43:LEU:HD12	1.74	0.51
28:a:20:ARG:NH1	28:a:76:TYR:OH	2.42	0.51
39:z:579:G:H2'	39:z:580:U:C6	2.45	0.51
1:2:297:C:H2'	1:2:298:G:C8	2.45	0.51
1:2:553:G:C2	1:2:554:A:C8	2.99	0.51
1:2:1164:G:H2'	1:2:1165:G:O4'	2.10	0.51
1:2:1195:A:H2'	1:2:1196:A:C8	2.45	0.51
1:2:1631:G:N7	35:h:41:ARG:NH1	2.58	0.51
4:C:112:ILE:HG13	4:C:112:ILE:O	2.10	0.51
9:H:28:VAL:O	9:H:42:LYS:NZ	2.40	0.51
9:H:122:ARG:HH22	31:d:58:LEU:N	2.09	0.51
13:L:50:LEU:HD11	13:L:100:LEU:CD1	2.40	0.51
19:R:85:ILE:HG22	19:R:112:ILE:HD13	1.92	0.51
31:d:12:ALA:HA	31:d:35:MET:HG2	1.92	0.51
31:d:31:ARG:HD2	31:d:43:ILE:HD11	1.92	0.51
1:2:77:A:O2'	10:I:176:ILE:N	2.43	0.51
1:2:435:A:H4'	12:K:50:GLY:HA2	1.93	0.51
1:2:518:A:H2'	1:2:519:A:C8	2.45	0.51
1:2:743:U:O2'	1:2:744:C:O5'	2.29	0.51
1:2:1015:C:H2'	1:2:1016:A:C4	2.45	0.51
1:2:1188:U:H2'	1:2:1189:U:C6	2.46	0.51
3:B:367:ILE:HA	3:B:434:CYS:HA	1.93	0.51
14:M:47:LYS:O	14:M:50:GLN:HB3	2.11	0.51
15:N:49:GLU:HG2	15:N:116:CYS:SG	2.51	0.51
34:g:122:SER:OG	34:g:132:TRP:NE1	2.38	0.51
1:2:127:C:O2'	1:2:212:G:OP2	2.29	0.51
1:2:1510:G:H2'	1:2:1511:G:H8	1.74	0.51
1:2:1612:G:H1	19:R:40:ARG:HH22	1.59	0.51
10:I:162:LEU:HD23	10:I:170:ARG:H	1.76	0.51
26:Y:77:PRO:HB2	27:Z:7:LEU:HD21	1.92	0.51
27:Z:25:LYS:HA	27:Z:28:LYS:HB3	1.91	0.51
1:2:520:U:H2'	1:2:521:A:C8	2.46	0.51
1:2:552:U:H2'	1:2:553:G:C8	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:837:G:H2'	1:2:838:C:C6	2.46	0.51
1:2:1099:C:H2'	1:2:1100:G:H8	1.74	0.51
1:2:1668:U:H2'	1:2:1669:G:O4'	2.11	0.51
7:F:23:GLU:HB3	32:e:46:TYR:OH	2.11	0.51
12:K:12:ARG:HG2	12:K:13:LYS:H	1.76	0.51
15:N:135:SER:H	15:N:138:VAL:HG12	1.76	0.51
24:W:69:PRO:HA	32:e:40:ARG:HH12	1.75	0.51
39:z:579:G:H2'	39:z:580:U:H6	1.74	0.51
1:2:432:C:H42	1:2:439:A:H62	0.71	0.51
1:2:978:G:H2'	1:2:979:A:C8	2.46	0.51
1:2:1445:G:H2'	1:2:1446:G:O4'	2.11	0.51
7:F:50:ILE:HG22	7:F:88:ALA:HA	1.93	0.51
14:M:36:ALA:HB1	14:M:39:ASN:HD21	1.76	0.51
1:2:1130:G:H2'	1:2:1131:C:C6	2.45	0.50
1:2:1611:U:HO2'	1:2:1656:A:HO2'	1.58	0.50
1:2:1688:G:OP2	29:b:89:ARG:NH2	2.41	0.50
4:C:74:VAL:HG22	4:C:121:LEU:HB2	1.93	0.50
21:T:33:ARG:O	21:T:36:GLU:HG3	2.11	0.50
27:Z:59:ALA:N	27:Z:65:ALA:O	2.44	0.50
29:b:26:CYS:SG	29:b:76:SER:OG	2.69	0.50
33:f:116:ARG:HH12	33:f:119:ARG:HA	1.76	0.50
39:z:589:C:H2'	39:z:590:A:H8	1.75	0.50
1:2:29:G:H2'	1:2:30:C:C6	2.46	0.50
1:2:232:A:H2'	1:2:233:A:C8	2.46	0.50
1:2:837:G:H2'	1:2:838:C:H6	1.76	0.50
1:2:899:A:H2'	1:2:900:A:C8	2.46	0.50
17:P:34:LYS:HD2	17:P:74:ILE:HG12	1.93	0.50
17:P:61:ALA:HB2	30:c:32:PHE:CZ	2.46	0.50
17:P:84:LEU:HD11	17:P:89:TYR:HB2	1.92	0.50
19:R:74:GLU:HG2	19:R:75:VAL:N	2.24	0.50
29:b:49:ALA:O	29:b:53:ILE:HG12	2.11	0.50
32:e:34:TYR:HB2	32:e:36:LEU:HD23	1.93	0.50
38:y:55:C:N3	38:y:56:G:N1	2.59	0.50
39:z:522:U:H2'	39:z:523:G:C8	2.46	0.50
1:2:943:G:H2'	1:2:944:C:H6	1.76	0.50
1:2:1361:G:H2'	1:2:1362:G:H8	1.75	0.50
1:2:1671:U:C4	1:2:1672:U:C4	2.99	0.50
4:C:80:ARG:NH1	4:C:165:ASN:O	2.44	0.50
5:D:135:LEU:HD23	5:D:217:MET:HA	1.93	0.50
8:G:249:ALA:HA	13:L:72:PHE:CE1	2.46	0.50
17:P:30:SER:O	17:P:34:LYS:HG2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:y:36:A:H3'	38:y:37:A:H8	1.76	0.50
1:2:349:U:H5''	27:Z:22:TRP:HH2	1.77	0.50
1:2:544:A:H2'	1:2:545:A:C8	2.47	0.50
1:2:1281:G:OP1	16:O:107:SER:OG	2.30	0.50
1:2:1286:G:N2	1:2:1306:U:H1'	2.27	0.50
1:2:1424:G:C2	1:2:1425:G:C8	2.99	0.50
1:2:1631:G:H1'	9:H:164:ARG:HH12	1.76	0.50
1:2:1799:G:H2'	1:2:1800:A:C8	2.47	0.50
1:2:1839:A:H2'	1:2:1840:G:C8	2.47	0.50
6:E:99:LYS:HB3	6:E:106:ARG:HD3	1.94	0.50
7:F:158:ILE:HD13	7:F:205:PRO:HB3	1.93	0.50
8:G:59:ASP:O	8:G:62:LYS:HG3	2.11	0.50
8:G:182:MET:N	8:G:226:PHE:O	2.45	0.50
9:H:174:ALA:O	9:H:178:ILE:HG12	2.11	0.50
10:I:44:GLU:HG3	10:I:119:LYS:HE3	1.92	0.50
11:J:126:HIS:HA	11:J:129:ILE:HG22	1.94	0.50
12:K:42:ARG:HE	12:K:59:ARG:HH21	1.58	0.50
22:U:143:GLY:C	22:U:144:ARG:HD3	2.36	0.50
29:b:25:ASN:OD1	29:b:26:CYS:N	2.44	0.50
33:f:118:ARG:HH21	33:f:133:ALA:HA	1.76	0.50
38:y:25:G:C6	38:y:43:A:N1	2.80	0.50
38:y:43:A:H2'	38:y:44:G:C6	2.46	0.50
1:2:217:U:H2'	1:2:218:A:C8	2.46	0.50
1:2:413:U:H2'	1:2:414:C:C6	2.46	0.50
1:2:623:C:O3'	36:i:87:ARG:NH2	2.45	0.50
1:2:910:U:O2'	11:J:120:ARG:NH2	2.45	0.50
1:2:1429:C:H2'	1:2:1430:C:C6	2.47	0.50
9:H:49:LEU:HD13	20:S:47:LEU:HD22	1.93	0.50
9:H:100:ILE:HD11	9:H:108:PRO:HB3	1.92	0.50
17:P:49:GLN:HA	17:P:52:VAL:HG22	1.94	0.50
21:T:20:TYR:CZ	21:T:38:ILE:HD11	2.47	0.50
23:V:129:ARG:HG3	23:V:133:ARG:HH21	1.76	0.50
1:2:1228:U:H2'	1:2:1229:G:C8	2.46	0.50
1:2:1397:A:H4'	24:W:52:GLY:HA3	1.92	0.50
1:2:1414:C:H4'	1:2:1415:C:H5'	1.94	0.50
1:2:1554:C:H2'	1:2:1555:U:O4'	2.12	0.50
1:2:1678:C:C5	31:d:24:GLN:HG3	2.47	0.50
1:2:1750:C:H2'	1:2:1751:G:H8	1.76	0.50
7:F:138:VAL:O	7:F:149:SER:HA	2.11	0.50
9:H:34:SER:HA	31:d:55:VAL:HG13	1.94	0.50
15:N:16:ILE:HG13	15:N:17:PHE:H	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:102:ILE:HG12	26:Y:113:HIS:HD2	1.76	0.50
1:2:577:A:H5'	1:2:582:C:H5	1.77	0.50
1:2:1228:U:H2'	1:2:1229:G:H8	1.75	0.50
1:2:1266:G:N2	1:2:1507:U:O2	2.36	0.50
5:D:167:LYS:HA	5:D:170:GLU:CD	2.36	0.50
13:L:50:LEU:HD11	13:L:100:LEU:HD11	1.94	0.50
20:S:102:GLU:OE2	34:g:58:ALA:N	2.45	0.50
34:g:10:THR:O	34:g:12:LYS:NZ	2.41	0.50
34:g:13:GLY:HA3	34:g:43:TRP:CH2	2.43	0.50
1:2:337:G:H2'	1:2:338:A:C8	2.47	0.50
1:2:843:A:H2'	1:2:844:U:O4'	2.12	0.50
1:2:976:A:H2'	1:2:977:A:C8	2.47	0.50
1:2:1093:G:H4'	4:C:32:PHE:CG	2.46	0.50
1:2:1394:G:H2'	1:2:1395:C:H6	1.77	0.50
1:2:1448:A:N1	1:2:1470:A:O2'	2.44	0.50
11:J:142:LYS:O	11:J:143:ARG:HD2	2.12	0.50
13:L:63:LEU:HB2	13:L:70:ARG:HH21	1.76	0.50
29:b:37:LYS:HZ1	29:b:70:LYS:HG2	1.76	0.50
1:2:30:C:H5''	27:Z:138:LYS:NZ	2.27	0.50
1:2:996:C:OP2	29:b:17:HIS:NE2	2.45	0.50
5:D:145:LYS:NZ	5:D:149:GLN:O	2.39	0.50
8:G:163:ASP:OD1	8:G:164:LEU:N	2.45	0.50
12:K:101:ILE:HG22	12:K:172:LEU:HD12	1.94	0.50
17:P:63:VAL:HG12	17:P:67:THR:OG1	2.12	0.50
29:b:9:GLY:HA3	29:b:12:LYS:HD2	1.94	0.50
35:h:90:GLU:O	35:h:93:SER:OG	2.25	0.50
38:y:11:C:N3	38:y:24:U:C2	2.79	0.50
39:z:523:G:H2'	39:z:524:C:H6	1.76	0.50
1:2:146:G:O2'	1:2:147:A:H5''	2.12	0.49
1:2:411:G:O3'	15:N:98:LYS:NZ	2.43	0.49
1:2:1244:U:C2	38:y:33:C:H5'	2.47	0.49
6:E:122:VAL:HG11	6:E:229:ILE:HD12	1.94	0.49
14:M:49:MET:HE3	14:M:69:TRP:CG	2.46	0.49
15:N:47:PRO:HG3	15:N:117:PHE:HE1	1.77	0.49
19:R:7:LYS:O	19:R:9:LYS:HG2	2.11	0.49
21:T:71:ILE:HG23	21:T:74:GLN:H	1.76	0.49
31:d:16:LYS:O	31:d:31:ARG:N	2.45	0.49
39:z:575:A:C8	39:z:576:C:H4'	2.47	0.49
1:2:656:U:H2'	1:2:657:U:C6	2.47	0.49
1:2:946:C:H2'	1:2:947:C:C6	2.46	0.49
1:2:977:A:H2'	1:2:978:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1541:G:H22	1:2:1650:C:H1'	1.76	0.49
4:C:9:GLN:HA	4:C:55:TRP:HH2	1.77	0.49
8:G:136:ILE:HG12	8:G:149:TYR:CZ	2.48	0.49
11:J:26:ALA:HA	11:J:29:GLU:CD	2.37	0.49
21:T:2:GLY:O	21:T:3:ARG:HG3	2.12	0.49
31:d:13:ARG:HG2	31:d:35:MET:SD	2.52	0.49
38:y:46:U:H4'	38:y:47:C:C5	2.46	0.49
38:y:50:U:H2'	38:y:51:G:C8	2.47	0.49
1:2:1419:C:O2'	1:2:1420:G:O5'	2.27	0.49
1:2:1561:G:O3'	1:2:1562:G:N2	2.40	0.49
1:2:1583:A:H2	1:2:1649:G:H1'	1.77	0.49
5:D:62:LEU:O	5:D:65:ARG:HG3	2.13	0.49
5:D:82:ARG:NH1	5:D:191:ASP:OD2	2.44	0.49
9:H:178:ILE:HG22	9:H:182:LYS:HZ2	1.78	0.49
12:K:194:GLU:OE1	12:K:194:GLU:N	2.43	0.49
26:Y:78:ARG:HB3	26:Y:124:LYS:HD2	1.93	0.49
35:h:85:ARG:HA	35:h:88:LEU:HG	1.94	0.49
1:2:354:A:H2'	1:2:355:C:C6	2.47	0.49
1:2:431:C:H4'	1:2:1733:C:H5'	1.95	0.49
1:2:671:U:H2'	1:2:672:U:C6	2.47	0.49
1:2:1332:C:H2'	1:2:1333:C:O4'	2.12	0.49
14:M:11:ILE:O	14:M:15:LEU:HG	2.13	0.49
17:P:113:PHE:O	17:P:117:LEU:HG	2.11	0.49
18:Q:142:ARG:NH1	18:Q:143:LYS:O	2.30	0.49
19:R:106:GLU:OE2	19:R:107:ILE:N	2.46	0.49
39:z:580:U:H2'	39:z:581:A:C8	2.48	0.49
1:2:648:U:O2	27:Z:17:ARG:NH1	2.45	0.49
1:2:951:A:H4'	18:Q:60:MET:HE1	1.95	0.49
1:2:1130:G:OP1	29:b:6:ARG:NH1	2.46	0.49
1:2:1373:U:H3'	4:C:102:ARG:HH21	1.76	0.49
1:2:1413:C:H2'	1:2:1415:C:C6	2.48	0.49
1:2:1567:C:H2'	1:2:1568:G:C8	2.47	0.49
1:2:1596:A:O5'	35:h:41:ARG:NH2	2.45	0.49
4:C:103:PHE:O	4:C:107:THR:OG1	2.29	0.49
7:F:36:GLY:C	7:F:51:LEU:HB3	2.38	0.49
10:I:64:LYS:HE2	10:I:82:SER:HB3	1.94	0.49
26:Y:124:LYS:HD3	26:Y:125:ILE:H	1.77	0.49
34:g:34:ALA:HA	34:g:40:ILE:HG22	1.94	0.49
1:2:91:A:OP1	1:2:436:G:N2	2.29	0.49
1:2:144:U:H2'	1:2:145:G:H8	1.78	0.49
1:2:379:A:H2'	1:2:380:C:C6	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:944:C:H2'	1:2:945:G:C8	2.48	0.49
1:2:1587:C:OP1	9:H:91:ARG:NH2	2.45	0.49
4:C:70:ASN:ND2	6:E:259:VAL:HG21	2.26	0.49
5:D:36:PRO:HB2	5:D:38:MET:HE1	1.94	0.49
9:H:125:SER:O	31:d:47:LYS:NZ	2.45	0.49
12:K:144:LYS:H	12:K:147:LYS:HE2	1.78	0.49
13:L:85:GLY:HA3	13:L:151:LEU:HD13	1.94	0.49
17:P:55:ARG:HA	17:P:60:VAL:O	2.13	0.49
19:R:39:ALA:HA	19:R:42:ARG:NE	2.28	0.49
24:W:67:LYS:HA	32:e:44:ARG:NH2	2.28	0.49
24:W:67:LYS:HD2	32:e:44:ARG:CZ	2.42	0.49
1:2:1:U:O5'	13:L:54:ARG:NH1	2.46	0.49
1:2:76:U:OP2	10:I:159:ARG:NH1	2.46	0.49
1:2:318:U:C2	1:2:319:G:C8	3.00	0.49
1:2:858:A:C8	26:Y:107:SER:HA	2.47	0.49
1:2:1271:G:N2	1:2:1502:A:OP2	2.45	0.49
1:2:1858:U:H3'	29:b:5:ARG:NH2	2.27	0.49
13:L:93:LYS:HB2	13:L:96:TYR:CD2	2.48	0.49
13:L:150:ARG:O	13:L:154:GLN:HG3	2.13	0.49
14:M:64:TRP:NE1	32:e:23:VAL:HA	2.28	0.49
14:M:73:ASN:HA	14:M:76:ILE:HD12	1.93	0.49
17:P:23:PRO:HD2	17:P:26:LEU:HD11	1.94	0.49
17:P:88:LEU:O	17:P:92:ILE:HG12	2.12	0.49
28:a:18:LEU:HD13	28:a:20:ARG:NH2	2.28	0.49
35:h:68:ILE:HB	35:h:109:TYR:HB2	1.95	0.49
38:y:27:U:H2'	38:y:28:G:C8	2.48	0.49
1:2:118:C:H1'	1:2:435:A:C4	2.47	0.49
1:2:191:C:H4'	1:2:191:C:OP1	2.12	0.49
1:2:797:U:C2	1:2:798:A:C8	3.01	0.49
1:2:1084:U:H4'	1:2:1085:G:OP2	2.12	0.49
1:2:1274:A:C4	1:2:1316:G:N2	2.81	0.49
1:2:1629:A:H2'	1:2:1630:C:O4'	2.13	0.49
4:C:158:ASP:OD1	25:X:32:ILE:HD11	2.13	0.49
4:C:176:TRP:CZ2	4:C:199:PRO:HD3	2.48	0.49
11:J:168:HIS:CE1	11:J:169:LYS:HE3	2.48	0.49
20:S:146:ARG:NE	38:y:31:C:OP2	2.35	0.49
1:2:149:A:N7	1:2:169:U:O4	2.46	0.49
1:2:296:U:H5''	1:2:297:C:C2	2.48	0.49
1:2:551:A:H2'	1:2:552:U:C6	2.48	0.49
1:2:1453:U:H2'	1:2:1454:G:C8	2.48	0.49
4:C:39:TYR:OH	4:C:50:ASN:ND2	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:191:SER:OG	6:E:196:LYS:HE3	2.13	0.49
8:G:71:LYS:HG3	8:G:76:VAL:HG22	1.95	0.49
8:G:87:MET:HE3	8:G:123:LEU:HB2	1.95	0.49
9:H:126:THR:HB	31:d:47:LYS:HE2	1.94	0.49
12:K:120:PRO:HB2	12:K:123:ARG:HE	1.77	0.49
16:O:119:GLN:HG2	16:O:121:LYS:NZ	2.27	0.49
17:P:46:THR:O	17:P:49:GLN:N	2.45	0.49
27:Z:121:LYS:NZ	27:Z:122:VAL:O	2.45	0.49
28:a:38:THR:HA	28:a:41:GLN:HG2	1.95	0.49
32:e:26:ASN:ND2	32:e:27:ARG:O	2.46	0.49
34:g:8:ARG:HH11	34:g:311:GLN:HB3	1.77	0.49
34:g:256:ILE:HB	34:g:270:LEU:HB2	1.94	0.49
38:y:48:G:H2'	38:y:49:A:C8	2.48	0.49
1:2:163:U:OP1	10:I:85:ARG:N	2.45	0.49
1:2:1138:G:OP1	6:E:172:ARG:NH1	2.40	0.49
1:2:1301:C:H2'	1:2:1302:U:C6	2.48	0.49
1:2:1562:G:H2'	1:2:1563:C:C6	2.47	0.49
6:E:57:ASP:OD2	6:E:257:HIS:ND1	2.46	0.49
11:J:23:ILE:HG13	11:J:87:PHE:CE2	2.44	0.49
11:J:160:LYS:HA	11:J:189:PHE:HZ	1.77	0.49
12:K:197:PHE:CZ	12:K:201:LYS:HD2	2.48	0.49
28:a:24:VAL:HA	28:a:72:PHE:HA	1.94	0.49
34:g:247:TRP:NE1	34:g:260:ASP:OD1	2.42	0.49
39:z:527:G:H2'	39:z:528:C:C6	2.48	0.49
1:2:17:C:H2'	1:2:18:C:C6	2.48	0.48
1:2:55:U:OP1	1:2:441:G:N1	2.46	0.48
1:2:370:G:N1	1:2:373:G:OP2	2.38	0.48
1:2:859:U:C2	1:2:860:A:C8	3.01	0.48
5:D:142:PHE:HB2	5:D:209:ASP:HB2	1.95	0.48
8:G:6:LYS:O	8:G:30:ARG:NH2	2.46	0.48
22:U:66:ARG:O	22:U:70:ILE:HG12	2.12	0.48
27:Z:95:GLU:OE1	27:Z:95:GLU:N	2.46	0.48
39:z:534:A:O2'	39:z:535:A:O5'	2.30	0.48
39:z:574:C:O2'	39:z:575:A:OP1	2.25	0.48
39:z:596:A:H2'	39:z:597:A:H8	1.78	0.48
1:2:191:C:H2'	1:2:192:U:H6	1.77	0.48
1:2:399:C:H2'	1:2:400:G:C8	2.48	0.48
1:2:528:U:H2'	1:2:529:C:C6	2.48	0.48
1:2:1125:G:H2'	1:2:1126:G:N9	2.28	0.48
1:2:1351:C:O2'	1:2:1352:G:H5'	2.13	0.48
1:2:1660:G:C4	23:V:88:MET:HE1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1710:A:N1	1:2:1812:A:H2	2.09	0.48
5:D:111:CYS:HA	5:D:114:VAL:HG12	1.96	0.48
5:D:133:TYR:CG	5:D:217:MET:HE1	2.48	0.48
8:G:34:GLY:HA3	8:G:83:PRO:HG3	1.96	0.48
12:K:40:PRO:O	12:K:59:ARG:NH1	2.46	0.48
12:K:42:ARG:NE	12:K:59:ARG:HH21	2.11	0.48
12:K:110:ARG:HG2	12:K:121:LEU:HG	1.95	0.48
13:L:36:GLY:HA3	13:L:123:ILE:HD12	1.94	0.48
31:d:27:CYS:SG	31:d:28:THR:N	2.86	0.48
1:2:110:U:O2'	15:N:71:ARG:NH1	2.46	0.48
1:2:307:G:H3'	10:I:183:ARG:HH22	1.77	0.48
1:2:409:G:H2'	1:2:410:G:C8	2.48	0.48
1:2:619:A:O2'	1:2:621:U:OP1	2.30	0.48
1:2:1151:U:O2'	1:2:1152:U:H5'	2.14	0.48
1:2:1169:A:H62	1:2:1183:G:H21	1.60	0.48
1:2:1681:G:H2'	1:2:1682:C:H6	1.78	0.48
1:2:1854:A:H3'	29:b:8:ASN:HD21	1.77	0.48
8:G:160:ILE:HD12	8:G:169:ILE:HG21	1.95	0.48
12:K:40:PRO:HG2	12:K:59:ARG:HH12	1.79	0.48
26:Y:35:VAL:O	26:Y:39:THR:HG23	2.13	0.48
28:a:35:VAL:HG21	28:a:40:ILE:HD11	1.94	0.48
30:c:33:MET:HE1	30:c:48:SER:HA	1.95	0.48
34:g:57:ARG:HB3	34:g:59:LEU:HD22	1.95	0.48
39:z:597:A:H2'	39:z:598:A:H8	1.77	0.48
1:2:1412:C:C4'	23:V:128:GLN:HE22	2.26	0.48
5:D:193:ILE:H	5:D:193:ILE:HD12	1.77	0.48
6:E:155:TRP:HZ2	26:Y:97:ARG:HH21	1.60	0.48
7:F:214:LYS:HD3	21:T:19:LYS:HB3	1.94	0.48
8:G:137:PRO:HB2	8:G:150:PRO:HD2	1.94	0.48
9:H:194:ASP:OD1	9:H:195:GLU:N	2.46	0.48
13:L:92:MET:HA	13:L:92:MET:HE2	1.94	0.48
13:L:134:HIS:CE1	13:L:164:PRO:HD2	2.39	0.48
1:2:559:A:H2'	1:2:560:C:H6	1.78	0.48
1:2:831:C:O3'	1:2:832:G:N2	2.46	0.48
1:2:865:A:C5	1:2:911:G:H1'	2.47	0.48
1:2:1195:A:H5''	29:b:2:THR:HG22	1.96	0.48
1:2:1290:G:H2'	1:2:1291:A:C8	2.48	0.48
6:E:63:LEU:HG	6:E:82:PHE:HD2	1.78	0.48
9:H:124:ASP:OD1	9:H:125:SER:N	2.46	0.48
11:J:75:ILE:O	11:J:77:VAL:HG22	2.13	0.48
12:K:125:LYS:HG3	12:K:128:LYS:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:11:THR:HA	19:R:16:THR:HG22	1.96	0.48
31:d:44:ARG:NH1	31:d:63:ARG:O	2.45	0.48
33:f:135:HIS:HB2	33:f:138:ARG:HB2	1.95	0.48
1:2:290:A:H2'	1:2:291:U:H6	1.79	0.48
1:2:1054:A:H2'	1:2:1055:G:O4'	2.14	0.48
1:2:1803:A:H2'	1:2:1804:U:C6	2.49	0.48
5:D:87:ILE:HG23	5:D:101:HIS:HB2	1.95	0.48
9:H:135:ARG:HG2	18:Q:66:ARG:HH22	1.78	0.48
34:g:251:ALA:HB2	34:g:289:LEU:HD23	1.96	0.48
35:h:97:ILE:HG21	35:h:109:TYR:HB3	1.96	0.48
38:y:67:C:H2'	38:y:68:U:C6	2.48	0.48
1:2:336:C:H5''	8:G:38:LEU:HB2	1.96	0.48
1:2:642:U:H2'	1:2:643:A:C8	2.48	0.48
1:2:1135:C:H2'	1:2:1136:G:O4'	2.14	0.48
1:2:1160:G:H2'	1:2:1161:G:C2	2.49	0.48
5:D:222:LYS:HG2	5:D:223:PHE:H	1.78	0.48
6:E:133:ALA:O	6:E:136:ILE:HG22	2.13	0.48
20:S:105:LYS:HA	20:S:108:ILE:HG12	1.96	0.48
23:V:37:VAL:HG12	23:V:39:LEU:H	1.79	0.48
28:a:124:ASN:OD1	28:a:125:VAL:N	2.46	0.48
29:b:60:ASP:OD2	29:b:60:ASP:N	2.45	0.48
31:d:17:VAL:HG23	31:d:30:VAL:HG22	1.96	0.48
34:g:88:ARG:HD3	34:g:97:THR:HG21	1.95	0.48
1:2:144:U:H2'	1:2:145:G:C8	2.48	0.48
1:2:317:G:H1'	1:2:318:U:C5	2.49	0.48
1:2:510:A:H2'	1:2:511:A:H8	1.77	0.48
1:2:560:C:H2'	1:2:561:U:C6	2.49	0.48
1:2:1139:A:H4'	1:2:1351:C:H42	1.79	0.48
1:2:1582:G:OP1	1:2:1582:G:N2	2.47	0.48
4:C:51:LEU:HD23	4:C:51:LEU:H	1.78	0.48
16:O:33:ARG:H	16:O:33:ARG:HD3	1.79	0.48
17:P:24:THR:O	17:P:24:THR:HG22	2.14	0.48
17:P:64:ARG:HD2	17:P:70:LYS:HE3	1.94	0.48
1:2:17:C:H2'	1:2:18:C:H6	1.79	0.48
1:2:376:C:H1'	12:K:5:ARG:HG3	1.95	0.48
1:2:413:U:H2'	1:2:414:C:H6	1.78	0.48
1:2:434:G:N1	12:K:26:LYS:HE3	2.24	0.48
1:2:630:A:H2'	1:2:631:A:C8	2.49	0.48
1:2:988:A:H2'	1:2:989:G:H8	1.79	0.48
1:2:1030:A:H2'	1:2:1031:A:O4'	2.13	0.48
1:2:1717:G:H2'	1:2:1718:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1834:U:H2'	1:2:1835:C:H6	1.79	0.48
27:Z:93:PHE:CD2	27:Z:133:LEU:HD13	2.48	0.48
30:c:14:GLU:HA	30:c:17:ARG:HB3	1.95	0.48
39:z:596:A:H2'	39:z:597:A:C8	2.49	0.48
1:2:835:C:N4	28:a:9:THR:O	2.47	0.48
1:2:909:A:N6	11:J:120:ARG:HA	2.29	0.48
1:2:995:G:H3'	29:b:17:HIS:HE1	1.78	0.48
1:2:1310:U:H4'	14:M:8:ARG:NH2	2.29	0.48
1:2:1382:A:N6	7:F:206:ASP:OD2	2.42	0.48
1:2:1469:G:N2	1:2:1471:G:H5''	2.29	0.48
1:2:1789:G:H2'	1:2:1790:G:C8	2.48	0.48
6:E:170:THR:O	6:E:231:LYS:NZ	2.40	0.48
6:E:255:THR:HA	6:E:258:LEU:HD12	1.96	0.48
19:R:25:LEU:HA	19:R:28:MET:SD	2.54	0.48
20:S:24:HIS:ND1	20:S:24:HIS:O	2.46	0.48
26:Y:46:TYR:HA	26:Y:68:ARG:HG2	1.95	0.48
32:e:23:VAL:HG21	32:e:42:CYS:HB2	1.95	0.48
32:e:52:PHE:CZ	32:e:54:LYS:HA	2.48	0.48
39:z:541:C:H2'	39:z:542:A:C8	2.48	0.48
1:2:867:U:OP2	17:P:76:LYS:NZ	2.29	0.47
1:2:873:C:O2	1:2:873:C:H2'	2.14	0.47
5:D:81:PHE:CD1	5:D:109:LYS:HE2	2.48	0.47
5:D:146:CYS:SG	5:D:147:ASN:ND2	2.87	0.47
8:G:62:LYS:HA	8:G:65:CYS:SG	2.54	0.47
14:M:3:MET:SD	14:M:8:ARG:HG3	2.54	0.47
14:M:13:GLU:HA	14:M:16:PHE:HB3	1.95	0.47
18:Q:29:GLY:O	18:Q:94:HIS:N	2.23	0.47
18:Q:37:PHE:HE1	18:Q:110:PRO:HD3	1.78	0.47
23:V:6:VAL:HA	23:V:9:VAL:HG22	1.95	0.47
38:y:10:G:P	38:y:45:G:H21	2.36	0.47
1:2:473:C:H5''	27:Z:48:LYS:HE3	1.96	0.47
1:2:742:C:H2'	1:2:743:U:C6	2.49	0.47
1:2:1370:C:H2'	1:2:1371:G:O4'	2.14	0.47
6:E:158:LYS:O	25:X:4:ASN:ND2	2.48	0.47
10:I:7:PHE:HD1	10:I:113:ILE:HG21	1.79	0.47
22:U:52:LEU:HD23	22:U:52:LEU:H	1.79	0.47
24:W:20:ILE:HG13	24:W:115:THR:O	2.13	0.47
38:y:12:G:C6	38:y:23:G:C6	3.02	0.47
38:y:71:U:H3'	38:y:73:C:OP2	2.14	0.47
39:z:523:G:H2'	39:z:524:C:C6	2.48	0.47
1:2:59:U:H5'	1:2:493:C:N4	2.26	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:517:C:H2'	1:2:518:A:H8	1.78	0.47
1:2:663:G:H2'	1:2:664:C:H6	1.79	0.47
1:2:1528:A:O2'	9:H:81:ARG:NH1	2.48	0.47
1:2:1692:A:H2	6:E:100:GLN:NE2	2.12	0.47
5:D:37:ALA:HA	5:D:42:ARG:HE	1.79	0.47
7:F:53:THR:O	7:F:90:LYS:HG3	2.14	0.47
8:G:246:LEU:HD21	8:G:250:GLU:HG3	1.97	0.47
10:I:182:PRO:HA	10:I:185:LEU:HD12	1.96	0.47
11:J:138:GLU:HG2	17:P:19:ARG:NH1	2.27	0.47
19:R:28:MET:HB2	19:R:32:GLN:HE21	1.79	0.47
22:U:25:LYS:HD2	22:U:55:ARG:HD3	1.95	0.47
25:X:38:GLU:N	25:X:38:GLU:OE1	2.47	0.47
27:Z:134:TYR:OH	36:i:87:ARG:NH2	2.46	0.47
34:g:133:ASN:OD1	34:g:139:LYS:HE2	2.14	0.47
38:y:68:U:H2'	38:y:69:G:C8	2.49	0.47
39:z:521:U:H2'	39:z:522:U:C6	2.49	0.47
1:2:12:U:H2'	1:2:13:C:C6	2.50	0.47
1:2:96:C:H2'	1:2:97:U:H6	1.79	0.47
1:2:145:G:H2'	1:2:146:G:C8	2.49	0.47
1:2:744:C:H2'	1:2:745:U:C2	2.49	0.47
1:2:871:A:H2'	1:2:872:C:C6	2.48	0.47
1:2:943:G:H2'	1:2:944:C:C6	2.49	0.47
1:2:957:G:N2	39:z:831:A:N1	2.61	0.47
1:2:1028:C:H5''	17:P:109:LYS:HZ2	1.80	0.47
1:2:1216:A:H2'	1:2:1217:G:O4'	2.14	0.47
1:2:1570:G:H2'	1:2:1571:G:H8	1.79	0.47
1:2:1672:U:P	9:H:71:ARG:HH21	2.37	0.47
9:H:45:TYR:HA	9:H:47:LYS:HZ1	1.80	0.47
13:L:60:LEU:O	13:L:70:ARG:NH2	2.46	0.47
13:L:152:ASP:O	13:L:155:LYS:HG2	2.13	0.47
15:N:111:VAL:HG22	15:N:140:PHE:HB2	1.96	0.47
17:P:113:PHE:CE2	17:P:117:LEU:HD11	2.49	0.47
21:T:17:ILE:HD11	21:T:21:TYR:HD1	1.79	0.47
1:2:215:U:H2'	1:2:216:U:C6	2.49	0.47
1:2:592:G:N2	1:2:611:C:N3	2.63	0.47
1:2:794:G:N7	11:J:106:ARG:HA	2.29	0.47
1:2:904:A:H2'	1:2:905:G:C8	2.50	0.47
1:2:959:A:H2'	1:2:960:A:O4'	2.14	0.47
1:2:1144:A:H4'	1:2:1145:A:O4'	2.15	0.47
1:2:1511:G:O3'	19:R:122:THR:OG1	2.21	0.47
1:2:1687:U:H2'	1:2:1688:G:C8	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1859:C:C4	29:b:5:ARG:HA	2.50	0.47
5:D:60:ASP:HA	5:D:63:LYS:HD2	1.96	0.47
5:D:135:LEU:HB3	5:D:137:LEU:HD21	1.96	0.47
17:P:91:LEU:HD11	17:P:121:ARG:HD2	1.97	0.47
38:y:52:G:N2	38:y:53:A:H62	2.11	0.47
1:2:96:C:H2'	1:2:97:U:C6	2.49	0.47
1:2:603:C:OP1	36:i:75:LYS:N	2.47	0.47
1:2:1375:A:H2'	1:2:1376:C:H6	1.79	0.47
20:S:25:CYS:SG	20:S:95:TYR:HB2	2.54	0.47
21:T:79:GLU:HA	21:T:82:ASP:HB3	1.96	0.47
26:Y:60:LYS:HZ2	26:Y:62:VAL:HG12	1.79	0.47
27:Z:90:CYS:O	27:Z:94:ILE:HG12	2.15	0.47
39:z:584:A:H2'	39:z:586:A:N7	2.29	0.47
1:2:3:C:C6	6:E:190:ILE:HD11	2.50	0.47
1:2:162:C:H2'	1:2:163:U:O4'	2.14	0.47
1:2:349:U:H5''	27:Z:22:TRP:CH2	2.50	0.47
1:2:361:A:H5'	12:K:10:LYS:NZ	2.30	0.47
1:2:492:C:C2	8:G:66:MET:HE1	2.50	0.47
1:2:876:G:H2'	1:2:877:G:C8	2.50	0.47
1:2:965:U:H3'	1:2:966:G:N2	2.29	0.47
1:2:1028:C:H2'	1:2:1029:G:O4'	2.15	0.47
1:2:1223:G:C2	1:2:1224:A:C8	3.02	0.47
1:2:1302:U:H2'	1:2:1303:U:O4'	2.15	0.47
1:2:1348:G:H2'	1:2:1349:A:H8	1.79	0.47
1:2:1666:G:H2'	1:2:1667:U:C6	2.49	0.47
1:2:1674:A:H5''	9:H:60:ARG:HH21	1.78	0.47
1:2:1718:G:H2'	1:2:1719:A:C8	2.50	0.47
1:2:1718:G:H2'	1:2:1719:A:H8	1.78	0.47
1:2:1795:A:H2'	1:2:1796:C:H6	1.79	0.47
1:2:1847:C:H5	37:l:5:TRP:CH2	2.33	0.47
4:C:35:GLU:O	4:C:38:ILE:HG22	2.15	0.47
6:E:95:MET:SD	6:E:110:LYS:HB3	2.55	0.47
8:G:125:LYS:HB3	8:G:226:PHE:HD1	1.79	0.47
9:H:49:LEU:HD21	20:S:50:LYS:HB2	1.97	0.47
10:I:202:ASN:OD1	10:I:203:LYS:N	2.47	0.47
11:J:78:ARG:HG3	11:J:81:ARG:NH2	2.29	0.47
16:O:22:LEU:HD22	16:O:88:TRP:HE3	1.80	0.47
16:O:46:GLN:NE2	16:O:113:ASP:OD2	2.48	0.47
23:V:42:HIS:CE1	23:V:43:LYS:HG2	2.49	0.47
27:Z:54:LYS:HG2	27:Z:70:VAL:HG12	1.96	0.47
34:g:119:GLN:HG2	34:g:139:LYS:NZ	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:98:LYS:O	36:i:99:LYS:HE2	2.14	0.47
1:2:552:U:O4	1:2:577:A:N7	2.48	0.47
1:2:553:G:O2'	1:2:554:A:O5'	2.29	0.47
1:2:827:G:H2'	1:2:828:G:H8	1.79	0.47
1:2:952:G:H2'	1:2:953:A:H8	1.80	0.47
1:2:1097:U:H2'	1:2:1098:G:C8	2.50	0.47
1:2:1333:C:H5'	24:W:67:LYS:HE3	1.96	0.47
1:2:1688:G:N2	1:2:1828:A:H8	2.13	0.47
1:2:1748:G:C6	1:2:1773:G:C6	3.02	0.47
4:C:89:LYS:HZ1	4:C:202:TYR:HA	1.80	0.47
5:D:229:MET:O	5:D:233:GLY:N	2.48	0.47
7:F:25:LEU:HD12	7:F:37:VAL:HG11	1.96	0.47
18:Q:95:ILE:HD13	18:Q:129:ILE:HG22	1.96	0.47
22:U:120:HIS:O	22:U:124:ARG:HG2	2.15	0.47
23:V:83:GLN:OE1	23:V:85:ASN:HB2	2.15	0.47
34:g:260:ASP:HB2	34:g:267:VAL:HG22	1.96	0.47
38:y:16:C:O2	38:y:58:A:N6	2.48	0.47
1:2:498:A:H3'	1:2:499:G:H8	1.80	0.47
1:2:845:A:H2'	1:2:846:C:C6	2.50	0.47
1:2:1431:C:H2'	1:2:1432:C:C4	2.50	0.47
1:2:1614:A:OP2	19:R:47:ARG:NH2	2.37	0.47
1:2:1649:G:H2'	1:2:1650:C:C6	2.50	0.47
1:2:1697:G:O6	1:2:1830:G:N2	2.48	0.47
8:G:9:LEU:HD12	8:G:30:ARG:HA	1.95	0.47
25:X:38:GLU:OE1	25:X:50:SER:HA	2.14	0.47
1:2:560:C:H2'	1:2:561:U:H6	1.80	0.47
1:2:599:U:H2'	1:2:600:G:H8	1.79	0.47
1:2:1413:C:H5''	1:2:1414:C:OP2	2.15	0.47
1:2:1624:C:H5''	22:U:39:ARG:HG2	1.96	0.47
20:S:39:LEU:HA	20:S:42:ILE:HD11	1.97	0.47
22:U:80:PRO:HB2	22:U:82:TRP:CD1	2.50	0.47
23:V:134:ILE:O	23:V:138:VAL:HG23	2.15	0.47
24:W:66:ARG:HE	24:W:77:TRP:NE1	2.13	0.47
27:Z:91:LEU:HB3	36:i:83:VAL:HG11	1.97	0.47
28:a:109:GLU:O	28:a:113:ARG:HG2	2.15	0.47
34:g:45:LEU:HB3	34:g:47:ARG:HH12	1.79	0.47
1:2:215:U:H2'	1:2:216:U:H6	1.80	0.46
1:2:962:U:H2'	1:2:963:C:H6	1.80	0.46
1:2:1560:C:H2'	1:2:1561:G:C8	2.50	0.46
1:2:1769:U:H2'	1:2:1770:G:C8	2.51	0.46
21:T:73:LEU:O	21:T:76:GLU:HG2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:l:12:ARG:HH21	37:l:15:ARG:CZ	2.28	0.46
1:2:424:G:H2'	1:2:425:A:C8	2.51	0.46
1:2:469:C:C2	1:2:470:G:C8	3.03	0.46
1:2:918:A:H2'	1:2:919:G:O4'	2.15	0.46
1:2:1031:A:H2'	1:2:1032:A:O4'	2.15	0.46
1:2:1160:G:C2	1:2:1161:G:C6	3.04	0.46
1:2:1301:C:O5'	1:2:1301:C:H6	1.98	0.46
1:2:1615:A:P	19:R:40:ARG:HH21	2.38	0.46
1:2:1811:G:H2'	1:2:1812:A:C8	2.51	0.46
4:C:141:ASN:HB3	25:X:32:ILE:HG22	1.97	0.46
12:K:22:HIS:HB2	12:K:25:ARG:NH1	2.30	0.46
18:Q:132:VAL:HG13	18:Q:132:VAL:O	2.16	0.46
19:R:25:LEU:HB3	19:R:87:PRO:HG3	1.97	0.46
27:Z:103:ALA:O	27:Z:121:LYS:N	2.44	0.46
1:2:3:C:C4	13:L:17:ARG:HD2	2.50	0.46
1:2:11:A:N1	1:2:1196:A:H2	2.13	0.46
1:2:410:G:H5''	15:N:97:ARG:HH22	1.80	0.46
1:2:553:G:O2'	1:2:554:A:H8	1.98	0.46
1:2:744:C:H2'	1:2:745:U:C4	2.50	0.46
1:2:915:A:O3'	26:Y:57:ARG:NH2	2.49	0.46
1:2:1560:C:OP2	23:V:102:ARG:NH2	2.38	0.46
1:2:1678:C:C4	31:d:24:GLN:HG3	2.50	0.46
1:2:1688:G:H5'	1:2:1857:A:H5''	1.97	0.46
1:2:1814:G:H2'	1:2:1815:U:C6	2.51	0.46
6:E:79:ILE:O	6:E:83:LEU:HB2	2.15	0.46
10:I:57:ASP:HA	10:I:106:LEU:HA	1.96	0.46
15:N:35:ARG:NH2	15:N:53:GLY:O	2.48	0.46
22:U:30:ILE:HG22	22:U:36:VAL:HG11	1.96	0.46
25:X:4:ASN:OD1	25:X:5:ALA:N	2.48	0.46
28:a:3:ASP:OD1	28:a:4:THR:N	2.47	0.46
38:y:27:U:H2'	38:y:28:G:H8	1.81	0.46
1:2:10:G:O4'	1:2:1692:A:O2'	2.33	0.46
1:2:51:U:H2'	1:2:52:G:C8	2.51	0.46
1:2:223:A:N6	1:2:278:U:OP1	2.45	0.46
1:2:366:A:H2'	1:2:367:G:O4'	2.15	0.46
1:2:521:A:H2'	1:2:522:C:C6	2.49	0.46
1:2:668:U:N3	1:2:1023:A:N6	2.53	0.46
1:2:1007:A:H5''	17:P:3:ARG:NH2	2.29	0.46
1:2:1179:A:H2'	1:2:1180:G:H8	1.79	0.46
1:2:1743:G:N2	1:2:1780:U:O2	2.36	0.46
1:2:1798:U:H2'	1:2:1799:G:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:184:ARG:HA	4:C:190:SER:HB3	1.97	0.46
12:K:53:LYS:HA	12:K:53:LYS:HD3	1.78	0.46
12:K:114:GLU:CD	12:K:123:ARG:HH22	2.23	0.46
15:N:50:ALA:HB2	15:N:116:CYS:SG	2.56	0.46
16:O:48:HIS:HB3	16:O:113:ASP:H	1.79	0.46
20:S:40:GLU:O	20:S:48:GLN:NE2	2.44	0.46
27:Z:72:VAL:HG21	27:Z:100:VAL:HG21	1.97	0.46
29:b:71:LEU:HD13	29:b:73:TYR:CE1	2.50	0.46
1:2:76:U:H5''	1:2:77:A:H5''	1.98	0.46
1:2:107:A:H2'	1:2:108:G:C8	2.51	0.46
1:2:110:U:H4'	15:N:71:ARG:HH12	1.81	0.46
1:2:151:C:H2'	1:2:152:U:C6	2.50	0.46
1:2:483:A:H62	1:2:499:G:N2	2.12	0.46
1:2:863:G:N3	1:2:864:G:N1	2.63	0.46
1:2:1029:G:N2	1:2:1076:A:HO2'	2.14	0.46
1:2:1214:C:H2'	1:2:1215:C:C6	2.50	0.46
1:2:1271:G:H1	1:2:1502:A:H2'	1.81	0.46
1:2:1294:G:H5''	19:R:77:LYS:HB2	1.97	0.46
1:2:1708:C:H2'	1:2:1709:U:C6	2.50	0.46
8:G:251:GLU:O	8:G:254:LYS:HG2	2.16	0.46
14:M:59:LYS:HE3	14:M:70:TYR:HB3	1.98	0.46
20:S:38:PRO:HG2	23:V:8:ASP:HA	1.98	0.46
21:T:45:LYS:HE2	21:T:49:LYS:HD2	1.97	0.46
26:Y:60:LYS:C	26:Y:60:LYS:HD3	2.41	0.46
1:2:308:C:OP2	10:I:183:ARG:NH2	2.49	0.46
1:2:592:G:OP2	1:2:593:C:O2'	2.30	0.46
1:2:865:A:C4	1:2:911:G:H1'	2.50	0.46
1:2:1702:U:H2'	1:2:1703:C:C6	2.50	0.46
1:2:1834:U:H2'	1:2:1835:C:C6	2.50	0.46
1:2:1861:U:H5'	29:b:97:PRO:HG3	1.96	0.46
9:H:40:ALA:HB1	9:H:45:TYR:CD2	2.50	0.46
11:J:65:PRO:HB2	11:J:67:PRO:HD3	1.98	0.46
11:J:75:ILE:HG13	11:J:78:ARG:HD3	1.98	0.46
11:J:168:HIS:HE1	11:J:169:LYS:HE3	1.80	0.46
15:N:38:LYS:NZ	15:N:39:ASN:OD1	2.33	0.46
20:S:146:ARG:HH21	38:y:31:C:P	2.39	0.46
38:y:10:G:C8	38:y:45:G:C2	3.04	0.46
1:2:160:U:O2'	1:2:161:U:H3'	2.15	0.46
1:2:318:U:H2'	1:2:319:G:H8	1.81	0.46
1:2:399:C:H2'	1:2:400:G:H8	1.80	0.46
1:2:730:C:H2'	1:2:731:C:C5	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:749:C:H2'	1:2:750:G:C8	2.50	0.46
1:2:833:A:OP2	28:a:8:ARG:NH1	2.49	0.46
1:2:1058:A:H2'	1:2:1059:C:C6	2.51	0.46
1:2:1123:C:H2'	1:2:1124:C:C6	2.50	0.46
1:2:1609:A:OP2	19:R:42:ARG:NH2	2.48	0.46
7:F:165:ASN:OD1	7:F:166:TYR:N	2.48	0.46
11:J:67:PRO:HG2	11:J:68:GLN:OE1	2.16	0.46
12:K:8:TRP:O	12:K:18:ARG:HD2	2.15	0.46
12:K:197:PHE:HA	12:K:200:ARG:HG2	1.98	0.46
14:M:21:MET:HB3	14:M:69:TRP:HB2	1.97	0.46
27:Z:1:MET:HE2	27:Z:5:ARG:HB2	1.98	0.46
34:g:101:PHE:HB3	34:g:132:TRP:CZ3	2.50	0.46
39:z:560:C:H2'	39:z:561:U:C6	2.51	0.46
1:2:29:G:C6	1:2:636:G:C6	3.04	0.46
1:2:147:A:H62	10:I:137:ARG:NH2	2.14	0.46
1:2:369:C:H2'	1:2:370:G:C8	2.51	0.46
1:2:517:C:O2	1:2:549:G:N2	2.48	0.46
1:2:1537:C:O2'	20:S:43:GLU:OE2	2.29	0.46
1:2:1596:A:H1'	1:2:1599:G:O6	2.16	0.46
1:2:1666:G:H2'	1:2:1667:U:H6	1.80	0.46
4:C:9:GLN:HG3	4:C:10:MET:H	1.81	0.46
7:F:26:THR:HG22	7:F:34:TYR:CE1	2.51	0.46
7:F:64:ARG:HG2	7:F:68:GLU:OE2	2.16	0.46
8:G:125:LYS:HE3	8:G:226:PHE:HD1	1.81	0.46
9:H:198:ARG:HA	9:H:201:LYS:HG2	1.97	0.46
11:J:51:ILE:HD11	11:J:176:VAL:HG23	1.97	0.46
14:M:25:LYS:HB3	14:M:65:ARG:HB3	1.97	0.46
19:R:14:LYS:HE2	39:z:563:C:H2'	1.98	0.46
19:R:38:SER:O	19:R:42:ARG:N	2.46	0.46
29:b:31:PRO:HG2	29:b:34:LYS:HB2	1.96	0.46
35:h:51:ASP:HB2	35:h:54:THR:HG23	1.98	0.46
1:2:121:U:H5''	8:G:77:ARG:NH1	2.30	0.46
1:2:841:G:C6	1:2:842:G:C6	3.04	0.46
1:2:1142:C:O2'	1:2:1146:A:N1	2.49	0.46
1:2:1234:U:H2'	1:2:1235:U:C6	2.51	0.46
1:2:1466:C:H2'	1:2:1467:C:H6	1.81	0.46
4:C:9:GLN:HA	4:C:55:TRP:CH2	2.51	0.46
5:D:134:LEU:HD12	5:D:219:LYS:HG3	1.97	0.46
6:E:108:ARG:HG2	6:E:130:LYS:HA	1.98	0.46
7:F:122:VAL:O	7:F:126:ILE:HG12	2.15	0.46
11:J:142:LYS:C	11:J:143:ARG:HD2	2.41	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:67:ASP:HB3	18:Q:70:SER:HB3	1.98	0.46
21:T:96:ILE:HD12	21:T:96:ILE:HA	1.85	0.46
28:a:44:LEU:HD23	28:a:55:ILE:HG23	1.98	0.46
33:f:135:HIS:CD2	33:f:140:TYR:HB3	2.51	0.46
39:z:547:G:N1	39:z:550:A:OP2	2.43	0.46
1:2:1226:C:H1'	1:2:1660:G:H22	1.81	0.46
1:2:1383:G:C2	1:2:1384:A:H1'	2.51	0.46
3:B:254:PRO:HA	3:B:286:GLY:HA3	1.98	0.46
4:C:87:VAL:HG12	4:C:175:TRP:CZ2	2.51	0.46
4:C:144:THR:N	4:C:158:ASP:OD2	2.38	0.46
5:D:133:TYR:HA	5:D:219:LYS:O	2.16	0.46
8:G:139:LEU:HD12	8:G:147:ILE:HB	1.97	0.46
12:K:197:PHE:O	12:K:200:ARG:HG2	2.16	0.46
14:M:5:LYS:O	14:M:9:ILE:HD12	2.16	0.46
33:f:111:ASN:HA	33:f:112:GLY:HA2	1.65	0.46
34:g:212:LYS:HA	34:g:235:ILE:HG13	1.98	0.46
1:2:29:G:H4'	27:Z:129:SER:HB3	1.98	0.45
1:2:121:U:O3'	8:G:77:ARG:NH2	2.43	0.45
1:2:422:G:H2'	1:2:423:A:C8	2.51	0.45
1:2:1035:C:N4	1:2:1073:A:H61	2.14	0.45
1:2:1200:A:H2'	1:2:1201:C:C6	2.50	0.45
1:2:1270:G:O4'	14:M:47:LYS:HE2	2.16	0.45
1:2:1587:C:H5''	9:H:91:ARG:HH22	1.81	0.45
1:2:1606:G:H2'	1:2:1607:G:C8	2.51	0.45
4:C:22:GLY:O	4:C:164:ASN:ND2	2.42	0.45
5:D:147:ASN:OD1	5:D:148:ASN:N	2.49	0.45
9:H:70:GLU:O	9:H:73:THR:OG1	2.24	0.45
12:K:200:ARG:O	12:K:203:LYS:HG3	2.16	0.45
17:P:141:TYR:CE2	17:P:146:ALA:HB2	2.50	0.45
24:W:80:PHE:HA	32:e:52:PHE:CE1	2.51	0.45
28:a:44:LEU:O	28:a:47:MET:HB3	2.16	0.45
30:c:33:MET:HB2	30:c:80:ARG:H	1.81	0.45
31:d:37:ASP:N	31:d:37:ASP:OD1	2.49	0.45
34:g:153:CYS:SG	34:g:155:ARG:NH2	2.88	0.45
38:y:8:U:O2'	38:y:10:G:OP1	2.29	0.45
38:y:30:G:H2'	38:y:31:C:H6	1.80	0.45
1:2:369:C:H4'	12:K:31:ARG:O	2.15	0.45
3:B:86:ALA:N	3:B:130:VAL:O	2.49	0.45
4:C:73:ASP:OD1	4:C:73:ASP:N	2.49	0.45
4:C:110:ASN:OD1	4:C:112:ILE:N	2.41	0.45
5:D:26:SER:O	5:D:51:ARG:NH2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:55:THR:HA	7:F:58:VAL:HB	1.98	0.45
7:F:66:ILE:O	7:F:70:THR:HG23	2.16	0.45
11:J:160:LYS:HA	11:J:189:PHE:CZ	2.51	0.45
12:K:198:TYR:HE1	15:N:10:TYR:HB2	1.81	0.45
13:L:147:PHE:CD2	13:L:149:VAL:HG22	2.50	0.45
22:U:24:ARG:HG3	22:U:25:LYS:N	2.32	0.45
27:Z:25:LYS:HG3	27:Z:28:LYS:HE2	1.98	0.45
34:g:123:GLY:HA3	34:g:151:VAL:HG11	1.98	0.45
34:g:259:TRP:C	34:g:267:VAL:HG23	2.41	0.45
1:2:354:A:H2'	1:2:355:C:H6	1.82	0.45
1:2:625:G:H2'	1:2:626:C:C6	2.52	0.45
1:2:1014:U:H2'	1:2:1015:C:C6	2.50	0.45
1:2:1240:U:H2'	1:2:1241:G:C8	2.46	0.45
1:2:1395:C:H5''	34:g:100:ARG:CZ	2.46	0.45
1:2:1414:C:H2'	1:2:1420:G:H5'	1.98	0.45
1:2:1506:G:H2'	1:2:1506:G:N3	2.31	0.45
1:2:1712:C:H2'	1:2:1713:G:O4'	2.17	0.45
5:D:129:THR:OG1	5:D:131:ASP:OD1	2.26	0.45
8:G:195:ILE:HG23	8:G:196:THR:N	2.30	0.45
12:K:116:HIS:CD2	12:K:152:ARG:HE	2.35	0.45
22:U:18:THR:HG21	22:U:33:ILE:HG13	1.99	0.45
24:W:36:CYS:O	24:W:40:ILE:HG12	2.16	0.45
29:b:89:ARG:O	29:b:92:ARG:HG2	2.15	0.45
39:z:552:A:H2'	39:z:553:G:C8	2.52	0.45
1:2:220:C:H2'	1:2:221:A:H8	1.81	0.45
1:2:310:G:N2	1:2:322:G:C4	2.84	0.45
1:2:541:U:H2'	1:2:542:G:C8	2.52	0.45
1:2:1013:U:H2'	1:2:1014:U:C6	2.51	0.45
6:E:241:TRP:HH2	26:Y:46:TYR:CE1	2.34	0.45
8:G:125:LYS:HB3	8:G:226:PHE:CD1	2.51	0.45
9:H:191:LYS:HE3	9:H:192:LYS:HE3	1.98	0.45
14:M:62:PHE:CZ	14:M:65:ARG:HA	2.51	0.45
17:P:19:ARG:NH2	17:P:21:SER:HB3	2.32	0.45
27:Z:61:GLN:OE1	27:Z:61:GLN:N	2.34	0.45
32:e:5:GLN:OE1	32:e:6:LEU:HG	2.17	0.45
34:g:21:ILE:HG22	34:g:33:SER:HA	1.98	0.45
34:g:208:ALA:HA	34:g:218:LEU:HD13	1.98	0.45
34:g:240:CYS:SG	34:g:241:PHE:N	2.89	0.45
1:2:5:U:H2'	1:2:6:G:H8	1.80	0.45
1:2:106:C:H5''	1:2:421:G:O2'	2.16	0.45
1:2:198:U:H3'	1:2:199:G:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:549:G:H2'	1:2:550:A:H8	1.82	0.45
1:2:847:C:H5''	1:2:848:G:C5'	2.46	0.45
1:2:1316:G:H2'	1:2:1317:G:O4'	2.16	0.45
1:2:1326:G:N2	1:2:1331:G:O6	2.50	0.45
1:2:1373:U:H3'	4:C:102:ARG:NH2	2.31	0.45
1:2:1427:G:C2	1:2:1428:U:C4	3.05	0.45
1:2:1589:A:H62	35:h:104:ARG:HD2	1.81	0.45
4:C:120:ARG:NH2	6:E:251:TYR:HB3	2.31	0.45
9:H:142:SER:O	9:H:146:ARG:N	2.46	0.45
10:I:16:ILE:HG22	10:I:18:VAL:HG13	1.99	0.45
10:I:76:LEU:HD23	10:I:94:ARG:HB2	1.99	0.45
13:L:18:ARG:O	13:L:24:ARG:NH1	2.50	0.45
15:N:101:ARG:HD2	27:Z:7:LEU:HA	1.98	0.45
38:y:17:G:O2'	38:y:59:A:N1	2.44	0.45
38:y:65:C:H2'	38:y:66:U:C6	2.52	0.45
1:2:664:C:H2'	1:2:665:U:C6	2.52	0.45
1:2:736:C:O4'	11:J:99:ARG:NH2	2.50	0.45
1:2:1232:G:O6	22:U:137:LYS:HE3	2.16	0.45
1:2:1236:A:H2'	1:2:1237:A:C8	2.52	0.45
1:2:1450:A:OP1	21:T:3:ARG:NH1	2.50	0.45
5:D:198:GLU:O	5:D:202:GLN:HG3	2.17	0.45
8:G:212:ASP:OD1	8:G:216:ASN:N	2.40	0.45
9:H:36:GLN:C	9:H:38:TYR:H	2.24	0.45
15:N:128:VAL:HG12	15:N:142:VAL:HA	1.97	0.45
16:O:53:ALA:HA	16:O:79:VAL:O	2.17	0.45
17:P:45:LEU:HD13	17:P:49:GLN:HB3	1.98	0.45
18:Q:72:TYR:O	18:Q:75:MET:HG3	2.16	0.45
23:V:139:ALA:HA	23:V:144:LYS:HB2	1.98	0.45
28:a:20:ARG:HD2	28:a:74:MET:CE	2.46	0.45
28:a:48:TYR:O	28:a:50:THR:HG23	2.17	0.45
1:2:373:G:H2'	1:2:374:U:C6	2.51	0.45
1:2:379:A:H2'	1:2:380:C:H6	1.81	0.45
1:2:1138:G:H2'	1:2:1140:A:OP2	2.17	0.45
5:D:144:LYS:NZ	5:D:146:CYS:HA	2.32	0.45
7:F:168:VAL:HG12	7:F:189:MET:HG3	1.98	0.45
8:G:137:PRO:HD2	8:G:149:TYR:CD1	2.51	0.45
11:J:116:ARG:NH2	11:J:121:THR:OG1	2.49	0.45
11:J:145:ARG:NH2	26:Y:51:GLU:HB2	2.32	0.45
26:Y:15:ASN:O	26:Y:19:LYS:HG3	2.17	0.45
28:a:101:LYS:HB3	28:a:103:SER:HB2	1.98	0.45
35:h:70:PRO:HG3	35:h:88:LEU:HD21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:641:U:H2'	1:2:642:U:C6	2.52	0.45
1:2:860:A:H2'	1:2:861:A:H8	1.81	0.45
1:2:1351:C:H4'	6:E:223:LYS:NZ	2.31	0.45
1:2:1562:G:H5''	23:V:98:SER:HB3	1.99	0.45
1:2:1588:C:H4'	20:S:45:ARG:HH21	1.82	0.45
1:2:1618:A:O5'	22:U:133:GLY:HA3	2.17	0.45
3:B:58:VAL:O	3:B:62:SER:N	2.41	0.45
8:G:212:ASP:CG	8:G:214:ASN:H	2.24	0.45
17:P:20:ARG:HG3	17:P:65:PHE:CE1	2.52	0.45
20:S:134:GLY:HA3	20:S:140:ARG:HA	1.98	0.45
22:U:90:VAL:HG12	22:U:91:LYS:HG3	1.99	0.45
1:2:344:U:OP1	15:N:90:ARG:NH1	2.50	0.45
1:2:422:G:H2'	1:2:423:A:H8	1.82	0.45
1:2:559:A:H2'	1:2:560:C:C6	2.52	0.45
1:2:1168:U:P	37:l:14:LYS:HZ1	2.40	0.45
1:2:1369:C:OP1	21:T:7:LYS:HG2	2.16	0.45
1:2:1402:G:H21	1:2:1439:C:N4	2.14	0.45
4:C:50:ASN:ND2	4:C:53:ARG:HG2	2.31	0.45
5:D:78:GLU:N	5:D:78:GLU:OE1	2.50	0.45
6:E:172:ARG:HE	6:E:172:ARG:HB3	1.57	0.45
17:P:96:VAL:O	17:P:99:ARG:HG3	2.16	0.45
18:Q:127:GLY:HA2	29:b:58:VAL:HG22	1.99	0.45
23:V:44:GLU:HG2	23:V:45:LEU:HG	1.99	0.45
34:g:154:VAL:HG13	34:g:166:VAL:O	2.17	0.45
1:2:284:C:H2'	1:2:286:C:H5'	1.99	0.45
1:2:384:G:O3'	15:N:82:MET:HE1	2.17	0.45
1:2:419:C:O2'	1:2:807:A:N1	2.42	0.45
1:2:554:A:H2'	1:2:555:G:O4'	2.17	0.45
1:2:1088:G:C2	1:2:1089:A:N7	2.85	0.45
1:2:1093:G:H2'	1:2:1094:C:H6	1.82	0.45
1:2:1194:G:H2'	1:2:1195:A:C8	2.52	0.45
4:C:198:MET:SD	4:C:199:PRO:HD2	2.56	0.45
5:D:210:VAL:O	5:D:210:VAL:HG13	2.17	0.45
6:E:62:SER:OG	6:E:65:GLU:OE1	2.27	0.45
6:E:185:ARG:O	13:L:98:LEU:HD11	2.17	0.45
6:E:196:LYS:HE2	6:E:199:LEU:HD12	1.99	0.45
17:P:71:ILE:HA	17:P:74:ILE:HD13	1.99	0.45
17:P:115:LEU:HA	17:P:118:ILE:HG12	1.99	0.45
23:V:96:SER:HB2	23:V:99:VAL:HG12	1.98	0.45
26:Y:102:ILE:HA	26:Y:128:PHE:HA	1.99	0.45
33:f:146:LEU:HD23	33:f:146:LEU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:152:SER:H	34:g:169:GLY:HA2	1.82	0.45
37:l:19:LYS:NZ	37:l:23:ARG:HH11	2.15	0.45
1:2:518:A:C4	1:2:548:G:N2	2.85	0.44
1:2:628:C:H2'	1:2:629:C:C6	2.52	0.44
1:2:656:U:H4'	1:2:1084:U:H5'	1.98	0.44
1:2:839:C:H2'	1:2:840:U:C6	2.52	0.44
1:2:1119:C:O3'	5:D:149:GLN:HG3	2.17	0.44
1:2:1301:C:OP1	33:f:92:LYS:HE3	2.16	0.44
1:2:1305:C:OP2	33:f:105:TYR:OH	2.21	0.44
1:2:1435:A:H2'	1:2:1436:C:C6	2.52	0.44
1:2:1472:A:OP1	1:2:1473:U:N3	2.38	0.44
6:E:186:GLY:HA3	13:L:98:LEU:HD21	1.98	0.44
18:Q:31:CYS:SG	18:Q:93:LEU:HD12	2.57	0.44
18:Q:119:LEU:O	18:Q:124:MET:HB2	2.17	0.44
30:c:34:ASP:HB2	30:c:82:LYS:HE2	1.98	0.44
33:f:121:CYS:SG	33:f:130:VAL:HG23	2.57	0.44
34:g:280:LYS:HD2	34:g:280:LYS:HA	1.81	0.44
1:2:235:C:H2'	1:2:236:C:C6	2.52	0.44
1:2:364:G:H2'	1:2:365:U:H6	1.82	0.44
1:2:479:A:H2'	1:2:480:C:C6	2.52	0.44
1:2:740:G:N3	11:J:109:ARG:HB2	2.32	0.44
1:2:853:U:H4'	8:G:201:HIS:HE2	1.82	0.44
1:2:959:A:P	18:Q:66:ARG:HB3	2.57	0.44
1:2:1626:U:H2'	1:2:1627:G:O4'	2.17	0.44
1:2:1685:U:H2'	1:2:1686:U:H6	1.82	0.44
1:2:1850:C:H2'	1:2:1851:G:C8	2.51	0.44
1:2:1853:A:H2'	1:2:1854:A:C8	2.53	0.44
3:B:85:ASN:HA	3:B:131:SER:HA	1.99	0.44
34:g:125:ARG:HG2	34:g:150:TRP:CD2	2.52	0.44
37:l:8:LYS:HG3	37:l:12:ARG:HH11	1.82	0.44
1:2:1191:A:H2'	1:2:1192:A:C8	2.52	0.44
1:2:1194:G:H2'	1:2:1195:A:H8	1.82	0.44
1:2:1223:G:H5'	1:2:1634:G:O6	2.17	0.44
1:2:1309:A:O2'	16:O:91:LEU:HB2	2.17	0.44
1:2:1331:G:H1	1:2:1488:U:H3	1.66	0.44
1:2:1595:G:OP1	35:h:44:LEU:HB2	2.16	0.44
1:2:1850:C:H2'	1:2:1851:G:H8	1.83	0.44
4:C:63:ARG:CZ	25:X:78:ILE:HB	2.47	0.44
5:D:37:ALA:N	5:D:231:LEU:O	2.30	0.44
5:D:223:PHE:CD2	5:D:225:LEU:HG	2.51	0.44
7:F:218:LEU:HD21	7:F:220:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:166:PHE:HA	12:K:171:LEU:HD21	1.99	0.44
25:X:39:VAL:HG23	25:X:41:LYS:H	1.82	0.44
34:g:42:MET:HE3	34:g:56:GLN:HG3	1.99	0.44
35:h:57:LYS:HG2	35:h:77:LEU:HD21	1.99	0.44
38:y:2:G:C6	38:y:71:U:H1'	2.53	0.44
39:z:520:U:H2'	39:z:521:U:C6	2.52	0.44
39:z:540:C:H2'	39:z:541:C:C6	2.52	0.44
39:z:581:A:H2'	39:z:582:U:C6	2.53	0.44
1:2:35:C:H2'	1:2:36:U:C6	2.52	0.44
1:2:152:U:H2'	1:2:153:G:C8	2.52	0.44
1:2:158:A:C2	1:2:453:C:H1'	2.53	0.44
1:2:168:C:H2'	1:2:169:U:O4'	2.16	0.44
1:2:308:C:H5	10:I:183:ARG:HH21	1.65	0.44
1:2:404:A:H2'	1:2:405:A:C8	2.52	0.44
1:2:678:U:O2	11:J:103:LYS:HE3	2.18	0.44
1:2:812:A:H2'	1:2:813:G:O4'	2.17	0.44
1:2:858:A:C5	1:2:859:U:C5	3.06	0.44
1:2:1098:G:H22	1:2:1126:G:N2	2.15	0.44
1:2:1109:A:H2'	1:2:1110:U:C6	2.52	0.44
1:2:1176:C:H2'	1:2:1177:A:O4'	2.17	0.44
1:2:1444:A:H3'	1:2:1445:G:H5''	1.99	0.44
1:2:1483:A:H2'	1:2:1484:C:C6	2.51	0.44
1:2:1767:C:H2'	1:2:1768:C:C6	2.53	0.44
5:D:171:ILE:HG23	5:D:174:ARG:HH21	1.82	0.44
7:F:22:ASN:OD1	7:F:23:GLU:N	2.50	0.44
8:G:64:ILE:HD12	28:a:17:LEU:CD2	2.47	0.44
12:K:12:ARG:NH2	12:K:18:ARG:HB3	2.33	0.44
17:P:93:LYS:HA	17:P:96:VAL:HG12	1.99	0.44
20:S:16:LYS:HD3	20:S:82:TYR:HB3	1.99	0.44
21:T:29:HIS:HA	21:T:32:LYS:HE3	2.00	0.44
23:V:125:PRO:O	23:V:128:GLN:NE2	2.50	0.44
25:X:11:LEU:HG	25:X:12:TYR:HD1	1.82	0.44
33:f:105:TYR:HB2	33:f:131:PHE:CE2	2.51	0.44
37:l:8:LYS:O	37:l:12:ARG:HG2	2.17	0.44
1:2:92:A:C8	1:2:437:A:C4	3.06	0.44
1:2:365:U:O2'	15:N:7:GLU:OE2	2.22	0.44
1:2:444:U:O3'	10:I:94:ARG:NH2	2.34	0.44
1:2:585:U:H2'	1:2:586:U:C6	2.53	0.44
1:2:1195:A:H2'	1:2:1196:A:H8	1.81	0.44
1:2:1289:A:H2'	1:2:1290:G:H8	1.82	0.44
1:2:1398:A:H2'	1:2:1401:A:C5	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1460:C:P	21:T:63:ARG:HH22	2.40	0.44
6:E:189:ILE:HB	6:E:196:LYS:HZ2	1.81	0.44
7:F:218:LEU:HD11	34:g:192:THR:HA	1.98	0.44
9:H:90:VAL:O	9:H:94:LYS:HG2	2.18	0.44
12:K:67:TRP:HE1	15:N:20:LYS:NZ	2.15	0.44
12:K:144:LYS:HA	12:K:147:LYS:HB2	1.99	0.44
12:K:199:LEU:HA	12:K:202:ILE:HG12	1.99	0.44
13:L:88:ASP:OD1	13:L:89:GLU:N	2.51	0.44
14:M:38:LYS:O	14:M:38:LYS:HD3	2.17	0.44
23:V:62:ARG:HH12	23:V:66:LEU:HD11	1.82	0.44
34:g:272:GLN:OE1	34:g:272:GLN:N	2.44	0.44
1:2:12:U:H2'	1:2:13:C:H6	1.81	0.44
1:2:332:C:H2'	1:2:333:A:C8	2.51	0.44
1:2:449:C:H3'	1:2:450:A:H8	1.83	0.44
1:2:539:C:H2'	1:2:540:C:O4'	2.17	0.44
1:2:548:G:H2'	1:2:549:G:N9	2.33	0.44
1:2:749:C:H2'	1:2:750:G:H8	1.82	0.44
1:2:818:U:H2'	1:2:820:C:OP2	2.17	0.44
1:2:1707:A:H2'	1:2:1708:C:C6	2.52	0.44
1:2:1732:G:C6	1:2:1791:U:O2	2.69	0.44
1:2:1799:G:H2'	1:2:1800:A:H8	1.82	0.44
8:G:173:ILE:HD11	8:G:235:TRP:CE2	2.52	0.44
17:P:47:PRO:HA	17:P:50:ILE:HD13	1.99	0.44
19:R:79:HIS:CE1	19:R:102:PHE:HZ	2.36	0.44
22:U:6:PRO:O	35:h:49:LEU:HD12	2.18	0.44
31:d:66:ARG:HA	31:d:66:ARG:HD2	1.85	0.44
1:2:364:G:H2'	1:2:365:U:C6	2.53	0.44
1:2:374:U:H4'	15:N:134:LEU:O	2.18	0.44
1:2:639:U:OP2	27:Z:106:GLY:HA2	2.17	0.44
1:2:932:G:H2'	1:2:933:C:H6	1.81	0.44
1:2:1088:G:OP1	17:P:2:GLY:N	2.51	0.44
1:2:1652:G:H2'	1:2:1653:G:C8	2.53	0.44
5:D:104:ASP:OD1	5:D:105:LEU:N	2.41	0.44
7:F:76:ARG:O	7:F:76:ARG:NH1	2.43	0.44
8:G:11:ARG:N	8:G:26:VAL:O	2.33	0.44
9:H:126:THR:OG1	31:d:26:GLN:OE1	2.35	0.44
10:I:106:LEU:HD13	10:I:109:LEU:HD11	2.00	0.44
12:K:162:LEU:HB3	12:K:166:PHE:HE2	1.83	0.44
22:U:70:ILE:HA	22:U:77:TYR:CE2	2.52	0.44
38:y:26:C:H2'	38:y:27:U:H6	1.83	0.44
1:2:51:U:H2'	1:2:52:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:323:G:H2'	1:2:324:C:H6	1.83	0.44
1:2:664:C:H2'	1:2:665:U:H6	1.83	0.44
1:2:959:A:H2'	1:2:960:A:C8	2.53	0.44
1:2:1076:A:OP2	1:2:1076:A:H8	2.01	0.44
1:2:1117:G:C6	1:2:1118:A:C5	3.05	0.44
1:2:1125:G:H2'	1:2:1126:G:C4	2.53	0.44
1:2:1413:C:C2	1:2:1415:C:C5	3.06	0.44
1:2:1487:G:H2'	1:2:1488:U:C6	2.53	0.44
1:2:1544:U:OP1	32:e:34:TYR:OH	2.36	0.44
1:2:1748:G:H2'	1:2:1749:C:H6	1.83	0.44
1:2:1853:A:O2'	1:2:1854:A:H5'	2.18	0.44
4:C:10:MET:HG2	21:T:111:PHE:CE2	2.47	0.44
4:C:66:VAL:HA	4:C:186:ARG:HH11	1.82	0.44
4:C:189:ILE:H	4:C:189:ILE:HD12	1.82	0.44
10:I:63:MET:SD	10:I:100:CYS:HA	2.57	0.44
17:P:110:ASP:O	17:P:114:ARG:HG2	2.17	0.44
31:d:16:LYS:HD2	31:d:16:LYS:HA	1.72	0.44
32:e:49:ASP:OD1	32:e:50:ILE:N	2.47	0.44
39:z:527:G:H2'	39:z:528:C:H6	1.83	0.44
1:2:414:C:H2'	1:2:415:G:O4'	2.17	0.44
1:2:1066:A:H2'	1:2:1067:G:O4'	2.18	0.44
1:2:1321:G:O2'	1:2:1323:G:OP1	2.35	0.44
1:2:1451:A:H2'	1:2:1452:G:H8	1.82	0.44
1:2:1561:G:N2	1:2:1563:C:H3'	2.33	0.44
4:C:175:TRP:CE3	4:C:178:LEU:HD11	2.53	0.44
9:H:122:ARG:NH2	31:d:9:ILE:HD11	2.33	0.44
11:J:6:ALA:HB1	11:J:21:SER:HB3	2.00	0.44
11:J:99:ARG:HE	11:J:100:ILE:H	1.65	0.44
14:M:33:PRO:O	14:M:34:GLU:HG2	2.18	0.44
19:R:94:VAL:O	19:R:104:GLN:HA	2.17	0.44
39:z:540:C:H2'	39:z:541:C:H6	1.83	0.44
1:2:217:U:O4	1:2:293:A:N6	2.50	0.43
1:2:674:G:H2'	1:2:675:A:H8	1.83	0.43
1:2:1108:U:H3	1:2:1109:A:H62	1.64	0.43
1:2:1179:A:O3'	37:l:11:ARG:NH2	2.50	0.43
1:2:1492:U:O2'	1:2:1494:A:OP1	2.28	0.43
1:2:1606:G:H2'	1:2:1607:G:H8	1.83	0.43
1:2:1704:G:N2	1:2:1818:A:N1	2.50	0.43
1:2:1860:A:H5'	29:b:95:ARG:HD2	2.00	0.43
11:J:75:ILE:HD11	11:J:78:ARG:HB2	2.00	0.43
23:V:62:ARG:O	23:V:65:TYR:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:34:ILE:H	26:Y:34:ILE:HD12	1.83	0.43
1:2:17:C:O2'	1:2:1190:A:N1	2.51	0.43
1:2:369:C:P	12:K:181:GLN:HE22	2.42	0.43
1:2:882:A:H61	1:2:896:C:H42	1.66	0.43
1:2:962:U:H2'	1:2:963:C:C6	2.53	0.43
1:2:1800:A:H2'	1:2:1801:C:C6	2.53	0.43
8:G:8:HIS:O	8:G:30:ARG:NH1	2.51	0.43
15:N:147:LYS:HD3	15:N:153:LYS:HB2	2.00	0.43
26:Y:26:LEU:HA	26:Y:60:LYS:NZ	2.33	0.43
37:l:4:LYS:H	37:l:4:LYS:HG2	1.56	0.43
1:2:237:G:H2'	1:2:238:G:O4'	2.18	0.43
1:2:285:U:O4	15:N:14:PRO:HG2	2.18	0.43
1:2:370:G:H1'	12:K:5:ARG:NE	2.33	0.43
1:2:533:C:H2'	1:2:534:G:O4'	2.18	0.43
1:2:646:G:H5'	1:2:652:G:N2	2.32	0.43
1:2:820:C:H5'	13:L:147:PHE:CD1	2.53	0.43
4:C:108:PHE:HB2	4:C:136:GLU:CD	2.42	0.43
5:D:86:LEU:HD12	5:D:98:THR:HG23	2.00	0.43
7:F:94:ARG:HB2	7:F:125:PHE:HZ	1.82	0.43
7:F:132:LYS:NZ	7:F:193:ASP:HB2	2.33	0.43
8:G:129:ILE:HA	8:G:138:HIS:O	2.18	0.43
11:J:41:ARG:HD2	11:J:41:ARG:HA	1.79	0.43
11:J:126:HIS:O	11:J:130:LEU:HD23	2.18	0.43
12:K:67:TRP:HA	12:K:189:VAL:HG22	2.00	0.43
15:N:35:ARG:HG2	15:N:51:ILE:O	2.18	0.43
17:P:33:VAL:O	17:P:36:GLN:HG2	2.18	0.43
19:R:111:MET:HE1	22:U:117:ILE:HG23	2.00	0.43
28:a:15:ASN:OD1	28:a:18:LEU:HB2	2.18	0.43
32:e:33:LYS:O	32:e:36:LEU:HD23	2.18	0.43
39:z:535:A:O2'	39:z:540:C:N3	2.43	0.43
39:z:541:C:H2'	39:z:542:A:H8	1.83	0.43
1:2:1279:C:H4'	33:f:99:LYS:HZ2	1.83	0.43
1:2:1369:C:H5'	21:T:7:LYS:HD3	2.00	0.43
1:2:1851:G:H2'	1:2:1852:G:H8	1.83	0.43
4:C:111:GLN:HG2	6:E:74:LYS:HB3	1.99	0.43
6:E:226:PHE:HA	6:E:229:ILE:HG12	2.00	0.43
11:J:142:LYS:HD3	17:P:18:TYR:OH	2.18	0.43
19:R:10:ARG:HG3	19:R:22:LEU:HD22	2.01	0.43
20:S:54:PRO:HG3	20:S:85:ARG:HG3	2.00	0.43
23:V:11:GLN:HA	23:V:14:PHE:HB3	2.00	0.43
30:c:18:LYS:C	30:c:23:ARG:HH12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:36:ARG:HG2	34:g:65:PHE:HB3	1.99	0.43
1:2:74:G:H2'	1:2:75:G:N3	2.32	0.43
1:2:84:A:N3	1:2:150:A:O2'	2.49	0.43
1:2:124:U:N3	1:2:330:C:N4	2.37	0.43
1:2:1386:U:H2'	1:2:1387:C:H6	1.84	0.43
1:2:1436:C:H2'	1:2:1437:U:C6	2.54	0.43
1:2:1460:C:H2'	1:2:1461:A:C8	2.54	0.43
1:2:1587:C:H5''	9:H:91:ARG:NH1	2.31	0.43
1:2:1637:U:H2'	1:2:1638:U:H6	1.83	0.43
1:2:1803:A:H2'	1:2:1804:U:H6	1.84	0.43
4:C:22:GLY:HA2	4:C:24:HIS:CE1	2.54	0.43
5:D:82:ARG:HG3	5:D:82:ARG:O	2.19	0.43
22:U:6:PRO:N	35:h:50:PHE:HB2	2.32	0.43
23:V:42:HIS:HB3	23:V:93:SER:OG	2.17	0.43
26:Y:90:GLN:O	26:Y:94:LEU:HB3	2.17	0.43
34:g:19:THR:O	34:g:288:SER:HB3	2.18	0.43
1:2:42:A:O2'	1:2:98:C:OP1	2.25	0.43
1:2:193:C:H2'	1:2:194:C:C6	2.53	0.43
1:2:1575:A:C8	24:W:56:MET:HE1	2.53	0.43
1:2:1833:U:H2'	1:2:1834:U:C6	2.53	0.43
5:D:227:LYS:O	5:D:231:LEU:HG	2.19	0.43
6:E:93:LYS:HD2	6:E:95:MET:HE3	1.99	0.43
8:G:155:LYS:HA	8:G:155:LYS:HD3	1.90	0.43
9:H:106:GLU:OE2	9:H:110:GLN:HB2	2.18	0.43
10:I:98:ARG:HD2	10:I:106:LEU:HD21	1.99	0.43
10:I:131:ARG:H	10:I:131:ARG:HG2	1.67	0.43
13:L:21:GLU:OE1	13:L:24:ARG:N	2.39	0.43
13:L:109:ARG:HE	13:L:111:GLN:HE22	1.65	0.43
15:N:5:GLN:OE1	15:N:10:TYR:HA	2.18	0.43
20:S:61:GLU:H	20:S:61:GLU:CD	2.27	0.43
23:V:74:SER:O	23:V:77:LYS:HG3	2.19	0.43
23:V:101:ARG:O	23:V:105:GLN:OE1	2.36	0.43
35:h:82:SER:HA	35:h:85:ARG:NE	2.34	0.43
38:y:38:C:H3'	38:y:39:C:C6	2.54	0.43
1:2:291:U:C2	1:2:292:A:N7	2.87	0.43
1:2:330:C:H2'	1:2:331:C:C6	2.53	0.43
1:2:442:G:H2'	1:2:443:C:H6	1.83	0.43
1:2:952:G:H2'	1:2:953:A:C8	2.53	0.43
1:2:1262:C:C4	1:2:1512:G:N2	2.87	0.43
1:2:1394:G:H2'	1:2:1395:C:C6	2.54	0.43
1:2:1552:C:OP1	32:e:13:LYS:NZ	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1734:C:H2'	1:2:1735:C:H6	1.84	0.43
1:2:1766:C:H2'	1:2:1767:C:C6	2.53	0.43
4:C:33:GLN:NE2	25:X:63:GLY:O	2.51	0.43
7:F:164:VAL:O	7:F:168:VAL:HG22	2.18	0.43
8:G:64:ILE:HG23	28:a:17:LEU:HD21	2.01	0.43
10:I:210:ALA:O	10:I:213:LEU:HG	2.19	0.43
16:O:19:GLN:HG2	16:O:88:TRP:CH2	2.54	0.43
17:P:98:VAL:O	17:P:102:LEU:HD23	2.18	0.43
22:U:23:ARG:CZ	35:h:48:VAL:HG22	2.48	0.43
35:h:97:ILE:CG2	35:h:109:TYR:HB3	2.48	0.43
38:y:10:G:N7	38:y:45:G:N1	2.67	0.43
1:2:384:G:H2'	1:2:385:G:H8	1.83	0.43
1:2:487:C:H2'	1:2:488:C:C6	2.53	0.43
1:2:1088:G:C2	1:2:1154:G:C6	3.07	0.43
1:2:1165:G:H3'	1:2:1166:A:H8	1.83	0.43
1:2:1372:A:OP2	21:T:67:ARG:NH1	2.49	0.43
1:2:1403:U:H2'	1:2:1404:U:C6	2.54	0.43
1:2:1535:G:C2	1:2:1536:G:C5	3.06	0.43
1:2:1641:C:P	20:S:138:ARG:HE	2.42	0.43
4:C:11:LYS:NZ	4:C:184:ARG:HH12	2.17	0.43
4:C:124:VAL:O	4:C:146:ALA:HA	2.19	0.43
6:E:118:TYR:HE1	6:E:201:MET:HA	1.84	0.43
6:E:233:TYR:HE1	25:X:14:PRO:HB3	1.83	0.43
8:G:86:PHE:HE1	8:G:102:ILE:HA	1.84	0.43
9:H:122:ARG:HA	9:H:146:ARG:HH22	1.83	0.43
14:M:7:ASN:O	14:M:11:ILE:HG12	2.19	0.43
17:P:96:VAL:O	17:P:100:LYS:HG3	2.18	0.43
29:b:38:LYS:O	29:b:71:LEU:HG	2.18	0.43
37:l:15:ARG:O	37:l:18:ARG:HG2	2.18	0.43
1:2:29:G:H2'	1:2:30:C:H6	1.84	0.43
1:2:545:A:H2'	1:2:546:U:C6	2.54	0.43
1:2:952:G:H4'	18:Q:60:MET:HE1	2.00	0.43
1:2:966:G:H5''	1:2:967:G:C8	2.54	0.43
1:2:1028:C:H5''	17:P:109:LYS:NZ	2.32	0.43
1:2:1273:C:H2'	1:2:1274:A:H8	1.82	0.43
1:2:1413:C:H2'	1:2:1415:C:H6	1.84	0.43
1:2:1557:C:H5''	23:V:71:GLY:HA3	2.00	0.43
6:E:239:ASP:OD2	25:X:1:MET:HE2	2.19	0.43
8:G:71:LYS:NZ	8:G:93:ASP:OD2	2.51	0.43
9:H:145:ARG:HA	9:H:148:ASN:HD22	1.82	0.43
9:H:192:LYS:HA	9:H:195:GLU:OE1	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:49:LYS:HG3	11:J:63:PHE:HE1	1.84	0.43
15:N:92:TYR:CZ	15:N:105:ARG:HB2	2.54	0.43
22:U:23:ARG:HH12	35:h:47:LEU:HA	1.82	0.43
22:U:70:ILE:HA	22:U:77:TYR:HE2	1.83	0.43
26:Y:70:ASN:C	26:Y:70:ASN:HD22	2.26	0.43
34:g:20:GLN:OE1	34:g:69:VAL:N	2.36	0.43
35:h:72:VAL:O	35:h:76:ARG:HB2	2.19	0.43
1:2:4:C:H4'	6:E:192:ALA:HB2	2.01	0.43
1:2:50:A:H2'	1:2:51:U:O4'	2.19	0.43
1:2:293:A:H1'	12:K:73:THR:CG2	2.48	0.43
1:2:516:A:H5''	36:i:109:ARG:HH12	1.83	0.43
1:2:868:A:O2'	1:2:869:G:O5'	2.37	0.43
1:2:929:G:N3	1:2:996:C:H2'	2.34	0.43
1:2:938:G:H2'	1:2:939:U:C6	2.54	0.43
1:2:957:G:C4	39:z:831:A:C6	3.04	0.43
1:2:992:A:H2'	1:2:993:A:C8	2.54	0.43
1:2:1013:U:OP1	17:P:14:SER:OG	2.23	0.43
1:2:1584:A:H2'	1:2:1585:C:O4'	2.19	0.43
1:2:1748:G:H2'	1:2:1749:C:C6	2.54	0.43
4:C:69:GLU:OE2	6:E:252:GLN:HA	2.19	0.43
5:D:112:SER:HA	29:b:68:TYR:HE2	1.83	0.43
8:G:9:LEU:HG	8:G:30:ARG:HG3	2.01	0.43
9:H:77:MET:HA	9:H:77:MET:HE3	2.01	0.43
15:N:77:VAL:HG13	15:N:86:ILE:HD11	2.00	0.43
17:P:4:MET:HE3	17:P:124:ARG:HD3	2.00	0.43
19:R:18:ARG:H	22:U:91:LYS:CA	2.27	0.43
21:T:38:ILE:HD12	21:T:38:ILE:HA	1.91	0.43
33:f:82:LYS:HE2	33:f:82:LYS:HB2	1.87	0.43
34:g:298:LEU:HD23	34:g:298:LEU:H	1.83	0.43
1:2:92:A:N6	1:2:434:G:H1'	2.34	0.42
1:2:517:C:H2'	1:2:518:A:C8	2.53	0.42
1:2:532:U:H2'	1:2:533:C:O4'	2.19	0.42
1:2:826:A:C6	1:2:841:G:N1	2.87	0.42
1:2:1119:C:H4'	5:D:149:GLN:HB2	2.00	0.42
1:2:1281:G:N2	33:f:104:LYS:HG2	2.30	0.42
1:2:1289:A:N6	1:2:1298:G:O6	2.52	0.42
1:2:1386:U:H2'	1:2:1387:C:C6	2.53	0.42
5:D:167:LYS:NZ	5:D:201:CYS:HA	2.34	0.42
7:F:29:LEU:O	7:F:34:TYR:HB2	2.19	0.42
7:F:167:TYR:OH	7:F:201:LYS:O	2.30	0.42
8:G:11:ARG:NE	8:G:27:PHE:O	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:12:ARG:HG2	12:K:13:LYS:N	2.34	0.42
12:K:22:HIS:HB2	12:K:25:ARG:HH12	1.84	0.42
15:N:30:LYS:HG3	15:N:31:GLU:OE1	2.19	0.42
16:O:32:ALA:HB3	16:O:110:VAL:HB	2.01	0.42
18:Q:124:MET:HA	18:Q:124:MET:HE3	2.01	0.42
19:R:127:LYS:HD2	19:R:127:LYS:HA	1.64	0.42
22:U:51:ASP:OD1	22:U:52:LEU:N	2.52	0.42
26:Y:36:ARG:NE	26:Y:36:ARG:HA	2.34	0.42
26:Y:82:GLN:O	26:Y:84:LYS:HG2	2.19	0.42
37:l:9:ARG:HG2	37:l:10:MET:HE2	2.01	0.42
38:y:9:G:N2	38:y:21:G:O6	2.51	0.42
1:2:56:G:C6	1:2:90:G:N1	2.87	0.42
1:2:370:G:H5''	12:K:31:ARG:NH2	2.31	0.42
1:2:859:U:H2'	1:2:860:A:H8	1.84	0.42
1:2:967:G:H4'	1:2:968:A:H8	1.84	0.42
1:2:1156:U:P	27:Z:5:ARG:H	2.42	0.42
1:2:1217:G:H2'	1:2:1218:G:H8	1.84	0.42
1:2:1380:C:H5''	7:F:157:MET:O	2.19	0.42
1:2:1644:U:OP1	20:S:127:CYS:HA	2.19	0.42
5:D:171:ILE:HG23	5:D:174:ARG:NH2	2.34	0.42
13:L:32:ILE:HD11	13:L:37:LEU:HB2	2.01	0.42
13:L:93:LYS:HD2	13:L:93:LYS:HA	1.89	0.42
17:P:20:ARG:HG3	17:P:65:PHE:CD1	2.54	0.42
26:Y:34:ILE:O	26:Y:38:LEU:HD23	2.18	0.42
26:Y:75:ILE:HG12	26:Y:127:GLY:HA2	2.00	0.42
34:g:271:LYS:HD2	34:g:271:LYS:HA	1.93	0.42
35:h:62:VAL:O	35:h:111:ARG:HG3	2.19	0.42
1:2:1307:C:H3'	1:2:1308:G:H8	1.83	0.42
1:2:1537:C:OP1	23:V:63:HIS:NE2	2.52	0.42
4:C:14:ASP:HA	4:C:17:LYS:HZ2	1.84	0.42
5:D:162:ARG:HG2	5:D:165:ARG:HH21	1.84	0.42
6:E:233:TYR:CE1	25:X:14:PRO:HB3	2.54	0.42
7:F:67:ARG:NE	14:M:93:THR:HA	2.34	0.42
9:H:92:ILE:HD12	9:H:169:ILE:HG21	2.01	0.42
10:I:48:TYR:CD1	10:I:113:ILE:HD11	2.55	0.42
13:L:42:GLU:OE1	13:L:42:GLU:N	2.46	0.42
19:R:123:TYR:OH	22:U:124:ARG:NH1	2.49	0.42
20:S:58:LEU:O	20:S:62:ARG:NH1	2.52	0.42
26:Y:80:ASP:OD1	26:Y:81:VAL:N	2.52	0.42
26:Y:104:LEU:HB3	26:Y:125:ILE:HD12	2.00	0.42
30:c:30:SER:HB2	30:c:48:SER:OG	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:90:TRP:N	34:g:90:TRP:CD1	2.87	0.42
36:i:114:ARG:HD2	36:i:114:ARG:HA	1.81	0.42
38:y:64:C:H2'	38:y:65:C:C6	2.55	0.42
39:z:547:G:C2	39:z:549:G:H8	2.36	0.42
1:2:499:G:H2'	1:2:500:G:C8	2.55	0.42
1:2:637:U:H2'	1:2:638:A:H8	1.84	0.42
1:2:924:G:C6	1:2:1010:G:C6	3.08	0.42
1:2:1469:G:H22	1:2:1471:G:H5''	1.85	0.42
1:2:1535:G:C6	1:2:1589:A:N1	2.88	0.42
1:2:1612:G:H1	19:R:40:ARG:NH2	2.18	0.42
1:2:1618:A:C8	22:U:132:ARG:HG2	2.55	0.42
1:2:1643:G:HO2'	1:2:1669:G:H1	1.67	0.42
1:2:1687:U:H5''	29:b:89:ARG:NH1	2.34	0.42
1:2:1784:A:H2'	1:2:1785:A:O4'	2.19	0.42
4:C:17:LYS:HE2	4:C:176:TRP:HZ3	1.84	0.42
9:H:55:ARG:HH22	20:S:124:PRO:HD2	1.85	0.42
9:H:69:VAL:O	9:H:73:THR:HG23	2.18	0.42
11:J:118:ARG:O	11:J:121:THR:HG22	2.19	0.42
12:K:159:SER:HB3	12:K:161:LEU:HG	2.01	0.42
13:L:163:SER:H	13:L:168:GLY:HA3	1.84	0.42
16:O:26:LEU:HD23	16:O:93:LYS:HB3	2.01	0.42
27:Z:48:LYS:O	27:Z:74:LEU:HD12	2.19	0.42
33:f:92:LYS:HE2	33:f:93:HIS:O	2.20	0.42
34:g:6:THR:CG2	34:g:8:ARG:HH12	2.26	0.42
38:y:48:G:H2'	38:y:49:A:H8	1.84	0.42
38:y:51:G:C6	38:y:62:A:N1	2.88	0.42
1:2:15:U:H2'	1:2:16:G:O4'	2.19	0.42
1:2:158:A:H2	1:2:453:C:H1'	1.83	0.42
1:2:368:U:H2'	1:2:369:C:O4'	2.18	0.42
1:2:800:U:H2'	1:2:801:U:C6	2.54	0.42
1:2:911:G:N2	1:2:911:G:OP2	2.53	0.42
1:2:942:U:H2'	1:2:943:G:C8	2.54	0.42
1:2:1198:U:H4'	6:E:99:LYS:HE2	2.00	0.42
1:2:1440:U:H2'	1:2:1441:U:C6	2.54	0.42
1:2:1537:C:OP1	23:V:59:SER:OG	2.37	0.42
1:2:1670:A:N7	1:2:1671:U:C5	2.87	0.42
4:C:62:ALA:O	4:C:66:VAL:HG23	2.20	0.42
7:F:216:GLU:OE2	21:T:20:TYR:HA	2.19	0.42
8:G:36:HIS:CE1	8:G:85:GLY:HA3	2.54	0.42
9:H:140:ASP:OD1	9:H:141:VAL:N	2.45	0.42
13:L:137:VAL:C	13:L:139:LYS:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:50:LYS:HE3	18:Q:50:LYS:HB3	1.76	0.42
24:W:81:GLN:C	24:W:82:MET:HE2	2.44	0.42
38:y:63:U:H2'	38:y:64:C:C6	2.53	0.42
39:z:831:A:H5''	39:z:832:A:C5	2.54	0.42
1:2:163:U:O3'	10:I:83:CYS:HA	2.19	0.42
1:2:471:C:H2'	1:2:472:G:C8	2.55	0.42
1:2:580:A:H4'	36:i:98:LYS:HE2	2.02	0.42
1:2:827:G:H2'	1:2:828:G:C8	2.54	0.42
1:2:849:C:C5	1:2:850:A:C8	3.08	0.42
1:2:895:U:H2'	1:2:896:C:O4'	2.19	0.42
1:2:1067:G:H2'	1:2:1068:U:O4'	2.19	0.42
1:2:1102:C:OP1	30:c:70:LYS:NZ	2.36	0.42
1:2:1175:G:N2	1:2:1178:A:OP2	2.39	0.42
1:2:1859:C:N3	29:b:6:ARG:N	2.55	0.42
4:C:8:LEU:HD11	25:X:39:VAL:HG21	2.01	0.42
4:C:80:ARG:HH12	4:C:165:ASN:C	2.28	0.42
6:E:163:HIS:CG	6:E:185:ARG:HG2	2.54	0.42
6:E:195:PRO:HA	6:E:198:LEU:HG	2.00	0.42
10:I:192:ILE:HD12	10:I:192:ILE:HA	1.96	0.42
1:2:191:C:H2'	1:2:192:U:C6	2.53	0.42
1:2:469:C:H2'	1:2:470:G:O4'	2.20	0.42
1:2:528:U:H2'	1:2:529:C:H6	1.84	0.42
1:2:1721:G:C6	1:2:1803:A:C6	3.07	0.42
10:I:229:ALA:HA	10:I:232:ARG:HG3	2.02	0.42
11:J:144:ILE:HG12	26:Y:52:ILE:HG22	2.02	0.42
12:K:190:LEU:C	12:K:195:LEU:HD21	2.45	0.42
14:M:37:ASP:OD1	14:M:38:LYS:N	2.53	0.42
20:S:9:SER:HA	20:S:25:CYS:O	2.19	0.42
25:X:58:ALA:O	25:X:62:MET:HG3	2.20	0.42
34:g:234:ASP:OD1	34:g:235:ILE:N	2.52	0.42
37:l:3:ALA:HA	37:l:6:ARG:NH1	2.35	0.42
38:y:51:G:C6	38:y:62:A:C6	3.08	0.42
1:2:342:U:C5'	15:N:139:ARG:HG2	2.49	0.42
1:2:343:C:H2'	1:2:344:U:C6	2.54	0.42
1:2:553:G:N3	1:2:554:A:C8	2.88	0.42
1:2:637:U:H2'	1:2:638:A:C8	2.55	0.42
1:2:674:G:H2'	1:2:675:A:C8	2.55	0.42
1:2:821:A:H2'	1:2:822:A:H8	1.85	0.42
1:2:1187:C:H2'	1:2:1188:U:C6	2.54	0.42
1:2:1353:A:H5''	6:E:97:VAL:HG11	2.01	0.42
1:2:1469:G:N2	1:2:1471:G:OP2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:283:ILE:O	3:B:334:GLY:N	2.52	0.42
5:D:225:LEU:HB3	5:D:229:MET:HE1	2.01	0.42
9:H:99:ILE:O	9:H:103:LEU:HG	2.20	0.42
10:I:39:ASP:OD1	10:I:40:ALA:N	2.53	0.42
12:K:129:LEU:O	12:K:134:GLU:HB2	2.20	0.42
17:P:126:ALA:HB1	17:P:139:TRP:HZ3	1.85	0.42
19:R:10:ARG:HA	19:R:10:ARG:HD2	1.91	0.42
21:T:122:PRO:HA	21:T:123:THR:HA	1.85	0.42
25:X:55:ILE:HG23	25:X:59:ILE:HD11	2.01	0.42
32:e:26:ASN:O	32:e:27:ARG:HG3	2.20	0.42
38:y:49:A:H4'	39:z:551:C:O3'	2.19	0.42
1:2:96:C:H1'	1:2:464:G:H5'	2.02	0.42
1:2:1089:A:H2'	1:2:1090:C:C6	2.55	0.42
8:G:120:LYS:HA	8:G:120:LYS:HD2	1.91	0.42
8:G:127:ARG:N	8:G:140:VAL:O	2.40	0.42
19:R:82:ASP:OD1	19:R:82:ASP:N	2.50	0.42
21:T:18:GLU:HG2	21:T:70:SER:H	1.85	0.42
24:W:69:PRO:HA	32:e:40:ARG:NH1	2.35	0.42
30:c:79:PHE:O	30:c:80:ARG:NH1	2.42	0.42
1:2:442:G:H2'	1:2:443:C:C6	2.55	0.42
1:2:645:A:H1'	1:2:648:U:OP1	2.19	0.42
1:2:1174:U:H2'	1:2:1175:G:O4'	2.20	0.42
1:2:1412:C:O2'	23:V:132:ASP:OD2	2.38	0.42
1:2:1450:A:H5''	21:T:3:ARG:NH1	2.32	0.42
1:2:1858:U:O2'	1:2:1860:A:N7	2.53	0.42
5:D:212:VAL:HG13	5:D:212:VAL:O	2.19	0.42
6:E:155:TRP:C	26:Y:98:GLN:HE22	2.28	0.42
8:G:29:PRO:HG3	8:G:45:ILE:HD11	2.01	0.42
8:G:40:GLU:OE2	8:G:103:TYR:OH	2.20	0.42
8:G:124:CYS:HB3	8:G:141:THR:HB	2.02	0.42
12:K:113:TYR:OH	12:K:158:ILE:HD11	2.20	0.42
14:M:5:LYS:O	14:M:8:ARG:HB2	2.20	0.42
18:Q:31:CYS:HB2	18:Q:95:ILE:HA	2.02	0.42
18:Q:97:LEU:O	18:Q:132:VAL:N	2.24	0.42
19:R:123:TYR:CD2	19:R:125:PRO:HA	2.55	0.42
21:T:24:LEU:O	34:g:212:LYS:NZ	2.53	0.42
1:2:152:U:H2'	1:2:153:G:O4'	2.20	0.41
1:2:161:U:C4	28:a:115:LYS:HB3	2.55	0.41
1:2:412:U:H2'	1:2:413:U:H6	1.82	0.41
1:2:525:G:H2'	1:2:526:A:H8	1.85	0.41
1:2:643:A:H2'	1:2:644:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:743:U:O2'	1:2:744:C:O4'	2.29	0.41
1:2:921:G:C2	1:2:922:A:C8	3.08	0.41
1:2:1245:C:H3'	1:2:1246:A:C8	2.55	0.41
1:2:1252:G:H3'	1:2:1252:G:N3	2.35	0.41
1:2:1307:C:H3'	1:2:1308:G:C8	2.55	0.41
1:2:1347:G:H2'	1:2:1348:G:C8	2.53	0.41
7:F:157:MET:HE3	7:F:158:ILE:O	2.19	0.41
9:H:133:THR:OG1	9:H:135:ARG:NH1	2.53	0.41
14:M:3:MET:HA	14:M:4:PRO:HD3	1.91	0.41
18:Q:61:LYS:NZ	18:Q:76:LEU:HG	2.35	0.41
22:U:130:ARG:HA	22:U:130:ARG:HD3	1.78	0.41
23:V:62:ARG:NH1	23:V:66:LEU:HD11	2.35	0.41
23:V:85:ASN:HB3	23:V:88:MET:HB2	2.02	0.41
34:g:22:ALA:HB1	34:g:71:ILE:HG23	2.02	0.41
35:h:72:VAL:O	35:h:76:ARG:HD3	2.19	0.41
1:2:79:A:O2'	1:2:80:G:O5'	2.38	0.41
1:2:370:G:H1'	12:K:5:ARG:CZ	2.50	0.41
1:2:746:C:H2'	1:2:747:G:C8	2.55	0.41
1:2:1000:U:H2'	1:2:1001:G:C8	2.54	0.41
1:2:1140:A:P	1:2:1351:C:H41	2.43	0.41
1:2:1164:G:H3'	1:2:1165:G:C8	2.55	0.41
1:2:1255:A:H62	1:2:1513:C:H3'	1.85	0.41
1:2:1355:U:H2'	1:2:1356:U:C6	2.54	0.41
1:2:1360:U:H3	1:2:1371:G:H21	1.68	0.41
1:2:1456:C:H2'	1:2:1457:G:C8	2.55	0.41
1:2:1652:G:H2'	1:2:1653:G:H8	1.84	0.41
1:2:1660:G:OP1	23:V:91:HIS:NE2	2.49	0.41
1:2:1741:U:H2'	1:2:1742:C:C6	2.56	0.41
6:E:174:GLY:HA3	6:E:220:ASN:HD21	1.86	0.41
7:F:141:LYS:C	7:F:142:LEU:HD12	2.44	0.41
8:G:249:ALA:HA	13:L:72:PHE:HE1	1.85	0.41
9:H:82:ASN:HA	9:H:85:LYS:HD3	2.02	0.41
10:I:45:TRP:HA	10:I:48:TYR:HD2	1.84	0.41
12:K:40:PRO:HG2	12:K:59:ARG:NH1	2.35	0.41
16:O:22:LEU:HA	16:O:25:ALA:HB3	2.01	0.41
19:R:10:ARG:NH1	19:R:21:ASP:HA	2.35	0.41
19:R:41:GLN:OE1	19:R:41:GLN:N	2.41	0.41
21:T:72:LYS:HD2	21:T:75:GLU:OE2	2.20	0.41
24:W:66:ARG:HE	24:W:77:TRP:HE1	1.68	0.41
24:W:66:ARG:HG3	24:W:68:THR:H	1.84	0.41
27:Z:68:LYS:NZ	36:i:83:VAL:HA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
29:b:10:ARG:H	29:b:12:LYS:NZ	2.19	0.41
31:d:9:ILE:O	31:d:10:LYS:HE2	2.20	0.41
35:h:71:ALA:O	35:h:75:GLU:OE1	2.38	0.41
35:h:103:HIS:CG	35:h:104:ARG:N	2.87	0.41
1:2:49:C:H2'	1:2:462:C:H41	1.85	0.41
1:2:812:A:H2'	1:2:813:G:C8	2.54	0.41
1:2:1032:A:H4'	1:2:1849:G:N2	2.34	0.41
1:2:1450:A:OP1	21:T:49:LYS:NZ	2.44	0.41
1:2:1815:U:H2'	1:2:1816:A:C8	2.34	0.41
4:C:160:ALA:N	25:X:66:ASP:OD1	2.53	0.41
9:H:39:ILE:HG23	9:H:68:ILE:HG13	2.03	0.41
10:I:161:PRO:HA	10:I:171:THR:HA	2.03	0.41
18:Q:133:THR:O	18:Q:135:ILE:N	2.50	0.41
21:T:109:LEU:CD2	21:T:111:PHE:HB2	2.50	0.41
23:V:14:PHE:HZ	23:V:131:LEU:HD12	1.84	0.41
26:Y:11:LEU:HB2	26:Y:72:CYS:SG	2.60	0.41
31:d:27:CYS:SG	31:d:45:ASN:HB3	2.61	0.41
32:e:16:GLN:OE1	32:e:16:GLN:N	2.45	0.41
39:z:549:G:H2'	39:z:550:A:C8	2.56	0.41
1:2:357:U:OP1	12:K:11:ARG:NH2	2.53	0.41
1:2:376:C:H1'	12:K:5:ARG:CG	2.50	0.41
1:2:573:A:N3	1:2:573:A:H2'	2.35	0.41
1:2:604:G:N2	27:Z:62:PRO:O	2.53	0.41
18:Q:34:PHE:O	18:Q:41:PHE:N	2.36	0.41
21:T:25:GLY:O	21:T:58:MET:HG2	2.19	0.41
28:a:12:PHE:CZ	28:a:21:LYS:HD2	2.55	0.41
28:a:102:THR:OG1	28:a:103:SER:HA	2.20	0.41
38:y:42:G:H2'	38:y:43:A:C8	2.56	0.41
39:z:582:U:H2'	39:z:584:A:N7	2.35	0.41
1:2:294:C:H2'	1:2:295:C:C6	2.55	0.41
1:2:342:U:H5'	15:N:139:ARG:HG2	2.01	0.41
1:2:565:A:H2'	1:2:566:A:O4'	2.21	0.41
1:2:839:C:H1'	8:G:263:GLY:H	1.84	0.41
1:2:940:A:H1'	18:Q:139:SER:OG	2.20	0.41
1:2:957:G:N1	39:z:831:A:N1	2.65	0.41
1:2:1123:C:C4'	30:c:17:ARG:HH22	2.34	0.41
1:2:1135:C:H5	1:2:1145:A:H62	1.68	0.41
1:2:1223:G:H1'	1:2:1633:G:H1'	2.01	0.41
1:2:1280:A:H2	16:O:33:ARG:HE	1.68	0.41
1:2:1453:U:H2'	1:2:1454:G:H8	1.84	0.41
1:2:1637:U:H2'	1:2:1638:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1676:U:H2'	1:2:1677:C:C6	2.55	0.41
1:2:1680:U:C4	1:2:1681:G:N7	2.88	0.41
1:2:1688:G:P	29:b:89:ARG:HH22	2.43	0.41
1:2:1860:A:C2	29:b:87:ARG:NH2	2.89	0.41
4:C:71:PRO:HD3	4:C:186:ARG:NH2	2.35	0.41
4:C:84:GLN:HA	4:C:87:VAL:HG22	2.02	0.41
5:D:77:ASP:OD1	5:D:77:ASP:N	2.51	0.41
5:D:214:LYS:HB3	5:D:216:LYS:HZ3	1.86	0.41
7:F:121:GLY:HA2	7:F:124:ARG:HE	1.84	0.41
9:H:28:VAL:HA	9:H:110:GLN:HG3	2.03	0.41
13:L:135:ILE:HD13	13:L:159:PHE:HA	2.02	0.41
19:R:88:GLU:HG3	19:R:89:MET:SD	2.61	0.41
19:R:119:PHE:HZ	22:U:117:ILE:HG22	1.85	0.41
21:T:41:ILE:HG12	21:T:47:ARG:HB2	2.02	0.41
25:X:23:ILE:HD12	25:X:23:ILE:HA	1.86	0.41
38:y:17:G:H5'	38:y:60:C:H5'	2.02	0.41
38:y:46:U:H4'	38:y:47:C:H5	1.83	0.41
39:z:529:A:H2'	39:z:530:G:C8	2.55	0.41
39:z:564:G:H22	39:z:574:C:H1'	1.85	0.41
1:2:21:U:H4'	13:L:19:PRO:HG3	2.02	0.41
1:2:558:C:H2'	1:2:559:A:O4'	2.20	0.41
1:2:744:C:H2'	1:2:745:U:N3	2.35	0.41
1:2:919:G:H2'	1:2:920:G:H8	1.86	0.41
1:2:1003:C:O2'	17:P:101:HIS:ND1	2.50	0.41
1:2:1117:G:C4	1:2:1118:A:C8	3.09	0.41
1:2:1132:U:N3	1:2:1133:U:O4	2.53	0.41
1:2:1171:G:H2'	1:2:1172:G:H8	1.85	0.41
1:2:1193:G:H2'	1:2:1194:G:C8	2.52	0.41
1:2:1287:A:O2'	33:f:145:CYS:HB2	2.21	0.41
1:2:1383:G:H3'	1:2:1384:A:H8	1.85	0.41
1:2:1592:C:N4	1:2:1593:G:O6	2.52	0.41
1:2:1739:G:H8	1:2:1739:G:OP2	2.04	0.41
1:2:1792:C:O2'	12:K:2:GLY:N	2.54	0.41
4:C:89:LYS:NZ	4:C:202:TYR:HA	2.35	0.41
6:E:124:LEU:HD11	6:E:222:ALA:HB1	2.02	0.41
6:E:152:ARG:HB3	6:E:162:PRO:HB2	2.02	0.41
6:E:158:LYS:HB2	25:X:4:ASN:H	1.86	0.41
7:F:44:THR:O	7:F:44:THR:HG22	2.21	0.41
7:F:75:LYS:NZ	14:M:21:MET:HA	2.36	0.41
7:F:173:ARG:HD3	7:F:173:ARG:HA	1.85	0.41
8:G:165:GLU:N	8:G:165:GLU:OE1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:83:GLN:HA	18:Q:86:LYS:HE3	2.03	0.41
23:V:39:LEU:HD12	23:V:39:LEU:HA	1.84	0.41
26:Y:78:ARG:CB	26:Y:124:LYS:HD2	2.50	0.41
27:Z:53:GLU:OE2	27:Z:71:ARG:HD3	2.19	0.41
34:g:299:PHE:CE1	34:g:309:VAL:HG13	2.56	0.41
1:2:280:G:H2'	1:2:281:U:C6	2.55	0.41
1:2:483:A:N6	1:2:499:G:H21	2.14	0.41
1:2:585:U:H2'	1:2:586:U:H6	1.86	0.41
1:2:668:U:C2	1:2:1023:A:N6	2.87	0.41
1:2:677:C:O3'	11:J:103:LYS:NZ	2.53	0.41
1:2:1007:A:H5''	17:P:3:ARG:HH12	1.86	0.41
1:2:1603:U:H2'	1:2:1604:C:O4'	2.21	0.41
1:2:1741:U:OP1	10:I:31:ARG:NH2	2.54	0.41
3:B:317:LYS:O	3:B:342:LYS:N	2.53	0.41
6:E:185:ARG:C	13:L:98:LEU:HD21	2.46	0.41
7:F:140:GLY:HA3	7:F:182:LEU:CD2	2.50	0.41
8:G:191:ARG:CZ	8:G:245:ARG:HE	2.34	0.41
14:M:31:LYS:HD3	14:M:31:LYS:HA	1.91	0.41
16:O:24:THR:OG1	16:O:121:LYS:HE3	2.20	0.41
18:Q:95:ILE:HB	18:Q:129:ILE:HG22	2.01	0.41
18:Q:113:GLN:H	18:Q:113:GLN:CD	2.26	0.41
22:U:10:GLN:NE2	22:U:57:GLY:HA2	2.36	0.41
25:X:56:CYS:SG	25:X:59:ILE:HG12	2.60	0.41
38:y:50:U:H2'	38:y:51:G:H8	1.85	0.41
1:2:153:G:H2'	1:2:154:U:C6	2.56	0.41
1:2:487:C:H2'	1:2:488:C:H6	1.84	0.41
1:2:904:A:H2'	1:2:905:G:H8	1.85	0.41
1:2:931:G:H2'	1:2:932:G:H8	1.86	0.41
1:2:1139:A:OP1	1:2:1139:A:H8	2.03	0.41
1:2:1171:G:H2'	1:2:1172:G:C8	2.56	0.41
1:2:1283:A:C6	1:2:1284:U:H1'	2.55	0.41
1:2:1473:U:O2	1:2:1473:U:H2'	2.20	0.41
1:2:1481:U:H2'	1:2:1482:A:O4'	2.19	0.41
1:2:1573:U:N3	7:F:1:MET:O	2.54	0.41
5:D:51:ARG:HG3	5:D:53:GLN:HE22	1.85	0.41
7:F:99:ILE:HD12	7:F:99:ILE:H	1.85	0.41
8:G:139:LEU:HG	8:G:150:PRO:HG3	2.03	0.41
9:H:122:ARG:HA	9:H:146:ARG:HH12	1.85	0.41
11:J:64:VAL:O	11:J:97:GLN:HG3	2.20	0.41
14:M:65:ARG:HH22	32:e:22:ARG:HA	1.86	0.41
18:Q:34:PHE:HD2	18:Q:41:PHE:CD2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:41:PHE:HB3	18:Q:55:ARG:HH22	1.84	0.41
21:T:6:THR:O	21:T:10:LYS:HG2	2.20	0.41
25:X:71:ARG:O	25:X:74:LYS:HG2	2.21	0.41
34:g:16:GLY:HA3	34:g:36:ARG:C	2.46	0.41
34:g:78:ALA:O	34:g:89:LEU:HD12	2.20	0.41
39:z:546:G:H2'	39:z:547:G:C8	2.56	0.41
1:2:3:C:C5	6:E:190:ILE:HD11	2.55	0.41
1:2:31:U:O2'	1:2:633:A:N1	2.48	0.41
1:2:36:U:H2'	1:2:37:C:C6	2.53	0.41
1:2:59:U:N3	1:2:62:G:OP1	2.54	0.41
1:2:149:A:C5	1:2:170:A:N6	2.89	0.41
1:2:479:A:H2'	1:2:480:C:H6	1.85	0.41
1:2:842:G:C5	8:G:19:MET:HE1	2.56	0.41
1:2:848:G:N7	1:2:849:C:HI'	2.36	0.41
1:2:878:U:H2'	1:2:879:U:C6	2.56	0.41
1:2:931:G:H2'	1:2:932:G:C8	2.55	0.41
1:2:1074:C:H2'	1:2:1075:C:N1	2.36	0.41
1:2:1175:G:O2'	1:2:1178:A:N6	2.53	0.41
1:2:1438:U:HI'	20:S:11:GLN:NE2	2.36	0.41
1:2:1553:C:H2'	1:2:1554:C:C6	2.56	0.41
1:2:1613:C:H2'	1:2:1614:A:O4'	2.21	0.41
1:2:1795:A:H2'	1:2:1796:C:C6	2.56	0.41
4:C:103:PHE:O	4:C:104:THR:OG1	2.37	0.41
6:E:45:TRP:CD1	6:E:77:GLU:HG3	2.55	0.41
6:E:180:LEU:HD12	6:E:207:CYS:SG	2.60	0.41
8:G:93:ASP:OD1	8:G:93:ASP:N	2.54	0.41
9:H:125:SER:HA	9:H:138:ALA:HA	2.02	0.41
10:I:38:ALA:N	10:I:48:TYR:O	2.53	0.41
10:I:50:VAL:HG11	10:I:111:LEU:HD12	2.03	0.41
11:J:69:LEU:O	11:J:73:GLN:HG2	2.21	0.41
11:J:157:HIS:HA	11:J:188:GLU:O	2.21	0.41
12:K:10:LYS:HD3	12:K:11:ARG:N	2.36	0.41
12:K:65:PHE:HE2	12:K:78:ILE:HG12	1.86	0.41
14:M:16:PHE:HB2	14:M:79:LEU:HD13	2.02	0.41
14:M:42:ASN:C	14:M:44:HIS:H	2.29	0.41
15:N:27:GLU:HA	15:N:28:THR:HA	1.64	0.41
15:N:111:VAL:HG11	15:N:128:VAL:HG11	2.03	0.41
17:P:128:TYR:O	17:P:131:THR:HG22	2.21	0.41
18:Q:142:ARG:CZ	29:b:27:ALA:HB1	2.51	0.41
20:S:128:GLU:OE1	20:S:128:GLU:N	2.44	0.41
21:T:24:LEU:HD21	21:T:58:MET:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:37:GLU:OE2	34:g:150:TRP:NE1	2.49	0.41
21:T:57:LEU:O	21:T:61:ILE:HG23	2.21	0.41
22:U:8:LYS:HD2	35:h:50:PHE:O	2.20	0.41
23:V:52:TRP:O	23:V:56:ARG:N	2.48	0.41
25:X:18:SER:H	25:X:54:ALA:HB3	1.84	0.41
26:Y:102:ILE:HG12	26:Y:113:HIS:CD2	2.55	0.41
27:Z:4:CYS:SG	27:Z:9:THR:HG21	2.60	0.41
28:a:16:ARG:O	28:a:19:GLN:NE2	2.49	0.41
37:l:12:ARG:HH21	37:l:15:ARG:NE	2.19	0.41
38:y:9:G:O6	38:y:19:A:O2'	2.39	0.41
39:z:577:G:C2	39:z:592:C:C2	3.09	0.41
1:2:485:U:H2'	1:2:486:C:H6	1.86	0.41
1:2:524:G:H2'	1:2:525:G:H8	1.86	0.41
1:2:533:C:H3'	1:2:534:G:H8	1.86	0.41
1:2:540:C:C2	1:2:541:U:C5	3.08	0.41
1:2:1018:U:H6	17:P:128:TYR:CZ	2.39	0.41
1:2:1053:C:H5'	39:z:832:A:H4'	2.02	0.41
1:2:1285:U:H5	33:f:97:LYS:HE2	1.85	0.41
1:2:1589:A:OP2	35:h:104:ARG:N	2.54	0.41
1:2:1685:U:H2'	1:2:1686:U:C6	2.56	0.41
1:2:1687:U:H5'	29:b:87:ARG:O	2.21	0.41
1:2:1825:A:H1'	37:l:2:ARG:NH2	2.36	0.41
4:C:110:ASN:OD1	4:C:111:GLN:N	2.54	0.41
4:C:163:CYS:SG	4:C:164:ASN:N	2.94	0.41
10:I:37:ALA:HA	10:I:49:VAL:HA	2.03	0.41
12:K:167:GLN:HG3	12:K:168:GLN:OE1	2.21	0.41
22:U:114:LEU:O	22:U:118:ARG:N	2.53	0.41
28:a:91:LEU:HB3	28:a:97:TYR:HB3	2.01	0.41
28:a:102:THR:N	28:a:103:SER:HB2	2.36	0.41
33:f:118:ARG:HG3	33:f:132:MET:HE3	2.03	0.41
34:g:302:TYR:HB2	34:g:304:ASP:OD1	2.21	0.41
36:i:105:ARG:NH1	36:i:106:ALA:HB2	2.36	0.41
38:y:19:A:H1'	38:y:58:A:C8	2.56	0.41
1:2:65:C:C6	10:I:174:PRO:HB3	2.56	0.40
1:2:77:A:C6	10:I:181:THR:HG21	2.56	0.40
1:2:105:U:H2'	1:2:106:C:O4'	2.21	0.40
1:2:217:U:H2'	1:2:218:A:H8	1.86	0.40
1:2:321:C:HO2'	1:2:322:G:H8	1.67	0.40
1:2:821:A:H2'	1:2:822:A:C8	2.57	0.40
1:2:889:U:H2'	1:2:890:G:H8	1.86	0.40
1:2:1346:U:O2'	4:C:110:ASN:ND2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:259:LYS:HG3	8:G:259:LYS:O	2.21	0.40
11:J:19:PHE:CE2	11:J:23:ILE:HD11	2.57	0.40
12:K:170:LYS:O	12:K:171:LEU:HD22	2.21	0.40
21:T:58:MET:HA	21:T:61:ILE:HG12	2.03	0.40
22:U:104:ASP:OD1	22:U:104:ASP:N	2.54	0.40
23:V:21:PHE:O	23:V:25:SER:OG	2.33	0.40
23:V:101:ARG:HE	23:V:102:ARG:NH2	2.19	0.40
24:W:18:HIS:O	24:W:92:HIS:HA	2.21	0.40
24:W:23:THR:HB	24:W:113:GLU:CG	2.51	0.40
28:a:111:LYS:HG2	28:a:115:LYS:HE2	2.03	0.40
38:y:4:A:C6	38:y:69:G:N1	2.88	0.40
38:y:8:U:O3'	38:y:9:G:H3'	2.21	0.40
38:y:30:G:H2'	38:y:31:C:C6	2.55	0.40
1:2:13:C:H4'	1:2:1352:G:H21	1.87	0.40
1:2:527:C:H2'	1:2:528:U:C6	2.56	0.40
1:2:553:G:HO2'	1:2:554:A:P	2.45	0.40
1:2:676:U:H5''	26:Y:32:LYS:HZ2	1.85	0.40
1:2:1087:C:H2'	1:2:1088:G:C8	2.57	0.40
1:2:1423:C:H2'	1:2:1424:G:O4'	2.21	0.40
1:2:1443:G:OP1	24:W:87:ARG:NH2	2.55	0.40
1:2:1517:A:C8	19:R:128:HIS:CD2	3.09	0.40
1:2:1525:U:H1'	23:V:87:VAL:HG23	2.03	0.40
1:2:1697:G:C5	1:2:1698:C:C4	3.09	0.40
1:2:1736:U:OP1	12:K:42:ARG:HD3	2.21	0.40
1:2:1800:A:H2'	1:2:1801:C:H6	1.85	0.40
4:C:54:THR:O	4:C:161:ILE:HD11	2.21	0.40
4:C:81:ASN:OD1	4:C:81:ASN:N	2.53	0.40
5:D:128:LYS:HG2	5:D:129:THR:O	2.21	0.40
5:D:208:HIS:O	5:D:208:HIS:CG	2.74	0.40
7:F:196:GLY:C	7:F:198:ILE:HA	2.47	0.40
8:G:42:LEU:HD23	8:G:43:PRO:O	2.22	0.40
8:G:85:GLY:O	8:G:101:LEU:HD23	2.21	0.40
8:G:100:ARG:NH2	8:G:122:LYS:HA	2.35	0.40
10:I:145:PHE:HE2	10:I:156:TYR:O	2.04	0.40
15:N:59:LYS:HD3	15:N:134:LEU:HD13	2.04	0.40
19:R:24:GLN:HB3	19:R:28:MET:HE1	2.03	0.40
25:X:67:ASP:HA	25:X:70:LEU:HG	2.02	0.40
28:a:9:THR:O	28:a:10:ARG:HD2	2.20	0.40
31:d:13:ARG:C	31:d:32:VAL:HG23	2.47	0.40
33:f:135:HIS:HD2	33:f:140:TYR:H	1.68	0.40
34:g:44:LYS:HG2	34:g:54:ILE:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:102:ARG:HH11	36:i:106:ALA:HB1	1.86	0.40
39:z:587:U:H2'	39:z:588:A:C8	2.57	0.40
1:2:73:C:O2'	1:2:74:G:O4'	2.36	0.40
1:2:385:G:OP1	15:N:79:LYS:HD2	2.21	0.40
1:2:445:A:H2'	1:2:446:C:H6	1.86	0.40
1:2:927:C:H2'	1:2:928:G:C8	2.56	0.40
1:2:1063:C:H2'	1:2:1064:G:C8	2.56	0.40
1:2:1285:U:C5	33:f:97:LYS:HE2	2.56	0.40
1:2:1517:A:O2'	22:U:144:ARG:NH1	2.54	0.40
1:2:1805:C:H2'	1:2:1806:U:C6	2.57	0.40
1:2:1854:A:O2'	1:2:1856:G:H8	2.05	0.40
4:C:23:THR:HA	4:C:164:ASN:ND2	2.36	0.40
8:G:127:ARG:HB2	8:G:140:VAL:HG12	2.04	0.40
8:G:182:MET:HE2	8:G:182:MET:HA	2.03	0.40
10:I:194:LEU:HA	10:I:197:GLN:OE1	2.21	0.40
12:K:195:LEU:O	12:K:199:LEU:HD23	2.22	0.40
18:Q:121:ARG:C	18:Q:123:GLY:H	2.29	0.40
22:U:73:ASN:HB3	22:U:76:GLN:HB2	2.04	0.40
26:Y:78:ARG:HH12	26:Y:126:LEU:HD13	1.86	0.40
28:a:111:LYS:O	28:a:115:LYS:HG3	2.21	0.40
1:2:536:G:H2'	1:2:537:G:C8	2.57	0.40
1:2:552:U:C4'	13:L:132:GLN:HE22	2.35	0.40
1:2:624:A:H2'	1:2:625:G:C8	2.56	0.40
1:2:746:C:H2'	1:2:747:G:N9	2.36	0.40
1:2:811:U:N3	1:2:812:A:N7	2.70	0.40
1:2:958:A:H5''	18:Q:66:ARG:HD2	2.02	0.40
1:2:1259:U:H4'	32:e:27:ARG:NH1	2.37	0.40
1:2:1741:U:H2'	1:2:1742:C:H6	1.86	0.40
5:D:47:THR:HB	5:D:65:ARG:NH1	2.37	0.40
5:D:133:TYR:CE1	5:D:221:PRO:HD2	2.57	0.40
6:E:231:LYS:HA	6:E:234:SER:OG	2.22	0.40
6:E:259:VAL:HG23	6:E:259:VAL:O	2.20	0.40
8:G:31:PRO:HA	8:G:81:THR:OG1	2.21	0.40
8:G:89:VAL:HA	8:G:99:PHE:O	2.21	0.40
10:I:197:GLN:O	10:I:201:LYS:HG2	2.21	0.40
11:J:53:VAL:HG22	11:J:57:ARG:O	2.21	0.40
13:L:22:LYS:HA	13:L:22:LYS:HD2	1.89	0.40
17:P:75:LEU:HD23	17:P:81:ALA:HA	2.04	0.40
20:S:97:GLN:NE2	20:S:98:LYS:HB3	2.36	0.40
27:Z:81:ILE:HD12	27:Z:81:ILE:HA	1.98	0.40
27:Z:130:LEU:HA	27:Z:133:LEU:HG	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:11:LYS:O	28:a:23:MET:HA	2.22	0.40
32:e:4:GLN:NE2	32:e:5:GLN:HB2	2.36	0.40
34:g:218:LEU:HG	34:g:228:TYR:CZ	2.57	0.40
38:y:4:A:H2'	38:y:5:G:C8	2.57	0.40
38:y:19:A:H2	38:y:59:A:C6	2.40	0.40
39:z:531:C:O2'	39:z:532:G:C6	2.74	0.40
1:2:198:U:H3'	1:2:199:G:C8	2.56	0.40
1:2:560:C:C2	1:2:561:U:C5	3.09	0.40
1:2:1088:G:N1	1:2:1154:G:O6	2.54	0.40
1:2:1349:A:C6	1:2:1350:G:C6	3.10	0.40
1:2:1683:C:H2'	1:2:1684:C:C6	2.56	0.40
1:2:1785:A:H2'	1:2:1786:G:O4'	2.21	0.40
1:2:1839:A:H2'	1:2:1840:G:H8	1.85	0.40
5:D:22:VAL:O	5:D:27:LYS:NZ	2.53	0.40
7:F:12:VAL:O	7:F:16:ILE:HG12	2.21	0.40
8:G:77:ARG:HG3	8:G:82:TYR:CE2	2.57	0.40
10:I:170:ARG:HD3	10:I:172:LYS:HG2	2.02	0.40
13:L:29:LEU:O	13:L:32:ILE:HG22	2.21	0.40
17:P:46:THR:HG22	17:P:49:GLN:OE1	2.21	0.40
27:Z:48:LYS:O	27:Z:75:ILE:HG22	2.22	0.40
34:g:57:ARG:NE	34:g:94:THR:HA	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	A	276/315 (88%)	267 (97%)	9 (3%)	0	100	100
3	B	462/485 (95%)	453 (98%)	9 (2%)	0	100	100
4	C	206/295 (70%)	179 (87%)	26 (13%)	1 (0%)	24	63
5	D	213/264 (81%)	195 (92%)	17 (8%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	E	220/226 (97%)	203 (92%)	16 (7%)	1 (0%)	24	63
7	F	225/243 (93%)	212 (94%)	12 (5%)	1 (0%)	30	67
8	G	261/263 (99%)	242 (93%)	19 (7%)	0	100	100
9	H	189/204 (93%)	174 (92%)	15 (8%)	0	100	100
10	I	235/249 (94%)	224 (95%)	11 (5%)	0	100	100
11	J	188/194 (97%)	172 (92%)	16 (8%)	0	100	100
12	K	204/206 (99%)	185 (91%)	17 (8%)	2 (1%)	12	47
13	L	180/194 (93%)	172 (96%)	7 (4%)	1 (1%)	21	58
14	M	96/225 (43%)	79 (82%)	16 (17%)	1 (1%)	12	47
15	N	156/158 (99%)	148 (95%)	8 (5%)	0	100	100
16	O	122/132 (92%)	108 (88%)	14 (12%)	0	100	100
17	P	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
18	Q	134/168 (80%)	117 (87%)	17 (13%)	0	100	100
19	R	133/145 (92%)	115 (86%)	18 (14%)	0	100	100
20	S	139/146 (95%)	127 (91%)	12 (9%)	0	100	100
21	T	124/135 (92%)	121 (98%)	3 (2%)	0	100	100
22	U	140/152 (92%)	124 (89%)	15 (11%)	1 (1%)	18	55
23	V	139/141 (99%)	126 (91%)	12 (9%)	1 (1%)	18	55
24	W	102/119 (86%)	96 (94%)	6 (6%)	0	100	100
25	X	80/82 (98%)	72 (90%)	8 (10%)	0	100	100
26	Y	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
27	Z	140/143 (98%)	132 (94%)	8 (6%)	0	100	100
28	a	124/126 (98%)	117 (94%)	7 (6%)	0	100	100
29	b	97/115 (84%)	91 (94%)	6 (6%)	0	100	100
30	c	82/84 (98%)	72 (88%)	10 (12%)	0	100	100
31	d	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
32	e	51/56 (91%)	42 (82%)	9 (18%)	0	100	100
33	f	69/156 (44%)	59 (86%)	10 (14%)	0	100	100
34	g	311/317 (98%)	286 (92%)	25 (8%)	0	100	100
35	h	73/125 (58%)	71 (97%)	2 (3%)	0	100	100
36	i	57/59 (97%)	51 (90%)	6 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	l	23/25 (92%)	23 (100%)	0	0	100	100
All	All	5588/6292 (89%)	5177 (93%)	401 (7%)	10 (0%)	44	77

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	M	34	GLU
22	U	144	ARG
7	F	193	ASP
12	K	156	ALA
12	K	158	ILE
23	V	40	ALA
5	D	207	LEU
13	L	148	ILE
6	E	246	PHE
4	C	206	ASP

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	C	174/244 (71%)	174 (100%)	0	100	100
5	D	196/231 (85%)	196 (100%)	0	100	100
6	E	186/187 (100%)	186 (100%)	0	100	100
7	F	190/202 (94%)	190 (100%)	0	100	100
8	G	225/225 (100%)	225 (100%)	0	100	100
9	H	161/170 (95%)	161 (100%)	0	100	100
10	I	207/218 (95%)	207 (100%)	0	100	100
11	J	170/174 (98%)	169 (99%)	1 (1%)	78	81
12	K	177/177 (100%)	177 (100%)	0	100	100
13	L	157/168 (94%)	157 (100%)	0	100	100
14	M	89/173 (51%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	N	142/142 (100%)	142 (100%)	0	100	100
16	O	104/108 (96%)	104 (100%)	0	100	100
17	P	130/131 (99%)	130 (100%)	0	100	100
18	Q	106/130 (82%)	106 (100%)	0	100	100
19	R	121/130 (93%)	121 (100%)	0	100	100
20	S	117/121 (97%)	117 (100%)	0	100	100
21	T	114/121 (94%)	114 (100%)	0	100	100
22	U	122/132 (92%)	122 (100%)	0	100	100
23	V	113/113 (100%)	113 (100%)	0	100	100
24	W	94/107 (88%)	94 (100%)	0	100	100
25	X	67/67 (100%)	67 (100%)	0	100	100
26	Y	112/113 (99%)	112 (100%)	0	100	100
27	Z	114/115 (99%)	114 (100%)	0	100	100
28	a	108/108 (100%)	108 (100%)	0	100	100
29	b	87/99 (88%)	87 (100%)	0	100	100
30	c	76/76 (100%)	76 (100%)	0	100	100
31	d	57/57 (100%)	57 (100%)	0	100	100
32	e	47/49 (96%)	47 (100%)	0	100	100
33	f	64/140 (46%)	64 (100%)	0	100	100
34	g	272/275 (99%)	272 (100%)	0	100	100
35	h	66/103 (64%)	66 (100%)	0	100	100
36	i	49/49 (100%)	49 (100%)	0	100	100
37	l	24/24 (100%)	24 (100%)	0	100	100
All	All	4238/4679 (91%)	4237 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
11	J	97	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
4	C	9	GLN
4	C	33	GLN
4	C	50	ASN
4	C	70	ASN
4	C	111	GLN
5	D	95	ASN
5	D	101	HIS
5	D	159	GLN
5	D	163	GLN
6	E	121	HIS
6	E	257	HIS
7	F	101	GLN
8	G	142	HIS
9	H	82	ASN
9	H	83	ASN
10	I	146	ASN
11	J	25	GLN
11	J	168	HIS
12	K	64	ASN
12	K	165	GLN
13	L	75	ASN
13	L	113	GLN
13	L	132	GLN
13	L	134	HIS
15	N	5	GLN
15	N	94	HIS
15	N	156	GLN
17	P	105	ASN
19	R	6	GLN
19	R	35	GLN
20	S	86	GLN
22	U	17	ASN
22	U	19	ASN
23	V	42	HIS
23	V	117	GLN
24	W	92	HIS
25	X	2	GLN
26	Y	15	ASN
26	Y	70	ASN
26	Y	90	GLN
27	Z	26	GLN
28	a	106	GLN
28	a	112	ASN

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Mol	Chain	Res	Type
29	b	80	HIS
32	e	26	ASN
33	f	135	HIS
34	g	76	GLN
34	g	178	ASN
35	h	89	GLN
35	h	106	GLN
36	i	113	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1736/1863 (93%)	362 (20%)	4 (0%)
38	y	74/75 (98%)	35 (47%)	0
39	z	91/93 (97%)	32 (35%)	0
All	All	1901/2031 (93%)	429 (22%)	4 (0%)

All (429) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	4	C
1	2	11	A
1	2	26	U
1	2	33	G
1	2	39	A
1	2	41	G
1	2	42	A
1	2	44	U
1	2	46	A
1	2	55	U
1	2	56	G
1	2	60	A
1	2	67	C
1	2	68	A
1	2	72	C
1	2	73	C
1	2	74	G
1	2	76	U
1	2	79	A
1	2	80	G
1	2	94	G

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Mol	Chain	Res	Type
1	2	99	A
1	2	101	U
1	2	103	A
1	2	110	U
1	2	111	A
1	2	113	G
1	2	114	G
1	2	115	U
1	2	126	G
1	2	127	C
1	2	143	U
1	2	147	A
1	2	148	U
1	2	162	C
1	2	168	C
1	2	169	U
1	2	170	A
1	2	171	A
1	2	172	U
1	2	173	A
1	2	178	C
1	2	179	C
1	2	181	A
1	2	182	C
1	2	183	G
1	2	191	C
1	2	197	U
1	2	202	U
1	2	204	G
1	2	223	A
1	2	224	U
1	2	225	C
1	2	226	A
1	2	239	U
1	2	271	G
1	2	277	U
1	2	278	U
1	2	285	U
1	2	293	A
1	2	296	U
1	2	297	C
1	2	298	G

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Mol	Chain	Res	Type
1	2	299	G
1	2	300	G
1	2	303	G
1	2	308	C
1	2	311	C
1	2	315	C
1	2	316	C
1	2	317	G
1	2	322	G
1	2	325	G
1	2	337	G
1	2	340	C
1	2	347	C
1	2	350	A
1	2	352	C
1	2	354	A
1	2	358	U
1	2	359	C
1	2	375	G
1	2	376	C
1	2	388	A
1	2	389	C
1	2	390	C
1	2	399	C
1	2	403	G
1	2	408	A
1	2	438	A
1	2	440	C
1	2	442	G
1	2	457	G
1	2	462	C
1	2	466	A
1	2	474	A
1	2	475	A
1	2	477	U
1	2	479	A
1	2	483	A
1	2	487	C
1	2	492	C
1	2	506	A
1	2	507	C
1	2	513	A

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Mol	Chain	Res	Type
1	2	515	A
1	2	518	A
1	2	541	U
1	2	542	G
1	2	547	U
1	2	548	G
1	2	553	G
1	2	554	A
1	2	563	U
1	2	566	A
1	2	577	A
1	2	579	G
1	2	580	A
1	2	581	U
1	2	583	C
1	2	596	G
1	2	597	U
1	2	598	C
1	2	604	G
1	2	607	G
1	2	613	G
1	2	617	U
1	2	621	U
1	2	633	A
1	2	650	C
1	2	658	A
1	2	659	A
1	2	661	A
1	2	662	A
1	2	663	G
1	2	673	G
1	2	674	G
1	2	678	U
1	2	679	U
1	2	680	G
1	2	682	G
1	2	729	C
1	2	730	C
1	2	731	C
1	2	732	C
1	2	735	C
1	2	736	C

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Mol	Chain	Res	Type
1	2	737	C
1	2	738	U
1	2	739	U
1	2	740	G
1	2	741	C
1	2	742	C
1	2	743	U
1	2	744	C
1	2	747	G
1	2	748	G
1	2	749	C
1	2	750	G
1	2	787	C
1	2	789	G
1	2	793	C
1	2	794	G
1	2	796	U
1	2	797	U
1	2	800	U
1	2	807	A
1	2	818	U
1	2	819	U
1	2	820	C
1	2	823	A
1	2	827	G
1	2	829	C
1	2	832	G
1	2	833	A
1	2	835	C
1	2	837	G
1	2	843	A
1	2	865	A
1	2	868	A
1	2	869	G
1	2	870	G
1	2	873	C
1	2	874	G
1	2	883	U
1	2	886	U
1	2	894	U
1	2	901	C
1	2	907	C

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Mol	Chain	Res	Type
1	2	909	A
1	2	910	U
1	2	913	U
1	2	915	A
1	2	916	A
1	2	918	A
1	2	929	G
1	2	930	G
1	2	951	A
1	2	952	G
1	2	956	U
1	2	966	G
1	2	967	G
1	2	986	A
1	2	988	A
1	2	1004	A
1	2	1013	U
1	2	1016	A
1	2	1019	A
1	2	1022	C
1	2	1023	A
1	2	1041	U
1	2	1045	A
1	2	1049	C
1	2	1051	A
1	2	1056	A
1	2	1057	U
1	2	1058	A
1	2	1076	A
1	2	1079	A
1	2	1081	C
1	2	1097	U
1	2	1107	U
1	2	1112	C
1	2	1113	C
1	2	1125	G
1	2	1129	A
1	2	1135	C
1	2	1139	A
1	2	1144	A
1	2	1145	A
1	2	1146	A

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Mol	Chain	Res	Type
1	2	1150	U
1	2	1151	U
1	2	1153	G
1	2	1160	G
1	2	1191	A
1	2	1199	G
1	2	1203	G
1	2	1204	A
1	2	1211	C
1	2	1212	C
1	2	1217	G
1	2	1220	G
1	2	1224	A
1	2	1238	U
1	2	1244	U
1	2	1245	C
1	2	1247	A
1	2	1249	A
1	2	1252	G
1	2	1253	G
1	2	1254	A
1	2	1261	A
1	2	1269	C
1	2	1271	G
1	2	1280	A
1	2	1285	U
1	2	1287	A
1	2	1297	A
1	2	1298	G
1	2	1317	G
1	2	1323	G
1	2	1333	C
1	2	1339	U
1	2	1352	G
1	2	1354	U
1	2	1359	C
1	2	1360	U
1	2	1365	A
1	2	1366	A
1	2	1367	U
1	2	1368	U
1	2	1374	A

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Mol	Chain	Res	Type
1	2	1386	U
1	2	1399	C
1	2	1407	G
1	2	1408	C
1	2	1409	G
1	2	1411	C
1	2	1412	C
1	2	1414	C
1	2	1415	C
1	2	1427	G
1	2	1431	C
1	2	1432	C
1	2	1433	C
1	2	1438	U
1	2	1445	G
1	2	1446	G
1	2	1449	C
1	2	1450	A
1	2	1451	A
1	2	1459	U
1	2	1471	G
1	2	1472	A
1	2	1473	U
1	2	1485	A
1	2	1486	G
1	2	1487	G
1	2	1489	C
1	2	1490	U
1	2	1491	G
1	2	1494	A
1	2	1506	G
1	2	1507	U
1	2	1516	C
1	2	1517	A
1	2	1528	A
1	2	1531	G
1	2	1539	C
1	2	1543	G
1	2	1547	G
1	2	1548	C
1	2	1549	C
1	2	1550	U

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Mol	Chain	Res	Type
1	2	1551	A
1	2	1555	U
1	2	1574	A
1	2	1575	A
1	2	1580	U
1	2	1583	A
1	2	1593	G
1	2	1596	A
1	2	1601	G
1	2	1616	U
1	2	1617	U
1	2	1618	A
1	2	1636	A
1	2	1643	G
1	2	1654	U
1	2	1656	A
1	2	1659	A
1	2	1660	G
1	2	1675	G
1	2	1694	A
1	2	1695	C
1	2	1696	C
1	2	1715	U
1	2	1716	U
1	2	1717	G
1	2	1724	U
1	2	1732	G
1	2	1739	G
1	2	1777	C
1	2	1778	G
1	2	1791	U
1	2	1792	C
1	2	1817	A
1	2	1823	G
1	2	1829	A
1	2	1832	U
1	2	1833	U
1	2	1837	G
1	2	1843	G
1	2	1846	C
1	2	1853	A
1	2	1854	A

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Mol	Chain	Res	Type
1	2	1855	G
1	2	1856	G
1	2	1857	A
1	2	1859	C
1	2	1862	U
38	y	2	G
38	y	4	A
38	y	6	A
38	y	8	U
38	y	9	G
38	y	10	G
38	y	11	C
38	y	12	G
38	y	14	A
38	y	15	G
38	y	17	G
38	y	18	G
38	y	19	A
38	y	20	A
38	y	21	G
38	y	26	C
38	y	32	C
38	y	40	C
38	y	44	G
38	y	45	G
38	y	46	U
38	y	47	C
38	y	48	G
38	y	52	G
38	y	53	A
38	y	54	U
38	y	55	C
38	y	58	A
38	y	60	C
38	y	62	A
38	y	71	U
38	y	72	A
38	y	73	C
38	y	74	C
38	y	75	A
39	z	525	A
39	z	531	C

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Mol	Chain	Res	Type
39	z	534	A
39	z	535	A
39	z	536	C
39	z	537	C
39	z	538	C
39	z	539	C
39	z	540	C
39	z	546	G
39	z	549	G
39	z	550	A
39	z	556	G
39	z	557	C
39	z	558	C
39	z	559	U
39	z	562	G
39	z	564	G
39	z	565	G
39	z	568	A
39	z	575	A
39	z	576	C
39	z	577	G
39	z	578	U
39	z	585	G
39	z	586	A
39	z	587	U
39	z	594	G
39	z	832	A
39	z	833	U
39	z	837	G
39	z	838	C

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	740	G
1	2	747	G
1	2	792	G
1	2	914	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
39	z	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	z	601:C	O3'	831:A	P	113.25

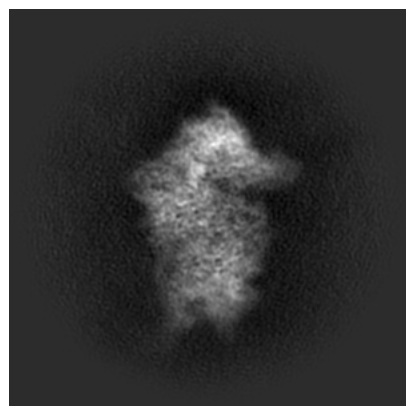
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64645. These allow visual inspection of the internal detail of the map and identification of artifacts.

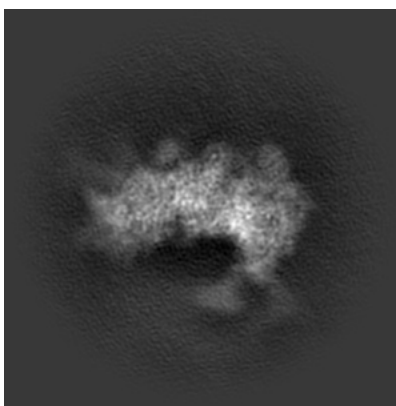
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

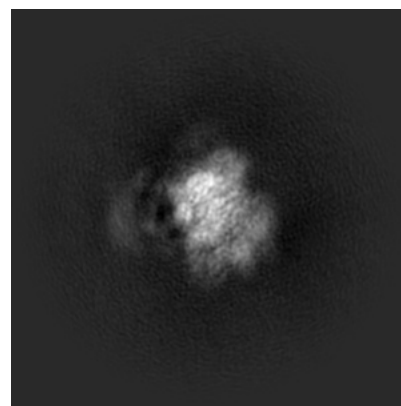
6.1.1 Primary map



X

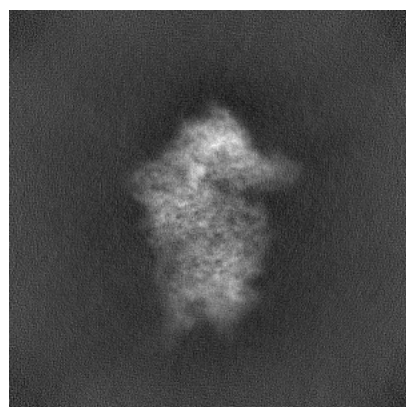


Y

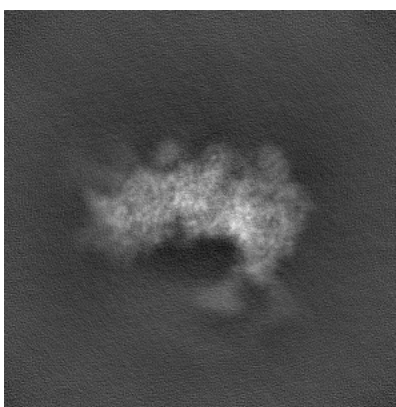


Z

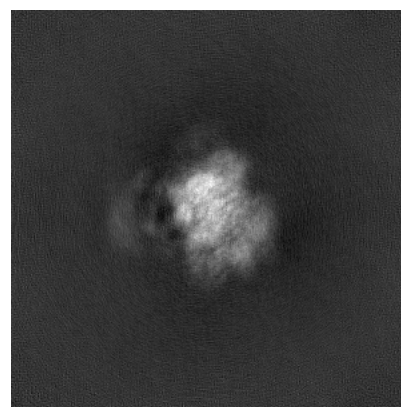
6.1.2 Raw map



X



Y

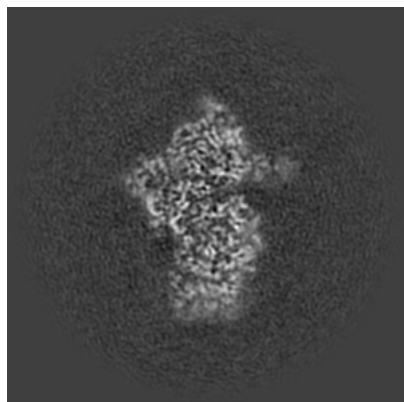


Z

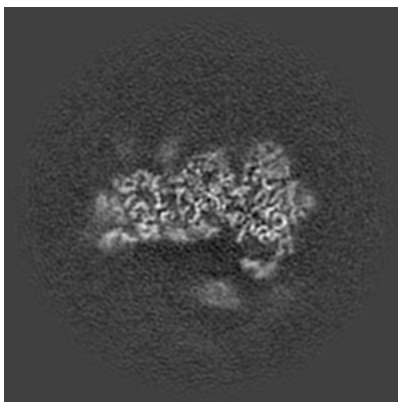
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

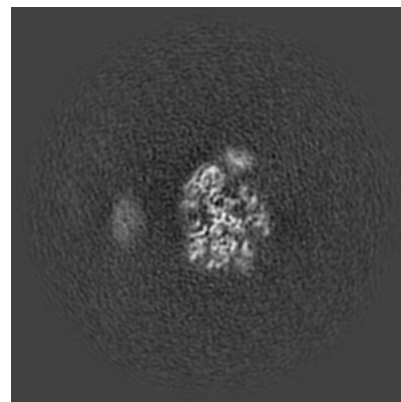
6.2.1 Primary map



X Index: 200

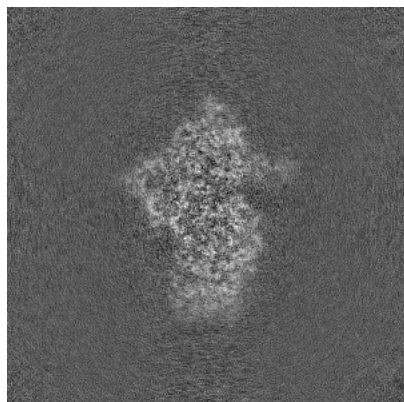


Y Index: 200

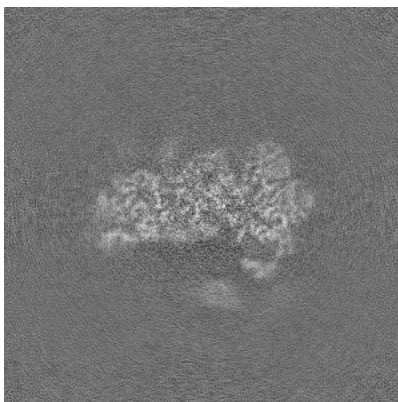


Z Index: 200

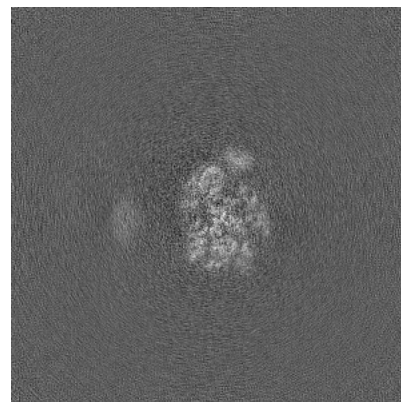
6.2.2 Raw map



X Index: 200



Y Index: 200

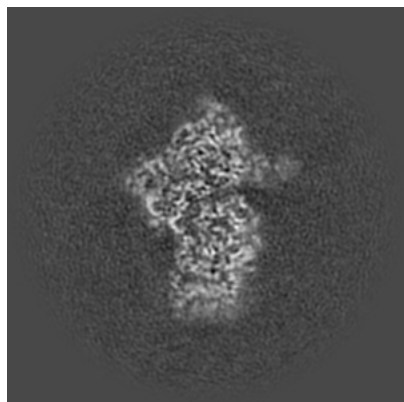


Z Index: 200

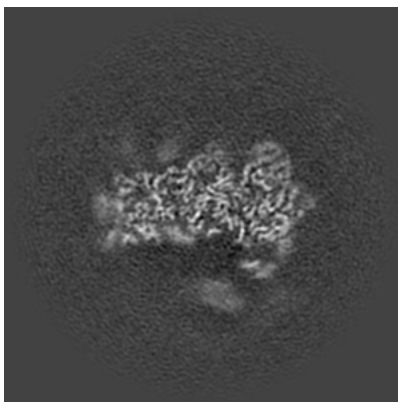
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

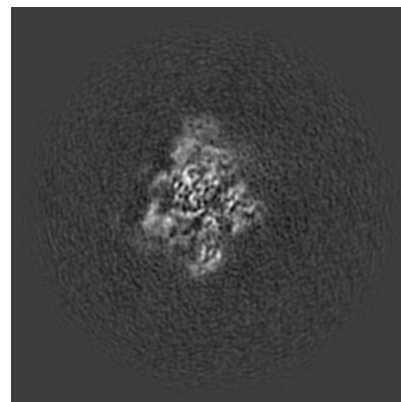
6.3.1 Primary map



X Index: 199

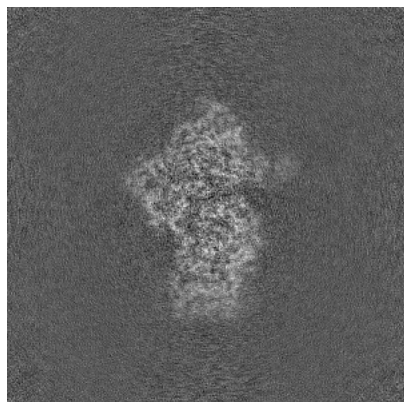


Y Index: 197

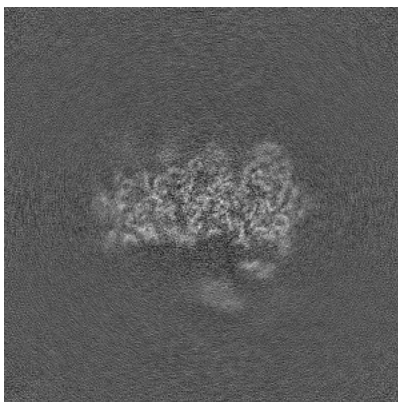


Z Index: 243

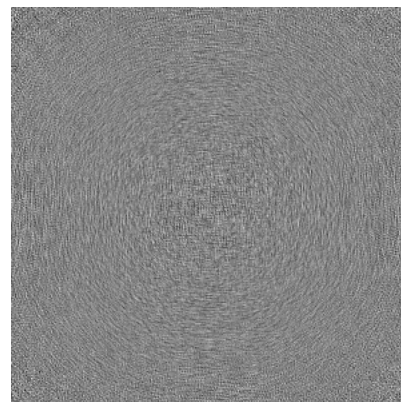
6.3.2 Raw map



X Index: 199



Y Index: 196

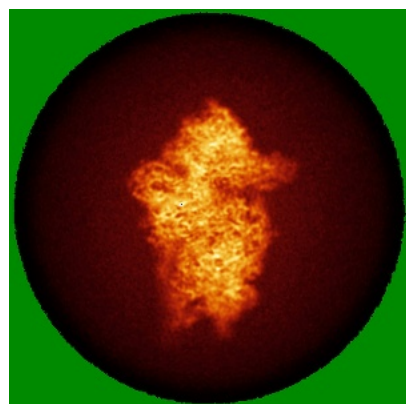


Z Index: 0

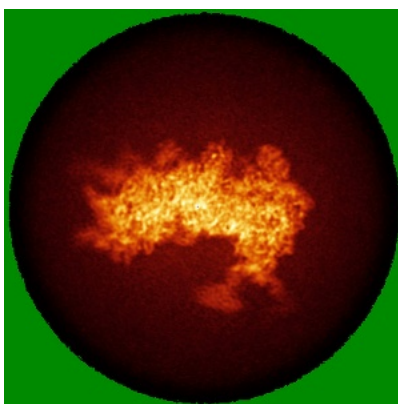
The images above show the largest variance slices of the map in three orthogonal directions.

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

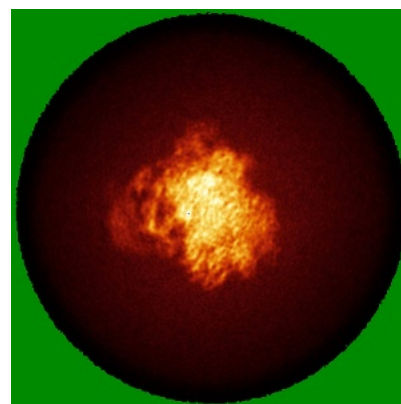
6.4.1 Primary map



X

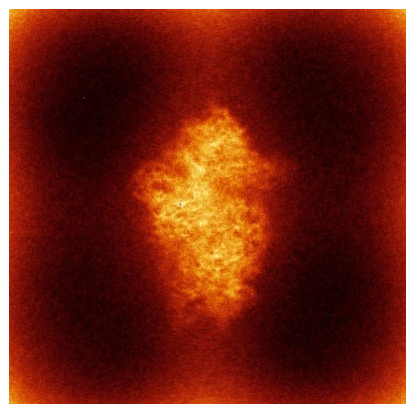


Y

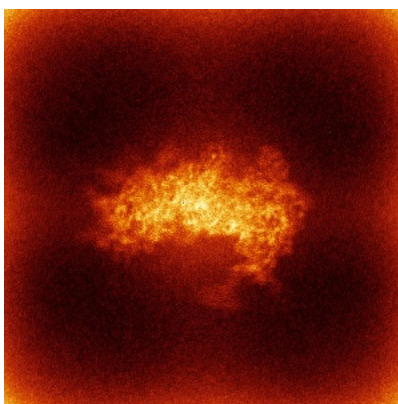


Z

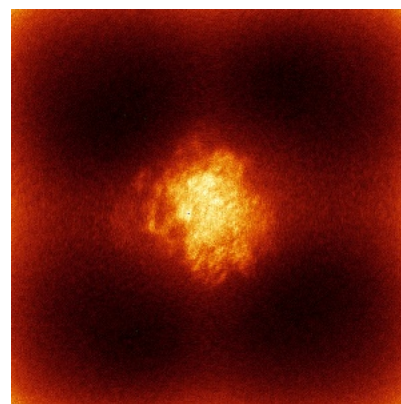
6.4.2 Raw map



X



Y

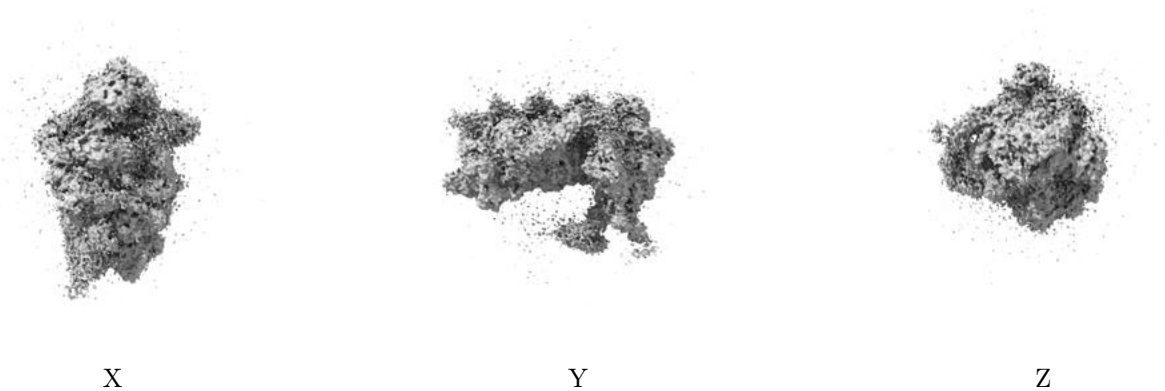


Z

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

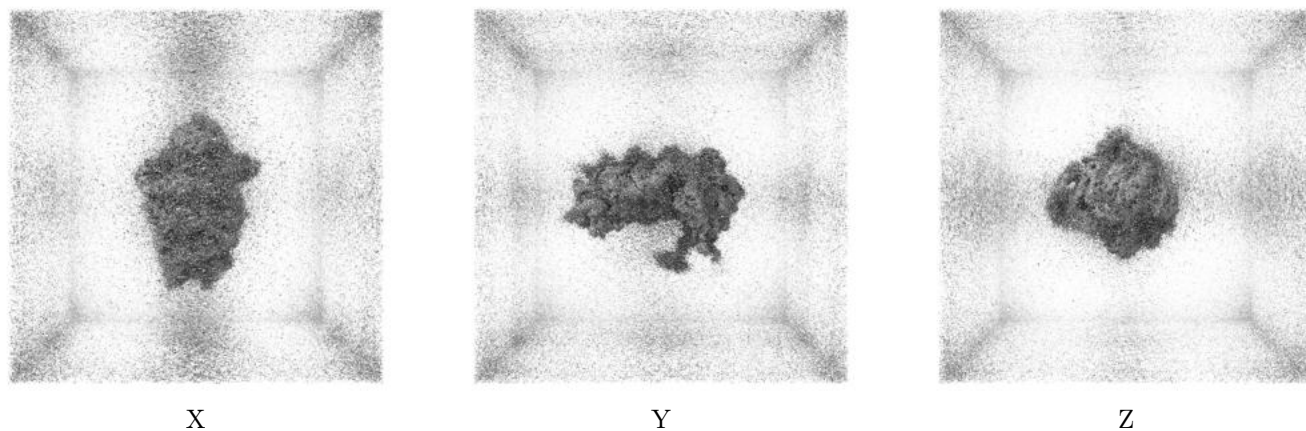
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0618. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

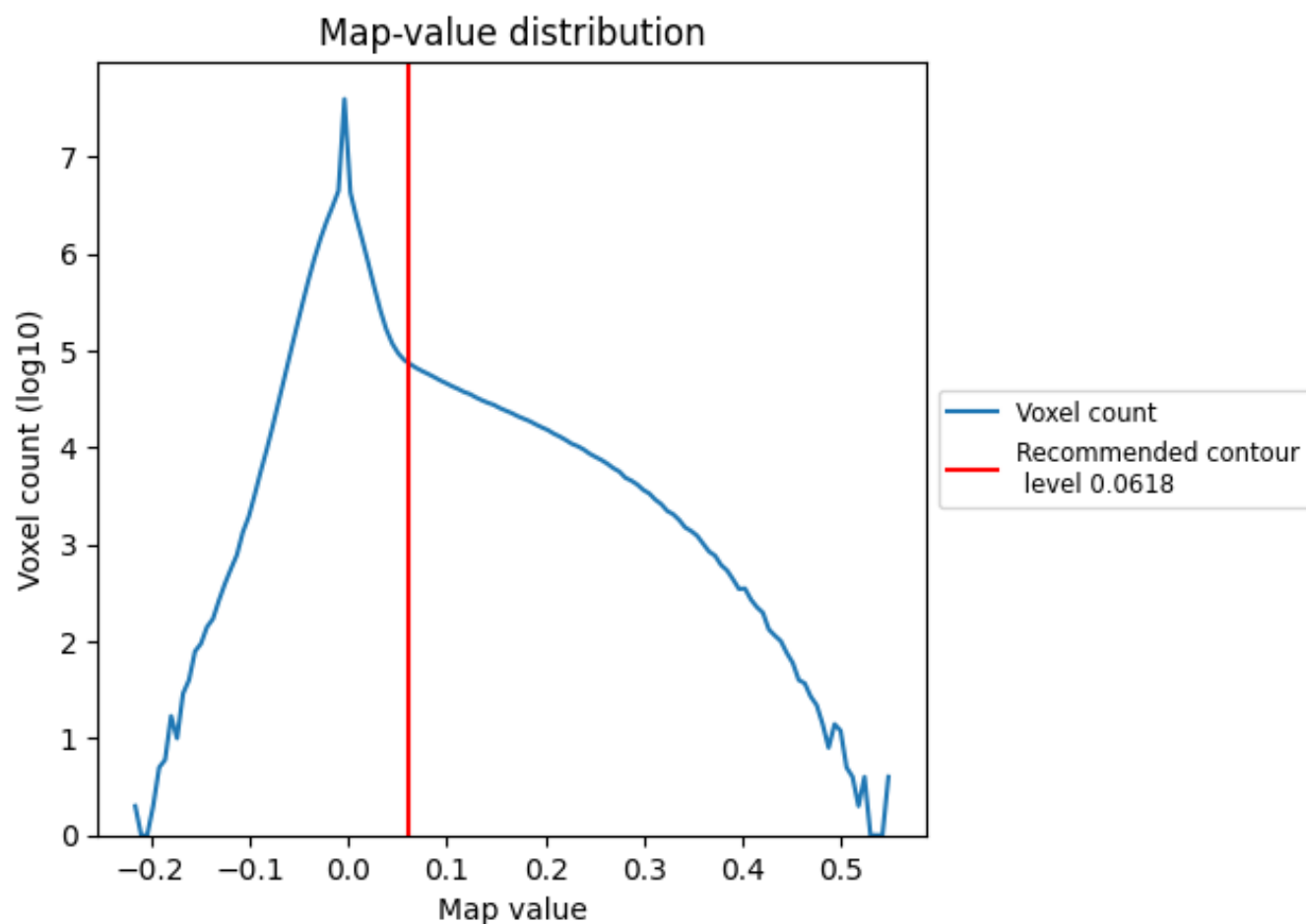
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

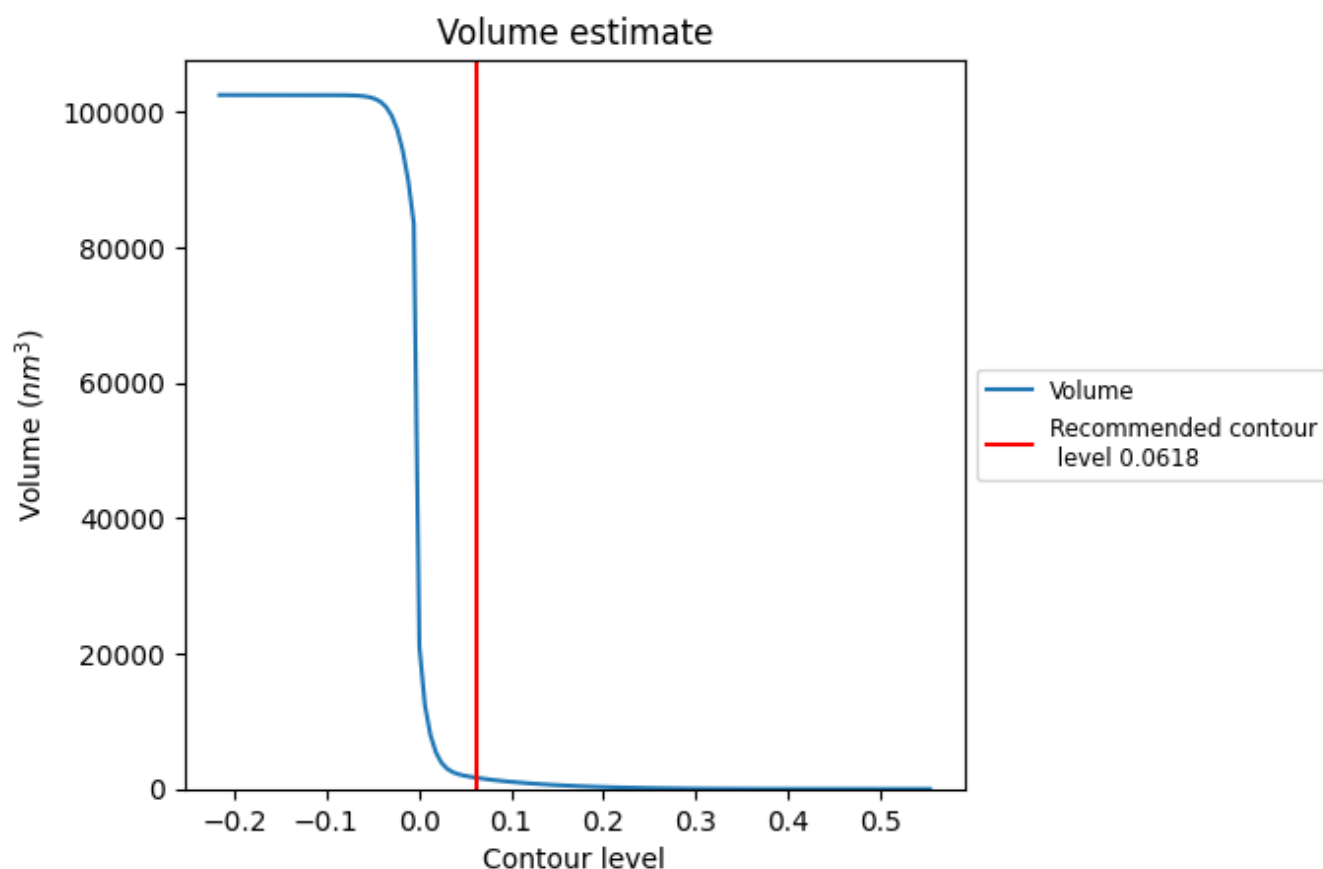
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

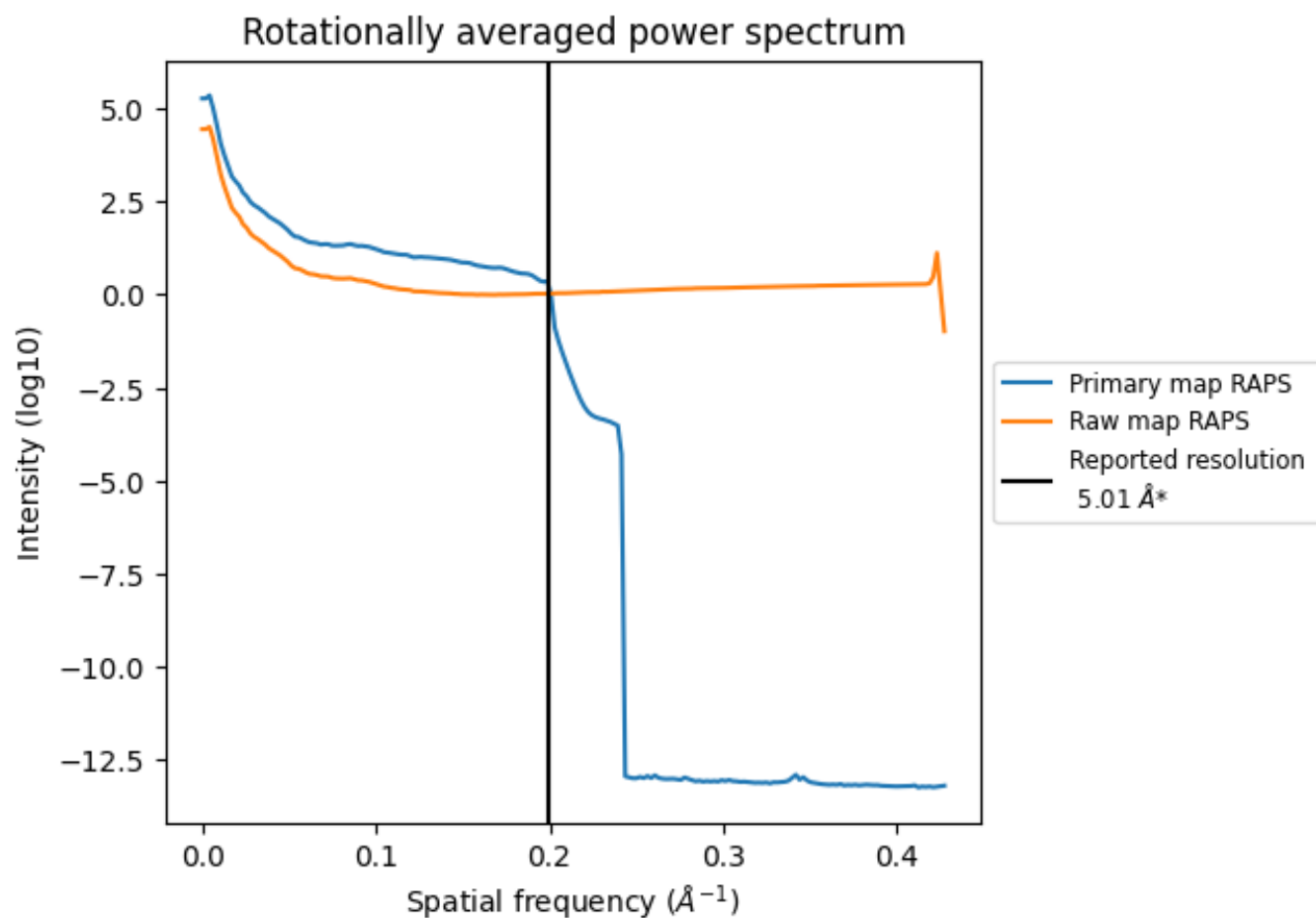
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1660 nm³; this corresponds to an approximate mass of 1500 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 ⓘ

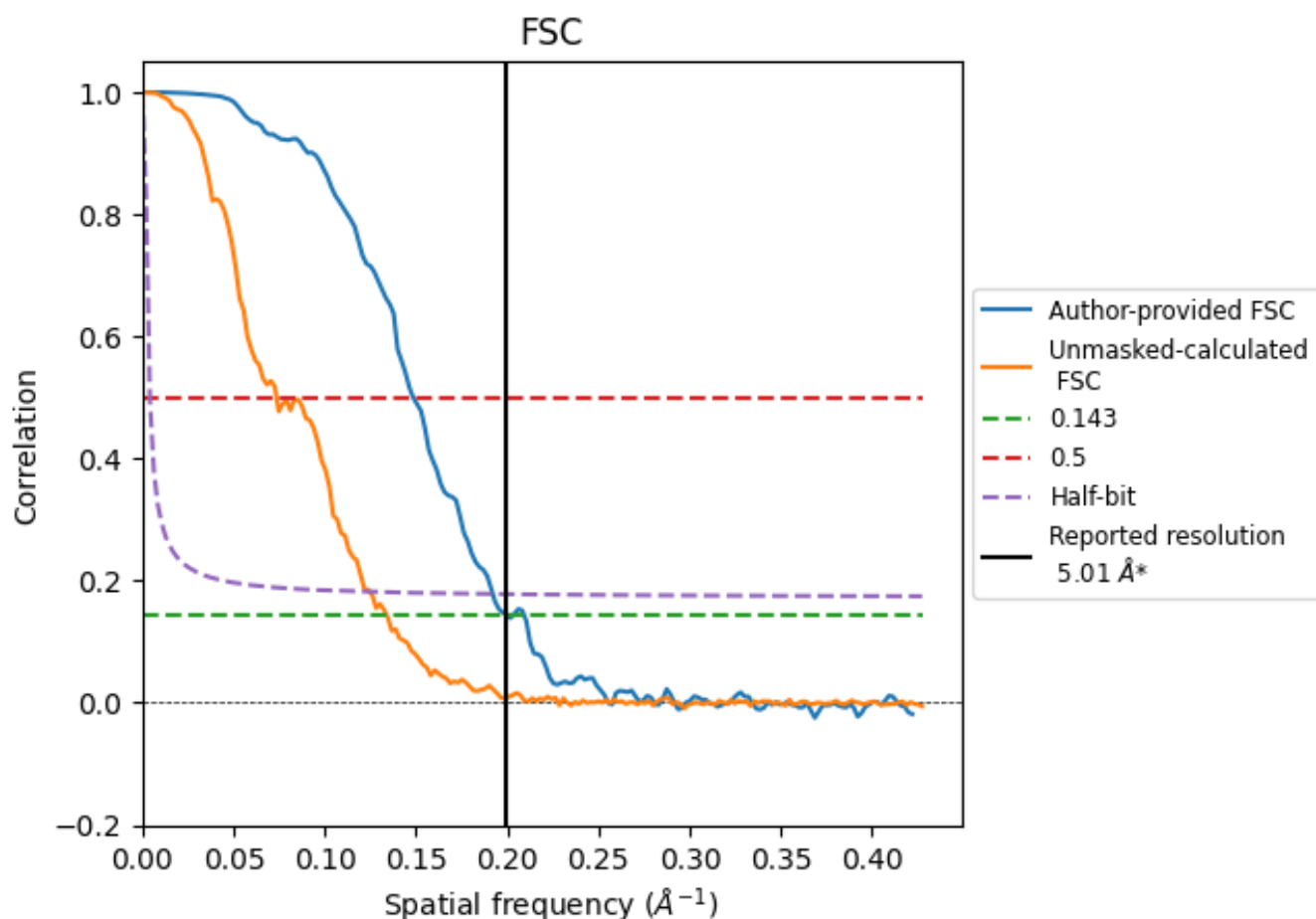


*Reported resolution corresponds to spatial frequency of 0.200 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.200 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

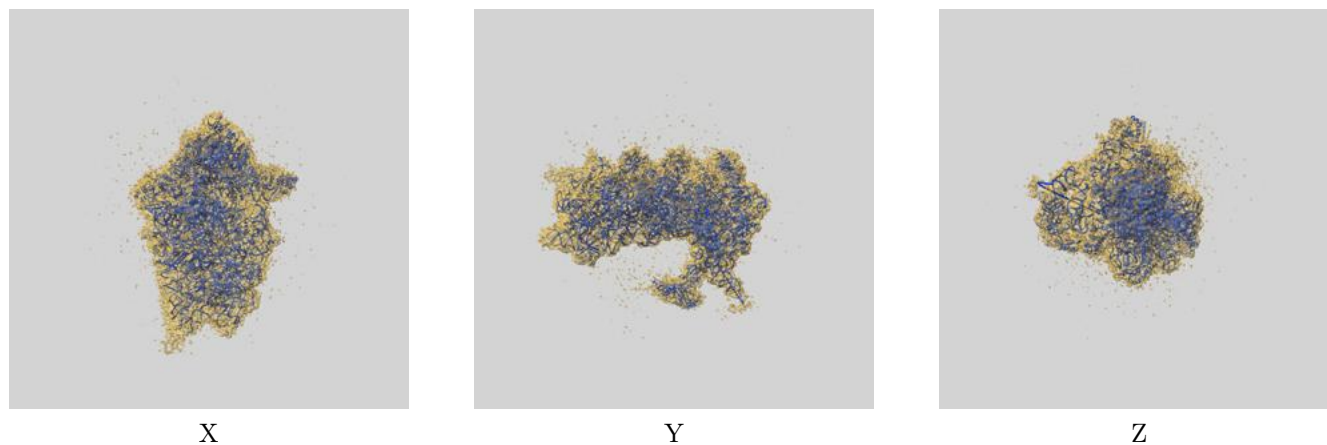
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.01	-	-
Author-provided FSC curve	5.01	6.73	5.21
Unmasked-calculated*	7.46	13.59	8.02

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 7.46 differs from the reported value 5.01 by more than 10 %

9 Map-model fit [i](#)

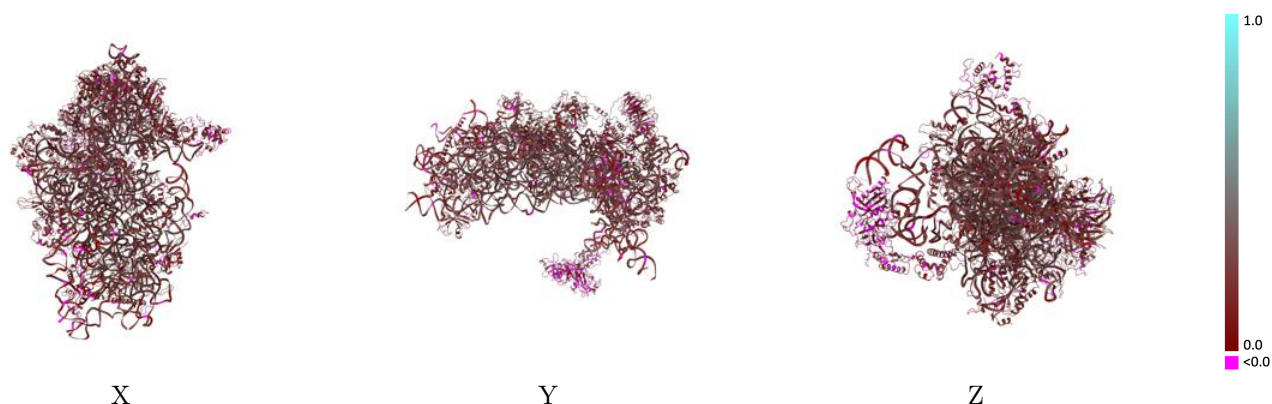
This section contains information regarding the fit between EMDB map EMD-64645 and PDB model 9UZL. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



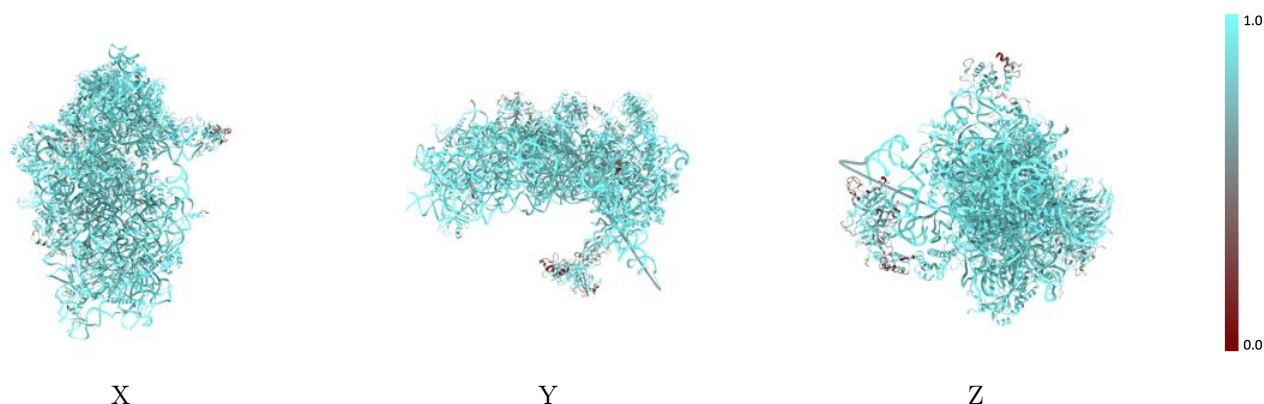
The images above show the 3D surface view of the map at the recommended contour level 0.0618 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



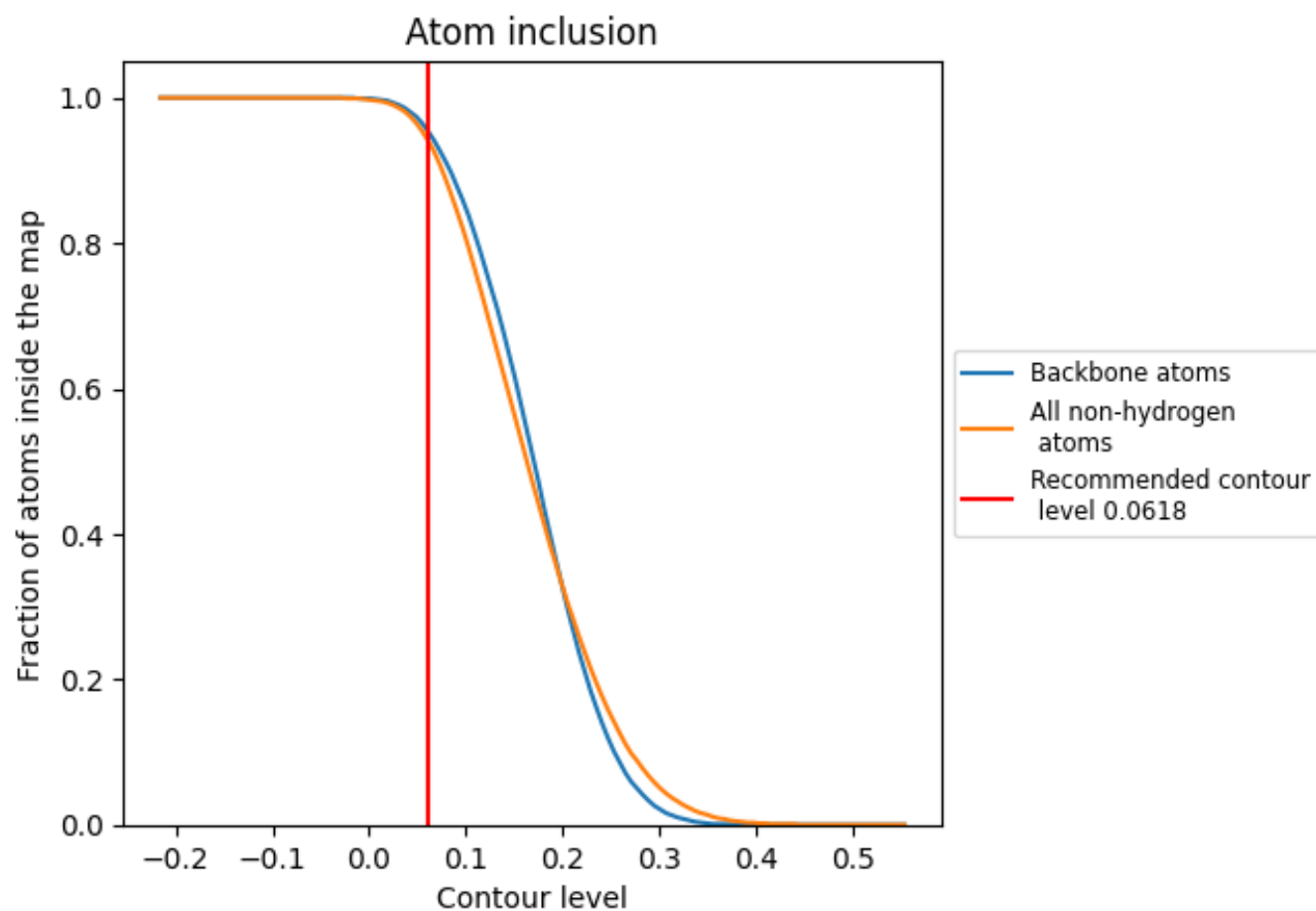
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0618).

9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0618) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9390	 0.2330
2	 0.9860	 0.2600
A	 0.8150	 0.1880
B	 0.7000	 0.1000
C	 0.8910	 0.2400
D	 0.9240	 0.2150
E	 0.9080	 0.2490
F	 0.9110	 0.2150
G	 0.9510	 0.2460
H	 0.9370	 0.2310
I	 0.9570	 0.1950
J	 0.7160	 0.1760
K	 0.9080	 0.2050
L	 0.9280	 0.2270
M	 0.9440	 0.2080
N	 0.8590	 0.2400
O	 0.6610	 0.1140
P	 0.9350	 0.2320
Q	 0.9310	 0.2080
R	 0.9560	 0.2150
S	 0.9380	 0.2270
T	 0.8650	 0.2280
U	 0.9420	 0.2230
V	 0.9670	 0.2240
W	 0.9480	 0.2100
X	 0.9290	 0.2390
Y	 0.8600	 0.2530
Z	 0.9370	 0.2650
a	 0.9630	 0.2130
b	 0.9430	 0.2720
c	 0.9180	 0.2380
d	 0.9690	 0.2480
e	 0.9560	 0.2330
f	 0.7390	 0.1330
g	 0.9390	 0.2030



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Chain	Atom inclusion	Q-score
h	 0.9470	 0.1970
i	 0.8880	 0.1830
l	 0.9680	 0.2520
y	 0.9780	 0.2060
z	 0.9670	 0.1930