Full wwPDB EM Validation Report ⓘ

Mar 13, 2024 – 01:32 PM JST

PDB ID	:	3JCM
EMDB ID	:	EMD-6561
Title	:	Cryo-EM structure of the spliceosomal U4/U6.U5 tri-snRNP
Authors	:	Wan, R.; Yan, C.; Bai, R.; Wang, L.; Huang, M.; Wong, C.C.; Shi, Y.
Deposited on	:	2015-12-23
Resolution	:	3.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

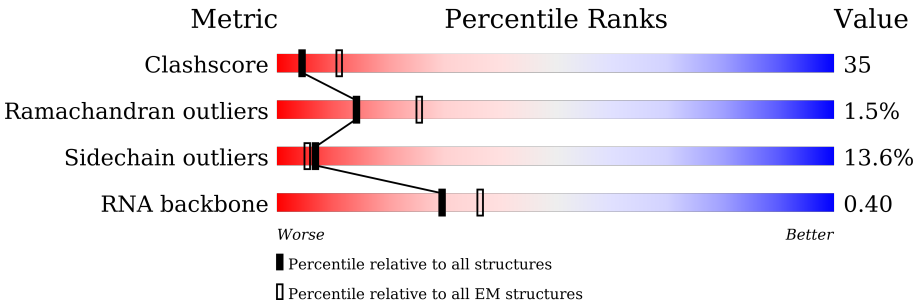
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance

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

The reported resolution of this entry is 3.80 Å.

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



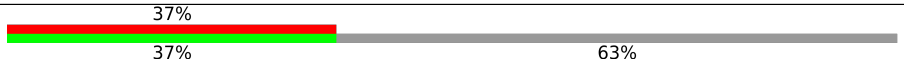
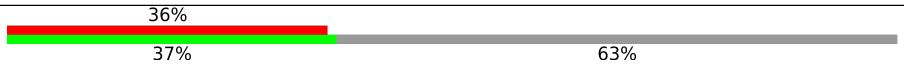
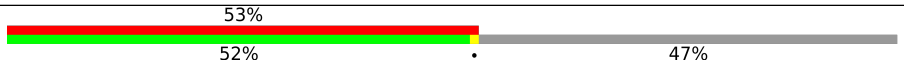
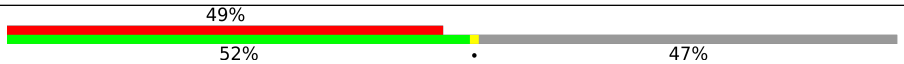
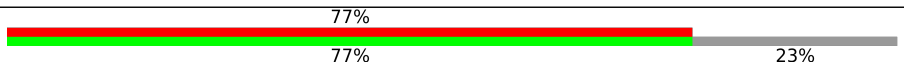
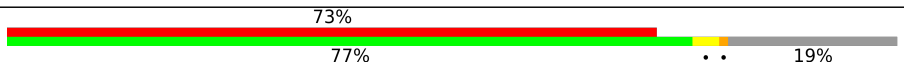
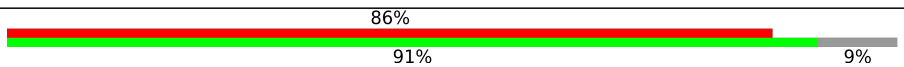
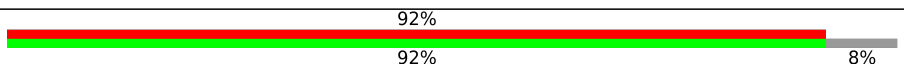
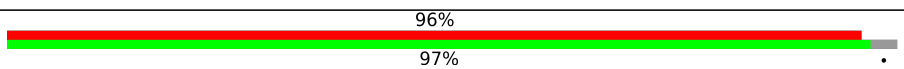
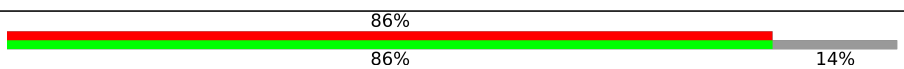
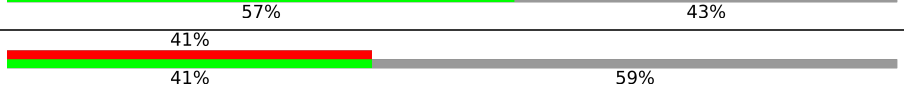
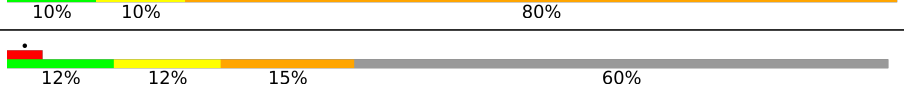
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2413	11% 54% 28% 8% 10%
2	B	465	40% 43% 9% 8%
3	I	494	42% 31% 10% 16%
4	G	899	53% 22% 7% 18%
5	K	469	35% 20% 41%
6	L	143	50% 38% 8%
7	M	126	75% 21% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
8	H	1008	
9	N	2163	
10	J	101	
10	R	101	
11	O	196	
11	S	196	
12	P	146	
12	T	146	
13	Q	110	
13	U	110	
14	V	94	
14	Y	94	
15	W	86	
15	Z	86	
16	X	77	
16	a	77	
17	b	109	
18	c	95	
19	d	89	
20	e	86	
21	f	93	
22	g	115	
23	h	187	
24	C	20	
25	D	112	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
26	E	160	13% 22% 18% 11% 47%
27	F	214	13% 13% 23% 15% 47%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
28	GTP	H	1500	-	-	X	-

2 Entry composition (i)

There are 29 unique types of molecules in this entry. The entry contains 58253 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 protein called Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2174	16889	10715	2978	3138	58	0	0

- Molecule 2 is a protein called U4/U6 small nuclear ribonucleoprotein PRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	429	3378	2102	610	652	14	0	0

- Molecule 3 is a protein called Pre-mRNA-processing factor 31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	I	416	3171	2001	573	585	12	0	0

- Molecule 4 is a protein called Pre-mRNA-splicing factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	G	734	4927	3063	911	939	14	0	0

- Molecule 5 is a protein called U4/U6 small nuclear ribonucleoprotein PRP3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	K	279	2328	1476	422	416	14	0	0

- Molecule 6 is a protein called Spliceosomal protein DIB1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	L	139	1146	725	199	211	11	0	0

- Molecule 7 is a protein called 13 kDa ribonucleoprotein-associated protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	126	Total	C	N	O	S	0	0
			950	605	163	177	5		

- Molecule 8 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	843	Total	C	N	O	S	0	0
			6732	4350	1119	1235	28		

- Molecule 9 is a protein called Pre-mRNA-splicing helicase BRR2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	1686	Total	C	N	O	0	0
			6744	3372	1686	1686		

- Molecule 10 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	R	79	Total	C	N	O	0	0
			316	158	79	79		
10	J	79	Total	C	N	O	0	0
			316	158	79	79		

- Molecule 11 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	S	73	Total	C	N	O	0	0
			292	146	73	73		
11	O	73	Total	C	N	O	0	0
			292	146	73	73		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	T	77	Total	C	N	O	0	0
			308	154	77	77		
12	P	77	Total	C	N	O	0	0
			308	154	77	77		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	U	90	Total 360	C 180	N 90	O 90	0	0
13	Q	89	Total 356	C 178	N 89	O 89	0	0

- Molecule 14 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	V	72	Total 288	C 144	N 72	O 72	0	0
14	Y	72	Total 288	C 144	N 72	O 72	0	0

- Molecule 15 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	W	70	Total 280	C 140	N 70	O 70	0	0
15	Z	70	Total 280	C 140	N 70	O 70	0	0

- Molecule 16 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	X	70	Total 280	C 140	N 70	O 70	0	0
16	a	71	Total 284	C 142	N 71	O 71	0	0

- Molecule 17 is a protein called U6 snRNA-associated Sm-like protein LSm8.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	b	65	Total 260	C 130	N 65	O 65	0	0

- Molecule 18 is a protein called U6 snRNA-associated Sm-like protein LSm2.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	c	92	Total 368	C 184	N 92	O 92	0	0

- Molecule 19 is a protein called U6 snRNA-associated Sm-like protein LSm3.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	d	77	Total 308	C 154	N 77	O 77	0	0

- Molecule 20 is a protein called U6 snRNA-associated Sm-like protein LSm6.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	e	74	Total 296	C 148	N 74	O 74	0	0

- Molecule 21 is a protein called U6 snRNA-associated Sm-like protein LSm5.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	f	77	Total 308	C 154	N 77	O 77	0	0

- Molecule 22 is a protein called U6 snRNA-associated Sm-like protein LSm7.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	g	66	Total 264	C 132	N 66	O 66	0	0

- Molecule 23 is a protein called U6 snRNA-associated Sm-like protein LSm4.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	h	77	Total 308	C 154	N 77	O 77	0	0

- Molecule 24 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	C	20	Total 429	C 193	N 79	O 137	P 20	0	0

- Molecule 25 is a RNA chain called SNR6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	D	45	Total 945	C 422	N 170	O 308	P 45	0	0

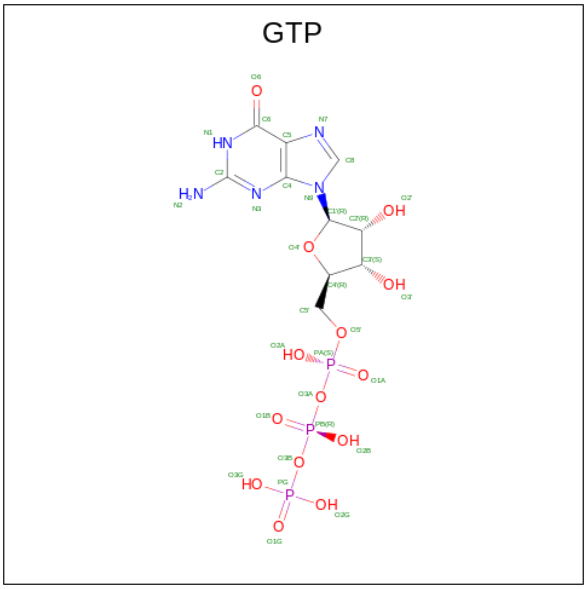
- Molecule 26 is a RNA chain called SNR14 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	E	85	Total	C	N	O	P	0	0
			1806	807	309	605	85		

- Molecule 27 is a RNA chain called SNR7-L snRNA.

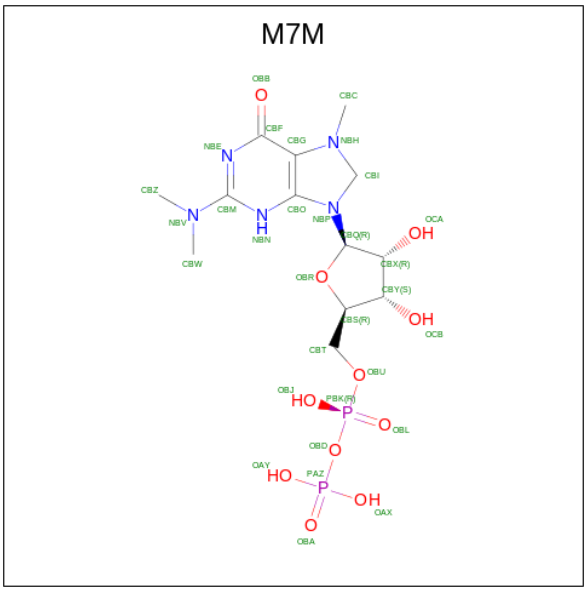
Mol	Chain	Residues	Atoms					AltConf	Trace
27	F	113	Total	C	N	O	P	0	0
			2385	1068	405	799	113		

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
28	H	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 29 is N,N,7-trimethylguanosine 5'-(trihydrogen diphosphate) (three-letter code: M7M) (formula: $C_{13}H_{23}N_5O_{11}P_2$).

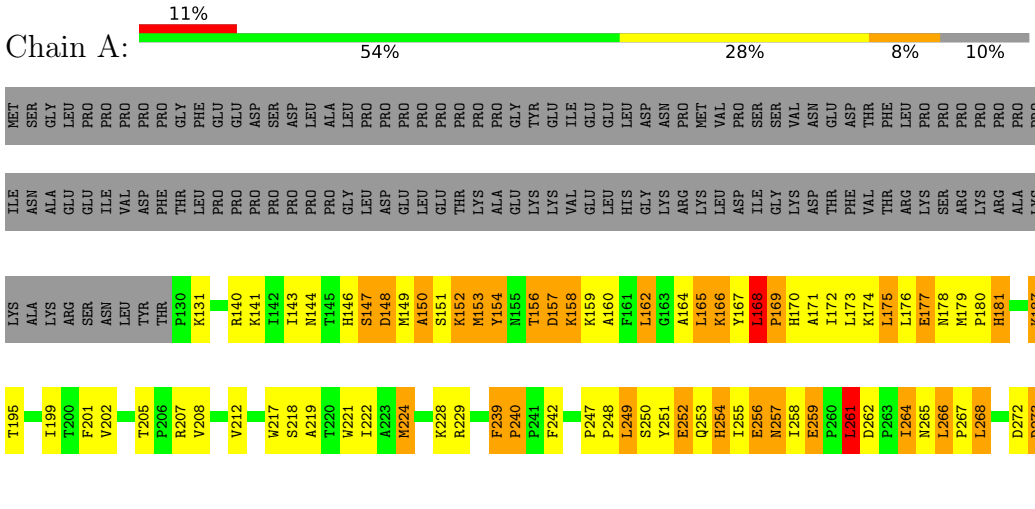


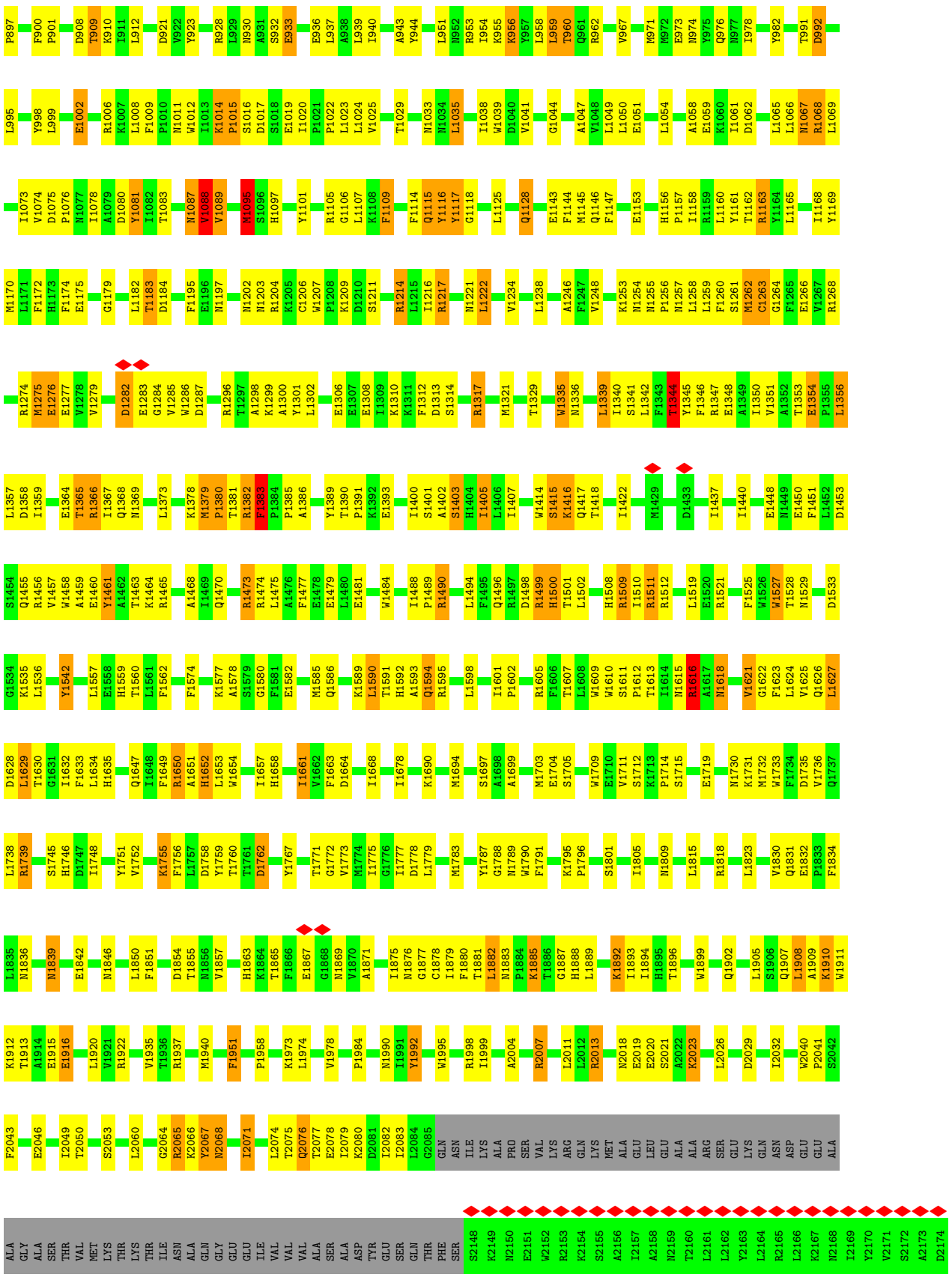
Mol	Chain	Residues	Atoms					AltConf
29	E	1	Total	C	N	O	P	0
			31	13	5	11	2	

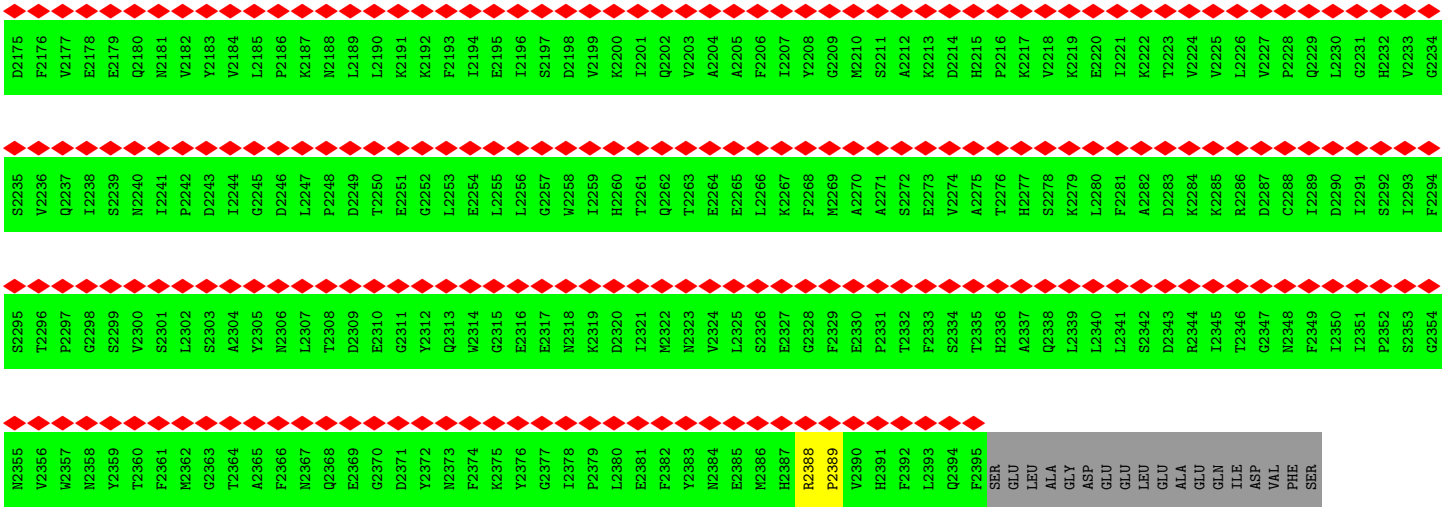
3 Residue-property plots (i)

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

- Molecule 1: Pre-mRNA-splicing factor 8

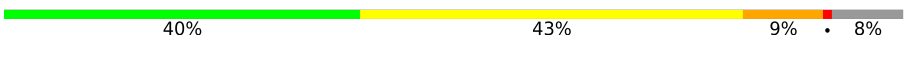


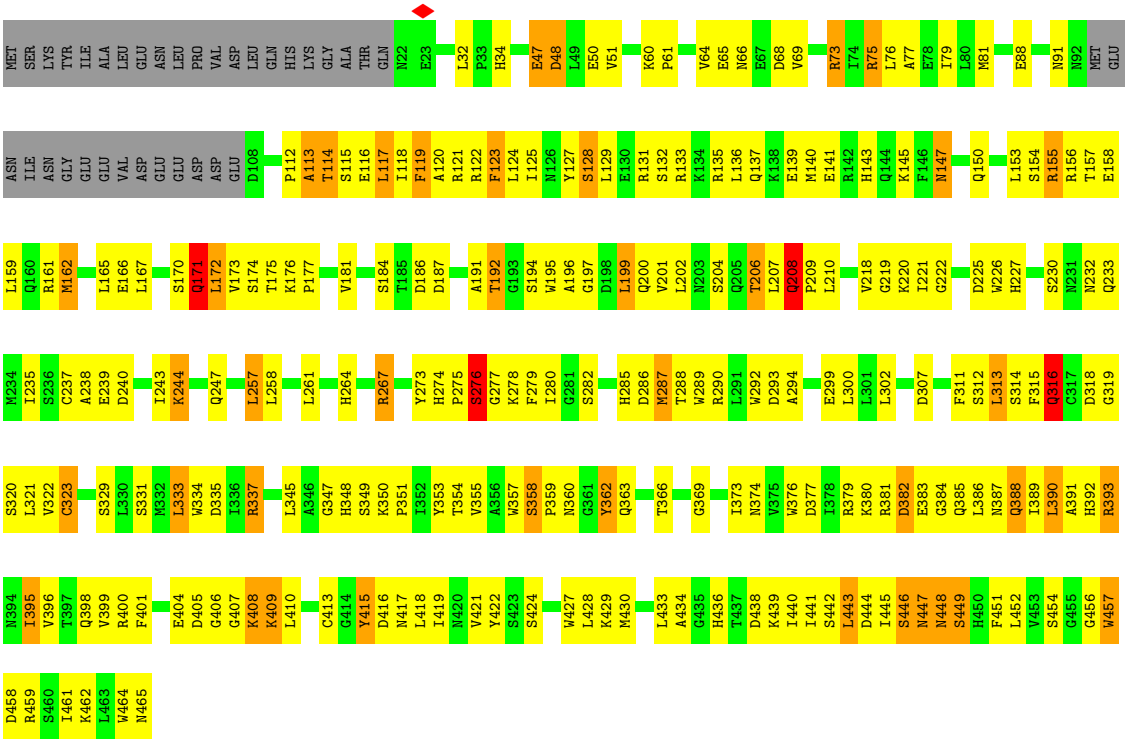

P897 F900 P901 D908 T909 K910 I911 L912 D921 V922 Y923 R928 L929 N930 A931 S932 E933 E936 L937 A938 L939 I940 A943 Y944 L951 N952 R953 I954 K955 K956 Y957 L958 L959 T960 Q961 R962 V967 M971 M972 E973 N974 Y975 Q976 N977 I978 Y982 T991 D992
L995 Y998 L999 E1002 R1006 K1007 L1008 F1009 P1010 N1011 W1012 I1013 K1014 P1015 S1016 D1017 S1018 E1019 I1020 P1021 P1022 L1023 L1024 V1025 T1029 N1033 N1034 L1035 I1038 W1039 D1040 V1041 G1044 A1047 V1048 L1049 L1050 E1051 L1054 A1058 E1059 K1060 I1061 D1062 L1065 L1066 N1067 R1068 L1069
I1073 V1074 D1075 P1076 N1077 I1078 A1079 D1080 Y1081 I1082 T1083 N1087 V1088 V1089 M1095 S1096 H1097 Y1101 R1105 G1106 L1107 K1108 F1109 F1114 Q1115 Y1116 Y1117 G1118 L1125 Q1128 E1143 F1144 M1145 Q1146 F1147 E1153 H1156 P1157 I1158 R1159 L1160 Y1161 T1162 R1163 Y1164 L1165 I1168 Y1169
M1170 L1171 F1172 H1173 F1174 E1175 G1179 L1182 T1183 D1184 F1195 E1196 N1197 N1202 N1203 R1204 K1205 C1206 W1207 P1208 K1209 D1210 S1211 R1214 L1215 I1216 R1217 N1221 L1222 V1234 L1238 A1246 F1247 V1248 K1253 N1254 N1255 P1256 N1257 L1258 L1259 F1260 S1261 M1262 C1263 G1264 F1265 E1266 V1267 R1268
R1274 M1275 E1276 E1277 V1278 V1279 D1282 E1283 G1284 V1285 W1286 D1287 R1296 T1297 A1298 K1299 A1300 Y1301 L1302 E1306 E1307 E1308 I1309 K1310 K1311 F1312 D1313 S1314 R1317 M1321 T1329 W1335 N1336 L1339 I1340 S1341 L1342 F1343 T1344 Y1345 F1346 R1347 E1348 A1349 I1350 V1351 A1352 T1353 E1354 P1355 L1356
L1357 D1358 I1359 E1364 T1365 R1366 I1367 Q1368 N1369 L1373 K1378 M1379 P1380 T1381 R1382 F1383 P1384 P1385 A1386 Y1389 T1390 P1391 K1392 E1393 I1400 S1401 A1402 S1403 H1404 I1405 L1406 I1407 W1414 S1415 K1416 Q1417 T1418 I1422 M1429 D1433 I1437 I1440 E1448 N1449 E1450 F1451 L1452 D1453
S1454 Q1455 R1456 V1457 W1458 A1459 E1460 Y1461 A1462 T1463 K1464 R1465 A1468 I1469 Q1470 R1473 R1474 L1475 A1476 F1477 E1478 E1479 L1480 E1481 W1484 I1488 P1489 R1490 L1494 F1495 Q1496 R1497 D1498 R1499 H1500 T1501 L1502 H1508 R1509 I1510 R1511 R1512 L1519 E1520 R1521 F1525 W1526 W1527 T1528 N1529 D1533
G1534 K1535 L1536 Y1542 L1557 E1558 H1559 T1560 L1561 F1562 F1574 K1577 A1578 S1579 G1580 F1581 E1582 M1585 Q1586 K1589 L1590 T1591 H1592 A1593 Q1594 R1595 L1598 I1601 P1602 R1605 F1606 T1607 L1608 W1609 W1610 S1611 P1612 T1613 T1614 N1615 R1616 A1617 N1618 V1621 G1622 F1623 L1624 V1625 Q1626 L1627
D1628 L1629 T1630 G1631 I1632 F1633 L1634 H1635 Q1647 I1648 F1649 R1650 A1651 H1652 L1653 W1654 I1657 H1658 I1661 V1662 F1663 D1664 I1668 I1678 K1690 M1694 S1697 A1698 A1699 M1703 E1704 S1705 W1709 E1710 V1711 S1712 K1713 P1714 S1715 E1719 N1730 K1731 M1732 W1733 F1734 D1735 V1736 Q1737
L1738 R1739 S1745 H1746 D1747 I1748 Y1751 V1752 K1755 F1756 L1757 D1758 Y1759 T1760 T1761 D1762 Y1767 T1771 G1772 V1773 M1774 I1775 G1776 I1777 D1778 L1779 M1783 Y1787 G1788 N1789 W1790 F1791 K1795 P1796 S1801 I1805 N1809 L1815 R1818 L1823 V1830 Q1831 E1832 P1833 F1834
L1835 N1836 N1839 E1842 N1846 L1850 F1851 D1854 T1855 N1856 V1857 H1863 K1864 T1865 F1866 E1867 G1868 N1869 V1870 A1871 I1875 N1876 G1877 C1878 I1879 F1880 T1881 L1882 N1883 P1884 K1885 T1886 G1887 H1888 L1889 K1892 I1893 I1894 H1895 T1896 W1899 Q1902 L1905 S1906 Q1907 L1908 A1909 K1910 W1911
K1912 T1913 A1914 E1915 E1916 L1920 V1921 R1922 V1935 T1936 R1937 M1940 F1951 P1958 K1973 L1974 V1978 P1984 N1990 I1991 Y1992 W1995 R1998 I1999 A2004 R2007 L2011 L2012 R2013 N2018 E2019 E2020 S2021 A2022 K2023 L2026 D2029 I2032 W2040 P2041 S2042
F2043 E2046 I2049 T2050 S2053 L2060 G2064 R2065 K2066 Y2067 N2068 I2071 L2074 T2075 Q2076 T2077 E2078 I2079 K2080 D2081 I2082 I2083 L2084 G2085 GLN ASN ILE LYS ALA PRO SER VAL LYS ARG GLN LYS MET ALA GLU LEU GLU ALA ALA ARG SER GLU LYS GLN ASN ASP GLU GLU ALA
ALA GLY ALA SER THR VAL MET LYS THR LYS THR ILE ASN ALA GLN GLY GLU GLU ILE VAL VAL VAL ALA SER ALA ASP TYR GLU SER GLN THR PHE SER S2148 K2149 N2150 E2151 W2152 R2153 K2154 S2155 A2156 I2157 A2158 N2159 T2160 L2161 L2162 Y2163 L2164 R2165 L2166 K2167 N2168 I2169 Y2170 V2171 S2172 A2173 D2174



• Molecule 2: U4/U6 small nuclear ribonucleoprotein PRP4

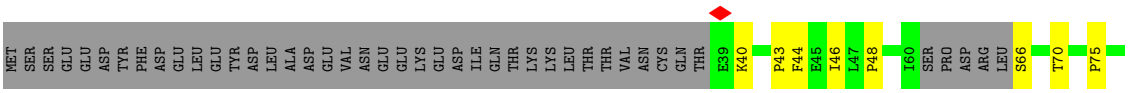
Chain B:

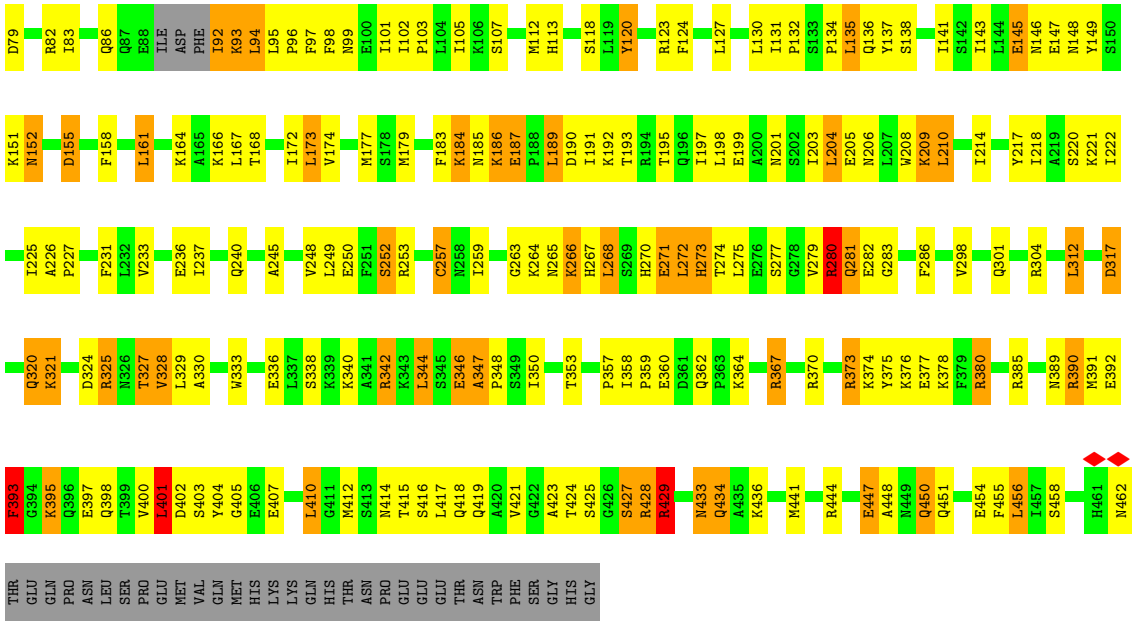




• Molecule 3: Pre-mRNA-processing factor 31

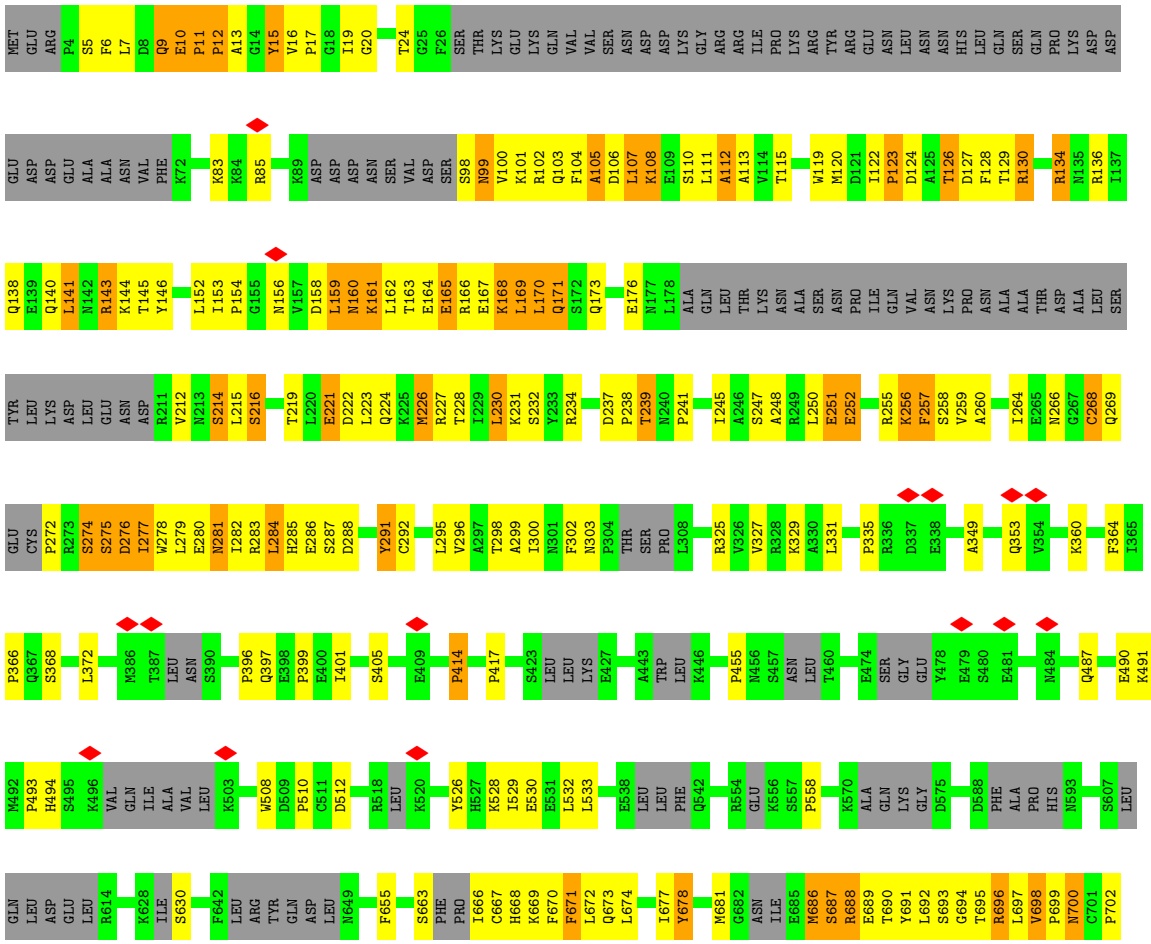
Chain I:

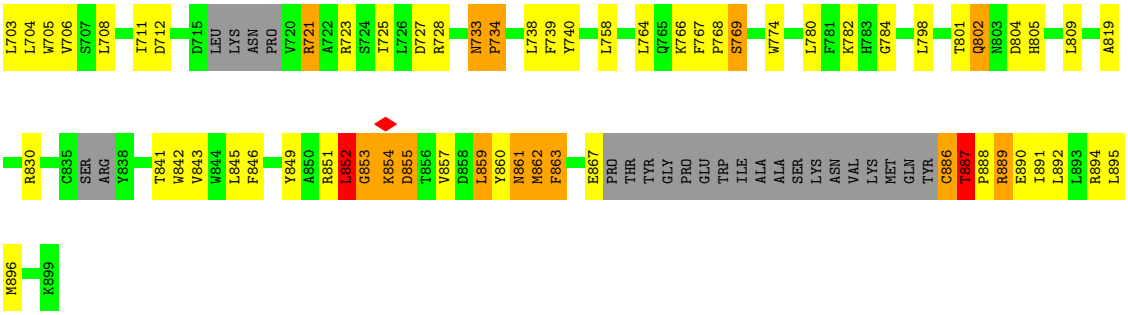




• Molecule 4: Pre-mRNA-splicing factor 6

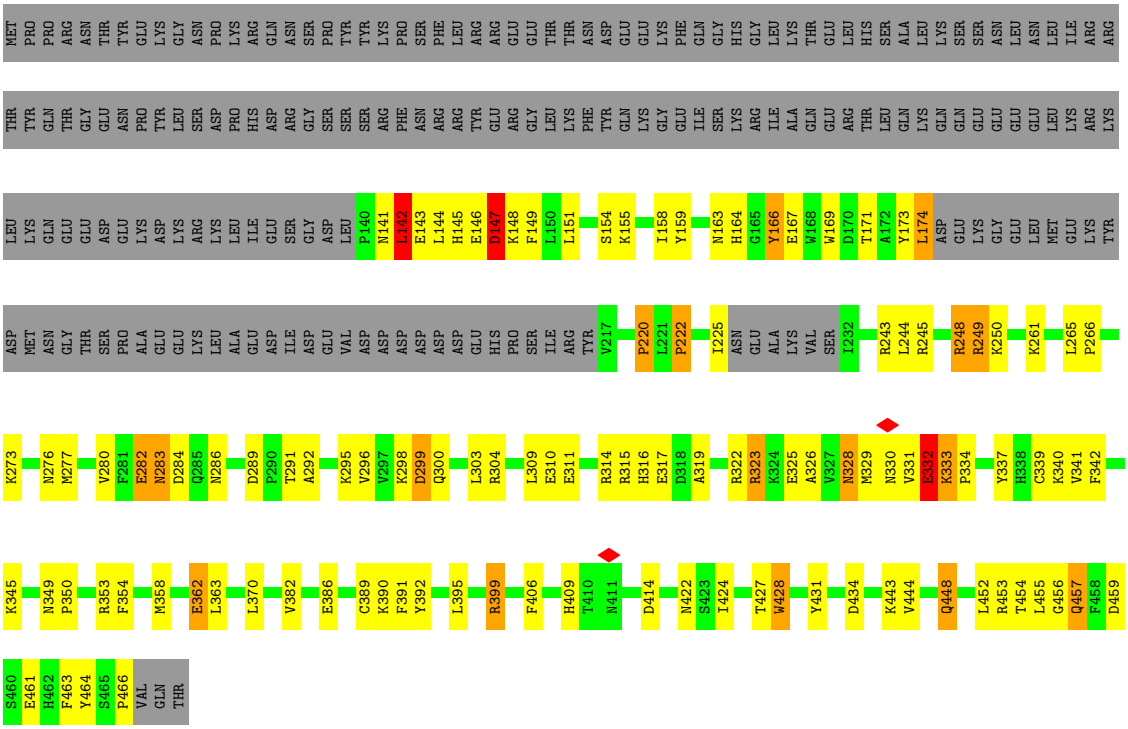
Chain G:





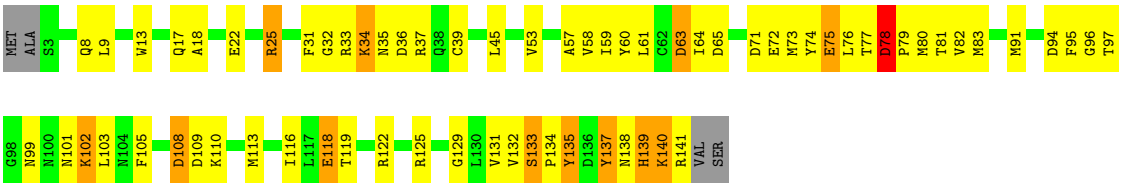
• Molecule 5: U4/U6 small nuclear ribonucleoprotein PRP3

Chain K:



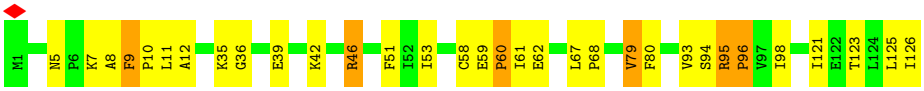
• Molecule 6: Spliceosomal protein DIB1

Chain L:

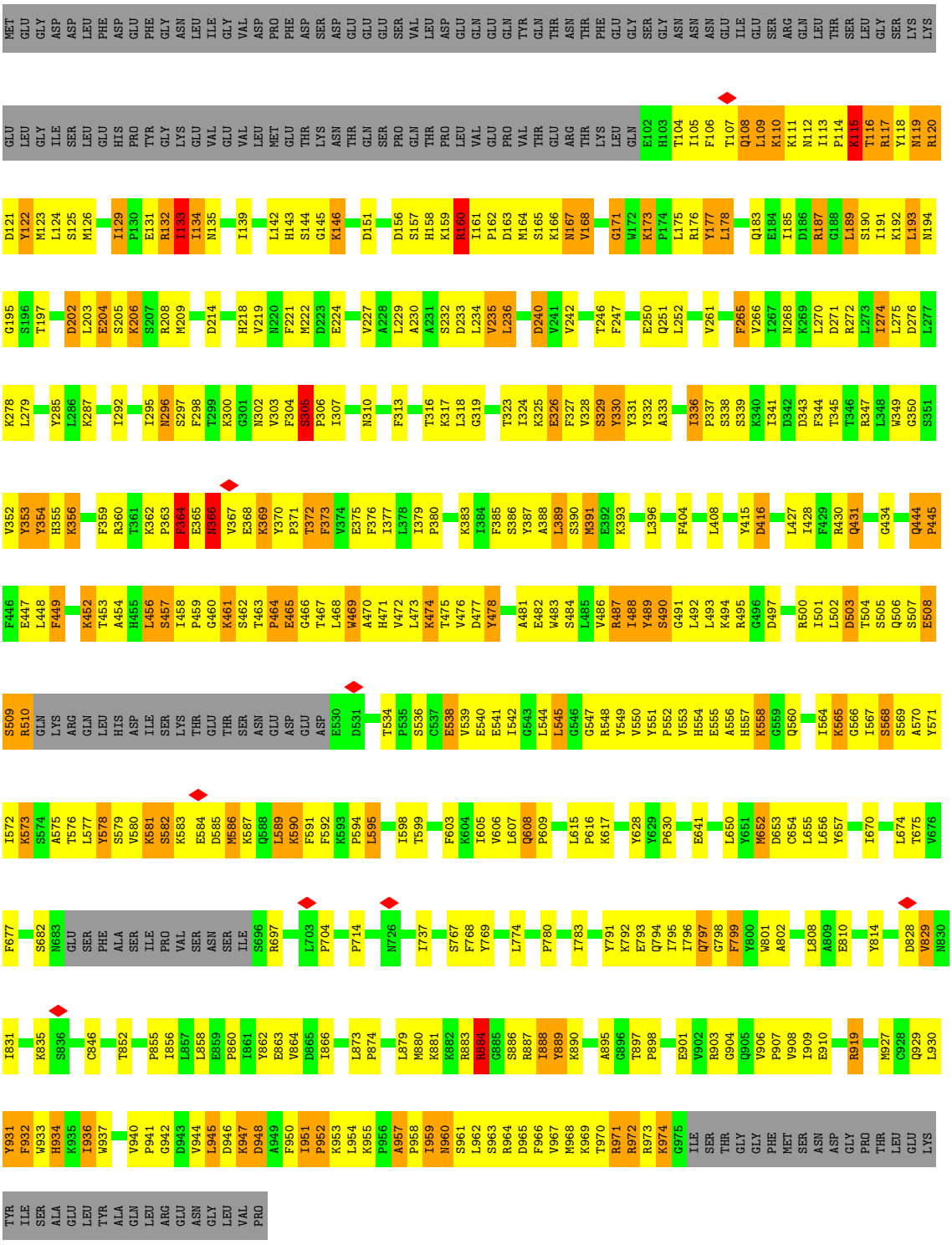


• Molecule 7: 13 kDa ribonucleoprotein-associated protein

Chain M:

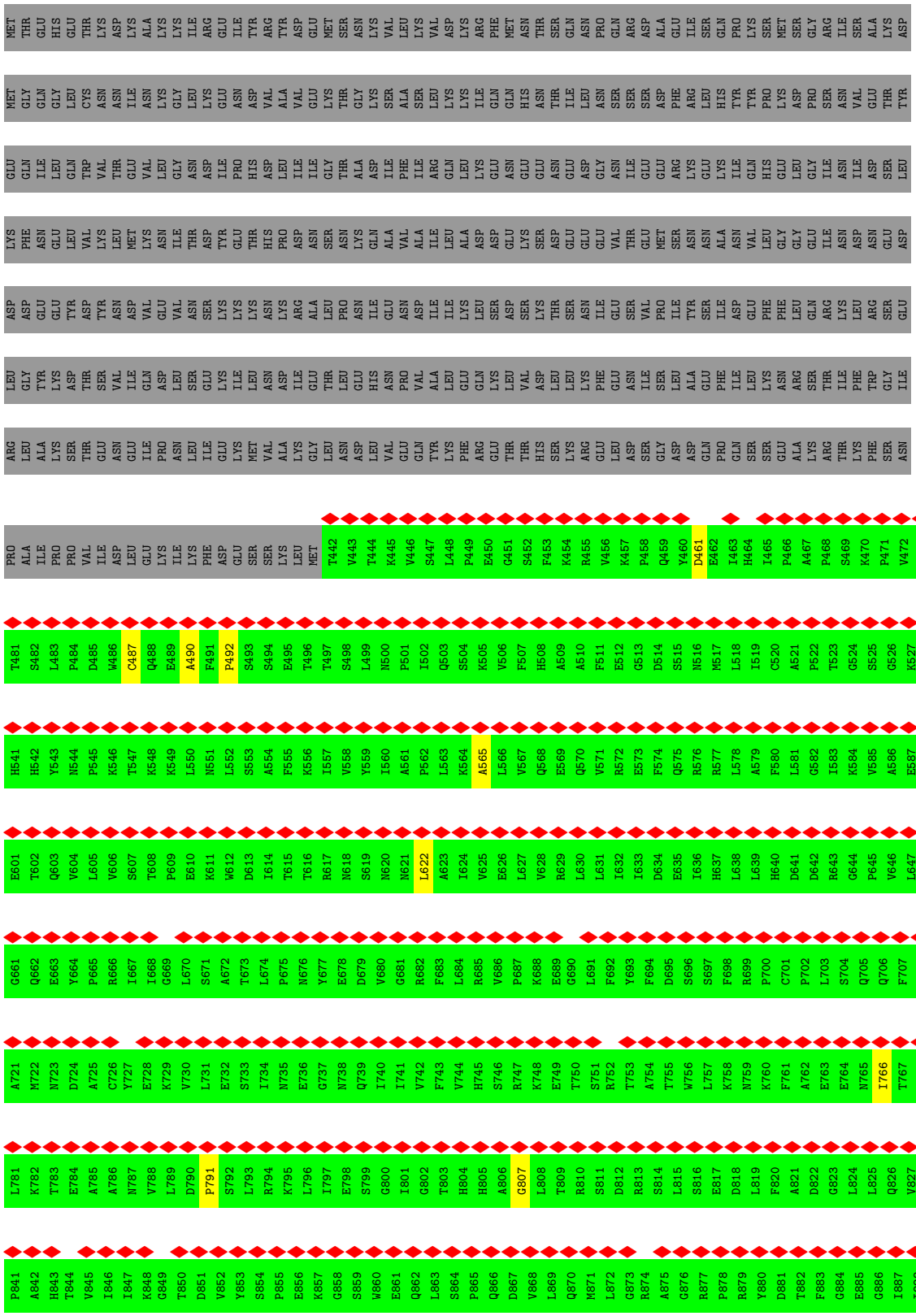


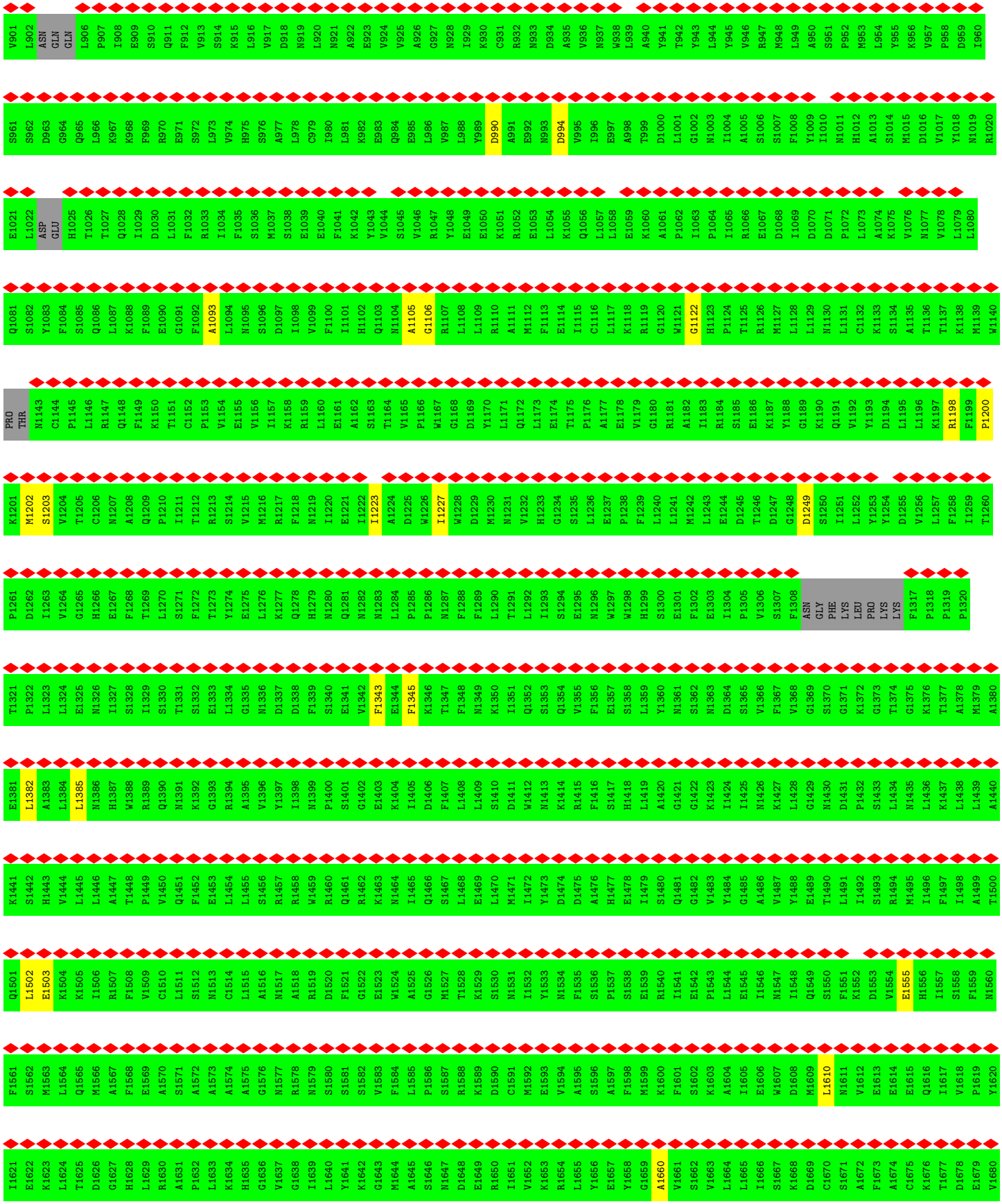
• Molecule 8: Pre-mRNA-splicing factor SNU114

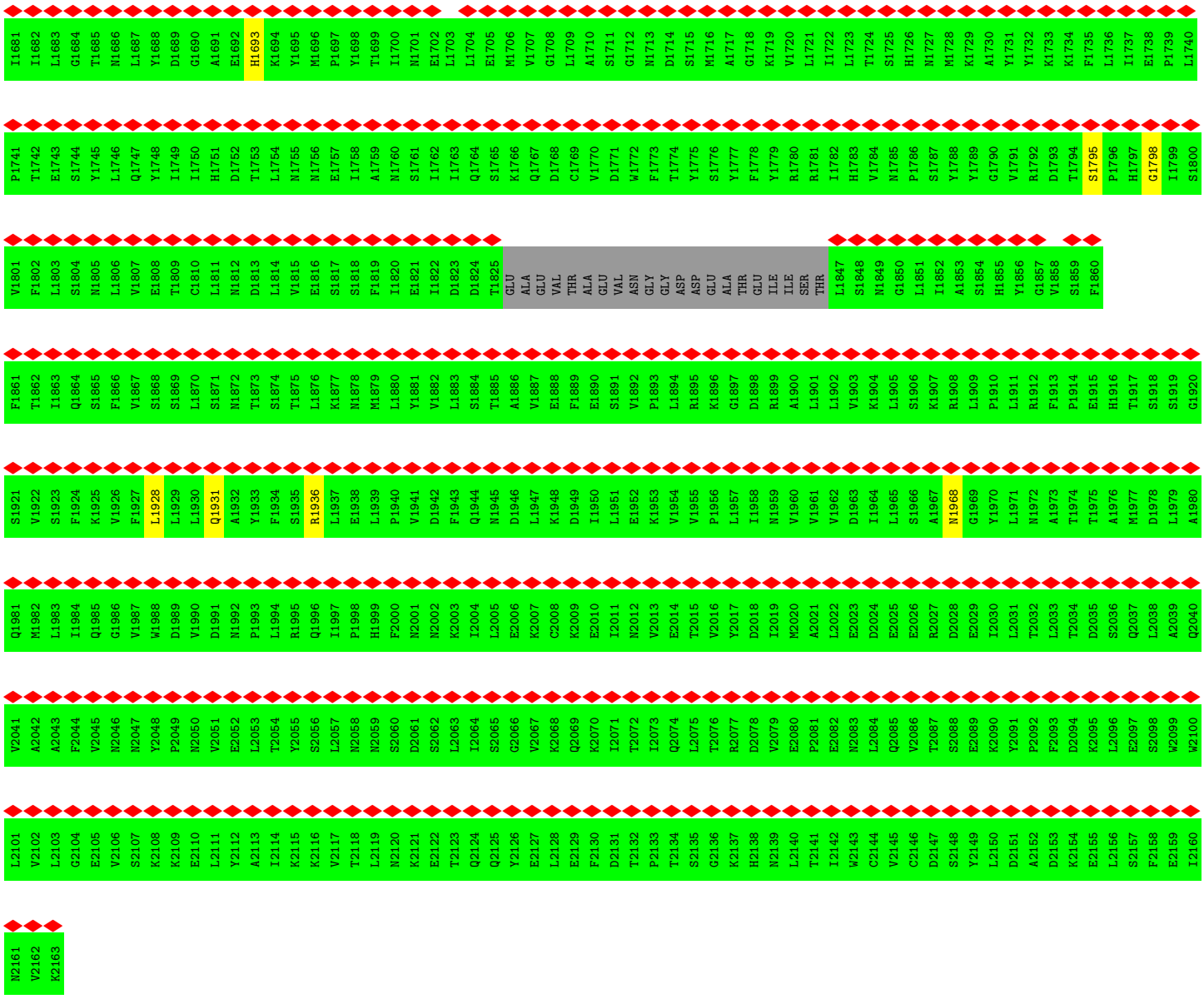


• Molecule 9: Pre-mRNA-splicing helicase BRR2

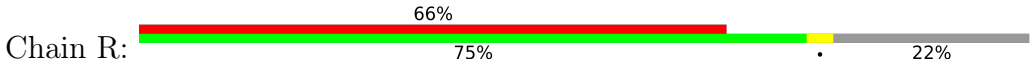
Chain N:

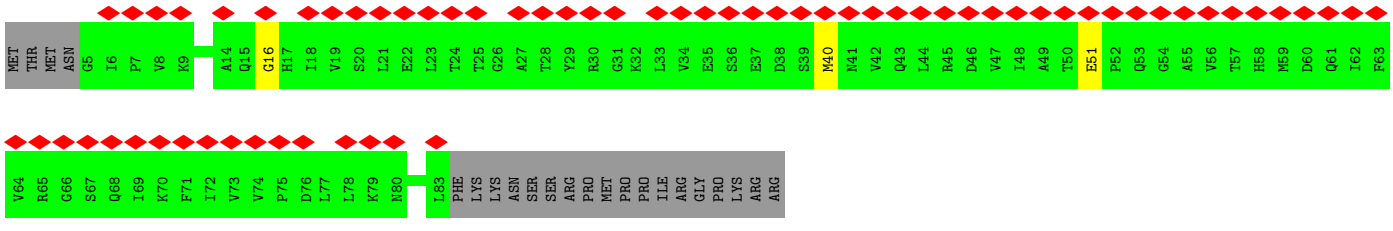



V901 L902 ASN GLN GLN L906 P907 I908 E909 S910 Q911 F912 V913 S914 K915 L916 V917 D918 N919 L920 N921 A922 E923 V924 V925 A926 G927 N928 I929 K930 C931 R932 N933 D934 A935 V936 N937 W938 L939 A940 Y941 T942 Y943 L944 Y945 V946 R947 M948 L949 A950 S951 P952 M953 L954 Y955 K956 V957 P958 D959 I960
S961 S962 D963 G964 Q965 L966 K967 K968 F969 R970 E971 S972 L973 V974 H975 S976 A977 L978 C979 I980 L981 K982 E983 Q984 E985 L986 V987 L988 Y989 D990 A991 E992 N993 D994 V995 I996 E997 A998 T999 D1000 L1001 G1002 N1003 I1004 A1005 S1006 S1007 F1008 Y1009 I1010 N1011 H1012 A1013 S1014 M1015 D1016 V1017 Y1018 N1019 R1020
E1021 L1022 ASP GLU H1025 T1026 T1027 Q1028 I1029 D1030 L1031 F1032 R1033 I1034 F1035 S1036 M1037 S1038 E1039 E1040 F1041 K1042 Y1043 V1044 S1045 V1046 R1047 Y1048 E1049 E1050 K1051 R1052 E1053 L1054 K1055 Q1056 L1057 L1058 E1059 K1060 A1061 P1062 I1063 P1064 I1065 R1066 E1067 D1068 I1069 D1070 D1071 P1072 L1073 A1074 K1075 V1076 N1077 V1078 L1079 L1080
Q1081 S1082 Y1083 F1084 S1085 Q1086 L1087 K1088 F1089 E1090 G1091 F1092 A1093 L1094 N1095 S1096 D1097 I1098 V1099 F1100 I1101 H1102 Q1103 N1104 A1105 G1106 R1107 L1108 L1109 R1110 A1111 M1112 F1113 E1114 I1115 C1116 L1117 K1118 R1119 G1120 W1121 G1122 H1123 P1124 T1125 R1126 M1127 L1128 L1129 N1130 L1131 C1132 K1133 S1134 A1135 T1136 T1137 K1138 M1139 W1140
PRO THR N1143 C1144 P1145 L1146 R1147 Q1148 F1149 K1150 T1151 C1152 P1153 V1154 E1155 V1156 I1157 K1158 R1159 L1160 E1161 A1162 S1163 T1164 V1165 P1166 W1167 G1168 D1169 Y1170 L1171 Q1172 L1173 E1174 T1175 P1176 A1177 E1178 V1179 G1180 R1181 A1182 I1183 R1184 S1185 E1186 K1187 Y1188 G1189 K1190 Q1191 V1192 Y1193 D1194 L1195 L1196 K1197 R1198 F1199 P1200
K1201 M1202 S1203 V1204 T1205 C1206 N1207 A1208 Q1209 P1210 I1211 T1212 R1213 S1214 V1215 M1216 R1217 F1218 N1219 I1220 E1221 I1222 I1223 A1224 D1225 W1226 I1227 W1228 D1229 M1230 N1231 V1232 H1233 G1234 S1235 L1236 E1237 P1238 F1239 L1240 L1241 M1242 L1243 R1244 E1245 D1246 D1247 G1248 D1249 S1250 I1251 L1252 Y1253 Y1254 D1255 V1256 L1257 F1258 I1259 T1260
P1261 D1262 I1263 V1264 G1265 H1266 E1267 F1268 T1269 L1270 S1271 F1272 T1273 Y1274 E1275 L1276 K1277 Q1278 H1279 N1280 Q1281 N1282 N1283 L1284 P1285 P1286 N1287 F1288 F1289 L1290 T1291 L1292 I1293 S1294 E1295 N1296 W1297 W1298 H1299 S1300 E1301 F1302 E1303 I1304 P1305 V1306 S1307 F1308 ASN GLY PHE LYS LEU PRO LYS LYS F1317 P1318 P1319 P1320
T1321 P1322 L1323 L1324 E1325 N1326 I1327 S1328 I1329 S1330 T1331 S1332 E1333 L1334 G1335 N1336 D1337 D1338 F1339 S1340 E1341 V1342 F1343 E1344 F1345 K1346 T1347 F1348 N1349 K1350 I1351 Q1352 S1353 Q1354 V1355 F1356 E1357 S1358 L1359 Y1360 N1361 S1362 N1363 D1364 S1365 V1366 F1367 V1368 G1369 S1370 G1371 K1372 G1373 T1374 G1375 K1376 T1377 A1378 M1379 A1380
E1381 L1382 A1383 L1384 L1385 N1386 H1387 W1388 R1389 Q1390 N1391 K1392 G1393 R1394 A1395 V1396 Y1397 I1398 N1399 P1400 S1401 G1402 E1403 K1404 I1405 D1406 F1407 L1408 L1409 S1410 D1411 W1412 N1413 K1414 R1415 F1416 S1417 H1418 L1419 A1420 G1421 G1422 K1423 I1424 I1425 N1426 K1427 L1428 G1429 N1430 D1431 P1432 S1433 L1434 N1435 L1436 K1437 L1438 L1439 A1440
K1441 S1442 H1443 V1444 L1445 L1446 A1447 T1448 P1449 V1450 Q1451 F1452 E1453 L1454 L1455 S1456 R1457 R1458 W1459 R1460 Q1461 R1462 K1463 N1464 I1465 Q1466 S1467 L1468 E1469 L1470 M1471 I1472 Y1473 D1474 D1475 A1476 H1477 E1478 I1479 A1480 Q1481 G1482 V1483 Y1484 G1485 A1486 V1487 Y1488 E1489 T1490 L1491 I1492 S1493 R1494 M1495 I1496 F1497 I1498 A1499 T1500
Q1501 L1502 E1503 K1504 K1505 I1506 R1507 F1508 V1509 C1510 L1511 S1512 N1513 C1514 L1515 A1516 N1517 A1518 R1519 D1520 F1521 G1522 E1523 W1524 A1525 G1526 M1527 T1528 K1529 S1530 N1531 I1532 Y1533 N1534 F1535 S1536 P1537 S1538 E1539 R1540 I1541 E1542 P1543 L1544 E1545 I1546 N1547 I1548 Q1549 S1550 F1551 K1552 D1553 V1554 E1555 H1556 I1557 S1558 F1559 N1560
F1561 S1562 M1563 L1564 Q1565 M1566 A1567 F1568 E1569 A1570 S1571 A1572 A1573 A1574 A1575 G1576 N1577 R1578 N1579 S1580 S1581 S1582 V1583 F1584 L1585 P1586 S1587 R1588 K1589 D1590 C1591 M1592 E1593 V1594 A1595 S1596 A1597 F1598 M1599 K1600 F1601 S1602 K1603 A1604 I1605 E1606 W1607 D1608 M1609 L1610 N1611 V1612 E1613 E1614 E1615 Q1616 I1617 V1618 P1619 Y1620
I1621 E1622 K1623 L1624 T1625 D1626 G1627 H1628 L1629 R1630 A1631 P1632 L1633 K1634 H1635 G1636 V1637 G1638 I1639 L1640 Y1641 K1642 G1643 M1644 A1645 S1646 N1647 D1648 E1649 R1650 I1651 V1652 K1653 R1654 L1655 Y1656 E1657 Y1658 G1659 A1660 V1661 S1662 V1663 L1664 L1665 I1666 S1667 K1668 D1669 C1670 S1671 A1672 F1673 A1674 C1675 K1676 T1677 D1678 E1679 V1680

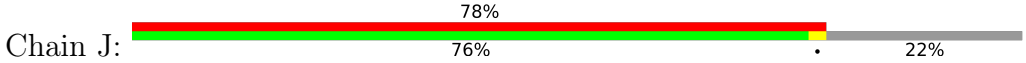


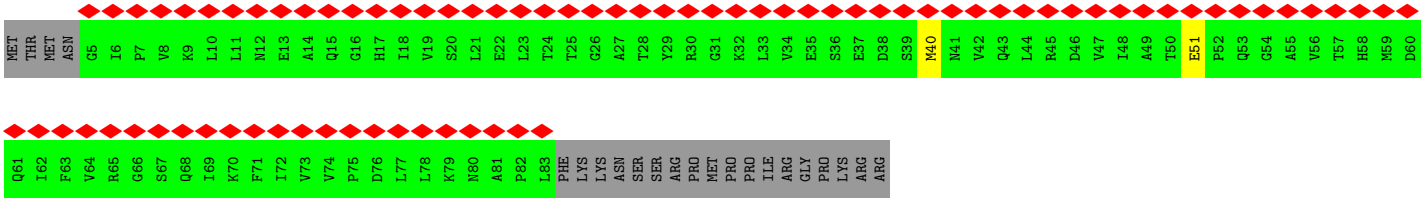
• Molecule 10: Small nuclear ribonucleoprotein Sm D3



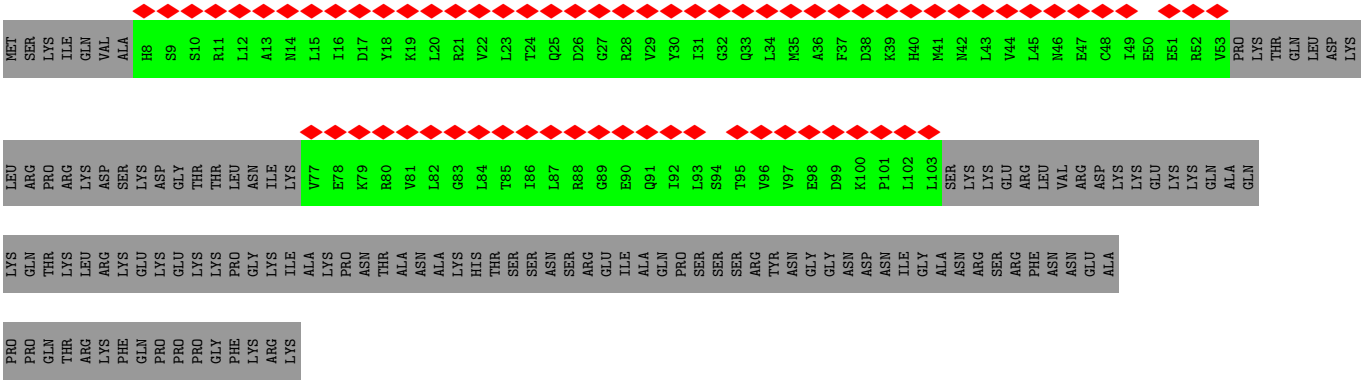


• Molecule 10: Small nuclear ribonucleoprotein Sm D3

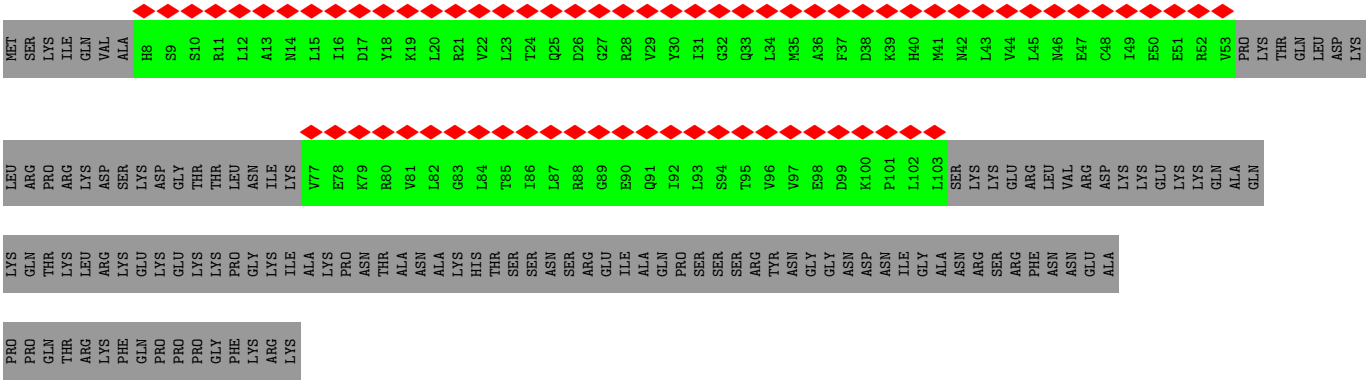




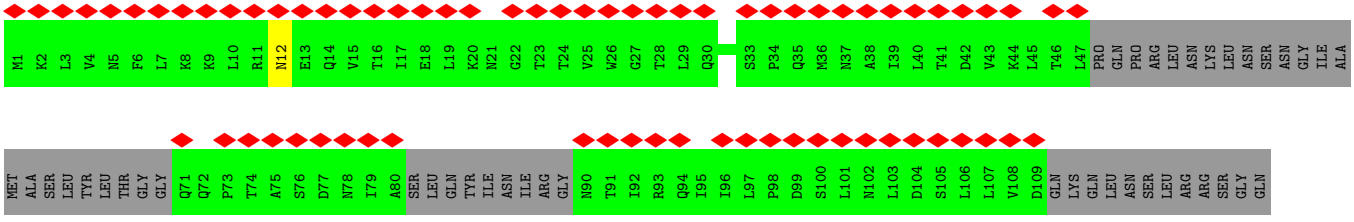
• Molecule 11: Small nuclear ribonucleoprotein-associated protein B



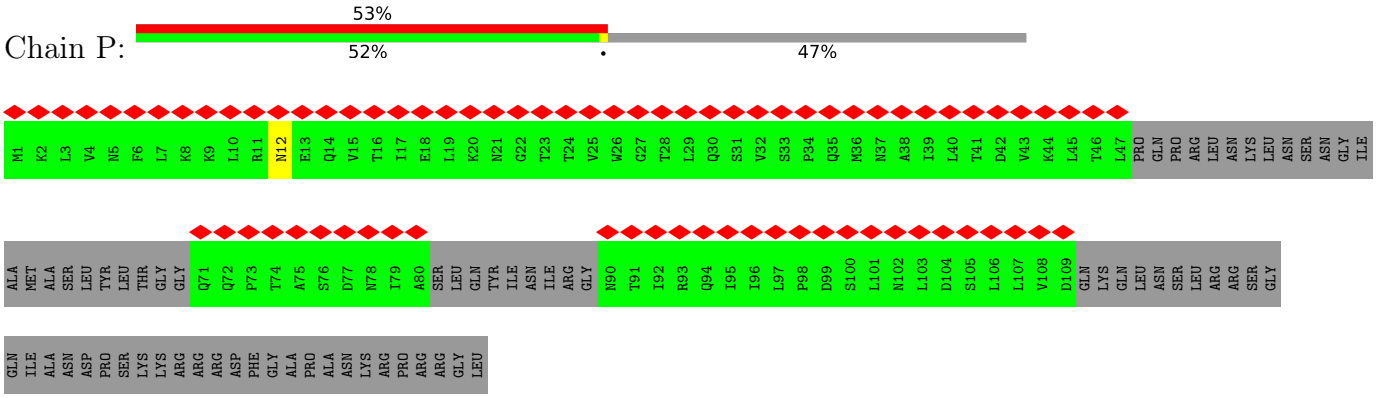
• Molecule 11: Small nuclear ribonucleoprotein-associated protein B



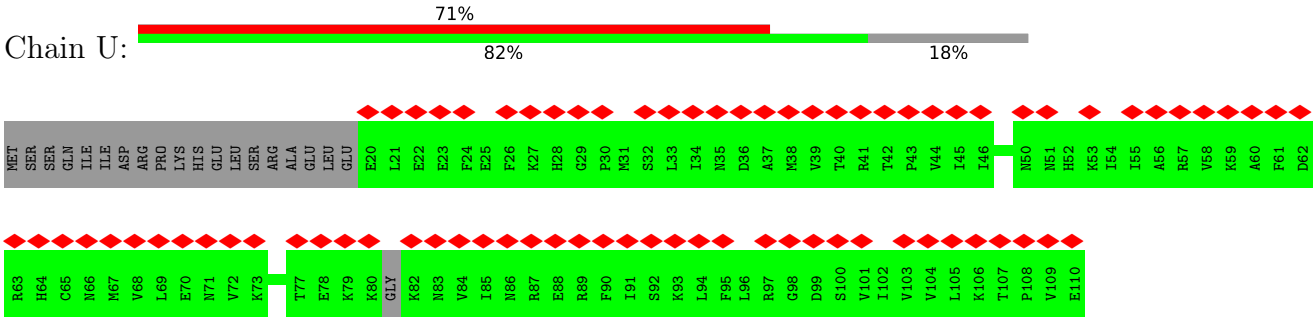
• Molecule 12: Small nuclear ribonucleoprotein Sm D1



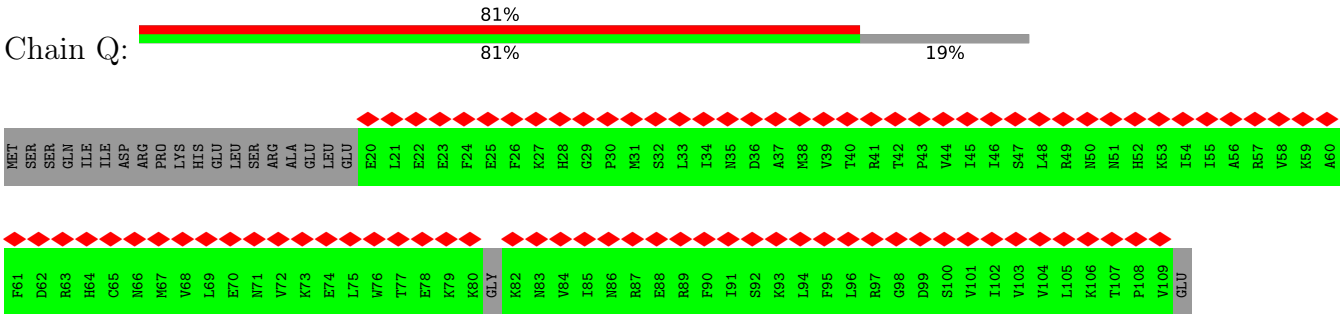
• Molecule 12: Small nuclear ribonucleoprotein Sm D1



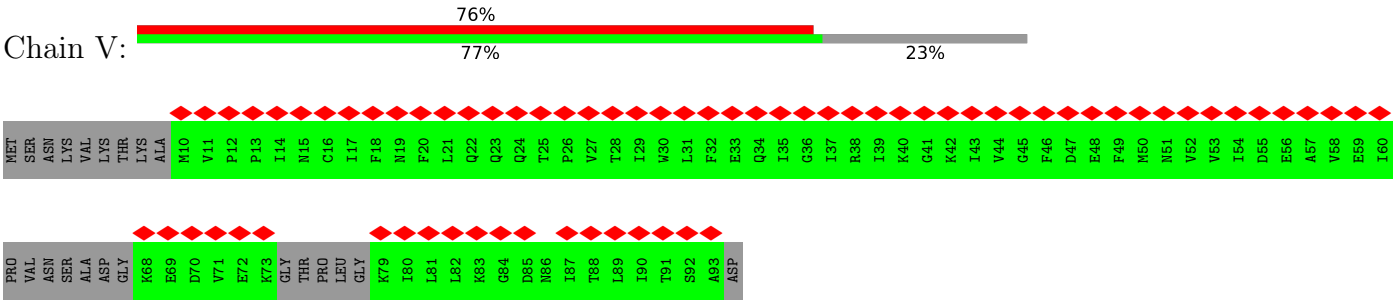
• Molecule 13: Small nuclear ribonucleoprotein Sm D2



• Molecule 13: Small nuclear ribonucleoprotein Sm D2

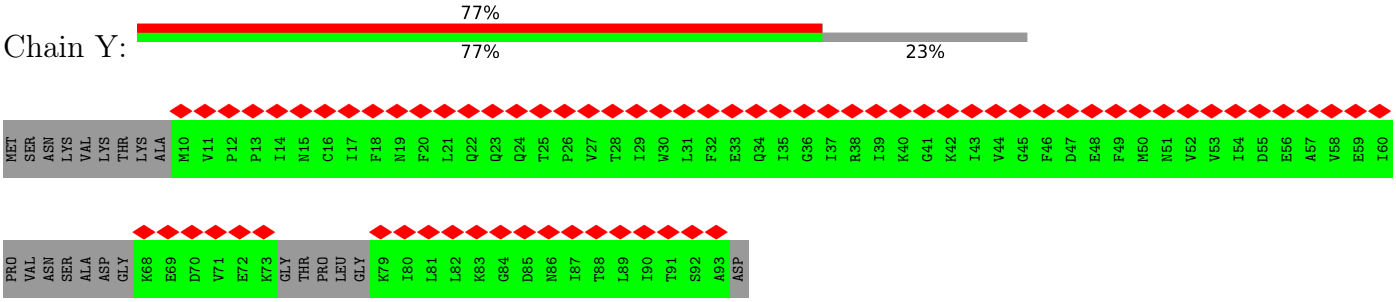


• Molecule 14: Small nuclear ribonucleoprotein E



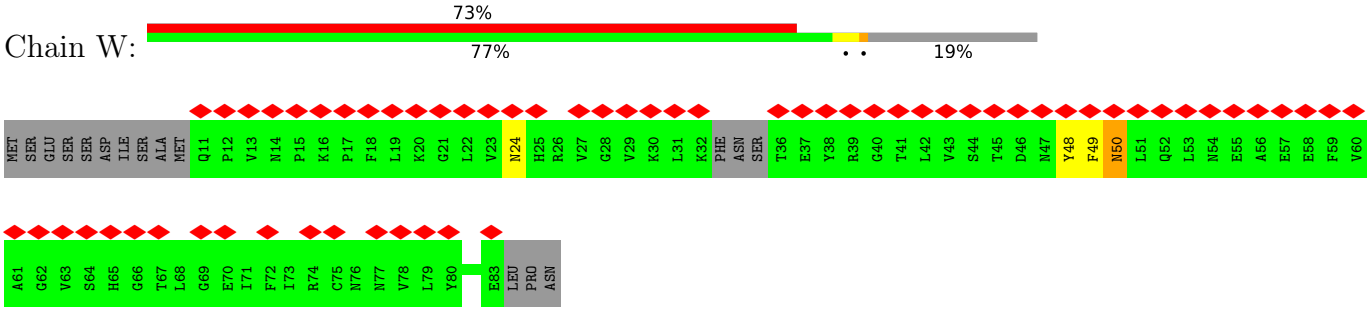
• Molecule 14: Small nuclear ribonucleoprotein E

Chain Y:



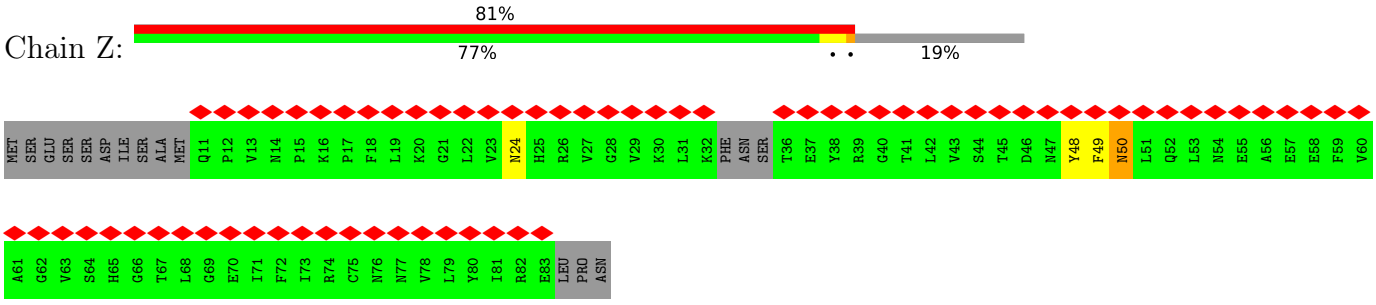
• Molecule 15: Small nuclear ribonucleoprotein F

Chain W:



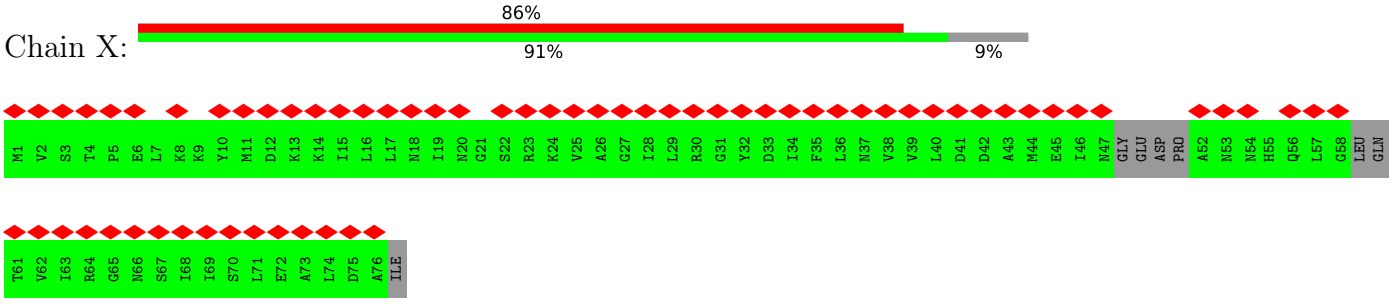
• Molecule 15: Small nuclear ribonucleoprotein F

Chain Z:



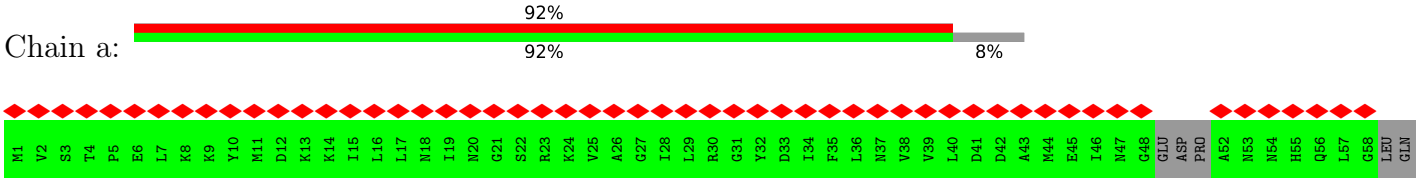
• Molecule 16: Small nuclear ribonucleoprotein G

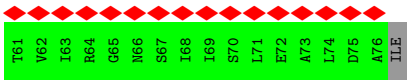
Chain X:



• Molecule 16: Small nuclear ribonucleoprotein G

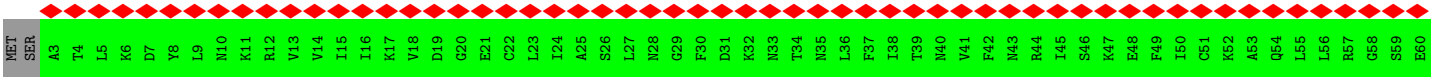
Chain a:

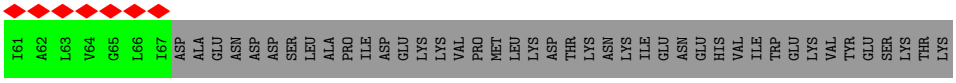




• Molecule 17: U6 snRNA-associated Sm-like protein LSm8

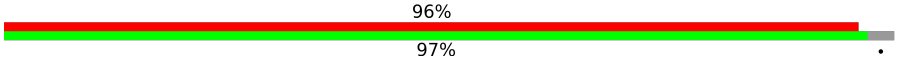
Chain b:

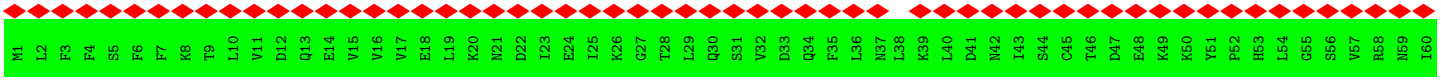


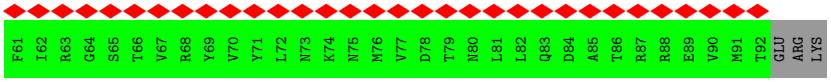


• Molecule 18: U6 snRNA-associated Sm-like protein LSm2

Chain c:

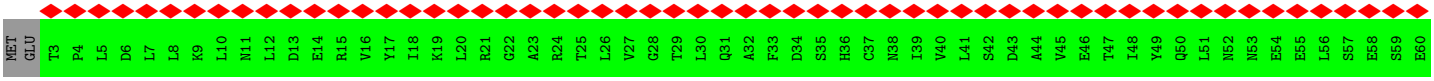


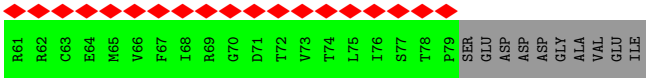




• Molecule 19: U6 snRNA-associated Sm-like protein LSm3

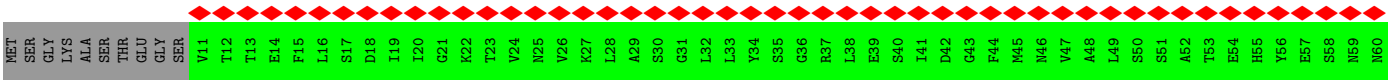
Chain d:





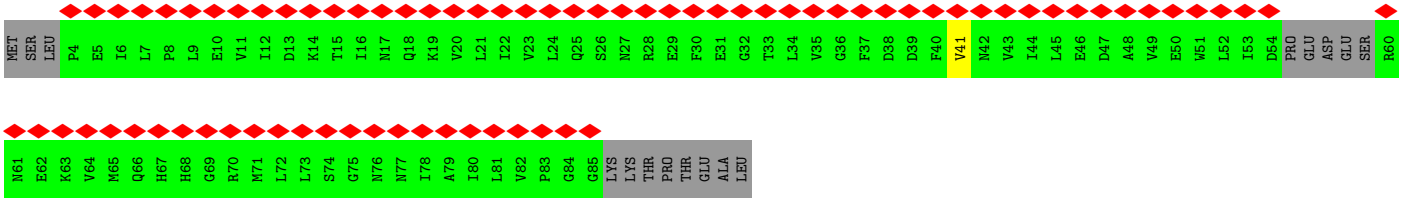
• Molecule 20: U6 snRNA-associated Sm-like protein LSm6

Chain e:



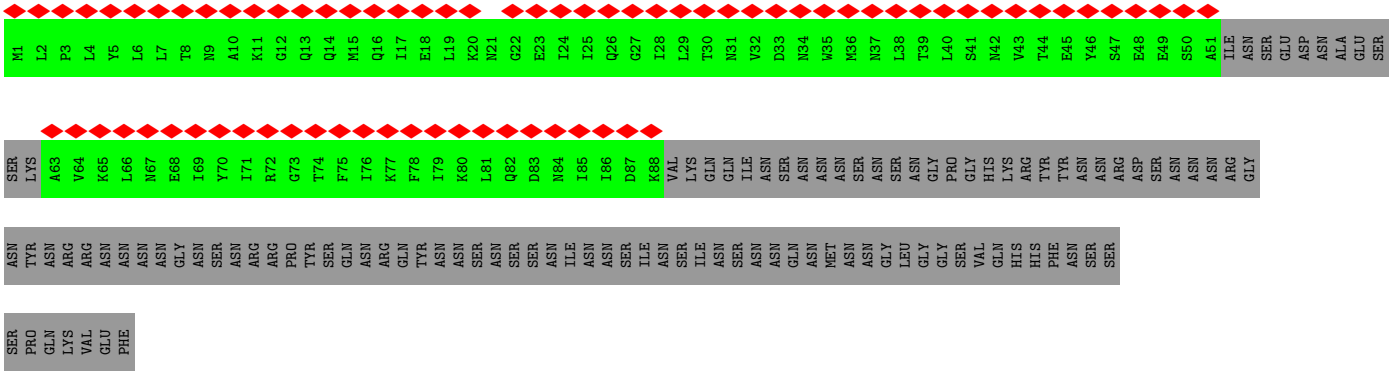
• Molecule 21: U6 snRNA-associated Sm-like protein LSm5

Chain f:

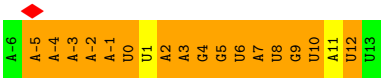


• Molecule 22: U6 snRNA-associated Sm-like protein LSm7

• Molecule 23: U6 snRNA-associated Sm-like protein LSm4



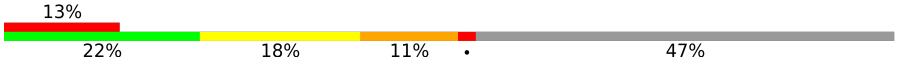
• Molecule 24: pre-mRNA

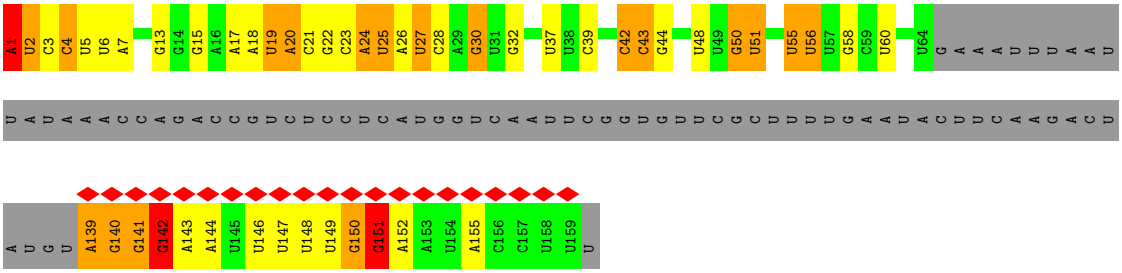


• Molecule 25: SNR6 snRNA

• Molecule 26: SNR14 snRNA

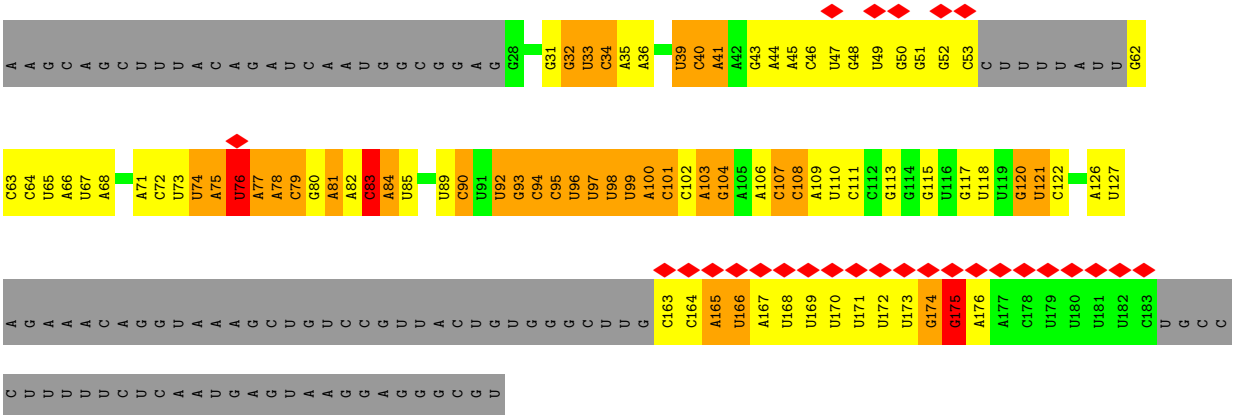
Chain E:





• Molecule 27: SNR7-L snRNA

Chain F:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	172134	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	Not provided	
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.204	Depositor
Minimum map value	-0.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0147	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: M7M, GTP

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.86	22/17296 (0.1%)	0.91	24/23336 (0.1%)
2	B	0.72	2/3434 (0.1%)	0.86	0/4635
3	I	0.84	1/3219 (0.0%)	0.99	13/4332 (0.3%)
4	G	0.62	3/4967 (0.1%)	0.79	14/6746 (0.2%)
5	K	0.67	1/2376 (0.0%)	0.83	3/3183 (0.1%)
6	L	0.73	0/1167	0.87	0/1571
7	M	0.95	0/963	1.02	2/1310 (0.2%)
8	H	0.55	2/6874 (0.0%)	0.78	8/9305 (0.1%)
9	N	0.52	0/6738	0.65	0/8412
10	J	0.29	0/315	0.46	0/392
10	R	0.29	0/315	0.46	0/392
11	O	0.28	0/290	0.46	0/359
11	S	0.28	0/290	0.46	0/359
12	P	0.27	0/305	0.47	0/376
12	T	0.27	0/305	0.46	0/376
13	Q	0.25	0/354	0.45	0/439
13	U	0.25	0/358	0.45	0/444
14	V	0.29	0/285	0.43	0/351
14	Y	0.29	0/285	0.43	0/351
15	W	0.30	0/278	0.45	0/344
15	Z	0.30	0/278	0.45	0/344
16	X	0.24	0/277	0.46	0/341
16	a	0.27	0/281	0.46	0/346
17	b	0.48	0/259	0.70	0/322
18	c	0.49	0/367	0.66	0/457
19	d	0.58	0/307	0.74	0/382
20	e	0.48	0/295	0.68	0/367
21	f	0.50	0/306	0.71	0/379
22	g	0.48	0/262	0.71	0/324
23	h	0.47	0/306	0.68	0/379
24	C	0.34	0/481	0.71	0/747
25	D	0.81	0/1054	0.93	3/1634 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
26	E	0.94	8/2016 (0.4%)	1.12	17/3136 (0.5%)
27	F	0.44	2/2659 (0.1%)	0.80	1/4131 (0.0%)
All	All	0.70	41/59562 (0.1%)	0.84	85/80302 (0.1%)

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
1	A	0	3
2	B	0	2
3	I	0	1
4	G	0	7
5	K	0	1
7	M	0	4
8	H	0	2
All	All	0	20

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	E	1	A	C5-C4	10.58	1.46	1.38
26	E	1	A	N7-C5	-8.64	1.34	1.39
1	A	1335	TRP	CG-CD2	-8.36	1.29	1.43
26	E	1	A	N9-C4	-8.09	1.32	1.37
26	E	1	A	C5-C6	7.52	1.47	1.41
1	A	1335	TRP	CE2-CZ2	-7.42	1.27	1.39
2	B	415	TYR	CE2-CZ	-7.38	1.28	1.38
5	K	428	TRP	CB-CG	-7.31	1.37	1.50
26	E	151	G	C1'-N9	-6.91	1.37	1.46
27	F	175	G	C1'-N9	-6.89	1.37	1.46
4	G	146	TYR	CE1-CZ	-6.75	1.29	1.38
26	E	142	G	C1'-N9	-6.75	1.37	1.46
1	A	856	TRP	CB-CG	-6.67	1.38	1.50
1	A	1335	TRP	CE3-CZ3	-6.46	1.27	1.38
1	A	1081	TYR	CE1-CZ	-6.35	1.30	1.38
1	A	1992	TYR	CE2-CZ	-6.32	1.30	1.38
4	G	146	TYR	CG-CD2	-6.10	1.31	1.39
26	E	155	A	C1'-N9	-6.08	1.38	1.46
1	A	1562	PHE	CB-CG	-6.06	1.41	1.51
1	A	1161	TYR	CB-CG	-5.89	1.42	1.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1383	PHE	CB-CG	-5.85	1.41	1.51
1	A	1012	TRP	CG-CD2	-5.79	1.33	1.43
2	B	415	TYR	CG-CD1	-5.71	1.31	1.39
26	E	17	A	O3'-P	-5.67	1.54	1.61
1	A	1542	TYR	CG-CD1	-5.61	1.31	1.39
1	A	1610	TRP	CD2-CE3	-5.56	1.32	1.40
4	G	774	TRP	CB-CG	-5.54	1.40	1.50
27	F	76	U	C1'-N1	5.45	1.56	1.48
1	A	1609	TRP	CB-CG	-5.42	1.40	1.50
1	A	708	TRP	CB-CG	-5.42	1.40	1.50
3	I	375	TYR	CG-CD1	-5.38	1.32	1.39
1	A	1116	TYR	CB-CG	-5.33	1.43	1.51
1	A	711	TRP	CB-CG	-5.32	1.40	1.50
8	H	958	PRO	N-CD	5.22	1.55	1.47
8	H	445	PRO	N-CD	5.15	1.55	1.47
1	A	1610	TRP	CG-CD2	-5.12	1.34	1.43
1	A	1117	TYR	CB-CG	-5.07	1.44	1.51
1	A	1542	TYR	CE1-CZ	-5.04	1.31	1.38
1	A	169	PRO	N-CD	5.04	1.54	1.47
1	A	1527	TRP	CE3-CZ3	-5.03	1.29	1.38
1	A	285	PRO	N-CD	5.01	1.54	1.47

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	E	1	A	C2-N3-C4	20.61	120.90	110.60
4	G	853	GLY	N-CA-C	12.86	145.25	113.10
26	E	1	A	N3-C4-C5	-11.57	118.70	126.80
8	H	951	ILE	C-N-CD	-10.75	96.95	120.60
1	A	1616	ARG	NE-CZ-NH1	10.12	125.36	120.30
26	E	1	A	N1-C2-N3	-9.87	124.37	129.30
26	E	1	A	N3-C4-N9	9.78	135.23	127.40
1	A	854	ARG	NE-CZ-NH2	-9.76	115.42	120.30
1	A	1268	ARG	NE-CZ-NH2	-9.14	115.73	120.30
25	D	61	C	O5'-P-OP2	-8.48	98.06	105.70
26	E	1	A	N9-C1'-C2'	-8.26	102.92	112.00
1	A	1616	ARG	NE-CZ-NH2	-8.16	116.22	120.30
4	G	852	LEU	N-CA-C	8.11	132.89	111.00
26	E	1	A	C4-C5-N7	-8.03	106.69	110.70
3	I	393	PHE	CB-CG-CD2	-7.84	115.31	120.80
26	E	50	G	O5'-P-OP2	7.67	119.91	110.70
3	I	393	PHE	CB-CG-CD1	7.51	126.06	120.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
26	E	1	A	C8-N9-C4	7.45	108.78	105.80
4	G	493	PRO	N-CA-CB	7.43	112.22	103.30
26	E	1	A	C5-N7-C8	7.38	107.59	103.90
1	A	1818	ARG	NE-CZ-NH2	-7.35	116.63	120.30
5	K	142	LEU	N-CA-C	7.25	130.59	111.00
1	A	1344	THR	CA-CB-CG2	-7.24	102.27	112.40
1	A	1095	MET	CG-SD-CE	-7.08	88.88	100.20
1	A	1263	CYS	CA-CB-SG	-7.00	101.40	114.00
3	I	304	ARG	NE-CZ-NH2	-6.98	116.81	120.30
4	G	396	PRO	N-CA-CB	6.84	111.51	103.30
4	G	399	PRO	N-CA-CB	6.77	111.42	103.30
7	M	79	VAL	CB-CA-C	-6.68	98.70	111.40
4	G	558	PRO	N-CA-CB	6.67	111.31	103.30
3	I	367	ARG	NE-CZ-NH1	-6.67	116.97	120.30
4	G	510	PRO	N-CA-CB	6.64	111.27	103.30
26	E	1	A	P-O3'-C3'	-6.63	111.74	119.70
5	K	222	PRO	N-CA-CB	6.58	111.20	103.30
1	A	668	ARG	NE-CZ-NH1	6.55	123.57	120.30
3	I	48	PRO	N-CA-CB	6.52	111.12	103.30
4	G	417	PRO	N-CA-CB	6.47	111.07	103.30
4	G	455	PRO	N-CA-CB	6.44	111.03	103.30
3	I	43	PRO	N-CA-CB	6.42	111.00	103.30
4	G	414	PRO	N-CA-CB	6.41	110.99	103.30
5	K	220	PRO	N-CA-CB	6.39	110.97	103.30
4	G	366	PRO	N-CA-CB	6.30	110.86	103.30
3	I	75	PRO	N-CA-CB	6.24	110.78	103.30
27	F	83	C	C4'-C3'-O3'	6.19	125.39	113.00
1	A	962	ARG	NE-CZ-NH1	-6.19	117.21	120.30
26	E	42	C	O5'-P-OP1	-6.15	100.16	105.70
1	A	1605	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	A	953	ARG	NE-CZ-NH2	-6.10	117.25	120.30
26	E	1	A	C6-C5-N7	6.00	136.50	132.30
8	H	464	PRO	N-CA-CB	5.95	110.44	103.30
3	I	390	ARG	NE-CZ-NH2	-5.94	117.33	120.30
3	I	401	LEU	CB-CG-CD1	-5.93	100.91	111.00
1	A	394	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	A	893	ARG	NE-CZ-NH2	-5.89	117.35	120.30
26	E	1	A	N7-C8-N9	-5.86	110.87	113.80
1	A	284	ARG	C-N-CD	5.80	140.57	128.40
8	H	370	TYR	C-N-CD	5.79	140.55	128.40
1	A	1823	LEU	CB-CG-CD1	-5.79	101.17	111.00
1	A	1335	TRP	CD1-NE1-CE2	-5.74	103.83	109.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	H	129	ILE	C-N-CD	5.74	140.45	128.40
1	A	168	LEU	C-N-CD	5.72	140.41	128.40
8	H	444	GLN	C-N-CD	5.68	140.34	128.40
8	H	957	ALA	C-N-CD	5.60	140.16	128.40
1	A	1089	VAL	N-CA-C	-5.58	95.92	111.00
4	G	152	LEU	CB-CG-CD1	-5.55	101.56	111.00
25	D	80	U	C5-C6-N1	-5.50	119.95	122.70
3	I	280	ARG	NE-CZ-NH2	-5.50	117.55	120.30
8	H	607	LEU	CB-CG-CD1	-5.49	101.67	111.00
1	A	1163	ARG	NE-CZ-NH2	-5.48	117.56	120.30
4	G	335	PRO	N-CA-CB	5.46	109.86	103.30
1	A	157	ASP	N-CA-C	5.46	125.73	111.00
26	E	1	A	O3'-P-O5'	5.40	114.25	104.00
3	I	429	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	1107	LEU	CB-CG-CD1	-5.26	102.06	111.00
1	A	1068	ARG	NE-CZ-NH2	-5.23	117.69	120.30
26	E	1	A	C3'-C2'-C1'	5.18	105.65	101.50
3	I	120	TYR	CB-CG-CD2	-5.17	117.90	121.00
26	E	50	G	O5'-P-OP1	-5.11	101.10	105.70
26	E	42	C	O5'-P-OP2	5.10	116.82	110.70
3	I	173	LEU	CB-CG-CD1	-5.09	102.35	111.00
25	D	80	U	N1-C2-N3	5.08	117.95	114.90
7	M	9	PHE	C-N-CD	-5.07	109.44	120.60
8	H	884	ARG	CG-CD-NE	-5.07	101.15	111.80
4	G	723	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	A	1739	ARG	NE-CZ-NH2	-5.04	117.78	120.30

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	1867	GLU	Peptide
1	A	694	ASN	Peptide
2	B	208	GLN	Peptide
2	B	316	GLN	Peptide
4	G	12	PRO	Peptide
4	G	123	PRO	Peptide
4	G	733	ASN	Mainchain,Peptide
4	G	767	PHE	Mainchain,Peptide
4	G	802	GLN	Peptide
8	H	160	ARG	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
8	H	171	GLY	Peptide
3	I	410	LEU	Peptide
5	K	282	GLU	Peptide
7	M	59	GLU	Mainchain,Peptide
7	M	9	PHE	Mainchain,Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	16889	0	16134	1106	0
2	B	3378	0	3342	372	0
3	I	3171	0	3140	274	0
4	G	4927	0	4006	390	0
5	K	2328	0	2314	156	0
6	L	1146	0	1133	126	0
7	M	950	0	1004	27	0
8	H	6732	0	6904	868	0
9	N	6744	0	1759	27	0
10	J	316	0	86	0	0
10	R	316	0	86	2	0
11	O	292	0	78	0	0
11	S	292	0	78	0	0
12	P	308	0	78	0	0
12	T	308	0	78	0	0
13	Q	356	0	88	0	0
13	U	360	0	89	0	0
14	V	288	0	74	0	0
14	Y	288	0	74	0	0
15	W	280	0	77	1	0
15	Z	280	0	77	1	0
16	X	280	0	79	0	0
16	a	284	0	82	0	0
17	b	260	0	72	0	0
18	c	368	0	99	0	0
19	d	308	0	80	0	0
20	e	296	0	83	0	0
21	f	308	0	85	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	g	264	0	76	0	0
23	h	308	0	85	0	0
24	C	429	0	214	48	0
25	D	945	0	478	73	0
26	E	1806	0	907	49	0
27	F	2385	0	1209	210	0
28	H	32	0	12	10	0
29	E	31	0	20	6	0
All	All	58253	0	44280	3557	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 35.

All (3557) 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)
8:H:856:ILE:HA	8:H:944:VAL:CG1	1.17	1.58
4:G:672:LEU:HD21	4:G:704:LEU:CD2	1.29	1.58
8:H:168:VAL:HG13	8:H:173:LYS:CD	1.09	1.56
8:H:364:PHE:CB	8:H:369:LYS:HG3	1.34	1.54
4:G:672:LEU:CD2	4:G:704:LEU:CD2	1.82	1.52
4:G:274:SER:HB3	4:G:277:ILE:CD1	1.38	1.52
4:G:274:SER:CB	4:G:277:ILE:HD11	1.30	1.50
8:H:168:VAL:CG1	8:H:173:LYS:HD3	1.39	1.50
8:H:500:ARG:CD	8:H:534:THR:HG21	1.40	1.49
8:H:364:PHE:HB2	8:H:369:LYS:CG	1.42	1.49
9:N:807:GLY:CA	9:N:1093:ALA:H	1.28	1.46
8:H:500:ARG:NE	8:H:534:THR:HG21	1.31	1.41
8:H:364:PHE:HD2	8:H:369:LYS:CD	1.33	1.41
6:L:105:PHE:CB	6:L:141:ARG:HG2	1.52	1.38
9:N:807:GLY:HA2	9:N:1093:ALA:N	1.10	1.38
1:A:781:THR:CA	1:A:784:GLN:OE1	1.71	1.37
8:H:488:ILE:CG2	8:H:558:LYS:HA	1.54	1.37
8:H:856:ILE:CA	8:H:944:VAL:CG1	2.00	1.36
8:H:855:PRO:C	8:H:944:VAL:HG11	1.43	1.36
1:A:289:ASP:OD2	1:A:292:LYS:N	1.59	1.36
2:B:389:ILE:CD1	2:B:427:TRP:HB3	1.54	1.35
8:H:168:VAL:CG1	8:H:173:LYS:CD	1.97	1.35
8:H:458:ILE:CG2	8:H:459:PRO:HD2	1.56	1.35
4:G:846:PHE:CE1	4:G:859:LEU:HD21	1.62	1.35
1:A:285:PRO:HD2	1:A:298:TYR:OH	1.27	1.34

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:268:CYS:SG	4:G:278:TRP:CH2	2.21	1.34
1:A:162:LEU:HD21	1:A:730:ILE:CG2	0.88	1.33
8:H:500:ARG:CD	8:H:534:THR:CG2	2.07	1.33
8:H:855:PRO:O	8:H:944:VAL:CG1	1.75	1.33
8:H:856:ILE:CA	8:H:944:VAL:HG11	1.56	1.33
3:I:197:ILE:O	3:I:201:ASN:ND2	1.61	1.32
4:G:672:LEU:CD2	4:G:704:LEU:HD21	1.50	1.32
4:G:630:SER:CB	4:G:670:PHE:CZ	2.11	1.32
1:A:162:LEU:CD2	1:A:730:ILE:HG21	0.85	1.32
9:N:807:GLY:CA	9:N:1093:ALA:N	1.86	1.31
8:H:856:ILE:N	8:H:944:VAL:HG11	1.45	1.30
8:H:810:GLU:OE2	8:H:974:LYS:HG3	1.13	1.28
4:G:863:PHE:CZ	4:G:892:LEU:HD21	1.67	1.28
27:F:73:U:C2'	27:F:74:U:H5'	1.64	1.27
1:A:289:ASP:O	1:A:293:VAL:HG12	1.29	1.27
8:H:486:VAL:CG1	8:H:564:ILE:HD11	1.65	1.27
6:L:105:PHE:CZ	6:L:137:TYR:CE2	2.23	1.26
1:A:611:LYS:CE	24:C:4:G:OP1	1.85	1.25
9:N:807:GLY:CA	9:N:1093:ALA:CA	2.14	1.25
25:D:48:C:O3'	25:D:49:A:C8	1.89	1.24
1:A:165:LEU:HD12	1:A:578:MET:SD	1.78	1.24
1:A:195:THR:HG23	1:A:556:TYR:O	1.34	1.24
8:H:364:PHE:CD2	8:H:369:LYS:HD2	1.73	1.24
8:H:500:ARG:HD3	8:H:534:THR:CG2	1.66	1.23
9:N:807:GLY:HA2	9:N:1093:ALA:CA	1.67	1.23
5:K:350:PRO:HA	5:K:353:ARG:CG	1.68	1.22
8:H:364:PHE:CD2	8:H:369:LYS:CD	2.22	1.22
3:I:226:ALA:HA	3:I:317:ASP:OD2	1.31	1.22
8:H:330:TYR:HE1	8:H:430:ARG:NH2	1.36	1.22
24:C:8:U:C6	25:D:51:A:N6	2.05	1.22
6:L:105:PHE:CE1	6:L:137:TYR:CE2	2.28	1.21
8:H:889:TYR:CD1	8:H:890:LYS:HG2	1.77	1.20
5:K:354:PHE:HE1	5:K:358:MET:CE	1.52	1.20
4:G:630:SER:CB	4:G:670:PHE:CE2	2.24	1.20
4:G:672:LEU:CD2	4:G:704:LEU:HD23	1.48	1.20
4:G:846:PHE:HE1	4:G:859:LEU:CD2	1.55	1.20
6:L:105:PHE:CZ	6:L:137:TYR:CD2	2.29	1.20
8:H:454:ALA:O	8:H:457:SER:O	1.55	1.20
25:D:48:C:H3'	25:D:49:A:N7	1.57	1.19
3:I:123:ARG:HD3	3:I:189:LEU:CD1	1.70	1.19
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD12	1.78	1.19

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1748:ILE:HG22	1:A:1752:VAL:HG22	1.21	1.19
4:G:655:PHE:CB	4:G:674:LEU:HD21	1.71	1.19
8:H:116:THR:HG23	8:H:158:HIS:CD2	1.78	1.18
25:D:48:C:C3'	25:D:49:A:C8	2.25	1.18
8:H:492:LEU:HD21	8:H:557:HIS:ND1	1.57	1.18
27:F:75:A:C8	27:F:77:A:H5'	1.78	1.18
1:A:286:LEU:HD21	1:A:292:LYS:HB2	1.25	1.17
8:H:510:ARG:HB2	8:H:591:PHE:CE2	1.78	1.17
2:B:389:ILE:HD11	2:B:427:TRP:CB	1.73	1.17
1:A:1755:LYS:O	1:A:1759:TYR:HD2	1.22	1.17
5:K:350:PRO:HA	5:K:353:ARG:HG2	1.20	1.16
1:A:1035:LEU:HD12	1:A:1038:ILE:HG21	1.17	1.16
8:H:354:TYR:CB	8:H:359:PHE:HB3	1.76	1.16
8:H:855:PRO:O	8:H:944:VAL:CG2	1.94	1.15
8:H:163:ASP:OD2	8:H:548:ARG:NH1	1.79	1.15
2:B:316:GLN:HB2	2:B:357:TRP:CD2	1.81	1.15
1:A:468:LEU:HD13	1:A:469:ILE:HD13	1.21	1.15
8:H:117:ARG:HD2	8:H:157:SER:O	1.42	1.15
1:A:162:LEU:HD21	1:A:730:ILE:HG22	1.22	1.15
1:A:1880:PHE:CE2	1:A:1889:LEU:HD21	1.81	1.15
8:H:501:ILE:CD1	8:H:567:ILE:CG2	2.24	1.15
24:C:-3:A:H8	24:C:-2:A:C6	1.65	1.14
6:L:105:PHE:CE1	6:L:137:TYR:CD2	2.35	1.14
1:A:252:GLU:O	1:A:256:GLU:HG2	1.48	1.14
1:A:779:ALA:HA	1:A:782:ILE:HD12	1.30	1.14
1:A:781:THR:HA	1:A:784:GLN:OE1	0.97	1.14
8:H:364:PHE:HD2	8:H:369:LYS:HD2	1.01	1.13
8:H:488:ILE:CD1	8:H:560:GLN:HG2	1.78	1.13
1:A:1490:ARG:NH1	1:A:1536:LEU:HA	1.62	1.13
1:A:1654:TRP:CZ3	1:A:1779:LEU:CD1	2.30	1.13
27:F:44:A:H2'	27:F:45:A:C8	1.83	1.13
8:H:501:ILE:HD11	8:H:567:ILE:CG2	1.78	1.12
8:H:330:TYR:CE1	8:H:430:ARG:NH2	2.17	1.12
8:H:810:GLU:OE2	8:H:974:LYS:CG	1.97	1.12
6:L:105:PHE:HB3	6:L:141:ARG:CG	1.79	1.11
27:F:44:A:H2'	27:F:45:A:H8	0.96	1.11
4:G:272:PRO:HB3	4:G:302:PHE:CD1	1.85	1.11
8:H:330:TYR:HE1	8:H:430:ARG:CZ	1.63	1.11
8:H:332:TYR:OH	8:H:376:PHE:HB3	1.50	1.11
8:H:488:ILE:HD12	8:H:560:GLN:HG2	1.29	1.11
25:D:48:C:O3'	25:D:49:A:H8	1.22	1.11

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:LYS:HA	1:A:144:ASN:ND2	1.64	1.11
1:A:362:GLU:HB3	1:A:1209:LYS:CE	1.81	1.11
2:B:329:SER:HB3	2:B:348:HIS:O	1.47	1.11
8:H:470:ALA:HB1	8:H:486:VAL:HG21	1.26	1.11
4:G:691:TYR:HB3	4:G:708:LEU:HD12	1.15	1.10
1:A:297:SER:HB3	27:F:32:G:OP1	1.48	1.10
8:H:486:VAL:HG12	8:H:564:ILE:HD11	1.13	1.10
1:A:162:LEU:HD23	1:A:730:ILE:HG21	1.20	1.10
8:H:168:VAL:HG13	8:H:173:LYS:HD2	1.18	1.10
8:H:677:PHE:CE1	8:H:966:PHE:CD2	2.39	1.10
1:A:2077:THR:O	1:A:2080:LYS:HG2	1.52	1.09
4:G:286:GLU:HB2	4:G:292:CYS:SG	1.90	1.09
8:H:364:PHE:HD2	8:H:369:LYS:HD3	1.17	1.08
1:A:141:LYS:HA	1:A:144:ASN:HD21	0.95	1.08
24:C:-3:A:H8	24:C:-2:A:C5	1.70	1.08
3:I:184:LYS:HD2	3:I:186:LYS:H	1.14	1.08
8:H:582:SER:CB	8:H:585:ASP:OD2	2.01	1.07
1:A:290:SER:OG	1:A:291:LYS:NZ	1.88	1.07
8:H:468:LEU:HD21	8:H:577:LEU:HD21	1.33	1.07
8:H:468:LEU:HD11	8:H:493:LEU:HD21	1.31	1.07
27:F:75:A:C8	27:F:77:A:C5'	2.37	1.07
2:B:323:CYS:SG	2:B:355:VAL:HG11	1.95	1.06
8:H:488:ILE:HD12	8:H:560:GLN:CG	1.82	1.06
4:G:252:GLU:HG2	4:G:256:LYS:HG3	1.37	1.06
8:H:598:ILE:HG22	8:H:933:TRP:CZ3	1.91	1.06
1:A:503:LYS:HA	1:A:506:PHE:CZ	1.89	1.06
8:H:197:THR:CG2	8:H:545:LEU:CD1	2.32	1.06
3:I:123:ARG:CD	3:I:189:LEU:HD13	1.84	1.06
4:G:668:HIS:HB3	4:G:698:VAL:HG11	1.32	1.06
4:G:672:LEU:HD23	4:G:704:LEU:CD2	1.68	1.06
8:H:458:ILE:HG23	8:H:459:PRO:HD2	1.08	1.06
3:I:135:LEU:HD23	3:I:136:GLN:N	1.70	1.06
5:K:354:PHE:HE1	5:K:358:MET:HE3	1.17	1.06
5:K:428:TRP:HZ2	5:K:463:PHE:CE2	1.74	1.06
8:H:168:VAL:HG13	8:H:173:LYS:CG	1.85	1.06
1:A:218:SER:N	1:A:318:LEU:HD21	1.71	1.05
4:G:274:SER:HB2	4:G:277:ILE:HD11	1.34	1.05
8:H:365:GLU:OE2	8:H:366:ASN:N	1.88	1.05
8:H:501:ILE:HD11	8:H:567:ILE:HG23	1.09	1.05
1:A:1755:LYS:O	1:A:1759:TYR:CD2	2.09	1.05
8:H:133:ILE:O	8:H:134:ILE:HG23	1.55	1.05

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1751:TYR:CE1	1:A:1755:LYS:HD3	1.92	1.05
1:A:1755:LYS:HG3	1:A:1759:TYR:HE2	1.19	1.05
6:L:116:ILE:HD11	6:L:137:TYR:OH	1.57	1.05
5:K:354:PHE:CE1	5:K:358:MET:CE	2.40	1.04
6:L:140:LYS:HG2	6:L:141:ARG:NH1	1.72	1.04
25:D:83:A:H1'	25:D:84:C:C5	1.93	1.04
24:C:-3:A:C8	24:C:-2:A:C6	2.45	1.04
8:H:501:ILE:CD1	8:H:567:ILE:HG23	1.87	1.04
4:G:846:PHE:CE1	4:G:859:LEU:CD2	2.35	1.04
1:A:611:LYS:HE2	24:C:4:G:OP1	1.55	1.03
1:A:1998:ARG:O	1:A:1999:ILE:HG13	1.58	1.03
1:A:1058:ALA:HB2	1:A:1114:PHE:HE1	1.23	1.03
8:H:500:ARG:NE	8:H:534:THR:CG2	2.15	1.03
2:B:389:ILE:HD11	2:B:427:TRP:HB3	1.04	1.03
8:H:510:ARG:HB2	8:H:591:PHE:HE2	0.86	1.03
1:A:611:LYS:HE3	24:C:4:G:OP1	1.54	1.02
8:H:488:ILE:HG22	8:H:558:LYS:CA	1.88	1.02
8:H:504:THR:HA	8:H:507:SER:OG	1.59	1.02
1:A:1748:ILE:O	1:A:1752:VAL:HG23	1.58	1.02
3:I:112:MET:HB3	3:I:204:LEU:HD21	1.38	1.02
4:G:695:THR:HB	4:G:705:TRP:NE1	1.73	1.02
8:H:227:VAL:HG11	8:H:474:LYS:HG3	1.37	1.02
1:A:1365:THR:O	1:A:1369:ASN:ND2	1.92	1.02
4:G:695:THR:O	4:G:699:PRO:HG3	1.58	1.02
27:F:78:A:O2'	27:F:79:C:O5'	1.76	1.02
1:A:1035:LEU:HD12	1:A:1038:ILE:CG2	1.90	1.02
3:I:217:TYR:HE1	3:I:221:LYS:NZ	1.58	1.02
8:H:110:LYS:HE2	8:H:552:PRO:HG2	1.42	1.02
1:A:294:ASN:HB2	1:A:299:LYS:O	1.59	1.02
9:N:807:GLY:N	9:N:1093:ALA:CA	2.22	1.02
1:A:470:LEU:O	1:A:473:THR:HG22	1.60	1.01
1:A:837:GLY:CA	1:A:1317:ARG:NH1	2.23	1.01
5:K:350:PRO:O	5:K:353:ARG:HG3	1.60	1.01
8:H:388:ALA:HA	8:H:396:LEU:HD11	1.42	1.01
27:F:95:C:O2'	27:F:96:U:H5'	1.60	1.01
8:H:472:VAL:HG11	8:H:571:TYR:CE2	1.96	1.01
2:B:127:TYR:CE2	2:B:276:SER:HB2	1.96	1.01
4:G:721:ARG:CD	4:G:725:ILE:HD11	1.90	1.01
8:H:354:TYR:HB2	8:H:359:PHE:HB3	1.40	1.01
8:H:504:THR:O	8:H:507:SER:OG	1.79	1.01
8:H:793:GLU:HA	8:H:796:ILE:HG22	1.39	1.01

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:283:ARG:HD2	4:G:284:LEU:HD22	1.43	1.00
8:H:608:GLN:HE22	8:H:641:GLU:HG2	1.25	1.00
1:A:192:LEU:HD11	1:A:557:PHE:HB3	1.42	1.00
2:B:446:SER:OG	2:B:451:PHE:HD2	1.42	1.00
27:F:43:G:H2'	27:F:44:A:C8	1.96	1.00
4:G:691:TYR:O	4:G:695:THR:HG23	1.62	1.00
27:F:39:U:H2'	27:F:40:C:H5'	1.43	1.00
1:A:837:GLY:HA3	1:A:1317:ARG:NH1	1.77	1.00
8:H:488:ILE:CG2	8:H:558:LYS:CA	2.39	1.00
27:F:73:U:H2'	27:F:74:U:C5'	1.90	1.00
1:A:1008:LEU:CD2	1:A:1073:ILE:HD11	1.91	0.99
8:H:488:ILE:HG21	8:H:557:HIS:C	1.81	0.99
8:H:862:TYR:HE1	8:H:908:VAL:HB	1.27	0.99
8:H:500:ARG:HD3	8:H:534:THR:HG23	1.42	0.99
8:H:481:ALA:HB3	8:H:565:LYS:HZ1	1.25	0.99
8:H:187:ARG:NH1	8:H:653:ASP:OD2	1.95	0.99
8:H:582:SER:HB2	8:H:585:ASP:HB2	1.44	0.99
8:H:133:ILE:O	8:H:134:ILE:CG2	2.11	0.99
8:H:304:PHE:HD2	8:H:310:ASN:CB	1.76	0.99
8:H:576:THR:HG22	8:H:592:PHE:HB2	1.40	0.99
8:H:901:GLU:OE2	8:H:903:ARG:NH2	1.95	0.99
1:A:912:LEU:HD11	1:A:951:LEU:HD21	1.42	0.98
4:G:274:SER:CB	4:G:277:ILE:CD1	2.13	0.98
8:H:387:TYR:O	8:H:391:MET:HB2	1.62	0.98
8:H:500:ARG:HE	8:H:534:THR:HG21	1.21	0.98
27:F:73:U:C2'	27:F:74:U:C5'	2.39	0.98
2:B:388:GLN:OE1	2:B:388:GLN:N	1.96	0.98
8:H:572:ILE:HD12	8:H:573:LYS:HG3	1.45	0.98
8:H:863:GLU:HB3	8:H:931:TYR:CE1	1.97	0.98
2:B:398:GLN:OE1	2:B:442:SER:OG	1.80	0.98
8:H:855:PRO:O	8:H:944:VAL:HG11	1.45	0.98
1:A:168:LEU:HB2	1:A:199:ILE:HD12	1.41	0.98
1:A:497:GLN:O	1:A:709:ARG:HD2	1.62	0.98
6:L:96:GLY:O	6:L:138:ASN:HB3	1.63	0.98
8:H:227:VAL:HG11	8:H:474:LYS:CG	1.92	0.98
8:H:677:PHE:HE1	8:H:966:PHE:CE2	1.82	0.98
4:G:230:LEU:HD12	4:G:247:SER:HA	1.40	0.98
8:H:168:VAL:CG1	8:H:173:LYS:CG	2.41	0.97
8:H:889:TYR:CE1	8:H:890:LYS:CG	2.47	0.97
3:I:358:ILE:HG23	3:I:359:PRO:HD2	1.44	0.97
8:H:855:PRO:HG2	8:H:944:VAL:HG21	1.42	0.97

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:465:GLU:OE1	8:H:466:GLY:N	1.97	0.97
1:A:322:VAL:HG21	1:A:327:TYR:CE2	1.99	0.97
2:B:235:ILE:CD1	2:B:280:ILE:HD13	1.95	0.97
3:I:266:LYS:HG3	3:I:267:HIS:H	1.26	0.97
8:H:855:PRO:C	8:H:944:VAL:CG1	2.26	0.97
24:C:-4:A:H1'	24:C:-3:A:OP1	1.64	0.97
8:H:304:PHE:HD2	8:H:310:ASN:HB3	1.25	0.97
27:F:43:G:H2'	27:F:44:A:H8	1.26	0.97
25:D:78:G:N2	26:E:4:C:C2	2.33	0.97
4:G:251:GLU:OE1	4:G:260:ALA:HB2	1.65	0.97
4:G:672:LEU:HD21	4:G:704:LEU:CG	1.93	0.97
3:I:282:GLU:HG2	3:I:286:PHE:CG	2.00	0.96
6:L:116:ILE:CD1	6:L:137:TYR:OH	2.13	0.96
8:H:677:PHE:CE1	8:H:966:PHE:CE2	2.53	0.96
4:G:846:PHE:HE1	4:G:859:LEU:HD21	0.91	0.96
8:H:492:LEU:CD2	8:H:557:HIS:ND1	2.28	0.96
1:A:773:SER:OG	1:A:774:ILE:CD1	2.13	0.96
8:H:576:THR:HG21	8:H:592:PHE:H	1.26	0.96
8:H:863:GLU:HB3	8:H:931:TYR:HE1	1.27	0.96
8:H:481:ALA:HB3	8:H:565:LYS:NZ	1.80	0.96
2:B:197:GLY:HA2	2:B:221:ILE:HG13	1.47	0.96
3:I:123:ARG:CD	3:I:189:LEU:CD1	2.41	0.96
8:H:324:ILE:O	8:H:328:VAL:HG23	1.66	0.96
1:A:1008:LEU:HD22	1:A:1073:ILE:HD11	1.46	0.95
3:I:226:ALA:CA	3:I:317:ASP:OD2	2.13	0.95
6:L:81:THR:HG21	6:L:102:LYS:NZ	1.80	0.95
6:L:105:PHE:CZ	6:L:137:TYR:HE2	1.72	0.95
8:H:458:ILE:CG2	8:H:459:PRO:CD	2.43	0.95
27:F:77:A:H4'	27:F:78:A:H5"	1.49	0.95
8:H:106:PHE:CE2	8:H:554:HIS:CE1	2.55	0.95
27:F:44:A:C2'	27:F:45:A:H8	1.78	0.95
4:G:663:SER:CA	4:G:667:CYS:SG	2.55	0.95
4:G:666:ILE:O	4:G:670:PHE:CD2	2.19	0.95
8:H:364:PHE:CD2	8:H:369:LYS:HD3	1.96	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE3	1.45	0.95
1:A:1654:TRP:HZ3	1:A:1779:LEU:HD12	1.29	0.95
8:H:131:GLU:OE1	8:H:445:PRO:HG3	1.66	0.95
8:H:458:ILE:HG22	8:H:459:PRO:HD2	1.47	0.95
8:H:501:ILE:CD1	8:H:567:ILE:HG22	1.95	0.95
25:D:49:A:H2'	25:D:50:G:H5"	1.46	0.95
8:H:331:TYR:CE1	8:H:404:PHE:HD1	1.84	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:372:THR:HG22	8:H:376:PHE:CD1	2.01	0.95
1:A:362:GLU:HB3	1:A:1209:LYS:HE2	1.47	0.94
27:F:99:U:O2'	27:F:100:A:OP1	1.84	0.94
27:F:175:G:N2	27:F:176:A:H62	1.65	0.94
1:A:1658:HIS:HA	1:A:1661:ILE:HD12	1.49	0.94
8:H:168:VAL:HG11	8:H:173:LYS:HD3	1.46	0.94
4:G:107:LEU:O	4:G:110:SER:OG	1.86	0.94
6:L:105:PHE:CB	6:L:141:ARG:CG	2.42	0.94
1:A:366:GLU:HB2	1:A:372:ARG:NH1	1.81	0.94
1:A:1490:ARG:HH12	1:A:1536:LEU:HA	1.33	0.94
4:G:663:SER:C	4:G:667:CYS:SG	2.45	0.94
8:H:383:LYS:O	8:H:387:TYR:HB2	1.68	0.94
26:E:151:G:N2	26:E:152:A:H62	1.65	0.94
27:F:175:G:N2	27:F:176:A:N6	2.16	0.94
2:B:235:ILE:HD12	2:B:280:ILE:HD13	1.47	0.94
8:H:488:ILE:CD1	8:H:560:GLN:CG	2.42	0.94
8:H:608:GLN:NE2	8:H:641:GLU:HG2	1.82	0.94
27:F:73:U:H2'	27:F:74:U:H5'	0.95	0.94
1:A:162:LEU:HG	1:A:734:PHE:HE2	1.32	0.94
1:A:165:LEU:O	1:A:168:LEU:HB3	1.68	0.94
4:G:692:LEU:CD2	4:G:708:LEU:HD11	1.98	0.94
2:B:290:ARG:NE	2:B:302:LEU:HD13	1.82	0.93
3:I:199:GLU:O	3:I:203:ILE:HG13	1.68	0.93
8:H:332:TYR:HH	8:H:376:PHE:HD2	1.06	0.93
1:A:168:LEU:HA	1:A:199:ILE:HD11	1.48	0.93
1:A:1022:PRO:HD3	1:A:1345:TYR:HE1	1.32	0.93
3:I:123:ARG:HD3	3:I:189:LEU:HD13	0.94	0.93
8:H:197:THR:CG2	8:H:545:LEU:HD13	1.96	0.93
24:C:2:A:H2	27:F:98:U:H3	1.06	0.93
6:L:96:GLY:O	6:L:138:ASN:CB	2.16	0.93
26:E:151:G:N2	26:E:152:A:N6	2.16	0.93
8:H:489:TYR:HD2	8:H:592:PHE:HZ	1.11	0.93
4:G:286:GLU:O	4:G:288:ASP:N	2.02	0.93
8:H:219:VAL:HG21	8:H:931:TYR:HB3	1.51	0.93
8:H:486:VAL:HG12	8:H:564:ILE:CD1	1.99	0.93
25:D:48:C:H3'	25:D:49:A:C8	1.99	0.93
1:A:212:VAL:HG11	1:A:285:PRO:HB3	1.46	0.93
8:H:192:LYS:HA	8:H:224:GLU:OE1	1.67	0.93
8:H:855:PRO:O	8:H:944:VAL:HG21	1.67	0.93
4:G:843:VAL:HG21	4:G:895:LEU:HD13	1.51	0.93
5:K:341:VAL:HG21	5:K:428:TRP:HE1	1.32	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:510:ARG:CB	8:H:591:PHE:HE2	1.80	0.93
27:F:45:A:C2	27:F:46:C:C5	2.56	0.93
8:H:449:PHE:CE1	8:H:453:THR:HG21	2.04	0.92
1:A:1621:VAL:HG12	1:A:1622:GLY:H	1.34	0.92
6:L:105:PHE:HZ	6:L:137:TYR:CE2	1.82	0.92
27:F:98:U:H4'	27:F:99:U:OP1	1.69	0.92
1:A:703:PHE:CE1	1:A:706:PRO:HD3	2.04	0.92
1:A:455:PRO:HB2	1:A:457:ASP:OD1	1.70	0.92
1:A:773:SER:OG	1:A:774:ILE:HD12	1.68	0.92
2:B:358:SER:OG	2:B:401:PHE:CE1	2.20	0.92
3:I:112:MET:CB	3:I:204:LEU:HD21	2.00	0.92
4:G:285:HIS:CE1	4:G:291:TYR:CE2	2.57	0.92
6:L:140:LYS:C	6:L:141:ARG:HD2	1.90	0.92
8:H:468:LEU:HD21	8:H:577:LEU:CD2	1.99	0.92
1:A:781:THR:HA	1:A:784:GLN:CD	1.89	0.92
1:A:1748:ILE:HG22	1:A:1752:VAL:CG2	1.98	0.92
5:K:154:SER:O	5:K:158:ILE:HG23	1.68	0.92
8:H:506:GLN:O	8:H:509:SER:HB2	1.69	0.92
8:H:500:ARG:HE	8:H:534:THR:CG2	1.77	0.92
8:H:856:ILE:HA	8:H:944:VAL:HG12	0.94	0.92
4:G:274:SER:HB3	4:G:277:ILE:HD12	1.50	0.92
8:H:458:ILE:HG23	8:H:459:PRO:CD	1.99	0.92
2:B:115:SER:HA	2:B:118:ILE:CD1	1.99	0.91
8:H:330:TYR:CE1	8:H:430:ARG:CZ	2.52	0.91
8:H:372:THR:CG2	8:H:376:PHE:CE1	2.52	0.91
8:H:889:TYR:CE1	8:H:890:LYS:HG2	2.04	0.91
1:A:1256:PRO:HA	1:A:1274:ARG:HH21	1.31	0.91
4:G:668:HIS:CB	4:G:698:VAL:HG11	2.00	0.91
4:G:663:SER:HA	4:G:667:CYS:SG	2.09	0.91
1:A:1755:LYS:HG3	1:A:1759:TYR:CE2	2.06	0.91
8:H:132:ARG:HG2	8:H:132:ARG:HH11	1.35	0.91
8:H:488:ILE:HG22	8:H:558:LYS:HA	0.93	0.91
8:H:582:SER:HB2	8:H:585:ASP:OD2	1.69	0.91
1:A:286:LEU:CD2	1:A:292:LYS:HB2	2.01	0.91
8:H:489:TYR:CD2	8:H:592:PHE:HZ	1.88	0.91
1:A:288:GLU:OE1	1:A:288:GLU:N	2.04	0.91
4:G:105:ALA:O	4:G:108:LYS:HG3	1.71	0.91
8:H:889:TYR:CD1	8:H:890:LYS:CG	2.53	0.90
7:M:95:ARG:HG2	7:M:95:ARG:HH11	1.34	0.90
8:H:329:SER:HA	8:H:333:ALA:HB2	1.53	0.90
1:A:298:TYR:O	1:A:493:MET:HG3	1.70	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:GLN:OE1	1:A:412:GLN:N	2.05	0.90
2:B:389:ILE:HD13	2:B:427:TRP:HB3	1.53	0.90
4:G:695:THR:HB	4:G:705:TRP:HE1	1.33	0.90
8:H:185:ILE:HD13	27:F:75:A:OP2	1.72	0.90
2:B:173:VAL:HG13	2:B:200:GLN:OE1	1.70	0.90
1:A:317:PRO:HG2	1:A:318:LEU:HD12	1.51	0.90
6:L:81:THR:HG21	6:L:102:LYS:HZ1	1.35	0.90
1:A:322:VAL:HG21	1:A:327:TYR:CD2	2.06	0.90
27:F:75:A:N7	27:F:77:A:C5'	2.35	0.90
2:B:313:LEU:CD1	2:B:322:VAL:HG23	2.02	0.90
4:G:668:HIS:O	4:G:672:LEU:HG	1.72	0.90
27:F:75:A:O2'	27:F:76:U:OP2	1.89	0.90
2:B:316:GLN:HB2	2:B:357:TRP:CE2	2.07	0.90
8:H:481:ALA:CB	8:H:565:LYS:NZ	2.35	0.90
1:A:165:LEU:HD22	1:A:730:ILE:HD11	1.51	0.89
8:H:168:VAL:HG13	8:H:173:LYS:HD3	0.93	0.89
3:I:184:LYS:CE	3:I:186:LYS:HB2	2.03	0.89
4:G:695:THR:O	4:G:699:PRO:CG	2.20	0.89
8:H:355:HIS:O	8:H:356:LYS:CG	2.19	0.89
1:A:218:SER:CA	1:A:318:LEU:HD21	2.02	0.89
4:G:272:PRO:HB3	4:G:302:PHE:HD1	1.35	0.89
6:L:105:PHE:CZ	6:L:137:TYR:HD2	1.84	0.89
8:H:598:ILE:HG22	8:H:933:TRP:HZ3	1.32	0.89
8:H:674:LEU:HD13	8:H:973:ARG:HH12	1.35	0.89
6:L:105:PHE:HB3	6:L:141:ARG:HG2	0.89	0.89
25:D:48:C:H4'	25:D:49:A:OP1	1.73	0.89
8:H:500:ARG:CG	8:H:534:THR:HG21	2.03	0.89
4:G:721:ARG:HD3	4:G:725:ILE:HD11	1.53	0.89
8:H:855:PRO:O	8:H:944:VAL:CB	2.21	0.89
4:G:266:ASN:O	4:G:269:GLN:HG3	1.73	0.88
8:H:889:TYR:CE1	8:H:890:LYS:HG3	2.06	0.88
1:A:294:ASN:CB	1:A:299:LYS:O	2.22	0.88
1:A:923:TYR:CE1	1:A:933:GLU:HG3	2.08	0.88
2:B:274:HIS:HD2	2:B:276:SER:H	1.20	0.88
8:H:855:PRO:O	8:H:944:VAL:HG13	1.72	0.88
25:D:83:A:O2'	25:D:84:C:OP2	1.92	0.88
4:G:277:ILE:HD12	4:G:277:ILE:H	1.36	0.88
5:K:428:TRP:CZ2	5:K:463:PHE:CE2	2.61	0.88
8:H:304:PHE:CD2	8:H:310:ASN:HB3	2.07	0.88
24:C:7:A:O2'	24:C:8:U:O5'	1.92	0.88
25:D:50:G:O2'	25:D:51:A:O5'	1.91	0.88

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:LEU:O	2:B:128:SER:OG	1.90	0.88
3:I:373:ARG:HB3	3:I:373:ARG:HH11	1.38	0.88
8:H:855:PRO:CG	8:H:944:VAL:HG21	2.03	0.88
1:A:466:GLU:N	1:A:466:GLU:OE2	2.06	0.88
1:A:850:GLY:O	1:A:853:THR:HG22	1.73	0.88
2:B:393:ARG:HG2	2:B:393:ARG:HH21	1.37	0.88
3:I:98:PHE:HE2	3:I:217:TYR:CD2	1.91	0.88
8:H:582:SER:HB2	8:H:585:ASP:CB	2.03	0.88
1:A:501:LEU:HD12	1:A:501:LEU:H	1.38	0.88
4:G:702:PRO:HB3	4:G:739:PHE:CZ	2.09	0.88
6:L:101:ASN:O	6:L:102:LYS:HG2	1.73	0.88
6:L:105:PHE:HB2	6:L:141:ARG:HG2	1.56	0.88
8:H:364:PHE:HB3	8:H:369:LYS:HG3	1.53	0.88
8:H:415:TYR:O	8:H:416:ASP:OD1	1.92	0.88
8:H:501:ILE:HD13	8:H:567:ILE:HG22	1.55	0.88
2:B:124:LEU:HD21	2:B:274:HIS:CE1	2.08	0.88
8:H:189:LEU:HD12	8:H:190:SER:N	1.89	0.88
1:A:297:SER:HB2	27:F:32:G:O5'	1.74	0.87
4:G:891:ILE:O	4:G:894:ARG:N	2.07	0.87
8:H:168:VAL:CG1	8:H:173:LYS:HG3	2.04	0.87
2:B:380:LYS:O	2:B:381:ARG:HG2	1.73	0.87
2:B:395:ILE:HG22	2:B:396:VAL:H	1.38	0.87
1:A:141:LYS:CA	1:A:144:ASN:HD21	1.86	0.87
3:I:282:GLU:CD	3:I:286:PHE:CD2	2.48	0.87
2:B:446:SER:OG	2:B:451:PHE:CD2	2.19	0.87
4:G:212:VAL:H	4:G:215:LEU:HD23	1.39	0.87
4:G:282:ILE:O	4:G:286:GLU:HG2	1.73	0.87
4:G:691:TYR:HB3	4:G:708:LEU:CD1	2.03	0.87
5:K:350:PRO:HA	5:K:353:ARG:CD	2.04	0.87
5:K:141:ASN:OD1	5:K:142:LEU:N	2.07	0.87
1:A:266:LEU:HD23	1:A:267:PRO:HD2	1.55	0.87
1:A:358:ARG:HB3	1:A:358:ARG:HH11	1.37	0.87
4:G:692:LEU:HD23	4:G:708:LEU:HD11	1.55	0.87
24:C:8:U:C5	25:D:51:A:N6	2.34	0.87
8:H:306:PRO:HG2	8:H:349:TRP:CZ3	2.09	0.87
27:F:98:U:O2'	27:F:99:U:O5'	1.92	0.87
1:A:1353:THR:O	1:A:1357:LEU:HD12	1.73	0.87
1:A:1373:LEU:HD13	6:L:139:HIS:HE1	1.36	0.86
3:I:282:GLU:OE2	3:I:286:PHE:CD2	2.27	0.86
8:H:250:GLU:HB3	8:H:298:PHE:CE2	2.09	0.86
1:A:168:LEU:HB2	1:A:199:ILE:CD1	2.03	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:837:GLY:HA3	1:A:1317:ARG:HH12	1.37	0.86
2:B:274:HIS:CD2	2:B:276:SER:HB3	2.10	0.86
1:A:1364:GLU:OE1	1:A:1389:TYR:OH	1.92	0.86
8:H:968:MET:HE2	8:H:968:MET:HA	1.57	0.86
2:B:177:PRO:HB3	2:B:457:TRP:HA	1.56	0.86
3:I:191:ILE:H	3:I:191:ILE:HD12	1.38	0.86
8:H:488:ILE:HD13	8:H:557:HIS:O	1.74	0.86
8:H:489:TYR:CD2	8:H:592:PHE:CZ	2.64	0.86
6:L:140:LYS:HB3	6:L:141:ARG:HD2	1.55	0.86
2:B:313:LEU:HD13	2:B:322:VAL:HG23	1.57	0.86
3:I:282:GLU:CD	3:I:286:PHE:CE2	2.49	0.86
4:G:892:LEU:O	4:G:896:MET:HG2	1.75	0.86
1:A:1373:LEU:CD1	6:L:139:HIS:HE1	1.88	0.86
1:A:149:MET:HB3	1:A:154:TYR:HD2	1.39	0.86
3:I:231:PHE:CD2	3:I:330:ALA:HB1	2.10	0.86
4:G:886:CYS:SG	4:G:888:PRO:HD2	2.16	0.86
8:H:197:THR:HG23	8:H:545:LEU:O	1.76	0.86
8:H:489:TYR:HD2	8:H:592:PHE:CZ	1.93	0.86
1:A:162:LEU:CD2	1:A:730:ILE:CG2	1.74	0.85
1:A:1490:ARG:NH1	1:A:1536:LEU:HD23	1.91	0.85
1:A:1875:ILE:HG22	1:A:1876:ASN:H	1.41	0.85
2:B:159:LEU:HD13	2:B:430:MET:CE	2.05	0.85
4:G:688:ARG:HH12	4:G:721:ARG:HE	1.24	0.85
8:H:481:ALA:CB	8:H:565:LYS:HZ3	1.89	0.85
1:A:286:LEU:HD21	1:A:292:LYS:CB	2.05	0.85
1:A:823:TRP:HZ3	1:A:855:LEU:HD21	1.39	0.85
2:B:197:GLY:HA2	2:B:221:ILE:CG1	2.07	0.85
8:H:197:THR:CG2	8:H:545:LEU:HD12	2.06	0.85
8:H:608:GLN:HE22	8:H:641:GLU:CG	1.89	0.85
1:A:936:GLU:O	1:A:940:ILE:HD12	1.77	0.85
8:H:117:ARG:CD	8:H:157:SER:O	2.23	0.85
8:H:492:LEU:HD21	8:H:557:HIS:HD1	1.34	0.85
4:G:691:TYR:CB	4:G:708:LEU:HD12	2.04	0.85
1:A:1756:PHE:O	1:A:1760:THR:HG23	1.75	0.85
2:B:115:SER:HA	2:B:118:ILE:HD12	1.57	0.85
8:H:120:ARG:HG3	8:H:551:TYR:CE1	2.11	0.85
8:H:235:VAL:HG22	8:H:261:VAL:HG12	1.59	0.85
8:H:586:MET:O	8:H:589:LEU:HD23	1.77	0.85
1:A:224:MET:HG3	1:A:701:CYS:O	1.77	0.85
1:A:928:ARG:HH21	4:G:145:THR:HG21	1.42	0.85
8:H:106:PHE:HE2	8:H:554:HIS:CE1	1.93	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:951:ILE:HB	8:H:952:PRO:HD2	1.58	0.85
1:A:162:LEU:HD21	1:A:730:ILE:CB	2.06	0.85
1:A:166:LYS:O	1:A:169:PRO:HD2	1.76	0.85
1:A:1498:ASP:OD1	1:A:1502:LEU:CD1	2.25	0.85
8:H:247:PHE:HA	8:H:250:GLU:OE1	1.76	0.85
8:H:855:PRO:HG2	8:H:944:VAL:CG2	2.05	0.85
1:A:176:LEU:HD23	1:A:708:TRP:HE1	1.42	0.84
2:B:117:LEU:HD23	2:B:300:LEU:HB3	1.58	0.84
2:B:124:LEU:CD2	2:B:274:HIS:CE1	2.60	0.84
8:H:605:ILE:HG13	8:H:652:MET:SD	2.17	0.84
3:I:158:PHE:HA	3:I:161:LEU:HD12	1.57	0.84
8:H:449:PHE:HE1	8:H:453:THR:HG21	1.40	0.84
8:H:486:VAL:HG11	8:H:564:ILE:HD11	1.57	0.84
8:H:501:ILE:HD13	8:H:567:ILE:CG2	2.05	0.84
8:H:951:ILE:O	8:H:952:PRO:O	1.95	0.84
1:A:251:TYR:HA	1:A:255:ILE:HD12	1.58	0.84
4:G:278:TRP:CZ2	4:G:298:THR:HB	2.12	0.84
6:L:33:ARG:HD3	6:L:65:ASP:CG	1.98	0.84
8:H:793:GLU:HA	8:H:796:ILE:CG2	2.06	0.84
1:A:691:PHE:CZ	1:A:701:CYS:HA	2.13	0.84
1:A:703:PHE:HE1	1:A:706:PRO:HD3	1.40	0.84
8:H:862:TYR:HE1	8:H:908:VAL:CB	1.90	0.84
1:A:175:LEU:HD12	1:A:175:LEU:O	1.76	0.84
1:A:1877:GLY:O	1:A:1894:ILE:N	2.11	0.84
2:B:320:SER:HB2	2:B:337:ARG:NH2	1.92	0.84
2:B:320:SER:HB2	2:B:337:ARG:HH22	1.42	0.84
4:G:888:PRO:O	4:G:892:LEU:HD23	1.77	0.84
8:H:504:THR:CA	8:H:507:SER:OG	2.25	0.84
27:F:39:U:C2'	27:F:40:C:H5'	2.06	0.84
27:F:175:G:H21	27:F:176:A:H62	1.23	0.84
25:D:86:G:H8	25:D:86:G:H5"	1.41	0.84
1:A:1073:ILE:HG23	1:A:1074:VAL:HG23	1.56	0.84
8:H:332:TYR:OH	8:H:376:PHE:CB	2.25	0.84
1:A:195:THR:CG2	1:A:556:TYR:O	2.24	0.84
1:A:1313:ASP:OD1	1:A:1359:ILE:HD13	1.78	0.84
8:H:449:PHE:O	8:H:453:THR:HG23	1.77	0.84
8:H:576:THR:CG2	8:H:592:PHE:HB2	2.07	0.84
1:A:160:ALA:HB1	1:A:194:HIS:CE1	2.12	0.84
1:A:176:LEU:CD2	1:A:708:TRP:HE1	1.90	0.84
1:A:218:SER:N	1:A:318:LEU:CD2	2.41	0.84
1:A:1909:ALA:O	1:A:1913:THR:HG23	1.78	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:98:PHE:CE2	3:I:217:TYR:CD2	2.65	0.84
3:I:401:LEU:HD12	4:G:214:SER:HB3	1.58	0.84
24:C:-3:A:C8	24:C:-2:A:C5	2.61	0.84
27:F:78:A:N1	27:F:81:A:C5	2.46	0.84
4:G:122:ILE:HG13	4:G:123:PRO:HD2	1.57	0.84
5:K:354:PHE:CE1	5:K:358:MET:HE3	2.08	0.84
8:H:542:ILE:O	8:H:553:VAL:HB	1.77	0.84
1:A:170:HIS:ND1	1:A:547:LEU:HD23	1.93	0.83
1:A:286:LEU:CD2	1:A:292:LYS:CB	2.56	0.83
1:A:1459:ALA:O	1:A:1463:THR:HG23	1.78	0.83
6:L:105:PHE:HE1	6:L:137:TYR:CE2	1.92	0.83
8:H:576:THR:HG21	8:H:592:PHE:N	1.92	0.83
4:G:863:PHE:HB3	4:G:889:ARG:HH22	1.41	0.83
5:K:350:PRO:CA	5:K:353:ARG:HG2	2.06	0.83
4:G:863:PHE:CE2	4:G:892:LEU:HD21	2.13	0.83
27:F:75:A:C5	27:F:77:A:H5”	2.13	0.83
1:A:1214:ARG:HB2	1:A:1255:ASN:OD1	1.78	0.83
2:B:335:ASP:OD1	2:B:337:ARG:HD2	1.77	0.83
8:H:576:THR:HB	8:H:592:PHE:HD2	1.41	0.83
27:F:75:A:N7	27:F:77:A:H5’	1.91	0.83
1:A:1453:ASP:O	1:A:1456:ARG:HG2	1.77	0.83
8:H:120:ARG:HG3	8:H:551:TYR:CZ	2.13	0.83
1:A:923:TYR:CE1	1:A:933:GLU:CG	2.62	0.83
2:B:441:ILE:HD11	2:B:457:TRP:HE1	1.42	0.83
3:I:373:ARG:HH11	3:I:373:ARG:CB	1.91	0.83
4:G:268:CYS:SG	4:G:278:TRP:CZ2	2.72	0.83
9:N:807:GLY:N	9:N:1093:ALA:N	2.23	0.83
26:E:151:G:H21	26:E:152:A:H62	1.23	0.83
27:F:33:U:O2’	27:F:34:C:P	2.37	0.83
2:B:47:GLU:O	2:B:51:VAL:HG23	1.78	0.83
2:B:197:GLY:HA2	2:B:221:ILE:CD1	2.08	0.83
4:G:696:ARG:C	4:G:699:PRO:HD3	1.98	0.83
8:H:307:ILE:HD12	8:H:324:ILE:HD11	1.59	0.83
1:A:753:TYR:HE1	6:L:37:ARG:HB3	1.44	0.83
3:I:98:PHE:O	3:I:101:ILE:HG22	1.78	0.83
25:D:62:A:C2	26:E:58:G:C2	2.66	0.83
5:K:341:VAL:HG21	5:K:428:TRP:NE1	1.93	0.82
5:K:146:GLU:HA	5:K:149:PHE:CD2	2.14	0.82
1:A:289:ASP:OD2	1:A:292:LYS:CG	2.27	0.82
5:K:428:TRP:HZ2	5:K:463:PHE:HE2	1.27	0.82
8:H:372:THR:HG23	8:H:376:PHE:CE1	2.12	0.82

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:116:THR:HG23	8:H:158:HIS:HD2	1.37	0.82
27:F:103:A:O2'	27:F:104:G:O5'	1.96	0.82
1:A:795:ALA:HA	1:A:1095:MET:CE	2.09	0.82
2:B:170:SER:O	2:B:171:GLN:HB2	1.79	0.82
2:B:389:ILE:HD11	2:B:427:TRP:CG	2.14	0.82
4:G:251:GLU:OE2	4:G:259:VAL:HB	1.79	0.82
8:H:488:ILE:HG21	8:H:558:LYS:HA	1.59	0.82
8:H:230:ALA:CB	8:H:595:LEU:HD21	2.09	0.82
25:D:62:A:H2'	25:D:63:G:H5'	1.61	0.82
2:B:419:ILE:HD11	2:B:443:LEU:CD1	2.10	0.82
5:K:164:HIS:ND1	5:K:164:HIS:O	2.13	0.82
8:H:674:LEU:CD1	8:H:973:ARG:HH12	1.93	0.82
8:H:797:GLN:HA	8:H:797:GLN:NE2	1.94	0.82
1:A:1350:ILE:HG23	1:A:1356:LEU:CD1	2.09	0.82
2:B:446:SER:OG	2:B:451:PHE:HB2	1.78	0.82
3:I:184:LYS:HD2	3:I:186:LYS:N	1.93	0.82
8:H:113:ILE:HG22	8:H:114:PRO:HD2	1.62	0.82
1:A:218:SER:CA	1:A:318:LEU:CD2	2.55	0.82
2:B:202:LEU:HD23	2:B:207:LEU:CD2	2.09	0.82
4:G:671:PHE:HZ	4:G:693:SER:HG	1.26	0.82
1:A:149:MET:HG2	1:A:154:TYR:CE2	2.15	0.82
1:A:1415:SER:OG	1:A:1746:HIS:NE2	2.12	0.82
1:A:923:TYR:HE1	1:A:933:GLU:HG3	1.44	0.81
1:A:1908:LEU:HD12	1:A:1908:LEU:O	1.80	0.81
2:B:323:CYS:SG	2:B:355:VAL:CG1	2.68	0.81
4:G:283:ARG:HD2	4:G:284:LEU:CD2	2.09	0.81
8:H:194:ASN:OD1	8:H:547:GLY:HA2	1.80	0.81
1:A:404:ASN:OD1	8:H:927:MET:CE	2.28	0.81
1:A:809:LYS:O	1:A:813:GLU:HG2	1.80	0.81
2:B:459:ARG:NH2	4:G:758:LEU:HD22	1.95	0.81
5:K:350:PRO:CA	5:K:353:ARG:CG	2.56	0.81
8:H:373:PHE:CD1	8:H:377:ILE:HD12	2.14	0.81
4:G:104:PHE:O	4:G:107:LEU:N	2.14	0.81
4:G:702:PRO:HB3	4:G:739:PHE:CE1	2.16	0.81
6:L:33:ARG:CD	6:L:65:ASP:CG	2.49	0.81
8:H:230:ALA:HB2	8:H:595:LEU:HD21	1.60	0.81
8:H:492:LEU:CD2	8:H:557:HIS:CG	2.62	0.81
2:B:51:VAL:HG13	2:B:76:LEU:CD1	2.09	0.81
3:I:184:LYS:CD	3:I:186:LYS:HB2	2.10	0.81
8:H:810:GLU:CD	8:H:974:LYS:HG3	2.00	0.81
1:A:289:ASP:O	1:A:293:VAL:CG1	2.24	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1496:GLN:O	1:A:1499:ARG:HG2	1.81	0.81
2:B:195:TRP:O	2:B:219:GLY:O	1.99	0.81
4:G:721:ARG:HD2	4:G:725:ILE:HD11	1.60	0.81
8:H:183:GLN:OE1	8:H:657:TYR:CD2	2.34	0.81
8:H:946:ASP:O	8:H:964:ARG:HG2	1.80	0.81
1:A:176:LEU:HD23	1:A:176:LEU:O	1.79	0.81
8:H:471:HIS:O	8:H:486:VAL:HG23	1.81	0.81
25:D:49:A:H2'	25:D:50:G:C5'	2.11	0.81
27:F:32:G:H5"	27:F:32:G:C8	2.15	0.81
8:H:175:LEU:HD23	8:H:176:ARG:N	1.96	0.81
27:F:95:C:C4'	27:F:96:U:OP1	2.29	0.81
4:G:144:LYS:NZ	26:E:55:U:O5'	2.14	0.80
1:A:149:MET:HG2	1:A:154:TYR:HE2	1.46	0.80
1:A:361:GLU:N	1:A:361:GLU:OE2	2.13	0.80
25:D:48:C:C3'	25:D:49:A:N7	2.34	0.80
6:L:140:LYS:HB3	6:L:141:ARG:CD	2.11	0.80
8:H:568:SER:HA	8:H:571:TYR:HE1	1.45	0.80
8:H:769:TYR:CE1	8:H:799:PHE:HE2	1.99	0.80
8:H:336:ILE:HD11	8:H:341:ILE:HG22	1.61	0.80
8:H:369:LYS:HE2	8:H:369:LYS:O	1.80	0.80
8:H:598:ILE:CG2	8:H:933:TRP:CZ3	2.64	0.80
1:A:301:TRP:CD1	1:A:491:GLY:O	2.34	0.80
3:I:268:LEU:HD12	3:I:271:GLU:CG	2.11	0.80
4:G:295:LEU:O	4:G:298:THR:OG1	1.98	0.80
8:H:468:LEU:CD1	8:H:493:LEU:HD21	2.09	0.80
1:A:289:ASP:OD2	1:A:292:LYS:HG2	1.81	0.80
1:A:703:PHE:HE1	1:A:705:GLN:HB3	1.45	0.80
8:H:296:ASN:HD21	8:H:304:PHE:H	1.26	0.80
8:H:793:GLU:CA	8:H:796:ILE:HG22	2.11	0.80
2:B:446:SER:HB2	2:B:451:PHE:H	1.46	0.80
8:H:470:ALA:HB1	8:H:486:VAL:CG2	2.10	0.80
8:H:769:TYR:CE1	8:H:799:PHE:CE2	2.70	0.80
1:A:162:LEU:CG	1:A:730:ILE:CG2	2.58	0.80
4:G:846:PHE:CD1	4:G:859:LEU:HD21	2.17	0.80
8:H:121:ASP:OD1	8:H:122:TYR:N	2.15	0.80
1:A:781:THR:N	1:A:784:GLN:OE1	2.14	0.80
1:A:912:LEU:CD1	1:A:951:LEU:HD21	2.12	0.80
2:B:441:ILE:HD11	2:B:457:TRP:NE1	1.97	0.80
8:H:168:VAL:HG12	8:H:173:LYS:HG3	1.63	0.80
8:H:470:ALA:HB3	8:H:577:LEU:HB3	1.61	0.80
27:F:78:A:C6	27:F:81:A:N7	2.50	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:LEU:HD11	1:A:476:ALA:HB2	1.63	0.80
1:A:1654:TRP:CH2	1:A:1779:LEU:HD12	2.17	0.80
4:G:688:ARG:HH12	4:G:721:ARG:NE	1.79	0.80
1:A:166:LYS:HD3	1:A:167:TYR:CE1	2.17	0.79
1:A:837:GLY:CA	1:A:1317:ARG:HH11	1.95	0.79
2:B:316:GLN:HG3	2:B:357:TRP:CZ2	2.16	0.79
3:I:46:ILE:O	3:I:97:PHE:CZ	2.35	0.79
4:G:696:ARG:O	4:G:699:PRO:CD	2.30	0.79
4:G:863:PHE:CE2	4:G:892:LEU:HG	2.17	0.79
27:F:32:G:H1	27:F:121:U:H3	1.31	0.79
4:G:251:GLU:OE2	4:G:259:VAL:CG1	2.30	0.79
4:G:695:THR:O	4:G:699:PRO:CD	2.30	0.79
1:A:585:ARG:HD2	1:A:733:GLN:CD	2.03	0.79
4:G:691:TYR:HE2	4:G:711:ILE:HD11	1.47	0.79
8:H:488:ILE:HG21	8:H:558:LYS:CA	2.10	0.79
8:H:488:ILE:HG21	8:H:558:LYS:N	1.97	0.79
1:A:1264:GLY:HA3	1:A:1308:GLU:OE1	1.83	0.79
3:I:123:ARG:NH1	3:I:187:GLU:O	2.14	0.79
8:H:856:ILE:HA	8:H:944:VAL:HG13	1.59	0.79
8:H:856:ILE:CA	8:H:944:VAL:HG12	1.85	0.79
3:I:197:ILE:C	3:I:201:ASN:HD22	1.85	0.79
1:A:456:GLU:OE1	1:A:456:GLU:N	2.14	0.79
2:B:389:ILE:CD1	2:B:427:TRP:CB	2.46	0.79
3:I:217:TYR:HE1	3:I:221:LYS:HZ3	0.81	0.79
4:G:672:LEU:CG	4:G:704:LEU:HD21	2.13	0.79
8:H:189:LEU:HD13	28:H:1500:GTP:O1G	1.82	0.79
2:B:380:LYS:C	2:B:381:ARG:HG2	2.02	0.79
4:G:691:TYR:CE2	4:G:711:ILE:CD1	2.66	0.79
4:G:691:TYR:CE2	4:G:711:ILE:HD11	2.18	0.79
8:H:449:PHE:CE1	8:H:453:THR:CG2	2.65	0.79
4:G:274:SER:HB3	4:G:277:ILE:HD11	0.79	0.79
5:K:159:TYR:O	5:K:163:ASN:ND2	2.16	0.79
25:D:83:A:H1'	25:D:84:C:H5	1.47	0.79
1:A:285:PRO:CD	1:A:298:TYR:OH	2.21	0.78
4:G:98:SER:OG	4:G:99:ASN:ND2	2.16	0.78
6:L:140:LYS:CG	6:L:141:ARG:NH1	2.46	0.78
8:H:197:THR:HG21	8:H:545:LEU:HD12	1.64	0.78
8:H:500:ARG:HE	8:H:534:THR:CB	1.96	0.78
7:M:93:VAL:HG12	7:M:95:ARG:H	1.48	0.78
8:H:167:ASN:ND2	8:H:173:LYS:HG2	1.98	0.78
27:F:77:A:C4'	27:F:78:A:H5"	2.14	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1038:ILE:HD11	1:A:1039:TRP:CD2	2.17	0.78
8:H:468:LEU:HD11	8:H:493:LEU:CD2	2.09	0.78
2:B:51:VAL:HG13	2:B:76:LEU:HD11	1.66	0.78
3:I:138:SER:HA	3:I:141:ILE:HD12	1.64	0.78
8:H:467:THR:O	8:H:490:SER:HB3	1.82	0.78
1:A:923:TYR:HE1	1:A:933:GLU:CG	1.95	0.78
2:B:290:ARG:HE	2:B:302:LEU:HD13	1.45	0.78
8:H:863:GLU:CB	8:H:931:TYR:HE1	1.96	0.78
1:A:1755:LYS:CG	1:A:1759:TYR:HE2	1.96	0.78
3:I:266:LYS:HG3	3:I:267:HIS:N	1.98	0.78
6:L:33:ARG:HD2	6:L:65:ASP:OD2	1.83	0.78
9:N:565:ALA:CA	9:N:837:GLY:HA2	2.13	0.78
3:I:184:LYS:HD2	3:I:186:LYS:HB2	1.63	0.78
1:A:2079:ILE:HA	1:A:2082:ILE:HD12	1.64	0.78
3:I:266:LYS:CG	3:I:267:HIS:H	1.96	0.78
4:G:863:PHE:CE2	4:G:892:LEU:CG	2.67	0.78
1:A:1468:ALA:HB1	1:A:1473:ARG:O	1.83	0.78
5:K:457:GLN:OE1	5:K:457:GLN:N	2.17	0.78
8:H:116:THR:CG2	8:H:158:HIS:CD2	2.65	0.78
8:H:355:HIS:O	8:H:356:LYS:HG3	1.82	0.78
1:A:287:GLU:HB2	1:A:288:GLU:OE1	1.84	0.78
4:G:251:GLU:OE2	4:G:259:VAL:HG12	1.84	0.78
4:G:702:PRO:O	4:G:706:VAL:HG23	1.83	0.78
8:H:472:VAL:CG1	8:H:571:TYR:CE2	2.67	0.78
27:F:78:A:N1	27:F:81:A:C4	2.53	0.77
1:A:1697:SER:OG	1:A:1759:TYR:CD1	2.37	0.77
6:L:25:ARG:HB2	6:L:25:ARG:HH11	1.49	0.77
8:H:769:TYR:CZ	8:H:799:PHE:HE2	2.01	0.77
1:A:511:ASP:HB2	1:A:514:TYR:CE1	2.19	0.77
4:G:282:ILE:HA	4:G:295:LEU:HD12	1.66	0.77
8:H:862:TYR:CE1	8:H:908:VAL:HB	2.18	0.77
1:A:377:VAL:HG13	1:A:378:PRO:HD2	1.67	0.77
1:A:1877:GLY:O	1:A:1894:ILE:HB	1.83	0.77
5:K:428:TRP:CZ2	5:K:463:PHE:HE2	2.01	0.77
27:F:75:A:O2'	27:F:76:U:P	2.41	0.77
1:A:212:VAL:HG11	1:A:285:PRO:CB	2.15	0.77
1:A:823:TRP:CZ3	1:A:855:LEU:HD21	2.19	0.77
1:A:1313:ASP:CG	1:A:1359:ILE:HD13	2.05	0.77
4:G:212:VAL:HG13	4:G:215:LEU:HB3	1.66	0.77
6:L:139:HIS:NE2	27:F:96:U:C5'	2.48	0.77
8:H:195:GLY:HA3	8:H:545:LEU:HD22	1.66	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ASP:HB3	1:A:276:VAL:CG2	2.14	0.77
27:F:31:G:C2	27:F:32:G:H1'	2.19	0.77
1:A:1654:TRP:CZ3	1:A:1779:LEU:HD11	2.17	0.77
4:G:695:THR:CB	4:G:705:TRP:HE1	1.98	0.77
8:H:794:GLN:OE1	8:H:835:LYS:HG3	1.84	0.77
8:H:947:LYS:CD	8:H:947:LYS:H	1.98	0.77
1:A:168:LEU:HA	1:A:199:ILE:CD1	2.14	0.77
5:K:146:GLU:O	5:K:148:LYS:N	2.18	0.77
1:A:1490:ARG:HH11	1:A:1536:LEU:HA	1.47	0.77
2:B:64:VAL:HG12	2:B:65:GLU:H	1.49	0.77
2:B:316:GLN:HG3	2:B:357:TRP:CE2	2.20	0.77
2:B:387:ASN:C	2:B:388:GLN:OE1	2.22	0.77
4:G:252:GLU:HG2	4:G:256:LYS:CG	2.15	0.77
8:H:151:ASP:OD1	8:H:175:LEU:HD22	1.85	0.77
1:A:317:PRO:HG2	1:A:318:LEU:CD1	2.15	0.77
1:A:2064:GLY:O	1:A:2068:ASN:N	2.18	0.77
9:N:1198:ARG:CA	9:N:1227:ILE:H	1.96	0.77
2:B:459:ARG:CZ	4:G:758:LEU:HD22	2.14	0.76
3:I:245:ALA:HB1	3:I:250:GLU:HB3	1.66	0.76
4:G:285:HIS:HE1	4:G:291:TYR:CE2	2.03	0.76
8:H:883:ARG:O	8:H:884:ARG:HB2	1.81	0.76
1:A:912:LEU:HD11	1:A:951:LEU:CD2	2.16	0.76
2:B:286:ASP:C	2:B:287:MET:HG2	2.05	0.76
8:H:189:LEU:HD21	8:H:218:HIS:HB2	1.67	0.76
8:H:265:PHE:CE2	8:H:295:ILE:HD12	2.20	0.76
8:H:492:LEU:HD23	8:H:557:HIS:HA	1.66	0.76
9:N:807:GLY:H	9:N:1093:ALA:CA	1.97	0.76
5:K:350:PRO:HB3	25:D:84:C:C5	2.21	0.76
8:H:492:LEU:HD21	8:H:557:HIS:CG	2.20	0.76
3:I:268:LEU:HD12	3:I:271:GLU:HG3	1.66	0.76
8:H:697:ARG:NE	8:H:697:ARG:HA	2.00	0.76
8:H:951:ILE:O	8:H:951:ILE:HD12	1.85	0.76
8:H:242:VAL:HG21	8:H:272:ARG:HD3	1.67	0.76
8:H:355:HIS:O	8:H:356:LYS:HG2	1.86	0.76
8:H:545:LEU:HD12	8:H:545:LEU:H	1.51	0.76
8:H:942:GLY:HA3	8:H:961:SER:HA	1.67	0.76
27:F:75:A:N7	27:F:77:A:H5"	2.00	0.76
27:F:106:A:C2'	27:F:107:C:H5'	2.16	0.76
1:A:162:LEU:HG	1:A:734:PHE:CE2	2.17	0.76
1:A:1073:ILE:HD12	1:A:1116:TYR:CE1	2.19	0.76
1:A:1902:GLN:O	1:A:1905:LEU:HD21	1.85	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2079:ILE:HG22	1:A:2083:ILE:HD11	1.65	0.76
1:A:1313:ASP:OD1	1:A:1359:ILE:HG21	1.85	0.76
4:G:251:GLU:OE2	4:G:259:VAL:CB	2.34	0.76
1:A:165:LEU:HD12	1:A:578:MET:CG	2.15	0.76
2:B:454:SER:HG	2:B:464:TRP:HE1	1.33	0.76
3:I:265:ASN:OD1	3:I:266:LYS:N	2.17	0.76
4:G:257:PHE:CG	4:G:258:SER:N	2.52	0.76
8:H:338:SER:HA	8:H:341:ILE:HD13	1.66	0.76
8:H:372:THR:HG22	8:H:376:PHE:CE1	2.16	0.76
1:A:218:SER:HA	1:A:318:LEU:HD21	1.66	0.76
1:A:217:TRP:C	1:A:318:LEU:HD21	2.05	0.75
8:H:197:THR:HG23	8:H:545:LEU:HD13	1.68	0.75
8:H:576:THR:HB	8:H:592:PHE:CD2	2.21	0.75
1:A:258:ILE:O	1:A:259:GLU:HB2	1.86	0.75
1:A:928:ARG:NH2	4:G:145:THR:HG21	2.00	0.75
1:A:1035:LEU:CD1	1:A:1038:ILE:HG21	2.09	0.75
1:A:1863:HIS:HB2	1:A:1871:ALA:HB3	1.67	0.75
2:B:154:SER:OG	2:B:155:ARG:HD3	1.85	0.75
1:A:253:GLN:O	1:A:257:ASN:ND2	2.19	0.75
8:H:118:TYR:HD1	8:H:119:ASN:O	1.69	0.75
8:H:468:LEU:CD1	8:H:493:LEU:CD2	2.63	0.75
1:A:296:THR:CG2	27:F:33:U:OP2	2.34	0.75
1:A:543:ASN:HD22	1:A:544:LYS:N	1.83	0.75
8:H:133:ILE:C	8:H:134:ILE:HG23	2.07	0.75
8:H:233:ASP:OD1	8:H:487:ARG:NH2	2.17	0.75
8:H:504:THR:C	8:H:507:SER:HG	1.89	0.75
2:B:345:LEU:HD13	2:B:376:TRP:CD2	2.20	0.75
8:H:146:LYS:HE2	28:H:1500:GTP:O3G	1.85	0.75
1:A:219:ALA:O	1:A:266:LEU:CD1	2.35	0.75
1:A:1058:ALA:HB2	1:A:1114:PHE:CE1	2.15	0.75
1:A:1647:GLN:HG2	25:D:52:G:OP2	1.86	0.75
8:H:304:PHE:CD2	8:H:310:ASN:CB	2.66	0.75
8:H:860:PRO:HB3	8:H:937:TRP:CZ3	2.21	0.75
1:A:276:VAL:HG11	1:A:310:ASN:HB3	1.68	0.75
1:A:322:VAL:CG2	1:A:327:TYR:CD2	2.69	0.75
4:G:672:LEU:HD21	4:G:704:LEU:HD23	1.15	0.75
6:L:139:HIS:CD2	27:F:96:U:H5”	2.21	0.75
8:H:331:TYR:CE1	8:H:404:PHE:CD1	2.73	0.75
8:H:456:LEU:N	8:H:456:LEU:HD23	2.02	0.75
1:A:1038:ILE:HD11	1:A:1039:TRP:CE3	2.21	0.75
3:I:151:LYS:O	3:I:152:ASN:HB2	1.85	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:806:ALA:O	1:A:810:LYS:HG2	1.87	0.75
8:H:510:ARG:HD3	8:H:591:PHE:CE2	2.21	0.75
1:A:180:PRO:HA	1:A:187:LYS:CD	2.17	0.74
2:B:121:ARG:O	2:B:125:ILE:HG13	1.86	0.74
2:B:155:ARG:O	2:B:159:LEU:HG	1.85	0.74
3:I:401:LEU:CD1	4:G:214:SER:HA	2.17	0.74
27:F:31:G:H2'	27:F:32:G:O4'	1.85	0.74
1:A:192:LEU:HD12	1:A:558:GLN:O	1.87	0.74
1:A:1035:LEU:HD21	1:A:1160:LEU:HD11	1.69	0.74
1:A:1629:LEU:HD23	1:A:1630:THR:HG23	1.68	0.74
3:I:192:LYS:O	3:I:195:THR:OG1	2.05	0.74
4:G:863:PHE:HB3	4:G:889:ARG:NH2	2.02	0.74
8:H:458:ILE:HG22	8:H:459:PRO:CD	2.14	0.74
1:A:1256:PRO:HA	1:A:1274:ARG:NH2	2.03	0.74
1:A:180:PRO:HA	1:A:187:LYS:HD3	1.67	0.74
1:A:289:ASP:OD2	1:A:292:LYS:CB	2.34	0.74
1:A:1275:MET:HE1	1:A:1299:LYS:HE3	1.69	0.74
4:G:863:PHE:HZ	4:G:892:LEU:HD21	1.47	0.74
5:K:315:ARG:NH1	25:D:72:C:O2	2.18	0.74
8:H:476:VAL:CG1	8:H:478:TYR:HD1	2.01	0.74
8:H:489:TYR:CE2	8:H:592:PHE:CE1	2.76	0.74
24:C:2:A:H2	27:F:98:U:N3	1.84	0.74
1:A:1275:MET:HE1	1:A:1299:LYS:CE	2.18	0.74
8:H:306:PRO:HG2	8:H:349:TRP:CE3	2.22	0.74
1:A:299:LYS:HA	1:A:493:MET:HG2	1.69	0.74
1:A:1922:ARG:HE	1:A:1951:PHE:HZ	1.35	0.74
8:H:504:THR:C	8:H:507:SER:OG	2.26	0.74
2:B:195:TRP:O	2:B:220:LYS:HA	1.86	0.74
26:E:139:A:O2'	26:E:140:G:OP2	2.05	0.74
4:G:281:ASN:ND2	4:G:295:LEU:CD1	2.51	0.74
24:C:-5:A:H4'	24:C:-4:A:OP2	1.88	0.74
1:A:173:LEU:HD11	1:A:712:LEU:HD11	1.68	0.74
1:A:404:ASN:OD1	8:H:927:MET:HE1	1.87	0.74
1:A:773:SER:OG	1:A:774:ILE:HD11	1.87	0.74
1:A:874:ILE:O	1:A:875:THR:OG1	2.06	0.74
2:B:410:LEU:HB2	2:B:422:TYR:HB2	1.68	0.74
3:I:231:PHE:HD2	3:I:330:ALA:HB1	1.50	0.74
3:I:272:LEU:O	3:I:272:LEU:HD13	1.87	0.74
4:G:863:PHE:CZ	4:G:892:LEU:CD2	2.61	0.74
5:K:146:GLU:HA	5:K:149:PHE:CE2	2.21	0.74
1:A:174:LYS:HD2	1:A:202:VAL:O	1.88	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:305:SER:OG	8:H:307:ILE:HG22	1.87	0.73
8:H:545:LEU:HD12	8:H:545:LEU:N	2.03	0.73
8:H:798:GLY:O	8:H:801:TRP:HB3	1.88	0.73
2:B:115:SER:HA	2:B:118:ILE:CG1	2.17	0.73
8:H:372:THR:HG23	8:H:376:PHE:HE1	1.53	0.73
1:A:297:SER:CB	27:F:32:G:OP1	2.33	0.73
1:A:365:ASN:OD1	1:A:366:GLU:N	2.22	0.73
2:B:374:ASN:HB3	2:B:376:TRP:HE1	1.53	0.73
8:H:354:TYR:CA	8:H:359:PHE:HB3	2.17	0.73
8:H:132:ARG:HG2	8:H:132:ARG:NH1	2.01	0.73
8:H:326:GLU:HG3	8:H:434:GLY:HA3	1.71	0.73
26:E:2:U:C5	26:E:3:C:C5	2.76	0.73
1:A:930:ASN:HB3	1:A:933:GLU:OE1	1.89	0.73
2:B:232:ASN:HB3	2:B:247:GLN:HE22	1.51	0.73
1:A:1498:ASP:OD1	1:A:1502:LEU:HD11	1.87	0.73
8:H:274:ILE:HG21	8:H:385:PHE:CE2	2.23	0.73
8:H:500:ARG:CG	8:H:534:THR:CG2	2.62	0.73
27:F:33:U:O2'	27:F:34:C:O5'	2.05	0.73
1:A:1065:LEU:HD23	1:A:1069:LEU:HD13	1.70	0.73
2:B:159:LEU:HD13	2:B:430:MET:HE2	1.71	0.73
4:G:99:ASN:O	4:G:103:GLN:HG3	1.88	0.73
1:A:1857:VAL:O	1:A:1877:GLY:HA3	1.89	0.73
3:I:123:ARG:O	3:I:183:PHE:HB2	1.89	0.73
4:G:655:PHE:CB	4:G:674:LEU:CD2	2.60	0.73
8:H:336:ILE:CD1	8:H:341:ILE:HG22	2.18	0.73
8:H:568:SER:HA	8:H:571:TYR:CE1	2.23	0.73
8:H:863:GLU:CB	8:H:931:TYR:CE1	2.71	0.73
24:C:8:U:H2'	24:C:9:G:H5'	1.68	0.73
1:A:151:SER:OG	1:A:152:LYS:N	2.22	0.73
1:A:289:ASP:OD2	1:A:292:LYS:CA	2.36	0.73
4:G:281:ASN:HD22	4:G:295:LEU:CD1	2.01	0.73
5:K:333:LYS:HE2	5:K:333:LYS:N	2.04	0.73
8:H:489:TYR:HE2	8:H:592:PHE:CE1	2.06	0.73
1:A:1414:TRP:HZ3	1:A:1416:LYS:HB2	1.54	0.72
2:B:127:TYR:CE2	2:B:276:SER:CB	2.71	0.72
9:N:1122:GLY:HA3	9:N:1249:ASP:CA	2.18	0.72
1:A:585:ARG:HD2	1:A:733:GLN:NE2	2.03	0.72
1:A:1195:PHE:HB3	1:A:1217:ARG:NH1	2.04	0.72
1:A:1461:TYR:CE2	1:A:1494:LEU:HD11	2.24	0.72
2:B:385:GLN:OE1	2:B:385:GLN:HA	1.88	0.72
27:F:44:A:C4	27:F:45:A:C8	2.76	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:751:ASP:OD1	1:A:752:ALA:N	2.22	0.72
1:A:842:LYS:O	1:A:842:LYS:HD2	1.89	0.72
1:A:1907:GLN:O	1:A:1910:LYS:HG2	1.89	0.72
8:H:197:THR:HG22	8:H:545:LEU:CD1	2.20	0.72
8:H:581:LYS:HZ2	8:H:581:LYS:HB3	1.52	0.72
8:H:959:ILE:CD1	8:H:960:ASN:H	2.00	0.72
1:A:1373:LEU:HD13	6:L:139:HIS:CE1	2.22	0.72
1:A:1464:LYS:O	1:A:1475:LEU:HD21	1.90	0.72
2:B:230:SER:HB2	2:B:232:ASN:HD22	1.53	0.72
8:H:274:ILE:HD13	8:H:274:ILE:O	1.90	0.72
8:H:336:ILE:CG1	8:H:341:ILE:HG22	2.19	0.72
8:H:476:VAL:HG12	8:H:478:TYR:HD1	1.55	0.72
24:C:2:A:C2	27:F:98:U:N3	2.57	0.72
1:A:286:LEU:HD12	1:A:287:GLU:N	2.05	0.72
2:B:199:LEU:N	2:B:199:LEU:HD23	2.04	0.72
8:H:197:THR:HG22	8:H:545:LEU:HD13	1.71	0.72
8:H:307:ILE:CD1	8:H:324:ILE:HD11	2.18	0.72
27:F:94:C:N4	27:F:96:U:O2'	2.22	0.72
1:A:468:LEU:HD13	1:A:469:ILE:CD1	2.10	0.72
1:A:1846:ASN:HA	1:A:1885:LYS:NZ	2.03	0.72
2:B:197:GLY:CA	2:B:221:ILE:HG13	2.18	0.72
2:B:374:ASN:OD1	2:B:388:GLN:HG3	1.90	0.72
3:I:346:GLU:O	3:I:347:ALA:HB3	1.87	0.72
3:I:427:SER:OG	3:I:428:ARG:N	2.20	0.72
5:K:354:PHE:CE1	5:K:358:MET:HE2	2.24	0.72
8:H:947:LYS:HG2	8:H:948:ASP:OD1	1.90	0.72
27:F:95:C:O4'	27:F:96:U:OP1	2.07	0.72
1:A:778:LYS:HA	1:A:778:LYS:CE	2.20	0.72
1:A:967:VAL:HG23	1:A:1088:VAL:HG11	1.72	0.72
1:A:1008:LEU:HD21	1:A:1073:ILE:HD11	1.70	0.72
1:A:1880:PHE:CE1	1:A:1882:LEU:HD12	2.25	0.72
8:H:967:VAL:HG12	8:H:968:MET:CE	2.20	0.72
2:B:369:GLY:HA2	2:B:395:ILE:HG23	1.72	0.71
1:A:298:TYR:O	1:A:493:MET:CG	2.37	0.71
1:A:1069:LEU:HB3	1:A:1116:TYR:HE2	1.55	0.71
1:A:1751:TYR:CZ	1:A:1755:LYS:HD3	2.25	0.71
8:H:347:ARG:O	8:H:352:VAL:HG11	1.90	0.71
27:F:73:U:O2'	27:F:74:U:C5'	2.39	0.71
1:A:779:ALA:HA	1:A:782:ILE:CD1	2.15	0.71
1:A:1216:ILE:HD12	1:A:1254:ASN:HB3	1.72	0.71
1:A:1629:LEU:HD23	1:A:1630:THR:CG2	2.20	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1653:LEU:HD12	1:A:1653:LEU:O	1.90	0.71
2:B:135:ARG:NH1	2:B:139:GLU:OE2	2.23	0.71
1:A:298:TYR:CE1	1:A:493:MET:HE1	2.26	0.71
1:A:315:SER:C	1:A:317:PRO:HD2	2.11	0.71
2:B:153:LEU:O	2:B:157:THR:HG23	1.90	0.71
3:I:401:LEU:HD11	4:G:214:SER:HA	1.72	0.71
8:H:168:VAL:HG12	8:H:173:LYS:CG	2.18	0.71
2:B:220:LYS:HB3	2:B:239:GLU:HB3	1.71	0.71
2:B:127:TYR:CD2	2:B:276:SER:HB2	2.26	0.71
3:I:135:LEU:CD2	3:I:136:GLN:HG3	2.20	0.71
8:H:944:VAL:HG23	8:H:945:LEU:HG	1.71	0.71
1:A:778:LYS:O	1:A:782:ILE:HG13	1.90	0.71
2:B:443:LEU:O	2:B:443:LEU:HD23	1.90	0.71
5:K:350:PRO:O	5:K:353:ARG:CG	2.37	0.71
8:H:265:PHE:CD2	8:H:295:ILE:HD12	2.25	0.71
1:A:171:ALA:HB2	1:A:201:PHE:CD1	2.25	0.71
2:B:313:LEU:CD1	2:B:322:VAL:CG2	2.68	0.71
2:B:415:TYR:OH	7:M:126:ILE:HA	1.91	0.71
4:G:666:ILE:HG22	4:G:667:CYS:N	2.05	0.71
6:L:139:HIS:NE2	27:F:96:U:H5”	2.06	0.71
27:F:75:A:C8	27:F:77:A:H5”	2.22	0.71
8:H:332:TYR:CZ	8:H:376:PHE:HB3	2.26	0.71
8:H:799:PHE:CE1	8:H:846:CYS:SG	2.84	0.71
27:F:77:A:H1’	27:F:78:A:H5’	1.71	0.71
1:A:410:ILE:HG13	8:H:276:ASP:OD1	1.90	0.71
1:A:1415:SER:OG	1:A:1746:HIS:CD2	2.43	0.71
2:B:446:SER:CB	2:B:451:PHE:HB2	2.20	0.71
8:H:354:TYR:HA	8:H:359:PHE:HA	1.72	0.71
8:H:677:PHE:CE1	8:H:966:PHE:HD2	2.08	0.71
2:B:359:PRO:HD2	2:B:407:GLY:HA3	1.73	0.70
4:G:696:ARG:O	4:G:699:PRO:HD3	1.89	0.70
27:F:94:C:H6	27:F:94:C:C5’	2.04	0.70
1:A:162:LEU:HD23	1:A:730:ILE:HD13	1.71	0.70
1:A:614:ARG:CZ	24:C:3:A:OP1	2.39	0.70
1:A:770:MET:HE3	1:A:778:LYS:HB2	1.72	0.70
8:H:129:ILE:N	8:H:129:ILE:HD12	2.06	0.70
8:H:501:ILE:HG21	8:H:570:ALA:HB3	1.73	0.70
1:A:774:ILE:HG23	1:A:777:LYS:HE3	1.73	0.70
2:B:359:PRO:HB2	2:B:406:GLY:O	1.91	0.70
2:B:390:LEU:HG	2:B:390:LEU:O	1.91	0.70
5:K:154:SER:O	5:K:158:ILE:CG2	2.39	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:TRP:CZ2	1:A:851:ARG:HG2	2.26	0.70
1:A:1489:PRO:O	1:A:1533:ASP:O	2.10	0.70
1:A:1877:GLY:O	1:A:1894:ILE:CB	2.38	0.70
1:A:2071:ILE:O	1:A:2071:ILE:HD13	1.91	0.70
4:G:143:ARG:HB3	4:G:143:ARG:CZ	2.20	0.70
5:K:350:PRO:HG3	5:K:353:ARG:CZ	2.21	0.70
27:F:39:U:H3	27:F:115:G:H1	1.38	0.70
1:A:1846:ASN:HA	1:A:1885:LYS:HZ1	1.56	0.70
1:A:2080:LYS:HA	1:A:2083:ILE:HD12	1.74	0.70
2:B:446:SER:HG	2:B:451:PHE:HD2	0.72	0.70
8:H:488:ILE:HG21	8:H:557:HIS:O	1.91	0.70
1:A:1704:GLU:HA	1:A:1731:LYS:HG2	1.74	0.70
1:A:1748:ILE:CG2	1:A:1752:VAL:HG22	2.12	0.70
3:I:145:GLU:OE2	3:I:145:GLU:HA	1.90	0.70
4:G:630:SER:CB	4:G:670:PHE:HZ	1.95	0.70
8:H:364:PHE:CB	8:H:369:LYS:CG	2.27	0.70
4:G:863:PHE:HE2	4:G:892:LEU:CG	2.04	0.70
27:F:31:G:C2	27:F:32:G:C4	2.80	0.70
1:A:149:MET:HB3	1:A:154:TYR:CD2	2.25	0.70
1:A:514:TYR:HB3	1:A:518:VAL:CG2	2.22	0.70
1:A:1615:ASN:HD21	1:A:1634:LEU:HD23	1.56	0.70
2:B:362:TYR:HD1	2:B:362:TYR:H	1.38	0.70
4:G:863:PHE:CE2	4:G:892:LEU:CD2	2.74	0.70
8:H:586:MET:HA	8:H:589:LEU:HD23	1.73	0.70
24:C:8:U:OP1	24:C:8:U:H4'	1.91	0.70
1:A:1647:GLN:O	1:A:1650:ARG:HG2	1.92	0.70
2:B:380:LYS:O	2:B:381:ARG:CG	2.39	0.70
4:G:98:SER:OG	4:G:99:ASN:N	2.24	0.70
6:L:31:PHE:O	6:L:80:MET:HA	1.92	0.70
1:A:1022:PRO:HD3	1:A:1345:TYR:CE1	2.22	0.69
8:H:132:ARG:O	8:H:133:ILE:HG12	1.91	0.69
8:H:135:ASN:HD22	8:H:487:ARG:NH2	1.90	0.69
4:G:251:GLU:OE2	4:G:260:ALA:N	2.25	0.69
4:G:666:ILE:HG22	4:G:667:CYS:H	1.57	0.69
8:H:105:ILE:HA	8:H:108:GLN:CD	2.12	0.69
8:H:474:LYS:NZ	8:H:630:PRO:HD3	2.06	0.69
8:H:580:VAL:HG22	8:H:582:SER:H	1.57	0.69
27:F:74:U:O2'	27:F:75:A:H5'	1.92	0.69
27:F:78:A:H61	27:F:81:A:N6	1.90	0.69
1:A:1756:PHE:CE1	1:A:1760:THR:HG21	2.27	0.69
4:G:862:MET:N	4:G:862:MET:SD	2.65	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:113:ILE:HG23	8:H:549:TYR:CD1	2.27	0.69
8:H:131:GLU:HA	8:H:131:GLU:OE2	1.92	0.69
26:E:4:C:O2'	26:E:5:U:H5'	1.92	0.69
1:A:1654:TRP:HZ3	1:A:1779:LEU:CD1	1.91	0.69
3:I:93:LYS:O	3:I:96:PRO:HD2	1.91	0.69
8:H:187:ARG:NH2	8:H:654:CYS:SG	2.66	0.69
8:H:959:ILE:N	8:H:959:ILE:HD12	2.06	0.69
27:F:78:A:C6	27:F:81:A:C5	2.80	0.69
1:A:305:LEU:HD11	1:A:476:ALA:CB	2.22	0.69
1:A:998:TYR:CE1	1:A:1002:GLU:HG3	2.28	0.69
1:A:1400:ILE:HG21	1:A:1440:ILE:HD11	1.75	0.69
8:H:143:HIS:HA	28:H:1500:GTP:O3B	1.91	0.69
8:H:161:ILE:HG23	8:H:162:PRO:HD2	1.75	0.69
2:B:115:SER:HA	2:B:118:ILE:HG13	1.75	0.69
2:B:177:PRO:HD2	2:B:195:TRP:CD1	2.28	0.69
2:B:274:HIS:CD2	2:B:276:SER:H	2.07	0.69
6:L:53:VAL:HG12	6:L:57:ALA:HB3	1.75	0.69
27:F:106:A:H2'	27:F:107:C:H5'	1.75	0.69
1:A:1051:GLU:OE2	1:A:1261:SER:N	2.21	0.69
1:A:1647:GLN:O	1:A:1650:ARG:CG	2.40	0.69
4:G:666:ILE:O	4:G:670:PHE:HD2	1.73	0.69
8:H:488:ILE:HD12	8:H:560:GLN:HG3	1.73	0.69
27:F:32:G:H4'	27:F:33:U:OP2	1.92	0.69
1:A:1574:PHE:CE1	3:I:390:ARG:HD3	2.27	0.69
2:B:235:ILE:HD12	2:B:280:ILE:CD1	2.20	0.69
4:G:851:ARG:O	4:G:852:LEU:HD12	1.92	0.69
5:K:141:ASN:HD21	5:K:144:LEU:HD23	1.58	0.69
8:H:495:ARG:HH21	8:H:541:GLU:CD	1.96	0.69
9:N:807:GLY:HA2	9:N:1093:ALA:H	0.66	0.69
1:A:431:ILE:HD11	8:H:287:LYS:HA	1.74	0.69
2:B:176:LYS:HB3	2:B:195:TRP:HB2	1.75	0.69
8:H:349:TRP:HZ3	8:H:373:PHE:CE2	2.10	0.69
8:H:582:SER:HB2	8:H:585:ASP:CG	2.12	0.69
2:B:117:LEU:HG	2:B:300:LEU:O	1.93	0.69
3:I:217:TYR:CE1	3:I:221:LYS:NZ	2.45	0.69
8:H:117:ARG:HD2	8:H:157:SER:C	2.13	0.69
8:H:572:ILE:HD12	8:H:573:LYS:CG	2.22	0.69
8:H:948:ASP:OD1	8:H:948:ASP:N	2.26	0.69
25:D:109:U:H3'	25:D:110:U:H5"	1.75	0.69
1:A:1882:LEU:O	1:A:1882:LEU:HD13	1.93	0.68
4:G:19:ILE:HD12	4:G:20:GLY:N	2.07	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:33:U:O2'	27:F:34:C:OP2	2.11	0.68
1:A:354:PRO:O	1:A:355:LEU:HB3	1.93	0.68
1:A:428:LEU:HD13	8:H:279:LEU:HD11	1.74	0.68
2:B:274:HIS:HD2	2:B:276:SER:N	1.89	0.68
4:G:687:SER:O	4:G:690:THR:HG22	1.92	0.68
5:K:350:PRO:HG3	5:K:353:ARG:NH1	2.07	0.68
6:L:101:ASN:O	6:L:102:LYS:CG	2.41	0.68
8:H:495:ARG:HG2	8:H:540:GLU:O	1.94	0.68
1:A:168:LEU:CA	1:A:199:ILE:HD11	2.21	0.68
1:A:431:ILE:HA	8:H:895:ALA:HB1	1.74	0.68
4:G:666:ILE:C	4:G:670:PHE:CD2	2.67	0.68
8:H:332:TYR:OH	8:H:376:PHE:CD2	2.44	0.68
27:F:78:A:N6	27:F:81:A:C5	2.61	0.68
2:B:419:ILE:HD11	2:B:443:LEU:HD12	1.73	0.68
3:I:183:PHE:CE2	3:I:185:ASN:ND2	2.58	0.68
5:K:303:LEU:C	5:K:303:LEU:HD23	2.13	0.68
8:H:470:ALA:HB3	8:H:577:LEU:HD22	1.76	0.68
3:I:98:PHE:CE2	3:I:217:TYR:HD2	2.09	0.68
4:G:166:ARG:O	4:G:169:LEU:N	2.27	0.68
6:L:25:ARG:HH11	6:L:25:ARG:CB	2.07	0.68
8:H:105:ILE:O	8:H:109:LEU:HD23	1.93	0.68
1:A:2075:THR:HG22	1:A:2077:THR:H	1.58	0.68
3:I:124:PHE:CE2	3:I:127:LEU:HB2	2.28	0.68
3:I:268:LEU:CD1	3:I:271:GLU:HG2	2.24	0.68
1:A:837:GLY:HA2	1:A:1317:ARG:HH11	1.56	0.68
2:B:359:PRO:HB2	2:B:406:GLY:C	2.14	0.68
4:G:264:ILE:HG21	4:G:281:ASN:HA	1.75	0.68
8:H:477:ASP:HB2	8:H:628:TYR:CE1	2.29	0.68
8:H:444:GLN:HE21	8:H:444:GLN:HA	1.57	0.68
1:A:404:ASN:OD1	8:H:927:MET:HE3	1.92	0.68
1:A:753:TYR:CE1	6:L:37:ARG:HB3	2.28	0.68
4:G:693:SER:O	4:G:697:LEU:HG	1.94	0.68
5:K:354:PHE:CE1	5:K:358:MET:SD	2.87	0.68
6:L:39:CYS:SG	6:L:80:MET:HB3	2.34	0.68
8:H:113:ILE:HD11	8:H:550:VAL:O	1.94	0.68
8:H:142:LEU:HD12	8:H:929:GLN:HE21	1.57	0.68
8:H:330:TYR:HE1	8:H:430:ARG:NE	1.91	0.68
27:F:40:C:O2'	27:F:41:A:H5"	1.93	0.68
27:F:78:A:N6	27:F:81:A:N7	2.41	0.68
1:A:176:LEU:CD2	1:A:708:TRP:NE1	2.56	0.68
1:A:358:ARG:HH11	1:A:358:ARG:CB	2.07	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:ARG:O	1:A:377:VAL:HB	1.93	0.68
1:A:276:VAL:HG13	1:A:310:ASN:HD22	1.59	0.67
1:A:296:THR:HG21	27:F:33:U:OP2	1.94	0.67
2:B:374:ASN:HB3	2:B:376:TRP:NE1	2.09	0.67
8:H:317:LYS:HB2	28:H:1500:GTP:C6	2.29	0.67
8:H:461:LYS:HD2	8:H:461:LYS:C	2.15	0.67
8:H:577:LEU:HD23	8:H:577:LEU:C	2.15	0.67
8:H:855:PRO:O	8:H:944:VAL:HG22	1.92	0.67
1:A:325:LYS:HB3	1:A:405:ASN:ND2	2.09	0.67
3:I:179:MET:HG3	3:I:183:PHE:CE1	2.28	0.67
8:H:197:THR:HG23	8:H:545:LEU:CD1	2.20	0.67
1:A:795:ALA:HA	1:A:1095:MET:HE3	1.75	0.67
1:A:939:LEU:HD11	3:I:441:MET:CE	2.24	0.67
2:B:159:LEU:HD13	2:B:430:MET:HE1	1.75	0.67
4:G:238:PRO:HD2	4:G:239:THR:H	1.59	0.67
4:G:281:ASN:ND2	4:G:295:LEU:HD13	2.10	0.67
8:H:246:THR:O	8:H:250:GLU:HG3	1.94	0.67
9:N:1122:GLY:CA	9:N:1249:ASP:CA	2.73	0.67
1:A:276:VAL:HG11	1:A:310:ASN:CB	2.24	0.67
1:A:691:PHE:HZ	1:A:701:CYS:HA	1.55	0.67
1:A:774:ILE:HG23	1:A:777:LYS:CE	2.24	0.67
1:A:1654:TRP:CH2	1:A:1779:LEU:CD1	2.78	0.67
8:H:116:THR:OG1	8:H:120:ARG:NH2	2.24	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CB	2.21	0.67
8:H:488:ILE:CD1	8:H:560:GLN:HG3	2.23	0.67
8:H:936:ILE:HD13	8:H:936:ILE:H	1.59	0.67
4:G:863:PHE:HE2	4:G:892:LEU:HG	1.58	0.67
8:H:364:PHE:HB2	8:H:369:LYS:CD	2.22	0.67
8:H:677:PHE:CZ	8:H:966:PHE:CD2	2.82	0.67
1:A:1197:ASN:ND2	1:A:1221:ASN:OD1	2.27	0.67
3:I:312:LEU:HB3	3:I:333:TRP:CH2	2.29	0.67
6:L:33:ARG:HD2	6:L:65:ASP:CG	2.15	0.67
1:A:175:LEU:HD12	1:A:175:LEU:C	2.15	0.67
1:A:1400:ILE:HG22	1:A:1401:SER:H	1.60	0.67
3:I:280:ARG:NH2	26:E:37:U:OP2	2.27	0.67
4:G:224:GLN:O	4:G:228:THR:HG23	1.95	0.67
8:H:105:ILE:HA	8:H:108:GLN:OE1	1.95	0.67
8:H:959:ILE:HD12	8:H:960:ASN:H	1.58	0.67
1:A:165:LEU:CD1	1:A:578:MET:SD	2.72	0.67
1:A:1651:ALA:C	1:A:1652:HIS:CD2	2.68	0.67
3:I:92:ILE:HD12	3:I:92:ILE:N	2.09	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:105:PHE:HZ	6:L:137:TYR:HE2	1.18	0.67
8:H:330:TYR:CE1	8:H:430:ARG:NE	2.61	0.67
8:H:338:SER:O	8:H:341:ILE:HG12	1.95	0.67
27:F:48:G:H1	27:F:67:U:H3	1.41	0.67
27:F:77:A:H4'	27:F:78:A:OP1	1.95	0.67
3:I:123:ARG:CD	3:I:189:LEU:HD12	2.23	0.67
8:H:486:VAL:CG1	8:H:564:ILE:CD1	2.59	0.67
1:A:1703:MET:HB2	1:A:1732:MET:HB2	1.75	0.67
5:K:350:PRO:CB	25:D:84:C:C5	2.78	0.67
8:H:316:THR:OG1	28:H:1500:GTP:N7	2.28	0.67
27:F:32:G:H5"	27:F:32:G:H8	1.60	0.67
1:A:371:ASP:O	8:H:969:LYS:HG3	1.94	0.66
1:A:511:ASP:HB2	1:A:514:TYR:HE1	1.60	0.66
1:A:1892:LYS:HD2	1:A:1916:GLU:CG	2.25	0.66
4:G:672:LEU:HD23	4:G:704:LEU:HD21	1.41	0.66
4:G:688:ARG:HH22	4:G:721:ARG:NH2	1.93	0.66
8:H:271:ASP:O	8:H:274:ILE:HG22	1.94	0.66
8:H:331:TYR:OH	8:H:428:ILE:HG23	1.95	0.66
8:H:415:TYR:C	8:H:416:ASP:OD1	2.33	0.66
1:A:362:GLU:HB2	1:A:1209:LYS:HG2	1.77	0.66
1:A:909:THR:CG2	1:A:910:LYS:N	2.57	0.66
2:B:360:ASN:HB3	2:B:362:TYR:CE1	2.31	0.66
3:I:231:PHE:CD2	3:I:330:ALA:CB	2.78	0.66
4:G:692:LEU:HD22	4:G:708:LEU:HD11	1.75	0.66
4:G:721:ARG:CD	4:G:725:ILE:CD1	2.72	0.66
5:K:292:ALA:O	5:K:296:VAL:HG23	1.94	0.66
8:H:189:LEU:HD12	8:H:189:LEU:C	2.14	0.66
8:H:329:SER:O	8:H:333:ALA:HB3	1.96	0.66
27:F:31:G:N2	27:F:32:G:H1'	2.10	0.66
27:F:31:G:N3	27:F:32:G:H1'	2.10	0.66
2:B:202:LEU:HD23	2:B:207:LEU:HD22	1.77	0.66
3:I:112:MET:HB3	3:I:204:LEU:CD2	2.22	0.66
3:I:358:ILE:HG23	3:I:359:PRO:CD	2.21	0.66
8:H:329:SER:HA	8:H:333:ALA:CB	2.25	0.66
8:H:472:VAL:HG11	8:H:571:TYR:CZ	2.30	0.66
1:A:1417:GLN:OE1	1:A:1422:ILE:HD11	1.96	0.66
2:B:380:LYS:O	2:B:382:ASP:OD1	2.13	0.66
2:B:456:GLY:O	2:B:459:ARG:N	2.21	0.66
8:H:219:VAL:CG2	8:H:931:TYR:HB3	2.25	0.66
8:H:317:LYS:HB2	28:H:1500:GTP:C5	2.30	0.66
8:H:354:TYR:HB3	8:H:359:PHE:HB3	1.75	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:458:ILE:HB	8:H:590:LYS:HD3	1.76	0.66
2:B:314:SER:OG	2:B:355:VAL:O	2.10	0.66
3:I:197:ILE:C	3:I:201:ASN:ND2	2.44	0.66
8:H:495:ARG:CG	8:H:540:GLU:O	2.43	0.66
25:D:51:A:H4'	25:D:51:A:OP1	1.96	0.66
1:A:558:GLN:OE1	1:A:558:GLN:HA	1.95	0.66
1:A:862:GLU:HA	1:A:862:GLU:OE2	1.96	0.66
2:B:177:PRO:HD2	2:B:195:TRP:HD1	1.61	0.66
8:H:444:GLN:HA	8:H:444:GLN:NE2	2.11	0.66
25:D:109:U:H4'	25:D:110:U:OP2	1.95	0.66
1:A:362:GLU:CB	1:A:1209:LYS:HE2	2.22	0.66
1:A:923:TYR:CE1	1:A:933:GLU:HG2	2.30	0.66
1:A:1657:ILE:O	1:A:1661:ILE:HG13	1.95	0.66
2:B:274:HIS:CD2	2:B:275:PRO:HD2	2.30	0.66
2:B:313:LEU:HD11	2:B:322:VAL:CG2	2.26	0.66
27:F:50:G:H1	27:F:65:U:H3	1.41	0.66
1:A:366:GLU:HB2	1:A:372:ARG:HH11	1.59	0.66
1:A:1038:ILE:CD1	1:A:1039:TRP:CE3	2.78	0.66
1:A:1041:VAL:HG11	1:A:1253:LYS:N	2.11	0.66
2:B:316:GLN:CB	2:B:357:TRP:CE2	2.78	0.66
4:G:256:LYS:HG2	4:G:257:PHE:H	1.61	0.66
5:K:141:ASN:O	5:K:142:LEU:HD22	1.96	0.66
8:H:126:MET:CE	8:H:132:ARG:HH12	2.09	0.66
3:I:124:PHE:CD2	3:I:127:LEU:HB2	2.30	0.66
5:K:349:ASN:HB2	5:K:406:PHE:CE1	2.31	0.66
8:H:564:ILE:CG2	8:H:567:ILE:HG12	2.26	0.66
25:D:78:G:N2	26:E:4:C:O2	2.28	0.66
27:F:73:U:O2'	27:F:74:U:H5"	1.96	0.66
1:A:1591:THR:HG22	1:A:1592:HIS:N	2.11	0.65
4:G:99:ASN:ND2	4:G:99:ASN:H	1.94	0.65
8:H:855:PRO:C	8:H:944:VAL:HG21	2.16	0.65
1:A:325:LYS:HB3	1:A:405:ASN:HD22	1.59	0.65
5:K:154:SER:O	5:K:158:ILE:CG1	2.44	0.65
5:K:155:LYS:O	5:K:158:ILE:HG13	1.96	0.65
8:H:110:LYS:HE2	8:H:552:PRO:CG	2.20	0.65
8:H:797:GLN:HA	8:H:797:GLN:HE21	1.61	0.65
1:A:319:ARG:NH1	1:A:485:PRO:HG2	2.11	0.65
2:B:227:HIS:HD2	2:B:273:TYR:CE1	2.14	0.65
3:I:93:LYS:HA	3:I:93:LYS:HZ1	1.61	0.65
3:I:197:ILE:CG2	3:I:201:ASN:HD21	2.09	0.65
5:K:154:SER:O	5:K:158:ILE:HG12	1.97	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:165:SER:OG	8:H:168:VAL:HG22	1.96	0.65
25:D:48:C:C2'	25:D:49:A:C8	2.79	0.65
1:A:875:THR:OG1	1:A:878:GLU:HB2	1.96	0.65
2:B:316:GLN:HB2	2:B:357:TRP:CE3	2.30	0.65
6:L:141:ARG:HD2	6:L:141:ARG:N	2.11	0.65
7:M:95:ARG:HG3	7:M:96:PRO:HD2	1.78	0.65
8:H:129:ILE:HG12	10:R:16:GLY:HA3	1.78	0.65
8:H:888:ILE:H	8:H:888:ILE:HD12	1.60	0.65
1:A:809:LYS:O	1:A:813:GLU:CG	2.43	0.65
2:B:202:LEU:HB3	2:B:207:LEU:HD23	1.79	0.65
3:I:120:TYR:HE2	3:I:141:ILE:HG12	1.59	0.65
2:B:147:ASN:HB3	2:B:150:GLN:OE1	1.95	0.65
2:B:280:ILE:O	2:B:292:TRP:N	2.29	0.65
2:B:329:SER:CB	2:B:348:HIS:O	2.36	0.65
3:I:358:ILE:CG2	3:I:360:GLU:H	2.10	0.65
4:G:212:VAL:CG1	4:G:215:LEU:HB3	2.25	0.65
8:H:274:ILE:O	8:H:278:LYS:HA	1.96	0.65
1:A:404:ASN:HA	8:H:919:ARG:HH12	1.61	0.65
1:A:1279:VAL:HG11	1:A:1301:TYR:OH	1.96	0.65
1:A:1578:ALA:HB1	1:A:1602:PRO:HB3	1.78	0.65
4:G:278:TRP:CH2	4:G:298:THR:HB	2.31	0.65
8:H:306:PRO:HG2	8:H:349:TRP:CH2	2.31	0.65
1:A:366:GLU:HB2	1:A:372:ARG:HH12	1.59	0.65
1:A:2060:LEU:HD21	1:A:2079:ILE:HG23	1.78	0.65
3:I:179:MET:HG3	3:I:183:PHE:HE1	1.62	0.65
8:H:799:PHE:HE1	8:H:846:CYS:SG	2.20	0.65
1:A:173:LEU:HD11	1:A:712:LEU:CD1	2.27	0.65
1:A:770:MET:CE	1:A:775:ARG:O	2.45	0.65
1:A:875:THR:OG1	1:A:878:GLU:OE1	2.15	0.65
2:B:381:ARG:HG3	2:B:382:ASP:OD1	1.97	0.65
8:H:503:ASP:OD1	8:H:571:TYR:HB2	1.97	0.65
1:A:1145:MET:O	1:A:1146:GLN:HG3	1.97	0.64
2:B:218:VAL:HG21	2:B:238:ALA:HB3	1.80	0.64
4:G:843:VAL:HG21	4:G:895:LEU:CD1	2.27	0.64
8:H:160:ARG:HB3	8:H:161:ILE:HA	1.78	0.64
27:F:95:C:O2'	27:F:96:U:C5'	2.43	0.64
27:F:97:U:C6	27:F:97:U:H5"	2.33	0.64
1:A:767:LEU:HD21	1:A:779:ALA:CB	2.27	0.64
1:A:1739:ARG:NH2	1:A:1745:SER:OG	2.31	0.64
3:I:184:LYS:HE2	3:I:186:LYS:HB2	1.78	0.64
1:A:168:LEU:CB	1:A:199:ILE:CD1	2.74	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:LEU:HD12	1:A:173:LEU:O	1.98	0.64
1:A:174:LYS:NZ	1:A:177:GLU:OE2	2.30	0.64
1:A:207:ARG:NH1	1:A:299:LYS:HG2	2.13	0.64
8:H:500:ARG:NE	8:H:534:THR:CB	2.57	0.64
8:H:599:THR:CG2	8:H:933:TRP:CZ3	2.80	0.64
8:H:599:THR:HG22	8:H:932:PHE:O	1.98	0.64
8:H:862:TYR:OH	8:H:908:VAL:HG23	1.98	0.64
1:A:250:SER:O	1:A:254:HIS:HB2	1.96	0.64
1:A:676:GLN:N	1:A:676:GLN:OE1	2.31	0.64
1:A:780:ARG:O	1:A:784:GLN:OE1	2.15	0.64
2:B:313:LEU:HD11	2:B:322:VAL:HG23	1.78	0.64
3:I:266:LYS:CG	3:I:267:HIS:N	2.56	0.64
5:K:146:GLU:HA	5:K:149:PHE:HD2	1.62	0.64
6:L:76:LEU:HD12	6:L:76:LEU:N	2.11	0.64
27:F:44:A:N3	27:F:45:A:C8	2.66	0.64
1:A:1017:ASP:O	1:A:1509:ARG:NH1	2.31	0.64
2:B:48:ASP:OD2	2:B:69:VAL:HG21	1.96	0.64
2:B:235:ILE:HD13	2:B:280:ILE:HD13	1.78	0.64
2:B:374:ASN:CB	2:B:376:TRP:HE1	2.11	0.64
2:B:393:ARG:HH21	2:B:393:ARG:CG	2.09	0.64
3:I:401:LEU:HD12	4:G:214:SER:CB	2.27	0.64
6:L:91:MET:HE1	6:L:129:GLY:HA2	1.79	0.64
8:H:129:ILE:HD12	8:H:129:ILE:H	1.59	0.64
26:E:24:A:C2	26:E:50:G:C2	2.86	0.64
1:A:273:ASP:O	1:A:276:VAL:HG22	1.97	0.64
1:A:784:GLN:O	1:A:788:GLU:HG2	1.98	0.64
1:A:1876:ASN:OD1	1:A:1896:THR:HG23	1.97	0.64
2:B:311:PHE:CE2	7:M:126:ILE:HD13	2.32	0.64
2:B:316:GLN:CG	2:B:357:TRP:CE2	2.81	0.64
4:G:281:ASN:ND2	4:G:295:LEU:HD11	2.13	0.64
4:G:721:ARG:HD3	4:G:725:ILE:CD1	2.26	0.64
8:H:197:THR:HG21	8:H:545:LEU:CD1	2.21	0.64
26:E:1:A:N6	29:E:201:M7M:HBZB	2.13	0.64
8:H:164:MET:HG2	8:H:175:LEU:HD12	1.80	0.64
8:H:292:ILE:O	8:H:295:ILE:HG12	1.97	0.64
27:F:76:U:OP2	27:F:76:U:H4'	1.97	0.64
1:A:294:ASN:OD1	1:A:300:LYS:CE	2.45	0.64
1:A:703:PHE:CE1	1:A:705:GLN:HB3	2.30	0.64
1:A:1621:VAL:HG12	1:A:1622:GLY:N	2.07	0.64
8:H:167:ASN:HD21	8:H:173:LYS:HG2	1.62	0.64
1:A:506:PHE:HA	1:A:522:TYR:CE1	2.33	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:304:ARG:NH1	26:E:13:G:OP1	2.31	0.64
5:K:325:GLU:HA	5:K:328:ASN:OD1	1.97	0.64
8:H:470:ALA:CB	8:H:577:LEU:HD22	2.28	0.64
3:I:120:TYR:CE2	3:I:141:ILE:HG12	2.33	0.64
4:G:693:SER:HA	4:G:696:ARG:HD2	1.80	0.64
26:E:23:C:O2'	26:E:24:A:H5'	1.97	0.64
1:A:1076:PRO:O	1:A:1080:ASP:OD2	2.16	0.63
1:A:1458:TRP:CZ3	1:A:1461:TYR:CD2	2.86	0.63
2:B:415:TYR:HD2	2:B:439:LYS:HD3	1.61	0.63
4:G:843:VAL:CG2	4:G:895:LEU:HD13	2.27	0.63
8:H:105:ILE:HA	8:H:108:GLN:NE2	2.13	0.63
1:A:273:ASP:N	1:A:273:ASP:OD1	2.31	0.63
1:A:293:VAL:HG13	1:A:295:GLY:N	2.13	0.63
1:A:767:LEU:HD21	1:A:779:ALA:HB2	1.78	0.63
8:H:227:VAL:O	8:H:473:LEU:HD13	1.99	0.63
25:D:62:A:C2'	25:D:63:G:H5'	2.28	0.63
1:A:1613:THR:O	1:A:1616:ARG:HD3	1.97	0.63
2:B:114:THR:O	2:B:118:ILE:HG13	1.99	0.63
2:B:273:TYR:CZ	2:B:280:ILE:HD11	2.33	0.63
3:I:197:ILE:HG23	3:I:201:ASN:HD21	1.61	0.63
8:H:118:TYR:CD1	8:H:119:ASN:O	2.50	0.63
8:H:463:THR:CB	8:H:585:ASP:OD1	2.47	0.63
8:H:880:MET:HB3	8:H:886:SER:HA	1.81	0.63
8:H:947:LYS:H	8:H:947:LYS:HD3	1.62	0.63
27:F:78:A:HO2'	27:F:79:C:P	2.18	0.63
1:A:173:LEU:CD1	1:A:712:LEU:CD1	2.76	0.63
6:L:25:ARG:HH11	6:L:25:ARG:CG	2.10	0.63
8:H:484:SER:HB3	8:H:571:TYR:OH	1.97	0.63
24:C:10:U:O2'	24:C:11:A:H5'	1.99	0.63
25:D:49:A:C2'	25:D:50:G:H5"	2.23	0.63
1:A:1935:VAL:HG11	1:A:1940:MET:HB2	1.81	0.63
3:I:98:PHE:CZ	3:I:217:TYR:HD2	2.15	0.63
3:I:225:ILE:C	3:I:325:ARG:HH12	2.01	0.63
3:I:282:GLU:OE1	3:I:286:PHE:CE2	2.52	0.63
4:G:134:ARG:HB3	4:G:134:ARG:CZ	2.28	0.63
8:H:945:LEU:HD12	8:H:945:LEU:H	1.63	0.63
27:F:40:C:H3'	27:F:40:C:OP2	1.99	0.63
1:A:175:LEU:HD11	1:A:564:TRP:CZ2	2.33	0.63
1:A:1317:ARG:HH21	1:A:1366:ARG:HH22	1.45	0.63
3:I:206:ASN:O	3:I:209:LYS:HG2	1.98	0.63
3:I:320:GLN:HG2	3:I:325:ARG:HA	1.80	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:358:ILE:HG22	3:I:360:GLU:H	1.64	0.63
8:H:469:TRP:CD1	8:H:578:TYR:HB3	2.34	0.63
8:H:968:MET:HE2	8:H:968:MET:CA	2.29	0.63
1:A:1618:ASN:N	1:A:1618:ASN:OD1	2.31	0.63
2:B:230:SER:OG	2:B:233:GLN:OE1	2.16	0.63
2:B:391:ALA:O	2:B:392:HIS:HB2	1.97	0.63
3:I:268:LEU:HD12	3:I:271:GLU:HG2	1.80	0.63
3:I:402:ASP:OD1	3:I:403:SER:N	2.31	0.63
4:G:886:CYS:C	4:G:888:PRO:HD2	2.19	0.63
8:H:363:PRO:O	8:H:364:PHE:HB3	1.98	0.63
8:H:889:TYR:HE1	8:H:890:LYS:HG3	1.57	0.63
27:F:94:C:H6	27:F:94:C:H5"	1.63	0.63
1:A:393:SER:O	1:A:394:ARG:HG2	1.98	0.63
1:A:1658:HIS:CA	1:A:1661:ILE:HD12	2.27	0.63
1:A:1748:ILE:O	1:A:1752:VAL:CG2	2.41	0.63
2:B:239:GLU:HA	2:B:267:ARG:HB2	1.81	0.63
3:I:429:ARG:CB	3:I:429:ARG:HH11	2.11	0.63
4:G:279:LEU:N	4:G:279:LEU:HD23	2.13	0.63
5:K:452:LEU:O	5:K:456:GLY:N	2.31	0.63
1:A:874:ILE:HD11	1:A:1062:ASP:HB2	1.81	0.63
1:A:1118:GLY:HA3	1:A:1163:ARG:NH2	2.14	0.63
4:G:666:ILE:C	4:G:670:PHE:HD2	2.02	0.63
4:G:702:PRO:HA	4:G:739:PHE:CE2	2.33	0.63
8:H:942:GLY:O	8:H:963:SER:OG	2.17	0.63
27:F:92:U:H6	27:F:92:U:H5"	1.64	0.63
1:A:297:SER:CB	27:F:32:G:O5'	2.47	0.62
1:A:1916:GLU:HA	1:A:1916:GLU:OE2	1.98	0.62
24:C:2:A:H8	24:C:2:A:O5'	1.82	0.62
1:A:1653:LEU:HD21	1:A:1815:LEU:HD23	1.80	0.62
4:G:703:LEU:HD13	4:G:703:LEU:C	2.19	0.62
4:G:859:LEU:O	4:G:862:MET:HG2	1.99	0.62
8:H:178:LEU:N	8:H:178:LEU:HD23	2.14	0.62
8:H:959:ILE:CD1	8:H:960:ASN:N	2.61	0.62
1:A:770:MET:HE1	1:A:779:ALA:N	2.15	0.62
1:A:2018:ASN:HB3	1:A:2021:SER:OG	2.00	0.62
2:B:405:ASP:OD2	2:B:408:LYS:HD3	1.98	0.62
3:I:102:ILE:HB	3:I:103:PRO:HD3	1.81	0.62
6:L:96:GLY:O	6:L:138:ASN:HB2	1.96	0.62
8:H:126:MET:SD	8:H:132:ARG:NH1	2.72	0.62
8:H:936:ILE:H	8:H:936:ILE:CD1	2.12	0.62
9:N:807:GLY:H	9:N:1093:ALA:N	1.93	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1275:MET:HE3	1:A:1299:LYS:HD2	1.81	0.62
3:I:146:ASN:ND2	3:I:148:ASN:ND2	2.47	0.62
4:G:268:CYS:SG	4:G:278:TRP:HH2	2.15	0.62
5:K:141:ASN:ND2	5:K:144:LEU:HD23	2.14	0.62
8:H:129:ILE:HB	8:H:132:ARG:HB2	1.81	0.62
8:H:793:GLU:O	8:H:796:ILE:HG22	1.99	0.62
24:C:3:A:H8	24:C:3:A:O5'	1.81	0.62
1:A:1880:PHE:CD2	1:A:1889:LEU:HD21	2.32	0.62
3:I:321:LYS:HD2	3:I:324:ASP:HB3	1.79	0.62
3:I:433:ASN:O	3:I:434:GLN:C	2.37	0.62
4:G:124:ASP:N	4:G:124:ASP:OD1	2.32	0.62
4:G:223:LEU:HD23	4:G:223:LEU:O	2.00	0.62
5:K:166:TYR:OH	5:K:174:LEU:HD12	2.00	0.62
1:A:376:ARG:NE	8:H:910:GLU:OE2	2.32	0.62
1:A:840:VAL:O	1:A:840:VAL:HG22	2.00	0.62
2:B:292:TRP:CD1	2:B:299:GLU:HA	2.34	0.62
3:I:373:ARG:HB3	3:I:373:ARG:NH1	2.14	0.62
3:I:433:ASN:O	3:I:434:GLN:O	2.18	0.62
4:G:857:VAL:O	4:G:860:TYR:HB2	1.99	0.62
8:H:202:ASP:N	8:H:202:ASP:OD1	2.31	0.62
8:H:483:TRP:CH2	8:H:565:LYS:HG3	2.34	0.62
24:C:5:G:H4'	24:C:6:U:OP1	1.98	0.62
1:A:219:ALA:O	1:A:266:LEU:HD12	1.99	0.62
1:A:1022:PRO:CD	1:A:1345:TYR:HE1	2.09	0.62
4:G:167:GLU:HG3	4:G:168:LYS:N	2.13	0.62
8:H:379:ILE:O	8:H:383:LYS:HG3	1.99	0.62
8:H:931:TYR:O	8:H:931:TYR:HD1	1.83	0.62
1:A:1458:TRP:CE3	1:A:1461:TYR:HD2	2.18	0.62
1:A:1887:GLY:HA3	1:A:1992:TYR:HD1	1.64	0.62
5:K:311:GLU:HA	5:K:311:GLU:OE1	2.00	0.62
1:A:175:LEU:CD1	1:A:564:TRP:CE2	2.83	0.62
1:A:286:LEU:CD2	1:A:292:LYS:HB3	2.28	0.62
1:A:780:ARG:C	1:A:784:GLN:OE1	2.38	0.62
2:B:165:LEU:N	2:B:165:LEU:HD23	2.14	0.62
4:G:688:ARG:HD3	4:G:692:LEU:HD21	1.81	0.62
8:H:326:GLU:OE1	8:H:330:TYR:HD2	1.82	0.62
8:H:582:SER:OG	8:H:585:ASP:OD2	2.17	0.62
8:H:674:LEU:CD1	8:H:973:ARG:HH22	2.12	0.62
9:N:487:CYS:O	9:N:490:ALA:N	2.33	0.62
1:A:169:PRO:HA	1:A:172:ILE:HD12	1.82	0.62
4:G:281:ASN:HD22	4:G:295:LEU:HD13	1.65	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:280:VAL:O	5:K:286:ASN:ND2	2.33	0.62
5:K:282:GLU:O	5:K:284:ASP:N	2.32	0.62
6:L:34:LYS:HD2	6:L:35:ASN:H	1.64	0.62
8:H:129:ILE:HG12	10:R:16:GLY:CA	2.30	0.62
1:A:1658:HIS:HA	1:A:1661:ILE:CD1	2.26	0.61
4:G:230:LEU:HD12	4:G:247:SER:CA	2.23	0.61
4:G:285:HIS:CE1	4:G:291:TYR:CZ	2.87	0.61
5:K:147:ASP:OD1	5:K:147:ASP:N	2.31	0.61
8:H:114:PRO:C	8:H:115:LYS:HG3	2.20	0.61
8:H:389:LEU:N	8:H:389:LEU:HD23	2.15	0.61
1:A:1585:MET:HB3	1:A:1598:LEU:HD13	1.81	0.61
2:B:124:LEU:CD2	2:B:274:HIS:HE1	2.10	0.61
2:B:192:THR:HB	2:B:461:ILE:HD11	1.82	0.61
2:B:313:LEU:HD13	2:B:322:VAL:CG2	2.26	0.61
3:I:400:VAL:HG21	4:G:154:PRO:HG2	1.81	0.61
4:G:671:PHE:CE2	4:G:694:GLY:HA2	2.35	0.61
4:G:721:ARG:HD2	4:G:725:ILE:CD1	2.30	0.61
4:G:888:PRO:O	4:G:892:LEU:CD2	2.48	0.61
8:H:373:PHE:CE1	8:H:377:ILE:HD12	2.34	0.61
8:H:881:LYS:HA	8:H:886:SER:CB	2.30	0.61
27:F:31:G:N1	27:F:32:G:C4	2.68	0.61
3:I:184:LYS:CD	3:I:186:LYS:H	2.01	0.61
8:H:168:VAL:HG12	8:H:173:LYS:O	2.00	0.61
8:H:581:LYS:HB3	8:H:581:LYS:NZ	2.11	0.61
24:C:11:A:H8	24:C:11:A:O5'	1.83	0.61
1:A:207:ARG:NH1	1:A:299:LYS:CG	2.63	0.61
1:A:837:GLY:O	1:A:1317:ARG:NH1	2.34	0.61
1:A:1907:GLN:O	1:A:1910:LYS:CG	2.48	0.61
2:B:395:ILE:HD11	7:M:123:THR:HG23	1.80	0.61
3:I:93:LYS:HA	3:I:93:LYS:NZ	2.15	0.61
3:I:263:GLY:O	3:I:283:GLY:HA2	2.00	0.61
3:I:450:GLN:HG3	3:I:451:GLN:N	2.14	0.61
4:G:143:ARG:HH21	4:G:143:ARG:CG	2.14	0.61
4:G:215:LEU:C	4:G:215:LEU:HD12	2.20	0.61
8:H:471:HIS:C	8:H:486:VAL:HG23	2.19	0.61
1:A:769:MET:CE	4:G:112:ALA:HA	2.29	0.61
1:A:843:THR:HG21	6:L:108:ASP:HB3	1.83	0.61
1:A:956:LYS:HD2	1:A:956:LYS:C	2.21	0.61
1:A:1340:ILE:O	1:A:1344:THR:OG1	2.18	0.61
4:G:6:PHE:CD1	4:G:7:LEU:N	2.68	0.61
4:G:238:PRO:CD	4:G:239:THR:H	2.14	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:674:LEU:HD13	8:H:973:ARG:NH1	2.13	0.61
1:A:147:SER:O	1:A:150:ALA:HB2	2.00	0.61
1:A:322:VAL:CG2	1:A:327:TYR:CE2	2.80	0.61
1:A:514:TYR:HB3	1:A:518:VAL:HG21	1.83	0.61
1:A:892:SER:CB	1:A:1128:GLN:HE22	2.13	0.61
8:H:139:ILE:HD12	8:H:252:LEU:HD22	1.81	0.61
8:H:379:ILE:HG22	8:H:383:LYS:HE3	1.81	0.61
9:N:807:GLY:C	9:N:1093:ALA:H	2.00	0.61
1:A:141:LYS:CA	1:A:144:ASN:ND2	2.54	0.61
1:A:1350:ILE:HG23	1:A:1356:LEU:HD12	1.81	0.61
2:B:206:THR:HB	2:B:208:GLN:OE1	2.00	0.61
2:B:320:SER:CB	2:B:337:ARG:HH22	2.13	0.61
2:B:456:GLY:O	2:B:458:ASP:N	2.34	0.61
8:H:106:PHE:O	8:H:110:LYS:HG2	2.00	0.61
8:H:968:MET:HA	8:H:968:MET:CE	2.30	0.61
27:F:32:G:O2’	27:F:33:U:OP1	2.19	0.61
1:A:217:TRP:CD1	1:A:703:PHE:CE2	2.89	0.61
1:A:1275:MET:CE	1:A:1299:LYS:HD2	2.31	0.61
1:A:1468:ALA:CB	1:A:1473:ARG:O	2.49	0.61
3:I:393:PHE:CD1	3:I:393:PHE:C	2.73	0.61
8:H:606:VAL:HG21	8:H:973:ARG:HH21	1.66	0.61
24:C:11:A:O2’	24:C:12:U:H5’	2.01	0.61
27:F:74:U:H5’	27:F:74:U:H6	1.65	0.61
1:A:355:LEU:HD13	1:A:356:TYR:N	2.16	0.61
1:A:495:ARG:CZ	1:A:497:GLN:HE21	2.12	0.61
1:A:1282:ASP:O	1:A:1285:VAL:HG23	2.01	0.61
1:A:1830:VAL:HG11	1:A:1958:PRO:HG3	1.80	0.61
8:H:132:ARG:HH21	8:H:206:LYS:HG3	1.66	0.61
8:H:235:VAL:HG22	8:H:261:VAL:CG1	2.29	0.61
8:H:369:LYS:NZ	8:H:369:LYS:H	1.99	0.61
8:H:883:ARG:NH2	8:H:910:GLU:O	2.34	0.61
1:A:293:VAL:HG22	1:A:294:ASN:H	1.65	0.61
1:A:1887:GLY:HA3	1:A:1992:TYR:CD1	2.35	0.61
3:I:135:LEU:HD23	3:I:136:GLN:HG3	1.83	0.61
3:I:402:ASP:O	3:I:405:GLY:N	2.33	0.61
4:G:668:HIS:HB3	4:G:698:VAL:CG1	2.21	0.61
4:G:702:PRO:CB	4:G:739:PHE:CZ	2.83	0.61
5:K:334:PRO:HG2	5:K:337:TYR:CE1	2.36	0.61
8:H:576:THR:CB	8:H:592:PHE:HD2	2.11	0.61
1:A:547:LEU:HD12	1:A:547:LEU:O	2.00	0.60
2:B:175:THR:HA	2:B:459:ARG:HD2	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:389:ILE:HD11	2:B:427:TRP:CD1	2.36	0.60
8:H:862:TYR:CE1	8:H:908:VAL:HG23	2.36	0.60
1:A:497:GLN:O	1:A:709:ARG:CD	2.46	0.60
1:A:547:LEU:HD12	1:A:547:LEU:C	2.20	0.60
1:A:1998:ARG:C	1:A:1999:ILE:HG13	2.21	0.60
1:A:842:LYS:HD2	1:A:842:LYS:C	2.19	0.60
1:A:1158:ILE:HG13	1:A:1172:PHE:HE1	1.65	0.60
1:A:1624:LEU:HD21	1:A:1635:HIS:CE1	2.36	0.60
3:I:158:PHE:HA	3:I:161:LEU:CD1	2.28	0.60
1:A:293:VAL:HG13	1:A:295:GLY:H	1.65	0.60
1:A:358:ARG:CD	1:A:360:GLU:HB2	2.31	0.60
1:A:861:GLN:HE21	1:A:1097:HIS:HB3	1.66	0.60
4:G:6:PHE:CE1	4:G:7:LEU:HD12	2.36	0.60
4:G:692:LEU:HD23	4:G:692:LEU:N	2.17	0.60
7:M:95:ARG:HG2	7:M:95:ARG:NH1	2.01	0.60
27:F:95:C:HO2'	27:F:96:U:H5'	1.63	0.60
1:A:325:LYS:HE2	1:A:325:LYS:HA	1.83	0.60
2:B:127:TYR:CE2	2:B:276:SER:CA	2.85	0.60
2:B:320:SER:HB2	2:B:337:ARG:CZ	2.30	0.60
4:G:630:SER:CA	4:G:670:PHE:CZ	2.84	0.60
5:K:457:GLN:CD	5:K:457:GLN:H	1.98	0.60
6:L:71:ASP:HA	6:L:76:LEU:HD13	1.82	0.60
3:I:123:ARG:HD2	3:I:189:LEU:CD1	2.31	0.60
5:K:244:LEU:O	5:K:248:ARG:HB2	2.02	0.60
6:L:74:TYR:CD1	6:L:83:MET:HE3	2.37	0.60
24:C:8:U:C5	25:D:51:A:C6	2.90	0.60
27:F:44:A:C4	27:F:45:A:N7	2.69	0.60
27:F:102:C:O5'	27:F:102:C:H6	1.85	0.60
2:B:187:ASP:OD2	2:B:447:ASN:HB3	2.01	0.60
3:I:135:LEU:HD23	3:I:136:GLN:H	1.62	0.60
4:G:855:ASP:N	4:G:855:ASP:OD1	2.34	0.60
5:K:341:VAL:CG2	5:K:428:TRP:NE1	2.65	0.60
8:H:113:ILE:HG23	8:H:549:TYR:CG	2.37	0.60
8:H:352:VAL:HG13	8:H:372:THR:OG1	2.02	0.60
2:B:331:SER:HB3	2:B:345:LEU:HB2	1.83	0.60
3:I:123:ARG:HD2	3:I:189:LEU:HD12	1.83	0.60
8:H:113:ILE:HG22	8:H:114:PRO:CD	2.30	0.60
1:A:255:ILE:HG23	1:A:640:ARG:HG2	1.83	0.60
1:A:1206:CYS:SG	1:A:1306:GLU:HG3	2.41	0.60
2:B:47:GLU:HB2	2:B:50:GLU:HG3	1.82	0.60
3:I:282:GLU:CG	3:I:286:PHE:CG	2.80	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:702:PRO:HB3	4:G:739:PHE:CE2	2.37	0.60
8:H:349:TRP:HZ3	8:H:373:PHE:HE2	1.47	0.60
24:C:8:U:N1	25:D:51:A:N6	2.48	0.60
27:F:32:G:N2	27:F:122:C:C2	2.70	0.60
27:F:97:U:C6	27:F:97:U:C5'	2.85	0.60
4:G:143:ARG:HH21	4:G:143:ARG:HG3	1.66	0.60
8:H:324:ILE:O	8:H:328:VAL:CG2	2.46	0.60
1:A:173:LEU:CD1	1:A:712:LEU:HD11	2.32	0.59
1:A:266:LEU:HD23	1:A:267:PRO:CD	2.32	0.59
1:A:1025:VAL:O	1:A:1029:THR:HG23	2.01	0.59
1:A:1354:GLU:N	1:A:1354:GLU:OE2	2.35	0.59
3:I:265:ASN:O	3:I:266:LYS:HB2	2.02	0.59
4:G:6:PHE:CZ	6:L:18:ALA:HB2	2.37	0.59
5:K:342:PHE:HB3	5:K:424:ILE:HD11	1.84	0.59
6:L:71:ASP:OD1	6:L:76:LEU:HB2	2.02	0.59
8:H:492:LEU:HD22	8:H:557:HIS:CG	2.36	0.59
27:F:97:U:H5"	27:F:97:U:H6	1.67	0.59
1:A:505:TRP:CZ3	1:A:690:LYS:HG3	2.37	0.59
1:A:1275:MET:CE	1:A:1299:LYS:CE	2.80	0.59
1:A:1450:GLU:HB3	1:A:1488:ILE:HD11	1.83	0.59
2:B:177:PRO:HB2	2:B:195:TRP:HE1	1.66	0.59
2:B:177:PRO:CD	2:B:195:TRP:CD1	2.85	0.59
4:G:863:PHE:HE2	4:G:892:LEU:CD1	2.16	0.59
6:L:81:THR:HG21	6:L:102:LYS:HZ3	1.62	0.59
1:A:1458:TRP:CZ3	1:A:1461:TYR:HD2	2.20	0.59
1:A:1857:VAL:O	1:A:1877:GLY:CA	2.49	0.59
3:I:98:PHE:CE2	3:I:217:TYR:CE2	2.91	0.59
3:I:184:LYS:HD2	3:I:186:LYS:CB	2.31	0.59
3:I:347:ALA:HB1	3:I:348:PRO:CD	2.31	0.59
5:K:350:PRO:HB3	5:K:353:ARG:HD2	1.84	0.59
7:M:125:LEU:O	7:M:126:ILE:C	2.39	0.59
2:B:177:PRO:HB2	2:B:195:TRP:NE1	2.17	0.59
3:I:98:PHE:HE2	3:I:217:TYR:CE2	2.19	0.59
8:H:332:TYR:OH	8:H:376:PHE:HD2	1.81	0.59
8:H:364:PHE:HB2	8:H:369:LYS:HG3	0.63	0.59
2:B:131:ARG:HG2	2:B:131:ARG:HH11	1.67	0.59
2:B:227:HIS:CD2	2:B:273:TYR:CE1	2.90	0.59
2:B:320:SER:CB	2:B:337:ARG:NH2	2.65	0.59
3:I:282:GLU:OE2	3:I:286:PHE:CE2	2.52	0.59
3:I:423:ALA:O	3:I:424:THR:HB	2.03	0.59
6:L:34:LYS:HD2	6:L:35:ASN:N	2.18	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ASN:OD1	1:A:300:LYS:HE2	2.01	0.59
1:A:362:GLU:OE2	1:A:1209:LYS:HE3	2.01	0.59
3:I:112:MET:CB	3:I:204:LEU:CD2	2.79	0.59
8:H:500:ARG:HD3	8:H:534:THR:CB	2.32	0.59
1:A:175:LEU:CD1	1:A:564:TRP:NE1	2.64	0.59
2:B:124:LEU:O	2:B:128:SER:N	2.31	0.59
3:I:301:GLN:OE1	3:I:344:LEU:HD13	2.01	0.59
5:K:146:GLU:O	5:K:149:PHE:N	2.33	0.59
8:H:385:PHE:O	8:H:389:LEU:HG	2.03	0.59
8:H:608:GLN:HG3	8:H:609:PRO:HD2	1.85	0.59
1:A:332:ASP:C	1:A:332:ASP:OD1	2.41	0.59
1:A:766:ILE:O	1:A:770:MET:HG2	2.03	0.59
2:B:177:PRO:CD	2:B:195:TRP:HD1	2.15	0.59
3:I:233:VAL:HG12	3:I:237:ILE:HB	1.84	0.59
3:I:393:PHE:C	3:I:393:PHE:HD1	2.05	0.59
8:H:230:ALA:HB3	8:H:473:LEU:HD13	1.84	0.59
8:H:323:THR:OG1	8:H:326:GLU:HB2	2.03	0.59
8:H:369:LYS:HE2	8:H:369:LYS:H	1.67	0.59
8:H:932:PHE:O	8:H:933:TRP:CE3	2.56	0.59
1:A:149:MET:O	1:A:153:MET:CG	2.51	0.59
1:A:316:THR:N	1:A:317:PRO:CD	2.66	0.59
1:A:390:LEU:HD13	8:H:652:MET:SD	2.42	0.59
1:A:546:LYS:O	1:A:550:SER:OG	2.18	0.59
1:A:1414:TRP:CZ3	1:A:1416:LYS:HB2	2.37	0.59
1:A:1577:LYS:NZ	3:I:397:GLU:OE2	2.36	0.59
2:B:51:VAL:HG13	2:B:76:LEU:HD12	1.85	0.59
3:I:94:LEU:HD13	3:I:98:PHE:CZ	2.38	0.59
4:G:277:ILE:HD12	4:G:277:ILE:N	2.15	0.59
5:K:141:ASN:HD21	5:K:144:LEU:CD2	2.15	0.59
5:K:249:ARG:HG2	5:K:249:ARG:HH11	1.67	0.59
6:L:75:GLU:C	6:L:76:LEU:HD12	2.24	0.59
8:H:959:ILE:HD13	8:H:960:ASN:N	2.17	0.59
27:F:44:A:C2'	27:F:45:A:C8	2.67	0.59
27:F:45:A:C2	27:F:46:C:C4	2.91	0.59
1:A:425:ASP:OD2	1:A:426:PRO:HD2	2.03	0.58
2:B:358:SER:OG	2:B:401:PHE:CZ	2.48	0.58
4:G:702:PRO:HG3	4:G:738:LEU:HB2	1.85	0.58
6:L:33:ARG:NE	6:L:64:ILE:HB	2.18	0.58
8:H:567:ILE:HD13	8:H:567:ILE:N	2.18	0.58
1:A:176:LEU:HD23	1:A:176:LEU:C	2.22	0.58
1:A:1147:PHE:CD2	1:A:1153:GLU:HG2	2.38	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1158:ILE:CG1	1:A:1172:PHE:CE1	2.86	0.58
1:A:1628:ASP:HB3	25:D:50:G:N2	2.18	0.58
2:B:405:ASP:OD2	2:B:408:LYS:CD	2.52	0.58
2:B:415:TYR:OH	7:M:126:ILE:CA	2.51	0.58
2:B:456:GLY:O	2:B:457:TRP:C	2.42	0.58
4:G:12:PRO:HB2	4:G:13:ALA:O	2.03	0.58
8:H:268:ASN:HD21	8:H:316:THR:CG2	2.17	0.58
8:H:362:LYS:HE2	8:H:365:GLU:HB2	1.84	0.58
8:H:386:SER:O	8:H:390:SER:HB3	2.03	0.58
8:H:449:PHE:CD1	8:H:453:THR:CG2	2.86	0.58
25:D:109:U:C3'	25:D:110:U:H5"	2.31	0.58
1:A:297:SER:HB3	27:F:32:G:P	2.41	0.58
2:B:115:SER:CA	2:B:118:ILE:HG13	2.32	0.58
1:A:165:LEU:CD2	1:A:730:ILE:HD11	2.29	0.58
1:A:1739:ARG:HD2	1:A:1751:TYR:CE2	2.38	0.58
1:A:1758:ASP:O	1:A:1762:ASP:HB2	2.04	0.58
1:A:1880:PHE:HE2	1:A:1889:LEU:HD21	1.57	0.58
2:B:127:TYR:OH	2:B:131:ARG:NH1	2.35	0.58
3:I:367:ARG:NH2	26:E:58:G:N7	2.52	0.58
6:L:74:TYR:CD1	6:L:83:MET:CE	2.86	0.58
8:H:191:ILE:HG23	8:H:221:PHE:CE1	2.38	0.58
8:H:881:LYS:HA	8:H:886:SER:HB2	1.84	0.58
1:A:168:LEU:CA	1:A:199:ILE:CD1	2.81	0.58
1:A:506:PHE:HA	1:A:522:TYR:CD1	2.39	0.58
1:A:1664:ASP:O	1:A:1668:ILE:HG13	2.04	0.58
1:A:1854:ASP:OD1	1:A:1879:ILE:HG23	2.04	0.58
5:K:363:LEU:HD11	5:K:391:PHE:HD2	1.68	0.58
8:H:145:GLY:N	28:H:1500:GTP:O2B	2.31	0.58
8:H:476:VAL:CG1	8:H:478:TYR:CD1	2.85	0.58
8:H:780:PRO:HA	8:H:783:ILE:HB	1.85	0.58
3:I:113:HIS:HD2	3:I:134:PRO:HA	1.68	0.58
1:A:1496:GLN:O	1:A:1499:ARG:CG	2.51	0.58
2:B:446:SER:HB2	2:B:451:PHE:N	2.16	0.58
4:G:630:SER:CA	4:G:670:PHE:HZ	2.16	0.58
4:G:849:TYR:O	4:G:853:GLY:N	2.35	0.58
7:M:8:ALA:HA	7:M:80:PHE:CE2	2.38	0.58
8:H:572:ILE:HD12	8:H:572:ILE:O	2.03	0.58
24:C:-1:A:N3	24:C:-1:A:H2'	2.18	0.58
1:A:255:ILE:O	1:A:258:ILE:HG22	2.03	0.58
1:A:457:ASP:OD1	1:A:457:ASP:N	2.37	0.58
1:A:839:HIS:NE2	27:F:96:U:C4	2.71	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1998:ARG:O	1:A:1999:ILE:CG1	2.44	0.58
3:I:282:GLU:HG2	3:I:286:PHE:CD1	2.36	0.58
6:L:133:SER:OG	6:L:135:TYR:O	2.20	0.58
8:H:307:ILE:CD1	8:H:324:ILE:CD1	2.81	0.58
8:H:369:LYS:HE2	8:H:369:LYS:CA	2.33	0.58
8:H:489:TYR:CE2	8:H:592:PHE:HE1	2.20	0.58
8:H:862:TYR:HD2	8:H:930:LEU:HB3	1.67	0.58
1:A:149:MET:CG	1:A:154:TYR:HE2	2.16	0.58
1:A:286:LEU:O	1:A:287:GLU:O	2.22	0.58
1:A:1256:PRO:CA	1:A:1274:ARG:HH21	2.12	0.58
1:A:1313:ASP:OD2	1:A:1359:ILE:HD13	2.03	0.58
5:K:295:LYS:O	5:K:299:ASP:HB2	2.04	0.58
8:H:296:ASN:HD21	8:H:304:PHE:N	2.00	0.58
8:H:507:SER:O	8:H:510:ARG:N	2.37	0.58
1:A:249:LEU:HD23	1:A:249:LEU:H	1.69	0.58
1:A:261:LEU:C	1:A:261:LEU:HD12	2.23	0.58
1:A:1751:TYR:CE1	1:A:1755:LYS:CD	2.77	0.58
2:B:197:GLY:C	2:B:221:ILE:HD11	2.24	0.58
3:I:421:VAL:HG21	4:G:250:LEU:CD1	2.33	0.58
4:G:278:TRP:HA	4:G:278:TRP:CE3	2.38	0.58
4:G:401:ILE:O	4:G:405:SER:N	2.35	0.58
4:G:672:LEU:HD23	4:G:704:LEU:HD23	1.45	0.58
4:G:697:LEU:N	4:G:697:LEU:HD23	2.17	0.58
1:A:1073:ILE:CG2	1:A:1074:VAL:HG23	2.29	0.57
1:A:1308:GLU:OE1	1:A:1346:PHE:HZ	1.87	0.57
2:B:286:ASP:C	2:B:287:MET:CG	2.72	0.57
4:G:248:ALA:HB1	4:G:264:ILE:HD11	1.86	0.57
4:G:867:GLU:OE2	4:G:888:PRO:CG	2.52	0.57
8:H:354:TYR:HA	8:H:359:PHE:CB	2.33	0.57
8:H:489:TYR:HE2	8:H:592:PHE:HE1	1.52	0.57
8:H:586:MET:CA	8:H:589:LEU:HD23	2.33	0.57
26:E:19:U:O2'	26:E:20:A:OP2	2.21	0.57
1:A:552:LYS:HG3	1:A:553:ASN:N	2.19	0.57
1:A:1256:PRO:CA	1:A:1274:ARG:NH2	2.67	0.57
2:B:264:HIS:HE1	2:B:290:ARG:HD2	1.69	0.57
2:B:278:LYS:C	2:B:279:PHE:HD1	2.08	0.57
4:G:764:LEU:O	4:G:768:PRO:HB3	2.04	0.57
4:G:846:PHE:CE1	4:G:859:LEU:HD23	2.36	0.57
8:H:349:TRP:CZ3	8:H:373:PHE:CE2	2.92	0.57
8:H:353:TYR:O	8:H:359:PHE:HB2	2.04	0.57
8:H:500:ARG:HG2	8:H:534:THR:CG2	2.33	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:833:ARG:HH21	1:A:840:VAL:HG23	1.69	0.57
2:B:124:LEU:C	2:B:128:SER:HG	2.01	0.57
2:B:443:LEU:HD11	2:B:452:LEU:HD11	1.86	0.57
3:I:147:GLU:CD	3:I:147:GLU:H	2.07	0.57
1:A:1283:GLU:HG2	1:A:1351:VAL:HB	1.84	0.57
4:G:170:LEU:C	4:G:170:LEU:HD13	2.24	0.57
6:L:119:THR:HG22	6:L:131:VAL:CG1	2.35	0.57
8:H:336:ILE:HG13	8:H:341:ILE:HG22	1.85	0.57
2:B:127:TYR:CE2	2:B:276:SER:HA	2.38	0.57
2:B:131:ARG:HG2	2:B:131:ARG:NH1	2.18	0.57
3:I:189:LEU:HD23	3:I:193:THR:OG1	2.03	0.57
3:I:346:GLU:O	3:I:347:ALA:CB	2.53	0.57
4:G:695:THR:CB	4:G:705:TRP:NE1	2.57	0.57
5:K:163:ASN:O	5:K:164:HIS:HB3	2.03	0.57
8:H:129:ILE:H	8:H:129:ILE:CD1	2.18	0.57
27:F:78:A:HO2’	27:F:79:C:C5’	2.10	0.57
1:A:251:TYR:CE2	1:A:566:GLU:OE1	2.58	0.57
1:A:1049:LEU:HD13	1:A:1260:PHE:HB3	1.87	0.57
1:A:2007:ARG:NH2	5:K:291:THR:OG1	2.35	0.57
3:I:217:TYR:O	3:I:220:SER:OG	2.18	0.57
5:K:144:LEU:HD22	5:K:144:LEU:H	1.69	0.57
6:L:74:TYR:HB2	6:L:76:LEU:HD11	1.86	0.57
8:H:132:ARG:NH2	8:H:206:LYS:HG3	2.19	0.57
8:H:369:LYS:H	8:H:369:LYS:CE	2.16	0.57
8:H:580:VAL:HG11	8:H:586:MET:HG2	1.85	0.57
1:A:224:MET:CE	1:A:702:GLY:HA3	2.34	0.57
1:A:301:TRP:CE2	1:A:491:GLY:HA3	2.40	0.57
4:G:698:VAL:N	4:G:699:PRO:HD3	2.20	0.57
8:H:227:VAL:CG1	8:H:474:LYS:HG3	2.25	0.57
8:H:306:PRO:O	8:H:324:ILE:HD13	2.04	0.57
1:A:258:ILE:O	1:A:259:GLU:CB	2.53	0.57
1:A:430:PRO:O	1:A:431:ILE:HG22	2.05	0.57
3:I:155:ASP:N	3:I:155:ASP:OD1	2.35	0.57
3:I:344:LEU:HD23	3:I:344:LEU:N	2.20	0.57
4:G:678:TYR:CZ	4:G:686:MET:HG2	2.40	0.57
4:G:846:PHE:CB	4:G:896:MET:SD	2.93	0.57
6:L:22:GLU:OE2	6:L:58:VAL:HG11	2.04	0.57
7:M:39:GLU:HB2	26:E:32:G:O6	2.05	0.57
8:H:488:ILE:HD13	8:H:560:GLN:HG2	1.81	0.57
1:A:165:LEU:CD2	1:A:726:ILE:HG21	2.35	0.57
1:A:543:ASN:ND2	1:A:544:LYS:N	2.53	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2068:ASN:N	1:A:2068:ASN:OD1	2.38	0.57
4:G:9:GLN:C	4:G:10:GLU:HG3	2.24	0.57
8:H:697:ARG:HA	8:H:697:ARG:CZ	2.35	0.57
27:F:99:U:HO2'	27:F:100:A:P	2.23	0.57
1:A:358:ARG:HD2	1:A:360:GLU:HB2	1.87	0.57
1:A:367:PHE:C	1:A:367:PHE:CD1	2.78	0.57
1:A:982:TYR:HB2	1:A:1106:GLY:HA3	1.87	0.57
1:A:1378:LYS:O	1:A:1379:MET:CB	2.53	0.57
1:A:1711:VAL:HG13	1:A:1789:ASN:HB3	1.87	0.57
8:H:133:ILE:O	8:H:134:ILE:HG22	2.01	0.57
8:H:251:GLN:HG2	8:H:933:TRP:CE2	2.39	0.57
8:H:331:TYR:HE1	8:H:404:PHE:HD1	1.50	0.57
8:H:468:LEU:CD1	8:H:493:LEU:HD23	2.35	0.57
1:A:299:LYS:HA	1:A:493:MET:CG	2.33	0.56
1:A:389:HIS:HB2	8:H:653:ASP:OD1	2.05	0.56
1:A:1020:ILE:HD13	1:A:1488:ILE:HG21	1.87	0.56
1:A:1158:ILE:HG13	1:A:1172:PHE:CE1	2.40	0.56
2:B:362:TYR:HB2	2:B:379:ARG:HD2	1.85	0.56
3:I:158:PHE:CA	3:I:161:LEU:HD12	2.34	0.56
8:H:251:GLN:HG2	8:H:933:TRP:CZ2	2.40	0.56
8:H:307:ILE:HD13	8:H:324:ILE:CD1	2.35	0.56
8:H:599:THR:HG23	8:H:933:TRP:CZ3	2.40	0.56
1:A:219:ALA:O	1:A:266:LEU:HD11	2.05	0.56
1:A:1073:ILE:HG23	1:A:1074:VAL:CG2	2.33	0.56
1:A:1464:LYS:C	1:A:1475:LEU:HD21	2.25	0.56
3:I:191:ILE:HD12	3:I:191:ILE:N	2.14	0.56
3:I:455:PHE:O	3:I:458:SER:OG	2.19	0.56
4:G:296:VAL:HG12	4:G:300:ILE:HD12	1.86	0.56
5:K:146:GLU:CA	5:K:149:PHE:HD2	2.18	0.56
27:F:103:A:O2'	27:F:104:G:P	2.63	0.56
1:A:170:HIS:ND1	1:A:547:LEU:CD2	2.68	0.56
1:A:180:PRO:HA	1:A:187:LYS:HD2	1.87	0.56
1:A:208:VAL:HG22	1:A:494:VAL:O	2.05	0.56
1:A:224:MET:HE2	1:A:702:GLY:HA3	1.86	0.56
1:A:325:LYS:HA	1:A:325:LYS:CE	2.35	0.56
1:A:770:MET:CE	1:A:778:LYS:CB	2.84	0.56
1:A:779:ALA:O	1:A:782:ILE:HB	2.04	0.56
1:A:909:THR:HG22	1:A:910:LYS:N	2.20	0.56
1:A:1038:ILE:HD11	1:A:1039:TRP:CE2	2.39	0.56
1:A:1498:ASP:HB2	4:G:159:LEU:HB2	1.86	0.56
1:A:1628:ASP:CB	25:D:50:G:N2	2.68	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:227:PRO:HG3	3:I:325:ARG:HB3	1.86	0.56
3:I:418:GLN:NE2	3:I:425:SER:HB2	2.20	0.56
5:K:296:VAL:O	5:K:300:GLN:HB2	2.05	0.56
6:L:53:VAL:CG1	6:L:57:ALA:HB3	2.35	0.56
6:L:82:VAL:HB	6:L:103:LEU:HB3	1.87	0.56
6:L:116:ILE:HD12	6:L:137:TYR:OH	2.02	0.56
8:H:146:LYS:CE	28:H:1500:GTP:O3G	2.51	0.56
8:H:268:ASN:HD21	8:H:316:THR:HG23	1.69	0.56
8:H:328:VAL:O	8:H:333:ALA:N	2.38	0.56
8:H:476:VAL:HG11	8:H:478:TYR:CD1	2.40	0.56
25:D:49:A:N6	25:D:50:G:C5	2.73	0.56
1:A:1115:GLN:HA	1:A:1115:GLN:NE2	2.20	0.56
1:A:1773:VAL:HG22	1:A:1788:GLY:HA2	1.86	0.56
8:H:328:VAL:HG21	8:H:345:THR:HG22	1.87	0.56
8:H:468:LEU:CD2	8:H:577:LEU:CD2	2.80	0.56
8:H:495:ARG:NH2	8:H:541:GLU:OE2	2.38	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CB	2.80	0.56
24:C:-3:A:C8	24:C:-2:A:N6	2.73	0.56
1:A:272:ASP:HB2	1:A:273:ASP:OD1	2.05	0.56
1:A:1275:MET:O	1:A:1277:GLU:O	2.24	0.56
1:A:1364:GLU:O	1:A:1368:GLN:HG3	2.06	0.56
1:A:2050:THR:O	1:A:2053:SER:OG	2.20	0.56
2:B:192:THR:CB	2:B:461:ILE:HD11	2.35	0.56
5:K:300:GLN:OE1	5:K:300:GLN:HA	2.06	0.56
7:M:95:ARG:CG	7:M:96:PRO:HD2	2.36	0.56
8:H:307:ILE:HA	8:H:324:ILE:HD11	1.87	0.56
8:H:369:LYS:HE2	8:H:369:LYS:N	2.20	0.56
8:H:489:TYR:CE2	8:H:592:PHE:CZ	2.94	0.56
9:N:461:ASP:O	9:N:709:GLY:N	2.35	0.56
25:D:86:G:H5"	25:D:86:G:C8	2.32	0.56
27:F:41:A:H5'	27:F:41:A:H8	1.71	0.56
1:A:273:ASP:HB3	1:A:276:VAL:HG22	1.86	0.56
2:B:115:SER:O	2:B:118:ILE:HB	2.06	0.56
2:B:127:TYR:HE2	2:B:276:SER:HB2	1.63	0.56
8:H:132:ARG:HH21	8:H:206:LYS:CD	2.18	0.56
1:A:406:PRO:HG2	28:H:1500:GTP:O2'	2.04	0.56
2:B:162:MET:CG	2:B:421:VAL:HG11	2.35	0.56
3:I:95:LEU:HA	3:I:98:PHE:HB2	1.88	0.56
3:I:217:TYR:HE1	3:I:221:LYS:CE	2.18	0.56
4:G:671:PHE:HZ	4:G:693:SER:OG	1.86	0.56
6:L:109:ASP:OD1	6:L:110:LYS:N	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:M:11:LEU:HD23	7:M:12:ALA:O	2.06	0.56
8:H:582:SER:CB	8:H:585:ASP:HB2	2.28	0.56
8:H:901:GLU:OE2	8:H:903:ARG:CZ	2.53	0.56
25:D:46:U:H2'	25:D:47:A:H8	1.69	0.56
1:A:148:ASP:OD1	1:A:148:ASP:N	2.38	0.56
1:A:360:GLU:OE1	1:A:360:GLU:HA	2.06	0.56
1:A:371:ASP:OD2	8:H:972:ARG:NH1	2.38	0.56
1:A:1379:MET:HG3	1:A:1380:PRO:HD2	1.87	0.56
8:H:118:TYR:CD1	8:H:119:ASN:N	2.74	0.56
1:A:165:LEU:CD1	1:A:578:MET:HB3	2.35	0.56
2:B:206:THR:O	2:B:207:LEU:HB2	2.05	0.56
3:I:95:LEU:HD23	3:I:98:PHE:HD2	1.69	0.56
4:G:288:ASP:OD1	4:G:291:TYR:HB2	2.05	0.56
8:H:341:ILE:O	8:H:344:PHE:HB3	2.06	0.56
1:A:167:TYR:N	1:A:167:TYR:CD1	2.73	0.56
1:A:176:LEU:O	1:A:179:MET:HG3	2.06	0.56
1:A:749:ARG:HD2	1:A:750:LEU:N	2.20	0.56
1:A:1389:TYR:CE2	1:A:1401:SER:HB3	2.40	0.56
2:B:320:SER:HB2	2:B:337:ARG:NH1	2.21	0.56
8:H:572:ILE:CD1	8:H:573:LYS:HG3	2.28	0.56
8:H:862:TYR:CE1	8:H:908:VAL:CG2	2.89	0.56
25:D:77:G:N2	26:E:4:C:O2	2.29	0.56
1:A:428:LEU:CD1	8:H:279:LEU:HD11	2.36	0.55
1:A:549:LYS:HG2	27:F:35:A:H5'	1.88	0.55
1:A:770:MET:CE	1:A:778:LYS:HB2	2.37	0.55
2:B:348:HIS:CD2	2:B:374:ASN:ND2	2.74	0.55
4:G:526:TYR:O	4:G:530:GLU:N	2.35	0.55
4:G:804:ASP:CG	4:G:805:HIS:H	2.10	0.55
1:A:355:LEU:HD13	1:A:355:LEU:C	2.26	0.55
1:A:939:LEU:HD11	3:I:441:MET:HE1	1.87	0.55
1:A:1400:ILE:HG22	1:A:1401:SER:N	2.21	0.55
1:A:1601:ILE:N	1:A:1602:PRO:HD2	2.22	0.55
1:A:2041:PRO:HG2	1:A:2043:PHE:CE2	2.41	0.55
3:I:329:LEU:HD12	3:I:333:TRP:CZ2	2.41	0.55
8:H:483:TRP:CZ3	8:H:565:LYS:CG	2.89	0.55
8:H:862:TYR:CZ	8:H:908:VAL:HG23	2.41	0.55
9:N:1795:SER:O	9:N:1798:GLY:N	2.39	0.55
27:F:33:U:O2	27:F:33:U:H2'	2.05	0.55
27:F:44:A:N1	27:F:71:A:N1	2.54	0.55
1:A:149:MET:O	1:A:153:MET:HG2	2.07	0.55
1:A:749:ARG:HD2	1:A:750:LEU:H	1.71	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:ASP:OD2	1:A:1109:PHE:CE2	2.60	0.55
2:B:389:ILE:HD12	2:B:427:TRP:O	2.05	0.55
8:H:229:LEU:HD21	8:H:235:VAL:HG11	1.87	0.55
25:D:48:C:C4'	25:D:49:A:OP1	2.52	0.55
27:F:78:A:N1	27:F:81:A:C8	2.74	0.55
27:F:95:C:H4'	27:F:96:U:OP1	2.05	0.55
1:A:503:LYS:HA	1:A:506:PHE:CE1	2.38	0.55
1:A:849:LEU:HG	1:A:973:GLU:HB3	1.88	0.55
1:A:1653:LEU:O	1:A:1657:ILE:HG13	2.05	0.55
1:A:1831:GLN:HG2	1:A:1832:GLU:N	2.20	0.55
4:G:282:ILE:O	4:G:286:GLU:CG	2.51	0.55
4:G:298:THR:O	4:G:302:PHE:HD2	1.88	0.55
8:H:332:TYR:CE2	8:H:376:PHE:HB3	2.41	0.55
8:H:605:ILE:CG1	8:H:652:MET:SD	2.92	0.55
25:D:44:A:H2'	25:D:45:A:H8	1.71	0.55
1:A:382:GLU:OE1	1:A:382:GLU:N	2.34	0.55
1:A:1065:LEU:HD23	1:A:1065:LEU:O	2.06	0.55
2:B:360:ASN:CB	2:B:362:TYR:HE1	2.20	0.55
4:G:695:THR:O	4:G:699:PRO:HD3	2.06	0.55
8:H:380:PRO:HA	8:H:383:LYS:HG3	1.88	0.55
8:H:430:ARG:O	8:H:431:GLN:O	2.23	0.55
8:H:586:MET:O	8:H:589:LEU:CD2	2.52	0.55
8:H:951:ILE:CD1	8:H:955:LYS:HB2	2.37	0.55
1:A:536:PRO:HG2	27:F:76:U:O4	2.06	0.55
1:A:1356:LEU:O	1:A:1356:LEU:HD22	2.06	0.55
1:A:1882:LEU:C	1:A:1882:LEU:HD22	2.26	0.55
1:A:2065:ARG:CD	1:A:2066:LYS:HE2	2.36	0.55
2:B:389:ILE:CD1	2:B:427:TRP:O	2.54	0.55
8:H:468:LEU:HB3	8:H:579:SER:HB3	1.89	0.55
8:H:506:GLN:O	8:H:509:SER:CB	2.49	0.55
1:A:160:ALA:CB	1:A:194:HIS:CE1	2.89	0.55
1:A:456:GLU:CD	1:A:456:GLU:H	1.97	0.55
1:A:1163:ARG:NH1	1:A:1165:LEU:O	2.39	0.55
1:A:1341:SER:HA	1:A:1525:PHE:HE1	1.72	0.55
2:B:166:GLU:O	2:B:465:ASN:N	2.39	0.55
3:I:135:LEU:HD23	3:I:135:LEU:C	2.25	0.55
5:K:350:PRO:HB3	25:D:84:C:C6	2.41	0.55
5:K:452:LEU:HB3	5:K:461:GLU:HG2	1.88	0.55
8:H:387:TYR:HB3	8:H:396:LEU:HD21	1.88	0.55
8:H:564:ILE:HG21	8:H:567:ILE:CG1	2.36	0.55
1:A:297:SER:CB	27:F:32:G:P	2.95	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:VAL:CB	1:A:327:TYR:CD2	2.90	0.55
1:A:672:LYS:O	1:A:674:MET:N	2.39	0.55
1:A:770:MET:HE2	1:A:775:ARG:O	2.06	0.55
1:A:1074:VAL:HG12	1:A:1075:ASP:N	2.21	0.55
2:B:141:GLU:OE1	2:B:141:GLU:HA	2.07	0.55
4:G:161:LYS:HA	4:G:161:LYS:HE3	1.89	0.55
5:K:332:GLU:O	5:K:332:GLU:HG2	2.05	0.55
8:H:272:ARG:HG3	8:H:276:ASP:HB2	1.89	0.55
25:D:51:A:O2'	25:D:52:G:O5'	2.22	0.55
1:A:1038:ILE:CD1	1:A:1039:TRP:CD2	2.90	0.55
2:B:446:SER:HB2	2:B:451:PHE:HB2	1.89	0.55
6:L:140:LYS:CB	6:L:141:ARG:HD2	2.32	0.55
8:H:354:TYR:HA	8:H:359:PHE:CA	2.35	0.55
8:H:474:LYS:HZ2	8:H:630:PRO:HD3	1.71	0.55
1:A:150:ALA:O	1:A:153:MET:HG2	2.07	0.55
1:A:1389:TYR:HE2	1:A:1401:SER:HB3	1.72	0.55
1:A:1559:HIS:O	1:A:1612:PRO:HG2	2.07	0.55
1:A:1627:LEU:HB2	1:A:1630:THR:OG1	2.07	0.55
2:B:275:PRO:HG3	2:B:319:GLY:CA	2.37	0.55
2:B:363:GLN:HG2	2:B:377:ASP:HB3	1.89	0.55
2:B:452:LEU:HB3	2:B:464:TRP:HB2	1.89	0.55
3:I:282:GLU:OE1	3:I:286:PHE:CZ	2.60	0.55
4:G:230:LEU:CD1	4:G:247:SER:HA	2.25	0.55
4:G:691:TYR:CD2	4:G:711:ILE:CD1	2.90	0.55
5:K:289:ASP:HB3	5:K:292:ALA:HB3	1.89	0.55
8:H:461:LYS:HD2	8:H:462:SER:N	2.22	0.55
8:H:829:VAL:O	8:H:829:VAL:HG12	2.07	0.55
1:A:373:VAL:O	8:H:969:LYS:HG2	2.07	0.54
1:A:867:ILE:HD13	1:A:1101:TYR:CD1	2.42	0.54
1:A:1458:TRP:HZ3	1:A:1461:TYR:CE2	2.24	0.54
2:B:441:ILE:HD11	2:B:457:TRP:CD1	2.41	0.54
3:I:338:SER:O	3:I:342:ARG:HG3	2.07	0.54
4:G:104:PHE:O	4:G:105:ALA:C	2.45	0.54
8:H:132:ARG:C	8:H:133:ILE:HG23	2.27	0.54
8:H:337:PRO:O	8:H:341:ILE:HG23	2.07	0.54
1:A:1910:LYS:HG3	1:A:1911:TRP:N	2.22	0.54
3:I:146:ASN:HD21	3:I:148:ASN:ND2	2.04	0.54
3:I:418:GLN:HE22	3:I:425:SER:HB2	1.71	0.54
6:L:140:LYS:HB3	6:L:141:ARG:HH11	1.70	0.54
8:H:303:VAL:HG23	8:H:303:VAL:O	2.07	0.54
8:H:968:MET:CE	8:H:968:MET:CA	2.85	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:ILE:HD12	1:A:410:ILE:N	2.22	0.54
2:B:206:THR:CG2	2:B:208:GLN:HE22	2.21	0.54
3:I:267:HIS:HE1	3:I:273:HIS:CE1	2.25	0.54
3:I:433:ASN:ND2	3:I:433:ASN:H	2.04	0.54
4:G:528:LYS:O	4:G:532:LEU:N	2.39	0.54
4:G:668:HIS:NE2	4:G:669:LYS:HG3	2.21	0.54
8:H:379:ILE:CG2	8:H:383:LYS:CE	2.86	0.54
8:H:582:SER:HB3	8:H:585:ASP:OD2	2.03	0.54
8:H:767:SER:OG	8:H:796:ILE:HD11	2.07	0.54
1:A:256:GLU:HG3	1:A:257:ASN:N	2.22	0.54
1:A:770:MET:SD	4:G:119:TRP:CZ3	3.01	0.54
1:A:1892:LYS:HD2	1:A:1916:GLU:CD	2.28	0.54
2:B:135:ARG:NH2	5:K:167:GLU:OE2	2.40	0.54
4:G:688:ARG:O	4:G:692:LEU:HG	2.07	0.54
4:G:696:ARG:C	4:G:699:PRO:CD	2.74	0.54
8:H:564:ILE:HG21	8:H:567:ILE:HG12	1.89	0.54
25:D:87:U:P	25:D:87:U:H3'	2.47	0.54
27:F:40:C:H3'	27:F:40:C:P	2.48	0.54
1:A:293:VAL:HG22	1:A:294:ASN:N	2.22	0.54
1:A:296:THR:HG22	27:F:33:U:OP2	2.06	0.54
1:A:363:ASP:N	1:A:363:ASP:OD1	2.39	0.54
1:A:413:ASN:ND2	1:A:413:ASN:H	2.06	0.54
1:A:1805:ILE:HG23	1:A:1809:ASN:HD21	1.72	0.54
4:G:846:PHE:HB2	4:G:896:MET:SD	2.48	0.54
1:A:221:TRP:CZ2	1:A:691:PHE:HB3	2.42	0.54
1:A:264:ILE:O	1:A:265:ASN:HB2	2.08	0.54
1:A:860:GLU:HA	1:A:860:GLU:OE1	2.07	0.54
3:I:191:ILE:H	3:I:191:ILE:CD1	2.14	0.54
5:K:141:ASN:OD1	5:K:144:LEU:HD23	2.08	0.54
8:H:470:ALA:CB	8:H:486:VAL:HG21	2.19	0.54
8:H:810:GLU:OE2	8:H:974:LYS:CB	2.56	0.54
1:A:158:LYS:HG2	1:A:159:LYS:N	2.23	0.54
1:A:1995:TRP:CZ3	1:A:2007:ARG:HD2	2.43	0.54
2:B:161:ARG:O	2:B:165:LEU:HD21	2.07	0.54
4:G:863:PHE:CE2	4:G:892:LEU:HD11	2.43	0.54
5:K:249:ARG:HG2	5:K:249:ARG:NH1	2.22	0.54
5:K:276:ASN:OD1	25:D:61:C:OP1	2.26	0.54
8:H:589:LEU:HD11	8:H:591:PHE:CE1	2.43	0.54
8:H:944:VAL:CG2	8:H:945:LEU:HG	2.37	0.54
27:F:74:U:C5'	27:F:74:U:H6	2.20	0.54
6:L:72:GLU:OE2	6:L:72:GLU:HA	2.08	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:140:LYS:HG2	6:L:141:ARG:CZ	2.37	0.54
25:D:78:G:C2	26:E:4:C:C2	2.96	0.54
1:A:322:VAL:HB	1:A:327:TYR:CD2	2.42	0.54
2:B:64:VAL:HG12	2:B:65:GLU:N	2.20	0.54
2:B:415:TYR:CD2	2:B:439:LYS:HD3	2.42	0.54
3:I:392:GLU:HB2	3:I:412:MET:SD	2.48	0.54
4:G:842:TRP:HA	4:G:845:LEU:HD12	1.90	0.54
8:H:769:TYR:CE1	8:H:799:PHE:CD2	2.96	0.54
8:H:862:TYR:HE1	8:H:908:VAL:CG2	2.20	0.54
27:F:31:G:C2	27:F:32:G:C1'	2.89	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CD	2.38	0.54
6:L:105:PHE:HB2	6:L:141:ARG:CG	2.25	0.54
8:H:502:LEU:O	8:H:575:ALA:HB1	2.08	0.54
27:F:78:A:C6	27:F:81:A:C8	2.95	0.54
1:A:266:LEU:CD2	1:A:267:PRO:HD2	2.33	0.53
1:A:614:ARG:NH1	24:C:3:A:OP1	2.41	0.53
1:A:1038:ILE:HD11	1:A:1039:TRP:CZ3	2.44	0.53
2:B:267:ARG:HG3	2:B:285:HIS:CD2	2.42	0.53
2:B:279:PHE:N	2:B:279:PHE:CD1	2.76	0.53
3:I:257:CYS:HB2	26:E:42:C:H41	1.72	0.53
3:I:421:VAL:O	3:I:421:VAL:HG12	2.06	0.53
5:K:455:LEU:C	5:K:457:GLN:OE1	2.47	0.53
8:H:177:TYR:C	8:H:178:LEU:HD23	2.29	0.53
8:H:578:TYR:CD2	8:H:589:LEU:HD13	2.43	0.53
24:C:7:A:HO2'	24:C:8:U:P	2.26	0.53
27:F:72:C:H2'	27:F:73:U:H6	1.73	0.53
1:A:166:LYS:HE3	1:A:723:GLU:HB3	1.90	0.53
1:A:176:LEU:HD21	1:A:708:TRP:CD1	2.43	0.53
1:A:1379:MET:HG3	1:A:1380:PRO:CD	2.39	0.53
1:A:1586:GLN:HG2	1:A:1595:ARG:NH1	2.23	0.53
2:B:201:VAL:C	2:B:202:LEU:HD12	2.28	0.53
4:G:891:ILE:O	4:G:892:LEU:C	2.45	0.53
5:K:167:GLU:HB3	5:K:169:TRP:CE3	2.43	0.53
6:L:33:ARG:HE	6:L:64:ILE:HB	1.73	0.53
8:H:307:ILE:CD1	8:H:345:THR:O	2.55	0.53
8:H:331:TYR:OH	8:H:428:ILE:CG2	2.57	0.53
8:H:494:LYS:HE2	8:H:555:GLU:OE1	2.08	0.53
24:C:11:A:C2'	24:C:12:U:H5'	2.39	0.53
1:A:167:TYR:O	1:A:201:PHE:HE1	1.91	0.53
1:A:284:ARG:NH1	27:F:33:U:O4	2.40	0.53
7:M:60:PRO:HB2	7:M:62:GLU:OE1	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:862:TYR:CD2	8:H:930:LEU:HB3	2.42	0.53
27:F:31:G:C2	27:F:32:G:N9	2.76	0.53
1:A:168:LEU:CB	1:A:199:ILE:HD11	2.38	0.53
1:A:1880:PHE:HE1	1:A:1882:LEU:HD12	1.71	0.53
5:K:167:GLU:HB3	5:K:169:TRP:HE3	1.73	0.53
8:H:114:PRO:O	8:H:115:LYS:O	2.27	0.53
8:H:447:GLU:HA	8:H:447:GLU:OE2	2.08	0.53
8:H:468:LEU:CD2	8:H:577:LEU:HD21	2.23	0.53
8:H:873:LEU:HB3	8:H:874:PRO:HD3	1.90	0.53
1:A:755:ASP:OD2	1:A:819:LYS:HE3	2.08	0.53
3:I:123:ARG:O	3:I:183:PHE:CB	2.56	0.53
1:A:469:ILE:O	1:A:470:LEU:HD22	2.09	0.53
1:A:674:MET:CE	1:A:678:ARG:HD3	2.38	0.53
1:A:2074:LEU:N	1:A:2074:LEU:HD23	2.22	0.53
2:B:199:LEU:HD23	2:B:199:LEU:H	1.73	0.53
2:B:322:VAL:HG13	2:B:334:TRP:HB2	1.91	0.53
2:B:360:ASN:HB3	2:B:362:TYR:CD1	2.44	0.53
4:G:292:CYS:O	4:G:296:VAL:HG23	2.09	0.53
4:G:708:LEU:HD22	4:G:725:ILE:HG21	1.90	0.53
8:H:113:ILE:CG2	8:H:114:PRO:HD2	2.34	0.53
8:H:599:THR:HG22	8:H:933:TRP:CZ3	2.43	0.53
8:H:677:PHE:HE1	8:H:966:PHE:HE2	1.45	0.53
8:H:697:ARG:NE	8:H:697:ARG:CA	2.71	0.53
26:E:19:U:C6	26:E:19:U:H3'	2.44	0.53
1:A:239:PHE:O	1:A:240:PRO:C	2.47	0.53
1:A:468:LEU:N	1:A:468:LEU:HD12	2.24	0.53
1:A:837:GLY:C	1:A:1317:ARG:NH1	2.62	0.53
1:A:1500:HIS:HB2	4:G:160:ASN:HD21	1.74	0.53
2:B:75:ARG:HG2	2:B:75:ARG:HH21	1.74	0.53
3:I:357:PRO:O	3:I:358:ILE:HG13	2.08	0.53
4:G:158:ASP:OD1	4:G:158:ASP:N	2.40	0.53
4:G:688:ARG:NH1	4:G:721:ARG:NE	2.54	0.53
4:G:691:TYR:CD2	4:G:711:ILE:HD12	2.44	0.53
25:D:49:A:C2'	25:D:50:G:C5'	2.84	0.53
1:A:954:ILE:HG23	1:A:991:THR:HG22	1.89	0.53
2:B:176:LYS:HB2	2:B:194:SER:OG	2.09	0.53
4:G:672:LEU:HD21	4:G:704:LEU:HG	1.83	0.53
4:G:846:PHE:HB3	4:G:896:MET:SD	2.49	0.53
8:H:504:THR:OG1	8:H:594:PRO:HG3	2.09	0.53
27:F:64:C:H2'	27:F:65:U:H6	1.74	0.53
27:F:73:U:C3'	27:F:74:U:C5'	2.87	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:PHE:CE1	1:A:249:LEU:HD21	2.44	0.53
1:A:774:ILE:HD12	1:A:774:ILE:N	2.24	0.53
1:A:944:TYR:O	4:G:166:ARG:NH1	2.41	0.53
2:B:162:MET:HE2	2:B:162:MET:N	2.24	0.53
4:G:104:PHE:O	4:G:106:ASP:N	2.41	0.53
8:H:227:VAL:HG11	8:H:474:LYS:CB	2.39	0.53
1:A:166:LYS:HD3	1:A:167:TYR:CZ	2.43	0.53
1:A:1125:LEU:HD21	1:A:1234:VAL:HG23	1.90	0.53
1:A:2065:ARG:HD2	1:A:2066:LYS:HE2	1.91	0.53
3:I:358:ILE:HG22	3:I:360:GLU:N	2.24	0.53
4:G:170:LEU:HD13	4:G:171:GLN:N	2.24	0.53
8:H:176:ARG:O	8:H:548:ARG:NH2	2.41	0.53
8:H:326:GLU:OE1	8:H:330:TYR:CD2	2.61	0.53
8:H:488:ILE:CD1	8:H:557:HIS:O	2.51	0.53
1:A:721:LEU:HD11	27:F:85:U:O2’	2.09	0.52
1:A:1511:ARG:NH2	1:A:1511:ARG:HG3	2.24	0.52
3:I:82:ARG:O	3:I:86:GLN:N	2.35	0.52
3:I:257:CYS:SG	26:E:44:G:O6	2.61	0.52
4:G:630:SER:HA	4:G:670:PHE:HZ	1.72	0.52
5:K:349:ASN:HB2	5:K:406:PHE:CD1	2.44	0.52
6:L:33:ARG:HD3	6:L:65:ASP:N	2.24	0.52
8:H:265:PHE:HE2	8:H:295:ILE:HB	1.73	0.52
1:A:881:THR:O	1:A:885:VAL:HG23	2.08	0.52
1:A:928:ARG:HH21	4:G:145:THR:CG2	2.17	0.52
1:A:1262:MET:O	1:A:1263:CYS:HB2	2.09	0.52
2:B:316:GLN:O	2:B:316:GLN:NE2	2.42	0.52
4:G:126:THR:HB	4:G:128:PHE:CZ	2.44	0.52
4:G:666:ILE:CG2	4:G:667:CYS:H	2.18	0.52
25:D:64:U:H5”	25:D:64:U:H6	1.74	0.52
1:A:778:LYS:HA	1:A:778:LYS:HE2	1.90	0.52
1:A:921:ASP:HB3	3:I:403:SER:HB2	1.91	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CE1	2.45	0.52
1:A:1468:ALA:O	1:A:1473:ARG:N	2.37	0.52
1:A:1699:ALA:HA	1:A:1735:ASP:OD1	2.09	0.52
3:I:327:THR:O	3:I:328:VAL:HG23	2.09	0.52
3:I:347:ALA:HA	4:G:130:ARG:HH11	1.74	0.52
5:K:143:GLU:HA	5:K:145:HIS:CE1	2.45	0.52
8:H:106:PHE:HE2	8:H:554:HIS:NE2	2.06	0.52
8:H:674:LEU:CD1	8:H:973:ARG:NH1	2.69	0.52
1:A:1380:PRO:HG3	1:A:1383:PHE:CD1	2.44	0.52
1:A:1613:THR:O	1:A:1616:ARG:CD	2.57	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:83:LYS:C	4:G:85:ARG:H	2.12	0.52
4:G:252:GLU:CG	4:G:256:LYS:HG3	2.26	0.52
4:G:283:ARG:NH1	4:G:284:LEU:HD21	2.24	0.52
4:G:672:LEU:HD21	4:G:704:LEU:HD21	1.28	0.52
7:M:95:ARG:HG3	7:M:96:PRO:CD	2.40	0.52
25:D:44:A:H2'	25:D:45:A:C8	2.44	0.52
26:E:19:U:O2'	26:E:20:A:P	2.67	0.52
26:E:19:U:C6	26:E:19:U:C3'	2.93	0.52
1:A:1065:LEU:CD2	1:A:1069:LEU:HD13	2.39	0.52
1:A:1902:GLN:O	1:A:1905:LEU:CD2	2.56	0.52
3:I:336:GLU:O	3:I:340:LYS:HB2	2.09	0.52
3:I:398:GLN:NE2	3:I:419:GLN:HG3	2.25	0.52
4:G:234:ARG:O	4:G:237:ASP:O	2.28	0.52
4:G:288:ASP:OD1	4:G:291:TYR:CB	2.58	0.52
4:G:671:PHE:CE1	4:G:690:THR:O	2.62	0.52
5:K:314:ARG:NH2	5:K:314:ARG:HG2	2.23	0.52
6:L:140:LYS:HB3	6:L:141:ARG:NH1	2.25	0.52
7:M:79:VAL:HG13	7:M:121:ILE:HG23	1.91	0.52
8:H:942:GLY:C	8:H:963:SER:OG	2.47	0.52
24:C:-4:A:C1'	24:C:-3:A:OP1	2.49	0.52
1:A:691:PHE:C	1:A:691:PHE:CD1	2.82	0.52
1:A:770:MET:HB2	1:A:775:ARG:HG3	1.92	0.52
1:A:1458:TRP:HZ3	1:A:1461:TYR:CD2	2.25	0.52
3:I:99:ASN:O	3:I:103:PRO:HD2	2.09	0.52
5:K:354:PHE:CE1	5:K:358:MET:HG2	2.45	0.52
6:L:140:LYS:CB	6:L:141:ARG:NH1	2.73	0.52
8:H:369:LYS:HE2	8:H:369:LYS:C	2.30	0.52
8:H:682:SER:HA	8:H:714:PRO:HG3	1.92	0.52
1:A:261:LEU:HD12	1:A:262:ASP:N	2.24	0.52
1:A:377:VAL:CG1	1:A:378:PRO:HD2	2.37	0.52
1:A:514:TYR:HD1	1:A:514:TYR:H	1.58	0.52
1:A:814:ARG:NH1	4:G:103:GLN:O	2.43	0.52
1:A:1342:LEU:C	1:A:1342:LEU:HD23	2.30	0.52
3:I:400:VAL:HG12	4:G:215:LEU:HA	1.92	0.52
4:G:712:ASP:OD2	4:G:721:ARG:HB3	2.09	0.52
4:G:863:PHE:HE2	4:G:892:LEU:HD11	1.73	0.52
8:H:126:MET:CE	8:H:132:ARG:NH1	2.73	0.52
27:F:95:C:O3'	27:F:96:U:C4'	2.58	0.52
8:H:332:TYR:CZ	8:H:376:PHE:HD2	2.27	0.52
8:H:884:ARG:HD3	8:H:884:ARG:C	2.30	0.52
1:A:362:GLU:CB	1:A:1209:LYS:CE	2.72	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:GLN:HB3	1:A:706:PRO:HD3	1.91	0.52
1:A:1468:ALA:HB1	1:A:1473:ARG:C	2.29	0.52
1:A:1899:TRP:CH2	1:A:1909:ALA:HB2	2.45	0.52
2:B:68:ASP:OD1	5:K:322:ARG:NH1	2.41	0.52
2:B:286:ASP:O	2:B:288:THR:HG23	2.10	0.52
2:B:438:ASP:HB2	2:B:458:ASP:HB3	1.91	0.52
3:I:101:ILE:O	3:I:105:ILE:HG13	2.10	0.52
3:I:217:TYR:CE1	3:I:221:LYS:CE	2.92	0.52
4:G:169:LEU:O	4:G:173:GLN:HG3	2.10	0.52
5:K:314:ARG:HG2	5:K:314:ARG:HH21	1.75	0.52
8:H:265:PHE:N	8:H:265:PHE:CD1	2.77	0.52
8:H:270:LEU:HD11	8:H:313:PHE:HB3	1.92	0.52
27:F:103:A:HO2'	27:F:104:G:P	2.29	0.52
1:A:644:VAL:O	1:A:645:ASP:HB2	2.10	0.52
1:A:703:PHE:HD1	1:A:704:TRP:N	2.08	0.52
1:A:1285:VAL:O	1:A:1448:GLU:OE2	2.29	0.52
2:B:316:GLN:HB2	2:B:357:TRP:CG	2.42	0.52
3:I:127:LEU:HD11	3:I:131:ILE:HD12	1.90	0.52
4:G:702:PRO:CA	4:G:739:PHE:CZ	2.93	0.52
8:H:168:VAL:HA	8:H:173:LYS:HG3	1.92	0.52
8:H:483:TRP:CZ3	8:H:565:LYS:HG2	2.45	0.52
1:A:321:GLU:HA	1:A:508:GLN:OE1	2.11	0.51
1:A:471:PRO:HG2	1:A:472:ASN:OD1	2.10	0.51
1:A:1416:LYS:HG2	1:A:1417:GLN:N	2.25	0.51
1:A:1992:TYR:CD2	1:A:2004:ALA:HB1	2.44	0.51
2:B:117:LEU:C	2:B:117:LEU:HD13	2.31	0.51
3:I:184:LYS:CD	3:I:186:LYS:CB	2.87	0.51
4:G:360:LYS:O	4:G:364:PHE:N	2.38	0.51
27:F:77:A:H4'	27:F:78:A:C5'	2.32	0.51
27:F:100:A:H5'	27:F:101:C:OP2	2.10	0.51
1:A:376:ARG:O	1:A:377:VAL:CB	2.56	0.51
1:A:769:MET:HE2	4:G:112:ALA:HA	1.91	0.51
2:B:360:ASN:CB	2:B:362:TYR:CE1	2.93	0.51
3:I:347:ALA:HB1	3:I:348:PRO:HD2	1.92	0.51
4:G:143:ARG:NH2	4:G:143:ARG:CB	2.73	0.51
8:H:227:VAL:HG13	8:H:473:LEU:HB3	1.90	0.51
8:H:497:ASP:O	8:H:538:GLU:HA	2.09	0.51
1:A:217:TRP:CD1	1:A:703:PHE:CZ	2.98	0.51
1:A:228:LYS:CD	1:A:691:PHE:HE1	2.23	0.51
1:A:286:LEU:HD12	1:A:287:GLU:H	1.72	0.51
1:A:1342:LEU:HD23	1:A:1350:ILE:HD11	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2013:ARG:HG3	1:A:2083:ILE:O	2.11	0.51
2:B:275:PRO:CG	2:B:319:GLY:CA	2.88	0.51
8:H:369:LYS:CE	8:H:369:LYS:N	2.73	0.51
8:H:478:TYR:HB2	8:H:483:TRP:HD1	1.76	0.51
9:N:1928:LEU:O	9:N:1931:GLN:N	2.40	0.51
1:A:249:LEU:HD23	1:A:249:LEU:N	2.25	0.51
1:A:823:TRP:CE2	1:A:851:ARG:HG2	2.45	0.51
1:A:861:GLN:NE2	1:A:1097:HIS:HB3	2.25	0.51
1:A:1464:LYS:NZ	1:A:1479:GLU:HB3	2.25	0.51
4:G:9:GLN:C	4:G:11:PRO:HD3	2.30	0.51
4:G:19:ILE:HD12	4:G:20:GLY:CA	2.40	0.51
4:G:327:VAL:O	4:G:331:LEU:N	2.39	0.51
8:H:135:ASN:HD22	8:H:487:ARG:HH21	1.57	0.51
8:H:354:TYR:CE1	8:H:376:PHE:HZ	2.28	0.51
8:H:478:TYR:HB2	8:H:483:TRP:CD1	2.45	0.51
8:H:860:PRO:HB3	8:H:937:TRP:HZ3	1.74	0.51
1:A:250:SER:HB2	1:A:252:GLU:OE1	2.11	0.51
1:A:1313:ASP:OD2	1:A:1359:ILE:CD1	2.59	0.51
1:A:1339:LEU:CD2	1:A:1440:ILE:HD12	2.40	0.51
5:K:316:HIS:C	5:K:316:HIS:CD2	2.83	0.51
5:K:350:PRO:C	5:K:353:ARG:HG3	2.30	0.51
6:L:135:TYR:N	6:L:135:TYR:CD1	2.79	0.51
8:H:113:ILE:CG2	8:H:114:PRO:CD	2.89	0.51
8:H:232:SER:OG	8:H:234:LEU:O	2.28	0.51
8:H:586:MET:C	8:H:589:LEU:HD23	2.30	0.51
8:H:951:ILE:CB	8:H:952:PRO:CD	2.88	0.51
8:H:959:ILE:HD13	8:H:960:ASN:H	1.72	0.51
27:F:62:G:H2'	27:F:63:C:H6	1.75	0.51
1:A:166:LYS:O	1:A:169:PRO:CD	2.53	0.51
1:A:366:GLU:HG3	1:A:367:PHE:N	2.26	0.51
2:B:171:GLN:O	2:B:172:LEU:CD1	2.59	0.51
2:B:436:HIS:CD2	2:B:440:ILE:HD11	2.45	0.51
3:I:401:LEU:HD12	4:G:214:SER:HA	1.93	0.51
4:G:101:LYS:O	4:G:105:ALA:N	2.36	0.51
6:L:94:ASP:OD1	6:L:132:VAL:HA	2.10	0.51
8:H:307:ILE:HD11	8:H:345:THR:C	2.30	0.51
8:H:354:TYR:HA	8:H:359:PHE:HB3	1.90	0.51
8:H:461:LYS:NZ	8:H:464:PRO:CB	2.73	0.51
1:A:291:LYS:NZ	1:A:291:LYS:H	2.09	0.51
1:A:497:GLN:HB3	1:A:712:LEU:HD23	1.92	0.51
1:A:1050:LEU:HD23	1:A:1248:VAL:HG22	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1065:LEU:CD2	1:A:1069:LEU:HD22	2.40	0.51
1:A:2067:TYR:N	1:A:2067:TYR:CD1	2.78	0.51
3:I:376:LYS:O	3:I:378:LYS:N	2.43	0.51
8:H:178:LEU:HD12	8:H:214:ASP:HB2	1.92	0.51
8:H:379:ILE:CG2	8:H:383:LYS:HE2	2.40	0.51
8:H:953:LYS:O	8:H:954:LEU:HB2	2.10	0.51
1:A:273:ASP:HB3	1:A:276:VAL:HG21	1.92	0.51
1:A:298:TYR:O	1:A:493:MET:SD	2.69	0.51
1:A:522:TYR:CE2	1:A:686:ILE:HD12	2.46	0.51
2:B:415:TYR:OH	7:M:126:ILE:C	2.49	0.51
27:F:74:U:H2'	27:F:75:A:H3'	1.92	0.51
1:A:976:GLN:HE22	1:A:1310:LYS:HB3	1.76	0.51
2:B:274:HIS:HD2	2:B:276:SER:HB3	1.72	0.51
3:I:112:MET:HB2	3:I:204:LEU:HD21	1.91	0.51
3:I:265:ASN:O	3:I:266:LYS:CB	2.57	0.51
8:H:697:ARG:NH1	8:H:852:THR:OG1	2.44	0.51
8:H:883:ARG:CZ	8:H:910:GLU:O	2.59	0.51
8:H:945:LEU:O	8:H:945:LEU:HD13	2.11	0.51
9:N:1502:LEU:O	9:N:1503:GLU:C	2.47	0.51
24:C:11:A:C2	24:C:12:U:C4	2.99	0.51
27:F:64:C:C2	27:F:65:U:C5	2.99	0.51
1:A:621:LEU:HD12	1:A:666:ILE:HD11	1.91	0.51
1:A:774:ILE:CG2	1:A:777:LYS:HE3	2.38	0.51
1:A:1511:ARG:HH21	1:A:1511:ARG:CG	2.22	0.51
1:A:1649:PHE:CE1	1:A:1815:LEU:HD21	2.46	0.51
1:A:1893:ILE:O	1:A:1984:PRO:HA	2.11	0.51
2:B:121:ARG:HD2	2:B:337:ARG:O	2.11	0.51
2:B:274:HIS:CD2	2:B:275:PRO:CD	2.93	0.51
7:M:46:ARG:NH1	26:E:43:C:OP1	2.44	0.51
8:H:143:HIS:HA	28:H:1500:GTP:PB	2.51	0.51
8:H:160:ARG:HB3	8:H:161:ILE:CA	2.40	0.51
8:H:376:PHE:CD1	8:H:376:PHE:N	2.79	0.51
27:F:72:C:C2	27:F:73:U:C5	2.98	0.51
1:A:767:LEU:CD2	1:A:779:ALA:HB2	2.40	0.50
1:A:806:ALA:N	1:A:807:PRO:HD2	2.26	0.50
1:A:1490:ARG:NH1	1:A:1535:LYS:O	2.44	0.50
2:B:127:TYR:HE2	2:B:276:SER:CB	2.19	0.50
2:B:167:LEU:O	4:G:728:ARG:NH2	2.44	0.50
2:B:243:ILE:HD12	2:B:292:TRP:CZ3	2.46	0.50
3:I:301:GLN:OE1	3:I:344:LEU:CD1	2.60	0.50
3:I:447:GLU:OE2	3:I:448:ALA:N	2.45	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:143:ARG:CG	4:G:143:ARG:NH2	2.73	0.50
8:H:116:THR:CG2	8:H:157:SER:OG	2.59	0.50
8:H:247:PHE:CB	8:H:931:TYR:OH	2.59	0.50
8:H:353:TYR:CE2	8:H:371:PRO:HG3	2.47	0.50
1:A:418:ASP:N	1:A:418:ASP:OD1	2.44	0.50
1:A:1477:PHE:O	1:A:1481:GLU:N	2.44	0.50
1:A:1498:ASP:OD1	1:A:1502:LEU:HD12	2.07	0.50
2:B:354:THR:HG21	2:B:399:VAL:H	1.75	0.50
3:I:210:LEU:O	3:I:214:ILE:HG13	2.12	0.50
3:I:447:GLU:HA	3:I:450:GLN:HG2	1.93	0.50
4:G:887:THR:N	4:G:888:PRO:CD	2.74	0.50
8:H:135:ASN:ND2	8:H:487:ARG:NH2	2.60	0.50
8:H:285:TYR:CD1	8:H:285:TYR:C	2.84	0.50
15:Z:48:TYR:O	15:Z:50:ASN:N	2.45	0.50
27:F:63:C:C2	27:F:64:C:C5	3.00	0.50
27:F:117:G:H2'	27:F:118:U:O4'	2.12	0.50
1:A:149:MET:CG	1:A:154:TYR:CE2	2.89	0.50
1:A:251:TYR:CA	1:A:255:ILE:HD12	2.34	0.50
1:A:774:ILE:O	1:A:774:ILE:HG22	2.11	0.50
1:A:1627:LEU:HD22	1:A:1632:ILE:HB	1.94	0.50
2:B:360:ASN:ND2	2:B:406:GLY:O	2.43	0.50
2:B:419:ILE:HD11	2:B:443:LEU:HD13	1.91	0.50
4:G:215:LEU:HD12	4:G:216:SER:O	2.11	0.50
8:H:305:SER:C	8:H:307:ILE:H	2.15	0.50
25:D:62:A:H2'	25:D:63:G:C5'	2.38	0.50
1:A:299:LYS:O	1:A:300:LYS:HB2	2.12	0.50
1:A:505:TRP:O	1:A:522:TYR:HE1	1.93	0.50
1:A:754:TYR:CE2	1:A:758:LEU:CD2	2.94	0.50
1:A:764:ASP:O	1:A:768:GLU:N	2.44	0.50
1:A:1158:ILE:HG12	1:A:1172:PHE:CE1	2.46	0.50
1:A:1336:ASN:O	1:A:1340:ILE:HG13	2.10	0.50
1:A:1373:LEU:HD21	1:A:1379:MET:SD	2.51	0.50
1:A:1461:TYR:CE2	1:A:1494:LEU:CD1	2.95	0.50
1:A:1709:TRP:HD1	1:A:1730:ASN:O	1.94	0.50
1:A:1735:ASP:O	1:A:1775:ILE:N	2.37	0.50
1:A:1880:PHE:CE2	1:A:1889:LEU:CD2	2.74	0.50
1:A:1882:LEU:HD22	1:A:1883:ASN:N	2.27	0.50
1:A:1892:LYS:HG3	1:A:1916:GLU:HG3	1.93	0.50
2:B:127:TYR:CZ	2:B:276:SER:HA	2.47	0.50
2:B:171:GLN:O	2:B:172:LEU:HD13	2.12	0.50
2:B:376:TRP:N	2:B:376:TRP:CD1	2.78	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:410:LEU:O	3:I:410:LEU:HD12	2.12	0.50
4:G:6:PHE:HE1	4:G:7:LEU:HD12	1.75	0.50
8:H:302:ASN:OD1	8:H:303:VAL:N	2.44	0.50
8:H:580:VAL:O	8:H:580:VAL:HG13	2.11	0.50
8:H:793:GLU:C	8:H:796:ILE:HG22	2.31	0.50
8:H:794:GLN:OE1	8:H:835:LYS:CG	2.57	0.50
1:A:1650:ARG:O	1:A:1651:ALA:HB3	2.12	0.50
6:L:32:GLY:O	6:L:63:ASP:HA	2.10	0.50
8:H:133:ILE:C	8:H:134:ILE:CG2	2.72	0.50
8:H:354:TYR:CA	8:H:359:PHE:CB	2.86	0.50
8:H:769:TYR:CD1	8:H:799:PHE:HD2	2.29	0.50
1:A:165:LEU:HD21	1:A:726:ILE:HG21	1.93	0.50
1:A:1317:ARG:O	1:A:1321:MET:HG2	2.11	0.50
1:A:1733:TRP:CE2	1:A:1772:GLY:HA3	2.46	0.50
1:A:1778:ASP:HB2	1:A:1783:MET:HB2	1.94	0.50
4:G:252:GLU:O	4:G:256:LYS:HB2	2.11	0.50
4:G:274:SER:HB2	4:G:277:ILE:CD1	2.15	0.50
4:G:702:PRO:CB	4:G:739:PHE:CE2	2.95	0.50
5:K:144:LEU:HD22	5:K:144:LEU:N	2.27	0.50
6:L:140:LYS:HG2	6:L:141:ARG:HH12	1.69	0.50
8:H:160:ARG:NH1	8:H:160:ARG:HG3	2.26	0.50
8:H:349:TRP:CZ3	8:H:373:PHE:CD2	2.99	0.50
15:W:48:TYR:O	15:W:50:ASN:N	2.45	0.50
25:D:81:G:C6	25:D:82:A:N7	2.80	0.50
27:F:39:U:O2'	27:F:40:C:H5'	2.11	0.50
1:A:286:LEU:HD21	1:A:289:ASP:HB3	1.92	0.50
1:A:289:ASP:CG	1:A:292:LYS:CG	2.80	0.50
1:A:367:PHE:O	1:A:367:PHE:HD1	1.95	0.50
1:A:897:PRO:O	1:A:1006:ARG:NH1	2.44	0.50
2:B:390:LEU:HD12	5:K:428:TRP:CD1	2.46	0.50
4:G:143:ARG:CZ	4:G:143:ARG:CB	2.86	0.50
4:G:241:PRO:HG3	4:G:274:SER:OG	2.12	0.50
8:H:133:ILE:HA	8:H:209:MET:O	2.11	0.50
8:H:379:ILE:HG22	8:H:383:LYS:CE	2.42	0.50
8:H:862:TYR:OH	8:H:908:VAL:CG2	2.59	0.50
1:A:547:LEU:O	1:A:551:LEU:HB2	2.12	0.50
2:B:290:ARG:NE	2:B:299:GLU:OE2	2.42	0.50
2:B:446:SER:OG	2:B:451:PHE:CB	2.54	0.50
2:B:462:LYS:HE2	4:G:727:ASP:OD2	2.12	0.50
4:G:161:LYS:O	4:G:165:GLU:HB2	2.12	0.50
26:E:139:A:O2'	26:E:140:G:P	2.69	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:97:U:O2	27:F:97:U:H2'	2.11	0.50
1:A:221:TRP:CH2	1:A:691:PHE:HB3	2.47	0.50
1:A:395:PRO:O	1:A:396:ARG:HG3	2.11	0.50
1:A:1008:LEU:HD21	1:A:1073:ILE:CD1	2.40	0.50
1:A:1264:GLY:HA3	1:A:1308:GLU:CD	2.33	0.50
4:G:141:LEU:O	4:G:141:LEU:HD13	2.11	0.50
4:G:299:ALA:O	4:G:303:ASN:N	2.43	0.50
5:K:363:LEU:HD11	5:K:391:PHE:CD2	2.47	0.50
6:L:140:LYS:CG	6:L:141:ARG:CZ	2.90	0.50
8:H:132:ARG:HH21	8:H:206:LYS:CG	2.25	0.50
8:H:347:ARG:HG3	8:H:359:PHE:CZ	2.47	0.50
8:H:501:ILE:HG21	8:H:570:ALA:CB	2.41	0.50
27:F:32:G:O3'	27:F:33:U:H4'	2.11	0.50
27:F:73:U:C2'	27:F:74:U:H5"	2.38	0.50
27:F:75:A:O2'	27:F:76:U:C3'	2.59	0.50
1:A:291:LYS:NZ	1:A:291:LYS:N	2.60	0.49
1:A:452:PHE:CZ	8:H:343:ASP:HB3	2.46	0.49
1:A:909:THR:HG22	1:A:910:LYS:H	1.77	0.49
1:A:1275:MET:CE	1:A:1299:LYS:NZ	2.75	0.49
1:A:1481:GLU:HA	1:A:1484:TRP:NE1	2.27	0.49
3:I:275:LEU:N	3:I:275:LEU:HD23	2.27	0.49
4:G:798:LEU:O	4:G:802:GLN:HA	2.12	0.49
5:K:319:ALA:O	5:K:323:ARG:N	2.44	0.49
8:H:250:GLU:HB3	8:H:298:PHE:CD2	2.47	0.49
1:A:201:PHE:CE2	1:A:551:LEU:HD21	2.47	0.49
1:A:1286:TRP:CZ2	1:A:1302:LEU:HD11	2.47	0.49
1:A:1709:TRP:HB3	1:A:1791:PHE:CE1	2.47	0.49
1:A:1759:TYR:HB3	1:A:1767:TYR:OH	2.12	0.49
1:A:1834:PHE:CD1	1:A:1958:PRO:HG2	2.48	0.49
1:A:2065:ARG:NE	1:A:2066:LYS:HE2	2.26	0.49
2:B:143:HIS:CE1	5:K:151:LEU:HD22	2.47	0.49
3:I:401:LEU:HD12	4:G:214:SER:CA	2.42	0.49
4:G:886:CYS:SG	4:G:888:PRO:CD	2.97	0.49
8:H:118:TYR:O	8:H:119:ASN:CB	2.60	0.49
8:H:474:LYS:HZ2	8:H:630:PRO:CD	2.25	0.49
8:H:503:ASP:OD1	8:H:571:TYR:CB	2.59	0.49
1:A:149:MET:O	1:A:153:MET:HG3	2.11	0.49
1:A:1490:ARG:HH11	1:A:1536:LEU:HD23	1.76	0.49
1:A:1591:THR:HG22	1:A:1592:HIS:H	1.76	0.49
2:B:448:ASN:O	2:B:449:SER:HB2	2.12	0.49
4:G:6:PHE:CD1	4:G:6:PHE:C	2.85	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:379:ILE:CG2	8:H:383:LYS:HE3	2.42	0.49
25:D:50:G:HO2'	25:D:51:A:P	2.27	0.49
26:E:141:G:O2'	26:E:142:G:OP2	2.27	0.49
27:F:62:G:C4	27:F:63:C:C5	3.00	0.49
1:A:1118:GLY:HA3	1:A:1163:ARG:CZ	2.42	0.49
8:H:336:ILE:HG13	8:H:341:ILE:CG2	2.43	0.49
8:H:430:ARG:O	8:H:431:GLN:C	2.50	0.49
1:A:356:TYR:HE2	1:A:396:ARG:HB2	1.76	0.49
1:A:470:LEU:HB2	1:A:473:THR:HB	1.95	0.49
1:A:908:ASP:HB3	1:A:951:LEU:HD11	1.94	0.49
1:A:912:LEU:CG	1:A:951:LEU:HD21	2.43	0.49
1:A:1014:LYS:HD3	1:A:1024:LEU:HD13	1.95	0.49
1:A:1074:VAL:HG12	1:A:1075:ASP:H	1.77	0.49
1:A:1365:THR:C	1:A:1369:ASN:ND2	2.63	0.49
1:A:1385:PRO:HG3	1:A:1407:ILE:HA	1.95	0.49
1:A:1590:LEU:HB2	1:A:1595:ARG:HH21	1.76	0.49
1:A:1922:ARG:NE	1:A:1951:PHE:HZ	2.06	0.49
2:B:276:SER:OG	2:B:277:GLY:N	2.46	0.49
3:I:98:PHE:O	3:I:102:ILE:HG12	2.12	0.49
5:K:331:VAL:O	5:K:332:GLU:HG2	2.13	0.49
8:H:160:ARG:HG3	8:H:160:ARG:HH11	1.77	0.49
8:H:191:ILE:HG23	8:H:221:PHE:CZ	2.48	0.49
8:H:539:VAL:HG13	8:H:564:ILE:HG23	1.93	0.49
27:F:31:G:N3	27:F:32:G:C1'	2.74	0.49
27:F:48:G:H2'	27:F:49:U:H6	1.77	0.49
27:F:73:U:H2'	27:F:74:U:H6	1.78	0.49
1:A:165:LEU:HD21	1:A:726:ILE:CG2	2.42	0.49
1:A:218:SER:HB2	1:A:317:PRO:HG2	1.95	0.49
1:A:272:ASP:CB	1:A:273:ASP:OD1	2.61	0.49
1:A:1207:TRP:HB3	1:A:1211:SER:OG	2.12	0.49
2:B:264:HIS:CE1	2:B:290:ARG:HD2	2.47	0.49
6:L:119:THR:HG22	6:L:131:VAL:HG11	1.94	0.49
8:H:470:ALA:HB3	8:H:577:LEU:CB	2.38	0.49
8:H:492:LEU:CD2	8:H:557:HIS:CE1	2.95	0.49
27:F:92:U:C4	27:F:93:G:N7	2.80	0.49
1:A:201:PHE:CE2	1:A:551:LEU:CD2	2.96	0.49
1:A:1204:ARG:HD2	1:A:1259:LEU:HB3	1.93	0.49
1:A:1373:LEU:CD1	6:L:139:HIS:CE1	2.80	0.49
4:G:672:LEU:HD22	4:G:703:LEU:HD12	1.93	0.49
4:G:712:ASP:OD2	4:G:721:ARG:HD2	2.13	0.49
4:G:843:VAL:CG2	4:G:895:LEU:CD1	2.88	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:571:TYR:HD2	8:H:573:LYS:O	1.96	0.49
8:H:864:VAL:HG12	8:H:866:ILE:HG13	1.94	0.49
24:C:11:A:N1	24:C:12:U:C4	2.81	0.49
25:D:83:A:HO2'	25:D:84:C:P	2.27	0.49
27:F:77:A:H1'	27:F:78:A:C5'	2.41	0.49
1:A:749:ARG:O	1:A:750:LEU:CB	2.61	0.49
3:I:93:LYS:HA	3:I:93:LYS:CE	2.43	0.49
8:H:268:ASN:ND2	8:H:316:THR:HG23	2.28	0.49
8:H:369:LYS:NZ	8:H:369:LYS:N	2.60	0.49
8:H:492:LEU:CD2	8:H:557:HIS:HA	2.39	0.49
1:A:165:LEU:CD2	1:A:726:ILE:CG2	2.90	0.49
1:A:277:LYS:HG3	1:A:278:ASP:N	2.28	0.49
1:A:1865:THR:OG1	1:A:1869:ASN:N	2.34	0.49
1:A:2071:ILE:HD13	1:A:2071:ILE:C	2.33	0.49
2:B:117:LEU:HD22	2:B:117:LEU:O	2.13	0.49
3:I:217:TYR:CE1	3:I:221:LYS:HE2	2.48	0.49
3:I:400:VAL:HB	4:G:214:SER:HB2	1.94	0.49
4:G:101:LYS:O	4:G:105:ALA:CB	2.61	0.49
4:G:276:ASP:OD1	4:G:276:ASP:N	2.38	0.49
6:L:105:PHE:CE1	6:L:137:TYR:HE2	2.01	0.49
8:H:589:LEU:HD11	8:H:591:PHE:HE1	1.78	0.49
27:F:63:C:H2'	27:F:64:C:H6	1.78	0.49
1:A:302:SER:HA	1:A:489:THR:O	2.13	0.49
1:A:1067:ASN:OD1	3:I:270:HIS:HB3	2.11	0.49
4:G:170:LEU:HD22	4:G:170:LEU:O	2.12	0.49
5:K:159:TYR:CG	5:K:163:ASN:ND2	2.77	0.49
8:H:383:LYS:O	8:H:387:TYR:CB	2.51	0.49
1:A:175:LEU:CD1	1:A:564:TRP:CZ2	2.96	0.48
1:A:276:VAL:CG1	1:A:310:ASN:CB	2.89	0.48
1:A:1038:ILE:HG13	1:A:1039:TRP:N	2.28	0.48
1:A:1629:LEU:H	1:A:1629:LEU:CD2	2.26	0.48
2:B:197:GLY:CA	2:B:221:ILE:CD1	2.87	0.48
5:K:265:LEU:HD12	5:K:266:PRO:HD2	1.94	0.48
5:K:354:PHE:CE1	5:K:358:MET:CG	2.96	0.48
5:K:448:GLN:HE21	5:K:464:TYR:HE2	1.61	0.48
8:H:165:SER:H	8:H:168:VAL:CG2	2.26	0.48
8:H:578:TYR:CD1	8:H:578:TYR:C	2.86	0.48
24:C:-4:A:H1'	24:C:-3:A:P	2.52	0.48
1:A:140:ARG:NH2	1:A:252:GLU:HB3	2.28	0.48
2:B:282:SER:O	2:B:290:ARG:N	2.40	0.48
4:G:136:ARG:NH1	26:E:51:U:OP2	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:306:PRO:O	8:H:324:ILE:CD1	2.60	0.48
8:H:677:PHE:CZ	8:H:966:PHE:CE2	3.00	0.48
8:H:791:TYR:O	8:H:795:ILE:HG13	2.13	0.48
1:A:192:LEU:HG	1:A:557:PHE:CD2	2.48	0.48
1:A:839:HIS:CE1	27:F:96:U:C5	3.02	0.48
1:A:1400:ILE:HG23	1:A:1542:TYR:CZ	2.48	0.48
1:A:1461:TYR:CZ	1:A:1494:LEU:HD13	2.48	0.48
1:A:1594:GLN:N	1:A:1594:GLN:HE21	2.11	0.48
3:I:376:LYS:O	3:I:377:GLU:C	2.51	0.48
4:G:99:ASN:H	4:G:99:ASN:HD22	1.61	0.48
4:G:780:LEU:O	4:G:784:GLY:N	2.45	0.48
8:H:177:TYR:O	8:H:178:LEU:HG	2.13	0.48
8:H:353:TYR:N	8:H:353:TYR:CD1	2.81	0.48
8:H:945:LEU:HD12	8:H:945:LEU:N	2.29	0.48
9:N:1198:ARG:CA	9:N:1227:ILE:N	2.71	0.48
27:F:45:A:H2'	27:F:45:A:N3	2.28	0.48
1:A:140:ARG:HH21	1:A:252:GLU:HB3	1.77	0.48
1:A:770:MET:HE1	1:A:778:LYS:C	2.33	0.48
1:A:1336:ASN:OD1	1:A:1400:ILE:HG13	2.13	0.48
1:A:1557:LEU:O	1:A:1560:THR:OG1	2.27	0.48
8:H:161:ILE:HB	8:H:164:MET:SD	2.54	0.48
8:H:161:ILE:CG2	8:H:162:PRO:HD2	2.41	0.48
8:H:489:TYR:O	8:H:558:LYS:HG3	2.13	0.48
8:H:674:LEU:HD11	8:H:973:ARG:HH22	1.77	0.48
8:H:936:ILE:HD13	8:H:936:ILE:N	2.27	0.48
24:C:8:U:H2'	24:C:9:G:C5'	2.42	0.48
27:F:46:C:H2'	27:F:47:U:H6	1.79	0.48
27:F:74:U:C2'	27:F:75:A:H5'	2.44	0.48
1:A:1183:THR:HG22	1:A:1184:ASP:N	2.29	0.48
1:A:1353:THR:O	1:A:1357:LEU:CD1	2.56	0.48
2:B:60:LYS:HG3	2:B:79:ILE:HD13	1.96	0.48
3:I:462:ASN:OD1	4:G:830:ARG:NE	2.47	0.48
8:H:881:LYS:HA	8:H:886:SER:HB3	1.95	0.48
8:H:884:ARG:CB	8:H:910:GLU:HG3	2.44	0.48
8:H:947:LYS:CD	8:H:947:LYS:N	2.73	0.48
24:C:8:U:C5	25:D:51:A:N1	2.81	0.48
1:A:1335:TRP:CZ2	1:A:1339:LEU:CD1	2.97	0.48
1:A:1650:ARG:HD2	25:D:52:G:P	2.53	0.48
1:A:1705:SER:HB3	1:A:1709:TRP:CD1	2.49	0.48
2:B:158:GLU:O	2:B:162:MET:HE3	2.14	0.48
2:B:177:PRO:HG2	2:B:195:TRP:HE1	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:K:350:PRO:C	5:K:353:ARG:CG	2.81	0.48
6:L:76:LEU:N	6:L:76:LEU:CD1	2.77	0.48
8:H:490:SER:HA	8:H:558:LYS:HG3	1.96	0.48
27:F:48:G:C4	27:F:49:U:C5	3.02	0.48
1:A:228:LYS:HD2	1:A:691:PHE:HE1	1.78	0.48
1:A:290:SER:HG	1:A:291:LYS:NZ	2.05	0.48
1:A:774:ILE:HG23	1:A:777:LYS:NZ	2.28	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CE3	2.48	0.48
2:B:357:TRP:CD1	2:B:358:SER:N	2.82	0.48
2:B:359:PRO:CD	2:B:407:GLY:HA3	2.41	0.48
3:I:130:LEU:HD22	3:I:174:VAL:HG11	1.96	0.48
5:K:146:GLU:C	5:K:148:LYS:N	2.66	0.48
6:L:81:THR:CG2	6:L:102:LYS:NZ	2.66	0.48
8:H:858:LEU:HB3	8:H:937:TRP:HB2	1.96	0.48
8:H:950:PHE:CZ	8:H:952:PRO:O	2.66	0.48
25:D:64:U:H5”	25:D:64:U:C6	2.49	0.48
27:F:46:C:C2	27:F:47:U:C5	3.01	0.48
1:A:305:LEU:C	1:A:305:LEU:HD23	2.34	0.48
1:A:553:ASN:C	1:A:554:THR:HG23	2.33	0.48
1:A:1657:ILE:O	1:A:1661:ILE:CD1	2.62	0.48
1:A:1875:ILE:HG22	1:A:1876:ASN:N	2.18	0.48
2:B:173:VAL:CG1	2:B:200:GLN:OE1	2.54	0.48
2:B:350:LYS:HE3	5:K:431:TYR:CG	2.49	0.48
2:B:386:LEU:C	2:B:386:LEU:HD12	2.34	0.48
5:K:159:TYR:CD2	5:K:163:ASN:ND2	2.82	0.48
7:M:42:LYS:NZ	26:E:44:G:O6	2.47	0.48
8:H:449:PHE:CD1	8:H:453:THR:HG21	2.45	0.48
8:H:491:GLY:O	8:H:492:LEU:HD23	2.14	0.48
27:F:52:G:C4	27:F:53:C:C5	3.01	0.48
27:F:71:A:H2’	27:F:72:C:H6	1.79	0.48
1:A:754:TYR:CE2	1:A:758:LEU:HD21	2.49	0.48
1:A:1061:ILE:HG12	1:A:1117:TYR:CE2	2.49	0.48
2:B:177:PRO:CB	2:B:195:TRP:HE1	2.27	0.48
2:B:293:ASP:OD1	2:B:294:ALA:N	2.46	0.48
2:B:320:SER:HB2	2:B:337:ARG:HH12	1.79	0.48
2:B:345:LEU:HD13	2:B:376:TRP:CG	2.49	0.48
2:B:395:ILE:HG22	2:B:396:VAL:N	2.18	0.48
4:G:886:CYS:CB	4:G:888:PRO:HD2	2.44	0.48
8:H:538:GLU:H	8:H:538:GLU:HG2	1.47	0.48
1:A:292:LYS:NZ	1:A:307:GLU:OE2	2.35	0.48
1:A:1908:LEU:HD12	1:A:1908:LEU:C	2.34	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:312:SER:HB2	2:B:353:TYR:O	2.14	0.48
3:I:248:VAL:O	3:I:252:SER:OG	2.30	0.48
4:G:284:LEU:CD2	4:G:284:LEU:N	2.77	0.48
5:K:141:ASN:C	5:K:142:LEU:HD22	2.33	0.48
26:E:1:A:OP2	29:E:201:M7M:HBI	2.13	0.48
1:A:2011:LEU:HB3	1:A:2040:TRP:CH2	2.49	0.47
2:B:60:LYS:HB3	2:B:61:PRO:HD2	1.95	0.47
2:B:404:GLU:O	2:B:405:ASP:HB3	2.13	0.47
3:I:79:ASP:O	3:I:83:ILE:N	2.31	0.47
4:G:286:GLU:OE2	4:G:292:CYS:SG	2.69	0.47
4:G:721:ARG:O	4:G:725:ILE:HD12	2.14	0.47
8:H:888:ILE:HA	8:H:904:GLY:HA2	1.96	0.47
26:E:24:A:O2'	26:E:25:U:OP1	2.28	0.47
1:A:501:LEU:HD13	1:A:705:GLN:HG2	1.96	0.47
1:A:874:ILE:O	1:A:874:ILE:HG22	2.15	0.47
1:A:1009:PHE:CE1	1:A:1115:GLN:HB3	2.49	0.47
1:A:1014:LYS:NZ	1:A:1016:SER:OG	2.39	0.47
1:A:1211:SER:HA	1:A:1257:ASN:ND2	2.30	0.47
1:A:1593:ALA:CB	6:L:118:GLU:OE1	2.63	0.47
3:I:95:LEU:HD23	3:I:98:PHE:CD2	2.49	0.47
4:G:809:LEU:HD12	4:G:841:THR:HG22	1.96	0.47
6:L:78:ASP:CG	6:L:79:PRO:HD3	2.34	0.47
6:L:118:GLU:OE2	6:L:122:ARG:NH2	2.26	0.47
8:H:132:ARG:HE	8:H:206:LYS:HD2	1.80	0.47
8:H:265:PHE:CE2	8:H:295:ILE:HB	2.49	0.47
8:H:577:LEU:HD23	8:H:577:LEU:O	2.13	0.47
9:N:1203:SER:N	9:N:1223:ILE:O	2.39	0.47
27:F:73:U:O2'	27:F:74:U:H5'	2.02	0.47
1:A:1156:HIS:CG	1:A:1157:PRO:HD2	2.50	0.47
1:A:1731:LYS:O	1:A:1771:THR:OG1	2.32	0.47
1:A:1877:GLY:O	1:A:1894:ILE:CA	2.62	0.47
2:B:77:ALA:O	2:B:81:MET:HG2	2.14	0.47
4:G:702:PRO:CA	4:G:739:PHE:CE2	2.98	0.47
6:L:18:ALA:HB1	6:L:60:TYR:CE2	2.49	0.47
8:H:444:GLN:NE2	8:H:444:GLN:CA	2.73	0.47
9:N:990:ASP:O	9:N:994:ASP:N	2.45	0.47
27:F:36:A:H61	27:F:118:U:H3	1.61	0.47
1:A:1033:ASN:HD21	1:A:1298:ALA:HB3	1.80	0.47
1:A:1586:GLN:CG	1:A:1595:ARG:NH1	2.77	0.47
1:A:2046:GLU:HG2	1:A:2049:ILE:HD12	1.96	0.47
2:B:446:SER:CB	2:B:451:PHE:H	2.22	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:209:LYS:HG3	3:I:210:LEU:N	2.29	0.47
4:G:740:TYR:OH	4:G:766:LYS:NZ	2.42	0.47
4:G:852:LEU:CD1	4:G:852:LEU:N	2.76	0.47
8:H:233:ASP:HA	8:H:452:LYS:NZ	2.29	0.47
8:H:373:PHE:CE1	8:H:377:ILE:CD1	2.97	0.47
8:H:889:TYR:N	8:H:903:ARG:O	2.47	0.47
27:F:32:G:HO2'	27:F:33:U:P	2.37	0.47
1:A:719:ILE:N	1:A:720:PRO:HD2	2.28	0.47
1:A:1286:TRP:NE1	1:A:1348:GLU:OE1	2.37	0.47
1:A:1607:THR:O	1:A:1611:SER:N	2.47	0.47
4:G:120:MET:O	4:G:122:ILE:N	2.44	0.47
4:G:291:TYR:O	4:G:291:TYR:HD1	1.97	0.47
5:K:350:PRO:CA	5:K:353:ARG:CD	2.85	0.47
8:H:118:TYR:O	8:H:119:ASN:HB3	2.14	0.47
8:H:247:PHE:CD1	8:H:903:ARG:NH1	2.83	0.47
8:H:769:TYR:CD1	8:H:799:PHE:CD2	3.02	0.47
8:H:860:PRO:HB3	8:H:937:TRP:CE3	2.48	0.47
8:H:941:PRO:HG2	8:H:962:LEU:HD12	1.97	0.47
25:D:86:G:H8	25:D:86:G:C5'	2.19	0.47
1:A:320:ASP:C	1:A:321:GLU:HG3	2.34	0.47
1:A:454:LEU:HD22	8:H:336:ILE:HB	1.96	0.47
1:A:495:ARG:NH1	1:A:497:GLN:HE21	2.12	0.47
1:A:790:TRP:CD2	1:A:819:LYS:HD3	2.49	0.47
1:A:2041:PRO:HG2	1:A:2043:PHE:CZ	2.50	0.47
5:K:282:GLU:C	5:K:284:ASP:H	2.16	0.47
8:H:104:THR:O	8:H:108:GLN:HG3	2.14	0.47
8:H:175:LEU:HD23	8:H:175:LEU:C	2.34	0.47
25:D:62:A:N3	26:E:58:G:N2	2.62	0.47
27:F:52:G:H2'	27:F:53:C:H6	1.79	0.47
27:F:71:A:C4	27:F:72:C:C5	3.02	0.47
1:A:301:TRP:CZ2	1:A:491:GLY:HA3	2.50	0.47
1:A:553:ASN:O	1:A:554:THR:HG23	2.15	0.47
1:A:1262:MET:O	1:A:1263:CYS:CB	2.61	0.47
1:A:1508:HIS:HA	1:A:1511:ARG:NH2	2.29	0.47
1:A:1730:ASN:C	1:A:1731:LYS:HG3	2.35	0.47
2:B:321:LEU:HD22	2:B:335:ASP:HA	1.97	0.47
2:B:362:TYR:CD2	2:B:379:ARG:HD2	2.49	0.47
2:B:413:CYS:SG	2:B:440:ILE:HG21	2.55	0.47
4:G:15:TYR:CE1	6:L:13:TRP:HD1	2.32	0.47
4:G:368:SER:O	4:G:372:LEU:N	2.47	0.47
4:G:672:LEU:HD13	4:G:703:LEU:HD12	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:853:GLY:O	4:G:854:LYS:HB2	2.14	0.47
8:H:492:LEU:HD22	8:H:557:HIS:ND1	2.24	0.47
8:H:581:LYS:NZ	8:H:581:LYS:CB	2.73	0.47
8:H:964:ARG:O	8:H:968:MET:HG2	2.15	0.47
1:A:174:LYS:O	1:A:178:ASN:ND2	2.39	0.47
1:A:239:PHE:CB	1:A:240:PRO:CD	2.92	0.47
1:A:767:LEU:HA	1:A:770:MET:HG3	1.96	0.47
1:A:1217:ARG:HD3	1:A:1217:ARG:HA	1.75	0.47
1:A:1527:TRP:CE3	1:A:1528:THR:HG23	2.50	0.47
1:A:1591:THR:CG2	1:A:1592:HIS:N	2.78	0.47
2:B:120:ALA:HB1	2:B:279:PHE:CE2	2.50	0.47
2:B:187:ASP:OD2	2:B:447:ASN:CB	2.63	0.47
2:B:225:ASP:OD1	2:B:226:TRP:N	2.48	0.47
2:B:275:PRO:HG3	2:B:319:GLY:N	2.30	0.47
4:G:144:LYS:O	4:G:145:THR:OG1	2.18	0.47
6:L:105:PHE:CB	6:L:141:ARG:CD	2.92	0.47
8:H:307:ILE:HD13	8:H:345:THR:O	2.15	0.47
8:H:336:ILE:HD11	8:H:341:ILE:CG2	2.38	0.47
27:F:66:A:C4	27:F:67:U:C5	3.02	0.47
1:A:175:LEU:HD11	1:A:564:TRP:CE2	2.50	0.47
1:A:470:LEU:H	1:A:473:THR:CG2	2.27	0.47
1:A:470:LEU:H	1:A:473:THR:HG21	1.80	0.47
1:A:691:PHE:HZ	1:A:701:CYS:CA	2.26	0.47
1:A:1115:GLN:NE2	1:A:1115:GLN:CA	2.78	0.47
1:A:1369:ASN:O	1:A:1373:LEU:HG	2.15	0.47
1:A:1623:PHE:CZ	24:C:5:G:C5	3.02	0.47
1:A:1651:ALA:C	1:A:1652:HIS:HD2	2.16	0.47
2:B:181:VAL:HA	2:B:191:ALA:O	2.15	0.47
2:B:243:ILE:HD12	2:B:292:TRP:HZ3	1.78	0.47
2:B:261:LEU:HD13	2:B:292:TRP:CE3	2.50	0.47
3:I:277:SER:HB3	3:I:279:VAL:HG23	1.97	0.47
4:G:288:ASP:O	4:G:292:CYS:SG	2.72	0.47
4:G:490:GLU:O	4:G:494:HIS:N	2.48	0.47
4:G:672:LEU:HD22	4:G:703:LEU:CD1	2.45	0.47
5:K:340:LYS:HE2	5:K:389:CYS:HB3	1.97	0.47
5:K:370:LEU:HD21	5:K:454:THR:HG21	1.95	0.47
1:A:840:VAL:C	1:A:841:GLU:HG3	2.34	0.47
1:A:845:VAL:HG21	1:A:1321:MET:CE	2.44	0.47
1:A:853:THR:OG1	1:A:971:MET:HG2	2.14	0.47
1:A:1145:MET:CE	1:A:1160:LEU:HD13	2.44	0.47
2:B:161:ARG:O	2:B:165:LEU:CD2	2.62	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:275:PRO:O	2:B:276:SER:O	2.33	0.47
4:G:698:VAL:N	4:G:699:PRO:CD	2.78	0.47
4:G:861:ASN:ND2	4:G:862:MET:SD	2.88	0.47
6:L:13:TRP:CH2	6:L:17:GLN:NE2	2.83	0.47
1:A:251:TYR:HA	1:A:255:ILE:CD1	2.37	0.46
1:A:289:ASP:HB3	1:A:292:LYS:HB2	1.97	0.46
2:B:206:THR:HB	2:B:208:GLN:CD	2.35	0.46
3:I:214:ILE:O	3:I:218:ILE:HG12	2.15	0.46
3:I:401:LEU:HD12	3:I:401:LEU:H	1.79	0.46
4:G:101:LYS:O	4:G:105:ALA:HB2	2.15	0.46
6:L:108:ASP:N	6:L:108:ASP:OD1	2.48	0.46
8:H:375:GLU:CG	8:H:376:PHE:CE1	2.99	0.46
8:H:500:ARG:CD	8:H:534:THR:HG23	2.10	0.46
8:H:564:ILE:HG22	8:H:567:ILE:HG12	1.95	0.46
8:H:855:PRO:CD	8:H:944:VAL:HG21	2.44	0.46
8:H:897:THR:HB	8:H:898:PRO:HD2	1.97	0.46
8:H:967:VAL:HB	8:H:968:MET:HE3	1.97	0.46
27:F:35:A:C4	27:F:120:G:N2	2.82	0.46
27:F:43:G:C2	27:F:44:A:C5	3.02	0.46
1:A:315:SER:C	1:A:317:PRO:CD	2.82	0.46
1:A:815:TYR:CD1	1:A:815:TYR:C	2.88	0.46
1:A:1115:GLN:N	1:A:1115:GLN:HE21	2.12	0.46
1:A:1156:HIS:ND1	1:A:1157:PRO:HD2	2.29	0.46
1:A:1704:GLU:HG2	1:A:1731:LYS:HD3	1.97	0.46
2:B:350:LYS:HB3	2:B:351:PRO:HD2	1.98	0.46
4:G:298:THR:O	4:G:302:PHE:CD2	2.67	0.46
5:K:395:LEU:HD13	5:K:399:ARG:CZ	2.45	0.46
8:H:941:PRO:HD2	8:H:962:LEU:HB2	1.98	0.46
25:D:48:C:H2'	25:D:49:A:C8	2.50	0.46
1:A:170:HIS:C	1:A:170:HIS:CD2	2.88	0.46
1:A:1366:ARG:HA	1:A:1369:ASN:HD22	1.80	0.46
2:B:362:TYR:HD2	2:B:379:ARG:HD2	1.81	0.46
2:B:387:ASN:CA	2:B:388:GLN:OE1	2.64	0.46
4:G:325:ARG:O	4:G:329:LYS:N	2.37	0.46
5:K:334:PRO:HG2	5:K:337:TYR:HE1	1.79	0.46
8:H:488:ILE:HD11	8:H:556:ALA:HB1	1.97	0.46
8:H:500:ARG:HE	8:H:534:THR:HB	1.75	0.46
27:F:165:A:O2'	27:F:166:U:OP2	2.27	0.46
1:A:505:TRP:HZ3	1:A:690:LYS:HG3	1.78	0.46
1:A:1275:MET:CE	1:A:1299:LYS:CD	2.93	0.46
1:A:1284:GLY:HA2	1:A:1348:GLU:HB3	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1899:TRP:CH2	1:A:1909:ALA:CB	2.98	0.46
2:B:184:SER:OG	2:B:186:ASP:OD1	2.18	0.46
4:G:122:ILE:CG1	4:G:123:PRO:HD2	2.36	0.46
4:G:691:TYR:CE2	4:G:711:ILE:HD12	2.49	0.46
8:H:167:ASN:ND2	8:H:167:ASN:C	2.69	0.46
8:H:296:ASN:OD1	8:H:303:VAL:HA	2.15	0.46
8:H:387:TYR:O	8:H:391:MET:CB	2.50	0.46
1:A:1402:ALA:O	1:A:1403:SER:CB	2.63	0.46
1:A:1878:CYS:O	1:A:1878:CYS:SG	2.73	0.46
1:A:2075:THR:HG22	1:A:2076:GLN:N	2.30	0.46
2:B:177:PRO:CG	2:B:195:TRP:HE1	2.27	0.46
2:B:279:PHE:HD1	2:B:279:PHE:N	2.12	0.46
2:B:307:ASP:OD1	5:K:225:ILE:HA	2.16	0.46
2:B:313:LEU:HD11	2:B:322:VAL:HG21	1.98	0.46
2:B:408:LYS:O	2:B:424:SER:HB3	2.15	0.46
3:I:281:GLN:NE2	26:E:37:U:O4	2.48	0.46
3:I:433:ASN:ND2	3:I:433:ASN:N	2.61	0.46
4:G:13:ALA:O	4:G:15:TYR:N	2.48	0.46
6:L:45:LEU:HD11	6:L:110:LYS:HA	1.97	0.46
8:H:449:PHE:CD1	8:H:449:PHE:C	2.88	0.46
1:A:286:LEU:HD22	1:A:292:LYS:HB3	1.96	0.46
1:A:514:TYR:N	1:A:514:TYR:CD1	2.84	0.46
1:A:1065:LEU:HG	3:I:177:MET:HE1	1.98	0.46
1:A:1216:ILE:HD12	1:A:1254:ASN:CB	2.44	0.46
1:A:1593:ALA:HB3	6:L:118:GLU:OE1	2.16	0.46
1:A:1756:PHE:CD1	1:A:1756:PHE:C	2.89	0.46
1:A:1995:TRP:CE3	1:A:2007:ARG:HD2	2.50	0.46
8:H:544:LEU:HG	8:H:553:VAL:HG21	1.97	0.46
8:H:801:TRP:O	8:H:801:TRP:HD1	1.98	0.46
1:A:247:PRO:HB2	1:A:248:PRO:HD2	1.98	0.46
1:A:810:LYS:HA	1:A:810:LYS:HE3	1.98	0.46
1:A:901:PRO:HD3	1:A:1078:ILE:HD11	1.98	0.46
1:A:1125:LEU:HD21	1:A:1234:VAL:CG2	2.46	0.46
1:A:1417:GLN:OE1	1:A:1422:ILE:CG1	2.64	0.46
2:B:290:ARG:CZ	2:B:302:LEU:HD13	2.45	0.46
4:G:703:LEU:HD13	4:G:703:LEU:O	2.16	0.46
8:H:247:PHE:HB3	8:H:931:TYR:OH	2.15	0.46
24:C:-4:A:C1'	24:C:-3:A:P	3.04	0.46
1:A:318:LEU:HD12	1:A:318:LEU:N	2.31	0.46
1:A:656:ILE:O	1:A:660:ILE:HG13	2.16	0.46
1:A:1038:ILE:HD12	1:A:1039:TRP:CE3	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1204:ARG:CD	1:A:1259:LEU:HB3	2.46	0.46
1:A:1287:ASP:OD2	1:A:1296:ARG:NH1	2.49	0.46
2:B:321:LEU:HD13	2:B:333:LEU:HD23	1.98	0.46
2:B:422:TYR:HD1	2:B:429:LYS:HA	1.81	0.46
3:I:136:GLN:NE2	3:I:166:LYS:O	2.49	0.46
3:I:226:ALA:CB	3:I:317:ASP:OD2	2.62	0.46
4:G:144:LYS:HE3	26:E:19:U:OP1	2.16	0.46
4:G:851:ARG:C	4:G:852:LEU:HD12	2.36	0.46
5:K:453:ARG:O	5:K:457:GLN:CD	2.54	0.46
7:M:51:PHE:CE2	7:M:53:ILE:HD11	2.50	0.46
8:H:571:TYR:CD2	8:H:573:LYS:O	2.69	0.46
8:H:967:VAL:HG12	8:H:971:ARG:HG3	1.97	0.46
1:A:141:LYS:HA	1:A:144:ASN:CG	2.19	0.46
1:A:665:GLY:O	1:A:668:ARG:HG2	2.15	0.46
2:B:171:GLN:OE1	2:B:172:LEU:O	2.34	0.46
3:I:143:ILE:HG23	3:I:149:TYR:HE2	1.81	0.46
4:G:16:VAL:HG13	4:G:17:PRO:HD2	1.98	0.46
4:G:103:GLN:O	4:G:106:ASP:OD1	2.34	0.46
8:H:362:LYS:HE2	8:H:365:GLU:CB	2.45	0.46
24:C:10:U:H2'	24:C:11:A:C8	2.50	0.46
26:E:2:U:C6	26:E:3:C:C5	3.03	0.46
27:F:89:U:C4	27:F:90:C:C5	3.04	0.46
1:A:175:LEU:HD12	1:A:564:TRP:NE1	2.31	0.46
1:A:275:TYR:O	1:A:279:TRP:CE2	2.69	0.46
1:A:532:ASN:ND2	27:F:83:C:O3'	2.49	0.46
1:A:1088:VAL:HG12	1:A:1089:VAL:H	1.79	0.46
1:A:1488:ILE:HB	1:A:1489:PRO:HD3	1.97	0.46
1:A:1521:ARG:CZ	3:I:404:TYR:CD2	2.99	0.46
1:A:1625:VAL:O	1:A:1633:PHE:HA	2.15	0.46
1:A:1790:TRP:CE3	1:A:1795:LYS:HG3	2.51	0.46
3:I:268:LEU:CD1	3:I:271:GLU:CG	2.83	0.46
4:G:223:LEU:HD23	4:G:223:LEU:C	2.36	0.46
4:G:692:LEU:O	4:G:696:ARG:HG3	2.15	0.46
4:G:769:SER:O	4:G:801:THR:HG22	2.15	0.46
6:L:78:ASP:CG	6:L:79:PRO:CD	2.85	0.46
8:H:831:ILE:O	8:H:831:ILE:HG22	2.16	0.46
26:E:32:G:N2	26:E:44:G:N3	2.64	0.46
1:A:853:THR:OG1	1:A:971:MET:CG	2.64	0.45
1:A:1711:VAL:HG12	1:A:1712:SER:N	2.31	0.45
5:K:159:TYR:CE1	5:K:163:ASN:ND2	2.83	0.45
6:L:36:ASP:HB2	6:L:39:CYS:HB2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:139:HIS:NE2	27:F:96:U:O5'	2.49	0.45
8:H:328:VAL:HG21	8:H:345:THR:CG2	2.45	0.45
27:F:73:U:C2	27:F:74:U:C5	3.03	0.45
1:A:971:MET:HE3	1:A:978:ILE:HG22	1.99	0.45
2:B:162:MET:N	2:B:162:MET:CE	2.79	0.45
2:B:244:LYS:HG2	2:B:257:LEU:HD23	1.97	0.45
2:B:261:LEU:HB3	2:B:292:TRP:CZ3	2.51	0.45
2:B:267:ARG:NH1	2:B:285:HIS:NE2	2.64	0.45
3:I:123:ARG:HB2	3:I:189:LEU:CD1	2.46	0.45
3:I:359:PRO:O	6:L:122:ARG:NH1	2.50	0.45
8:H:204:GLU:OE1	8:H:204:GLU:HA	2.17	0.45
8:H:963:SER:O	8:H:967:VAL:HG23	2.17	0.45
26:E:21:C:H2'	26:E:22:G:O4'	2.15	0.45
27:F:75:A:C4	27:F:77:A:H5"	2.50	0.45
1:A:388:PRO:HB2	1:A:398:VAL:HG11	1.98	0.45
1:A:495:ARG:CZ	1:A:497:GLN:NE2	2.78	0.45
1:A:1839:ASN:ND2	1:A:1842:GLU:OE1	2.50	0.45
3:I:98:PHE:CZ	3:I:217:TYR:CD2	2.98	0.45
3:I:424:THR:HG22	3:I:425:SER:N	2.30	0.45
4:G:487:GLN:O	4:G:491:LYS:N	2.43	0.45
5:K:337:TYR:CE2	5:K:434:ASP:HA	2.51	0.45
1:A:362:GLU:CB	1:A:1209:LYS:HG2	2.45	0.45
1:A:770:MET:HE1	1:A:778:LYS:CB	2.45	0.45
1:A:883:PHE:HB2	3:I:177:MET:SD	2.56	0.45
1:A:1335:TRP:CD1	1:A:1367:ILE:HD12	2.52	0.45
1:A:1589:LYS:O	1:A:1590:LEU:HD13	2.16	0.45
1:A:2066:LYS:HB2	1:A:2067:TYR:HD1	1.80	0.45
2:B:135:ARG:HD3	2:B:360:ASN:O	2.16	0.45
2:B:443:LEU:CD1	2:B:452:LEU:HD11	2.47	0.45
4:G:219:THR:HG22	4:G:221:GLU:H	1.81	0.45
4:G:238:PRO:CD	4:G:239:THR:N	2.79	0.45
4:G:255:ARG:HH11	4:G:255:ARG:HG3	1.80	0.45
4:G:285:HIS:HE1	4:G:291:TYR:HE2	1.56	0.45
4:G:668:HIS:HB2	4:G:698:VAL:HG11	1.95	0.45
4:G:691:TYR:HE2	4:G:711:ILE:CD1	2.14	0.45
5:K:144:LEU:CD2	5:K:144:LEU:H	2.29	0.45
5:K:273:LYS:O	5:K:277:MET:HB2	2.16	0.45
7:M:67:LEU:HB2	7:M:68:PRO:HD3	1.98	0.45
8:H:247:PHE:CD1	8:H:250:GLU:OE1	2.70	0.45
8:H:379:ILE:HG23	8:H:383:LYS:HE2	1.98	0.45
1:A:162:LEU:CD2	1:A:730:ILE:HD13	2.42	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:874:ILE:O	1:A:875:THR:O	2.34	0.45
1:A:1453:ASP:O	1:A:1457:VAL:HG23	2.16	0.45
2:B:155:ARG:CD	2:B:155:ARG:N	2.79	0.45
3:I:237:ILE:O	3:I:240:GLN:N	2.49	0.45
4:G:733:ASN:HB2	4:G:734:PRO:HA	1.99	0.45
6:L:102:LYS:CG	6:L:103:LEU:N	2.78	0.45
8:H:968:MET:HE2	8:H:971:ARG:HG3	1.98	0.45
9:N:1105:ALA:O	9:N:1106:GLY:C	2.54	0.45
27:F:77:A:C1'	27:F:78:A:C5'	2.95	0.45
1:A:251:TYR:O	1:A:255:ILE:HB	2.16	0.45
1:A:366:GLU:O	1:A:372:ARG:HD2	2.16	0.45
1:A:795:ALA:O	1:A:796:ASN:HB2	2.17	0.45
1:A:820:ALA:O	1:A:824:VAL:HG23	2.16	0.45
2:B:428:LEU:HD11	5:K:466:PRO:HD2	1.97	0.45
3:I:245:ALA:CB	3:I:250:GLU:HB3	2.40	0.45
4:G:252:GLU:CG	4:G:256:LYS:HE3	2.47	0.45
8:H:113:ILE:CG2	8:H:549:TYR:CD1	2.99	0.45
8:H:121:ASP:O	8:H:125:SER:N	2.49	0.45
8:H:270:LEU:CD1	8:H:313:PHE:HB3	2.45	0.45
8:H:306:PRO:HD2	8:H:349:TRP:CE2	2.51	0.45
1:A:205:THR:HG23	1:A:205:THR:O	2.16	0.45
1:A:373:VAL:CG1	1:A:374:ILE:N	2.80	0.45
1:A:1974:LEU:O	1:A:1978:VAL:HG23	2.17	0.45
2:B:88:GLU:HA	2:B:91:ASN:HB3	1.98	0.45
2:B:192:THR:CG2	2:B:200:GLN:HG3	2.47	0.45
2:B:202:LEU:N	2:B:202:LEU:CD1	2.80	0.45
3:I:92:ILE:O	3:I:96:PRO:HD3	2.16	0.45
6:L:74:TYR:CG	6:L:83:MET:CE	3.00	0.45
8:H:272:ARG:O	8:H:276:ASP:HB2	2.16	0.45
8:H:274:ILE:HD13	8:H:274:ILE:C	2.37	0.45
8:H:675:THR:HG22	8:H:909:ILE:HD13	1.98	0.45
27:F:66:A:H2'	27:F:67:U:H6	1.81	0.45
27:F:102:C:H2'	27:F:103:A:H5'	1.99	0.45
1:A:176:LEU:CD2	1:A:176:LEU:C	2.85	0.45
1:A:776:GLN:HG2	1:A:777:LYS:N	2.32	0.45
1:A:1611:SER:N	1:A:1612:PRO:HD2	2.32	0.45
2:B:447:ASN:ND2	2:B:447:ASN:C	2.70	0.45
2:B:454:SER:OG	2:B:464:TRP:NE1	2.29	0.45
3:I:66:SER:O	3:I:70:THR:N	2.50	0.45
5:K:409:HIS:ND1	5:K:414:ASP:OD1	2.44	0.45
8:H:500:ARG:HG2	8:H:534:THR:HG21	1.87	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:578:TYR:CD1	8:H:578:TYR:O	2.70	0.45
9:N:1343:PHE:O	9:N:1345:PHE:N	2.49	0.45
25:D:49:A:H2'	25:D:50:G:O5'	2.16	0.45
27:F:84:A:C2	27:F:111:C:C2	3.05	0.45
1:A:151:SER:H	1:A:577:ASN:ND2	2.14	0.45
1:A:505:TRP:HD1	1:A:505:TRP:H	1.64	0.45
1:A:505:TRP:CE3	1:A:690:LYS:HG3	2.50	0.45
1:A:956:LYS:C	1:A:956:LYS:CD	2.83	0.45
2:B:419:ILE:CG2	2:B:433:LEU:HB2	2.47	0.45
3:I:46:ILE:O	3:I:97:PHE:CE1	2.69	0.45
3:I:358:ILE:CG2	3:I:359:PRO:CD	2.94	0.45
4:G:890:GLU:OE1	4:G:890:GLU:HA	2.17	0.45
8:H:167:ASN:ND2	8:H:173:LYS:CG	2.76	0.45
8:H:471:HIS:O	8:H:486:VAL:HA	2.17	0.45
8:H:950:PHE:CE1	8:H:951:ILE:O	2.70	0.45
29:E:201:M7M:NBN	29:E:201:M7M:HBX	2.32	0.45
27:F:107:C:H2'	27:F:108:C:O4'	2.16	0.45
1:A:298:TYR:O	1:A:298:TYR:CD1	2.70	0.45
5:K:141:ASN:CG	5:K:144:LEU:HD23	2.37	0.45
24:C:11:A:C2	25:D:47:A:C6	3.05	0.45
1:A:484:PHE:CD1	27:F:81:A:C6	3.05	0.44
1:A:770:MET:HE3	1:A:775:ARG:O	2.17	0.44
1:A:860:GLU:OE2	1:A:863:ARG:NH1	2.51	0.44
1:A:1047:ALA:HA	1:A:1172:PHE:O	2.17	0.44
1:A:2029:ASP:HB2	1:A:2032:ILE:HD12	1.98	0.44
2:B:357:TRP:HD1	2:B:358:SER:N	2.15	0.44
2:B:393:ARG:CG	2:B:393:ARG:NH2	2.74	0.44
8:H:133:ILE:HG13	8:H:134:ILE:N	2.32	0.44
8:H:234:LEU:HD23	8:H:234:LEU:H	1.82	0.44
8:H:470:ALA:HB3	8:H:577:LEU:CD2	2.46	0.44
8:H:481:ALA:HB2	8:H:565:LYS:HZ3	1.77	0.44
8:H:539:VAL:HG22	8:H:567:ILE:HD11	1.99	0.44
27:F:79:C:O2	27:F:79:C:H3'	2.17	0.44
1:A:176:LEU:HD21	1:A:708:TRP:NE1	2.31	0.44
1:A:874:ILE:C	1:A:875:THR:OG1	2.55	0.44
2:B:116:GLU:CD	2:B:117:LEU:N	2.70	0.44
3:I:113:HIS:HD2	3:I:134:PRO:CA	2.30	0.44
3:I:400:VAL:CG2	4:G:154:PRO:HG2	2.47	0.44
3:I:401:LEU:HA	3:I:407:GLU:HA	1.97	0.44
4:G:688:ARG:HH11	4:G:712:ASP:CG	2.20	0.44
5:K:341:VAL:HG21	5:K:428:TRP:CD1	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:110:LYS:HA	8:H:110:LYS:HD3	1.79	0.44
8:H:354:TYR:CD1	8:H:354:TYR:O	2.70	0.44
8:H:599:THR:HG23	8:H:933:TRP:HZ3	1.80	0.44
8:H:942:GLY:HA2	8:H:960:ASN:O	2.17	0.44
24:C:-3:A:H1'	24:C:-2:A:C8	2.52	0.44
25:D:83:A:O2'	25:D:84:C:P	2.75	0.44
27:F:103:A:C4	27:F:104:G:N7	2.86	0.44
1:A:165:LEU:HD23	1:A:726:ILE:HG21	1.99	0.44
1:A:1020:ILE:HD12	1:A:1020:ILE:N	2.32	0.44
1:A:1364:GLU:OE1	1:A:1405:ILE:HD11	2.17	0.44
1:A:1378:LYS:O	1:A:1379:MET:HB2	2.16	0.44
1:A:2075:THR:O	1:A:2079:ILE:HD12	2.17	0.44
1:A:2076:GLN:HA	1:A:2079:ILE:HD12	1.98	0.44
2:B:154:SER:HG	2:B:155:ARG:HD3	1.79	0.44
3:I:429:ARG:HH11	3:I:429:ARG:HA	1.82	0.44
5:K:143:GLU:O	5:K:145:HIS:CE1	2.70	0.44
6:L:133:SER:HA	6:L:134:PRO:HD2	1.84	0.44
6:L:140:LYS:CB	6:L:141:ARG:HH11	2.30	0.44
8:H:449:PHE:O	8:H:449:PHE:CD1	2.70	0.44
27:F:50:G:H2'	27:F:51:G:H8	1.82	0.44
27:F:95:C:O3'	27:F:96:U:H4'	2.17	0.44
1:A:1144:PHE:CD2	1:A:1145:MET:HG2	2.53	0.44
1:A:1373:LEU:HD11	27:F:96:U:OP1	2.17	0.44
1:A:1417:GLN:HE22	1:A:1783:MET:HA	1.83	0.44
1:A:1474:ARG:HG2	1:A:1475:LEU:N	2.33	0.44
1:A:1851:PHE:O	1:A:1881:THR:HA	2.17	0.44
1:A:1857:VAL:HG13	1:A:1894:ILE:CD1	2.47	0.44
1:A:1880:PHE:CD2	1:A:1889:LEU:CD2	3.00	0.44
2:B:32:LEU:HD23	2:B:34:HIS:H	1.82	0.44
2:B:359:PRO:HG2	2:B:407:GLY:CA	2.47	0.44
2:B:390:LEU:CD1	5:K:428:TRP:CD1	3.01	0.44
2:B:393:ARG:HG2	2:B:393:ARG:NH2	2.17	0.44
3:I:456:LEU:HD23	3:I:456:LEU:O	2.18	0.44
8:H:120:ARG:HA	8:H:120:ARG:HD3	1.67	0.44
8:H:354:TYR:HB2	8:H:359:PHE:CB	2.28	0.44
8:H:472:VAL:CG1	8:H:571:TYR:HE2	2.29	0.44
8:H:595:LEU:HD13	8:H:595:LEU:HA	1.83	0.44
24:C:7:A:N6	25:D:51:A:C8	2.85	0.44
1:A:162:LEU:CG	1:A:734:PHE:CE2	2.96	0.44
1:A:275:TYR:CD1	1:A:275:TYR:N	2.72	0.44
1:A:325:LYS:CE	1:A:325:LYS:CA	2.96	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:543:ASN:HD22	1:A:543:ASN:C	2.21	0.44
1:A:807:PRO:O	1:A:811:ILE:HG13	2.18	0.44
1:A:1073:ILE:HD12	1:A:1116:TYR:HE1	1.77	0.44
1:A:1275:MET:HE1	1:A:1299:LYS:CD	2.47	0.44
4:G:98:SER:HG	4:G:99:ASN:ND2	2.14	0.44
8:H:375:GLU:HB3	8:H:376:PHE:CD1	2.52	0.44
8:H:950:PHE:CZ	8:H:951:ILE:O	2.70	0.44
27:F:102:C:C2'	27:F:103:A:H5'	2.47	0.44
1:A:170:HIS:CD2	1:A:170:HIS:O	2.70	0.44
1:A:358:ARG:CB	1:A:358:ARG:NH1	2.80	0.44
1:A:429:ASN:HB3	1:A:430:PRO:HD2	1.98	0.44
2:B:293:ASP:HB2	2:B:300:LEU:HD11	1.99	0.44
3:I:137:TYR:O	3:I:141:ILE:HG13	2.17	0.44
3:I:398:GLN:OE1	3:I:414:ASN:ND2	2.49	0.44
4:G:111:LEU:O	4:G:113:ALA:N	2.51	0.44
6:L:25:ARG:CG	6:L:25:ARG:NH1	2.75	0.44
8:H:229:LEU:CD2	8:H:235:VAL:HG11	2.48	0.44
8:H:230:ALA:HB3	8:H:473:LEU:CD1	2.48	0.44
8:H:769:TYR:CZ	8:H:799:PHE:CE2	2.92	0.44
9:N:1382:LEU:O	9:N:1385:LEU:N	2.50	0.44
26:E:151:G:C2	26:E:152:A:N6	2.84	0.44
1:A:164:ALA:HB2	1:A:194:HIS:CD2	2.53	0.44
1:A:807:PRO:HB2	4:G:111:LEU:HD23	1.99	0.44
1:A:1015:PRO:HG2	1:A:1510:ILE:HG12	1.98	0.44
1:A:1661:ILE:HB	1:A:1736:VAL:HG11	2.00	0.44
2:B:154:SER:O	2:B:158:GLU:HG3	2.18	0.44
2:B:416:ASP:O	2:B:417:ASN:HB2	2.18	0.44
3:I:277:SER:CB	3:I:279:VAL:HG23	2.48	0.44
4:G:867:GLU:OE2	4:G:888:PRO:HG2	2.17	0.44
5:K:345:LYS:HB2	5:K:422:ASN:HA	2.00	0.44
8:H:123:MET:SD	8:H:209:MET:HE3	2.58	0.44
8:H:132:ARG:O	8:H:133:ILE:HG23	2.17	0.44
8:H:304:PHE:N	8:H:304:PHE:CD1	2.86	0.44
8:H:460:GLY:HA3	8:H:461:LYS:HA	1.67	0.44
1:A:171:ALA:HB2	1:A:201:PHE:CE1	2.51	0.44
1:A:180:PRO:O	1:A:181:HIS:HB2	2.17	0.44
1:A:613:SER:O	1:A:614:ARG:C	2.55	0.44
2:B:171:GLN:NE2	2:B:172:LEU:H	2.15	0.44
2:B:448:ASN:O	2:B:449:SER:CB	2.65	0.44
3:I:263:GLY:C	3:I:283:GLY:HA2	2.38	0.44
4:G:6:PHE:CE1	4:G:7:LEU:CD1	2.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:166:ARG:O	4:G:167:GLU:C	2.56	0.44
8:H:484:SER:O	8:H:564:ILE:HD12	2.17	0.44
26:E:6:U:H2'	26:E:7:A:H8	1.83	0.44
27:F:99:U:O2'	27:F:100:A:P	2.73	0.44
1:A:413:ASN:ND2	1:A:413:ASN:N	2.66	0.44
1:A:1276:GLU:N	1:A:1276:GLU:OE2	2.50	0.44
1:A:1836:ASN:H	1:A:1839:ASN:HB3	1.83	0.44
3:I:282:GLU:CG	3:I:286:PHE:CD2	3.00	0.44
3:I:400:VAL:HG21	4:G:154:PRO:CG	2.46	0.44
4:G:161:LYS:HA	4:G:161:LYS:CE	2.48	0.44
4:G:212:VAL:HG22	4:G:214:SER:H	1.83	0.44
4:G:272:PRO:CB	4:G:302:PHE:CD1	2.77	0.44
6:L:25:ARG:HH11	6:L:25:ARG:HG3	1.82	0.44
8:H:185:ILE:CD1	27:F:75:A:OP2	2.55	0.44
8:H:306:PRO:HG2	8:H:349:TRP:CD2	2.52	0.44
8:H:354:TYR:CD1	8:H:376:PHE:HZ	2.36	0.44
27:F:175:G:H4'	27:F:176:A:O4'	2.18	0.44
1:A:379:ILE:HG22	1:A:379:ILE:O	2.17	0.43
1:A:689:TYR:O	1:A:689:TYR:CD1	2.71	0.43
1:A:900:PHE:CZ	1:A:959:LEU:HD12	2.52	0.43
1:A:1285:VAL:HA	1:A:1300:ALA:O	2.18	0.43
1:A:1393:GLU:HG2	3:I:395:LYS:O	2.18	0.43
2:B:316:GLN:O	2:B:319:GLY:N	2.45	0.43
2:B:447:ASN:C	2:B:447:ASN:HD22	2.22	0.43
3:I:267:HIS:CE1	3:I:273:HIS:CE1	3.05	0.43
4:G:702:PRO:HB3	4:G:739:PHE:CD1	2.52	0.43
6:L:95:PHE:CE2	6:L:103:LEU:HD13	2.53	0.43
25:D:84:C:O2	25:D:84:C:C2'	2.66	0.43
27:F:175:G:C2	27:F:176:A:N6	2.84	0.43
1:A:1276:GLU:H	1:A:1276:GLU:CD	2.21	0.43
1:A:1501:THR:HG21	4:G:163:THR:HG21	1.99	0.43
1:A:1894:ILE:HG21	1:A:1899:TRP:CZ2	2.52	0.43
1:A:2067:TYR:N	1:A:2067:TYR:HD1	2.15	0.43
2:B:316:GLN:CG	2:B:357:TRP:CZ2	2.97	0.43
5:K:144:LEU:HB3	5:K:146:GLU:OE2	2.18	0.43
5:K:341:VAL:CG2	5:K:428:TRP:CD1	3.01	0.43
6:L:74:TYR:CD1	6:L:83:MET:HE1	2.52	0.43
8:H:347:ARG:HG3	8:H:359:PHE:HZ	1.81	0.43
8:H:488:ILE:HD11	8:H:560:GLN:CG	2.42	0.43
1:A:505:TRP:CD1	1:A:505:TRP:N	2.86	0.43
1:A:750:LEU:HG	1:A:751:ASP:N	2.34	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:357:TRP:O	2:B:401:PHE:CD2	2.72	0.43
2:B:395:ILE:CG2	2:B:396:VAL:H	2.16	0.43
2:B:409:LYS:HA	2:B:422:TYR:O	2.18	0.43
3:I:298:VAL:O	3:I:298:VAL:HG12	2.18	0.43
3:I:327:THR:O	3:I:328:VAL:CB	2.67	0.43
3:I:391:MET:SD	3:I:397:GLU:HG3	2.58	0.43
5:K:333:LYS:HD2	5:K:333:LYS:O	2.17	0.43
27:F:44:A:H61	27:F:71:A:H61	1.66	0.43
1:A:415:GLU:OE1	1:A:416:GLU:HB2	2.18	0.43
1:A:1019:GLU:HA	1:A:1023:LEU:HD23	2.00	0.43
1:A:1335:TRP:CD1	1:A:1367:ILE:CD1	3.01	0.43
1:A:1342:LEU:HD23	1:A:1350:ILE:CD1	2.49	0.43
2:B:127:TYR:HE2	2:B:276:SER:CA	2.31	0.43
3:I:450:GLN:HG3	3:I:451:GLN:H	1.83	0.43
4:G:231:LYS:HA	4:G:234:ARG:HD3	2.00	0.43
8:H:144:SER:HA	8:H:240:ASP:OD2	2.18	0.43
8:H:330:TYR:HE1	8:H:430:ARG:HH21	1.25	0.43
8:H:373:PHE:O	8:H:377:ILE:HB	2.17	0.43
8:H:566:GLY:C	8:H:567:ILE:HD13	2.39	0.43
24:C:-4:A:H4’	24:C:-3:A:OP2	2.18	0.43
27:F:47:U:H2’	27:F:48:G:H8	1.83	0.43
27:F:67:U:H2’	27:F:68:A:H8	1.82	0.43
1:A:162:LEU:HD11	1:A:730:ILE:HG22	2.01	0.43
1:A:1381:THR:OG1	1:A:1382:ARG:HG3	2.19	0.43
1:A:1664:ASP:O	1:A:1668:ILE:CG1	2.66	0.43
1:A:1739:ARG:HD2	1:A:1751:TYR:CD2	2.53	0.43
2:B:192:THR:HG23	2:B:200:GLN:CG	2.48	0.43
2:B:337:ARG:HD3	5:K:173:TYR:OH	2.18	0.43
3:I:137:TYR:CE2	3:I:141:ILE:HD11	2.54	0.43
3:I:183:PHE:CD2	3:I:185:ASN:ND2	2.86	0.43
6:L:33:ARG:HD3	6:L:65:ASP:H	1.84	0.43
8:H:349:TRP:CZ3	8:H:373:PHE:HE2	2.31	0.43
8:H:360:ARG:HG2	8:H:362:LYS:H	1.82	0.43
1:A:1168:ILE:O	1:A:1169:TYR:CD1	2.72	0.43
1:A:1580:GLY:HA3	3:I:389:ASN:ND2	2.33	0.43
2:B:222:GLY:N	2:B:237:CYS:O	2.44	0.43
3:I:143:ILE:HG23	3:I:149:TYR:CE2	2.52	0.43
3:I:380:ARG:CZ	3:I:380:ARG:CB	2.96	0.43
4:G:127:ASP:C	4:G:127:ASP:OD1	2.57	0.43
5:K:146:GLU:C	5:K:148:LYS:H	2.21	0.43
8:H:769:TYR:HE1	8:H:774:LEU:HB2	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:D:109:U:H3'	25:D:110:U:C5'	2.47	0.43
26:E:151:G:H4'	26:E:152:A:O4'	2.18	0.43
27:F:31:G:C6	27:F:32:G:C5	3.06	0.43
27:F:83:C:H4'	27:F:84:A:OP1	2.18	0.43
27:F:102:C:N4	27:F:103:A:H62	2.16	0.43
1:A:484:PHE:HB3	1:A:485:PRO:HD3	2.00	0.43
1:A:839:HIS:CE1	27:F:96:U:C6	3.07	0.43
1:A:1222:LEU:HD23	1:A:1222:LEU:HA	1.76	0.43
1:A:1855:THR:HA	1:A:1937:ARG:NH2	2.34	0.43
1:A:2076:GLN:OE1	5:K:283:ASN:O	2.37	0.43
2:B:382:ASP:OD1	2:B:382:ASP:N	2.50	0.43
3:I:93:LYS:CE	3:I:93:LYS:CA	2.95	0.43
3:I:416:SER:HA	3:I:419:GLN:OE1	2.19	0.43
4:G:153:ILE:HG23	4:G:154:PRO:HD2	1.99	0.43
4:G:529:ILE:O	4:G:533:LEU:N	2.52	0.43
4:G:666:ILE:N	4:G:668:HIS:CD2	2.86	0.43
4:G:697:LEU:C	4:G:699:PRO:HD3	2.39	0.43
5:K:382:VAL:HG11	5:K:392:TYR:CE2	2.53	0.43
8:H:132:ARG:NH1	8:H:132:ARG:CG	2.73	0.43
8:H:364:PHE:CG	8:H:369:LYS:CD	2.94	0.43
8:H:571:TYR:CB	8:H:575:ALA:HB2	2.49	0.43
8:H:964:ARG:NH1	8:H:968:MET:CE	2.82	0.43
26:E:150:G:C2	26:E:152:A:H4'	2.54	0.43
29:E:201:M7M:HBX	29:E:201:M7M:HNBN	1.82	0.43
1:A:222:ILE:HB	1:A:266:LEU:HD11	2.01	0.43
1:A:287:GLU:HB2	1:A:288:GLU:H	1.64	0.43
1:A:755:ASP:CG	1:A:819:LYS:HE3	2.39	0.43
1:A:960:THR:HG21	3:I:455:PHE:CZ	2.54	0.43
1:A:1668:ILE:HD13	1:A:1801:SER:HB2	2.01	0.43
1:A:2046:GLU:HA	1:A:2049:ILE:HD12	2.01	0.43
2:B:73:ARG:O	2:B:76:LEU:HB2	2.19	0.43
2:B:202:LEU:HD12	2:B:202:LEU:N	2.33	0.43
5:K:337:TYR:HE2	5:K:434:ASP:HA	1.82	0.43
6:L:25:ARG:NH1	6:L:25:ARG:HG3	2.34	0.43
8:H:355:HIS:C	8:H:356:LYS:CG	2.86	0.43
8:H:379:ILE:O	8:H:383:LYS:CG	2.65	0.43
27:F:174:G:C2	27:F:176:A:H4'	2.54	0.43
1:A:207:ARG:NH1	1:A:299:LYS:HG3	2.34	0.43
1:A:883:PHE:O	1:A:887:VAL:HG23	2.19	0.43
1:A:1286:TRP:HA	1:A:1448:GLU:OE2	2.19	0.43
1:A:1451:PHE:O	1:A:1455:GLN:OE1	2.35	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1647:GLN:O	1:A:1650:ARG:HG3	2.17	0.43
1:A:1657:ILE:O	1:A:1661:ILE:CG1	2.64	0.43
1:A:1992:TYR:HD2	1:A:2004:ALA:HB1	1.83	0.43
2:B:208:GLN:HA	2:B:209:PRO:HA	1.66	0.43
5:K:142:LEU:HD13	5:K:142:LEU:HA	1.74	0.43
5:K:146:GLU:O	5:K:149:PHE:HD2	2.01	0.43
6:L:33:ARG:HD3	6:L:65:ASP:CB	2.49	0.43
8:H:488:ILE:HD11	8:H:560:GLN:HG3	1.99	0.43
8:H:858:LEU:HB3	8:H:937:TRP:CB	2.48	0.43
27:F:62:G:H2'	27:F:63:C:C6	2.54	0.43
27:F:98:U:O2'	27:F:99:U:P	2.76	0.43
1:A:410:ILE:N	1:A:410:ILE:CD1	2.82	0.43
1:A:617:ASN:ND2	27:F:99:U:O2'	2.46	0.43
1:A:1087:ASN:ND2	3:I:274:THR:OG1	2.45	0.43
1:A:1511:ARG:HG3	1:A:1511:ARG:HH21	1.81	0.43
2:B:458:ASP:OD2	2:B:462:LYS:NZ	2.52	0.43
3:I:321:LYS:O	3:I:324:ASP:O	2.35	0.43
3:I:429:ARG:HH11	3:I:429:ARG:CG	2.32	0.43
4:G:127:ASP:OD1	4:G:128:PHE:N	2.52	0.43
8:H:114:PRO:O	8:H:115:LYS:HG3	2.18	0.43
8:H:373:PHE:HE1	8:H:377:ILE:HG21	1.84	0.43
8:H:598:ILE:CG2	8:H:933:TRP:CH2	3.01	0.43
24:C:6:U:O2	24:C:6:U:O2'	2.28	0.43
26:E:6:U:H2'	26:E:7:A:C8	2.53	0.43
1:A:291:LYS:H	1:A:291:LYS:HZ2	1.67	0.42
1:A:294:ASN:HB2	1:A:300:LYS:HB2	2.01	0.42
1:A:1020:ILE:HD12	1:A:1020:ILE:H	1.84	0.42
1:A:1386:ALA:O	1:A:1390:THR:HG23	2.19	0.42
1:A:1468:ALA:C	1:A:1473:ARG:O	2.57	0.42
2:B:446:SER:OG	2:B:451:PHE:CG	2.69	0.42
3:I:120:TYR:OH	3:I:141:ILE:HG23	2.19	0.42
3:I:417:LEU:HB3	4:G:226:MET:HE3	2.00	0.42
4:G:702:PRO:HA	4:G:739:PHE:CZ	2.54	0.42
5:K:155:LYS:HA	5:K:158:ILE:HG12	1.99	0.42
6:L:8:GLN:HG2	6:L:61:LEU:HB2	2.01	0.42
8:H:862:TYR:N	8:H:862:TYR:CD1	2.87	0.42
8:H:884:ARG:HD3	8:H:884:ARG:O	2.19	0.42
8:H:940:VAL:HA	8:H:941:PRO:HD3	1.89	0.42
1:A:268:LEU:HD12	1:A:268:LEU:O	2.19	0.42
1:A:689:TYR:CD1	1:A:689:TYR:C	2.93	0.42
1:A:770:MET:SD	4:G:119:TRP:HZ3	2.41	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:883:PHE:CD1	3:I:177:MET:SD	3.13	0.42
1:A:940:ILE:O	1:A:943:ALA:HB3	2.18	0.42
1:A:1615:ASN:ND2	1:A:1634:LEU:HD23	2.31	0.42
2:B:247:GLN:HB2	2:B:258:LEU:HD21	1.99	0.42
2:B:349:SER:O	2:B:350:LYS:HG3	2.19	0.42
2:B:353:TYR:HE2	2:B:395:ILE:HG21	1.84	0.42
2:B:422:TYR:CD1	2:B:429:LYS:HA	2.54	0.42
4:G:245:ILE:HG23	4:G:280:GLU:HG2	2.01	0.42
8:H:129:ILE:N	8:H:129:ILE:CD1	2.73	0.42
8:H:160:ARG:HA	8:H:160:ARG:HD2	1.70	0.42
8:H:189:LEU:CD1	8:H:190:SER:O	2.66	0.42
8:H:236:LEU:HD23	8:H:266:VAL:HG21	2.00	0.42
8:H:305:SER:C	8:H:307:ILE:N	2.72	0.42
8:H:408:LEU:HD21	8:H:427:LEU:HD22	2.01	0.42
8:H:801:TRP:CD1	8:H:801:TRP:C	2.92	0.42
8:H:828:ASP:O	8:H:829:VAL:C	2.57	0.42
25:D:62:A:C2	26:E:58:G:N1	2.87	0.42
27:F:73:U:H2'	27:F:74:U:C6	2.54	0.42
1:A:396:ARG:O	1:A:398:VAL:HG23	2.19	0.42
1:A:901:PRO:HG3	1:A:998:TYR:CD2	2.54	0.42
1:A:1739:ARG:O	1:A:1778:ASP:HA	2.18	0.42
2:B:123:PHE:CD1	2:B:123:PHE:C	2.93	0.42
2:B:321:LEU:CD2	2:B:335:ASP:HA	2.49	0.42
3:I:376:LYS:HE2	26:E:56:U:OP2	2.20	0.42
3:I:400:VAL:O	3:I:400:VAL:HG23	2.19	0.42
4:G:264:ILE:HG22	4:G:281:ASN:OD1	2.19	0.42
4:G:364:PHE:O	4:G:368:SER:N	2.38	0.42
5:K:323:ARG:O	5:K:326:ALA:HB3	2.19	0.42
5:K:333:LYS:O	5:K:333:LYS:CE	2.67	0.42
8:H:124:LEU:HD12	8:H:124:LEU:O	2.18	0.42
8:H:470:ALA:N	8:H:577:LEU:O	2.48	0.42
8:H:483:TRP:CH2	8:H:565:LYS:CG	3.01	0.42
8:H:933:TRP:HB2	8:H:934:HIS:CE1	2.55	0.42
1:A:703:PHE:CD1	1:A:703:PHE:C	2.93	0.42
1:A:1206:CYS:HB2	1:A:1266:GLU:OE1	2.19	0.42
1:A:1846:ASN:CA	1:A:1885:LYS:NZ	2.79	0.42
2:B:119:PHE:CD1	2:B:119:PHE:C	2.93	0.42
2:B:315:PHE:CE1	2:B:322:VAL:HB	2.54	0.42
3:I:135:LEU:HD21	3:I:136:GLN:HG3	2.01	0.42
3:I:168:THR:O	3:I:172:ILE:HD12	2.19	0.42
3:I:385:ARG:CZ	4:G:153:ILE:HD11	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:134:ARG:CZ	4:G:134:ARG:CB	2.96	0.42
4:G:275:SER:O	4:G:279:LEU:HG	2.19	0.42
5:K:443:LYS:HG2	5:K:444:VAL:H	1.84	0.42
8:H:167:ASN:HD22	8:H:168:VAL:N	2.16	0.42
1:A:1559:HIS:ND1	1:A:1613:THR:HG21	2.34	0.42
1:A:1697:SER:CB	1:A:1759:TYR:CE1	3.02	0.42
1:A:1877:GLY:C	1:A:1894:ILE:HB	2.40	0.42
2:B:112:PRO:O	2:B:113:ALA:HB3	2.19	0.42
2:B:125:ILE:HA	2:B:128:SER:OG	2.20	0.42
4:G:846:PHE:CD1	4:G:859:LEU:CD2	2.88	0.42
5:K:164:HIS:O	5:K:164:HIS:CG	2.71	0.42
5:K:309:LEU:HD23	5:K:309:LEU:HA	1.79	0.42
8:H:234:LEU:HD23	8:H:234:LEU:N	2.34	0.42
8:H:510:ARG:HD3	8:H:591:PHE:CZ	2.54	0.42
8:H:652:MET:HA	8:H:655:LEU:HD12	2.01	0.42
8:H:957:ALA:HB2	8:H:965:ASP:OD2	2.19	0.42
27:F:95:C:C1'	27:F:96:U:OP1	2.67	0.42
1:A:294:ASN:C	1:A:294:ASN:ND2	2.73	0.42
1:A:410:ILE:CG1	8:H:276:ASP:OD1	2.65	0.42
1:A:779:ALA:CA	1:A:782:ILE:HD12	2.23	0.42
1:A:1834:PHE:CE1	1:A:1958:PRO:HG2	2.53	0.42
2:B:124:LEU:HD22	2:B:274:HIS:HE1	1.84	0.42
2:B:320:SER:O	2:B:321:LEU:HD23	2.20	0.42
3:I:95:LEU:O	3:I:98:PHE:HB2	2.20	0.42
3:I:227:PRO:HG3	3:I:325:ARG:HG2	2.02	0.42
8:H:968:MET:CE	8:H:971:ARG:HG3	2.49	0.42
1:A:173:LEU:CD1	1:A:712:LEU:HD12	2.50	0.42
1:A:939:LEU:HA	1:A:939:LEU:HD23	1.85	0.42
1:A:1335:TRP:HZ3	1:A:1400:ILE:O	2.03	0.42
1:A:1344:THR:HG22	1:A:1347:ARG:HH21	1.83	0.42
1:A:1586:GLN:HB3	1:A:1595:ARG:HH12	1.84	0.42
4:G:251:GLU:CD	4:G:260:ALA:HB2	2.37	0.42
5:K:143:GLU:HA	5:K:145:HIS:HE1	1.84	0.42
6:L:33:ARG:HD3	6:L:65:ASP:OD1	2.17	0.42
8:H:500:ARG:HD3	8:H:534:THR:OG1	2.19	0.42
8:H:964:ARG:HA	8:H:964:ARG:HD2	1.77	0.42
24:C:-1:A:O2'	24:C:0:U:C6	2.73	0.42
26:E:26:A:O2'	26:E:27:U:P	2.78	0.42
1:A:193:TYR:CZ	1:A:558:GLN:HB3	2.55	0.42
1:A:370:ILE:HD12	8:H:953:LYS:HD2	2.00	0.42
1:A:908:ASP:HB3	1:A:951:LEU:CD1	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:974:ASN:C	1:A:976:GLN:H	2.23	0.42
1:A:1274:ARG:O	1:A:1277:GLU:OE1	2.37	0.42
1:A:1629:LEU:CD2	1:A:1629:LEU:N	2.82	0.42
1:A:1850:LEU:HD23	1:A:1883:ASN:HB3	2.00	0.42
1:A:2066:LYS:HB2	1:A:2067:TYR:CD1	2.54	0.42
2:B:159:LEU:N	2:B:159:LEU:HD23	2.34	0.42
2:B:275:PRO:O	2:B:276:SER:C	2.57	0.42
2:B:418:LEU:CD2	2:B:434:ALA:HB2	2.50	0.42
3:I:93:LYS:HD2	3:I:93:LYS:N	2.34	0.42
3:I:102:ILE:HB	3:I:103:PRO:CD	2.48	0.42
4:G:15:TYR:O	4:G:15:TYR:CD1	2.72	0.42
4:G:508:TRP:O	4:G:512:ASP:N	2.52	0.42
4:G:678:TYR:HD1	4:G:678:TYR:HA	1.74	0.42
8:H:271:ASP:OD2	8:H:318:LEU:HG	2.20	0.42
1:A:1629:LEU:HD23	1:A:1630:THR:HG22	1.98	0.42
1:A:1652:HIS:CD2	1:A:1652:HIS:N	2.87	0.42
1:A:1715:SER:HB2	1:A:1719:GLU:OE1	2.19	0.42
1:A:2075:THR:CG2	1:A:2076:GLN:N	2.82	0.42
1:A:2079:ILE:HG22	1:A:2083:ILE:CD1	2.44	0.42
1:A:2388:ARG:O	1:A:2389:PRO:C	2.57	0.42
2:B:345:LEU:HB3	2:B:376:TRP:CH2	2.54	0.42
3:I:123:ARG:HB2	3:I:189:LEU:HD11	2.02	0.42
3:I:424:THR:CG2	3:I:425:SER:N	2.83	0.42
4:G:282:ILE:HG12	4:G:295:LEU:HB3	2.01	0.42
4:G:349:ALA:O	4:G:353:GLN:N	2.48	0.42
4:G:671:PHE:CZ	4:G:693:SER:OG	2.64	0.42
5:K:280:VAL:HG12	5:K:282:GLU:H	1.85	0.42
5:K:350:PRO:CB	5:K:353:ARG:HD2	2.48	0.42
8:H:449:PHE:O	8:H:449:PHE:HD1	2.02	0.42
8:H:483:TRP:CZ3	8:H:565:LYS:HG3	2.54	0.42
8:H:572:ILE:HD12	8:H:572:ILE:C	2.40	0.42
1:A:276:VAL:CG1	1:A:310:ASN:HB2	2.49	0.42
1:A:465:GLU:HG3	8:H:387:TYR:OH	2.20	0.42
1:A:843:THR:HG21	6:L:108:ASP:CB	2.49	0.42
1:A:999:LEU:HD23	1:A:999:LEU:HA	1.78	0.42
1:A:1453:ASP:O	1:A:1456:ARG:CG	2.58	0.42
1:A:1851:PHE:HB2	1:A:1882:LEU:HD13	2.01	0.42
1:A:2026:LEU:HD11	1:A:2040:TRP:HZ3	1.85	0.42
4:G:19:ILE:HD12	4:G:20:GLY:HA2	2.02	0.42
4:G:252:GLU:HG3	4:G:284:LEU:CD1	2.50	0.42
4:G:281:ASN:HD22	4:G:281:ASN:C	2.23	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:78:ASP:OD2	6:L:79:PRO:HD2	2.20	0.42
8:H:475:THR:HG22	8:H:483:TRP:O	2.20	0.42
8:H:798:GLY:O	8:H:802:ALA:N	2.53	0.42
8:H:968:MET:CE	8:H:968:MET:N	2.82	0.42
1:A:358:ARG:HD3	1:A:360:GLU:HB2	2.00	0.41
1:A:1390:THR:HA	1:A:1391:PRO:HD3	1.75	0.41
2:B:171:GLN:CD	2:B:172:LEU:H	2.23	0.41
2:B:280:ILE:N	2:B:292:TRP:O	2.45	0.41
2:B:445:ILE:HG12	2:B:446:SER:N	2.35	0.41
3:I:429:ARG:HH11	3:I:429:ARG:CA	2.33	0.41
4:G:83:LYS:C	4:G:85:ARG:N	2.73	0.41
5:K:146:GLU:CA	5:K:149:PHE:CD2	2.91	0.41
7:M:95:ARG:NH1	7:M:95:ARG:CG	2.73	0.41
9:N:1610:LEU:O	9:N:1660:ALA:O	2.38	0.41
27:F:48:G:H2'	27:F:49:U:C6	2.55	0.41
1:A:474:LYS:C	1:A:474:LYS:CD	2.89	0.41
1:A:703:PHE:HD1	1:A:703:PHE:C	2.23	0.41
1:A:774:ILE:CG2	1:A:777:LYS:NZ	2.83	0.41
1:A:958:LEU:HD22	1:A:1081:TYR:CD2	2.56	0.41
2:B:218:VAL:HG23	2:B:240:ASP:CG	2.40	0.41
2:B:335:ASP:OD1	2:B:337:ARG:CD	2.58	0.41
3:I:390:ARG:O	3:I:412:MET:HG2	2.20	0.41
4:G:397:GLN:O	4:G:401:ILE:N	2.38	0.41
5:K:300:GLN:OE1	5:K:300:GLN:CA	2.68	0.41
6:L:39:CYS:SG	6:L:79:PRO:O	2.78	0.41
6:L:59:ILE:HG22	6:L:60:TYR:N	2.33	0.41
6:L:74:TYR:CG	6:L:83:MET:HE1	2.55	0.41
8:H:159:LYS:H	8:H:159:LYS:HG2	1.53	0.41
8:H:191:ILE:O	8:H:224:GLU:OE1	2.38	0.41
8:H:372:THR:O	8:H:373:PHE:C	2.58	0.41
8:H:656:LEU:HD13	8:H:670:ILE:HD13	2.02	0.41
8:H:933:TRP:C	8:H:934:HIS:CG	2.92	0.41
27:F:77:A:C4'	27:F:78:A:C5'	2.93	0.41
1:A:217:TRP:NE1	1:A:703:PHE:CE1	2.89	0.41
1:A:276:VAL:HG11	1:A:310:ASN:HB2	2.01	0.41
1:A:286:LEU:HD22	1:A:292:LYS:CB	2.47	0.41
1:A:329:TYR:CD2	1:A:330:LEU:HG	2.55	0.41
1:A:594:ASP:C	1:A:594:ASP:OD1	2.59	0.41
1:A:1512:ARG:HD2	1:A:1529:ASN:OD1	2.20	0.41
1:A:1626:GLN:HE22	1:A:1694:MET:HG2	1.84	0.41
1:A:1714:PRO:HB2	1:A:1787:TYR:CE2	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:289:TRP:HB2	2:B:313:LEU:HD23	2.01	0.41
2:B:316:GLN:OE1	2:B:321:LEU:HB2	2.20	0.41
3:I:92:ILE:HB	3:I:93:LYS:HD2	2.01	0.41
3:I:441:MET:SD	3:I:444:ARG:NH2	2.93	0.41
4:G:115:THR:O	4:G:119:TRP:HD1	2.03	0.41
8:H:108:GLN:OE1	8:H:109:LEU:HD23	2.19	0.41
8:H:507:SER:C	8:H:509:SER:N	2.71	0.41
8:H:571:TYR:H	8:H:571:TYR:HD1	1.69	0.41
8:H:879:LEU:O	8:H:883:ARG:HG2	2.20	0.41
27:F:32:G:O2'	27:F:33:U:P	2.79	0.41
27:F:45:A:N3	27:F:46:C:C5	2.87	0.41
1:A:672:LYS:C	1:A:674:MET:N	2.72	0.41
1:A:1115:GLN:CA	1:A:1115:GLN:HE21	2.33	0.41
1:A:1216:ILE:HG21	1:A:1254:ASN:ND2	2.36	0.41
1:A:1697:SER:OG	1:A:1759:TYR:CE1	2.64	0.41
1:A:1738:LEU:HD23	1:A:1777:ILE:HB	2.01	0.41
1:A:2020:GLU:HA	1:A:2023:LYS:HB2	2.01	0.41
3:I:329:LEU:HD12	3:I:333:TRP:CH2	2.55	0.41
5:K:354:PHE:CZ	5:K:358:MET:SD	3.14	0.41
5:K:362:GLU:HG2	29:E:201:M7M:NBN	2.35	0.41
7:M:126:ILE:HG22	7:M:126:ILE:O	2.21	0.41
8:H:177:TYR:O	8:H:178:LEU:CB	2.69	0.41
8:H:482:GLU:HG2	8:H:482:GLU:O	2.20	0.41
8:H:608:GLN:NE2	8:H:641:GLU:CG	2.61	0.41
1:A:458:PHE:O	1:A:458:PHE:CD1	2.74	0.41
1:A:484:PHE:N	1:A:485:PRO:CD	2.83	0.41
1:A:1204:ARG:HG3	1:A:1259:LEU:HD13	2.00	0.41
1:A:1417:GLN:OE1	1:A:1422:ILE:CD1	2.65	0.41
1:A:1678:ILE:HD13	1:A:1703:MET:CE	2.50	0.41
2:B:174:SER:OG	2:B:175:THR:N	2.54	0.41
2:B:316:GLN:HE21	2:B:318:ASP:H	1.67	0.41
2:B:362:TYR:CB	2:B:379:ARG:HD2	2.48	0.41
3:I:141:ILE:HG21	3:I:197:ILE:HG23	2.03	0.41
5:K:159:TYR:CE2	5:K:163:ASN:ND2	2.89	0.41
5:K:386:GLU:HG2	5:K:390:LYS:HE2	2.01	0.41
8:H:193:LEU:CB	8:H:214:ASP:O	2.67	0.41
8:H:325:LYS:HD2	8:H:325:LYS:HA	1.92	0.41
8:H:327:PHE:HE1	8:H:331:TYR:CD2	2.39	0.41
8:H:467:THR:HG23	8:H:579:SER:O	2.21	0.41
8:H:578:TYR:C	8:H:578:TYR:HD1	2.24	0.41
8:H:950:PHE:CD1	8:H:951:ILE:N	2.88	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:F:63:C:H2'	27:F:64:C:C6	2.55	0.41
1:A:294:ASN:ND2	27:F:32:G:OP1	2.53	0.41
1:A:1054:LEU:HD23	1:A:1054:LEU:HA	1.86	0.41
1:A:1175:GLU:O	1:A:1179:GLY:N	2.49	0.41
1:A:1312:PHE:CD1	1:A:1342:LEU:HD12	2.55	0.41
1:A:1335:TRP:CH2	1:A:1339:LEU:HD13	2.56	0.41
1:A:1405:ILE:HB	1:A:1437:ILE:HD12	2.03	0.41
1:A:1461:TYR:CD1	1:A:1461:TYR:O	2.74	0.41
1:A:1578:ALA:CB	1:A:1602:PRO:HB3	2.48	0.41
1:A:1582:GLU:OE2	1:A:1586:GLN:NE2	2.53	0.41
1:A:1594:GLN:NE2	1:A:1594:GLN:CA	2.83	0.41
2:B:405:ASP:OD2	2:B:408:LYS:HD2	2.21	0.41
2:B:456:GLY:C	2:B:458:ASP:N	2.71	0.41
4:G:255:ARG:O	4:G:256:LYS:CB	2.68	0.41
5:K:159:TYR:CZ	5:K:163:ASN:ND2	2.88	0.41
7:M:5:ASN:HD21	7:M:61:ILE:HG21	1.85	0.41
7:M:58:CYS:SG	7:M:98:ILE:HG21	2.60	0.41
8:H:362:LYS:CG	8:H:363:PRO:HD2	2.50	0.41
8:H:461:LYS:HZ2	8:H:464:PRO:CB	2.34	0.41
8:H:475:THR:CG2	8:H:483:TRP:O	2.68	0.41
25:D:87:U:O5'	25:D:87:U:H6	2.04	0.41
27:F:49:U:H2'	27:F:50:G:H8	1.84	0.41
1:A:166:LYS:C	1:A:169:PRO:HD2	2.39	0.41
1:A:473:THR:HG23	1:A:474:LYS:N	2.35	0.41
1:A:778:LYS:HE2	1:A:778:LYS:CA	2.50	0.41
1:A:1051:GLU:O	1:A:1246:ALA:HA	2.21	0.41
1:A:1088:VAL:HG12	1:A:1089:VAL:N	2.36	0.41
1:A:1308:GLU:OE1	1:A:1346:PHE:CZ	2.70	0.41
2:B:177:PRO:N	2:B:195:TRP:HD1	2.18	0.41
2:B:408:LYS:O	2:B:424:SER:CB	2.68	0.41
4:G:677:ILE:O	4:G:681:MET:HG2	2.20	0.41
5:K:158:ILE:HG13	5:K:159:TYR:N	2.34	0.41
5:K:159:TYR:CD1	5:K:163:ASN:ND2	2.76	0.41
8:H:352:VAL:HG13	8:H:352:VAL:O	2.21	0.41
8:H:365:GLU:O	8:H:366:ASN:HB2	2.20	0.41
8:H:792:LYS:O	8:H:796:ILE:N	2.43	0.41
25:D:49:A:N6	25:D:50:G:C6	2.88	0.41
1:A:258:ILE:HG21	1:A:640:ARG:HG3	2.03	0.41
1:A:691:PHE:CD1	1:A:691:PHE:O	2.73	0.41
1:A:750:LEU:HD23	1:A:752:ALA:HB3	2.03	0.41
1:A:1011:ASN:ND2	1:A:1143:GLU:O	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1144:PHE:HZ	1:A:1162:THR:HG21	1.85	0.41
1:A:1195:PHE:HB3	1:A:1217:ARG:HH11	1.82	0.41
1:A:1795:LYS:N	1:A:1796:PRO:HD2	2.36	0.41
2:B:196:ALA:C	2:B:219:GLY:O	2.58	0.41
3:I:259:ILE:HD13	3:I:259:ILE:HG21	1.76	0.41
3:I:321:LYS:HG3	3:I:324:ASP:O	2.21	0.41
3:I:358:ILE:CG2	3:I:359:PRO:N	2.84	0.41
4:G:19:ILE:CD1	4:G:20:GLY:N	2.81	0.41
4:G:669:LYS:O	4:G:673:GLN:HG3	2.21	0.41
4:G:804:ASP:OD1	4:G:805:HIS:N	2.53	0.41
4:G:851:ARG:C	4:G:852:LEU:CD1	2.89	0.41
5:K:303:LEU:C	5:K:303:LEU:CD2	2.84	0.41
5:K:330:ASN:HD22	5:K:331:VAL:HG23	1.85	0.41
6:L:95:PHE:HD1	6:L:133:SER:CB	2.33	0.41
8:H:132:ARG:O	8:H:133:ILE:CG1	2.66	0.41
8:H:178:LEU:N	8:H:178:LEU:CD2	2.83	0.41
8:H:386:SER:O	8:H:390:SER:CB	2.69	0.41
24:C:9:G:O5'	24:C:9:G:H8	2.04	0.41
25:D:48:C:H2'	25:D:48:C:O2	2.20	0.41
27:F:46:C:H2'	27:F:47:U:C6	2.55	0.41
1:A:331:PHE:CD2	1:A:509:HIS:CE1	3.09	0.41
1:A:767:LEU:HD21	1:A:779:ALA:HB1	2.00	0.41
1:A:882:ILE:HD13	1:A:1238:LEU:HD21	2.03	0.41
1:A:1067:ASN:HD22	1:A:1067:ASN:HA	1.62	0.41
1:A:1174:PHE:HD2	1:A:1222:LEU:HD11	1.85	0.41
1:A:1183:THR:CG2	1:A:1184:ASP:N	2.83	0.41
1:A:1461:TYR:CD1	1:A:1461:TYR:C	2.94	0.41
1:A:1464:LYS:HZ2	1:A:1479:GLU:HB3	1.86	0.41
1:A:1594:GLN:HE21	1:A:1594:GLN:CA	2.33	0.41
1:A:2032:ILE:HD13	1:A:2043:PHE:CE1	2.56	0.41
2:B:68:ASP:OD1	2:B:69:VAL:N	2.53	0.41
2:B:267:ARG:HG3	2:B:285:HIS:HD2	1.82	0.41
2:B:275:PRO:HG3	2:B:319:GLY:HA2	2.02	0.41
2:B:383:GLU:OE1	2:B:383:GLU:HA	2.21	0.41
2:B:419:ILE:HG21	2:B:419:ILE:HD13	1.89	0.41
3:I:40:LYS:O	3:I:44:PHE:N	2.44	0.41
3:I:271:GLU:O	3:I:272:LEU:HB3	2.19	0.41
4:G:284:LEU:HD22	4:G:284:LEU:N	2.36	0.41
6:L:33:ARG:CD	6:L:65:ASP:OD2	2.54	0.41
7:M:36:GLY:CA	26:E:30:G:O2'	2.69	0.41
8:H:449:PHE:CD1	8:H:453:THR:HG23	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:578:TYR:CE2	8:H:589:LEU:CD1	3.04	0.41
8:H:586:MET:O	8:H:586:MET:SD	2.79	0.41
8:H:615:LEU:HB3	8:H:616:PRO:HD3	2.02	0.41
8:H:808:LEU:HD11	8:H:855:PRO:HB2	2.01	0.41
8:H:906:VAL:HA	8:H:907:PRO:HD3	1.97	0.41
8:H:908:VAL:HG13	8:H:909:ILE:N	2.34	0.41
8:H:950:PHE:CG	8:H:951:ILE:N	2.89	0.41
25:D:49:A:C2'	25:D:50:G:O5'	2.69	0.41
26:E:2:U:C5	26:E:3:C:H5	2.32	0.41
27:F:96:U:P	27:F:96:U:O4'	2.79	0.41
1:A:160:ALA:HB1	1:A:194:HIS:HE1	1.79	0.41
1:A:294:ASN:OD1	1:A:300:LYS:HE3	2.18	0.41
1:A:795:ALA:HA	1:A:1095:MET:HE2	1.94	0.41
1:A:863:ARG:NH2	1:A:1059:GLU:HB3	2.36	0.41
2:B:235:ILE:CD1	2:B:280:ILE:HG21	2.51	0.41
2:B:418:LEU:HD23	2:B:434:ALA:HB2	2.02	0.41
5:K:158:ILE:HG13	5:K:159:TYR:H	1.86	0.41
5:K:427:THR:OG1	5:K:428:TRP:N	2.54	0.41
8:H:116:THR:CG2	8:H:158:HIS:HD2	2.16	0.41
8:H:117:ARG:NE	8:H:156:ASP:O	2.54	0.41
8:H:486:VAL:HG22	8:H:487:ARG:N	2.36	0.41
8:H:576:THR:CG2	8:H:592:PHE:H	2.14	0.41
25:D:87:U:H3'	25:D:87:U:H6	1.86	0.41
1:A:543:ASN:ND2	1:A:544:LYS:HB2	2.36	0.40
1:A:867:ILE:HG22	1:A:867:ILE:O	2.21	0.40
1:A:1481:GLU:OE2	4:G:256:LYS:HD3	2.20	0.40
1:A:1623:PHE:CZ	24:C:5:G:C4	3.09	0.40
6:L:9:LEU:HD11	6:L:60:TYR:CB	2.51	0.40
6:L:97:THR:HG23	6:L:99:ASN:H	1.86	0.40
8:H:122:TYR:HD1	8:H:122:TYR:O	2.05	0.40
8:H:123:MET:SD	8:H:209:MET:SD	3.19	0.40
8:H:164:MET:HG2	8:H:175:LEU:CD1	2.50	0.40
8:H:305:SER:O	8:H:307:ILE:N	2.55	0.40
1:A:175:LEU:HD12	1:A:564:TRP:HE1	1.86	0.40
1:A:574:GLN:HA	1:A:574:GLN:OE1	2.21	0.40
1:A:1029:THR:HG22	1:A:1260:PHE:HZ	1.85	0.40
1:A:1049:LEU:HD11	1:A:1258:LEU:HD21	2.04	0.40
1:A:1203:ASN:N	1:A:1203:ASN:OD1	2.54	0.40
2:B:162:MET:HG3	2:B:421:VAL:HG11	2.03	0.40
2:B:366:THR:O	2:B:373:ILE:HA	2.22	0.40
4:G:302:PHE:O	4:G:303:ASN:OD1	2.39	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:178:LEU:HD13	8:H:194:ASN:O	2.20	0.40
8:H:187:ARG:HD3	8:H:650:LEU:HD11	2.02	0.40
8:H:589:LEU:O	8:H:589:LEU:HG	2.20	0.40
8:H:737:ILE:HG12	8:H:768:PHE:HB3	2.03	0.40
26:E:1:A:C6	29:E:201:M7M:HBZB	2.56	0.40
1:A:141:LYS:CA	1:A:144:ASN:CG	2.89	0.40
1:A:1182:LEU:HD23	1:A:1182:LEU:HA	1.91	0.40
1:A:1653:LEU:CD2	1:A:1815:LEU:HD23	2.48	0.40
3:I:161:LEU:HB3	3:I:167:LEU:HD12	2.03	0.40
3:I:222:ILE:HD13	3:I:222:ILE:HA	1.89	0.40
4:G:278:TRP:CE2	4:G:298:THR:HB	2.52	0.40
6:L:25:ARG:HB2	6:L:25:ARG:NH1	2.27	0.40
6:L:34:LYS:HD2	6:L:34:LYS:N	2.35	0.40
8:H:500:ARG:CD	8:H:534:THR:CB	2.88	0.40
8:H:796:ILE:HD12	8:H:796:ILE:HA	1.87	0.40
8:H:951:ILE:CB	8:H:952:PRO:HD2	2.30	0.40
25:D:62:A:C2'	25:D:63:G:C5'	2.98	0.40
27:F:103:A:C4	27:F:104:G:C8	3.10	0.40
1:A:287:GLU:H	1:A:287:GLU:HG3	1.47	0.40
1:A:297:SER:HB2	27:F:32:G:P	2.59	0.40
1:A:510:PRO:O	1:A:514:TYR:CE1	2.74	0.40
1:A:766:ILE:HG21	1:A:782:ILE:HG21	2.03	0.40
1:A:1790:TRP:CD1	1:A:1795:LYS:HE3	2.56	0.40
1:A:1887:GLY:O	1:A:1990:ASN:HA	2.21	0.40
2:B:173:VAL:HA	2:B:200:GLN:OE1	2.20	0.40
2:B:311:PHE:HE2	7:M:126:ILE:HD13	1.84	0.40
3:I:248:VAL:HG11	3:I:317:ASP:HB3	2.03	0.40
3:I:415:THR:O	3:I:418:GLN:N	2.52	0.40
5:K:339:CYS:SG	5:K:340:LYS:N	2.94	0.40
8:H:135:ASN:ND2	8:H:487:ARG:HH21	2.18	0.40
8:H:189:LEU:HD12	8:H:190:SER:O	2.22	0.40
8:H:247:PHE:HD1	8:H:903:ARG:NH1	2.18	0.40
8:H:586:MET:C	8:H:586:MET:SD	3.00	0.40
27:F:43:G:N3	27:F:44:A:N7	2.69	0.40
27:F:77:A:C1'	27:F:78:A:H5'	2.45	0.40
1:A:143:ILE:HA	1:A:146:HIS:HB3	2.03	0.40
1:A:168:LEU:N	1:A:169:PRO:HD2	2.36	0.40
1:A:298:TYR:CE1	1:A:493:MET:CE	3.00	0.40
1:A:305:LEU:N	1:A:306:PRO:HD2	2.36	0.40
1:A:770:MET:CE	1:A:778:LYS:HB3	2.51	0.40
3:I:402:ASP:O	3:I:403:SER:C	2.60	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:256:LYS:O	4:G:257:PHE:HB3	2.21	0.40
5:K:244:LEU:HD23	5:K:244:LEU:HA	1.69	0.40
8:H:375:GLU:HG2	8:H:376:PHE:CE1	2.57	0.40
8:H:942:GLY:CA	8:H:960:ASN:O	2.70	0.40
25:D:49:A:C3'	25:D:50:G:C5'	2.99	0.40
27:F:94:C:H5"	27:F:94:C:C6	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	2166/2413 (90%)	2019 (93%)	110 (5%)	37 (2%)	9 43
2	B	425/465 (91%)	380 (89%)	36 (8%)	9 (2%)	7 40
3	I	410/494 (83%)	380 (93%)	24 (6%)	6 (2%)	10 46
4	G	684/899 (76%)	604 (88%)	64 (9%)	16 (2%)	6 38
5	K	273/469 (58%)	247 (90%)	21 (8%)	5 (2%)	8 42
6	L	137/143 (96%)	129 (94%)	6 (4%)	2 (2%)	10 46
7	M	124/126 (98%)	118 (95%)	4 (3%)	2 (2%)	9 44
8	H	837/1008 (83%)	770 (92%)	47 (6%)	20 (2%)	6 37
9	N	1674/2163 (77%)	1555 (93%)	109 (6%)	10 (1%)	25 62
10	J	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	5 36
10	R	77/101 (76%)	69 (90%)	6 (8%)	2 (3%)	5 36
11	O	69/196 (35%)	63 (91%)	6 (9%)	0	100 100
11	S	69/196 (35%)	63 (91%)	6 (9%)	0	100 100
12	P	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	11 46
12	T	71/146 (49%)	66 (93%)	4 (6%)	1 (1%)	11 46

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	Q	85/110 (77%)	82 (96%)	3 (4%)	0	100	100
13	U	86/110 (78%)	83 (96%)	3 (4%)	0	100	100
14	V	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
14	Y	66/94 (70%)	62 (94%)	4 (6%)	0	100	100
15	W	66/86 (77%)	59 (89%)	4 (6%)	3 (4%)	2	25
15	Z	66/86 (77%)	60 (91%)	3 (4%)	3 (4%)	2	25
16	X	64/77 (83%)	58 (91%)	6 (9%)	0	100	100
16	a	65/77 (84%)	59 (91%)	6 (9%)	0	100	100
17	b	63/109 (58%)	61 (97%)	2 (3%)	0	100	100
18	c	90/95 (95%)	83 (92%)	7 (8%)	0	100	100
19	d	75/89 (84%)	71 (95%)	4 (5%)	0	100	100
20	e	72/86 (84%)	70 (97%)	2 (3%)	0	100	100
21	f	73/93 (78%)	69 (94%)	3 (4%)	1 (1%)	11	46
22	g	62/115 (54%)	62 (100%)	0	0	100	100
23	h	73/187 (39%)	72 (99%)	1 (1%)	0	100	100
All	All	8236/10574 (78%)	7611 (92%)	505 (6%)	120 (2%)	14	46

All (120) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ALA
1	A	157	ASP
1	A	239	PHE
1	A	240	PRO
1	A	259	GLU
1	A	264	ILE
1	A	287	GLU
1	A	546	LYS
1	A	645	ASP
1	A	699	PRO
1	A	1044	GLY
1	A	1403	SER
2	B	113	ALA
2	B	171	GLN
2	B	276	SER
2	B	395	ILE
3	I	266	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	I	328	VAL
3	I	434	GLN
4	G	10	GLU
4	G	287	SER
4	G	700	ASN
5	K	147	ASP
8	H	115	LYS
8	H	133	ILE
8	H	356	LYS
8	H	364	PHE
8	H	431	GLN
8	H	704	PRO
8	H	829	VAL
8	H	884	ARG
8	H	952	PRO
9	N	766	ILE
9	N	1200	PRO
1	A	156	THR
1	A	554	THR
1	A	803	GLY
1	A	1088	VAL
2	B	449	SER
3	I	152	ASN
4	G	112	ALA
5	K	220	PRO
5	K	332	GLU
8	H	146	LYS
8	H	350	GLY
8	H	366	ASN
8	H	367	VAL
8	H	508	GLU
9	N	1693	HIS
10	R	40	MET
12	T	12	ASN
15	W	24	ASN
15	W	49	PHE
10	J	40	MET
12	P	12	ASN
15	Z	24	ASN
15	Z	49	PHE
1	A	261	LEU
1	A	539	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	750	LEU
1	A	875	THR
1	A	1015	PRO
2	B	384	GLY
4	G	11	PRO
4	G	105	ALA
4	G	734	PRO
6	L	75	GLU
8	H	488	ILE
9	N	492	PRO
9	N	1936	ARG
1	A	407	VAL
1	A	511	ASP
1	A	538	LEU
1	A	701	CYS
1	A	1087	ASN
1	A	1621	VAL
1	A	2019	GLU
2	B	204	SER
2	B	210	LEU
2	B	347	GLY
4	G	256	LYS
4	G	769	SER
4	G	819	ALA
5	K	283	ASN
8	H	119	ASN
9	N	1555	GLU
9	N	1968	ASN
1	A	300	LYS
1	A	377	VAL
1	A	841	GLU
1	A	1379	MET
1	A	1380	PRO
4	G	782	LYS
8	H	171	GLY
8	H	305	SER
15	W	50	ASN
15	Z	50	ASN
1	A	802	PRO
4	G	239	THR
4	G	257	PHE
4	G	887	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	L	78	ASP
7	M	60	PRO
8	H	134	ILE
9	N	622	LEU
9	N	1202	MET
10	R	51	GLU
10	J	51	GLU
1	A	406	PRO
4	G	698	VAL
7	M	10	PRO
9	N	791	PRO
4	G	414	PRO
1	A	644	VAL
5	K	222	PRO
21	f	41	VAL
1	A	181	HIS
3	I	132	PRO
3	I	347	ALA
8	H	319	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1749/2182 (80%)	1543 (88%)	206 (12%)	5 26
2	B	374/410 (91%)	321 (86%)	53 (14%)	3 21
3	I	327/445 (74%)	264 (81%)	63 (19%)	1 10
4	G	361/813 (44%)	295 (82%)	66 (18%)	1 11
5	K	253/436 (58%)	228 (90%)	25 (10%)	8 32
6	L	129/132 (98%)	113 (88%)	16 (12%)	4 24
7	M	104/104 (100%)	98 (94%)	6 (6%)	20 51
8	H	757/910 (83%)	639 (84%)	118 (16%)	2 17
All	All	4054/5432 (75%)	3501 (86%)	553 (14%)	7 22

All (553) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	131	LYS
1	A	147	SER
1	A	148	ASP
1	A	152	LYS
1	A	153	MET
1	A	154	TYR
1	A	156	THR
1	A	158	LYS
1	A	162	LEU
1	A	165	LEU
1	A	166	LYS
1	A	168	LEU
1	A	175	LEU
1	A	177	GLU
1	A	187	LYS
1	A	224	MET
1	A	229	ARG
1	A	249	LEU
1	A	252	GLU
1	A	254	HIS
1	A	256	GLU
1	A	257	ASN
1	A	261	LEU
1	A	266	LEU
1	A	268	LEU
1	A	273	ASP
1	A	275	TYR
1	A	279	TRP
1	A	283	SER
1	A	287	GLU
1	A	288	GLU
1	A	291	LYS
1	A	294	ASN
1	A	298	TYR
1	A	299	LYS
1	A	313	ARG
1	A	321	GLU
1	A	324	ASP
1	A	325	LYS
1	A	328	TYR
1	A	331	PHE
1	A	351	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	353	GLU
1	A	355	LEU
1	A	358	ARG
1	A	360	GLU
1	A	361	GLU
1	A	362	GLU
1	A	363	ASP
1	A	364	TYR
1	A	367	PHE
1	A	371	ASP
1	A	372	ARG
1	A	376	ARG
1	A	408	SER
1	A	409	CYS
1	A	412	GLN
1	A	413	ASN
1	A	414	ASP
1	A	416	GLU
1	A	418	ASP
1	A	425	ASP
1	A	427	SER
1	A	454	LEU
1	A	456	GLU
1	A	458	PHE
1	A	462	LEU
1	A	468	LEU
1	A	469	ILE
1	A	472	ASN
1	A	474	LYS
1	A	501	LEU
1	A	503	LYS
1	A	504	LYS
1	A	507	LEU
1	A	511	ASP
1	A	514	TYR
1	A	543	ASN
1	A	544	LYS
1	A	545	THR
1	A	546	LYS
1	A	547	LEU
1	A	549	LYS
1	A	555	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	581	LEU
1	A	608	LYS
1	A	611	LYS
1	A	614	ARG
1	A	678	ARG
1	A	691	PHE
1	A	703	PHE
1	A	749	ARG
1	A	758	LEU
1	A	768	GLU
1	A	774	ILE
1	A	776	GLN
1	A	777	LYS
1	A	778	LYS
1	A	786	LEU
1	A	813	GLU
1	A	815	TYR
1	A	817	LYS
1	A	841	GLU
1	A	842	LYS
1	A	844	MET
1	A	849	LEU
1	A	852	LEU
1	A	858	LYS
1	A	861	GLN
1	A	862	GLU
1	A	878	GLU
1	A	880	THR
1	A	909	THR
1	A	932	SER
1	A	933	GLU
1	A	937	LEU
1	A	955	LYS
1	A	956	LYS
1	A	959	LEU
1	A	960	THR
1	A	992	ASP
1	A	995	LEU
1	A	1002	GLU
1	A	1035	LEU
1	A	1066	LEU
1	A	1067	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1068	ARG
1	A	1083	THR
1	A	1088	VAL
1	A	1095	MET
1	A	1105	ARG
1	A	1109	PHE
1	A	1115	GLN
1	A	1128	GLN
1	A	1170	MET
1	A	1183	THR
1	A	1202	ASN
1	A	1214	ARG
1	A	1217	ARG
1	A	1222	LEU
1	A	1262	MET
1	A	1275	MET
1	A	1276	GLU
1	A	1282	ASP
1	A	1314	SER
1	A	1317	ARG
1	A	1329	THR
1	A	1339	LEU
1	A	1344	THR
1	A	1354	GLU
1	A	1356	LEU
1	A	1358	ASP
1	A	1365	THR
1	A	1366	ARG
1	A	1382	ARG
1	A	1383	PHE
1	A	1405	ILE
1	A	1415	SER
1	A	1416	LYS
1	A	1418	THR
1	A	1460	GLU
1	A	1461	TYR
1	A	1465	ARG
1	A	1470	GLN
1	A	1473	ARG
1	A	1490	ARG
1	A	1499	ARG
1	A	1500	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1509	ARG
1	A	1511	ARG
1	A	1519	LEU
1	A	1590	LEU
1	A	1594	GLN
1	A	1616	ARG
1	A	1618	ASN
1	A	1627	LEU
1	A	1629	LEU
1	A	1650	ARG
1	A	1652	HIS
1	A	1661	ILE
1	A	1663	PHE
1	A	1690	LYS
1	A	1755	LYS
1	A	1762	ASP
1	A	1839	ASN
1	A	1882	LEU
1	A	1885	LYS
1	A	1888	HIS
1	A	1892	LYS
1	A	1908	LEU
1	A	1910	LYS
1	A	1912	LYS
1	A	1915	GLU
1	A	1916	GLU
1	A	1920	LEU
1	A	1951	PHE
1	A	1973	LYS
1	A	2007	ARG
1	A	2013	ARG
1	A	2023	LYS
1	A	2065	ARG
1	A	2067	TYR
1	A	2068	ASN
1	A	2071	ILE
1	A	2076	GLN
1	A	2078	GLU
2	B	47	GLU
2	B	48	ASP
2	B	66	ASN
2	B	73	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	75	ARG
2	B	114	THR
2	B	117	LEU
2	B	119	PHE
2	B	122	ARG
2	B	123	PHE
2	B	128	SER
2	B	129	LEU
2	B	132	SER
2	B	133	ARG
2	B	136	LEU
2	B	137	GLN
2	B	140	MET
2	B	145	LYS
2	B	147	ASN
2	B	155	ARG
2	B	156	ARG
2	B	162	MET
2	B	171	GLN
2	B	172	LEU
2	B	192	THR
2	B	199	LEU
2	B	206	THR
2	B	208	GLN
2	B	244	LYS
2	B	257	LEU
2	B	267	ARG
2	B	276	SER
2	B	287	MET
2	B	313	LEU
2	B	316	GLN
2	B	323	CYS
2	B	333	LEU
2	B	337	ARG
2	B	358	SER
2	B	362	TYR
2	B	382	ASP
2	B	388	GLN
2	B	390	LEU
2	B	393	ARG
2	B	400	ARG
2	B	408	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	409	LYS
2	B	443	LEU
2	B	444	ASP
2	B	446	SER
2	B	447	ASN
2	B	448	ASN
2	B	457	TRP
3	I	92	ILE
3	I	93	LYS
3	I	94	LEU
3	I	107	SER
3	I	118	SER
3	I	135	LEU
3	I	145	GLU
3	I	155	ASP
3	I	161	LEU
3	I	164	LYS
3	I	173	LEU
3	I	184	LYS
3	I	186	LYS
3	I	187	GLU
3	I	189	LEU
3	I	190	ASP
3	I	198	LEU
3	I	204	LEU
3	I	205	GLU
3	I	208	TRP
3	I	209	LYS
3	I	210	LEU
3	I	236	GLU
3	I	249	LEU
3	I	252	SER
3	I	253	ARG
3	I	257	CYS
3	I	264	LYS
3	I	268	LEU
3	I	271	GLU
3	I	272	LEU
3	I	273	HIS
3	I	280	ARG
3	I	281	GLN
3	I	312	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	I	317	ASP
3	I	320	GLN
3	I	321	LYS
3	I	325	ARG
3	I	327	THR
3	I	342	ARG
3	I	344	LEU
3	I	346	GLU
3	I	350	ILE
3	I	353	THR
3	I	362	GLN
3	I	364	LYS
3	I	370	ARG
3	I	373	ARG
3	I	374	LYS
3	I	380	ARG
3	I	393	PHE
3	I	395	LYS
3	I	401	LEU
3	I	427	SER
3	I	428	ARG
3	I	429	ARG
3	I	433	ASN
3	I	436	LYS
3	I	447	GLU
3	I	450	GLN
3	I	454	GLU
3	I	456	LEU
4	G	5	SER
4	G	9	GLN
4	G	15	TYR
4	G	24	THR
4	G	99	ASN
4	G	100	VAL
4	G	102	ARG
4	G	107	LEU
4	G	108	LYS
4	G	126	THR
4	G	129	THR
4	G	130	ARG
4	G	134	ARG
4	G	138	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	G	140	GLN
4	G	141	LEU
4	G	143	ARG
4	G	156	ASN
4	G	159	LEU
4	G	160	ASN
4	G	161	LYS
4	G	162	LEU
4	G	164	GLU
4	G	165	GLU
4	G	168	LYS
4	G	169	LEU
4	G	170	LEU
4	G	171	GLN
4	G	176	GLU
4	G	214	SER
4	G	216	SER
4	G	221	GLU
4	G	222	ASP
4	G	226	MET
4	G	227	ARG
4	G	230	LEU
4	G	232	SER
4	G	251	GLU
4	G	252	GLU
4	G	268	CYS
4	G	274	SER
4	G	275	SER
4	G	276	ASP
4	G	277	ILE
4	G	281	ASN
4	G	284	LEU
4	G	291	TYR
4	G	671	PHE
4	G	678	TYR
4	G	686	MET
4	G	687	SER
4	G	688	ARG
4	G	689	GLU
4	G	696	ARG
4	G	700	ASN
4	G	721	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	G	852	LEU
4	G	854	LYS
4	G	855	ASP
4	G	859	LEU
4	G	861	ASN
4	G	862	MET
4	G	863	PHE
4	G	886	CYS
4	G	887	THR
4	G	889	ARG
5	K	142	LEU
5	K	147	ASP
5	K	166	TYR
5	K	171	THR
5	K	174	LEU
5	K	243	ARG
5	K	245	ARG
5	K	248	ARG
5	K	249	ARG
5	K	250	LYS
5	K	261	LYS
5	K	298	LYS
5	K	299	ASP
5	K	310	GLU
5	K	317	GLU
5	K	323	ARG
5	K	328	ASN
5	K	329	MET
5	K	332	GLU
5	K	333	LYS
5	K	362	GLU
5	K	399	ARG
5	K	448	GLN
5	K	457	GLN
5	K	459	ASP
6	L	25	ARG
6	L	34	LYS
6	L	63	ASP
6	L	73	MET
6	L	77	THR
6	L	78	ASP
6	L	102	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
6	L	108	ASP
6	L	113	MET
6	L	118	GLU
6	L	125	ARG
6	L	133	SER
6	L	135	TYR
6	L	137	TYR
6	L	139	HIS
6	L	140	LYS
7	M	7	LYS
7	M	35	LYS
7	M	46	ARG
7	M	94	SER
7	M	95	ARG
7	M	96	PRO
8	H	107	THR
8	H	108	GLN
8	H	109	LEU
8	H	110	LYS
8	H	111	LYS
8	H	112	ASN
8	H	115	LYS
8	H	116	THR
8	H	117	ARG
8	H	120	ARG
8	H	122	TYR
8	H	132	ARG
8	H	133	ILE
8	H	160	ARG
8	H	166	LYS
8	H	167	ASN
8	H	168	VAL
8	H	173	LYS
8	H	177	TYR
8	H	178	LEU
8	H	187	ARG
8	H	189	LEU
8	H	193	LEU
8	H	202	ASP
8	H	203	LEU
8	H	204	GLU
8	H	205	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	206	LYS
8	H	208	ARG
8	H	222	MET
8	H	235	VAL
8	H	236	LEU
8	H	240	ASP
8	H	265	PHE
8	H	274	ILE
8	H	275	LEU
8	H	296	ASN
8	H	297	SER
8	H	300	LYS
8	H	305	SER
8	H	326	GLU
8	H	329	SER
8	H	330	TYR
8	H	336	ILE
8	H	339	SER
8	H	353	TYR
8	H	354	TYR
8	H	364	PHE
8	H	366	ASN
8	H	368	GLU
8	H	369	LYS
8	H	372	THR
8	H	373	PHE
8	H	389	LEU
8	H	391	MET
8	H	393	LYS
8	H	416	ASP
8	H	448	LEU
8	H	449	PHE
8	H	452	LYS
8	H	456	LEU
8	H	457	SER
8	H	461	LYS
8	H	465	GLU
8	H	469	TRP
8	H	474	LYS
8	H	478	TYR
8	H	487	ARG
8	H	489	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	490	SER
8	H	503	ASP
8	H	505	SER
8	H	508	GLU
8	H	509	SER
8	H	510	ARG
8	H	536	SER
8	H	538	GLU
8	H	545	LEU
8	H	558	LYS
8	H	565	LYS
8	H	568	SER
8	H	569	SER
8	H	573	LYS
8	H	578	TYR
8	H	581	LYS
8	H	582	SER
8	H	583	LYS
8	H	584	GLU
8	H	586	MET
8	H	587	LYS
8	H	589	LEU
8	H	590	LYS
8	H	595	LEU
8	H	603	PHE
8	H	608	GLN
8	H	617	LYS
8	H	652	MET
8	H	797	GLN
8	H	799	PHE
8	H	814	TYR
8	H	884	ARG
8	H	887	ARG
8	H	888	ILE
8	H	889	TYR
8	H	919	ARG
8	H	931	TYR
8	H	932	PHE
8	H	934	HIS
8	H	936	ILE
8	H	945	LEU
8	H	947	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	948	ASP
8	H	959	ILE
8	H	960	ASN
8	H	970	THR
8	H	971	ARG
8	H	972	ARG
8	H	974	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	HIS
1	A	254	HIS
1	A	310	ASN
1	A	326	ASN
1	A	344	ASN
1	A	392	ASN
1	A	413	ASN
1	A	429	ASN
1	A	497	GLN
1	A	543	ASN
1	A	592	HIS
1	A	868	GLN
1	A	948	HIS
1	A	976	GLN
1	A	1067	ASN
1	A	1115	GLN
1	A	1128	GLN
1	A	1156	HIS
1	A	1496	GLN
1	A	1594	GLN
1	A	1603	ASN
1	A	1615	ASN
1	A	1652	HIS
1	A	1809	ASN
1	A	1839	ASN
2	B	144	GLN
2	B	208	GLN
2	B	227	HIS
2	B	232	ASN
2	B	247	GLN
2	B	274	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	316	GLN
2	B	374	ASN
2	B	392	HIS
2	B	420	ASN
2	B	447	ASN
2	B	448	ASN
2	B	450	HIS
3	I	113	HIS
3	I	146	ASN
3	I	148	ASN
3	I	152	ASN
3	I	196	GLN
3	I	201	ASN
3	I	211	GLN
3	I	267	HIS
3	I	281	GLN
3	I	398	GLN
3	I	414	ASN
3	I	433	ASN
3	I	449	ASN
3	I	461	HIS
4	G	99	ASN
4	G	138	GLN
4	G	140	GLN
4	G	160	ASN
4	G	281	ASN
4	G	285	HIS
4	G	668	HIS
4	G	700	ASN
4	G	805	HIS
5	K	163	ASN
5	K	316	HIS
5	K	330	ASN
6	L	14	HIS
6	L	17	GLN
6	L	87	HIS
6	L	139	HIS
7	M	45	ASN
8	H	112	ASN
8	H	135	ASN
8	H	158	HIS
8	H	167	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
8	H	211	ASN
8	H	296	ASN
8	H	334	HIS
8	H	355	HIS
8	H	418	GLN
8	H	444	GLN
8	H	554	HIS
8	H	608	GLN
8	H	721	GLN
8	H	797	GLN
8	H	929	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
24	C	19/20 (95%)	17 (89%)	2 (10%)
25	D	41/112 (36%)	22 (53%)	4 (9%)
26	E	85/160 (53%)	28 (32%)	7 (8%)
27	F	111/214 (51%)	51 (45%)	14 (12%)
All	All	256/506 (50%)	118 (46%)	27 (10%)

All (118) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
24	C	-5	A
24	C	-4	A
24	C	-3	A
24	C	-2	A
24	C	-1	A
24	C	0	U
24	C	1	U
24	C	2	A
24	C	3	A
24	C	4	G
24	C	5	G
24	C	6	U
24	C	7	A
24	C	8	U
24	C	9	G
24	C	10	U
24	C	12	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
25	D	48	C
25	D	49	A
25	D	50	G
25	D	51	A
25	D	52	G
25	D	57	U
25	D	62	A
25	D	63	G
25	D	66	C
25	D	72	C
25	D	75	A
25	D	76	A
25	D	77	G
25	D	78	G
25	D	79	A
25	D	83	A
25	D	84	C
25	D	85	C
25	D	86	G
25	D	87	U
25	D	109	U
25	D	110	U
26	E	2	U
26	E	4	C
26	E	15	G
26	E	18	A
26	E	19	U
26	E	20	A
26	E	25	U
26	E	27	U
26	E	28	C
26	E	30	G
26	E	39	C
26	E	43	C
26	E	48	U
26	E	51	U
26	E	55	U
26	E	56	U
26	E	60	U
26	E	140	G
26	E	141	G
26	E	142	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
26	E	143	A
26	E	144	A
26	E	146	U
26	E	147	U
26	E	148	U
26	E	149	U
26	E	150	G
26	E	151	G
27	F	32	G
27	F	33	U
27	F	34	C
27	F	39	U
27	F	40	C
27	F	41	A
27	F	74	U
27	F	75	A
27	F	76	U
27	F	77	A
27	F	78	A
27	F	79	C
27	F	80	G
27	F	81	A
27	F	82	A
27	F	83	C
27	F	84	A
27	F	90	C
27	F	92	U
27	F	93	G
27	F	94	C
27	F	95	C
27	F	96	U
27	F	97	U
27	F	98	U
27	F	99	U
27	F	100	A
27	F	101	C
27	F	103	A
27	F	104	G
27	F	107	C
27	F	108	C
27	F	109	A
27	F	110	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	F	113	G
27	F	120	G
27	F	121	U
27	F	126	A
27	F	127	U
27	F	164	C
27	F	165	A
27	F	166	U
27	F	167	A
27	F	168	U
27	F	169	U
27	F	170	U
27	F	171	U
27	F	172	U
27	F	173	U
27	F	174	G
27	F	175	G

All (27) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	C	-4	A
24	C	6	U
25	D	48	C
25	D	50	G
25	D	83	A
25	D	85	C
26	E	1	A
26	E	18	A
26	E	19	U
26	E	24	A
26	E	139	A
26	E	142	G
26	E	148	U
27	F	32	G
27	F	33	U
27	F	75	A
27	F	77	A
27	F	81	A
27	F	83	C
27	F	95	C
27	F	97	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
27	F	98	U
27	F	107	C
27	F	163	C
27	F	166	U
27	F	168	U
27	F	172	U

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
29	M7M	E	201	26	29,33,33	1.50	5 (17%)	39,52,52	2.02	7 (17%)
28	GTP	H	1500	-	26,34,34	0.93	1 (3%)	32,54,54	1.62	4 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	M7M	E	201	26	-	6/20/48/48	0/3/3/3
28	GTP	H	1500	-	-	4/18/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	E	201	M7M	CBG-CBO	4.47	1.46	1.37
29	E	201	M7M	CBG-NBH	-3.22	1.32	1.35
29	E	201	M7M	CBF-NBE	-2.80	1.33	1.38
28	H	1500	GTP	C6-N1	-2.41	1.34	1.37
29	E	201	M7M	CBO-NBP	-2.12	1.32	1.35
29	E	201	M7M	CBO-NBN	-2.10	1.33	1.37

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
29	E	201	M7M	NBP-CBI-NBH	-5.79	95.09	103.38
29	E	201	M7M	PBK-OBD-PAZ	-5.05	115.50	132.83
28	H	1500	GTP	PB-O3B-PG	-4.56	117.19	132.83
29	E	201	M7M	PBK-OBU-CBT	4.44	147.72	121.68
28	H	1500	GTP	PA-O3A-PB	-4.06	118.89	132.83
29	E	201	M7M	NBN-CBM-NBV	-3.59	114.98	118.04
29	E	201	M7M	CBG-CBO-NBN	-3.56	117.72	124.00
28	H	1500	GTP	C3'-C2'-C1'	3.39	106.08	100.98
29	E	201	M7M	OBU-PBK-OBL	-3.39	95.83	109.07
29	E	201	M7M	OAY-PAZ-OBA	2.93	122.13	110.68
28	H	1500	GTP	C8-N7-C5	2.50	107.75	102.99

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
29	E	201	M7M	NBE-CBM-NBV-CBW
29	E	201	M7M	NBE-CBM-NBV-CBZ
29	E	201	M7M	NBN-CBM-NBV-CBZ
29	E	201	M7M	CBS-CBT-OBU-PBK
28	H	1500	GTP	O4'-C4'-C5'-O5'
28	H	1500	GTP	C3'-C4'-C5'-O5'
29	E	201	M7M	NBN-CBM-NBV-CBW
29	E	201	M7M	CBX-CBQ-NBP-CBI
28	H	1500	GTP	PB-O3A-PA-O2A
28	H	1500	GTP	PB-O3A-PA-O1A

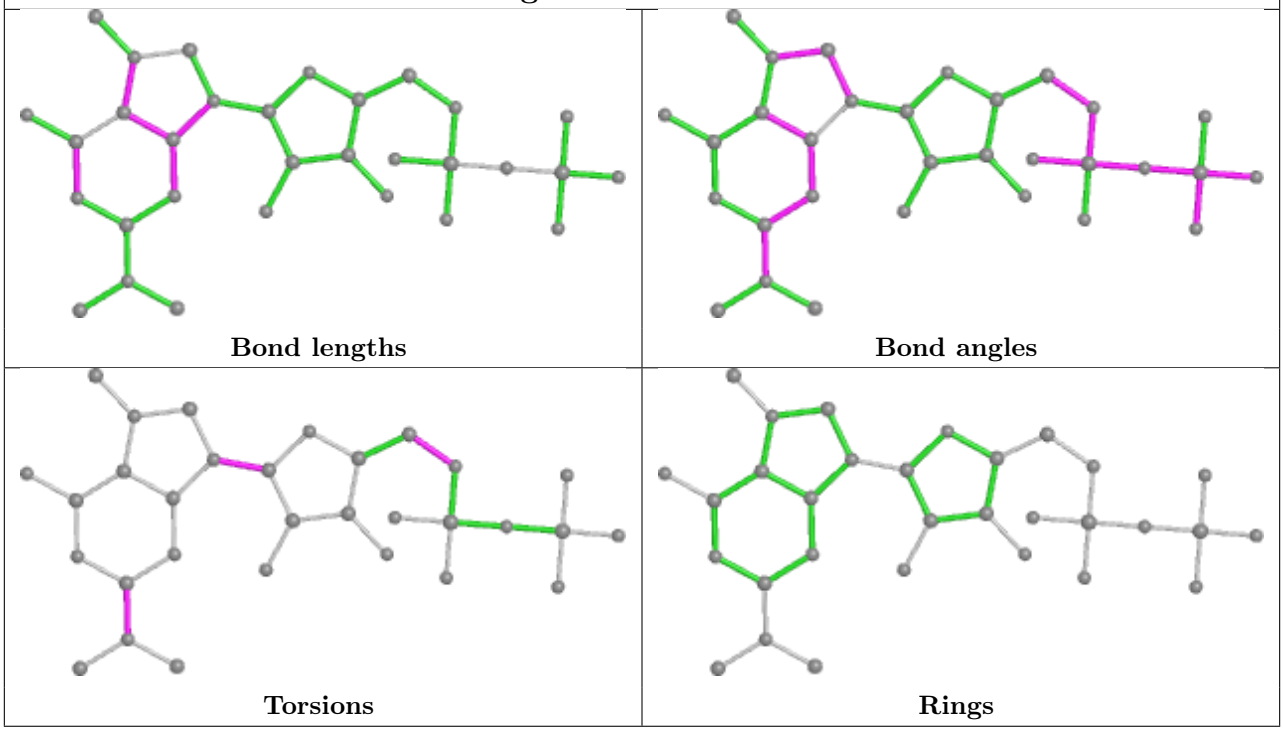
There are no ring outliers.

2 monomers are involved in 16 short contacts:

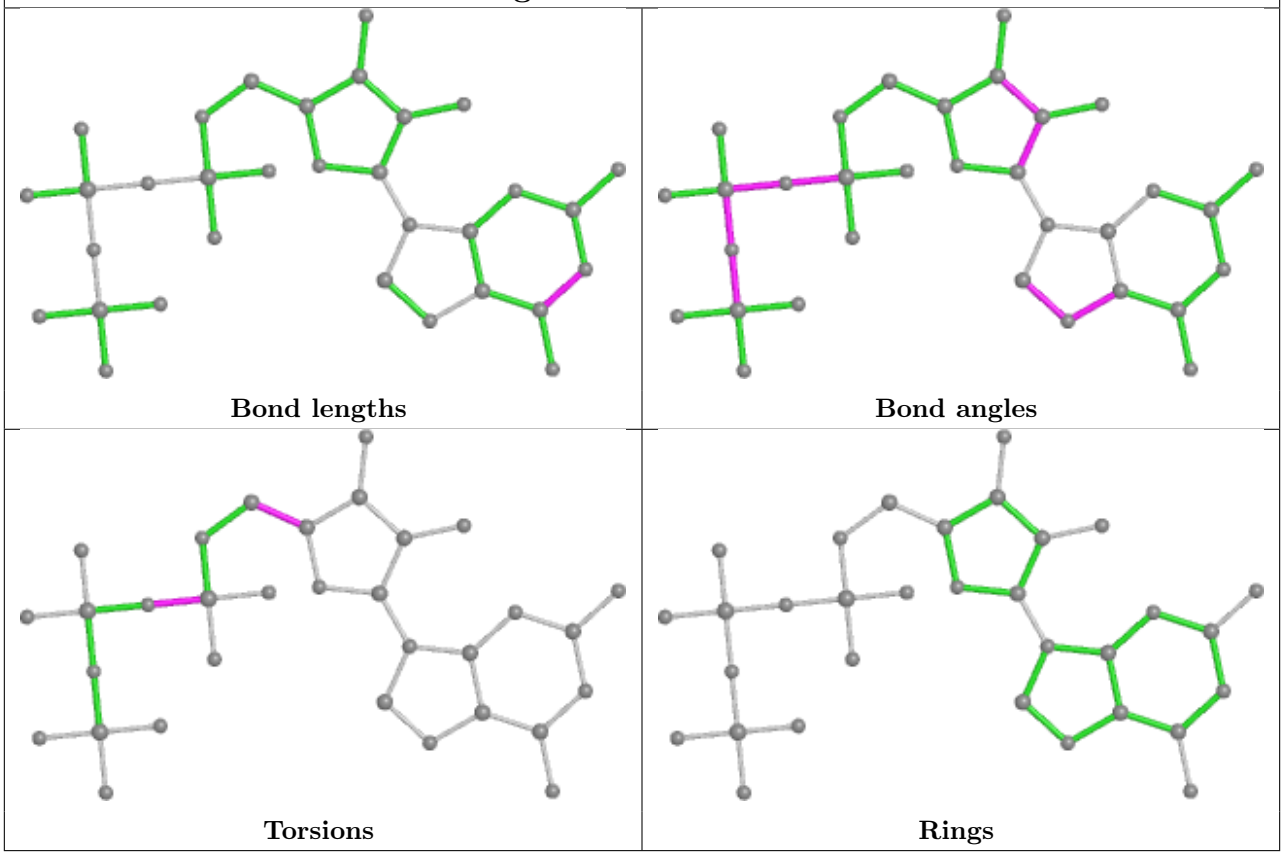
Mol	Chain	Res	Type	Clashes	Symm-Clashes
29	E	201	M7M	6	0
28	H	1500	GTP	10	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand M7M E 201



Ligand GTP H 1500



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

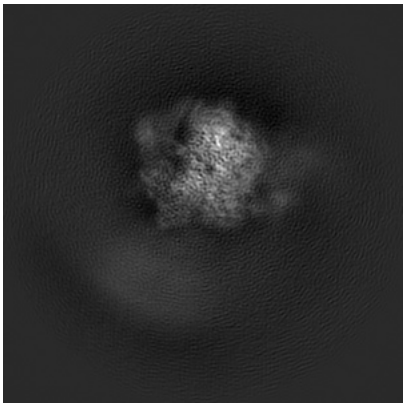
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6561. These allow visual inspection of the internal detail of the map and identification of artifacts.

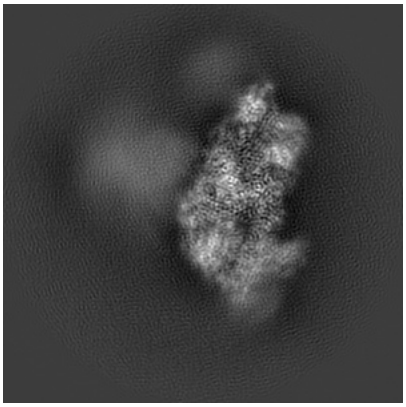
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

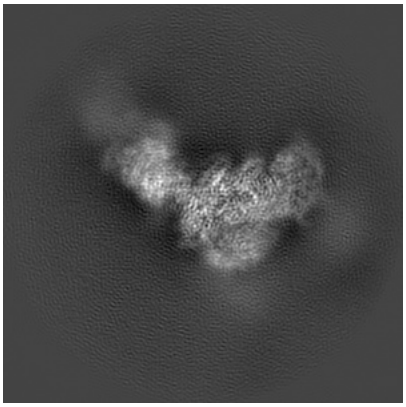
6.1.1 Primary map



X



Y

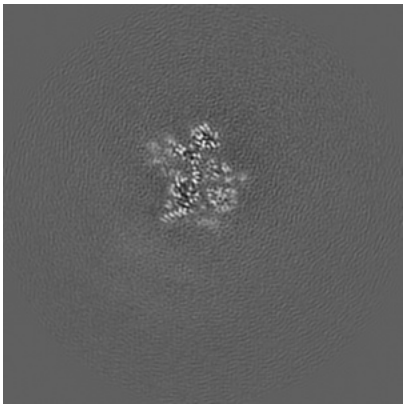


Z

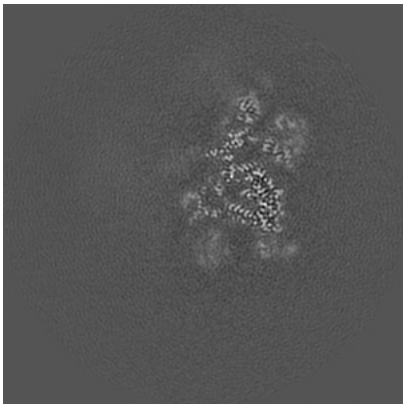
The images above show the map projected in three orthogonal directions.

6.2 Central slices

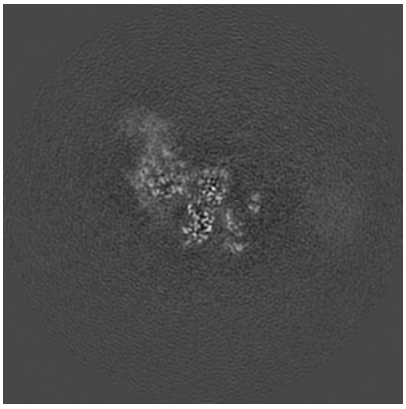
6.2.1 Primary map



X Index: 160



Y Index: 160

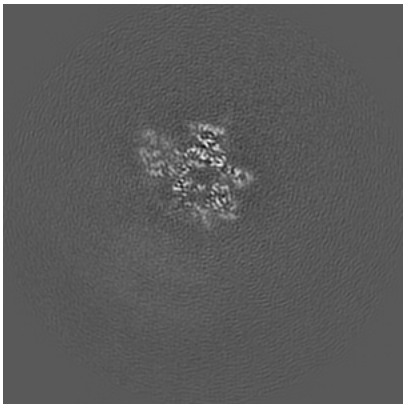


Z Index: 160

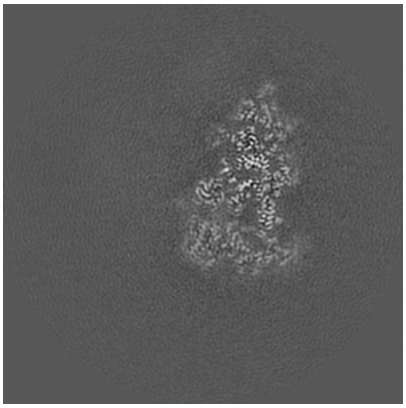
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

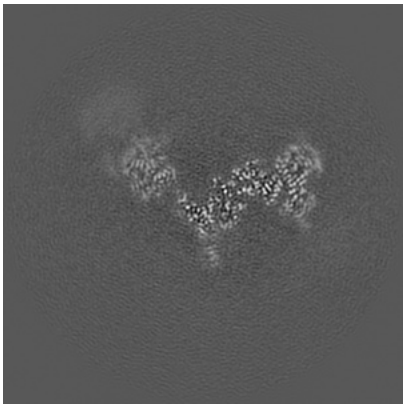
6.3.1 Primary map



X Index: 167



Y Index: 171

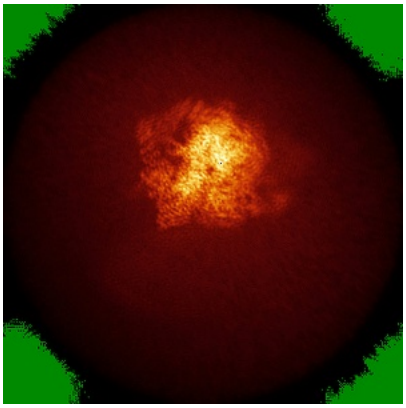


Z Index: 199

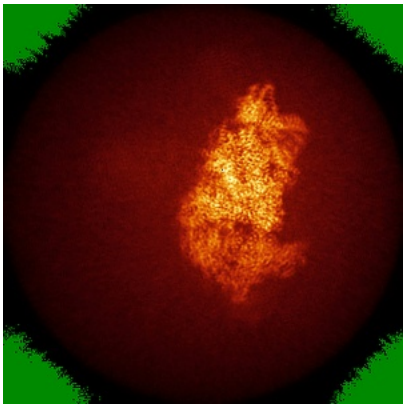
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

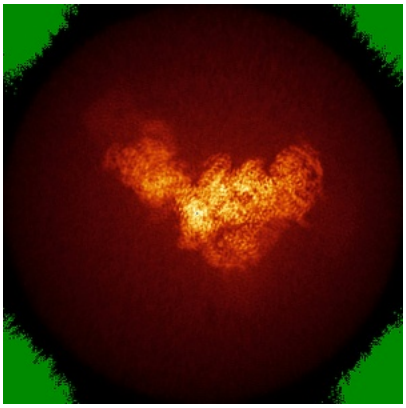
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0147. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

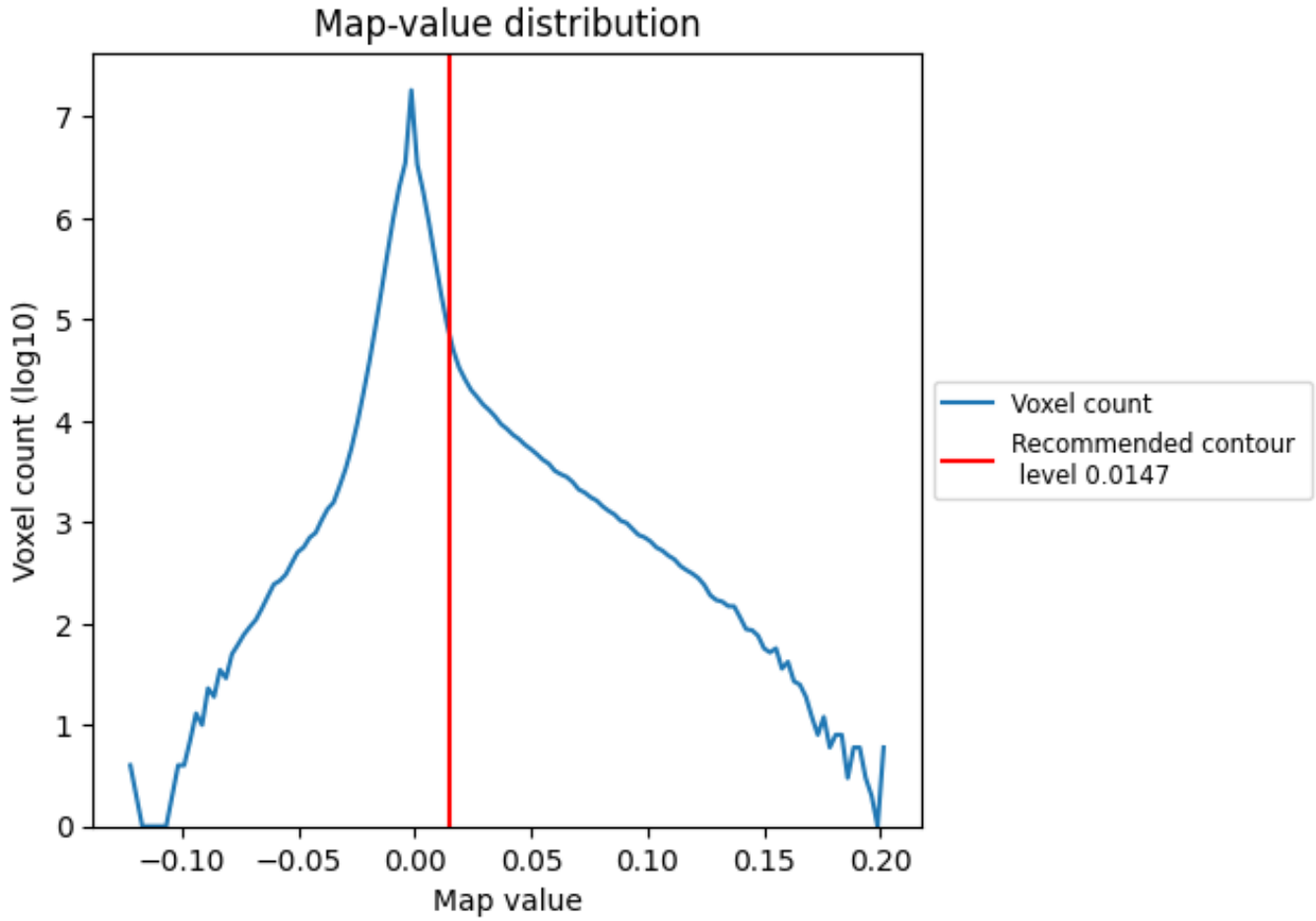
6.6 Mask visualisation (i)

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

7 Map analysis

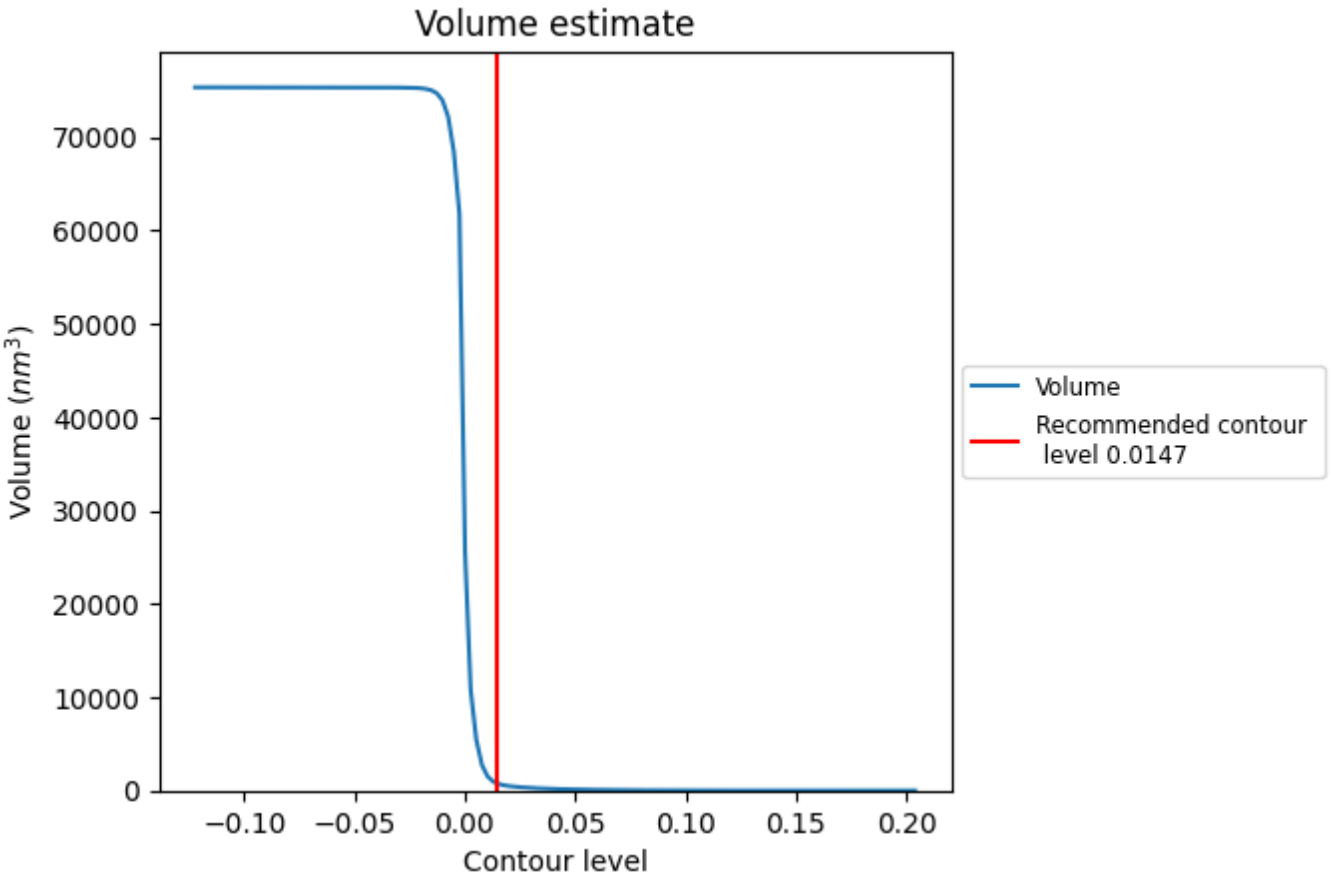
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

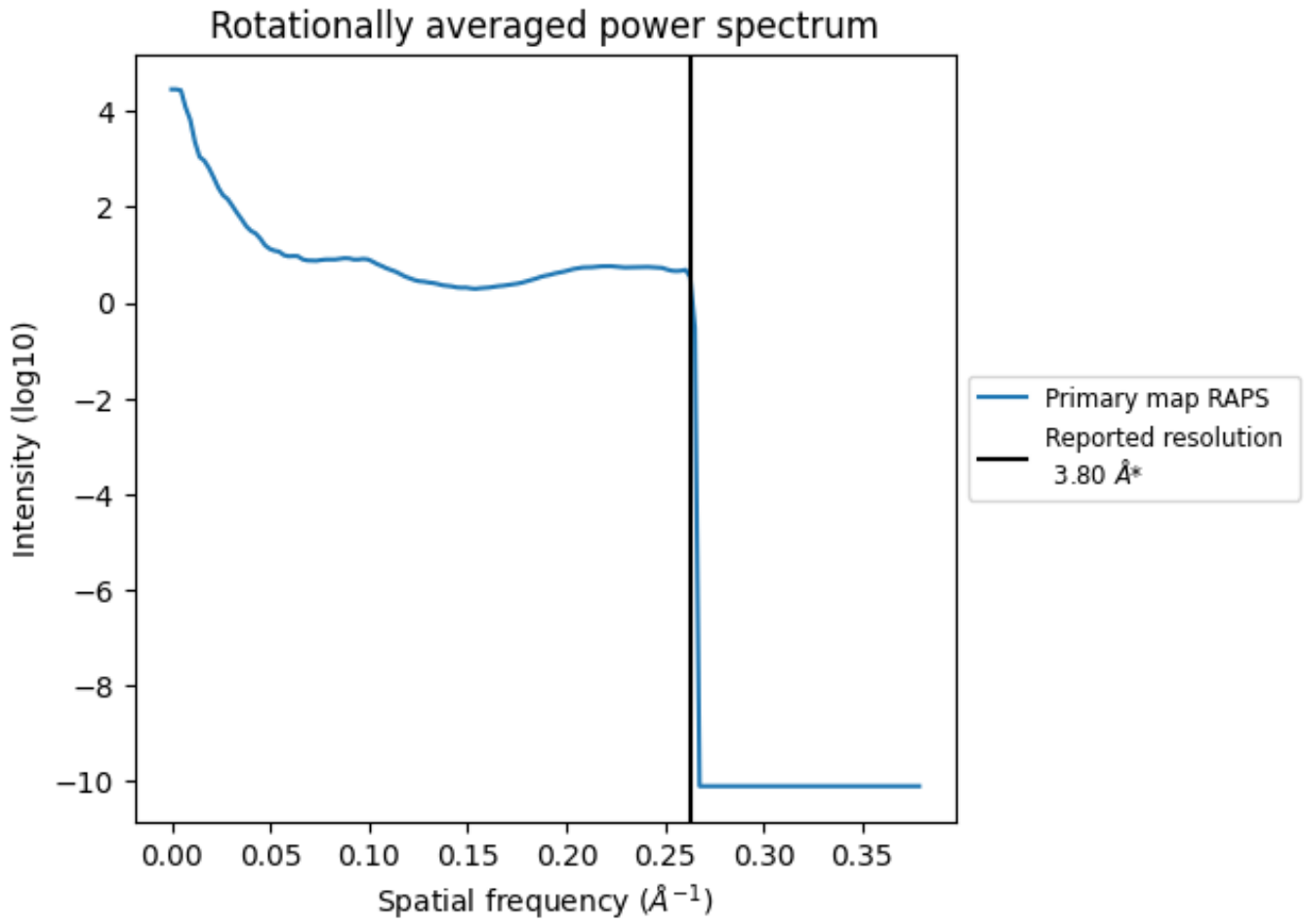
7.2 Volume estimate



The volume at the recommended contour level is 773 nm^3; this corresponds to an approximate mass of 699 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 (i)



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

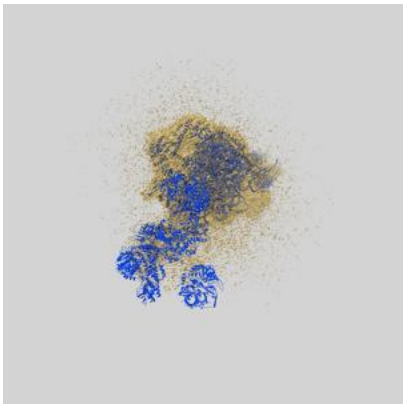
8 Fourier-Shell correlation (i)

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

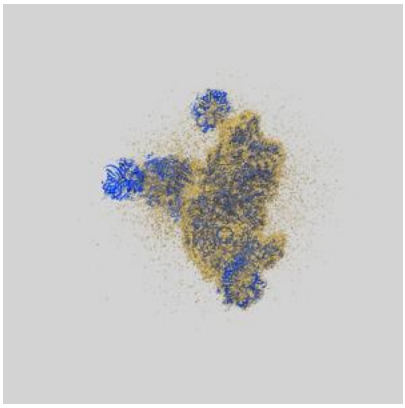
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-6561 and PDB model 3JCM. Per-residue inclusion information can be found in section 3 on page 11.

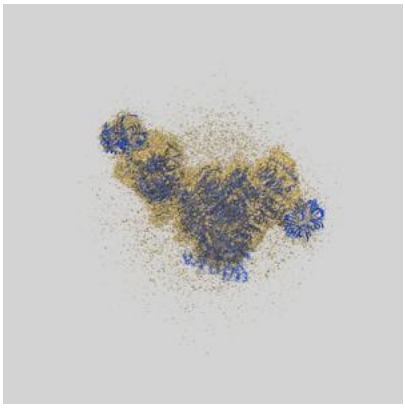
9.1 Map-model overlay



X



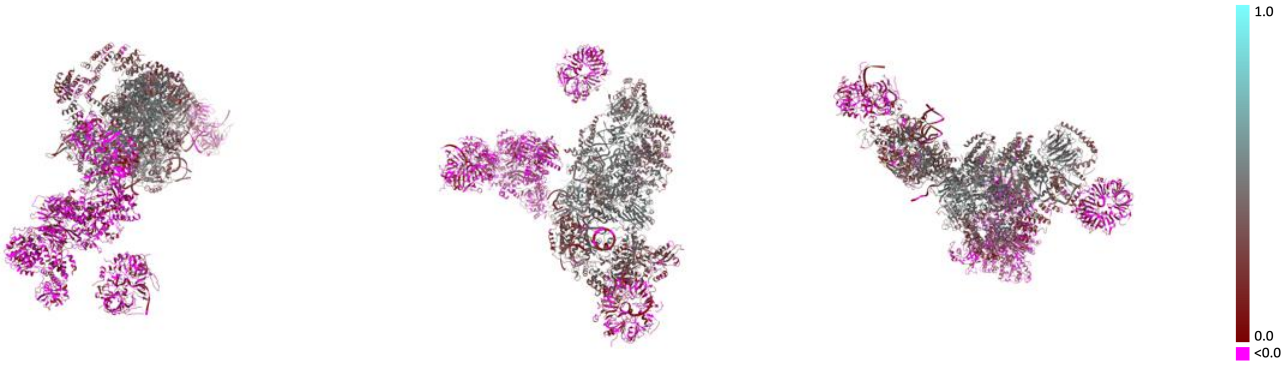
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0147 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.

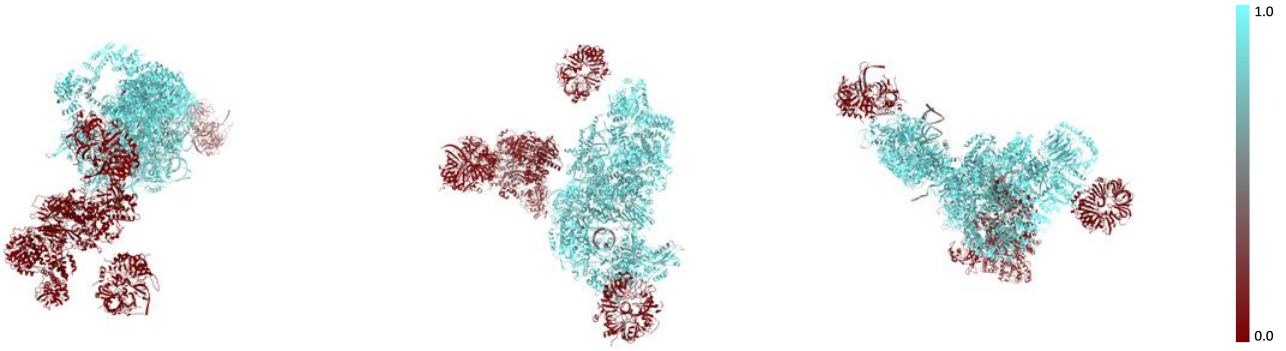
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

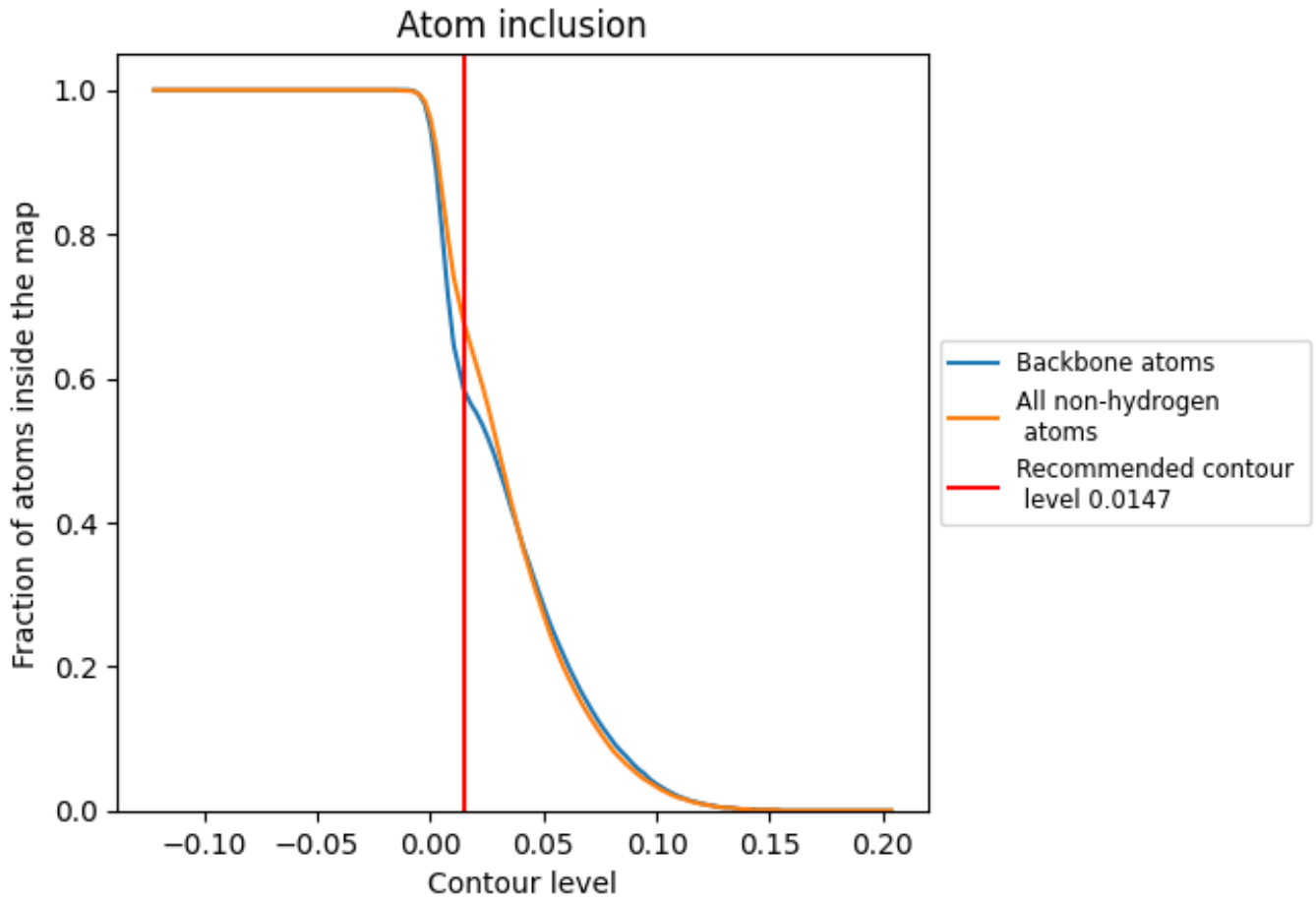
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.0147).

9.4 Atom inclusion (i)



At the recommended contour level, 58% of all backbone atoms, 68% 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 (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6780	0.2940
A	0.8560	0.3990
B	0.9060	0.4200
C	0.8700	0.2880
D	0.8910	0.3730
E	0.7470	0.3630
F	0.7110	0.2090
G	0.9070	0.3400
H	0.8910	0.3210
I	0.9220	0.4400
J	0.0000	-0.0190
K	0.9070	0.4070
L	0.9240	0.4570
M	0.9270	0.4890
N	0.0230	0.0020
O	0.0000	0.0160
P	0.0030	0.0440
Q	0.0000	0.0460
R	0.1490	0.0620
S	0.0510	0.0240
T	0.0910	0.0940
U	0.1220	0.0370
V	0.0490	-0.0010
W	0.1320	0.0400
X	0.0500	0.0310
Y	0.0000	-0.0070
Z	0.0040	0.0190
a	0.0000	0.0330
b	0.0110	0.0180
c	0.0110	0.0280
d	0.0100	0.0140
e	0.0270	0.0190
f	0.0130	0.0250
g	0.0110	0.0220
h	0.0160	-0.0580