Full wwPDB EM Validation Report

Oct 27, 2024 – 01:16 PM JST

PDB ID	:	5Z58
EMDB ID	:	EMD-6891
Title	:	Cryo-EM structure of a human activated spliceosome (early Bact) at 4.9 angstrom.
Authors	:	Zhang, X.; Yan, C.; Zhan, X.; Li, L.; Lei, J.; Shi, Y.
Deposited on	:	2018-01-17
Resolution	:	4.90 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:

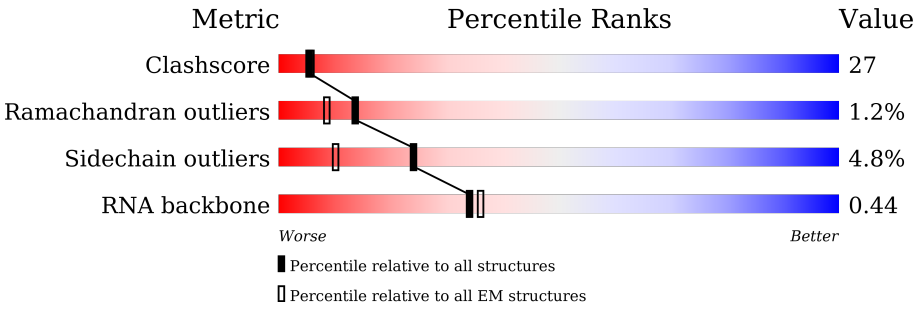
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 4.90 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.



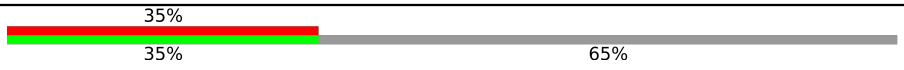
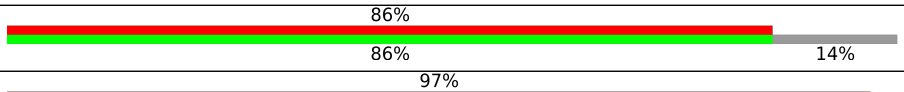
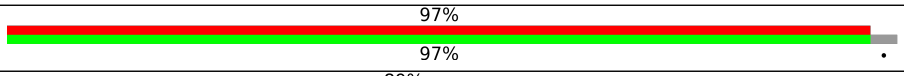
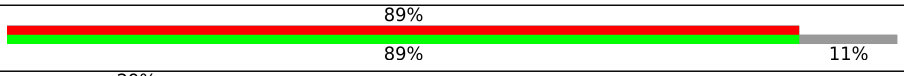
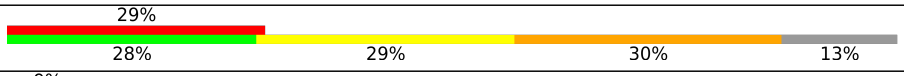
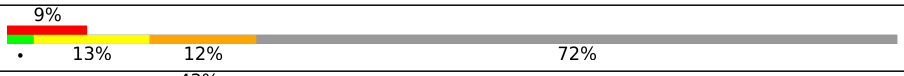
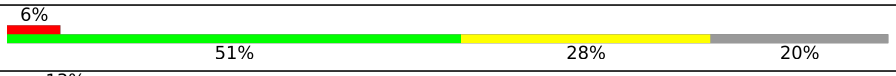
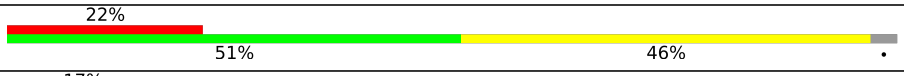
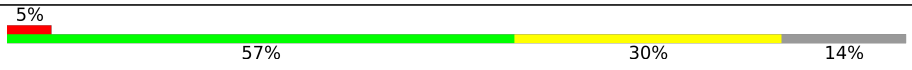
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2335	24% 54% 36% • • 5%
2	B	117	20% 28% 27% 13% • 28%
3	C	972	38% 47% 33% 7% • 12%
4	D	2136	73% 79% • 19%
5	E	357	83% 59% 21% • 16%
6	a	126	64% 64% 36%
6	h	126	63% 63% 37%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
7	b	231	
7	i	231	
8	c	119	
8	j	119	
9	d	118	
9	k	118	
10	f	86	
10	m	86	
11	e	92	
11	l	92	
12	g	76	
12	n	76	
13	F	107	
14	G	274	
15	H	188	
16	o	255	
17	p	225	
18	w	501	
19	u	793	
20	v	464	
21	1	1304	
22	2	895	
23	3	1217	
24	4	424	
25	5	125	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
26	6	110	32% 55% 26% 19%
27	7	86	10% 43% 33% 23%
28	J	848	45% 54% 6% 38%
29	L	802	6% 12% 84%
30	M	343	7% 90%
31	P	229	26% 18% 18% 5% 58%
32	R	540	29% 28% 20% 8% 43%
33	T	514	36% 20% 39%
34	V	908	32% 45% 5% 50%
35	X	396	7% 31% 9% 60%
36	Y	322	6% 15% 17% 68%
37	Z	619	5% 9% 7% 82%
38	z	472	13% 38% 62%
39	x	1041	55% 55% 44%

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
41	GTP	C	1500	-	-	X	-

2 Entry composition

There are 43 unique types of molecules in this entry. The entry contains 94673 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-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	2211	18165	11706	3163	3220	76	0	0

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	84	1768	792	295	597	84	0	0

- Molecule 3 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	860	6716	4294	1120	1270	32	0	0

- Molecule 4 is a protein called U5 small nuclear ribonucleoprotein 200 kDa helicase.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	D	1722	8528	5084	1722	1722	0	0

- Molecule 5 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	299	2338	1470	410	445	13	0	0

- Molecule 6 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	a	81	399	237	81	81	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
6	h	80	Total 393	C 233	N 80	O 80	0	0

- Molecule 7 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	b	82	Total 405	C 241	N 82	O 82	0	0
7	i	86	Total 422	C 250	N 86	O 86	0	0

- Molecule 8 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	c	82	Total 406	C 242	N 82	O 82	0	0
8	j	82	Total 406	C 242	N 82	O 82	0	0

- Molecule 9 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	d	97	Total 480	C 286	N 97	O 97	0	0
9	k	85	Total 422	C 252	N 85	O 85	0	0

- Molecule 10 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	f	74	Total 361	C 213	N 74	O 74	0	0
10	m	74	Total 361	C 213	N 74	O 74	0	0

- Molecule 11 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	e	79	Total 391	C 233	N 79	O 79	0	0
11	l	79	Total 391	C 233	N 79	O 79	0	0

- Molecule 12 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	g	74	Total 363	C 215	N 74	O 74	0	0
12	n	68	Total 334	C 198	N 68	O 68	0	0

- Molecule 13 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	93	Total 1988	C 889	N 363	O 643	P 93	0	0

- Molecule 14 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	77	Total 1545	C 689	N 240	O 539	P 77	0	0

- Molecule 15 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	136	Total 2886	C 1289	N 499	O 962	P 136	0	0

- Molecule 16 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	o	162	Total 804	C 480	N 162	O 162	0	0

- Molecule 17 is a protein called U2 small nuclear ribonucleoprotein B".

Mol	Chain	Residues	Atoms				AltConf	Trace
17	p	165	Total 813	C 483	N 165	O 165	0	0

- Molecule 18 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	w	437	Total 2369	C 1448	N 460	O 458	S 3	0	0

- Molecule 19 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	u	105	Total	C	N	O	0	0
			525	315	105	105		

- Molecule 20 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	v	98	Total	C	N	O	0	0
			486	290	98	98		

- Molecule 21 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	1	1038	Total	C	N	O	S	0	0
			7702	4900	1347	1415	40		

- Molecule 22 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	2	183	Total	C	N	O	S	0	0
			1252	809	213	226	4		

- Molecule 23 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	3	1177	Total	C	N	O	S	0	0
			9220	5854	1566	1755	45		

- Molecule 24 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	4	78	Total	C	N	O	0	0
			527	345	83	99		

- Molecule 25 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	5	108	Total	C	N	O	S	0	0
			807	512	142	150	3		

- Molecule 26 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	6	89	Total	C	N	O	S	0	0
			670	410	119	128	13		

- Molecule 27 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	7	66	Total	C	N	O	S	0	0
			540	343	94	98	5		

- Molecule 28 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	J	522	Total	C	N	O	S	0	0
			3463	2156	653	648	6		

- Molecule 29 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	L	132	Total	C	N	O	S	0	0
			1077	691	188	194	4		

- Molecule 30 is a protein called RING finger protein 113A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	M	36	Total	C	N	O	S	0	0
			267	167	45	52	3		

- Molecule 31 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	P	96	Total	C	N	O	S	0	0
			829	508	162	157	2		

- Molecule 32 is a protein called Skip.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	R	309	Total	C	N	O	S	0	0
			2314	1454	413	435	12		

- Molecule 33 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	T	313	Total	C	N	O	S	0	0
			2457	1552	447	450	8		

- Molecule 34 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	V	451	Total	C	N	O	0	0
			2238	1336	451	451		

- Molecule 35 is a protein called Smad nuclear-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	X	158	Total	C	N	O	S	0	0
			1012	645	172	194	1		

- Molecule 36 is a protein called RNA-binding motif protein, X-linked 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Y	104	Total	C	N	O	S	0	0
			737	466	126	143	2		

- Molecule 37 is a protein called BUD13 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	Z	113	Total	C	N	O	0	0
			755	474	147	134		

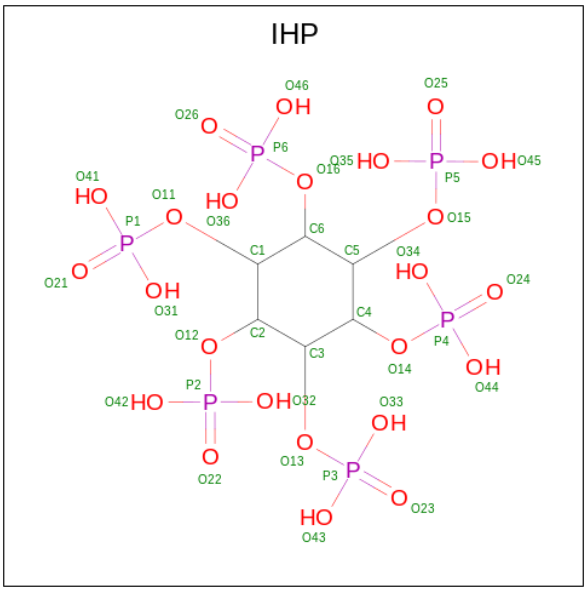
- Molecule 38 is a protein called Peptidyl-prolyl cis-trans isomerase CWC27 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	z	177	Total	C	N	O	S	1	0
			1381	869	241	266	5		

- Molecule 39 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16.

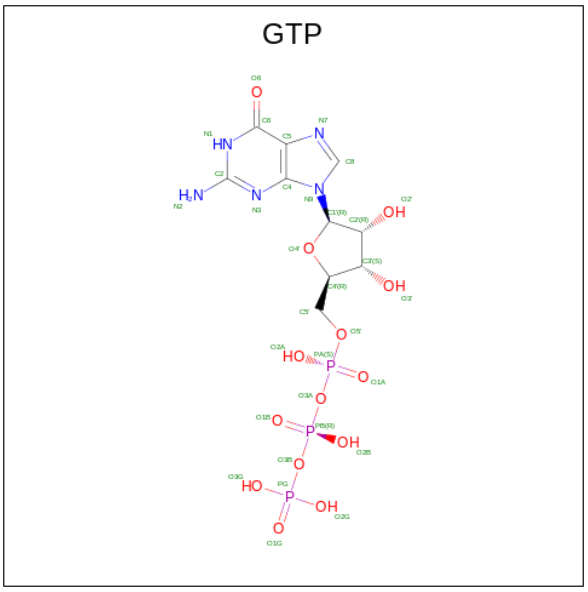
Mol	Chain	Residues	Atoms				AltConf	Trace
39	x	583	Total	C	N	O	0	0
			2882	1715	583	584		

- Molecule 40 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
40	A	1	36	6	24	6	0

- Molecule 41 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

- Molecule 42 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
42	C	1	Total Mg 1 1	0
42	F	5	Total Mg 5 5	0

- Molecule 43 is ZINC ION (three-letter code: ZN) (formula: Zn).

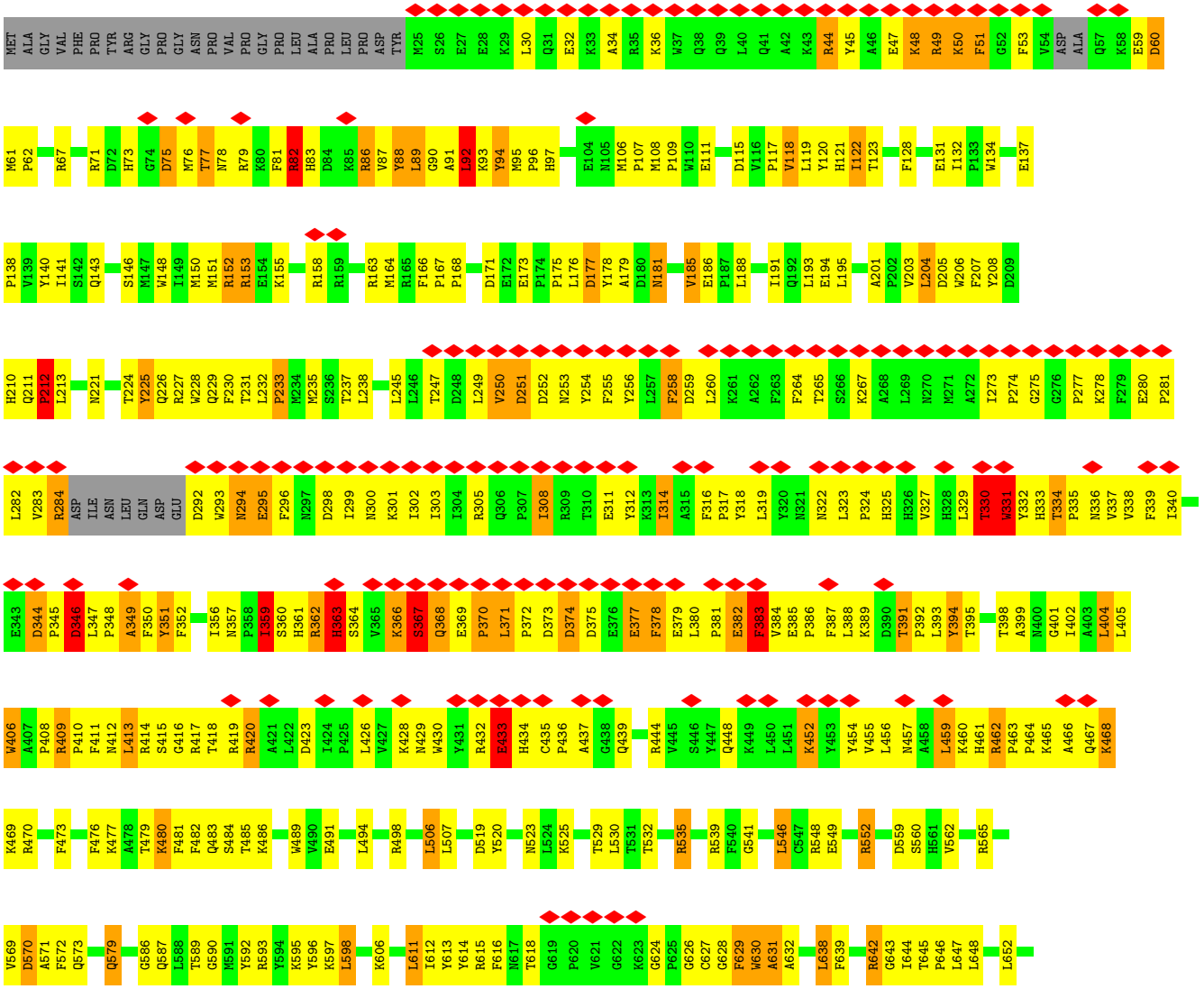
Mol	Chain	Residues	Atoms	AltConf
43	6	3	Total Zn 3 3	0
43	M	1	Total Zn 1 1	0

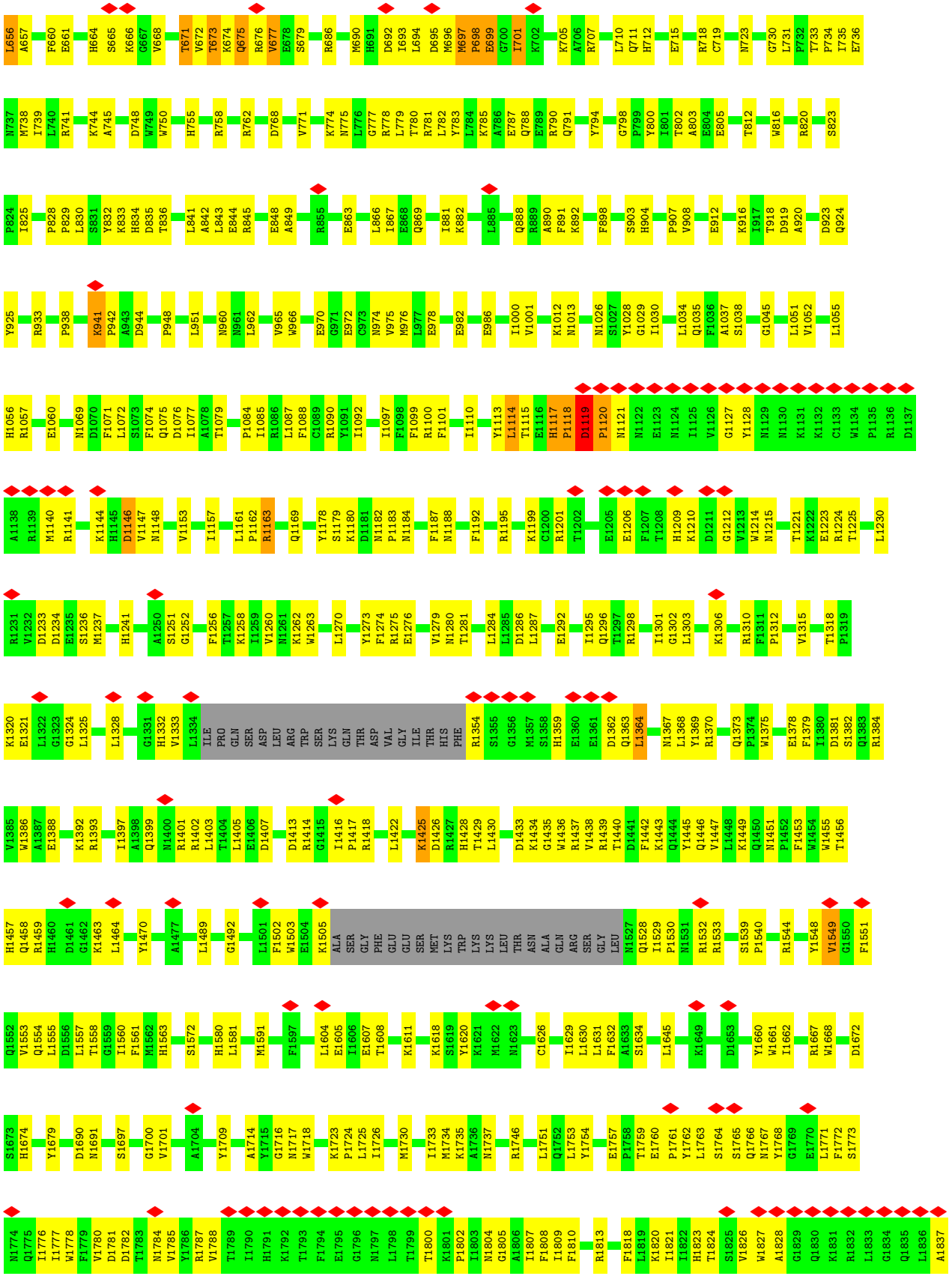
3 Residue-property plots (i)

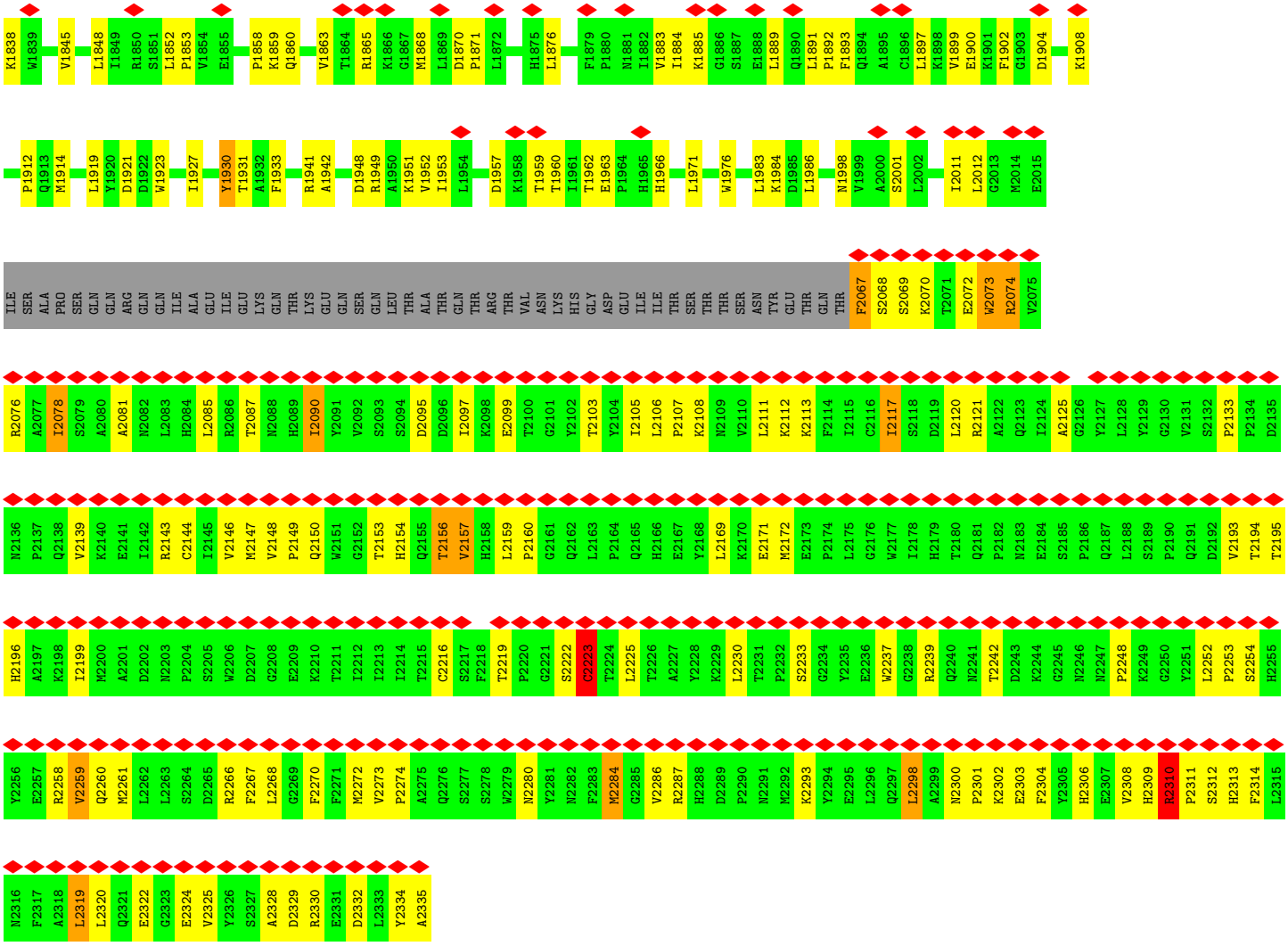
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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-processing-splicing factor 8

Chain A:

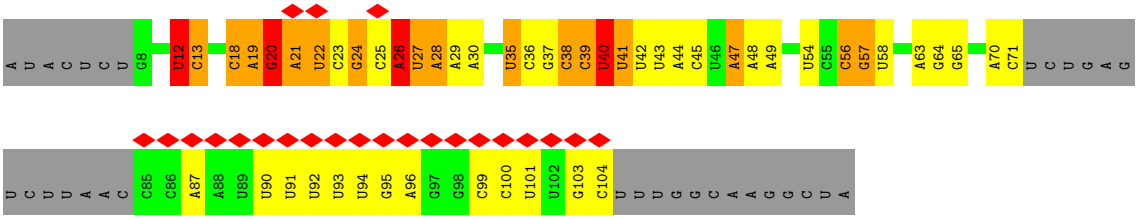



L656 A657 F660 E661 H664 S665 K666 G667 V668 T671 V672 T673 K674 Q675 R676 V677 E678 S679 R686 M690 H691 D692 I693 L694 D695 M696 M697 P698 E699 G700 I701 K702 K705 A706 R707 L710 Q711 H712 E715 R718 C719 N723 G730 L731 P732 T733 P734 I735 E736
N737 M738 I739 L740 R741 K744 A745 D748 W749 W750 H755 R758 R762 D768 V771 K774 N775 L776 G777 R778 L779 T780 R781 L782 Y783 L784 K785 A786 E787 Q788 E789 R790 Q791 Y794 G798 P799 Y800 I801 T802 A803 E804 E805 T812 W816 R820 S823
P824 I825 P828 P829 L830 S831 Y832 K833 H834 D835 T836 L841 A842 L843 E844 R845 E848 A849 R855 E863 L866 I867 E868 Q869 I881 K882 L885 Q888 R889 A890 F891 K892 F898 S903 H904 P907 V908 E912 K916 I917 T918 D919 A920 D923 Q924
Y925 R933 P938 K941 P942 A943 D944 P948 L951 N960 N961 L962 V965 W966 E970 G971 E972 C973 N974 V975 M976 L977 E978 E982 E986 I1000 V1001 K1012 N1013 N1026 S1027 Y1028 G1029 I1030 L1034 Q1035 F1036 A1037 S1038 G1045 L1051 V1052 L1055
H1056 R1057 E1060 N1069 D1070 F1071 L1072 S1073 F1074 Q1075 D1076 I1077 A1078 T1079 P1084 I1085 R1086 L1087 F1088 C1089 R1090 Y1091 I1092 I1097 F1098 F1099 R1100 F1101 I1110 Y1113 L1114 T1115 E1116 H1117 P1118 D1119 P1120 N1121 N1122 E1123 N1124 I1125 V1126 G1127 Y1128 N1129 N1130 K1131 K1132 C1133 W1134 P1135 R1136 D1137
A1138 R1139 M1140 R1141 K1144 H1145 D1146 V1147 N1148 V1153 I1157 L1161 P1162 R1163 Q1169 Y1178 S1179 K1180 D1181 N1182 P1183 N1184 F1187 N1188 F1192 R1195 K1199 C1200 R1201 T1202 E1205 E1206 F1207 T1208 H1209 K1210 D1211 G1212 V1213 W1214 N1215 T1221 K1222 E1223 R1224 T1225 L1230
R1231 V1232 D1233 D1234 E1235 S1236 M1237 H1241 A1250 S1251 G1252 F1256 T1257 K1258 T1259 V1260 N1261 K1262 W1263 L1270 Y1273 F1274 R1275 E1276 V1279 N1280 T1281 L1284 L1285 D1286 L1287 E1292 I1295 Q1296 T1297 R1298 I1301 G1302 L1303 K1306 R1310 F1311 P1312 V1315 T1318 P1319
K1320 E1321 L1322 G1323 G1324 L1325 L1328 G1331 H1332 V1333 L1334 ILE PRO GLN SER ASP LEU ARG TRP SER LYS GLN THR ASP VAL GLY ILE THR HIS PHE R1354 S1355 G1356 M1357 S1358 H1359 E1360 E1361 D1362 Q1363 L1364 N1367 L1368 Y1369 R1370 Q1373 P1374 W1375 E1378 F1379 I1380 D1381 S1382 Q1383 R1384
V1385 W1386 A1387 E1388 K1392 R1393 I1397 A1398 Q1399 N1400 R1401 R1402 L1403 T1404 L1405 E1406 D1407 D1413 R1414 G1415 I1416 P1417 R1418 L1422 K1425 D1426 R1427 H1428 T1429 L1430 D1433 K1434 G1435 W1436 R1437 V1438 R1439 T1440 D1441 F1442 K1443 Q1444 Y1445 Q1446 V1447 L1448 K1449 Q1450 N1451 P1452 F1453 W1454 W1455 T1456
H1457 Q1458 R1459 H1460 D1461 G1462 K1463 L1464 Y1470 A1477 L1489 G1492 L1501 F1502 W1503 E1504 K1505 ALA SER GLY PHE GLU GLU SER MET LYS TRP LYS LYS LEU THR ASN ALA GLN ARG SER GLY LEU N1527 Q1528 I1529 P1530 N1531 R1532 R1533 S1539 P1540 R1544 Y1548 V1549 G1550 F1551
Q1552 V1553 Q1554 L1555 D1556 L1557 T1558 G1559 I1560 F1561 M1562 H1563 S1572 H1580 L1581 M1591 F1597 L1604 E1605 I1606 E1607 T1608 K1611 K1618 S1619 Y1620 K1621 M1622 N1623 C1626 I1629 L1630 L1631 F1632 A1633 S1634 L1645 K1649 D1653 Y1660 W1661 I1662 R1667 W1668 D1672
S1673 H1674 Y1679 D1690 N1691 S1697 G1700 V1701 A1704 Y1709 A1714 Y1715 G1716 N1717 W1718 K1723 P1724 L1725 I1726 M1730 I1733 M1734 K1735 A1736 N1737 R1746 L1751 Q1752 L1753 Y1754 E1757 P1758 T1759 E1760 P1761 Y1762 L1763 S1764 S1765 Q1766 N1767 Y1768 G1769 E1770 L1771 F1772 S1773
N1774 Q1775 I1776 I1777 W1778 F1779 V1780 D1781 D1782 T1783 N1784 V1785 Y1786 R1787 V1788 T1789 I1790 H1791 K1792 T1793 F1794 E1795 G1796 N1797 L1798 T1799 T1800 K1801 P1802 I1803 N1804 G1805 A1806 I1807 F1808 I1809 F1810 R1813 F1818 L1819 K1820 I1821 I1822 H1823 T1824 S1825 V1826 W1827 A1828 G1829 Q1830 K1831 R1832 L1833 G1834 Q1835 L1836 A1837



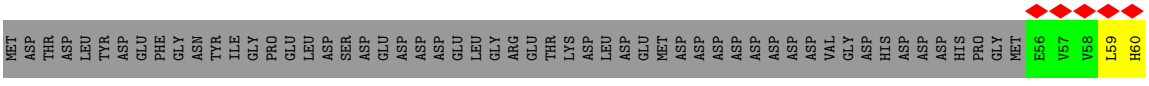
• Molecule 2: U5 snRNA

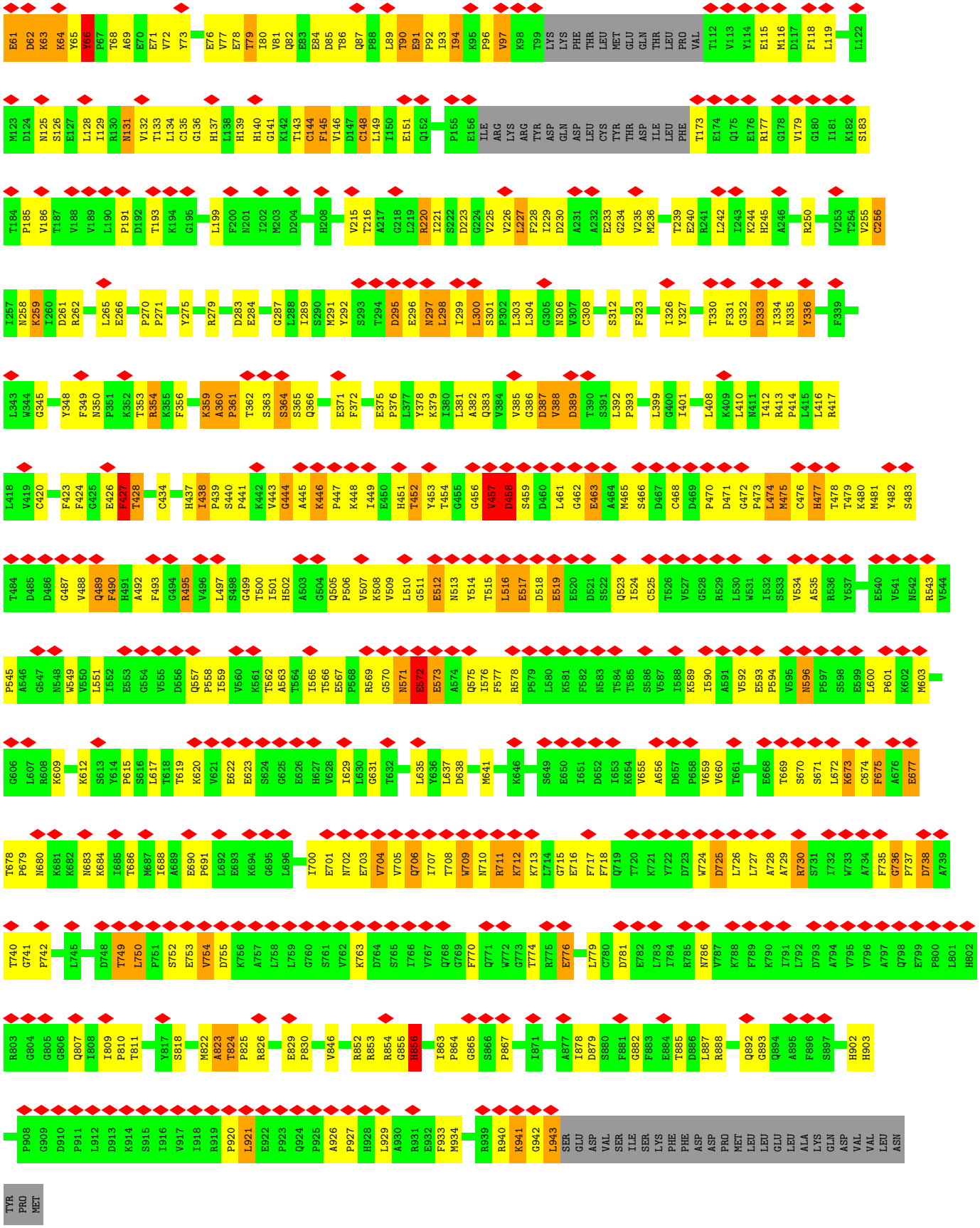
Chain B:



• Molecule 3: 116 kDa U5 small nuclear ribonucleoprotein component

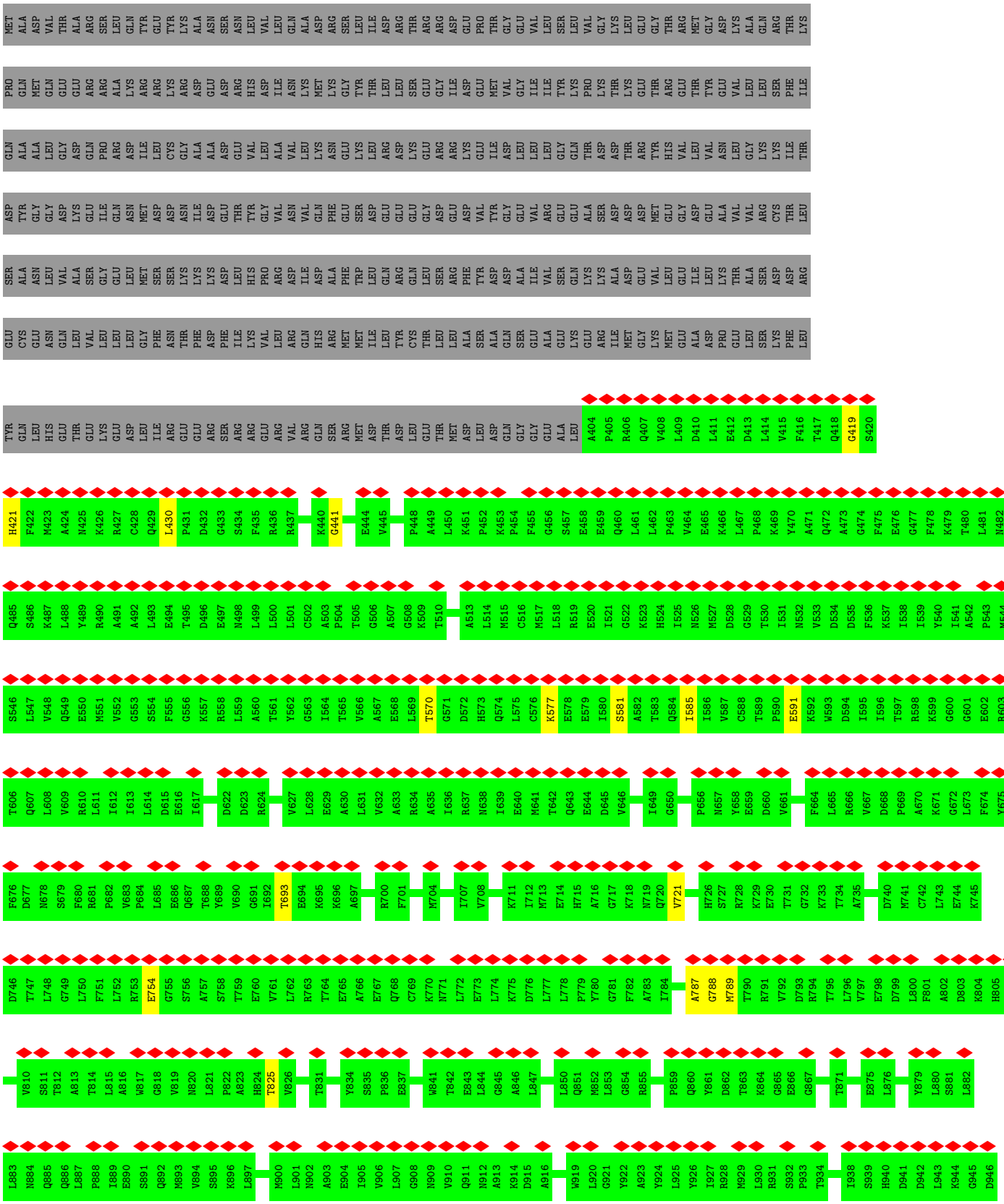
Chain C:

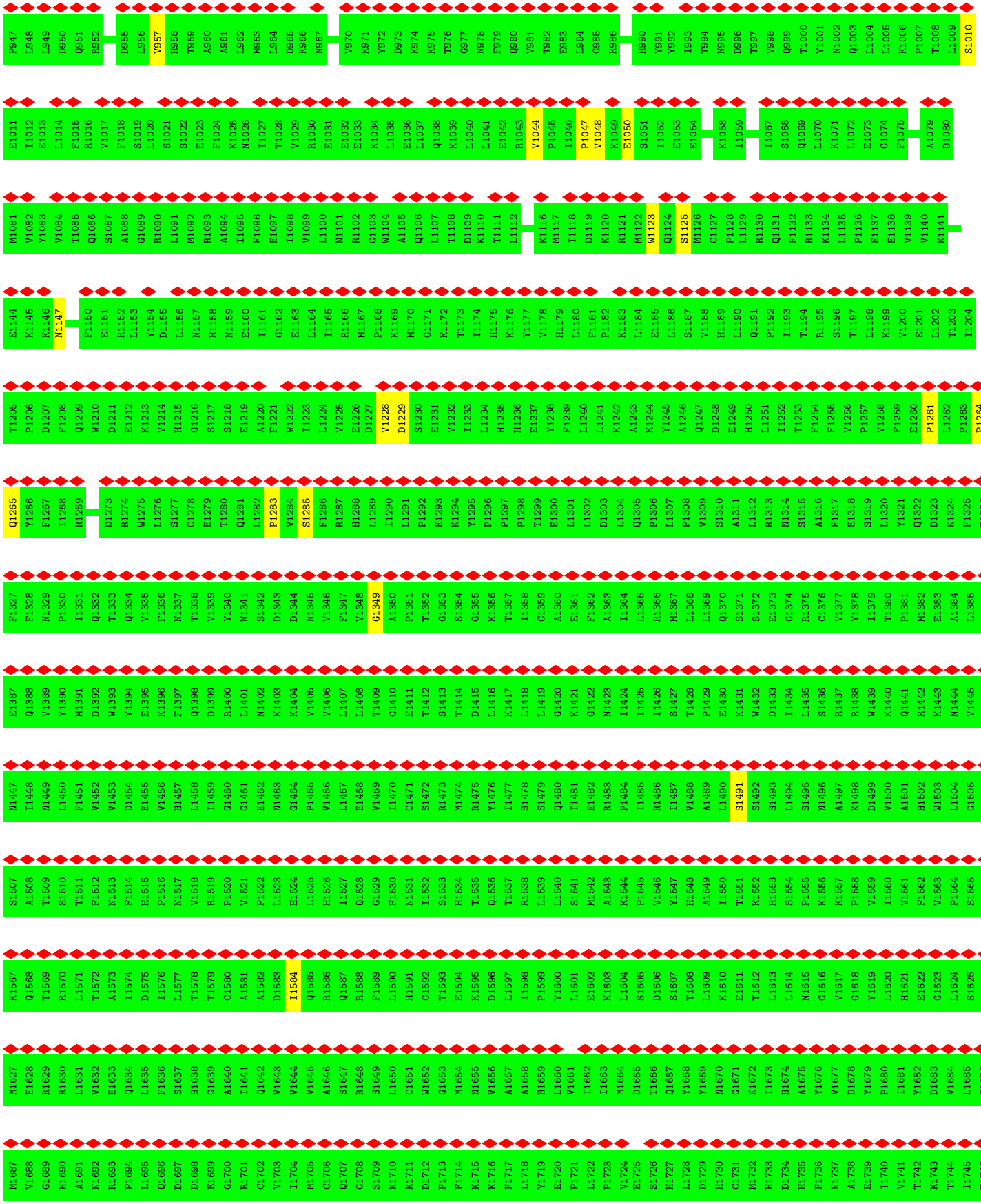


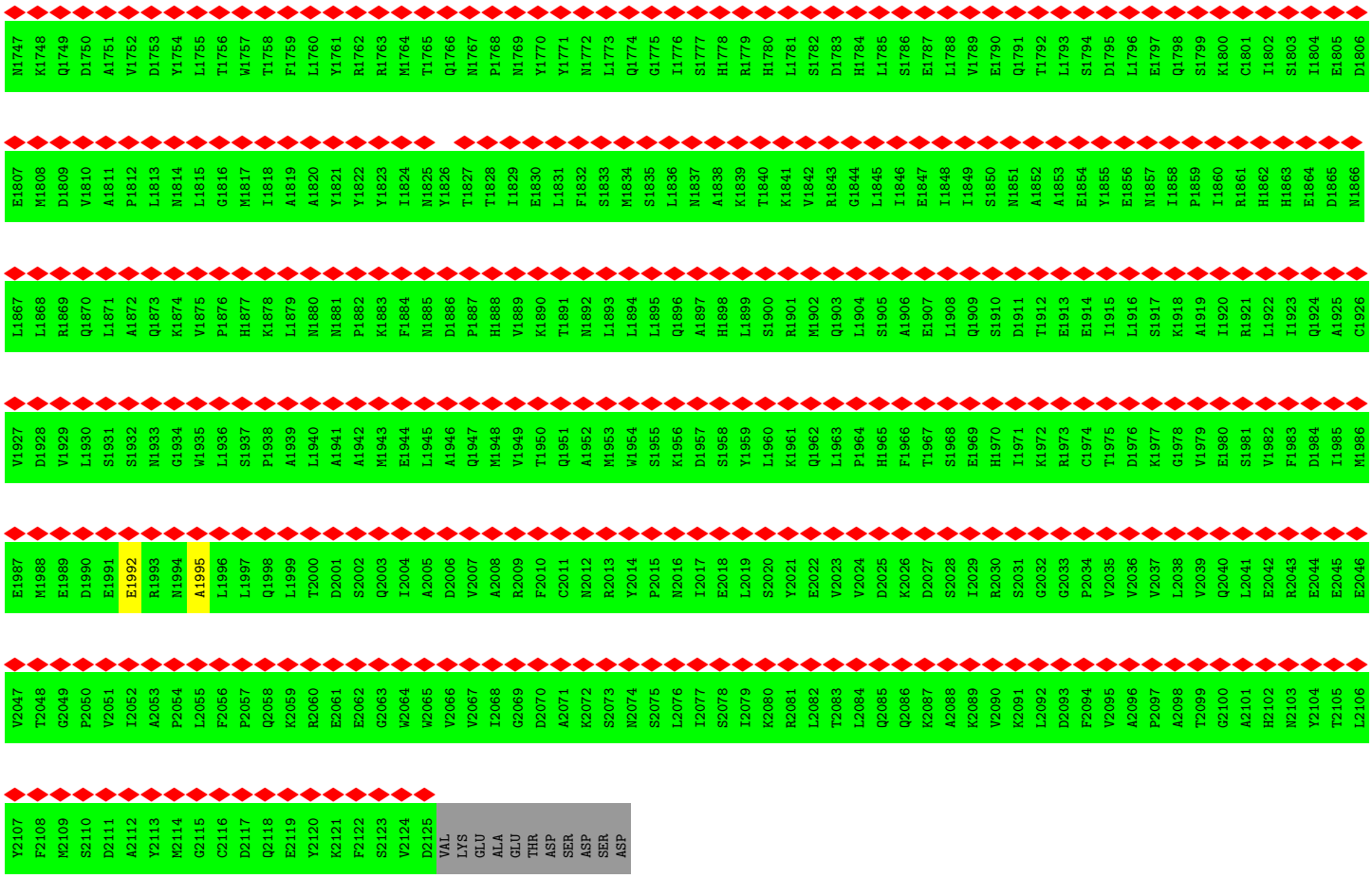

TYR
PRO
MET

• Molecule 4: U5 small nuclear ribonucleoprotein 200 kDa helicase

Chain D:

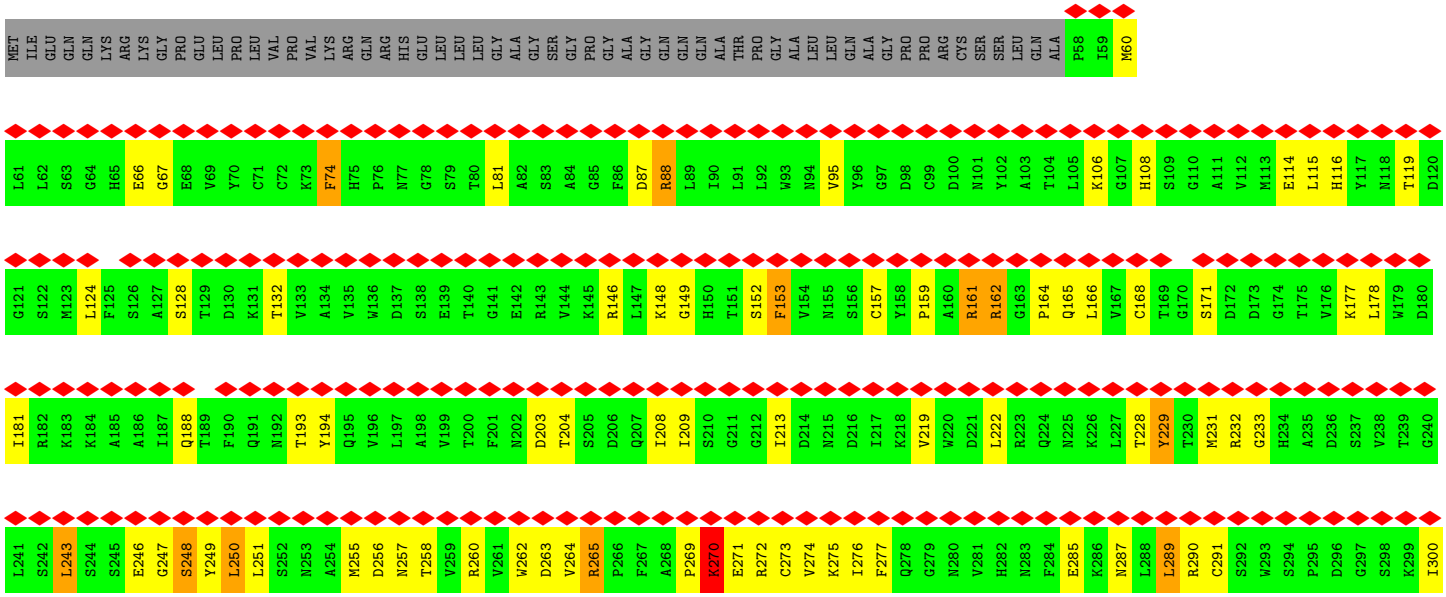


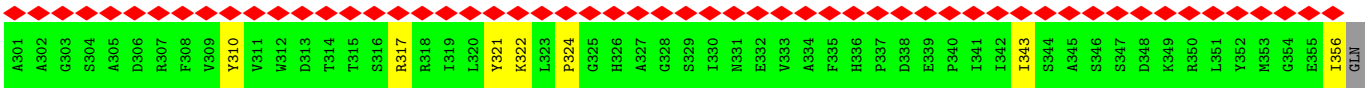

P947 L948 L949 D950 Q951 R952 D955 L956 V957 H958 T959 A960 A961 L962 M963 L964 D965 K966 N967 V970 K971 Y972 D973 K974 K975 T976 G977 N978 F979 Q980 V981 T982 E983 L984 G985 R986 H990 Y991 Y992 I993 T994 N995 D996 T997 V998 Q999 T1000 Y1001 N1002 Q1003 L1004 L1005 K1006 P1007 T1008 L1009 S1010
E1011 I1012 E1013 L1014 F1015 R1016 V1017 F1018 S1019 L1020 S1021 S1022 E1023 F1024 K1025 N1026 I1027 T1028 V1029 R1030 E1031 E1032 E1033 K1034 L1035 E1036 L1037 Q1038 K1039 L1040 L1041 E1042 R1043 V1044 P1045 I1046 P1047 V1048 K1049 E1050 S1051 I1052 E1053 E1054 K1058 I1059 I1067 S1068 Q1069 L1070 K1071 L1072 E1073 G1074 F1075 A1079 D1080
M1081 V1082 Y1083 V1084 T1085 Q1086 S1087 A1088 G1089 R1090 L1091 M1092 R1093 A1094 I1095 F1096 E1097 I1098 V1099 L1100 N1101 R1102 G1103 W1104 A1105 Q1106 L1107 T1108 D1109 K1110 T1111 L1112 K1116 M1117 I1118 D1119 K1120 R1121 M1122 W1123 Q1124 S1125 M1126 C1127 P1128 L1129 R1130 Q1131 F1132 R1133 K1134 L1135 P1136 E1137 E1138 V1139 V1140 K1141
E1144 K1145 K1146 N1147 F1150 E1151 R1152 L1153 Y1154 D1155 L1156 N1157 H1158 N1159 E1160 I1161 G1162 E1163 L1164 I1165 R1166 M1167 P1168 K1169 M1170 G1171 K1172 T1173 I1174 H1175 K1176 Y1177 V1178 H1179 L1180 F1181 P1182 K1183 L1184 E1185 L1186 S1187 V1188 H1189 L1190 Q1191 P1192 I1193 T1194 R1195 S1196 T1197 L1198 K1199 V1200 E1201 L1202 T1203 I1204
T1205 P1206 D1207 F1208 Q1209 W1210 D1211 E1212 K1213 V1214 H1215 G1216 S1217 S1218 E1219 A1220 F1221 W1222 I1223 L1224 V1225 E1226 D1227 V1228 D1229 S1230 E1231 V1232 I1233 L1234 H1235 H1236 E1237 Y1238 F1239 L1240 L1241 K1242 A1243 K1244 Y1245 A1246 Q1247 D1248 E1249 H1250 L1251 I1252 T1253 F1254 F1255 V1256 P1257 V1258 F1259 E1260 P1261 L1262 P1263 P1264
Q1265 Y1266 F1267 I1268 R1269 D1273 R1274 W1275 L1276 S1277 C1278 E1279 T1280 Q1281 L1282 P1283 V1284 S1285 F1286 R1287 H1288 L1289 I1290 L1291 P1292 E1293 K1294 Y1295 P1296 P1297 P1298 T1299 E1300 L1301 L1302 D1303 L1304 Q1305 P1306 L1307 P1308 V1309 S1310 A1311 L1312 R1313 N1314 S1315 A1316 F1317 E1318 S1319 L1320 Y1321 Q1322 D1323 K1324 F1325 P1326
F1327 F1328 N1329 P1330 I1331 Q1332 T1333 Q1334 V1335 F1336 N1337 T1338 V1339 Y1340 N1341 S1342 D1343 D1344 N1345 V1346 F1347 V1348 G1349 A1350 P1351 T1352 G1353 S1354 G1355 K1356 T1357 I1358 C1359 A1360 E1361 F1362 A1363 I1364 L1365 R1366 M1367 L1368 L1369 Q1370 S1371 S1372 E1373 G1374 R1375 C1376 V1377 Y1378 I1379 T1380 P1381 M1382 E1383 A1384 L1385 A1386
E1387 Q1388 V1389 Y1390 M1391 D1392 W1393 Y1394 E1396 K1396 F1397 Q1398 D1399 R1400 L1401 N1402 K1403 K1404 V1405 V1406 L1407 L1408 T1409 G1410 E1411 T1412 S1413 R1473 T1414 M1474 D1415 R1475 L1416 K1417 I1418 L1419 G1420 K1421 G1422 N1423 I1424 I1425 I1426 S1427 T1428 P1429 E1430 K1431 L1490 W1432 D1433 I1434 L1435 S1436 R1437 R1438 W1439 K1440 Q1441 R1442 K1443 N1444 V1445 Q1446
N1447 I1448 N1449 L1450 F1451 V1452 V1453 D1454 E1455 V1456 H1457 L1458 I1459 G1460 G1461 E1462 N1463 G1464 P1465 V1466 L1467 E1468 V1469 I1470 C1471 S1472 S1473 M1474 R1475 Y1476 I1477 S1478 S1479 Q1480 I1481 E1482 R1483 P1484 I1485 R1486 I1487 V1488 A1489 L1490 S1491 S1492 S1493 L1494 S1495 N1496 A1497 K1498 D1499 V1500 A1501 H1502 W1503 L1504 G1505 C1506
S1507 A1508 T1509 S1510 T1511 F1512 N1513 F1514 H1515 P1516 N1517 V1518 R1519 P1520 V1521 P1522 L1523 E1524 L1525 H1526 I1527 Q1528 G1529 F1530 N1531 I1532 S1533 H1534 T1535 Q1536 T1537 R1538 L1539 L1540 S1541 M1542 A1543 K1544 P1545 V1546 Y1547 H1548 A1549 I1550 T1551 K1552 H1553 S1554 P1555 K1556 K1557 P1558 V1559 I1560 V1561 F1562 V1563 P1564 S1565 R1566
K1567 Q1568 T1569 R1570 L1571 T1572 A1573 I1574 D1575 I1576 L1577 T1578 T1579 C1580 A1581 A1582 D1583 I1584 Q1585 R1586 Q1587 R1588 F1589 L1590 H1591 C1592 T1593 E1594 K1595 D1596 L1597 I1598 P1599 Y1600 L1601 E1602 K1603 L1604 S1605 D1606 S1607 T1608 L1609 K1610 E1611 T1612 L1613 L1614 N1615 G1616 V1617 G1618 Y1619 L1620 H1621 E1622 G1623 L1624 S1625 P1626
M1627 E1628 R1629 R1630 L1631 V1632 E1633 Q1634 L1635 F1636 S1637 S1638 G1639 A1640 I1641 Q1642 V1643 V1644 V1645 A1646 S1647 R1648 S1649 L1650 C1651 W1652 G1653 M1654 N1655 V1656 A1657 A1658 H1659 L1660 V1661 I1662 I1663 M1664 D1665 T1666 Q1667 Y1668 Y1669 N1670 G1671 K1672 I1673 H1674 A1675 Y1676 V1677 D1678 Y1679 P1680 I1681 Y1682 D1683 V1684 L1685 Q1686
M1687 V1688 G1689 H1690 A1691 N1692 R1693 P1694 L1695 Q1696 D1697 D1698 E1699 G1700 R1701 C1702 V1703 I1704 M1705 C1706 Q1707 G1708 S1709 K1710 K1711 D1712 F1713 F1714 K1715 K1716 F1717 L1718 Y1719 E1720 P1721 L1722 P1723 V1724 E1725 S1726 H1727 L1728 D1729 H1730 C1731 M1732 H1733 D1734 H1735 F1736 N1737 A1738 E1739 I1740 V1741 T1742 K1743 T1744 I1745 E1746



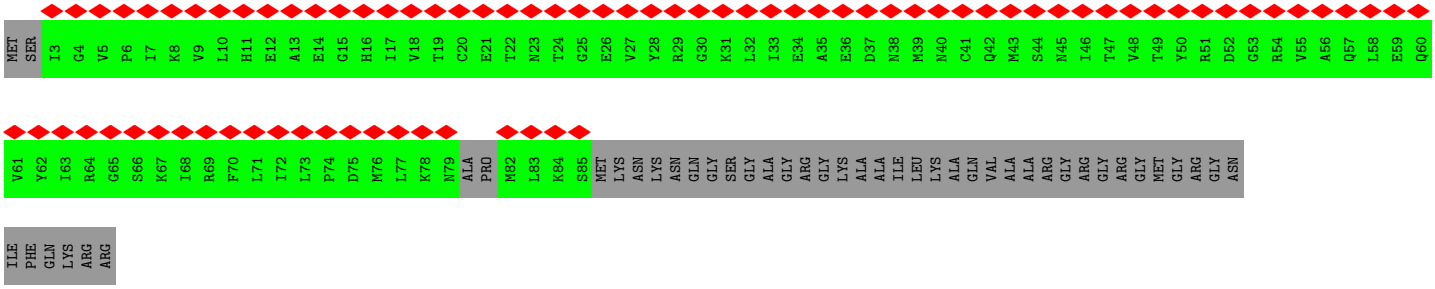
• Molecule 5: U5 small nuclear ribonucleoprotein 40 kDa protein

Chain E:

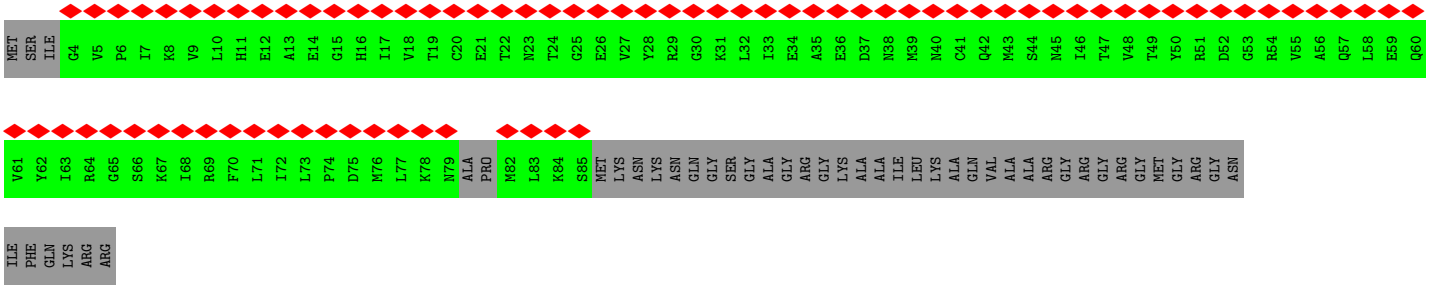




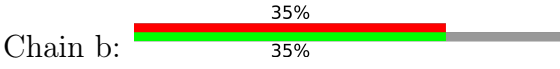
• Molecule 6: Small nuclear ribonucleoprotein Sm D3

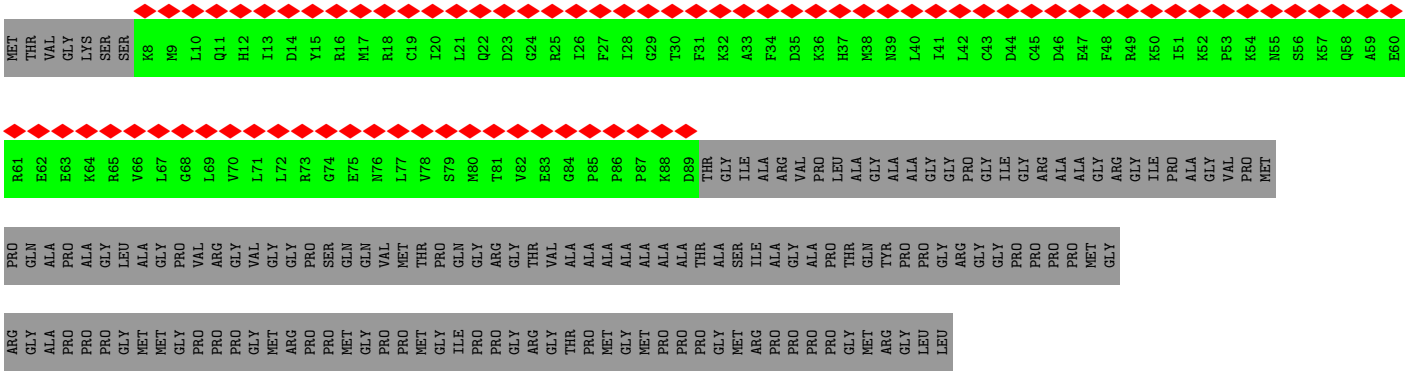


• Molecule 6: Small nuclear ribonucleoprotein Sm D3

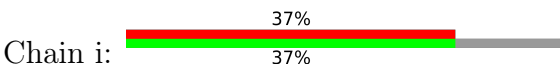


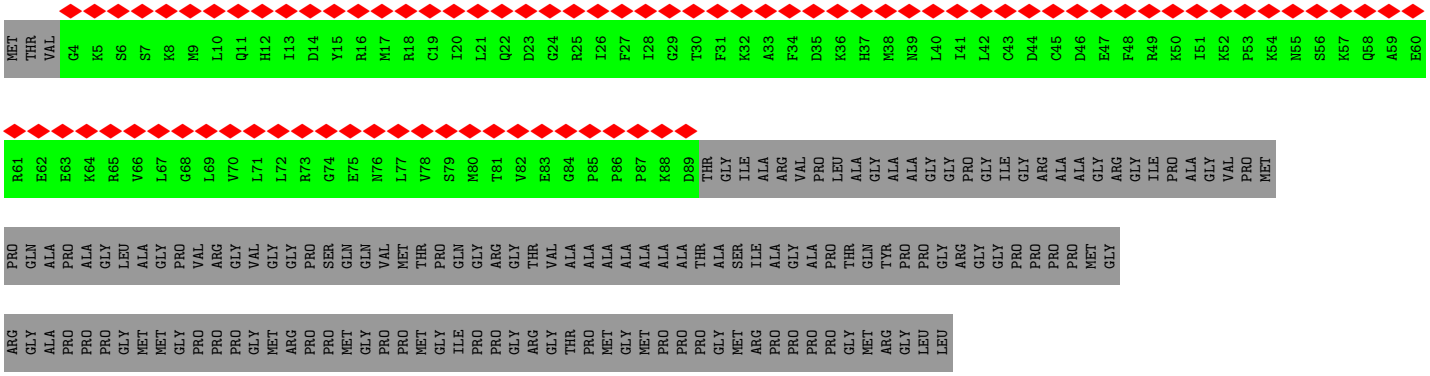
• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'



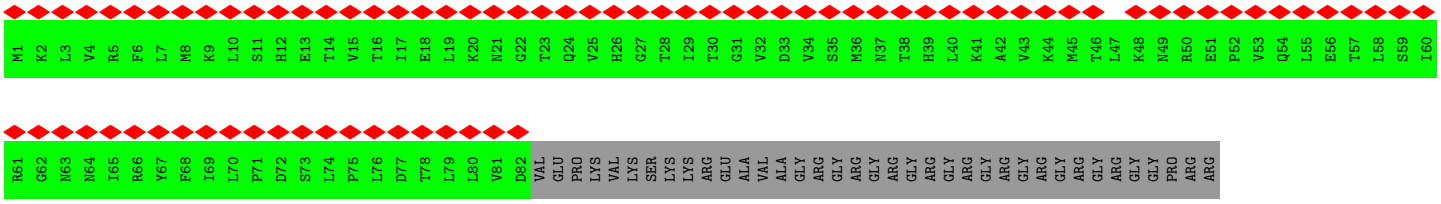


• Molecule 7: Small nuclear ribonucleoprotein-associated proteins B and B'

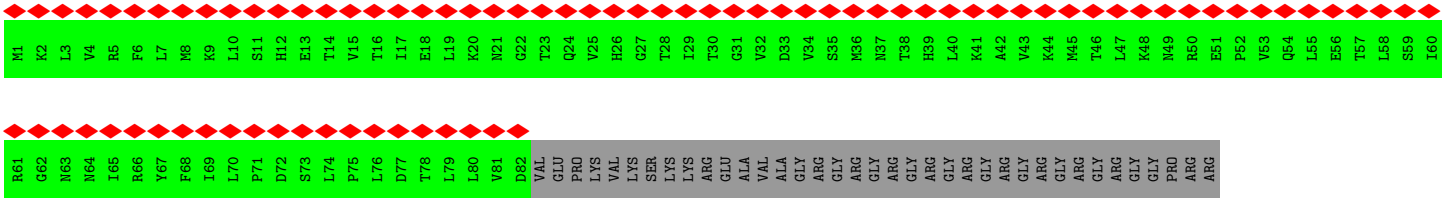




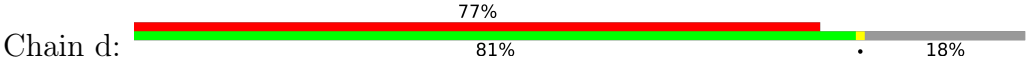
• Molecule 8: Small nuclear ribonucleoprotein Sm D1

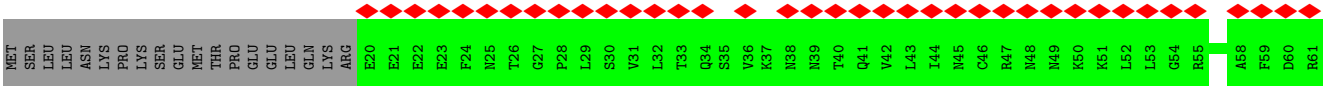


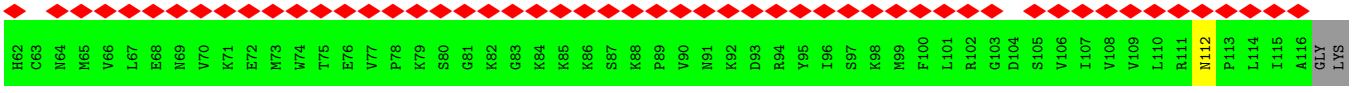
• Molecule 8: Small nuclear ribonucleoprotein Sm D1



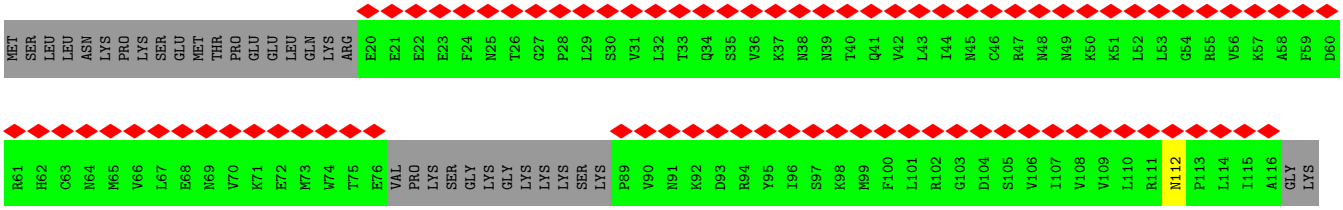
• Molecule 9: Small nuclear ribonucleoprotein Sm D2





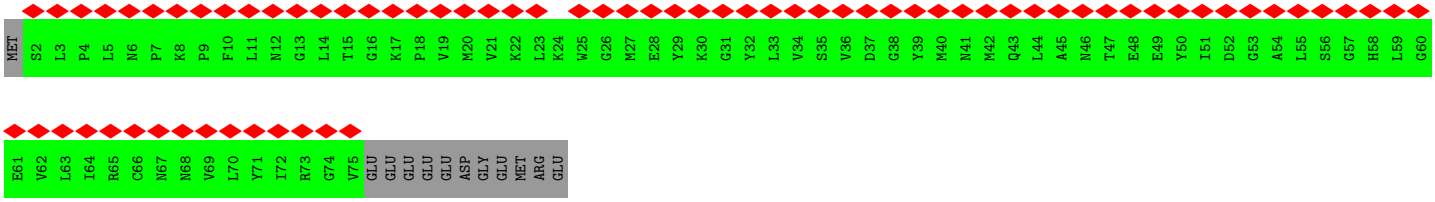


• Molecule 9: Small nuclear ribonucleoprotein Sm D2



• Molecule 10: Small nuclear ribonucleoprotein F

Chain f:

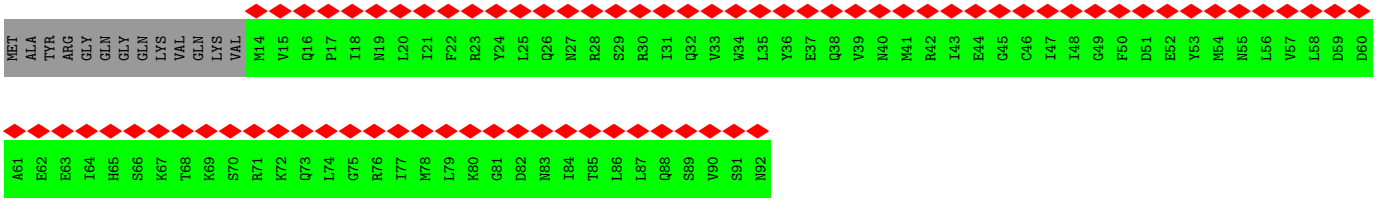


• Molecule 10: Small nuclear ribonucleoprotein F

Chain m:

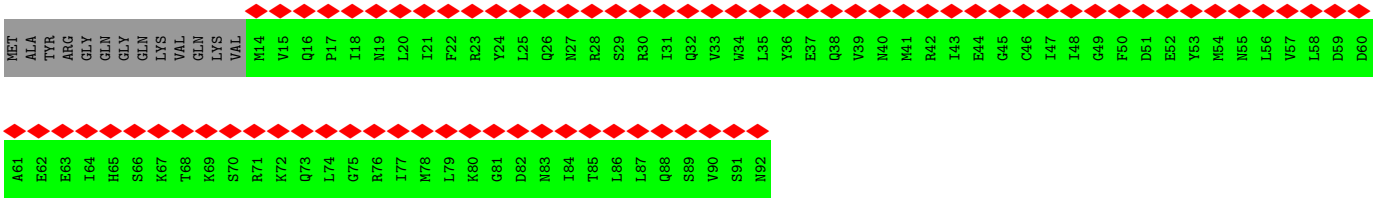
• Molecule 11: Small nuclear ribonucleoprotein E

Chain e:



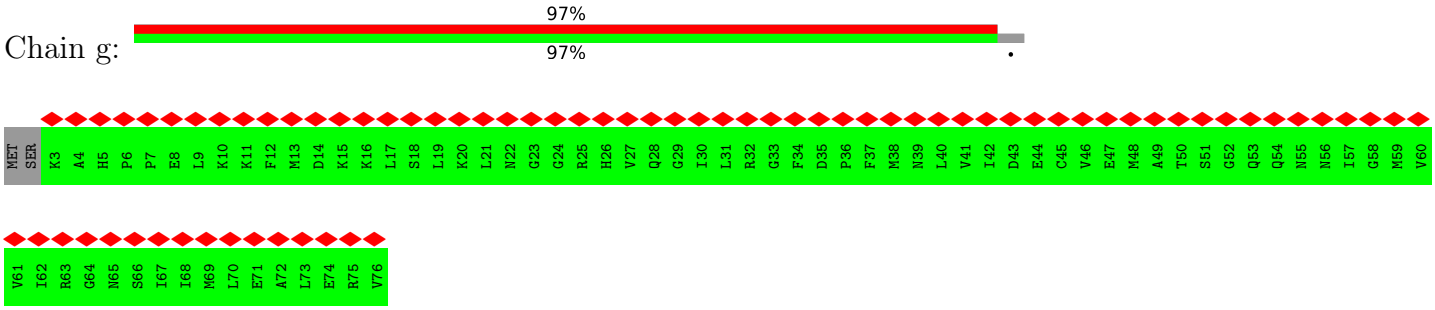
• Molecule 11: Small nuclear ribonucleoprotein E

Chain l:



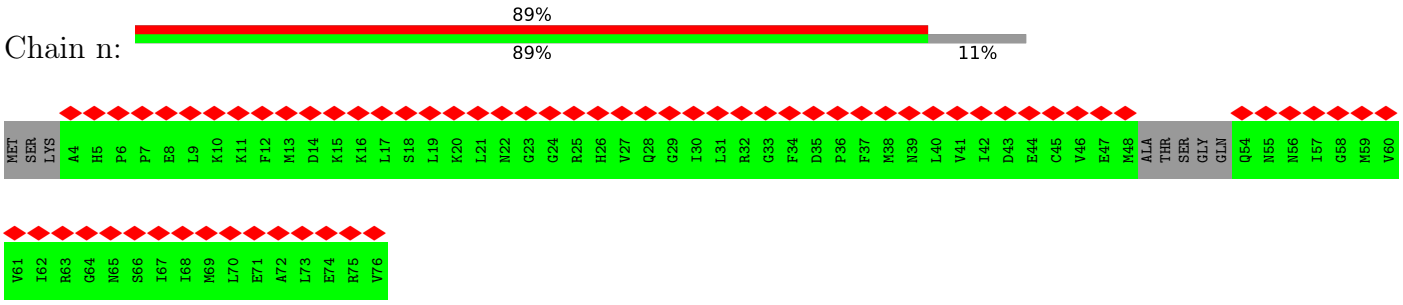
• Molecule 12: Small nuclear ribonucleoprotein G

Chain g:



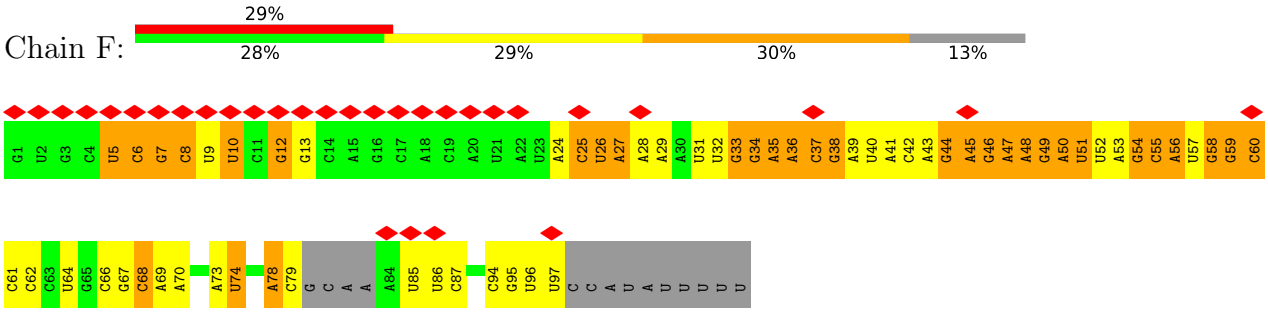
• Molecule 12: Small nuclear ribonucleoprotein G

Chain n:



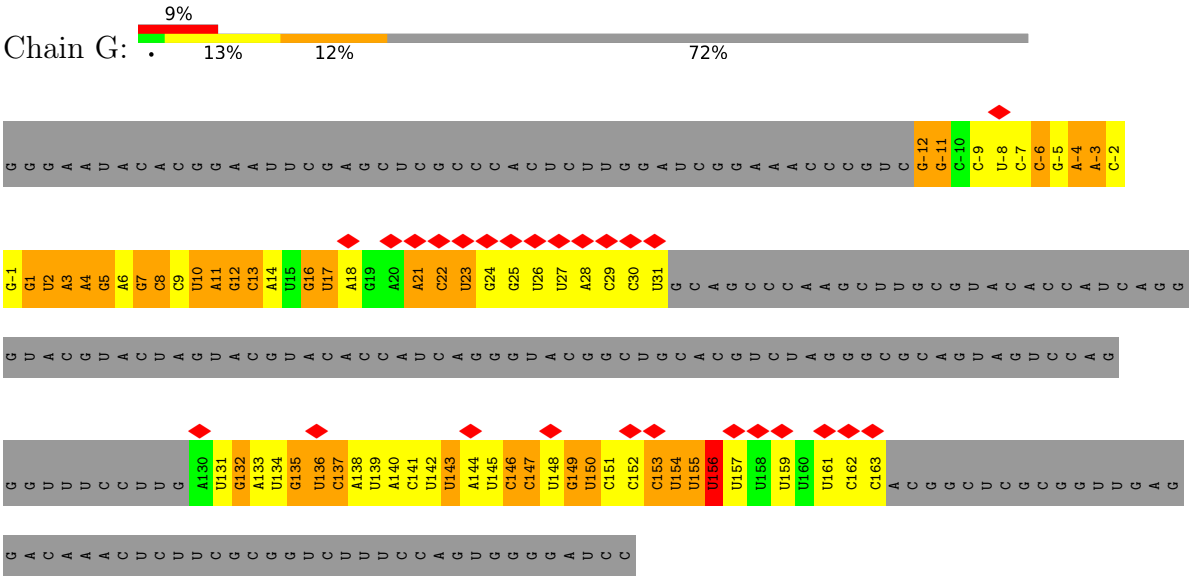
• Molecule 13: U6 snRNA

Chain F:



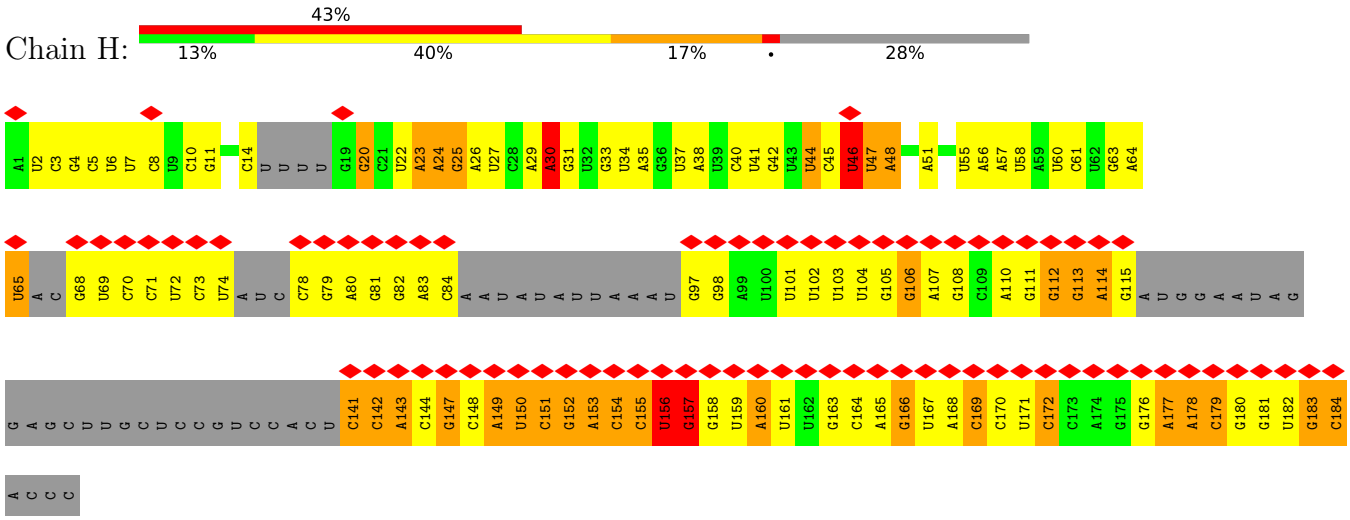
• Molecule 14: pre-mRNA

Chain G:



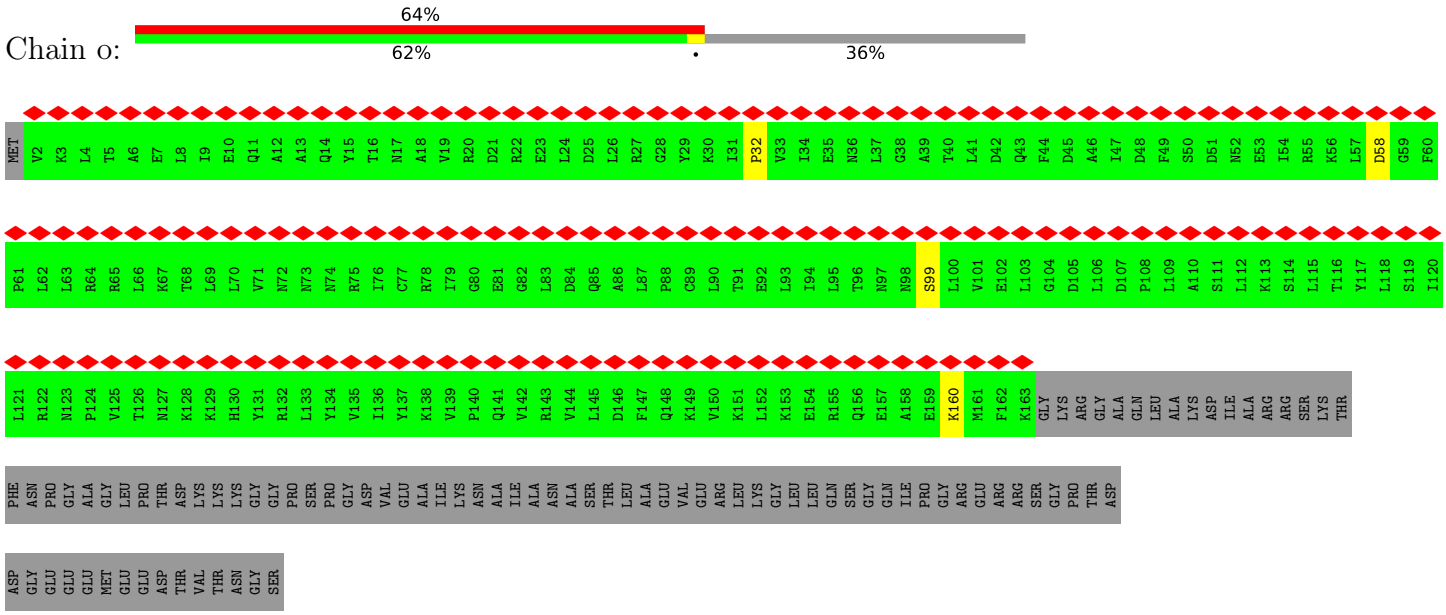
• Molecule 15: U2 snRNA

Chain H:



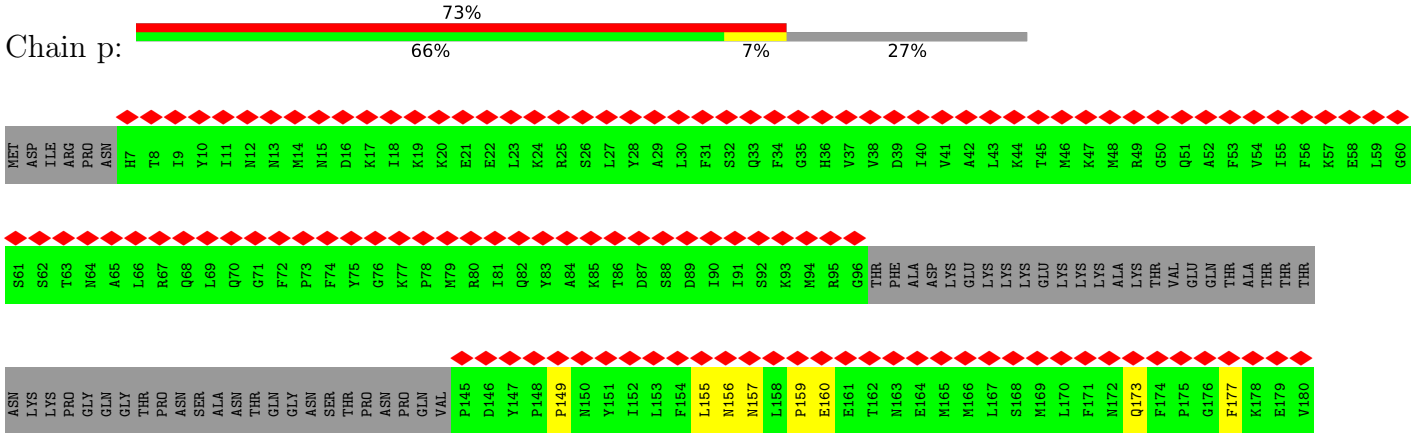
• Molecule 16: U2 small nuclear ribonucleoprotein A'

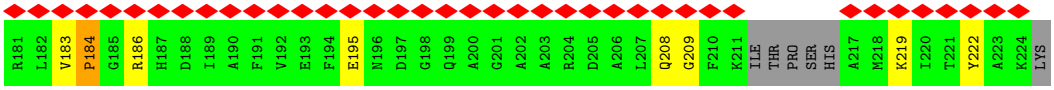
Chain o:



• Molecule 17: U2 small nuclear ribonucleoprotein B"

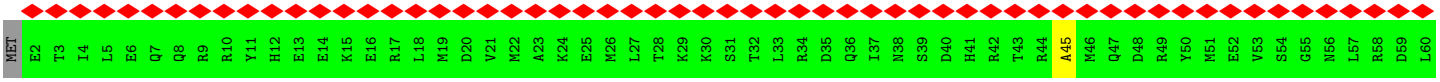
Chain p:

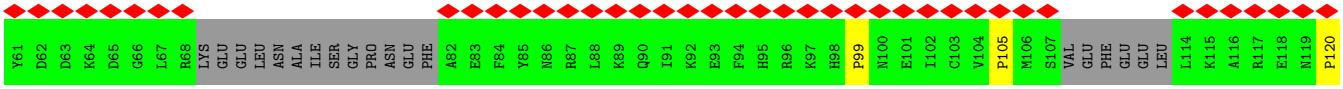


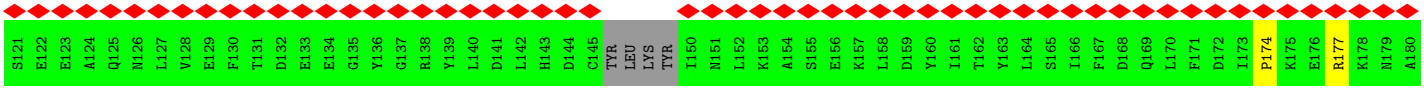


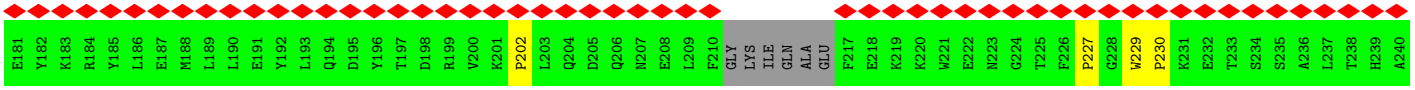
• Molecule 18: Splicing factor 3A subunit 3

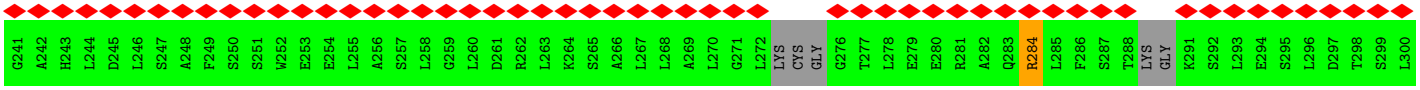
Chain w:

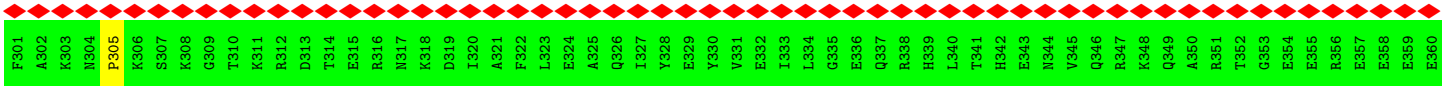


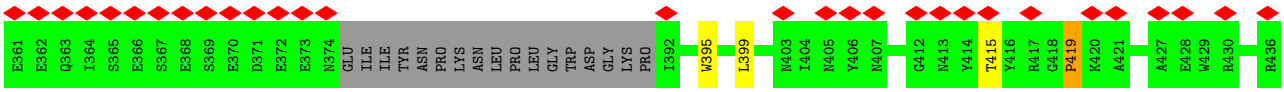


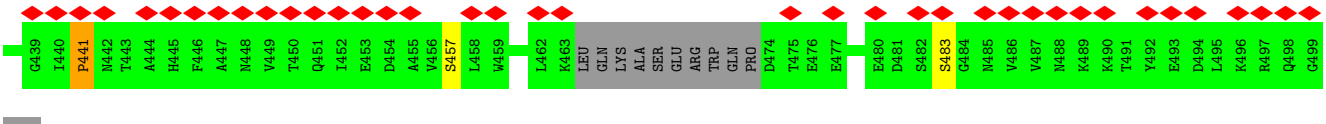






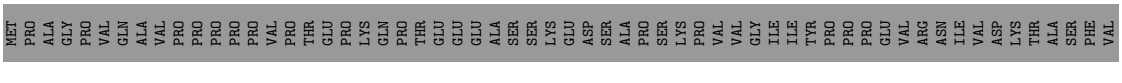


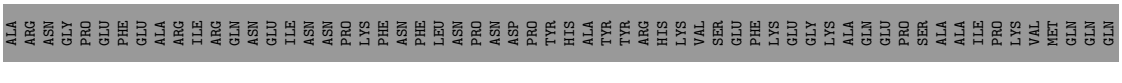


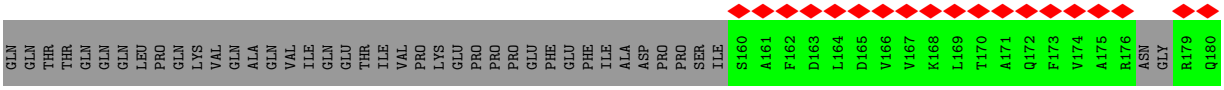


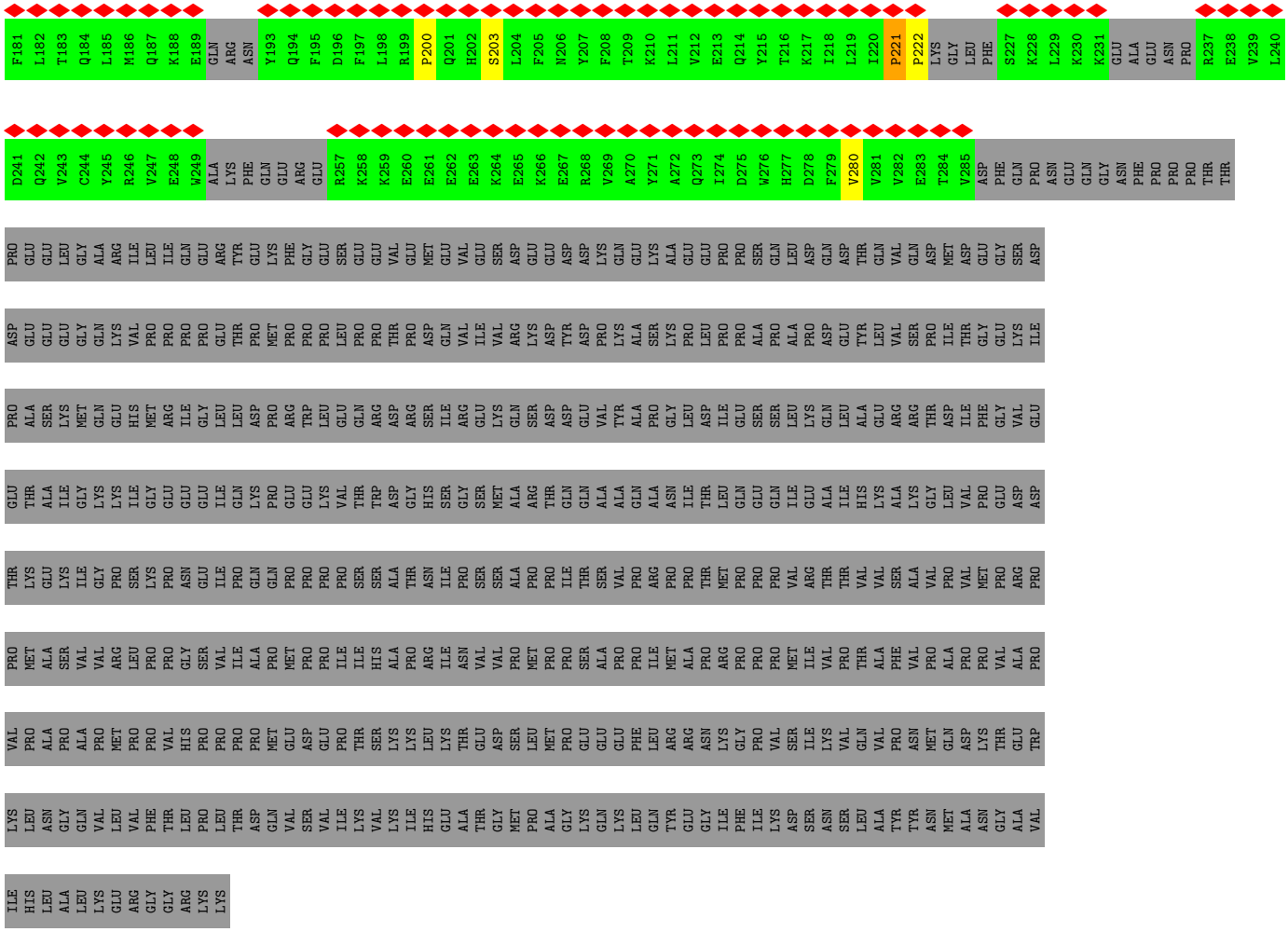
• Molecule 19: Splicing factor 3A subunit 1

Chain u:

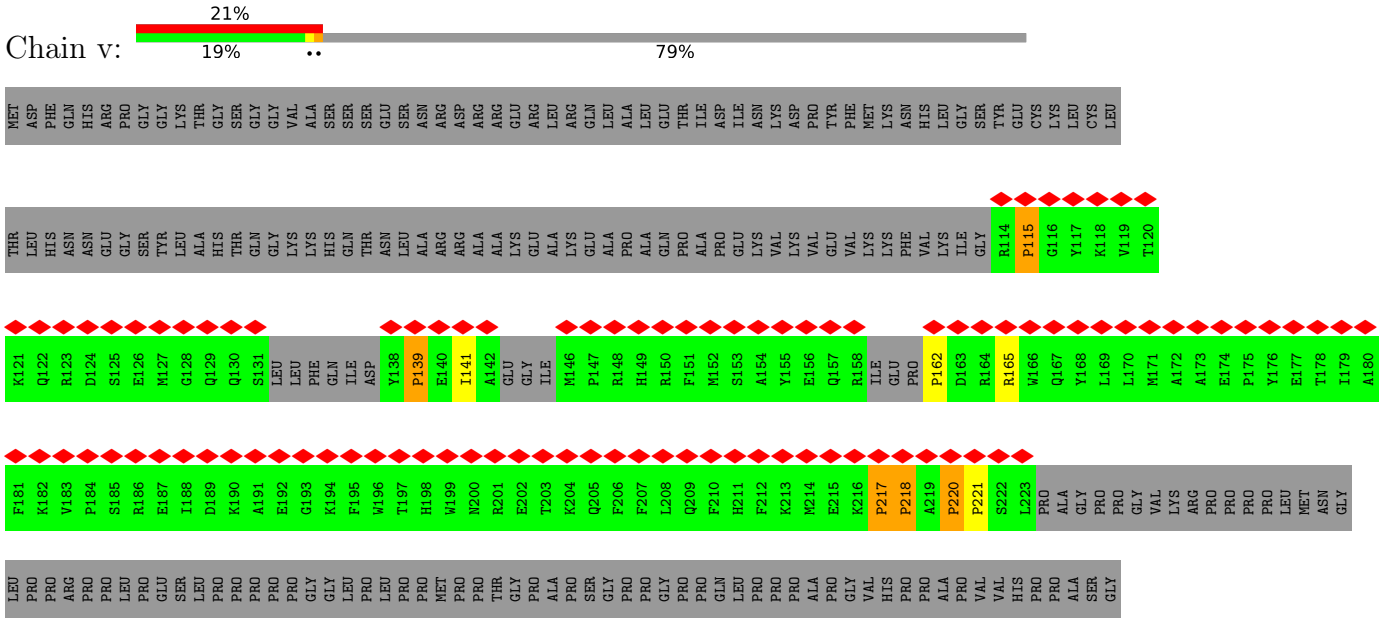


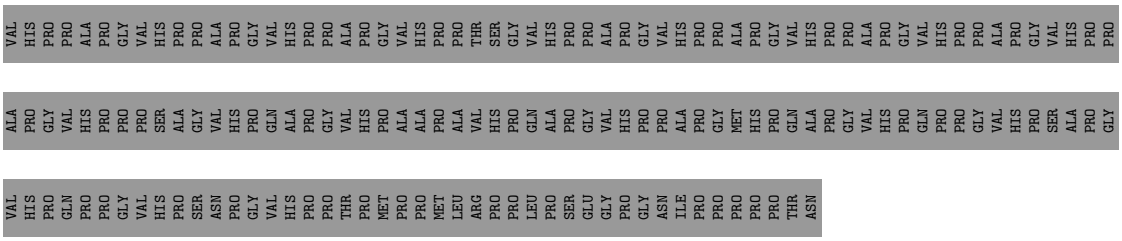






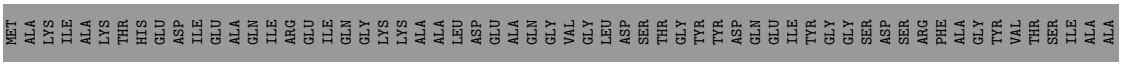
• Molecule 20: Splicing factor 3A subunit 2

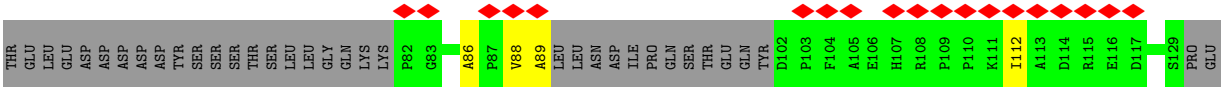


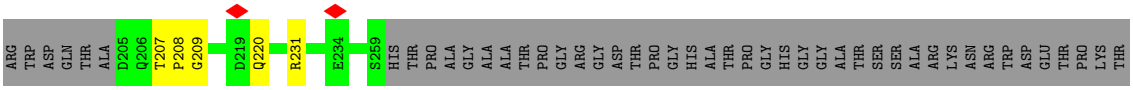


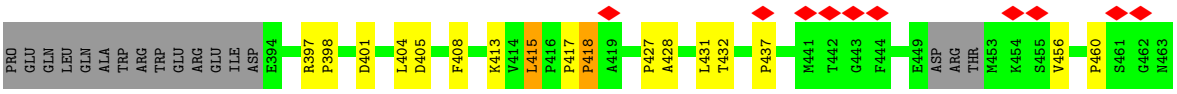
• Molecule 21: Splicing factor 3B subunit 1

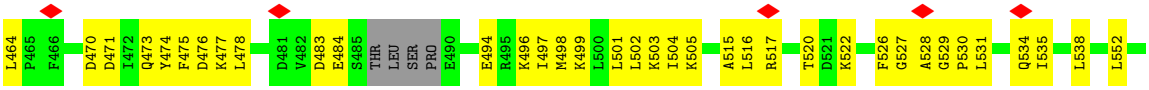
Chain 1:

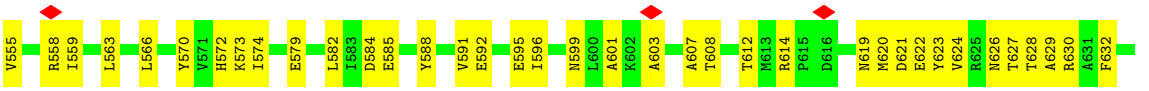


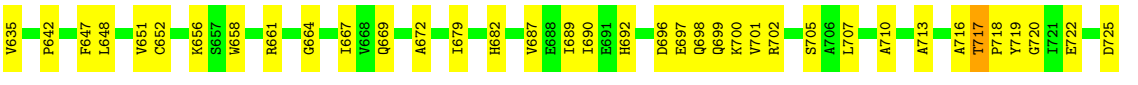


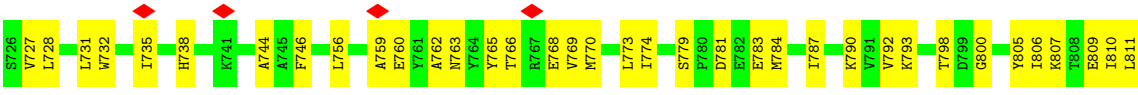


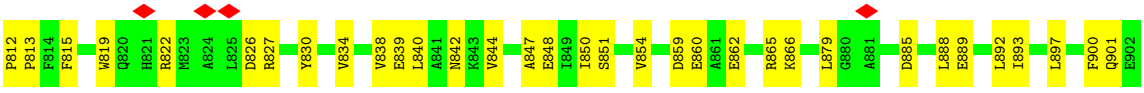


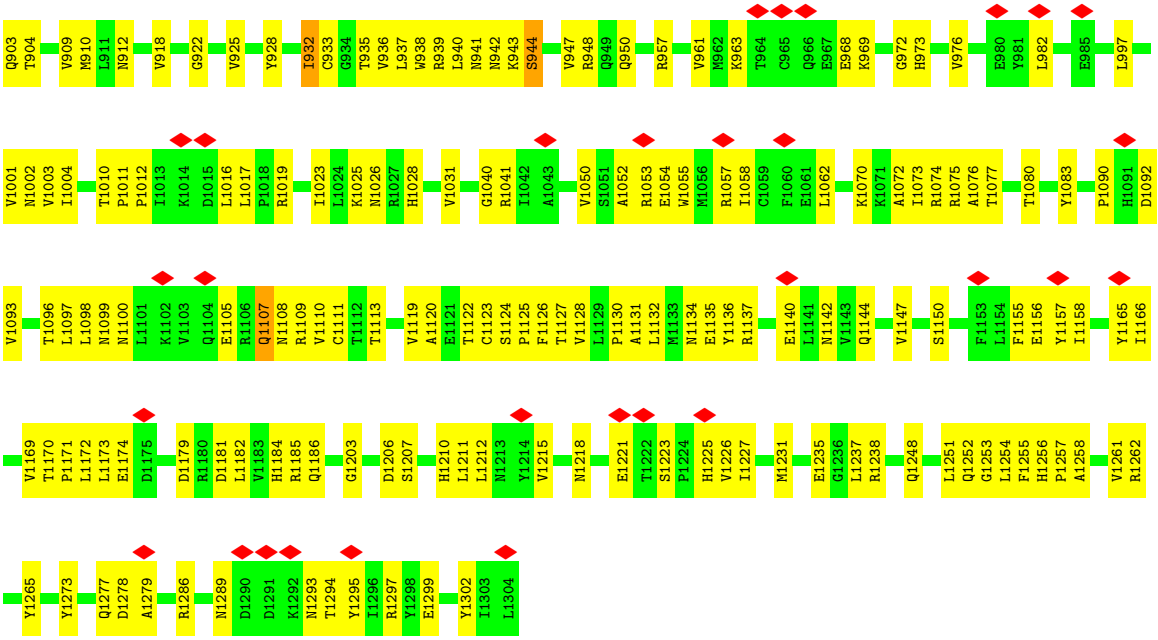






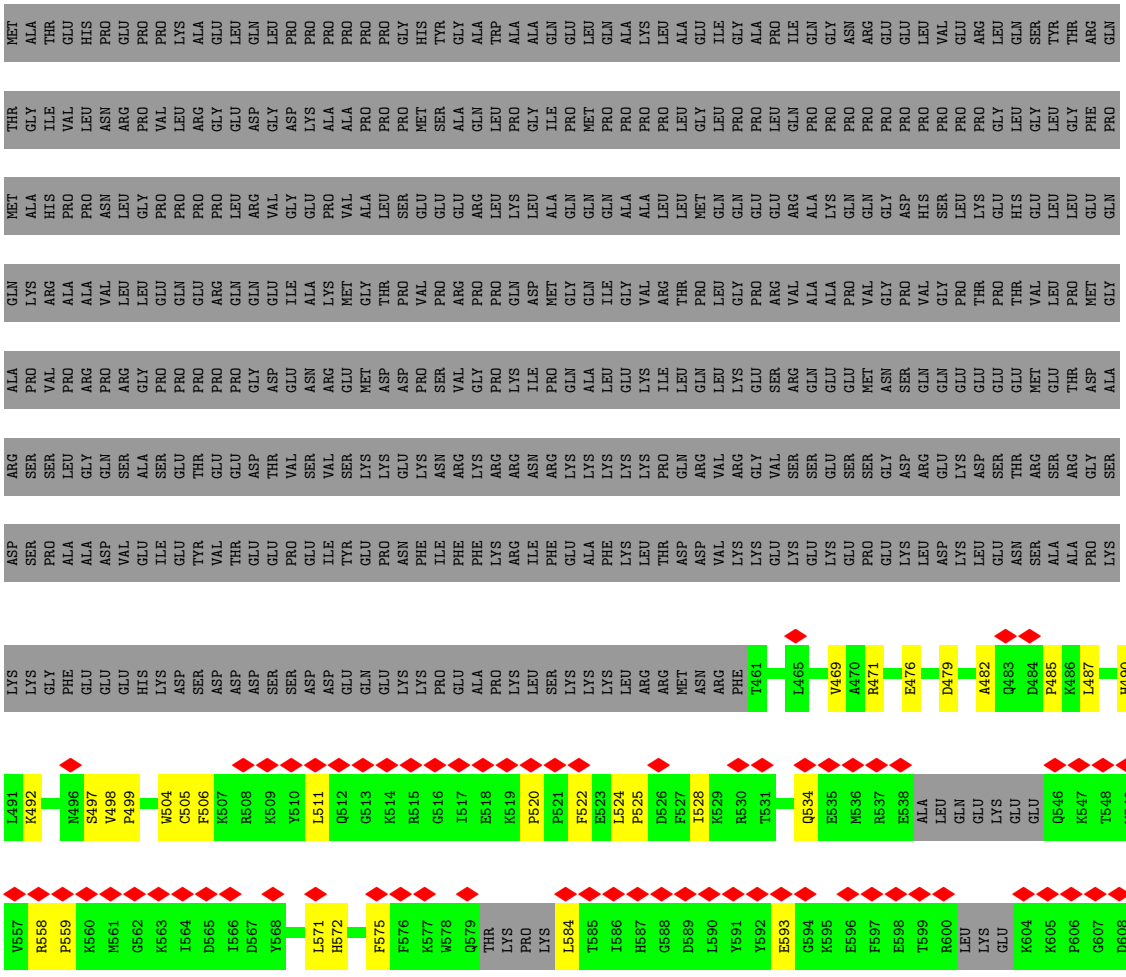


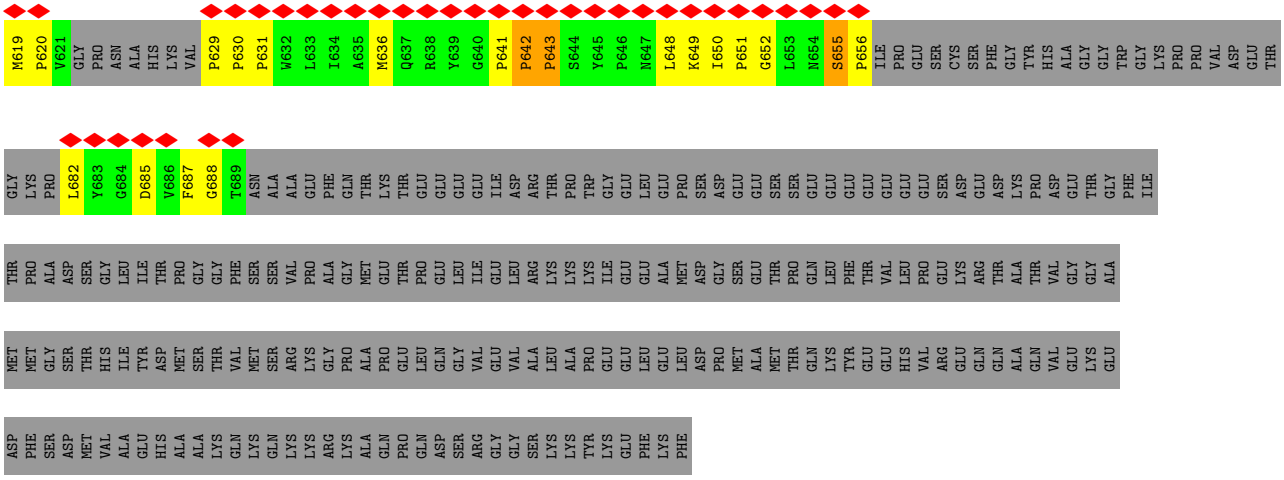




• Molecule 22: Splicing factor 3B subunit 2

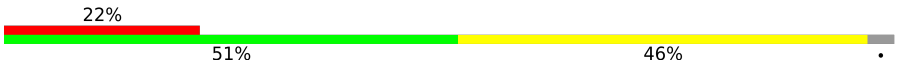
Chain 2:

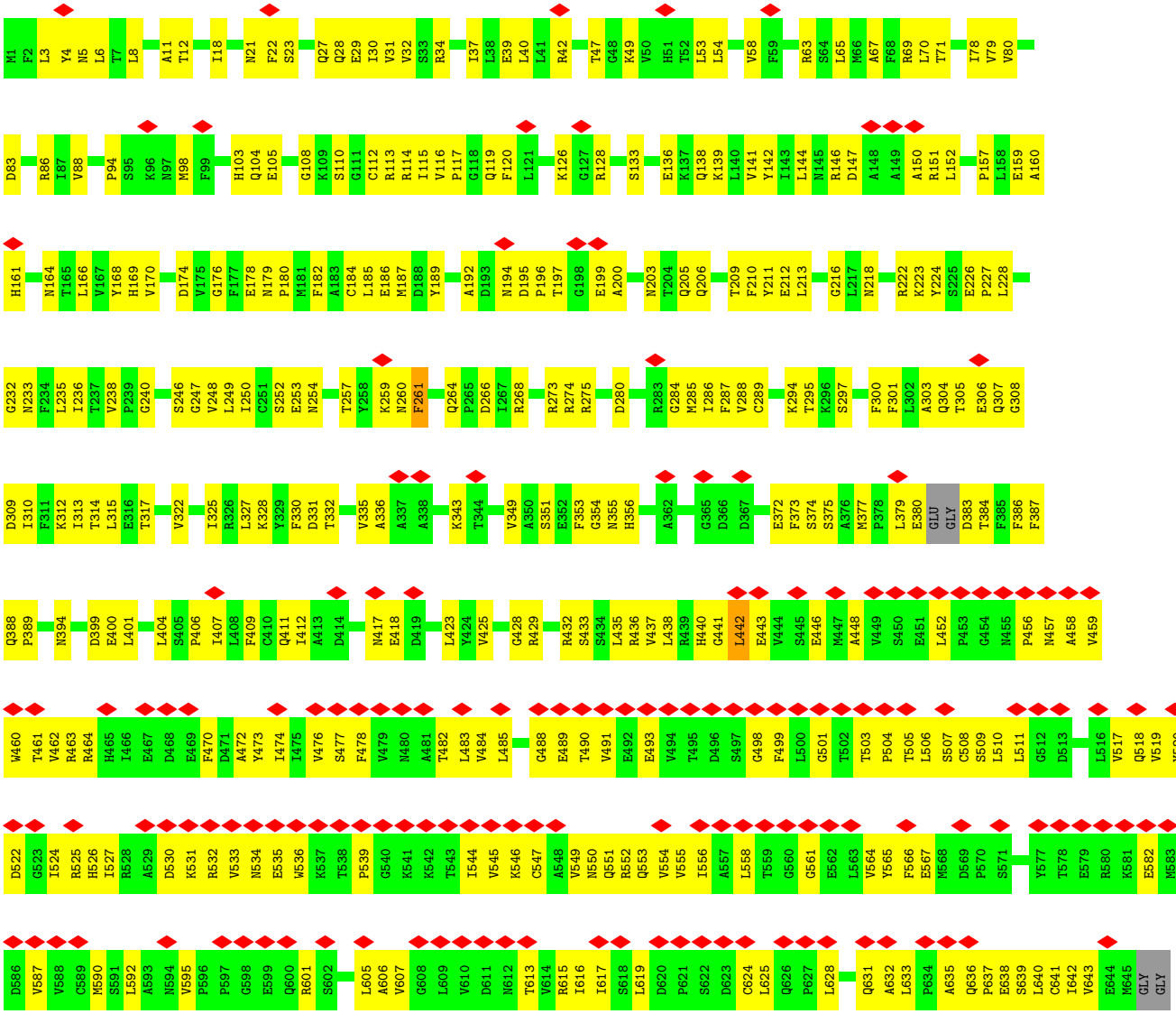


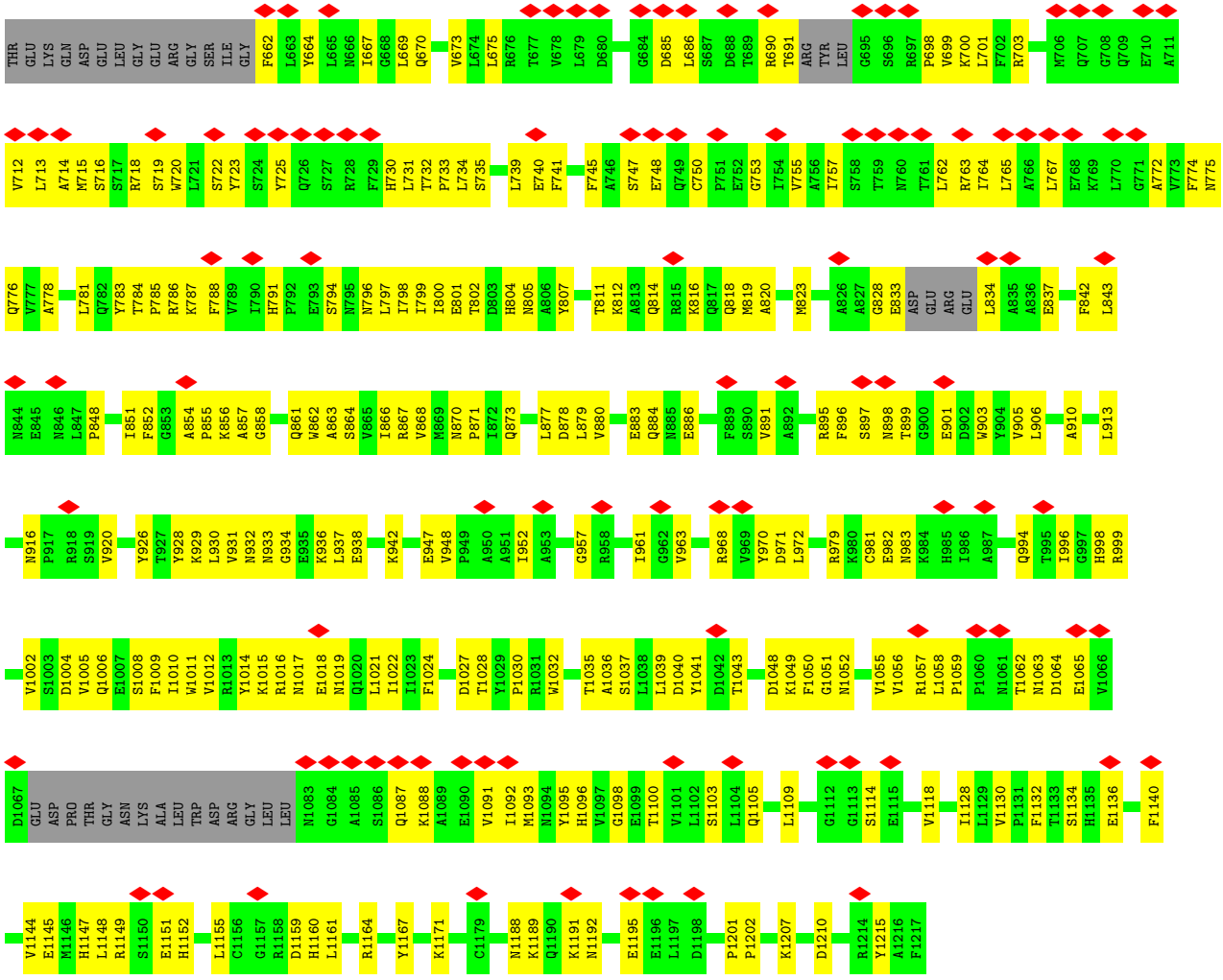


• Molecule 23: Splicing factor 3B subunit 3

Chain 3:

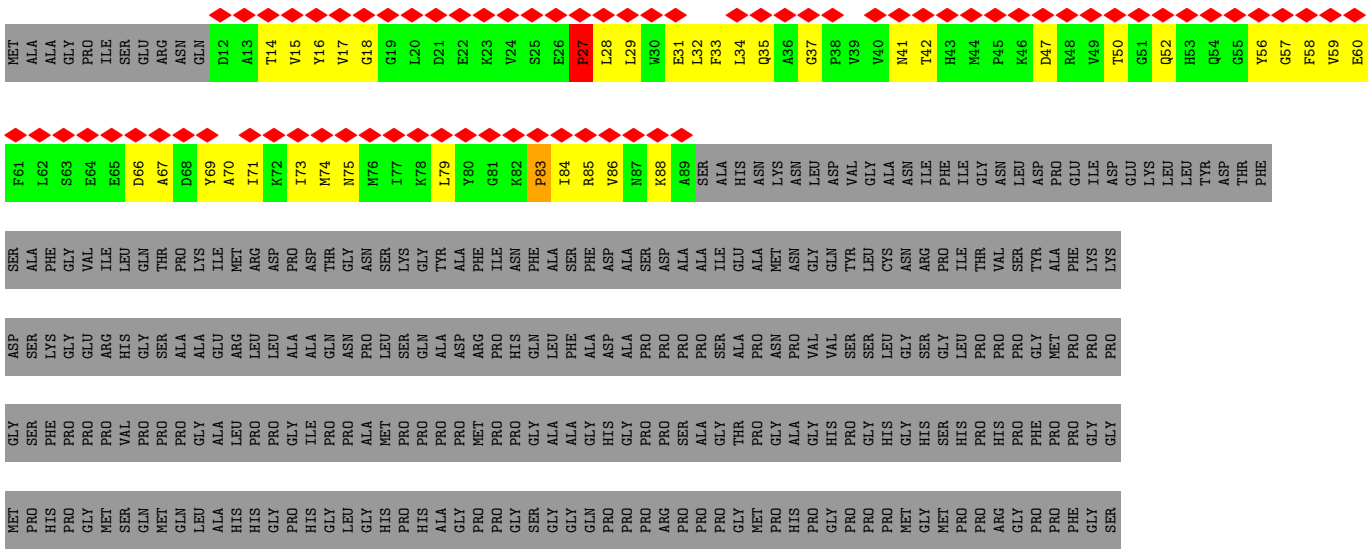






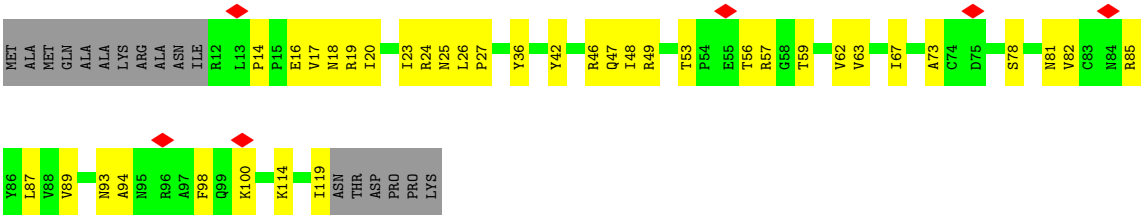
• Molecule 24: Splicing factor 3B subunit 4

Chain 4:



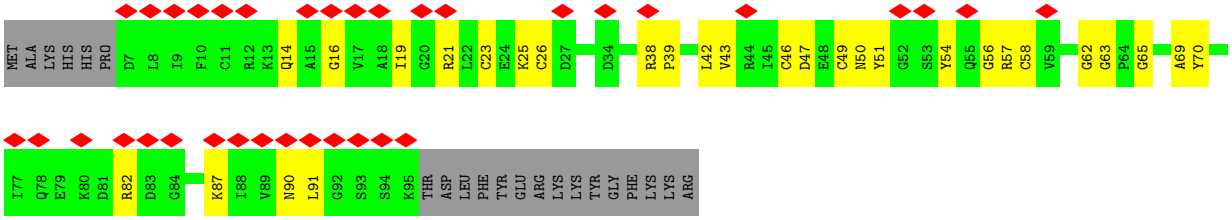
• Molecule 25: Splicing factor 3B subunit 6

Chain 5:



• Molecule 26: PHD finger-like domain-containing protein 5A

Chain 6:

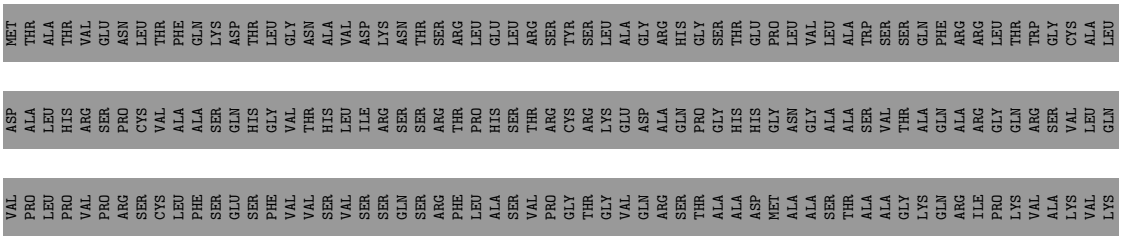


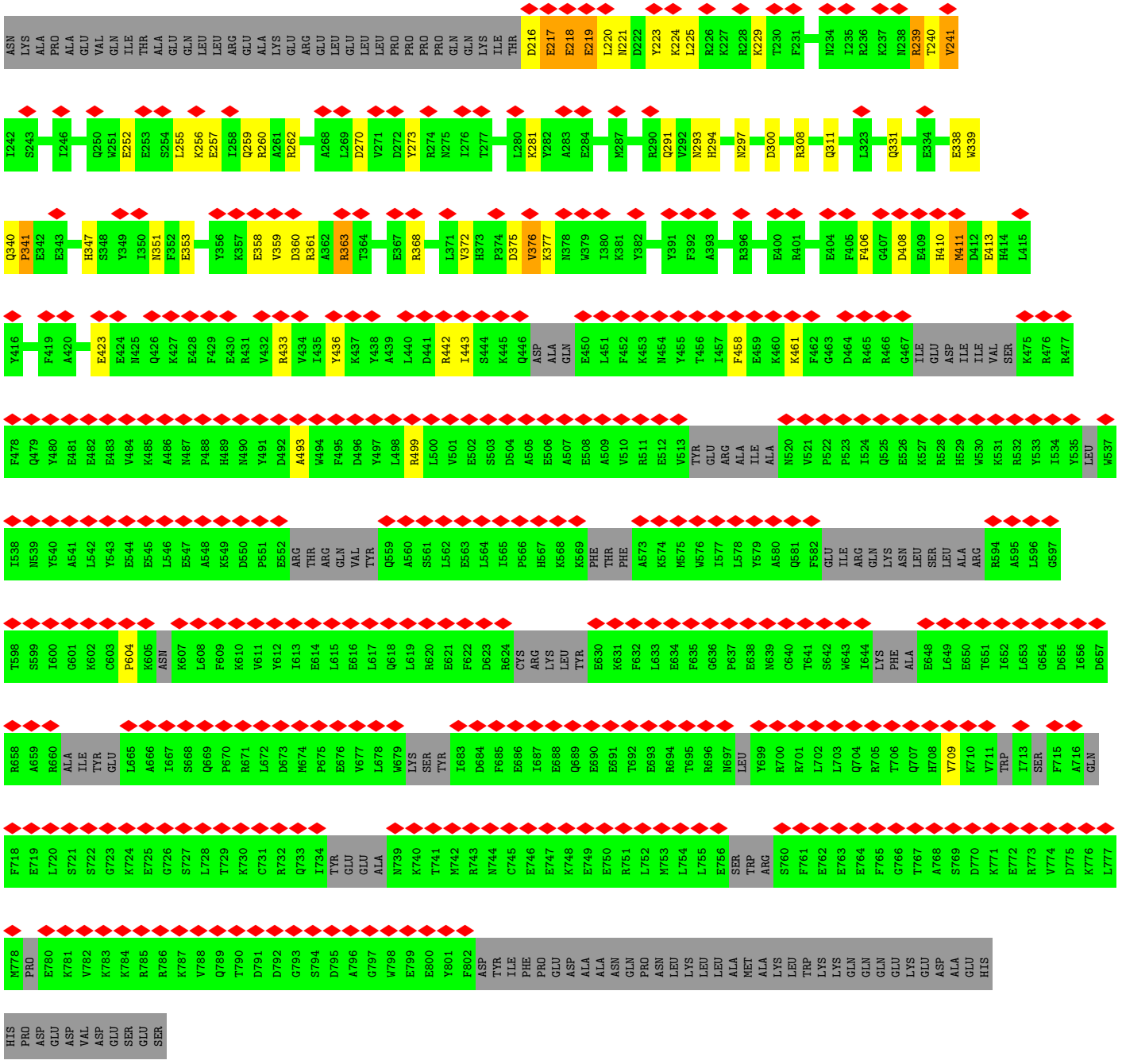
• Molecule 27: Splicing factor 3B subunit 5

Chain 7:

• Molecule 28: Crooked neck-like protein 1

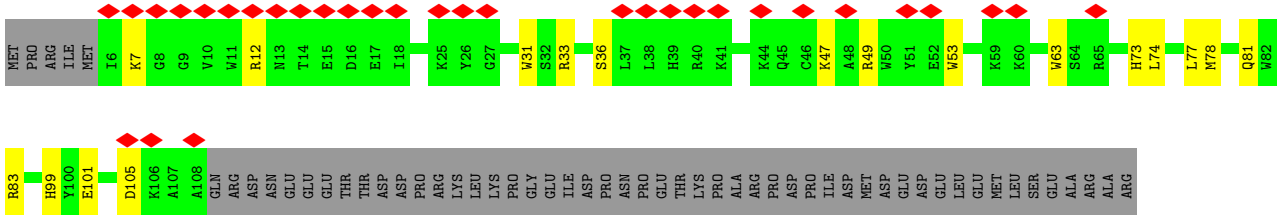
Chain J:

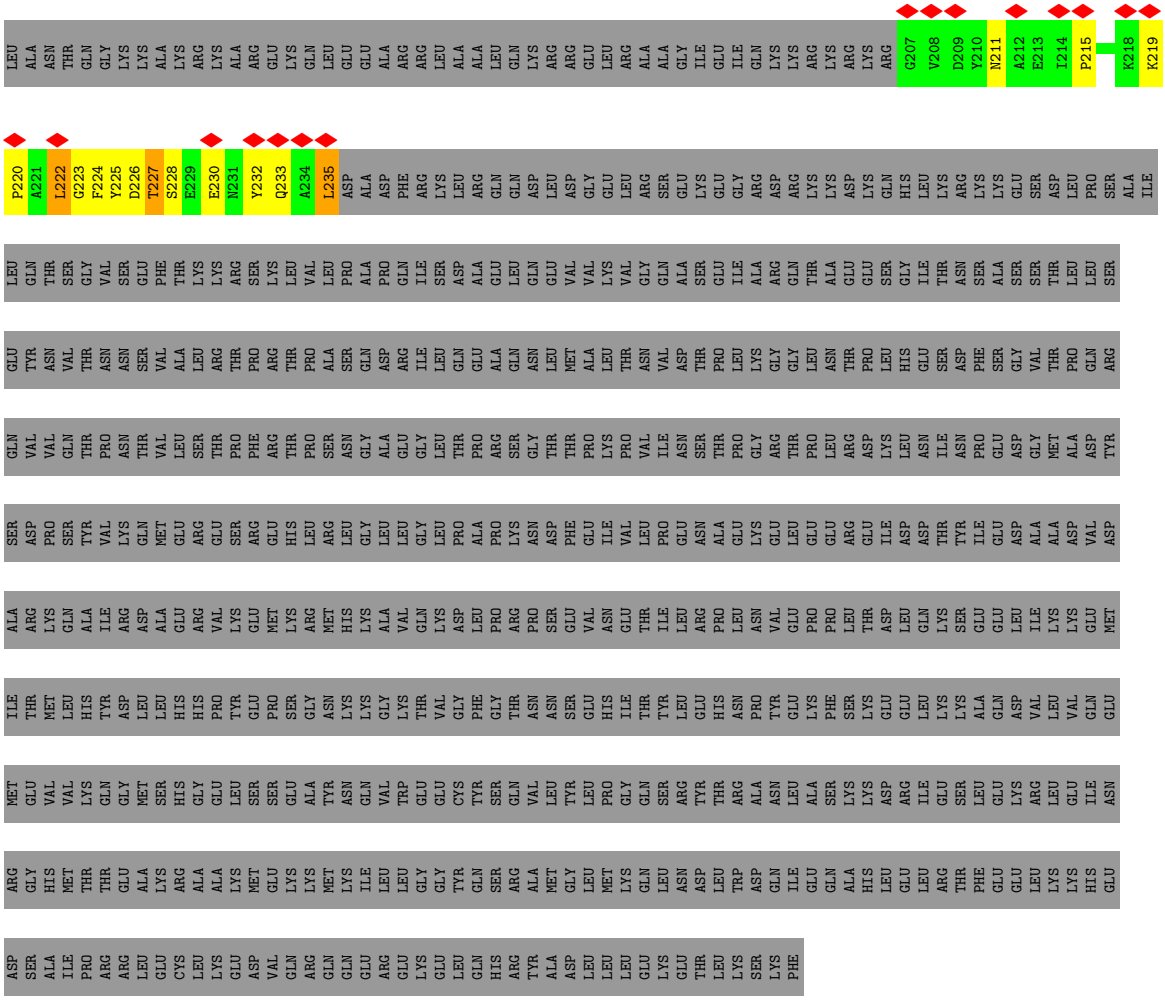




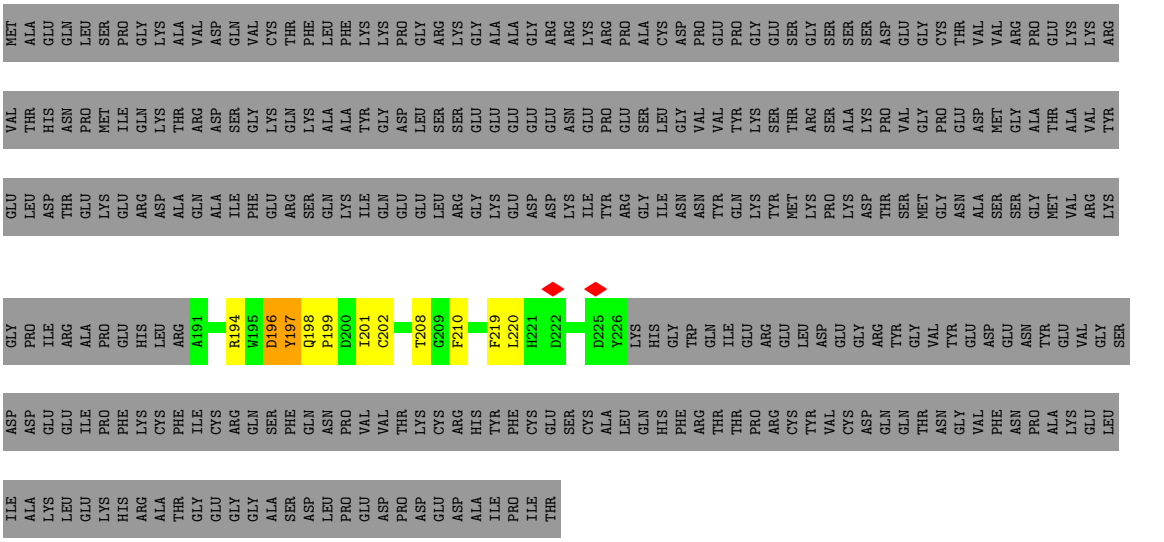
• Molecule 29: Cell division cycle 5-like protein

Chain L:

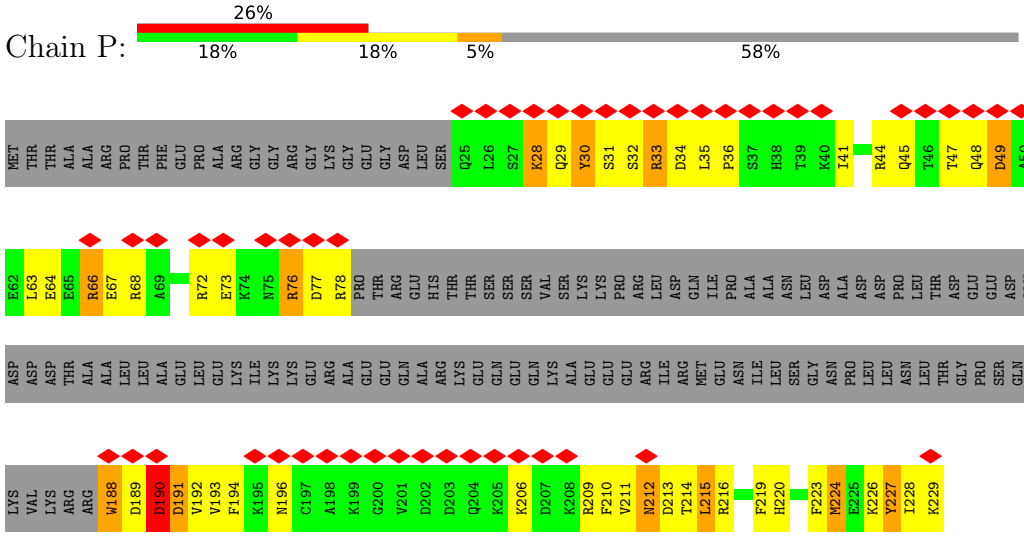




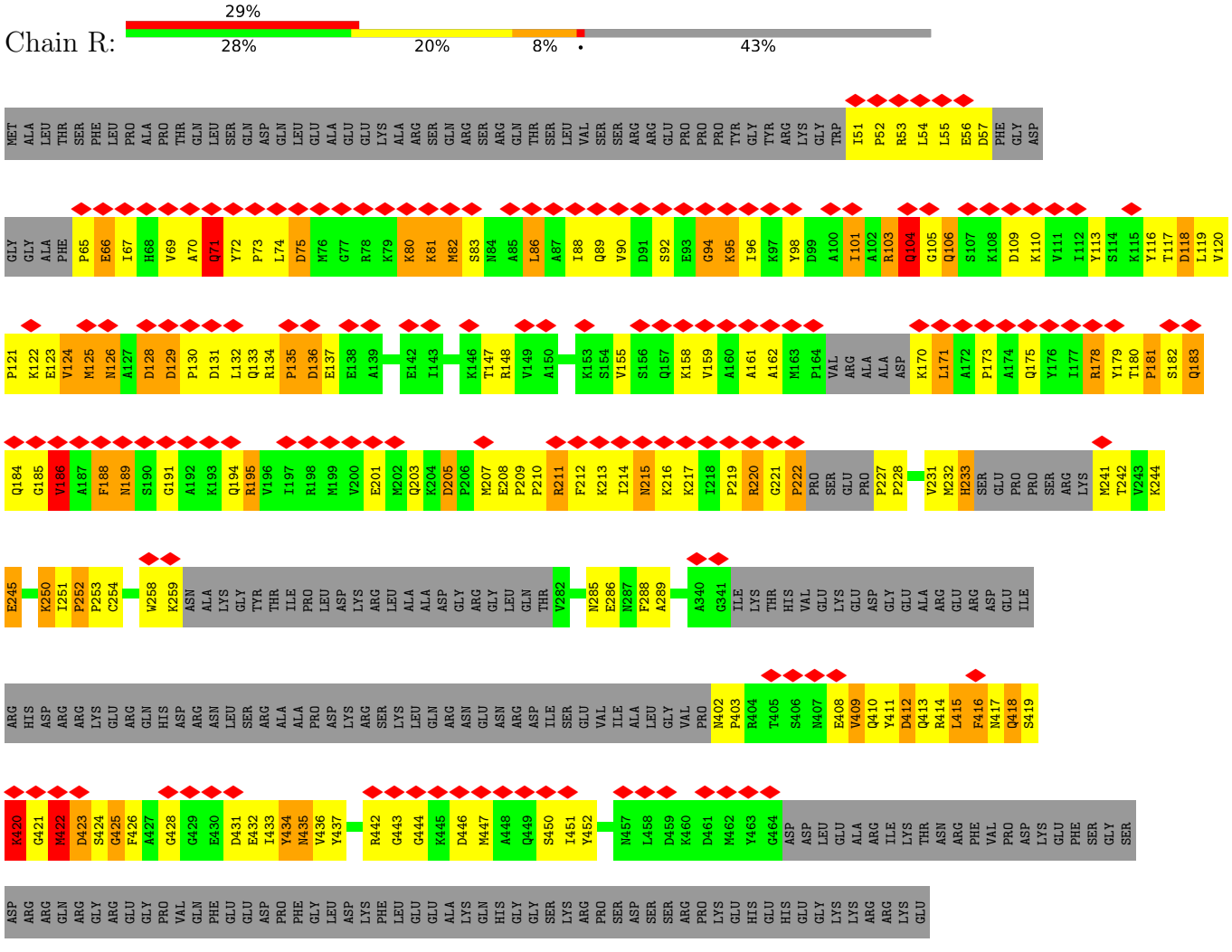
• Molecule 30: RING finger protein 113A



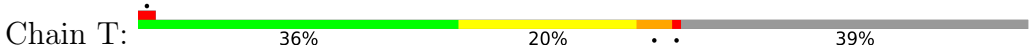
• Molecule 31: Spliceosome-associated protein CWC15 homolog

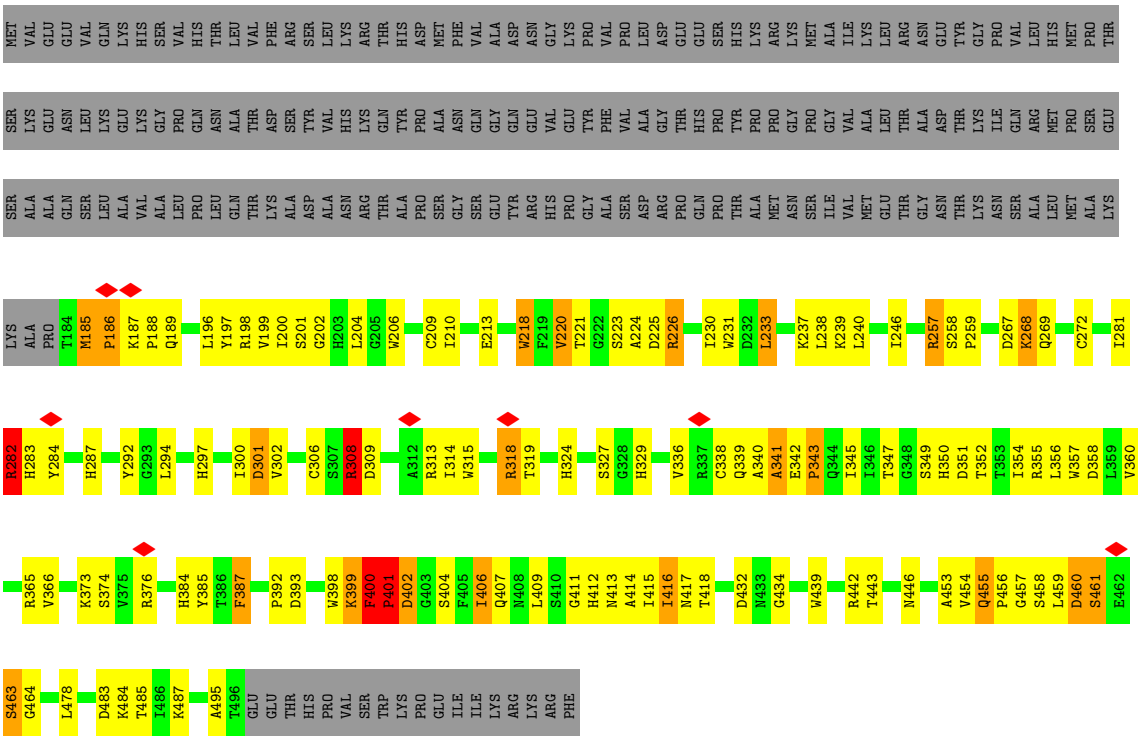


• Molecule 32: Skip



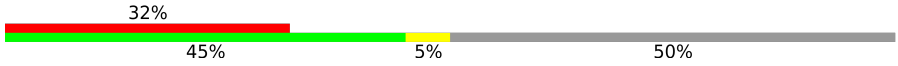
• Molecule 33: Pleiotropic regulator 1

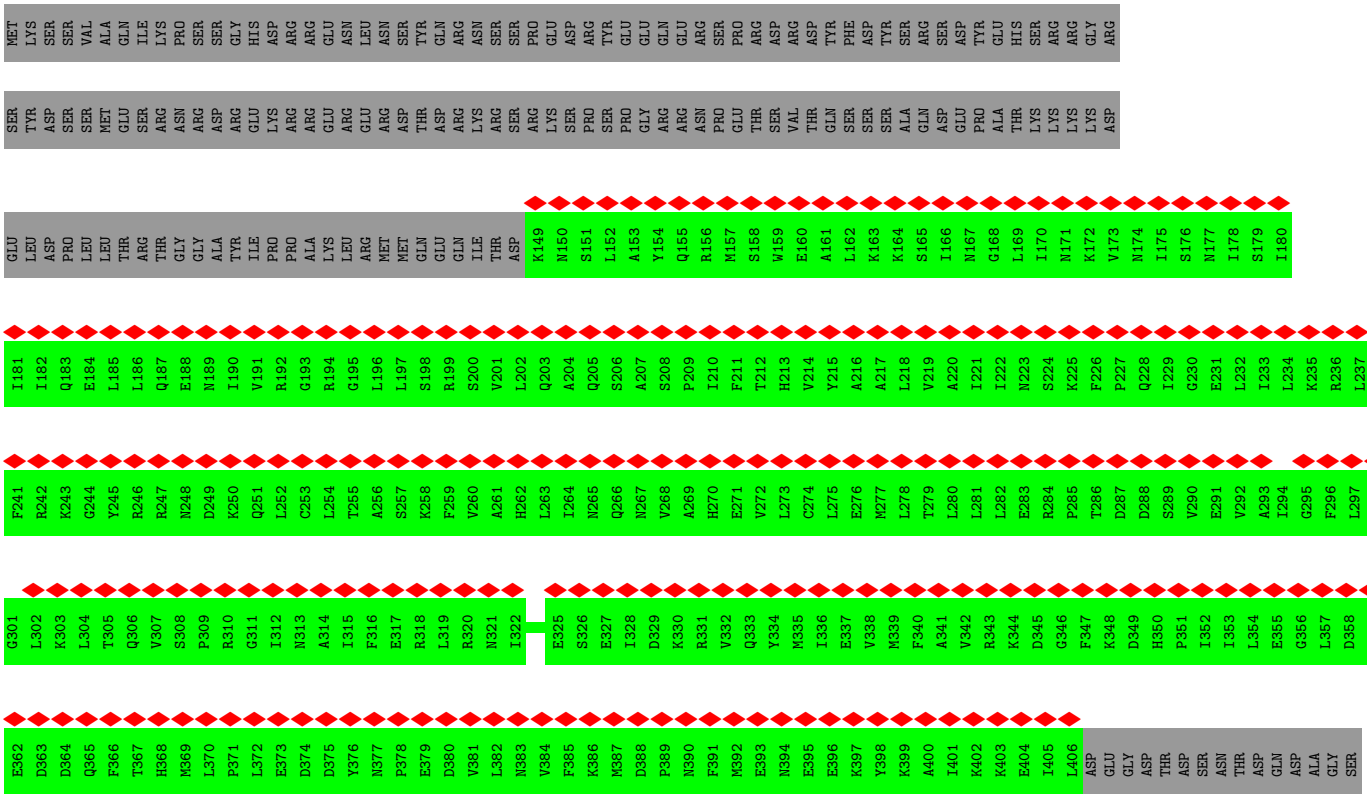


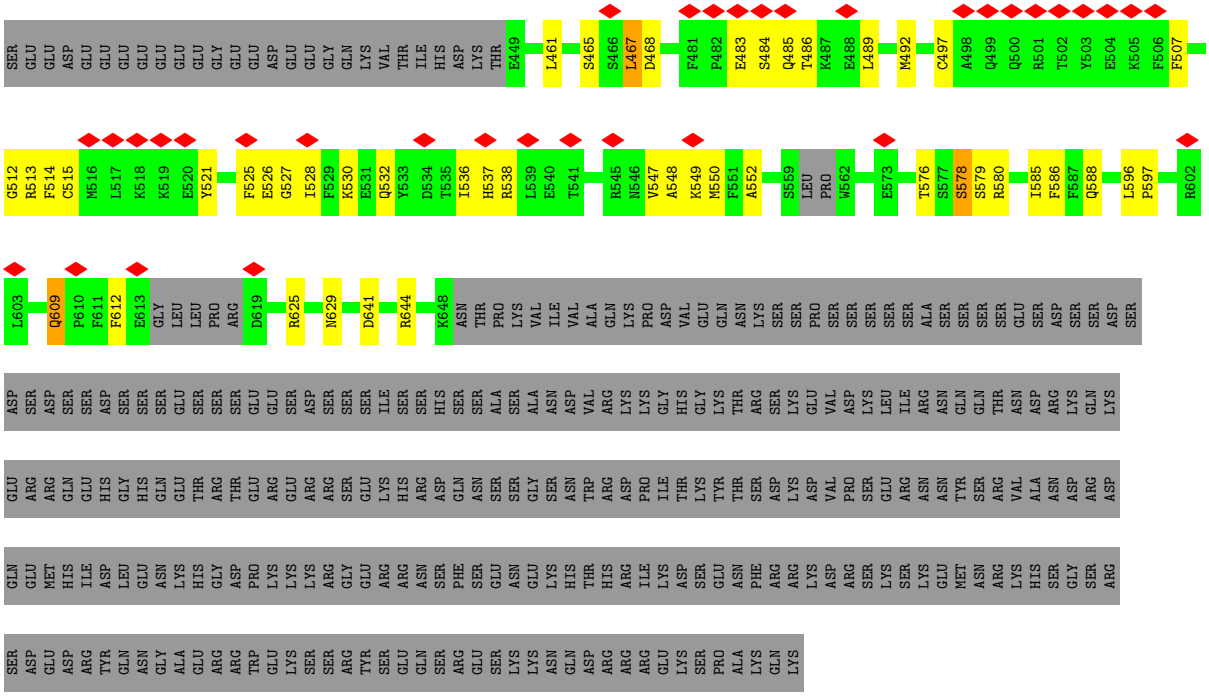


• Molecule 34: Pre-mRNA-splicing factor CWC22 homolog

Chain V:

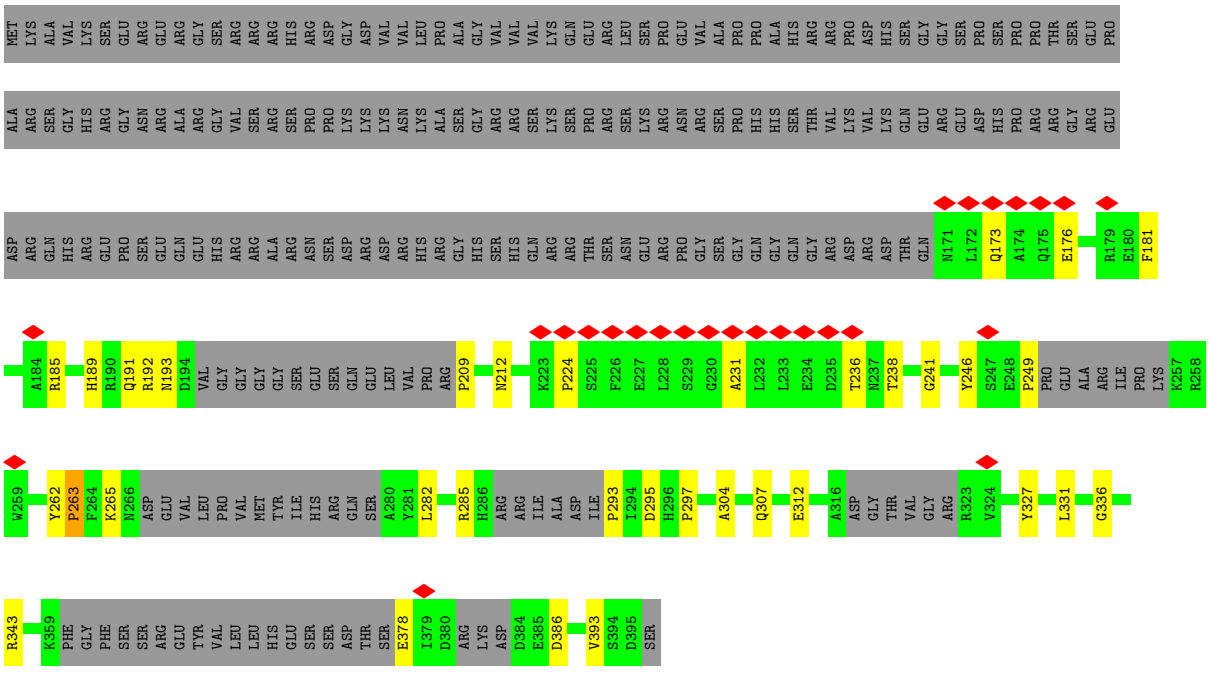






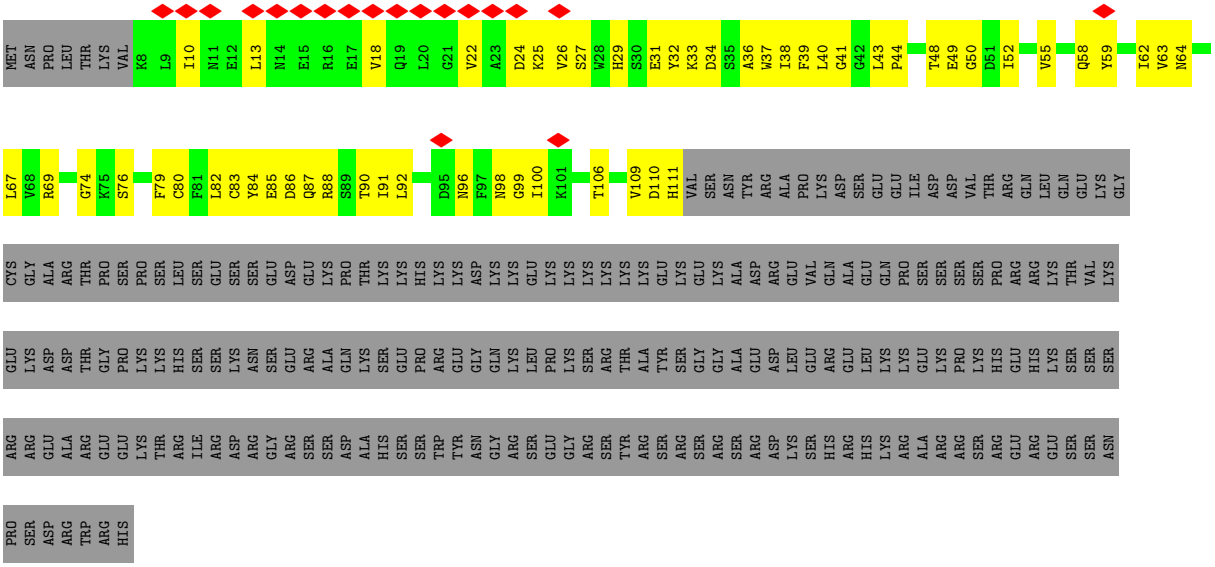
• Molecule 35: Smad nuclear-interacting protein 1

Chain X:



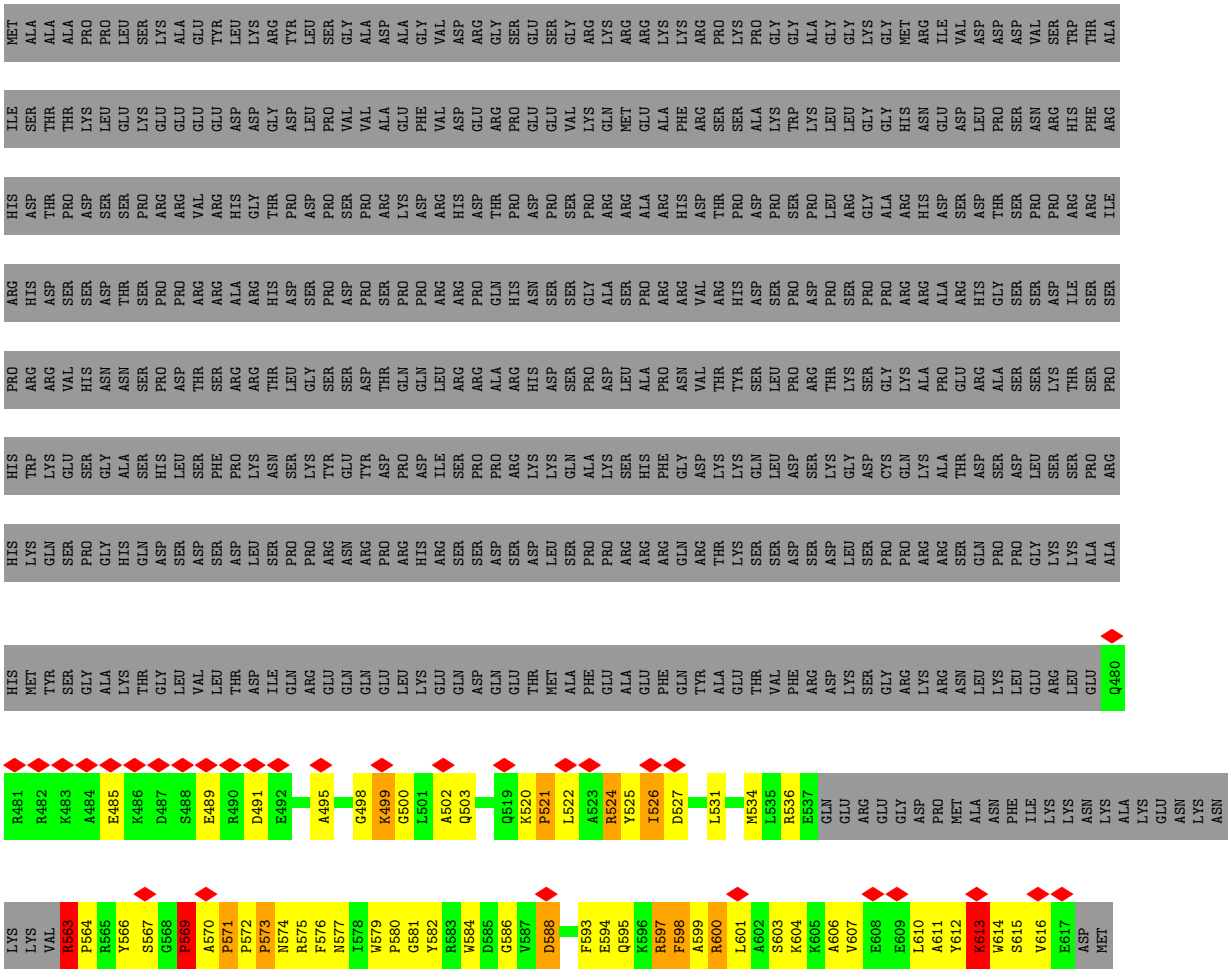
• Molecule 36: RNA-binding motif protein, X-linked 2

Chain Y:



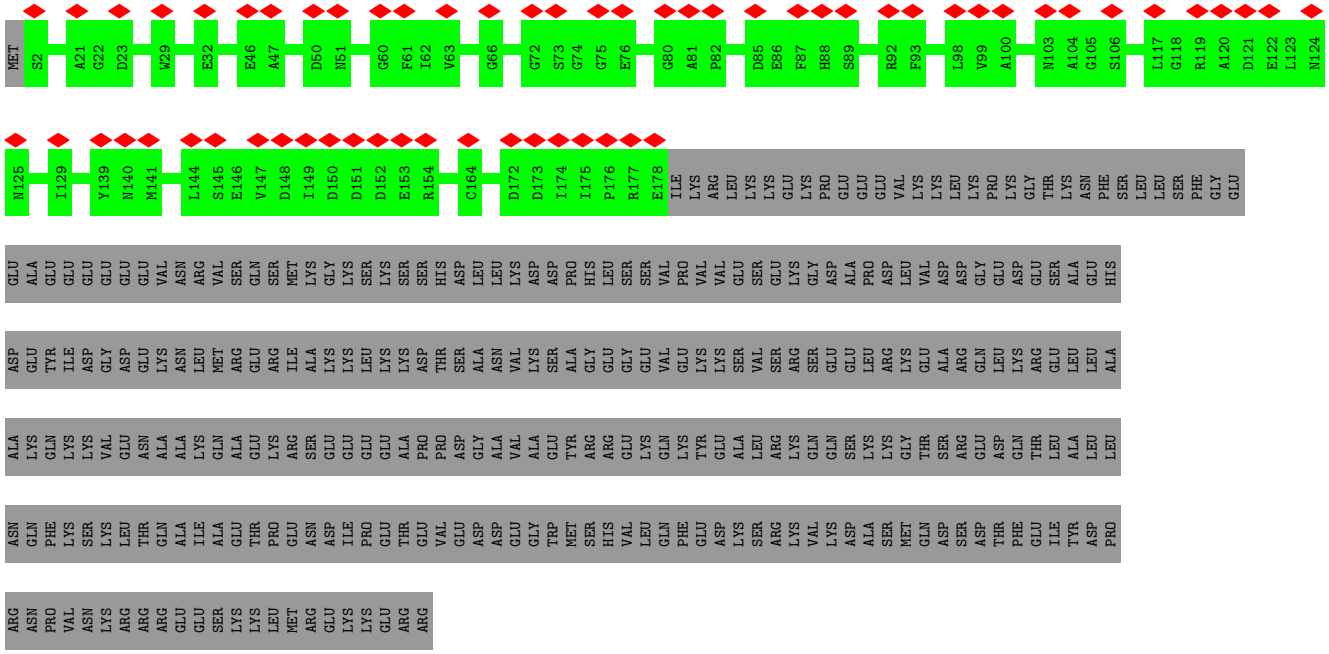
• Molecule 37: BUD13 homolog

Chain Z:



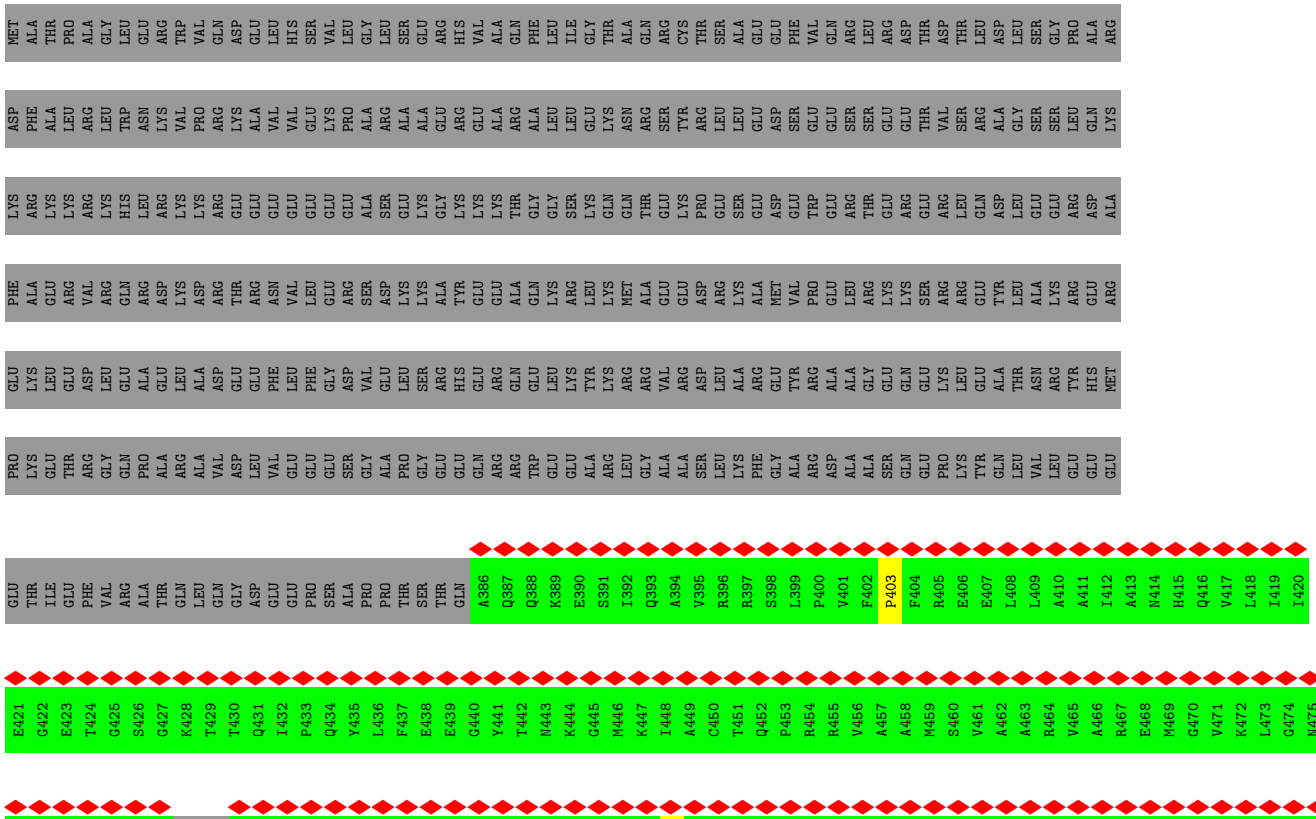
• Molecule 38: Peptidyl-prolyl cis-trans isomerase CWC27 homolog

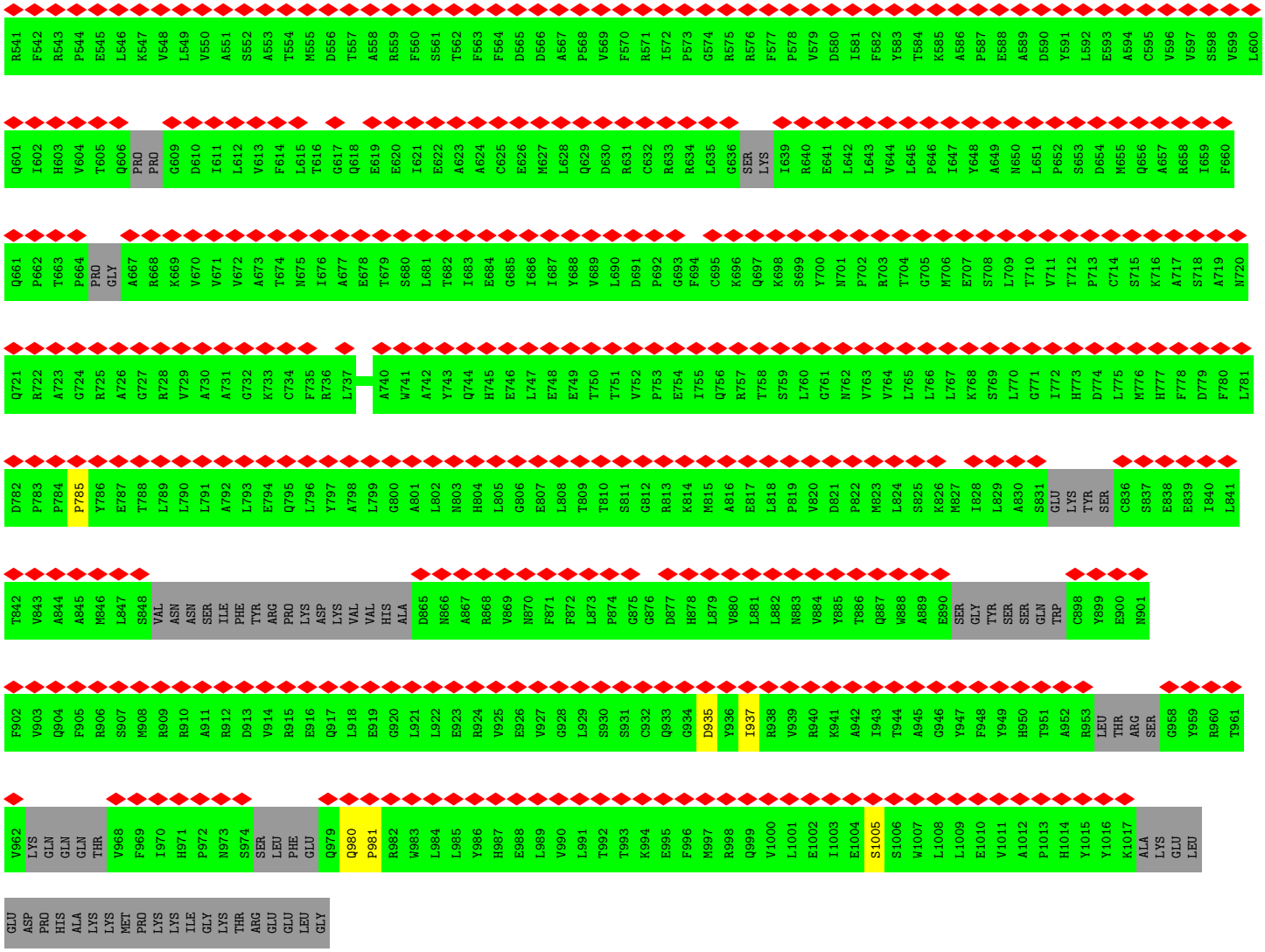
Chain z:



• Molecule 39: Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16

Chain x:




R541 F542 R543 P544 E545 L546 K547 V548 L549 V550 A551 S552 A553 T554 M555 D556 T557 A558 R559 F560 S561 T562 F563 F564 D565 D566 A567 P568 V569 F570 R571 I572 P573 G574 R575 R576 F577 P578 V579 D580 I581 F582 Y583 T584 K585 A586 P587 E588 A589 D590 Y591 L592 E593 A594 C595 V596 V597 S598 V599 L600
Q601 I602 H603 V604 T605 Q606 PRO PRO G609 D610 I611 L612 V613 F614 L615 T616 G617 Q618 E619 E620 I621 E622 A623 A624 C625 E626 M627 L628 Q629 D630 R631 C632 R633 R634 L635 G636 SER LYS I639 R640 E641 L642 L643 V644 L645 P646 I647 Y648 A649 N650 L651 P652 S653 D654 M655 Q656 A657 R658 I659 F660
Q661 P662 T663 P664 PRO GLY A667 R668 K669 V670 V671 V672 A673 T674 N675 I676 A677 E678 T679 S680 L681 T682 I683 E684 G685 I686 I687 Y688 V689 L690 D691 P692 G693 F694 C695 K696 Q697 K698 S699 Y700 N701 P702 R703 T704 G705 M706 E707 S708 L709 T710 V711 T712 P713 C714 S715 K716 A717 S718 A719 N720
Q721 R722 A723 G724 R725 A726 G727 R728 V729 A730 A731 G732 K733 C734 F735 R736 L737 A740 W741 A742 Y743 Q744 H745 E746 L747 E748 E749 T750 T751 V752 P753 E754 I755 Q756 R757 T758 S759 L760 G761 N762 V763 V764 L765 L766 L767 K768 S769 L770 G771 I772 H773 D774 L775 M776 H777 F778 D779 F780 L781
D782 P783 P784 P785 Y786 E787 T788 L789 L790 L791 A792 L793 E794 Q795 L796 Y797 A798 L799 G800 A801 L802 N803 H804 L805 G806 E807 L808 T809 T810 S811 G812 R813 K814 M815 A816 E817 L818 P819 V820 D821 P822 M823 L824 S825 K826 M827 I828 L829 A830 S831 GLU LYS TYR SER C836 S837 E838 E839 I840 L841
T842 V843 A844 A845 M846 L847 S848 VAL ASN ASN SER ILE PHE TYR ARG PRO LYS ASP LYS VAL VAL VAL HIS ALA D865 N866 A867 R868 V869 N870 F871 F872 L873 P874 G875 G876 D877 H878 L879 V880 L881 L882 N883 V884 Y885 T886 Q887 W888 A889 E890 SER GLY TYR SER SER GLN TRP C898 Y899 E900 N901
P902 V903 Q904 F905 R906 S907 M908 R909 R910 A911 R912 D913 V914 R915 E916 Q917 L918 E919 G920 L921 L922 E923 R924 V925 E926 V927 G928 L929 S930 S931 C932 Q933 G934 D935 Y936 I937 R938 V939 R940 K941 A942 I943 T944 A945 G946 Y947 F948 Y949 H950 T951 A952 R953 LEU THR ARG SER G958 Y959 R960 T961
V962 LYS GLN GLN GLN THR V968 F969 I970 H971 P972 N973 S974 SER LEU PHE GLU Q979 Q980 P981 R982 W983 L984 L985 Y986 H987 E988 L989 V990 L991 T992 T993 K994 E995 F996 M997 R998 Q999 V1000 L1001 E1002 I1003 E1004 S1005 S1006 W1007 L1008 L1009 E1010 V1011 A1012 P1013 H1014 Y1015 Y1016 K1017 ALA LYS GLU LEU
GLU ASP PRO HIS ALA LYS LYS MET PRO LYS LYS ILE GLY LYS THR ARG GLU GLU LEU GLY

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	96523	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	48	Depositor
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	0.184	Depositor
Minimum map value	-0.094	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0346	Depositor
Map size (Å)	535.2, 535.2, 535.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.338, 1.338, 1.338	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.69	10/18665 (0.1%)	0.77	26/25340 (0.1%)
2	B	0.73	2/1970 (0.1%)	0.91	7/3060 (0.2%)
3	C	0.79	1/6864 (0.0%)	0.96	10/9334 (0.1%)
4	D	0.33	0/8527	0.59	0/11887
5	E	0.64	0/2392	0.79	0/3242
6	a	0.47	0/397	0.61	0/549
6	h	0.46	0/391	0.61	0/540
7	b	0.49	0/404	0.72	0/561
7	i	0.50	0/421	0.73	0/583
8	c	0.57	0/405	0.73	0/563
8	j	0.57	0/405	0.73	0/563
9	d	0.68	0/479	0.84	0/666
9	k	0.70	0/420	0.85	0/583
10	f	0.75	0/360	0.81	0/497
10	m	0.75	0/360	0.81	0/497
11	e	0.65	0/390	0.80	0/542
11	l	0.64	0/390	0.80	0/542
12	g	0.54	0/362	0.71	0/501
12	n	0.54	0/332	0.72	0/458
13	F	0.39	0/2224	0.86	0/3462
14	G	0.35	0/1717	0.95	1/2664 (0.0%)
15	H	0.59	7/3217 (0.2%)	1.06	18/4997 (0.4%)
16	o	0.61	0/803	1.41	2/1119 (0.2%)
17	p	1.01	1/810 (0.1%)	1.46	4/1122 (0.4%)
18	w	0.53	5/2376 (0.2%)	0.67	13/3269 (0.4%)
19	u	0.23	0/519	0.62	4/717 (0.6%)
20	v	0.36	0/482	0.81	7/666 (1.1%)
21	1	0.33	0/7826	0.51	0/10617
22	2	0.52	3/1277 (0.2%)	0.73	7/1724 (0.4%)
23	3	0.32	0/9408	0.53	0/12767
24	4	0.83	2/535 (0.4%)	0.98	4/724 (0.6%)
25	5	0.29	0/823	0.48	0/1123

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
26	6	0.29	0/678	0.51	0/909
27	7	0.31	0/556	0.45	0/751
28	J	0.62	0/3500	0.73	0/4750
29	L	0.41	0/1103	0.57	0/1487
30	M	0.29	0/272	0.49	0/363
31	P	0.83	1/841 (0.1%)	1.01	2/1117 (0.2%)
32	R	0.66	5/2351 (0.2%)	0.86	7/3163 (0.2%)
33	T	1.05	1/2522 (0.0%)	1.11	4/3438 (0.1%)
34	V	0.55	0/2234	0.67	1/3111 (0.0%)
35	X	0.27	0/1011	0.48	0/1348
36	Y	0.31	0/747	0.48	0/1006
37	Z	0.57	2/772 (0.3%)	0.79	7/1056 (0.7%)
38	z	0.29	0/1414	0.51	0/1916
39	x	0.35	0/2871	0.53	3/3981 (0.1%)
All	All	0.57	40/96823 (0.0%)	0.76	127/133875 (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	7
3	C	0	3
4	D	0	1
9	d	0	1
9	k	0	1
21	1	0	9
22	2	0	1
23	3	0	4
27	7	0	1
30	M	0	1
32	R	0	1
33	T	0	2
35	X	0	1
All	All	0	33

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
18	w	457	SER	CB-OG	8.21	1.52	1.42
18	w	483	SER	CB-OG	7.46	1.51	1.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	H	142	C	C1'-N1	7.35	1.59	1.48
22	2	655	SER	CB-OG	7.35	1.51	1.42
1	A	406	TRP	CB-CG	-7.08	1.37	1.50
2	B	103	G	C1'-N9	-6.95	1.37	1.46
15	H	150	U	C1'-N1	6.76	1.58	1.48
1	A	2223	CYS	CB-SG	-6.76	1.70	1.82
31	P	227	TYR	CG-CD2	-6.70	1.30	1.39
1	A	476	PHE	CG-CD2	6.63	1.48	1.38
15	H	97	G	C1'-N9	-6.48	1.37	1.46
15	H	151	C	C1'-N1	6.44	1.58	1.48
15	H	184	C	C1'-N1	6.37	1.58	1.48
15	H	141	C	C1'-N1	6.31	1.58	1.48
24	4	50	THR	CB-OG1	5.94	1.55	1.43
18	w	395	TRP	CZ3-CH2	5.86	1.49	1.40
24	4	42	THR	CB-OG1	5.85	1.54	1.43
33	T	218	TRP	CB-CG	-5.71	1.40	1.50
1	A	212	PRO	N-CA	-5.44	1.38	1.47
37	Z	569	PRO	N-CD	5.43	1.55	1.47
2	B	56	C	O3'-P	-5.41	1.54	1.61
22	2	620	PRO	N-CD	5.41	1.55	1.47
18	w	284	ARG	CA-CB	-5.37	1.42	1.53
1	A	94	TYR	CB-CG	-5.34	1.43	1.51
1	A	1120	PRO	N-CD	5.29	1.55	1.47
22	2	643	PRO	N-CD	5.24	1.55	1.47
17	p	156	ASN	C-N	-5.21	1.22	1.34
18	w	415	THR	CB-OG1	5.21	1.53	1.43
1	A	140	TYR	CG-CD2	-5.19	1.32	1.39
32	R	130	PRO	N-CD	5.18	1.55	1.47
37	Z	521	PRO	N-CD	5.15	1.55	1.47
15	H	110	A	C1'-N9	-5.13	1.39	1.46
32	R	222	PRO	N-CD	5.13	1.55	1.47
1	A	351	TYR	CB-CG	-5.10	1.44	1.51
1	A	225	TYR	CB-CG	-5.06	1.44	1.51
32	R	253	PRO	N-CD	5.05	1.54	1.47
3	C	145	PHE	CB-CG	-5.04	1.42	1.51
32	R	252	PRO	N-CD	5.04	1.54	1.47
32	R	227	PRO	N-CD	5.03	1.54	1.47
1	A	406	TRP	CG-CD2	-5.03	1.35	1.43

All (127) bond angle outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	4	83	PRO	CA-CB-CG	10.19	124.17	104.80
22	2	636	MET	CG-SD-CE	9.28	115.05	100.20
37	Z	569	PRO	CA-N-CD	-8.56	99.52	111.50
37	Z	573	PRO	CA-N-CD	-8.45	99.67	111.50
1	A	404	LEU	CB-CG-CD1	8.13	124.82	111.00
1	A	552	ARG	NE-CZ-NH1	7.48	124.04	120.30
1	A	153	ARG	NE-CZ-NH2	-7.36	116.62	120.30
2	B	20	G	N9-C1'-C2'	7.28	123.46	114.00
15	H	113	G	OP2-P-O3'	7.25	121.15	105.20
15	H	141	C	OP2-P-O3'	7.24	121.14	105.20
15	H	114	A	OP2-P-O3'	7.22	121.09	105.20
3	C	144	CYS	N-CA-CB	7.20	123.56	110.60
15	H	150	U	OP2-P-O3'	7.19	121.01	105.20
32	R	180	THR	C-N-CD	-7.16	104.85	120.60
18	w	441	PRO	N-CA-CB	7.16	111.89	103.30
19	u	222	PRO	N-CA-CB	7.14	111.87	103.30
1	A	611	LEU	CB-CG-CD1	-7.13	98.88	111.00
22	2	656	PRO	N-CA-CB	6.88	111.56	103.30
1	A	565	ARG	NE-CZ-NH2	-6.81	116.90	120.30
15	H	155	C	P-O3'-C3'	6.78	127.84	119.70
2	B	26	A	O5'-P-OP2	6.77	118.83	110.70
15	H	141	C	O3'-P-O5'	-6.77	91.14	104.00
15	H	150	U	O3'-P-O5'	-6.77	91.14	104.00
2	B	104	C	C2'-C3'-O3'	-6.77	94.61	109.50
15	H	113	G	O3'-P-O5'	-6.73	91.21	104.00
15	H	114	A	O3'-P-O5'	-6.72	91.23	104.00
15	H	30	A	O5'-P-OP1	-6.71	99.66	105.70
2	B	12	U	N1-C1'-C2'	-6.66	104.67	112.00
20	v	115	PRO	N-CA-CB	6.65	111.28	103.30
3	C	420	CYS	CA-CB-SG	-6.63	102.07	114.00
31	P	215	LEU	CB-CG-CD1	-6.61	99.76	111.00
20	v	139	PRO	N-CA-CB	6.54	111.15	103.30
24	4	27	PRO	N-CA-CB	6.50	111.10	103.30
1	A	598	LEU	CB-CG-CD2	-6.48	99.98	111.00
31	P	215	LEU	CB-CG-CD2	6.47	122.00	111.00
18	w	120	PRO	N-CA-CB	6.47	111.06	103.30
18	w	227	PRO	N-CA-CB	6.47	111.06	103.30
3	C	921	LEU	CB-CG-CD1	6.41	121.89	111.00
39	x	403	PRO	N-CA-CB	6.35	110.92	103.30
19	u	200	PRO	N-CA-CB	6.31	110.87	103.30
32	R	205	ASP	CB-CG-OD2	6.30	123.97	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
20	v	218	PRO	N-CA-CB	6.28	110.83	103.30
37	Z	570	ALA	C-N-CD	6.25	141.52	128.40
1	A	476	PHE	CB-CG-CD1	6.24	125.17	120.80
18	w	105	PRO	N-CA-CB	6.24	110.79	103.30
18	w	305	PRO	N-CA-CB	6.23	110.77	103.30
22	2	641	PRO	N-CA-CB	6.21	110.76	103.30
18	w	174	PRO	N-CA-CB	6.21	110.75	103.30
1	A	153	ARG	NE-CZ-NH1	6.20	123.40	120.30
33	T	220	VAL	CB-CA-C	-6.18	99.65	111.40
33	T	282	ARG	NE-CZ-NH2	-6.18	117.21	120.30
1	A	506	LEU	CB-CG-CD1	-6.17	100.51	111.00
19	u	221	PRO	N-CA-CB	6.17	110.70	103.30
39	x	509	PRO	N-CA-CB	6.14	110.66	103.30
17	p	184	PRO	N-CA-CB	6.10	110.62	103.30
1	A	1117	HIS	C-N-CD	6.05	141.11	128.40
18	w	202	PRO	N-CA-CB	6.04	110.55	103.30
20	v	221	PRO	N-CA-CB	6.04	110.55	103.30
17	p	155	LEU	N-CA-CB	5.99	122.37	110.40
14	G	156	U	C2-N1-C1'	5.97	124.87	117.70
20	v	162	PRO	N-CA-CB	5.96	110.45	103.30
18	w	99	PRO	N-CA-CB	5.96	110.45	103.30
32	R	252	PRO	C-N-CD	5.93	140.85	128.40
18	w	230	PRO	N-CA-CB	5.86	110.33	103.30
17	p	219	LYS	O-C-N	5.86	132.07	122.70
20	v	220	PRO	N-CA-CB	5.86	110.33	103.30
18	w	419	PRO	N-CA-CB	5.85	110.32	103.30
20	v	217	PRO	N-CA-CB	5.84	110.31	103.30
15	H	172	C	P-O3'-C3'	5.84	126.71	119.70
3	C	148	CYS	CB-CA-C	5.82	122.04	110.40
3	C	446	LYS	C-N-CD	5.81	140.61	128.40
15	H	156	U	P-O3'-C3'	-5.77	112.78	119.70
22	2	629	PRO	N-CA-CB	5.77	110.22	103.30
37	Z	563	ARG	C-N-CD	5.76	140.49	128.40
32	R	221	GLY	C-N-CD	5.66	140.29	128.40
22	2	642	PRO	C-N-CD	5.65	140.27	128.40
24	4	27	PRO	CA-CB-CG	5.64	115.51	104.80
1	A	1364	LEU	CA-CB-CG	5.63	128.25	115.30
37	Z	520	LYS	C-N-CD	5.61	140.18	128.40
1	A	565	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	1119	ASP	C-N-CD	5.58	140.12	128.40
15	H	46	U	P-O3'-C3'	5.57	126.39	119.70
39	x	785	PRO	N-CA-CB	5.56	109.97	103.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	o	58	ASP	N-CA-CB	-5.52	100.66	110.60
1	A	656	LEU	CB-CG-CD1	-5.48	101.68	111.00
1	A	118	VAL	CB-CA-C	-5.47	101.01	111.40
15	H	157	G	O4'-C1'-N9	-5.47	103.83	108.20
3	C	146	VAL	CA-CB-CG2	-5.46	102.70	110.90
1	A	420	ARG	NE-CZ-NH2	-5.46	117.57	120.30
18	w	399	LEU	CB-CG-CD1	-5.42	101.78	111.00
3	C	91	GLU	C-N-CD	-5.42	108.68	120.60
1	A	2310	ARG	CG-CD-NE	5.41	123.16	111.80
22	2	651	PRO	N-CA-CB	5.39	109.77	103.30
1	A	251	ASP	CB-CG-OD1	5.38	123.14	118.30
33	T	308	ARG	NE-CZ-NH2	-5.36	117.62	120.30
22	2	619	MET	C-N-CD	5.36	139.66	128.40
15	H	106	G	O5'-P-OP1	5.34	117.10	110.70
15	H	156	U	OP2-P-O3'	5.33	116.93	105.20
1	A	92	LEU	CB-CG-CD1	-5.30	101.99	111.00
32	R	178	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	656	LEU	CA-CB-CG	-5.30	103.12	115.30
1	A	314	ILE	CA-CB-CG1	-5.29	100.95	111.00
2	B	40	U	N1-C1'-C2'	5.28	120.86	114.00
2	B	37	G	O5'-P-OP2	-5.27	100.96	105.70
24	4	50	THR	CA-CB-OG1	5.25	120.02	109.00
3	C	921	LEU	CB-CG-CD2	-5.24	102.09	111.00
17	p	149	PRO	N-CA-CB	5.23	109.58	103.30
1	A	656	LEU	CB-CG-CD2	5.21	119.85	111.00
37	Z	588	ASP	CB-CG-OD2	5.20	122.98	118.30
3	C	776	GLU	N-CA-C	5.19	125.02	111.00
32	R	178	ARG	NE-CZ-NH1	5.19	122.90	120.30
37	Z	527	ASP	CB-CG-OD2	5.19	122.97	118.30
19	u	203	SER	N-CA-CB	-5.18	102.73	110.50
1	A	330	THR	CA-CB-CG2	-5.15	105.19	112.40
15	H	157	G	P-O5'-C5'	-5.13	112.69	120.90
34	V	467	LEU	CB-CA-C	-5.12	100.47	110.20
1	A	647	LEU	CB-CG-CD1	-5.12	102.31	111.00
1	A	638	LEU	CA-CB-CG	-5.11	103.55	115.30
2	B	20	G	O4'-C1'-N9	5.09	112.28	108.20
18	w	399	LEU	CD1-CG-CD2	5.09	125.76	110.50
15	H	156	U	C4'-C3'-C2'	5.08	107.68	102.60
1	A	677	VAL	CB-CA-C	-5.07	101.78	111.40
33	T	233	LEU	CB-CG-CD1	-5.06	102.40	111.00
18	w	45	ALA	N-CA-CB	-5.04	103.04	110.10
32	R	101	ILE	CB-CA-C	-5.04	101.53	111.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
16	o	99	SER	N-CA-CB	-5.03	102.96	110.50
3	C	220	ARG	NE-CZ-NH2	-5.01	117.79	120.30

There are no chirality outliers.

All (33) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
21	1	1028	HIS	Peptide
21	1	1105	GLU	Peptide
21	1	1107	GLN	Peptide
21	1	220	GLN	Peptide
21	1	415	LEU	Peptide
21	1	418	PRO	Peptide
21	1	460	PRO	Peptide
21	1	717	THR	Peptide
21	1	943	LYS	Peptide
22	2	558	ARG	Peptide
23	3	261	PHE	Peptide
23	3	530	ASP	Peptide
23	3	552	ARG	Peptide
23	3	916	ASN	Peptide
27	7	74	GLN	Peptide
1	A	1119	ASP	Peptide
1	A	166	PHE	Peptide
1	A	346	ASP	Peptide
1	A	408	PRO	Peptide
1	A	433	GLU	Peptide
1	A	697	MET	Peptide
1	A	941	LYS	Peptide
3	C	622	GLU	Peptide
3	C	736	GLY	Peptide
3	C	823	ALA	Peptide
4	D	430	LEU	Peptide
30	M	196	ASP	Peptide
32	R	94	GLY	Peptide
33	T	400	PHE	Peptide,Mainchain
35	X	193	ASN	Peptide
9	d	112	ASN	Peptide
9	k	112	ASN	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	18165	0	17930	1529	0
2	B	1768	0	897	123	0
3	C	6716	0	6691	968	0
4	D	8528	0	3745	69	0
5	E	2338	0	2272	136	0
6	a	399	0	173	0	0
6	h	393	0	170	0	0
7	b	405	0	170	0	0
7	i	422	0	177	0	0
8	c	406	0	170	0	0
8	j	406	0	170	0	0
9	d	480	0	200	0	0
9	k	422	0	175	0	0
10	f	361	0	158	0	0
10	m	361	0	158	0	0
11	e	391	0	163	0	0
11	l	391	0	163	0	0
12	g	363	0	160	0	0
12	n	334	0	143	0	0
13	F	1988	0	1005	133	0
14	G	1545	0	786	121	0
15	H	2886	0	1463	239	0
16	o	804	0	350	0	0
17	p	813	0	365	0	0
18	w	2369	0	1298	0	0
19	u	525	0	216	0	0
20	v	486	0	206	0	0
21	1	7702	0	7389	291	0
22	2	1252	0	1040	56	0
23	3	9220	0	9139	481	0
24	4	527	0	438	40	0
25	5	807	0	729	27	0
26	6	670	0	654	21	0
27	7	540	0	509	25	0
28	J	3463	0	2544	106	0
29	L	1077	0	1067	54	0
30	M	267	0	225	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	P	829	0	814	187	0
32	R	2314	0	2189	405	0
33	T	2457	0	2416	251	0
34	V	2238	0	969	49	0
35	X	1012	0	731	18	0
36	Y	737	0	608	67	0
37	Z	755	0	591	155	0
38	z	1381	0	1298	0	0
39	x	2882	0	1308	0	0
40	A	36	0	6	0	0
41	C	32	0	12	11	0
42	C	1	0	0	0	0
42	F	5	0	0	0	0
43	6	3	0	0	0	0
43	M	1	0	0	0	0
All	All	94673	0	74250	4461	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 27.

All (4461) 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)
36:Y:37:TRP:CH2	37:Z:498:GLY:HA2	1.23	1.65
1:A:2270:PHE:HB3	4:D:1264:PRO:CB	1.34	1.57
1:A:2270:PHE:CG	4:D:1264:PRO:CB	1.89	1.56
3:C:149:LEU:HD13	3:C:427:PHE:CD2	1.38	1.54
3:C:77:VAL:HG11	33:T:196:LEU:CG	1.39	1.52
36:Y:37:TRP:CH2	37:Z:498:GLY:CA	1.93	1.51
1:A:2270:PHE:CB	4:D:1264:PRO:CB	1.86	1.50
37:Z:564:PRO:HB2	37:Z:582:TYR:CG	1.45	1.49
31:P:193:VAL:HG23	31:P:194:PHE:CD2	1.46	1.47
32:R:442:ARG:HH11	32:R:443:GLY:C	1.17	1.45
1:A:844:GLU:CB	32:R:422:MET:CE	1.94	1.45
31:P:193:VAL:CG2	31:P:194:PHE:HD2	1.28	1.45
23:3:440:HIS:CE1	23:3:733:PRO:HD3	1.50	1.43
32:R:414:ARG:NH1	37:Z:598:PHE:CZ	1.86	1.43
1:A:73:HIS:HD2	1:A:81:PHE:CE2	1.37	1.42
1:A:530:LEU:H	30:M:198:GLN:NE2	1.18	1.42
1:A:2270:PHE:CD1	4:D:1264:PRO:CB	2.03	1.41
3:C:705:VAL:HG23	3:C:717:PHE:CD2	1.55	1.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:79:THR:CG2	33:T:199:VAL:HB	1.51	1.40
28:J:293:ASN:CB	29:L:225:TYR:CB	1.98	1.39
1:A:312:TYR:CE2	3:C:882:GLY:HA3	1.58	1.39
3:C:79:THR:HG23	33:T:199:VAL:CB	1.49	1.39
5:E:260:ARG:NH1	5:E:273:CYS:SG	1.95	1.39
1:A:530:LEU:HB2	30:M:198:GLN:NE2	1.38	1.38
28:J:339:TRP:HA	32:R:116:TYR:CE2	1.58	1.38
3:C:387:ASP:O	3:C:388:VAL:HG12	1.20	1.37
32:R:442:ARG:CD	32:R:443:GLY:H	1.37	1.37
1:A:393:LEU:HA	3:C:379:LYS:CG	1.52	1.36
3:C:77:VAL:HG12	33:T:196:LEU:C	1.46	1.36
1:A:762:ARG:HH22	31:P:226:LYS:NZ	1.19	1.35
28:J:339:TRP:HA	32:R:116:TYR:CD2	1.60	1.35
32:R:414:ARG:NH1	37:Z:598:PHE:CE2	1.93	1.35
3:C:77:VAL:CG1	33:T:196:LEU:C	1.94	1.35
1:A:393:LEU:N	3:C:379:LYS:HE2	1.42	1.34
3:C:149:LEU:CD1	3:C:427:PHE:CD2	2.08	1.34
32:R:442:ARG:HD3	32:R:443:GLY:N	1.05	1.34
1:A:121:HIS:NE2	1:A:481:PHE:HB3	1.42	1.34
32:R:414:ARG:NE	37:Z:598:PHE:CZ	1.95	1.34
3:C:452:THR:CG2	3:C:577:PHE:HD2	1.40	1.34
1:A:312:TYR:CZ	3:C:882:GLY:HA3	1.61	1.34
1:A:1962:THR:CG2	37:Z:524:ARG:HB2	1.57	1.33
1:A:384:VAL:HG12	3:C:331:PHE:CB	1.58	1.32
1:A:388:LEU:CD1	3:C:399:LEU:HD21	1.58	1.32
3:C:145:PHE:CA	3:C:312:SER:HB2	1.57	1.31
32:R:414:ARG:CZ	37:Z:598:PHE:CZ	2.14	1.31
3:C:670:SER:HA	3:C:823:ALA:CB	1.60	1.31
31:P:212:ASN:O	33:T:458:SER:HA	1.30	1.30
1:A:73:HIS:CD2	1:A:81:PHE:CE2	2.20	1.30
1:A:384:VAL:HA	3:C:331:PHE:CD2	1.67	1.30
1:A:844:GLU:CB	32:R:422:MET:HE3	1.54	1.30
1:A:305:ARG:HB3	3:C:879:ASP:OD1	1.28	1.29
1:A:73:HIS:CD2	1:A:81:PHE:CZ	2.20	1.29
31:P:211:VAL:HG13	33:T:457:GLY:CA	1.62	1.29
3:C:77:VAL:CG1	33:T:196:LEU:HG	1.63	1.28
3:C:705:VAL:CG2	3:C:717:PHE:CE2	2.15	1.28
1:A:264:PHE:CZ	1:A:459:LEU:HD13	1.66	1.27
23:3:440:HIS:CE1	23:3:733:PRO:CD	2.14	1.27
1:A:384:VAL:CG1	3:C:331:PHE:HB3	1.64	1.27
1:A:2268:LEU:HD23	4:D:1261:PRO:O	1.21	1.27

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:LEU:HD11	3:C:399:LEU:CD2	1.63	1.27
1:A:2268:LEU:HD22	4:D:1261:PRO:CB	1.65	1.26
1:A:666:LYS:CB	1:A:668:VAL:HG22	1.64	1.26
3:C:78:GLU:O	33:T:198:ARG:HA	1.35	1.26
1:A:530:LEU:CA	30:M:198:GLN:HE22	1.49	1.26
3:C:145:PHE:HA	3:C:312:SER:CB	1.65	1.26
31:P:211:VAL:CG1	33:T:457:GLY:HA3	1.65	1.26
1:A:406:TRP:HZ3	3:C:265:LEU:O	1.14	1.26
1:A:392:PRO:C	3:C:379:LYS:HE2	1.54	1.26
31:P:193:VAL:CG2	31:P:194:PHE:CD2	2.09	1.26
5:E:146:ARG:NH1	5:E:148:LYS:CE	1.98	1.25
32:R:414:ARG:CZ	37:Z:598:PHE:HZ	1.47	1.25
1:A:2113:LYS:HE3	4:D:1229:ASP:O	1.33	1.25
1:A:530:LEU:CB	30:M:198:GLN:HE22	1.47	1.24
24:4:14:THR:HA	24:4:59:VAL:O	1.32	1.24
32:R:442:ARG:HD2	32:R:444:GLY:N	1.50	1.24
3:C:679:PRO:HB2	3:C:807:GLN:OE1	1.25	1.24
3:C:84:GLU:O	33:T:238:LEU:HD23	1.34	1.24
1:A:530:LEU:N	30:M:198:GLN:NE2	1.84	1.23
36:Y:37:TRP:CZ3	37:Z:498:GLY:CA	2.20	1.23
36:Y:37:TRP:CZ3	37:Z:498:GLY:HA2	1.73	1.23
3:C:140:HIS:CG	3:C:230:ASP:HB2	1.74	1.22
1:A:121:HIS:CE1	1:A:481:PHE:HB3	1.73	1.22
23:3:440:HIS:NE2	23:3:733:PRO:CD	2.03	1.22
2:B:42:U:N3	14:G:-3:A:C2	2.07	1.22
1:A:762:ARG:HH22	31:P:226:LYS:CE	1.51	1.22
3:C:78:GLU:HG2	3:C:80:ILE:CD1	1.69	1.22
3:C:145:PHE:CA	3:C:312:SER:CB	2.18	1.22
28:J:256:LYS:O	29:L:232:TYR:CD2	1.93	1.22
1:A:530:LEU:CB	30:M:198:GLN:NE2	2.02	1.21
3:C:77:VAL:HG13	33:T:196:LEU:O	1.40	1.21
3:C:497:LEU:HD13	3:C:577:PHE:CZ	1.76	1.21
36:Y:18:VAL:CB	37:Z:600:ARG:HH21	1.53	1.21
1:A:2325:VAL:HG13	4:D:788:GLY:O	1.40	1.21
1:A:1320:LYS:HE2	32:R:434:TYR:CE1	1.76	1.21
3:C:137:HIS:CD2	3:C:236:MET:HB2	1.75	1.21
32:R:442:ARG:CD	32:R:443:GLY:N	1.95	1.20
1:A:2298:LEU:HB3	4:D:1283:PRO:CB	1.71	1.20
23:3:699:VAL:HA	23:3:715:MET:O	1.40	1.20
1:A:384:VAL:CG2	3:C:334:ILE:HG21	1.72	1.19
1:A:755:HIS:ND1	31:P:223:PHE:CG	2.10	1.19

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:705:VAL:HG23	3:C:717:PHE:CE2	1.75	1.19
1:A:227:ARG:HA	1:A:416:GLY:O	1.39	1.19
1:A:401:GLY:HA3	3:C:386:GLY:HA2	1.20	1.19
5:E:146:ARG:NH1	5:E:148:LYS:HE3	1.53	1.19
13:F:68:C:N4	31:P:33:ARG:HB3	1.55	1.18
1:A:695:ASP:HB3	33:T:374:SER:OG	1.40	1.18
1:A:2268:LEU:CD2	4:D:1261:PRO:O	1.91	1.17
3:C:149:LEU:HD13	3:C:427:PHE:CG	1.79	1.17
1:A:232:LEU:CD1	1:A:404:LEU:HD12	1.75	1.17
1:A:705:LYS:CB	32:R:251:ILE:HD12	1.72	1.17
3:C:140:HIS:CG	3:C:230:ASP:CB	2.27	1.17
1:A:151:MET:HE3	1:A:628:GLY:O	1.41	1.17
1:A:406:TRP:CZ3	3:C:265:LEU:O	1.98	1.17
1:A:696:MET:CB	33:T:415:ILE:CD1	2.22	1.17
3:C:465:MET:HE1	3:C:475:MET:HG3	1.26	1.17
3:C:77:VAL:CG1	33:T:196:LEU:O	1.89	1.16
1:A:393:LEU:HA	3:C:379:LYS:HG3	1.28	1.16
3:C:78:GLU:CG	3:C:80:ILE:HD11	1.72	1.16
3:C:221:ILE:HD11	3:C:479:THR:OG1	1.46	1.16
1:A:758:ARG:HB3	31:P:227:TYR:CE2	1.79	1.16
1:A:384:VAL:HG21	3:C:334:ILE:CG2	1.76	1.15
3:C:679:PRO:CB	3:C:807:GLN:OE1	1.95	1.15
1:A:1900:GLU:OE1	37:Z:522:LEU:HB2	1.47	1.15
1:A:755:HIS:CE1	31:P:223:PHE:CG	2.35	1.14
1:A:1262:LYS:HG2	32:R:431:ASP:CB	1.77	1.14
3:C:670:SER:HA	3:C:823:ALA:HB1	1.27	1.14
5:E:74:PHE:CE1	5:E:81:LEU:HD21	1.82	1.14
24:4:28:LEU:O	24:4:32:LEU:HB2	1.48	1.14
32:R:101:ILE:O	32:R:104:GLN:HG3	1.48	1.14
1:A:1405:LEU:HB3	32:R:415:LEU:HD23	1.29	1.14
15:H:156:U:H6	15:H:156:U:H5”	1.10	1.14
36:Y:18:VAL:CB	37:Z:600:ARG:NH2	2.10	1.14
1:A:1405:LEU:HB3	32:R:415:LEU:CD2	1.78	1.14
1:A:2298:LEU:O	4:D:1283:PRO:CB	1.95	1.14
3:C:77:VAL:HG12	33:T:197:TYR:N	1.61	1.14
32:R:442:ARG:NH1	32:R:443:GLY:C	2.00	1.14
1:A:1757:GLU:OE1	32:R:451:ILE:HG12	1.49	1.13
14:G:11:A:C2	14:G:12:G:C8	2.36	1.13
3:C:452:THR:CG2	3:C:577:PHE:CD2	2.31	1.13
3:C:679:PRO:HD2	3:C:807:GLN:HB3	1.16	1.13
1:A:252:ASP:CB	1:A:334:THR:HG21	1.79	1.13

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:705:LYS:HB2	32:R:251:ILE:HD12	1.28	1.13
1:A:762:ARG:NH2	31:P:226:LYS:NZ	1.95	1.13
3:C:216:THR:HG22	3:C:245:HIS:HE1	0.97	1.12
23:3:440:HIS:ND1	23:3:733:PRO:HG3	1.63	1.12
1:A:299:ILE:CD1	3:C:921:LEU:HB2	1.79	1.12
3:C:81:VAL:HG13	33:T:201:SER:CB	1.77	1.12
3:C:140:HIS:CB	3:C:230:ASP:HB2	1.79	1.12
3:C:507:VAL:HG11	3:C:565:ILE:HG23	1.30	1.12
3:C:216:THR:HG22	3:C:245:HIS:CE1	1.85	1.12
13:F:68:C:C4	31:P:33:ARG:HB3	1.85	1.12
1:A:696:MET:CB	33:T:415:ILE:HD11	1.80	1.11
1:A:758:ARG:HB3	31:P:227:TYR:HE2	0.96	1.11
1:A:1548:TYR:CD2	1:A:1549:VAL:HG22	1.83	1.11
1:A:439:GLN:NE2	1:A:614:TYR:CZ	2.18	1.11
3:C:77:VAL:HG11	33:T:196:LEU:CB	1.79	1.11
1:A:762:ARG:NH2	31:P:226:LYS:CE	2.14	1.11
1:A:1548:TYR:HD2	1:A:1549:VAL:HG22	1.14	1.11
32:R:420:LYS:HE3	32:R:420:LYS:HA	1.18	1.11
37:Z:566:TYR:CE2	37:Z:584:TRP:CZ3	2.39	1.11
1:A:692:ASP:HA	33:T:376:ARG:NH2	1.65	1.10
23:3:440:HIS:HE1	23:3:720:TRP:CZ3	1.67	1.10
1:A:73:HIS:HD2	1:A:81:PHE:CD2	1.69	1.10
1:A:264:PHE:HE1	1:A:455:VAL:HG13	1.15	1.10
1:A:1505:LYS:CE	37:Z:615:SER:OG	1.99	1.10
1:A:349:ALA:HB2	1:A:399:ALA:HB2	1.27	1.10
1:A:1900:GLU:HG2	37:Z:521:PRO:HG2	1.33	1.10
1:A:2287:ARG:NH2	4:D:1147:ASN:CB	2.14	1.10
28:J:225:LEU:HD21	29:L:211:ASN:HB2	1.29	1.10
1:A:86:ARG:HH22	32:R:211:ARG:HG3	1.08	1.10
1:A:232:LEU:HD23	3:C:388:VAL:CG1	1.80	1.10
1:A:1962:THR:HG22	37:Z:524:ARG:HB2	1.18	1.10
3:C:470:PRO:HB3	3:C:500:THR:HG23	1.34	1.10
1:A:252:ASP:HB2	1:A:334:THR:CG2	1.81	1.09
1:A:73:HIS:NE2	1:A:81:PHE:CE1	2.20	1.09
1:A:299:ILE:HD11	3:C:921:LEU:HB2	1.33	1.09
1:A:762:ARG:NH2	31:P:226:LYS:HE2	1.66	1.09
1:A:232:LEU:HD23	3:C:388:VAL:HG12	1.21	1.09
1:A:312:TYR:OH	3:C:853:ARG:NH2	1.85	1.09
1:A:666:LYS:HB2	1:A:668:VAL:HG22	1.18	1.09
3:C:66:TYR:CD2	33:T:457:GLY:HA2	1.87	1.09
36:Y:85:GLU:O	37:Z:502:ALA:N	1.85	1.08

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:MET:CE	1:A:88:TYR:CD2	2.36	1.08
1:A:76:MET:HE1	1:A:88:TYR:CD2	1.89	1.08
1:A:393:LEU:N	3:C:379:LYS:CE	2.15	1.08
1:A:349:ALA:CB	1:A:399:ALA:HB2	1.82	1.08
3:C:465:MET:CE	3:C:475:MET:HG3	1.82	1.08
37:Z:566:TYR:CE2	37:Z:584:TRP:HZ3	1.71	1.08
1:A:384:VAL:HG21	3:C:334:ILE:HG21	1.21	1.08
1:A:529:THR:HG22	30:M:197:TYR:O	1.52	1.08
1:A:783:TYR:CE1	31:P:228:ILE:HG21	1.88	1.08
1:A:666:LYS:HB2	1:A:668:VAL:CG2	1.82	1.08
28:J:259:GLN:HE22	29:L:220:PRO:CD	1.66	1.08
1:A:417:ARG:NH1	2:B:58:U:O3'	1.87	1.07
3:C:497:LEU:CD1	3:C:577:PHE:CZ	2.36	1.07
1:A:395:THR:CG2	3:C:383:GLN:HE22	1.65	1.07
24:4:17:VAL:HA	24:4:85:ARG:O	1.53	1.07
3:C:670:SER:CB	3:C:823:ALA:HB3	1.85	1.07
1:A:546:LEU:HD11	1:A:595:LYS:HD2	1.12	1.06
1:A:744:LYS:CE	31:P:213:ASP:HA	1.84	1.06
1:A:1146:ASP:OD2	1:A:1182:ASN:ND2	1.89	1.06
13:F:68:C:C4	31:P:33:ARG:CB	2.38	1.06
1:A:369:GLU:O	1:A:371:LEU:N	1.88	1.06
1:A:393:LEU:HA	3:C:379:LYS:HG2	1.34	1.06
28:J:406:PHE:CD2	28:J:411:MET:HE3	1.90	1.06
1:A:91:ALA:CB	32:R:207:MET:HE2	1.85	1.05
1:A:264:PHE:CE1	1:A:455:VAL:HG13	1.90	1.05
2:B:39:C:H4'	2:B:40:U:OP1	1.23	1.05
1:A:168:PRO:HG3	1:A:559:ASP:HB3	1.39	1.05
1:A:387:PHE:HE1	3:C:327:TYR:HA	1.14	1.05
1:A:705:LYS:CG	32:R:251:ILE:HD12	1.86	1.05
3:C:452:THR:HG22	3:C:577:PHE:HD2	1.21	1.05
1:A:664:HIS:CE1	1:A:668:VAL:HG23	1.92	1.04
1:A:664:HIS:HE1	1:A:668:VAL:HG23	1.21	1.04
1:A:844:GLU:CB	32:R:422:MET:HE1	1.83	1.04
33:T:399:LYS:CG	33:T:406:ILE:HD11	1.87	1.04
1:A:692:ASP:HA	33:T:376:ARG:HH22	1.18	1.04
3:C:228:PHE:HA	3:C:256:CYS:O	1.57	1.04
32:R:178:ARG:HD3	32:R:194:GLN:HE22	1.17	1.04
1:A:1449:LYS:HE3	32:R:428:GLY:HA3	1.37	1.04
3:C:78:GLU:HG2	3:C:80:ILE:HD11	1.06	1.04
1:A:331:TRP:CE3	3:C:179:VAL:HG21	1.91	1.04
1:A:755:HIS:ND1	31:P:223:PHE:CD1	2.26	1.04

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:488:VAL:HG13	3:C:609:LYS:HE2	1.39	1.04
13:F:25:C:H4'	13:F:26:U:OP2	1.22	1.04
32:R:436:VAL:HG23	32:R:437:TYR:CD1	1.93	1.04
1:A:232:LEU:HD12	1:A:404:LEU:HD12	1.04	1.04
24:4:70:ALA:O	24:4:74:MET:CB	2.04	1.03
1:A:168:PRO:CG	1:A:559:ASP:HB3	1.87	1.03
1:A:755:HIS:CE1	31:P:223:PHE:CD2	2.46	1.03
29:L:224:PHE:CD1	32:R:86:LEU:HD12	1.93	1.03
28:J:273:TYR:CZ	32:R:228:PRO:HB3	1.94	1.03
4:D:754:GLU:CB	23:3:662:PHE:CZ	2.41	1.03
15:H:105:G:H2'	15:H:106:G:H5"	1.37	1.03
1:A:254:TYR:CZ	1:A:434:HIS:HB3	1.93	1.02
3:C:452:THR:HG22	3:C:577:PHE:CD2	1.94	1.02
28:J:331:GLN:HG2	32:R:98:TYR:OH	1.59	1.02
37:Z:564:PRO:CB	37:Z:582:TYR:CG	2.41	1.02
1:A:250:VAL:HB	1:A:337:VAL:HG11	1.41	1.02
3:C:387:ASP:O	3:C:388:VAL:CG1	2.07	1.02
32:R:420:LYS:HG3	32:R:421:GLY:H	1.20	1.02
1:A:338:VAL:HG23	3:C:867:PRO:HG3	1.39	1.02
13:F:68:C:C5	31:P:33:ARG:CB	2.42	1.02
32:R:434:TYR:O	32:R:435:ASN:ND2	1.90	1.02
36:Y:37:TRP:CD1	36:Y:83:CYS:HB2	1.92	1.02
1:A:254:TYR:CE2	1:A:434:HIS:HB2	1.94	1.02
13:F:36:A:H3'	13:F:37:C:H5"	1.39	1.02
32:R:442:ARG:HD2	32:R:444:GLY:H	0.97	1.02
1:A:299:ILE:HD11	3:C:921:LEU:CB	1.90	1.01
1:A:305:ARG:CB	3:C:879:ASP:OD1	2.07	1.01
23:3:440:HIS:CE1	23:3:720:TRP:CZ3	2.47	1.01
37:Z:525:TYR:CD1	37:Z:526:ILE:HG23	1.95	1.01
3:C:511:GLY:O	3:C:576:ILE:CD1	2.07	1.01
1:A:1457:HIS:HE1	1:A:1459:ARG:CG	1.74	1.01
1:A:1900:GLU:HG2	37:Z:521:PRO:CG	1.91	1.01
3:C:132:VAL:HG12	3:C:226:VAL:HG23	1.43	1.01
3:C:349:PHE:CD1	3:C:356:PHE:CE1	2.49	1.01
1:A:299:ILE:HD11	3:C:921:LEU:CA	1.91	1.00
1:A:1900:GLU:OE2	37:Z:521:PRO:HB2	1.59	1.00
23:3:440:HIS:O	23:3:733:PRO:HG2	1.61	1.00
3:C:261:ASP:OD2	41:C:1500:GTP:N1	1.92	1.00
3:C:703:GLU:OE2	3:C:740:THR:HG21	1.61	1.00
15:H:179:C:H2'	15:H:180:G:H8	1.25	1.00
1:A:312:TYR:CZ	3:C:882:GLY:CA	2.45	1.00

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1301:ILE:CD1	1:A:1306:LYS:HE2	1.92	1.00
2:B:42:U:N3	14:G:-3:A:H2	1.50	1.00
3:C:705:VAL:CG2	3:C:717:PHE:CD2	2.39	1.00
31:P:193:VAL:HG21	31:P:194:PHE:HD2	1.26	1.00
1:A:264:PHE:CE1	1:A:459:LEU:HD13	1.96	1.00
3:C:81:VAL:CG1	33:T:201:SER:HB3	1.90	1.00
23:3:303:ALA:O	23:3:310:ILE:HA	1.61	1.00
2:B:64:G:H5'	5:E:106:LYS:HZ3	1.26	1.00
3:C:85:ASP:HB3	33:T:238:LEU:HG	1.43	1.00
3:C:129:ILE:HG22	3:C:199:LEU:HB3	1.44	1.00
1:A:1162:PRO:HG2	31:P:194:PHE:CE2	1.97	1.00
37:Z:525:TYR:CE1	37:Z:526:ILE:HG23	1.96	1.00
1:A:779:LEU:HD21	31:P:223:PHE:CE2	1.97	0.99
23:3:440:HIS:CE1	23:3:733:PRO:CG	2.45	0.99
32:R:414:ARG:NE	37:Z:598:PHE:HZ	1.38	0.99
1:A:783:TYR:HB2	31:P:228:ILE:HG12	1.43	0.99
28:J:270:ASP:OD2	32:R:222:PRO:CG	2.10	0.99
1:A:232:LEU:HD12	1:A:404:LEU:CD1	1.91	0.99
1:A:267:LYS:NZ	2:B:49:A:OP1	1.94	0.99
1:A:1505:LYS:HE3	37:Z:615:SER:OG	1.62	0.99
1:A:696:MET:CB	33:T:415:ILE:HD13	1.89	0.99
33:T:434:GLY:HA2	33:T:464:GLY:HA2	1.41	0.99
1:A:715:GLU:OE2	32:R:258:TRP:HZ3	1.43	0.99
37:Z:600:ARG:HB3	37:Z:600:ARG:HH11	1.24	0.99
1:A:384:VAL:CG1	3:C:332:GLY:H	1.76	0.99
3:C:64:LYS:HE3	31:P:206:LYS:HE2	1.45	0.99
3:C:137:HIS:CD2	3:C:236:MET:CB	2.45	0.99
13:F:68:C:C5	31:P:33:ARG:HB2	1.97	0.99
1:A:1457:HIS:NE2	32:R:425:GLY:N	2.09	0.99
1:A:2287:ARG:HH21	4:D:1147:ASN:CB	1.72	0.99
1:A:232:LEU:CD1	1:A:404:LEU:CD1	2.41	0.99
1:A:1900:GLU:OE1	37:Z:522:LEU:CB	2.10	0.98
3:C:78:GLU:O	33:T:198:ARG:CA	2.11	0.98
1:A:1084:PRO:HG2	31:P:188:TRP:HZ2	1.26	0.98
23:3:440:HIS:CE1	23:3:733:PRO:HG3	1.99	0.98
31:P:210:PHE:CD2	33:T:455:GLN:OE1	2.16	0.98
32:R:420:LYS:HB2	37:Z:610:LEU:HD11	1.44	0.98
3:C:306:ASN:OD1	3:C:437:HIS:CE1	2.16	0.98
31:P:30:TYR:OH	32:R:162:ALA:HA	1.63	0.98
1:A:417:ARG:NH2	2:B:58:U:H5"	1.79	0.98
1:A:2074:ARG:NH2	4:D:1044:VAL:O	1.96	0.98

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:GLU:OE2	1:A:369:GLU:N	1.97	0.98
15:H:83:A:H2'	15:H:84:C:O4'	1.64	0.98
3:C:84:GLU:O	33:T:238:LEU:CD2	2.12	0.97
3:C:670:SER:CA	3:C:823:ALA:HB3	1.94	0.97
3:C:66:TYR:HB3	33:T:456:PRO:O	1.64	0.97
3:C:81:VAL:HG13	33:T:201:SER:HB3	0.99	0.97
36:Y:37:TRP:CZ3	37:Z:498:GLY:HA3	2.00	0.97
34:V:548:ALA:CB	34:V:585:ILE:CB	2.42	0.97
37:Z:566:TYR:HE2	37:Z:584:TRP:HZ3	1.05	0.97
3:C:711:ARG:HD3	3:C:730:ARG:HH11	1.29	0.97
3:C:500:THR:HG22	3:C:545:PRO:HA	1.47	0.97
3:C:670:SER:HA	3:C:823:ALA:HB3	1.43	0.97
1:A:299:ILE:HG12	3:C:920:PRO:O	1.64	0.97
1:A:546:LEU:HD11	1:A:595:LYS:CD	1.94	0.97
1:A:1320:LYS:HE2	32:R:434:TYR:HE1	1.15	0.97
1:A:2328:ALA:HB2	4:D:788:GLY:HA2	1.43	0.97
1:A:256:TYR:CE1	3:C:888:ARG:NH1	2.33	0.96
3:C:670:SER:CA	3:C:823:ALA:CB	2.43	0.96
28:J:300:ASP:OD2	32:R:101:ILE:HG13	1.65	0.96
23:3:440:HIS:NE2	23:3:733:PRO:HD3	1.70	0.96
1:A:121:HIS:NE2	1:A:481:PHE:CB	2.29	0.96
3:C:855:GLY:O	3:C:856:HIS:HB3	1.63	0.96
33:T:352:THR:HG22	33:T:373:LYS:O	1.65	0.96
36:Y:37:TRP:HH2	37:Z:498:GLY:CA	1.70	0.96
1:A:47:GLU:O	1:A:50:LYS:HB2	1.64	0.96
3:C:135:CYS:SG	3:C:227:LEU:HD12	2.06	0.96
15:H:78:C:H2'	15:H:79:G:H8	1.27	0.96
1:A:748:ASP:OD1	31:P:214:THR:HG22	1.64	0.96
1:A:1900:GLU:CD	37:Z:522:LEU:HB2	1.85	0.96
3:C:115:GLU:O	3:C:118:PHE:N	1.98	0.95
1:A:232:LEU:CD2	3:C:388:VAL:CG1	2.43	0.95
1:A:783:TYR:CD1	31:P:228:ILE:HG21	2.01	0.95
1:A:2298:LEU:CB	4:D:1283:PRO:CB	2.44	0.95
5:E:146:ARG:HH11	5:E:148:LYS:HE2	1.27	0.95
14:G:11:A:N3	14:G:12:G:H8	1.64	0.95
36:Y:37:TRP:CH2	37:Z:498:GLY:HA3	1.96	0.95
23:3:440:HIS:NE2	23:3:733:PRO:HD2	1.77	0.95
32:R:442:ARG:HD3	32:R:443:GLY:CA	1.96	0.95
1:A:171:ASP:O	1:A:520:TYR:CD2	2.20	0.95
1:A:664:HIS:CE1	1:A:666:LYS:HB2	2.02	0.95
15:H:156:U:H5"	15:H:156:U:C6	2.02	0.95

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2335:ALA:O	4:D:570:THR:HA	1.65	0.95
3:C:145:PHE:CB	3:C:312:SER:HB3	1.97	0.95
32:R:442:ARG:HH11	32:R:444:GLY:N	1.64	0.95
1:A:86:ARG:HH22	32:R:211:ARG:CG	1.79	0.95
3:C:700:ILE:HG23	3:C:735:PHE:CD2	2.01	0.95
1:A:393:LEU:CA	3:C:379:LYS:CG	2.45	0.95
1:A:705:LYS:HG2	32:R:251:ILE:HB	1.49	0.95
1:A:221:ASN:OD1	2:B:12:U:OP1	1.83	0.95
1:A:1505:LYS:HE2	37:Z:615:SER:OG	1.65	0.95
1:A:305:ARG:HH21	3:C:854:ARG:NH1	1.65	0.94
1:A:785:LYS:CE	31:P:215:LEU:HD11	1.97	0.94
14:G:11:A:C2	14:G:12:G:N7	2.34	0.94
1:A:384:VAL:CG2	3:C:334:ILE:CG2	2.42	0.94
1:A:1162:PRO:HG3	31:P:194:PHE:CD2	2.02	0.94
1:A:1457:HIS:CE1	32:R:424:SER:HA	2.01	0.94
28:J:339:TRP:CA	32:R:116:TYR:CE2	2.48	0.94
3:C:711:ARG:NH2	3:C:730:ARG:O	2.00	0.94
13:F:49:G:N7	29:L:33:ARG:NH1	2.15	0.94
1:A:278:LYS:NZ	14:G:-9:C:OP1	1.99	0.94
1:A:386:PRO:HD3	3:C:372:PHE:HE1	1.28	0.94
5:E:119:THR:CG2	5:E:161:ARG:HB3	1.97	0.94
15:H:180:G:H2'	15:H:181:G:H8	1.30	0.94
33:T:352:THR:HG22	33:T:373:LYS:C	1.86	0.94
1:A:264:PHE:CZ	1:A:459:LEU:CD1	2.50	0.94
1:A:402:ILE:HG13	3:C:385:VAL:HG21	1.45	0.94
1:A:530:LEU:N	30:M:198:GLN:HE22	1.52	0.94
1:A:1405:LEU:CB	32:R:415:LEU:CD2	2.45	0.94
1:A:1459:ARG:HE	32:R:423:ASP:HB2	1.31	0.94
1:A:1962:THR:CG2	37:Z:524:ARG:CB	2.45	0.94
3:C:145:PHE:HA	3:C:312:SER:HB2	0.95	0.94
3:C:445:ALA:HB3	3:C:466:SER:HA	1.50	0.94
15:H:79:G:H2'	15:H:80:A:H8	1.33	0.94
24:4:69:TYR:CZ	24:4:73:ILE:HG13	2.03	0.94
3:C:349:PHE:HD1	3:C:356:PHE:CD1	1.85	0.94
1:A:2113:LYS:CE	4:D:1229:ASP:O	2.16	0.93
13:F:8:C:H6	13:F:8:C:H5"	1.31	0.93
1:A:2268:LEU:CD2	4:D:1261:PRO:CB	2.46	0.93
1:A:158:ARG:NH2	1:A:570:ASP:OD2	2.01	0.93
1:A:256:TYR:CZ	3:C:888:ARG:NH1	2.36	0.93
13:F:25:C:C4'	13:F:26:U:OP2	2.16	0.93
32:R:171:LEU:HD12	32:R:201:GLU:OE1	1.67	0.93

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:HIS:CD2	1:A:81:PHE:CE1	2.56	0.93
1:A:151:MET:CE	1:A:628:GLY:O	2.15	0.93
1:A:366:LYS:HE3	1:A:366:LYS:H	1.29	0.93
3:C:76:GLU:OE1	3:C:76:GLU:N	2.01	0.93
5:E:146:ARG:NH1	5:E:148:LYS:HE2	1.82	0.93
1:A:76:MET:HE1	1:A:88:TYR:CG	2.03	0.93
3:C:149:LEU:CD1	3:C:427:PHE:HD2	1.80	0.93
1:A:695:ASP:CB	33:T:374:SER:OG	2.15	0.93
3:C:449:ILE:HG21	3:C:457:VAL:CG1	1.99	0.93
28:J:259:GLN:NE2	29:L:220:PRO:CD	2.30	0.93
28:J:294:HIS:CE1	29:L:227:THR:HB	2.04	0.93
1:A:523:ASN:OD1	1:A:552:ARG:NH2	2.02	0.93
1:A:1900:GLU:OE2	37:Z:521:PRO:C	2.06	0.93
1:A:2314:PHE:CB	4:D:1125:SER:CA	2.47	0.93
3:C:497:LEU:HD13	3:C:577:PHE:HZ	1.17	0.93
13:F:68:C:C4	31:P:33:ARG:CG	2.52	0.93
2:B:40:U:H3	14:G:-1:G:H1	1.14	0.92
32:R:101:ILE:O	32:R:104:GLN:CG	2.16	0.92
3:C:69:ALA:HA	33:T:456:PRO:HG3	1.49	0.92
3:C:449:ILE:CG2	3:C:457:VAL:CG1	2.46	0.92
3:C:678:THR:HG21	3:C:683:ASN:HD22	1.35	0.92
1:A:228:TRP:O	1:A:415:SER:HA	1.70	0.92
1:A:402:ILE:HG12	3:C:265:LEU:CD2	1.99	0.92
1:A:548:ARG:NH2	1:A:549:GLU:OE2	2.01	0.92
1:A:2113:LYS:HE2	4:D:1229:ASP:CB	1.98	0.92
2:B:43:U:N3	14:G:-4:A:N1	2.17	0.92
32:R:412:ASP:CG	32:R:413:GLN:H	1.69	0.92
3:C:77:VAL:CG1	33:T:196:LEU:CB	2.45	0.92
3:C:140:HIS:CG	3:C:230:ASP:HB3	2.03	0.92
32:R:414:ARG:NH1	37:Z:598:PHE:HE2	1.58	0.92
1:A:305:ARG:HA	1:A:305:ARG:HH11	1.33	0.92
2:B:44:A:C2	14:G:-5:G:N1	2.36	0.92
3:C:445:ALA:O	3:C:449:ILE:N	2.03	0.92
3:C:476:CYS:HB3	3:C:565:ILE:HB	1.51	0.92
28:J:339:TRP:CA	32:R:116:TYR:CD2	2.51	0.92
1:A:1301:ILE:HD11	1:A:1306:LYS:HE2	1.51	0.92
23:3:440:HIS:HE1	23:3:720:TRP:HZ3	1.06	0.92
1:A:387:PHE:CE1	3:C:327:TYR:HA	2.05	0.92
1:A:539:ARG:NH2	13:F:64:U:O2'	2.02	0.92
2:B:39:C:C4'	2:B:40:U:OP1	2.16	0.92
3:C:670:SER:HB3	3:C:823:ALA:HB3	1.48	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:J:259:GLN:HE22	29:L:220:PRO:HD2	1.32	0.92
1:A:762:ARG:HH22	31:P:226:LYS:HZ1	1.08	0.92
1:A:779:LEU:HD21	31:P:223:PHE:CZ	2.05	0.92
3:C:244:LYS:HA	3:C:292:TYR:HD2	1.34	0.91
32:R:106:GLN:HG2	32:R:110:LYS:HE2	1.51	0.91
1:A:67:ARG:HD3	1:A:179:ALA:HB2	1.51	0.91
1:A:235:MET:CE	1:A:411:PHE:HA	1.99	0.91
3:C:483:SER:HA	3:C:490:PHE:HB3	1.52	0.91
3:C:674:CYS:SG	3:C:822:MET:SD	2.67	0.91
3:C:86:THR:O	33:T:239:LYS:O	1.88	0.91
3:C:132:VAL:CG1	3:C:226:VAL:HG23	2.00	0.91
2:B:64:G:H5'	5:E:106:LYS:NZ	1.83	0.91
2:B:41:U:O4	14:G:-2:C:N4	2.03	0.91
1:A:1761:PRO:HB2	1:A:1930:TYR:OH	1.71	0.91
1:A:1962:THR:HG22	37:Z:524:ARG:CB	2.00	0.91
1:A:417:ARG:HH12	2:B:58:U:C3'	1.84	0.91
1:A:463:PRO:HB3	2:B:20:G:O2'	1.69	0.91
1:A:1320:LYS:CE	32:R:434:TYR:CE1	2.54	0.91
23:3:699:VAL:HG22	23:3:716:SER:HB2	1.53	0.91
1:A:2328:ALA:CB	4:D:788:GLY:HA2	1.99	0.91
3:C:452:THR:HG22	3:C:577:PHE:HB3	1.52	0.91
29:L:224:PHE:CD1	32:R:86:LEU:CD1	2.53	0.91
1:A:384:VAL:HA	3:C:331:PHE:HD2	1.03	0.90
3:C:145:PHE:N	3:C:312:SER:HB2	1.85	0.90
13:F:35:A:C8	14:G:12:G:C6	2.59	0.90
23:3:34:ARG:HB2	23:3:37:ILE:HB	1.51	0.90
1:A:393:LEU:CA	3:C:379:LYS:CE	2.48	0.90
1:A:666:LYS:HB3	1:A:668:VAL:HG22	1.52	0.90
3:C:230:ASP:OD2	3:C:233:GLU:HG2	1.70	0.90
1:A:1457:HIS:CE1	32:R:425:GLY:H	1.88	0.90
3:C:678:THR:OG1	3:C:680:ASN:O	1.89	0.90
1:A:171:ASP:HB3	1:A:519:ASP:HB2	1.53	0.90
1:A:1320:LYS:CE	32:R:434:TYR:HE1	1.85	0.90
36:Y:37:TRP:NE1	36:Y:83:CYS:HB2	1.87	0.90
1:A:312:TYR:CE2	3:C:882:GLY:CA	2.53	0.90
1:A:1426:ASP:CG	32:R:421:GLY:HA3	1.91	0.90
1:A:254:TYR:CZ	1:A:434:HIS:CB	2.54	0.90
3:C:221:ILE:CD1	3:C:479:THR:OG1	2.19	0.90
13:F:94:C:P	28:J:351:ASN:HD22	1.95	0.90
1:A:782:LEU:HD13	31:P:220:HIS:HE1	1.34	0.90
3:C:711:ARG:HD3	3:C:730:ARG:NH1	1.86	0.90

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:228:PHE:CA	3:C:256:CYS:O	2.20	0.90
1:A:705:LYS:HG2	32:R:251:ILE:CB	2.01	0.89
33:T:399:LYS:HG3	33:T:406:ILE:HD11	1.54	0.89
1:A:419:ARG:NH2	1:A:423:ASP:O	2.06	0.89
36:Y:36:ALA:HB2	37:Z:499:LYS:O	1.72	0.89
1:A:744:LYS:HE2	31:P:213:ASP:HA	1.52	0.89
1:A:227:ARG:CA	1:A:416:GLY:O	2.20	0.89
31:P:192:VAL:HG12	31:P:194:PHE:H	1.35	0.89
1:A:748:ASP:HA	31:P:214:THR:HG21	1.54	0.89
15:H:80:A:H2'	15:H:81:G:H8	1.36	0.89
32:R:81:LYS:HA	32:R:81:LYS:CE	2.02	0.89
1:A:232:LEU:CD2	3:C:388:VAL:HG11	2.03	0.89
28:J:220:LEU:HD11	28:J:224:LYS:HE3	1.53	0.89
1:A:90:GLY:HA3	32:R:207:MET:O	1.73	0.89
1:A:175:PRO:HG2	1:A:498:ARG:NH2	1.88	0.89
1:A:333:HIS:CA	3:C:139:HIS:NE2	2.36	0.89
15:H:81:G:H2'	15:H:82:G:H8	1.35	0.89
15:H:82:G:H2'	15:H:83:A:H8	1.38	0.89
32:R:442:ARG:CD	32:R:444:GLY:H	1.85	0.89
3:C:64:LYS:HZ1	31:P:206:LYS:HG2	1.38	0.88
31:P:193:VAL:HG21	31:P:194:PHE:CD2	2.02	0.88
14:G:11:A:N3	14:G:12:G:C8	2.38	0.88
32:R:81:LYS:HA	32:R:81:LYS:NZ	1.88	0.88
1:A:785:LYS:HE2	31:P:215:LEU:HD11	1.54	0.88
3:C:78:GLU:O	33:T:199:VAL:N	2.06	0.88
3:C:140:HIS:CE1	3:C:233:GLU:HB2	2.07	0.88
3:C:679:PRO:CG	3:C:807:GLN:OE1	2.21	0.88
3:C:678:THR:CG2	3:C:683:ASN:HB2	2.04	0.88
13:F:68:C:C4	31:P:33:ARG:HG2	2.07	0.88
1:A:251:ASP:HB3	1:A:337:VAL:HG23	1.54	0.88
32:R:442:ARG:CD	32:R:444:GLY:N	2.34	0.88
1:A:715:GLU:OE2	32:R:258:TRP:CZ3	2.25	0.88
1:A:2314:PHE:HB2	4:D:1125:SER:CA	2.02	0.88
22:2:614:ARG:HH11	22:2:614:ARG:HG3	1.38	0.88
3:C:261:ASP:OD1	41:C:1500:GTP:O6	1.92	0.88
1:A:1457:HIS:CE1	32:R:425:GLY:N	2.41	0.88
1:A:1459:ARG:HG3	32:R:422:MET:O	1.74	0.88
23:3:440:HIS:O	23:3:733:PRO:CG	2.22	0.88
31:P:224:MET:CE	31:P:228:ILE:HD13	2.04	0.88
1:A:305:ARG:NH2	3:C:854:ARG:HH11	1.72	0.87
3:C:97:VAL:CG2	31:P:45:GLN:HG3	2.03	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:179:C:O2'	15:H:180:G:H5'	1.74	0.87
1:A:48:LYS:O	1:A:53:PHE:CD2	2.27	0.87
3:C:149:LEU:HD12	3:C:427:PHE:HD2	1.39	0.87
3:C:700:ILE:HG23	3:C:735:PHE:CE2	2.09	0.87
23:3:812:LYS:O	23:3:816:LYS:HB2	1.74	0.87
2:B:42:U:N3	14:G:-3:A:N1	2.16	0.87
14:G:137:C:H42	15:H:40:C:H42	1.22	0.87
23:3:545:VAL:HG12	23:3:546:LYS:HG2	1.57	0.87
24:4:75:ASN:OD1	24:4:86:VAL:HB	1.74	0.87
3:C:523:GLN:OE1	3:C:524:ILE:N	2.07	0.87
1:A:393:LEU:CA	3:C:379:LYS:HG2	2.02	0.87
1:A:1118:PRO:C	1:A:1120:PRO:HA	1.94	0.87
3:C:705:VAL:HG21	3:C:717:PHE:CE2	2.07	0.87
5:E:243:LEU:CD1	5:E:247:GLY:HA2	2.04	0.87
15:H:68:G:O2'	15:H:69:U:H5'	1.74	0.87
15:H:78:C:H2'	15:H:79:G:C8	2.10	0.87
1:A:1162:PRO:CG	31:P:194:PHE:CE2	2.57	0.87
3:C:488:VAL:HG13	3:C:609:LYS:CE	2.05	0.87
15:H:154:C:O2	15:H:176:G:N2	2.07	0.87
28:J:339:TRP:CD2	32:R:116:TYR:HD2	1.93	0.87
32:R:423:ASP:O	32:R:424:SER:OG	1.92	0.87
1:A:86:ARG:NH2	32:R:211:ARG:HG3	1.88	0.87
1:A:384:VAL:HG12	3:C:332:GLY:H	1.38	0.87
1:A:395:THR:HG21	3:C:383:GLN:HE22	1.38	0.87
15:H:180:G:H2'	15:H:181:G:C8	2.10	0.87
3:C:701:GLU:HA	3:C:740:THR:OG1	1.75	0.87
28:J:255:LEU:HD22	29:L:235:LEU:HD13	1.56	0.87
3:C:216:THR:CG2	3:C:245:HIS:HE1	1.84	0.86
32:R:442:ARG:NH1	32:R:443:GLY:O	2.07	0.86
1:A:420:ARG:NH1	2:B:56:C:O2'	2.07	0.86
1:A:91:ALA:HB1	32:R:207:MET:HE2	1.57	0.86
1:A:331:TRP:CE3	3:C:179:VAL:CG2	2.59	0.86
15:H:179:C:H2'	15:H:180:G:C8	2.09	0.86
1:A:1757:GLU:CD	32:R:451:ILE:HG12	1.96	0.86
15:H:148:C:O2'	15:H:149:A:H5'	1.75	0.86
21:1:1179:ASP:OD2	21:1:1185:ARG:NH1	2.08	0.86
33:T:399:LYS:HG2	33:T:406:ILE:HD11	1.53	0.86
1:A:401:GLY:HA3	3:C:386:GLY:CA	2.03	0.86
5:E:269:PRO:O	5:E:270:LYS:HB3	1.76	0.86
13:F:26:U:H3'	13:F:27:A:H5"	1.56	0.86
28:J:256:LYS:O	29:L:232:TYR:CE2	2.29	0.86

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:210:PHE:HD2	33:T:455:GLN:OE1	1.53	0.86
32:R:147:THR:HG23	33:T:360:VAL:HG12	1.57	0.86
23:3:442:LEU:HD12	23:3:733:PRO:O	1.76	0.86
33:T:417:ASN:OD1	33:T:432:ASP:OD1	1.94	0.86
1:A:386:PRO:HA	3:C:327:TYR:CE2	2.10	0.86
1:A:152:ARG:HB3	1:A:152:ARG:HH11	1.39	0.85
32:R:135:PRO:O	32:R:136:ASP:OD1	1.94	0.85
1:A:433:GLU:OE1	1:A:436:PRO:HB3	1.74	0.85
32:R:420:LYS:HE3	32:R:420:LYS:CA	1.98	0.85
1:A:252:ASP:HB2	1:A:334:THR:HG21	0.90	0.85
3:C:72:VAL:HG22	33:T:453:ALA:HB1	1.58	0.85
3:C:149:LEU:HD12	3:C:427:PHE:CD2	2.07	0.85
15:H:79:G:O2'	15:H:80:A:H5'	1.76	0.85
3:C:145:PHE:HB2	3:C:312:SER:HB3	1.57	0.85
21:1:672:ALA:HA	21:1:679:ILE:HD11	1.58	0.85
1:A:363:HIS:NE2	3:C:287:GLY:HA3	1.91	0.85
2:B:95:G:H4'	2:B:96:A:O4'	1.76	0.85
32:R:414:ARG:NH1	37:Z:598:PHE:HZ	1.44	0.85
5:E:162:ARG:NH2	5:E:203:ASP:O	2.10	0.85
1:A:388:LEU:HD11	3:C:399:LEU:HD21	0.86	0.85
32:R:414:ARG:HB2	32:R:414:ARG:NH2	1.92	0.85
3:C:133:THR:O	3:C:226:VAL:N	2.10	0.85
1:A:386:PRO:HA	3:C:327:TYR:CZ	2.11	0.85
2:B:42:U:H3	14:G:-3:A:H2	0.90	0.85
14:G:1:G:N2	30:M:202:CYS:SG	2.50	0.85
1:A:232:LEU:CD2	3:C:388:VAL:HG12	2.05	0.84
1:A:595:LYS:HE3	1:A:644:ILE:HD11	1.58	0.84
1:A:1900:GLU:CG	37:Z:521:PRO:CG	2.55	0.84
3:C:94:ILE:HD13	31:P:44:ARG:NH1	1.92	0.84
15:H:156:U:H6	15:H:156:U:C5'	1.88	0.84
37:Z:600:ARG:HH11	37:Z:600:ARG:CB	1.90	0.84
1:A:73:HIS:CD2	1:A:81:PHE:CD2	2.57	0.84
1:A:1370:ARG:HH11	34:V:467:LEU:CA	1.89	0.84
1:A:1900:GLU:OE2	37:Z:522:LEU:N	2.11	0.84
3:C:444:GLY:O	3:C:447:PRO:HD2	1.77	0.84
3:C:516:LEU:HD12	3:C:517:GLU:HG3	1.59	0.84
1:A:121:HIS:CG	1:A:481:PHE:O	2.30	0.84
13:F:36:A:H2'	13:F:38:G:OP2	1.78	0.84
15:H:80:A:O2'	15:H:81:G:H5'	1.78	0.84
15:H:181:G:O2'	15:H:182:U:H5'	1.77	0.84
15:H:182:U:O2'	15:H:183:G:H5'	1.75	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:356:HIS:HB2	23:3:401:LEU:HB2	1.60	0.84
3:C:80:ILE:O	33:T:200:ILE:HA	1.78	0.84
32:R:415:LEU:O	32:R:417:ASN:N	2.09	0.84
1:A:91:ALA:CB	32:R:207:MET:CE	2.56	0.84
1:A:755:HIS:CE1	31:P:223:PHE:CB	2.60	0.84
3:C:711:ARG:HD3	3:C:730:ARG:HE	1.42	0.84
1:A:232:LEU:HD11	3:C:412:ILE:HD11	1.59	0.84
1:A:1505:LYS:HE2	37:Z:615:SER:CB	2.07	0.84
3:C:244:LYS:HA	3:C:292:TYR:CD2	2.13	0.84
3:C:365:SER:OG	3:C:371:GLU:OE2	1.95	0.84
3:C:725:ASP:OD1	3:C:727:LEU:N	2.10	0.84
15:H:78:C:O2'	15:H:79:G:H5'	1.77	0.84
32:R:178:ARG:HD3	32:R:194:GLN:NE2	1.91	0.84
1:A:393:LEU:CA	3:C:379:LYS:HE3	2.07	0.84
1:A:1426:ASP:CB	32:R:421:GLY:HA3	2.08	0.84
1:A:1457:HIS:CE1	1:A:1459:ARG:CG	2.61	0.84
1:A:1457:HIS:NE2	32:R:424:SER:HA	1.93	0.83
3:C:705:VAL:HG21	3:C:717:PHE:HE2	1.40	0.83
1:A:333:HIS:O	3:C:139:HIS:CE1	2.31	0.83
3:C:79:THR:C	3:C:80:ILE:HD12	1.98	0.83
3:C:348:TYR:CD1	3:C:359:LYS:HB3	2.13	0.83
15:H:71:C:O2'	15:H:72:U:H5'	1.78	0.83
37:Z:566:TYR:CE2	37:Z:584:TRP:CE3	2.66	0.83
1:A:168:PRO:HG3	1:A:559:ASP:CB	2.07	0.83
1:A:254:TYR:CE2	1:A:434:HIS:CB	2.61	0.83
1:A:1301:ILE:HD12	2:B:39:C:H5"	1.60	0.83
3:C:488:VAL:CG1	3:C:609:LYS:HE2	2.08	0.83
14:G:22:C:O2'	14:G:23:U:OP1	1.95	0.83
15:H:152:G:N2	15:H:153:A:N7	2.27	0.83
1:A:338:VAL:CG2	3:C:867:PRO:HG3	2.07	0.83
5:E:74:PHE:CE1	5:E:81:LEU:CD2	2.62	0.83
36:Y:37:TRP:CZ2	37:Z:498:GLY:HA2	2.08	0.83
1:A:1757:GLU:CD	32:R:451:ILE:CG1	2.47	0.83
3:C:151:GLU:OE1	3:C:417:ARG:NH2	2.11	0.83
15:H:70:C:O2'	15:H:71:C:H5'	1.78	0.83
23:3:442:LEU:O	23:3:735:SER:N	2.10	0.83
32:R:117:THR:O	32:R:120:VAL:HG12	1.78	0.83
3:C:77:VAL:CG1	33:T:196:LEU:CG	2.35	0.83
1:A:1301:ILE:CD1	2:B:39:C:H5"	2.09	0.83
3:C:80:ILE:N	33:T:199:VAL:O	2.12	0.83
1:A:387:PHE:CZ	3:C:326:ILE:HG22	2.13	0.83

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:824:THR:HG23	3:C:824:THR:O	1.77	0.83
28:J:270:ASP:CG	32:R:222:PRO:HB3	1.99	0.83
32:R:134:ARG:O	32:R:136:ASP:N	2.12	0.83
1:A:1457:HIS:HE1	1:A:1459:ARG:HG2	1.43	0.83
1:A:1900:GLU:OE2	37:Z:521:PRO:CB	2.26	0.83
3:C:145:PHE:CA	3:C:312:SER:HB3	2.04	0.83
15:H:72:U:O2'	15:H:73:C:H5'	1.77	0.83
3:C:470:PRO:HB3	3:C:500:THR:CG2	2.08	0.82
21:1:1108:ASN:ND2	21:1:1111:CYS:SG	2.52	0.82
1:A:91:ALA:HB1	32:R:207:MET:CE	2.09	0.82
1:A:529:THR:CG2	30:M:197:TYR:O	2.26	0.82
1:A:615:ARG:O	1:A:618:THR:OG1	1.96	0.82
15:H:73:C:O2'	15:H:74:U:H5'	1.79	0.82
1:A:319:LEU:HD11	3:C:590:ILE:HD11	1.60	0.82
1:A:1084:PRO:HG2	31:P:188:TRP:CZ2	2.12	0.82
3:C:220:ARG:NH1	3:C:578:ARG:O	2.12	0.82
3:C:228:PHE:CB	3:C:256:CYS:O	2.27	0.82
3:C:482:TYR:HE2	3:C:493:PHE:CG	1.97	0.82
5:E:165:GLN:O	5:E:166:LEU:HD23	1.79	0.82
28:J:259:GLN:NE2	29:L:220:PRO:HD2	1.94	0.82
2:B:42:U:C2	14:G:-3:A:H2	1.97	0.82
3:C:705:VAL:CB	3:C:717:PHE:CE2	2.61	0.82
14:G:11:A:C4	14:G:12:G:C8	2.67	0.82
15:H:69:U:O2'	15:H:70:C:H5'	1.80	0.82
32:R:103:ARG:HB3	32:R:103:ARG:HH11	1.44	0.82
15:H:81:G:O2'	15:H:82:G:H5'	1.78	0.82
3:C:140:HIS:ND1	3:C:230:ASP:HB3	1.94	0.82
23:3:304:GLN:HE21	23:3:308:GLY:HA2	1.44	0.82
1:A:393:LEU:HD12	3:C:379:LYS:HG3	1.60	0.82
1:A:417:ARG:HH12	2:B:58:U:C4'	1.92	0.82
1:A:1370:ARG:HH12	34:V:468:ASP:N	1.77	0.82
3:C:489:GLN:O	3:C:489:GLN:NE2	2.13	0.82
15:H:105:G:C2'	15:H:106:G:H5"	2.10	0.82
31:P:30:TYR:OH	32:R:162:ALA:CA	2.27	0.82
1:A:1457:HIS:CE1	1:A:1459:ARG:HG2	2.15	0.82
3:C:259:LYS:HG2	3:C:262:ARG:CD	2.09	0.82
31:P:212:ASN:HB3	33:T:458:SER:HB2	1.61	0.82
2:B:18:C:O2'	2:B:19:A:O5'	1.98	0.82
1:A:331:TRP:CZ3	3:C:179:VAL:HG21	2.14	0.81
1:A:2113:LYS:HE3	4:D:1229:ASP:C	2.01	0.81
5:E:74:PHE:CE2	5:E:343:ILE:HG12	2.14	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:37:TRP:HA	36:Y:82:LEU:O	1.80	0.81
1:A:305:ARG:HG2	3:C:878:ILE:HG21	1.60	0.81
1:A:331:TRP:CZ3	3:C:179:VAL:CG2	2.64	0.81
1:A:1900:GLU:CG	37:Z:521:PRO:HG2	2.09	0.81
3:C:64:LYS:HE3	31:P:206:LYS:CE	2.10	0.81
3:C:244:LYS:HB2	3:C:292:TYR:CE2	2.15	0.81
3:C:306:ASN:OD1	3:C:437:HIS:ND1	2.14	0.81
3:C:507:VAL:CG1	3:C:565:ILE:HG23	2.10	0.81
22:2:643:PRO:HD2	24:4:69:TYR:CD2	2.16	0.81
23:3:42:ARG:HE	23:3:53:LEU:HD11	1.45	0.81
23:3:210:PHE:HB2	23:3:224:TYR:HB2	1.60	0.81
26:6:49:CYS:HB3	26:6:87:LYS:HD3	1.61	0.81
1:A:247:THR:OG1	1:A:429:ASN:HB3	1.80	0.81
31:P:193:VAL:HG23	31:P:194:PHE:CG	2.15	0.81
1:A:232:LEU:HD11	3:C:412:ILE:CD1	2.10	0.81
1:A:235:MET:HE1	1:A:411:PHE:HA	1.61	0.81
1:A:250:VAL:HG23	1:A:337:VAL:HB	1.60	0.81
23:3:772:ALA:HB1	23:3:775:ASN:HD21	1.44	0.81
33:T:213:GLU:HG3	33:T:218:TRP:CE2	2.16	0.81
1:A:1301:ILE:HD13	1:A:1306:LYS:HE2	1.63	0.81
3:C:511:GLY:O	3:C:576:ILE:HD13	1.79	0.81
32:R:443:GLY:HA2	32:R:446:ASP:HB3	1.62	0.81
1:A:1184:ASN:OD1	1:A:1195:ARG:NH1	2.14	0.81
1:A:1426:ASP:HB2	32:R:421:GLY:CA	2.11	0.81
3:C:452:THR:HG21	3:C:577:PHE:HD2	1.43	0.81
5:E:74:PHE:CZ	5:E:81:LEU:HD21	2.16	0.81
1:A:705:LYS:HB2	32:R:251:ILE:CD1	2.07	0.81
1:A:439:GLN:O	1:A:444:ARG:NH1	2.14	0.81
1:A:907:PRO:HD3	31:P:229:LYS:HB2	1.63	0.81
3:C:96:PRO:HA	31:P:48:GLN:HE21	1.44	0.81
3:C:140:HIS:NE2	3:C:233:GLU:HG3	1.95	0.81
1:A:660:PHE:CD2	32:R:209:PRO:HB2	2.16	0.81
3:C:140:HIS:ND1	3:C:230:ASP:N	2.28	0.81
3:C:452:THR:CB	3:C:577:PHE:HD2	1.93	0.81
3:C:507:VAL:HG11	3:C:565:ILE:CG2	2.09	0.81
3:C:711:ARG:HD3	3:C:730:ARG:NE	1.96	0.81
1:A:228:TRP:N	1:A:416:GLY:O	2.14	0.80
15:H:183:G:H2'	15:H:184:C:H6	1.44	0.80
1:A:245:LEU:HA	1:A:430:TRP:HZ2	1.46	0.80
15:H:83:A:H2'	15:H:84:C:C1'	2.10	0.80
23:3:440:HIS:CG	23:3:733:PRO:HG3	2.15	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:68:C:H41	31:P:33:ARG:HB3	1.45	0.80
28:J:273:TYR:CE1	32:R:228:PRO:HB3	2.17	0.80
14:G:134:U:H3	15:H:42:G:H1	1.24	0.80
23:3:979:ARG:HD2	23:3:982:GLU:HB2	1.63	0.80
32:R:65:PRO:HG2	32:R:66:GLU:OE2	1.79	0.80
15:H:149:A:H2'	15:H:150:U:H6	1.44	0.80
22:2:682:LEU:HD13	22:2:687:PHE:HA	1.63	0.80
1:A:357:ASN:O	3:C:865:GLY:N	2.15	0.80
1:A:417:ARG:HH22	2:B:58:U:H5"	1.42	0.80
1:A:748:ASP:CA	31:P:214:THR:HG21	2.11	0.80
3:C:705:VAL:CG2	3:C:717:PHE:HE2	1.84	0.80
15:H:82:G:O2'	15:H:83:A:H5'	1.81	0.80
1:A:121:HIS:HA	1:A:482:PHE:HA	1.62	0.80
1:A:384:VAL:CG1	3:C:332:GLY:N	2.45	0.80
3:C:87:GLN:OE1	3:C:91:GLU:HG2	1.82	0.80
3:C:140:HIS:CE1	3:C:230:ASP:HB3	2.16	0.80
3:C:776:GLU:O	3:C:781:ASP:OD1	2.00	0.80
5:E:265:ARG:H	5:E:272:ARG:NH2	1.80	0.80
13:F:68:C:N3	31:P:33:ARG:HG2	1.97	0.80
15:H:152:G:H5"	15:H:153:A:OP2	1.80	0.80
21:1:732:TRP:HE1	21:1:768:GLU:HG2	1.47	0.80
1:A:1144:LYS:O	1:A:1147:VAL:HG22	1.82	0.80
1:A:1764:SER:HB3	1:A:1766:GLN:HG2	1.64	0.80
3:C:445:ALA:HB1	3:C:449:ILE:HD11	1.63	0.80
3:C:738:ASP:HB2	3:C:740:THR:O	1.82	0.80
1:A:305:ARG:NH2	3:C:854:ARG:NH1	2.29	0.80
1:A:401:GLY:CA	3:C:386:GLY:HA2	2.08	0.80
1:A:402:ILE:HG12	3:C:265:LEU:HD23	1.61	0.80
1:A:1370:ARG:HH11	34:V:467:LEU:HA	1.43	0.80
1:A:2314:PHE:HB3	4:D:1125:SER:CA	2.11	0.80
5:E:248:SER:HB2	5:E:249:TYR:CD1	2.17	0.80
23:3:637:PRO:HA	23:3:669:LEU:HA	1.63	0.80
24:4:28:LEU:O	24:4:32:LEU:CB	2.27	0.80
2:B:90:U:H5"	2:B:91:U:H5'	1.65	0.79
5:E:209:ILE:HG21	5:E:250:LEU:CD1	2.12	0.79
23:3:442:LEU:HD12	23:3:734:LEU:HD23	1.64	0.79
23:3:477:SER:HA	23:3:482:THR:HG22	1.65	0.79
29:L:222:LEU:H	29:L:222:LEU:HD22	1.45	0.79
1:A:264:PHE:HE1	1:A:455:VAL:CG1	1.94	0.79
1:A:299:ILE:CG1	3:C:920:PRO:O	2.30	0.79
1:A:362:ARG:NH2	3:C:284:GLU:OE2	2.15	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:ILE:HB	1:A:1001:VAL:HG12	1.65	0.79
3:C:145:PHE:N	3:C:312:SER:CB	2.41	0.79
33:T:292:TYR:CZ	33:T:308:ARG:HG3	2.18	0.79
1:A:168:PRO:HG2	1:A:559:ASP:HB3	1.64	0.79
1:A:232:LEU:HD13	1:A:404:LEU:CD1	2.12	0.79
1:A:318:TYR:N	3:C:638:ASP:OD1	2.14	0.79
3:C:77:VAL:HG11	33:T:196:LEU:HG	0.79	0.79
5:E:310:TYR:CE1	5:E:322:LYS:HD2	2.18	0.79
33:T:306:CYS:SG	33:T:336:VAL:HB	2.22	0.79
23:3:772:ALA:CB	23:3:775:ASN:HD21	1.95	0.79
1:A:312:TYR:CD2	3:C:882:GLY:HA3	2.16	0.79
1:A:1876:LEU:HD12	1:A:1884:ILE:HD11	1.65	0.79
3:C:244:LYS:HB2	3:C:292:TYR:HE2	1.47	0.79
1:A:283:VAL:O	1:A:284:ARG:NE	2.15	0.79
15:H:153:A:H2'	15:H:154:C:H5'	1.65	0.79
32:R:67:ILE:HG22	32:R:69:VAL:HG23	1.65	0.79
31:P:212:ASN:O	33:T:458:SER:CA	2.23	0.79
32:R:420:LYS:HG3	32:R:421:GLY:N	1.97	0.79
33:T:351:ASP:O	33:T:352:THR:OG1	1.98	0.79
3:C:515:THR:O	3:C:517:GLU:N	2.16	0.79
3:C:705:VAL:HB	3:C:717:PHE:CE2	2.18	0.79
1:A:393:LEU:HB2	3:C:379:LYS:HE3	1.65	0.79
3:C:140:HIS:ND1	3:C:230:ASP:CB	2.46	0.79
3:C:259:LYS:HE2	3:C:262:ARG:CD	2.13	0.79
15:H:68:G:H1	15:H:84:C:H42	1.29	0.79
15:H:79:G:H2'	15:H:80:A:C8	2.17	0.79
1:A:256:TYR:CD1	3:C:888:ARG:NH2	2.51	0.78
1:A:293:TRP:CZ3	1:A:295:GLU:OE1	2.35	0.78
1:A:435:CYS:HB2	3:C:892:GLN:NE2	1.98	0.78
13:F:34:G:N7	14:G:12:G:O6	2.16	0.78
15:H:101:U:H5"	15:H:102:U:H5'	1.64	0.78
37:Z:593:PHE:O	37:Z:597:ARG:HB2	1.83	0.78
1:A:1767:ASN:O	1:A:1771:LEU:HB2	1.82	0.78
1:A:48:LYS:O	1:A:53:PHE:CG	2.37	0.78
1:A:718:ARG:NH2	32:R:259:LYS:HE3	1.98	0.78
15:H:82:G:H2'	15:H:83:A:C8	2.17	0.78
23:3:1109:LEU:HD11	23:3:1128:ILE:HG21	1.65	0.78
1:A:250:VAL:CB	1:A:337:VAL:HG11	2.14	0.78
1:A:695:ASP:OD2	33:T:350:HIS:HB3	1.83	0.78
23:3:641:CYS:HB2	23:3:701:LEU:HB3	1.64	0.78
23:3:435:LEU:HD22	23:3:799:ILE:HD11	1.66	0.78

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:440:HIS:HE1	23:3:733:PRO:HD3	1.46	0.78
1:A:1370:ARG:NH1	34:V:468:ASP:N	2.32	0.78
32:R:132:LEU:HB3	33:T:399:LYS:NZ	1.99	0.78
1:A:705:LYS:HG2	32:R:251:ILE:HD12	1.65	0.78
1:A:758:ARG:CB	31:P:227:TYR:CE2	2.64	0.78
2:B:43:U:H4'	13:F:67:G:H1	1.48	0.78
33:T:387:PHE:CE1	33:T:398:TRP:CD1	2.72	0.78
1:A:152:ARG:HH11	1:A:152:ARG:CB	1.96	0.78
24:4:17:VAL:HG22	24:4:86:VAL:HG22	1.66	0.78
33:T:434:GLY:HA2	33:T:464:GLY:CA	2.14	0.78
1:A:1505:LYS:HD2	37:Z:615:SER:HB3	1.66	0.78
3:C:133:THR:HB	3:C:225:VAL:HG23	1.65	0.78
23:3:295:THR:HG22	23:3:297:SER:H	1.48	0.78
3:C:452:THR:HG21	3:C:577:PHE:CD2	2.16	0.78
22:2:649:LYS:HB3	22:2:655:SER:HB2	1.65	0.78
24:4:17:VAL:O	24:4:56:TYR:HA	1.83	0.78
31:P:224:MET:HE2	31:P:228:ILE:HD13	1.63	0.78
33:T:267:ASP:HB3	33:T:269:GLN:HG2	1.64	0.78
1:A:468:LYS:HD3	1:A:469:LYS:N	1.99	0.77
1:A:692:ASP:CA	33:T:376:ARG:HH22	1.97	0.77
1:A:919:ASP:OD2	1:A:1012:LYS:NZ	2.17	0.77
1:A:1838:LYS:HG2	1:A:1871:PRO:HG2	1.66	0.77
21:1:1053:ARG:NH1	22:2:559:PRO:O	2.17	0.77
23:3:590:MET:HG2	23:3:607:VAL:HA	1.63	0.77
23:3:805:ASN:ND2	23:3:858:GLY:O	2.14	0.77
1:A:398:THR:HG23	3:C:382:ALA:HB1	1.67	0.77
2:B:42:U:C4	14:G:-3:A:N1	2.53	0.77
1:A:329:LEU:HB3	3:C:177:ARG:NE	1.98	0.77
3:C:449:ILE:HG21	3:C:457:VAL:HG12	1.66	0.77
3:C:677:GLU:OE2	3:C:684:LYS:HG2	1.83	0.77
21:1:941:ASN:HA	21:1:948:ARG:HH22	1.48	0.77
1:A:91:ALA:HA	32:R:207:MET:CE	2.14	0.77
1:A:203:VAL:HG21	1:A:237:THR:CG2	2.14	0.77
1:A:1405:LEU:CA	32:R:415:LEU:CD2	2.62	0.77
3:C:449:ILE:CD1	3:C:466:SER:OG	2.33	0.77
15:H:80:A:H2'	15:H:81:G:C8	2.19	0.77
24:4:69:TYR:CE1	24:4:73:ILE:HG13	2.19	0.77
37:Z:595:GLN:O	37:Z:599:ALA:N	2.14	0.77
1:A:456:LEU:O	1:A:460:LYS:HG2	1.84	0.77
3:C:140:HIS:HA	3:C:259:LYS:HZ3	1.47	0.77
3:C:349:PHE:CD1	3:C:356:PHE:CD1	2.68	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:277:PHE:HE2	5:E:300:ILE:CD1	1.98	0.77
13:F:8:C:H5"	13:F:8:C:C6	2.19	0.77
23:3:474:ILE:O	23:3:485:LEU:HB2	1.83	0.77
23:3:772:ALA:HB1	23:3:775:ASN:ND2	1.99	0.77
3:C:85:ASP:CB	33:T:238:LEU:HG	2.14	0.77
3:C:151:GLU:OE1	3:C:417:ARG:CZ	2.33	0.77
14:G:11:A:H2'	14:G:12:G:O4'	1.84	0.77
36:Y:86:ASP:HA	37:Z:502:ALA:HB3	1.65	0.77
1:A:1505:LYS:CE	37:Z:615:SER:CB	2.62	0.77
28:J:291:GLN:NE2	29:L:230:GLU:OE2	2.17	0.77
33:T:318:ARG:HG3	33:T:319:THR:HG23	1.67	0.77
1:A:664:HIS:CE1	1:A:668:VAL:CG2	2.66	0.77
1:A:1757:GLU:OE2	32:R:451:ILE:HD11	1.85	0.77
3:C:482:TYR:HE2	3:C:493:PHE:CB	1.98	0.77
37:Z:603:SER:O	37:Z:607:VAL:HG23	1.84	0.77
1:A:1426:ASP:HB2	32:R:421:GLY:HA3	1.64	0.77
3:C:145:PHE:CZ	3:C:427:PHE:CE1	2.73	0.77
3:C:471:ASP:H	3:C:499:GLY:HA2	1.47	0.77
5:E:74:PHE:CD1	5:E:81:LEU:CD2	2.67	0.77
23:3:785:PRO:HA	23:3:800:ILE:O	1.84	0.77
3:C:567:GLU:HG2	3:C:572:GLU:OE2	1.85	0.77
15:H:177:A:H5"	15:H:178:A:OP1	1.84	0.77
23:3:981:CYS:SG	23:3:982:GLU:N	2.57	0.77
1:A:232:LEU:HD21	3:C:388:VAL:HG11	1.67	0.76
1:A:630:TRP:O	1:A:632:ALA:N	2.18	0.76
1:A:782:LEU:HD13	31:P:220:HIS:CE1	2.18	0.76
3:C:82:GLN:CB	33:T:231:TRP:HZ3	1.98	0.76
3:C:711:ARG:HD3	3:C:730:ARG:CZ	2.16	0.76
5:E:146:ARG:HH12	5:E:148:LYS:HE3	1.49	0.76
1:A:232:LEU:HD13	1:A:404:LEU:HD13	1.66	0.76
21:1:473:GLN:HE22	25:5:93:ASN:H	1.33	0.76
32:R:420:LYS:HG2	32:R:423:ASP:OD2	1.84	0.76
1:A:705:LYS:CB	32:R:251:ILE:CD1	2.59	0.76
2:B:44:A:H2	14:G:-5:G:N1	1.81	0.76
3:C:449:ILE:HD11	3:C:466:SER:N	1.99	0.76
15:H:143:A:H3'	15:H:143:A:N3	2.01	0.76
1:A:362:ARG:O	1:A:362:ARG:NE	2.18	0.76
3:C:261:ASP:CG	41:C:1500:GTP:HN1	1.88	0.76
5:E:162:ARG:NH2	5:E:204:THR:HA	1.99	0.76
15:H:148:C:H2'	15:H:149:A:H8	1.48	0.76
1:A:417:ARG:CZ	2:B:58:U:H5"	2.14	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:471:ASP:OD1	3:C:472:GLY:N	2.19	0.76
22:2:611:ASP:O	22:2:614:ARG:HB3	1.86	0.76
32:R:412:ASP:CG	32:R:413:GLN:N	2.39	0.76
1:A:755:HIS:HA	31:P:223:PHE:CE1	2.20	0.76
1:A:1119:ASP:N	1:A:1120:PRO:HA	2.01	0.76
23:3:423:LEU:HB2	23:3:438:LEU:HB2	1.66	0.76
34:V:548:ALA:HB1	34:V:586:PHE:N	2.00	0.76
15:H:168:A:H5'	15:H:169:C:OP2	1.86	0.76
37:Z:566:TYR:HD2	37:Z:580:PRO:HG2	1.50	0.76
3:C:750:LEU:O	3:C:754:VAL:HG23	1.84	0.76
13:F:40:U:H2'	13:F:41:A:C8	2.20	0.76
23:3:328:LYS:HB2	23:3:372:GLU:HG3	1.68	0.76
1:A:229:GLN:HG2	1:A:415:SER:HB2	1.68	0.76
1:A:405:LEU:CD1	3:C:265:LEU:HD13	2.15	0.76
1:A:779:LEU:CD2	31:P:223:PHE:CE2	2.69	0.76
5:E:231:MET:HB3	5:E:262:TRP:CZ3	2.21	0.76
1:A:305:ARG:HH21	3:C:854:ARG:HH11	1.28	0.75
1:A:435:CYS:SG	3:C:892:GLN:NE2	2.57	0.75
1:A:1162:PRO:CG	31:P:194:PHE:CD2	2.69	0.75
23:3:11:ALA:O	23:3:34:ARG:NH1	2.17	0.75
37:Z:594:GLU:O	37:Z:598:PHE:HB2	1.86	0.75
3:C:149:LEU:CD1	3:C:427:PHE:CG	2.53	0.75
3:C:593:GLU:HG3	3:C:594:PRO:HD2	1.67	0.75
14:G:132:G:H1	15:H:44:U:H3	1.34	0.75
23:3:784:THR:O	23:3:786:ARG:NH1	2.18	0.75
32:R:66:GLU:OE2	32:R:66:GLU:N	2.19	0.75
32:R:181:PRO:O	32:R:182:SER:HB2	1.84	0.75
1:A:319:LEU:HD11	3:C:590:ILE:CD1	2.16	0.75
1:A:378:PHE:HZ	3:C:335:ASN:HB2	1.51	0.75
14:G:11:A:C4	14:G:12:G:H8	2.04	0.75
15:H:81:G:H2'	15:H:82:G:C8	2.19	0.75
23:3:905:VAL:HB	23:3:928:TYR:HB2	1.68	0.75
1:A:1951:LYS:HD3	37:Z:521:PRO:O	1.85	0.75
23:3:720:TRP:HB3	23:3:731:LEU:HD11	1.69	0.75
1:A:230:PHE:N	1:A:414:ARG:O	2.18	0.75
1:A:305:ARG:HD3	3:C:933:PHE:CZ	2.22	0.75
3:C:470:PRO:HA	3:C:499:GLY:HA2	1.67	0.75
3:C:711:ARG:CD	3:C:730:ARG:HE	1.99	0.75
15:H:10:C:H2'	15:H:11:G:H8	1.52	0.75
23:3:441:GLY:HA3	23:3:734:LEU:O	1.85	0.75
23:3:1105:GLN:O	23:3:1118:VAL:HB	1.87	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:LEU:HD12	1:A:484:SER:HB2	1.67	0.75
1:A:221:ASN:CG	2:B:12:U:OP1	2.25	0.75
1:A:1762:TYR:O	1:A:1768:TYR:OH	2.05	0.75
13:F:36:A:C3'	13:F:37:C:H5"	2.16	0.75
28:J:339:TRP:CE3	32:R:116:TYR:HD2	2.04	0.75
34:V:515:CYS:HA	34:V:521:TYR:CB	2.17	0.75
3:C:82:GLN:HB2	33:T:231:TRP:HZ3	1.50	0.75
3:C:465:MET:HE1	3:C:475:MET:CG	2.13	0.75
15:H:71:C:H2'	15:H:72:U:C6	2.21	0.75
1:A:384:VAL:HG21	3:C:334:ILE:HG12	1.69	0.75
15:H:153:A:C2'	15:H:154:C:H5'	2.17	0.75
34:V:538:ARG:HA	37:Z:534:MET:CB	2.16	0.75
1:A:405:LEU:HD13	3:C:265:LEU:HD13	1.68	0.74
3:C:348:TYR:CE1	3:C:359:LYS:HB3	2.22	0.74
3:C:510:LEU:HD22	3:C:514:TYR:CE2	2.22	0.74
28:J:256:LYS:O	29:L:232:TYR:HD2	1.66	0.74
28:J:273:TYR:CG	32:R:228:PRO:HG2	2.21	0.74
1:A:231:THR:HA	3:C:389:ASP:OD2	1.86	0.74
1:A:1405:LEU:CA	32:R:415:LEU:HD21	2.15	0.74
1:A:1784:ASN:HD22	1:A:1897:LEU:HD12	1.50	0.74
1:A:2073:TRP:CD1	1:A:2074:ARG:HD2	2.22	0.74
3:C:449:ILE:CG2	3:C:457:VAL:HG12	2.17	0.74
1:A:203:VAL:CG2	1:A:237:THR:CG2	2.66	0.74
1:A:783:TYR:CB	31:P:228:ILE:HG12	2.17	0.74
37:Z:525:TYR:HD1	37:Z:526:ILE:HG23	1.52	0.74
23:3:437:VAL:O	23:3:776:GLN:HA	1.87	0.74
1:A:463:PRO:CB	2:B:20:G:O2'	2.35	0.74
1:A:1457:HIS:CD2	32:R:425:GLY:H	2.04	0.74
3:C:137:HIS:CG	3:C:236:MET:HB2	2.22	0.74
15:H:180:G:O2'	15:H:181:G:H5'	1.88	0.74
32:R:70:ALA:O	32:R:71:GLN:O	2.05	0.74
1:A:1301:ILE:HG13	2:B:39:C:OP1	1.87	0.74
1:A:1405:LEU:HA	32:R:415:LEU:CD2	2.17	0.74
23:3:294:LYS:O	23:3:343:LYS:NZ	2.21	0.74
23:3:931:VAL:HG12	23:3:932:ASN:H	1.53	0.74
28:J:270:ASP:OD2	32:R:222:PRO:HG2	1.88	0.74
1:A:168:PRO:CG	1:A:559:ASP:CB	2.64	0.74
1:A:388:LEU:CD1	3:C:399:LEU:CD2	2.41	0.74
5:E:258:THR:HG22	5:E:260:ARG:HG2	1.68	0.74
1:A:76:MET:HE3	1:A:506:LEU:HD11	1.70	0.74
1:A:744:LYS:HE3	31:P:213:ASP:HA	1.70	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:140:HIS:CA	3:C:230:ASP:HB2	2.17	0.74
13:F:34:G:H5”	13:F:34:G:N3	2.03	0.74
32:R:422:MET:O	32:R:424:SER:N	2.17	0.74
33:T:385:TYR:O	33:T:400:PHE:HB2	1.88	0.74
3:C:445:ALA:HB1	3:C:449:ILE:CD1	2.17	0.74
1:A:748:ASP:OD1	31:P:214:THR:CG2	2.36	0.73
5:E:243:LEU:HD11	5:E:247:GLY:HA2	1.68	0.73
23:3:555:VAL:HG23	23:3:592:LEU:HD22	1.70	0.73
28:J:406:PHE:CD2	28:J:411:MET:CE	2.70	0.73
1:A:546:LEU:CD1	1:A:595:LYS:HD2	2.06	0.73
5:E:119:THR:HG21	5:E:161:ARG:CB	2.17	0.73
1:A:378:PHE:CZ	3:C:335:ASN:HB2	2.22	0.73
3:C:97:VAL:HG21	31:P:45:GLN:HG3	1.69	0.73
21:1:563:LEU:HD22	21:1:566:LEU:HD22	1.70	0.73
1:A:231:THR:CB	3:C:389:ASP:OD2	2.37	0.73
1:A:253:ASN:ND2	1:A:334:THR:O	2.21	0.73
1:A:1900:GLU:CD	37:Z:522:LEU:CB	2.55	0.73
3:C:94:ILE:HD11	31:P:44:ARG:NH2	2.03	0.73
23:3:772:ALA:O	23:3:775:ASN:ND2	2.21	0.73
1:A:260:LEU:HD23	1:A:455:VAL:HG22	1.70	0.73
2:B:42:U:O4	14:G:-3:A:N1	2.21	0.73
3:C:516:LEU:CD1	3:C:517:GLU:HG3	2.18	0.73
3:C:671:SER:O	3:C:672:LEU:HD13	1.89	0.73
15:H:69:U:H2’	15:H:70:C:C6	2.23	0.73
15:H:165:A:O2’	15:H:166:G:H5’	1.88	0.73
5:E:287:ASN:O	5:E:289:LEU:HD23	1.88	0.73
26:6:51:TYR:H	26:6:54:TYR:HB2	1.53	0.73
32:R:67:ILE:HG22	32:R:69:VAL:CG2	2.18	0.73
1:A:1301:ILE:O	1:A:1303:LEU:O	2.06	0.73
1:A:2325:VAL:HG13	4:D:788:GLY:C	2.07	0.73
1:A:91:ALA:HB2	32:R:207:MET:HE2	1.71	0.73
1:A:2078:ILE:CG2	4:D:1047:PRO:CB	2.66	0.73
15:H:106:G:H4’	15:H:107:A:O4’	1.89	0.73
23:3:1145:GLU:OE2	23:3:1149:ARG:NH2	2.21	0.73
28:J:339:TRP:CE3	32:R:116:TYR:CD2	2.76	0.73
3:C:711:ARG:CD	3:C:730:ARG:HH11	2.01	0.73
28:J:259:GLN:NE2	29:L:220:PRO:HD3	2.02	0.73
3:C:449:ILE:HG22	3:C:457:VAL:CG1	2.18	0.72
5:E:146:ARG:HH12	5:E:148:LYS:CE	1.99	0.72
5:E:250:LEU:HD23	5:E:250:LEU:O	1.88	0.72
15:H:70:C:H2’	15:H:71:C:C6	2.24	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:HIS:ND1	1:A:435:CYS:SG	2.62	0.72
3:C:508:LYS:HE3	3:C:566:THR:HG21	1.70	0.72
23:3:547:CYS:HA	23:3:555:VAL:O	1.89	0.72
33:T:434:GLY:CA	33:T:464:GLY:HA2	2.19	0.72
3:C:93:ILE:HD13	33:T:230:ILE:HD13	1.72	0.72
15:H:106:G:H21	15:H:107:A:N6	1.87	0.72
15:H:182:U:H2'	15:H:183:G:H8	1.53	0.72
21:1:428:ALA:O	21:1:432:THR:N	2.21	0.72
1:A:368:GLN:OE1	1:A:368:GLN:HA	1.88	0.72
1:A:541:GLY:HA3	13:F:66:C:OP1	1.87	0.72
1:A:675:GLN:OE1	13:F:70:A:OP1	2.08	0.72
3:C:519:GLU:N	3:C:519:GLU:OE2	2.21	0.72
13:F:34:G:N3	13:F:34:G:H3'	2.05	0.72
1:A:1457:HIS:HE2	32:R:424:SER:CA	2.02	0.72
1:A:2324:GLU:HG2	1:A:2330:ARG:HH12	1.54	0.72
3:C:125:ASN:O	3:C:126:SER:OG	2.04	0.72
3:C:726:LEU:HD12	3:C:726:LEU:O	1.89	0.72
33:T:352:THR:CG2	33:T:373:LYS:C	2.58	0.72
1:A:712:HIS:CE1	32:R:254:CYS:HB2	2.24	0.72
3:C:77:VAL:CG1	33:T:196:LEU:CA	2.68	0.72
3:C:449:ILE:HG21	3:C:457:VAL:HG11	1.70	0.72
13:F:5:U:H3'	13:F:7:G:H5"	1.71	0.72
1:A:107:PRO:O	1:A:111:GLU:OE1	2.08	0.72
1:A:193:LEU:HD12	1:A:194:GLU:H	1.55	0.72
1:A:462:ARG:HD2	1:A:462:ARG:N	2.05	0.72
1:A:1413:ASP:O	1:A:1418:ARG:NH1	2.21	0.72
1:A:2325:VAL:CG1	4:D:789:MET:HA	2.20	0.72
3:C:250:ARG:HE	3:C:451:HIS:CD2	2.07	0.72
23:3:442:LEU:CD1	23:3:734:LEU:HD23	2.19	0.72
34:V:548:ALA:HB3	34:V:585:ILE:CB	2.19	0.72
1:A:150:MET:SD	1:A:153:ARG:NH2	2.62	0.72
1:A:335:PRO:HG3	3:C:139:HIS:HB3	1.70	0.72
13:F:39:A:H61	14:G:8:C:H42	1.36	0.72
22:2:614:ARG:HG3	22:2:614:ARG:NH1	1.98	0.72
1:A:332:TYR:CB	3:C:177:ARG:O	2.38	0.72
1:A:718:ARG:CZ	32:R:259:LYS:HE3	2.20	0.72
1:A:2078:ILE:HG21	4:D:1047:PRO:CB	2.20	0.72
5:E:264:VAL:HA	5:E:272:ARG:HH21	1.55	0.72
23:3:783:TYR:HB2	23:3:801:GLU:HB3	1.72	0.72
1:A:386:PRO:HD3	3:C:372:PHE:CE1	2.20	0.72
1:A:785:LYS:HE3	31:P:215:LEU:HD11	1.71	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:165:A:C2'	15:H:166:G:H5'	2.20	0.72
23:3:440:HIS:CE1	23:3:720:TRP:HZ3	1.96	0.72
1:A:228:TRP:O	1:A:415:SER:CA	2.38	0.71
1:A:480:LYS:HE2	32:R:203:GLN:OE1	1.90	0.71
3:C:64:LYS:NZ	31:P:206:LYS:HG2	2.05	0.71
3:C:129:ILE:HA	3:C:199:LEU:O	1.90	0.71
1:A:176:LEU:HD13	1:A:181:ASN:HD22	1.52	0.71
1:A:549:GLU:OE1	1:A:552:ARG:NH1	2.23	0.71
1:A:1301:ILE:CG1	2:B:39:C:OP1	2.38	0.71
28:J:273:TYR:CE1	32:R:228:PRO:CB	2.72	0.71
29:L:224:PHE:CE1	32:R:86:LEU:CD1	2.73	0.71
31:P:66:ARG:HB2	31:P:66:ARG:HH11	1.55	0.71
1:A:231:THR:HB	3:C:389:ASP:OD2	1.89	0.71
1:A:730:GLY:O	32:R:252:PRO:HG2	1.90	0.71
1:A:1364:LEU:HD22	34:V:465:SER:CB	2.20	0.71
1:A:1402:ARG:HH22	37:Z:572:PRO:HA	1.53	0.71
2:B:44:A:H2	14:G:-5:G:C6	2.08	0.71
21:1:1206:ASP:OD1	21:1:1207:SER:N	2.21	0.71
23:3:446:GLU:OE1	23:3:763:ARG:NH1	2.24	0.71
1:A:264:PHE:CE2	1:A:459:LEU:CD1	2.73	0.71
1:A:384:VAL:HG12	3:C:332:GLY:N	2.04	0.71
15:H:153:A:H2'	15:H:154:C:C5'	2.19	0.71
21:1:405:ASP:HA	25:5:49:ARG:HH22	1.55	0.71
1:A:529:THR:HG22	30:M:197:TYR:C	2.11	0.71
3:C:706:GLN:HE21	3:C:708:THR:H	1.38	0.71
5:E:74:PHE:CE2	5:E:343:ILE:CG1	2.73	0.71
31:P:224:MET:CE	31:P:224:MET:HA	2.21	0.71
32:R:414:ARG:CZ	32:R:414:ARG:HB2	2.18	0.71
1:A:1962:THR:HG23	37:Z:524:ARG:HB2	1.68	0.71
3:C:700:ILE:HA	3:C:705:VAL:CG1	2.21	0.71
3:C:705:VAL:HG23	3:C:717:PHE:HD2	1.48	0.71
15:H:72:U:H2'	15:H:73:C:C6	2.26	0.71
1:A:203:VAL:HG23	1:A:237:THR:HG21	1.72	0.71
1:A:393:LEU:CB	3:C:379:LYS:HE3	2.21	0.71
1:A:1529:ILE:O	1:A:1532:ARG:N	2.24	0.71
3:C:80:ILE:HD12	3:C:80:ILE:N	2.05	0.71
3:C:94:ILE:HD13	31:P:44:ARG:CZ	2.20	0.71
3:C:441:PRO:O	3:C:444:GLY:HA3	1.90	0.71
3:C:490:PHE:CZ	3:C:612:LYS:HD2	2.26	0.71
31:P:191:ASP:N	31:P:191:ASP:OD1	2.23	0.71
37:Z:612:TYR:O	37:Z:614:TRP:N	2.23	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:43:U:C4	14:G:-4:A:N1	2.58	0.71
1:A:81:PHE:O	1:A:83:HIS:N	2.24	0.71
1:A:171:ASP:O	1:A:520:TYR:CG	2.44	0.71
1:A:1459:ARG:CG	32:R:422:MET:O	2.39	0.71
1:A:2156:THR:OG1	1:A:2157:VAL:N	2.21	0.71
3:C:679:PRO:HG2	3:C:807:GLN:OE1	1.91	0.71
28:J:270:ASP:OD2	32:R:222:PRO:HG3	1.88	0.71
32:R:422:MET:HG2	32:R:423:ASP:N	2.05	0.71
34:V:549:LYS:O	34:V:552:ALA:HB3	1.91	0.71
1:A:76:MET:CE	1:A:88:TYR:CG	2.70	0.71
1:A:377:GLU:O	1:A:378:PHE:HB3	1.91	0.71
1:A:705:LYS:HG2	32:R:251:ILE:CD1	2.21	0.71
1:A:1085:ILE:HG12	1:A:1099:PHE:HE1	1.56	0.71
1:A:1306:LYS:NZ	2:B:38:C:H2'	2.05	0.71
21:1:1221:GLU:HG3	21:1:1223:SER:H	1.56	0.71
28:J:353:GLU:OE1	28:J:358:GLU:HB3	1.91	0.71
31:P:189:ASP:OD2	31:P:192:VAL:HG21	1.91	0.71
33:T:366:VAL:HG21	33:T:402:ASP:HA	1.72	0.71
1:A:73:HIS:NE2	1:A:81:PHE:CZ	2.51	0.70
1:A:181:ASN:O	1:A:185:VAL:HG22	1.90	0.70
1:A:719:CYS:SG	32:R:258:TRP:CH2	2.84	0.70
3:C:259:LYS:HG3	41:C:1500:GTP:C6	2.26	0.70
1:A:301:LYS:HG2	3:C:940:ARG:N	2.06	0.70
1:A:2328:ALA:HB3	4:D:788:GLY:N	2.05	0.70
15:H:160:A:O2'	15:H:161:U:H5'	1.90	0.70
14:G:11:A:N3	14:G:11:A:H5"	2.05	0.70
15:H:168:A:N3	15:H:168:A:H2'	2.06	0.70
13:F:24:A:H2	13:F:26:U:C2	2.09	0.70
32:R:189:ASN:HD21	32:R:195:ARG:NH2	1.90	0.70
33:T:267:ASP:O	33:T:268:LYS:HG3	1.91	0.70
1:A:251:ASP:CB	1:A:337:VAL:HG23	2.20	0.70
1:A:316:PHE:CE1	3:C:635:LEU:HA	2.27	0.70
2:B:40:U:H4'	2:B:41:U:OP2	1.89	0.70
2:B:43:U:N3	14:G:-4:A:C2	2.51	0.70
3:C:449:ILE:HD13	3:C:466:SER:OG	1.92	0.70
13:F:94:C:OP1	28:J:351:ASN:ND2	2.25	0.70
15:H:181:G:H2'	15:H:182:U:C6	2.26	0.70
21:1:901:GLN:HA	21:1:939:ARG:NH2	2.07	0.70
32:R:103:ARG:HH11	32:R:103:ARG:CB	2.04	0.70
34:V:536:ILE:O	34:V:578:SER:CB	2.39	0.70
1:A:76:MET:CE	1:A:506:LEU:HD11	2.21	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:457:VAL:CB	3:C:462:GLY:HA3	2.22	0.70
13:F:38:G:P	13:F:38:G:H8	2.14	0.70
13:F:68:C:C2	31:P:33:ARG:HG2	2.27	0.70
14:G:12:G:N3	14:G:12:G:H2'	2.07	0.70
21:1:1108:ASN:OD1	21:1:1110:VAL:N	2.25	0.70
1:A:1860:GLN:HG2	1:A:1883:VAL:HB	1.74	0.70
2:B:40:U:C4'	2:B:41:U:OP2	2.39	0.70
3:C:132:VAL:CG1	3:C:226:VAL:CG2	2.70	0.70
3:C:135:CYS:SG	3:C:227:LEU:CD1	2.80	0.70
32:R:220:ARG:NH1	32:R:220:ARG:HB2	2.06	0.70
1:A:664:HIS:NE2	1:A:666:LYS:HG2	2.06	0.70
1:A:675:GLN:O	13:F:55:C:O2'	2.10	0.70
1:A:1318:THR:HB	1:A:1324:GLY:HA3	1.73	0.70
15:H:154:C:H2'	15:H:155:C:C6	2.27	0.70
21:1:1155:PHE:HA	21:1:1158:ILE:HG12	1.73	0.70
32:R:80:LYS:O	32:R:81:LYS:NZ	2.25	0.70
1:A:231:THR:CA	3:C:389:ASP:OD2	2.40	0.70
1:A:719:CYS:SG	32:R:258:TRP:HH2	2.13	0.70
3:C:137:HIS:CE1	3:C:236:MET:SD	2.85	0.70
1:A:299:ILE:HD12	3:C:921:LEU:HB2	1.74	0.69
1:A:718:ARG:NE	32:R:259:LYS:HE3	2.06	0.69
3:C:452:THR:HB	3:C:577:PHE:CD2	2.26	0.69
23:3:722:SER:HA	23:3:730:HIS:O	1.92	0.69
1:A:76:MET:SD	1:A:88:TYR:CG	2.85	0.69
1:A:363:HIS:CE1	3:C:287:GLY:HA3	2.27	0.69
1:A:673:THR:O	1:A:677:VAL:HG23	1.91	0.69
3:C:64:LYS:NZ	31:P:206:LYS:CG	2.55	0.69
3:C:452:THR:O	3:C:577:PHE:HA	1.92	0.69
5:E:74:PHE:HE2	5:E:343:ILE:HG12	1.54	0.69
5:E:264:VAL:HA	5:E:272:ARG:NH2	2.07	0.69
1:A:232:LEU:HD23	3:C:387:ASP:O	1.92	0.69
1:A:250:VAL:CG2	1:A:337:VAL:CG1	2.70	0.69
1:A:311:GLU:HB3	3:C:885:THR:CG2	2.21	0.69
1:A:461:HIS:CD2	2:B:26:A:H61	2.10	0.69
1:A:974:ASN:HB2	1:A:1178:TYR:HB3	1.73	0.69
1:A:439:GLN:NE2	1:A:614:TYR:CE2	2.49	0.69
1:A:805:GLU:CB	31:P:194:PHE:HZ	2.04	0.69
1:A:2314:PHE:HD2	4:D:1123:TRP:CB	2.05	0.69
3:C:709:TRP:HB3	3:C:713:LYS:HD2	1.73	0.69
23:3:280:ASP:H	23:3:857:ALA:HB3	1.58	0.69
31:P:30:TYR:OH	32:R:161:ALA:O	2.10	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:436:VAL:HG23	32:R:437:TYR:CE1	2.26	0.69
1:A:645:THR:HB	1:A:646:PRO:HD3	1.74	0.69
1:A:755:HIS:HE1	31:P:223:PHE:CD2	2.06	0.69
15:H:149:A:H2'	15:H:150:U:C6	2.27	0.69
15:H:153:A:N6	15:H:177:A:C2	2.60	0.69
15:H:183:G:H2'	15:H:184:C:C6	2.26	0.69
32:R:408:GLU:CG	32:R:409:VAL:H	2.04	0.69
1:A:71:ARG:HD2	1:A:177:ASP:OD2	1.91	0.69
1:A:1180:LYS:HA	1:A:1201:ARG:HH12	1.58	0.69
23:3:428:GLY:HA3	23:3:433:SER:HA	1.73	0.69
1:A:203:VAL:CG2	1:A:237:THR:HG21	2.23	0.69
1:A:256:TYR:CE1	3:C:888:ARG:CZ	2.76	0.69
1:A:367:SER:CB	3:C:299:ILE:HD12	2.23	0.69
1:A:384:VAL:CA	3:C:331:PHE:CD2	2.61	0.69
1:A:762:ARG:NH2	31:P:226:LYS:HZ3	1.87	0.69
1:A:1505:LYS:CD	37:Z:615:SER:HB3	2.22	0.69
3:C:89:LEU:HD23	3:C:89:LEU:C	2.14	0.69
3:C:482:TYR:CE2	3:C:493:PHE:HB2	2.28	0.69
5:E:178:LEU:CD1	5:E:222:LEU:CD2	2.71	0.69
15:H:83:A:C2'	15:H:84:C:O4'	2.39	0.69
23:3:452:LEU:HD11	23:3:762:LEU:HB2	1.74	0.69
25:5:18:ASN:OD1	25:5:19:ARG:N	2.25	0.69
35:X:185:ARG:O	35:X:189:HIS:HB2	1.93	0.69
1:A:1459:ARG:HG3	32:R:424:SER:H	1.57	0.69
1:A:2267:PHE:HA	4:D:1261:PRO:CB	2.23	0.69
3:C:93:ILE:CG2	33:T:218:TRP:CE2	2.76	0.69
3:C:736:GLY:CA	3:C:770:PHE:CE2	2.75	0.69
15:H:152:G:O3'	15:H:153:A:O4'	2.11	0.69
23:3:236:ILE:HB	23:3:249:LEU:HB2	1.75	0.69
28:J:353:GLU:OE1	28:J:358:GLU:CB	2.41	0.69
31:P:30:TYR:CZ	32:R:162:ALA:HA	2.28	0.69
31:P:224:MET:CE	31:P:228:ILE:CD1	2.71	0.69
1:A:299:ILE:HD11	3:C:921:LEU:HA	1.74	0.69
1:A:392:PRO:C	3:C:379:LYS:CE	2.48	0.69
3:C:72:VAL:HG22	33:T:453:ALA:CB	2.23	0.69
3:C:256:CYS:SG	3:C:308:CYS:HB2	2.33	0.69
5:E:74:PHE:CD1	5:E:81:LEU:HD23	2.28	0.69
1:A:229:GLN:CG	1:A:415:SER:HB2	2.21	0.68
1:A:253:ASN:OD1	1:A:334:THR:OG1	2.03	0.68
1:A:388:LEU:HD12	3:C:399:LEU:HD21	1.72	0.68
1:A:755:HIS:CE1	31:P:223:PHE:HB3	2.28	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1076:ASP:O	1:A:1079:THR:OG1	2.11	0.68
13:F:37:C:H4'	13:F:38:G:OP2	1.91	0.68
22:2:487:LEU:O	22:2:490:HIS:N	2.26	0.68
23:3:718:ARG:NH2	23:3:734:LEU:O	2.25	0.68
1:A:255:PHE:HE1	1:A:432:ARG:O	1.75	0.68
3:C:140:HIS:CD2	3:C:230:ASP:HB3	2.28	0.68
3:C:445:ALA:CB	3:C:466:SER:HA	2.20	0.68
3:C:725:ASP:OD1	3:C:728:ALA:N	2.25	0.68
32:R:434:TYR:HE2	32:R:436:VAL:HG22	1.57	0.68
1:A:73:HIS:NE2	1:A:81:PHE:CD1	2.59	0.68
1:A:1301:ILE:CD1	1:A:1306:LYS:CE	2.70	0.68
2:B:21:A:O3'	2:B:22:U:H4'	1.94	0.68
22:2:643:PRO:HD2	24:4:69:TYR:CG	2.27	0.68
31:P:72:ARG:NH1	31:P:72:ARG:HB2	2.08	0.68
32:R:106:GLN:CG	32:R:110:LYS:HE2	2.22	0.68
32:R:420:LYS:HG2	32:R:423:ASP:CG	2.13	0.68
36:Y:33:LYS:HA	36:Y:87:GLN:HE22	1.59	0.68
1:A:32:GLU:HG3	1:A:36:LYS:HE3	1.74	0.68
1:A:402:ILE:HG12	3:C:265:LEU:HD22	1.75	0.68
3:C:453:TYR:CZ	3:C:575:GLN:HB2	2.28	0.68
36:Y:86:ASP:HB2	37:Z:502:ALA:CB	2.23	0.68
1:A:44:ARG:HD2	1:A:45:TYR:CE2	2.28	0.68
1:A:1900:GLU:OE2	37:Z:522:LEU:HB2	1.93	0.68
1:A:2146:VAL:HG22	1:A:2272:MET:HB2	1.74	0.68
3:C:482:TYR:CE2	3:C:493:PHE:CB	2.77	0.68
3:C:678:THR:HG21	3:C:683:ASN:ND2	2.06	0.68
14:G:-2:C:H2'	14:G:-1:G:C8	2.28	0.68
23:3:441:GLY:O	23:3:775:ASN:CG	2.31	0.68
23:3:868:VAL:O	23:3:877:LEU:N	2.27	0.68
5:E:108:HIS:CE1	5:E:128:SER:CB	2.77	0.68
15:H:147:G:O2'	15:H:148:C:H5'	1.94	0.68
23:3:524:ILE:HD11	23:3:556:ILE:HG21	1.74	0.68
31:P:63:LEU:O	31:P:63:LEU:HD23	1.94	0.68
32:R:414:ARG:NE	37:Z:598:PHE:CE1	2.47	0.68
1:A:338:VAL:HG21	3:C:867:PRO:CD	2.24	0.68
1:A:779:LEU:CD2	31:P:223:PHE:HE2	2.06	0.68
1:A:1457:HIS:HE2	32:R:424:SER:HA	1.55	0.68
13:F:68:C:C5	31:P:33:ARG:HB3	2.20	0.68
32:R:88:ILE:CG2	32:R:96:ILE:CG2	2.71	0.68
3:C:79:THR:HG23	33:T:199:VAL:CG2	2.24	0.68
3:C:452:THR:HG22	3:C:577:PHE:CB	2.23	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:74:PHE:CD1	5:E:81:LEU:HD21	2.29	0.68
34:V:547:VAL:O	34:V:550:MET:N	2.27	0.68
37:Z:597:ARG:NH1	37:Z:601:LEU:CD1	2.57	0.68
1:A:660:PHE:CD2	32:R:209:PRO:CB	2.76	0.68
1:A:758:ARG:HG3	1:A:779:LEU:HD11	1.75	0.68
1:A:1210:LYS:NZ	1:A:1369:TYR:OH	2.27	0.68
2:B:19:A:O2'	2:B:20:G:OP1	2.12	0.68
3:C:141:GLY:O	3:C:258:ASN:ND2	2.27	0.68
22:2:614:ARG:NH2	22:2:685:ASP:OD1	2.26	0.68
23:3:301:PHE:HB2	23:3:313:ILE:HB	1.76	0.68
27:7:48:ASP:O	27:7:51:ASN:N	2.27	0.68
28:J:360:ASP:O	28:J:363:ARG:HG3	1.93	0.68
36:Y:86:ASP:CA	37:Z:502:ALA:HB3	2.23	0.68
1:A:91:ALA:O	1:A:93:LYS:N	2.27	0.68
1:A:121:HIS:HE2	1:A:481:PHE:HB3	1.51	0.68
1:A:245:LEU:HA	1:A:430:TRP:CZ2	2.28	0.68
3:C:94:ILE:CD1	31:P:44:ARG:NH1	2.57	0.68
13:F:35:A:H5"	13:F:35:A:N3	2.09	0.68
15:H:159:U:O2'	15:H:160:A:H5'	1.94	0.68
23:3:374:SER:HB3	23:3:377:MET:HG3	1.76	0.68
28:J:353:GLU:OE2	28:J:361:ARG:NH2	2.27	0.68
1:A:76:MET:HE1	1:A:88:TYR:CB	2.23	0.67
3:C:94:ILE:CD1	31:P:44:ARG:CZ	2.72	0.67
3:C:360:ALA:H	3:C:361:PRO:HD3	1.59	0.67
3:C:534:VAL:HG12	3:C:535:ALA:H	1.59	0.67
32:R:420:LYS:HB2	37:Z:610:LEU:CD1	2.22	0.67
1:A:122:ILE:CD1	1:A:483:GLN:HG3	2.24	0.67
1:A:298:ASP:O	1:A:302:ILE:HG12	1.95	0.67
1:A:305:ARG:HG3	3:C:878:ILE:HB	1.77	0.67
1:A:2270:PHE:HD1	4:D:1264:PRO:CB	1.96	0.67
3:C:140:HIS:HB3	3:C:230:ASP:HB2	1.71	0.67
23:3:18:ILE:HD12	23:3:67:ALA:HB2	1.77	0.67
32:R:147:THR:CG2	33:T:360:VAL:HG12	2.23	0.67
1:A:91:ALA:CA	32:R:207:MET:CE	2.71	0.67
3:C:140:HIS:CD2	3:C:230:ASP:CB	2.77	0.67
3:C:737:PRO:HG3	3:C:774:THR:OG1	1.93	0.67
21:1:437:PRO:O	35:X:262:TYR:HA	1.94	0.67
23:3:753:GLY:HA3	23:3:765:LEU:O	1.94	0.67
1:A:75:ASP:OD1	1:A:75:ASP:N	2.26	0.67
1:A:228:TRP:O	1:A:416:GLY:N	2.26	0.67
1:A:1072:LEU:HD22	1:A:1087:LEU:HD22	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1118:PRO:HD2	1:A:1119:ASP:H	1.59	0.67
1:A:1962:THR:HG23	37:Z:524:ARG:HG3	1.74	0.67
3:C:259:LYS:HE2	3:C:262:ARG:HD2	1.74	0.67
21:1:1097:LEU:O	21:1:1100:ASN:ND2	2.24	0.67
23:3:412:ILE:HG12	23:3:423:LEU:HG	1.76	0.67
1:A:76:MET:SD	1:A:88:TYR:CD1	2.88	0.67
1:A:89:LEU:HD22	1:A:656:LEU:HD22	1.76	0.67
1:A:1422:LEU:HD22	21:1:88:VAL:CB	2.25	0.67
1:A:2113:LYS:CE	4:D:1229:ASP:CB	2.71	0.67
3:C:389:ASP:OD1	3:C:389:ASP:N	2.26	0.67
5:E:66:GLU:HB2	5:E:87:ASP:OD2	1.94	0.67
21:1:474:TYR:OH	25:5:93:ASN:ND2	2.27	0.67
21:1:798:THR:HG22	21:1:800:GLY:H	1.60	0.67
32:R:119:LEU:CB	32:R:232:MET:HG3	2.24	0.67
32:R:285:ASN:OD1	32:R:286:GLU:N	2.27	0.67
33:T:185:MET:CB	33:T:186:PRO:HD3	2.24	0.67
1:A:1281:THR:HG22	1:A:1284:LEU:H	1.59	0.67
3:C:94:ILE:HD11	31:P:44:ARG:HH22	1.60	0.67
3:C:132:VAL:HG12	3:C:226:VAL:CG2	2.23	0.67
5:E:246:GLU:HB2	5:E:248:SER:OG	1.94	0.67
33:T:455:GLN:HG3	33:T:485:THR:HG21	1.76	0.67
1:A:435:CYS:CB	3:C:892:GLN:NE2	2.57	0.67
1:A:1258:LYS:HE2	32:R:432:GLU:HA	1.77	0.67
1:A:1661:TRP:CE2	1:A:1700:GLY:HA3	2.30	0.67
1:A:2300:ASN:OD1	4:D:1228:VAL:O	2.12	0.67
3:C:736:GLY:CA	3:C:770:PHE:HE2	2.07	0.67
36:Y:62:ILE:HA	36:Y:84:TYR:HA	1.75	0.67
36:Y:100:ILE:O	36:Y:106:THR:HA	1.94	0.67
37:Z:597:ARG:NH1	37:Z:601:LEU:HD12	2.08	0.67
1:A:171:ASP:OD2	1:A:519:ASP:OD2	2.12	0.67
1:A:299:ILE:CD1	3:C:920:PRO:O	2.43	0.67
1:A:393:LEU:HA	3:C:379:LYS:CD	2.24	0.67
1:A:696:MET:C	1:A:698:PRO:HD3	2.15	0.67
2:B:40:U:C5'	2:B:41:U:OP2	2.43	0.67
3:C:572:GLU:HG3	3:C:573:GLU:H	1.60	0.67
15:H:151:C:C2	15:H:152:G:C8	2.83	0.67
32:R:81:LYS:HA	32:R:81:LYS:HZ1	1.59	0.67
32:R:119:LEU:HA	32:R:232:MET:SD	2.34	0.67
33:T:272:CYS:HB3	33:T:282:ARG:HG3	1.76	0.67
1:A:229:GLN:HA	1:A:414:ARG:O	1.94	0.67
1:A:293:TRP:HZ3	1:A:295:GLU:OE1	1.76	0.67

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:452:THR:CB	3:C:577:PHE:CD2	2.73	0.67
5:E:243:LEU:HD12	5:E:247:GLY:HA2	1.76	0.67
14:G:10:U:O5'	14:G:10:U:H6	1.78	0.67
15:H:169:C:O2'	15:H:170:C:H5'	1.95	0.67
23:3:63:ARG:NH2	23:3:119:GLN:OE1	2.22	0.67
23:3:470:PHE:HB3	23:3:747:SER:HA	1.75	0.67
23:3:802:THR:HA	23:3:863:ALA:O	1.95	0.67
1:A:91:ALA:HA	32:R:207:MET:HE3	1.74	0.67
1:A:439:GLN:NE2	1:A:614:TYR:OH	2.27	0.67
3:C:149:LEU:HD13	3:C:427:PHE:CE2	2.22	0.67
3:C:510:LEU:HD22	3:C:514:TYR:CD2	2.30	0.67
15:H:153:A:C3'	15:H:154:C:H5'	2.25	0.67
21:1:1126:PHE:HA	21:1:1165:TYR:OH	1.94	0.67
32:R:135:PRO:O	32:R:136:ASP:CG	2.33	0.67
1:A:406:TRP:CZ3	3:C:265:LEU:C	2.69	0.66
1:A:417:ARG:HH22	2:B:58:U:C5'	2.07	0.66
1:A:1984:LYS:HG3	1:A:2011:ILE:HD11	1.76	0.66
1:A:2306:HIS:CD2	1:A:2308:VAL:H	2.13	0.66
3:C:77:VAL:CG1	33:T:196:LEU:HB3	2.24	0.66
3:C:129:ILE:HG22	3:C:199:LEU:CB	2.23	0.66
23:3:1035:THR:HG21	23:3:1103:SER:HA	1.75	0.66
24:4:17:VAL:HG13	24:4:84:ILE:HG23	1.77	0.66
1:A:398:THR:CG2	3:C:382:ALA:HB1	2.23	0.66
3:C:230:ASP:OD1	3:C:259:LYS:CB	2.43	0.66
15:H:143:A:H2'	15:H:144:C:H6	1.59	0.66
15:H:151:C:O2	15:H:152:G:C8	2.48	0.66
1:A:676:ARG:NE	13:F:56:A:OP1	2.28	0.66
1:A:1768:TYR:HA	1:A:1771:LEU:HB3	1.75	0.66
3:C:62:ASP:OD1	3:C:62:ASP:N	2.28	0.66
3:C:244:LYS:CB	3:C:292:TYR:CE2	2.79	0.66
15:H:151:C:H2'	15:H:152:G:H8	1.59	0.66
23:3:147:ASP:OD1	23:3:151:ARG:N	2.25	0.66
23:3:546:LYS:O	23:3:556:ILE:HA	1.94	0.66
23:3:947:GLU:HB3	23:3:963:VAL:HG22	1.75	0.66
1:A:338:VAL:CG2	3:C:867:PRO:CG	2.73	0.66
1:A:377:GLU:O	1:A:378:PHE:CB	2.44	0.66
1:A:748:ASP:OD2	33:T:204:LEU:O	2.13	0.66
1:A:1386:TRP:HE1	1:A:1417:PRO:HD2	1.61	0.66
1:A:1457:HIS:CE1	1:A:1459:ARG:HB2	2.30	0.66
5:E:146:ARG:HH11	5:E:148:LYS:CE	1.83	0.66
15:H:73:C:H2'	15:H:74:U:C6	2.30	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:114:A:H61	15:H:142:C:H42	1.44	0.66
21:1:397:ARG:HD3	21:1:398:PRO:HD2	1.78	0.66
26:6:25:LYS:NZ	26:6:26:CYS:SG	2.68	0.66
1:A:480:LYS:HG2	32:R:203:GLN:OE1	1.95	0.66
2:B:19:A:H2'	2:B:20:G:H5"	1.78	0.66
2:B:47:A:HO2'	2:B:48:A:H8	1.42	0.66
1:A:134:TRP:HB3	1:A:418:THR:CG2	2.25	0.66
3:C:473:PRO:O	3:C:474:LEU:HB3	1.96	0.66
3:C:474:LEU:HD23	3:C:474:LEU:C	2.16	0.66
15:H:47:U:H1'	15:H:48:A:H8	1.61	0.66
23:3:1017:ASN:OD1	23:3:1018:GLU:N	2.29	0.66
31:P:212:ASN:OD1	33:T:483:ASP:HA	1.96	0.66
33:T:314:ILE:HD12	33:T:324:HIS:HB2	1.75	0.66
36:Y:39:PHE:O	36:Y:109:VAL:HA	1.95	0.66
36:Y:98:ASN:OD1	36:Y:99:GLY:N	2.25	0.66
37:Z:525:TYR:HE1	37:Z:526:ILE:HG23	1.57	0.66
1:A:1370:ARG:NH1	34:V:467:LEU:C	2.49	0.66
3:C:145:PHE:CE1	3:C:427:PHE:HE1	2.14	0.66
3:C:221:ILE:CG1	3:C:479:THR:OG1	2.43	0.66
33:T:342:GLU:HB3	33:T:343:PRO:CD	2.26	0.66
34:V:548:ALA:HB1	34:V:585:ILE:CB	2.25	0.66
1:A:76:MET:HE2	1:A:88:TYR:CD2	2.30	0.66
1:A:312:TYR:CE1	3:C:882:GLY:CA	2.78	0.66
1:A:395:THR:CG2	3:C:383:GLN:NE2	2.49	0.66
1:A:718:ARG:HH21	32:R:259:LYS:HE3	1.58	0.66
1:A:785:LYS:HE3	31:P:215:LEU:CD1	2.26	0.66
3:C:140:HIS:HA	3:C:259:LYS:NZ	2.10	0.66
5:E:116:HIS:O	5:E:124:LEU:HD12	1.95	0.66
23:3:355:ASN:OD1	23:3:436:ARG:NH2	2.26	0.66
1:A:366:LYS:HE3	1:A:366:LYS:N	2.07	0.66
14:G:146:C:H41	21:1:1107:GLN:HG3	1.60	0.66
23:3:952:ILE:HG12	23:3:961:ILE:HG12	1.78	0.66
27:7:63:ARG:O	27:7:67:ASN:ND2	2.29	0.66
28:J:300:ASP:OD2	32:R:101:ILE:CG1	2.44	0.66
1:A:225:TYR:O	1:A:418:THR:OG1	2.11	0.66
1:A:755:HIS:HE1	31:P:223:PHE:HB3	1.61	0.66
1:A:829:PRO:O	1:A:882:LYS:NZ	2.27	0.66
1:A:1457:HIS:NE2	32:R:424:SER:CA	2.59	0.66
3:C:87:GLN:HE21	33:T:239:LYS:HD3	1.61	0.66
23:3:330:PHE:O	23:3:394:ASN:ND2	2.29	0.66
3:C:77:VAL:HG12	33:T:197:TYR:CA	2.25	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:136:GLY:HA2	3:C:239:THR:HG22	1.77	0.65
5:E:178:LEU:HD11	5:E:222:LEU:CD2	2.26	0.65
32:R:124:VAL:HG13	32:R:125:MET:H	1.60	0.65
1:A:333:HIS:O	3:C:139:HIS:NE2	2.29	0.65
1:A:344:ASP:N	1:A:344:ASP:OD1	2.28	0.65
1:A:1459:ARG:HE	32:R:423:ASP:CB	2.06	0.65
14:G:-12:G:H2'	14:G:-11:G:C8	2.30	0.65
23:3:440:HIS:CG	23:3:733:PRO:CG	2.79	0.65
33:T:439:TRP:CZ3	33:T:446:ASN:HB2	2.32	0.65
21:1:1171:PRO:O	21:1:1174:GLU:HB2	1.96	0.65
31:P:210:PHE:HB3	33:T:455:GLN:HE22	1.61	0.65
1:A:1459:ARG:CD	32:R:422:MET:O	2.45	0.65
1:A:1962:THR:O	37:Z:524:ARG:CG	2.45	0.65
21:1:713:ALA:HA	21:1:716:ALA:HB3	1.77	0.65
31:P:66:ARG:HH11	31:P:66:ARG:CB	2.09	0.65
3:C:457:VAL:HB	3:C:462:GLY:HA3	1.78	0.65
33:T:327:SER:O	33:T:357:TRP:HH2	1.79	0.65
1:A:254:TYR:OH	1:A:434:HIS:HB3	1.95	0.65
1:A:435:CYS:CB	3:C:892:GLN:HE22	2.09	0.65
3:C:700:ILE:HG21	3:C:741:GLY:O	1.97	0.65
14:G:137:C:H42	15:H:40:C:N4	1.95	0.65
21:1:584:ASP:OD1	21:1:585:GLU:N	2.29	0.65
22:2:487:LEU:HD12	27:7:28:LYS:HE3	1.78	0.65
22:2:511:LEU:HD23	22:2:593:GLU:HG3	1.79	0.65
23:3:458:ALA:HA	23:3:741:PHE:HB3	1.78	0.65
33:T:459:LEU:HD12	33:T:460:ASP:H	1.61	0.65
1:A:91:ALA:CA	32:R:207:MET:HE3	2.26	0.65
1:A:333:HIS:C	3:C:139:HIS:NE2	2.49	0.65
1:A:361:HIS:HD2	3:C:279:ARG:NH1	1.95	0.65
5:E:108:HIS:CE1	5:E:128:SER:HB3	2.31	0.65
13:F:24:A:H2	13:F:26:U:N3	1.94	0.65
1:A:134:TRP:HB3	1:A:418:THR:HG21	1.79	0.65
1:A:405:LEU:HD11	3:C:385:VAL:HG11	1.78	0.65
2:B:40:U:H5'	2:B:41:U:OP2	1.97	0.65
3:C:572:GLU:HG3	3:C:573:GLU:N	2.12	0.65
23:3:866:ILE:HB	23:3:880:VAL:HB	1.79	0.65
32:R:451:ILE:HD13	32:R:451:ILE:N	2.12	0.65
33:T:458:SER:OG	33:T:459:LEU:N	2.30	0.65
2:B:43:U:O4	14:G:-4:A:N1	2.29	0.65
23:3:791:HIS:HE1	23:3:934:GLY:HA3	1.62	0.65
24:4:75:ASN:OD1	24:4:86:VAL:CB	2.45	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:HIS:HD2	1:A:473:PHE:CZ	2.15	0.65
1:A:2314:PHE:CD2	4:D:1123:TRP:CB	2.80	0.65
3:C:749:THR:O	3:C:753:GLU:N	2.27	0.65
13:F:33:G:OP2	13:F:33:G:H8	1.80	0.65
15:H:153:A:H3'	15:H:154:C:H5'	1.79	0.65
15:H:156:U:C6	15:H:156:U:C5'	2.72	0.65
21:1:1026:ASN:HD22	21:1:1031:VAL:HG11	1.60	0.65
31:P:210:PHE:CE2	33:T:455:GLN:OE1	2.50	0.65
3:C:97:VAL:CG1	31:P:47:THR:OG1	2.45	0.64
3:C:463:GLU:OE1	3:C:463:GLU:N	2.29	0.64
3:C:488:VAL:HG13	3:C:609:LYS:NZ	2.12	0.64
5:E:277:PHE:HE2	5:E:300:ILE:HD13	1.61	0.64
21:1:912:ASN:OD1	21:1:957:ARG:NH1	2.30	0.64
32:R:171:LEU:CD1	32:R:201:GLU:OE1	2.44	0.64
1:A:664:HIS:NE2	1:A:666:LYS:HB2	2.11	0.64
3:C:72:VAL:CG2	33:T:453:ALA:HB1	2.26	0.64
14:G:11:A:N3	14:G:11:A:H3'	2.12	0.64
15:H:148:C:H2'	15:H:149:A:C8	2.30	0.64
1:A:378:PHE:CD1	1:A:379:GLU:N	2.65	0.64
3:C:141:GLY:C	3:C:258:ASN:HD22	2.01	0.64
5:E:153:PHE:O	5:E:171:SER:HB2	1.97	0.64
23:3:429:ARG:HH12	27:7:58:ASN:HA	1.62	0.64
23:3:635:ALA:HB3	23:3:669:LEU:HD23	1.79	0.64
1:A:363:HIS:CD2	3:C:283:ASP:O	2.50	0.64
1:A:779:LEU:HD21	31:P:223:PHE:HE2	1.59	0.64
1:A:1051:LEU:CD2	31:P:193:VAL:HG11	2.27	0.64
3:C:256:CYS:SG	3:C:308:CYS:CB	2.86	0.64
23:3:206:GLN:HG3	23:3:228:LEU:HD12	1.78	0.64
23:3:670:GLN:HA	23:3:698:PRO:HA	1.78	0.64
32:R:88:ILE:H	32:R:88:ILE:HD12	1.61	0.64
36:Y:24:ASP:O	36:Y:27:SER:N	2.30	0.64
37:Z:594:GLU:O	37:Z:598:PHE:N	2.25	0.64
1:A:976:MET:HG2	1:A:1187:PHE:HB3	1.78	0.64
1:A:1069:ASN:OD1	1:A:1075:GLN:NE2	2.31	0.64
1:A:2328:ALA:CB	4:D:788:GLY:CA	2.74	0.64
3:C:97:VAL:HG22	31:P:45:GLN:HG3	1.77	0.64
3:C:482:TYR:HE2	3:C:493:PHE:CD2	2.14	0.64
1:A:305:ARG:HA	1:A:305:ARG:NH1	2.09	0.64
15:H:68:G:H1	15:H:84:C:N4	1.95	0.64
23:3:714:ALA:O	23:3:720:TRP:HB2	1.97	0.64
32:R:419:SER:O	32:R:420:LYS:O	2.16	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:ILE:CG2	3:C:933:PHE:CE1	2.81	0.64
3:C:350:ASN:ND2	3:C:353:THR:HG23	2.13	0.64
3:C:705:VAL:HB	3:C:717:PHE:CZ	2.33	0.64
14:G:149:G:C2	14:G:150:U:H2'	2.32	0.64
21:1:847:ALA:O	21:1:851:SER:CB	2.46	0.64
32:R:433:ILE:HD12	32:R:435:ASN:ND2	2.12	0.64
1:A:250:VAL:CG2	1:A:337:VAL:HG11	2.28	0.64
1:A:305:ARG:HG2	3:C:878:ILE:CG2	2.27	0.64
1:A:1118:PRO:O	1:A:1119:ASP:CB	2.44	0.64
3:C:824:THR:O	3:C:824:THR:CG2	2.45	0.64
13:F:38:G:H8	13:F:38:G:O5'	1.79	0.64
21:1:599:ASN:O	21:1:603:ALA:HB2	1.98	0.64
21:1:702:ARG:O	21:1:705:SER:OG	2.13	0.64
23:3:525:ARG:HG3	23:3:533:VAL:HG13	1.78	0.64
24:4:15:VAL:O	24:4:58:PHE:HA	1.97	0.64
29:L:224:PHE:HD1	32:R:86:LEU:HD12	1.54	0.64
1:A:406:TRP:CH2	3:C:266:GLU:HB2	2.33	0.64
1:A:1252:GLY:HA2	1:A:1298:ARG:NH2	2.13	0.64
1:A:1370:ARG:NH1	34:V:467:LEU:HA	2.12	0.64
3:C:363:SER:O	3:C:364:SER:OG	2.11	0.64
15:H:25:G:H2'	15:H:26:A:H8	1.62	0.64
28:J:294:HIS:CE1	29:L:227:THR:CB	2.80	0.64
1:A:176:LEU:HD13	1:A:181:ASN:ND2	2.13	0.64
1:A:338:VAL:HG23	3:C:867:PRO:CG	2.24	0.64
1:A:384:VAL:CG1	3:C:331:PHE:CB	2.46	0.64
1:A:393:LEU:HA	3:C:379:LYS:CE	2.18	0.64
1:A:1215:ASN:HB3	1:A:1224:ARG:HD2	1.79	0.64
1:A:1457:HIS:CE1	32:R:424:SER:CA	2.79	0.64
3:C:678:THR:HG21	3:C:683:ASN:HB2	1.76	0.64
14:G:155:U:H4'	14:G:156:U:H5'	1.79	0.64
1:A:1962:THR:HG23	37:Z:524:ARG:CG	2.27	0.63
1:A:2319:LEU:HG	1:A:2320:LEU:N	2.11	0.63
3:C:482:TYR:CE2	3:C:493:PHE:CD2	2.86	0.63
4:D:1992:GLU:HA	4:D:1995:ALA:HB3	1.80	0.63
23:3:673:VAL:HA	23:3:691:THR:H	1.63	0.63
1:A:175:PRO:HG2	1:A:498:ARG:CZ	2.27	0.63
1:A:366:LYS:H	1:A:366:LYS:CE	2.09	0.63
2:B:12:U:O2'	2:B:13:C:O5'	2.14	0.63
3:C:481:MET:SD	3:C:492:ALA:HB2	2.37	0.63
3:C:596:ASN:HD22	3:C:596:ASN:N	1.96	0.63
13:F:94:C:OP1	28:J:351:ASN:HB2	1.98	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:152:G:C2	15:H:153:A:C5	2.87	0.63
23:3:524:ILE:HD11	23:3:556:ILE:HD13	1.80	0.63
24:4:75:ASN:OD1	24:4:86:VAL:N	2.31	0.63
1:A:109:PRO:HD3	1:A:630:TRP:CZ2	2.33	0.63
3:C:77:VAL:HG12	33:T:196:LEU:O	1.70	0.63
5:E:119:THR:HG23	5:E:161:ARG:HB3	1.80	0.63
13:F:35:A:H2'	13:F:36:A:C5'	2.28	0.63
23:3:187:MET:HE2	23:3:206:GLN:HB3	1.80	0.63
23:3:931:VAL:N	23:3:936:LYS:O	2.29	0.63
25:5:20:ILE:HG12	25:5:63:VAL:HG22	1.78	0.63
1:A:305:ARG:HD3	3:C:933:PHE:HZ	1.64	0.63
1:A:755:HIS:CD2	31:P:219:PHE:HE2	2.15	0.63
13:F:58:G:H2'	13:F:59:G:C8	2.32	0.63
23:3:86:ARG:HA	23:3:105:GLU:O	1.98	0.63
23:3:174:ASP:OD2	23:3:240:GLY:N	2.31	0.63
23:3:489:GLU:HG2	23:3:748:GLU:HB3	1.80	0.63
35:X:241:GLY:N	35:X:262:TYR:O	2.31	0.63
1:A:44:ARG:HD2	1:A:45:TYR:CZ	2.34	0.63
3:C:129:ILE:CG2	3:C:199:LEU:HB3	2.27	0.63
3:C:295:ASP:OD1	3:C:297:ASN:N	2.32	0.63
3:C:350:ASN:CG	3:C:353:THR:HG23	2.19	0.63
3:C:456:GLY:O	3:C:457:VAL:HG22	1.99	0.63
13:F:36:A:C5'	13:F:36:A:H8	2.12	0.63
32:R:132:LEU:HD23	32:R:132:LEU:H	1.63	0.63
1:A:251:ASP:HB3	1:A:337:VAL:CG2	2.25	0.63
1:A:468:LYS:HD3	1:A:469:LYS:H	1.61	0.63
1:A:1852:LEU:HD12	1:A:1853:PRO:HD2	1.80	0.63
23:3:794:SER:OG	23:3:796:ASN:OD1	2.15	0.63
32:R:123:GLU:OE1	32:R:124:VAL:N	2.30	0.63
1:A:97:HIS:CD2	1:A:473:PHE:CZ	2.87	0.63
1:A:1260:VAL:HG21	1:A:1325:LEU:HB3	1.80	0.63
1:A:1787:ARG:NH2	1:A:1804:ASN:O	2.31	0.63
1:A:1820:LYS:HD3	1:A:1914:MET:HE2	1.78	0.63
5:E:178:LEU:HD21	5:E:208:ILE:CD1	2.28	0.63
15:H:47:U:H1'	15:H:48:A:C8	2.34	0.63
21:1:812:PRO:HB2	21:1:813:PRO:HD3	1.81	0.63
25:5:23:ILE:HD12	25:5:89:VAL:HG12	1.81	0.63
1:A:331:TRP:CZ3	3:C:179:VAL:HG22	2.33	0.63
1:A:693:ILE:HG13	1:A:738:MET:SD	2.38	0.63
1:A:1000:ILE:HG22	1:A:1001:VAL:HG13	1.81	0.63
3:C:93:ILE:CD1	33:T:230:ILE:HD13	2.29	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:476:CYS:CB	3:C:565:ILE:HB	2.27	0.63
21:1:698:GLN:O	21:1:702:ARG:NH1	2.32	0.63
23:3:399:ASP:OD1	23:3:400:GLU:N	2.32	0.63
23:3:521:PRO:HA	23:3:544:ILE:HG22	1.81	0.63
32:R:67:ILE:HD13	32:R:67:ILE:N	2.13	0.63
1:A:155:LYS:NZ	1:A:624:GLY:O	2.29	0.63
3:C:259:LYS:HE2	3:C:262:ARG:HD3	1.79	0.63
13:F:26:U:C3'	13:F:27:A:H5"	2.29	0.63
13:F:40:U:H2'	13:F:41:A:H8	1.61	0.63
32:R:418:GLN:O	37:Z:606:ALA:HB2	1.97	0.63
1:A:768:ASP:HB2	1:A:771:VAL:HG12	1.79	0.62
3:C:250:ARG:NE	3:C:451:HIS:NE2	2.47	0.62
5:E:265:ARG:H	5:E:272:ARG:HH21	1.47	0.62
15:H:179:C:C2	15:H:180:G:N7	2.67	0.62
32:R:250:LYS:HD3	32:R:251:ILE:N	2.13	0.62
34:V:549:LYS:O	34:V:552:ALA:N	2.32	0.62
37:Z:566:TYR:HB2	37:Z:581:GLY:O	1.98	0.62
1:A:1085:ILE:HG12	1:A:1099:PHE:CE1	2.34	0.62
5:E:251:LEU:HG	5:E:291:CYS:SG	2.39	0.62
1:A:203:VAL:HG21	1:A:237:THR:HG22	1.81	0.62
1:A:312:TYR:CE1	3:C:882:GLY:O	2.52	0.62
1:A:312:TYR:CE1	3:C:882:GLY:HA3	2.28	0.62
3:C:79:THR:HG23	33:T:199:VAL:HB	0.68	0.62
21:1:1010:THR:OG1	21:1:1011:PRO:HD3	1.98	0.62
1:A:395:THR:HG23	3:C:383:GLN:HE22	1.58	0.62
1:A:417:ARG:NH1	2:B:58:U:H5"	2.14	0.62
1:A:755:HIS:ND1	31:P:223:PHE:CD2	2.60	0.62
1:A:1301:ILE:HD11	1:A:1306:LYS:CE	2.25	0.62
3:C:360:ALA:N	3:C:361:PRO:HD3	2.14	0.62
21:1:1257:PRO:HG3	22:2:482:ALA:HB2	1.81	0.62
23:3:553:GLN:NE2	23:3:565:TYR:OH	2.31	0.62
37:Z:566:TYR:CD2	37:Z:584:TRP:CE3	2.88	0.62
1:A:386:PRO:CD	3:C:372:PHE:HE1	2.07	0.62
3:C:132:VAL:HG11	3:C:434:CYS:SG	2.39	0.62
23:3:27:GLN:OE1	23:3:42:ARG:NH1	2.32	0.62
23:3:380:GLU:O	23:3:383:ASP:N	2.32	0.62
32:R:250:LYS:HA	32:R:250:LYS:HE3	1.81	0.62
33:T:185:MET:HB3	33:T:186:PRO:HD3	1.81	0.62
1:A:755:HIS:HE1	31:P:223:PHE:CG	2.11	0.62
3:C:259:LYS:HG2	3:C:262:ARG:HD2	1.81	0.62
15:H:182:U:H2'	15:H:183:G:C8	2.34	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:273:ARG:O	23:3:386:PHE:HA	2.00	0.62
1:A:361:HIS:CD2	3:C:279:ARG:NH1	2.68	0.62
1:A:393:LEU:HD11	3:C:378:TYR:HB2	1.81	0.62
1:A:414:ARG:HD3	3:C:410:LEU:O	1.99	0.62
1:A:800:TYR:CG	3:C:59:LEU:HD13	2.34	0.62
1:A:2105:ILE:HD13	1:A:2266:ARG:HH22	1.64	0.62
5:E:119:THR:HG21	5:E:161:ARG:HB3	1.72	0.62
23:3:440:HIS:CD2	23:3:733:PRO:CD	2.82	0.62
23:3:567:GLU:OE2	23:3:601:ARG:NE	2.29	0.62
31:P:211:VAL:HG13	33:T:457:GLY:HA3	0.75	0.62
33:T:356:LEU:N	33:T:356:LEU:HD12	2.15	0.62
1:A:282:LEU:C	1:A:282:LEU:HD23	2.20	0.62
5:E:146:ARG:CZ	5:E:148:LYS:HE3	2.27	0.62
21:1:847:ALA:O	21:1:851:SER:HB3	1.99	0.62
23:3:440:HIS:CE1	23:3:720:TRP:CH2	2.87	0.62
37:Z:600:ARG:HH11	37:Z:600:ARG:CG	2.13	0.62
1:A:155:LYS:HD2	1:A:626:GLY:O	2.00	0.62
1:A:303:ILE:HG21	3:C:933:PHE:CE1	2.34	0.62
1:A:344:ASP:OD1	1:A:347:LEU:HD12	2.00	0.62
1:A:762:ARG:NH2	31:P:226:LYS:HZ1	1.79	0.62
1:A:2328:ALA:HB3	4:D:788:GLY:CA	2.30	0.62
15:H:154:C:H2'	15:H:155:C:H6	1.63	0.62
15:H:161:U:H6	15:H:161:U:O5'	1.83	0.62
21:1:664:GLY:HA2	21:1:667:ILE:HD12	1.80	0.62
21:1:696:ASP:OD1	21:1:697:GLU:N	2.33	0.62
21:1:1052:ALA:HA	21:1:1055:TRP:HD1	1.64	0.62
22:2:612:GLU:O	22:2:615:ILE:N	2.33	0.62
23:3:642:ILE:O	23:3:703:ARG:NH2	2.32	0.62
28:J:406:PHE:CE2	28:J:411:MET:CE	2.83	0.62
37:Z:573:PRO:HD2	37:Z:573:PRO:O	1.99	0.62
1:A:141:ILE:HG12	1:A:426:LEU:CD2	2.30	0.62
3:C:230:ASP:OD1	3:C:259:LYS:HB3	2.00	0.62
4:D:754:GLU:CB	23:3:662:PHE:CE1	2.83	0.62
25:5:53:THR:OG1	25:5:56:THR:OG1	2.14	0.62
1:A:256:TYR:CD1	3:C:888:ARG:CZ	2.83	0.61
1:A:329:LEU:CD1	3:C:173:THR:HG23	2.30	0.61
1:A:835:ASP:OD1	1:A:836:THR:N	2.32	0.61
5:E:277:PHE:HE2	5:E:300:ILE:HD12	1.63	0.61
23:3:811:THR:OG1	23:3:884:GLN:OE1	2.14	0.61
23:3:1004:ASP:OD1	23:3:1005:VAL:N	2.33	0.61
31:P:194:PHE:O	31:P:196:ASN:N	4.26	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:LEU:CD2	1:A:455:VAL:HG22	2.30	0.61
1:A:2068:SER:HB2	1:A:2072:GLU:HB2	1.81	0.61
3:C:141:GLY:C	3:C:258:ASN:ND2	2.53	0.61
13:F:24:A:C2	13:F:26:U:C2	2.88	0.61
14:G:13:C:H2'	14:G:14:A:C8	2.36	0.61
23:3:786:ARG:NH1	23:3:802:THR:O	2.33	0.61
28:J:262:ARG:HD3	29:L:220:PRO:HG2	1.82	0.61
37:Z:597:ARG:HH12	37:Z:601:LEU:HD12	1.66	0.61
1:A:783:TYR:HB2	31:P:228:ILE:CG1	2.26	0.61
13:F:38:G:P	13:F:38:G:C8	2.94	0.61
21:1:866:LYS:HG3	21:1:909:VAL:HG11	1.82	0.61
23:3:317:THR:HA	23:3:322:VAL:HA	1.81	0.61
1:A:203:VAL:CG2	1:A:237:THR:HB	2.30	0.61
1:A:630:TRP:O	1:A:631:ALA:C	2.37	0.61
1:A:1900:GLU:HG2	37:Z:521:PRO:HG3	1.82	0.61
14:G:146:C:H1'	15:H:33:G:N2	2.15	0.61
15:H:165:A:H8	15:H:165:A:O5'	1.84	0.61
32:R:55:LEU:O	32:R:73:PRO:O	2.19	0.61
35:X:343:ARG:HB3	35:X:378:GLU:HG3	1.83	0.61
37:Z:566:TYR:CD1	37:Z:567:SER:N	2.69	0.61
1:A:2106:LEU:HD12	1:A:2107:PRO:HD2	1.83	0.61
3:C:679:PRO:HD3	3:C:811:THR:OG1	1.99	0.61
3:C:750:LEU:C	3:C:750:LEU:HD12	2.21	0.61
15:H:56:A:H61	22:2:505:CYS:HA	1.66	0.61
15:H:68:G:H2'	15:H:69:U:C6	2.35	0.61
21:1:648:LEU:O	21:1:651:VAL:N	2.33	0.61
23:3:288:VAL:HG23	23:3:289:CYS:H	1.65	0.61
23:3:994:GLN:NE2	23:3:1036:ALA:O	2.33	0.61
33:T:327:SER:O	33:T:357:TRP:CH2	2.53	0.61
1:A:158:ARG:HH12	1:A:573:GLN:HE21	1.48	0.61
1:A:530:LEU:H	30:M:198:GLN:CD	1.96	0.61
3:C:64:LYS:HZ2	31:P:206:LYS:HG3	1.63	0.61
3:C:97:VAL:HG13	31:P:47:THR:OG1	2.00	0.61
3:C:140:HIS:CG	3:C:230:ASP:H	2.18	0.61
3:C:809:ILE:HB	3:C:810:PRO:HD3	1.82	0.61
23:3:1191:LYS:NZ	23:3:1195:GLU:OE2	2.33	0.61
1:A:349:ALA:HB1	1:A:399:ALA:HB2	1.78	0.61
2:B:43:U:H3	14:G:-4:A:H2	1.45	0.61
3:C:471:ASP:N	3:C:499:GLY:HA2	2.15	0.61
3:C:495:ARG:HD2	3:C:497:LEU:HD23	1.81	0.61
21:1:720:GLY:N	23:3:216:GLY:O	2.29	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:185:GLY:O	32:R:186:VAL:HG22	2.00	0.61
33:T:339:GLN:NE2	33:T:342:GLU:O	2.34	0.61
33:T:355:ARG:C	33:T:356:LEU:HD12	2.21	0.61
34:V:537:HIS:HA	34:V:578:SER:CB	2.31	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CD1	2.88	0.61
1:A:283:VAL:HG13	1:A:284:ARG:H	1.64	0.61
1:A:1286:ASP:OD1	1:A:1354:ARG:NH2	2.33	0.61
3:C:151:GLU:OE1	3:C:417:ARG:NH1	2.34	0.61
3:C:470:PRO:HA	3:C:499:GLY:CA	2.29	0.61
3:C:675:PHE:HD1	3:C:675:PHE:H	1.47	0.61
14:G:8:C:H2'	14:G:9:C:C6	2.35	0.61
15:H:106:G:N2	15:H:107:A:C6	2.67	0.61
15:H:142:C:C2'	15:H:143:A:H5'	2.30	0.61
15:H:157:G:H5"	15:H:157:G:H8	1.65	0.61
28:J:408:ASP:OD1	28:J:442:ARG:HG2	2.01	0.61
3:C:478:THR:OG1	3:C:563:ALA:O	2.14	0.61
3:C:705:VAL:HG22	3:C:705:VAL:O	2.00	0.61
15:H:153:A:N6	15:H:177:A:H2	1.98	0.61
23:3:452:LEU:HB3	23:3:478:PHE:HE1	1.66	0.61
29:L:74:LEU:HD23	29:L:77:LEU:HD12	1.83	0.61
36:Y:87:GLN:O	36:Y:90:THR:N	2.33	0.61
1:A:73:HIS:CD2	1:A:81:PHE:CG	2.89	0.61
1:A:402:ILE:CG1	3:C:385:VAL:HG21	2.25	0.61
5:E:108:HIS:CE1	5:E:128:SER:HB2	2.35	0.61
13:F:6:C:OP2	13:F:6:C:H4'	1.99	0.61
21:1:1203:GLY:O	23:3:1171:LYS:NZ	2.34	0.61
23:3:226:GLU:HG3	23:3:261:PHE:HZ	1.65	0.61
24:4:71:ILE:HD11	24:4:88:LYS:HB3	1.83	0.61
33:T:349:SER:OG	33:T:351:ASP:OD1	2.18	0.61
1:A:122:ILE:N	1:A:481:PHE:O	2.34	0.60
1:A:1405:LEU:HA	32:R:415:LEU:HD21	1.78	0.60
3:C:133:THR:O	3:C:226:VAL:HB	2.01	0.60
3:C:135:CYS:O	3:C:228:PHE:N	2.28	0.60
3:C:449:ILE:HD11	3:C:466:SER:CA	2.31	0.60
3:C:710:ASN:O	3:C:713:LYS:N	2.31	0.60
15:H:143:A:H2'	15:H:144:C:C6	2.35	0.60
21:1:1293:ASN:HB3	27:7:76:CYS:HB3	1.83	0.60
28:J:406:PHE:CG	28:J:411:MET:HE3	2.36	0.60
37:Z:524:ARG:NE	37:Z:524:ARG:O	2.34	0.60
1:A:121:HIS:CE1	1:A:481:PHE:CB	2.68	0.60
1:A:800:TYR:CD2	3:C:59:LEU:HD13	2.36	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1457:HIS:CE1	1:A:1459:ARG:CB	2.83	0.60
13:F:26:U:O2'	13:F:27:A:OP1	2.18	0.60
21:1:918:VAL:HG12	21:1:961:VAL:HG21	1.83	0.60
23:3:505:THR:HG21	23:3:508:CYS:SG	2.40	0.60
28:J:338:GLU:O	32:R:116:TYR:CD1	2.54	0.60
37:Z:491:ASP:O	37:Z:495:ALA:CB	2.48	0.60
1:A:151:MET:SD	1:A:628:GLY:C	2.80	0.60
1:A:387:PHE:CZ	3:C:330:THR:HB	2.35	0.60
28:J:291:GLN:OE1	29:L:230:GLU:HG3	2.01	0.60
33:T:339:GLN:HG2	33:T:340:ALA:N	2.16	0.60
37:Z:491:ASP:O	37:Z:495:ALA:HB2	2.01	0.60
1:A:82:ARG:HB3	1:A:83:HIS:ND1	2.17	0.60
1:A:301:LYS:HG2	3:C:940:ARG:CA	2.31	0.60
14:G:13:C:H2'	14:G:14:A:H8	1.66	0.60
23:3:441:GLY:O	23:3:775:ASN:HB2	2.00	0.60
24:4:31:GLU:O	24:4:35:GLN:HG2	2.02	0.60
33:T:292:TYR:CE2	33:T:308:ARG:HG3	2.36	0.60
1:A:351:TYR:HA	3:C:270:PRO:HG3	1.84	0.60
1:A:461:HIS:CD2	2:B:26:A:N6	2.68	0.60
1:A:664:HIS:HE1	1:A:668:VAL:CG2	2.04	0.60
1:A:1827:TRP:HH2	1:A:1837:ALA:HB2	1.67	0.60
1:A:2073:TRP:CZ3	1:A:2310:ARG:HG2	2.36	0.60
5:E:178:LEU:HD21	5:E:208:ILE:HD13	1.82	0.60
23:3:833:GLU:HA	23:3:834:LEU:HB2	1.84	0.60
29:L:233:GLN:OE1	29:L:233:GLN:HA	2.01	0.60
32:R:171:LEU:CD1	32:R:201:GLU:CD	2.70	0.60
1:A:392:PRO:O	3:C:379:LYS:HG2	2.01	0.60
1:A:1447:VAL:HG11	1:A:1449:LYS:HE2	1.82	0.60
3:C:86:THR:HG22	33:T:238:LEU:O	2.01	0.60
3:C:452:THR:HG22	3:C:577:PHE:CG	2.37	0.60
3:C:706:GLN:NE2	3:C:708:THR:OG1	2.35	0.60
34:V:483:GLU:O	34:V:486:THR:CB	2.49	0.60
1:A:344:ASP:OD1	1:A:347:LEU:CD1	2.49	0.60
1:A:924:GLN:HE22	1:A:1439:ARG:CZ	2.14	0.60
3:C:221:ILE:HD11	3:C:479:THR:HG1	1.65	0.60
23:3:898:ASN:OD1	23:3:899:THR:N	2.34	0.60
1:A:384:VAL:HG12	3:C:331:PHE:HB3	0.71	0.60
1:A:705:LYS:HE2	32:R:251:ILE:HB	1.82	0.60
1:A:960:ASN:ND2	1:A:1225:THR:OG1	2.32	0.60
1:A:2298:LEU:CD1	4:D:1265:GLN:CB	2.79	0.60
3:C:77:VAL:HG21	33:T:196:LEU:HD23	1.83	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:148:CYS:HA	3:C:417:ARG:NH2	2.16	0.60
23:3:325:ILE:O	23:3:375:SER:N	2.35	0.60
33:T:267:ASP:O	33:T:268:LYS:CB	2.47	0.60
33:T:455:GLN:HG2	33:T:456:PRO:HD3	1.83	0.60
1:A:661:GLU:HG3	32:R:210:PRO:CB	2.32	0.60
3:C:140:HIS:HA	3:C:230:ASP:HB2	1.83	0.60
3:C:567:GLU:OE2	3:C:570:GLY:HA3	2.02	0.60
13:F:7:G:H5'	13:F:7:G:H8	1.66	0.60
13:F:37:C:H41	14:G:5:G:P	2.24	0.60
15:H:83:A:C2	15:H:84:C:C2	2.90	0.60
29:L:77:LEU:HD22	32:R:289:ALA:HA	1.84	0.60
33:T:342:GLU:HB3	33:T:343:PRO:HD3	1.83	0.60
37:Z:563:ARG:HH21	37:Z:563:ARG:CG	2.14	0.60
1:A:1384:ARG:HH21	1:A:1414:ARG:HH12	1.50	0.60
1:A:1426:ASP:OD2	32:R:421:GLY:HA3	2.01	0.60
3:C:79:THR:CG2	33:T:199:VAL:CB	2.37	0.60
3:C:82:GLN:HB2	33:T:231:TRP:CZ3	2.36	0.60
3:C:94:ILE:CD1	31:P:44:ARG:NH2	2.65	0.60
3:C:443:VAL:O	3:C:447:PRO:HD3	2.02	0.60
3:C:678:THR:CG2	3:C:683:ASN:CB	2.79	0.60
21:1:862:GLU:OE1	21:1:904:THR:OG1	2.19	0.60
23:3:457:ASN:ND2	23:3:478:PHE:O	2.35	0.60
32:R:106:GLN:HG2	32:R:110:LYS:CE	2.28	0.60
33:T:185:MET:SD	33:T:442:ARG:NH1	2.71	0.60
23:3:968:ARG:HD3	23:3:979:ARG:HD3	1.84	0.59
1:A:329:LEU:HD13	3:C:173:THR:HG23	1.82	0.59
3:C:73:TYR:CD2	33:T:199:VAL:HG21	2.36	0.59
3:C:73:TYR:CZ	33:T:487:LYS:HE3	2.37	0.59
3:C:669:THR:HG22	3:C:690:GLU:HB3	1.84	0.59
28:J:406:PHE:CE2	28:J:411:MET:HE3	2.36	0.59
31:P:72:ARG:HB2	31:P:72:ARG:HH11	1.66	0.59
33:T:455:GLN:HG2	33:T:456:PRO:CD	2.32	0.59
1:A:718:ARG:HE	32:R:259:LYS:HE3	1.67	0.59
3:C:186:VAL:HG22	3:C:535:ALA:HA	1.85	0.59
23:3:883:GLU:HG3	23:3:884:GLN:H	1.66	0.59
32:R:104:GLN:NE2	32:R:105:GLY:N	2.50	0.59
37:Z:574:ASN:O	37:Z:575:ARG:C	2.40	0.59
5:E:233:GLY:O	5:E:260:ARG:NH2	2.35	0.59
14:G:22:C:O2'	14:G:23:U:P	2.60	0.59
28:J:493:ALA:HB1	28:J:499:ARG:CB	2.32	0.59
32:R:124:VAL:HG22	32:R:125:MET:N	2.16	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:420:LYS:HA	32:R:420:LYS:CE	2.12	0.59
1:A:398:THR:HG23	3:C:382:ALA:CB	2.32	0.59
1:A:944:ASP:OD2	1:A:1435:GLY:N	2.34	0.59
1:A:1262:LYS:CG	32:R:431:ASP:CB	2.69	0.59
1:A:1405:LEU:HA	32:R:415:LEU:HD22	1.84	0.59
1:A:1962:THR:O	37:Z:524:ARG:HG3	2.02	0.59
3:C:298:LEU:HD13	3:C:298:LEU:N	2.18	0.59
15:H:56:A:H2'	15:H:57:A:C8	2.38	0.59
23:3:895:ARG:NH2	23:3:901:GLU:OE1	2.34	0.59
23:3:1040:ASP:OD1	23:3:1043:THR:N	2.35	0.59
34:V:514:PHE:O	34:V:521:TYR:CB	2.51	0.59
1:A:181:ASN:N	1:A:181:ASN:OD1	2.35	0.59
1:A:435:CYS:HB2	3:C:892:GLN:CD	2.22	0.59
1:A:692:ASP:O	1:A:696:MET:CB	2.50	0.59
1:A:942:PRO:HB2	1:A:1438:VAL:HG12	1.84	0.59
1:A:1076:ASP:OD1	1:A:1077:ILE:N	2.35	0.59
1:A:1363:GLN:HG2	1:A:1364:LEU:H	1.66	0.59
3:C:66:TYR:HE2	31:P:211:VAL:HG11	1.67	0.59
3:C:91:GLU:OE1	3:C:91:GLU:HA	2.01	0.59
3:C:145:PHE:CB	3:C:312:SER:CB	2.65	0.59
13:F:36:A:C5'	13:F:36:A:C8	2.85	0.59
15:H:112:G:H2'	15:H:113:G:H8	1.65	0.59
21:1:936:VAL:O	21:1:940:LEU:HB2	2.03	0.59
21:1:1125:PRO:HA	21:1:1128:VAL:HG22	1.84	0.59
23:3:740:GLU:HB2	23:3:757:ILE:HD12	1.83	0.59
33:T:345:ILE:HB	33:T:357:TRP:HB2	1.85	0.59
1:A:86:ARG:HG3	1:A:87:VAL:N	2.17	0.59
1:A:132:ILE:HD13	2:B:57:G:OP1	2.02	0.59
1:A:367:SER:HB3	3:C:299:ILE:HD12	1.85	0.59
1:A:1405:LEU:CB	32:R:415:LEU:HD22	2.33	0.59
1:A:2095:ASP:OD2	1:A:2258:ARG:NE	2.36	0.59
3:C:149:LEU:CD1	3:C:427:PHE:CB	2.80	0.59
23:3:224:TYR:HB3	23:3:261:PHE:HE2	1.66	0.59
23:3:1015:LYS:HE2	23:3:1065:GLU:HG2	1.85	0.59
28:J:225:LEU:CD2	29:L:211:ASN:HB2	2.20	0.59
32:R:90:VAL:CG1	32:R:94:GLY:O	2.50	0.59
32:R:110:LYS:HD2	32:R:110:LYS:C	2.23	0.59
36:Y:88:ARG:HH11	37:Z:576:PHE:HB3	1.68	0.59
1:A:44:ARG:CG	1:A:45:TYR:CD2	2.85	0.59
1:A:417:ARG:NH1	2:B:58:U:C4'	2.65	0.59
1:A:569:VAL:O	1:A:570:ASP:CB	2.50	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:GLN:NE2	1:A:890:ALA:O	2.19	0.59
3:C:227:LEU:O	3:C:255:VAL:HA	2.03	0.59
23:3:613:THR:HG22	23:3:632:ALA:HA	1.84	0.59
23:3:784:THR:HB	23:3:786:ARG:HH12	1.67	0.59
23:3:1027:ASP:OD1	23:3:1028:THR:N	2.35	0.59
26:6:56:GLY:O	26:6:65:GLY:N	2.21	0.59
32:R:420:LYS:HG2	32:R:423:ASP:OD1	2.02	0.59
32:R:421:GLY:O	32:R:423:ASP:N	2.35	0.59
1:A:122:ILE:HD13	1:A:483:GLN:CG	2.32	0.59
1:A:303:ILE:HG21	3:C:933:PHE:CD1	2.38	0.59
2:B:44:A:C2	14:G:-5:G:C6	2.89	0.59
3:C:137:HIS:CD2	3:C:236:MET:HB3	2.35	0.59
3:C:497:LEU:HD11	3:C:577:PHE:CZ	2.32	0.59
21:1:1223:SER:HB2	21:1:1226:VAL:HG12	1.83	0.59
3:C:145:PHE:CE1	3:C:427:PHE:CE1	2.91	0.59
3:C:465:MET:CE	3:C:475:MET:CG	2.70	0.59
3:C:736:GLY:HA2	3:C:770:PHE:CE2	2.38	0.59
13:F:45:A:H1'	13:F:73:A:C2	2.38	0.59
21:1:522:LYS:HD3	21:1:526:PHE:CZ	2.38	0.59
23:3:22:PHE:HD2	23:3:29:GLU:HB2	1.68	0.59
23:3:587:VAL:HG11	23:3:590:MET:HG3	1.85	0.59
28:J:259:GLN:HE22	29:L:220:PRO:CG	2.15	0.59
32:R:125:MET:CE	32:R:131:ASP:OD1	2.51	0.59
32:R:148:ARG:HG3	32:R:148:ARG:HH11	1.68	0.59
1:A:44:ARG:HG3	1:A:45:TYR:CD2	2.37	0.58
1:A:480:LYS:CD	32:R:203:GLN:OE1	2.50	0.58
1:A:723:ASN:HB2	1:A:785:LYS:HG2	1.83	0.58
1:A:1370:ARG:HH11	34:V:467:LEU:C	2.06	0.58
3:C:69:ALA:CA	33:T:456:PRO:HG3	2.28	0.58
3:C:359:LYS:HE3	3:C:359:LYS:O	2.02	0.58
13:F:35:A:O2'	13:F:36:A:OP1	2.21	0.58
21:1:1278:ASP:OD2	23:3:112:CYS:N	2.36	0.58
22:2:648:LEU:HD11	22:2:650:ILE:HG13	1.85	0.58
23:3:336:ALA:HA	23:3:351:SER:HA	1.85	0.58
23:3:463:ARG:HB2	23:3:510:LEU:HD22	1.85	0.58
28:J:339:TRP:CG	32:R:116:TYR:HD2	2.21	0.58
33:T:185:MET:SD	33:T:442:ARG:NH2	2.75	0.58
36:Y:52:ILE:HA	36:Y:55:VAL:HG22	1.84	0.58
1:A:695:ASP:CG	33:T:374:SER:OG	2.41	0.58
1:A:2073:TRP:CD1	1:A:2074:ARG:N	2.71	0.58
1:A:2073:TRP:HD1	1:A:2074:ARG:HD2	1.67	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2268:LEU:HD22	4:D:1261:PRO:O	1.96	0.58
3:C:78:GLU:CD	33:T:198:ARG:HE	2.07	0.58
3:C:474:LEU:HD11	3:C:501:ILE:HG12	1.85	0.58
21:1:982:LEU:HD11	21:1:997:LEU:HD11	1.83	0.58
21:1:1147:VAL:O	21:1:1150:SER:OG	2.17	0.58
23:3:417:ASN:OD1	23:3:418:GLU:N	2.36	0.58
23:3:673:VAL:HG12	23:3:690:ARG:HA	1.84	0.58
23:3:797:LEU:HG	23:3:871:PRO:HG3	1.85	0.58
23:3:903:TRP:HB3	23:3:930:LEU:HD23	1.84	0.58
32:R:433:ILE:CD1	32:R:435:ASN:ND2	2.67	0.58
36:Y:86:ASP:CB	37:Z:502:ALA:HB3	2.33	0.58
1:A:32:GLU:OE2	1:A:36:LYS:HE3	2.03	0.58
1:A:305:ARG:HD3	3:C:933:PHE:CE1	2.38	0.58
1:A:316:PHE:HE1	3:C:635:LEU:HA	1.67	0.58
3:C:133:THR:O	3:C:226:VAL:CA	2.51	0.58
5:E:87:ASP:O	5:E:88:ARG:HG3	2.04	0.58
21:1:773:LEU:HD21	21:1:792:VAL:HG22	1.84	0.58
23:3:304:GLN:NE2	23:3:335:VAL:HA	2.18	0.58
23:3:638:GLU:H	23:3:669:LEU:HA	1.68	0.58
31:P:210:PHE:HD2	33:T:455:GLN:CD	2.05	0.58
32:R:233:HIS:CD2	32:R:233:HIS:H	2.22	0.58
34:V:497:CYS:CB	34:V:507:PHE:CB	2.81	0.58
1:A:480:LYS:CE	32:R:203:GLN:OE1	2.50	0.58
1:A:657:ALA:HA	32:R:210:PRO:HG2	1.84	0.58
1:A:1180:LYS:HA	1:A:1201:ARG:NH1	2.18	0.58
3:C:679:PRO:HD2	3:C:807:GLN:CB	2.10	0.58
23:3:440:HIS:O	23:3:718:ARG:NH2	2.36	0.58
28:J:338:GLU:O	32:R:116:TYR:CG	2.57	0.58
1:A:388:LEU:HD11	3:C:399:LEU:CG	2.31	0.58
1:A:1367:ASN:OD1	1:A:1368:LEU:N	2.37	0.58
1:A:1900:GLU:OE1	37:Z:522:LEU:HB3	2.00	0.58
3:C:750:LEU:O	3:C:750:LEU:HD12	2.03	0.58
5:E:263:ASP:HB3	5:E:274:VAL:HG21	1.84	0.58
37:Z:566:TYR:CD2	37:Z:584:TRP:HE3	2.20	0.58
1:A:60:ASP:OD1	1:A:60:ASP:N	2.36	0.58
1:A:229:GLN:HA	1:A:415:SER:HA	1.85	0.58
1:A:357:ASN:HB2	3:C:863:ILE:O	2.04	0.58
1:A:1863:VAL:HG11	1:A:1868:MET:HB2	1.84	0.58
1:A:2310:ARG:NH1	1:A:2314:PHE:HE1	2.02	0.58
5:E:87:ASP:O	5:E:88:ARG:CB	2.51	0.58
23:3:224:TYR:HB3	23:3:261:PHE:CE2	2.39	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:4:18:GLY:H	24:4:85:ARG:HB2	1.67	0.58
31:P:35:LEU:HB3	31:P:36:PRO:HD2	1.86	0.58
34:V:609:GLN:O	34:V:612:PHE:N	2.36	0.58
1:A:303:ILE:CG2	3:C:933:PHE:CD1	2.87	0.58
1:A:329:LEU:HB3	3:C:177:ARG:CZ	2.33	0.58
1:A:798:GLY:HA2	32:R:288:PHE:CE2	2.39	0.58
1:A:1962:THR:O	37:Z:524:ARG:HG2	2.03	0.58
1:A:2325:VAL:O	4:D:788:GLY:HA2	2.03	0.58
3:C:509:VAL:O	3:C:510:LEU:HD23	2.04	0.58
15:H:147:G:H2'	15:H:148:C:C6	2.38	0.58
30:M:196:ASP:O	30:M:198:GLN:N	2.36	0.58
1:A:76:MET:SD	1:A:88:TYR:CD2	2.95	0.58
1:A:280:GLU:OE2	1:A:281:PRO:HD2	2.03	0.58
1:A:392:PRO:CA	3:C:379:LYS:HE2	2.32	0.58
1:A:417:ARG:NH2	2:B:58:U:OP1	2.37	0.58
1:A:1757:GLU:OE1	32:R:451:ILE:CG1	2.36	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CG	2.66	0.58
15:H:80:A:C2	15:H:81:G:C5	2.92	0.58
23:3:461:THR:HA	23:3:473:TYR:O	2.03	0.58
25:5:24:ARG:HG2	25:5:59:THR:HG22	1.86	0.58
31:P:188:TRP:C	31:P:190:ASP:N	2.52	0.58
3:C:140:HIS:NE2	3:C:233:GLU:CB	2.67	0.58
14:G:141:C:H2'	14:G:142:U:H6	1.69	0.58
21:1:415:LEU:O	25:5:36:TYR:OH	2.21	0.58
21:1:1109:ARG:NH2	21:1:1142:ASN:HB2	2.19	0.58
21:1:1165:TYR:HE1	22:2:575:PHE:CD1	2.21	0.58
23:3:878:ASP:OD1	23:3:879:LEU:N	2.37	0.58
32:R:124:VAL:HG22	32:R:126:ASN:H	1.68	0.58
37:Z:566:TYR:HE2	37:Z:584:TRP:CZ3	1.92	0.58
1:A:378:PHE:HZ	3:C:335:ASN:CB	2.16	0.58
1:A:593:ARG:HH22	1:A:1551:PHE:CB	2.17	0.58
3:C:573:GLU:N	3:C:573:GLU:OE1	2.37	0.58
23:3:8:LEU:HD23	23:3:774:PHE:HZ	1.68	0.58
23:3:753:GLY:CA	23:3:765:LEU:O	2.51	0.58
32:R:125:MET:HE3	32:R:131:ASP:OD1	2.03	0.58
32:R:171:LEU:HD23	32:R:171:LEU:O	2.03	0.58
1:A:121:HIS:ND1	1:A:481:PHE:O	2.36	0.57
1:A:301:LYS:HG2	3:C:940:ARG:HA	1.85	0.57
3:C:145:PHE:CD1	3:C:312:SER:HB3	2.39	0.57
5:E:165:GLN:HG3	5:E:181:ILE:HD11	1.85	0.57
32:R:189:ASN:HD21	32:R:195:ARG:HH22	1.50	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:415:LEU:C	32:R:417:ASN:H	2.05	0.57
33:T:399:LYS:HG2	33:T:406:ILE:CD1	2.31	0.57
5:E:277:PHE:CE2	5:E:300:ILE:CD1	2.85	0.57
13:F:39:A:N6	14:G:8:C:H42	2.02	0.57
14:G:12:G:N2	14:G:13:C:O4'	2.38	0.57
23:3:440:HIS:CD2	23:3:733:PRO:HD2	2.39	0.57
23:3:781:LEU:HB3	23:3:801:GLU:OE2	2.04	0.57
31:P:188:TRP:O	31:P:189:ASP:C	2.42	0.57
1:A:152:ARG:HH11	1:A:152:ARG:CG	2.16	0.57
1:A:224:THR:CG2	2:B:13:C:OP2	2.52	0.57
1:A:384:VAL:HG13	3:C:332:GLY:H	1.67	0.57
3:C:749:THR:OG1	3:C:752:SER:HB2	2.04	0.57
35:X:285:ARG:NH1	35:X:304:ALA:O	2.35	0.57
1:A:82:ARG:NH1	14:G:16:G:O6	2.37	0.57
1:A:322:ASN:OD1	3:C:655:VAL:N	2.38	0.57
1:A:535:ARG:CZ	1:A:535:ARG:HB3	2.33	0.57
1:A:800:TYR:HB3	3:C:59:LEU:CD1	2.34	0.57
3:C:617:LEU:HD11	3:C:629:ILE:HG23	1.87	0.57
23:3:306:GLU:OE2	27:7:63:ARG:HG3	2.03	0.57
23:3:1050:PHE:HB3	23:3:1167:TYR:CE2	2.38	0.57
29:L:73:HIS:O	29:L:77:LEU:HG	2.04	0.57
32:R:171:LEU:HD12	32:R:201:GLU:CD	2.25	0.57
1:A:50:LYS:O	1:A:51:PHE:C	2.43	0.57
1:A:1771:LEU:HD11	1:A:1777:ILE:HG21	1.86	0.57
3:C:79:THR:HG23	33:T:199:VAL:CG1	2.27	0.57
21:1:850:ILE:O	21:1:854:VAL:HG23	2.04	0.57
23:3:791:HIS:CE1	23:3:934:GLY:HA3	2.39	0.57
32:R:55:LEU:CB	32:R:73:PRO:O	2.53	0.57
1:A:785:LYS:CE	31:P:215:LEU:CD1	2.78	0.57
3:C:93:ILE:O	3:C:94:ILE:HB	2.04	0.57
3:C:572:GLU:O	3:C:573:GLU:HB2	2.04	0.57
3:C:669:THR:CG2	3:C:690:GLU:OE1	2.52	0.57
14:G:137:C:N4	15:H:40:C:H42	1.99	0.57
23:3:211:TYR:CE1	23:3:222:ARG:HG2	2.40	0.57
23:3:429:ARG:NH1	27:7:58:ASN:OD1	2.38	0.57
23:3:635:ALA:H	23:3:669:LEU:HD21	1.70	0.57
31:P:73:GLU:O	31:P:76:ARG:HG2	2.04	0.57
31:P:188:TRP:N	31:P:188:TRP:CE3	2.73	0.57
1:A:226:GLN:OE1	1:A:417:ARG:NE	2.31	0.57
1:A:356:ILE:HG22	1:A:357:ASN:N	2.20	0.57
1:A:461:HIS:NE2	2:B:26:A:N6	2.49	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:745:ALA:HB2	33:T:206:TRP:CZ2	2.40	0.57
1:A:783:TYR:CG	31:P:228:ILE:HG12	2.39	0.57
2:B:20:G:O6	2:B:24:G:OP1	2.21	0.57
3:C:140:HIS:HE2	3:C:233:GLU:HG3	1.68	0.57
15:H:166:G:OP2	15:H:166:G:N2	2.27	0.57
29:L:33:ARG:O	29:L:36:SER:OG	2.20	0.57
31:P:31:SER:N	31:P:34:ASP:OD2	2.37	0.57
34:V:483:GLU:O	34:V:486:THR:N	2.33	0.57
1:A:71:ARG:NH1	1:A:177:ASP:OD2	2.32	0.57
1:A:282:LEU:HD23	1:A:282:LEU:O	2.05	0.57
1:A:705:LYS:CG	32:R:251:ILE:HB	2.27	0.57
1:A:1370:ARG:NH1	34:V:467:LEU:CA	2.64	0.57
1:A:2153:THR:HG22	1:A:2154:HIS:H	1.70	0.57
3:C:140:HIS:CE1	3:C:233:GLU:CB	2.83	0.57
3:C:487:GLY:HA3	3:C:489:GLN:OE1	2.05	0.57
3:C:490:PHE:HZ	3:C:612:LYS:HD2	1.69	0.57
3:C:511:GLY:O	3:C:576:ILE:HD12	2.02	0.57
15:H:148:C:O5'	15:H:148:C:H6	1.87	0.57
21:1:1109:ARG:HH22	21:1:1142:ASN:HB2	1.69	0.57
21:1:1258:ALA:HB3	21:1:1261:VAL:HG12	1.86	0.57
23:3:184:CYS:SG	23:3:209:THR:OG1	2.56	0.57
23:3:275:ARG:HE	23:3:386:PHE:HD2	1.51	0.57
32:R:434:TYR:CD2	32:R:435:ASN:N	2.73	0.57
34:V:489:LEU:O	34:V:492:MET:CB	2.53	0.57
1:A:178:TYR:CD2	1:A:491:GLU:HB2	2.40	0.57
1:A:692:ASP:CA	33:T:376:ARG:NH2	2.53	0.57
1:A:705:LYS:CG	32:R:251:ILE:CD1	2.70	0.57
1:A:1757:GLU:HG3	32:R:451:ILE:HG13	1.87	0.57
5:E:310:TYR:CE1	5:E:322:LYS:CD	2.86	0.57
15:H:152:G:N2	15:H:153:A:C5	2.73	0.57
21:1:1098:LEU:HD13	21:1:1135:GLU:HG3	1.85	0.57
21:1:1126:PHE:CE2	22:2:572:HIS:HA	2.39	0.57
28:J:224:LYS:HE2	28:J:255:LEU:HD13	1.85	0.57
37:Z:525:TYR:CD1	37:Z:526:ILE:N	2.73	0.57
1:A:249:LEU:HD22	1:A:254:TYR:HB2	1.86	0.57
1:A:250:VAL:HG23	1:A:337:VAL:CB	2.32	0.57
1:A:299:ILE:HD11	3:C:920:PRO:C	2.25	0.57
1:A:434:HIS:CE1	1:A:435:CYS:SG	2.98	0.57
1:A:570:ASP:OD1	1:A:571:ALA:N	2.38	0.57
1:A:832:TYR:CE2	1:A:834:HIS:HB2	2.40	0.57
3:C:508:LYS:HE3	3:C:566:THR:CG2	2.34	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:807:LYS:HA	21:1:811:LEU:HD12	1.87	0.57
21:1:942:ASN:HD22	21:1:947:VAL:HG11	1.70	0.57
23:3:442:LEU:CD1	23:3:733:PRO:O	2.50	0.57
33:T:347:THR:CG2	33:T:357:TRP:HE1	2.18	0.57
37:Z:611:ALA:O	37:Z:614:TRP:HB3	2.05	0.57
1:A:32:GLU:CG	1:A:36:LYS:HE3	2.35	0.56
1:A:393:LEU:CD1	3:C:375:GLU:O	2.53	0.56
1:A:464:PRO:O	1:A:465:LYS:HB3	2.05	0.56
3:C:261:ASP:OD1	41:C:1500:GTP:C6	2.57	0.56
3:C:456:GLY:C	3:C:457:VAL:HG13	2.25	0.56
28:J:270:ASP:OD2	32:R:222:PRO:CB	2.52	0.56
33:T:306:CYS:SG	33:T:336:VAL:CG1	2.93	0.56
1:A:89:LEU:HD13	1:A:660:PHE:CZ	2.41	0.56
1:A:378:PHE:C	1:A:379:GLU:HG2	2.25	0.56
1:A:385:GLU:HB3	1:A:386:PRO:HD2	1.86	0.56
1:A:790:ARG:NE	1:A:986:GLU:OE2	2.38	0.56
1:A:1233:ASP:OD1	1:A:1234:ASP:N	2.37	0.56
1:A:1252:GLY:HA2	1:A:1298:ARG:HH21	1.69	0.56
13:F:57:U:H2'	13:F:58:G:H8	1.69	0.56
14:G:7:G:H2'	14:G:8:C:C6	2.40	0.56
15:H:78:C:HO2'	15:H:79:G:H5'	1.70	0.56
15:H:141:C:C2	15:H:142:C:C5	2.94	0.56
23:3:327:LEU:O	23:3:373:PHE:HB2	2.05	0.56
23:3:478:PHE:O	23:3:504:PRO:HB3	2.05	0.56
28:J:273:TYR:CG	32:R:228:PRO:CG	2.88	0.56
32:R:409:VAL:O	32:R:410:GLN:HG2	2.05	0.56
37:Z:524:ARG:HB3	37:Z:524:ARG:CZ	2.35	0.56
1:A:296:PHE:CG	3:C:656:ALA:HB2	2.40	0.56
1:A:587:GLN:O	1:A:587:GLN:HG2	2.04	0.56
1:A:593:ARG:HH22	1:A:1551:PHE:HB3	1.71	0.56
1:A:1386:TRP:HZ2	1:A:1417:PRO:HB2	1.69	0.56
1:A:1548:TYR:CD2	1:A:1549:VAL:CG2	2.75	0.56
2:B:40:U:H3'	2:B:40:U:O2	2.05	0.56
3:C:426:GLU:O	3:C:427:PHE:HB2	2.05	0.56
3:C:449:ILE:CG2	3:C:457:VAL:HG11	2.30	0.56
5:E:250:LEU:CD2	5:E:262:TRP:HB2	2.35	0.56
15:H:152:G:N2	15:H:153:A:C8	2.73	0.56
21:1:847:ALA:O	21:1:851:SER:OG	2.24	0.56
22:2:643:PRO:CD	24:4:69:TYR:CG	2.88	0.56
23:3:438:LEU:HA	23:3:775:ASN:O	2.06	0.56
23:3:520:TYR:HB2	23:3:521:PRO:HD2	1.87	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:633:LEU:HD13	23:3:667:ILE:HG21	1.87	0.56
31:P:76:ARG:HG3	31:P:77:ASP:N	2.19	0.56
3:C:223:ASP:OD1	3:C:495:ARG:NH2	2.38	0.56
3:C:457:VAL:HA	3:C:462:GLY:HA3	1.88	0.56
3:C:673:LYS:HG3	3:C:686:THR:CG2	2.36	0.56
3:C:701:GLU:HA	3:C:740:THR:HG1	1.70	0.56
14:G:22:C:O2	14:G:22:C:H2'	2.06	0.56
21:1:944:SER:O	21:1:948:ARG:HG3	2.04	0.56
21:1:1279:ALA:HA	23:3:1167:TYR:CE1	2.41	0.56
24:4:75:ASN:ND2	24:4:86:VAL:O	2.38	0.56
30:M:201:ILE:HA	30:M:220:LEU:HB3	1.85	0.56
1:A:283:VAL:HG22	1:A:284:ARG:HG2	1.88	0.56
1:A:299:ILE:HD11	3:C:921:LEU:N	2.20	0.56
1:A:378:PHE:CZ	3:C:335:ASN:CB	2.89	0.56
1:A:569:VAL:O	1:A:570:ASP:HB2	2.04	0.56
1:A:692:ASP:OD1	33:T:376:ARG:NH2	2.38	0.56
1:A:1163:ARG:NH2	3:C:61:GLU:OE2	2.35	0.56
23:3:550:ASN:HD21	23:3:595:VAL:H	1.53	0.56
27:7:32:LEU:O	27:7:36:HIS:ND1	2.23	0.56
28:J:311:GLN:OE1	28:J:311:GLN:N	2.33	0.56
1:A:226:GLN:HA	1:A:418:THR:OG1	2.06	0.56
1:A:229:GLN:HG2	1:A:415:SER:CB	2.36	0.56
1:A:250:VAL:HG23	1:A:337:VAL:CG1	2.36	0.56
2:B:35:U:H6	2:B:35:U:OP2	1.89	0.56
3:C:301:SER:O	3:C:304:LEU:N	2.30	0.56
3:C:619:THR:C	3:C:620:LYS:HG3	2.25	0.56
13:F:50:A:O2'	13:F:51:U:OP1	2.23	0.56
1:A:402:ILE:HG13	3:C:385:VAL:CG2	2.28	0.56
1:A:579:GLN:NE2	1:A:613:TYR:CE1	2.74	0.56
1:A:812:THR:HG23	1:A:1055:LEU:HD11	1.88	0.56
1:A:2320:LEU:HD23	1:A:2322:GLU:H	1.71	0.56
3:C:140:HIS:CB	3:C:230:ASP:CB	2.66	0.56
24:4:79:LEU:HB2	24:4:84:ILE:HD11	1.88	0.56
1:A:44:ARG:NH2	5:E:285:GLU:O	2.38	0.56
1:A:849:ALA:O	1:A:1449:LYS:NZ	2.36	0.56
3:C:85:ASP:HB3	33:T:238:LEU:CG	2.27	0.56
3:C:677:GLU:HA	3:C:683:ASN:O	2.05	0.56
5:E:277:PHE:CE2	5:E:300:ILE:HD13	2.40	0.56
21:1:1026:ASN:ND2	21:1:1031:VAL:HG11	2.21	0.56
23:3:745:PHE:HE2	23:3:750:CYS:HB3	1.71	0.56
1:A:251:ASP:CA	1:A:337:VAL:HG21	2.36	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1306:LYS:NZ	2:B:38:C:C2'	2.68	0.56
3:C:385:VAL:HG23	3:C:386:GLY:N	2.20	0.56
5:E:153:PHE:HD1	5:E:153:PHE:H	1.54	0.56
15:H:150:U:C2	15:H:151:C:C5	2.94	0.56
21:1:689:ILE:O	21:1:692:HIS:ND1	2.39	0.56
21:1:718:PRO:HA	21:1:756:LEU:HG	1.88	0.56
23:3:669:LEU:HB2	23:3:673:VAL:HG22	1.88	0.56
25:5:93:ASN:OD1	25:5:94:ALA:N	2.34	0.56
28:J:433:ARG:HH12	28:J:461:LYS:CB	2.19	0.56
33:T:342:GLU:CB	33:T:343:PRO:CD	2.83	0.56
37:Z:612:TYR:O	37:Z:613:LYS:C	2.43	0.56
1:A:311:GLU:CB	3:C:885:THR:CG2	2.84	0.56
1:A:395:THR:HG21	3:C:383:GLN:NE2	2.15	0.56
1:A:1451:ASN:OD1	1:A:1453:PHE:N	2.39	0.56
3:C:631:GLY:HA3	3:C:637:LEU:HD21	1.88	0.56
15:H:83:A:N1	15:H:84:C:C4	2.74	0.56
21:1:1293:ASN:HA	27:7:76:CYS:O	2.05	0.56
21:1:1295:TYR:CE2	27:7:28:LYS:HE2	2.41	0.56
23:3:29:GLU:HB3	23:3:40:LEU:HD11	1.87	0.56
23:3:804:HIS:HD2	23:3:862:TRP:CZ2	2.24	0.56
23:3:1028:THR:HG22	23:3:1088:LYS:HD3	1.86	0.56
1:A:251:ASP:CA	1:A:337:VAL:CG2	2.84	0.55
1:A:319:LEU:HD13	3:C:637:LEU:HB3	1.86	0.55
1:A:434:HIS:HB3	3:C:892:GLN:OE1	2.07	0.55
1:A:783:TYR:CD1	31:P:228:ILE:HG12	2.41	0.55
14:G:16:G:H4'	14:G:17:U:O5'	2.04	0.55
15:H:154:C:O2'	15:H:155:C:H5'	2.04	0.55
21:1:570:TYR:HD1	21:1:573:LYS:HD2	1.71	0.55
1:A:89:LEU:O	1:A:89:LEU:HD23	2.06	0.55
1:A:91:ALA:O	1:A:92:LEU:C	2.45	0.55
1:A:387:PHE:HE1	3:C:327:TYR:CA	2.05	0.55
1:A:2113:LYS:CE	4:D:1229:ASP:CA	2.84	0.55
15:H:141:C:H2'	15:H:142:C:H6	1.71	0.55
15:H:149:A:C4	15:H:150:U:C5	2.95	0.55
15:H:180:G:C2	15:H:181:G:C5	2.94	0.55
1:A:530:LEU:CA	30:M:198:GLN:NE2	2.27	0.55
1:A:1321:GLU:O	1:A:1503:TRP:NE1	2.39	0.55
1:A:1418:ARG:HE	1:A:1464:LEU:HD23	1.72	0.55
1:A:2325:VAL:CG1	4:D:788:GLY:O	2.33	0.55
3:C:674:CYS:HG	3:C:822:MET:CE	2.16	0.55
5:E:250:LEU:HD22	5:E:262:TRP:HB2	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1137:ARG:HH21	22:2:524:LEU:HD13	1.72	0.55
31:P:224:MET:HA	31:P:224:MET:HE3	1.88	0.55
1:A:89:LEU:HD13	1:A:660:PHE:HZ	1.71	0.55
1:A:280:GLU:HB2	2:B:48:A:C4'	2.36	0.55
3:C:77:VAL:HG13	33:T:196:LEU:C	1.90	0.55
3:C:706:GLN:NE2	3:C:708:THR:H	2.02	0.55
22:2:650:ILE:HG12	22:2:688:GLY:HA3	1.89	0.55
1:A:151:MET:SD	1:A:628:GLY:O	2.65	0.55
1:A:305:ARG:CG	3:C:878:ILE:CG2	2.85	0.55
1:A:1035:GLN:HA	1:A:1446:GLN:NE2	2.21	0.55
1:A:1690:ASP:OD1	1:A:1691:ASN:N	2.39	0.55
2:B:94:U:H2'	2:B:95:G:H5"	1.89	0.55
3:C:185:PRO:HG3	3:C:482:TYR:CZ	2.41	0.55
3:C:439:PRO:HB2	3:C:443:VAL:HB	1.88	0.55
21:1:1166:ILE:O	21:1:1170:THR:HG23	2.07	0.55
23:3:526:HIS:HB3	23:3:534:ASN:HB2	1.88	0.55
24:4:29:LEU:HD22	24:4:33:PHE:HE2	1.72	0.55
34:V:641:ASP:O	34:V:644:ARG:N	2.39	0.55
37:Z:566:TYR:CD2	37:Z:580:PRO:HG2	2.36	0.55
1:A:356:ILE:HG22	1:A:357:ASN:H	1.72	0.55
1:A:1607:GLU:N	1:A:1632:PHE:O	2.38	0.55
1:A:1930:TYR:O	1:A:1933:PHE:HB3	2.06	0.55
1:A:2073:TRP:HD1	1:A:2074:ARG:N	2.04	0.55
3:C:516:LEU:HD13	3:C:516:LEU:C	2.26	0.55
3:C:702:ASN:O	3:C:703:GLU:HB2	2.07	0.55
5:E:162:ARG:CZ	5:E:203:ASP:O	2.55	0.55
15:H:165:A:H2'	15:H:166:G:H5'	1.88	0.55
23:3:996:ILE:HG23	23:3:999:ARG:H	1.72	0.55
1:A:319:LEU:HB2	3:C:638:ASP:HA	1.89	0.55
1:A:1233:ASP:O	1:A:1236:SER:OG	2.23	0.55
1:A:1899:VAL:HB	1:A:1902:PHE:HD2	1.71	0.55
3:C:78:GLU:OE1	33:T:198:ARG:NE	2.36	0.55
3:C:79:THR:CG2	33:T:199:VAL:CG1	2.84	0.55
3:C:567:GLU:OE1	3:C:572:GLU:HB3	2.06	0.55
5:E:260:ARG:NH1	5:E:276:ILE:HD11	2.22	0.55
14:G:23:U:O2	14:G:23:U:H2'	2.07	0.55
21:1:1255:PHE:CD2	22:2:487:LEU:HD22	2.42	0.55
31:P:33:ARG:HG3	31:P:33:ARG:HH11	1.72	0.55
36:Y:22:VAL:HG22	36:Y:26:VAL:HG13	1.88	0.55
37:Z:600:ARG:HB3	37:Z:600:ARG:NH1	2.08	0.55
1:A:283:VAL:HG13	1:A:284:ARG:N	2.22	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:TYR:CD2	3:C:882:GLY:CA	2.86	0.55
1:A:715:GLU:CD	32:R:258:TRP:CZ3	2.79	0.55
1:A:1099:PHE:HE2	1:A:1153:VAL:HG13	1.72	0.55
1:A:1457:HIS:HE1	1:A:1459:ARG:HG3	1.68	0.55
1:A:1971:LEU:HB2	1:A:1976:TRP:CE2	2.42	0.55
2:B:63:A:O2'	5:E:106:LYS:NZ	2.39	0.55
21:1:1017:LEU:HD13	21:1:1050:VAL:HG21	1.89	0.55
21:1:1076:ALA:O	21:1:1080:THR:HG23	2.07	0.55
23:3:441:GLY:O	23:3:775:ASN:CB	2.55	0.55
32:R:74:LEU:HD23	32:R:75:ASP:OD1	2.06	0.55
32:R:436:VAL:CG2	32:R:437:TYR:CE1	2.89	0.55
36:Y:85:GLU:O	37:Z:502:ALA:CB	2.55	0.55
1:A:151:MET:CE	1:A:628:GLY:C	2.75	0.55
3:C:149:LEU:HA	3:C:427:PHE:CD2	2.41	0.55
5:E:114:GLU:CD	5:E:116:HIS:HE2	2.09	0.55
14:G:142:U:H2'	14:G:143:U:C6	2.42	0.55
15:H:150:U:H2'	15:H:151:C:H6	1.71	0.55
25:5:17:VAL:HG23	25:5:67:ILE:HD11	1.89	0.55
36:Y:37:TRP:HZ3	37:Z:498:GLY:HA3	1.66	0.55
1:A:1457:HIS:HE2	32:R:425:GLY:H	1.46	0.55
1:A:1505:LYS:HE3	37:Z:615:SER:HG	1.68	0.55
1:A:1645:LEU:HB2	1:A:1714:ALA:HB3	1.88	0.55
1:A:2306:HIS:HD2	1:A:2308:VAL:H	1.54	0.55
3:C:220:ARG:HG2	3:C:479:THR:HG21	1.89	0.55
21:1:1174:GLU:OE2	21:1:1210:HIS:NE2	2.35	0.55
23:3:452:LEU:HB3	23:3:478:PHE:CE1	2.42	0.55
29:L:224:PHE:CD1	32:R:86:LEU:O	2.59	0.55
31:P:188:TRP:O	31:P:190:ASP:N	2.39	0.55
32:R:74:LEU:HD23	32:R:74:LEU:C	2.27	0.55
37:Z:574:ASN:O	37:Z:577:ASN:N	2.33	0.55
1:A:311:GLU:HB3	3:C:885:THR:HG21	1.89	0.54
4:D:1048:VAL:O	4:D:1050:GLU:N	2.40	0.54
23:3:309:ASP:HA	23:3:332:THR:HG22	1.88	0.54
23:3:848:PRO:HB2	23:3:851:ILE:HG22	1.89	0.54
24:4:14:THR:CA	24:4:59:VAL:O	2.28	0.54
26:6:39:PRO:HB3	26:6:70:TYR:HB2	1.88	0.54
28:J:294:HIS:HE1	29:L:227:THR:HB	1.70	0.54
31:P:228:ILE:O	31:P:229:LYS:C	2.45	0.54
32:R:86:LEU:HD12	32:R:86:LEU:O	2.06	0.54
1:A:350:PHE:CE2	1:A:398:THR:HG21	2.43	0.54
5:E:119:THR:HG21	5:E:161:ARG:HB2	1.87	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:153:A:C3'	15:H:154:C:C5'	2.86	0.54
21:1:1179:ASP:HB3	22:2:511:LEU:CD1	2.37	0.54
21:1:1279:ALA:HA	23:3:1167:TYR:HE1	1.70	0.54
35:X:312:GLU:O	35:X:327:TYR:HB2	2.07	0.54
1:A:148:TRP:CH2	1:A:616:PHE:HB2	2.42	0.54
1:A:420:ARG:CZ	2:B:56:C:O2'	2.55	0.54
1:A:436:PRO:O	1:A:437:ALA:HB3	2.07	0.54
3:C:140:HIS:CD2	3:C:233:GLU:HG3	2.41	0.54
3:C:510:LEU:HB3	3:C:576:ILE:HD11	1.89	0.54
13:F:36:A:H2'	13:F:37:C:H4'	1.89	0.54
13:F:38:G:H2'	13:F:39:A:C8	2.42	0.54
13:F:56:A:C2	15:H:20:G:C2	2.96	0.54
23:3:553:GLN:HA	23:3:566:PHE:O	2.07	0.54
23:3:1014:TYR:OH	23:3:1019:ASN:OD1	2.24	0.54
28:J:218:GLU:HG3	28:J:219:GLU:OE2	2.07	0.54
1:A:529:THR:HB	30:M:199:PRO:HD3	1.88	0.54
1:A:676:ARG:HG3	13:F:56:A:P	2.48	0.54
3:C:749:THR:HG1	3:C:752:SER:HB2	1.72	0.54
32:R:402:ASN:HB3	35:X:191:GLN:HB2	1.90	0.54
36:Y:10:ILE:HD13	36:Y:98:ASN:HD21	1.73	0.54
1:A:387:PHE:CD1	3:C:327:TYR:CD1	2.95	0.54
1:A:699:GLU:O	1:A:701:ILE:HD12	2.07	0.54
1:A:1306:LYS:HB2	14:G:-6:C:H4'	1.89	0.54
1:A:1459:ARG:HG3	32:R:424:SER:N	2.22	0.54
3:C:145:PHE:CZ	3:C:427:PHE:HE1	2.21	0.54
5:E:161:ARG:NH1	5:E:203:ASP:OD1	2.40	0.54
23:3:913:LEU:HD23	23:3:920:VAL:HG12	1.89	0.54
28:J:262:ARG:HD3	29:L:220:PRO:CG	2.38	0.54
29:L:224:PHE:HD1	32:R:86:LEU:O	1.91	0.54
31:P:63:LEU:HD23	31:P:63:LEU:C	2.28	0.54
33:T:455:GLN:NE2	33:T:456:PRO:HD2	2.22	0.54
1:A:705:LYS:HG2	32:R:251:ILE:CG1	2.38	0.54
1:A:1333:VAL:HG11	1:A:1367:ASN:HD22	1.73	0.54
1:A:2095:ASP:OD1	1:A:2095:ASP:N	2.41	0.54
5:E:108:HIS:ND1	5:E:128:SER:CB	2.70	0.54
5:E:310:TYR:CZ	5:E:322:LYS:HD2	2.42	0.54
23:3:138:GLN:HG2	23:3:161:HIS:CE1	2.43	0.54
23:3:336:ALA:HB2	23:3:349:VAL:HG13	1.90	0.54
32:R:131:ASP:OD2	32:R:132:LEU:HD23	2.07	0.54
1:A:592:TYR:HA	1:A:595:LYS:O	2.08	0.54
1:A:978:GLU:OE2	1:A:1187:PHE:HB2	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1328:LEU:HD22	1:A:1368:LEU:HD21	1.89	0.54
1:A:2325:VAL:O	4:D:788:GLY:CA	2.56	0.54
3:C:259:LYS:CE	3:C:262:ARG:HD2	2.36	0.54
3:C:482:TYR:CD2	3:C:493:PHE:HB2	2.42	0.54
3:C:700:ILE:CG2	3:C:735:PHE:CD2	2.83	0.54
21:1:470:ASP:OD1	21:1:471:ASP:N	2.41	0.54
21:1:624:VAL:O	21:1:628:THR:OG1	2.14	0.54
21:1:632:PHE:HA	21:1:635:VAL:HG22	1.90	0.54
23:3:144:LEU:HB3	23:3:152:LEU:HD11	1.89	0.54
23:3:253:GLU:OE2	23:3:254:ASN:ND2	2.41	0.54
23:3:440:HIS:C	23:3:733:PRO:HG2	2.28	0.54
28:J:408:ASP:OD1	28:J:443:ILE:HG22	2.07	0.54
1:A:119:LEU:HD11	1:A:477:LYS:HG3	1.88	0.54
1:A:173:GLU:O	1:A:520:TYR:CD2	2.61	0.54
3:C:230:ASP:CG	3:C:259:LYS:NZ	2.61	0.54
15:H:183:G:C4	15:H:184:C:C5	2.95	0.54
21:1:331:ALA:O	21:1:335:LYS:N	2.34	0.54
31:P:228:ILE:HD12	31:P:228:ILE:N	2.23	0.54
33:T:356:LEU:N	33:T:356:LEU:CD1	2.70	0.54
37:Z:612:TYR:O	37:Z:615:SER:N	2.29	0.54
1:A:120:TYR:N	1:A:483:GLN:O	2.33	0.54
1:A:122:ILE:HD13	1:A:483:GLN:HG3	1.90	0.54
1:A:254:TYR:O	1:A:434:HIS:HD2	1.91	0.54
1:A:278:LYS:O	1:A:452:LYS:HD2	2.08	0.54
1:A:384:VAL:CG2	3:C:334:ILE:HG23	2.35	0.54
1:A:384:VAL:HG21	3:C:334:ILE:CG1	2.38	0.54
1:A:465:LYS:HG3	1:A:465:LYS:O	2.08	0.54
1:A:1778:TRP:CE2	1:A:1858:PRO:HG3	2.42	0.54
1:A:2067:PHE:CE2	1:A:2069:SER:HA	2.43	0.54
3:C:135:CYS:SG	3:C:227:LEU:HB2	2.47	0.54
21:1:893:ILE:HG13	21:1:928:TYR:CD2	2.43	0.54
22:2:476:GLU:N	22:2:479:ASP:OD2	2.41	0.54
27:7:15:GLN:O	27:7:21:THR:OG1	2.22	0.54
28:J:255:LEU:HD22	29:L:235:LEU:CD1	2.35	0.54
32:R:232:MET:O	32:R:232:MET:HG2	2.07	0.54
1:A:256:TYR:CZ	3:C:888:ARG:CZ	2.91	0.54
1:A:264:PHE:CE1	1:A:455:VAL:CG1	2.75	0.54
1:A:1838:LYS:HG3	1:A:1868:MET:SD	2.49	0.54
1:A:2113:LYS:HE3	4:D:1229:ASP:CA	2.38	0.54
1:A:2325:VAL:HG13	4:D:789:MET:HA	1.88	0.54
3:C:79:THR:HA	33:T:199:VAL:H	1.73	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:137:C:H2'	14:G:138:A:O4'	2.07	0.54
15:H:3:C:H2'	15:H:4:G:H8	1.73	0.54
21:1:826:ASP:OD1	21:1:827:ARG:N	2.39	0.54
21:1:1010:THR:O	21:1:1012:PRO:HD3	2.08	0.54
27:7:60:SER:HG	27:7:63:ARG:H	1.55	0.54
32:R:135:PRO:HD2	33:T:341:ALA:HB1	1.90	0.54
32:R:442:ARG:CD	32:R:443:GLY:CA	2.70	0.54
1:A:335:PRO:HG3	3:C:139:HIS:CB	2.36	0.53
1:A:2117:ILE:O	1:A:2304:PHE:HB2	2.07	0.53
3:C:700:ILE:HA	3:C:705:VAL:HG12	1.89	0.53
3:C:742:PRO:HB2	3:C:786:ASN:H	1.72	0.53
5:E:178:LEU:CD1	5:E:222:LEU:HD22	2.37	0.53
32:R:442:ARG:NH1	32:R:444:GLY:N	2.41	0.53
33:T:287:HIS:CE1	33:T:313:ARG:HG3	2.43	0.53
37:Z:485:GLU:O	37:Z:489:GLU:CB	2.56	0.53
1:A:705:LYS:HG2	32:R:251:ILE:CG2	2.38	0.53
1:A:1403:LEU:O	32:R:412:ASP:HB2	2.08	0.53
1:A:1930:TYR:CD2	1:A:1931:THR:N	2.76	0.53
14:G:135:G:H1	15:H:41:U:H3	1.56	0.53
15:H:84:C:O2	15:H:84:C:H2'	2.09	0.53
23:3:166:LEU:O	23:3:186:GLU:HA	2.08	0.53
33:T:454:VAL:HG12	33:T:455:GLN:N	2.24	0.53
34:V:525:PHE:O	34:V:528:ILE:N	2.41	0.53
1:A:386:PRO:HB3	3:C:372:PHE:CD1	2.43	0.53
1:A:628:GLY:O	1:A:629:PHE:HB2	2.09	0.53
1:A:1118:PRO:CD	1:A:1119:ASP:H	2.19	0.53
1:A:1605:GLU:OE2	1:A:2286:VAL:HG21	2.07	0.53
1:A:1962:THR:CG2	37:Z:524:ARG:CG	2.86	0.53
5:E:87:ASP:O	5:E:88:ARG:HB2	2.07	0.53
13:F:53:A:H2'	13:F:54:G:O4'	2.09	0.53
21:1:626:ASN:ND2	21:1:630:ARG:HH12	2.06	0.53
21:1:1299:GLU:HA	21:1:1302:TYR:CE2	2.44	0.53
33:T:384:HIS:O	33:T:385:TYR:CB	2.55	0.53
35:X:181:PHE:HA	36:Y:50:GLY:H	1.73	0.53
1:A:664:HIS:CE1	1:A:666:LYS:CB	2.85	0.53
3:C:449:ILE:CD1	3:C:466:SER:N	2.71	0.53
21:1:822:ARG:HH11	36:Y:31:GLU:HG2	1.74	0.53
21:1:1077:THR:O	21:1:1080:THR:OG1	2.22	0.53
21:1:1127:THR:HA	22:2:571:LEU:HB3	1.88	0.53
23:3:3:LEU:HD12	23:3:1093:MET:SD	2.48	0.53
28:J:218:GLU:HG3	28:J:219:GLU:N	2.23	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:103:ARG:HH11	32:R:103:ARG:CG	2.21	0.53
1:A:2073:TRP:CH2	1:A:2310:ARG:HG2	2.44	0.53
1:A:2298:LEU:HD13	4:D:1265:GLN:CB	2.39	0.53
3:C:481:MET:SD	3:C:559:ILE:HD11	2.48	0.53
23:3:712:VAL:HG23	23:3:722:SER:HB3	1.91	0.53
1:A:115:ASP:HB3	1:A:486:LYS:HE2	1.91	0.53
1:A:665:SER:HB3	32:R:215:ASN:HB2	1.90	0.53
1:A:881:ILE:HG23	1:A:918:THR:HG23	1.88	0.53
1:A:1457:HIS:HE2	32:R:425:GLY:N	2.04	0.53
1:A:2310:ARG:HH12	1:A:2314:PHE:HE1	1.56	0.53
2:B:18:C:C2'	2:B:19:A:O5'	2.56	0.53
3:C:115:GLU:O	3:C:116:MET:C	2.43	0.53
3:C:220:ARG:O	3:C:448:LYS:HE2	2.08	0.53
3:C:360:ALA:N	3:C:361:PRO:CD	2.71	0.53
15:H:147:G:C2	15:H:148:C:C2	2.97	0.53
15:H:153:A:H3'	15:H:154:C:C5'	2.38	0.53
21:1:1157:TYR:O	26:6:38:ARG:NH2	2.40	0.53
23:3:195:ASP:OD1	23:3:197:THR:OG1	2.23	0.53
23:3:250:ILE:HD13	23:3:259:LYS:HB3	1.91	0.53
23:3:547:CYS:HB3	23:3:556:ILE:HG22	1.90	0.53
23:3:667:ILE:HB	23:3:675:LEU:HB2	1.91	0.53
31:P:41:ILE:HD11	33:T:318:ARG:HB2	1.90	0.53
1:A:393:LEU:HD13	3:C:375:GLU:O	2.08	0.53
1:A:586:GLY:O	1:A:1549:VAL:HG12	2.08	0.53
3:C:449:ILE:HG22	3:C:457:VAL:HG13	1.88	0.53
5:E:108:HIS:ND1	5:E:128:SER:HB2	2.24	0.53
5:E:178:LEU:CD2	5:E:208:ILE:CD1	2.87	0.53
15:H:68:G:C2'	15:H:69:U:H5'	2.37	0.53
23:3:141:VAL:HG11	23:3:213:LEU:HD12	1.89	0.53
23:3:440:HIS:CD2	23:3:733:PRO:CG	2.92	0.53
1:A:203:VAL:HG23	1:A:237:THR:CG2	2.35	0.53
1:A:308:ILE:HG22	1:A:308:ILE:O	2.09	0.53
1:A:384:VAL:HG21	3:C:334:ILE:HG23	1.80	0.53
3:C:82:GLN:CG	33:T:237:LYS:HA	2.38	0.53
15:H:79:G:C2	15:H:80:A:C5	2.97	0.53
21:1:944:SER:HA	21:1:948:ARG:NE	2.23	0.53
28:J:359:VAL:O	28:J:363:ARG:HG2	2.08	0.53
32:R:132:LEU:HB3	33:T:399:LYS:HZ2	1.70	0.53
33:T:318:ARG:HH11	33:T:318:ARG:CG	2.22	0.53
37:Z:571:PRO:HD3	37:Z:579:TRP:CH2	2.43	0.53
1:A:299:ILE:HD11	3:C:920:PRO:O	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:ARG:HH12	2:B:58:U:C5'	2.21	0.53
1:A:1199:LYS:NZ	1:A:1206:GLU:OE2	2.32	0.53
3:C:259:LYS:HG2	3:C:262:ARG:HG3	1.90	0.53
5:E:232:ARG:O	5:E:262:TRP:HH2	1.91	0.53
21:1:516:LEU:O	21:1:520:THR:HG23	2.08	0.53
24:4:47:ASP:HB3	24:4:52:GLN:O	2.08	0.53
1:A:148:TRP:CZ2	1:A:616:PHE:HA	2.44	0.53
1:A:264:PHE:CE1	1:A:459:LEU:CD1	2.81	0.53
1:A:405:LEU:CD1	3:C:265:LEU:HD22	2.39	0.53
1:A:723:ASN:ND2	1:A:788:GLN:OE1	2.41	0.53
1:A:748:ASP:HA	31:P:214:THR:CG2	2.34	0.53
1:A:1275:ARG:HD2	1:A:1375:TRP:CD1	2.44	0.53
1:A:1425:LYS:CG	32:R:417:ASN:OD1	2.56	0.53
1:A:1781:ASP:HB3	1:A:1808:PHE:HB3	1.90	0.53
3:C:250:ARG:NE	3:C:451:HIS:CD2	2.76	0.53
3:C:516:LEU:HB2	3:C:575:GLN:HE22	1.73	0.53
13:F:50:A:H2'	13:F:51:U:C6	2.44	0.53
13:F:56:A:C6	15:H:20:G:C6	2.96	0.53
22:2:614:ARG:HH11	22:2:614:ARG:CG	2.14	0.53
23:3:211:TYR:HE1	23:3:222:ARG:HG2	1.74	0.53
23:3:605:LEU:O	23:3:616:ILE:HA	2.08	0.53
23:3:719:SER:OG	23:3:739:LEU:HD11	2.09	0.53
34:V:530:LYS:O	34:V:532:GLN:N	2.42	0.53
1:A:121:HIS:CD2	1:A:481:PHE:HB3	2.36	0.52
1:A:891:PHE:O	29:L:83:ARG:NH1	2.42	0.52
3:C:671:SER:C	3:C:672:LEU:HD22	2.30	0.52
21:1:599:ASN:O	21:1:603:ALA:CB	2.57	0.52
23:3:519:VAL:HG22	23:3:524:ILE:HG12	1.90	0.52
23:3:639:SER:OG	23:3:701:LEU:N	2.42	0.52
23:3:1148:LEU:O	23:3:1152:HIS:N	2.39	0.52
32:R:95:LYS:HD3	32:R:95:LYS:N	2.25	0.52
1:A:1701:VAL:HA	1:A:1716:GLY:HA3	1.90	0.52
3:C:943:LEU:HD23	3:C:943:LEU:N	2.24	0.52
13:F:48:A:N3	29:L:33:ARG:NH2	2.57	0.52
13:F:94:C:OP1	28:J:351:ASN:CB	2.57	0.52
14:G:153:C:H4'	14:G:154:U:OP1	2.10	0.52
15:H:81:G:C2	15:H:82:G:C5	2.97	0.52
23:3:550:ASN:HB3	23:3:553:GLN:HB2	1.90	0.52
3:C:97:VAL:HG12	31:P:47:THR:OG1	2.10	0.52
13:F:34:G:H2'	13:F:35:A:O5'	2.10	0.52
14:G:-4:A:H2'	14:G:-3:A:C8	2.44	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:148:C:C2'	15:H:149:A:H5'	2.39	0.52
21:1:516:LEU:HD11	21:1:558:ARG:HD3	1.91	0.52
21:1:1090:PRO:HG3	21:1:1123:CYS:HB2	1.91	0.52
23:3:128:ARG:HH21	23:3:180:PRO:HG3	1.73	0.52
23:3:159:GLU:OE2	26:6:14:GLN:HB2	2.09	0.52
23:3:755:VAL:HG22	23:3:764:ILE:HD12	1.89	0.52
31:P:189:ASP:O	31:P:191:ASP:N	2.43	0.52
32:R:233:HIS:H	32:R:233:HIS:HD2	1.56	0.52
33:T:351:ASP:C	33:T:352:THR:HG1	2.11	0.52
1:A:830:LEU:HA	1:A:882:LYS:HZ2	1.74	0.52
1:A:1214:TRP:CE2	1:A:1230:LEU:HD11	2.45	0.52
1:A:1301:ILE:HD13	1:A:1306:LYS:CE	2.35	0.52
5:E:178:LEU:N	5:E:178:LEU:HD23	2.25	0.52
14:G:-12:G:H4'	14:G:-11:G:OP1	2.09	0.52
21:1:1108:ASN:OD1	21:1:1109:ARG:N	2.43	0.52
23:3:114:ARG:NE	23:3:136:GLU:OE1	2.32	0.52
32:R:52:PRO:O	32:R:53:ARG:HB2	2.09	0.52
32:R:81:LYS:HA	32:R:81:LYS:HE3	1.87	0.52
1:A:204:LEU:HD23	1:A:205:ASP:OD1	2.09	0.52
1:A:267:LYS:HZ1	2:B:49:A:P	2.24	0.52
1:A:338:VAL:O	3:C:266:GLU:HG2	2.10	0.52
1:A:384:VAL:HG22	3:C:334:ILE:CG2	2.33	0.52
1:A:387:PHE:CE1	3:C:326:ILE:HG22	2.45	0.52
1:A:664:HIS:NE2	1:A:666:LYS:CG	2.73	0.52
1:A:666:LYS:HB2	1:A:668:VAL:HG23	1.83	0.52
1:A:1275:ARG:NH1	1:A:1378:GLU:OE1	2.43	0.52
3:C:80:ILE:CD1	3:C:80:ILE:N	2.73	0.52
3:C:143:THR:HB	41:C:1500:GTP:O1A	2.09	0.52
3:C:700:ILE:CG2	3:C:741:GLY:O	2.57	0.52
13:F:36:A:C8	13:F:36:A:C4'	2.93	0.52
13:F:57:U:H2'	13:F:58:G:C8	2.45	0.52
21:1:717:THR:HG22	21:1:718:PRO:CD	2.39	0.52
21:1:762:ALA:O	21:1:766:THR:OG1	2.19	0.52
23:3:159:GLU:HB3	23:3:161:HIS:CD2	2.44	0.52
37:Z:524:ARG:HD2	37:Z:525:TYR:HB3	1.92	0.52
1:A:128:PHE:CD1	1:A:473:PHE:CZ	2.98	0.52
1:A:665:SER:OG	1:A:666:LYS:HD3	2.10	0.52
1:A:1113:TYR:C	1:A:1115:THR:H	2.13	0.52
1:A:1631:LEU:HD12	1:A:1660:TYR:HD2	1.74	0.52
1:A:2133:PRO:HD2	1:A:2139:VAL:HG13	1.92	0.52
3:C:78:GLU:O	33:T:198:ARG:C	2.47	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:78:GLU:CG	3:C:80:ILE:CD1	2.54	0.52
3:C:139:HIS:O	3:C:259:LYS:NZ	2.36	0.52
3:C:449:ILE:HD11	3:C:466:SER:HA	1.91	0.52
3:C:508:LYS:HB3	3:C:566:THR:CG2	2.39	0.52
3:C:710:ASN:O	3:C:712:LYS:N	2.42	0.52
21:1:1254:LEU:O	21:1:1262:ARG:HG2	2.09	0.52
23:3:1059:PRO:O	23:3:1062:THR:HG23	2.08	0.52
33:T:267:ASP:O	33:T:268:LYS:CG	2.56	0.52
33:T:351:ASP:C	33:T:352:THR:OG1	2.48	0.52
37:Z:597:ARG:NH1	37:Z:601:LEU:HD13	2.24	0.52
1:A:203:VAL:CG2	1:A:237:THR:CB	2.88	0.52
1:A:433:GLU:OE1	1:A:436:PRO:CB	2.54	0.52
1:A:661:GLU:CG	32:R:210:PRO:CB	2.88	0.52
1:A:1162:PRO:HG3	31:P:194:PHE:CG	2.44	0.52
1:A:1459:ARG:HD2	32:R:422:MET:O	2.09	0.52
2:B:27:U:O2'	2:B:28:A:O5'	2.23	0.52
14:G:11:A:N1	14:G:12:G:C8	2.77	0.52
23:3:285:MET:SD	23:3:305:THR:HB	2.49	0.52
23:3:304:GLN:HE22	23:3:335:VAL:HA	1.73	0.52
24:4:41:ASN:HB2	24:4:60:GLU:HB3	1.92	0.52
33:T:318:ARG:HH11	33:T:319:THR:HG23	1.74	0.52
1:A:47:GLU:OE1	1:A:47:GLU:N	2.35	0.52
3:C:711:ARG:CZ	3:C:730:ARG:O	2.57	0.52
3:C:902:HIS:ND1	3:C:903:HIS:HB2	2.25	0.52
21:1:1289:ASN:HB3	21:1:1295:TYR:H	1.75	0.52
23:3:108:GLY:O	26:6:82:ARG:HD3	2.09	0.52
23:3:232:GLY:HA2	23:3:252:SER:HA	1.90	0.52
24:4:34:LEU:HA	24:4:37:GLY:O	2.10	0.52
32:R:135:PRO:O	32:R:136:ASP:CB	2.58	0.52
1:A:191:ILE:HG23	1:A:572:PHE:CZ	2.44	0.52
1:A:339:PHE:C	1:A:340:ILE:HD13	2.31	0.52
3:C:259:LYS:HG2	3:C:262:ARG:CG	2.39	0.52
3:C:510:LEU:HD22	3:C:514:TYR:HE2	1.75	0.52
21:1:901:GLN:HA	21:1:939:ARG:HH22	1.72	0.52
31:P:193:VAL:HG23	31:P:194:PHE:N	2.25	0.52
33:T:347:THR:O	33:T:354:ILE:HG23	2.10	0.52
1:A:676:ARG:HG3	13:F:55:C:O3'	2.09	0.52
2:B:42:U:H3	14:G:-3:A:N1	1.47	0.52
3:C:449:ILE:CD1	3:C:466:SER:CA	2.88	0.52
3:C:600:LEU:N	3:C:601:PRO:HD2	2.25	0.52
21:1:661:ARG:NH1	21:1:696:ASP:OD2	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:1070:LYS:HB3	21:1:1073:ILE:HD12	1.91	0.52
21:1:1096:THR:HA	21:1:1099:ASN:ND2	2.25	0.52
23:3:259:LYS:HG3	23:3:266:ASP:OD1	2.09	0.52
23:3:1048:ASP:HB3	23:3:1052:ASN:H	1.75	0.52
31:P:189:ASP:OD2	31:P:192:VAL:CG2	2.59	0.52
32:R:70:ALA:O	32:R:71:GLN:C	2.48	0.52
32:R:442:ARG:CD	32:R:443:GLY:C	2.77	0.52
36:Y:69:ARG:NH2	36:Y:74:GLY:O	2.34	0.52
1:A:312:TYR:N	1:A:312:TYR:CD1	2.78	0.51
1:A:941:LYS:HG3	1:A:1071:PHE:CE1	2.46	0.51
1:A:1275:ARG:HD2	1:A:1375:TRP:NE1	2.25	0.51
1:A:1425:LYS:C	1:A:1425:LYS:HD3	2.31	0.51
3:C:64:LYS:NZ	31:P:206:LYS:HG3	2.22	0.51
3:C:89:LEU:O	3:C:91:GLU:N	2.43	0.51
21:1:1256:HIS:ND1	21:1:1261:VAL:HG11	2.24	0.51
23:3:460:TRP:CZ2	23:3:507:SER:HA	2.46	0.51
23:3:476:VAL:HG22	23:3:762:LEU:HD22	1.91	0.51
23:3:1134:SER:HB2	23:3:1136:GLU:OE1	2.09	0.51
31:P:32:SER:O	31:P:35:LEU:HD12	2.09	0.51
1:A:107:PRO:O	1:A:111:GLU:CD	2.48	0.51
1:A:245:LEU:HD22	1:A:430:TRP:CH2	2.44	0.51
1:A:664:HIS:NE2	1:A:666:LYS:CB	2.73	0.51
1:A:672:VAL:HG21	33:T:267:ASP:OD1	2.10	0.51
1:A:805:GLU:CB	31:P:194:PHE:CZ	2.89	0.51
3:C:77:VAL:HG13	33:T:196:LEU:HB3	1.91	0.51
13:F:36:A:H3'	13:F:37:C:C5'	2.26	0.51
21:1:1253:GLY:HA3	21:1:1265:TYR:CG	2.45	0.51
26:6:54:TYR:HA	26:6:57:ARG:HB2	1.92	0.51
29:L:224:PHE:CE1	32:R:86:LEU:HD13	2.44	0.51
33:T:392:PRO:HA	33:T:414:ALA:O	2.09	0.51
1:A:296:PHE:HB3	3:C:656:ALA:HB2	1.92	0.51
1:A:366:LYS:N	1:A:366:LYS:CD	2.73	0.51
1:A:589:THR:OG1	1:A:590:GLY:N	2.44	0.51
1:A:642:ARG:NH2	2:B:56:C:C2	2.78	0.51
1:A:750:TRP:CZ2	1:A:778:ARG:HG2	2.45	0.51
1:A:1179:SER:O	1:A:1182:ASN:N	2.44	0.51
1:A:1784:ASN:ND2	1:A:1897:LEU:HD12	2.22	0.51
3:C:674:CYS:SG	3:C:822:MET:CE	2.99	0.51
13:F:45:A:N1	22:2:554:ARG:NH2	2.53	0.51
21:1:1179:ASP:HB2	21:1:1185:ARG:HD3	1.93	0.51
23:3:331:ASP:OD2	23:3:394:ASN:HB2	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:125:MET:O	32:R:126:ASN:HB3	2.11	0.51
33:T:267:ASP:O	33:T:268:LYS:HB2	2.09	0.51
33:T:454:VAL:CG2	33:T:463:SER:OG	2.58	0.51
1:A:221:ASN:ND2	2:B:12:U:OP1	2.43	0.51
1:A:232:LEU:HB2	1:A:233:PRO:HD3	1.93	0.51
1:A:782:LEU:HB3	31:P:224:MET:SD	2.50	0.51
3:C:300:LEU:HD13	3:C:300:LEU:N	2.25	0.51
3:C:388:VAL:O	3:C:388:VAL:HG22	2.10	0.51
15:H:55:U:H1'	15:H:58:U:H5	1.74	0.51
15:H:107:A:C6	15:H:108:G:C5	2.99	0.51
37:Z:593:PHE:O	37:Z:597:ARG:CB	2.57	0.51
1:A:152:ARG:CG	1:A:152:ARG:NH1	2.73	0.51
1:A:227:ARG:H	1:A:417:ARG:HA	1.75	0.51
1:A:227:ARG:C	1:A:416:GLY:O	2.48	0.51
1:A:1667:ARG:HD2	1:A:1679:TYR:CE2	2.46	0.51
1:A:2147:MET:O	1:A:2274:PRO:HD3	2.10	0.51
3:C:678:THR:HG23	3:C:683:ASN:H	1.75	0.51
5:E:231:MET:SD	5:E:262:TRP:CE3	3.04	0.51
13:F:68:C:N4	31:P:33:ARG:CB	2.45	0.51
21:1:1054:GLU:OE1	21:1:1057:ARG:NH1	2.36	0.51
23:3:854:ALA:HB1	23:3:856:LYS:HD2	1.93	0.51
23:3:1002:VAL:HB	23:3:1010:ILE:HB	1.93	0.51
1:A:1447:VAL:HG12	1:A:1449:LYS:HG2	1.92	0.51
13:F:43:A:O2'	13:F:44:G:H5'	2.11	0.51
21:1:231:ARG:HA	21:1:607:ALA:HB2	1.92	0.51
23:3:264:GLN:HE22	23:3:322:VAL:H	1.58	0.51
23:3:745:PHE:CZ	23:3:747:SER:HB3	2.46	0.51
33:T:318:ARG:HG3	33:T:318:ARG:HH11	1.76	0.51
1:A:349:ALA:HB2	1:A:399:ALA:CB	2.19	0.51
1:A:978:GLU:CD	1:A:1188:ASN:H	2.14	0.51
1:A:1320:LYS:NZ	32:R:434:TYR:CD1	2.77	0.51
1:A:1962:THR:HG23	37:Z:524:ARG:CB	2.28	0.51
1:A:2090:ILE:HA	1:A:2223:CYS:O	2.10	0.51
3:C:220:ARG:O	3:C:448:LYS:CE	2.58	0.51
13:F:34:G:N3	13:F:34:G:C3'	2.72	0.51
13:F:94:C:H5"	28:J:347:HIS:HB3	1.92	0.51
22:2:469:VAL:HG12	22:2:471:ARG:H	1.76	0.51
23:3:113:ARG:HB2	23:3:116:VAL:HB	1.91	0.51
23:3:971:ASP:OD1	23:3:972:LEU:N	2.43	0.51
33:T:459:LEU:HD12	33:T:460:ASP:N	2.25	0.51
36:Y:37:TRP:CH2	37:Z:498:GLY:N	2.74	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:MET:N	1:A:96:PRO:HD2	2.26	0.51
1:A:1629:ILE:HB	1:A:1662:ILE:HB	1.92	0.51
1:A:1923:TRP:HB3	1:A:1927:ILE:HD11	1.93	0.51
1:A:2081:ALA:HB1	4:D:1010:SER:CB	2.40	0.51
3:C:133:THR:O	3:C:226:VAL:O	2.29	0.51
13:F:34:G:N3	13:F:34:G:C5'	2.73	0.51
13:F:35:A:N3	13:F:35:A:C5'	2.73	0.51
23:3:354:GLY:HA3	23:3:432:ARG:HH12	1.76	0.51
24:4:16:TYR:HA	24:4:57:GLY:O	2.10	0.51
24:4:16:TYR:HD1	24:4:58:PHE:CE2	2.28	0.51
28:J:257:GLU:HA	29:L:232:TYR:CE2	2.46	0.51
28:J:273:TYR:CD2	32:R:228:PRO:CG	2.94	0.51
1:A:206:TRP:CD1	1:A:213:LEU:HD21	2.45	0.51
1:A:331:TRP:C	1:A:331:TRP:HE3	2.14	0.51
1:A:744:LYS:HZ1	31:P:212:ASN:C	2.14	0.51
1:A:975:VAL:HB	1:A:1099:PHE:HB2	1.93	0.51
1:A:1373:GLN:HB3	1:A:1378:GLU:OE2	2.11	0.51
1:A:1502:PHE:CZ	1:A:1505:LYS:HB3	2.45	0.51
3:C:131:ASN:ND2	3:C:223:ASP:OD2	2.44	0.51
14:G:11:A:N3	14:G:11:A:C5'	2.73	0.51
14:G:11:A:N1	14:G:12:G:N7	2.59	0.51
21:1:669:GLN:O	21:1:672:ALA:N	2.44	0.51
23:3:246:SER:O	23:3:260:ASN:ND2	2.44	0.51
23:3:404:LEU:HD23	23:3:407:ILE:HD11	1.92	0.51
23:3:520:TYR:CE1	23:3:522:ASP:HB2	2.46	0.51
23:3:896:PHE:HB2	23:3:899:THR:HG22	1.93	0.51
28:J:273:TYR:CD1	32:R:228:PRO:HG2	2.46	0.51
33:T:300:ILE:O	33:T:301:ASP:HB2	2.11	0.51
1:A:331:TRP:CE2	3:C:635:LEU:HD22	2.46	0.51
1:A:748:ASP:OD2	33:T:484:LYS:NZ	2.43	0.51
1:A:823:SER:OG	1:A:933:ARG:NH1	2.44	0.51
1:A:1276:GLU:O	1:A:1279:VAL:HG12	2.11	0.51
3:C:93:ILE:CD1	33:T:230:ILE:CD1	2.89	0.51
15:H:111:G:O3'	15:H:112:G:O4'	2.29	0.51
21:1:475:PHE:CE1	21:1:502:LEU:HB2	2.46	0.51
21:1:582:LEU:HD23	21:1:630:ARG:HB3	1.93	0.51
23:3:556:ILE:HD11	23:3:564:VAL:HB	1.93	0.51
23:3:1144:VAL:O	23:3:1148:LEU:HB2	2.11	0.51
33:T:385:TYR:CE2	33:T:400:PHE:HB3	2.46	0.51
34:V:576:THR:O	34:V:580:ARG:N	2.36	0.51
1:A:1435:GLY:O	1:A:1438:VAL:HG22	2.10	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:215:VAL:HG11	3:C:242:LEU:HD22	1.93	0.50
3:C:559:ILE:C	3:C:559:ILE:HD12	2.31	0.50
23:3:28:GLN:HE22	23:3:343:LYS:HG2	1.77	0.50
23:3:80:VAL:HB	23:3:88:VAL:HG23	1.93	0.50
23:3:110:SER:HB3	26:6:82:ARG:HH12	1.75	0.50
28:J:252:GLU:OE1	28:J:260:ARG:HB3	2.12	0.50
28:J:360:ASP:HA	28:J:363:ARG:HD2	1.91	0.50
32:R:220:ARG:CB	32:R:220:ARG:HH11	2.24	0.50
33:T:233:LEU:HD23	33:T:233:LEU:C	2.32	0.50
1:A:251:ASP:N	1:A:337:VAL:HG21	2.26	0.50
1:A:863:GLU:OE2	1:A:916:LYS:NZ	2.36	0.50
1:A:1757:GLU:CD	32:R:451:ILE:HD11	2.30	0.50
1:A:1930:TYR:HD2	1:A:1931:THR:N	2.09	0.50
1:A:2298:LEU:CD1	4:D:1285:SER:CA	2.89	0.50
3:C:452:THR:O	3:C:578:ARG:N	2.43	0.50
3:C:457:VAL:HG12	3:C:462:GLY:CA	2.41	0.50
3:C:619:THR:O	3:C:620:LYS:HG3	2.11	0.50
5:E:229:TYR:CE2	5:E:272:ARG:NH1	2.77	0.50
15:H:51:A:N6	15:H:63:G:O6	2.44	0.50
23:3:506:LEU:HB3	23:3:547:CYS:SG	2.52	0.50
23:3:669:LEU:HD22	23:3:673:VAL:HG21	1.93	0.50
37:Z:574:ASN:O	37:Z:576:PHE:N	2.44	0.50
1:A:844:GLU:CB	32:R:422:MET:HE2	2.23	0.50
3:C:94:ILE:HG21	33:T:259:PRO:HB3	1.92	0.50
3:C:387:ASP:O	3:C:389:ASP:OD1	2.30	0.50
3:C:659:VAL:HG12	3:C:660:VAL:N	2.26	0.50
14:G:-12:G:O2'	14:G:-11:G:O5'	2.30	0.50
15:H:153:A:C2'	15:H:154:C:C5'	2.86	0.50
15:H:182:U:C2'	15:H:183:G:H5'	2.41	0.50
21:1:1156:GLU:O	26:6:38:ARG:NH1	2.45	0.50
27:7:32:LEU:HA	27:7:35:GLN:HG2	1.93	0.50
32:R:178:ARG:CD	32:R:194:GLN:HE22	2.07	0.50
32:R:422:MET:C	32:R:424:SER:H	2.12	0.50
32:R:434:TYR:CD1	37:Z:616:VAL:CB	2.95	0.50
33:T:329:HIS:CE1	33:T:355:ARG:HG3	2.46	0.50
1:A:89:LEU:CD2	1:A:656:LEU:HD22	2.42	0.50
1:A:232:LEU:CD1	3:C:412:ILE:HD11	2.37	0.50
1:A:329:LEU:HB3	3:C:177:ARG:HE	1.74	0.50
1:A:368:GLN:HA	1:A:369:GLU:OE2	2.10	0.50
1:A:480:LYS:CG	32:R:203:GLN:OE1	2.58	0.50
1:A:596:TYR:O	1:A:597:LYS:C	2.50	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:GLU:OE2	31:P:28:LYS:HB2	2.11	0.50
1:A:1379:PHE:O	1:A:1382:SER:OG	2.17	0.50
1:A:2073:TRP:HH2	1:A:2310:ARG:NH1	2.09	0.50
3:C:134:LEU:HD23	3:C:226:VAL:HB	1.94	0.50
3:C:140:HIS:HB3	3:C:230:ASP:N	2.26	0.50
3:C:456:GLY:O	3:C:457:VAL:HG13	2.11	0.50
5:E:277:PHE:CE2	5:E:300:ILE:HD12	2.46	0.50
13:F:35:A:C8	14:G:12:G:N1	2.80	0.50
13:F:37:C:N4	14:G:5:G:OP1	2.44	0.50
14:G:-4:A:H2'	14:G:-3:A:H8	1.76	0.50
21:1:897:LEU:HD11	21:1:932:ILE:HD13	1.93	0.50
23:3:757:ILE:HG23	23:3:762:LEU:HD13	1.94	0.50
23:3:996:ILE:HD13	23:3:1041:TYR:HD1	1.75	0.50
32:R:434:TYR:CE2	32:R:436:VAL:HG22	2.43	0.50
33:T:306:CYS:SG	33:T:336:VAL:CB	2.97	0.50
36:Y:86:ASP:HB2	37:Z:502:ALA:HB3	1.93	0.50
1:A:76:MET:SD	1:A:88:TYR:CE1	3.05	0.50
1:A:393:LEU:HD11	3:C:378:TYR:CB	2.41	0.50
1:A:393:LEU:CD1	3:C:379:LYS:HG3	2.36	0.50
1:A:693:ILE:O	1:A:697:MET:N	2.42	0.50
2:B:42:U:C2	14:G:-3:A:C2	2.82	0.50
3:C:93:ILE:HG21	33:T:218:TRP:CE2	2.46	0.50
3:C:846:VAL:HG22	3:C:887:LEU:HD11	1.94	0.50
14:G:132:G:H2'	14:G:133:A:C8	2.46	0.50
21:1:822:ARG:HD3	36:Y:32:TYR:OH	2.12	0.50
23:3:550:ASN:OD1	23:3:551:GLN:N	2.41	0.50
23:3:685:ASP:OD1	23:3:686:LEU:N	2.44	0.50
23:3:807:TYR:HE1	23:3:861:GLN:HG3	1.76	0.50
32:R:101:ILE:O	32:R:104:GLN:HG2	2.08	0.50
32:R:442:ARG:HH11	32:R:443:GLY:CA	2.15	0.50
33:T:297:HIS:HD2	33:T:338:CYS:SG	2.34	0.50
34:V:484:SER:C	34:V:486:THR:H	2.15	0.50
1:A:338:VAL:HG21	3:C:867:PRO:CG	2.42	0.50
1:A:361:HIS:HE2	3:C:279:ARG:NH2	2.10	0.50
1:A:848:GLU:CD	32:R:424:SER:OG	2.50	0.50
1:A:2073:TRP:CH2	1:A:2310:ARG:NH1	2.80	0.50
2:B:100:C:H2'	2:B:101:U:C6	2.47	0.50
13:F:36:A:C3'	13:F:37:C:C5'	2.85	0.50
15:H:25:G:H2'	15:H:26:A:C8	2.45	0.50
15:H:46:U:O2'	15:H:47:U:OP2	2.25	0.50
15:H:70:C:O5'	15:H:70:C:H6	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:147:G:N2	15:H:148:C:C2	2.80	0.50
21:1:1003:VAL:HG23	21:1:1004:ILE:H	1.77	0.50
21:1:1132:LEU:O	21:1:1135:GLU:N	2.45	0.50
23:3:300:PHE:CG	23:3:312:LYS:HE2	2.46	0.50
31:P:41:ILE:HD11	33:T:318:ARG:HA	1.92	0.50
31:P:210:PHE:CG	33:T:201:SER:OG	2.64	0.50
1:A:117:PRO:HG2	1:A:131:GLU:HB2	1.94	0.50
1:A:121:HIS:HA	1:A:481:PHE:O	2.12	0.50
1:A:253:ASN:HB3	3:C:893:GLY:O	2.12	0.50
1:A:386:PRO:HB3	3:C:372:PHE:HD1	1.77	0.50
1:A:1209:HIS:CG	1:A:1210:LYS:H	2.30	0.50
1:A:316:PHE:CE1	3:C:635:LEU:CA	2.94	0.50
1:A:948:PRO:O	1:A:951:LEU:HB2	2.12	0.50
1:A:1505:LYS:HE2	37:Z:615:SER:CA	2.40	0.50
1:A:1757:GLU:CD	32:R:451:ILE:CD1	2.80	0.50
3:C:66:TYR:CD2	33:T:457:GLY:CA	2.79	0.50
3:C:244:LYS:CA	3:C:292:TYR:CD2	2.92	0.50
15:H:148:C:HO2'	15:H:149:A:H5'	1.77	0.50
23:3:1050:PHE:HB3	23:3:1167:TYR:HE2	1.75	0.50
23:3:1147:HIS:O	23:3:1151:GLU:HB2	2.10	0.50
33:T:281:ILE:HD12	33:T:282:ARG:HG2	1.92	0.50
1:A:1119:ASP:N	1:A:1120:PRO:CA	2.74	0.50
1:A:1402:ARG:HH21	37:Z:573:PRO:HG3	1.77	0.50
3:C:259:LYS:HE2	3:C:262:ARG:HH11	1.77	0.50
5:E:228:THR:HG22	5:E:229:TYR:HD1	1.77	0.50
13:F:41:A:H2'	13:F:42:C:C6	2.47	0.50
15:H:74:U:O5'	15:H:74:U:H6	1.95	0.50
21:1:595:GLU:O	21:1:599:ASN:ND2	2.45	0.50
23:3:12:THR:HA	23:3:34:ARG:NH1	2.27	0.50
23:3:819:MET:O	23:3:823:MET:HG3	2.12	0.50
35:X:282:LEU:HD23	35:X:295:ASP:HA	1.94	0.50
1:A:122:ILE:HD12	1:A:483:GLN:HG3	1.94	0.49
1:A:686:ARG:HH11	1:A:710:LEU:HD13	1.77	0.49
1:A:1127:GLY:O	1:A:1128:TYR:C	2.48	0.49
3:C:144:CYS:C	3:C:312:SER:HB2	2.33	0.49
3:C:499:GLY:O	3:C:500:THR:CG2	2.60	0.49
21:1:1040:GLY:HA2	21:1:1080:THR:HG22	1.94	0.49
23:3:4:TYR:HB2	23:3:1132:PHE:CZ	2.47	0.49
23:3:458:ALA:HB3	23:3:477:SER:HB3	1.94	0.49
23:3:550:ASN:HD21	23:3:595:VAL:N	2.10	0.49
23:3:1188:ASN:O	23:3:1192:ASN:ND2	2.31	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:66:ARG:HH11	31:P:66:ARG:CG	2.24	0.49
37:Z:612:TYR:C	37:Z:614:TRP:N	2.63	0.49
37:Z:614:TRP:CD1	37:Z:614:TRP:C	2.85	0.49
1:A:348:PRO:O	1:A:350:PHE:N	2.45	0.49
1:A:965:VAL:HG13	1:A:966:TRP:CD1	2.47	0.49
1:A:1403:LEU:O	32:R:412:ASP:CB	2.60	0.49
1:A:1700:GLY:H	1:A:1717:ASN:HD22	1.60	0.49
3:C:116:MET:O	3:C:119:LEU:HB3	2.12	0.49
3:C:854:ARG:NH1	3:C:879:ASP:OD2	2.45	0.49
5:E:265:ARG:N	5:E:272:ARG:HH21	2.10	0.49
15:H:181:G:N2	15:H:182:U:C2	2.80	0.49
21:1:717:THR:HG22	21:1:718:PRO:HD3	1.93	0.49
23:3:274:ARG:HG2	23:3:387:PHE:CE1	2.47	0.49
23:3:755:VAL:HG13	23:3:762:LEU:HD11	1.93	0.49
32:R:132:LEU:HB3	33:T:399:LYS:HZ1	1.77	0.49
36:Y:48:THR:OG1	36:Y:49:GLU:OE1	2.30	0.49
1:A:387:PHE:CZ	3:C:330:THR:CB	2.96	0.49
1:A:1120:PRO:HG2	1:A:1121:ASN:H	1.78	0.49
1:A:2298:LEU:C	4:D:1283:PRO:CB	2.78	0.49
2:B:20:G:H1'	2:B:21:A:OP1	2.12	0.49
3:C:65:TYR:C	3:C:66:TYR:CG	2.86	0.49
3:C:78:GLU:OE1	33:T:198:ARG:NH2	2.45	0.49
3:C:297:ASN:HB3	3:C:298:LEU:HD13	1.95	0.49
3:C:493:PHE:HD2	3:C:551:LEU:HD21	1.76	0.49
3:C:715:GLY:HA2	3:C:729:ALA:HB1	1.93	0.49
5:E:164:PRO:O	5:E:166:LEU:HG	2.13	0.49
21:1:499:LYS:HD3	21:1:534:GLN:NE2	2.27	0.49
21:1:652:CYS:HB3	21:1:692:HIS:CE1	2.46	0.49
21:1:827:ARG:O	21:1:830:TYR:HB3	2.12	0.49
23:3:235:LEU:HG	23:3:250:ILE:HG13	1.93	0.49
23:3:1008:SER:OG	23:3:1009:PHE:N	2.45	0.49
1:A:235:MET:CE	1:A:411:PHE:CA	2.84	0.49
1:A:800:TYR:CB	3:C:59:LEU:HD13	2.43	0.49
1:A:1056:HIS:NE2	1:A:1060:GLU:OE2	2.44	0.49
1:A:1310:ARG:NH2	1:A:1563:HIS:O	2.45	0.49
1:A:1760:GLU:HB2	1:A:1761:PRO:HD2	1.93	0.49
1:A:1807:ILE:HB	1:A:1820:LYS:HB3	1.92	0.49
1:A:2325:VAL:HG11	4:D:789:MET:HA	1.94	0.49
3:C:62:ASP:HB3	31:P:206:LYS:NZ	2.27	0.49
3:C:66:TYR:CE2	31:P:211:VAL:HG11	2.45	0.49
3:C:349:PHE:CD1	3:C:356:PHE:HE1	2.22	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:37:U:H2'	15:H:38:A:H8	1.77	0.49
23:3:253:GLU:OE2	23:3:284:GLY:HA3	2.12	0.49
23:3:483:LEU:HD11	23:3:493:GLU:HG3	1.94	0.49
28:J:220:LEU:HD13	28:J:220:LEU:C	2.32	0.49
32:R:433:ILE:HG13	32:R:434:TYR:O	2.12	0.49
1:A:115:ASP:CB	1:A:486:LYS:HE2	2.42	0.49
1:A:366:LYS:N	1:A:366:LYS:CE	2.73	0.49
1:A:409:ARG:N	1:A:410:PRO:HD2	2.26	0.49
1:A:1405:LEU:N	32:R:415:LEU:HD21	2.27	0.49
1:A:1818:PHE:CD2	1:A:1848:LEU:HD21	2.47	0.49
1:A:1930:TYR:CD2	1:A:1930:TYR:C	2.85	0.49
3:C:133:THR:O	3:C:226:VAL:CB	2.60	0.49
3:C:335:ASN:OD1	3:C:336:TYR:N	2.45	0.49
3:C:709:TRP:N	3:C:709:TRP:CD1	2.79	0.49
23:3:994:GLN:HE22	23:3:1037:SER:HA	1.78	0.49
32:R:231:VAL:HG23	32:R:232:MET:N	2.26	0.49
32:R:241:MET:SD	32:R:245:GLU:CD	2.91	0.49
32:R:450:SER:OG	32:R:452:TYR:O	2.30	0.49
37:Z:563:ARG:CG	37:Z:563:ARG:NH2	2.73	0.49
1:A:690:MET:HG3	1:A:694:LEU:HD12	1.95	0.49
1:A:1723:LYS:HB3	1:A:1724:PRO:HD3	1.95	0.49
1:A:1809:ILE:HD11	1:A:1845:VAL:HG22	1.93	0.49
13:F:36:A:C8	13:F:36:A:H5'	2.48	0.49
21:1:805:TYR:CE1	21:1:809:GLU:HG3	2.46	0.49
23:3:23:SER:HA	23:3:94:PRO:HG3	1.95	0.49
23:3:794:SER:HB2	23:3:933:ASN:O	2.12	0.49
23:3:1048:ASP:OD1	23:3:1049:LYS:N	2.45	0.49
28:J:331:GLN:CG	32:R:98:TYR:OH	2.47	0.49
37:Z:526:ILE:N	37:Z:526:ILE:HD12	2.27	0.49
1:A:347:LEU:HD13	1:A:351:TYR:OH	2.12	0.49
1:A:800:TYR:HB3	3:C:59:LEU:HD13	1.95	0.49
1:A:2097:ILE:HD12	1:A:2099:GLU:HB2	1.93	0.49
3:C:140:HIS:O	3:C:258:ASN:HB3	2.13	0.49
3:C:363:SER:O	3:C:364:SER:CB	2.60	0.49
21:1:498:MET:HE1	21:1:531:LEU:HD12	1.93	0.49
21:1:1017:LEU:HD21	21:1:1058:ILE:HD11	1.93	0.49
21:1:1273:TYR:OH	21:1:1277:GLN:NE2	2.46	0.49
23:3:31:VAL:HG21	23:3:78:ILE:HD11	1.95	0.49
23:3:440:HIS:ND1	23:3:720:TRP:CH2	2.80	0.49
23:3:527:ILE:HA	23:3:532:ARG:O	2.12	0.49
31:P:30:TYR:OH	32:R:162:ALA:C	2.50	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:Z:597:ARG:HH12	37:Z:601:LEU:CD1	2.22	0.49
1:A:251:ASP:HA	1:A:337:VAL:HG21	1.94	0.49
1:A:1618:LYS:HD2	1:A:1626:CYS:H	1.78	0.49
1:A:1718:TRP:HZ3	1:A:1726:ILE:HD12	1.77	0.49
1:A:2287:ARG:HH22	4:D:1147:ASN:CB	2.15	0.49
3:C:73:TYR:CZ	33:T:487:LYS:CE	2.95	0.49
3:C:137:HIS:NE2	3:C:236:MET:CE	2.75	0.49
3:C:705:VAL:HG21	3:C:718:PHE:CZ	2.47	0.49
5:E:74:PHE:HE1	5:E:95:VAL:CG2	2.25	0.49
13:F:53:A:C6	13:F:54:G:C5	3.00	0.49
14:G:5:G:H2'	14:G:5:G:N3	2.28	0.49
14:G:155:U:H4'	14:G:156:U:OP2	2.13	0.49
15:H:107:A:C2	15:H:108:G:C4	3.01	0.49
15:H:143:A:N3	15:H:143:A:C3'	2.73	0.49
21:1:175:LYS:O	21:1:179:GLY:HA3	2.11	0.49
21:1:1134:ASN:ND2	22:2:534:GLN:HA	2.28	0.49
23:3:47:THR:HG23	23:3:49:LYS:H	1.77	0.49
23:3:785:PRO:HA	23:3:801:GLU:HA	1.95	0.49
24:4:32:LEU:HD21	24:4:79:LEU:HD21	1.94	0.49
32:R:55:LEU:CA	32:R:73:PRO:O	2.61	0.49
1:A:87:VAL:HG13	32:R:205:ASP:OD2	2.13	0.49
1:A:1393:ARG:O	1:A:1397:ILE:HG13	2.12	0.49
3:C:301:SER:O	3:C:303:LEU:N	2.44	0.49
3:C:499:GLY:O	3:C:500:THR:HG23	2.13	0.49
5:E:219:VAL:HB	5:E:229:TYR:HB2	1.95	0.49
26:6:43:VAL:HG21	26:6:69:ALA:HB3	1.94	0.49
32:R:131:ASP:OD2	32:R:132:LEU:CD2	2.60	0.49
32:R:171:LEU:HD11	32:R:201:GLU:CD	2.32	0.49
33:T:442:ARG:HB3	33:T:443:THR:HG23	1.95	0.49
36:Y:38:ILE:HG22	36:Y:90:THR:HG23	1.95	0.49
1:A:91:ALA:O	1:A:94:TYR:N	2.43	0.49
1:A:273:ILE:CG2	1:A:274:PRO:HD2	2.42	0.49
1:A:660:PHE:HB3	32:R:210:PRO:O	2.13	0.49
1:A:2113:LYS:HE2	4:D:1229:ASP:CA	2.41	0.49
3:C:381:LEU:CD2	3:C:416:LEU:HD22	2.42	0.49
5:E:74:PHE:HE1	5:E:95:VAL:HG22	1.77	0.49
15:H:71:C:H2'	15:H:72:U:H6	1.75	0.49
32:R:433:ILE:O	32:R:434:TYR:HB3	2.13	0.49
36:Y:24:ASP:CG	36:Y:25:LYS:H	2.14	0.49
1:A:44:ARG:CG	1:A:45:TYR:CE2	2.95	0.48
1:A:529:THR:HG22	30:M:197:TYR:HB3	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1870:ASP:HB2	1:A:1871:PRO:HD3	1.95	0.48
1:A:1998:ASN:O	1:A:2001:SER:OG	2.23	0.48
3:C:82:GLN:HG3	33:T:237:LYS:HA	1.94	0.48
3:C:334:ILE:HD12	3:C:334:ILE:O	2.13	0.48
5:E:153:PHE:N	5:E:153:PHE:CD1	2.78	0.48
13:F:26:U:H3'	13:F:27:A:C5'	2.37	0.48
15:H:182:U:HO2'	15:H:183:G:H5'	1.76	0.48
21:1:408:PHE:HB2	25:5:49:ARG:NH1	2.28	0.48
23:3:734:LEU:HD13	23:3:767:LEU:HD21	1.94	0.48
32:R:82:MET:HE2	32:R:82:MET:O	2.13	0.48
36:Y:32:TYR:C	36:Y:34:ASP:H	2.15	0.48
1:A:794:TYR:CD2	1:A:1028:TYR:HB2	2.47	0.48
1:A:1301:ILE:HD11	2:B:39:C:H5"	1.91	0.48
3:C:78:GLU:C	33:T:198:ARG:HA	2.25	0.48
3:C:508:LYS:HB3	3:C:566:THR:HG23	1.95	0.48
3:C:855:GLY:O	3:C:856:HIS:CB	2.44	0.48
5:E:162:ARG:HH22	5:E:204:THR:HA	1.74	0.48
13:F:54:G:N2	15:H:22:U:C2	2.81	0.48
14:G:11:A:N3	14:G:11:A:C3'	2.76	0.48
15:H:5:C:H2'	15:H:6:U:H6	1.78	0.48
21:1:483:ASP:OD1	21:1:484:GLU:N	2.46	0.48
28:J:360:ASP:HA	28:J:363:ARG:CG	2.44	0.48
1:A:267:LYS:NZ	2:B:49:A:P	2.85	0.48
1:A:494:LEU:HD21	1:A:562:VAL:HG21	1.95	0.48
1:A:828:PRO:HG3	1:A:925:TYR:CZ	2.48	0.48
1:A:1214:TRP:CZ2	1:A:1230:LEU:HD11	2.48	0.48
1:A:2298:LEU:HD11	4:D:1285:SER:CA	2.43	0.48
3:C:73:TYR:CE1	33:T:453:ALA:O	2.67	0.48
3:C:297:ASN:HD22	3:C:298:LEU:CD1	2.26	0.48
3:C:333:ASP:OD1	3:C:333:ASP:N	2.42	0.48
3:C:401:ILE:HD11	3:C:423:PHE:HB2	1.96	0.48
13:F:49:G:H2'	13:F:50:A:H8	1.78	0.48
14:G:138:A:H5"	29:L:12:ARG:NE	2.28	0.48
15:H:10:C:H2'	15:H:11:G:C8	2.40	0.48
23:3:157:PRO:HD2	26:6:16:GLY:HA2	1.95	0.48
23:3:870:ASN:ND2	23:3:873:GLN:H	2.10	0.48
32:R:433:ILE:HG13	32:R:434:TYR:N	2.27	0.48
33:T:302:VAL:HG23	33:T:315:TRP:O	2.14	0.48
37:Z:604:LYS:HA	37:Z:607:VAL:HG23	1.94	0.48
1:A:412:ASN:OD1	1:A:413:LEU:HD23	2.13	0.48
1:A:2149:PRO:O	1:A:2160:PRO:HD3	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:291:MET:CG	3:C:292:TYR:CE1	2.96	0.48
3:C:443:VAL:O	3:C:447:PRO:CD	2.62	0.48
3:C:452:THR:O	3:C:577:PHE:CA	2.60	0.48
13:F:8:C:H6	13:F:8:C:C5'	2.15	0.48
13:F:66:C:H2'	13:F:67:G:O4'	2.12	0.48
14:G:-8:U:H2'	14:G:-7:C:O4'	2.13	0.48
14:G:9:C:H2'	14:G:10:U:C6	2.48	0.48
15:H:25:G:N3	15:H:26:A:C8	2.82	0.48
23:3:886:GLU:OE1	23:3:926:TYR:OH	2.24	0.48
23:3:1149:ARG:HH12	23:3:1161:LEU:HD13	1.79	0.48
28:J:406:PHE:HB3	28:J:411:MET:HG2	1.96	0.48
35:X:212:ASN:H	35:X:307:GLN:HE22	1.60	0.48
1:A:258:PHE:HZ	1:A:275:GLY:O	1.96	0.48
1:A:387:PHE:HD1	3:C:327:TYR:CD1	2.31	0.48
1:A:774:LYS:HG2	15:H:23:A:C8	2.48	0.48
1:A:1214:TRP:NE1	1:A:1276:GLU:OE1	2.23	0.48
13:F:45:A:H4'	13:F:46:G:OP2	2.14	0.48
13:F:53:A:C6	15:H:25:G:C4	3.02	0.48
23:3:457:ASN:HD21	23:3:504:PRO:HB3	1.79	0.48
23:3:624:CYS:SG	23:3:625:LEU:HD13	2.54	0.48
23:3:930:LEU:HA	23:3:937:LEU:HD23	1.95	0.48
27:7:40:TYR:HA	27:7:43:TYR:CD2	2.49	0.48
32:R:103:ARG:CG	32:R:103:ARG:NH1	2.75	0.48
33:T:185:MET:CB	33:T:186:PRO:CD	2.90	0.48
33:T:213:GLU:HB2	33:T:218:TRP:O	2.14	0.48
34:V:549:LYS:O	34:V:552:ALA:CB	2.60	0.48
1:A:299:ILE:CD1	3:C:920:PRO:C	2.82	0.48
1:A:323:LEU:N	1:A:324:PRO:CD	2.77	0.48
1:A:366:LYS:N	1:A:366:LYS:HD3	2.27	0.48
1:A:595:LYS:CE	1:A:644:ILE:HD11	2.38	0.48
1:A:718:ARG:HH21	32:R:259:LYS:CE	2.25	0.48
1:A:1370:ARG:NH1	34:V:468:ASP:H	2.09	0.48
3:C:350:ASN:HB3	3:C:353:THR:HG23	1.94	0.48
3:C:445:ALA:O	3:C:449:ILE:HG13	2.12	0.48
3:C:678:THR:HG23	3:C:683:ASN:CA	2.43	0.48
3:C:736:GLY:N	3:C:770:PHE:HE2	2.10	0.48
21:1:1212:LEU:HD13	21:1:1237:LEU:HD13	1.96	0.48
23:3:142:TYR:CE1	23:3:157:PRO:HB3	2.48	0.48
23:3:565:TYR:CG	23:3:619:LEU:HD13	2.48	0.48
32:R:215:ASN:HD22	32:R:216:LYS:N	2.11	0.48
1:A:338:VAL:HG21	3:C:867:PRO:HD2	1.96	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1295:ILE:HG13	1:A:1296:GLN:N	2.29	0.48
3:C:135:CYS:SG	3:C:227:LEU:HA	2.54	0.48
3:C:149:LEU:CA	3:C:427:PHE:CE2	2.97	0.48
3:C:349:PHE:HB2	3:C:356:PHE:CE1	2.48	0.48
3:C:514:TYR:CD1	3:C:515:THR:N	2.82	0.48
15:H:83:A:C2	15:H:84:C:N3	2.82	0.48
23:3:842:PHE:HD2	23:3:843:LEU:HD12	1.78	0.48
23:3:926:TYR:HE1	23:3:942:LYS:HG3	1.77	0.48
28:J:273:TYR:CZ	32:R:228:PRO:CB	2.82	0.48
33:T:387:PHE:CD1	33:T:387:PHE:C	2.87	0.48
1:A:1332:HIS:HB3	1:A:1359:HIS:HE1	1.78	0.48
1:A:2298:LEU:HD11	4:D:1265:GLN:CB	2.44	0.48
3:C:82:GLN:O	33:T:202:GLY:HA3	2.13	0.48
3:C:457:VAL:HG12	3:C:462:GLY:HA3	1.96	0.48
3:C:477:HIS:HD1	3:C:478:THR:N	2.12	0.48
5:E:243:LEU:HD11	5:E:247:GLY:CA	2.41	0.48
14:G:17:U:H2'	14:G:18:A:C8	2.49	0.48
15:H:83:A:C2	15:H:84:C:C4	3.01	0.48
21:1:1297:ARG:NH1	27:7:39:SER:OG	2.46	0.48
22:2:504:TRP:C	22:2:506:PHE:H	2.17	0.48
33:T:384:HIS:O	33:T:385:TYR:HB3	2.13	0.48
1:A:405:LEU:HD11	3:C:265:LEU:HD22	1.96	0.48
1:A:1892:PRO:HD3	1:A:1941:ARG:HH21	1.79	0.48
3:C:128:LEU:O	3:C:199:LEU:N	2.37	0.48
3:C:690:GLU:HB2	3:C:691:PRO:HD2	1.95	0.48
13:F:44:G:H2'	22:2:554:ARG:HG2	1.96	0.48
15:H:37:U:H2'	15:H:38:A:C8	2.49	0.48
22:2:652:GLY:N	22:2:655:SER:O	2.45	0.48
23:3:21:ASN:HD21	23:3:28:GLN:HG2	1.77	0.48
23:3:58:VAL:HG12	23:3:1155:LEU:HB3	1.95	0.48
23:3:539:PRO:HD2	23:3:558:LEU:HD21	1.95	0.48
23:3:891:VAL:HA	23:3:906:LEU:O	2.13	0.48
23:3:1057:ARG:HG2	23:3:1058:LEU:O	2.13	0.48
32:R:184:GLN:O	32:R:188:PHE:HB2	2.13	0.48
34:V:576:THR:O	34:V:579:SER:N	2.47	0.48
36:Y:110:ASP:OD1	36:Y:111:HIS:N	2.43	0.48
1:A:356:ILE:CG2	3:C:865:GLY:C	2.82	0.48
1:A:417:ARG:NH1	2:B:58:U:C5'	2.77	0.48
1:A:529:THR:HB	30:M:199:PRO:CD	2.44	0.48
1:A:546:LEU:HD11	1:A:595:LYS:CG	2.43	0.48
1:A:731:LEU:HD23	1:A:736:GLU:HB2	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2310:ARG:HH11	1:A:2310:ARG:CG	2.27	0.48
2:B:42:U:H2'	2:B:43:U:O4'	2.13	0.48
3:C:93:ILE:O	3:C:94:ILE:CB	2.62	0.48
3:C:145:PHE:HB2	3:C:312:SER:CB	2.32	0.48
21:1:208:PRO:N	21:1:656:LYS:HE3	2.29	0.48
23:3:476:VAL:O	23:3:482:THR:HA	2.14	0.48
23:3:981:CYS:SG	23:3:1021:LEU:HG	2.54	0.48
32:R:402:ASN:HB2	35:X:192:ARG:CG	2.43	0.48
34:V:527:GLY:O	34:V:530:LYS:N	2.47	0.48
1:A:171:ASP:CG	1:A:519:ASP:OD2	2.53	0.47
1:A:238:LEU:HB3	1:A:411:PHE:HE2	1.79	0.47
1:A:406:TRP:CH2	3:C:265:LEU:C	2.87	0.47
1:A:409:ARG:HD2	1:A:409:ARG:O	2.14	0.47
1:A:735:ILE:O	1:A:738:MET:HE2	2.14	0.47
1:A:758:ARG:HD2	1:A:775:ASN:ND2	2.28	0.47
1:A:1183:PRO:HA	1:A:1201:ARG:HE	1.78	0.47
1:A:1754:TYR:CD1	21:1:948:ARG:NH1	2.82	0.47
1:A:1768:TYR:HA	1:A:1771:LEU:CB	2.40	0.47
3:C:557:GLN:N	3:C:558:PRO:HD2	2.29	0.47
5:E:263:ASP:OD1	5:E:272:ARG:HB3	2.13	0.47
13:F:44:G:N2	14:G:3:A:C8	2.82	0.47
21:1:209:GLY:HA3	21:1:614:ARG:NH1	2.29	0.47
23:3:353:PHE:HB3	23:3:406:PRO:HD3	1.96	0.47
23:3:814:GLN:O	23:3:818:GLN:HB2	2.13	0.47
26:6:19:ILE:HD12	26:6:42:LEU:HD21	1.96	0.47
28:J:273:TYR:CD2	32:R:228:PRO:HG3	2.49	0.47
32:R:120:VAL:CG2	32:R:121:PRO:HD2	2.44	0.47
34:V:484:SER:C	34:V:486:THR:N	2.67	0.47
35:X:246:TYR:H	35:X:386:ASP:HA	1.79	0.47
1:A:134:TRP:HB3	1:A:418:THR:HG22	1.95	0.47
1:A:312:TYR:CZ	3:C:882:GLY:C	2.87	0.47
1:A:330:THR:O	1:A:331:TRP:CB	2.62	0.47
1:A:666:LYS:HE2	32:R:217:LYS:HG3	1.96	0.47
1:A:1045:GLY:HA3	1:A:1090:ARG:NH2	2.29	0.47
1:A:1270:LEU:HD12	1:A:1274:PHE:CD2	2.49	0.47
1:A:1551:PHE:O	1:A:1553:VAL:HG23	2.14	0.47
3:C:753:GLU:O	3:C:755:ASP:N	2.45	0.47
5:E:269:PRO:O	5:E:270:LYS:CB	2.54	0.47
13:F:12:G:H2'	13:F:13:G:O4'	2.14	0.47
15:H:151:C:C2	15:H:152:G:N7	2.82	0.47
23:3:675:LEU:HD23	23:3:686:LEU:HD11	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:1095:TYR:CZ	23:3:1164:ARG:HD2	2.49	0.47
26:6:23:CYS:HB3	26:6:58:CYS:HB2	1.97	0.47
27:7:69:MET:HA	27:7:72:MET:HG2	1.96	0.47
28:J:436:TYR:OH	28:J:458:PHE:HA	2.14	0.47
33:T:416:ILE:O	33:T:416:ILE:HD13	2.14	0.47
1:A:350:PHE:HE2	1:A:398:THR:HG21	1.79	0.47
1:A:1258:LYS:HE2	32:R:432:GLU:CA	2.44	0.47
1:A:2148:VAL:O	1:A:2150:GLN:HG2	2.14	0.47
3:C:66:TYR:OH	31:P:216:ARG:HD2	2.13	0.47
3:C:73:TYR:HE1	33:T:453:ALA:O	1.97	0.47
3:C:441:PRO:O	3:C:444:GLY:CA	2.61	0.47
3:C:449:ILE:HD12	3:C:466:SER:OG	2.13	0.47
3:C:673:LYS:HB3	3:C:688:ILE:HG22	1.96	0.47
5:E:178:LEU:CD2	5:E:208:ILE:HD13	2.44	0.47
14:G:138:A:H2'	14:G:139:U:C6	2.49	0.47
21:1:1252:GLN:HG2	22:2:492:LYS:HA	1.96	0.47
23:3:240:GLY:HA3	23:3:246:SER:HB2	1.95	0.47
27:7:33:VAL:HG23	27:7:75:PRO:HG2	1.96	0.47
32:R:73:PRO:HG2	32:R:74:LEU:H	1.79	0.47
32:R:189:ASN:HD21	32:R:195:ARG:CZ	2.26	0.47
34:V:625:ARG:O	34:V:629:ASN:CB	2.62	0.47
36:Y:63:VAL:HG23	36:Y:64:ASN:H	1.78	0.47
1:A:121:HIS:O	1:A:123:THR:N	2.47	0.47
1:A:1192:PHE:HE1	1:A:1274:PHE:CD1	2.32	0.47
1:A:1439:ARG:O	1:A:1443:LYS:HG2	2.15	0.47
2:B:20:G:OP1	2:B:20:G:H4'	2.12	0.47
3:C:240:GLU:OE2	3:C:292:TYR:OH	2.18	0.47
3:C:438:ILE:CD1	3:C:438:ILE:N	2.76	0.47
14:G:17:U:H2'	14:G:18:A:H8	1.79	0.47
14:G:149:G:N2	14:G:150:U:H2'	2.29	0.47
21:1:464:LEU:HD23	21:1:478:LEU:HD21	1.95	0.47
21:1:781:ASP:HB3	21:1:784:MET:HB2	1.95	0.47
23:3:54:LEU:HD22	23:3:98:MET:HA	1.97	0.47
23:3:120:PHE:HB2	23:3:133:SER:OG	2.15	0.47
26:6:21:ARG:HG3	26:6:56:GLY:HA2	1.96	0.47
31:P:224:MET:HE2	31:P:228:ILE:CD1	2.39	0.47
31:P:228:ILE:CD1	31:P:228:ILE:N	2.78	0.47
1:A:203:VAL:HG12	1:A:207:PHE:CD1	2.49	0.47
1:A:2252:LEU:HD23	1:A:2253:PRO:HD2	1.96	0.47
2:B:44:A:H2	14:G:-5:G:O6	1.97	0.47
3:C:73:TYR:OH	33:T:487:LYS:CE	2.62	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:185:PRO:HD3	3:C:482:TYR:CE1	2.50	0.47
5:E:161:ARG:HH11	5:E:161:ARG:CG	2.26	0.47
21:1:1172:LEU:HA	22:2:522:PHE:HE1	1.79	0.47
23:3:354:GLY:HA3	23:3:432:ARG:NH1	2.30	0.47
31:P:192:VAL:HG12	31:P:193:VAL:N	2.29	0.47
32:R:103:ARG:NH2	32:R:110:LYS:O	2.40	0.47
32:R:178:ARG:CD	32:R:194:GLN:NE2	2.72	0.47
1:A:393:LEU:HD13	3:C:375:GLU:HG3	1.95	0.47
3:C:507:VAL:HG12	3:C:508:LYS:N	2.29	0.47
3:C:710:ASN:O	3:C:711:ARG:C	2.53	0.47
14:G:-5:G:O2'	14:G:-4:A:H8	1.98	0.47
15:H:57:A:H2'	15:H:58:U:O4'	2.14	0.47
21:1:1140:GLU:O	21:1:1144:GLN:HG3	2.15	0.47
23:3:459:VAL:HB	23:3:757:ILE:HG23	1.97	0.47
23:3:554:VAL:HB	23:3:566:PHE:HB2	1.97	0.47
28:J:216:ASP:O	28:J:219:GLU:N	2.47	0.47
32:R:51:ILE:N	32:R:52:PRO:CD	2.77	0.47
33:T:318:ARG:HH11	33:T:319:THR:CG2	2.28	0.47
1:A:121:HIS:HE2	1:A:481:PHE:CB	2.14	0.47
1:A:340:ILE:HD13	1:A:340:ILE:N	2.29	0.47
1:A:363:HIS:HD2	3:C:283:ASP:O	1.98	0.47
1:A:639:PHE:O	2:B:28:A:O2'	2.31	0.47
1:A:664:HIS:HE1	1:A:666:LYS:HB2	1.71	0.47
1:A:735:ILE:O	1:A:738:MET:HB3	2.15	0.47
1:A:1241:HIS:ND1	1:A:1287:LEU:HD11	2.29	0.47
2:B:41:U:H2'	2:B:42:U:C6	2.49	0.47
3:C:78:GLU:CD	3:C:80:ILE:HD11	2.30	0.47
3:C:749:THR:O	3:C:753:GLU:HB2	2.14	0.47
21:1:903:GLN:HE22	21:1:910:MET:HG3	1.80	0.47
23:3:18:ILE:HD13	23:3:65:LEU:HG	1.96	0.47
23:3:931:VAL:O	23:3:936:LYS:N	2.40	0.47
23:3:1032:TRP:O	23:3:1048:ASP:HA	2.15	0.47
28:J:273:TYR:CE2	32:R:228:PRO:HB3	2.46	0.47
31:P:227:TYR:N	31:P:227:TYR:CD1	2.81	0.47
33:T:257:ARG:HD3	33:T:301:ASP:OD1	2.14	0.47
36:Y:40:LEU:HB2	36:Y:43:LEU:HD11	1.96	0.47
1:A:195:LEU:H	1:A:195:LEU:HD12	1.80	0.47
1:A:592:TYR:O	1:A:595:LYS:O	2.32	0.47
1:A:1455:TRP:CE3	1:A:1456:THR:HB	2.50	0.47
2:B:43:U:H5'	13:F:67:G:H22	1.79	0.47
3:C:115:GLU:O	3:C:118:PHE:CA	2.61	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:457:VAL:CA	3:C:462:GLY:HA3	2.44	0.47
21:1:207:THR:HA	21:1:656:LYS:NZ	2.28	0.47
21:1:699:GLN:HA	21:1:702:ARG:CZ	2.45	0.47
23:3:164:ASN:ND2	23:3:189:TYR:OH	2.34	0.47
23:3:304:GLN:HA	23:3:309:ASP:O	2.15	0.47
23:3:931:VAL:HG12	23:3:932:ASN:N	2.26	0.47
25:5:14:PRO:HB2	25:5:16:GLU:OE1	2.15	0.47
33:T:246:ILE:HB	33:T:267:ASP:OD1	2.15	0.47
1:A:97:HIS:HD2	1:A:473:PHE:HZ	1.59	0.47
1:A:695:ASP:HB3	33:T:374:SER:CB	2.38	0.47
1:A:1608:THR:HG22	1:A:1632:PHE:HB2	1.97	0.47
21:1:535:ILE:O	21:1:538:LEU:N	2.47	0.47
21:1:760:GLU:N	21:1:760:GLU:OE1	2.47	0.47
21:1:1132:LEU:HD11	21:1:1150:SER:OG	2.14	0.47
23:3:5:ASN:OD1	23:3:6:LEU:N	2.47	0.47
23:3:212:GLU:OE1	23:3:223:LYS:HD2	2.15	0.47
23:3:498:GLY:HA3	23:3:531:LYS:NZ	2.30	0.47
32:R:67:ILE:HG22	32:R:69:VAL:HG21	1.97	0.47
32:R:82:MET:HE3	32:R:82:MET:C	2.36	0.47
34:V:467:LEU:O	34:V:468:ASP:CB	2.62	0.47
2:B:12:U:H3	2:B:65:G:H1	1.62	0.47
2:B:41:U:C4	14:G:-1:G:N1	2.83	0.47
3:C:470:PRO:CA	3:C:499:GLY:HA2	2.42	0.47
3:C:490:PHE:CE1	3:C:612:LYS:HD2	2.49	0.47
13:F:49:G:H2'	13:F:50:A:C8	2.50	0.47
14:G:156:U:P	14:G:156:U:H3'	2.54	0.47
15:H:6:U:H2'	15:H:7:U:H6	1.80	0.47
15:H:47:U:H4'	15:H:48:A:OP1	2.15	0.47
15:H:153:A:C8	15:H:154:C:H5'	2.50	0.47
21:1:1185:ARG:HD2	21:1:1218:ASN:CG	2.35	0.47
22:2:642:PRO:HG3	22:2:648:LEU:HD22	1.97	0.47
23:3:182:PHE:O	23:3:210:PHE:HA	2.15	0.47
23:3:458:ALA:HA	23:3:741:PHE:CB	2.45	0.47
28:J:255:LEU:CD2	29:L:235:LEU:HD13	2.38	0.47
1:A:67:ARG:HD3	1:A:179:ALA:CB	2.34	0.46
1:A:277:PRO:HA	1:A:448:GLN:HG3	1.96	0.46
1:A:316:PHE:HE1	3:C:635:LEU:CA	2.27	0.46
1:A:437:ALA:O	1:A:439:GLN:HG2	2.15	0.46
1:A:519:ASP:C	1:A:519:ASP:OD1	2.54	0.46
1:A:755:HIS:HE1	31:P:223:PHE:CB	2.14	0.46
1:A:1256:PHE:CZ	1:A:1302:GLY:HA3	2.51	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1364:LEU:HD13	34:V:461:LEU:O	2.15	0.46
1:A:1718:TRP:CZ3	1:A:1723:LYS:HA	2.50	0.46
2:B:43:U:O4	14:G:-4:A:C6	2.68	0.46
3:C:82:GLN:HG3	33:T:238:LEU:N	2.30	0.46
3:C:244:LYS:HG3	3:C:292:TYR:CD2	2.50	0.46
3:C:449:ILE:HD11	3:C:465:MET:C	2.35	0.46
3:C:571:ASN:O	3:C:572:GLU:HB3	2.16	0.46
21:1:815:PHE:HA	21:1:819:TRP:HD1	1.81	0.46
21:1:1058:ILE:O	21:1:1062:LEU:HG	2.16	0.46
23:3:248:VAL:HG23	23:3:250:ILE:HD11	1.96	0.46
31:P:64:GLU:OE2	31:P:68:ARG:NE	2.48	0.46
1:A:280:GLU:HB2	2:B:48:A:O4'	2.15	0.46
1:A:414:ARG:NH1	3:C:408:LEU:O	2.43	0.46
1:A:1209:HIS:CG	1:A:1210:LYS:N	2.83	0.46
1:A:1212:GLY:HA3	1:A:1280:ASN:ND2	2.31	0.46
1:A:1824:THR:HA	1:A:1827:TRP:HD1	1.80	0.46
1:A:1892:PRO:HG3	1:A:1941:ARG:HE	1.81	0.46
2:B:42:U:O5'	2:B:42:U:H6	1.97	0.46
2:B:44:A:C2	14:G:-5:G:O6	2.69	0.46
3:C:262:ARG:HG2	41:C:1500:GTP:N2	2.30	0.46
3:C:350:ASN:CB	3:C:353:THR:HG23	2.45	0.46
13:F:78:A:H8	13:F:78:A:OP2	1.98	0.46
15:H:150:U:H2'	15:H:151:C:C6	2.50	0.46
21:1:732:TRP:HB2	21:1:765:TYR:HE1	1.79	0.46
21:1:738:HIS:CE1	21:1:746:PHE:HE2	2.32	0.46
21:1:1169:VAL:HG12	21:1:1173:LEU:HG	1.97	0.46
23:3:28:GLN:NE2	23:3:343:LYS:HG2	2.31	0.46
23:3:1005:VAL:O	23:3:1032:TRP:HA	2.15	0.46
36:Y:48:THR:HG1	36:Y:49:GLU:H	1.63	0.46
1:A:388:LEU:HB3	1:A:391:THR:OG1	2.16	0.46
1:A:405:LEU:HD21	3:C:385:VAL:HG12	1.98	0.46
1:A:844:GLU:O	1:A:848:GLU:HG2	2.15	0.46
1:A:982:GLU:HG3	1:A:1169:GLN:HG3	1.97	0.46
1:A:1761:PRO:CB	1:A:1930:TYR:OH	2.55	0.46
1:A:1821:ILE:O	1:A:1912:PRO:HA	2.15	0.46
3:C:221:ILE:HG23	3:C:495:ARG:HB3	1.96	0.46
5:E:87:ASP:O	5:E:88:ARG:CG	2.63	0.46
21:1:728:LEU:O	21:1:731:LEU:N	2.48	0.46
23:3:274:ARG:NH2	23:3:307:GLN:OE1	2.48	0.46
32:R:195:ARG:HB3	32:R:195:ARG:HH11	1.80	0.46
36:Y:37:TRP:CZ3	37:Z:498:GLY:C	2.86	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ILE:CD1	1:A:483:GLN:CG	2.89	0.46
1:A:201:ALA:HA	1:A:204:LEU:HB3	1.98	0.46
1:A:468:LYS:HD3	1:A:468:LYS:C	2.35	0.46
1:A:1607:GLU:HB2	1:A:1634:SER:HA	1.96	0.46
1:A:1733:ILE:HG23	1:A:1737:ASN:HB2	1.98	0.46
1:A:2070:LYS:HA	1:A:2070:LYS:HD3	1.67	0.46
1:A:2121:ARG:O	1:A:2154:HIS:HA	2.15	0.46
1:A:2314:PHE:HB3	4:D:1125:SER:N	2.29	0.46
2:B:29:A:O2'	2:B:30:A:H5'	2.15	0.46
3:C:66:TYR:CG	33:T:457:GLY:HA2	2.46	0.46
3:C:80:ILE:HD13	33:T:198:ARG:HG3	1.98	0.46
3:C:678:THR:HG21	3:C:683:ASN:CB	2.43	0.46
5:E:260:ARG:CZ	5:E:276:ILE:HD11	2.46	0.46
13:F:37:C:O2	13:F:37:C:H2'	2.15	0.46
14:G:149:G:H2'	14:G:150:U:C6	2.50	0.46
15:H:71:C:O5'	15:H:71:C:H6	1.98	0.46
15:H:79:G:N3	15:H:80:A:C8	2.83	0.46
15:H:142:C:H2'	15:H:143:A:H5'	1.98	0.46
21:1:572:HIS:HB2	21:1:612:THR:HG23	1.96	0.46
21:1:722:GLU:O	21:1:725:ASP:HB2	2.14	0.46
21:1:842:ASN:HA	21:1:879:LEU:HD11	1.96	0.46
21:1:1210:HIS:CD2	22:2:584:LEU:HD22	2.51	0.46
23:3:30:ILE:HG22	23:3:32:VAL:HG13	1.98	0.46
23:3:228:LEU:HD23	23:3:259:LYS:NZ	2.30	0.46
23:3:238:VAL:HB	23:3:247:GLY:O	2.16	0.46
23:3:718:ARG:HG2	23:3:719:SER:N	2.30	0.46
23:3:801:GLU:O	23:3:864:SER:HA	2.16	0.46
33:T:213:GLU:HG3	33:T:218:TRP:NE1	2.29	0.46
1:A:232:LEU:HD11	3:C:412:ILE:HD13	1.95	0.46
1:A:298:ASP:OD1	1:A:300:ASN:N	2.48	0.46
1:A:1370:ARG:HH12	34:V:468:ASP:H	1.58	0.46
1:A:1700:GLY:O	1:A:1717:ASN:N	2.41	0.46
1:A:1782:ASP:OD1	1:A:1865:ARG:HD3	2.15	0.46
3:C:385:VAL:CG2	3:C:386:GLY:N	2.78	0.46
15:H:80:A:N3	15:H:81:G:C8	2.84	0.46
21:1:478:LEU:HA	21:1:496:LYS:HE3	1.97	0.46
21:1:579:GLU:HB3	21:1:627:THR:OG1	2.16	0.46
21:1:903:GLN:HG3	21:1:950:GLN:HE22	1.81	0.46
21:1:1186:GLN:HE22	21:1:1225:HIS:HB3	1.79	0.46
21:1:1253:GLY:HA3	21:1:1265:TYR:CD1	2.51	0.46
23:3:195:ASP:OD2	23:3:200:ALA:N	2.43	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:787:LYS:HB3	23:3:800:ILE:HD11	1.96	0.46
23:3:828:GLY:O	23:3:834:LEU:N	2.49	0.46
23:3:851:ILE:HG23	23:3:852:PHE:CD2	2.50	0.46
25:5:78:SER:HA	25:5:89:VAL:HG21	1.97	0.46
32:R:134:ARG:O	32:R:135:PRO:C	2.54	0.46
1:A:91:ALA:CA	32:R:207:MET:HE2	2.38	0.46
1:A:229:GLN:CB	1:A:415:SER:HB2	2.45	0.46
1:A:748:ASP:CB	31:P:214:THR:HG21	2.46	0.46
1:A:1306:LYS:HZ2	2:B:38:C:C2'	2.27	0.46
1:A:1397:ILE:HG12	32:R:408:GLU:CG	2.45	0.46
3:C:145:PHE:CG	3:C:312:SER:HB3	2.49	0.46
3:C:149:LEU:N	3:C:427:PHE:HE2	2.14	0.46
21:1:862:GLU:O	21:1:865:ARG:N	2.48	0.46
21:1:972:GLY:O	21:1:976:VAL:HG22	2.15	0.46
23:3:253:GLU:HG3	23:3:254:ASN:HD22	1.81	0.46
23:3:488:GLY:C	23:3:490:THR:H	2.19	0.46
25:5:81:ASN:OD1	25:5:82:VAL:N	2.48	0.46
33:T:185:MET:HB2	33:T:186:PRO:HD3	1.98	0.46
1:A:132:ILE:CD1	2:B:57:G:OP1	2.64	0.46
1:A:374:ASP:O	1:A:375:ASP:HB3	2.16	0.46
1:A:384:VAL:HG22	3:C:334:ILE:HG21	1.82	0.46
1:A:1306:LYS:NZ	2:B:38:C:O2'	2.47	0.46
3:C:66:TYR:N	3:C:66:TYR:CD1	2.81	0.46
3:C:507:VAL:HG13	3:C:566:THR:O	2.16	0.46
3:C:559:ILE:HD12	3:C:559:ILE:O	2.15	0.46
3:C:569:ARG:O	3:C:569:ARG:HG2	2.16	0.46
3:C:671:SER:OG	3:C:672:LEU:HD22	2.15	0.46
3:C:853:ARG:O	3:C:854:ARG:CB	2.62	0.46
3:C:934:MET:HE2	3:C:934:MET:HB2	1.77	0.46
5:E:276:ILE:C	5:E:277:PHE:HD1	2.19	0.46
14:G:135:G:O6	14:G:137:C:N4	2.48	0.46
15:H:30:A:C8	29:L:7:LYS:HD3	2.51	0.46
15:H:107:A:C6	15:H:108:G:C6	3.04	0.46
21:1:859:ASP:OD1	21:1:860:GLU:N	2.47	0.46
23:3:448:ALA:HB3	23:3:764:ILE:HB	1.97	0.46
29:L:78:MET:HB3	29:L:81:GLN:OE1	2.16	0.46
37:Z:604:LYS:HA	37:Z:607:VAL:CG2	2.46	0.46
1:A:780:THR:HG22	1:A:898:PHE:CD2	2.50	0.46
1:A:802:THR:HG22	1:A:803:ALA:H	1.80	0.46
1:A:1237:MET:HG2	1:A:1284:LEU:HD21	1.98	0.46
1:A:1312:PRO:O	1:A:1315:VAL:HG22	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1399:GLN:HB3	1:A:1401:ARG:HG2	1.98	0.46
1:A:2112:LYS:HE2	1:A:2112:LYS:HB3	1.67	0.46
13:F:56:A:N1	15:H:20:G:C6	2.84	0.46
15:H:78:C:O5'	15:H:78:C:H6	1.98	0.46
21:1:588:TYR:HA	21:1:591:VAL:HG12	1.98	0.46
21:1:608:THR:O	21:1:612:THR:OG1	2.15	0.46
21:1:759:ALA:O	21:1:763:ASN:HB2	2.16	0.46
23:3:69:ARG:HG2	23:3:70:LEU:O	2.16	0.46
23:3:509:SER:CB	23:3:549:VAL:HG21	2.45	0.46
32:R:88:ILE:HG22	32:R:96:ILE:HG23	1.98	0.46
32:R:220:ARG:NH1	32:R:220:ARG:CB	2.76	0.46
1:A:232:LEU:N	1:A:233:PRO:CD	2.78	0.46
1:A:434:HIS:C	1:A:434:HIS:HD1	2.19	0.46
1:A:841:LEU:HD13	1:A:1433:ASP:HB2	1.98	0.46
1:A:1388:GLU:O	1:A:1392:LYS:HG2	2.16	0.46
1:A:1718:TRP:CZ3	1:A:1726:ILE:HD12	2.50	0.46
3:C:725:ASP:OD1	3:C:727:LEU:CA	2.64	0.46
5:E:276:ILE:C	5:E:277:PHE:CD1	2.89	0.46
13:F:43:A:H2	14:G:4:A:H61	1.64	0.46
15:H:114:A:H2'	15:H:115:G:H8	1.81	0.46
21:1:647:PHE:O	21:1:651:VAL:HG23	2.16	0.46
21:1:1125:PRO:O	21:1:1128:VAL:N	2.49	0.46
21:1:1181:ASP:H	21:1:1184:HIS:HD2	1.64	0.46
23:3:71:THR:HG23	23:3:126:LYS:HD2	1.98	0.46
23:3:482:THR:HG23	23:3:503:THR:O	2.15	0.46
23:3:616:ILE:O	23:3:628:LEU:HB2	2.16	0.46
24:4:29:LEU:HD22	24:4:33:PHE:CE2	2.49	0.46
24:4:32:LEU:CD2	24:4:79:LEU:HD21	2.46	0.46
25:5:46:ARG:HB3	25:5:63:VAL:HG12	1.97	0.46
28:J:406:PHE:CG	28:J:411:MET:CE	2.97	0.46
31:P:54:VAL:HG13	31:P:59:PHE:HZ	1.80	0.46
32:R:185:GLY:C	32:R:186:VAL:HG13	2.35	0.46
1:A:34:ALA:HA	5:E:213:ILE:CD1	2.46	0.46
1:A:121:HIS:HD2	1:A:482:PHE:CE1	2.34	0.46
1:A:738:MET:HE3	1:A:739:ILE:HG13	1.97	0.46
1:A:1328:LEU:HD23	1:A:1470:TYR:CE2	2.51	0.46
1:A:1505:LYS:CD	37:Z:615:SER:CB	2.91	0.46
1:A:2272:MET:HB3	1:A:2272:MET:HE3	1.68	0.46
3:C:678:THR:HG23	3:C:683:ASN:N	2.31	0.46
5:E:248:SER:HB2	5:E:249:TYR:HD1	1.75	0.46
21:1:888:LEU:O	21:1:892:LEU:HG	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:287:PHE:CD1	23:3:303:ALA:HB1	2.50	0.46
31:P:48:GLN:O	31:P:49:ASP:CB	2.64	0.46
32:R:148:ARG:HG3	32:R:148:ARG:NH1	2.31	0.46
1:A:378:PHE:HE2	3:C:335:ASN:HD22	1.62	0.45
1:A:892:LYS:HD2	1:A:912:GLU:OE1	2.16	0.45
1:A:903:SER:OG	1:A:904:HIS:N	2.48	0.45
1:A:1026:ASN:ND2	1:A:1029:GLY:O	2.45	0.45
2:B:22:U:O2	2:B:22:U:H2'	2.15	0.45
2:B:47:A:O2'	2:B:48:A:H8	1.98	0.45
5:E:232:ARG:O	5:E:262:TRP:CH2	2.69	0.45
21:1:744:ALA:O	21:1:787:ILE:HG21	2.16	0.45
21:1:1165:TYR:HE1	22:2:575:PHE:CG	2.33	0.45
23:3:58:VAL:HG12	23:3:1155:LEU:HD23	1.98	0.45
23:3:233:ASN:ND2	23:3:286:ILE:HD12	2.31	0.45
23:3:462:VAL:HG21	23:3:508:CYS:HB3	1.98	0.45
23:3:1012:VAL:HA	23:3:1022:ILE:O	2.17	0.45
1:A:666:LYS:HD3	1:A:666:LYS:N	2.31	0.45
1:A:671:THR:OG1	13:F:69:A:OP1	2.34	0.45
1:A:1084:PRO:HB3	1:A:1101:PHE:CE1	2.51	0.45
3:C:136:GLY:HA3	3:C:228:PHE:O	2.16	0.45
3:C:301:SER:C	3:C:303:LEU:N	2.68	0.45
3:C:499:GLY:C	3:C:500:THR:HG23	2.36	0.45
3:C:753:GLU:C	3:C:755:ASP:H	2.19	0.45
13:F:57:U:C2	13:F:58:G:N7	2.84	0.45
14:G:10:U:O2'	14:G:11:A:OP1	2.28	0.45
21:1:701:VAL:O	21:1:705:SER:HB3	2.16	0.45
23:3:536:TRP:CG	23:3:566:PHE:HZ	2.33	0.45
23:3:700:LYS:NZ	23:3:740:GLU:O	2.41	0.45
23:3:701:LEU:HA	23:3:713:LEU:O	2.16	0.45
1:A:61:MET:HB3	1:A:62:PRO:HD2	1.98	0.45
1:A:305:ARG:NH2	3:C:854:ARG:HD3	2.31	0.45
1:A:907:PRO:CD	31:P:229:LYS:HB2	2.39	0.45
1:A:1957:ASP:HB3	1:A:1960:THR:HG23	1.98	0.45
3:C:336:TYR:CD1	3:C:336:TYR:C	2.89	0.45
5:E:146:ARG:NH1	5:E:148:LYS:NZ	2.62	0.45
15:H:60:U:H2'	15:H:61:C:H6	1.81	0.45
21:1:1074:ARG:HD2	21:1:1111:CYS:SG	2.55	0.45
23:3:169:HIS:CD2	23:3:170:VAL:H	2.34	0.45
23:3:526:HIS:HB3	23:3:534:ASN:O	2.17	0.45
23:3:544:ILE:HD11	23:3:556:ILE:HG21	1.98	0.45
23:3:805:ASN:O	23:3:856:LYS:HB3	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:P:227:TYR:N	31:P:227:TYR:HD1	2.14	0.45
33:T:306:CYS:SG	33:T:336:VAL:HG12	2.56	0.45
1:A:305:ARG:HH21	3:C:854:ARG:CZ	2.29	0.45
1:A:1434:LYS:O	1:A:1439:ARG:NH1	2.45	0.45
2:B:57:G:H2'	2:B:58:U:H5'	1.99	0.45
3:C:193:THR:HG22	3:C:428:THR:HG21	1.97	0.45
3:C:482:TYR:CE2	3:C:493:PHE:CG	2.89	0.45
5:E:119:THR:CG2	5:E:161:ARG:CB	2.73	0.45
5:E:157:CYS:HA	5:E:168:CYS:O	2.16	0.45
15:H:181:G:C2	15:H:182:U:N3	2.84	0.45
21:1:427:PRO:O	21:1:431:LEU:N	2.45	0.45
21:1:834:VAL:O	21:1:838:VAL:HG23	2.16	0.45
21:1:1181:ASP:OD1	21:1:1182:LEU:N	2.46	0.45
23:3:257:THR:OG1	23:3:268:ARG:HG2	2.16	0.45
23:3:482:THR:HG21	23:3:505:THR:OG1	2.17	0.45
23:3:897:SER:HB2	23:3:957:GLY:HA3	1.97	0.45
23:3:905:VAL:HG23	23:3:930:LEU:HB2	1.98	0.45
27:7:73:LEU:HD12	27:7:74:GLN:N	2.32	0.45
31:P:193:VAL:CG2	31:P:194:PHE:N	2.79	0.45
32:R:88:ILE:HD12	32:R:88:ILE:N	2.29	0.45
32:R:181:PRO:O	32:R:182:SER:CB	2.58	0.45
1:A:966:TRP:HE3	1:A:1178:TYR:CZ	2.35	0.45
1:A:1426:ASP:OD2	32:R:421:GLY:CA	2.64	0.45
1:A:1809:ILE:HB	1:A:1818:PHE:HB2	1.97	0.45
1:A:1900:GLU:OE2	37:Z:521:PRO:CA	2.64	0.45
3:C:183:SER:OG	3:C:480:LYS:NZ	2.50	0.45
3:C:230:ASP:CG	3:C:259:LYS:HZ1	2.19	0.45
5:E:243:LEU:CD1	5:E:247:GLY:CA	2.84	0.45
15:H:25:G:C2	15:H:26:A:C5	3.04	0.45
15:H:150:U:H3	15:H:181:G:H1	1.62	0.45
15:H:152:G:O2'	15:H:153:A:H1'	2.16	0.45
23:3:796:ASN:HA	23:3:871:PRO:HD3	1.98	0.45
28:J:360:ASP:HA	28:J:363:ARG:CD	2.46	0.45
33:T:409:LEU:HD12	33:T:409:LEU:N	2.31	0.45
1:A:75:ASP:HB2	1:A:77:THR:OG1	2.16	0.45
1:A:168:PRO:HG2	1:A:559:ASP:CB	2.36	0.45
1:A:466:ALA:HB3	2:B:54:U:OP2	2.17	0.45
1:A:730:GLY:O	1:A:731:LEU:HB2	2.16	0.45
1:A:1413:ASP:OD1	1:A:1414:ARG:HG3	2.17	0.45
1:A:1604:LEU:HD11	1:A:1725:LEU:HD22	1.98	0.45
1:A:2169:LEU:HD21	1:A:2272:MET:HG3	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2303:GLU:CD	1:A:2303:GLU:H	2.19	0.45
3:C:66:TYR:CB	33:T:456:PRO:O	2.51	0.45
3:C:495:ARG:HG3	3:C:495:ARG:O	2.16	0.45
3:C:497:LEU:CD1	3:C:577:PHE:CE1	2.94	0.45
3:C:852:ARG:NH2	14:G:-12:G:OP1	2.50	0.45
4:D:1349:GLY:HA2	4:D:1491:SER:O	2.16	0.45
5:E:260:ARG:CD	5:E:276:ILE:HG12	2.47	0.45
13:F:94:C:H2'	13:F:95:G:H8	1.82	0.45
14:G:-12:G:HO2'	14:G:-11:G:C5'	2.29	0.45
23:3:115:ILE:HD11	27:7:18:TYR:CE1	2.51	0.45
32:R:179:TYR:CE2	32:R:181:PRO:HG3	2.52	0.45
33:T:297:HIS:CD2	33:T:338:CYS:SG	3.09	0.45
37:Z:525:TYR:CE1	37:Z:526:ILE:CG2	2.86	0.45
1:A:193:LEU:HB3	1:A:208:TYR:OH	2.17	0.45
1:A:331:TRP:CE3	1:A:331:TRP:C	2.90	0.45
1:A:648:LEU:HD23	1:A:648:LEU:HA	1.79	0.45
1:A:1768:TYR:HE1	1:A:1930:TYR:CE1	2.34	0.45
3:C:926:ALA:N	3:C:927:PRO:HD2	2.32	0.45
5:E:178:LEU:HG	5:E:188:GLN:HB2	1.98	0.45
5:E:277:PHE:CD1	5:E:277:PHE:N	2.83	0.45
21:1:86:ALA:O	21:1:89:ALA:HB3	2.17	0.45
21:1:476:ASP:OD1	21:1:477:LYS:N	2.49	0.45
21:1:1110:VAL:O	21:1:1113:THR:HB	2.17	0.45
21:1:1251:LEU:HD12	22:2:497:SER:OG	2.16	0.45
23:3:223:LYS:HE2	23:3:224:TYR:CZ	2.52	0.45
23:3:429:ARG:HH12	27:7:59:GLU:H	1.65	0.45
23:3:1114:SER:HB2	23:3:1215:TYR:CE1	2.51	0.45
28:J:338:GLU:O	32:R:116:TYR:CE1	2.69	0.45
32:R:128:ASP:OD2	32:R:133:GLN:OE1	2.34	0.45
33:T:393:ASP:O	33:T:413:ASN:ND2	2.49	0.45
37:Z:564:PRO:O	37:Z:582:TYR:CG	2.69	0.45
37:Z:600:ARG:CG	37:Z:600:ARG:NH1	2.73	0.45
1:A:259:ASP:C	1:A:259:ASP:OD1	2.55	0.45
1:A:586:GLY:O	1:A:592:TYR:CE2	2.69	0.45
1:A:755:HIS:CG	31:P:219:PHE:HE2	2.35	0.45
1:A:833:LYS:HG3	1:A:834:HIS:CD2	2.52	0.45
1:A:975:VAL:HG11	1:A:1153:VAL:HG21	1.98	0.45
1:A:1963:GLU:HB2	1:A:1966:HIS:HD2	1.81	0.45
3:C:144:CYS:SG	3:C:148:CYS:SG	3.15	0.45
13:F:38:G:OP2	13:F:38:G:C8	2.70	0.45
14:G:6:A:H2'	14:G:7:G:H8	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:501:LEU:O	21:1:504:ILE:N	2.48	0.45
21:1:592:GLU:O	21:1:596:ILE:HG23	2.16	0.45
21:1:629:ALA:HA	21:1:667:ILE:HG12	1.99	0.45
23:3:383:ASP:OD1	23:3:384:THR:N	2.50	0.45
23:3:1057:ARG:HB2	23:3:1092:ILE:HD13	1.98	0.45
32:R:82:MET:C	32:R:82:MET:CE	2.86	0.45
36:Y:41:GLY:HA2	36:Y:79:PHE:HB3	1.99	0.45
1:A:305:ARG:HG3	3:C:878:ILE:CB	2.46	0.45
1:A:318:TYR:O	3:C:641:MET:CB	2.65	0.45
1:A:660:PHE:CE2	32:R:209:PRO:CB	3.00	0.45
1:A:733:THR:OG1	1:A:734:PRO:HD3	2.16	0.45
1:A:1013:ASN:OD1	1:A:1030:ILE:HG13	2.16	0.45
1:A:1904:ASP:O	1:A:1908:LYS:HG2	2.16	0.45
1:A:1949:ARG:HA	1:A:1952:VAL:HG23	1.98	0.45
1:A:2074:ARG:O	1:A:2078:ILE:HD13	2.17	0.45
2:B:40:U:O4	14:G:-1:G:O6	2.35	0.45
3:C:137:HIS:HD2	3:C:236:MET:HB2	1.61	0.45
3:C:191:PRO:HG2	3:C:426:GLU:OE1	2.17	0.45
3:C:445:ALA:HB1	3:C:449:ILE:CG1	2.45	0.45
5:E:162:ARG:HH21	5:E:204:THR:HA	1.78	0.45
13:F:51:U:H2'	13:F:52:U:O4'	2.17	0.45
21:1:552:LEU:HA	21:1:555:VAL:HG12	1.98	0.45
21:1:822:ARG:NH1	36:Y:31:GLU:HG2	2.32	0.45
21:1:897:LEU:O	21:1:901:GLN:HG3	2.17	0.45
21:1:1186:GLN:NE2	21:1:1225:HIS:HB3	2.31	0.45
23:3:643:VAL:HG12	23:3:664:TYR:O	2.17	0.45
25:5:48:ILE:HG12	25:5:62:VAL:HG23	1.99	0.45
28:J:406:PHE:CB	28:J:411:MET:HG2	2.47	0.45
33:T:342:GLU:CB	33:T:343:PRO:HD2	2.47	0.45
33:T:454:VAL:HG22	33:T:463:SER:OG	2.16	0.45
33:T:455:GLN:CG	33:T:456:PRO:CD	2.94	0.45
1:A:44:ARG:CD	1:A:45:TYR:CE2	2.99	0.45
1:A:256:TYR:CG	3:C:888:ARG:NH2	2.85	0.45
1:A:382:GLU:O	1:A:383:PHE:CD2	2.70	0.45
1:A:507:LEU:HD12	1:A:507:LEU:HA	1.79	0.45
1:A:661:GLU:CG	32:R:210:PRO:HB3	2.47	0.45
1:A:845:ARG:NH2	1:A:1439:ARG:HE	2.15	0.45
1:A:1258:LYS:HE2	32:R:432:GLU:CB	2.47	0.45
1:A:1780:VAL:HG22	1:A:1809:ILE:HG12	1.99	0.45
3:C:65:TYR:O	3:C:66:TYR:CB	2.65	0.45
3:C:230:ASP:OD2	3:C:233:GLU:CG	2.55	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:502:HIS:ND1	3:C:543:ARG:HB3	2.32	0.45
3:C:926:ALA:HA	3:C:929:LEU:HG	1.98	0.45
13:F:50:A:H2'	13:F:51:U:H6	1.82	0.45
14:G:6:A:H2'	14:G:7:G:C8	2.52	0.45
14:G:12:G:N3	14:G:12:G:C2'	2.79	0.45
14:G:157:U:H5'	21:1:622:GLU:OE1	2.17	0.45
15:H:113:G:H2'	15:H:114:A:H8	1.82	0.45
21:1:1002:ASN:OD1	21:1:1041:ARG:NH2	2.50	0.45
22:2:611:ASP:O	22:2:614:ARG:CB	2.60	0.45
23:3:462:VAL:O	23:3:472:ALA:N	2.46	0.45
23:3:509:SER:OG	23:3:517:VAL:O	2.20	0.45
23:3:883:GLU:HG3	23:3:884:GLN:N	2.32	0.45
23:3:1051:GLY:HA2	23:3:1100:THR:HA	1.99	0.45
25:5:26:LEU:HD12	25:5:87:LEU:HD22	1.98	0.45
27:7:31:TRP:HE3	27:7:32:LEU:HD12	1.82	0.45
29:L:226:ASP:OD1	32:R:83:SER:HB2	2.16	0.45
32:R:88:ILE:HG21	32:R:96:ILE:CG2	2.46	0.45
32:R:408:GLU:CG	32:R:409:VAL:N	2.78	0.45
35:X:336:GLY:HA3	35:X:378:GLU:HB2	1.99	0.45
37:Z:524:ARG:HD2	37:Z:525:TYR:CB	2.46	0.45
1:A:76:MET:SD	1:A:88:TYR:CE2	3.10	0.44
1:A:193:LEU:HD12	1:A:194:GLU:N	2.29	0.44
1:A:1147:VAL:HG23	1:A:1148:ASN:N	2.33	0.44
3:C:93:ILE:CG2	33:T:218:TRP:NE1	2.80	0.44
5:E:276:ILE:O	5:E:277:PHE:HD1	2.00	0.44
13:F:68:C:C5	31:P:33:ARG:HG2	2.52	0.44
13:F:94:C:H2'	13:F:95:G:C8	2.52	0.44
15:H:7:U:H2'	15:H:8:C:C6	2.52	0.44
15:H:81:G:N3	15:H:82:G:C8	2.85	0.44
15:H:141:C:H2'	15:H:142:C:C6	2.50	0.44
21:1:810:ILE:O	21:1:813:PRO:HD2	2.17	0.44
23:3:460:TRP:CE2	23:3:507:SER:HA	2.52	0.44
23:3:723:TYR:CD1	23:3:725:TYR:HB2	2.53	0.44
23:3:1140:PHE:O	23:3:1144:VAL:HG23	2.17	0.44
32:R:147:THR:HG23	33:T:360:VAL:CG1	2.40	0.44
32:R:416:PHE:O	32:R:416:PHE:CG	2.70	0.44
1:A:89:LEU:CD2	1:A:656:LEU:CD2	2.95	0.44
1:A:1088:PHE:HD1	1:A:1097:ILE:HG12	1.82	0.44
1:A:1430:LEU:HD11	32:R:422:MET:HA	1.98	0.44
1:A:1591:MET:SD	1:A:1611:LYS:NZ	2.75	0.44
1:A:1788:VAL:HA	1:A:1802:PRO:HA	1.98	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2196:HIS:HB3	1:A:2230:LEU:HD11	1.98	0.44
1:A:2222:SER:OG	1:A:2223:CYS:N	2.50	0.44
1:A:2334:TYR:CE1	4:D:591:GLU:CB	3.00	0.44
2:B:40:U:OP2	2:B:40:U:C6	2.70	0.44
3:C:93:ILE:CG2	33:T:218:TRP:CZ2	3.00	0.44
3:C:388:VAL:HA	3:C:392:LEU:HB2	1.99	0.44
5:E:132:THR:HG21	5:E:146:ARG:HG2	1.98	0.44
13:F:58:G:O2'	13:F:59:G:OP1	2.31	0.44
15:H:143:A:OP2	15:H:143:A:C2	2.71	0.44
15:H:157:G:H5"	15:H:157:G:C8	2.50	0.44
21:1:762:ALA:O	21:1:766:THR:CB	2.64	0.44
21:1:1252:GLN:NE2	22:2:492:LYS:O	2.51	0.44
22:2:613:LEU:HD21	24:4:32:LEU:HD13	1.99	0.44
23:3:404:LEU:HB3	23:3:407:ILE:HD11	1.99	0.44
23:3:536:TRP:CD1	23:3:566:PHE:HZ	2.35	0.44
23:3:607:VAL:HB	23:3:615:ARG:O	2.17	0.44
23:3:1159:ASP:OD1	23:3:1160:HIS:N	2.49	0.44
28:J:297:ASN:OD1	29:L:223:GLY:O	2.34	0.44
34:V:548:ALA:HB2	34:V:585:ILE:CB	2.42	0.44
1:A:317:PRO:HB2	1:A:327:VAL:HG11	1.98	0.44
1:A:1459:ARG:HD3	1:A:1459:ARG:HA	1.75	0.44
1:A:1785:VAL:O	1:A:1805:GLY:HA3	2.17	0.44
1:A:2328:ALA:CB	4:D:788:GLY:N	2.79	0.44
3:C:140:HIS:HB3	3:C:230:ASP:CB	2.43	0.44
3:C:671:SER:CB	3:C:672:LEU:HD22	2.46	0.44
4:D:721:VAL:HA	4:D:825:THR:O	2.17	0.44
5:E:209:ILE:HG21	5:E:250:LEU:HD11	1.94	0.44
13:F:39:A:H2'	13:F:40:U:C6	2.52	0.44
21:1:529:GLY:HA2	21:1:570:TYR:CZ	2.51	0.44
23:3:205:GLN:HB2	23:3:228:LEU:O	2.17	0.44
23:3:747:SER:N	23:3:750:CYS:O	2.51	0.44
25:5:98:PHE:O	25:5:100:LYS:N	2.50	0.44
31:P:188:TRP:N	31:P:188:TRP:CD2	2.86	0.44
32:R:416:PHE:O	32:R:416:PHE:CD1	2.70	0.44
33:T:387:PHE:CZ	33:T:398:TRP:CD1	3.04	0.44
37:Z:500:GLY:O	37:Z:503:GLN:N	2.50	0.44
37:Z:573:PRO:O	37:Z:573:PRO:CD	2.65	0.44
37:Z:597:ARG:CZ	37:Z:601:LEU:HD13	2.47	0.44
1:A:777:GLY:O	1:A:780:THR:OG1	2.25	0.44
1:A:1074:PHE:HB3	1:A:1079:THR:OG1	2.17	0.44
1:A:1631:LEU:HD12	1:A:1660:TYR:CD2	2.51	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:42:U:O2	14:G:-3:A:H2	2.00	0.44
13:F:5:U:H5'	13:F:6:C:OP2	2.17	0.44
15:H:159:U:H2'	15:H:160:A:C8	2.52	0.44
15:H:165:A:C6	15:H:166:G:O6	2.71	0.44
21:1:937:LEU:O	21:1:940:LEU:HB3	2.18	0.44
22:2:611:ASP:O	22:2:614:ARG:N	2.50	0.44
23:3:1063:ASN:H	23:3:1087:GLN:HE22	1.65	0.44
23:3:1096:HIS:NE2	23:3:1098:GLY:HA2	2.33	0.44
31:P:189:ASP:C	31:P:191:ASP:N	2.68	0.44
33:T:439:TRP:CE3	33:T:446:ASN:HB2	2.52	0.44
34:V:525:PHE:O	34:V:526:GLU:C	2.55	0.44
36:Y:36:ALA:CB	37:Z:499:LYS:O	2.54	0.44
1:A:359:ILE:O	1:A:360:SER:HB3	2.16	0.44
1:A:373:ASP:OD1	1:A:374:ASP:N	2.51	0.44
1:A:638:LEU:HA	1:A:638:LEU:HD23	1.70	0.44
1:A:1110:ILE:HG22	1:A:1114:LEU:HD12	1.98	0.44
1:A:1402:ARG:HD2	32:R:412:ASP:HA	1.98	0.44
1:A:1533:ARG:HD2	1:A:1751:LEU:O	2.18	0.44
1:A:1553:VAL:O	1:A:1561:PHE:HA	2.18	0.44
1:A:1957:ASP:O	1:A:1960:THR:OG1	2.19	0.44
1:A:2073:TRP:CZ3	1:A:2313:HIS:CE1	3.05	0.44
3:C:135:CYS:SG	3:C:227:LEU:CB	3.06	0.44
3:C:259:LYS:HD2	41:C:1500:GTP:C5	2.52	0.44
3:C:673:LYS:HG3	3:C:686:THR:HG23	2.00	0.44
14:G:21:A:O3'	14:G:22:C:C6	2.71	0.44
15:H:60:U:H2'	15:H:61:C:C6	2.52	0.44
21:1:1211:LEU:O	21:1:1215:VAL:HG23	2.17	0.44
23:3:442:LEU:HD11	23:3:732:THR:OG1	2.17	0.44
23:3:636:GLN:O	23:3:670:GLN:HG2	2.17	0.44
26:6:58:CYS:N	26:6:63:GLY:O	2.46	0.44
36:Y:58:GLN:HB2	37:Z:584:TRP:NE1	2.33	0.44
1:A:121:HIS:CD2	1:A:481:PHE:O	2.70	0.44
1:A:381:PRO:HG2	3:C:333:ASP:HB2	2.00	0.44
1:A:707:ARG:O	1:A:711:GLN:HG3	2.17	0.44
1:A:978:GLU:OE2	1:A:1188:ASN:N	2.36	0.44
1:A:1364:LEU:CD1	34:V:461:LEU:O	2.66	0.44
1:A:1407:ASP:OD1	1:A:1407:ASP:N	2.51	0.44
1:A:1667:ARG:HD2	1:A:1679:TYR:CD2	2.52	0.44
1:A:2125:ALA:O	1:A:2150:GLN:NE2	2.50	0.44
1:A:2237:TRP:HZ2	1:A:2248:PRO:HB2	1.81	0.44
3:C:457:VAL:CG1	3:C:462:GLY:HA3	2.46	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:34:U:C4	15:H:35:A:N7	2.85	0.44
15:H:73:C:O5'	15:H:73:C:H6	2.01	0.44
15:H:142:C:O2'	15:H:143:A:H5'	2.18	0.44
15:H:147:G:C6	15:H:148:C:N4	2.86	0.44
21:1:1108:ASN:OD1	21:1:1110:VAL:HG12	2.17	0.44
23:3:812:LYS:O	23:3:816:LYS:CB	2.57	0.44
31:P:193:VAL:HG23	31:P:194:PHE:CB	2.47	0.44
36:Y:63:VAL:HG23	36:Y:64:ASN:N	2.33	0.44
1:A:369:GLU:HB2	1:A:370:PRO:HD2	2.00	0.44
1:A:1362:ASP:OD1	1:A:1362:ASP:N	2.51	0.44
1:A:1674:HIS:HB3	1:A:1709:TYR:CE2	2.53	0.44
1:A:2121:ARG:HA	1:A:2121:ARG:HD2	1.55	0.44
3:C:145:PHE:HD1	3:C:312:SER:HB3	1.83	0.44
13:F:9:U:H2'	13:F:10:U:C6	2.52	0.44
13:F:68:C:C5	31:P:33:ARG:CG	2.95	0.44
15:H:26:A:C6	15:H:27:U:C4	3.05	0.44
21:1:1072:ALA:O	21:1:1075:ARG:HB3	2.18	0.44
23:3:929:LYS:HD3	23:3:938:GLU:OE2	2.17	0.44
29:L:224:PHE:CE1	32:R:86:LEU:HD12	2.43	0.44
33:T:342:GLU:O	33:T:343:PRO:C	2.56	0.44
37:Z:584:TRP:CZ3	37:Z:586:GLY:HA2	2.53	0.44
1:A:73:HIS:HA	1:A:81:PHE:CE2	2.53	0.44
1:A:121:HIS:CA	1:A:481:PHE:O	2.66	0.44
1:A:251:ASP:HA	1:A:337:VAL:CG2	2.48	0.44
1:A:363:HIS:CE1	3:C:287:GLY:CA	3.00	0.44
1:A:1034:LEU:HB2	1:A:1037:ALA:HB2	1.98	0.44
1:A:1457:HIS:CE1	32:R:424:SER:C	2.90	0.44
1:A:1555:LEU:HD12	1:A:1560:ILE:HB	2.00	0.44
1:A:1557:LEU:HD13	1:A:1580:HIS:CE1	2.53	0.44
1:A:2280:ASN:HB3	1:A:2309:HIS:CD2	2.53	0.44
21:1:601:ALA:HB2	21:1:635:VAL:HG12	2.00	0.44
21:1:969:LYS:O	21:1:973:HIS:ND1	2.36	0.44
23:3:353:PHE:CD1	23:3:406:PRO:HD3	2.53	0.44
23:3:607:VAL:HG21	23:3:617:ILE:HD12	1.99	0.44
23:3:930:LEU:HG	23:3:934:GLY:HA2	1.98	0.44
24:4:79:LEU:HG	24:4:84:ILE:HG13	2.00	0.44
31:P:66:ARG:HB2	31:P:66:ARG:NH1	2.30	0.44
32:R:124:VAL:HG22	32:R:125:MET:H	1.83	0.44
32:R:132:LEU:HD23	32:R:132:LEU:N	2.31	0.44
32:R:208:GLU:OE2	32:R:211:ARG:NH1	2.51	0.44
32:R:415:LEU:H	32:R:415:LEU:HG	1.56	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:358:ASP:HB2	33:T:365:ARG:HD2	2.00	0.44
37:Z:524:ARG:CD	37:Z:524:ARG:C	2.85	0.44
1:A:86:ARG:NH2	32:R:211:ARG:CG	2.63	0.44
1:A:94:TYR:CD2	32:R:207:MET:SD	3.11	0.44
1:A:941:LYS:HE3	1:A:951:LEU:HD21	2.00	0.44
1:A:1038:SER:HA	1:A:1442:PHE:HE2	1.83	0.44
1:A:1900:GLU:CG	37:Z:521:PRO:HG3	2.39	0.44
3:C:439:PRO:O	3:C:440:SER:CB	2.66	0.44
3:C:465:MET:HE1	3:C:475:MET:CE	2.47	0.44
3:C:779:LEU:HD11	3:C:825:PRO:HB2	1.99	0.44
14:G:11:A:C5	14:G:12:G:C8	3.06	0.44
14:G:21:A:O3'	14:G:22:C:H6	2.00	0.44
15:H:6:U:H2'	15:H:7:U:C6	2.53	0.44
21:1:503:LYS:HD2	21:1:515:ALA:HB2	2.00	0.44
21:1:779:SER:HB3	21:1:784:MET:HG2	2.00	0.44
21:1:1131:ALA:O	21:1:1135:GLU:HG2	2.17	0.44
23:3:411:GLN:HA	23:3:1105:GLN:OE1	2.18	0.44
23:3:798:ILE:HA	23:3:867:ARG:O	2.18	0.44
25:5:46:ARG:N	25:5:63:VAL:O	2.50	0.44
1:A:44:ARG:HG2	1:A:45:TYR:CD2	2.53	0.43
1:A:79:ARG:HD2	1:A:79:ARG:O	2.18	0.43
1:A:394:TYR:CD1	1:A:394:TYR:N	2.86	0.43
1:A:1118:PRO:O	1:A:1120:PRO:O	2.36	0.43
1:A:2073:TRP:CH2	1:A:2313:HIS:CG	3.06	0.43
3:C:229:ILE:CG2	3:C:234:GLY:O	2.66	0.43
5:E:248:SER:HB2	5:E:249:TYR:CE1	2.53	0.43
13:F:35:A:C8	14:G:12:G:O6	2.71	0.43
13:F:68:C:H42	33:T:283:HIS:CE1	2.35	0.43
21:1:903:GLN:HG3	21:1:950:GLN:NE2	2.33	0.43
23:3:176:GLY:O	23:3:178:GLU:HG2	2.17	0.43
23:3:446:GLU:CD	23:3:763:ARG:HD3	2.38	0.43
23:3:745:PHE:HB2	23:3:755:VAL:HG23	2.00	0.43
23:3:998:HIS:HE1	23:3:1064:ASP:OD2	2.00	0.43
23:3:1207:LYS:HA	23:3:1210:ASP:OD2	2.18	0.43
25:5:53:THR:O	25:5:57:ARG:HG3	2.18	0.43
28:J:339:TRP:C	32:R:116:TYR:CE2	2.92	0.43
32:R:109:ASP:OD1	32:R:110:LYS:N	2.51	0.43
33:T:454:VAL:CG1	33:T:455:GLN:N	2.81	0.43
1:A:106:MET:HG2	1:A:489:TRP:CZ2	2.53	0.43
1:A:210:HIS:CD2	1:A:210:HIS:C	2.92	0.43
1:A:330:THR:O	1:A:331:TRP:HB2	2.17	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:LEU:O	1:A:698:PRO:HG3	2.18	0.43
1:A:970:GLU:HB2	1:A:972:GLU:OE2	2.17	0.43
1:A:1301:ILE:HD11	2:B:39:C:OP1	2.18	0.43
1:A:1532:ARG:HG2	1:A:1572:SER:OG	2.18	0.43
1:A:2310:ARG:HH11	1:A:2310:ARG:HB3	1.83	0.43
3:C:135:CYS:N	3:C:226:VAL:O	2.50	0.43
3:C:392:LEU:HD12	3:C:392:LEU:O	2.18	0.43
3:C:508:LYS:O	3:C:566:THR:HG22	2.18	0.43
3:C:674:CYS:HB2	3:C:818:SER:HB3	2.00	0.43
3:C:703:GLU:OE2	3:C:740:THR:CG2	2.50	0.43
5:E:251:LEU:CG	5:E:291:CYS:SG	3.05	0.43
15:H:159:U:H2'	15:H:160:A:H8	1.83	0.43
15:H:182:U:H6	15:H:182:U:O5'	2.01	0.43
21:1:528:ALA:HB2	21:1:563:LEU:HD13	2.00	0.43
21:1:732:TRP:O	21:1:735:ILE:HB	2.19	0.43
22:2:556:LYS:O	22:2:559:PRO:HD3	2.18	0.43
23:3:409:PHE:HD2	23:3:788:PHE:CE2	2.36	0.43
23:3:484:VAL:HG21	23:3:499:PHE:HB2	1.99	0.43
23:3:791:HIS:ND1	23:3:794:SER:HB3	2.33	0.43
23:3:837:GLU:O	23:3:837:GLU:HG2	2.17	0.43
32:R:419:SER:C	32:R:420:LYS:O	2.55	0.43
1:A:345:PRO:O	1:A:346:ASP:O	2.35	0.43
1:A:525:LYS:HG2	30:M:194:ARG:CG	2.48	0.43
1:A:908:VAL:HA	1:A:1445:TYR:O	2.18	0.43
1:A:1071:PHE:CD2	1:A:1072:LEU:HG	2.53	0.43
1:A:1544:ARG:HB3	1:A:1672:ASP:OD2	2.19	0.43
1:A:2067:PHE:HB2	1:A:2072:GLU:HG2	2.00	0.43
2:B:12:U:O2'	2:B:13:C:P	2.77	0.43
3:C:131:ASN:HB3	3:C:549:TRP:CZ2	2.52	0.43
3:C:524:ILE:O	3:C:525:CYS:SG	2.74	0.43
15:H:64:A:H2'	15:H:65:U:C6	2.53	0.43
15:H:153:A:H2'	15:H:154:C:H5"	1.99	0.43
21:1:840:LEU:O	21:1:844:VAL:HG12	2.19	0.43
22:2:482:ALA:O	22:2:485:PRO:HD3	2.18	0.43
23:3:88:VAL:HA	23:3:103:HIS:O	2.18	0.43
23:3:458:ALA:C	23:3:757:ILE:HG12	2.39	0.43
23:3:511:LEU:HB2	23:3:517:VAL:HG23	1.99	0.43
23:3:1056:VAL:HG22	23:3:1091:VAL:HG22	2.01	0.43
24:4:67:ALA:HA	24:4:70:ALA:HB3	2.00	0.43
32:R:88:ILE:HG22	32:R:96:ILE:CG2	2.49	0.43
33:T:406:ILE:HG22	33:T:407:GLN:N	2.33	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:LEU:HD21	3:C:388:VAL:CG1	2.32	0.43
1:A:305:ARG:CG	3:C:878:ILE:HG21	2.38	0.43
1:A:318:TYR:O	3:C:641:MET:HB2	2.19	0.43
1:A:459:LEU:HD12	1:A:459:LEU:HA	1.75	0.43
1:A:741:ARG:NH2	33:T:432:ASP:O	2.41	0.43
1:A:1113:TYR:O	1:A:1117:HIS:CB	2.66	0.43
1:A:1263:TRP:CE3	1:A:1295:ILE:HD13	2.53	0.43
2:B:64:G:C5'	5:E:106:LYS:HZ3	2.13	0.43
2:B:99:C:H2'	2:B:100:C:C6	2.53	0.43
3:C:133:THR:CB	3:C:225:VAL:HG23	2.43	0.43
3:C:297:ASN:HD22	3:C:298:LEU:HD12	1.83	0.43
3:C:350:ASN:HB3	3:C:353:THR:CG2	2.49	0.43
3:C:505:GLN:HG2	3:C:506:PRO:HD2	2.00	0.43
3:C:776:GLU:O	3:C:781:ASP:HA	2.18	0.43
13:F:42:C:H2'	13:F:43:A:C8	2.53	0.43
21:1:885:ASP:OD1	21:1:888:LEU:HB3	2.18	0.43
21:1:1119:VAL:O	21:1:1122:THR:HG22	2.17	0.43
21:1:1120:ALA:HB1	21:1:1125:PRO:HB3	2.01	0.43
21:1:1179:ASP:HB3	22:2:511:LEU:HD12	2.00	0.43
22:2:630:PRO:HA	22:2:631:PRO:HD3	1.77	0.43
23:3:136:GLU:OE2	23:3:189:TYR:OH	2.10	0.43
29:L:63:TRP:CH2	29:L:99:HIS:HB2	2.54	0.43
29:L:101:GLU:O	29:L:105:ASP:HB2	2.18	0.43
32:R:54:LEU:HD12	32:R:54:LEU:HA	1.86	0.43
32:R:55:LEU:C	32:R:73:PRO:O	2.56	0.43
33:T:399:LYS:HG3	33:T:406:ILE:CD1	2.37	0.43
36:Y:36:ALA:HB3	37:Z:498:GLY:O	2.18	0.43
1:A:141:ILE:HG12	1:A:426:LEU:HD23	1.99	0.43
1:A:643:GLY:O	1:A:646:PRO:HD2	2.19	0.43
3:C:145:PHE:N	3:C:312:SER:OG	2.50	0.43
3:C:736:GLY:HA3	3:C:770:PHE:CE2	2.53	0.43
5:E:67:GLY:N	5:E:87:ASP:OD1	2.42	0.43
14:G:-5:G:O2'	14:G:-4:A:H5"	2.18	0.43
15:H:83:A:C4	15:H:84:C:C6	3.07	0.43
15:H:98:G:H5'	15:H:104:U:OP2	2.18	0.43
15:H:154:C:O2'	15:H:155:C:C5'	2.66	0.43
15:H:181:G:C2	15:H:182:U:C4	3.07	0.43
21:1:897:LEU:HD21	21:1:932:ILE:HD13	2.00	0.43
21:1:1235:GLU:O	21:1:1238:ARG:HB3	2.18	0.43
23:3:139:LYS:HB2	23:3:160:ALA:HB3	2.00	0.43
23:3:868:VAL:HG12	23:3:877:LEU:HB2	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:R:126:ASN:HD22	32:R:128:ASP:H	1.66	0.43
36:Y:29:HIS:CG	36:Y:91:ILE:HG23	2.53	0.43
1:A:148:TRP:HE3	1:A:629:PHE:CD1	2.35	0.43
1:A:253:ASN:CG	1:A:334:THR:O	2.57	0.43
1:A:417:ARG:NH1	2:B:58:U:H4'	2.33	0.43
1:A:549:GLU:CD	1:A:552:ARG:NH1	2.72	0.43
1:A:1382:SER:HB3	1:A:1416:ILE:HG12	2.00	0.43
1:A:1771:LEU:HD12	1:A:1777:ILE:HD13	2.00	0.43
1:A:2284:MET:HE1	1:A:2311:PRO:HG3	2.01	0.43
3:C:60:HIS:ND1	3:C:60:HIS:O	2.51	0.43
13:F:36:A:C3'	13:F:36:A:C8	3.01	0.43
15:H:157:G:H2'	15:H:158:G:O4'	2.19	0.43
21:1:889:GLU:HA	21:1:892:LEU:HD12	2.00	0.43
22:2:613:LEU:HD11	24:4:32:LEU:HD13	1.99	0.43
23:3:32:VAL:HG23	23:3:39:GLU:HB3	1.99	0.43
25:5:114:LYS:HA	25:5:119:ILE:O	2.19	0.43
29:L:73:HIS:CD2	29:L:77:LEU:HD11	2.53	0.43
32:R:52:PRO:HB3	32:R:57:ASP:OD2	2.17	0.43
32:R:119:LEU:HA	32:R:232:MET:CE	2.49	0.43
32:R:120:VAL:HG23	32:R:121:PRO:HD2	2.01	0.43
33:T:459:LEU:HG	33:T:461:SER:OG	2.18	0.43
1:A:661:GLU:HG3	32:R:210:PRO:HB2	2.00	0.43
1:A:790:ARG:HG3	3:C:60:HIS:HD2	1.82	0.43
1:A:1921:ASP:OD2	1:A:1966:HIS:HB3	2.19	0.43
1:A:2073:TRP:CD1	1:A:2073:TRP:C	2.91	0.43
1:A:2328:ALA:HB3	4:D:787:ALA:C	2.38	0.43
2:B:87:A:H5'	2:B:93:U:OP2	2.19	0.43
3:C:61:GLU:OE1	3:C:62:ASP:N	2.51	0.43
3:C:295:ASP:OD1	3:C:297:ASN:HB2	2.19	0.43
3:C:461:LEU:HD23	3:C:461:LEU:HA	1.78	0.43
4:D:441:GLY:O	4:D:693:THR:N	2.36	0.43
21:1:471:ASP:OD2	21:1:505:LYS:NZ	2.34	0.43
32:R:242:THR:HG22	32:R:244:LYS:H	1.84	0.43
32:R:443:GLY:O	32:R:447:MET:CB	2.67	0.43
1:A:356:ILE:HG23	3:C:865:GLY:C	2.39	0.43
1:A:781:ARG:NH2	15:H:24:A:H5'	2.34	0.43
1:A:1433:ASP:O	1:A:1434:LYS:HD3	2.19	0.43
1:A:1437:ARG:O	1:A:1440:THR:OG1	2.36	0.43
3:C:73:TYR:CE1	33:T:487:LYS:HE2	2.52	0.43
3:C:137:HIS:HD2	3:C:236:MET:CB	2.22	0.43
3:C:275:TYR:OH	3:C:345:GLY:HA2	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:349:PHE:CG	3:C:356:PHE:HE1	2.36	0.43
3:C:941:LYS:HG2	3:C:942:GLY:N	2.34	0.43
13:F:46:G:H2'	13:F:47:A:C8	2.54	0.43
15:H:166:G:N3	15:H:166:G:H2'	2.33	0.43
15:H:180:G:N3	15:H:181:G:C8	2.87	0.43
21:1:892:LEU:HD23	21:1:892:LEU:HA	1.91	0.43
27:7:51:ASN:OD1	27:7:61:LYS:HE2	2.18	0.43
31:P:191:ASP:O	31:P:192:VAL:HG23	2.18	0.43
33:T:225:ASP:O	33:T:226:ARG:HB2	2.18	0.43
1:A:151:MET:SD	1:A:628:GLY:HA3	2.59	0.43
1:A:175:PRO:CG	1:A:498:ARG:NH2	2.73	0.43
1:A:331:TRP:HZ3	3:C:179:VAL:HG22	1.82	0.43
1:A:843:LEU:HD22	1:A:867:ILE:HG23	2.01	0.43
3:C:289:ILE:CD1	3:C:300:LEU:HD21	2.49	0.43
3:C:381:LEU:HD23	3:C:416:LEU:HD22	1.99	0.43
5:E:255:MET:C	5:E:257:ASN:H	2.22	0.43
13:F:39:A:H61	14:G:8:C:N4	2.11	0.43
14:G:12:G:C2	14:G:13:C:O4'	2.71	0.43
21:1:184:VAL:O	21:1:188:ALA:CB	2.66	0.43
23:3:633:LEU:HD12	23:3:637:PRO:HG2	2.00	0.43
28:J:339:TRP:CG	32:R:116:TYR:CD2	3.06	0.43
32:R:250:LYS:HD3	32:R:250:LYS:C	2.39	0.43
33:T:347:THR:HG21	33:T:357:TRP:HE1	1.82	0.43
35:X:307:GLN:HB3	35:X:331:LEU:HD13	2.01	0.43
1:A:30:LEU:HB3	5:E:194:TYR:CZ	2.53	0.43
1:A:1735:LYS:NZ	1:A:1765:SER:O	2.50	0.43
3:C:669:THR:HG22	3:C:690:GLU:CB	2.48	0.43
5:E:178:LEU:CD1	5:E:222:LEU:HD21	2.46	0.43
5:E:321:TYR:OH	5:E:356:ILE:HG23	2.19	0.43
15:H:68:G:C6	15:H:84:C:N4	2.85	0.43
21:1:900:PHE:HA	21:1:903:GLN:HE21	1.83	0.43
21:1:968:GLU:OE1	21:1:968:GLU:N	2.51	0.43
23:3:253:GLU:HA	23:3:286:ILE:HG22	2.01	0.43
23:3:820:ALA:HB2	23:3:843:LEU:HD11	2.00	0.43
23:3:1055:VAL:HB	23:3:1093:MET:HB3	2.00	0.43
26:6:14:GLN:O	26:6:46:CYS:HB3	2.18	0.43
32:R:113:TYR:CG	32:R:118:ASP:OD2	2.72	0.43
33:T:399:LYS:CG	33:T:406:ILE:CD1	2.78	0.43
34:V:585:ILE:O	34:V:586:PHE:C	2.58	0.43
36:Y:37:TRP:CE2	36:Y:83:CYS:SG	3.11	0.43
36:Y:85:GLU:O	37:Z:502:ALA:CA	2.65	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:TYR:CE1	1:A:485:THR:HG22	2.54	0.42
1:A:405:LEU:HD11	3:C:265:LEU:HD13	2.00	0.42
1:A:532:THR:HG21	14:G:2:U:O5'	2.19	0.42
1:A:1373:GLN:NE2	1:A:1381:ASP:OD2	2.52	0.42
1:A:1539:SER:OG	1:A:1540:PRO:HD3	2.19	0.42
1:A:1630:LEU:HA	1:A:1630:LEU:HD23	1.80	0.42
1:A:1900:GLU:CD	37:Z:521:PRO:HB2	2.34	0.42
1:A:2302:LYS:HD2	1:A:2306:HIS:CE1	2.54	0.42
1:A:2328:ALA:CB	4:D:787:ALA:C	2.87	0.42
3:C:77:VAL:CB	33:T:196:LEU:HG	2.41	0.42
3:C:457:VAL:O	3:C:458:ASP:CB	2.67	0.42
13:F:55:C:OP2	13:F:74:U:O2'	2.36	0.42
23:3:169:HIS:H	23:3:185:LEU:HB2	1.83	0.42
23:3:226:GLU:HG3	23:3:261:PHE:CZ	2.51	0.42
23:3:498:GLY:HA3	23:3:531:LYS:HZ3	1.83	0.42
23:3:520:TYR:HE1	23:3:522:ASP:HB2	1.83	0.42
23:3:640:LEU:HD22	23:3:667:ILE:HG12	2.01	0.42
23:3:1188:ASN:OD1	23:3:1189:LYS:N	2.51	0.42
26:6:57:ARG:HD2	26:6:62:GLY:C	2.40	0.42
32:R:124:VAL:HG22	32:R:126:ASN:N	2.34	0.42
33:T:284:TYR:N	33:T:284:TYR:CD1	2.87	0.42
36:Y:92:LEU:O	36:Y:96:ASN:CB	2.67	0.42
1:A:250:VAL:HG21	1:A:337:VAL:HG12	2.01	0.42
1:A:284:ARG:HE	1:A:284:ARG:HB3	1.70	0.42
1:A:311:GLU:CB	3:C:885:THR:HG21	2.47	0.42
1:A:349:ALA:CB	1:A:399:ALA:CB	2.74	0.42
1:A:1425:LYS:HG2	32:R:417:ASN:OD1	2.18	0.42
1:A:2072:GLU:O	1:A:2076:ARG:HG3	2.18	0.42
1:A:2310:ARG:HG2	1:A:2310:ARG:HH11	1.84	0.42
3:C:93:ILE:HG21	33:T:218:TRP:CZ2	2.54	0.42
3:C:481:MET:SD	3:C:492:ALA:CB	3.06	0.42
15:H:168:A:N3	15:H:168:A:C2'	2.77	0.42
21:1:404:LEU:HD23	25:5:47:GLN:CD	2.39	0.42
21:1:744:ALA:HB2	21:1:784:MET:SD	2.59	0.42
21:1:1289:ASN:HB2	21:1:1294:THR:HA	2.00	0.42
23:3:274:ARG:NH2	23:3:309:ASP:OD2	2.50	0.42
32:R:118:ASP:OD1	32:R:232:MET:HE1	2.19	0.42
32:R:220:ARG:HB2	32:R:220:ARG:CZ	2.49	0.42
36:Y:37:TRP:NE1	36:Y:83:CYS:CB	2.70	0.42
1:A:32:GLU:OE2	1:A:36:LYS:CE	2.68	0.42
1:A:962:LEU:HB2	1:A:965:VAL:HB	1.99	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1052:VAL:HG22	1:A:1161:LEU:HD21	2.01	0.42
1:A:1099:PHE:HZ	1:A:1157:ILE:HD11	1.85	0.42
1:A:1457:HIS:HE2	32:R:424:SER:CB	2.32	0.42
1:A:1772:PHE:CD1	1:A:1773:SER:N	2.87	0.42
1:A:1810:PHE:CE1	1:A:1919:LEU:HD12	2.55	0.42
3:C:242:LEU:HD23	3:C:242:LEU:HA	1.84	0.42
3:C:413:ARG:HB2	3:C:414:PRO:HD3	1.99	0.42
15:H:3:C:H2'	15:H:4:G:C8	2.53	0.42
15:H:178:A:N3	15:H:178:A:H2'	2.34	0.42
21:1:707:LEU:O	21:1:710:ALA:HB3	2.20	0.42
21:1:811:LEU:HB2	21:1:812:PRO:HD3	2.00	0.42
21:1:1040:GLY:CA	21:1:1080:THR:HG22	2.48	0.42
22:2:613:LEU:HA	22:2:616:SER:OG	2.20	0.42
23:3:310:ILE:O	23:3:330:PHE:HB3	2.19	0.42
23:3:961:ILE:HB	23:3:970:TYR:CD2	2.54	0.42
28:J:375:ASP:O	28:J:376:VAL:C	2.58	0.42
1:A:32:GLU:CD	1:A:36:LYS:HE3	2.39	0.42
1:A:94:TYR:HD2	32:R:207:MET:SD	2.43	0.42
1:A:319:LEU:CD1	3:C:637:LEU:HB3	2.48	0.42
1:A:361:HIS:CD2	3:C:279:ARG:CZ	3.03	0.42
2:B:94:U:O2'	2:B:95:G:H3'	2.18	0.42
3:C:323:PHE:CE1	3:C:424:PHE:HE1	2.37	0.42
3:C:706:GLN:HE21	3:C:708:THR:N	2.12	0.42
3:C:863:ILE:HA	3:C:864:PRO:HD3	1.88	0.42
5:E:67:GLY:H	5:E:87:ASP:CG	2.20	0.42
15:H:5:C:H2'	15:H:6:U:C6	2.54	0.42
21:1:413:LYS:HG3	21:1:415:LEU:HD11	2.01	0.42
21:1:619:ASN:ND2	21:1:624:VAL:HG21	2.34	0.42
21:1:619:ASN:OD1	21:1:620:MET:N	2.52	0.42
21:1:722:GLU:O	21:1:725:ASP:CB	2.67	0.42
23:3:185:LEU:HD11	23:3:235:LEU:HD13	2.01	0.42
23:3:287:PHE:HA	23:3:304:GLN:O	2.19	0.42
23:3:1014:TYR:CE2	23:3:1016:ARG:HA	2.55	0.42
23:3:1052:ASN:OD1	23:3:1096:HIS:ND1	2.39	0.42
23:3:1201:PRO:HB2	23:3:1202:PRO:HD3	2.02	0.42
26:6:47:ASP:HA	26:6:50:ASN:O	2.20	0.42
28:J:331:GLN:HG2	32:R:98:TYR:HH	1.76	0.42
28:J:339:TRP:CD2	32:R:116:TYR:CD2	2.85	0.42
29:L:63:TRP:CZ2	29:L:99:HIS:HB2	2.54	0.42
31:P:188:TRP:C	31:P:190:ASP:H	2.21	0.42
32:R:183:GLN:HB3	32:R:188:PHE:CD2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:Y:69:ARG:HA	36:Y:76:SER:HA	2.02	0.42
1:A:211:GLN:HA	1:A:212:PRO:HD3	1.82	0.42
1:A:258:PHE:CD2	1:A:434:HIS:HA	2.55	0.42
1:A:303:ILE:HG23	3:C:933:PHE:CD1	2.53	0.42
1:A:378:PHE:CD1	1:A:378:PHE:C	2.93	0.42
1:A:380:LEU:H	1:A:380:LEU:HD22	1.84	0.42
1:A:718:ARG:NH2	32:R:259:LYS:CE	2.78	0.42
1:A:1263:TRP:CD2	1:A:1295:ILE:HD13	2.54	0.42
1:A:1363:GLN:O	1:A:1364:LEU:HG	2.18	0.42
3:C:669:THR:HG22	3:C:690:GLU:OE1	2.19	0.42
3:C:712:LYS:O	3:C:716:GLU:HG3	2.18	0.42
5:E:277:PHE:CE1	5:E:317:ARG:HG2	2.53	0.42
14:G:5:G:C2	14:G:6:A:C5	3.08	0.42
14:G:136:U:O4	21:1:515:ALA:HA	2.19	0.42
21:1:494:GLU:HA	21:1:497:ILE:HG22	2.01	0.42
21:1:940:LEU:O	21:1:948:ARG:NH2	2.51	0.42
21:1:1255:PHE:HD2	22:2:487:LEU:HD22	1.81	0.42
23:3:456:PRO:HB2	23:3:757:ILE:HD13	2.02	0.42
23:3:508:CYS:SG	23:3:518:GLN:NE2	2.92	0.42
23:3:784:THR:HB	23:3:786:ARG:NH1	2.32	0.42
32:R:129:ASP:HB3	32:R:131:ASP:CG	2.40	0.42
33:T:318:ARG:CG	33:T:318:ARG:NH1	2.82	0.42
34:V:484:SER:O	34:V:486:THR:N	2.53	0.42
1:A:715:GLU:OE1	32:R:258:TRP:CE3	2.73	0.42
1:A:791:GLN:NE2	1:A:1026:ASN:OD1	2.52	0.42
1:A:1759:THR:N	21:1:938:TRP:CD1	2.88	0.42
1:A:1948:ASP:O	1:A:1951:LYS:HB2	2.20	0.42
1:A:1953:ILE:HD11	1:A:1986:LEU:HD13	2.01	0.42
1:A:2216:CYS:HA	1:A:2225:LEU:HB3	2.01	0.42
3:C:85:ASP:OD2	33:T:240:LEU:HA	2.20	0.42
3:C:90:THR:O	3:C:92:PRO:HD3	2.19	0.42
15:H:107:A:N1	15:H:108:G:C5	2.88	0.42
21:1:1075:ARG:HE	21:1:1075:ARG:HB2	1.64	0.42
23:3:146:ARG:HB2	23:3:150:ALA:HA	2.02	0.42
23:3:353:PHE:O	23:3:432:ARG:NH1	2.44	0.42
23:3:774:PHE:N	23:3:774:PHE:CD2	2.86	0.42
27:7:30:GLU:HA	27:7:33:VAL:HG12	2.02	0.42
30:M:202:CYS:HB2	30:M:219:PHE:HB2	2.02	0.42
32:R:71:GLN:HE21	32:R:71:GLN:HB2	1.61	0.42
33:T:188:PRO:HG3	33:T:443:THR:HG21	2.01	0.42
36:Y:38:ILE:HG12	36:Y:82:LEU:HB3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:LYS:HG2	1:A:49:ARG:N	2.35	0.42
1:A:1560:ILE:HG12	1:A:1668:TRP:CB	2.49	0.42
1:A:1889:LEU:HD11	1:A:2012:LEU:HG	2.02	0.42
3:C:77:VAL:HG13	33:T:196:LEU:CB	2.41	0.42
3:C:140:HIS:CB	3:C:230:ASP:H	2.33	0.42
3:C:259:LYS:HD2	41:C:1500:GTP:C4	2.55	0.42
3:C:452:THR:HB	3:C:577:PHE:CE2	2.55	0.42
5:E:152:SER:OG	5:E:153:PHE:HD1	2.03	0.42
13:F:58:G:O2'	13:F:59:G:P	2.78	0.42
14:G:141:C:H2'	14:G:142:U:C6	2.52	0.42
15:H:179:C:C2	15:H:180:G:C8	3.07	0.42
21:1:401:ASP:HA	21:1:404:LEU:HB2	2.00	0.42
21:1:848:GLU:O	21:1:851:SER:OG	2.32	0.42
21:1:1179:ASP:OD1	21:1:1181:ASP:N	2.52	0.42
23:3:3:LEU:HA	23:3:1130:VAL:O	2.20	0.42
23:3:228:LEU:HD23	23:3:259:LYS:HZ2	1.84	0.42
23:3:482:THR:OG1	23:3:501:GLY:HA3	2.19	0.42
23:3:691:THR:HG22	23:3:716:SER:HB3	2.02	0.42
23:3:718:ARG:HG2	23:3:719:SER:H	1.84	0.42
25:5:25:ASN:HB3	25:5:87:LEU:HA	2.02	0.42
28:J:294:HIS:HE1	29:L:227:THR:CB	2.26	0.42
31:P:226:LYS:HD3	31:P:227:TYR:HE1	1.83	0.42
32:R:67:ILE:CG1	32:R:71:GLN:OE1	2.68	0.42
34:V:547:VAL:O	34:V:548:ALA:C	2.58	0.42
1:A:371:LEU:HD12	1:A:372:PRO:HD2	2.00	0.42
1:A:380:LEU:HD12	3:C:334:ILE:HA	2.02	0.42
1:A:382:GLU:O	1:A:383:PHE:CG	2.73	0.42
1:A:611:LEU:HA	1:A:611:LEU:HD12	1.85	0.42
1:A:816:TRP:CE2	1:A:820:ARG:HG3	2.55	0.42
1:A:1436:TRP:HA	1:A:1439:ARG:CZ	2.50	0.42
3:C:149:LEU:HA	3:C:427:PHE:HD2	1.82	0.42
14:G:-3:A:H2'	14:G:-2:C:C6	2.55	0.42
15:H:82:G:C2	15:H:83:A:C5	3.08	0.42
21:1:527:GLY:O	21:1:531:LEU:HD13	2.20	0.42
22:2:525:PRO:HD2	22:2:528:ILE:HD12	2.00	0.42
23:3:412:ILE:HD12	23:3:1118:VAL:HG11	2.01	0.42
33:T:187:LYS:N	33:T:188:PRO:CD	2.83	0.42
33:T:233:LEU:HD23	33:T:233:LEU:O	2.20	0.42
36:Y:37:TRP:HH2	37:Z:498:GLY:N	2.15	0.42
36:Y:59:TYR:HB3	36:Y:92:LEU:HD23	2.01	0.42
1:A:109:PRO:HD3	1:A:630:TRP:HZ2	1.83	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:TYR:HH	3:C:853:ARG:NH2	2.07	0.42
1:A:697:MET:N	1:A:698:PRO:HD3	2.34	0.42
1:A:833:LYS:HE3	1:A:834:HIS:NE2	2.35	0.42
1:A:1301:ILE:CD1	2:B:39:C:OP1	2.67	0.42
1:A:1416:ILE:HB	1:A:1417:PRO:HD3	2.01	0.42
1:A:1457:HIS:HE1	32:R:424:SER:HA	1.74	0.42
1:A:1529:ILE:O	1:A:1530:PRO:C	2.59	0.42
2:B:41:U:C4	2:B:42:U:O4	2.73	0.42
2:B:92:U:C3'	2:B:93:U:H5'	2.50	0.42
3:C:140:HIS:HB3	3:C:230:ASP:H	1.85	0.42
3:C:149:LEU:HA	3:C:427:PHE:CE2	2.54	0.42
14:G:139:U:H2'	14:G:140:A:C8	2.55	0.42
15:H:26:A:C5	15:H:27:U:C5	3.08	0.42
21:1:687:VAL:HA	21:1:690:ILE:HG22	2.01	0.42
21:1:727:VAL:HG12	21:1:731:LEU:HD11	2.02	0.42
21:1:790:LYS:O	21:1:793:LYS:HB3	2.19	0.42
23:3:1039:LEU:HB2	23:3:1043:THR:OG1	2.20	0.42
28:J:240:THR:O	28:J:241:VAL:HB	2.19	0.42
28:J:259:GLN:HE21	29:L:220:PRO:HD3	1.82	0.42
31:P:58:ASP:OD2	31:P:61:ARG:HB2	2.19	0.42
31:P:192:VAL:CG1	31:P:193:VAL:N	2.83	0.42
1:A:428:LYS:HE3	1:A:454:TYR:CE1	2.55	0.42
1:A:479:THR:HG23	32:R:203:GLN:NE2	2.35	0.42
1:A:1188:ASN:ND2	1:A:1233:ASP:OD2	2.47	0.42
1:A:1399:GLN:C	1:A:1401:ARG:H	2.24	0.42
1:A:1489:LEU:O	1:A:1492:GLY:N	2.45	0.42
1:A:1503:TRP:CZ2	1:A:1753:LEU:HD21	2.55	0.42
1:A:1555:LEU:HB2	1:A:1558:THR:OG1	2.19	0.42
1:A:1763:LEU:HD23	1:A:1764:SER:O	2.20	0.42
1:A:2117:ILE:H	1:A:2117:ILE:HG12	1.64	0.42
3:C:220:ARG:HD3	3:C:477:HIS:NE2	2.34	0.42
3:C:474:LEU:HD12	3:C:500:THR:O	2.20	0.42
5:E:274:VAL:C	5:E:275:LYS:HG3	2.40	0.42
15:H:147:G:C2	15:H:148:C:N3	2.87	0.42
15:H:155:C:H2'	15:H:156:U:H5"	2.02	0.42
15:H:179:C:O2	15:H:180:G:C8	2.72	0.42
21:1:555:VAL:O	21:1:559:ILE:HG12	2.19	0.42
22:2:643:PRO:HG2	24:4:66:ASP:HA	2.01	0.42
23:3:259:LYS:HE3	23:3:266:ASP:OD2	2.20	0.42
23:3:261:PHE:HD1	23:3:261:PHE:HA	1.72	0.42
23:3:288:VAL:HG23	23:3:289:CYS:N	2.33	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:3:519:VAL:HG22	23:3:524:ILE:HG23	2.02	0.42
23:3:673:VAL:HA	23:3:690:ARG:HA	2.02	0.42
23:3:968:ARG:CZ	23:3:979:ARG:HH11	2.33	0.42
23:3:1011:TRP:HB3	23:3:1024:PHE:CZ	2.55	0.42
28:J:216:ASP:O	28:J:218:GLU:N	2.53	0.42
33:T:281:ILE:CD1	33:T:282:ARG:HG2	2.50	0.42
1:A:121:HIS:C	1:A:123:THR:H	2.23	0.41
1:A:1320:LYS:NZ	32:R:434:TYR:CE1	2.88	0.41
1:A:1402:ARG:CD	32:R:412:ASP:HA	2.50	0.41
1:A:1942:ALA:CB	1:A:1983:LEU:HD22	2.50	0.41
3:C:291:MET:HG2	3:C:292:TYR:CE1	2.54	0.41
3:C:445:ALA:HB1	3:C:449:ILE:HG13	2.02	0.41
3:C:829:GLU:HG3	3:C:830:PRO:HD2	2.01	0.41
13:F:8:C:C6	13:F:8:C:C5'	2.98	0.41
13:F:31:U:H2'	13:F:32:U:C6	2.55	0.41
15:H:68:G:H2'	15:H:69:U:H6	1.82	0.41
21:1:783:GLU:O	21:1:787:ILE:HG12	2.20	0.41
21:1:1025:LYS:HE2	30:M:210:PHE:CE1	2.55	0.41
23:3:443:GLU:HA	23:3:735:SER:OG	2.20	0.41
23:3:812:LYS:NZ	23:3:855:PRO:HG2	2.35	0.41
27:7:23:HIS:H	27:7:26:THR:HG1	1.68	0.41
28:J:239:ARG:C	28:J:239:ARG:HD3	2.40	0.41
28:J:262:ARG:HB3	29:L:220:PRO:HG3	2.02	0.41
28:J:368:ARG:O	28:J:372:VAL:HG23	2.20	0.41
32:R:131:ASP:OD2	32:R:132:LEU:N	2.53	0.41
1:A:120:TYR:HE1	1:A:485:THR:HB	1.84	0.41
1:A:137:GLU:N	1:A:138:PRO:HD2	2.35	0.41
1:A:143:GLN:O	1:A:146:SER:HB3	2.20	0.41
1:A:148:TRP:CZ2	1:A:616:PHE:CA	3.02	0.41
1:A:252:ASP:HB2	1:A:334:THR:CB	2.48	0.41
1:A:344:ASP:OD1	1:A:347:LEU:HD11	2.19	0.41
1:A:470:ARG:CZ	1:A:470:ARG:HB2	2.49	0.41
1:A:615:ARG:HE	1:A:615:ARG:HB2	1.59	0.41
1:A:1051:LEU:HD22	31:P:193:VAL:HG11	2.00	0.41
1:A:1428:HIS:O	1:A:1429:THR:C	2.59	0.41
1:A:1823:HIS:O	1:A:1826:VAL:HG22	2.20	0.41
3:C:73:TYR:HB3	3:C:77:VAL:HG21	2.02	0.41
3:C:89:LEU:C	3:C:89:LEU:CD2	2.82	0.41
3:C:259:LYS:HG2	3:C:262:ARG:HD3	1.99	0.41
3:C:449:ILE:CD1	3:C:466:SER:HA	2.50	0.41
15:H:80:A:C2	15:H:81:G:N7	2.88	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:153:A:H62	15:H:177:A:H2	1.67	0.41
21:1:1185:ARG:HD2	21:1:1218:ASN:OD1	2.20	0.41
23:3:425:VAL:O	23:3:435:LEU:HD12	2.20	0.41
23:3:436:ARG:HG2	23:3:778:ALA:HA	2.01	0.41
29:L:31:TRP:CH2	29:L:47:LYS:HA	2.55	0.41
32:R:88:ILE:CG2	32:R:96:ILE:HG23	2.48	0.41
32:R:418:GLN:HE21	32:R:418:GLN:HB2	1.64	0.41
32:R:442:ARG:NH1	32:R:443:GLY:CA	2.78	0.41
36:Y:64:ASN:O	36:Y:83:CYS:HB3	2.19	0.41
37:Z:572:PRO:CG	37:Z:588:ASP:OD2	2.67	0.41
1:A:305:ARG:HE	3:C:854:ARG:NH1	2.18	0.41
1:A:629:PHE:CD2	1:A:629:PHE:O	2.73	0.41
1:A:1118:PRO:CD	1:A:1119:ASP:N	2.82	0.41
1:A:1883:VAL:HG12	1:A:1885:LYS:HG3	2.01	0.41
1:A:2111:LEU:HD21	1:A:2225:LEU:HD21	2.03	0.41
2:B:35:U:OP2	2:B:35:U:C6	2.70	0.41
3:C:148:CYS:SG	3:C:312:SER:O	2.78	0.41
3:C:512:GLU:HG3	3:C:562:THR:O	2.19	0.41
5:E:263:ASP:O	5:E:272:ARG:NE	2.32	0.41
21:1:520:THR:HG21	21:1:558:ARG:HE	1.85	0.41
21:1:1124:SER:O	21:1:1127:THR:OG1	2.28	0.41
23:3:8:LEU:HD23	23:3:774:PHE:CZ	2.52	0.41
33:T:225:ASP:O	33:T:226:ARG:CB	2.67	0.41
1:A:206:TRP:CE3	1:A:212:PRO:HB3	2.55	0.41
1:A:592:TYR:O	1:A:593:ARG:C	2.59	0.41
1:A:800:TYR:HB3	3:C:59:LEU:HD11	2.02	0.41
1:A:1554:GLN:NE2	1:A:1620:TYR:O	2.49	0.41
1:A:1730:MET:O	1:A:1734:MET:HG2	2.19	0.41
1:A:2172:MET:HB2	1:A:2172:MET:HE3	1.79	0.41
3:C:261:ASP:CG	41:C:1500:GTP:N1	2.61	0.41
3:C:445:ALA:CB	3:C:449:ILE:HD11	2.43	0.41
3:C:853:ARG:O	3:C:854:ARG:HB3	2.20	0.41
15:H:152:G:H2'	15:H:152:G:N3	2.36	0.41
15:H:154:C:N3	15:H:176:G:N1	2.61	0.41
21:1:642:PRO:HB3	21:1:682:HIS:NE2	2.36	0.41
21:1:1136:TYR:CE1	21:1:1144:GLN:HB3	2.55	0.41
23:3:199:GLU:HB3	23:3:203:ASN:HD21	1.85	0.41
28:J:220:LEU:O	28:J:223:TYR:HB3	2.21	0.41
32:R:155:VAL:O	32:R:159:VAL:HG23	2.20	0.41
1:A:368:GLN:C	1:A:369:GLU:OE2	2.57	0.41
1:A:387:PHE:HD1	3:C:327:TYR:CE1	2.38	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:589:LYS:HB3	3:C:659:VAL:O	2.20	0.41
3:C:704:VAL:O	3:C:709:TRP:CZ2	2.74	0.41
3:C:707:ILE:HD11	3:C:735:PHE:HB2	2.01	0.41
13:F:40:U:O4	13:F:41:A:N6	2.54	0.41
15:H:103:U:C3'	15:H:104:U:H5'	2.51	0.41
21:1:621:ASP:OD2	21:1:623:TYR:HB3	2.19	0.41
21:1:719:TYR:CD1	23:3:218:ASN:HB2	2.56	0.41
23:3:116:VAL:HA	23:3:117:PRO:HD3	1.95	0.41
23:3:896:PHE:CZ	23:3:972:LEU:HB2	2.55	0.41
24:4:69:TYR:OH	24:4:73:ILE:HG13	2.20	0.41
28:J:340:GLN:N	28:J:341:PRO:HD3	2.35	0.41
31:P:189:ASP:O	31:P:190:ASP:C	2.58	0.41
33:T:223:SER:OG	33:T:224:ALA:N	2.53	0.41
35:X:173:GLN:NE2	35:X:176:GLU:HA	2.36	0.41
1:A:151:MET:SD	1:A:628:GLY:CA	3.09	0.41
1:A:280:GLU:HB2	2:B:48:A:H4'	2.01	0.41
1:A:335:PRO:HG3	3:C:139:HIS:CG	2.56	0.41
1:A:362:ARG:CD	1:A:362:ARG:C	2.88	0.41
1:A:398:THR:CG2	3:C:382:ALA:CB	2.96	0.41
1:A:434:HIS:ND1	1:A:434:HIS:C	2.73	0.41
1:A:1325:LEU:HD23	1:A:1325:LEU:HA	1.86	0.41
1:A:1948:ASP:HA	1:A:1951:LYS:HD2	2.01	0.41
1:A:2073:TRP:CZ3	1:A:2313:HIS:CG	3.09	0.41
1:A:2117:ILE:HG21	1:A:2301:PRO:HB2	2.02	0.41
1:A:2120:LEU:HD12	1:A:2120:LEU:N	2.35	0.41
3:C:97:VAL:HG21	31:P:45:GLN:CG	2.46	0.41
3:C:137:HIS:NE2	3:C:236:MET:SD	2.93	0.41
13:F:39:A:H2'	13:F:40:U:O4'	2.21	0.41
14:G:-2:C:H2'	14:G:-1:G:H8	1.82	0.41
15:H:72:U:H6	15:H:72:U:O5'	2.03	0.41
15:H:171:U:H2'	15:H:172:C:O4'	2.21	0.41
21:1:815:PHE:HA	21:1:819:TRP:CD1	2.56	0.41
23:3:168:TYR:CE1	27:7:69:MET:HB3	2.55	0.41
23:3:442:LEU:HD13	23:3:734:LEU:HD23	1.99	0.41
23:3:587:VAL:CG1	23:3:590:MET:HG3	2.49	0.41
33:T:297:HIS:CE1	33:T:300:ILE:HD12	2.56	0.41
33:T:455:GLN:CG	33:T:456:PRO:HD2	2.51	0.41
36:Y:24:ASP:O	36:Y:26:VAL:N	2.54	0.41
1:A:296:PHE:CZ	3:C:593:GLU:HB2	2.56	0.41
1:A:530:LEU:CB	30:M:198:GLN:HE21	2.17	0.41
1:A:866:LEU:O	1:A:869:GLN:HB3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1035:GLN:HA	1:A:1446:GLN:HE22	1.84	0.41
1:A:1099:PHE:CE2	1:A:1153:VAL:HG13	2.53	0.41
1:A:1221:THR:O	1:A:1223:GLU:HG3	2.20	0.41
1:A:1430:LEU:HD21	32:R:422:MET:HA	2.03	0.41
1:A:1458:GLN:HE21	1:A:1463:LYS:HG3	1.86	0.41
3:C:230:ASP:OD1	3:C:259:LYS:HB2	2.17	0.41
3:C:270:PRO:HA	3:C:271:PRO:HD3	1.87	0.41
4:D:577:LYS:O	4:D:581:SER:N	2.54	0.41
14:G:155:U:C4'	14:G:156:U:H5'	2.49	0.41
15:H:4:G:H2'	15:H:5:C:C6	2.55	0.41
15:H:83:A:H2'	15:H:84:C:H1'	2.00	0.41
21:1:1127:THR:O	22:2:571:LEU:HD13	2.21	0.41
23:3:314:THR:HG22	23:3:315:LEU:N	2.36	0.41
23:3:521:PRO:HA	23:3:544:ILE:CG2	2.49	0.41
23:3:524:ILE:CD1	23:3:556:ILE:HD13	2.49	0.41
24:4:67:ALA:O	24:4:70:ALA:HB3	2.21	0.41
28:J:273:TYR:CD1	32:R:228:PRO:CB	3.04	0.41
1:A:61:MET:HB3	1:A:62:PRO:CD	2.50	0.41
1:A:1891:LEU:HB2	1:A:1893:PHE:CE2	2.55	0.41
1:A:2090:ILE:H	1:A:2090:ILE:HD13	1.86	0.41
1:A:2259:VAL:HG22	1:A:2260:GLN:H	1.86	0.41
2:B:20:G:C1'	2:B:21:A:OP1	2.69	0.41
3:C:300:LEU:N	3:C:300:LEU:CD1	2.84	0.41
13:F:60:C:H5"	32:R:219:PRO:HB3	2.01	0.41
15:H:160:A:H2'	15:H:161:U:C6	2.55	0.41
21:1:719:TYR:HB3	23:3:216:GLY:O	2.20	0.41
21:1:1016:LEU:O	21:1:1019:ARG:HB3	2.20	0.41
21:1:1055:TRP:O	21:1:1058:ILE:HB	2.20	0.41
21:1:1092:ASP:OD1	21:1:1092:ASP:N	2.53	0.41
23:3:86:ARG:CD	23:3:104:GLN:HE21	2.33	0.41
23:3:205:GLN:HE21	23:3:227:PRO:HB3	1.85	0.41
23:3:554:VAL:HG12	23:3:556:ILE:HG23	2.01	0.41
26:6:90:ASN:OD1	26:6:91:LEU:N	2.54	0.41
30:M:208:THR:HG22	30:M:210:PHE:HD2	1.85	0.41
32:R:129:ASP:C	32:R:131:ASP:N	2.73	0.41
33:T:309:ASP:C	33:T:309:ASP:OD1	2.59	0.41
37:Z:522:LEU:HD13	37:Z:522:LEU:C	2.41	0.41
37:Z:525:TYR:HD1	37:Z:526:ILE:CG2	2.29	0.41
1:A:121:HIS:C	1:A:123:THR:N	2.74	0.41
1:A:128:PHE:CD1	1:A:473:PHE:CE1	3.09	0.41
1:A:155:LYS:CE	1:A:624:GLY:O	2.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:GLU:O	1:A:520:TYR:HD2	2.02	0.41
1:A:292:ASP:O	1:A:294:ASN:ND2	2.54	0.41
1:A:331:TRP:CD1	3:C:635:LEU:HD13	2.55	0.41
1:A:596:TYR:O	1:A:598:LEU:N	2.54	0.41
1:A:965:VAL:O	1:A:1100:ARG:NH1	2.54	0.41
1:A:1052:VAL:CG2	1:A:1161:LEU:HD21	2.51	0.41
1:A:1661:TRP:NE1	1:A:1697:SER:O	2.53	0.41
1:A:1757:GLU:CG	32:R:451:ILE:HG13	2.51	0.41
1:A:1776:ILE:O	1:A:1859:LYS:N	2.48	0.41
1:A:1788:VAL:HG21	1:A:1800:THR:HB	2.03	0.41
1:A:2117:ILE:HG22	1:A:2303:GLU:HA	2.03	0.41
1:A:2320:LEU:HD21	1:A:2322:GLU:CD	2.41	0.41
2:B:27:U:HO2'	2:B:28:A:P	2.42	0.41
2:B:64:G:H5'	5:E:106:LYS:HZ2	1.78	0.41
3:C:64:LYS:HE2	3:C:64:LYS:HA	2.02	0.41
3:C:65:TYR:O	3:C:66:TYR:CG	2.73	0.41
3:C:79:THR:HA	33:T:199:VAL:O	2.20	0.41
3:C:132:VAL:HG11	3:C:226:VAL:CG2	2.49	0.41
3:C:133:THR:HB	3:C:225:VAL:HA	2.02	0.41
3:C:513:ASN:O	3:C:513:ASN:ND2	2.54	0.41
3:C:518:ASP:N	3:C:519:GLU:OE2	2.54	0.41
5:E:115:LEU:O	5:E:116:HIS:CD2	2.74	0.41
5:E:177:LYS:C	5:E:178:LEU:HD23	2.41	0.41
5:E:243:LEU:HD22	5:E:243:LEU:HA	1.80	0.41
15:H:152:G:H2'	15:H:153:A:C1'	2.51	0.41
21:1:184:VAL:O	21:1:188:ALA:HB2	2.21	0.41
21:1:517:ARG:O	21:1:520:THR:OG1	2.20	0.41
21:1:664:GLY:O	21:1:667:ILE:HB	2.21	0.41
21:1:770:MET:O	21:1:774:ILE:HG12	2.21	0.41
21:1:963:LYS:HG2	21:1:1003:VAL:HB	2.02	0.41
21:1:1080:THR:HA	21:1:1083:TYR:CD2	2.56	0.41
21:1:1092:ASP:OD1	21:1:1093:VAL:N	2.54	0.41
21:1:1227:ILE:O	21:1:1231:MET:HG2	2.20	0.41
21:1:1252:GLN:OE1	22:2:499:PRO:HA	2.20	0.41
23:3:65:LEU:HD12	23:3:79:VAL:O	2.21	0.41
23:3:631:GLN:HG2	23:3:632:ALA:O	2.21	0.41
23:3:910:ALA:HB2	23:3:948:VAL:HG23	2.02	0.41
32:R:69:VAL:HG12	32:R:70:ALA:N	2.36	0.41
32:R:132:LEU:HD13	33:T:399:LYS:HE3	2.02	0.41
32:R:414:ARG:NH2	32:R:414:ARG:CB	2.73	0.41
33:T:209:CYS:O	33:T:221:THR:HA	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:T:210:ILE:HG12	33:T:221:THR:HG22	2.03	0.41
33:T:294:LEU:N	33:T:294:LEU:HD23	2.36	0.41
33:T:400:PHE:HD1	33:T:401:PRO:HA	1.86	0.41
36:Y:10:ILE:O	36:Y:13:LEU:N	2.53	0.41
36:Y:67:LEU:HA	36:Y:80:CYS:HA	2.02	0.41
37:Z:566:TYR:CE2	37:Z:584:TRP:HE3	2.29	0.41
1:A:107:PRO:O	1:A:108:MET:HB2	2.21	0.41
1:A:118:VAL:HG12	1:A:119:LEU:N	2.36	0.41
1:A:164:MET:CE	1:A:560:SER:HA	2.51	0.41
1:A:247:THR:OG1	1:A:429:ASN:CB	2.60	0.41
1:A:384:VAL:O	1:A:385:GLU:HG2	2.21	0.41
1:A:395:THR:HG23	3:C:383:GLN:NE2	2.24	0.41
1:A:842:ALA:HB1	1:A:920:ALA:HB1	2.03	0.41
1:A:1425:LYS:CB	32:R:417:ASN:OD1	2.69	0.41
1:A:1771:LEU:O	1:A:1777:ILE:HD12	2.20	0.41
1:A:1776:ILE:HD13	1:A:1813:ARG:HD3	2.03	0.41
2:B:19:A:HO2'	2:B:20:G:P	2.38	0.41
3:C:149:LEU:HD11	3:C:427:PHE:CB	2.51	0.41
3:C:354:ARG:CG	3:C:354:ARG:HH11	2.34	0.41
13:F:42:C:C2	13:F:43:A:C8	3.09	0.41
21:1:1286:ARG:N	23:3:1006:GLN:HE22	2.19	0.41
23:3:274:ARG:HD2	23:3:389:PRO:HD3	2.02	0.41
25:5:14:PRO:O	25:5:17:VAL:HG22	2.21	0.41
28:J:423:GLU:OE1	28:J:423:GLU:HA	2.21	0.41
29:L:49:ARG:NH1	29:L:53:TRP:HB3	2.36	0.41
33:T:399:LYS:HB2	33:T:404:SER:HB3	2.03	0.41
33:T:434:GLY:HA2	33:T:464:GLY:N	2.36	0.41
34:V:512:GLY:O	34:V:513:ARG:C	2.60	0.41
1:A:265:THR:HG22	1:A:314:ILE:HG12	2.03	0.40
1:A:393:LEU:N	3:C:379:LYS:HE3	2.13	0.40
1:A:1528:GLN:HG3	1:A:1530:PRO:CD	2.51	0.40
1:A:1957:ASP:OD2	1:A:1959:THR:OG1	2.37	0.40
2:B:19:A:H2'	2:B:20:G:C5'	2.49	0.40
3:C:221:ILE:HG13	3:C:479:THR:OG1	2.21	0.40
3:C:235:VAL:HG13	3:C:239:THR:OG1	2.22	0.40
3:C:392:LEU:N	3:C:393:PRO:CD	2.84	0.40
4:D:419:GLY:C	4:D:421:HIS:H	2.25	0.40
5:E:178:LEU:CD2	5:E:208:ILE:HD11	2.51	0.40
14:G:146:C:C4	14:G:147:C:N4	2.89	0.40
15:H:112:G:O5'	15:H:112:G:H8	2.04	0.40
21:1:498:MET:HE1	21:1:530:PRO:HB2	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:1:765:TYR:O	21:1:769:VAL:HG23	2.20	0.40
21:1:806:ILE:HG12	21:1:810:ILE:HD12	2.03	0.40
21:1:997:LEU:O	21:1:1001:VAL:HG23	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CZ	2.56	0.40
23:3:6:LEU:HD12	23:3:1128:ILE:HD11	2.03	0.40
23:3:194:ASN:O	23:3:196:PRO:HD3	2.21	0.40
23:3:259:LYS:HG3	23:3:266:ASP:CG	2.42	0.40
25:5:27:PRO:HG3	25:5:85:ARG:NH1	2.36	0.40
34:V:585:ILE:O	34:V:588:GLN:N	2.54	0.40
35:X:263:PRO:CG	35:X:265:LYS:H	2.34	0.40
37:Z:563:ARG:HH21	37:Z:563:ARG:HG3	1.83	0.40
1:A:76:MET:SD	1:A:88:TYR:CZ	3.15	0.40
1:A:212:PRO:HD2	1:A:225:TYR:OH	2.21	0.40
1:A:225:TYR:O	1:A:418:THR:CB	2.68	0.40
1:A:254:TYR:HH	1:A:434:HIS:HB3	1.85	0.40
1:A:363:HIS:NE2	3:C:287:GLY:CA	2.74	0.40
1:A:1251:SER:O	1:A:1298:ARG:NH2	2.55	0.40
1:A:1263:TRP:CZ2	1:A:1292:GLU:HG2	2.56	0.40
1:A:1451:ASN:HB2	32:R:428:GLY:O	2.21	0.40
1:A:1529:ILE:HG13	1:A:1530:PRO:HD3	2.03	0.40
3:C:64:LYS:NZ	31:P:209:ARG:NH1	2.70	0.40
3:C:85:ASP:HA	33:T:238:LEU:HB3	2.03	0.40
3:C:534:VAL:HG12	3:C:535:ALA:N	2.31	0.40
13:F:42:C:H2'	13:F:43:A:O4'	2.21	0.40
15:H:2:U:H2'	15:H:3:C:C6	2.55	0.40
15:H:149:A:N3	15:H:150:U:C6	2.89	0.40
21:1:658:TRP:CZ3	21:1:700:LYS:HD2	2.55	0.40
21:1:935:THR:O	21:1:939:ARG:HG2	2.21	0.40
21:1:1126:PHE:HA	21:1:1165:TYR:CE2	2.56	0.40
22:2:614:ARG:O	22:2:618:GLY:N	2.51	0.40
22:2:648:LEU:O	22:2:649:LYS:HD3	2.21	0.40
23:3:983:ASN:HB2	23:3:1021:LEU:HB2	2.03	0.40
24:4:17:VAL:HG13	24:4:84:ILE:CG2	2.48	0.40
28:J:338:GLU:O	32:R:116:TYR:CD2	2.75	0.40
28:J:376:VAL:HG13	28:J:377:LYS:N	2.36	0.40
31:P:44:ARG:HG3	33:T:258:SER:CA	2.51	0.40
34:V:530:LYS:C	34:V:532:GLN:N	2.74	0.40
35:X:238:THR:O	35:X:393:VAL:HG23	2.21	0.40
1:A:82:ARG:HB3	1:A:83:HIS:HD1	1.86	0.40
1:A:247:THR:HG23	1:A:249:LEU:HD12	2.03	0.40
1:A:378:PHE:CE2	3:C:335:ASN:HB2	2.56	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:LEU:HD23	1:A:652:LEU:HA	1.84	0.40
1:A:1057:ARG:O	1:A:1060:GLU:HB2	2.22	0.40
1:A:1273:TYR:HD2	1:A:1274:PHE:CD2	2.39	0.40
1:A:1581:LEU:HD22	1:A:1746:ARG:NH1	2.36	0.40
1:A:2144:CYS:HB2	1:A:2270:PHE:CE1	2.57	0.40
3:C:375:GLU:N	3:C:376:PRO:HD2	2.37	0.40
5:E:255:MET:O	5:E:257:ASN:N	2.54	0.40
21:1:922:GLY:O	21:1:925:VAL:HG12	2.22	0.40
21:1:933:CYS:HA	21:1:936:VAL:HB	2.02	0.40
21:1:1130:PRO:HB3	22:2:528:ILE:HG23	2.04	0.40
23:3:63:ARG:HD2	23:3:83:ASP:HA	2.03	0.40
23:3:379:LEU:HB2	23:3:383:ASP:HB3	2.04	0.40
23:3:388:GLN:NE2	23:3:389:PRO:HD2	2.36	0.40
23:3:606:ALA:HA	23:3:616:ILE:HD13	2.04	0.40
33:T:339:GLN:CG	33:T:340:ALA:N	2.84	0.40
36:Y:37:TRP:HH2	37:Z:498:GLY:HA3	1.59	0.40
37:Z:491:ASP:O	37:Z:495:ALA:HB3	2.21	0.40
1:A:293:TRP:CE3	1:A:293:TRP:C	2.94	0.40
1:A:457:ASN:ND2	2:B:27:U:H3'	2.36	0.40
1:A:938:PRO:O	1:A:941:LYS:HD3	2.22	0.40
1:A:2120:LEU:HD12	1:A:2120:LEU:H	1.86	0.40
3:C:229:ILE:HG12	3:C:239:THR:HG21	2.04	0.40
3:C:567:GLU:O	3:C:567:GLU:HG3	2.20	0.40
13:F:96:U:H2'	13:F:97:U:C6	2.56	0.40
21:1:1052:ALA:HA	21:1:1055:TRP:CD1	2.51	0.40
21:1:1248:GLN:NE2	23:3:1030:PRO:HD3	2.36	0.40
23:3:179:ASN:HB3	23:3:213:LEU:O	2.22	0.40
23:3:192:ALA:HA	23:3:200:ALA:HB3	2.02	0.40
23:3:464:ARG:NH1	23:3:473:TYR:OH	2.53	0.40
23:3:535:GLU:HG2	23:3:536:TRP:N	2.36	0.40
25:5:42:TYR:CZ	25:5:73:ALA:HA	2.56	0.40
33:T:220:VAL:HG12	33:T:221:THR:N	2.37	0.40
1:A:148:TRP:CZ3	1:A:612:ILE:HG23	2.56	0.40
1:A:283:VAL:O	1:A:284:ARG:CZ	2.67	0.40
1:A:361:HIS:HE2	3:C:279:ARG:HH22	1.68	0.40
1:A:692:ASP:HA	33:T:376:ARG:HH21	1.72	0.40
1:A:718:ARG:NH2	32:R:259:LYS:HG3	2.36	0.40
1:A:787:GLU:OE1	1:A:790:ARG:NH2	2.53	0.40
1:A:923:ASP:OD2	1:A:1439:ARG:HD3	2.22	0.40
1:A:1161:LEU:HD23	1:A:1161:LEU:HA	1.85	0.40
1:A:2195:THR:O	1:A:2199:ILE:HG12	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2332:ASP:O	1:A:2334:TYR:N	2.54	0.40
3:C:259:LYS:HG3	41:C:1500:GTP:C5	2.57	0.40
3:C:592:VAL:HG12	3:C:603:MET:SD	2.62	0.40
3:C:673:LYS:HD3	3:C:673:LYS:H	1.86	0.40
3:C:738:ASP:N	3:C:738:ASP:OD1	2.54	0.40
3:C:926:ALA:N	3:C:927:PRO:CD	2.84	0.40
13:F:58:G:HO2'	13:F:59:G:P	2.44	0.40
21:1:570:TYR:O	21:1:574:ILE:HG12	2.22	0.40
21:1:839:GLU:O	21:1:842:ASN:HB2	2.22	0.40
21:1:1023:ILE:O	21:1:1026:ASN:HB2	2.21	0.40
23:3:561:GLY:O	23:3:582:GLU:HA	2.22	0.40
23:3:999:ARG:NE	23:3:1041:TYR:OH	2.54	0.40
32:R:123:GLU:C	32:R:124:VAL:HG12	2.41	0.40
33:T:218:TRP:HZ3	33:T:220:VAL:CG2	2.35	0.40
35:X:231:ALA:O	35:X:236:THR:OG1	2.39	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	2199/2335 (94%)	2049 (93%)	117 (5%)	33 (2%)	8 39
3	C	854/972 (88%)	777 (91%)	57 (7%)	20 (2%)	5 28
4	D	1720/2136 (80%)	1632 (95%)	85 (5%)	3 (0%)	44 78
5	E	297/357 (83%)	272 (92%)	16 (5%)	9 (3%)	3 22
6	a	77/126 (61%)	76 (99%)	1 (1%)	0	100 100
6	h	76/126 (60%)	75 (99%)	1 (1%)	0	100 100
7	b	80/231 (35%)	78 (98%)	2 (2%)	0	100 100
7	i	84/231 (36%)	82 (98%)	2 (2%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	c	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
8	j	80/119 (67%)	77 (96%)	3 (4%)	0	100	100
9	d	95/118 (80%)	91 (96%)	4 (4%)	0	100	100
9	k	81/118 (69%)	78 (96%)	3 (4%)	0	100	100
10	f	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
10	m	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
11	e	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
11	l	77/92 (84%)	76 (99%)	1 (1%)	0	100	100
12	g	72/76 (95%)	70 (97%)	2 (3%)	0	100	100
12	n	64/76 (84%)	62 (97%)	2 (3%)	0	100	100
16	o	160/255 (63%)	146 (91%)	12 (8%)	2 (1%)	10	42
17	p	159/225 (71%)	138 (87%)	9 (6%)	12 (8%)	1	10
18	w	419/501 (84%)	379 (90%)	37 (9%)	3 (1%)	19	56
19	u	93/793 (12%)	87 (94%)	4 (4%)	2 (2%)	5	29
20	v	90/464 (19%)	67 (74%)	16 (18%)	7 (8%)	1	10
21	1	1022/1304 (78%)	897 (88%)	119 (12%)	6 (1%)	22	59
22	2	171/895 (19%)	154 (90%)	17 (10%)	0	100	100
23	3	1165/1217 (96%)	1086 (93%)	78 (7%)	1 (0%)	48	83
24	4	76/424 (18%)	69 (91%)	6 (8%)	1 (1%)	10	42
25	5	106/125 (85%)	90 (85%)	16 (15%)	0	100	100
26	6	87/110 (79%)	80 (92%)	7 (8%)	0	100	100
27	7	64/86 (74%)	55 (86%)	9 (14%)	0	100	100
28	J	483/848 (57%)	452 (94%)	24 (5%)	7 (1%)	9	40
29	L	128/802 (16%)	119 (93%)	8 (6%)	1 (1%)	16	54
30	M	34/343 (10%)	30 (88%)	3 (9%)	1 (3%)	3	23
31	P	92/229 (40%)	82 (89%)	8 (9%)	2 (2%)	5	29
32	R	295/540 (55%)	249 (84%)	31 (10%)	15 (5%)	1	15
33	T	311/514 (60%)	282 (91%)	17 (6%)	12 (4%)	2	18
34	V	443/908 (49%)	412 (93%)	26 (6%)	5 (1%)	12	46
35	X	142/396 (36%)	131 (92%)	11 (8%)	0	100	100
36	Y	102/322 (32%)	91 (89%)	11 (11%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
37	Z	109/619 (18%)	93 (85%)	10 (9%)	6 (6%)	1 15
38	z	176/472 (37%)	170 (97%)	6 (3%)	0	100 100
39	x	561/1041 (54%)	536 (96%)	20 (4%)	5 (1%)	14 50
All	All	12645/20929 (60%)	11680 (92%)	812 (6%)	153 (1%)	14 44

All (153) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ARG
1	A	92	LEU
1	A	167	PRO
1	A	188	LEU
1	A	331	TRP
1	A	346	ASP
1	A	383	PHE
1	A	570	ASP
1	A	629	PHE
1	A	701	ILE
1	A	1119	ASP
3	C	388	VAL
3	C	427	PHE
3	C	444	GLY
3	C	457	VAL
3	C	458	ASP
3	C	516	LEU
3	C	824	THR
4	D	957	VAL
4	D	1584	ILE
5	E	193	THR
17	p	157	ASN
17	p	183	VAL
17	p	195	GLU
18	w	284	ARG
20	v	139	PRO
20	v	165	ARG
20	v	218	PRO
28	J	413	GLU
31	P	49	ASP
32	R	71	GLN
32	R	135	PRO
32	R	136	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R	186	VAL
32	R	412	ASP
32	R	416	PHE
32	R	420	LYS
32	R	425	GLY
33	T	186	PRO
33	T	268	LYS
33	T	341	ALA
33	T	343	PRO
33	T	495	ALA
34	V	596	LEU
34	V	597	PRO
37	Z	499	LYS
37	Z	531	LEU
37	Z	536	ARG
37	Z	569	PRO
39	x	937	ILE
1	A	122	ILE
1	A	308	ILE
1	A	349	ALA
1	A	367	SER
1	A	370	PRO
1	A	374	ASP
1	A	631	ALA
1	A	1141	ARG
3	C	90	THR
3	C	364	SER
3	C	572	GLU
3	C	711	ARG
16	o	160	LYS
17	p	159	PRO
17	p	160	GLU
17	p	177	PHE
17	p	186	ARG
19	u	280	VAL
20	v	115	PRO
21	1	112	ILE
28	J	217	GLU
28	J	341	PRO
28	J	376	VAL
28	J	709	VAL
31	P	190	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R	191	GLY
32	R	422	MET
33	T	301	ASP
34	V	485	GLN
37	Z	613	LYS
1	A	51	PHE
1	A	212	PRO
1	A	378	PHE
1	A	699	GLU
1	A	1118	PRO
1	A	1140	MET
5	E	60	MET
5	E	88	ARG
5	E	256	ASP
17	p	222	TYR
18	w	177	ARG
30	M	197	TYR
32	R	104	GLN
32	R	173	PRO
33	T	406	ILE
34	V	578	SER
39	x	1005	SER
1	A	363	HIS
1	A	480	LYS
1	A	698	PRO
1	A	1092	ILE
1	A	1114	LEU
1	A	1828	ALA
3	C	63	LYS
3	C	754	VAL
3	C	856	HIS
5	E	162	ARG
16	o	32	PRO
17	p	208	GLN
17	p	209	GLY
21	1	417	PRO
21	1	456	VAL
28	J	604	PRO
32	R	124	VAL
33	T	401	PRO
39	x	935	ASP
1	A	359	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	361	PRO
3	C	615	PRO
5	E	159	PRO
20	v	217	PRO
32	R	126	ASN
32	R	423	ASP
33	T	185	MET
33	T	189	GLN
33	T	226	ARG
39	x	980	GLN
39	x	981	PRO
3	C	94	ILE
3	C	360	ALA
3	C	623	GLU
5	E	270	LYS
17	p	173	GLN
20	v	141	ILE
20	v	220	PRO
21	1	944	SER
29	L	215	PRO
34	V	609	GLN
3	C	66	TYR
5	E	149	GLY
37	Z	571	PRO
1	A	186	GLU
19	u	221	PRO
18	w	229	TRP
21	1	418	PRO
24	4	27	PRO
28	J	241	VAL
33	T	411	GLY
4	D	585	ILE
5	E	324	PRO
17	p	184	PRO
21	1	932	ILE
23	3	491	VAL

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	1954/2108 (93%)	1850 (95%)	104 (5%)	19 41
3	C	745/866 (86%)	677 (91%)	68 (9%)	7 25
5	E	256/300 (85%)	244 (95%)	12 (5%)	22 44
18	w	49/446 (11%)	47 (96%)	2 (4%)	26 48
21	1	735/1104 (67%)	735 (100%)	0	100 100
22	2	94/776 (12%)	90 (96%)	4 (4%)	25 47
23	3	1018/1051 (97%)	1017 (100%)	1 (0%)	92 94
24	4	39/336 (12%)	37 (95%)	2 (5%)	20 42
25	5	74/109 (68%)	74 (100%)	0	100 100
26	6	76/95 (80%)	76 (100%)	0	100 100
27	7	57/77 (74%)	57 (100%)	0	100 100
28	J	205/751 (27%)	194 (95%)	11 (5%)	18 40
29	L	110/709 (16%)	105 (96%)	5 (4%)	23 45
30	M	25/294 (8%)	25 (100%)	0	100 100
31	P	90/203 (44%)	77 (86%)	13 (14%)	2 13
32	R	220/463 (48%)	170 (77%)	50 (23%)	0 5
33	T	268/441 (61%)	251 (94%)	17 (6%)	15 36
35	X	50/349 (14%)	44 (88%)	6 (12%)	4 17
36	Y	57/291 (20%)	56 (98%)	1 (2%)	54 71
37	Z	47/545 (9%)	39 (83%)	8 (17%)	1 10
38	z	146/416 (35%)	146 (100%)	0	100 100
39	x	1/897 (0%)	1 (100%)	0	100 100
All	All	6316/12627 (50%)	6012 (95%)	304 (5%)	24 43

All (304) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	ARG
1	A	48	LYS
1	A	49	ARG
1	A	50	LYS
1	A	59	GLU
1	A	60	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	75	ASP
1	A	77	THR
1	A	78	ASN
1	A	82	ARG
1	A	86	ARG
1	A	88	TYR
1	A	89	LEU
1	A	152	ARG
1	A	163	ARG
1	A	177	ASP
1	A	181	ASN
1	A	185	VAL
1	A	204	LEU
1	A	233	PRO
1	A	250	VAL
1	A	258	PHE
1	A	284	ARG
1	A	294	ASN
1	A	295	GLU
1	A	325	HIS
1	A	330	THR
1	A	331	TRP
1	A	334	THR
1	A	336	ASN
1	A	344	ASP
1	A	352	PHE
1	A	359	ILE
1	A	362	ARG
1	A	363	HIS
1	A	364	SER
1	A	366	LYS
1	A	367	SER
1	A	368	GLN
1	A	371	LEU
1	A	377	GLU
1	A	382	GLU
1	A	383	PHE
1	A	389	LYS
1	A	391	THR
1	A	394	TYR
1	A	409	ARG
1	A	413	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	433	GLU
1	A	452	LYS
1	A	459	LEU
1	A	462	ARG
1	A	467	GLN
1	A	468	LYS
1	A	535	ARG
1	A	546	LEU
1	A	579	GLN
1	A	606	LYS
1	A	627	CYS
1	A	630	TRP
1	A	642	ARG
1	A	671	THR
1	A	673	THR
1	A	674	LYS
1	A	675	GLN
1	A	679	SER
1	A	1146	ASP
1	A	1163	ARG
1	A	1425	LYS
1	A	1549	VAL
1	A	1930	TYR
1	A	2067	PHE
1	A	2073	TRP
1	A	2074	ARG
1	A	2078	ILE
1	A	2085	LEU
1	A	2087	THR
1	A	2090	ILE
1	A	2103	THR
1	A	2108	LYS
1	A	2117	ILE
1	A	2143	ARG
1	A	2156	THR
1	A	2157	VAL
1	A	2159	LEU
1	A	2171	GLU
1	A	2193	VAL
1	A	2194	THR
1	A	2219	THR
1	A	2223	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2233	SER
1	A	2239	ARG
1	A	2242	THR
1	A	2254	SER
1	A	2259	VAL
1	A	2261	MET
1	A	2273	VAL
1	A	2284	MET
1	A	2293	LYS
1	A	2298	LEU
1	A	2310	ARG
1	A	2312	SER
1	A	2319	LEU
1	A	2329	ASP
3	C	61	GLU
3	C	62	ASP
3	C	63	LYS
3	C	64	LYS
3	C	66	TYR
3	C	68	THR
3	C	71	GLU
3	C	79	THR
3	C	97	VAL
3	C	131	ASN
3	C	227	LEU
3	C	256	CYS
3	C	259	LYS
3	C	295	ASP
3	C	296	GLU
3	C	297	ASN
3	C	298	LEU
3	C	300	LEU
3	C	333	ASP
3	C	336	TYR
3	C	354	ARG
3	C	359	LYS
3	C	362	THR
3	C	366	GLN
3	C	387	ASP
3	C	389	ASP
3	C	427	PHE
3	C	428	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	438	ILE
3	C	446	LYS
3	C	452	THR
3	C	454	THR
3	C	457	VAL
3	C	458	ASP
3	C	459	SER
3	C	463	GLU
3	C	468	CYS
3	C	474	LEU
3	C	475	MET
3	C	477	HIS
3	C	489	GLN
3	C	490	PHE
3	C	495	ARG
3	C	512	GLU
3	C	517	GLU
3	C	519	GLU
3	C	571	ASN
3	C	572	GLU
3	C	573	GLU
3	C	596	ASN
3	C	673	LYS
3	C	675	PHE
3	C	677	GLU
3	C	704	VAL
3	C	706	GLN
3	C	709	TRP
3	C	712	LYS
3	C	724	TRP
3	C	725	ASP
3	C	730	ARG
3	C	738	ASP
3	C	749	THR
3	C	750	LEU
3	C	763	LYS
3	C	826	ARG
3	C	856	HIS
3	C	941	LYS
3	C	943	LEU
5	E	74	PHE
5	E	153	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	E	161	ARG
5	E	229	TYR
5	E	243	LEU
5	E	248	SER
5	E	250	LEU
5	E	265	ARG
5	E	270	LYS
5	E	271	GLU
5	E	289	LEU
5	E	290	ARG
18	w	419	PRO
18	w	441	PRO
22	2	498	VAL
22	2	520	PRO
22	2	614	ARG
22	2	616	SER
23	3	442	LEU
24	4	27	PRO
24	4	83	PRO
28	J	217	GLU
28	J	218	GLU
28	J	219	GLU
28	J	221	ASN
28	J	229	LYS
28	J	239	ARG
28	J	281	LYS
28	J	308	ARG
28	J	363	ARG
28	J	410	HIS
28	J	411	MET
29	L	219	LYS
29	L	222	LEU
29	L	227	THR
29	L	228	SER
29	L	235	LEU
31	P	28	LYS
31	P	29	GLN
31	P	30	TYR
31	P	33	ARG
31	P	66	ARG
31	P	67	GLU
31	P	76	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
31	P	78	ARG
31	P	188	TRP
31	P	190	ASP
31	P	191	ASP
31	P	212	ASN
31	P	224	MET
32	R	56	GLU
32	R	66	GLU
32	R	71	GLN
32	R	72	TYR
32	R	75	ASP
32	R	80	LYS
32	R	81	LYS
32	R	82	MET
32	R	86	LEU
32	R	89	GLN
32	R	92	SER
32	R	95	LYS
32	R	103	ARG
32	R	104	GLN
32	R	106	GLN
32	R	118	ASP
32	R	122	LYS
32	R	125	MET
32	R	128	ASP
32	R	129	ASP
32	R	137	GLU
32	R	158	LYS
32	R	170	LYS
32	R	171	LEU
32	R	175	GLN
32	R	181	PRO
32	R	183	GLN
32	R	186	VAL
32	R	188	PHE
32	R	189	ASN
32	R	195	ARG
32	R	211	ARG
32	R	212	PHE
32	R	213	LYS
32	R	214	ILE
32	R	215	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R	220	ARG
32	R	233	HIS
32	R	245	GLU
32	R	250	LYS
32	R	403	PRO
32	R	409	VAL
32	R	411	TYR
32	R	415	LEU
32	R	418	GLN
32	R	420	LYS
32	R	422	MET
32	R	426	PHE
32	R	434	TYR
32	R	435	ASN
33	T	257	ARG
33	T	282	ARG
33	T	308	ARG
33	T	318	ARG
33	T	387	PHE
33	T	399	LYS
33	T	400	PHE
33	T	401	PRO
33	T	402	ASP
33	T	412	HIS
33	T	416	ILE
33	T	418	THR
33	T	455	GLN
33	T	460	ASP
33	T	461	SER
33	T	463	SER
33	T	478	LEU
35	X	209	PRO
35	X	224	PRO
35	X	249	PRO
35	X	263	PRO
35	X	293	PRO
35	X	297	PRO
36	Y	44	PRO
37	Z	524	ARG
37	Z	526	ILE
37	Z	563	ARG
37	Z	569	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
37	Z	597	ARG
37	Z	598	PHE
37	Z	600	ARG
37	Z	613	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (96) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	73	HIS
1	A	78	ASN
1	A	97	HIS
1	A	210	HIS
1	A	297	ASN
1	A	325	HIS
1	A	363	HIS
1	A	573	GLN
1	A	584	HIS
1	A	601	GLN
1	A	675	GLN
1	A	775	ASN
1	A	924	GLN
1	A	1024	HIS
1	A	1069	ASN
1	A	1075	GLN
1	A	1096	HIS
1	A	1296	GLN
1	A	1359	HIS
1	A	1458	GLN
1	A	1460	HIS
1	A	1527	ASN
1	A	1580	HIS
1	A	1717	ASN
1	A	1784	ASN
1	A	1966	HIS
1	A	2123	GLN
1	A	2300	ASN
1	A	2306	HIS
3	C	87	GLN
3	C	245	HIS
3	C	297	ASN
3	C	383	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	C	437	HIS
3	C	513	ASN
3	C	575	GLN
3	C	583	ASN
3	C	596	ASN
3	C	706	GLN
3	C	924	GLN
5	E	165	GLN
18	w	425	HIS
18	w	485	ASN
21	1	473	GLN
21	1	599	ASN
21	1	903	GLN
21	1	942	ASN
21	1	1026	ASN
21	1	1186	GLN
21	1	1209	ASN
21	1	1248	GLN
21	1	1277	GLN
22	2	490	HIS
23	3	21	ASN
23	3	104	GLN
23	3	254	ASN
23	3	264	GLN
23	3	293	HIS
23	3	304	GLN
23	3	388	GLN
23	3	440	HIS
23	3	518	GLN
23	3	775	ASN
23	3	870	ASN
23	3	1087	GLN
28	J	221	ASN
28	J	259	GLN
28	J	294	HIS
28	J	351	ASN
29	L	73	HIS
30	M	198	GLN
31	P	212	ASN
31	P	220	HIS
32	R	89	GLN
32	R	104	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
32	R	106	GLN
32	R	126	ASN
32	R	189	ASN
32	R	194	GLN
32	R	215	ASN
32	R	233	HIS
32	R	283	HIS
32	R	418	GLN
33	T	217	GLN
33	T	278	ASN
33	T	297	HIS
33	T	413	ASN
33	T	417	ASN
33	T	446	ASN
33	T	451	HIS
33	T	455	GLN
35	X	307	GLN
36	Y	87	GLN
38	z	112	GLN
38	z	127	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	F	91/107 (85%)	37 (40%)	12 (13%)
14	G	76/274 (27%)	48 (63%)	9 (11%)
15	H	130/188 (69%)	33 (25%)	4 (3%)
2	B	82/117 (70%)	21 (25%)	10 (12%)
All	All	379/686 (55%)	139 (36%)	35 (9%)

All (139) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	13	C
2	B	19	A
2	B	20	G
2	B	21	A
2	B	22	U
2	B	23	C
2	B	24	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	25	C
2	B	26	A
2	B	28	A
2	B	35	U
2	B	36	C
2	B	38	C
2	B	40	U
2	B	41	U
2	B	45	C
2	B	47	A
2	B	57	G
2	B	70	A
2	B	71	C
13	F	6	C
13	F	7	G
13	F	8	C
13	F	10	U
13	F	12	G
13	F	25	C
13	F	26	U
13	F	27	A
13	F	28	A
13	F	29	A
13	F	33	G
13	F	34	G
13	F	36	A
13	F	37	C
13	F	38	G
13	F	44	G
13	F	45	A
13	F	46	G
13	F	47	A
13	F	48	A
13	F	49	G
13	F	51	U
13	F	54	G
13	F	55	C
13	F	56	A
13	F	58	G
13	F	59	G
13	F	60	C
13	F	61	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
13	F	62	C
13	F	68	C
13	F	74	U
13	F	78	A
13	F	79	C
13	F	85	U
13	F	86	U
13	F	87	C
14	G	-11	G
14	G	-6	C
14	G	-4	A
14	G	-3	A
14	G	1	G
14	G	2	U
14	G	3	A
14	G	4	A
14	G	5	G
14	G	7	G
14	G	8	C
14	G	10	U
14	G	11	A
14	G	12	G
14	G	13	C
14	G	17	U
14	G	21	A
14	G	22	C
14	G	23	U
14	G	24	G
14	G	25	G
14	G	26	U
14	G	27	U
14	G	28	A
14	G	29	C
14	G	30	C
14	G	31	U
14	G	131	U
14	G	132	G
14	G	135	G
14	G	136	U
14	G	137	C
14	G	143	U
14	G	144	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	G	145	U
14	G	146	C
14	G	147	C
14	G	148	U
14	G	149	G
14	G	150	U
14	G	151	C
14	G	152	C
14	G	154	U
14	G	156	U
14	G	159	U
14	G	161	U
14	G	162	C
14	G	163	C
15	H	14	C
15	H	20	G
15	H	23	A
15	H	24	A
15	H	25	G
15	H	29	A
15	H	30	A
15	H	31	G
15	H	44	U
15	H	45	C
15	H	46	U
15	H	47	U
15	H	48	A
15	H	65	U
15	H	112	G
15	H	143	A
15	H	147	G
15	H	149	A
15	H	152	G
15	H	153	A
15	H	154	C
15	H	156	U
15	H	157	G
15	H	160	A
15	H	163	G
15	H	164	C
15	H	166	G
15	H	167	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	H	169	C
15	H	177	A
15	H	178	A
15	H	179	C
15	H	183	G

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	12	U
2	B	18	C
2	B	19	A
2	B	20	G
2	B	23	C
2	B	24	G
2	B	25	C
2	B	27	U
2	B	39	C
2	B	40	U
13	F	5	U
13	F	7	G
13	F	25	C
13	F	33	G
13	F	35	A
13	F	36	A
13	F	37	C
13	F	47	A
13	F	48	A
13	F	50	A
13	F	58	G
13	F	59	G
14	G	-12	G
14	G	16	G
14	G	21	A
14	G	22	C
14	G	136	U
14	G	148	U
14	G	151	C
14	G	153	C
14	G	155	U
15	H	29	A
15	H	46	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
15	H	47	U
15	H	156	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 10 are monoatomic - leaving 2 for Mogul analysis.

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	$\#\|Z\| > 2$
40	IHP	A	3000	-	36,36,36	1.01	2 (5%)	54,60,60	1.62	12 (22%)
41	GTP	C	1500	42	26,34,34	1.18	1 (3%)	32,54,54	1.81	8 (25%)

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
40	IHP	A	3000	-	-	6/30/54/54	0/1/1/1
41	GTP	C	1500	42	-	7/18/38/38	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	C	1500	GTP	C6-N1	-3.52	1.32	1.37
40	A	3000	IHP	P5-O45	-2.86	1.43	1.54
40	A	3000	IHP	P2-O12	2.65	1.64	1.59

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
40	A	3000	IHP	O45-P5-O35	4.10	123.30	107.64
40	A	3000	IHP	O35-P5-O15	-3.97	88.19	105.99
41	C	1500	GTP	C5-C6-N1	3.79	120.64	113.95
41	C	1500	GTP	PA-O3A-PB	-3.79	119.84	132.83
41	C	1500	GTP	O6-C6-C5	-3.73	117.08	124.37
40	A	3000	IHP	O16-C6-C1	3.32	116.50	108.69
40	A	3000	IHP	C6-C1-C2	-3.22	103.37	110.41
41	C	1500	GTP	PB-O3B-PG	-3.16	121.97	132.83
41	C	1500	GTP	C2-N1-C6	-3.02	119.53	125.10
41	C	1500	GTP	O2G-PG-O3B	2.89	114.34	104.64
40	A	3000	IHP	O44-P4-O34	2.73	118.06	107.64
40	A	3000	IHP	C5-C6-C1	-2.65	104.62	110.41
41	C	1500	GTP	C3'-C2'-C1'	2.32	104.47	100.98
41	C	1500	GTP	O4'-C4'-C3'	2.30	109.66	105.11
40	A	3000	IHP	O35-P5-O25	2.25	119.48	110.68
40	A	3000	IHP	O12-C2-C3	2.14	113.74	108.69
40	A	3000	IHP	O15-C5-C4	-2.13	103.66	108.69
40	A	3000	IHP	O42-P2-O22	2.10	118.91	110.68
40	A	3000	IHP	O31-P1-O11	-2.09	96.62	105.99
40	A	3000	IHP	C4-C3-C2	2.08	114.96	110.41

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
40	A	3000	IHP	C4-C5-O15-P5
40	A	3000	IHP	C6-C5-O15-P5
41	C	1500	GTP	PB-O3B-PG-O3G
41	C	1500	GTP	C5'-O5'-PA-O3A
41	C	1500	GTP	C5'-O5'-PA-O1A
41	C	1500	GTP	C5'-O5'-PA-O2A
41	C	1500	GTP	O4'-C4'-C5'-O5'
41	C	1500	GTP	C3'-C4'-C5'-O5'
40	A	3000	IHP	C2-O12-P2-O22
40	A	3000	IHP	C1-O11-P1-O21

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
40	A	3000	IHP	C1-O11-P1-O31
40	A	3000	IHP	C5-O15-P5-O35
41	C	1500	GTP	PG-O3B-PB-O2B

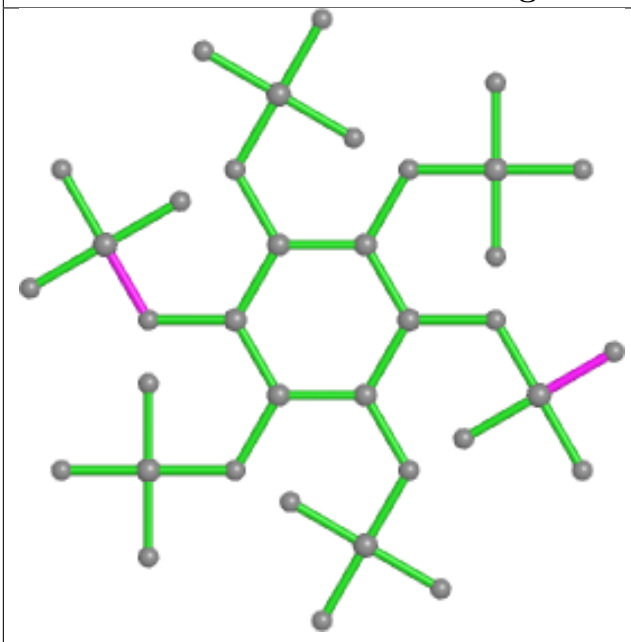
There are no ring outliers.

1 monomer is involved in 11 short contacts:

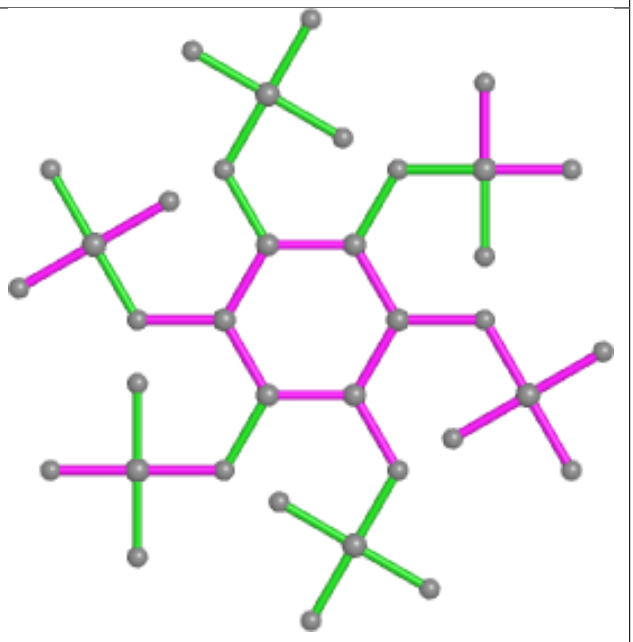
Mol	Chain	Res	Type	Clashes	Symm-Clashes
41	C	1500	GTP	11	0

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.

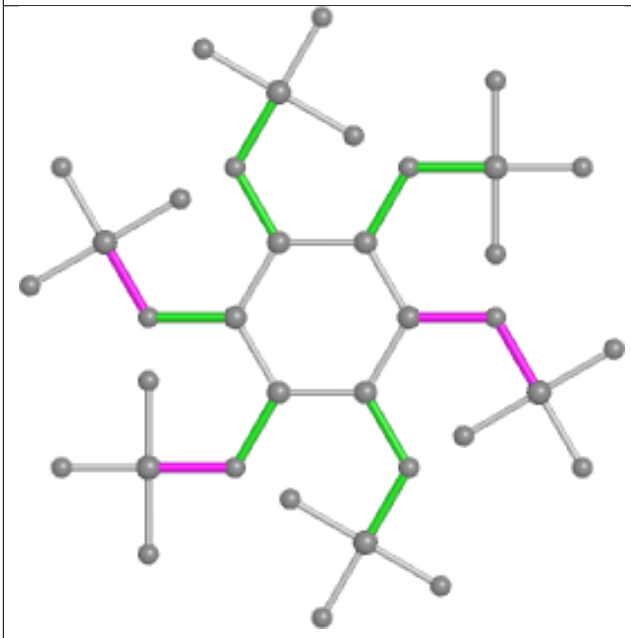
Ligand IHP A 3000



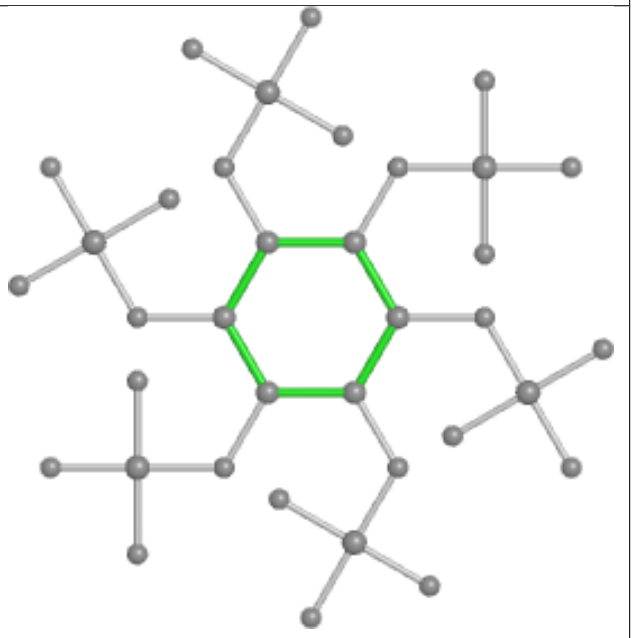
Bond lengths



Bond angles

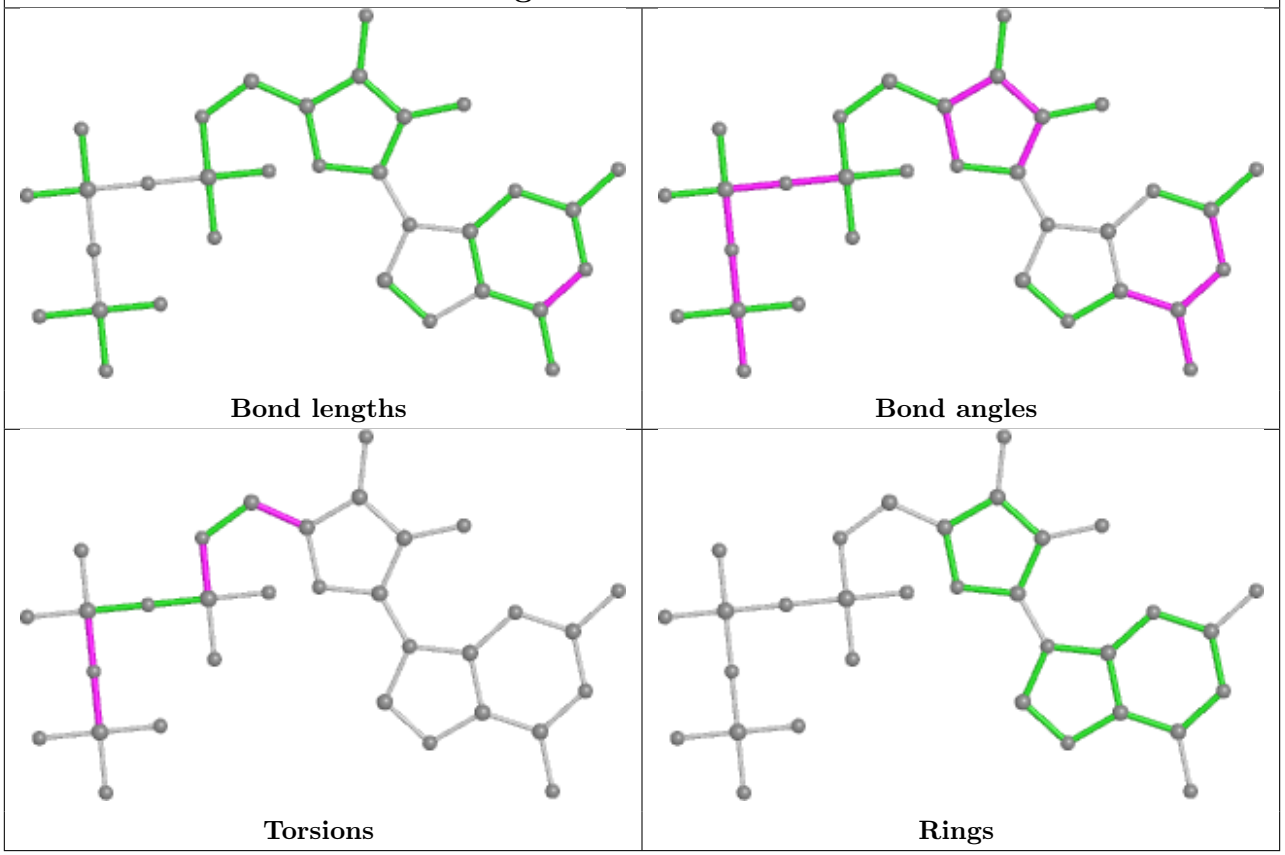


Torsions



Rings

Ligand GTP C 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.

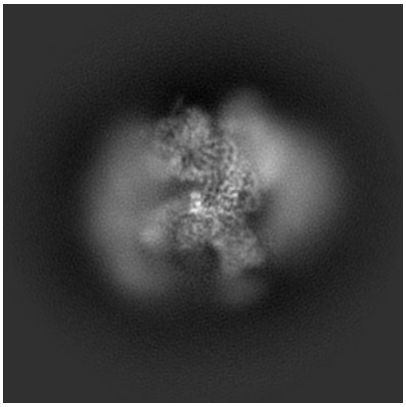
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-6891. These allow visual inspection of the internal detail of the map and identification of artifacts.

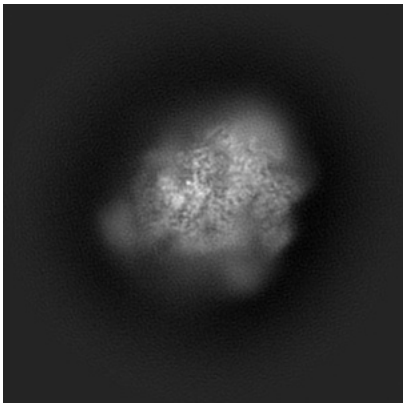
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

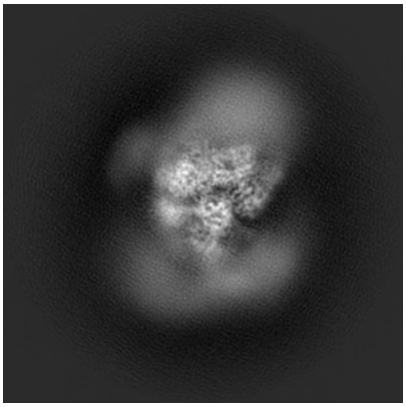
6.1.1 Primary map



X



Y

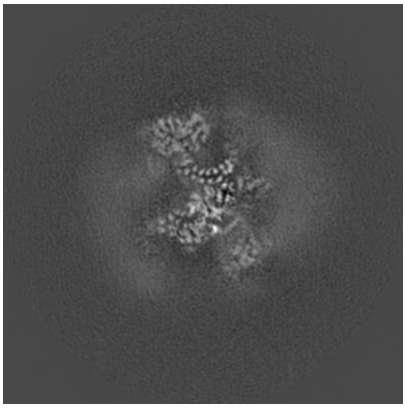


Z

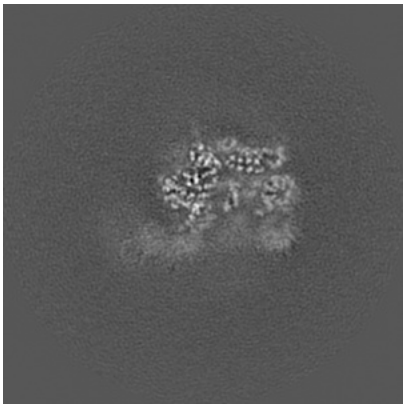
The images above show the map projected in three orthogonal directions.

6.2 Central slices

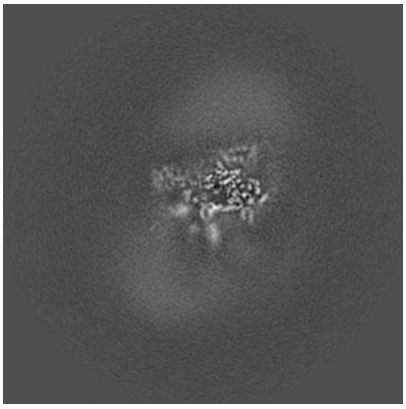
6.2.1 Primary map



X Index: 200



Y Index: 200

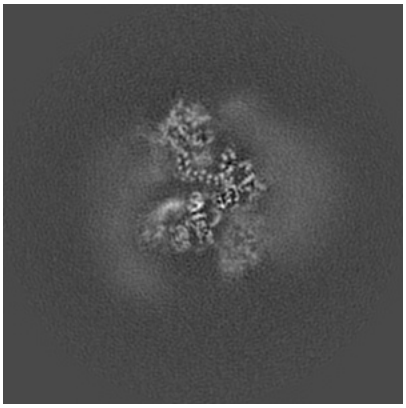


Z Index: 200

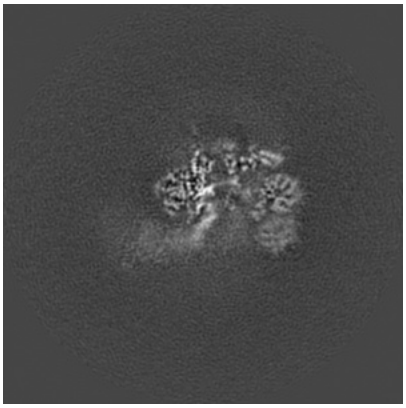
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

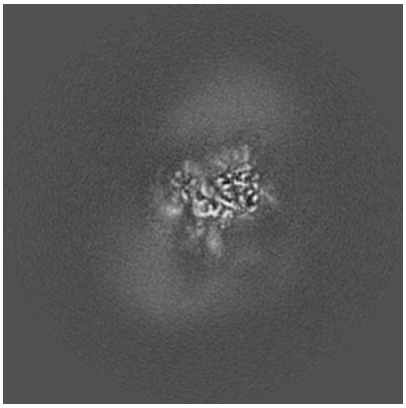
6.3.1 Primary map



X Index: 210



Y Index: 195

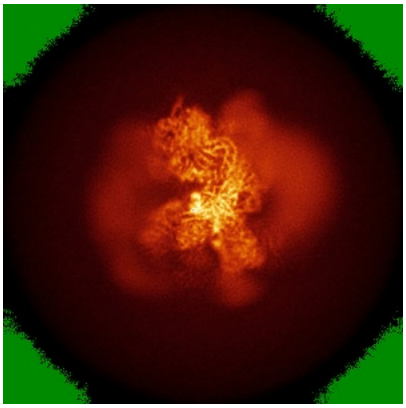


Z Index: 193

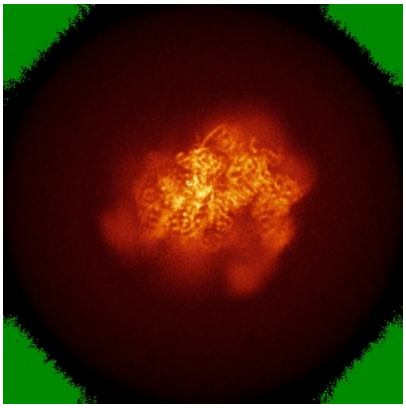
The images above show the largest variance slices of the map in three orthogonal directions.

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

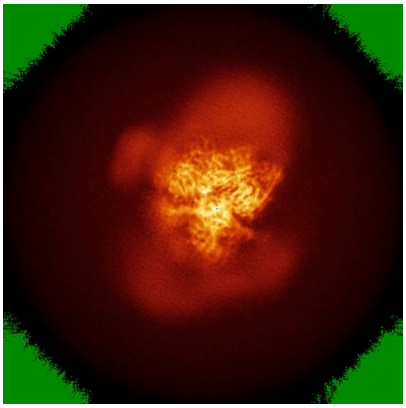
6.4.1 Primary map



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 0.0346. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

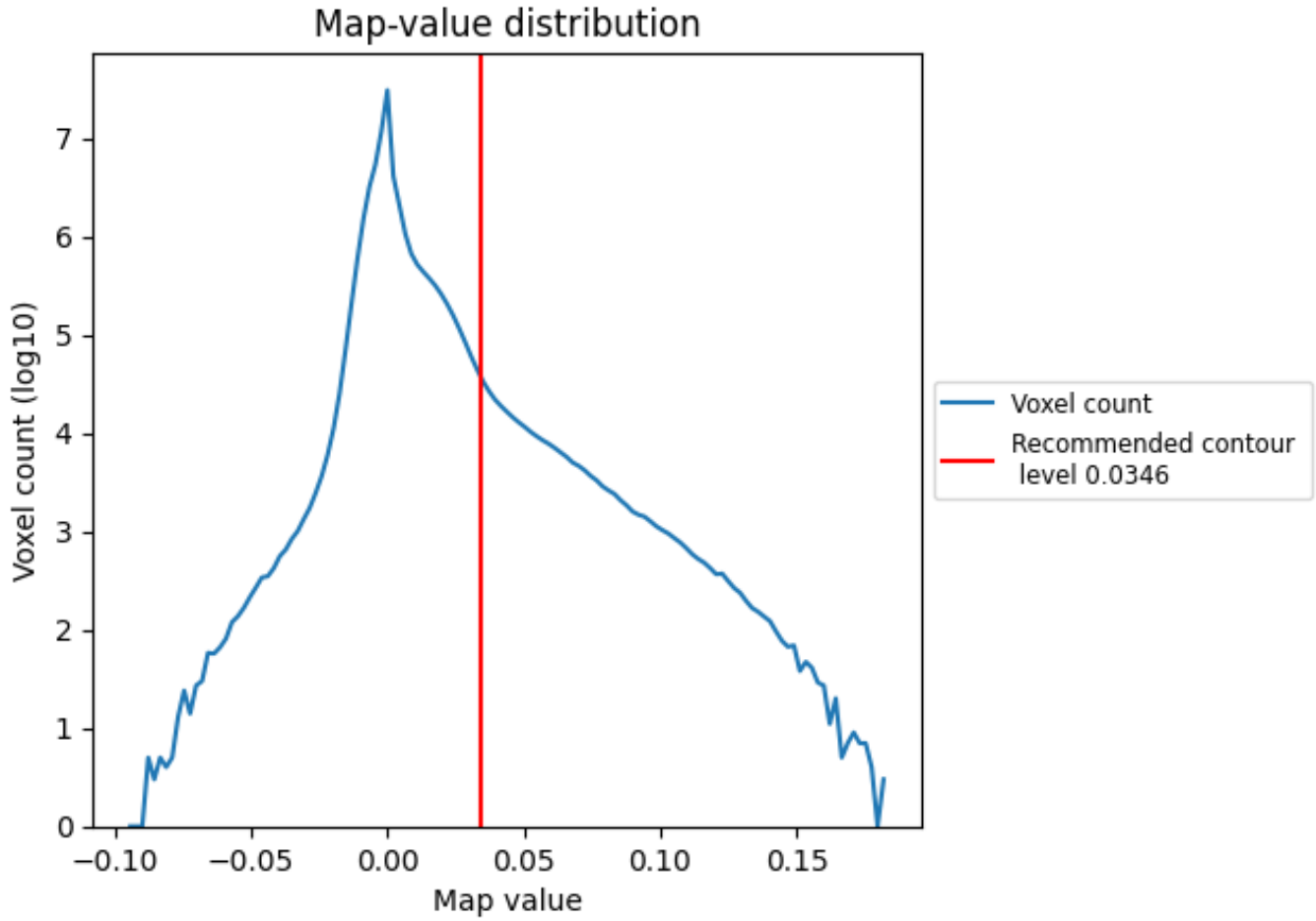
6.6 Mask visualisation (i)

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

7 Map analysis

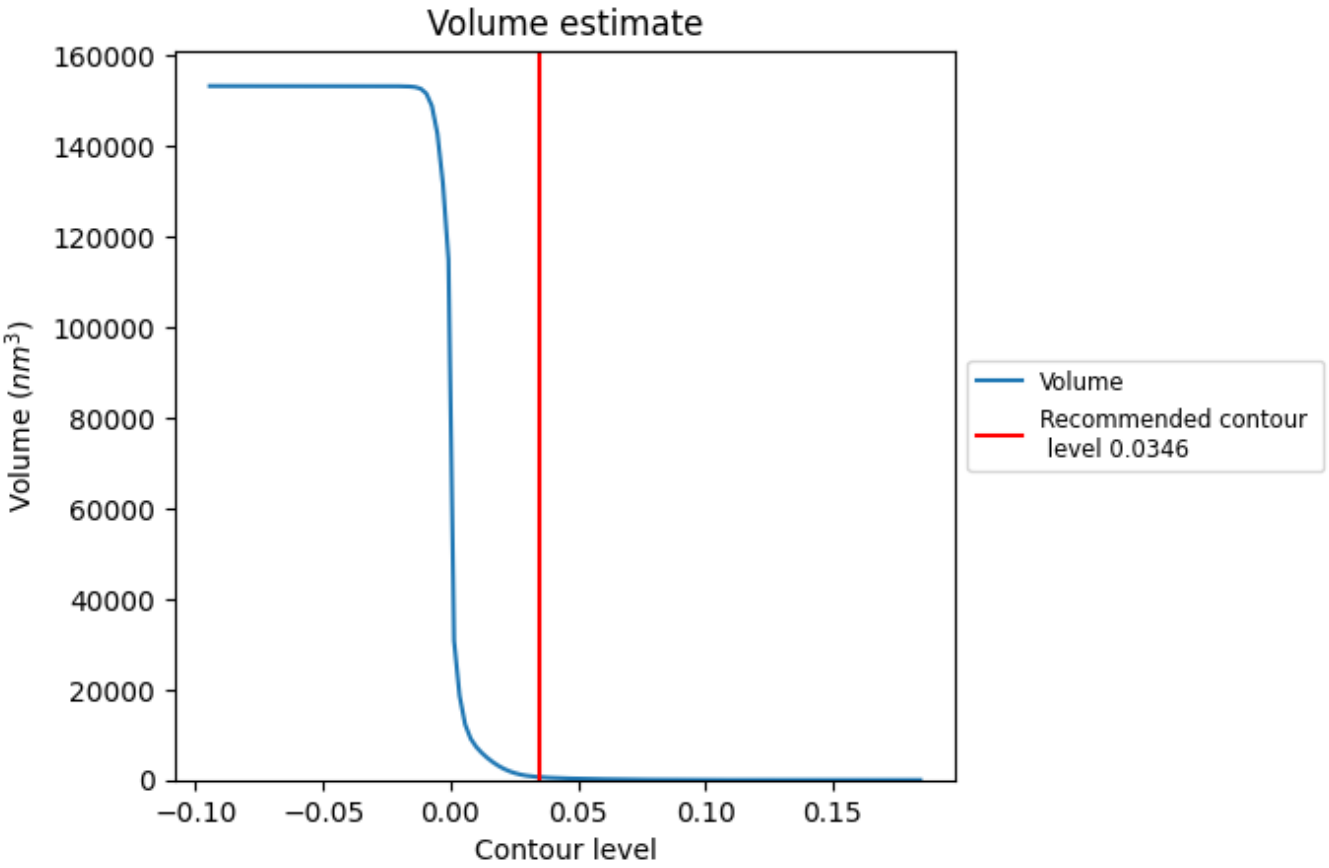
This section contains the results of statistical analysis of the map.

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.

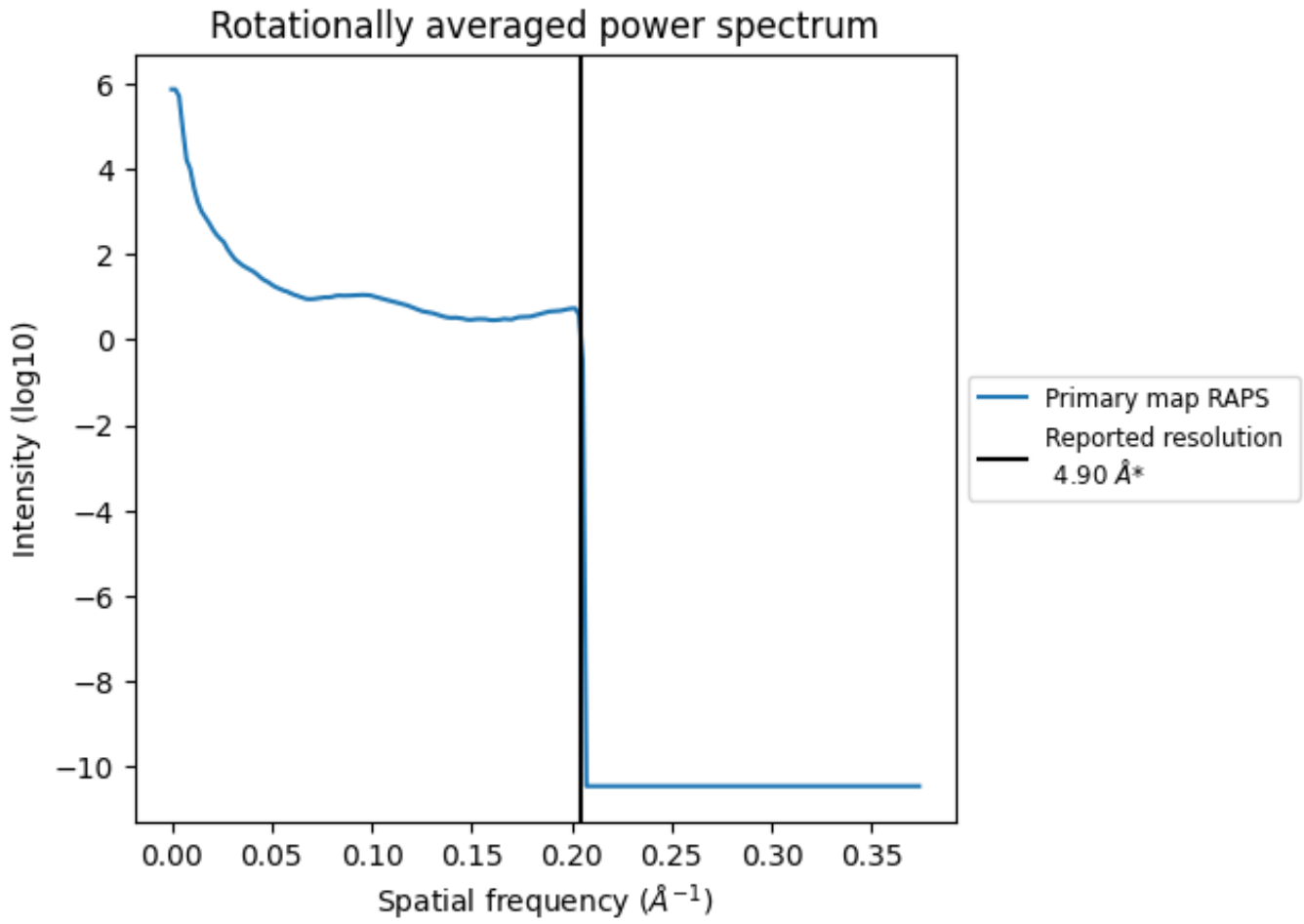
7.2 Volume estimate



The volume at the recommended contour level is 642 nm^3; this corresponds to an approximate mass of 580 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 0.204 Å^{-1}

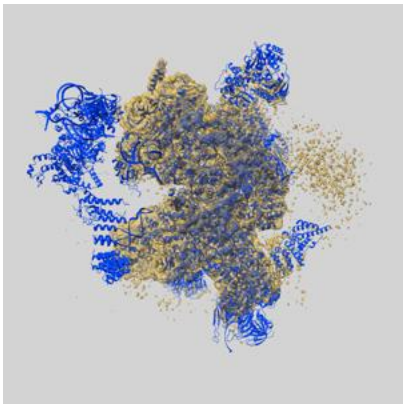
8 Fourier-Shell correlation

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

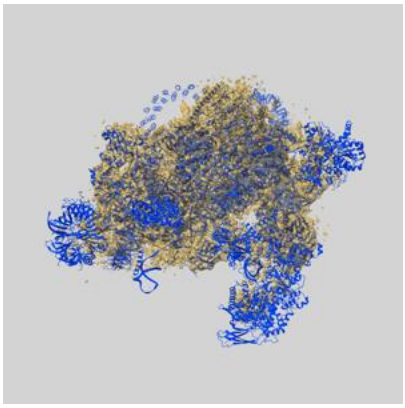
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-6891 and PDB model 5Z58. Per-residue inclusion information can be found in section 3 on page 13.

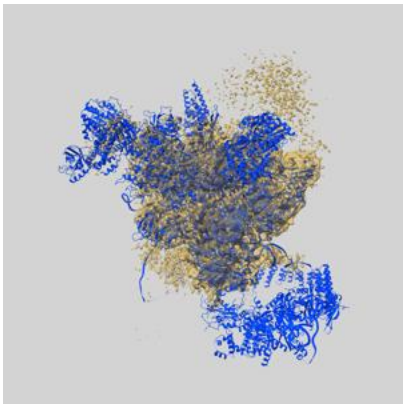
9.1 Map-model overlay



X



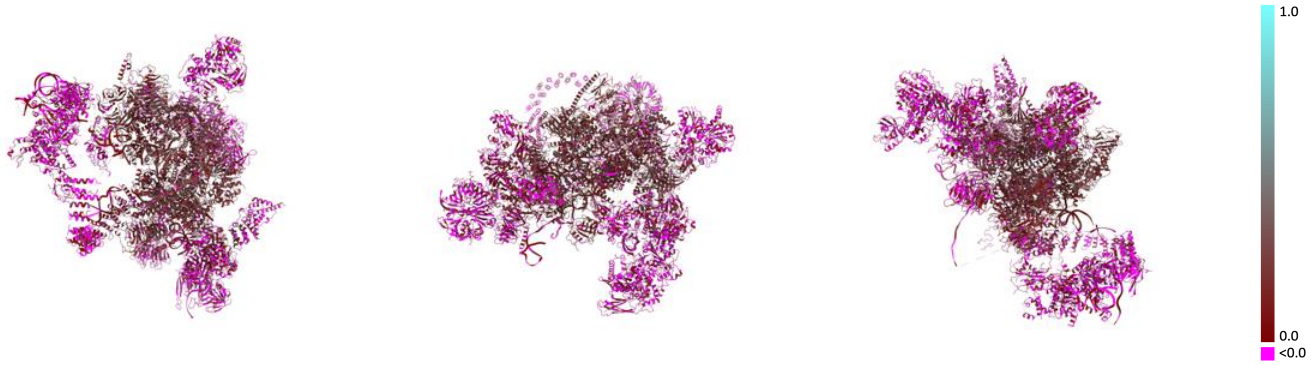
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0346 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.

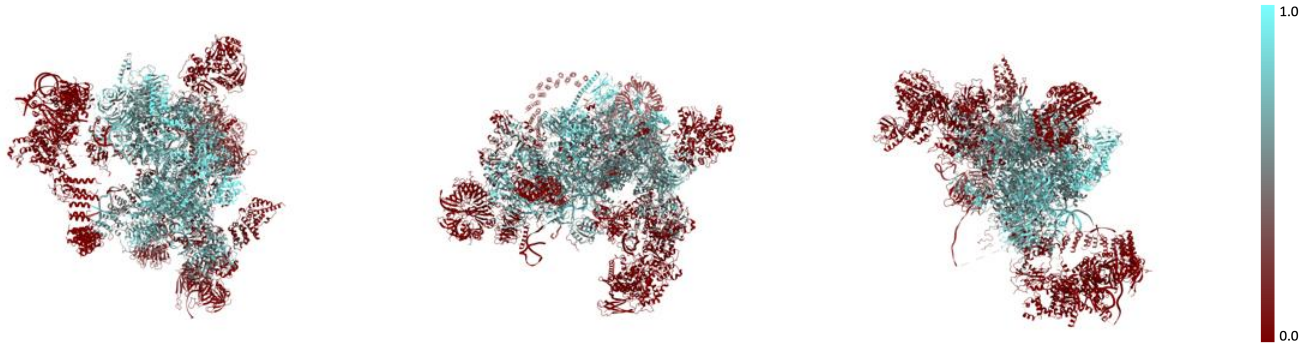
9.2 Q-score mapped to coordinate model (i)



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.

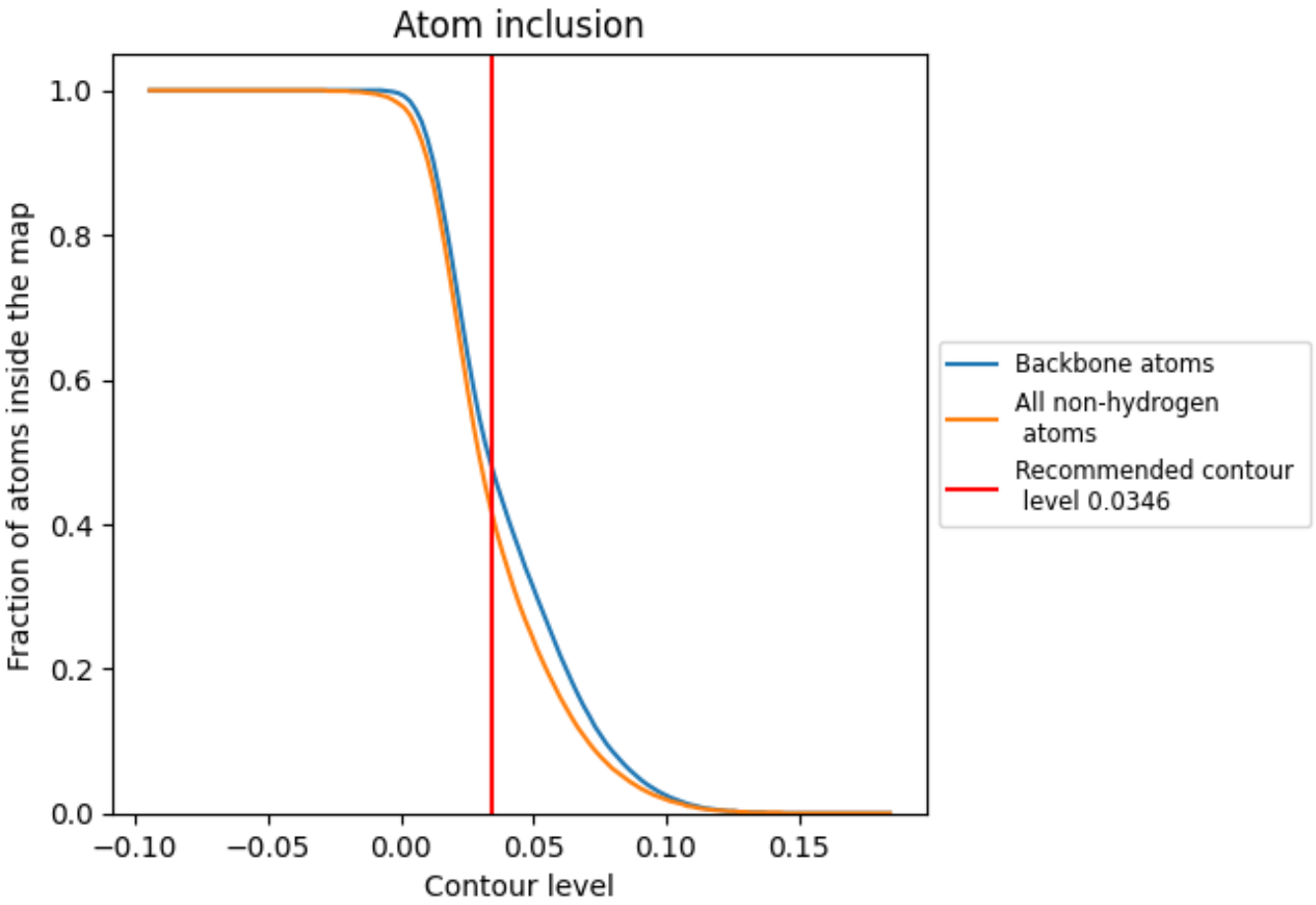
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0346).

9.4 Atom inclusion (i)



At the recommended contour level, 48% of all backbone atoms, 41% 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 (0.0346) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4120	0.1310
1	0.6670	0.2300
2	0.2970	0.1480
3	0.6080	0.1670
4	0.0730	0.0080
5	0.7300	0.2390
6	0.5060	0.1590
7	0.6800	0.2240
A	0.5570	0.1970
B	0.5980	0.1040
C	0.4530	0.0950
D	0.1160	0.0400
E	0.0260	0.0260
F	0.5990	0.1470
G	0.6230	0.1490
H	0.3420	0.0880
J	0.2790	0.0660
L	0.4750	0.2070
M	0.7170	0.2530
P	0.3090	0.1160
R	0.4080	0.1660
T	0.7530	0.2280
V	0.3420	0.1200
X	0.7090	0.2160
Y	0.6250	0.2470
Z	0.5950	0.2670
a	0.0000	0.0170
b	0.0050	0.0410
c	0.0220	0.0060
d	0.0940	-0.0040
e	0.0050	0.0020
f	0.0170	-0.0230
g	0.0000	0.0030
h	0.0000	0.0340
i	0.0000	0.0210

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
j	0.0000	-0.0440
k	0.0000	0.0110
l	0.0000	0.0140
m	0.0000	-0.0500
n	0.0000	0.0110
o	0.0000	0.0280
p	0.0000	0.0160
u	0.0000	0.0040
v	0.0000	0.0460
w	0.1150	0.0420
x	0.0290	0.0110
z	0.4980	0.1870