



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 05:18 AM UTC

PDB ID : 6EMK / pdb_00006emk
EMDB ID : EMD-3896
Title : Cryo-EM Structure of Saccharomyces cerevisiae Target of Rapamycin Complex 2
Authors : Karuppasamy, M.; Kusmider, B.; Oliveira, T.M.; Gaubitz, C.; Prouteau, M.; Loewith, R.; Schaffitzel, C.
Deposited on : 2017-10-02
Resolution : 7.90 Å (reported)
Based on initial model : 5FVM

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

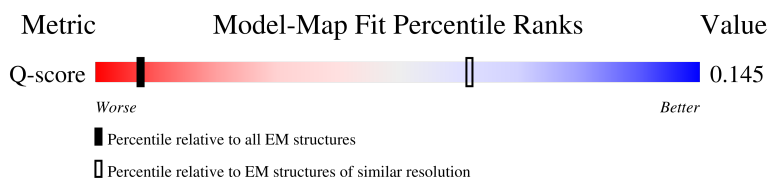
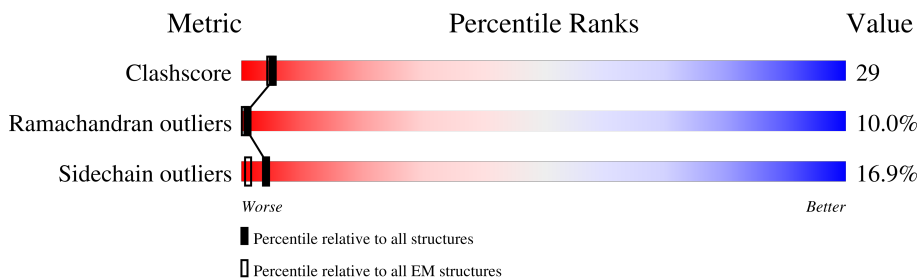
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.90 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	366 (7.40 - 8.40)

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

Mol	Chain	Length	Quality of chain
1	A	2474	
1	C	2474	
2	B	303	
2	D	303	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	E	303	91%9%
3	F	303	88%12%
4	G	426	33%64%
4	H	426	29%6%64%
5	I	1176	6%5%88%
5	J	1176	6%88%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 48012 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 Serine/threonine-protein kinase TOR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2262	Total	C	N	O	S	0	0
			18186	11650	3110	3345	81		
1	C	2262	Total	C	N	O	S	0	0
			18186	11650	3110	3345	81		

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	300	Total	C	N	O	S	0	0
			2372	1468	433	460	11		
2	D	300	Total	C	N	O	S	0	0
			2372	1468	433	460	11		

- Molecule 3 is a protein called Target of rapamycin complex 2 subunit TSC11.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	E	303	Total	C	N	O	0	0
			1515	909	303	303		
3	F	303	Total	C	N	O	0	0
			1515	909	303	303		

- Molecule 4 is a protein called Target of rapamycin complex 2 subunit AVO2.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	G	155	Total	C	N	O	0	0
			762	452	155	155		
4	H	155	Total	C	N	O	0	0
			762	452	155	155		

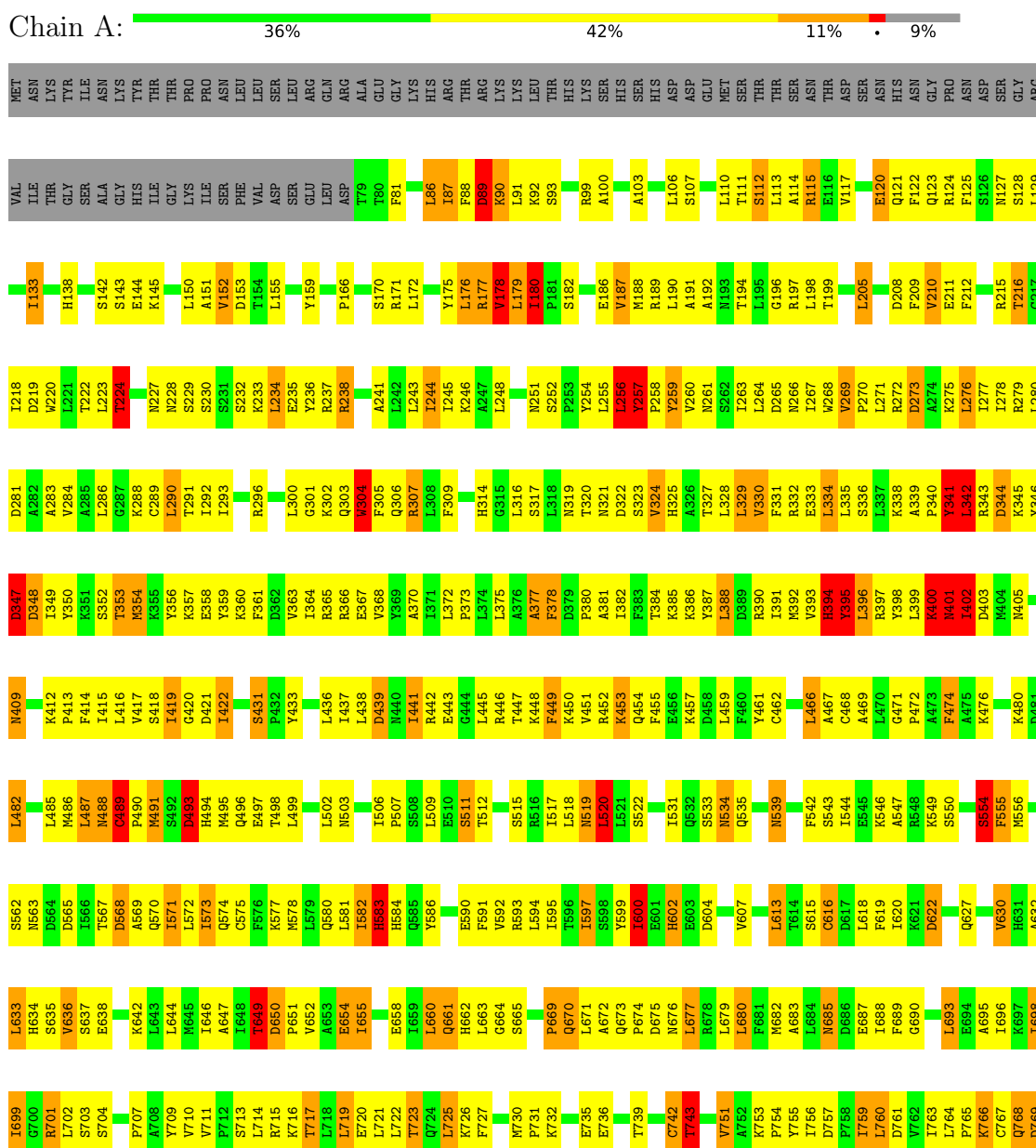
- Molecule 5 is a protein called Target of rapamycin complex 2 subunit AVO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	146	Total	C	N	O	S	0	0
			1171	739	187	242	3		
5	J	146	Total	C	N	O	S	0	0
			1171	739	187	242	3		

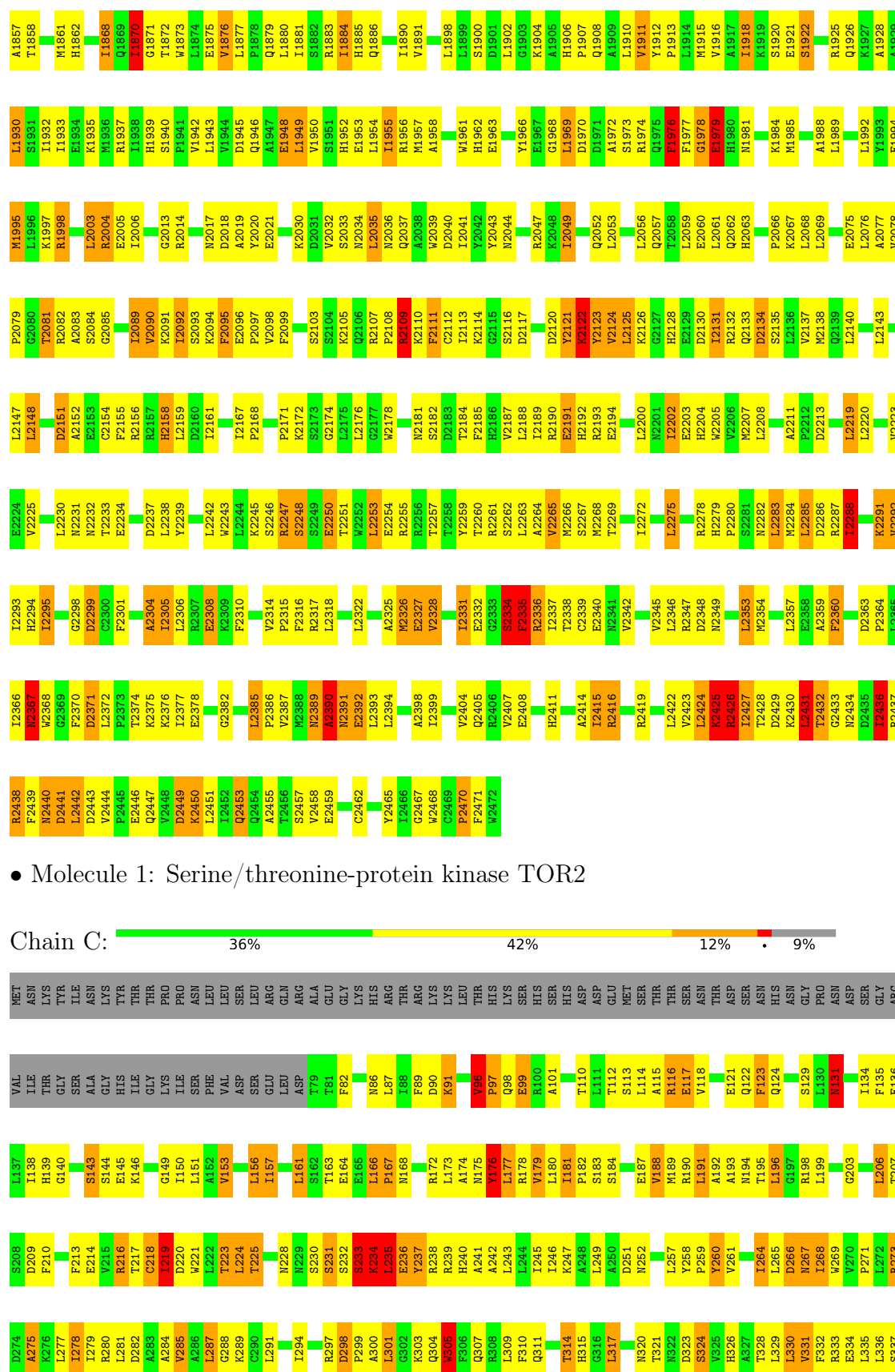
3 Residue-property plots

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

- Molecule 1: Serine/threonine-protein kinase TOR2



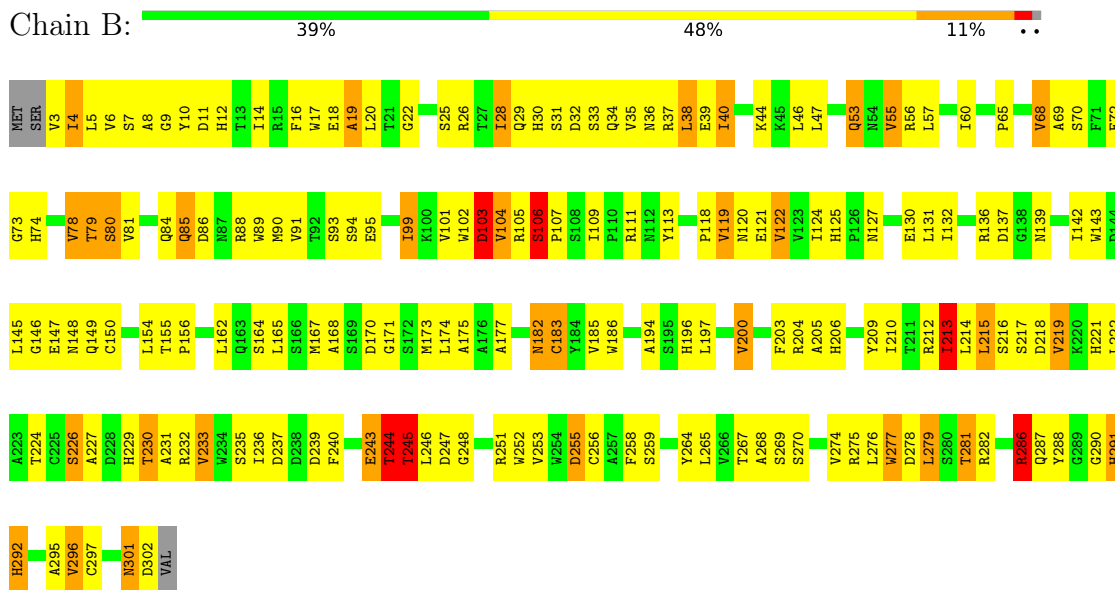
GLU	Q1728	Y1653	T1577	I1502	A1415	I1332	S1266	I1193	V1126	Q1084	F982	VAL	G846	A770
PHE	P1729	A1654	R1578	C1504	E1418	P1333	V1267	N1199	R1127	K1057	Q983	SER	I847	S771
ASN	K1730	Q1655	L1579	C1504	K1419	I1334	Y1268	N1199	R1128	R1058	Q984	PRO	L848	S772
GLY	R1732	K1657	L1580	F1510	E1418	K1339	A1272	V1201	L1129	L1065	L985	ASN	R849	A773
MET	L1733	G1581	K1511	K1511	K1419	Y1340	R1273	F1202	N1130	V1060	I851	ASP	N850	V774
ILE	S1734	Q1582	K1512	A1513	G1423	A1341	E1274	E1203	R1134	I1062	V992	E914	L852	A775
GLY	W1735	L1659	A1513	A1513	E1424	Q1342	L1275	R1204	E1136	R1063	K993	Y915	K853	S776
VAL	P1736	W1660	E1514	E1514	D1425	K1343	F1276	K1205	L1135	I1064	Q994	Y916	T854	T777
ASN	D1666	E1667	V1515	V1515	V1426	C1344	N1277	N1206	L1136	L1063	H995	P917	E855	A778
THR	A1667	L1667	H1516	H1516	E1427	H1345	A1278	Y1207	T1137	L1065	Y996	T918	N856	K780
PHE	E1668	V1588	F1517	F1517	E1428		S1279	K1207	K1138	K1066	R997	V919	K780	V781
ASP	L1669	V1589	G1518	G1518	V1429	A1348	F1280	E1208	A1139	S1067	F998	V920	I860	E784
ALA	K1670	Q1590	M1519	M1519	M1430		S1281	D1209	T1140	L1068	H999	I921	R861	E784
LYS	Q1671	T1591	A1520	A1520	K1433	L1351	S1282		M1141	R861	V1000	R922	R862	E784
GLU	L1672	T1592	L1523	L1523	L1434	H1352	C1283	Q1212	N1142	I1070	E1001	N923	G863	V788
VAL	L1744	L1593	L1523	L1523	L1434	Y1353	W1284	V1213	T1143	F1071	K1002	N923	T864	
HIS	A1746	R1594	L1524	L1524	R1435	K1354	V1285	T1214	L1144	G1072	I1003	I927	V965	K791
TYR	T1747	V1595	V1525	V1525	S1436	E1355	E1266	K1215	S1445	P1073	Y1004	L928	R866	M793
S1811		M1679	T1526	T1526	L1437	V1356	L1287	K1216	L1146		G1005	H929	L867	K793
S1812	D1760		E1527	E1527	T1438	E1357	Q1288	P1217	L1147	E1076	V1006	D930	I868	T794
N1813	N1751	D1682	L1528	L1528	A1439	F1358	T1289	V1218	L1148	D1077	I1007	P930	R869	M795
L1814	T1752	L1683	L1528	L1528	L1440	L1359	S1290	M1219	L1149	Y1078	R1008	S932	ILE	Y796
L1815	W1753	GLY	E1534	E1534	S1447		Y1291	Q1220	Q1150	S1079	E1009	L933	LEU	L797
H1816	Y1754	LEU	S1535	S1535	S1446	P1362	Q1292	M1221	L1151		F1010		GLY	K798
V1819	K1755	ASP	A1539	A1539	S1447		E1293	L1222	G1152	I1082		H937	ALA	E799
P1820	A1756	PRO	Y1540	Y1540	R1448	T1366	L1294	L1223	T1153	M1083	T1013	T938	L800	L800
I1821	T1757	ASN			L1449	I1367	LEU	K1224	D1154	P1084	I1014	A939	ASP	M801
A1822	H1758	ASN			A1450	E1368	ILE		F1155	I1085	K1015	PRO	TYR	I804
L1823	N1759	MET	V1544	V1544	S1451	A1369	GLN	W1227	V1156	I1086	L1016	Q942	L928	I805
K1824	A1762	ALA	R1545	R1545	E1452	L1370	ALA	I1228	V1157	V1087	Q1017	I944	HIS	T806
G1825	A1763	GLN	A1546	A1546	K1453	I1371	LEU	C1229	F1158	R1088	Q1017	I944	ARG	N907
F1826	N1764	GLN	Q1547	Q1547	L1456	S1372	CYS	S1230	V1159	M1089	T1019	H946	GLU	F808
F1827		SER	K1611	K1611	T1456	I1373	LYS	Q1231	P1160	T1090	I1020	I947	ILE	Q809
		VAL	F1612	F1612	A1457		ALA	Q1232	V1161	E1091	I1021		GLU	D810
V1767		PRO	A1550	A1550	K1458	L1377	LEU	K1233	K1164	Y1092	S1022		VAL	S812
S1768		GLN	E1551	E1551	P1459	H1378	SER	E1236	A1165	L1097	V1023	THR	THR	S812
MET		GLN	L1552	L1552	L1459	Q1379	SER	D1237	L1166	K1098	I1024	SER	SER	N813
S1831		SER	E1553	E1553	M1465	T1380	GLU	W1238	L1167	C955	E1025	ASN	ASN	N813
L1832		LYS	E1554	E1554			ASN			I1100	S1026	SER	SER	F815
S1835		ARG	I1555	I1555	L1468	A1383				S1101	I1027	S957	L936	R816
S1836		VAL	I1556	I1556	L1476	I1384	PRO	K1241	R1170	I1102	S1028	SER	SER	R817
S1837		PRO	K1557	K1557	E1477	G1385	PRO	I1242	I1171	I1103	K1029	D960	VAL	D818
L1838		ARG	Y1558	Y1558	E1477	I1386	GLU	R1243	Q1172	T1104		G1033	VAL	
L1838		SER	K1559	K1559		L1387	ILE	R1244	H1173	L1104		E1034	GLN	
Q1839		HIS			D1480	K1388	TYR	L1245	S1174	L1105	G1033	Q961	GLU	L821
D1840		V1706	P1562	P1562		H1389	GLN	I1247	Y1175	G1106	F1035	I962	GLN	
A1841		K1711	Q1563	Q1563	V1488	A1390	MET	Q1247	V1176			I963	ASN	
L1842		L1712	D1566	D1566	M1489	Q1391	LEU	L1247	D1177	K1110	V1039	P964	ALA	L824
R1843		L1713	K1567	K1567	K1490		LEU	L1249	Q1178	N1111	P1040	G965	PRO	L827
L1844		A1714	R1567	R1567	S1491	T1401	ASN	E1252	N1181	I1112	E1041	SER	SER	
		ASP	L1568	L1568	Q1492	W1402	V1320	S1253	K1182	I967	T1042	I967	ILE	V835
		C1716	L1569	L1569	S1493	E1403			L1183	L968	L1043	V969	ASP	
			T1570	T1570		A1404			L1184	E1116	T1044	F1045	ILE	L838
		K1719	M1571	M1571	K1496	K1405	D1326	L1258		M1117	T1045	R971	ALA	
			R1572	R1572	E1497	L1406	P1327	R1259			F1046		LEU	Y841
			E1573	E1573	F1498	Q1407	D1327	S1262	L1189	R1120	T1049	Q977	LEU	P842
		W1723	T1574	T1574	F1498	L1407	P1329	S1263	P1190	I1121	T1049	L978	MET	E843
		ASP	V1575	V1575	D1500	R1408	L1330	S1263	T1191	V1122	F1045	L978	GLN	L844
		V1725							N1192	Q1123		D979	GLY	L845



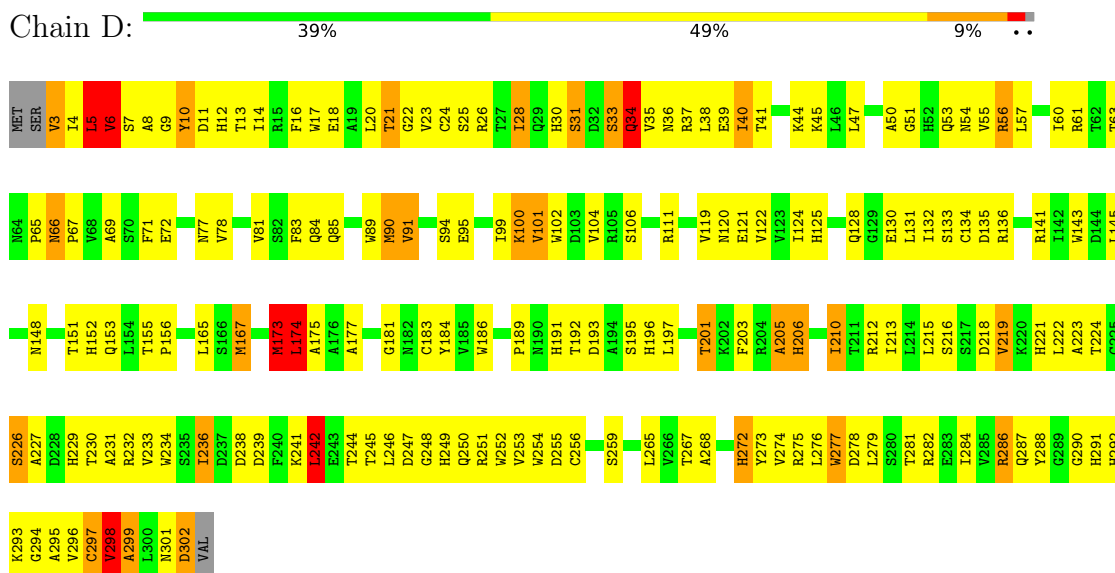


L2433	L2434	G2435	N2436	D2437	I2438	N2442	D2443	L2444	D2445	V2446	P2447	E2448	Q2449	V2450	D2451	K2452	L2453	S2459	V2460	E2461	T2468	G2469	W2470	C2471	P2472	F2473	N2474	L2483	L2484	L2485	L2486	L2487	L2488	L2489	L2490	L2491	L2492	L2493	L2494	L2495	L2496	L2497	L2498	L2499	F1500	I1504	L1505	C1506	L1507	H1508	R1509	A1510	L1511	G1512	F1513	K1514	A1515	E1516	F1517	H1518	L1519	F1520	N1521	L1525	L1526	E1529	L1530	S1531	A1532	V1533	L1534	M1535	E1536	S1537	R1540	A1541	Y1542	N1543	V1544	V1545	V1546	R1547	E1548	Q1549	I1550	L1551	A1552	E1553	Q1554	Y1555	T1556	E1557	L1558	S1559	K1560	Y1561	K1562	L1563	D1568	K1569	R1570	L1571	T1572	M1573	R1574	E1575	T1576	N1577	V1578	G1579	A1580	L1581	L1582	G1583	E1584	Q1585	L1586	W1587	V1588	D1589	V1590	Y1591	Q1592	R1593	L1594	R1595	V1596	L1597	A1598	S1599	M1600	E1601	S1602	K1603	P1604	K1605	E1606	Q1609	V1610	R1611	L1612	K1613	F1614	G1615	N1616	V1617	W1618	L1619	R1620	M1621	A1622	S1623	L1624	Y1625	K1626	Y1627	Y1628	Y1629	Y1630	Y1631	Y1632	T1633	L1634	E1635	E1636	E1637	S1650	V1653	V1654	V1655	A1656	G1657	L1658	L1659	W1660	L1661	W1662	A1663	L1666	Q1667	D1668	E1669	A1670	L1671	L1674	T1678	M1681	A1682	H1683	D1684	L1685	GLY	LEU	ASP	PRO	ASN	ASN	MET	ILE	ALA	GLN	SER	VAL	PRO	GLN	GLN	L1623	M1624	A1625	L1626	Y1627	Y1628	Y1629	Y1630	Y1631	Y1632	Y1633	Y1634	Y1635	Y1636	Y1637	Y1638	Y1639	Y1640	Y1641	Y1642	Y1643	Y1644	Y1645	Y1646	Y1647	Y1648	Y1649	Y1650	Y1651	Y1652	Y1653	Y1654	Y1655	Y1656	Y1657	Y1658	Y1659	Y1660	Y1661	Y1662	Y1663	Y1664	Y1665	Y1666	Y1667	Y1668	Y1669	Y1670	Y1671	Y1672	Y1673	Y1674	Y1675	Y1676	Y1677	Y1678	Y1679	Y1680	Y1681	Y1682	Y1683	Y1684	Y1685	Y1686	Y1687	Y1688	Y1689	Y1690	Y1691	Y1692	Y1693	Y1694	Y1695	Y1696	Y1697	Y1698	Y1699	Y1700	Y1701	Y1702	Y1703	Y1704	Y1705	Y1706	Y1707	Y1708	Y1709	Y1710	Y1711	Y1712	Y1713	Y1714	Y1715	Y1716	Y1717	Y1718	Y1719	Y1720	Y1721	Y1722	Y1723	Y1724	Y1725	Y1726	Y1727	Y1728	Y1729	Y1730	Y1731	Y1732	Y1733	Y1734	Y1735	Y1736	Y1737	Y1738	Y1739	Y1740	Y1741	Y1742	Y1743	Y1744	Y1745	Y1746	Y1747	Y1748	Y1749	Y1750	Y1751	Y1752	Y1753	Y1754	Y1755	Y1756	Y1757	Y1758	Y1759	Y1760	Y1761	Y1762	Y1763	Y1764	Y1765	Y1766	Y1767	Y1768	Y1769	Y1770	Y1771	Y1772	Y1773	Y1774	Y1775	Y1776	Y1777	Y1778	Y1779	Y1780	Y1781	Y1782	Y1783	Y1784	Y1785	Y1786	Y1787	Y1788	Y1789	Y1790	Y1791	Y1792	Y1793	Y1794	Y1795	Y1796	Y1797	Y1798	Y1799	Y1800	Y1801	Y1802	Y1803	Y1804	Y1805	Y1806	Y1807	Y1808	Y1809	Y1810	Y1811	Y1812	Y1813	Y1814	Y1815	Y1816	Y1817	Y1818	Y1819	Y1820	Y1821	Y1822	Y1823	Y1824	Y1825	Y1826	Y1827	Y1828	Y1829	Y1830	Y1831	Y1832	Y1833	Y1834	Y1835	Y1836	Y1837	Y1838	Y1839	Y1840	Y1841	Y1842	Y1843	Y1844	Y1845	Y1846	Y1847	Y1848	Y1849	Y1850	Y1851	Y1852	Y1853	Y1854	Y1855	Y1856	Y1857	Y1858	Y1859	Y1860	Y1861	Y1862	Y1863	Y1864	Y1865	Y1866	Y1867	Y1868	Y1869	Y1870	Y1871	Y1872	Y1873	Y1874	Y1875	Y1876	Y1877	Y1878	Y1879	Y1880	Y1881	Y1882	Y1883	Y1884	Y1885	Y1886	Y1887	Y1888	Y1889	Y1890	Y1891	Y1892	Y1893	Y1894	Y1895	Y1896	Y1897	Y1898	Y1899	Y1900	Y1901	Y1902	Y1903	Y1904	Y1905	Y1906	Y1907	Y1908	Y1909	Y1910	Y1911	Y1912	Y1913	Y1914	Y1915	Y1916	Y1917	Y1918	Y1919	Y1920	Y1921	Y1922	Y1923	Y1924	Y1925	Y1926	Y1927	Y1928	Y1929	Y1930	Y1931	Y1932	Y1933	Y1934	Y1935	Y1936	Y1937	Y1938	Y1939	Y1940	Y1941	Y1942	Y1943	Y1944	Y1945	Y1946	Y1947	Y1948	Y1949	Y1950	Y1951	Y1952	Y1953	Y1954	Y1955	Y1956	Y1957	Y1958	Y1959	Y1960	Y1961	Y1962	Y1963	Y1964	Y1965	Y1966	Y1967	Y1968	Y1969	Y1970	Y1971	Y1972	Y1973	Y1974	Y1975	Y1976	Y1977	Y1978	Y1979	Y1980	Y1981	Y1982	Y1983	Y1984	Y1985	Y1986	Y1987	Y1988	Y1989	Y1990	Y1991	Y1992	Y1993	Y1994	Y1995	Y1996	Y1997	Y1998	Y1999	Y2000	Y2001	Y2002	Y2003	Y2004	Y2005	Y2006	Y2007	Y2008	Y2009	Y2010	Y2011	Y2012	Y2013	Y2014	Y2015	Y2016	Y2017	Y2018	Y2019	Y2020	Y2021	Y2022	Y2023	Y2024	Y2025	Y2026	Y2027	Y2028	Y2029	Y2030	Y2031	Y2032	Y2033	Y2034	Y2035	Y2036	Y2037	Y2038	Y2039	Y2040	Y2041	Y2042	Y2043	Y2044	Y2045	Y2046	Y2047	Y2048	Y2049	Y2050	Y2051	Y2052	Y2053	Y2054	Y2055	Y2056	Y2057	Y2058	Y2059	Y2060	Y2061	Y2062	Y2063	Y2064	Y2065	Y2066	Y2067	Y2068	Y2069	Y2070	Y2071	Y2072	Y2073	Y2074	Y2075	Y2076	Y2077	Y2078	Y2079	Y2080	Y2081	Y2082	Y2083	Y2084	Y2085	Y2086	Y2087	Y2088	Y2089	Y2090	Y2091	Y2092	Y2093	Y2094	Y2095	Y2096	Y2097	Y2098	Y2099	Y2100	Y2101	Y2102	Y2103	Y2104	Y2105	Y2106	Y2107	Y2108	Y2109	Y2110	Y2111	Y2112	Y2113	Y2114	Y2115	Y2116	Y2117	Y2118	Y2119	Y2120	Y2121	Y2122	Y2123	Y2124	Y2125	Y2126	Y2127	Y2128	Y2129	Y2130	Y2131	Y2132	Y2133	Y2134	Y2135	Y2136	Y2137	Y2138	Y2139	Y2140	Y2141	Y2142	Y2143	Y2144	Y2145	Y2146	Y2147	Y2148	Y2149	Y2150	Y2151	Y2152	Y2153	Y2154	Y2155	Y2156	Y2157	Y2158	Y2159	Y2160	Y2161	Y2162	Y2163	Y2164	Y2165	Y2166	Y2167	Y2168	Y2169	Y2170	Y2171	Y2172	Y2173	Y2174	Y2175	Y2176	Y2177	Y2178	Y2179	Y2180	Y2181	Y2182	Y2183	Y2184	Y2185	Y2186	Y2187	Y2188	Y2189	Y2190	Y2191	Y2192	Y2193	Y2194	Y2195	Y2196	Y2197	Y2198	Y2199	Y2200	Y2201	Y2202	Y2203	Y2204	Y2205	Y2206	Y2207	Y2208	Y2209	Y2210	Y2211	Y2212	Y2213	Y2214	Y2215	Y2216	Y2217	Y2218	Y2219	Y2220	Y2221	Y2222	Y2223	Y2224	Y2225	Y2226	Y2227	Y2228	Y2229	Y2230	Y2231	Y2232	Y2233	Y2234	Y2235	Y2236	Y2237	Y2238	Y2239	Y2240	Y2241	Y2242	Y2243	Y2244	Y2245	Y2246	Y2247	Y2248	Y2249	Y2250	Y2251	Y2252	Y2253	Y2254	Y2255	Y2256	Y2257	Y2258	Y2259	Y2260	Y2261	Y2262	Y2263	Y2264	Y2265	Y2266	Y2267	Y2268	Y2269	Y2270	Y2271	Y2272	Y2273	Y2274	Y2275	Y2276	Y2277	Y2278	Y2279	Y2280	Y2281	Y2282	Y2283	Y2284	Y2285	Y2286	Y2287	Y2288	Y2289	Y2290	Y2291	Y2292	Y2293	Y2294	Y2295	Y2296	Y2297	Y2298	Y2299	Y2300	Y2301	Y2302	Y2303	Y2304	Y2305	Y2306	Y2307	Y2308	Y2309	Y2310	Y2311	Y2312	Y2313	Y2314	Y2315	Y2316	Y2317	Y2318	Y2319	Y2320	Y2321	Y2322	Y2323	Y2324	Y2325	Y2326	Y2327	Y2328	Y2329	Y2330	Y2331	Y2332	Y2333	Y2334	Y2335	Y2336	Y2337	Y2338	Y2339	Y2340	Y2341	Y2342	Y2343	Y2344	Y2345	Y2346	Y2347	Y2348	Y2349	Y2350	Y2351	Y2352	Y2353	Y2354	Y2355	Y2356	Y2357	Y2358	Y2359	Y2360	Y2361	Y2362	Y2363	Y2364	Y2365	Y2366	Y2367	Y2368	Y2369	Y2370	Y2371	Y2372	Y2373	Y2374	Y2375	Y2376	Y2377	Y2378	Y2379	Y2380	Y2381	Y2382	Y2383	Y2384	Y2385	Y2386	Y2387	Y2388	Y2389	Y2390	Y2391	Y2392	Y2393	Y2394	Y2395	Y2396	Y2397	Y2398	Y2399	Y2400	Y2401	Y2402	Y2403	Y2404	Y2405	Y2406	Y2407	Y2408	Y2409	Y2410	Y2411	Y2412	Y2413	Y2414	Y2415	Y2416	Y2417	Y2418	Y2419	Y2420	Y2421	Y2422	Y2423	Y2424	Y2425	Y2426	Y2427	Y2428	Y2429	Y2430	Y2431	Y2432	Y2433	Y2434	Y2435	Y2436	Y2437	Y2438	Y2439	Y2440	Y2441	Y2442	Y2443	Y2444	Y2445	Y2446	Y2447	Y2448	Y2449	Y2450	Y2451	Y2452	Y2453	Y2454	Y2455	Y2456	Y2457	Y2458	Y2459	Y2460	Y2461	Y2462	Y2463	Y2464	Y2465	Y2466	Y2467	Y2468	Y2469	Y2470	Y2471	Y2472	Y2473	Y2474	Y2475	Y2476	Y2477	Y2478	Y2479	Y2480	Y2481	Y2482	Y2483	Y2484	Y2485	Y2486	Y2487	Y2488	Y2489	Y2490	Y2491	Y2492	Y2493	Y2494	Y2495	Y2496	Y2497	Y2498	Y2499	Y2500	Y2501	Y2502	Y2503	Y2504	Y2505	Y2506	Y2507	Y2508	Y2509	Y2510	Y2511	Y2512	Y2513	Y2514	Y2515	Y2516	Y2517	Y2518	Y2519	Y2520	Y2521	Y2522	Y2523	Y2524	Y2525	Y2526	Y2527	Y2528	Y2529	Y2530	Y2531	Y2532	Y2533	Y2534	Y2535	Y2536	Y2537	Y2538	Y2539	Y2540	Y2541	Y2542	Y2543	Y2544	Y2545	Y2546	Y2547	Y2548	Y2549	Y2550	Y2551	Y2552	Y2553	Y2554	Y2555	Y2556	Y2557	Y2558	Y2559	Y2560	Y2561	Y2562	Y2563	Y2564	Y2565	Y2566	Y2567	Y2568	Y2569	Y2570	Y2571	Y2572	Y2573	Y2574	Y2575	Y2576	Y2577	Y2578	Y2579	Y2580	Y2581	Y2582	Y2583	Y2584	Y2585	Y2586	Y2587	Y2588	Y2589	Y2590	Y2591	Y2592	Y2593	Y2594	Y2595	Y2596	Y2597	Y2598	Y2599	Y2600	Y2601	Y2602	Y2603	Y2604	Y2605	Y2606	Y2607	Y2608	Y2609	Y2610	Y2611	Y2612	Y2613	Y2614	Y2615	Y2616	Y2617	Y2618	Y2619	Y2620	Y2621	Y2622	Y2623	Y2624	Y2625	Y2626	Y2627	Y2628	Y2629	Y2630	Y2631	Y2632	Y2633	Y2634	Y2635	Y2636	Y2637	Y2638	Y2639	Y2640	Y2641	Y2642	Y2643	Y2644	Y2645	Y2646	Y2647	Y2648	Y2649	Y2650	Y2651	Y2652	Y2653	Y2654	Y2655	Y2656	Y2657	Y2658	Y2659	Y2660	Y2661	Y2662
-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

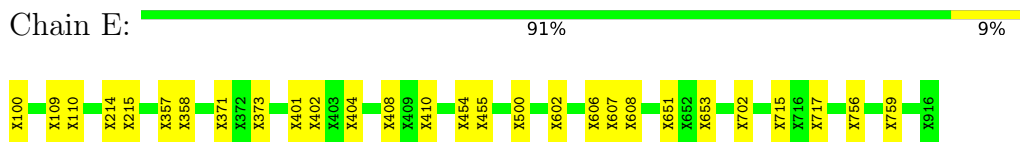
- Molecule 2: Target of rapamycin complex subunit LST8



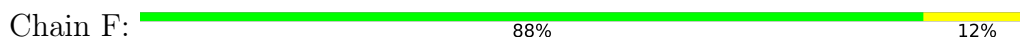
- Molecule 2: Target of rapamycin complex subunit LST8



- Molecule 3: Target of rapamycin complex 2 subunit TSC11



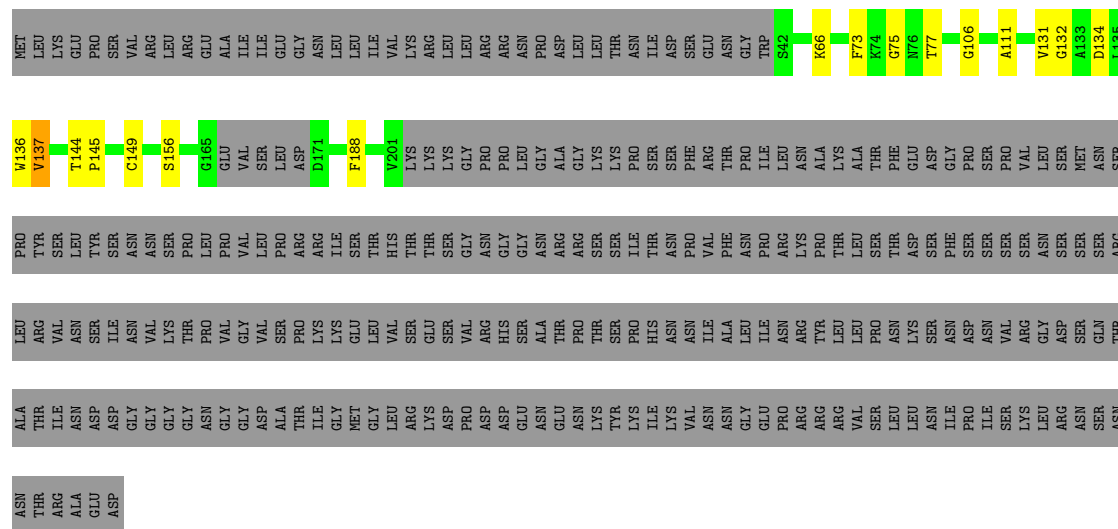
- Molecule 3: Target of rapamycin complex 2 subunit TSC11





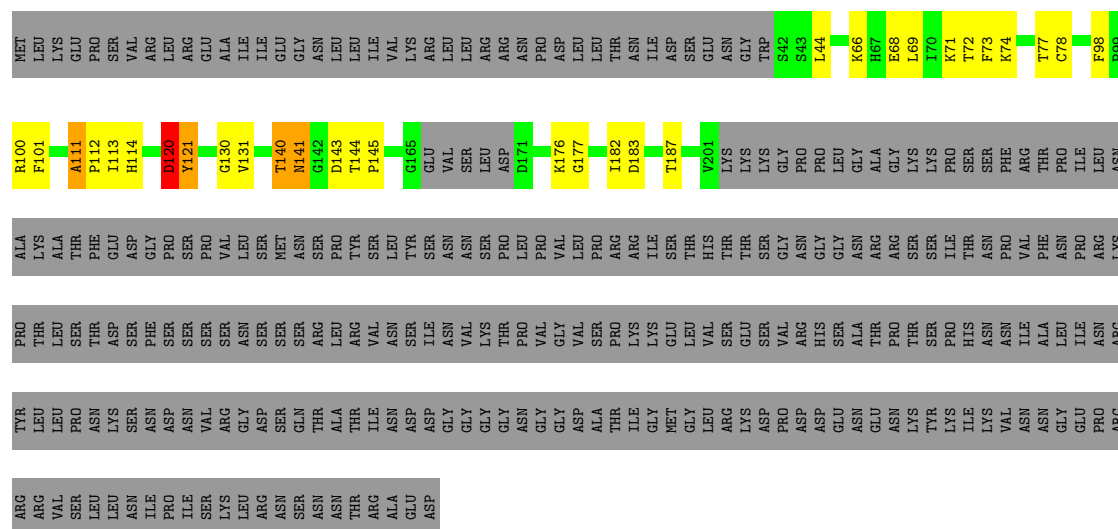
- Molecule 4: Target of rapamycin complex 2 subunit AVO2

Chain G: 33% 64%



- Molecule 4: Target of rapamycin complex 2 subunit AVO2

Chain H: 29% 6% 64%



- Molecule 5: Target of rapamycin complex 2 subunit AVO1

Chain I: 6% 5% 88%





ASN	PHE	GLN	VAL	ASP	LEU	PHE	THR	GLY	ALA	TYR	HIS	ARG	LYS	TYR	PRO	GLU	GLY	THR	ARG	ILE	HIS	TRP	VAL	PHE	ILE	ARG	LYS	GLN	GLY	ASN	ASP	LYS	HIS	GLU	ILE	ARG	THR	LEU	ALA	ILE	ASP	GLY	ASP	TYR	ILE	TYR	ILE	ILE	VAL	PRO	GLU	GLY	THR	ARG	ILE	HIS	TRP	HIS	ASP	ASN	VAL	LYS	TYR	LYS	SER	LEU	HIS	ILE				
SER	GLN	VAL	VAL	VAL	VAL	LYS	LYS	SER	LYS	ARG	VAL	PRO	GLU	GLY	THR	ARG	ILE	HIS	TRP	VAL	PHE	ILE	ARG	LYS	GLN	GLY	ASN	ASP	ILE	GLU	ILE	ARG	THR	LEU	TYR	ALA	ILE	PHE	GLU	ALA	VAL	SER	GLY	GLN	GLU	GLY	THR	ILE	ILE	VAL	ILE	THR	ARG	ILE	HIS	LEU	GLN	ASN	ASN	LEU	SER	VAL	LYS	ALA	TYR	ARG	MET	ASN	ASN	LEU	HIS	LYS

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, POINT	Depositor
Number of particles used	16190, 10663	Depositor
Resolution determination method	FSC 0.143 CUT-OFF, FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION, PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50, 47	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	105000	Depositor
Image detector	FEI FALCON II (4k x 4k), GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.101	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0147	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.83	14/18019 (0.1%)	1.21	142/23495 (0.6%)
1	C	0.82	19/17986 (0.1%)	1.20	158/23389 (0.7%)
2	B	0.85	1/2362 (0.0%)	1.21	19/3108 (0.6%)
2	D	0.83	2/2353 (0.1%)	1.14	23/3080 (0.7%)
4	G	0.69	0/715	1.23	6/918 (0.7%)
4	H	0.72	0/718	1.46	18/927 (1.9%)
5	I	1.48	12/1165 (1.0%)	1.43	12/1526 (0.8%)
5	J	1.23	8/1160 (0.7%)	1.29	12/1509 (0.8%)
All	All	0.86	56/44478 (0.1%)	1.22	390/57952 (0.7%)

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	1	28
1	C	0	25
2	B	0	4
2	D	0	2
5	I	0	2
5	J	0	2
All	All	1	63

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2389	ASN	CA-C	12.01	1.58	1.52
1	A	768	GLN	CA-C	9.03	1.58	1.53
1	C	1205	ARG	CA-C	8.96	1.60	1.52
5	I	713	LEU	CA-C	8.78	1.64	1.52
1	C	1205	ARG	N-CA	8.66	1.54	1.46
5	I	713	LEU	N-CA	8.52	1.57	1.45

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	714	TYR	N-CA	8.30	1.56	1.46
1	A	2084	SER	CA-C	8.17	1.56	1.52
1	A	2392	GLU	N-CA	7.67	1.56	1.46
1	A	1205	LYS	N-CA	7.26	1.55	1.46
5	I	685	SER	CA-C	7.17	1.59	1.52
1	C	1016	LYS	N-CA	7.08	1.54	1.45
5	I	670	VAL	CA-C	6.96	1.60	1.52
1	C	1019	ILE	N-CA	6.93	1.55	1.46
1	C	1019	ILE	CA-C	6.86	1.61	1.52
1	C	2393	ASN	CA-C	6.66	1.60	1.52
1	C	1204	GLU	CA-C	6.58	1.61	1.52
1	C	1020	THR	N-CA	6.54	1.54	1.46
1	A	2386	PRO	CA-C	6.48	1.60	1.53
5	I	712	PHE	CA-C	6.47	1.61	1.52
1	A	177	ARG	CA-C	6.45	1.60	1.52
5	J	713	LEU	CA-C	6.41	1.61	1.52
1	C	1586	LYS	N-CA	6.40	1.54	1.46
1	C	1204	GLU	N-CA	6.27	1.54	1.46
1	A	2393	LEU	CA-C	6.14	1.58	1.52
1	A	1204	ARG	CA-C	6.14	1.62	1.53
1	C	2391	ASN	CA-C	6.08	1.57	1.52
1	A	1205	LYS	CA-C	6.06	1.60	1.52
5	J	764	ILE	N-CA	6.01	1.53	1.46
5	I	714	TYR	CA-C	5.94	1.60	1.52
1	C	2394	GLU	N-CA	5.93	1.53	1.46
1	A	1204	ARG	N-CA	5.71	1.54	1.45
5	I	769	ASP	CA-C	5.71	1.56	1.53
5	I	764	ILE	N-CA	5.64	1.53	1.46
2	B	264	TYR	CA-C	5.63	1.59	1.52
1	C	225	THR	CA-C	5.63	1.60	1.52
1	C	2155	GLU	CA-C	5.62	1.58	1.52
2	D	5	LEU	N-CA	5.59	1.53	1.46
1	A	2392	GLU	CA-C	5.55	1.60	1.52
5	J	743	ILE	N-CA	5.51	1.52	1.46
1	C	1019	ILE	CA-CB	5.46	1.61	1.54
1	A	224	THR	CA-C	5.44	1.60	1.52
5	J	744	VAL	N-CA	5.43	1.53	1.46
5	J	713	LEU	N-CA	5.42	1.53	1.46
5	J	743	ILE	CA-CB	5.32	1.60	1.54
2	D	25	SER	N-CA	5.22	1.52	1.46
1	A	210	VAL	CA-C	5.17	1.58	1.52
5	J	681	TYR	CA-CB	5.17	1.59	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	96	VAL	N-CA	5.14	1.52	1.46
5	I	668	ASP	CA-C	5.13	1.59	1.52
5	I	685	SER	N-CA	5.12	1.52	1.46
5	I	723	PHE	CA-C	5.04	1.59	1.53
5	J	787	ILE	N-CA	5.04	1.50	1.46
1	C	1287	GLU	N-CA	5.03	1.52	1.46
1	C	96	VAL	CA-CB	5.03	1.60	1.54
1	C	117	GLU	CA-C	5.03	1.59	1.52

All (390) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	104	VAL	N-CA-C	-20.80	93.95	113.71
1	A	2335	PHE	N-CA-C	-14.30	95.79	113.38
1	A	768	GLN	N-CA-C	-13.76	97.50	108.78
1	C	2077	GLU	N-CA-C	13.26	125.75	111.03
1	C	1996	GLU	N-CA-C	11.32	128.43	113.72
4	G	111	ALA	CA-C-N	11.05	133.65	119.84
4	G	111	ALA	C-N-CA	11.05	133.65	119.84
1	C	2155	GLU	N-CA-C	10.90	127.42	112.93
1	A	1814	LEU	N-CA-C	9.95	122.13	111.28
4	H	66	LYS	N-CA-C	9.76	125.72	111.96
1	C	1856	ILE	CA-C-N	9.50	131.72	119.84
1	C	1856	ILE	C-N-CA	9.50	131.72	119.84
1	C	175	ASN	CA-C-N	9.46	138.72	121.70
1	C	175	ASN	C-N-CA	9.46	138.72	121.70
1	A	1090	THR	N-CA-C	9.35	122.42	111.02
1	C	1084	MET	C-N-CD	-9.18	100.41	120.60
5	I	685	SER	CA-C-N	9.17	138.21	121.70
5	I	685	SER	C-N-CA	9.17	138.21	121.70
4	H	144	THR	CA-C-N	9.16	131.30	119.84
4	H	144	THR	C-N-CA	9.16	131.30	119.84
1	A	554	SER	N-CA-C	9.09	124.48	113.12
1	A	1731	TRP	CA-C-N	8.82	137.58	121.70
1	A	1731	TRP	C-N-CA	8.82	137.58	121.70
5	J	701	SER	CA-C-N	8.75	137.45	121.70
5	J	701	SER	C-N-CA	8.75	137.45	121.70
1	C	1587	ASN	N-CA-C	8.61	120.02	107.88
1	A	344	ASP	CA-C-N	8.55	137.09	121.70
1	A	344	ASP	C-N-CA	8.55	137.09	121.70
1	C	783	LEU	N-CA-C	8.52	124.33	114.62
1	A	180	ILE	N-CA-CB	8.50	115.86	110.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	424	ALA	CA-C-N	8.48	136.96	121.70
1	C	424	ALA	C-N-CA	8.48	136.96	121.70
1	A	1976	PHE	N-CA-C	8.45	124.28	113.88
5	I	685	SER	N-CA-C	8.37	123.33	112.12
4	G	144	THR	CA-C-N	8.31	130.22	119.84
4	G	144	THR	C-N-CA	8.31	130.22	119.84
1	A	347	ASP	CA-C-N	8.23	136.52	121.70
1	A	347	ASP	C-N-CA	8.23	136.52	121.70
1	C	997	ILE	N-CA-C	-8.20	104.49	113.43
1	A	400	LYS	N-CA-C	8.20	122.06	112.72
1	A	742	CYS	CA-C-N	8.19	136.44	121.70
1	A	742	CYS	C-N-CA	8.19	136.44	121.70
1	A	2440	ASN	CA-C-N	8.12	136.31	121.70
1	A	2440	ASN	C-N-CA	8.12	136.31	121.70
1	C	1286	VAL	CA-C-N	8.05	136.91	121.54
1	C	1286	VAL	C-N-CA	8.05	136.91	121.54
1	A	1090	THR	CA-C-N	7.99	136.07	121.70
1	A	1090	THR	C-N-CA	7.99	136.07	121.70
1	A	996	ILE	N-CA-C	-7.95	104.62	112.17
1	C	839	LEU	N-CA-C	7.94	120.71	111.02
1	A	1446	LEU	N-CA-C	7.88	123.35	113.43
1	A	768	GLN	CA-C-N	7.86	135.84	121.70
1	A	768	GLN	C-N-CA	7.86	135.84	121.70
2	B	104	VAL	CB-CA-C	-7.86	103.25	110.63
1	C	674	GLN	N-CA-C	7.80	123.36	112.75
1	A	1386	ILE	N-CA-C	-7.76	104.80	112.17
2	B	103	ASP	CA-C-N	7.72	132.34	121.53
2	B	103	ASP	C-N-CA	7.72	132.34	121.53
1	C	996	HIS	N-CA-C	7.71	119.41	108.54
1	A	2425	LYS	CA-C-N	7.71	135.57	121.70
1	A	2425	LYS	C-N-CA	7.71	135.57	121.70
2	B	106	SER	C-N-CD	-7.69	103.69	120.60
5	J	701	SER	N-CA-C	7.66	127.11	110.80
1	A	2018	ASP	CA-C-N	7.63	135.43	121.70
1	A	2018	ASP	C-N-CA	7.63	135.43	121.70
1	A	394	HIS	CA-C-N	7.62	135.42	121.70
1	A	394	HIS	C-N-CA	7.62	135.42	121.70
1	A	1446	LEU	CA-C-N	7.62	135.41	121.70
1	A	1446	LEU	C-N-CA	7.62	135.41	121.70
1	A	2426	ARG	N-CA-C	7.59	132.25	111.00
1	C	1996	GLU	CA-C-N	7.58	135.34	121.70
1	C	1996	GLU	C-N-CA	7.58	135.34	121.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1981	GLU	N-CA-C	7.56	126.90	110.80
1	C	1585	GLN	N-CA-C	7.53	126.85	110.80
1	C	1293	GLN	N-CA-C	7.50	126.78	110.80
1	A	2018	ASP	N-CA-C	7.50	126.77	110.80
1	C	354	THR	N-CA-C	7.47	122.42	113.16
1	A	2390	ALA	CA-C-N	7.46	135.14	121.70
1	A	2390	ALA	C-N-CA	7.46	135.14	121.70
1	C	600	TYR	N-CA-C	7.43	119.34	108.86
1	A	1457	ALA	N-CA-C	7.41	119.81	109.15
1	A	573	ILE	N-CA-C	-7.39	103.26	110.72
1	A	2436	ILE	N-CA-C	7.39	124.71	109.34
1	C	404	ASP	N-CA-C	-7.37	102.94	112.23
1	A	1082	ILE	CA-C-N	7.30	134.84	121.70
1	A	1082	ILE	C-N-CA	7.30	134.84	121.70
5	I	706	VAL	N-CA-C	-7.29	106.03	113.10
4	H	182	ILE	CA-C-N	7.28	134.81	121.70
4	H	182	ILE	C-N-CA	7.28	134.81	121.70
2	D	294	GLY	N-CA-C	7.21	123.78	112.31
2	D	36	ASN	N-CA-C	-7.21	102.25	112.13
1	A	1584	LYS	N-CA-C	7.18	126.10	110.80
1	A	1498	PHE	CA-C-N	7.09	134.47	121.70
1	A	1498	PHE	C-N-CA	7.09	134.47	121.70
1	A	491	MET	N-CA-C	7.09	120.12	108.99
1	A	649	THR	CA-C-N	7.09	134.46	121.70
1	A	649	THR	C-N-CA	7.09	134.46	121.70
1	C	347	TYR	CA-C-N	7.08	134.45	121.70
1	C	347	TYR	C-N-CA	7.08	134.45	121.70
1	C	1293	GLN	CA-C-N	7.07	134.43	121.70
1	C	1293	GLN	C-N-CA	7.07	134.43	121.70
1	A	1147	LEU	N-CA-C	7.06	119.63	111.02
1	A	1341	ALA	CA-C-N	7.05	134.40	121.70
1	A	1341	ALA	C-N-CA	7.05	134.40	121.70
1	A	1587	ASP	CA-C-N	7.03	134.35	121.70
1	A	1587	ASP	C-N-CA	7.03	134.35	121.70
1	C	232	SER	CA-C-N	7.03	134.35	121.70
1	C	232	SER	C-N-CA	7.03	134.35	121.70
1	A	1733	LEU	CA-C-N	7.01	134.33	121.70
1	A	1733	LEU	C-N-CA	7.01	134.33	121.70
1	A	520	LEU	N-CA-C	6.98	120.13	108.20
1	A	403	ASP	N-CA-C	-6.95	104.55	113.16
1	A	2449	ASP	N-CA-C	6.94	122.41	113.18
1	C	2355	LEU	N-CA-C	6.90	130.33	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1199	ASN	CA-C-N	6.88	134.09	121.70
1	A	1199	ASN	C-N-CA	6.88	134.09	121.70
1	C	721	GLU	CA-C-N	6.87	134.07	121.70
1	C	721	GLU	C-N-CA	6.87	134.07	121.70
2	D	100	LYS	CA-C-N	6.87	134.06	121.70
2	D	100	LYS	C-N-CA	6.87	134.06	121.70
4	H	111	ALA	CA-C-N	6.86	128.41	119.84
4	H	111	ALA	C-N-CA	6.86	128.41	119.84
2	B	244	THR	CA-C-N	6.85	134.03	121.70
2	B	244	THR	C-N-CA	6.85	134.03	121.70
1	A	995	HIS	N-CA-C	6.84	118.19	108.54
4	H	73	PHE	CA-C-N	6.84	134.01	121.70
4	H	73	PHE	C-N-CA	6.84	134.01	121.70
1	C	1019	ILE	N-CA-C	6.83	123.56	109.34
2	B	36	ASN	N-CA-C	-6.83	102.96	112.45
1	C	233	SER	N-CA-C	6.78	129.97	111.00
1	A	178	VAL	CB-CA-C	6.77	124.26	111.40
1	C	2354	SER	CA-C-N	6.77	133.88	121.70
1	C	2354	SER	C-N-CA	6.77	133.88	121.70
1	A	768	GLN	O-C-N	-6.71	116.43	121.47
1	C	1009	ARG	N-CA-C	6.70	118.49	110.19
1	A	531	ILE	N-CA-C	6.69	116.71	110.42
1	C	655	GLU	CA-C-N	6.68	133.72	121.70
1	C	655	GLU	C-N-CA	6.68	133.72	121.70
1	A	2327	GLU	N-CA-C	6.64	119.23	108.34
2	B	245	THR	N-CA-C	6.62	129.54	111.00
1	C	2146	VAL	N-CA-CB	6.62	122.15	111.23
1	A	1731	TRP	N-CA-C	6.57	124.80	110.80
1	A	554	SER	CA-C-N	6.56	133.51	121.70
1	A	554	SER	C-N-CA	6.56	133.51	121.70
4	H	140	THR	CA-C-N	6.56	133.50	121.70
4	H	140	THR	C-N-CA	6.56	133.50	121.70
1	A	958	PHE	CA-C-N	6.55	133.50	121.70
1	A	958	PHE	C-N-CA	6.55	133.50	121.70
1	C	1007	VAL	CA-C-N	6.55	133.49	121.70
1	C	1007	VAL	C-N-CA	6.55	133.49	121.70
1	C	577	PHE	N-CA-C	6.54	119.23	111.71
1	A	1161	VAL	N-CA-C	-6.53	106.63	112.90
1	C	223	THR	CA-C-N	6.53	133.44	121.70
1	C	223	THR	C-N-CA	6.53	133.44	121.70
5	J	678	LEU	N-CA-C	6.52	118.43	110.41
5	I	662	PHE	N-CA-C	6.51	118.46	111.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	764	ILE	N-CA-C	6.50	122.86	109.34
1	C	2176	GLY	N-CA-C	6.50	120.10	110.42
2	B	213	ILE	CB-CA-C	6.49	121.93	111.29
2	B	19	ALA	N-CA-C	6.49	121.25	112.88
2	D	5	LEU	CA-C-N	6.48	133.36	121.70
2	D	5	LEU	C-N-CA	6.48	133.36	121.70
2	B	243	GLU	N-CA-C	-6.44	107.28	114.62
1	C	2356	MET	N-CA-C	6.44	118.09	111.14
1	C	1062	PRO	N-CA-C	6.42	121.98	113.57
2	D	218	ASP	N-CA-C	6.41	118.35	111.36
2	D	297	CYS	CA-C-N	6.41	133.23	121.70
2	D	297	CYS	C-N-CA	6.41	133.23	121.70
1	A	841	TYR	N-CA-C	-6.37	101.55	109.64
1	C	1386	ILE	N-CA-C	-6.35	106.14	112.17
1	A	353	THR	N-CA-C	6.34	121.03	113.16
1	C	219	ILE	CB-CA-C	6.33	119.47	112.19
2	D	226	SER	N-CA-C	6.29	118.74	109.24
1	C	1409	GLN	N-CA-C	6.27	122.40	114.31
1	C	829	ALA	N-CA-C	6.26	120.94	113.12
1	C	305	TRP	CA-CB-CG	6.25	125.48	113.60
1	C	2261	TYR	N-CA-C	6.18	117.81	111.14
1	C	1942	SER	CA-C-N	6.17	125.86	119.56
1	C	1942	SER	C-N-CA	6.17	125.86	119.56
1	C	1328	ASP	N-CA-C	6.15	117.65	111.07
2	B	286	ARG	N-CA-C	6.14	118.11	108.96
1	C	966	GLY	N-CA-C	6.14	120.08	112.64
5	I	764	ILE	N-CA-C	6.13	122.10	109.34
2	D	205	ALA	N-CA-C	6.12	118.49	111.02
5	I	770	SER	N-CA-C	6.12	116.64	108.38
5	J	720	PRO	CA-C-N	6.12	132.72	121.70
5	J	720	PRO	C-N-CA	6.12	132.72	121.70
1	C	415	PHE	CA-C-N	6.10	132.69	121.70
1	C	415	PHE	C-N-CA	6.10	132.69	121.70
1	A	1241	TRP	CA-C-N	6.10	132.68	121.70
1	A	1241	TRP	C-N-CA	6.10	132.68	121.70
2	B	244	THR	N-CA-C	-6.09	98.68	108.55
1	A	1058	ARG	N-CA-C	-6.09	106.49	114.04
1	A	1023	VAL	N-CA-C	6.06	116.23	110.53
1	C	266	ASP	CA-C-N	6.06	132.61	121.70
1	C	266	ASP	C-N-CA	6.06	132.61	121.70
1	C	305	TRP	N-CA-CB	6.04	118.07	110.45
1	C	2064	GLN	N-CA-C	-6.04	105.74	113.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	279	LEU	N-CA-C	6.04	117.53	111.07
1	C	2184	SER	CA-C-N	6.02	132.53	121.70
1	C	2184	SER	C-N-CA	6.02	132.53	121.70
1	C	1205	ARG	N-CA-C	6.01	120.29	111.34
1	A	257	TYR	N-CA-C	6.00	123.08	109.81
1	A	1354	LYS	N-CA-C	5.99	117.61	111.14
1	C	218	CYS	N-CA-C	5.97	120.69	113.41
1	A	1083	MET	N-CA-C	5.96	127.70	111.00
1	A	1976	PHE	CA-C-N	5.96	132.44	121.70
1	A	1976	PHE	C-N-CA	5.96	132.44	121.70
1	A	1419	LYS	N-CA-C	-5.96	106.66	114.04
1	C	1059	ARG	N-CA-C	-5.94	106.00	113.72
1	A	1500	ASP	N-CA-C	-5.94	106.58	113.88
1	C	1148	LEU	N-CA-C	5.92	121.08	111.37
1	C	1637	GLU	N-CA-C	-5.92	105.80	114.39
1	C	1610	VAL	N-CA-C	-5.91	105.95	111.45
1	C	1012	PHE	CA-C-N	5.91	127.22	119.84
1	C	1012	PHE	C-N-CA	5.91	127.22	119.84
1	A	503	ASN	CA-C-N	5.90	132.32	121.70
1	A	503	ASN	C-N-CA	5.90	132.32	121.70
1	A	613	LEU	N-CA-C	5.90	117.79	111.36
2	D	205	ALA	CA-C-N	5.89	132.30	121.70
2	D	205	ALA	C-N-CA	5.89	132.30	121.70
1	A	774	VAL	N-CA-CB	5.89	117.05	110.51
1	A	1498	PHE	N-CA-C	5.89	123.34	110.80
2	D	173	MET	CA-C-N	5.87	132.27	121.70
2	D	173	MET	C-N-CA	5.87	132.27	121.70
1	C	305	TRP	N-CA-C	5.85	118.81	110.68
1	C	131	ASN	CA-C-N	5.85	132.23	121.70
1	C	131	ASN	C-N-CA	5.85	132.23	121.70
1	A	1840	ASP	N-CA-C	5.83	118.41	111.71
1	A	1022	SER	N-CA-C	5.83	123.21	110.80
1	A	2425	LYS	N-CA-C	5.83	118.86	109.83
1	C	2104	ILE	CA-C-N	5.79	132.12	121.70
1	C	2104	ILE	C-N-CA	5.79	132.12	121.70
1	A	693	LEU	N-CA-C	5.78	118.33	111.33
1	C	2145	LEU	CA-C-N	5.75	132.33	121.97
1	C	2145	LEU	C-N-CA	5.75	132.33	121.97
1	C	527	SER	N-CA-C	5.75	117.81	109.07
1	C	2417	ILE	N-CA-C	-5.74	104.61	113.16
1	C	489	ASN	N-CA-C	5.74	117.40	111.03
1	C	1586	LYS	N-CA-C	5.74	123.02	110.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	34	GLN	CA-C-N	5.73	132.01	121.70
2	D	34	GLN	C-N-CA	5.73	132.01	121.70
1	A	2264	ALA	N-CA-C	5.72	118.25	111.33
1	A	938	THR	CA-C-N	5.70	131.96	121.70
1	A	938	THR	C-N-CA	5.70	131.96	121.70
1	A	259	TYR	N-CA-C	5.69	119.40	112.23
1	C	673	ALA	N-CA-C	5.69	122.91	110.80
2	D	124	ILE	N-CA-C	5.67	116.11	108.17
1	A	2328	VAL	N-CA-C	5.65	121.09	109.34
4	H	120	ASP	CA-C-N	5.65	131.87	121.70
4	H	120	ASP	C-N-CA	5.65	131.87	121.70
1	A	176	LEU	N-CA-C	-5.62	103.77	110.41
5	I	699	LYS	N-CA-C	-5.62	106.38	113.18
1	A	661	GLN	CA-C-N	5.61	131.79	121.70
1	A	661	GLN	C-N-CA	5.61	131.79	121.70
1	C	164	GLU	N-CA-C	5.61	119.86	113.19
1	C	691	GLY	N-CA-C	5.60	126.46	113.18
1	C	1861	GLN	N-CA-C	5.60	118.92	111.75
1	A	401	ASN	N-CA-C	-5.58	97.68	107.73
1	C	1399	GLN	N-CA-C	5.58	117.11	110.19
1	A	563	ASN	N-CA-C	5.58	122.69	110.80
2	B	226	SER	N-CA-C	5.57	118.65	109.85
4	H	66	LYS	CA-C-N	5.57	131.72	121.70
4	H	66	LYS	C-N-CA	5.57	131.72	121.70
1	A	1626	LYS	CA-C-N	5.56	131.71	121.70
1	A	1626	LYS	C-N-CA	5.56	131.71	121.70
1	A	177	ARG	CA-C-N	5.56	131.70	121.70
1	A	177	ARG	C-N-CA	5.56	131.70	121.70
1	C	1016	LYS	N-CA-C	5.56	118.68	110.46
1	A	1218	VAL	N-CA-C	5.55	116.95	110.62
1	A	2432	THR	N-CA-C	-5.53	103.37	111.17
1	C	721	GLU	N-CA-C	5.51	122.55	110.80
5	J	785	ASN	N-CA-C	5.51	116.31	108.54
2	D	24	CYS	N-CA-C	5.51	119.39	107.49
1	C	1409	GLN	CA-C-N	5.50	131.59	121.70
1	C	1409	GLN	C-N-CA	5.50	131.59	121.70
5	I	760	ARG	N-CA-C	-5.49	107.15	112.97
1	A	1135	GLU	N-CA-C	5.48	122.48	110.80
1	C	829	ALA	CA-C-N	5.48	131.57	121.70
1	C	829	ALA	C-N-CA	5.48	131.57	121.70
5	J	681	TYR	CA-CB-CG	5.48	123.77	113.90
2	B	109	ILE	N-CA-C	5.48	112.98	107.55

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2359	LEU	N-CA-C	-5.47	106.57	113.18
2	D	299	ALA	N-CA-C	5.46	118.66	107.37
1	C	826	GLY	CA-C-N	5.45	131.51	121.70
1	C	826	GLY	C-N-CA	5.45	131.51	121.70
1	A	1208	GLU	CA-C-N	5.45	131.51	121.70
1	A	1208	GLU	C-N-CA	5.45	131.51	121.70
4	H	98	PHE	CA-C-N	5.45	126.65	119.84
4	H	98	PHE	C-N-CA	5.45	126.65	119.84
1	C	96	VAL	N-CA-C	5.45	120.65	108.88
1	C	428	GLY	N-CA-C	5.45	119.08	112.49
1	A	2084	SER	N-CA-C	5.45	116.78	108.12
1	A	304	TRP	N-CA-C	5.44	122.39	110.80
1	C	2391	ASN	N-CA-C	5.44	119.45	111.34
1	A	342	LEU	N-CA-C	5.43	122.37	110.80
1	C	1856	ILE	N-CA-C	5.43	114.07	109.02
1	C	339	LYS	CA-C-N	5.42	131.46	121.70
1	C	339	LYS	C-N-CA	5.42	131.46	121.70
1	C	1616	ASN	N-CA-C	-5.42	106.51	113.23
1	A	420	GLY	CA-C-N	5.40	127.83	120.54
1	A	420	GLY	C-N-CA	5.40	127.83	120.54
1	C	1733	TRP	N-CA-C	5.40	122.31	110.80
1	C	285	VAL	N-CA-C	-5.39	105.68	113.07
1	C	278	ILE	N-CA-C	5.37	117.27	112.17
1	A	2371	ASP	N-CA-C	5.36	119.56	113.19
1	A	2109	ARG	N-CA-C	5.33	117.82	110.35
1	A	2392	GLU	N-CA-C	5.33	122.15	110.80
1	C	1020	THR	N-CA-C	5.33	117.58	108.90
2	D	174	LEU	CA-CB-CG	5.33	134.94	116.30
1	C	1529	GLU	N-CA-C	5.32	118.56	111.75
1	C	2062	GLU	CA-C-N	5.30	131.25	121.70
1	C	2062	GLU	C-N-CA	5.30	131.25	121.70
1	C	1459	ALA	CA-C-N	5.30	131.23	121.70
1	C	1459	ALA	C-N-CA	5.30	131.23	121.70
1	C	718	THR	CA-C-N	5.29	131.23	121.70
1	C	718	THR	C-N-CA	5.29	131.23	121.70
1	A	1732	ARG	N-CA-CB	5.28	119.48	110.50
1	A	2158	HIS	N-CA-C	5.26	117.94	110.10
2	B	32	ASP	N-CA-C	-5.25	105.52	112.24
1	C	1541	ALA	CA-C-N	5.25	131.15	121.70
1	C	1541	ALA	C-N-CA	5.25	131.15	121.70
5	I	711	LEU	N-CA-C	5.25	116.60	110.41
1	A	1854	ILE	CA-C-N	5.24	126.39	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1854	ILE	C-N-CA	5.24	126.39	119.84
1	C	694	LEU	N-CA-C	5.24	117.07	111.36
1	C	1981	GLU	CA-C-N	5.24	131.13	121.70
1	C	1981	GLU	C-N-CA	5.24	131.13	121.70
1	C	1728	CYS	N-CA-C	-5.24	107.54	114.04
1	A	317	SER	N-CA-C	5.24	117.47	110.35
5	J	662	PHE	N-CA-C	5.23	119.37	112.89
1	A	1013	ILE	N-CA-C	5.23	116.43	108.80
1	C	576	CYS	N-CA-C	5.21	116.65	110.97
1	A	2441	ASP	N-CA-C	5.21	125.59	111.00
1	A	1408	ARG	CB-CA-C	-5.21	109.57	117.07
1	A	2367	ASN	CA-C-N	5.20	131.06	121.70
1	A	2367	ASN	C-N-CA	5.20	131.06	121.70
1	C	2096	LYS	CA-C-N	5.20	131.06	121.70
1	C	2096	LYS	C-N-CA	5.20	131.06	121.70
1	C	831	SER	N-CA-C	-5.20	106.89	113.18
1	C	1074	PRO	CA-C-N	5.20	131.06	121.70
1	C	1074	PRO	C-N-CA	5.20	131.06	121.70
4	G	156	SER	CA-C-N	5.20	131.06	121.70
4	G	156	SER	C-N-CA	5.20	131.06	121.70
1	A	2021	GLU	N-CA-C	5.20	120.54	113.37
1	C	1328	ASP	CA-C-N	5.20	131.05	121.70
1	C	1328	ASP	C-N-CA	5.20	131.05	121.70
5	J	731	GLU	N-CA-C	5.20	117.83	110.50
1	C	2005	LEU	N-CA-C	5.18	116.61	109.15
1	C	149	GLY	N-CA-C	5.15	119.37	112.77
1	C	1611	ARG	N-CA-C	-5.14	99.84	110.80
1	C	705	SER	CA-C-N	5.14	130.95	121.70
1	C	705	SER	C-N-CA	5.14	130.95	121.70
1	C	757	ILE	N-CA-C	-5.13	105.49	110.42
1	C	1421	LYS	N-CA-C	-5.13	107.69	114.31
1	C	1480	GLN	N-CA-C	5.11	117.94	109.46
1	C	2155	GLU	CA-C-N	5.11	131.29	121.54
1	C	2155	GLU	C-N-CA	5.11	131.29	121.54
1	A	2415	ILE	N-CA-C	-5.11	105.15	112.35
1	A	1450	ALA	N-CA-C	5.10	117.74	109.83
1	C	1488	THR	N-CA-C	5.10	117.58	111.71
5	J	784	GLN	N-CA-C	-5.10	107.06	113.28
1	A	2034	ASN	CA-C-N	5.10	130.88	121.70
1	A	2034	ASN	C-N-CA	5.10	130.88	121.70
2	B	120	ASN	N-CA-C	5.09	117.61	111.40
2	D	31	SER	N-CA-C	5.09	114.76	108.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1288	LEU	N-CA-C	-5.08	107.08	113.28
5	I	712	PHE	N-CA-C	5.08	121.63	110.80
2	D	18	GLU	N-CA-C	5.07	117.16	108.90
1	C	1204	GLU	CA-C-N	5.07	128.29	121.90
1	C	1204	GLU	C-N-CA	5.07	128.29	121.90
1	C	602	GLU	CA-C-N	5.07	130.82	121.70
1	C	602	GLU	C-N-CA	5.07	130.82	121.70
4	H	140	THR	N-CA-C	5.06	121.58	110.80
1	A	1922	SER	N-CA-C	-5.05	106.53	113.30
1	C	1135	ARG	CA-C-N	5.05	130.79	121.70
1	C	1135	ARG	C-N-CA	5.05	130.79	121.70
1	C	1286	VAL	N-CA-C	5.05	119.84	109.34
1	C	131	ASN	CB-CA-C	5.04	119.69	110.10
1	C	1036	PHE	N-CA-C	-5.04	106.98	113.23
1	A	87	ILE	CB-CA-C	5.03	115.57	110.65
1	A	2014	ARG	N-CA-C	5.03	116.45	111.07
1	A	180	ILE	CB-CA-C	-5.02	109.03	114.35
1	C	645	LEU	N-CA-C	5.02	116.44	111.07
1	A	2003	LEU	N-CA-C	5.02	117.58	110.10
5	I	746	GLU	N-CA-C	5.02	117.71	108.58
1	A	2359	ALA	N-CA-C	-5.02	107.01	113.23
1	A	2334	SER	N-CA-C	-5.01	100.12	110.80
1	C	175	ASN	N-CA-C	5.01	121.46	110.80
1	C	2253	THR	N-CA-C	-5.00	106.68	112.89

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	257	TYR	CA

All (63) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1089	MET	Peptide
1	A	1241	TRP	Peptide
1	A	1385	GLY	Peptide
1	A	1523	LEU	Peptide
1	A	1587	ASP	Peptide
1	A	1731	TRP	Peptide
1	A	178	VAL	Peptide
1	A	180	ILE	Peptide
1	A	1976	PHE	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	2121	TYR	Peptide
1	A	2123	TYR	Peptide
1	A	2334	SER	Peptide
1	A	2367	ASN	Peptide
1	A	2385	LEU	Peptide
1	A	2431	LEU	Peptide
1	A	2436	ILE	Peptide
1	A	256	LEU	Peptide
1	A	257	TYR	Peptide
1	A	347	ASP	Peptide
1	A	394	HIS	Peptide
1	A	400	LYS	Peptide
1	A	401	ASN	Peptide
1	A	402	ILE	Peptide
1	A	488	ASN	Peptide
1	A	489	CYS	Peptide
1	A	604	ASP	Peptide
1	A	649	THR	Peptide
1	A	958	PHE	Peptide
2	B	103	ASP	Peptide
2	B	244	THR	Peptide
2	B	291	HIS	Peptide
2	B	31	SER	Peptide
1	C	1084	MET	Peptide
1	C	1151	GLN	Peptide
1	C	1152	LEU	Peptide
1	C	1286	VAL	Peptide
1	C	131	ASN	Peptide
1	C	1610	VAL	Peptide
1	C	1611	ARG	Peptide
1	C	1636	GLU	Peptide
1	C	1670	ALA	Peptide
1	C	1995	TYR	Peptide
1	C	2027	ASN	Peptide
1	C	2076	LEU	Peptide
1	C	2077	GLU	Peptide
1	C	2078	LEU	Peptide
1	C	2145	LEU	Peptide
1	C	2155	GLU	Peptide
1	C	2308	LEU	Peptide
1	C	235	LEU	Peptide
1	C	2416	ALA	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	C	403	ILE	Peptide
1	C	646	MET	Peptide
1	C	651	ASP	Peptide
1	C	665	GLY	Peptide
1	C	712	VAL	Peptide
1	C	916	TYR	Peptide
2	D	173	MET	Peptide
2	D	34	GLN	Peptide
5	I	682	ILE	Peptide
5	I	697	VAL	Peptide
5	J	736	PRO	Peptide
5	J	760	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	18186	0	18002	1109	0
1	C	18186	0	17976	1109	0
2	B	2372	0	2199	141	0
2	D	2372	0	2191	151	0
3	E	1515	0	491	15	0
3	F	1515	0	490	24	0
4	G	762	0	290	6	0
4	H	762	0	293	11	0
5	I	1171	0	1119	62	0
5	J	1171	0	1116	55	0
All	All	48012	0	44167	2653	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 29.

All (2653) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2060:GLU:HB3	1:A:2062:GLN:HG2	1.25	1.18

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:841:TYR:HB2	1:A:843:GLU:HG2	1.16	1.13
1:C:983:PHE:HB3	1:C:1022:ILE:HG12	1.31	1.10
1:A:179:LEU:HD22	1:A:233:LYS:HG3	1.31	1.10
2:D:297:CYS:HA	2:D:298:VAL:HB	1.25	1.09
1:A:1083:MET:HB3	1:A:1084:PRO:HD3	1.34	1.08
1:C:265:LEU:HA	1:C:307:GLN:HB3	1.29	1.07
1:C:2337:PHE:HZ	1:C:2450:VAL:HG13	1.16	1.07
1:C:230:SER:HB3	1:C:233:SER:HB2	1.34	1.07
2:D:4:ILE:HG12	2:D:60:ILE:HG12	1.36	1.05
2:B:4:ILE:HG12	2:B:60:ILE:HG12	1.38	1.05
1:C:1442:LEU:HB3	1:C:1624:MET:HG2	1.36	1.05
1:A:650:ASP:H	1:A:651:PRO:HD3	1.20	1.04
5:J:655:SER:HA	5:J:659:LEU:HB2	1.40	1.02
1:C:2374:LEU:HD11	1:C:2417:ILE:HB	1.39	1.02
1:A:652:VAL:HB	3:F:100:UNK:H2	1.22	1.01
1:A:1151:LEU:CB	1:A:1152:GLY:HA2	1.90	1.01
1:C:1612:ILE:HG23	1:C:1615:ALA:HB3	1.39	1.00
1:C:842:TYR:HB3	1:C:844:GLU:HG2	1.41	1.00
5:J:699:LYS:HE2	5:J:737:ASN:HB2	1.44	0.99
2:D:84:GLN:HB3	2:D:89:TRP:HB2	1.45	0.99
1:A:2121:TYR:HA	1:A:2122:LYS:HB2	1.45	0.96
1:A:1263:SER:HB3	1:A:1268:TYR:HE2	1.30	0.96
1:C:297:ARG:HD2	1:C:339:LYS:HG3	1.48	0.96
1:C:1763:ALA:HB1	1:C:1825:ILE:HA	1.45	0.96
1:C:857:ASN:HB3	1:C:1586:LYS:HA	1.47	0.96
5:I:693:PHE:CE2	5:I:760:ARG:HB3	2.01	0.95
1:A:2126:LYS:HD3	1:A:2131:ILE:HD11	1.48	0.95
1:C:2062:GLU:HA	1:C:2063:LEU:HB2	1.48	0.94
1:A:581:LEU:HA	1:A:583:HIS:N	1.81	0.94
1:C:401:LYS:HA	1:C:403:ILE:HG23	1.49	0.94
2:B:265:LEU:HB2	2:B:279:LEU:HD12	1.46	0.94
1:C:1011:PHE:HD1	1:C:1022:ILE:HG23	1.29	0.94
1:A:801:MET:HA	1:A:804:ILE:HB	1.47	0.94
1:A:280:LEU:HA	1:A:330:VAL:HG22	1.48	0.94
1:A:771:SER:HB2	1:A:774:VAL:HB	1.50	0.94
2:B:4:ILE:HG21	2:B:40:ILE:HD11	1.47	0.93
1:C:1630:VAL:HB	1:C:1634:LEU:HG	1.50	0.93
1:C:346:LYS:HD3	1:C:350:ILE:HG12	1.51	0.93
1:A:1043:LEU:HD11	1:C:702:ARG:HD3	1.52	0.92
1:A:650:ASP:H	1:A:651:PRO:CD	1.80	0.92
1:C:2045:TYR:HB3	1:C:2049:ARG:HH12	1.33	0.91

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1850:TRP:HZ2	1:C:1859:ALA:HB1	1.36	0.91
1:C:2337:PHE:CZ	1:C:2450:VAL:HG13	2.05	0.91
1:A:281:ASP:HA	1:A:284:VAL:HB	1.52	0.90
1:A:2112:CYS:HB2	1:A:2120:ASP:HB3	1.51	0.90
2:D:229:HIS:HB3	2:D:251:ARG:HB2	1.53	0.90
1:A:636:VAL:HG13	1:A:675:ASP:HB3	1.52	0.89
1:C:2004:THR:HG1	1:C:2008:ILE:N	1.68	0.89
1:A:1371:ILE:HD13	1:A:1387:LEU:HG	1.53	0.89
1:A:2078:VAL:HG13	1:A:2089:ILE:HA	1.53	0.89
1:A:856:ASN:HB2	1:A:1580:LEU:HA	1.54	0.89
1:C:188:VAL:HG21	1:C:233:SER:HB3	1.52	0.89
1:A:704:SER:HB2	1:A:709:TYR:HB2	1.55	0.88
1:A:824:LEU:HD21	1:A:1534:GLU:HB2	1.55	0.88
1:A:1212:GLN:HB2	1:A:1252:GLU:HG3	1.55	0.88
1:A:2337:ILE:HA	1:A:2340:GLU:HG2	1.55	0.87
1:C:113:SER:C	1:C:114:LEU:HA	2.00	0.87
2:B:9:GLY:HA2	2:B:296:VAL:HG23	1.54	0.87
1:A:1617:ARG:HE	1:A:1657:LYS:HB3	1.39	0.87
1:A:117:VAL:HB	1:A:120:GLU:HA	1.57	0.86
1:A:768:GLN:HB2	1:A:770:ALA:H	1.40	0.86
1:A:849:ILE:HG12	1:A:1548:ILE:HA	1.57	0.86
1:A:1045:PHE:HZ	1:A:1064:ILE:HA	1.40	0.86
1:C:1547:ARG:HA	1:C:1550:ILE:HD12	1.57	0.86
1:C:1850:TRP:CZ2	1:C:1859:ALA:HB1	2.10	0.86
1:A:835:VAL:HG11	1:A:844:LEU:HB2	1.58	0.86
1:A:1820:ILE:H	1:A:1821:PRO:HD3	1.40	0.86
1:C:333:ARG:HB3	1:C:373:LEU:HB2	1.55	0.86
1:A:177:ARG:H	1:A:178:VAL:CG2	1.88	0.86
1:A:581:LEU:HA	1:A:583:HIS:H	1.36	0.85
2:B:210:ILE:HD13	2:B:224:THR:CG2	2.06	0.85
1:C:1011:PHE:CD1	1:C:1022:ILE:HG23	2.11	0.85
1:C:1619:ARG:HA	1:C:1626:LEU:HG	1.58	0.85
2:B:210:ILE:HD13	2:B:224:THR:HG23	1.58	0.85
1:C:2145:LEU:HB3	1:C:2146:VAL:HG13	1.59	0.85
1:A:1151:LEU:HB3	1:A:1152:GLY:HA2	1.58	0.85
2:D:26:ARG:HE	2:D:60:ILE:HD12	1.38	0.84
1:A:1151:LEU:HB2	1:A:1152:GLY:HA2	1.57	0.84
1:A:1589:TRP:HE3	1:A:1612:PHE:HE1	1.23	0.84
1:C:2064:GLN:HG3	1:C:2065:HIS:CD2	2.13	0.84
1:A:1216:LEU:HA	1:A:1217:PRO:HA	1.59	0.84
1:C:2247:LYS:HA	1:C:2249:ARG:H	1.41	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:127:ASN:HD21	2:B:130:GLU:HB2	1.41	0.84
1:C:634:LEU:HD22	1:C:675:PRO:HG2	1.58	0.84
1:A:257:TYR:HB3	1:A:258:PRO:C	2.03	0.84
1:A:1545:ARG:HA	1:A:1548:ILE:HD12	1.60	0.83
1:A:2259:TYR:HA	1:A:2262:SER:HB2	1.58	0.83
1:A:860:ILE:HG22	1:A:863:GLY:HA3	1.59	0.83
1:C:1615:ALA:HB2	1:C:1629:LYS:HE2	1.60	0.83
2:D:14:ILE:HG22	2:D:38:LEU:HD23	1.60	0.83
4:H:120:ASP:HA	4:H:121:TYR:CB	2.08	0.83
1:A:1116:GLU:O	1:C:664:LEU:HB2	1.77	0.83
1:A:177:ARG:H	1:A:178:VAL:HG23	1.41	0.83
2:B:14:ILE:HG22	2:B:38:LEU:HD23	1.60	0.83
1:A:1587:ASP:N	1:A:1588:VAL:HB	1.94	0.83
1:A:2091:LYS:C	1:A:2092:ILE:HA	2.03	0.83
5:I:647:LYS:HD3	5:I:649:LYS:HE3	1.61	0.83
1:C:1246:LEU:HA	1:C:1276:LEU:HD23	1.59	0.83
2:D:286:ARG:HB3	2:D:288:TYR:OH	1.79	0.83
1:A:1341:ALA:HB3	1:A:1342:GLN:HB2	1.61	0.82
1:A:345:LYS:HE3	1:A:349:ILE:HG12	1.61	0.82
1:C:1491:MET:HG3	1:C:1492:LYS:N	1.93	0.82
1:A:124:ARG:HG3	1:A:155:LEU:HD11	1.59	0.82
1:A:331:PHE:HE2	1:A:349:ILE:HG21	1.44	0.82
1:A:2200:LEU:HG	1:A:2471:PHE:HZ	1.45	0.82
1:A:124:ARG:HH21	1:A:170:SER:HB3	1.44	0.82
3:F:507:UNK:C	3:F:508:UNK:HA	2.10	0.81
1:C:721:GLU:HB3	1:C:722:LEU:HB2	1.62	0.81
1:C:1722:GLN:HG2	1:C:1748:ALA:HB1	1.60	0.81
1:A:722:LEU:HA	1:A:760:LEU:HD13	1.63	0.81
1:A:652:VAL:HB	3:F:100:UNK:N	1.95	0.81
1:A:1104:THR:OG1	1:A:1141:MET:HE1	1.81	0.81
2:B:90:MET:N	2:B:104:VAL:HG22	1.95	0.81
1:C:335:LEU:HD23	1:C:338:LEU:HD22	1.63	0.81
1:C:189:MET:HA	1:C:193:ALA:HB3	1.63	0.81
1:A:138:HIS:NE2	1:A:178:VAL:HG12	1.97	0.80
1:C:1414:ALA:HB1	1:C:1442:LEU:HD11	1.64	0.80
1:A:2075:GLU:HA	1:A:2091:LYS:HG2	1.62	0.80
1:C:346:LYS:HA	1:C:349:ASP:HB2	1.62	0.80
1:A:1446:LEU:H	1:A:1447:SER:HB2	1.47	0.80
1:A:1263:SER:HB3	1:A:1268:TYR:CE2	2.17	0.80
1:C:346:LYS:HD3	1:C:350:ILE:CG1	2.12	0.80
1:C:726:LEU:HB2	1:C:761:LEU:HB3	1.64	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:ARG:HD3	1:A:413:PRO:HB2	1.64	0.80
5:I:757:LYS:HG3	5:I:784:GLN:HG2	1.63	0.80
1:A:1097:LEU:HA	1:A:1100:ILE:HB	1.65	0.79
1:C:240:HIS:HA	1:C:241:ALA:C	2.08	0.79
1:C:2288:ASP:HB3	1:C:2290:ILE:HG13	1.65	0.79
1:A:188:MET:HG3	1:A:236:TYR:HB3	1.63	0.79
2:B:46:LEU:HD22	2:B:68:VAL:HG11	1.64	0.79
1:A:356:TYR:HB3	1:A:365:ARG:HE	1.48	0.79
1:C:569:ASP:HA	1:C:573:LEU:HD12	1.63	0.79
1:A:91:LEU:HD11	1:A:143:SER:HB3	1.64	0.79
1:C:332:PHE:HZ	1:C:350:ILE:HG12	1.48	0.79
1:A:2426:ARG:O	1:A:2433:GLY:HA2	1.82	0.79
1:C:2061:LEU:O	1:C:2100:VAL:HA	1.82	0.79
1:C:918:PRO:HB3	1:C:1214:VAL:HG21	1.63	0.79
1:A:113:LEU:HB2	1:A:117:VAL:HG22	1.65	0.79
1:A:1814:LEU:HD23	1:A:1819:VAL:HG21	1.65	0.78
1:A:1820:ILE:N	1:A:1821:PRO:HD3	1.97	0.78
1:C:1590:VAL:O	1:C:1594:ILE:HG13	1.83	0.78
1:C:188:VAL:CG1	1:C:234:LYS:HA	2.13	0.78
1:C:1454:GLU:O	1:C:1458:THR:HG23	1.84	0.78
1:C:1612:ILE:CG2	1:C:1615:ALA:HB3	2.13	0.78
5:I:785:ASN:HB3	5:I:788:GLU:N	1.98	0.78
1:A:178:VAL:HG11	1:A:190:LEU:HD12	1.65	0.78
1:C:266:ASP:N	1:C:267:ASN:HB2	1.98	0.78
1:C:1496:PRO:HB3	1:C:1525:LEU:HB3	1.64	0.78
1:A:1730:LYS:HB3	1:A:1735:ASN:HB3	1.65	0.78
1:C:337:SER:HB2	1:C:376:LEU:HB2	1.64	0.78
1:A:1588:VAL:O	1:A:1592:ILE:HG12	1.84	0.78
1:A:436:LEU:HA	1:A:439:ASP:HB2	1.65	0.77
1:C:437:LEU:HA	1:C:440:ASP:HB2	1.65	0.77
5:J:699:LYS:HB2	5:J:760:ARG:HB2	1.66	0.77
1:A:1492:GLN:HA	1:A:1493:SER:N	1.99	0.77
1:C:700:ILE:HD12	1:C:718:THR:HG22	1.66	0.77
1:C:983:PHE:HB3	1:C:1022:ILE:CG1	2.12	0.77
1:C:2339:ILE:HA	1:C:2342:GLU:HG2	1.66	0.77
1:A:1083:MET:HB3	1:A:1084:PRO:CD	2.13	0.77
5:I:730:VAL:HG11	5:I:790:PRO:HD2	1.67	0.77
1:C:2007:GLU:HB3	1:C:2065:HIS:HB3	1.65	0.77
1:A:1900:SER:HB3	1:A:1932:ILE:HD12	1.64	0.77
1:C:1011:PHE:HD1	1:C:1022:ILE:CG2	1.98	0.77
1:A:270:PRO:HB2	1:A:279:ARG:HB2	1.64	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2425:LYS:HA	1:A:2434:ASN:HD22	1.49	0.77
1:C:1108:ARG:HA	1:C:1150:LEU:HD11	1.66	0.77
1:C:2265:LEU:HD11	1:C:2328:MET:HE1	1.67	0.77
1:A:399:LEU:O	1:A:402:ILE:HG23	1.85	0.76
4:H:100:ARG:C	4:H:101:PHE:HA	2.09	0.76
5:J:710:ALA:HB1	5:J:718:LYS:HG2	1.65	0.76
5:I:700:SER:HA	5:I:731:GLU:HB3	1.67	0.76
1:A:2283:LEU:HD21	1:A:2317:ARG:HD3	1.67	0.76
2:B:8:ALA:HB1	2:B:12:HIS:HA	1.66	0.76
1:C:1952:VAL:HA	1:C:1955:GLU:HB2	1.68	0.76
1:A:234:LEU:HD11	1:A:270:PRO:HG3	1.68	0.76
1:A:1110:LYS:HD3	1:A:1148:LEU:HD21	1.67	0.76
1:C:468:ALA:HA	1:C:469:CYS:HA	1.67	0.76
1:C:992:ILE:N	1:C:993:VAL:HA	2.00	0.76
1:C:98:GLN:HA	1:C:101:ALA:HB3	1.66	0.76
5:J:693:PHE:CZ	5:J:760:ARG:HB3	2.21	0.76
1:A:1601:LYS:HB2	1:A:1602:PRO:HD2	1.68	0.75
2:B:79:THR:HG1	2:B:95:GLU:N	1.83	0.75
1:C:261:VAL:HG11	1:C:303:LYS:HD2	1.68	0.75
1:C:1140:ALA:HB1	1:C:1173:GLN:CB	2.15	0.75
1:C:1557:ILE:HD13	1:C:1577:TRP:CZ2	2.22	0.75
5:J:698:ARG:HG3	5:J:788:GLU:HG2	1.65	0.75
1:A:1969:LEU:HB3	1:A:1970:ASP:HA	1.66	0.75
1:A:1848:TRP:HZ2	1:A:1857:ALA:HB1	1.50	0.75
2:B:122:VAL:HG13	2:B:131:LEU:HD11	1.69	0.75
1:A:1215:LYS:HD2	1:A:1249:LEU:HA	1.68	0.75
1:A:367:GLU:HA	1:A:370:ALA:HB3	1.69	0.75
1:C:2222:LEU:HD21	2:D:227:ALA:HB2	1.69	0.75
1:A:391:ILE:HA	1:A:395:TYR:HD2	1.51	0.75
1:A:2161:ILE:HG12	1:A:2266:MET:HB2	1.67	0.74
1:C:395:HIS:HE1	1:C:438:ILE:HG21	1.52	0.74
1:C:1013:PRO:HA	1:C:1022:ILE:O	1.85	0.74
1:C:1111:LYS:HD2	1:C:1149:LEU:HD21	1.68	0.74
1:A:2325:ALA:HA	1:A:2326:MET:C	2.11	0.74
1:C:2104:ILE:HA	1:C:2105:SER:HB2	1.68	0.74
1:C:332:PHE:CZ	1:C:350:ILE:HG12	2.21	0.74
1:A:2266:MET:HB2	1:A:2292:VAL:HG21	1.68	0.74
1:C:1100:LYS:HA	1:C:1103:ILE:HB	1.67	0.74
1:C:2131:GLU:HB3	1:C:2132:ASP:N	2.03	0.74
1:C:2263:ARG:HG2	1:C:2339:ILE:HD13	1.70	0.74
1:C:1971:LEU:HD13	1:C:1991:LEU:HD21	1.70	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:40:ILE:HG23	2:B:47:LEU:HB3	1.70	0.73
1:C:688:GLU:C	1:C:691:GLY:H	1.97	0.73
1:C:1430:GLU:HB2	1:C:1431:VAL:N	2.02	0.73
1:A:1734:SER:HB3	1:A:1735:ASN:HB2	1.69	0.73
4:H:68:GLU:O	4:H:71:LYS:N	2.21	0.73
2:B:12:HIS:CE1	2:B:35:VAL:H	2.07	0.73
1:C:1058:LYS:HD2	1:C:1060:ILE:HD12	1.69	0.73
1:C:1611:ARG:C	1:C:1613:LYS:H	1.96	0.73
1:A:533:SER:HA	1:A:534:ASN:C	2.14	0.73
1:A:2185:PHE:HA	1:A:2188:LEU:HG	1.70	0.73
1:C:1978:PHE:HA	1:C:1983:ASN:HB2	1.71	0.73
1:A:188:MET:HA	1:A:192:ALA:HB3	1.71	0.73
1:A:677:LEU:HG	1:A:726:LYS:HB3	1.71	0.73
1:A:698:ILE:HG23	1:C:1079:TYR:CE2	2.24	0.73
1:A:1060:VAL:HA	1:A:1063:ARG:HD2	1.71	0.73
1:A:1723:TRP:HE1	1:A:1739:ILE:HG23	1.54	0.73
1:A:2061:LEU:HD12	1:A:2097:PRO:HA	1.69	0.73
1:A:2423:VAL:O	1:A:2426:ARG:HB3	1.89	0.72
1:C:2126:VAL:HG12	1:C:2180:TRP:HE3	1.53	0.72
1:C:674:GLN:OE1	1:C:720:LEU:HD22	1.89	0.72
5:J:694:THR:C	5:J:696:LYS:H	1.97	0.72
1:C:315:HIS:CD2	1:C:320:ASN:HD21	2.08	0.72
1:C:1140:ALA:HB1	1:C:1173:GLN:HB2	1.69	0.72
1:C:1026:GLU:HG3	1:C:1030:LYS:HE2	1.69	0.72
1:C:1533:LEU:C	1:C:1534:VAL:HA	2.14	0.72
1:A:1223:LEU:HD13	1:A:1244:ARG:HH22	1.54	0.72
1:A:303:GLN:HB3	1:A:307:ARG:HB2	1.72	0.72
1:A:1440:LEU:HD22	1:A:1622:MET:HG2	1.71	0.72
1:C:842:TYR:HB3	1:C:844:GLU:CG	2.20	0.72
1:C:518:ILE:HG22	1:C:520:ASN:H	1.54	0.72
1:A:673:GLN:HA	1:A:676:ASN:ND2	2.04	0.72
1:A:2223:VAL:HG22	1:A:2459:GLU:HB3	1.71	0.72
1:C:401:LYS:HG3	1:C:403:ILE:HG12	1.72	0.72
1:C:797:TYR:CE2	1:C:844:GLU:HB3	2.25	0.72
1:C:2096:LYS:HA	1:C:2097:PHE:CG	2.25	0.72
2:B:53:GLN:HE21	2:B:94:SER:HB3	1.55	0.71
5:I:703:ILE:HG13	5:I:703:ILE:O	1.89	0.71
1:A:1027:ILE:HG21	1:A:1071:PHE:HA	1.72	0.71
5:J:690:ARG:HG2	5:J:691:ASN:HB2	1.72	0.71
1:C:235:LEU:HG	1:C:236:GLU:HA	1.71	0.71
1:A:1849:PHE:HB3	1:A:1886:GLN:HG3	1.72	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:704:SER:OG	1:A:714:LEU:HA	1.89	0.71
1:C:836:VAL:HG21	1:C:845:LEU:HB2	1.73	0.71
1:C:1505:LEU:HB3	1:C:1514:LYS:HG2	1.73	0.71
1:A:284:VAL:HG22	1:A:334:LEU:HD11	1.72	0.71
1:C:947:HIS:HA	1:C:950:GLN:HB2	1.72	0.71
1:A:1957:MET:HE2	1:A:2059:LEU:HD13	1.73	0.70
1:A:1630:ASN:HA	1:A:1633:LEU:HD13	1.72	0.70
1:C:674:GLN:HB3	1:C:720:LEU:HB3	1.72	0.70
1:A:197:ARG:C	1:A:199:THR:HG23	2.16	0.70
1:A:687:GLU:C	1:A:690:GLY:H	1.99	0.70
1:A:856:ASN:HB3	1:A:1584:LYS:HG2	1.73	0.70
1:C:956:CYS:HG	1:C:957:VAL:N	1.89	0.70
1:A:1151:LEU:HB2	1:A:1152:GLY:CA	2.21	0.70
1:C:242:ALA:HA	1:C:245:ILE:HB	1.73	0.70
1:A:845:LEU:HG	1:A:1525:VAL:HG23	1.73	0.70
1:C:2114:CYS:HB3	1:C:2123:TYR:C	2.17	0.70
1:C:2145:LEU:CB	1:C:2146:VAL:HG13	2.22	0.70
1:C:797:TYR:HE2	1:C:844:GLU:HB3	1.55	0.70
1:C:1451:LEU:O	1:C:1455:LYS:N	2.16	0.70
1:C:2077:GLU:HA	1:C:2093:LYS:HG2	1.74	0.70
2:D:201:THR:HB	2:D:203:PHE:HE1	1.54	0.70
1:A:797:LEU:O	1:A:800:LEU:HB2	1.90	0.70
1:C:89:PHE:HA	1:C:101:ALA:HB2	1.71	0.70
1:C:260:TYR:HE1	1:C:300:ALA:HB1	1.56	0.70
1:C:490:CYS:HB3	1:C:491:PRO:HD3	1.74	0.70
1:C:777:SER:HA	1:C:780:LEU:HB3	1.71	0.70
1:A:142:SER:HA	1:A:145:LYS:HE3	1.74	0.70
1:A:2035:LEU:HD21	5:I:648:LYS:HE2	1.72	0.70
1:A:2053:LEU:HG	1:A:2056:LEU:HD22	1.73	0.70
1:C:157:ILE:HG12	1:C:172:ARG:HH22	1.55	0.70
1:C:336:LEU:HD22	1:C:342:TYR:HB3	1.74	0.70
5:J:730:VAL:HG21	5:J:789:THR:HA	1.72	0.70
1:C:1832:ILE:HD13	1:C:1837:SER:HB3	1.72	0.70
1:C:1920:ILE:HD13	1:C:1935:ILE:HD11	1.74	0.70
1:A:702:LEU:HD23	1:A:713:SER:HB3	1.74	0.70
1:C:1409:GLN:H	1:C:1410:ARG:HB3	1.56	0.69
1:A:91:LEU:HD11	1:A:143:SER:CB	2.21	0.69
1:A:841:TYR:CB	1:A:843:GLU:HG2	2.09	0.69
1:C:1983:ASN:HB3	1:C:1986:LYS:HB3	1.73	0.69
2:B:253:VAL:HB	2:B:267:THR:HG23	1.73	0.69
1:C:1718:CYS:HB2	1:C:1759:TRP:CH2	2.26	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1503:LEU:HB3	1:A:1512:LYS:HG2	1.73	0.69
1:A:394:HIS:HB2	1:A:395:TYR:CG	2.27	0.69
1:A:1380:THR:HA	1:A:1383:ALA:HB3	1.75	0.69
1:A:1555:ILE:HG13	1:A:1556:ILE:H	1.57	0.69
1:C:329:LEU:HD21	1:C:357:TYR:CD2	2.26	0.69
1:C:1088:VAL:HA	1:C:1100:LYS:HD2	1.73	0.69
1:C:1818:HIS:HA	1:C:1821:VAL:H	1.58	0.69
1:A:180:ILE:HG22	1:A:223:LEU:CD1	2.22	0.69
2:D:278:ASP:HB3	2:D:281:THR:HB	1.75	0.69
1:A:187:VAL:HG11	1:A:233:LYS:HA	1.73	0.69
1:C:179:VAL:HG11	1:C:191:LEU:HD13	1.74	0.69
1:C:1070:VAL:HG11	1:C:1109:LEU:HD23	1.74	0.69
2:D:83:PHE:CE1	2:D:104:VAL:HG21	2.27	0.69
1:A:296:ARG:HH11	1:A:338:LYS:HG2	1.58	0.69
1:A:361:PHE:HE1	1:A:414:PHE:CZ	2.10	0.69
1:A:1082:ILE:HG23	1:A:1085:ILE:HG12	1.74	0.69
1:A:1415:ALA:HA	1:A:1418:GLU:HB2	1.74	0.69
1:C:280:ARG:HH12	1:C:328:THR:HB	1.58	0.69
1:C:533:GLN:C	1:C:535:ASN:H	2.00	0.69
5:I:730:VAL:HB	5:I:788:GLU:O	1.92	0.69
1:C:681:LEU:HD11	1:C:724:THR:HG22	1.75	0.69
1:A:1668:ALA:HA	1:A:1671:GLN:HB2	1.74	0.69
1:A:2184:THR:HB	1:A:2284:MET:HB2	1.75	0.69
1:C:1612:ILE:HG23	1:C:1615:ALA:CB	2.22	0.69
1:C:260:TYR:CE1	1:C:300:ALA:HB1	2.28	0.68
1:C:628:GLN:O	1:C:631:VAL:HG22	1.92	0.68
1:C:818:ARG:HD2	1:C:868:LEU:HD13	1.76	0.68
1:C:2193:GLU:HA	1:C:2196:GLU:HB2	1.76	0.68
1:C:2319:ARG:HG2	1:C:2470:TRP:HZ3	1.58	0.68
1:C:378:ALA:HA	1:C:379:PHE:N	2.08	0.68
1:C:334:GLU:HG3	1:C:372:ILE:HD12	1.75	0.68
2:D:120:ASN:HD21	2:D:136:ARG:HA	1.59	0.68
1:A:453:LYS:N	1:A:454:GLN:HA	2.08	0.68
1:C:1421:LYS:HE2	1:C:1435:LYS:HD2	1.76	0.68
1:C:2186:THR:HA	1:C:2286:MET:HA	1.75	0.68
2:B:53:GLN:HG3	2:B:78:VAL:HG13	1.75	0.68
1:C:783:LEU:H	1:C:784:GLY:HA3	1.57	0.68
1:C:1474:ALA:HA	1:C:1478:LEU:H	1.57	0.68
2:B:12:HIS:HB3	2:B:30:HIS:O	1.93	0.68
1:A:300:LEU:HA	1:A:303:GLN:HB2	1.75	0.68
1:A:841:TYR:HB2	1:A:843:GLU:CG	2.10	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2411:HIS:HA	1:A:2414:ALA:HB3	1.76	0.68
1:A:452:ARG:HD3	1:A:453:LYS:HB2	1.76	0.68
1:C:115:ALA:HB1	1:C:161:LEU:HB2	1.76	0.68
1:A:2211:ALA:HB2	1:A:2225:VAL:HG21	1.76	0.68
1:C:2141:GLN:C	1:C:2142:LEU:HA	2.19	0.68
2:D:232:ARG:HG2	2:D:245:THR:HA	1.76	0.68
1:C:115:ALA:C	1:C:117:GLU:H	2.02	0.67
1:A:1087:VAL:HB	1:A:1102:ILE:HG21	1.76	0.67
1:A:2315:PRO:HB3	1:A:2451:LEU:HB3	1.77	0.67
1:C:2409:VAL:N	1:C:2410:GLU:HG2	2.09	0.67
1:A:627:GLN:O	1:A:630:VAL:HG12	1.94	0.67
1:A:1516:HIS:HA	1:A:1519:ASN:HB2	1.75	0.67
1:A:1159:VAL:HG21	1:C:622:LYS:HD3	1.75	0.67
1:C:2142:LEU:HD11	1:C:2362:PHE:CE2	2.28	0.67
1:C:2370:TRP:N	1:C:2371:GLY:HA3	2.10	0.67
1:A:314:HIS:HD2	1:A:328:LEU:HD11	1.60	0.67
1:A:1906:HIS:HA	1:A:1908:GLN:HB3	1.76	0.67
5:I:685:SER:HB3	5:I:686:LYS:HB2	1.77	0.67
1:A:1573:GLU:O	1:A:1577:THR:N	2.27	0.67
1:C:1920:ILE:HG12	1:C:1932:LEU:HG	1.74	0.67
2:D:10:TYR:HE2	2:D:293:LYS:HG3	1.60	0.67
1:A:835:VAL:HG13	1:A:1525:VAL:HG11	1.76	0.67
1:C:1542:TYR:H	1:C:1543:ASN:HA	1.58	0.67
2:B:5:LEU:HA	2:B:6:VAL:N	2.10	0.67
1:C:268:ILE:HG23	1:C:311:GLN:HG3	1.77	0.67
1:C:1844:LEU:HB2	1:C:2358:ILE:HG21	1.77	0.67
1:A:396:LEU:HD23	1:A:400:LYS:HG2	1.76	0.67
1:A:1558:TYR:HA	1:A:1562:PRO:HD2	1.77	0.67
1:C:1382:THR:HA	1:C:1385:ALA:HB3	1.77	0.66
1:C:961:ASP:HB3	1:C:965:PRO:HG2	1.77	0.66
1:C:1455:LYS:HE3	1:C:1467:MET:HE3	1.77	0.66
1:C:2354:SER:HA	1:C:2356:MET:H	1.60	0.66
1:A:650:ASP:N	1:A:651:PRO:HD3	2.04	0.66
1:A:2363:ASP:HB2	1:A:2367:ASN:O	1.96	0.66
1:A:257:TYR:CG	1:A:286:LEU:HD11	2.31	0.66
2:B:22:GLY:HA3	2:B:286:ARG:HD3	1.76	0.66
2:B:255:ASP:OD1	2:B:297:CYS:HA	1.95	0.66
1:C:188:VAL:HA	1:C:192:ALA:HB3	1.76	0.66
1:A:855:GLU:O	1:A:1588:VAL:HG22	1.94	0.66
1:A:1228:TYR:HE1	1:A:1293:GLU:HB2	1.61	0.66
1:C:271:PRO:HG2	1:C:280:ARG:HB2	1.78	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:418:VAL:HB	1:C:419:SER:N	2.11	0.66
1:A:695:ALA:HA	1:A:698:ILE:HB	1.76	0.66
1:A:2283:LEU:HD21	1:A:2317:ARG:CD	2.25	0.66
1:C:2374:LEU:HD21	1:C:2417:ILE:HD12	1.78	0.66
1:A:178:VAL:HB	1:A:179:LEU:HG	1.78	0.66
1:A:179:LEU:HD13	1:A:233:LYS:HE3	1.76	0.66
1:A:1020:ILE:HG21	1:A:1024:ILE:HB	1.78	0.66
1:A:1918:ILE:HG12	1:A:1930:LEU:HG	1.78	0.66
2:D:205:ALA:HB3	2:D:206:HIS:HB2	1.78	0.66
2:D:229:HIS:CB	2:D:251:ARG:HB2	2.25	0.66
1:A:664:GLY:HA2	1:A:671:LEU:HG	1.77	0.66
1:A:2251:THR:HA	1:A:2254:GLU:HB3	1.75	0.66
1:C:181:ILE:HG22	1:C:228:ASN:HD21	1.60	0.66
1:C:188:VAL:HG11	1:C:234:LYS:HA	1.76	0.66
1:C:1056:SER:HG	1:C:1057:ASN:N	1.94	0.66
1:C:1295:ASP:CG	1:C:1342:TYR:OH	2.38	0.66
1:C:1440:TYR:HE1	1:C:1473:GLY:HA3	1.61	0.66
1:A:1829:SER:HG	1:A:1830:ILE:N	1.94	0.66
1:C:268:ILE:CG2	1:C:311:GLN:HG3	2.26	0.66
1:A:835:VAL:HG21	1:A:844:LEU:H	1.61	0.66
1:C:90:ASP:HB3	1:C:91:LYS:HG2	1.77	0.66
1:A:391:ILE:HA	1:A:395:TYR:CD2	2.31	0.65
1:A:1848:TRP:CZ2	1:A:1857:ALA:HB1	2.30	0.65
1:A:1858:THR:HA	1:A:1862:HIS:HB3	1.78	0.65
1:A:2078:VAL:HG22	1:A:2089:ILE:HG23	1.78	0.65
1:A:2407:VAL:HG13	1:A:2408:GLU:OE1	1.97	0.65
2:B:216:SER:HG	2:B:221:HIS:N	1.95	0.65
1:C:1505:LEU:HB3	1:C:1514:LYS:CG	2.26	0.65
1:C:1906:LYS:C	1:C:1909:PRO:HD3	2.21	0.65
2:B:3:VAL:HG11	2:B:19:ALA:HB3	1.79	0.65
1:C:1284:CYS:SG	1:C:1288:LEU:HB3	2.36	0.65
1:C:2114:CYS:HB2	1:C:2122:ASP:HB3	1.78	0.65
2:D:272:HIS:HA	2:D:293:LYS:O	1.95	0.65
2:D:297:CYS:CA	2:D:298:VAL:HB	2.15	0.65
1:A:280:LEU:O	1:A:283:ALA:N	2.30	0.65
1:A:2261:ARG:HG2	1:A:2337:ILE:HD13	1.78	0.65
1:C:572:ILE:HG22	1:C:573:LEU:HG	1.78	0.65
2:D:33:SER:CB	2:D:51:GLY:HA2	2.27	0.65
1:A:259:TYR:CD1	1:A:260:VAL:HG23	2.32	0.65
1:A:632:ALA:HA	1:A:635:SER:HB2	1.77	0.65
1:A:2286:ASP:HB3	1:A:2288:ILE:HG13	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1248:ILE:HG12	1:C:1260:ARG:HH12	1.61	0.65
1:A:254:TYR:N	1:A:293:ILE:HA	2.12	0.65
1:A:1723:TRP:NE1	1:A:1739:ILE:HG23	2.11	0.65
1:C:2015:GLY:HA2	1:C:2018:LEU:HG	1.79	0.65
1:A:345:LYS:O	1:A:372:LEU:HD21	1.96	0.65
2:D:101:VAL:HG11	2:D:143:TRP:CH2	2.31	0.65
1:A:682:MET:O	1:A:685:ASN:HB2	1.97	0.64
1:A:2432:THR:H	1:A:2447:GLN:NE2	1.95	0.64
1:C:402:ASN:HA	1:C:414:PRO:HG3	1.80	0.64
1:C:662:GLN:HE22	1:C:677:ASN:HA	1.60	0.64
1:C:1007:VAL:HG13	1:C:1009:ARG:CZ	2.27	0.64
1:C:1575:GLU:O	1:C:1579:THR:N	2.30	0.64
1:C:1495:SER:HG	1:C:1498:LYS:N	1.94	0.64
1:C:1954:HIS:HA	1:C:1957:ILE:HG22	1.78	0.64
5:J:694:THR:HG22	5:J:696:LYS:HB2	1.78	0.64
1:A:854:THR:HB	1:A:1579:LEU:HB2	1.80	0.64
1:A:2095:PHE:HB2	1:A:2096:GLU:N	2.11	0.64
1:C:1578:ASN:C	1:C:1579:THR:N	2.55	0.64
1:C:1725:TRP:HE1	1:C:1741:ILE:HG22	1.63	0.64
1:A:360:LYS:HE2	1:A:365:ARG:HH22	1.62	0.64
1:A:1627:LYS:O	1:A:1630:ASN:N	2.31	0.64
1:C:601:ILE:HG12	1:C:603:HIS:HB2	1.79	0.64
1:C:1510:ASN:ND2	4:G:73:PHE:HA	2.12	0.64
1:A:1517:ILE:HG12	1:A:1553:GLU:HB3	1.78	0.64
1:A:1559:LYS:N	1:A:1572:ARG:HH22	1.95	0.64
1:A:1041:GLU:HA	1:A:1044:THR:HG22	1.80	0.64
1:A:1453:LYS:HE3	1:A:1465:MET:CE	2.28	0.64
2:B:217:SER:HG	2:B:218:ASP:N	1.96	0.64
5:I:740:SER:HB2	5:I:768:SER:HA	1.80	0.64
1:A:633:LEU:HA	1:A:636:VAL:HB	1.79	0.64
1:A:742:CYS:HB2	1:A:743:THR:OG1	1.97	0.64
1:C:2374:LEU:HB3	1:C:2375:PRO:HD3	1.79	0.64
2:D:201:THR:HB	2:D:203:PHE:CE1	2.32	0.64
1:A:1963:GLU:HG2	1:A:2056:LEU:HD21	1.80	0.64
1:C:2244:LEU:HD11	1:C:2328:MET:HA	1.79	0.64
1:A:331:PHE:HZ	1:A:345:LYS:HE2	1.63	0.63
1:A:2060:GLU:HG2	1:A:2097:PRO:C	2.23	0.63
1:C:1725:TRP:NE1	1:C:1741:ILE:HG22	2.13	0.63
1:A:613:LEU:HA	1:A:616:CYS:HB3	1.80	0.63
1:A:856:ASN:HA	1:A:1584:LYS:HA	1.80	0.63
1:A:124:ARG:NH2	1:A:170:SER:HB3	2.12	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1291:TYR:HE1	1:A:1340:TYR:HE2	1.45	0.63
1:C:188:VAL:HG13	1:C:234:LYS:HA	1.79	0.63
1:C:948:ILE:HG13	1:C:952:LEU:HD13	1.81	0.63
5:J:730:VAL:HG11	5:J:790:PRO:HD2	1.81	0.63
1:A:2259:TYR:HA	1:A:2262:SER:CB	2.26	0.63
1:A:1617:ARG:HA	1:A:1624:LEU:HD22	1.81	0.63
1:C:1758:ALA:HA	1:C:1761:ASN:HD22	1.62	0.63
1:A:1969:LEU:HD13	1:A:1989:LEU:HD21	1.80	0.63
1:A:2266:MET:HA	1:A:2269:THR:HB	1.79	0.63
1:C:1965:GLU:OE1	1:C:2054:GLN:HG3	1.99	0.63
2:B:55:VAL:HA	2:B:81:VAL:HG21	1.80	0.63
1:C:453:ARG:HD3	1:C:454:LYS:HB2	1.81	0.63
5:I:678:LEU:HD21	5:I:688:TYR:CE2	2.34	0.63
1:C:1119:SER:HG	1:C:1120:SER:N	1.97	0.62
1:C:1978:PHE:HB2	1:C:1987:MET:HB2	1.79	0.62
1:C:1983:ASN:HD22	1:C:1987:MET:HG3	1.64	0.62
1:C:2433:LEU:HD22	1:C:2449:GLN:HA	1.81	0.62
3:E:404:UNK:O	3:E:408:UNK:N	2.27	0.62
1:C:825:LEU:HA	1:C:828:LEU:HB2	1.81	0.62
1:C:1440:TYR:HD1	1:C:1445:TRP:HE1	1.45	0.62
3:E:401:UNK:C	3:E:402:UNK:HA	2.29	0.62
5:I:655:SER:HA	5:I:659:LEU:CB	2.29	0.62
5:I:707:ILE:HD13	5:I:728:LEU:HG	1.80	0.62
1:C:379:PHE:HB2	1:C:381:PRO:HD2	1.80	0.62
1:C:849:LEU:HD22	1:C:1549:GLN:HB3	1.82	0.62
1:A:341:TYR:CE2	1:A:345:LYS:HE2	2.35	0.62
1:C:865:THR:HA	1:C:868:LEU:HD12	1.81	0.62
1:A:1555:ILE:HD13	1:A:1575:TRP:CZ2	2.34	0.62
1:A:1566:ASP:HB3	1:A:1568:ARG:HG3	1.81	0.62
2:B:232:ARG:HG2	2:B:245:THR:HA	1.79	0.62
5:I:655:SER:HA	5:I:659:LEU:HB2	1.81	0.62
1:A:2059:LEU:HD21	1:A:2099:PHE:HB2	1.81	0.62
1:C:181:ILE:H	1:C:182:PRO:N	1.96	0.62
1:C:305:TRP:HE1	1:C:341:PRO:HG2	1.64	0.62
1:C:670:PRO:HD2	1:C:671:GLN:N	2.14	0.62
1:C:760:ILE:HG13	1:C:761:LEU:HA	1.82	0.62
1:C:1956:LEU:HD21	1:C:2127:LEU:HD22	1.80	0.62
1:A:187:VAL:HG11	1:A:232:SER:O	1.99	0.62
1:A:600:ILE:H	1:A:602:HIS:HB2	1.64	0.62
1:A:1596:ARG:C	1:A:1598:LEU:H	2.06	0.62
1:A:2043:TYR:HB3	1:A:2047:ARG:HH12	1.63	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:ARG:O	1:A:597:ILE:N	2.33	0.62
1:A:849:ILE:HB	1:A:1551:GLU:N	2.15	0.62
1:A:993:LYS:HA	1:A:994:GLN:HB2	1.80	0.62
1:A:1555:ILE:HG13	1:A:1556:ILE:N	2.15	0.62
1:A:2457:SER:HA	1:A:2458:VAL:HA	1.82	0.62
5:J:701:SER:H	5:J:702:THR:HB	1.65	0.62
1:A:300:LEU:HD13	1:A:303:GLN:HB2	1.81	0.62
1:A:499:LEU:HA	1:A:502:LEU:HB2	1.81	0.62
1:A:845:LEU:HD22	1:A:1547:GLN:HG3	1.80	0.62
1:A:1453:LYS:HE3	1:A:1465:MET:HE2	1.81	0.62
1:C:764:ILE:HA	1:C:806:ILE:HG21	1.80	0.62
1:C:1274:ARG:HB2	1:C:1327:HIS:HE1	1.64	0.62
2:D:254:TRP:CD1	2:D:296:VAL:HA	2.35	0.62
1:A:1291:TYR:HE1	1:A:1340:TYR:CE2	2.17	0.62
1:A:1371:ILE:CD1	1:A:1387:LEU:HG	2.28	0.62
1:A:1634:GLU:HG3	1:A:1651:VAL:HG11	1.82	0.62
1:A:1820:ILE:N	1:A:1821:PRO:CD	2.63	0.62
1:A:2078:VAL:N	1:A:2090:VAL:O	2.32	0.62
1:C:221:TRP:HA	1:C:235:LEU:HD13	1.82	0.62
1:C:309:LEU:HA	1:C:346:LYS:HZ1	1.64	0.62
1:C:355:MET:SD	1:C:389:LEU:HD13	2.40	0.62
1:A:1592:ILE:HD12	1:A:1596:ARG:HD3	1.82	0.61
1:C:1218:PRO:HB2	1:C:1221:GLN:HB2	1.81	0.61
1:A:517:ILE:HG22	1:A:519:ASN:H	1.65	0.61
1:A:1440:LEU:HD13	1:A:1622:MET:HE3	1.82	0.61
1:C:793:GLU:HG3	1:C:795:THR:OG1	2.00	0.61
1:C:1964:HIS:NE2	1:C:2008:ILE:HA	2.15	0.61
1:C:2062:GLU:HG2	1:C:2064:GLN:H	1.64	0.61
1:A:443:GLU:HB3	1:A:446:ARG:HH11	1.64	0.61
1:A:471:GLY:C	4:H:187:THR:HA	2.25	0.61
1:C:1831:SER:HG	1:C:1832:ILE:N	1.97	0.61
1:A:280:LEU:HA	1:A:330:VAL:CG2	2.26	0.61
1:A:776:SER:HA	1:A:779:LEU:HB3	1.81	0.61
1:A:1224:LYS:HB2	1:A:1241:TRP:CE2	2.36	0.61
1:C:203:GLY:HA2	1:C:206:LEU:HB3	1.82	0.61
2:B:210:ILE:HD13	2:B:224:THR:HG22	1.82	0.61
1:C:1557:ILE:CG2	1:C:1577:TRP:HE1	2.13	0.61
1:C:2096:LYS:HA	1:C:2097:PHE:CB	2.30	0.61
1:C:2097:PHE:HD1	1:C:2097:PHE:C	2.09	0.61
2:B:233:VAL:O	2:B:243:GLU:HB3	1.99	0.61
1:C:264:ILE:O	1:C:268:ILE:HB	2.00	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:938:HIS:HE1	1:C:978:GLN:HA	1.65	0.61
5:J:730:VAL:HG21	5:J:790:PRO:HD2	1.81	0.61
1:A:1592:ILE:HB	1:A:1596:ARG:HB3	1.82	0.61
1:C:2185:ASP:O	1:C:2287:LEU:HG	2.01	0.61
1:C:2354:SER:HA	1:C:2356:MET:N	2.15	0.61
1:A:331:PHE:HZ	1:A:345:LYS:CE	2.13	0.61
1:A:1084:PRO:HG2	1:A:1117:MET:SD	2.41	0.61
2:B:127:ASN:ND2	2:B:130:GLU:HB2	2.14	0.61
1:C:1074:PRO:HA	1:C:1075:ASN:HB2	1.81	0.61
1:C:1151:GLN:HA	1:C:1151:GLN:NE2	2.15	0.61
1:C:1391:HIS:HB2	1:C:2334:GLU:HG2	1.81	0.61
1:C:2448:GLU:C	1:C:2449:GLN:N	2.59	0.61
1:A:345:LYS:HG3	1:A:349:ILE:CG1	2.31	0.61
1:C:213:PHE:O	1:C:217:THR:N	2.33	0.61
1:C:265:LEU:CA	1:C:307:GLN:HB3	2.20	0.61
1:C:630:SER:O	1:C:634:LEU:HG	2.01	0.61
1:A:346:TYR:OH	1:A:382:ILE:HG13	2.00	0.61
1:A:360:LYS:HE2	1:A:365:ARG:NH2	2.16	0.61
1:C:362:PHE:CD1	1:C:393:MET:HE1	2.36	0.61
1:C:1591:TRP:HE3	1:C:1614:PHE:HE1	1.49	0.61
1:C:2268:MET:HA	1:C:2271:THR:HB	1.81	0.61
2:D:183:CYS:SG	2:D:213:ILE:HG21	2.41	0.61
1:A:835:VAL:HB	1:A:844:LEU:HD23	1.83	0.60
2:D:9:GLY:O	2:D:12:HIS:CE1	2.54	0.60
3:E:408:UNK:C	3:E:410:UNK:H	2.13	0.60
1:C:766:PRO:HG3	1:C:809:PHE:HB3	1.83	0.60
1:C:1140:ALA:HB1	1:C:1173:GLN:HB3	1.83	0.60
1:C:1938:MET:HB3	1:C:1946:VAL:HG11	1.82	0.60
1:A:182:SER:HB3	1:A:187:VAL:HG23	1.81	0.60
1:A:324:VAL:HG22	1:A:327:THR:CG2	2.31	0.60
2:B:182:ASN:HA	2:B:183:CYS:HB2	1.82	0.60
1:C:681:LEU:HD22	1:C:728:PHE:HD1	1.66	0.60
1:C:1661:LEU:HG	1:C:1666:LEU:HB2	1.83	0.60
5:I:759:ASP:HB2	5:I:761:LYS:H	1.66	0.60
1:A:1164:LYS:C	1:A:1166:LEU:H	2.09	0.60
1:A:1679:MET:HA	1:A:1682:ASP:HB2	1.84	0.60
1:C:173:LEU:HD21	1:C:209:ASP:HA	1.81	0.60
3:E:214:UNK:C	3:E:215:UNK:H2	2.13	0.60
5:J:699:LYS:HD3	5:J:760:ARG:HD2	1.84	0.60
1:A:699:ILE:HG23	1:A:717:THR:HG22	1.82	0.60
1:A:1716:CYS:HB2	1:A:1757:TRP:CH2	2.37	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:235:LEU:CG	1:C:236:GLU:HA	2.31	0.60
1:C:1389:LEU:HD11	1:C:1403:THR:HA	1.83	0.60
1:C:1625:ALA:O	1:C:1626:LEU:N	2.34	0.60
1:C:2026:MET:HG3	1:C:2027:ASN:H	1.66	0.60
2:D:206:HIS:CD2	2:D:224:THR:HG22	2.36	0.60
1:A:381:ALA:HB1	1:A:385:LYS:HD3	1.84	0.60
1:A:2132:ARG:HA	1:A:2135:SER:HB2	1.83	0.60
2:B:99:ILE:HD13	2:B:122:VAL:HG21	1.82	0.60
1:C:285:VAL:HG22	1:C:335:LEU:CD1	2.31	0.60
1:C:1025:ILE:HA	1:C:1028:ILE:HG12	1.82	0.60
1:A:1885:HIS:HA	1:A:1886:GLN:N	2.17	0.60
1:A:2336:ARG:HA	1:A:2339:CYS:HB2	1.83	0.60
2:B:246:LEU:HD11	2:B:282:ARG:O	2.02	0.60
1:C:181:ILE:HG22	1:C:224:LEU:HD13	1.82	0.60
1:C:767:LYS:HB3	1:C:772:SER:HA	1.83	0.60
2:D:100:LYS:HA	2:D:101:VAL:HG12	1.83	0.60
1:C:1881:GLN:HG2	1:C:2134:ARG:HH21	1.65	0.60
2:D:37:ARG:HH22	2:D:212:ARG:HH22	1.48	0.60
1:A:1139:ALA:HB1	1:A:1172:GLN:OE1	2.02	0.60
2:B:206:HIS:CE1	2:B:226:SER:HB2	2.37	0.60
1:C:2063:LEU:H	1:C:2066:VAL:H	1.50	0.60
1:C:2407:GLN:O	1:C:2409:VAL:N	2.34	0.60
5:J:730:VAL:CG2	5:J:789:THR:HA	2.32	0.60
1:A:2238:LEU:HB3	1:A:2326:MET:H	1.67	0.60
1:C:997:ILE:HA	1:C:1000:HIS:HD2	1.67	0.60
1:C:2124:LYS:HB3	1:C:2180:TRP:C	2.27	0.60
1:A:683:ALA:HA	1:A:688:ILE:HD13	1.84	0.59
1:A:1283:CYS:HA	1:A:1287:LEU:N	2.17	0.59
1:A:2187:VAL:HA	1:A:2190:ARG:HG2	1.84	0.59
1:A:2266:MET:CB	1:A:2292:VAL:HG21	2.32	0.59
1:C:351:TYR:HH	1:C:386:LYS:N	1.99	0.59
1:C:1541:ALA:CB	1:C:1542:TYR:HA	2.32	0.59
1:C:2062:GLU:CA	1:C:2063:LEU:HB2	2.28	0.59
3:E:607:UNK:HA	3:E:608:UNK:C	2.32	0.59
5:J:781:GLU:C	5:J:784:GLN:HB3	2.27	0.59
1:A:233:LYS:HE2	1:A:237:ARG:HG2	1.83	0.59
1:A:314:HIS:HB2	1:A:328:LEU:HD21	1.85	0.59
1:A:347:ASP:N	1:A:348:ASP:HB2	2.17	0.59
1:A:1600:ILE:HG13	1:A:1601:LYS:H	1.65	0.59
1:C:1612:ILE:HG21	1:C:1656:ALA:HB1	1.83	0.59
1:A:1020:ILE:C	1:A:1025:GLU:HB2	2.27	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1563:GLN:C	1:A:1568:ARG:HD2	2.27	0.59
1:A:1837:SER:HG	1:A:1839:GLN:N	2.00	0.59
1:C:176:TYR:CE1	1:C:191:LEU:HD22	2.37	0.59
1:A:569:ALA:O	1:A:573:ILE:HG13	2.03	0.59
1:A:1945:ASP:HA	1:A:1948:GLU:HB2	1.85	0.59
1:C:280:ARG:HH22	1:C:328:THR:HB	1.68	0.59
1:C:801:LEU:HD23	1:C:805:ILE:HD11	1.83	0.59
1:C:1474:ALA:HB1	1:C:1478:LEU:HD23	1.84	0.59
1:C:1661:LEU:O	1:C:1666:LEU:N	2.35	0.59
1:A:824:LEU:CD2	1:A:1534:GLU:HB2	2.31	0.59
2:B:276:LEU:O	2:B:286:ARG:N	2.35	0.59
1:C:2064:GLN:HG3	1:C:2065:HIS:HD2	1.64	0.59
1:C:2247:LYS:HA	1:C:2249:ARG:N	2.16	0.59
5:J:674:GLU:HB2	5:J:693:PHE:CE2	2.37	0.59
1:A:818:ASP:HA	1:A:821:LEU:HB3	1.83	0.59
1:A:864:THR:HG23	1:A:867:LEU:HD12	1.84	0.59
1:A:1320:VAL:HG22	1:A:1345:HIS:CE1	2.38	0.59
1:A:1423:GLY:HA3	1:A:1424:GLU:HG3	1.84	0.59
1:A:2301:PHE:N	1:A:2374:THR:HG1	2.01	0.59
1:C:1674:LEU:O	1:C:1678:THR:N	2.36	0.59
1:C:1844:LEU:HD11	1:C:1878:VAL:HG11	1.84	0.59
1:C:2024:TRP:HB2	1:C:2039:GLN:HG2	1.85	0.59
2:D:17:TRP:HZ2	2:D:290:GLY:HA3	1.67	0.59
1:A:211:GLU:HG3	1:A:211:GLU:O	2.01	0.59
1:A:300:LEU:HD12	1:A:339:ALA:HB2	1.85	0.59
1:A:419:ILE:HG21	1:A:462:CYS:HB3	1.85	0.59
1:A:732:LYS:HB3	1:A:735:GLU:HB2	1.84	0.59
1:A:2079:PRO:HD3	1:A:2090:VAL:HG13	1.83	0.59
1:A:2394:LEU:HD21	1:A:2404:VAL:HG13	1.83	0.59
1:C:1757:LYS:HA	1:C:1832:ILE:HG21	1.85	0.59
1:C:2080:VAL:HA	1:C:2092:VAL:HG12	1.84	0.59
1:C:2360:GLU:C	1:C:2361:ALA:HA	2.28	0.59
1:A:2204:HIS:CE1	1:A:2470:PRO:HD2	2.37	0.59
5:I:676:MET:HE3	5:I:699:LYS:HZ1	1.66	0.59
1:A:2242:LEU:HD11	1:A:2326:MET:HA	1.83	0.59
2:B:229:HIS:HD2	2:B:252:TRP:H	1.50	0.59
1:A:594:LEU:HD23	1:A:597:ILE:HD12	1.84	0.59
1:A:1049:ILE:HD12	1:A:1064:ILE:HG12	1.85	0.59
1:C:188:VAL:CG2	1:C:233:SER:HB3	2.31	0.59
1:C:2062:GLU:O	1:C:2065:HIS:HB2	2.03	0.59
1:A:194:THR:HG22	1:A:197:ARG:HH21	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:VAL:HG22	1:A:303:GLN:HE21	1.68	0.58
1:A:336:SER:HB2	1:A:375:LEU:HB2	1.85	0.58
1:A:392:MET:HE3	1:A:414:PHE:CE1	2.38	0.58
1:A:688:ILE:HG13	1:A:689:PHE:N	2.18	0.58
1:A:1054:GLN:HE21	1:A:1057:LYS:HG2	1.68	0.58
1:A:1178:GLN:HA	1:A:1181:ASN:HB2	1.83	0.58
1:A:1232:GLN:O	1:A:1233:LYS:HB2	2.03	0.58
1:C:353:SER:HB3	1:C:357:TYR:CE2	2.38	0.58
1:C:1611:ARG:C	1:C:1613:LYS:N	2.61	0.58
1:C:2258:ARG:O	1:C:2262:THR:N	2.36	0.58
1:A:515:SER:O	1:A:518:LEU:HG	2.03	0.58
1:C:1294:GLU:HA	1:C:1295:ASP:HA	1.85	0.58
1:C:1494:GLN:HA	1:C:1495:SER:N	2.19	0.58
5:J:698:ARG:C	5:J:700:SER:H	2.09	0.58
1:A:241:ALA:HA	1:A:244:ILE:HB	1.83	0.58
1:A:554:SER:H	1:A:555:PHE:HB2	1.66	0.58
1:C:116:ARG:NH2	1:C:156:LEU:HD23	2.18	0.58
1:C:260:TYR:H	1:C:260:TYR:HD2	1.50	0.58
1:C:651:ASP:HB3	1:C:652:PRO:HA	1.85	0.58
1:C:1430:GLU:HA	1:C:1458:THR:HG22	1.85	0.58
1:A:353:THR:OG1	1:A:368:VAL:HG12	2.03	0.58
1:A:1273:ARG:HE	1:A:1277:ASN:HD22	1.49	0.58
1:C:857:ASN:HB3	1:C:1586:LYS:CA	2.27	0.58
1:C:1459:ALA:HA	1:C:1460:LYS:C	2.27	0.58
1:C:2080:VAL:HG12	1:C:2083:THR:HB	1.84	0.58
1:A:445:LEU:HG	1:A:449:PHE:CE2	2.39	0.58
1:A:960:ASP:C	1:A:961:GLN:N	2.61	0.58
1:A:1574:THR:HG22	1:A:1578:ARG:HB2	1.86	0.58
1:A:2425:LYS:HA	1:A:2434:ASN:ND2	2.16	0.58
1:C:471:LEU:HD13	1:C:475:PHE:HB2	1.84	0.58
1:C:1373:ILE:HD13	1:C:1389:LEU:HD23	1.84	0.58
1:C:1384:SER:HB3	1:C:2335:GLY:HA3	1.84	0.58
1:C:1451:LEU:O	1:C:1454:GLU:N	2.37	0.58
1:C:1914:TYR:O	1:C:1918:VAL:HG23	2.03	0.58
2:D:216:SER:HG	2:D:221:HIS:N	2.00	0.58
1:A:276:LEU:HB3	1:A:279:ARG:HH21	1.68	0.58
1:C:2446:VAL:O	1:C:2450:VAL:HB	2.03	0.58
1:A:187:VAL:HA	1:A:191:ALA:HB3	1.85	0.58
1:A:1870:ILE:HG22	1:A:1873:TRP:N	2.17	0.58
2:B:105:ARG:O	2:B:106:SER:HB2	2.04	0.58
1:C:542:GLN:C	1:C:543:PHE:N	2.61	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:681:LEU:HD13	1:C:728:PHE:HA	1.85	0.58
1:C:1097:SER:HG	1:C:1098:LEU:N	2.01	0.58
1:A:1113:ASN:HB3	1:A:1149:LEU:HB3	1.86	0.58
1:A:1602:PRO:HG2	1:A:1635:GLU:HG2	1.86	0.58
1:C:378:ALA:HB2	1:C:386:LYS:HD2	1.85	0.58
1:C:2268:MET:SD	1:C:2296:HIS:N	2.77	0.58
2:D:16:PHE:HB2	2:D:26:ARG:HB3	1.84	0.58
2:D:233:VAL:HG21	2:D:279:LEU:HD11	1.86	0.58
1:C:213:PHE:CE1	1:C:239:ARG:HA	2.38	0.58
1:C:214:GLU:HA	1:C:217:THR:HG22	1.86	0.58
1:C:1629:LYS:HE3	1:C:1633:THR:HG21	1.86	0.58
1:C:1743:GLY:HA3	1:C:1746:LEU:HB2	1.85	0.58
1:C:1832:ILE:HD13	1:C:1837:SER:CB	2.32	0.58
1:C:2115:ILE:HG13	1:C:2125:TYR:CE2	2.39	0.58
1:A:1049:ILE:HG23	1:A:1064:ILE:HD13	1.86	0.58
1:A:1446:LEU:N	1:A:1447:SER:HB2	2.17	0.58
1:A:331:PHE:CE2	1:A:349:ILE:HG21	2.34	0.57
1:A:519:ASN:HB3	1:A:520:LEU:HD13	1.85	0.57
1:A:680:LEU:HD13	1:A:727:PHE:HA	1.84	0.57
1:A:1139:ALA:HA	1:A:1172:GLN:HB3	1.84	0.57
1:C:89:PHE:HE2	1:C:131:ASN:ND2	2.01	0.57
1:C:1819:ARG:HE	1:C:1853:PHE:HZ	1.51	0.57
1:A:1061:PRO:HA	1:A:1064:ILE:HD12	1.86	0.57
1:A:1972:ALA:C	1:A:1974:ARG:H	2.12	0.57
1:C:213:PHE:HE1	1:C:239:ARG:HA	1.68	0.57
1:C:1009:ARG:HB2	1:C:1011:PHE:CD2	2.40	0.57
1:C:2112:LYS:HD2	1:C:2180:TRP:HZ3	1.69	0.57
1:A:344:ASP:HB2	1:A:345:LYS:HB2	1.86	0.57
1:A:345:LYS:HG3	1:A:349:ILE:HG12	1.86	0.57
1:A:669:PRO:HG2	1:A:719:LEU:HD21	1.86	0.57
1:A:693:LEU:HA	1:A:696:ILE:HD12	1.85	0.57
1:A:1821:PRO:HA	1:A:1824:LYS:HG3	1.86	0.57
2:B:29:GLN:HB3	5:I:682:ILE:HG21	1.84	0.57
1:C:2180:TRP:HA	1:C:2181:VAL:HB	1.84	0.57
2:D:186:TRP:HB3	2:D:197:LEU:HB3	1.86	0.57
1:A:232:SER:HB2	1:A:236:TYR:HE2	1.69	0.57
1:A:848:LEU:H	1:A:1547:GLN:HE22	1.52	0.57
1:A:947:ILE:HG13	1:A:951:LEU:HD13	1.85	0.57
1:A:1010:PHE:HD1	1:A:1021:ILE:HG23	1.70	0.57
1:A:1034:GLU:HA	1:A:1035:PHE:N	2.19	0.57
1:A:1099:LYS:HA	1:A:1102:ILE:HB	1.85	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1502:ILE:HB	1:A:1594:ARG:HH22	1.69	0.57
1:C:135:PHE:HA	1:C:145:GLU:O	2.04	0.57
1:C:694:LEU:HD12	1:C:697:ILE:HD12	1.86	0.57
1:C:2138:LEU:O	1:C:2142:LEU:N	2.37	0.57
1:A:1384:ILE:HD13	1:A:1408:ARG:NH2	2.20	0.57
1:C:359:GLU:HG3	1:C:389:LEU:HD21	1.85	0.57
1:A:1856:GLU:O	1:A:1861:MET:N	2.37	0.57
1:A:1935:LYS:O	1:A:1939:HIS:N	2.37	0.57
1:A:2059:LEU:C	1:A:2098:VAL:HA	2.29	0.57
1:C:193:ALA:HA	1:C:196:LEU:HB3	1.86	0.57
1:C:689:ILE:HG13	1:C:690:PHE:N	2.20	0.57
1:C:1448:LEU:HD13	1:C:1470:LEU:HA	1.85	0.57
5:I:693:PHE:CZ	5:I:760:ARG:HB3	2.39	0.57
1:A:1191:THR:C	1:A:1193:ILE:H	2.13	0.57
2:B:231:ALA:HB1	2:B:265:LEU:HD21	1.86	0.57
1:C:1443:GLY:HA3	1:C:1628:LYS:HD2	1.85	0.57
1:C:1771:SER:HB2	1:C:1845:ARG:HH22	1.70	0.57
1:C:2344:VAL:O	1:C:2348:LEU:HG	2.03	0.57
1:A:1039:VAL:HG23	1:A:1040:PRO:HD3	1.85	0.57
1:C:1283:SER:HG	1:C:1285:TRP:CD1	2.22	0.57
1:A:768:GLN:HB2	1:A:770:ALA:N	2.16	0.57
1:A:1969:LEU:CB	1:A:1970:ASP:HA	2.35	0.57
2:B:278:ASP:HB3	2:B:281:THR:HB	1.87	0.57
1:C:280:ARG:HH12	1:C:328:THR:CB	2.18	0.57
1:C:347:TYR:OH	1:C:383:ILE:O	2.22	0.57
1:C:700:ILE:HD12	1:C:718:THR:CG2	2.35	0.57
1:C:860:HIS:O	1:C:862:ARG:N	2.34	0.57
1:C:2097:PHE:C	1:C:2097:PHE:CD1	2.81	0.57
1:C:2288:ASP:HB3	1:C:2290:ILE:CG1	2.35	0.57
2:D:231:ALA:HB2	2:D:253:VAL:HG11	1.86	0.57
1:A:259:TYR:HD1	1:A:260:VAL:HG23	1.68	0.57
1:A:569:ALA:HA	1:A:591:PHE:HE1	1.69	0.57
1:A:766:LYS:O	1:A:768:GLN:N	2.31	0.57
1:A:1001:GLU:HG2	1:A:1044:THR:HG21	1.86	0.57
1:A:1020:ILE:CG2	1:A:1024:ILE:HB	2.35	0.57
1:A:1406:LEU:HD13	1:A:1412:ALA:HA	1.85	0.57
2:B:125:HIS:HA	2:B:167:MET:HE1	1.87	0.57
1:C:450:PHE:HB3	1:C:453:ARG:HD2	1.87	0.57
1:C:2352:LYS:O	1:C:2356:MET:HG2	2.04	0.57
5:J:755:PHE:CE2	5:J:781:GLU:HB3	2.39	0.57
1:A:177:ARG:H	1:A:178:VAL:HG22	1.69	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1010:PHE:HE1	1:A:1022:SER:HB2	1.69	0.56
1:A:2112:CYS:HB3	1:A:2122:LYS:N	2.20	0.56
1:C:216:ARG:HD2	1:C:234:LYS:NZ	2.20	0.56
1:C:346:LYS:HB3	1:C:350:ILE:HG13	1.87	0.56
1:C:828:LEU:HD11	1:C:848:ILE:HG21	1.87	0.56
1:C:1407:LYS:HD2	1:C:1413:ASP:N	2.20	0.56
2:D:276:LEU:HB3	2:D:286:ARG:HB2	1.87	0.56
1:A:457:LYS:HB3	1:A:485:LEU:HD11	1.87	0.56
1:A:1076:GLU:HB3	1:A:1079:SER:OG	2.05	0.56
1:A:1090:THR:HG23	1:A:1091:GLU:HB2	1.86	0.56
1:A:2453:GLN:O	1:A:2457:SER:N	2.34	0.56
2:B:17:TRP:HZ2	2:B:290:GLY:HA2	1.69	0.56
1:C:121:GLU:C	1:C:123:PHE:H	2.12	0.56
1:C:234:LYS:HE3	1:C:238:ARG:HG2	1.86	0.56
1:C:804:LEU:HD23	1:C:851:ASN:HB2	1.87	0.56
1:C:862:ARG:HG3	1:C:863:ARG:H	1.70	0.56
1:C:2125:TYR:HA	1:C:2179:GLY:HA2	1.86	0.56
1:C:2432:LYS:HE2	1:C:2433:LEU:N	2.20	0.56
1:A:198:LEU:HA	1:A:248:LEU:HG	1.88	0.56
1:A:856:ASN:CB	1:A:1580:LEU:HA	2.31	0.56
1:A:861:ARG:HB3	1:A:1540:TYR:CD2	2.41	0.56
1:A:1510:PHE:CZ	1:A:1514:GLU:HA	2.40	0.56
1:A:2301:PHE:HZ	1:A:2423:VAL:HG22	1.70	0.56
2:B:33:SER:HG	2:B:34:GLN:N	2.04	0.56
1:C:112:THR:HG22	1:C:114:LEU:HD12	1.85	0.56
1:C:853:LEU:HD12	1:C:1580:ARG:HD3	1.87	0.56
1:C:1349:PHE:HD2	1:C:1351:LYS:N	2.03	0.56
1:C:1594:ILE:HB	1:C:1598:ARG:HB3	1.87	0.56
1:C:2437:ASP:HB3	1:C:2438:ILE:HG12	1.86	0.56
2:D:10:TYR:CE2	2:D:293:LYS:HG3	2.38	0.56
1:A:246:LYS:N	1:A:289:CYS:HG	2.02	0.56
1:A:581:LEU:HA	1:A:582:ILE:C	2.31	0.56
1:A:1427:VAL:HG23	1:A:1428:GLU:H	1.70	0.56
1:A:1584:LYS:O	1:A:1585:ASN:HB3	2.05	0.56
1:A:1666:ASP:O	1:A:1670:LYS:N	2.38	0.56
1:C:2157:PHE:O	1:C:2160:HIS:HB2	2.05	0.56
1:A:387:TYR:O	1:A:391:ILE:N	2.38	0.56
1:A:655:ILE:HA	1:A:658:GLU:HB2	1.88	0.56
1:A:2060:GLU:HG3	1:A:2098:VAL:HG23	1.85	0.56
1:C:444:GLU:HA	1:C:447:ARG:HB2	1.88	0.56
1:C:1370:GLU:HA	1:C:1373:ILE:HD12	1.88	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1584:CYS:O	1:C:1585:GLN:HB2	2.05	0.56
1:C:1743:GLY:HA2	1:C:1744:SER:C	2.30	0.56
1:A:280:LEU:C	1:A:284:VAL:HG23	2.31	0.56
1:A:827:LEU:HD11	1:A:847:ILE:HG21	1.86	0.56
1:A:1243:ARG:HH21	1:A:1259:ARG:HG2	1.71	0.56
1:C:2126:VAL:HG12	1:C:2180:TRP:CE3	2.38	0.56
1:A:1458:LYS:HB3	1:A:1459:PRO:HD3	1.87	0.56
1:C:285:VAL:HG22	1:C:335:LEU:HD11	1.86	0.56
1:C:1421:LYS:HG3	1:C:1435:LYS:HD2	1.87	0.56
1:A:233:LYS:HE2	1:A:237:ARG:CG	2.35	0.56
1:A:1100:ILE:HG23	1:A:1141:MET:SD	2.46	0.56
1:A:1140:THR:HG22	1:A:1172:GLN:NE2	2.21	0.56
1:A:2318:LEU:HD11	1:A:2455:ALA:HB1	1.86	0.56
5:I:693:PHE:HE2	5:I:760:ARG:HH21	1.54	0.56
1:A:1428:GLU:HA	1:A:1456:THR:HG22	1.87	0.56
1:C:221:TRP:HA	1:C:235:LEU:CD1	2.36	0.56
1:C:1410:ARG:HG3	1:C:1411:TRP:N	2.20	0.56
1:C:2171:LEU:H	1:C:2176:GLY:HA2	1.71	0.56
2:D:3:VAL:C	2:D:4:ILE:HG13	2.31	0.56
2:D:40:ILE:HG23	2:D:47:LEU:HD23	1.87	0.56
5:J:655:SER:HA	5:J:659:LEU:CB	2.27	0.56
1:A:993:LYS:HZ2	1:A:1029:LYS:HE3	1.71	0.56
1:C:297:ARG:HD2	1:C:339:LYS:CG	2.31	0.56
1:C:1061:VAL:N	1:C:1062:PRO:CD	2.70	0.56
1:C:1085:PRO:HG3	1:C:1118:MET:SD	2.46	0.56
1:C:1406:GLU:HG3	1:C:1409:GLN:HG3	1.88	0.56
1:C:1761:ASN:HA	1:C:1764:LEU:HD12	1.88	0.56
1:C:281:LEU:CD1	1:C:330:LEU:HB3	2.36	0.55
1:C:515:ASN:HA	1:C:518:ILE:HD12	1.87	0.55
1:C:2323:MET:HA	1:C:2326:TYR:HB3	1.87	0.55
5:I:720:PRO:HD3	5:I:723:PHE:HB2	1.87	0.55
1:A:215:ARG:HG3	1:A:233:LYS:HZ3	1.71	0.55
1:A:1252:GLU:HG2	1:A:1253:SER:H	1.70	0.55
1:A:1961:TRP:HB2	1:A:2006:ILE:HG12	1.87	0.55
1:C:146:LYS:HG2	1:C:191:LEU:HD11	1.87	0.55
1:C:195:THR:HG22	1:C:198:ARG:HH21	1.71	0.55
1:C:1594:ILE:HA	1:C:1597:VAL:HB	1.88	0.55
1:C:2374:LEU:HD12	1:C:2421:ARG:HH22	1.70	0.55
1:A:821:LEU:HA	1:A:824:LEU:HB2	1.87	0.55
1:A:1143:THR:HB	1:A:1177:ASP:HB2	1.88	0.55
1:A:1830:ILE:HG22	1:A:1832:LEU:HD22	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1952:HIS:HA	1:A:1955:ILE:HG22	1.88	0.55
2:B:236:ILE:HG23	2:B:237:ASP:HB3	1.88	0.55
1:C:2079:ALA:HB2	1:C:2094:ILE:HG12	1.88	0.55
2:D:223:ALA:HB2	2:D:233:VAL:HG23	1.88	0.55
1:A:89:ASP:HB3	1:A:90:LYS:HG2	1.87	0.55
1:A:487:LEU:HD23	1:A:488:ASN:H	1.71	0.55
1:C:329:LEU:HD23	1:C:366:ARG:HD3	1.89	0.55
1:C:1222:ASN:HA	1:C:1225:LYS:HD2	1.89	0.55
1:C:2098:GLU:HB3	1:C:2100:VAL:C	2.31	0.55
1:C:2103:VAL:HA	1:C:2111:ARG:HA	1.88	0.55
1:A:352:SER:HB3	1:A:356:TYR:CE2	2.42	0.55
1:A:392:MET:HE1	1:A:396:LEU:HD22	1.88	0.55
1:A:1452:GLU:O	1:A:1456:THR:HG23	2.07	0.55
1:A:1821:PRO:HA	1:A:1824:LYS:CG	2.36	0.55
1:A:2436:ILE:HG13	1:A:2438:ARG:H	1.72	0.55
1:A:2442:LEU:O	1:A:2446:GLU:HB2	2.06	0.55
2:D:12:HIS:O	2:D:13:THR:N	2.39	0.55
2:D:14:ILE:HD11	2:D:28:ILE:HD12	1.89	0.55
1:A:1609:ARG:C	1:A:1610:ILE:N	2.65	0.55
1:A:2035:LEU:HD21	5:I:648:LYS:HG3	1.89	0.55
1:C:2008:ILE:HD11	1:C:2066:VAL:HG23	1.87	0.55
1:A:187:VAL:CG1	1:A:233:LYS:HA	2.37	0.55
1:A:1183:LEU:HD13	1:A:1189:LEU:HD22	1.89	0.55
1:A:1502:ILE:HB	1:A:1594:ARG:NH2	2.22	0.55
1:C:2207:TRP:HA	1:C:2210:LEU:HD12	1.88	0.55
5:I:690:ARG:HG2	5:I:691:ASN:HB2	1.88	0.55
1:A:1215:LYS:HB2	1:A:1249:LEU:HB3	1.89	0.55
1:A:1621:ARG:HG2	1:A:1624:LEU:HD23	1.88	0.55
1:A:1962:HIS:NE2	1:A:2006:ILE:HA	2.22	0.55
2:B:46:LEU:HD13	2:B:57:LEU:HD13	1.89	0.55
5:I:659:LEU:HD21	5:I:690:ARG:HH12	1.72	0.55
1:C:866:VAL:N	1:C:1537:SER:HG	2.03	0.55
1:C:1014:ILE:HG23	1:C:1064:ARG:HE	1.72	0.55
1:C:1598:ARG:C	1:C:1600:LEU:H	2.14	0.55
1:C:2222:LEU:HB3	2:D:254:TRP:HZ3	1.72	0.55
1:A:1238:TRP:O	1:A:1241:TRP:N	2.40	0.55
1:A:1291:TYR:CE1	1:A:1340:TYR:HE2	2.24	0.55
1:A:2429:ASP:HB2	1:A:2439:PHE:HB3	1.88	0.55
1:C:282:ASP:HA	1:C:285:VAL:HB	1.89	0.55
1:C:780:LEU:HD11	1:C:816:PHE:HB2	1.89	0.55
3:E:715:UNK:C	3:E:717:UNK:H	2.20	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:7:SER:HB3	2:B:295:ALA:CB	2.36	0.54
1:C:1009:ARG:HB2	1:C:1011:PHE:CE2	2.41	0.54
1:A:954:ARG:NH1	1:A:992:VAL:H	2.06	0.54
1:A:1419:LYS:HG3	1:A:1433:LYS:HD2	1.89	0.54
1:C:1114:ASN:HB3	1:C:1150:LEU:HA	1.88	0.54
1:C:1165:LYS:HE3	1:C:1171:ARG:HG3	1.89	0.54
1:C:2191:ILE:HD12	1:C:2194:HIS:HD2	1.72	0.54
1:A:455:PHE:HB2	1:A:491:MET:HG3	1.89	0.54
1:A:849:ILE:HG23	1:A:853:LYS:N	2.22	0.54
1:A:993:LYS:HA	1:A:994:GLN:CB	2.38	0.54
1:A:1217:PRO:HB2	1:A:1220:GLN:HB2	1.88	0.54
1:A:1291:TYR:CE1	1:A:1340:TYR:CE2	2.95	0.54
1:C:347:TYR:HE2	1:C:383:ILE:HG12	1.72	0.54
1:C:1031:ALA:HB1	1:C:1034:GLY:O	2.07	0.54
5:J:754:ASN:HB3	5:J:760:ARG:HG3	1.89	0.54
2:D:35:VAL:HG22	2:D:38:LEU:HD21	1.89	0.54
3:F:102:UNK:C	3:F:103:UNK:HA	2.36	0.54
1:A:177:ARG:N	1:A:178:VAL:HG23	2.16	0.54
1:C:97:PRO:HB2	1:C:144:SER:HB3	1.90	0.54
1:C:1504:ILE:HG21	1:C:1596:ARG:HH12	1.72	0.54
2:D:165:LEU:HD11	2:D:174:LEU:HD23	1.88	0.54
5:J:658:VAL:HG23	5:J:659:LEU:HD12	1.89	0.54
1:A:1010:PHE:HD1	1:A:1021:ILE:CG2	2.21	0.54
2:B:113:TYR:OH	2:B:150:CYS:HA	2.07	0.54
1:C:2147:ASN:HA	1:C:2150:LEU:HB2	1.88	0.54
2:D:259:SER:HB2	2:D:302:ASP:OD2	2.07	0.54
5:I:700:SER:HA	5:I:731:GLU:CB	2.35	0.54
5:J:698:ARG:C	5:J:700:SER:N	2.65	0.54
1:A:152:VAL:HA	1:A:155:LEU:HB3	1.89	0.54
1:A:378:PHE:HB2	1:A:380:PRO:HD2	1.89	0.54
1:A:1499:TYR:H	1:A:1594:ARG:NH2	2.05	0.54
1:A:1713:LEU:HA	1:A:1752:THR:HG21	1.89	0.54
1:A:2044:ASN:HA	1:A:2047:ARG:NH1	2.21	0.54
1:A:2135:SER:HA	1:A:2138:MET:HE3	1.89	0.54
1:C:2038:ASN:HA	1:C:2041:TRP:HB2	1.88	0.54
2:D:54:ASN:HA	2:D:72:GLU:HG2	1.90	0.54
1:A:358:GLU:HG3	1:A:388:LEU:HD21	1.90	0.54
1:A:542:PHE:HB2	1:A:544:ILE:HG23	1.90	0.54
1:A:635:SER:HA	1:A:638:GLU:HB3	1.89	0.54
1:A:699:ILE:HD12	1:A:717:THR:CG2	2.37	0.54
1:C:1165:LYS:C	1:C:1167:LEU:H	2.15	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2308:LEU:HB3	1:C:2309:ARG:HB2	1.90	0.54
1:C:2412:GLU:HA	1:C:2415:ASN:HB2	1.90	0.54
1:A:650:ASP:N	1:A:651:PRO:CD	2.61	0.54
1:A:1876:VAL:O	1:A:1880:LEU:HG	2.08	0.54
1:A:2043:TYR:CE1	5:I:660:GLU:HG3	2.42	0.54
1:C:168:ASN:HD21	1:C:172:ARG:HH21	1.56	0.54
1:C:358:LYS:HD3	1:C:393:MET:HG3	1.90	0.54
1:C:1585:GLN:O	1:C:1586:LYS:HB2	2.08	0.54
1:C:1662:TRP:HZ3	1:C:1726:ARG:CZ	2.20	0.54
1:C:2102:SER:H	1:C:2113:PHE:HE2	1.56	0.54
2:D:215:LEU:HD22	2:D:236:ILE:HD12	1.90	0.54
5:I:730:VAL:HG21	5:I:789:THR:HA	1.89	0.54
1:A:322:ASP:O	1:A:324:VAL:HG23	2.08	0.54
1:A:445:LEU:HA	1:A:448:LYS:HB2	1.89	0.54
1:A:673:GLN:HG2	1:A:719:LEU:HD13	1.88	0.54
1:A:1040:PRO:HA	1:A:1043:LEU:HG	1.90	0.54
1:A:1232:GLN:HG3	1:A:1294:ASP:O	2.08	0.54
1:A:1437:LEU:HB3	1:A:1446:LEU:HD21	1.88	0.54
2:B:84:GLN:HB3	2:B:89:TRP:HB2	1.90	0.54
2:B:91:VAL:HG22	2:B:99:ILE:HD11	1.90	0.54
2:B:275:ARG:HG3	2:B:287:GLN:HG3	1.90	0.54
1:C:421:GLY:HA2	1:C:424:ALA:HB2	1.90	0.54
1:C:745:LEU:HD22	1:C:782:VAL:HG21	1.90	0.54
1:C:2062:GLU:HA	1:C:2063:LEU:CB	2.31	0.54
1:C:2255:LEU:O	1:C:2259:THR:N	2.37	0.54
1:C:2273:TYR:CD1	1:C:2317:PRO:HA	2.43	0.54
1:C:2373:ASP:HB3	1:C:2418:ARG:HH21	1.73	0.54
1:A:235:GLU:HB3	1:A:278:ILE:HB	1.90	0.53
1:A:1588:VAL:HG12	1:A:1612:PHE:CD1	2.43	0.53
1:A:1589:TRP:HE3	1:A:1612:PHE:CE1	2.15	0.53
1:A:1950:VAL:HA	1:A:1953:GLU:HB2	1.89	0.53
1:C:138:ILE:C	1:C:140:GLY:H	2.14	0.53
1:C:473:PRO:O	1:C:477:LYS:HG2	2.08	0.53
1:C:682:PHE:C	1:C:684:ALA:H	2.15	0.53
1:C:951:ASN:HB3	1:C:954:LEU:H	1.72	0.53
1:C:1444:GLU:C	1:C:1445:TRP:HA	2.33	0.53
1:C:1857:PRO:C	1:C:1859:ALA:N	2.65	0.53
3:E:109:UNK:C	3:E:110:UNK:HA	2.39	0.53
1:C:763:VAL:HG12	1:C:806:ILE:HB	1.90	0.53
1:C:818:ARG:HD2	1:C:868:LEU:CD1	2.38	0.53
1:C:1982:HIS:HB3	1:C:1984:THR:N	2.22	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2080:VAL:HB	1:C:2084:ARG:HG3	1.90	0.53
1:C:2109:ARG:N	1:C:2110:PRO:HD3	2.22	0.53
2:D:231:ALA:H	2:D:246:LEU:C	2.16	0.53
3:F:659:UNK:O	3:F:661:UNK:N	2.41	0.53
1:A:264:LEU:HB2	1:A:306:GLN:CD	2.33	0.53
1:A:397:ARG:HB3	1:A:399:LEU:HB2	1.91	0.53
1:A:725:LEU:HG	1:A:726:LYS:N	2.23	0.53
1:A:1103:ILE:HB	1:A:1141:MET:HE2	1.88	0.53
1:A:1652:VAL:HG12	1:A:1656:LEU:HB2	1.91	0.53
1:A:1916:VAL:HG11	1:A:2168:PRO:HB2	1.89	0.53
1:A:2032:VAL:HA	1:A:2035:LEU:HD22	1.90	0.53
1:A:2253:LEU:O	1:A:2257:THR:N	2.42	0.53
1:A:2306:LEU:HD12	1:A:2376:LYS:H	1.73	0.53
1:C:573:LEU:HD23	1:C:576:CYS:HB2	1.91	0.53
1:C:1340:GLY:HA2	1:C:1343:ALA:H	1.73	0.53
1:C:1655:TYR:HE1	1:C:1720:LEU:HD21	1.73	0.53
1:C:2172:SER:HB3	1:C:2173:PRO:HD2	1.88	0.53
1:C:2445:ASP:O	1:C:2449:GLN:HB2	2.07	0.53
1:A:689:PHE:HZ	1:A:732:LYS:HD3	1.73	0.53
1:A:1046:PHE:HA	1:A:1049:ILE:HG12	1.90	0.53
1:A:1498:PHE:HD2	1:A:1499:TYR:CD2	2.26	0.53
1:A:1928:ALA:O	1:A:1932:ILE:HG12	2.09	0.53
2:B:231:ALA:HB3	2:B:246:LEU:HB3	1.89	0.53
1:C:862:ARG:HB2	1:C:1537:SER:HA	1.91	0.53
1:C:1581:LEU:HD12	1:C:1582:LEU:HD23	1.91	0.53
2:D:246:LEU:HD11	2:D:282:ARG:HA	1.89	0.53
1:A:770:ALA:HA	1:A:810:ASP:HB2	1.91	0.53
1:A:1089:MET:HB3	1:A:1092:TYR:CD2	2.44	0.53
1:A:2111:PHE:HD1	1:A:2112:CYS:HA	1.74	0.53
2:B:235:SER:HB3	2:B:239:ASP:HB3	1.89	0.53
1:C:395:HIS:CE1	1:C:438:ILE:HG21	2.38	0.53
1:C:852:ILE:HG21	1:C:1584:CYS:HB2	1.90	0.53
1:C:1192:THR:C	1:C:1194:ILE:H	2.17	0.53
2:D:84:GLN:HB2	2:D:145:LEU:HD22	1.90	0.53
1:A:212:PHE:HE1	1:A:238:ARG:HA	1.72	0.53
1:A:1406:LEU:HD21	1:A:1436:SER:HB3	1.90	0.53
1:A:2057:GLN:HE22	1:A:2103:SER:HB2	1.74	0.53
2:B:16:PHE:HB3	2:B:60:ILE:HD13	1.91	0.53
2:B:79:THR:HG23	2:B:95:GLU:HG3	1.91	0.53
2:B:131:LEU:HB3	2:B:143:TRP:O	2.08	0.53
1:C:214:GLU:HG2	1:C:218:CYS:SG	2.48	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:366:ARG:HA	1:C:369:VAL:HB	1.90	0.53
1:C:1962:LEU:HB2	1:C:1965:GLU:N	2.23	0.53
2:D:156:PRO:HB3	2:D:184:TYR:HB2	1.91	0.53
5:J:676:MET:HE3	5:J:699:LYS:HE3	1.91	0.53
1:A:520:LEU:O	1:A:522:SER:HA	2.08	0.53
1:A:1586:ILE:C	1:A:1587:ASP:HB2	2.34	0.53
1:C:636:SER:HA	1:C:639:GLU:HB3	1.90	0.53
1:A:354:MET:SD	1:A:388:LEU:HD13	2.48	0.53
1:A:1213:VAL:HG22	1:A:1248:GLN:HE21	1.72	0.53
1:A:1352:HIS:NE2	1:A:2250:GLU:HG3	2.24	0.53
1:A:2262:SER:HB3	1:A:2292:VAL:N	2.24	0.53
2:B:143:TRP:HE1	2:B:148:ASN:HA	1.74	0.53
2:B:258:PHE:CE1	2:B:279:LEU:HD13	2.43	0.53
1:C:173:LEU:HD21	1:C:209:ASP:OD1	2.09	0.53
1:C:284:ALA:HB3	1:C:331:VAL:HG11	1.91	0.53
1:C:333:ARG:NH1	1:C:354:THR:HB	2.24	0.53
1:C:1082:LEU:HA	1:C:1085:PRO:HG2	1.90	0.53
1:C:2304:GLU:O	1:C:2308:LEU:HD13	2.09	0.53
2:D:268:ALA:HB2	2:D:298:VAL:HG21	1.90	0.53
1:A:304:TRP:HB2	1:A:341:TYR:CE2	2.44	0.53
1:A:765:PRO:O	1:A:766:LYS:C	2.51	0.53
1:A:774:VAL:O	1:A:777:THR:OG1	2.22	0.53
1:A:920:VAL:HG12	1:A:923:ASN:HB2	1.91	0.53
1:A:1328:LYS:HB2	1:A:1329:PRO:HD3	1.91	0.53
1:A:1559:LYS:N	1:A:1572:ARG:NH2	2.57	0.53
1:A:2132:ARG:HB3	1:A:2366:ILE:HG21	1.91	0.53
1:C:236:GLU:HG2	1:C:279:ILE:HB	1.90	0.53
1:C:332:PHE:CE1	1:C:336:LEU:HD11	2.44	0.53
1:C:862:ARG:HG3	1:C:863:ARG:N	2.24	0.53
1:C:1510:ASN:HD21	4:G:73:PHE:HA	1.72	0.53
1:C:2081:PRO:HB2	1:C:2123:TYR:CE2	2.44	0.53
2:D:12:HIS:HB3	2:D:30:HIS:O	2.09	0.53
2:B:7:SER:HB2	2:B:274:VAL:HB	1.91	0.53
1:C:938:HIS:CE1	1:C:978:GLN:HA	2.44	0.53
1:C:1030:LYS:C	1:C:1032:LEU:H	2.17	0.53
1:C:1149:LEU:HD12	1:C:1194:ILE:HG21	1.91	0.53
1:C:1344:GLN:CD	1:C:1350:ALA:H	2.17	0.53
1:C:1504:ILE:HG12	1:C:1508:HIS:NE2	2.24	0.53
5:I:737:ASN:HB3	5:I:754:ASN:O	2.08	0.53
1:A:273:ASP:HA	1:A:276:LEU:HD11	1.89	0.52
1:A:853:LYS:HG3	1:A:1582:CYS:HB3	1.89	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1419:LYS:HG3	1:A:1433:LYS:HZ3	1.74	0.52
1:A:2121:TYR:HA	1:A:2122:LYS:CB	2.30	0.52
1:A:2347:ARG:HH22	1:A:2444:VAL:H	1.56	0.52
1:C:705:SER:HB2	1:C:710:TYR:HB3	1.91	0.52
1:C:857:ASN:CB	1:C:1586:LYS:HA	2.29	0.52
1:C:1021:ILE:HG21	1:C:1025:ILE:HB	1.89	0.52
4:G:75:GLY:HA3	4:G:106:GLY:HA2	1.91	0.52
1:A:590:GLU:C	1:A:594:LEU:H	2.16	0.52
1:A:2345:VAL:HA	1:A:2348:ASP:OD1	2.09	0.52
1:C:443:ARG:O	1:C:447:ARG:N	2.43	0.52
1:A:267:ILE:O	1:A:279:ARG:HD2	2.08	0.52
1:A:283:ALA:O	1:A:307:ARG:NH2	2.41	0.52
1:A:2155:PHE:HA	1:A:2158:HIS:HB2	1.91	0.52
2:B:154:LEU:HD23	2:B:197:LEU:HD12	1.91	0.52
1:C:265:LEU:HA	1:C:307:GLN:CB	2.19	0.52
1:C:1403:THR:HG23	1:C:1407:LYS:HE2	1.91	0.52
1:C:1505:LEU:HD22	1:C:1514:LYS:HE2	1.90	0.52
1:C:1816:LEU:N	1:C:1817:ILE:HA	2.23	0.52
1:C:2097:PHE:HB3	1:C:2115:ILE:HA	1.92	0.52
2:D:56:ARG:HD3	2:D:67:PRO:HD3	1.90	0.52
1:A:176:LEU:HA	1:A:179:LEU:HB2	1.90	0.52
1:A:565:ASP:O	1:A:570:GLN:N	2.42	0.52
1:A:1852:GLY:HA2	1:A:1891:VAL:HG21	1.91	0.52
1:C:842:TYR:O	1:C:844:GLU:N	2.42	0.52
1:C:2369:ASN:O	1:C:2418:ARG:NH2	2.43	0.52
2:D:44:LYS:HE2	2:D:61:ARG:NH2	2.24	0.52
3:F:353:UNK:C	3:F:354:UNK:H	2.22	0.52
4:H:141:ASN:O	4:H:176:LYS:N	2.43	0.52
5:J:703:ILE:HG21	5:J:732:ASP:CG	2.34	0.52
1:A:572:LEU:HA	1:A:575:CYS:HB2	1.92	0.52
1:A:963:ILE:HG23	1:A:964:PRO:HD3	1.90	0.52
1:A:1100:ILE:O	1:A:1141:MET:HE2	2.09	0.52
1:A:2061:LEU:H	1:A:2097:PRO:C	2.16	0.52
2:B:8:ALA:HB3	2:B:38:LEU:HD21	1.92	0.52
2:B:156:PRO:HA	2:B:186:TRP:HZ2	1.73	0.52
1:C:1050:ILE:HD12	1:C:1065:ILE:HG12	1.91	0.52
1:C:1144:THR:HG22	1:C:1178:ASP:HB2	1.92	0.52
1:A:436:LEU:HD22	1:A:474:PHE:HZ	1.74	0.52
2:B:55:VAL:HG22	2:B:57:LEU:HD21	1.90	0.52
1:C:573:LEU:HB3	1:C:577:PHE:HD2	1.74	0.52
1:C:1388:ILE:HA	1:C:1391:HIS:HB3	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2047:VAL:HA	1:C:2050:LYS:HD2	1.90	0.52
1:C:2084:ARG:HH22	1:C:2169:ILE:HG12	1.75	0.52
1:C:2280:ARG:HB3	1:C:2319:ARG:HH11	1.74	0.52
2:D:101:VAL:HG13	2:D:111:ARG:HB2	1.92	0.52
3:E:357:UNK:C	3:E:358:UNK:H	2.22	0.52
1:A:669:PRO:CG	1:A:719:LEU:HD21	2.39	0.52
1:A:1351:LEU:O	1:A:1355:GLU:HB2	2.10	0.52
1:A:1908:GLN:HB2	1:A:1939:HIS:NE2	2.25	0.52
1:A:1962:HIS:NE2	1:A:2005:GLU:O	2.37	0.52
1:C:231:SER:HA	1:C:234:LYS:HB3	1.90	0.52
1:C:490:CYS:HB3	1:C:491:PRO:CD	2.40	0.52
1:C:998:ARG:NE	1:C:1035:GLU:H	2.08	0.52
1:C:2194:HIS:CE1	1:C:2243:VAL:HB	2.45	0.52
2:D:71:PHE:HB3	2:D:90:MET:HE1	1.92	0.52
1:A:2049:ILE:O	1:A:2052:GLN:HB3	2.10	0.52
1:C:310:PHE:HA	1:C:317:LEU:HD11	1.92	0.52
1:C:855:THR:HA	1:C:1550:ILE:HG21	1.91	0.52
2:B:227:ALA:HA	2:B:252:TRP:HA	1.92	0.52
1:C:446:LEU:HA	1:C:449:LYS:HB2	1.91	0.52
1:C:450:PHE:CD1	1:C:456:PHE:HA	2.45	0.52
1:C:462:TYR:CD2	1:C:498:GLU:HB3	2.45	0.52
1:C:573:LEU:HB3	1:C:577:PHE:CD2	2.45	0.52
2:D:77:ASN:H	2:D:95:GLU:HB2	1.75	0.52
2:D:212:ARG:NH2	2:D:297:CYS:SG	2.83	0.52
2:D:233:VAL:HG12	2:D:244:THR:HB	1.91	0.52
1:A:290:LEU:HA	1:A:293:ILE:HB	1.92	0.52
1:A:1465:MET:HE1	1:A:1488:VAL:HB	1.91	0.52
1:A:1920:SER:HB3	1:A:2171:PRO:HD3	1.91	0.52
1:A:2275:LEU:HG	1:A:2299:ASP:C	2.35	0.52
1:C:90:ASP:HA	1:C:131:ASN:O	2.10	0.52
1:C:998:ARG:C	1:C:999:PRO:N	2.68	0.52
1:C:2063:LEU:HB3	1:C:2099:PRO:HA	1.90	0.52
1:C:2261:TYR:HA	1:C:2264:SER:HB2	1.91	0.52
1:A:409:ASN:HB2	1:A:452:ARG:HD2	1.90	0.51
1:A:1968:GLY:HA3	1:A:1992:LEU:HD21	1.92	0.51
1:A:2066:PRO:HA	1:A:2069:LEU:HB3	1.92	0.51
1:A:2078:VAL:HG12	1:A:2081:THR:HG22	1.92	0.51
2:B:229:HIS:HA	2:B:251:ARG:HB2	1.91	0.51
2:B:278:ASP:O	2:B:282:ARG:N	2.42	0.51
1:C:264:ILE:HG23	1:C:268:ILE:HD12	1.91	0.51
1:A:436:LEU:HD12	1:A:439:ASP:HB3	1.91	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:LEU:HD13	1:A:474:PHE:CE1	2.45	0.51
1:A:1134:ARG:HG3	1:A:1138:LYS:HB2	1.91	0.51
1:A:1592:ILE:HA	1:A:1595:VAL:HB	1.93	0.51
2:B:229:HIS:CD2	2:B:252:TRP:H	2.29	0.51
2:B:253:VAL:HA	2:B:268:ALA:O	2.10	0.51
1:C:180:LEU:HG	1:C:234:LYS:HD2	1.92	0.51
1:C:424:ALA:HB3	1:C:425:PHE:HB2	1.93	0.51
1:C:919:THR:HA	1:C:922:ILE:HB	1.91	0.51
1:C:1512:PHE:CZ	1:C:1516:GLU:HA	2.46	0.51
1:C:2100:VAL:O	1:C:2101:PHE:N	2.44	0.51
1:C:2187:PHE:N	1:C:2285:LEU:O	2.43	0.51
2:D:12:HIS:HE1	2:D:35:VAL:HB	1.75	0.51
1:A:220:TRP:HA	1:A:270:PRO:HG3	1.92	0.51
1:A:1045:PHE:CZ	1:A:1064:ILE:HA	2.33	0.51
1:A:1883:ARG:HG2	1:A:2364:PRO:HG2	1.91	0.51
1:A:2282:ASN:HA	1:A:2295:ILE:O	2.09	0.51
2:B:111:ARG:HH12	2:B:146:GLY:HA3	1.75	0.51
1:C:307:GLN:HA	1:C:310:PHE:HB3	1.91	0.51
1:C:382:ALA:C	1:C:386:LYS:HD3	2.35	0.51
1:C:983:PHE:HA	1:C:986:LEU:HD22	1.93	0.51
1:C:1261:SER:HG	1:C:1263:SER:N	2.08	0.51
1:C:1570:ARG:HA	1:C:1573:MET:HG2	1.92	0.51
1:C:2139:VAL:O	1:C:2142:LEU:N	2.43	0.51
1:C:2266:ALA:HB1	1:C:2343:ASN:HD21	1.76	0.51
4:H:120:ASP:CA	4:H:121:TYR:CB	2.85	0.51
1:A:324:VAL:HG22	1:A:327:THR:HG22	1.92	0.51
1:A:1368:GLU:HA	1:A:1371:ILE:HD12	1.92	0.51
1:A:1449:LEU:HB3	1:A:1452:GLU:HB2	1.93	0.51
1:A:2239:TYR:HA	1:A:2242:LEU:HD12	1.92	0.51
1:C:260:TYR:HA	1:C:287:LEU:HD11	1.92	0.51
1:C:569:ASP:HB3	1:C:570:ALA:N	2.25	0.51
1:C:992:ILE:HD12	1:C:994:LYS:HB3	1.91	0.51
1:C:1500:PHE:CD1	1:C:1551:ILE:HG23	2.46	0.51
1:C:1670:ALA:O	1:C:1674:LEU:N	2.43	0.51
1:C:1901:LEU:HA	1:C:1904:LEU:HB2	1.91	0.51
2:D:212:ARG:HE	2:D:255:ASP:HB3	1.75	0.51
1:A:138:HIS:NE2	1:A:178:VAL:CG1	2.73	0.51
1:A:1589:TRP:CD1	1:A:1590:GLN:H	2.28	0.51
1:A:1978:GLY:O	1:A:1979:GLU:HB2	2.10	0.51
1:A:2124:VAL:HG12	1:A:2178:TRP:HE3	1.75	0.51
1:C:446:LEU:HD12	1:C:449:LYS:HD2	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1100:LYS:O	1:C:1104:ILE:HG12	2.11	0.51
1:C:1429:VAL:HG23	1:C:1430:GLU:H	1.76	0.51
1:C:2128:LYS:HD3	1:C:2131:GLU:HG3	1.92	0.51
1:C:2355:LEU:HB3	1:C:2356:MET:HE2	1.91	0.51
1:C:2365:ASP:HB3	1:C:2369:ASN:O	2.10	0.51
1:C:2429:ILE:HD13	1:C:2435:GLY:N	2.25	0.51
5:J:736:PRO:HA	5:J:755:PHE:CD1	2.46	0.51
1:A:288:LYS:O	1:A:292:ILE:HG23	2.11	0.51
1:A:304:TRP:HE1	1:A:340:PRO:HG2	1.76	0.51
1:A:1010:PHE:CD1	1:A:1021:ILE:HG23	2.45	0.51
1:A:2411:HIS:O	1:A:2415:ILE:N	2.43	0.51
1:A:2430:LYS:HA	1:A:2450:LYS:HG3	1.93	0.51
2:B:37:ARG:HH21	2:B:80:SER:HA	1.76	0.51
1:C:1002:GLU:HG2	1:C:1042:GLU:HG3	1.93	0.51
1:C:1570:ARG:O	1:C:1574:ARG:HB2	2.10	0.51
3:E:454:UNK:HA	3:E:455:UNK:C	2.41	0.51
1:A:1065:LEU:HD13	1:A:1101:SER:HB3	1.93	0.51
1:C:314:THR:HA	1:C:317:LEU:HB2	1.93	0.51
1:C:1475:ALA:HB1	1:C:1484:ILE:HG13	1.93	0.51
1:C:1598:ARG:HA	1:C:1600:LEU:HG	1.92	0.51
1:C:2346:LYS:HG3	1:C:2350:ASP:OD2	2.10	0.51
1:A:722:LEU:CA	1:A:760:LEU:HD13	2.38	0.51
1:A:2044:ASN:HA	1:A:2047:ARG:HH11	1.76	0.51
1:A:2191:GLU:HA	1:A:2194:GLU:HB2	1.93	0.51
2:B:14:ILE:HD11	2:B:28:ILE:HD12	1.93	0.51
2:B:121:GLU:OE1	2:B:165:LEU:HB3	2.11	0.51
2:B:175:ALA:C	2:B:222:LEU:HD21	2.36	0.51
2:B:186:TRP:HB3	2:B:197:LEU:HB3	1.92	0.51
1:C:183:SER:HB3	1:C:230:SER:O	2.10	0.51
1:C:1547:ARG:HB3	1:C:1593:ARG:HH21	1.75	0.51
3:F:250:UNK:O	3:F:254:UNK:N	2.44	0.51
5:I:699:LYS:HZ1	5:I:702:THR:HG21	1.75	0.51
5:I:699:LYS:HB2	5:I:760:ARG:HB2	1.91	0.51
1:A:590:GLU:HB3	1:A:594:LEU:HB2	1.93	0.51
1:A:721:LEU:HD22	1:A:757:ASP:HB3	1.93	0.51
1:A:1524:LEU:HD11	1:A:1549:ILE:HB	1.91	0.51
1:A:2200:LEU:HG	1:A:2471:PHE:CZ	2.35	0.51
1:A:2211:ALA:HB1	1:A:2213:ASP:C	2.36	0.51
1:A:2239:TYR:O	1:A:2243:TRP:N	2.44	0.51
1:C:805:ILE:HG12	1:C:851:ASN:CG	2.36	0.51
1:C:1105:THR:OG1	1:C:1142:MET:HE1	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1518:HIS:HA	1:C:1521:ASN:HB2	1.93	0.51
1:C:1554:LEU:HA	1:C:1557:ILE:HG23	1.92	0.51
1:C:1909:PRO:HB2	1:C:1913:VAL:HB	1.92	0.51
1:C:2026:MET:HG3	1:C:2027:ASN:N	2.25	0.51
2:D:83:PHE:HE1	2:D:104:VAL:HG21	1.74	0.51
4:H:111:ALA:C	4:H:113:ILE:H	2.18	0.51
5:I:699:LYS:HD3	5:I:737:ASN:HD22	1.74	0.51
5:I:709:PHE:CE2	5:I:716:THR:HB	2.46	0.51
1:A:347:ASP:N	1:A:348:ASP:CB	2.74	0.51
1:A:361:PHE:HE1	1:A:414:PHE:CE1	2.29	0.51
1:A:1069:VAL:CG1	1:A:1105:LEU:HG	2.41	0.51
1:A:1453:LYS:HG2	1:A:1465:MET:HG2	1.93	0.51
1:A:1879:GLN:HG2	1:A:2132:ARG:HH21	1.76	0.51
1:C:1661:LEU:HD21	1:C:1669:GLU:HB3	1.91	0.51
1:C:1822:ILE:HG23	1:C:1826:LYS:HD2	1.92	0.51
2:D:90:MET:HB3	2:D:102:TRP:HB2	1.92	0.51
2:D:265:LEU:HA	2:D:279:LEU:HD12	1.92	0.51
5:I:664:PHE:HE1	5:I:691:ASN:HD22	1.57	0.51
1:A:120:GLU:HG2	1:A:123:GLN:HB3	1.93	0.50
1:A:341:TYR:CG	1:A:345:LYS:HG2	2.46	0.50
1:A:1008:ARG:HB2	1:A:1010:PHE:CE2	2.46	0.50
1:A:1127:ARG:HG2	1:A:1128:ILE:N	2.26	0.50
1:C:674:GLN:HG2	1:C:720:LEU:HD13	1.92	0.50
1:C:1386:ILE:HG12	1:C:1406:GLU:HB3	1.92	0.50
1:C:2346:LYS:O	1:C:2350:ASP:N	2.44	0.50
1:C:2446:VAL:HB	1:C:2447:PRO:HD3	1.92	0.50
1:A:1544:VAL:O	1:A:1548:ILE:HG13	2.11	0.50
2:B:132:ILE:HG21	2:B:174:LEU:HD11	1.93	0.50
1:C:1015:ILE:HD11	1:C:1067:LYS:HE2	1.93	0.50
1:C:1084:MET:SD	1:C:1084:MET:O	2.69	0.50
1:C:1429:VAL:HB	1:C:1435:LYS:HZ2	1.75	0.50
1:C:2112:LYS:HA	1:C:2126:VAL:HA	1.93	0.50
2:D:13:THR:HG21	2:D:292:HIS:H	1.75	0.50
2:D:44:LYS:HE2	2:D:61:ARG:HH22	1.75	0.50
5:J:661:TYR:CD2	5:J:697:VAL:HG11	2.47	0.50
5:J:730:VAL:HG21	5:J:790:PRO:CD	2.40	0.50
5:J:730:VAL:HB	5:J:788:GLU:O	2.12	0.50
1:A:256:LEU:HD22	1:A:259:TYR:CE2	2.47	0.50
1:A:272:ARG:N	1:A:322:ASP:OD1	2.45	0.50
1:A:673:GLN:OE1	1:A:719:LEU:HD22	2.12	0.50
1:A:1862:HIS:CD2	1:A:1898:LEU:HD23	2.46	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2192:HIS:CG	1:A:2237:ASP:HB3	2.46	0.50
1:A:2423:VAL:C	1:A:2426:ARG:HB3	2.36	0.50
1:C:362:PHE:CE1	1:C:393:MET:HE1	2.46	0.50
1:A:1013:ILE:HG23	1:A:1063:ARG:HE	1.76	0.50
1:A:2334:SER:HA	1:A:2337:ILE:HD12	1.92	0.50
2:B:121:GLU:HG3	2:B:165:LEU:N	2.26	0.50
1:C:502:ILE:HA	1:C:505:GLU:HG2	1.94	0.50
1:C:747:ASN:C	1:C:749:SER:H	2.20	0.50
1:C:1135:ARG:HB2	1:C:1136:GLU:HA	1.94	0.50
1:C:1900:LEU:O	1:C:1904:LEU:HG	2.11	0.50
1:A:86:LEU:HA	1:A:89:ASP:HB2	1.92	0.50
1:A:595:ILE:HG13	1:A:599:TYR:HD2	1.76	0.50
1:A:835:VAL:HG13	1:A:1525:VAL:CG1	2.42	0.50
1:A:2092:ILE:HG22	1:A:2114:LYS:O	2.11	0.50
1:A:2121:TYR:CA	1:A:2122:LYS:HB2	2.30	0.50
1:A:2268:MET:HG2	1:A:2342:VAL:HA	1.94	0.50
2:B:99:ILE:CD1	2:B:122:VAL:HG21	2.41	0.50
1:C:1059:ARG:HD2	1:C:1099:LYS:HB3	1.94	0.50
1:C:1483:GLU:HA	1:C:1486:GLN:HE22	1.77	0.50
1:C:1960:ALA:O	1:C:2111:ARG:NH1	2.45	0.50
1:A:81:PHE:HB3	1:A:107:SER:HA	1.92	0.50
1:A:256:LEU:HD22	1:A:259:TYR:HE2	1.77	0.50
1:A:1527:GLU:O	1:A:1528:LEU:N	2.44	0.50
1:A:1759:ASN:HA	1:A:1762:LEU:HD12	1.93	0.50
1:C:143:SER:CB	1:C:190:ARG:HE	2.25	0.50
1:C:1445:TRP:O	1:C:1448:LEU:N	2.44	0.50
1:C:2026:MET:CG	1:C:2027:ASN:H	2.24	0.50
1:C:2061:LEU:HG	1:C:2101:PHE:N	2.27	0.50
2:D:242:LEU:HD11	2:D:245:THR:HG23	1.94	0.50
5:I:709:PHE:HE2	5:I:716:THR:HB	1.77	0.50
1:A:263:ILE:HA	1:A:266:ASN:HB2	1.93	0.50
1:A:781:VAL:O	1:A:784:GLU:HB3	2.12	0.50
1:A:815:PHE:HB3	1:A:818:ASP:C	2.36	0.50
1:A:848:LEU:HD22	1:A:1547:GLN:HB3	1.94	0.50
1:A:1004:TYR:O	1:A:1007:ILE:N	2.44	0.50
1:C:166:LEU:HB3	1:C:167:PRO:HD3	1.94	0.50
1:C:710:TYR:N	1:C:714:SER:HG	2.10	0.50
1:C:757:ILE:O	1:C:761:LEU:HG	2.10	0.50
1:C:799:LYS:C	1:C:800:GLU:N	2.70	0.50
1:C:1285:TRP:O	1:C:1286:VAL:HB	2.11	0.50
1:C:1844:LEU:HD21	1:C:1878:VAL:HG21	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2153:ASP:HB2	1:C:2346:LYS:HG2	1.93	0.50
2:D:83:PHE:CD1	2:D:104:VAL:HG11	2.47	0.50
5:I:698:ARG:HB2	5:I:700:SER:H	1.77	0.50
5:I:730:VAL:CG2	5:I:789:THR:HA	2.41	0.50
1:A:2367:ASN:HB3	1:A:2371:ASP:HB2	1.93	0.50
2:B:274:VAL:HG12	2:B:291:HIS:HE1	1.75	0.50
1:C:458:LYS:HE3	1:C:461:PHE:HD2	1.77	0.50
1:C:982:TYR:HA	1:C:985:GLN:HB2	1.94	0.50
1:C:1127:VAL:HG23	1:C:1167:LEU:HD11	1.94	0.50
1:C:1487:TYR:HE2	1:C:1498:LYS:HE3	1.77	0.50
1:C:2284:ASN:HB3	1:C:2296:HIS:NE2	2.27	0.50
1:A:260:VAL:O	1:A:263:ILE:N	2.45	0.50
1:A:569:ALA:HA	1:A:591:PHE:CE1	2.47	0.50
2:B:26:ARG:HE	2:B:60:ILE:HD12	1.76	0.50
1:C:571:GLN:O	1:C:575:GLN:N	2.44	0.50
1:A:1245:LEU:HA	1:A:1275:LEU:HD23	1.94	0.49
2:B:7:SER:CB	2:B:274:VAL:HB	2.42	0.49
2:B:182:ASN:CG	2:B:204:ARG:HE	2.20	0.49
1:C:595:LEU:HA	1:C:598:ILE:HB	1.94	0.49
1:C:998:ARG:HE	1:C:1035:GLU:H	1.60	0.49
1:C:1712:THR:HA	1:C:1715:LEU:HG	1.94	0.49
1:C:2288:ASP:OD2	1:C:2293:LYS:HG3	2.12	0.49
2:D:229:HIS:HD2	2:D:252:TRP:H	1.60	0.49
1:A:971:ARG:HD3	1:A:977:GLN:HE21	1.77	0.49
1:A:1606:ALA:O	1:A:1610:ILE:N	2.44	0.49
1:C:822:LEU:HA	1:C:825:LEU:HB2	1.94	0.49
2:D:121:GLU:HG3	2:D:165:LEU:H	1.77	0.49
2:D:125:HIS:HB3	2:D:130:GLU:HB2	1.94	0.49
3:F:704:UNK:O	3:F:708:UNK:N	2.45	0.49
5:I:650:ARG:HG3	5:I:651:THR:HG23	1.93	0.49
1:A:633:LEU:HB3	1:A:674:PRO:HG2	1.94	0.49
1:A:1976:PHE:HB2	1:A:1985:MET:HB2	1.93	0.49
2:B:57:LEU:HD12	2:B:69:ALA:HB3	1.94	0.49
1:C:157:ILE:HG12	1:C:172:ARG:NH2	2.25	0.49
1:C:926:MET:HE1	1:C:944:ALA:HA	1.94	0.49
1:C:1839:SER:OG	1:C:1841:GLN:HB3	2.12	0.49
1:C:2352:LYS:HD3	1:C:2356:MET:HE3	1.93	0.49
1:A:363:VAL:HA	1:A:366:ARG:HG3	1.94	0.49
1:A:438:LEU:O	1:A:442:ARG:N	2.45	0.49
1:A:633:LEU:HD21	1:A:665:SER:HA	1.94	0.49
1:A:849:ILE:HG21	1:A:1548:ILE:HG23	1.95	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1660:TRP:HZ3	1:A:1724:ARG:CZ	2.25	0.49
1:A:1811:SER:HB2	1:A:1843:ARG:HH22	1.78	0.49
2:B:16:PHE:HB2	2:B:26:ARG:HB3	1.95	0.49
1:C:1425:GLY:HA2	1:C:1429:VAL:HG13	1.94	0.49
1:C:1531:SER:C	1:C:1532:ALA:HA	2.37	0.49
1:C:2339:ILE:HA	1:C:2342:GLU:CG	2.41	0.49
2:D:37:ARG:NH2	2:D:212:ARG:HH22	2.10	0.49
2:D:65:PRO:HB2	2:D:66:ASN:C	2.37	0.49
2:D:183:CYS:SG	2:D:222:LEU:HD21	2.52	0.49
5:J:789:THR:O	5:J:791:LEU:N	2.45	0.49
1:A:180:ILE:O	1:A:230:SER:OG	2.30	0.49
1:A:954:ARG:H	1:A:955:CYS:N	2.11	0.49
1:A:2390:ALA:HB3	1:A:2391:ASN:HB2	1.94	0.49
2:B:12:HIS:CB	2:B:30:HIS:O	2.61	0.49
1:C:173:LEU:CD2	1:C:209:ASP:HA	2.42	0.49
1:C:366:ARG:HA	1:C:369:VAL:CG2	2.43	0.49
1:C:1118:MET:HG3	1:C:1121:ARG:CG	2.42	0.49
1:C:2409:VAL:HA	1:C:2410:GLU:C	2.37	0.49
1:A:636:VAL:CG1	1:A:675:ASP:HB3	2.34	0.49
1:C:281:LEU:HD11	1:C:330:LEU:HB3	1.95	0.49
1:C:690:PHE:HD1	1:C:728:PHE:HZ	1.60	0.49
1:C:1578:ASN:C	1:C:1581:LEU:HG	2.36	0.49
1:C:1732:LYS:HA	1:C:1737:ASN:HB2	1.94	0.49
2:D:101:VAL:HG11	2:D:143:TRP:HH2	1.74	0.49
1:A:649:THR:HB	1:A:650:ASP:HB2	1.95	0.49
1:A:1608:VAL:HA	1:A:1611:LYS:HB2	1.94	0.49
1:A:2286:ASP:HB2	1:A:2291:LYS:H	1.77	0.49
1:C:537:TYR:HB2	1:C:543:PHE:CE2	2.48	0.49
1:C:626:CYS:HB2	1:C:629:THR:HG22	1.93	0.49
1:C:826:GLY:HA3	1:C:827:GLN:HG2	1.93	0.49
1:C:939:THR:HG21	1:C:1262:CYS:SG	2.53	0.49
1:C:1429:VAL:HB	1:C:1435:LYS:NZ	2.27	0.49
1:C:2046:ASN:HA	1:C:2049:ARG:HH11	1.78	0.49
1:A:534:ASN:C	1:A:535:GLN:N	2.71	0.49
1:A:704:SER:HB2	1:A:709:TYR:CB	2.33	0.49
1:A:933:LEU:HD13	1:A:939:ALA:HB2	1.93	0.49
1:A:1120:ARG:HA	1:A:1123:GLN:HG2	1.95	0.49
1:A:1155:PHE:CE2	1:C:622:LYS:HB3	2.47	0.49
1:A:1383:ALA:HA	1:A:1386:ILE:HG22	1.95	0.49
1:A:2126:LYS:HD2	1:A:2176:LEU:HG	1.95	0.49
1:A:2354:MET:SD	1:A:2427:ILE:HG21	2.53	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:244:THR:HG22	2:B:245:THR:O	2.13	0.49
1:C:543:PHE:CD1	1:C:545:ILE:HG23	2.47	0.49
1:C:573:LEU:HD13	1:C:577:PHE:HE2	1.76	0.49
1:C:1887:HIS:HB2	1:C:1927:ARG:HG2	1.95	0.49
2:D:205:ALA:O	2:D:224:THR:HG21	2.12	0.49
5:J:680:ILE:C	5:J:682:ILE:H	2.21	0.49
1:A:412:LYS:HZ1	1:A:442:ARG:HD3	1.77	0.49
1:A:1341:ALA:H	1:A:1342:GLN:HB3	1.77	0.49
1:A:2043:TYR:HE1	5:I:660:GLU:HG3	1.78	0.49
1:A:2116:SER:C	1:A:2117:ASP:HA	2.37	0.49
2:B:26:ARG:NH2	2:B:47:LEU:HD21	2.28	0.49
1:C:1061:VAL:N	1:C:1062:PRO:HD3	2.27	0.49
1:C:1295:ASP:CG	1:C:1342:TYR:HH	2.18	0.49
1:A:232:SER:HB2	1:A:236:TYR:CE2	2.48	0.49
1:A:1177:ASP:O	1:A:1181:ASN:N	2.46	0.49
1:A:1729:PRO:HD2	1:A:1730:LYS:HD2	1.95	0.49
1:A:2111:PHE:HD1	1:A:2112:CYS:CA	2.25	0.49
1:C:424:ALA:N	1:C:425:PHE:HB2	2.28	0.49
1:C:1760:HIS:CD2	1:C:1832:ILE:HG13	2.48	0.49
1:C:2309:ARG:C	1:C:2380:GLU:OE2	2.55	0.49
1:A:642:LYS:HE2	1:A:646:ILE:HG12	1.94	0.48
1:A:690:GLY:HA2	1:A:693:LEU:H	1.77	0.48
1:A:792:GLU:HB3	1:A:795:ARG:H	1.78	0.48
1:A:964:PRO:HB3	1:A:967:ILE:HB	1.95	0.48
1:A:1458:LYS:HB3	1:A:1459:PRO:CD	2.42	0.48
2:B:40:ILE:HG21	2:B:44:LYS:HA	1.94	0.48
2:B:78:VAL:HA	2:B:94:SER:HA	1.94	0.48
1:C:439:LEU:HA	1:C:442:ILE:HG12	1.95	0.48
1:C:678:LEU:HD23	1:C:727:LYS:HB3	1.94	0.48
1:C:700:ILE:HG13	1:C:721:GLU:CD	2.38	0.48
1:C:1763:ALA:HB2	1:C:1828:PHE:HB3	1.94	0.48
1:C:1826:LYS:HB2	1:C:1863:MET:SD	2.53	0.48
2:D:12:HIS:NE2	2:D:34:GLN:HG3	2.28	0.48
5:I:698:ARG:HA	5:I:759:ASP:HA	1.93	0.48
5:J:730:VAL:HG21	5:J:789:THR:CA	2.41	0.48
1:A:817:ARG:HD2	1:A:867:LEU:CD1	2.43	0.48
1:A:1440:LEU:HB3	1:A:1622:MET:SD	2.53	0.48
1:A:1755:LYS:C	1:A:1758:HIS:HB3	2.38	0.48
1:C:91:LYS:HD3	1:C:134:ILE:HG21	1.95	0.48
1:C:285:VAL:HA	1:C:335:LEU:HD13	1.95	0.48
1:C:1515:ALA:O	1:C:1518:HIS:N	2.47	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2157:PHE:HD1	1:C:2160:HIS:CD2	2.30	0.48
1:C:2227:VAL:C	1:C:2228:PHE:N	2.71	0.48
2:D:131:LEU:O	2:D:143:TRP:N	2.46	0.48
2:D:297:CYS:HA	2:D:298:VAL:CB	2.18	0.48
4:G:132:GLY:O	4:G:134:ASP:N	2.46	0.48
1:A:90:LYS:HB3	1:A:133:ILE:HG21	1.95	0.48
1:A:1245:LEU:HD12	1:A:1275:LEU:HD23	1.94	0.48
1:A:1724:ARG:HG3	1:A:1725:VAL:HG13	1.96	0.48
1:C:332:PHE:C	1:C:333:ARG:HA	2.38	0.48
1:C:842:TYR:CB	1:C:844:GLU:HG2	2.30	0.48
1:C:969:LEU:HD13	1:C:985:GLN:HB3	1.95	0.48
1:C:1088:VAL:HG22	1:C:1103:ILE:HG21	1.94	0.48
1:C:1356:LYS:HD2	1:C:1375:ILE:HD13	1.96	0.48
1:C:2444:LEU:HD13	1:C:2452:LYS:HE3	1.96	0.48
1:A:215:ARG:O	1:A:219:ASP:HB2	2.14	0.48
1:A:335:LEU:HD13	1:A:341:TYR:HB3	1.94	0.48
1:A:546:LYS:O	1:A:550:SER:N	2.45	0.48
1:A:1069:VAL:HG13	1:A:1105:LEU:HG	1.95	0.48
1:A:1130:ASN:HB3	1:A:1166:LEU:HB3	1.96	0.48
1:A:2305:ILE:HB	1:A:2375:LYS:HD3	1.94	0.48
2:B:18:GLU:HG2	2:B:25:SER:HB2	1.95	0.48
1:C:818:ARG:HB2	1:C:818:ARG:HH11	1.77	0.48
1:C:1069:LEU:HD22	1:C:1106:LEU:O	2.13	0.48
1:C:1273:ALA:HB3	1:C:1324:PHE:CE1	2.48	0.48
3:F:507:UNK:C	3:F:508:UNK:CA	2.88	0.48
1:A:1164:LYS:HB3	1:A:1170:ARG:HG3	1.95	0.48
1:A:1946:GLN:C	1:A:1949:LEU:HB2	2.38	0.48
1:A:2147:LEU:HD22	1:A:2353:LEU:HD13	1.96	0.48
1:C:581:GLN:HG3	1:C:589:LEU:HD22	1.95	0.48
1:C:1668:ASP:HA	1:C:1671:LEU:HD12	1.94	0.48
1:C:1902:SER:HB3	1:C:1934:ILE:HD12	1.96	0.48
2:D:39:GLU:HA	2:D:299:ALA:HB2	1.96	0.48
2:D:210:ILE:HD11	2:D:224:THR:HA	1.95	0.48
1:A:698:ILE:HG23	1:C:1079:TYR:HE2	1.73	0.48
1:A:1548:ILE:HG22	1:A:1552:LEU:HD22	1.96	0.48
1:A:1994:GLU:O	1:A:1997:LYS:HB2	2.12	0.48
1:A:2133:GLN:HG3	1:A:2370:PHE:CZ	2.49	0.48
1:C:377:ALA:HB1	1:C:382:ALA:HB1	1.95	0.48
1:C:1084:MET:HE2	1:C:1103:ILE:HG23	1.95	0.48
1:C:1460:LYS:HB2	1:C:1461:PRO:HD2	1.95	0.48
1:C:1557:ILE:HG22	1:C:1577:TRP:HE1	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1578:ASN:HA	1:C:1581:LEU:HG	1.95	0.48
1:C:2279:ASP:HA	1:C:2309:ARG:HH22	1.79	0.48
2:D:37:ARG:HG3	2:D:81:VAL:N	2.29	0.48
5:J:693:PHE:CZ	5:J:760:ARG:HD3	2.48	0.48
1:A:594:LEU:O	1:A:595:ILE:HD12	2.14	0.48
1:A:1966:TYR:HB2	1:A:2049:ILE:HD12	1.95	0.48
1:A:2459:GLU:HA	1:A:2462:CYS:HB3	1.94	0.48
1:C:533:GLN:C	1:C:535:ASN:N	2.68	0.48
1:C:601:ILE:HA	1:C:602:GLU:HA	1.72	0.48
1:C:915:GLU:HB3	1:C:917:TYR:HB2	1.94	0.48
1:C:1244:ARG:HG3	1:C:1269:TYR:HH	1.79	0.48
1:C:1244:ARG:HG3	1:C:1269:TYR:OH	2.14	0.48
1:C:2062:GLU:CG	1:C:2099:PRO:HB2	2.44	0.48
5:J:698:ARG:HB2	5:J:700:SER:H	1.78	0.48
1:A:280:LEU:HD11	1:A:333:GLU:OE1	2.14	0.48
1:A:412:LYS:HZ1	1:A:445:LEU:HD22	1.78	0.48
1:A:731:PRO:HB3	1:A:736:GLU:HB2	1.95	0.48
1:A:1814:LEU:HB2	1:A:1816:HIS:CD2	2.48	0.48
2:B:6:VAL:HG22	2:B:38:LEU:HD22	1.94	0.48
2:B:185:VAL:C	2:B:200:VAL:H	2.21	0.48
1:C:280:ARG:NH1	1:C:328:THR:HB	2.27	0.48
1:C:640:VAL:HG13	1:C:643:LYS:HB3	1.96	0.48
1:C:857:ASN:CG	1:C:1586:LYS:HG2	2.39	0.48
1:C:1121:ARG:HA	1:C:1124:GLN:HG2	1.95	0.48
1:C:1623:ARG:CZ	1:C:1663:ALA:HB1	2.44	0.48
1:C:1826:LYS:HE3	1:C:1863:MET:HB2	1.95	0.48
2:D:275:ARG:HD3	2:D:284:ILE:HG12	1.95	0.48
3:F:556:UNK:O	3:F:559:UNK:N	2.47	0.48
1:A:468:CYS:SG	1:A:469:ALA:N	2.87	0.48
1:A:619:PHE:HA	1:A:622:ASP:HB3	1.94	0.48
1:A:1060:VAL:N	1:A:1061:PRO:HD2	2.29	0.48
1:A:1434:LEU:HD13	1:A:1468:LEU:HD21	1.95	0.48
1:C:508:PRO:HG3	4:G:188:PHE:HA	1.94	0.48
1:C:631:VAL:HA	1:C:634:LEU:HB2	1.95	0.48
1:C:849:LEU:HD21	1:C:1546:VAL:HB	1.96	0.48
1:C:1014:ILE:HD11	1:C:1022:ILE:HD12	1.96	0.48
1:C:1195:ILE:O	1:C:1195:ILE:HG22	2.14	0.48
1:C:2138:LEU:HD11	1:C:2362:PHE:CZ	2.49	0.48
5:J:707:ILE:HD13	5:J:728:LEU:HD22	1.95	0.48
1:A:323:SER:HB2	1:A:325:HIS:CD2	2.49	0.48
1:A:754:PRO:C	1:A:755:TYR:HA	2.39	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1489:MET:SD	1:A:1490:LYS:HG2	2.54	0.48
1:A:1556:ILE:O	1:A:1559:LYS:N	2.46	0.48
1:A:1823:ILE:HG23	1:A:1824:LYS:H	1.79	0.48
1:C:705:SER:HA	1:C:706:VAL:C	2.38	0.48
1:C:1050:ILE:CD1	1:C:1065:ILE:HG12	2.43	0.48
1:C:1178:ASP:C	1:C:1182:ASN:H	2.22	0.48
1:C:1496:PRO:HA	1:C:1525:LEU:HD22	1.95	0.48
1:C:1591:TRP:HB3	1:C:1614:PHE:HZ	1.79	0.48
1:C:1612:ILE:HG21	1:C:1656:ALA:CB	2.43	0.48
1:C:1745:TYR:O	1:C:1762:TRP:NE1	2.47	0.48
1:C:1866:GLY:HA2	1:C:1869:LEU:HG	1.95	0.48
1:C:1918:VAL:HG22	1:C:2170:PRO:O	2.14	0.48
1:C:2062:GLU:CD	1:C:2064:GLN:HG2	2.39	0.48
3:F:554:UNK:C	3:F:556:UNK:N	2.73	0.48
1:A:284:VAL:HG13	1:A:334:LEU:HD21	1.96	0.47
1:A:367:GLU:HA	1:A:370:ALA:CB	2.43	0.47
1:A:1440:LEU:HD13	1:A:1622:MET:CE	2.44	0.47
1:A:1922:SER:HB2	1:A:1926:GLN:HB3	1.96	0.47
1:C:2255:LEU:HG	1:C:2259:THR:HB	1.96	0.47
5:I:699:LYS:NZ	5:I:702:THR:HG21	2.29	0.47
1:A:461:TYR:CD2	1:A:497:GLU:HB3	2.48	0.47
1:A:1736:PRO:HA	1:A:1739:ILE:HB	1.95	0.47
1:A:1972:ALA:HB1	1:A:1988:ALA:CB	2.44	0.47
1:A:2265:VAL:HG23	1:A:2266:MET:H	1.78	0.47
2:B:9:GLY:O	2:B:12:HIS:CE1	2.67	0.47
1:C:401:LYS:O	1:C:414:PRO:HG3	2.14	0.47
1:C:414:PRO:C	1:C:417:LEU:HB3	2.39	0.47
1:C:454:LYS:C	1:C:455:GLN:HA	2.38	0.47
1:C:948:ILE:HA	1:C:952:LEU:HB2	1.95	0.47
1:C:1244:ARG:NH2	1:C:1260:ARG:HD3	2.29	0.47
1:C:1626:LEU:O	1:C:1630:VAL:HG22	2.13	0.47
1:C:2279:ASP:HB3	1:C:2284:ASN:ND2	2.29	0.47
1:C:2421:ARG:HA	1:C:2424:LEU:HB3	1.94	0.47
3:E:602:UNK:O	3:E:606:UNK:N	2.47	0.47
1:A:453:LYS:H	1:A:454:GLN:HA	1.76	0.47
1:A:1339:LYS:C	1:A:1343:LYS:HG2	2.38	0.47
1:A:1558:TYR:HB2	1:A:1572:ARG:HE	1.80	0.47
1:A:1601:LYS:O	1:A:1603:LYS:N	2.46	0.47
2:B:68:VAL:HG12	2:B:69:ALA:N	2.29	0.47
1:C:347:TYR:O	1:C:351:TYR:HB3	2.15	0.47
1:C:1448:LEU:HD23	1:C:1451:LEU:HD13	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2194:HIS:O	1:C:2198:LYS:HD3	2.14	0.47
1:C:2432:LYS:O	1:C:2449:GLN:HG2	2.14	0.47
2:D:10:TYR:O	2:D:12:HIS:CD2	2.67	0.47
1:A:89:ASP:HB3	1:A:90:LYS:H	1.29	0.47
1:A:357:LYS:HZ3	1:A:366:ARG:HA	1.80	0.47
1:A:759:ILE:O	1:A:763:ILE:N	2.47	0.47
1:A:862:ARG:HB3	1:A:2156:ARG:HA	1.96	0.47
1:A:1449:LEU:O	1:A:1453:LYS:N	2.32	0.47
1:A:2107:ARG:N	1:A:2108:PRO:CD	2.77	0.47
1:C:368:GLU:HA	1:C:371:ALA:HB2	1.96	0.47
1:C:661:LEU:C	1:C:664:LEU:HB3	2.39	0.47
1:C:814:ASN:C	1:C:818:ARG:HG3	2.39	0.47
1:C:1574:ARG:C	1:C:1575:GLU:N	2.73	0.47
1:C:2337:PHE:O	1:C:2341:CYS:N	2.47	0.47
2:D:40:ILE:HD13	2:D:301:ASN:HB2	1.95	0.47
2:D:84:GLN:CB	2:D:89:TRP:HB2	2.33	0.47
2:D:246:LEU:HD22	2:D:277:TRP:CZ3	2.49	0.47
3:E:756:UNK:HA	3:E:759:UNK:H2	1.79	0.47
1:A:272:ARG:HG2	1:A:273:ASP:H	1.79	0.47
1:A:400:LYS:HG3	1:A:402:ILE:HG12	1.95	0.47
1:A:673:GLN:HA	1:A:676:ASN:HD21	1.76	0.47
1:A:710:VAL:HG12	1:A:711:VAL:HA	1.96	0.47
1:A:1027:ILE:HB	1:A:1070:THR:HB	1.96	0.47
1:A:2075:GLU:O	1:A:2091:LYS:HA	2.15	0.47
1:C:235:LEU:CB	1:C:236:GLU:HA	2.44	0.47
1:C:260:TYR:HD2	1:C:260:TYR:N	2.12	0.47
1:C:301:LEU:HG	1:C:340:ALA:HA	1.96	0.47
1:C:506:LYS:HD3	1:C:508:PRO:O	2.14	0.47
1:C:690:PHE:CE1	1:C:731:MET:HB3	2.50	0.47
1:C:793:GLU:HG2	1:C:796:ARG:HG3	1.97	0.47
5:I:698:ARG:HG3	5:I:788:GLU:HG2	1.95	0.47
1:A:180:ILE:HG22	1:A:223:LEU:HD13	1.93	0.47
1:A:461:TYR:C	1:A:462:CYS:N	2.72	0.47
1:A:937:HIS:HE1	1:A:977:GLN:HA	1.79	0.47
1:A:1073:PRO:HB3	1:A:1110:LYS:H	1.79	0.47
1:A:1427:VAL:O	1:A:1433:LYS:HE2	2.13	0.47
1:A:2082:ARG:HH12	1:A:2167:ILE:HD13	1.79	0.47
1:A:2189:ILE:O	1:A:2193:ARG:HG3	2.15	0.47
1:C:634:LEU:HA	1:C:637:VAL:HB	1.96	0.47
1:C:651:ASP:CB	1:C:652:PRO:HA	2.44	0.47
1:C:1655:TYR:HA	1:C:1658:LEU:HB2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:11:ASP:HB3	2:D:293:LYS:H	1.80	0.47
2:D:213:ILE:HG22	2:D:224:THR:HG23	1.97	0.47
5:I:693:PHE:O	5:I:694:THR:N	2.48	0.47
1:A:115:ARG:HB2	1:A:159:TYR:HB3	1.97	0.47
1:A:125:PHE:O	1:A:129:LEU:HB3	2.14	0.47
1:A:259:TYR:HB3	1:A:293:ILE:HD13	1.95	0.47
1:A:300:LEU:HD22	1:A:303:GLN:HG3	1.95	0.47
1:A:796:TYR:HE2	1:A:843:GLU:HB3	1.79	0.47
1:A:841:TYR:O	1:A:843:GLU:N	2.47	0.47
1:A:848:LEU:H	1:A:1547:GLN:NE2	2.13	0.47
1:A:1516:HIS:O	1:A:1520:ALA:N	2.47	0.47
1:A:1613:ALA:O	1:A:1617:ARG:HG2	2.13	0.47
1:A:1870:ILE:HG12	1:A:1902:LEU:HA	1.96	0.47
1:A:2245:LYS:HE3	1:A:2287:ARG:HH11	1.78	0.47
1:A:2266:MET:HE1	1:A:2294:HIS:HB2	1.97	0.47
1:A:2405:GLN:C	1:A:2407:VAL:H	2.22	0.47
1:A:2449:ASP:O	1:A:2453:GLN:HB2	2.15	0.47
2:B:91:VAL:HB	2:B:145:LEU:HD21	1.97	0.47
1:C:112:THR:O	1:C:114:LEU:HG	2.15	0.47
1:C:157:ILE:O	1:C:163:THR:HG21	2.15	0.47
1:C:260:TYR:N	1:C:260:TYR:CD2	2.80	0.47
1:C:500:LEU:HD12	1:C:503:LEU:HD12	1.96	0.47
1:C:573:LEU:O	1:C:577:PHE:HB2	2.14	0.47
1:C:620:PHE:HD1	1:C:623:ASP:HB3	1.78	0.47
1:C:688:GLU:C	1:C:690:PHE:N	2.72	0.47
1:C:712:VAL:HB	1:C:713:PRO:CD	2.45	0.47
1:C:926:MET:HA	1:C:929:LEU:HD23	1.95	0.47
1:C:1541:ALA:HB1	1:C:1542:TYR:HA	1.97	0.47
1:C:1561:LYS:HA	1:C:1570:ARG:HH21	1.78	0.47
1:C:1893:VAL:O	1:C:1896:SER:HB2	2.15	0.47
1:C:1916:LEU:HA	1:C:1919:ALA:HB2	1.96	0.47
2:D:83:PHE:HD1	2:D:104:VAL:HG11	1.78	0.47
2:D:173:MET:HB3	2:D:174:LEU:CA	2.44	0.47
1:A:324:VAL:HA	1:A:325:HIS:N	2.30	0.47
1:A:2220:LEU:HD13	2:B:209:TYR:HD2	1.79	0.47
2:B:7:SER:OG	2:B:274:VAL:HB	2.14	0.47
2:B:233:VAL:HG11	2:B:279:LEU:HD21	1.97	0.47
1:C:818:ARG:O	1:C:822:LEU:HB3	2.15	0.47
1:C:1239:TRP:O	1:C:1243:ILE:HG12	2.15	0.47
2:D:4:ILE:O	2:D:5:LEU:HB3	2.14	0.47
5:J:681:TYR:O	5:J:681:TYR:CD1	2.68	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:GLU:CD	1:A:275:LYS:HB2	2.39	0.47
1:A:259:TYR:HB2	1:A:290:LEU:CD1	2.45	0.47
1:A:377:ALA:HA	1:A:385:LYS:HZ2	1.78	0.47
1:A:1126:VAL:HG23	1:A:1166:LEU:HD11	1.97	0.47
1:A:2113:ILE:HG13	1:A:2123:TYR:CE2	2.49	0.47
1:A:2151:ASP:C	1:A:2155:PHE:HB2	2.40	0.47
1:C:260:TYR:HE1	1:C:300:ALA:CB	2.27	0.47
1:C:410:ASN:O	1:C:450:PHE:HD2	1.97	0.47
1:C:417:LEU:HD13	1:C:460:LEU:HD11	1.97	0.47
1:C:1513:LYS:HA	1:C:1516:GLU:HB3	1.97	0.47
1:C:1587:ASN:O	1:C:1590:VAL:HG23	2.14	0.47
1:C:2432:LYS:HD3	1:C:2437:ASP:HB2	1.97	0.47
2:D:221:HIS:HB3	2:D:233:VAL:HG22	1.97	0.47
4:G:136:TRP:HA	4:G:137:VAL:O	2.15	0.47
5:I:737:ASN:OD1	5:I:768:SER:HB2	2.15	0.47
1:A:328:LEU:O	1:A:368:VAL:HG13	2.15	0.47
1:A:398:TYR:CG	1:A:441:ILE:HB	2.50	0.47
1:A:556:MET:HA	1:A:590:GLU:CD	2.40	0.47
1:A:620:ILE:HA	1:A:660:LEU:HD21	1.97	0.47
1:A:946:HIS:C	1:A:947:ILE:N	2.73	0.47
1:A:947:ILE:HA	1:A:951:LEU:HD13	1.96	0.47
1:A:1087:VAL:HA	1:A:1099:LYS:HD2	1.97	0.47
1:A:1227:TRP:CH2	1:A:1238:TRP:HE3	2.33	0.47
1:C:721:GLU:CB	1:C:722:LEU:HB2	2.40	0.47
1:C:836:VAL:CG2	1:C:845:LEU:HD12	2.45	0.47
1:C:1070:VAL:CG2	1:C:1106:LEU:HG	2.45	0.47
1:C:1521:ASN:HB3	1:C:1525:LEU:HD21	1.95	0.47
1:C:1636:GLU:HG2	1:C:1653:VAL:HG21	1.96	0.47
1:A:145:LYS:HD3	1:A:186:GLU:HG3	1.97	0.46
1:A:357:LYS:HZ2	1:A:414:PHE:HD1	1.61	0.46
1:A:399:LEU:HB3	1:A:405:ASN:O	2.15	0.46
1:A:759:ILE:HG21	1:A:798:LYS:C	2.40	0.46
1:A:1555:ILE:HG21	1:A:1575:TRP:NE1	2.30	0.46
1:A:2304:ALA:C	1:A:2306:LEU:H	2.22	0.46
2:B:221:HIS:CE1	2:B:279:LEU:HD22	2.49	0.46
1:C:216:ARG:HD2	1:C:234:LYS:HZ1	1.79	0.46
1:C:1757:LYS:HD2	1:C:1832:ILE:HG21	1.97	0.46
1:A:676:ASN:HB3	1:A:723:THR:HA	1.96	0.46
1:A:788:VAL:HB	1:A:795:ARG:HH11	1.80	0.46
1:A:1820:ILE:HG23	1:A:1824:LYS:HG2	1.97	0.46
1:A:1877:LEU:HD23	1:A:1913:PRO:HD2	1.96	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2424:LEU:C	1:A:2427:ILE:H	2.23	0.46
2:B:40:ILE:HG23	2:B:47:LEU:HD23	1.96	0.46
2:B:105:ARG:O	2:B:106:SER:CB	2.62	0.46
2:B:168:ALA:HB3	2:B:171:GLY:H	1.80	0.46
1:C:1044:LEU:O	1:C:1048:LEU:HB2	2.15	0.46
1:C:2112:LYS:C	1:C:2113:PHE:N	2.73	0.46
1:C:2192:ARG:O	1:C:2196:GLU:N	2.46	0.46
5:I:647:LYS:HZ3	5:I:649:LYS:HZ3	1.62	0.46
1:A:91:LEU:HD13	1:A:144:GLU:HG3	1.97	0.46
1:A:698:ILE:O	1:C:1079:TYR:HE2	1.98	0.46
1:A:843:GLU:C	1:A:845:LEU:H	2.23	0.46
1:A:1504:CYS:SG	1:A:1510:PHE:HA	2.55	0.46
1:A:2182:SER:HA	1:A:2287:ARG:H	1.81	0.46
2:B:91:VAL:HG11	2:B:131:LEU:HD13	1.97	0.46
2:B:233:VAL:HG21	2:B:279:LEU:HG	1.96	0.46
1:C:269:TRP:HB2	1:C:310:PHE:HE2	1.80	0.46
1:C:601:ILE:HA	1:C:603:HIS:HB2	1.98	0.46
1:C:703:LEU:HD13	1:C:714:SER:HB3	1.96	0.46
1:C:1369:ILE:HA	1:C:1372:LEU:HD23	1.97	0.46
1:C:1432:MET:O	1:C:1435:LYS:HG3	2.14	0.46
1:C:1609:GLN:C	1:C:1611:ARG:O	2.59	0.46
1:C:1627:ALA:O	1:C:1631:LEU:HG	2.16	0.46
1:C:2133:ILE:CD1	1:C:2176:GLY:HA3	2.45	0.46
1:C:2194:HIS:CE1	1:C:2239:ASP:HB3	2.51	0.46
1:A:301:GLY:HA2	1:A:304:TRP:NE1	2.31	0.46
1:A:644:LEU:HA	1:A:647:ALA:HB3	1.98	0.46
1:A:689:PHE:CZ	1:A:732:LYS:HD3	2.51	0.46
1:A:1555:ILE:HG13	1:A:1556:ILE:HG13	1.98	0.46
1:A:1730:LYS:HB3	1:A:1735:ASN:CB	2.41	0.46
1:C:1601:VAL:O	1:C:1602:ILE:HB	2.14	0.46
1:C:2253:THR:HG22	1:C:2257:ARG:HD2	1.97	0.46
2:D:6:VAL:HG13	2:D:7:SER:HB3	1.97	0.46
1:A:328:LEU:HB3	1:A:368:VAL:HG13	1.98	0.46
1:A:1351:LEU:HD22	1:A:1377:LEU:HD22	1.97	0.46
2:B:60:ILE:O	2:B:60:ILE:HG13	2.15	0.46
1:C:1445:TRP:HB2	1:C:1478:LEU:HB3	1.97	0.46
1:C:1760:HIS:CG	1:C:1832:ILE:HG13	2.50	0.46
2:D:16:PHE:O	2:D:26:ARG:N	2.48	0.46
2:D:181:GLY:HA2	2:D:210:ILE:HB	1.96	0.46
1:A:763:ILE:HG23	1:A:805:ILE:HD12	1.98	0.46
1:A:1084:PRO:HA	1:A:1087:VAL:HG13	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1628:VAL:HB	1:A:1632:LEU:HD12	1.98	0.46
1:A:1884:ILE:HB	1:A:1925:ARG:HD2	1.97	0.46
1:A:2134:ASP:HA	1:A:2137:VAL:HB	1.97	0.46
1:A:2246:SER:O	1:A:2248:SER:N	2.49	0.46
1:C:640:VAL:HB	1:C:679:ARG:HH22	1.79	0.46
1:C:715:LEU:O	1:C:719:LEU:HB3	2.15	0.46
1:C:850:ILE:HG12	1:C:1550:ILE:HA	1.96	0.46
1:C:1478:LEU:C	1:C:1479:GLU:N	2.73	0.46
1:C:1655:TYR:CE1	1:C:1720:LEU:HD21	2.51	0.46
1:C:2128:LYS:HD2	1:C:2133:ILE:HD11	1.98	0.46
1:C:2222:LEU:HG	2:D:252:TRP:CZ3	2.50	0.46
5:J:701:SER:N	5:J:702:THR:HB	2.29	0.46
1:A:774:VAL:N	1:A:775:ALA:HB2	2.31	0.46
1:A:1610:ILE:HG23	1:A:1654:ALA:HB2	1.98	0.46
1:A:2185:PHE:HB3	1:A:2280:PRO:HA	1.96	0.46
1:A:2368:TRP:HA	1:A:2416:ARG:HH22	1.79	0.46
1:C:89:PHE:HD1	1:C:101:ALA:HB1	1.81	0.46
1:C:1090:MET:HB3	1:C:1093:TYR:CD2	2.50	0.46
1:C:1871:GLN:HE21	1:C:1873:GLY:HA3	1.81	0.46
4:H:111:ALA:O	4:H:114:HIS:N	2.49	0.46
5:J:725:GLU:HG3	5:J:726:ASP:H	1.80	0.46
1:A:227:ASN:O	1:A:230:SER:HB2	2.15	0.46
1:A:365:ARG:HD2	1:A:368:VAL:HG21	1.98	0.46
1:A:449:PHE:HB3	1:A:452:ARG:HD2	1.97	0.46
1:A:636:VAL:HG13	1:A:675:ASP:CB	2.37	0.46
1:A:773:ALA:N	1:A:775:ALA:HB2	2.30	0.46
1:A:1280:PHE:HA	1:A:1281:SER:HA	1.76	0.46
1:A:1587:ASP:N	1:A:1588:VAL:CB	2.75	0.46
1:A:1588:VAL:HG11	1:A:1615:LEU:CD2	2.46	0.46
1:A:1601:LYS:HD2	1:A:1635:GLU:HG3	1.98	0.46
1:A:2099:PHE:HA	1:A:2111:PHE:HE2	1.79	0.46
2:B:230:THR:HG22	2:B:246:LEU:H	1.81	0.46
1:C:346:LYS:HD3	1:C:350:ILE:HG13	1.97	0.46
1:C:1734:ARG:HH12	1:C:1771:SER:HB3	1.80	0.46
1:C:2082:GLY:HA3	1:C:2123:TYR:CE1	2.50	0.46
2:D:53:GLN:HE21	2:D:94:SER:HB3	1.80	0.46
5:I:730:VAL:HG21	5:I:790:PRO:N	2.31	0.46
1:A:361:PHE:CE1	1:A:414:PHE:CZ	2.99	0.46
1:A:1599:VAL:HA	1:A:1600:ILE:HA	1.70	0.46
1:A:1622:MET:O	1:A:1626:LYS:HD3	2.15	0.46
1:A:1911:VAL:O	1:A:1915:MET:N	2.49	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2109:ARG:HG3	1:A:2125:LEU:HD13	1.98	0.46
1:A:2112:CYS:HB3	1:A:2122:LYS:H	1.79	0.46
1:A:2190:ARG:O	1:A:2194:GLU:N	2.43	0.46
2:B:74:HIS:HE1	2:B:102:TRP:HE1	1.64	0.46
1:C:1526:LEU:HD22	1:C:1548:ALA:HB1	1.98	0.46
1:C:1857:PRO:C	1:C:1859:ALA:H	2.24	0.46
1:C:2061:LEU:HD21	1:C:2101:PHE:HB2	1.97	0.46
1:C:2080:VAL:HA	1:C:2092:VAL:CG1	2.46	0.46
1:C:2404:GLU:HB3	1:C:2405:GLU:N	2.30	0.46
1:A:145:LYS:HB3	1:A:189:ARG:HB3	1.98	0.46
1:A:1384:ILE:HD13	1:A:1408:ARG:HH21	1.80	0.46
1:A:1740:LEU:O	1:A:1744:LEU:HG	2.16	0.46
1:A:2030:LYS:HD2	1:A:2033:SER:HB2	1.98	0.46
1:A:2368:TRP:HA	1:A:2416:ARG:NH2	2.31	0.46
2:B:147:GLU:HG2	2:B:149:GLN:HB3	1.98	0.46
2:B:156:PRO:HB3	2:B:186:TRP:HE1	1.81	0.46
1:C:289:LYS:HG3	1:C:338:LEU:HD21	1.98	0.46
1:C:462:TYR:OH	1:C:501:MET:HB2	2.15	0.46
2:D:4:ILE:O	2:D:5:LEU:CB	2.64	0.46
5:I:675:SER:HB3	5:I:687:LYS:HD3	1.97	0.46
5:I:698:ARG:HA	5:I:759:ASP:N	2.31	0.46
1:A:233:LYS:HE2	1:A:237:ARG:CD	2.46	0.45
1:A:305:PHE:HD2	1:A:306:GLN:HE21	1.64	0.45
1:A:725:LEU:HB3	1:A:760:LEU:HB3	1.97	0.45
1:A:1216:LEU:HA	1:A:1217:PRO:CA	2.39	0.45
1:A:2004:ARG:HB3	1:A:2063:HIS:CD2	2.52	0.45
1:A:2377:ILE:HD11	1:A:2415:ILE:HD13	1.98	0.45
1:C:163:THR:O	1:C:168:ASN:HB3	2.16	0.45
1:C:245:ILE:HG12	1:C:249:LEU:HD12	1.97	0.45
1:C:265:LEU:HD13	1:C:307:GLN:HE21	1.82	0.45
1:C:362:PHE:C	1:C:362:PHE:CD2	2.94	0.45
1:C:682:PHE:O	1:C:684:ALA:N	2.46	0.45
1:C:824:THR:C	1:C:826:GLY:H	2.24	0.45
1:C:1559:LYS:HG2	1:C:1563:LEU:HD13	1.98	0.45
2:D:4:ILE:HG23	2:D:60:ILE:HD13	1.97	0.45
2:D:6:VAL:O	2:D:274:VAL:HG21	2.16	0.45
3:E:651:UNK:O	3:E:653:UNK:N	2.49	0.45
1:A:1286:GLU:HA	1:A:1289:THR:HG22	1.97	0.45
1:A:1838:LEU:HA	1:A:1841:ALA:HB3	1.98	0.45
2:B:11:ASP:HB2	2:B:292:HIS:HB2	1.98	0.45
2:B:185:VAL:HG11	2:B:240:PHE:CZ	2.52	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:596:ILE:CD1	1:C:600:TYR:HD2	2.29	0.45
1:C:1069:LEU:HD13	1:C:1106:LEU:C	2.42	0.45
2:D:156:PRO:HA	2:D:186:TRP:HZ2	1.81	0.45
3:F:756:UNK:C	3:F:757:UNK:HA	2.45	0.45
1:A:220:TRP:N	1:A:234:LEU:HD13	2.32	0.45
1:A:354:MET:HG3	1:A:388:LEU:HD22	1.98	0.45
1:A:574:GLN:O	1:A:578:MET:HG2	2.16	0.45
1:A:1555:ILE:O	1:A:1572:ARG:NH2	2.50	0.45
1:A:1758:HIS:CG	1:A:1830:ILE:HD11	2.51	0.45
1:A:2278:ARG:O	1:A:2317:ARG:HD2	2.17	0.45
1:A:2446:GLU:O	1:A:2450:LYS:N	2.43	0.45
2:B:8:ALA:HB3	2:B:35:VAL:HG21	1.97	0.45
2:B:164:SER:CB	2:B:212:ARG:HA	2.46	0.45
2:B:248:GLY:HA3	2:B:251:ARG:NE	2.31	0.45
1:C:329:LEU:O	1:C:369:VAL:HG13	2.16	0.45
1:C:361:LYS:HE3	1:C:366:ARG:NH2	2.31	0.45
1:C:397:LEU:HD23	1:C:401:LYS:HG2	1.99	0.45
1:C:859:PRO:HG3	1:C:1543:ASN:CG	2.42	0.45
1:C:1430:GLU:HA	1:C:1458:THR:CG2	2.45	0.45
1:C:1556:GLU:HA	1:C:1559:LYS:HE3	1.98	0.45
1:C:2258:ARG:O	1:C:2261:TYR:N	2.50	0.45
1:A:115:ARG:HE	1:A:166:PRO:HB2	1.81	0.45
1:A:1142:ASN:HA	1:A:1145:SER:HB3	1.98	0.45
1:A:1181:ASN:HA	1:A:1184:LEU:HB3	1.97	0.45
1:A:1764:ASN:C	1:A:1767:VAL:HG22	2.41	0.45
1:A:2203:GLU:O	1:A:2207:MET:N	2.49	0.45
1:C:176:TYR:HA	1:C:179:VAL:HG22	1.98	0.45
1:C:715:LEU:HD21	1:C:754:LYS:HG3	1.99	0.45
1:C:923:HIS:O	1:C:923:HIS:CG	2.69	0.45
1:C:1860:THR:HA	1:C:1864:HIS:HB3	1.97	0.45
1:C:1880:PRO:HA	1:C:1883:ILE:HG12	1.97	0.45
1:C:2157:PHE:HD1	1:C:2160:HIS:CG	2.34	0.45
1:C:2189:VAL:HA	1:C:2192:ARG:HG2	1.98	0.45
1:A:482:LEU:HD11	1:A:498:THR:HG21	1.98	0.45
1:A:768:GLN:HG3	1:A:770:ALA:O	2.16	0.45
1:A:918:THR:HA	1:A:921:ILE:HB	1.99	0.45
1:A:1634:GLU:HB3	1:A:1636:THR:H	1.81	0.45
1:A:1675:PHE:HB3	1:A:1715:ARG:CZ	2.46	0.45
1:A:2128:HIS:HA	1:A:2172:LYS:HG3	1.97	0.45
1:A:2130:ASP:HB2	1:A:2366:ILE:HG23	1.97	0.45
1:A:2282:ASN:HB3	1:A:2294:HIS:CD2	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2377:ILE:HD12	1:A:2415:ILE:HG21	1.99	0.45
2:B:137:ASP:HB3	2:B:139:ASN:N	2.30	0.45
1:C:97:PRO:C	1:C:99:GLU:H	2.24	0.45
1:C:271:PRO:CG	1:C:280:ARG:HB2	2.47	0.45
1:C:469:CYS:HG	1:C:470:ALA:N	2.15	0.45
1:C:801:LEU:HB3	1:C:805:ILE:HG13	1.98	0.45
1:C:981:PHE:C	1:C:985:GLN:HG2	2.42	0.45
1:C:1007:VAL:H	1:C:1008:ILE:HG12	1.82	0.45
1:C:1924:SER:HB3	1:C:1927:ARG:HD2	1.97	0.45
5:J:707:ILE:HD13	5:J:728:LEU:CD2	2.47	0.45
1:A:1155:PHE:HE2	1:C:622:LYS:HB3	1.82	0.45
1:A:1953:GLU:O	1:A:1957:MET:N	2.50	0.45
1:A:2077:ALA:HB2	1:A:2091:LYS:C	2.42	0.45
2:B:85:GLN:H	2:B:124:ILE:HD13	1.82	0.45
2:B:230:THR:HA	2:B:247:ASP:HA	1.99	0.45
1:C:275:ALA:O	1:C:277:LEU:N	2.50	0.45
1:C:389:LEU:C	1:C:391:ARG:H	2.24	0.45
1:C:856:GLU:HG3	1:C:1590:VAL:HG13	1.98	0.45
1:C:952:LEU:HD21	1:C:988:SER:O	2.16	0.45
1:C:1005:TYR:C	1:C:1007:VAL:N	2.72	0.45
1:C:1734:ARG:NH2	1:C:1771:SER:O	2.49	0.45
1:C:2109:ARG:N	1:C:2110:PRO:CD	2.80	0.45
1:C:2269:SER:HB3	1:C:2318:PHE:CE2	2.51	0.45
2:D:239:ASP:C	2:D:241:LYS:N	2.73	0.45
2:D:275:ARG:HB3	2:D:284:ILE:HG23	1.99	0.45
5:J:676:MET:CE	5:J:699:LYS:HE3	2.47	0.45
1:A:103:ALA:HA	1:A:106:LEU:HB2	1.98	0.45
1:A:179:LEU:CD2	1:A:233:LYS:HG3	2.23	0.45
1:A:366:ARG:HD3	1:A:413:PRO:CB	2.41	0.45
1:A:663:LEU:N	1:C:1117:GLU:HB2	2.31	0.45
1:A:999:HIS:HA	1:A:1002:LYS:HB2	1.98	0.45
1:A:1419:LYS:HE2	1:A:1433:LYS:NZ	2.32	0.45
1:A:1672:LEU:HD11	1:A:1719:LYS:HG3	1.99	0.45
1:A:2082:ARG:NH1	1:A:2167:ILE:HG21	2.31	0.45
1:A:2155:PHE:HD1	1:A:2158:HIS:CG	2.35	0.45
2:B:93:SER:HB2	2:B:119:VAL:HG22	1.99	0.45
1:C:138:ILE:HG22	1:C:140:GLY:H	1.82	0.45
1:C:763:VAL:HG11	1:C:803:PRO:HA	1.97	0.45
1:C:857:ASN:O	1:C:1585:GLN:N	2.49	0.45
1:C:1173:GLN:O	1:C:1177:TYR:HB2	2.17	0.45
1:C:1504:ILE:HB	1:C:1596:ARG:HH22	1.82	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:703:ILE:HD12	5:I:706:VAL:HG21	1.98	0.45
5:J:709:PHE:HE2	5:J:716:THR:HG1	1.61	0.45
1:A:234:LEU:HD11	1:A:270:PRO:CG	2.41	0.45
1:A:431:SER:C	1:A:433:TYR:H	2.25	0.45
1:A:765:PRO:HG3	1:A:805:ILE:HG22	1.99	0.45
1:A:1279:SER:O	1:A:1282:SER:N	2.50	0.45
1:A:1910:LEU:C	1:A:1911:VAL:HG12	2.42	0.45
1:A:2279:HIS:HA	1:A:2467:GLY:O	2.17	0.45
2:B:44:LYS:HD2	2:B:301:ASN:HB3	1.98	0.45
1:C:174:ALA:HB1	1:C:178:ARG:CZ	2.47	0.45
1:C:269:TRP:HB2	1:C:310:PHE:CE2	2.52	0.45
1:C:281:LEU:O	1:C:285:VAL:N	2.50	0.45
1:C:291:LEU:HA	1:C:294:ILE:HD12	1.97	0.45
1:C:690:PHE:CD1	1:C:728:PHE:HZ	2.34	0.45
1:C:2063:LEU:HD12	1:C:2099:PRO:HA	1.99	0.45
1:C:2133:ILE:HD13	1:C:2176:GLY:HA3	1.99	0.45
1:C:2264:SER:O	1:C:2267:VAL:HG12	2.16	0.45
1:C:2280:ARG:HB3	1:C:2319:ARG:HD2	1.98	0.45
1:C:2407:GLN:O	1:C:2409:VAL:CA	2.65	0.45
2:D:13:THR:OG1	2:D:291:HIS:HA	2.16	0.45
3:F:651:UNK:O	3:F:653:UNK:N	2.50	0.45
1:A:1065:LEU:HA	1:A:1068:LEU:HB2	1.98	0.45
1:A:1077:ASP:HB2	1:C:699:ILE:HG12	1.97	0.45
1:A:2067:LYS:C	1:A:2068:LEU:HA	2.42	0.45
2:B:44:LYS:HB3	2:B:301:ASN:HB3	1.98	0.45
1:C:731:MET:HA	1:C:732:PRO:HD2	1.85	0.45
1:C:969:LEU:HD22	1:C:985:GLN:HG3	1.98	0.45
1:C:1104:ILE:HB	1:C:1142:MET:HB3	1.99	0.45
1:C:1619:ARG:CA	1:C:1626:LEU:HG	2.37	0.45
1:C:1912:LEU:C	1:C:1914:TYR:H	2.24	0.45
1:C:1974:ALA:HB1	1:C:1990:ALA:HB3	1.98	0.45
1:C:2017:ASP:O	1:C:2020:ASP:N	2.50	0.45
3:F:606:UNK:HA	3:F:607:UNK:C	2.47	0.45
5:I:736:PRO:HA	5:I:755:PHE:HE1	1.81	0.45
5:J:736:PRO:HA	5:J:755:PHE:HD1	1.80	0.45
1:A:303:GLN:HB3	1:A:307:ARG:CB	2.46	0.45
1:A:449:PHE:CD1	1:A:455:PHE:HA	2.52	0.45
1:A:673:GLN:C	1:A:674:PRO:N	2.75	0.45
1:A:721:LEU:O	1:A:760:LEU:HB2	2.16	0.45
1:A:964:PRO:HA	1:A:965:GLY:HA3	1.72	0.45
1:A:2043:TYR:HB3	1:A:2047:ARG:HH22	1.81	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2060:GLU:CB	1:A:2062:GLN:HG2	2.18	0.45
1:A:2205:TRP:HA	1:A:2208:LEU:HB2	1.98	0.45
1:A:2284:MET:C	1:A:2293:ILE:HB	2.42	0.45
2:B:229:HIS:CB	2:B:251:ARG:HB2	2.47	0.45
1:C:1545:VAL:C	1:C:1546:VAL:HA	2.42	0.45
1:A:244:ILE:HA	1:A:248:LEU:HB2	2.00	0.44
1:A:381:ALA:CB	1:A:385:LYS:HD3	2.46	0.44
1:A:1258:LEU:HD23	1:A:1258:LEU:HA	1.92	0.44
1:A:1586:ILE:N	1:A:1615:LEU:HD21	2.32	0.44
1:A:1730:LYS:C	1:A:1731:TRP:CD1	2.95	0.44
1:C:917:TYR:N	1:C:918:PRO:CD	2.79	0.44
1:C:1214:VAL:HG22	1:C:1249:GLN:HE21	1.81	0.44
1:C:1732:LYS:CA	1:C:1737:ASN:HB2	2.47	0.44
2:D:205:ALA:N	2:D:206:HIS:O	2.50	0.44
2:D:274:VAL:N	2:D:288:TYR:O	2.50	0.44
1:A:87:ILE:HG12	1:A:99:ARG:HH21	1.83	0.44
1:A:914:GLU:O	1:A:915:TYR:N	2.50	0.44
1:A:1117:MET:HG3	1:A:1120:ARG:HG3	1.99	0.44
2:B:70:SER:HB3	2:B:72:GLU:HG3	1.98	0.44
1:C:632:HIS:O	1:C:636:SER:N	2.51	0.44
1:C:2153:ASP:OD1	1:C:2156:CYS:C	2.60	0.44
2:D:143:TRP:HE1	2:D:148:ASN:HA	1.81	0.44
1:A:1354:LYS:HE3	1:A:1373:ILE:HD13	1.98	0.44
1:C:177:LEU:HD12	1:C:238:ARG:NH2	2.33	0.44
1:C:288:GLY:O	1:C:338:LEU:HD23	2.17	0.44
1:C:444:GLU:HB3	1:C:447:ARG:HH11	1.82	0.44
1:C:541:ASN:C	1:C:542:GLN:C	2.85	0.44
1:C:1000:HIS:HA	1:C:1003:LYS:HB2	1.98	0.44
1:C:1216:LYS:HB3	1:C:1249:GLN:O	2.18	0.44
1:C:1602:ILE:HG22	1:C:1606:GLU:HB2	2.00	0.44
1:C:1610:VAL:C	1:C:1611:ARG:O	2.58	0.44
1:C:1749:THR:HB	1:C:1762:TRP:CE3	2.53	0.44
1:A:314:HIS:NE2	1:A:319:ASN:OD1	2.51	0.44
1:A:600:ILE:N	1:A:602:HIS:HB2	2.32	0.44
1:A:1961:TRP:HB3	1:A:1995:MET:HE1	1.99	0.44
1:C:143:SER:HB3	1:C:190:ARG:HE	1.83	0.44
1:C:220:ASP:O	1:C:235:LEU:HD22	2.18	0.44
1:C:560:THR:O	1:C:562:GLU:N	2.51	0.44
1:C:850:ILE:CD1	1:C:1553:GLU:HB2	2.46	0.44
1:C:1185:LEU:HD13	1:C:1189:CYS:HA	2.00	0.44
2:D:254:TRP:HD1	2:D:296:VAL:HA	1.80	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:252:UNK:O	3:F:253:UNK:N	2.47	0.44
5:J:737:ASN:HB3	5:J:754:ASN:HB2	1.98	0.44
1:A:370:ALA:CB	1:A:417:VAL:HA	2.48	0.44
1:A:1567:LYS:O	1:A:1568:ARG:N	2.50	0.44
1:A:2111:PHE:CD1	1:A:2123:TYR:HE2	2.36	0.44
1:A:2148:LEU:O	1:A:2158:HIS:NE2	2.50	0.44
1:A:2260:THR:HA	1:A:2327:GLU:OE1	2.18	0.44
1:A:2430:LYS:N	1:A:2442:LEU:HD12	2.33	0.44
2:B:121:GLU:CD	2:B:165:LEU:HB3	2.42	0.44
1:C:297:ARG:HH21	1:C:341:PRO:HA	1.81	0.44
1:C:359:GLU:HG2	1:C:393:MET:HG2	2.00	0.44
1:C:660:ILE:HA	1:C:663:HIS:HB3	1.98	0.44
1:C:1749:THR:HG23	1:C:1759:TRP:HE3	1.82	0.44
1:C:1752:ASP:HA	1:C:1759:TRP:CZ3	2.52	0.44
2:D:4:ILE:HG23	2:D:16:PHE:CD1	2.52	0.44
2:D:12:HIS:CE1	2:D:35:VAL:HB	2.52	0.44
1:A:172:LEU:HD23	1:A:176:LEU:HD13	1.99	0.44
1:A:554:SER:N	1:A:555:PHE:HB2	2.31	0.44
1:A:1589:TRP:O	1:A:1593:LEU:N	2.49	0.44
1:A:1621:ARG:HA	1:A:1624:LEU:HB3	1.99	0.44
1:A:1732:ARG:NH2	1:A:1733:LEU:HG	2.32	0.44
1:A:2181:ASN:HA	1:A:2182:SER:N	2.32	0.44
2:B:86:ASP:HB3	2:B:88:ARG:H	1.81	0.44
1:C:176:TYR:H	1:C:179:VAL:HG22	1.82	0.44
1:C:811:ASP:C	1:C:812:GLN:HA	2.43	0.44
1:C:827:GLN:H	1:C:830:ALA:HB1	1.83	0.44
1:C:1561:LYS:HE3	1:C:1601:VAL:HB	1.99	0.44
1:C:2187:PHE:C	1:C:2282:PRO:HB3	2.42	0.44
1:A:461:TYR:CE1	1:A:498:THR:HA	2.52	0.44
1:A:466:LEU:O	1:A:467:ALA:HB3	2.17	0.44
1:A:507:PRO:HB2	1:A:509:LEU:HD23	1.99	0.44
1:A:574:GLN:HE21	1:A:578:MET:HE3	1.81	0.44
1:A:675:ASP:N	1:A:675:ASP:OD1	2.50	0.44
1:A:699:ILE:HD13	1:A:699:ILE:HA	1.89	0.44
1:A:796:TYR:OH	1:A:844:LEU:HD22	2.18	0.44
1:A:1025:GLU:HG3	1:A:1029:LYS:HE2	1.98	0.44
1:A:1088:ARG:NH2	1:A:1120:ARG:HB2	2.32	0.44
1:A:1389:HIS:HB2	1:A:2332:GLU:HG2	1.98	0.44
1:A:1725:VAL:HA	1:A:1728:GLN:HB3	1.99	0.44
1:C:249:LEU:HA	1:C:252:ASN:HB3	2.00	0.44
1:C:355:MET:HB2	1:C:389:LEU:HD22	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:688:GLU:HB3	1:C:692:ILE:HG13	2.00	0.44
1:C:771:ALA:HA	1:C:811:ASP:HB2	1.99	0.44
1:C:1238:ASP:HA	1:C:1241:GLU:HB2	1.98	0.44
1:C:1554:LEU:HA	1:C:1557:ILE:CG2	2.47	0.44
1:C:2116:LYS:HA	1:C:2122:ASP:HA	1.99	0.44
2:D:131:LEU:HB3	2:D:143:TRP:O	2.18	0.44
1:A:114:ALA:C	1:A:159:TYR:HD1	2.25	0.44
1:A:328:LEU:HD12	1:A:365:ARG:HD2	1.99	0.44
1:A:676:ASN:HB3	1:A:726:LYS:HE2	2.00	0.44
1:A:861:ARG:NH1	1:A:1540:TYR:HB3	2.33	0.44
1:A:1112:ILE:HG22	1:A:1112:ILE:O	2.18	0.44
1:A:1558:TYR:C	1:A:1572:ARG:HH21	2.25	0.44
1:A:2110:LYS:HD2	1:A:2178:TRP:HZ3	1.83	0.44
1:A:2465:TYR:HA	1:A:2468:TRP:HB3	2.00	0.44
1:C:181:ILE:CG2	1:C:224:LEU:HD13	2.47	0.44
1:C:458:LYS:C	1:C:461:PHE:HB3	2.43	0.44
1:C:655:GLU:CG	1:C:658:LEU:HB3	2.48	0.44
1:C:856:GLU:O	1:C:1590:VAL:HA	2.18	0.44
1:C:1344:GLN:HE22	1:C:1351:LYS:N	2.16	0.44
1:C:1435:LYS:HZ1	1:C:1436:LEU:HG	1.82	0.44
1:C:1504:ILE:HB	1:C:1596:ARG:NH2	2.33	0.44
1:C:2264:SER:HB3	1:C:2294:VAL:H	1.82	0.44
1:C:2265:LEU:CD1	1:C:2333:ILE:HG22	2.48	0.44
1:C:2317:PRO:HB3	1:C:2453:LEU:HD13	2.00	0.44
1:A:142:SER:HB3	1:A:189:ARG:NE	2.33	0.44
1:A:256:LEU:HB3	1:A:258:PRO:HA	1.99	0.44
1:A:1060:VAL:N	1:A:1061:PRO:CD	2.81	0.44
1:A:2335:PHE:O	1:A:2339:CYS:N	2.51	0.44
1:A:2446:GLU:O	1:A:2450:LYS:HG2	2.18	0.44
1:C:399:TYR:CZ	1:C:442:ILE:HG21	2.53	0.44
1:C:819:ASP:O	1:C:823:THR:N	2.51	0.44
1:C:1007:VAL:N	1:C:1008:ILE:HG12	2.32	0.44
1:C:1996:GLU:O	1:C:1999:LYS:HB3	2.18	0.44
1:C:2346:LYS:HD2	1:C:2346:LYS:HA	1.87	0.44
2:D:57:LEU:HD12	2:D:69:ALA:HB3	1.98	0.44
1:A:113:LEU:HD13	1:A:117:VAL:HG13	1.98	0.43
1:A:807:THR:HA	1:A:1578:ARG:CZ	2.47	0.43
1:A:1134:ARG:HG2	1:A:1138:LYS:HE2	1.99	0.43
1:A:1352:HIS:C	1:A:1355:GLU:H	2.25	0.43
1:C:239:ARG:NH1	1:C:271:PRO:HG2	2.33	0.43
1:C:583:ILE:HA	1:C:584:HIS:HA	1.76	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:586:GLN:HB3	1:C:629:THR:OG1	2.18	0.43
1:C:845:LEU:C	1:C:846:LEU:HA	2.43	0.43
1:C:950:GLN:O	1:C:953:GLY:N	2.51	0.43
1:C:963:ILE:HG13	1:C:964:ILE:N	2.33	0.43
1:C:965:PRO:O	1:C:969:LEU:HG	2.18	0.43
1:C:1259:LEU:C	1:C:1261:SER:H	2.26	0.43
1:C:1322:VAL:HG22	1:C:1347:HIS:CE1	2.53	0.43
1:C:1421:LYS:NZ	1:C:1451:LEU:HD11	2.33	0.43
1:C:1923:GLU:HB2	1:C:1925:LEU:HG	1.98	0.43
1:C:1975:SER:HA	1:C:1978:PHE:HB3	1.99	0.43
2:D:125:HIS:HB2	2:D:167:MET:SD	2.58	0.43
3:F:367:UNK:C	3:F:369:UNK:N	2.80	0.43
5:J:676:MET:HB3	5:J:688:TYR:HD2	1.82	0.43
1:A:568:ASP:HA	1:A:572:LEU:HD22	2.00	0.43
1:A:1138:LYS:HA	1:A:1141:MET:HB2	2.00	0.43
1:A:1653:TYR:HA	1:A:1656:LEU:HB3	2.00	0.43
1:A:1904:LYS:HA	1:A:1907:PRO:HG3	2.00	0.43
1:A:2308:GLU:HB2	1:A:2378:GLU:CD	2.43	0.43
1:C:346:LYS:HB3	1:C:350:ILE:CG1	2.48	0.43
1:C:783:LEU:HG	1:C:800:GLU:HG2	1.99	0.43
1:C:846:LEU:HD22	1:C:1549:GLN:HG3	1.99	0.43
1:C:1046:PHE:O	1:C:1050:ILE:HG12	2.18	0.43
2:D:37:ARG:O	2:D:50:ALA:N	2.51	0.43
2:D:151:THR:HA	2:D:152:HIS:HA	2.00	0.43
3:F:659:UNK:C	3:F:661:UNK:N	2.82	0.43
1:A:329:LEU:HD11	1:A:367:GLU:HB2	2.01	0.43
1:A:1391:GLN:NE2	1:A:1405:LYS:HE2	2.34	0.43
1:A:1830:ILE:HD13	1:A:1835:SER:CB	2.47	0.43
1:A:2154:CYS:SG	1:A:2340:GLU:HB3	2.58	0.43
1:A:2185:PHE:C	1:A:2280:PRO:HB3	2.43	0.43
1:C:138:ILE:C	1:C:140:GLY:N	2.76	0.43
1:C:291:LEU:HD22	1:C:301:LEU:HD22	2.00	0.43
1:C:456:PHE:N	1:C:492:MET:HG3	2.32	0.43
1:C:1070:VAL:HG13	1:C:1106:LEU:HA	2.00	0.43
1:C:1192:THR:C	1:C:1194:ILE:N	2.76	0.43
1:C:1492:LYS:O	1:C:1498:LYS:HB2	2.19	0.43
1:C:2400:ALA:O	1:C:2401:ILE:HG13	2.19	0.43
2:D:12:HIS:CE1	2:D:34:GLN:HG3	2.54	0.43
2:D:134:CYS:SG	2:D:165:LEU:HD13	2.58	0.43
2:D:206:HIS:CD2	2:D:226:SER:HB2	2.53	0.43
1:A:151:ALA:O	1:A:155:LEU:HB2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:PRO:O	1:A:377:ALA:HB2	2.17	0.43
1:A:502:LEU:HB3	1:A:511:SER:OG	2.18	0.43
1:A:796:TYR:CE2	1:A:843:GLU:HB3	2.53	0.43
1:A:805:ILE:O	1:A:808:PHE:HB3	2.19	0.43
1:A:1077:ASP:CG	1:C:699:ILE:HG23	2.44	0.43
1:A:2140:LEU:HD21	1:A:2360:PHE:HE2	1.83	0.43
1:C:461:PHE:HE2	1:C:483:LEU:HD13	1.82	0.43
1:C:802:MET:C	1:C:806:ILE:HG12	2.43	0.43
1:C:994:LYS:HA	1:C:995:GLN:HB2	1.99	0.43
1:C:2064:GLN:CG	1:C:2065:HIS:CD2	2.93	0.43
1:C:2104:ILE:HD12	1:C:2110:PRO:HD2	2.01	0.43
1:C:2104:ILE:HG12	1:C:2112:LYS:HD3	2.00	0.43
1:A:235:GLU:OE1	1:A:275:LYS:HB2	2.19	0.43
1:A:280:LEU:CD1	1:A:329:LEU:HB3	2.48	0.43
1:A:370:ALA:HB1	1:A:417:VAL:HA	2.01	0.43
1:A:634:HIS:HA	1:A:637:SER:HB2	2.00	0.43
1:A:1156:VAL:HG13	1:A:1157:VAL:HG13	2.01	0.43
1:A:1167:LEU:HG	1:A:1167:LEU:O	2.18	0.43
1:A:1258:LEU:HD22	1:A:1268:TYR:CE2	2.53	0.43
1:A:1436:SER:HB2	1:A:1440:LEU:CD1	2.49	0.43
1:A:2205:TRP:CA	1:A:2208:LEU:HB2	2.48	0.43
1:A:2430:LYS:O	1:A:2447:GLN:HG2	2.19	0.43
1:C:257:LEU:HD22	1:C:260:TYR:CG	2.53	0.43
1:C:389:LEU:HA	1:C:392:ILE:HB	1.99	0.43
1:C:717:LYS:C	1:C:721:GLU:HB2	2.44	0.43
1:C:1421:LYS:HZ2	1:C:1451:LEU:HD11	1.84	0.43
1:C:1930:ALA:O	1:C:1934:ILE:HG12	2.18	0.43
1:C:2286:MET:HB3	1:C:2295:ILE:HB	2.00	0.43
1:C:2308:LEU:HD12	1:C:2377:LYS:C	2.44	0.43
1:C:2333:ILE:O	1:C:2333:ILE:HG13	2.18	0.43
2:D:4:ILE:HG23	2:D:16:PHE:HD1	1.84	0.43
5:I:720:PRO:CD	5:I:723:PHE:HB2	2.49	0.43
1:A:142:SER:C	1:A:145:LYS:HB2	2.43	0.43
1:A:345:LYS:HD2	1:A:348:ASP:OD2	2.18	0.43
1:A:852:LEU:HD13	1:A:1575:TRP:HA	1.99	0.43
1:A:1898:LEU:O	1:A:1902:LEU:HG	2.19	0.43
1:A:2019:ALA:C	1:A:2020:TYR:N	2.76	0.43
1:A:2037:GLN:NE2	1:A:2040:ASP:HB3	2.34	0.43
2:B:269:SER:N	2:B:295:ALA:HB3	2.34	0.43
1:C:1063:ILE:HG22	1:C:1064:ARG:N	2.32	0.43
1:C:1256:SER:C	1:C:1258:CYS:H	2.27	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1568:ASP:C	1:C:1570:ARG:H	2.25	0.43
1:C:1654:VAL:O	1:C:1658:LEU:N	2.50	0.43
1:C:1767:PHE:HD1	1:C:1825:ILE:HG21	1.84	0.43
1:C:2062:GLU:HG2	1:C:2064:GLN:N	2.32	0.43
2:D:6:VAL:HG22	2:D:7:SER:HA	2.00	0.43
2:D:291:HIS:HB3	2:D:293:LYS:O	2.19	0.43
1:A:88:PHE:HD1	1:A:100:ALA:HB1	1.83	0.43
1:A:257:TYR:CD1	1:A:286:LEU:HD11	2.53	0.43
1:A:715:ARG:O	1:A:719:LEU:N	2.52	0.43
1:A:1088:ARG:HH22	1:A:1120:ARG:HB2	1.84	0.43
1:A:1097:LEU:HD23	1:A:1100:ILE:HG21	2.00	0.43
1:A:2268:MET:SD	1:A:2342:VAL:HG23	2.59	0.43
2:B:274:VAL:HG13	2:B:288:TYR:HB2	2.01	0.43
1:C:188:VAL:HB	1:C:237:TYR:CD2	2.54	0.43
1:C:763:VAL:HG12	1:C:763:VAL:O	2.19	0.43
1:C:1841:GLN:O	1:C:1844:LEU:N	2.51	0.43
2:D:26:ARG:HH22	2:D:47:LEU:HD11	1.83	0.43
2:D:248:GLY:HA3	2:D:251:ARG:CZ	2.48	0.43
4:H:141:ASN:C	4:H:143:ASP:H	2.27	0.43
5:J:676:MET:O	5:J:688:TYR:N	2.51	0.43
1:A:234:LEU:HD21	1:A:270:PRO:HB3	2.01	0.43
1:A:699:ILE:HD12	1:A:717:THR:HG23	1.99	0.43
1:A:701:ARG:O	1:C:1044:LEU:HD11	2.18	0.43
1:A:1073:PRO:HB3	1:A:1110:LYS:N	2.34	0.43
1:A:1241:TRP:N	1:A:1243:ARG:H	2.16	0.43
1:A:2053:LEU:HA	1:A:2056:LEU:HD13	2.00	0.43
1:A:2306:LEU:HG	1:A:2376:LYS:HB2	2.00	0.43
1:C:1407:LYS:HB3	1:C:1412:GLU:HB3	2.00	0.43
1:C:1435:LYS:HE3	1:C:1436:LEU:HG	2.01	0.43
1:C:1749:THR:HB	1:C:1762:TRP:CD2	2.54	0.43
1:A:268:TRP:CZ3	1:A:316:LEU:HD23	2.54	0.43
1:A:331:PHE:HZ	1:A:345:LYS:HE3	1.84	0.43
1:A:409:ASN:O	1:A:449:PHE:HD2	2.01	0.43
1:A:486:MET:HE1	1:A:495:MET:HE2	2.01	0.43
1:A:954:ARG:NH1	1:A:958:PHE:HE2	2.16	0.43
1:A:1953:GLU:HB3	1:A:2068:LEU:HG	2.00	0.43
1:A:2036:ASN:HA	1:A:2039:TRP:CB	2.49	0.43
1:A:2314:VAL:HB	1:A:2315:PRO:HD2	2.01	0.43
2:B:136:ARG:C	2:B:137:ASP:N	2.77	0.43
1:C:326:HIS:HB3	1:C:365:ILE:HB	2.01	0.43
1:C:388:TYR:O	1:C:392:ILE:N	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:389:LEU:O	1:C:393:MET:N	2.52	0.43
1:C:537:TYR:OH	1:C:545:ILE:HD13	2.19	0.43
1:C:700:ILE:HD13	1:C:703:LEU:HD12	2.01	0.43
1:C:840:LEU:O	1:C:842:TYR:N	2.51	0.43
1:C:1615:ALA:HB2	1:C:1629:LYS:HG2	2.00	0.43
1:C:2007:GLU:HG2	1:C:2066:VAL:HB	2.00	0.43
1:C:2063:LEU:O	1:C:2068:PRO:HA	2.19	0.43
2:D:267:THR:OG1	2:D:277:TRP:NE1	2.51	0.43
1:A:442:ARG:O	1:A:446:ARG:N	2.49	0.43
1:A:714:LEU:HD13	1:A:753:LYS:HE2	2.01	0.43
1:A:771:SER:O	1:A:773:ALA:N	2.52	0.43
1:A:1617:ARG:HD2	1:A:1624:LEU:CD2	2.48	0.43
1:A:2109:ARG:H	1:A:2109:ARG:HG2	1.58	0.43
2:B:30:HIS:CE1	2:B:35:VAL:HG23	2.53	0.43
1:C:121:GLU:OE2	1:C:124:GLN:N	2.52	0.43
1:C:246:ILE:CD1	1:C:258:TYR:N	2.81	0.43
1:C:333:ARG:HG2	1:C:350:ILE:HD13	2.01	0.43
1:C:378:ALA:O	1:C:379:PHE:N	2.52	0.43
1:C:1878:VAL:O	1:C:1878:VAL:HG12	2.18	0.43
1:C:1974:ALA:HB1	1:C:1990:ALA:CB	2.49	0.43
1:C:2340:THR:O	1:C:2344:VAL:HG12	2.19	0.43
2:D:21:THR:O	2:D:286:ARG:CZ	2.67	0.43
2:D:177:ALA:HB2	2:D:183:CYS:HA	2.01	0.43
2:D:232:ARG:HA	2:D:244:THR:HG22	2.01	0.43
2:D:247:ASP:CG	2:D:248:GLY:H	2.27	0.43
5:J:729:THR:HB	5:J:730:VAL:HG22	2.00	0.43
5:J:734:SER:HB3	5:J:773:VAL:HB	2.01	0.43
1:A:115:ARG:HH12	1:A:124:ARG:HG3	1.84	0.42
1:A:422:ILE:HG23	1:A:466:LEU:HB2	2.01	0.42
1:A:1904:LYS:HG3	1:A:1939:HIS:HB2	2.00	0.42
1:C:570:ALA:HA	1:C:596:ILE:CD1	2.49	0.42
1:C:1108:ARG:HD2	1:C:1145:LEU:HB3	1.99	0.42
1:C:1138:THR:HG22	1:C:1142:MET:HG2	2.00	0.42
1:C:1148:LEU:O	1:C:1151:GLN:HB2	2.18	0.42
2:D:78:VAL:HG21	2:D:81:VAL:HG13	2.01	0.42
2:D:248:GLY:HA3	2:D:251:ARG:NE	2.34	0.42
1:A:280:LEU:HD13	1:A:329:LEU:HB3	2.02	0.42
1:A:388:LEU:HA	1:A:391:ILE:HB	2.01	0.42
1:A:390:ARG:HA	1:A:393:VAL:HB	2.00	0.42
1:A:413:PRO:HA	1:A:416:LEU:HB3	2.02	0.42
1:A:676:ASN:CB	1:A:726:LYS:HE2	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:861:ARG:O	1:A:865:VAL:HG23	2.19	0.42
1:A:862:ARG:NH1	1:A:2152:ALA:O	2.51	0.42
1:A:1126:VAL:HG23	1:A:1166:LEU:HD21	2.01	0.42
1:A:1371:ILE:HG21	1:A:1387:LEU:CD1	2.49	0.42
1:A:1430:MET:O	1:A:1433:LYS:HE3	2.17	0.42
1:A:1585:ASN:C	1:A:1588:VAL:HG21	2.44	0.42
1:A:1950:VAL:HG13	1:A:2068:LEU:HD21	2.01	0.42
1:A:2342:VAL:O	1:A:2346:LEU:HG	2.19	0.42
1:C:724:THR:O	1:C:728:PHE:N	2.53	0.42
1:C:1355:TYR:HA	1:C:1358:VAL:HG12	1.99	0.42
1:C:1658:LEU:C	1:C:1661:LEU:H	2.27	0.42
1:C:2104:ILE:O	1:C:2109:ARG:HA	2.20	0.42
5:I:647:LYS:NZ	5:I:649:LYS:NZ	2.67	0.42
5:I:676:MET:HB2	5:I:702:THR:CG2	2.49	0.42
1:A:443:GLU:HA	1:A:446:ARG:HB2	2.01	0.42
1:A:482:LEU:HA	1:A:485:LEU:HB2	1.99	0.42
1:A:489:CYS:HA	1:A:539:ASN:HD22	1.84	0.42
1:A:916:TYR:N	1:A:917:PRO:CD	2.82	0.42
1:A:1013:ILE:HD11	1:A:1021:ILE:HD12	2.01	0.42
1:A:1244:ARG:HA	1:A:1247:ILE:HD12	2.01	0.42
1:A:1607:GLN:HA	1:A:1610:ILE:HD12	2.01	0.42
1:A:1943:LEU:HB3	1:A:2076:LEU:HD22	2.01	0.42
1:A:2349:ASN:O	1:A:2353:LEU:N	2.52	0.42
1:C:124:GLN:OE1	1:C:124:GLN:HA	2.17	0.42
1:C:240:HIS:CA	1:C:241:ALA:C	2.87	0.42
1:C:521:LEU:HD23	1:C:537:TYR:HD1	1.84	0.42
1:C:990:ILE:HD11	1:C:1208:TYR:HE2	1.84	0.42
2:D:85:GLN:HG2	2:D:128:GLN:CD	2.43	0.42
5:I:676:MET:HB3	5:I:688:TYR:HB2	2.00	0.42
1:A:212:PHE:O	1:A:216:THR:HG22	2.19	0.42
1:A:673:GLN:HB3	1:A:719:LEU:HB3	2.01	0.42
1:A:730:MET:HA	1:A:731:PRO:HD2	1.75	0.42
1:A:824:LEU:HA	1:A:827:LEU:HB2	2.01	0.42
1:A:944:ILE:O	1:A:947:ILE:HB	2.19	0.42
1:A:1117:MET:HG2	1:A:1121:ILE:HG13	2.01	0.42
1:A:1525:VAL:O	1:A:1528:LEU:HD23	2.19	0.42
1:A:1567:LYS:O	1:A:1570:THR:N	2.52	0.42
2:B:40:ILE:CG2	2:B:44:LYS:HA	2.49	0.42
1:C:333:ARG:HH11	1:C:354:THR:HB	1.84	0.42
1:C:377:ALA:O	1:C:382:ALA:HB3	2.20	0.42
1:C:458:LYS:HE3	1:C:461:PHE:CD2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1430:GLU:O	1:C:1436:LEU:HD11	2.20	0.42
1:C:1681:MET:HA	1:C:1684:ASP:HB3	2.00	0.42
1:C:1766:ASN:O	1:C:1769:VAL:HB	2.19	0.42
5:I:736:PRO:HA	5:I:755:PHE:CE1	2.54	0.42
1:A:171:ARG:O	1:A:171:ARG:HG2	2.19	0.42
1:A:583:HIS:HB3	1:A:584:HIS:H	1.61	0.42
1:A:856:ASN:C	1:A:1584:LYS:H	2.27	0.42
1:A:865:VAL:HG22	1:A:1535:SER:HB3	2.01	0.42
1:A:1242:ILE:HD12	1:A:1272:ALA:HB1	2.02	0.42
1:A:1586:ILE:HA	1:A:1587:ASP:N	2.34	0.42
1:A:1981:ASN:HB3	1:A:1984:LYS:HB3	2.01	0.42
1:C:115:ALA:C	1:C:117:GLU:N	2.74	0.42
1:C:964:ILE:C	1:C:965:PRO:N	2.77	0.42
1:C:1452:ALA:HA	1:C:1455:LYS:HE2	2.00	0.42
1:C:2225:VAL:HG22	1:C:2461:GLU:HB2	2.02	0.42
2:D:222:LEU:HB3	2:D:234:TRP:HB2	2.01	0.42
5:I:668:ASP:HA	5:I:669:LYS:HA	1.93	0.42
1:A:928:LEU:HD21	1:A:942:GLN:CB	2.48	0.42
1:A:1287:LEU:HA	1:A:1290:SER:OG	2.20	0.42
1:A:1435:ARG:O	1:A:1439:ALA:N	2.52	0.42
1:A:1839:GLN:CD	1:A:2353:LEU:HA	2.45	0.42
1:A:2299:ASP:O	1:A:2301:PHE:N	2.53	0.42
1:A:2331:ILE:HA	1:A:2334:SER:HB2	2.02	0.42
2:B:246:LEU:HG	2:B:277:TRP:CZ3	2.55	0.42
1:C:247:LYS:O	1:C:251:ASP:N	2.53	0.42
1:C:654:ALA:HA	1:C:657:ARG:HB2	2.02	0.42
1:C:827:GLN:H	1:C:830:ALA:CB	2.32	0.42
1:C:1161:PRO:HB2	1:C:1162:VAL:N	2.34	0.42
1:C:1674:LEU:HD11	1:C:1721:LYS:HG3	2.02	0.42
1:C:1980:GLY:HA2	5:J:648:LYS:NZ	2.34	0.42
1:C:2021:ALA:C	1:C:2022:TYR:N	2.78	0.42
2:D:213:ILE:HD12	2:D:222:LEU:HD11	2.02	0.42
4:H:100:ARG:O	4:H:101:PHE:HA	2.19	0.42
5:J:782:LYS:HA	5:J:785:ASN:O	2.20	0.42
1:A:331:PHE:CZ	1:A:345:LYS:HE3	2.54	0.42
1:A:577:LYS:HE3	1:A:618:LEU:HD13	2.02	0.42
1:A:1490:LYS:O	1:A:1496:LYS:HB3	2.20	0.42
1:A:1617:ARG:HD2	1:A:1624:LEU:HD21	2.02	0.42
1:A:1666:ASP:HA	1:A:1669:LEU:HB2	2.01	0.42
1:A:2114:LYS:HA	1:A:2120:ASP:HA	2.01	0.42
1:C:146:LYS:HD2	1:C:190:ARG:HG3	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:189:MET:HG3	1:C:237:TYR:HB3	2.02	0.42
1:C:213:PHE:CE1	1:C:217:THR:HB	2.55	0.42
1:C:268:ILE:HG21	1:C:311:GLN:HG3	2.00	0.42
1:C:801:LEU:O	1:C:805:ILE:N	2.52	0.42
1:C:917:TYR:N	1:C:918:PRO:HD2	2.35	0.42
2:D:8:ALA:C	2:D:295:ALA:HA	2.45	0.42
2:D:30:HIS:CE1	2:D:34:GLN:C	2.98	0.42
5:I:655:SER:HA	5:I:659:LEU:HB3	1.99	0.42
5:I:699:LYS:HG2	5:I:755:PHE:HA	2.01	0.42
5:J:710:ALA:HB1	5:J:718:LYS:CG	2.43	0.42
1:A:259:TYR:HB2	1:A:290:LEU:HD11	2.01	0.42
1:A:300:LEU:HD13	1:A:303:GLN:CB	2.49	0.42
1:A:533:SER:CA	1:A:534:ASN:C	2.88	0.42
1:A:807:THR:HA	1:A:1578:ARG:NE	2.35	0.42
1:A:969:VAL:HG22	1:A:1003:ILE:HD11	2.00	0.42
1:A:1981:ASN:HD22	1:A:1985:MET:HE2	1.85	0.42
1:A:2062:GLN:HG3	1:A:2063:HIS:N	2.34	0.42
1:A:2094:LYS:HD2	1:A:2095:PHE:CZ	2.55	0.42
1:C:398:ARG:O	1:C:401:LYS:HB2	2.19	0.42
1:C:500:LEU:O	1:C:503:LEU:HB2	2.20	0.42
1:C:955:ARG:HH11	1:C:959:PHE:HE2	1.67	0.42
1:C:1098:LEU:N	1:C:1101:ILE:HD12	2.35	0.42
1:C:1952:VAL:O	1:C:1956:LEU:N	2.53	0.42
1:C:2045:TYR:HB3	1:C:2049:ARG:NH1	2.16	0.42
1:C:2362:PHE:N	1:C:2362:PHE:CD1	2.86	0.42
1:A:930:ASP:HA	1:A:931:PRO:HD3	1.92	0.42
1:A:1006:VAL:O	1:A:1007:ILE:N	2.53	0.42
2:B:84:GLN:OE1	2:B:89:TRP:HB2	2.20	0.42
1:C:146:LYS:HD3	1:C:187:GLU:HG2	2.01	0.42
1:C:781:LYS:O	1:C:785:GLU:N	2.50	0.42
1:C:1504:ILE:HD13	1:C:1596:ARG:CZ	2.50	0.42
1:C:1925:LEU:N	1:C:1928:GLN:HG2	2.34	0.42
1:C:2303:PHE:HB3	1:C:2377:LYS:HG3	2.02	0.42
1:C:2317:PRO:HB2	1:C:2318:PHE:CD2	2.55	0.42
1:C:2429:ILE:HA	1:C:2434:THR:C	2.44	0.42
1:A:248:LEU:O	1:A:251:ASN:HB3	2.20	0.42
1:A:415:ILE:HG12	1:A:438:LEU:HD13	2.02	0.42
1:A:486:MET:HG3	1:A:494:HIS:HB2	2.02	0.42
1:A:661:GLN:HE21	1:A:672:ALA:HB1	1.84	0.42
1:A:1191:THR:C	1:A:1193:ILE:N	2.78	0.42
1:A:1600:ILE:HG13	1:A:1601:LYS:N	2.33	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1627:LYS:C	1:A:1629:LEU:H	2.28	0.42
1:A:1732:ARG:O	1:A:1734:SER:HB2	2.20	0.42
1:A:1754:TYR:HD1	1:A:1826:PHE:CZ	2.38	0.42
1:A:2334:SER:HB3	1:A:2335:PHE:HA	2.02	0.42
1:A:2398:ALA:HB1	1:A:2399:ILE:HG13	2.02	0.42
1:A:2436:ILE:HG13	1:A:2438:ARG:N	2.35	0.42
2:B:91:VAL:HA	2:B:101:VAL:HA	2.01	0.42
2:B:118:PRO:C	2:B:136:ARG:HG3	2.45	0.42
1:C:136:GLU:HA	1:C:179:VAL:HA	2.01	0.42
1:C:2203:ASN:O	1:C:2207:TRP:N	2.48	0.42
2:D:7:SER:HB2	2:D:38:LEU:HB2	2.02	0.42
2:D:14:ILE:HD12	2:D:16:PHE:HE2	1.85	0.42
2:D:173:MET:HB3	2:D:174:LEU:HA	2.02	0.42
5:I:698:ARG:HA	5:I:759:ASP:CA	2.50	0.42
5:I:698:ARG:O	5:I:701:SER:N	2.53	0.42
5:J:725:GLU:HG3	5:J:726:ASP:N	2.35	0.42
1:A:212:PHE:CE1	1:A:238:ARG:HA	2.53	0.41
1:A:577:LYS:HZ3	1:A:615:SER:HA	1.85	0.41
1:A:660:LEU:HA	1:A:663:LEU:HB3	2.01	0.41
1:A:1933:ILE:C	1:A:1937:ARG:HE	2.27	0.41
1:A:1954:LEU:O	1:A:1958:ALA:N	2.53	0.41
1:A:1962:HIS:HE2	1:A:2006:ILE:HA	1.85	0.41
1:A:2140:LEU:HD21	1:A:2360:PHE:CE2	2.55	0.41
1:A:2232:ASN:OD1	1:A:2233:THR:N	2.53	0.41
1:A:2266:MET:HE2	1:A:2266:MET:HB3	1.95	0.41
1:A:2436:ILE:HD11	1:A:2438:ARG:HB2	2.02	0.41
2:B:267:THR:HB	2:B:277:TRP:HE1	1.84	0.41
1:C:236:GLU:OE2	1:C:271:PRO:HB3	2.19	0.41
1:C:315:HIS:CD2	1:C:320:ASN:ND2	2.83	0.41
1:C:315:HIS:NE2	1:C:320:ASN:OD1	2.53	0.41
1:C:333:ARG:HG2	1:C:373:LEU:HD13	2.02	0.41
1:C:474:ALA:HA	1:C:477:LYS:NZ	2.35	0.41
1:C:602:GLU:HA	1:C:603:HIS:C	2.45	0.41
1:C:836:VAL:HG22	1:C:845:LEU:HD12	2.02	0.41
1:C:1365:LYS:H	1:C:1368:THR:HG22	1.84	0.41
1:C:2340:THR:HA	1:C:2343:ASN:ND2	2.35	0.41
2:D:26:ARG:HD2	2:D:63:THR:HA	2.02	0.41
2:D:191:HIS:CG	2:D:192:THR:H	2.38	0.41
1:A:335:LEU:HD22	1:A:341:TYR:HB2	2.02	0.41
1:A:350:TYR:OH	1:A:385:LYS:HA	2.19	0.41
1:A:493:ASP:HA	1:A:496:GLN:HG2	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:675:ASP:O	1:A:679:LEU:N	2.53	0.41
1:A:709:TYR:HA	1:A:713:SER:HB2	2.02	0.41
1:A:1060:VAL:O	1:A:1063:ARG:HB2	2.21	0.41
1:A:1351:LEU:HD23	1:A:1373:ILE:HD12	2.02	0.41
1:A:1408:ARG:CZ	1:A:1408:ARG:HB2	2.50	0.41
1:A:1763:ALA:O	1:A:1767:VAL:HG13	2.19	0.41
1:A:2107:ARG:N	1:A:2108:PRO:HD3	2.35	0.41
2:B:183:CYS:SG	2:B:205:ALA:HB2	2.60	0.41
1:C:1061:VAL:HA	1:C:1064:ARG:HB2	2.02	0.41
1:C:1274:ARG:HB2	1:C:1327:HIS:CE1	2.50	0.41
1:C:1281:PHE:CD2	1:C:1332:LEU:HD22	2.56	0.41
1:C:1408:LEU:HD21	1:C:1438:SER:HB3	2.01	0.41
1:C:2261:TYR:O	1:C:2262:THR:C	2.63	0.41
1:C:2307:ILE:HB	1:C:2377:LYS:HD3	2.01	0.41
1:C:2317:PRO:HB3	1:C:2453:LEU:HD22	2.01	0.41
2:D:91:VAL:HG23	2:D:101:VAL:HB	2.01	0.41
2:D:174:LEU:HB3	2:D:175:ALA:H	1.75	0.41
4:H:68:GLU:O	4:H:69:LEU:C	2.63	0.41
5:J:741:LEU:HB3	5:J:742:LYS:H	1.66	0.41
1:A:281:ASP:CA	1:A:284:VAL:HB	2.35	0.41
1:A:506:ILE:N	1:A:507:PRO:HD2	2.35	0.41
1:A:547:ALA:HA	1:A:550:SER:OG	2.19	0.41
1:A:567:THR:HA	1:A:571:ILE:HG13	2.02	0.41
1:A:769:ASP:HA	1:A:809:GLN:HB2	2.02	0.41
1:A:804:ILE:HG22	1:A:805:ILE:HD13	2.01	0.41
1:A:923:ASN:HD22	1:A:923:ASN:N	2.18	0.41
1:A:1384:ILE:HA	1:A:1385:GLY:HA2	1.74	0.41
1:A:1824:LYS:O	1:A:1827:PHE:HB3	2.20	0.41
1:A:1881:ILE:HG21	1:A:1913:PRO:O	2.20	0.41
1:A:2247:ARG:O	1:A:2248:SER:HB3	2.20	0.41
1:A:2407:VAL:HA	1:A:2411:HIS:HB2	2.01	0.41
1:C:136:GLU:HA	1:C:179:VAL:HG12	2.01	0.41
1:C:153:VAL:HB	1:C:176:TYR:HE2	1.84	0.41
1:C:285:VAL:HG22	1:C:335:LEU:HD13	2.02	0.41
1:C:929:LEU:HD21	1:C:943:GLN:HB2	2.02	0.41
1:C:998:ARG:HG2	1:C:1038:ARG:HG2	2.02	0.41
1:C:1589:ASP:HA	1:C:1591:TRP:CE2	2.55	0.41
1:C:1846:LEU:O	1:C:1847:LEU:HA	2.21	0.41
1:C:1984:THR:O	1:C:1986:LYS:N	2.53	0.41
1:C:2206:HIS:NE2	1:C:2472:PRO:HD2	2.35	0.41
1:C:2274:ILE:HD13	1:C:2274:ILE:HA	1.98	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2459:SER:HA	1:C:2460:VAL:HA	1.47	0.41
2:D:132:ILE:HG21	2:D:174:LEU:HD11	2.00	0.41
1:A:175:TYR:HD1	1:A:190:LEU:HD13	1.85	0.41
1:A:196:GLY:HA2	1:A:198:LEU:HD12	2.01	0.41
1:A:800:LEU:HB3	1:A:804:ILE:HD12	2.02	0.41
1:A:1593:LEU:HD23	1:A:1596:ARG:HH21	1.85	0.41
1:A:2267:SER:HB3	1:A:2316:PHE:CE2	2.54	0.41
1:C:180:LEU:HD21	1:C:192:ALA:HB2	2.01	0.41
1:C:219:ILE:O	1:C:219:ILE:CG2	2.68	0.41
1:C:233:SER:C	1:C:235:LEU:H	2.28	0.41
1:C:257:LEU:HD21	1:C:294:ILE:HG21	2.03	0.41
1:C:798:LEU:O	1:C:801:LEU:HB2	2.21	0.41
1:C:849:LEU:HD21	1:C:1546:VAL:CG2	2.51	0.41
1:C:1033:GLU:OE1	1:C:1075:ASN:ND2	2.53	0.41
1:C:1569:LYS:O	1:C:1573:MET:N	2.44	0.41
1:C:1766:ASN:O	1:C:1767:PHE:N	2.53	0.41
1:C:2174:LYS:O	1:C:2175:SER:HB2	2.20	0.41
1:A:271:LEU:O	1:A:272:ARG:HB2	2.21	0.41
1:A:332:ARG:HA	1:A:372:LEU:HD13	2.02	0.41
1:A:928:LEU:HD21	1:A:942:GLN:HB3	2.02	0.41
1:A:1629:LEU:O	1:A:1630:ASN:N	2.53	0.41
1:C:631:VAL:HA	1:C:634:LEU:HD12	2.01	0.41
1:C:854:LYS:HG3	1:C:1584:CYS:HB2	2.02	0.41
1:C:1113:ILE:N	1:C:1150:LEU:HD22	2.36	0.41
1:C:1817:ILE:O	1:C:1821:VAL:HG23	2.21	0.41
1:C:2157:PHE:CD1	1:C:2160:HIS:CG	3.09	0.41
2:D:84:GLN:HB3	2:D:89:TRP:CB	2.32	0.41
3:F:107:UNK:C	3:F:108:UNK:HA	2.50	0.41
1:A:87:ILE:HG23	1:A:99:ARG:HE	1.86	0.41
1:A:971:ARG:HH22	1:A:984:GLN:HG3	1.84	0.41
1:A:1626:LYS:HB2	1:A:1629:LEU:HG	2.01	0.41
1:A:2419:ARG:HA	1:A:2422:LEU:HB3	2.02	0.41
2:B:173:MET:HB2	2:B:215:LEU:HD11	2.01	0.41
1:C:1131:ASN:CG	1:C:1132:ASN:H	2.28	0.41
1:C:1249:GLN:NE2	1:C:1275:GLU:HG2	2.36	0.41
1:C:1430:GLU:CB	1:C:1431:VAL:N	2.81	0.41
1:C:1909:PRO:HA	1:C:1912:LEU:N	2.35	0.41
1:C:2113:PHE:N	1:C:2125:TYR:O	2.53	0.41
2:D:189:PRO:HG2	2:D:196:HIS:H	1.86	0.41
3:F:711:UNK:O	3:F:713:UNK:N	2.53	0.41
5:I:703:ILE:HA	5:I:706:VAL:HG23	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:I:719:LYS:HA	5:I:720:PRO:HA	1.91	0.41
5:J:705:GLU:O	5:J:709:PHE:N	2.53	0.41
1:A:88:PHE:HZ	1:A:151:ALA:HB2	1.85	0.41
1:A:305:PHE:O	1:A:309:PHE:HB2	2.20	0.41
1:A:854:THR:HG22	1:A:855:GLU:N	2.35	0.41
1:A:1280:PHE:CZ	1:A:1330:LEU:HD13	2.55	0.41
1:A:1386:ILE:HA	1:A:1389:HIS:HB3	2.02	0.41
1:A:2219:LEU:O	1:A:2223:VAL:HG23	2.20	0.41
2:B:17:TRP:CE2	2:B:288:TYR:HB3	2.56	0.41
1:C:131:ASN:HB3	1:C:135:PHE:CE2	2.55	0.41
1:C:153:VAL:HG11	1:C:172:ARG:HG3	2.03	0.41
1:C:653:VAL:CG2	3:E:100:UNK:HA	2.51	0.41
1:C:766:PRO:HD3	1:C:806:ILE:HG22	2.03	0.41
1:C:1720:LEU:O	1:C:1724:GLU:HB3	2.21	0.41
1:C:2080:VAL:HG13	1:C:2091:ILE:HA	2.01	0.41
2:D:41:THR:C	2:D:44:LYS:H	2.28	0.41
1:A:291:THR:HG22	1:A:296:ARG:HB3	2.03	0.41
1:A:472:PRO:HG2	1:A:476:LYS:HB3	2.03	0.41
1:A:671:LEU:C	1:A:672:ALA:N	2.78	0.41
1:A:687:GLU:O	1:A:689:PHE:N	2.53	0.41
1:A:784:GLU:O	1:A:788:VAL:HG22	2.21	0.41
1:A:792:GLU:HG3	1:A:794:THR:OG1	2.21	0.41
1:A:812:SER:HB2	1:A:851:ILE:HG13	2.02	0.41
1:A:1222:ILE:HG12	1:A:1285:VAL:HG11	2.03	0.41
1:A:1824:LYS:HD2	1:A:1861:MET:HB2	2.01	0.41
1:A:1870:ILE:O	1:A:1872:THR:N	2.54	0.41
1:C:268:ILE:HG12	1:C:311:GLN:CD	2.45	0.41
1:C:437:LEU:HA	1:C:440:ASP:CB	2.44	0.41
1:C:783:LEU:N	1:C:784:GLY:HA3	2.28	0.41
1:C:862:ARG:HH22	1:C:1542:TYR:HB3	1.85	0.41
1:C:1360:PHE:HB3	1:C:1372:LEU:HD22	2.03	0.41
1:C:1431:VAL:HG22	1:C:1463:VAL:HG13	2.03	0.41
1:C:1512:PHE:O	1:C:1515:ALA:N	2.53	0.41
1:C:1541:ALA:CB	1:C:1542:TYR:CA	2.97	0.41
1:C:1576:THR:O	1:C:1580:ARG:N	2.49	0.41
1:C:1615:ALA:O	1:C:1619:ARG:N	2.53	0.41
1:C:1714:LEU:HD21	1:C:1751:PHE:O	2.20	0.41
1:C:2187:PHE:HE1	1:C:2324:LEU:HD13	1.85	0.41
1:C:2242:LYS:O	1:C:2243:VAL:N	2.53	0.41
1:C:2414:LYS:HA	1:C:2417:ILE:HG13	2.03	0.41
3:F:704:UNK:O	3:F:707:UNK:N	2.54	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:LEU:HA	1:A:209:PHE:HB3	2.03	0.41
1:A:260:VAL:HG22	1:A:303:GLN:HG2	2.03	0.41
1:A:417:VAL:HB	1:A:418:SER:N	2.36	0.41
1:A:422:ILE:HG12	1:A:466:LEU:HD13	2.03	0.41
1:A:422:ILE:CG1	1:A:466:LEU:HD13	2.50	0.41
1:A:735:GLU:CD	3:F:117:UNK:HA	2.46	0.41
1:A:817:ARG:HD2	1:A:867:LEU:HD13	2.02	0.41
1:A:979:ASP:HA	1:A:982:PHE:CD2	2.56	0.41
1:A:1366:THR:HA	1:A:1369:ALA:HB3	2.02	0.41
1:A:1499:TYR:H	1:A:1594:ARG:HH21	1.68	0.41
1:A:1630:ASN:O	1:A:1633:LEU:HB2	2.21	0.41
1:A:1669:LEU:O	1:A:1672:LEU:HB3	2.20	0.41
1:A:1715:ARG:HH21	1:A:1719:LYS:HE3	1.85	0.41
1:A:1910:LEU:HB3	1:A:1912:TYR:H	1.85	0.41
1:A:1968:GLY:C	1:A:1992:LEU:HD11	2.46	0.41
1:A:1997:LYS:H	1:A:1998:ARG:N	2.19	0.41
1:A:2124:VAL:HG12	1:A:2178:TRP:CE3	2.54	0.41
1:A:2285:LEU:HB2	1:A:2286:ASP:H	1.78	0.41
1:A:2404:VAL:HB	1:A:2408:GLU:HB2	2.03	0.41
1:A:2431:LEU:HA	1:A:2447:GLN:CG	2.51	0.41
2:B:55:VAL:HG13	2:B:57:LEU:HG	2.03	0.41
2:B:232:ARG:HA	2:B:244:THR:HB	2.02	0.41
1:C:114:LEU:N	1:C:118:VAL:HG22	2.35	0.41
1:C:143:SER:HA	1:C:146:LYS:HE3	2.02	0.41
1:C:217:THR:O	1:C:221:TRP:CG	2.74	0.41
1:C:234:LYS:NZ	1:C:238:ARG:HE	2.18	0.41
1:C:330:LEU:O	1:C:334:GLU:HB2	2.20	0.41
1:C:378:ALA:CA	1:C:379:PHE:N	2.80	0.41
1:C:487:MET:HE2	1:C:487:MET:HB3	2.01	0.41
1:C:613:ALA:HB1	1:C:643:LYS:NZ	2.36	0.41
1:C:683:MET:O	1:C:686:ASN:HB2	2.21	0.41
1:C:721:GLU:HG3	1:C:722:LEU:HD12	2.03	0.41
1:C:801:LEU:O	1:C:802:MET:N	2.53	0.41
1:C:1053:ASN:HD21	1:C:1061:VAL:HG21	1.85	0.41
1:C:1066:LEU:HD11	1:C:1103:ILE:HG13	2.02	0.41
1:C:1088:VAL:HG22	1:C:1103:ILE:CG2	2.50	0.41
1:C:1281:PHE:CE1	1:C:1332:LEU:HD13	2.56	0.41
1:C:1421:LYS:HB2	1:C:1435:LYS:HB2	2.01	0.41
1:C:1655:TYR:O	1:C:1659:LYS:N	2.53	0.41
1:C:1726:ARG:HG3	1:C:1727:VAL:H	1.84	0.41
1:C:2134:ARG:HB3	1:C:2368:ILE:HB	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2172:SER:HB2	1:C:2174:LYS:C	2.46	0.41
1:C:2185:ASP:O	1:C:2286:MET:HG3	2.21	0.41
1:C:2258:ARG:HD2	1:C:2329:GLU:HB2	2.03	0.41
2:D:9:GLY:HA2	2:D:296:VAL:HG23	2.03	0.41
2:D:141:ARG:HG2	2:D:153:GLN:HB3	2.02	0.41
1:A:449:PHE:C	1:A:451:VAL:N	2.79	0.41
1:A:543:SER:O	1:A:544:ILE:HG13	2.21	0.41
1:A:759:ILE:HG13	1:A:760:LEU:N	2.36	0.41
1:A:1049:ILE:HD13	1:A:1049:ILE:N	2.36	0.41
1:A:1756:ALA:O	1:A:1759:ASN:HB2	2.21	0.41
1:A:1972:ALA:C	1:A:1973:SER:HA	2.46	0.41
1:C:280:ARG:NH2	1:C:328:THR:HB	2.34	0.41
1:C:500:LEU:HA	1:C:503:LEU:HD12	2.04	0.41
1:C:576:CYS:HB3	1:C:580:LEU:HD22	2.03	0.41
1:C:678:LEU:HB2	1:C:727:LYS:HD2	2.03	0.41
1:C:963:ILE:HG13	1:C:964:ILE:H	1.85	0.41
1:C:968:ILE:HA	1:C:971:MET:HB3	2.01	0.41
1:C:969:LEU:C	1:C:972:ARG:HG2	2.46	0.41
1:C:994:LYS:HA	1:C:995:GLN:CB	2.51	0.41
1:C:1093:TYR:O	1:C:1100:LYS:HD3	2.21	0.41
1:C:1097:SER:C	1:C:1098:LEU:N	2.79	0.41
1:C:1967:TRP:CD1	1:C:1994:LEU:O	2.74	0.41
1:C:2068:PRO:HB3	1:C:2071:LEU:HD13	2.02	0.41
1:C:2089:LYS:N	1:C:2090:PRO:CD	2.84	0.41
2:D:275:ARG:HG2	2:D:287:GLN:CD	2.46	0.41
5:J:757:LYS:HB2	5:J:784:GLN:HG2	2.02	0.41
1:A:180:ILE:H	1:A:180:ILE:HG12	1.78	0.40
1:A:1173:HIS:CD2	1:A:1178:GLN:HB2	2.56	0.40
1:A:1523:LEU:HD12	1:A:1524:LEU:HG	2.03	0.40
1:A:1985:MET:HA	1:A:1988:ALA:HB2	2.02	0.40
1:A:2251:THR:CG2	1:A:2255:ARG:HD2	2.51	0.40
2:B:213:ILE:HB	2:B:214:LEU:CA	2.51	0.40
1:C:1991:LEU:HA	1:C:1994:LEU:HG	2.03	0.40
1:C:2133:ILE:C	1:C:2170:PRO:HG3	2.46	0.40
1:C:2470:TRP:CD1	1:C:2472:PRO:HD3	2.56	0.40
1:A:661:GLN:HG2	1:A:672:ALA:HB1	2.03	0.40
1:A:1580:LEU:HB3	1:A:1584:LYS:NZ	2.36	0.40
1:A:2431:LEU:HA	1:A:2447:GLN:HG2	2.03	0.40
2:B:25:SER:OG	2:B:60:ILE:HD11	2.22	0.40
2:B:40:ILE:HD12	2:B:301:ASN:HB2	2.03	0.40
2:B:194:ALA:HB1	2:B:196:HIS:NE2	2.36	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:857:ASN:HB3	1:C:1586:LYS:N	2.37	0.40
1:C:861:ILE:HG22	1:C:864:GLY:N	2.36	0.40
1:C:976:PRO:HA	1:C:979:LEU:HB2	2.03	0.40
1:C:2000:ARG:HG3	1:C:2003:GLU:OE1	2.21	0.40
1:C:2108:GLN:HE22	1:C:2130:HIS:HB2	1.86	0.40
1:A:120:GLU:HG3	1:A:159:TYR:CZ	2.56	0.40
1:A:172:LEU:HD21	1:A:208:ASP:OD1	2.21	0.40
1:A:813:ASN:C	1:A:817:ARG:HG3	2.47	0.40
1:A:1151:LEU:HD11	1:A:1184:LEU:HD21	2.03	0.40
1:A:1165:ALA:C	1:A:1166:LEU:HD12	2.46	0.40
1:A:2095:PHE:CD2	1:A:2113:ILE:HG12	2.56	0.40
1:A:2140:LEU:HA	1:A:2143:LEU:HB2	2.04	0.40
1:A:2202:ILE:HA	1:A:2205:TRP:HB3	2.03	0.40
1:A:2398:ALA:HA	1:A:2399:ILE:HA	1.82	0.40
1:C:194:ASN:H	1:C:195:THR:N	2.19	0.40
1:C:277:LEU:HD11	1:C:324:SER:HB2	2.02	0.40
1:C:439:LEU:O	1:C:443:ARG:HG2	2.20	0.40
1:C:446:LEU:HG	1:C:450:PHE:CE2	2.56	0.40
1:C:546:GLU:HA	1:C:549:ARG:CB	2.52	0.40
1:C:763:VAL:HG21	1:C:803:PRO:HB3	2.02	0.40
1:C:983:PHE:CB	1:C:1022:ILE:HG12	2.23	0.40
1:C:1005:TYR:C	1:C:1007:VAL:H	2.29	0.40
1:C:1452:ALA:HA	1:C:1455:LYS:HB3	2.03	0.40
1:C:1723:GLY:HA2	1:C:1726:ARG:HD3	2.03	0.40
3:F:251:UNK:HA	3:F:254:UNK:CB	2.51	0.40
3:F:262:UNK:O	3:F:265:UNK:N	2.53	0.40
5:I:654:ASN:O	5:I:659:LEU:HB2	2.20	0.40
1:A:277:ILE:H	1:A:277:ILE:HG13	1.78	0.40
1:A:416:LEU:HD12	1:A:459:LEU:HD21	2.03	0.40
1:A:654:GLU:O	1:A:658:GLU:N	2.54	0.40
1:A:670:GLN:HE22	1:A:716:LYS:HB2	1.86	0.40
1:A:1024:ILE:O	1:A:1024:ILE:HG22	2.22	0.40
1:A:1033:GLY:HA2	1:A:1034:GLU:HA	1.77	0.40
1:A:1440:LEU:CD2	1:A:1622:MET:HG2	2.47	0.40
1:A:2131:ILE:HD13	1:A:2174:GLY:HA3	2.03	0.40
1:A:2450:LYS:HD3	1:A:2450:LYS:HA	1.89	0.40
1:C:86:ASN:HD21	1:C:124:GLN:HB3	1.86	0.40
1:C:366:ARG:HA	1:C:369:VAL:CB	2.51	0.40
1:C:602:GLU:HA	1:C:603:HIS:O	2.22	0.40
1:C:726:LEU:HD13	1:C:761:LEU:HD23	2.03	0.40
1:C:1151:GLN:HB3	1:C:1152:LEU:H	1.61	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1226:ASN:HD22	1:C:1286:VAL:HG13	1.86	0.40
1:C:1259:LEU:HD23	1:C:1259:LEU:HA	1.93	0.40
1:C:1541:ALA:HB3	1:C:1542:TYR:HA	2.04	0.40
1:C:2005:LEU:O	1:C:2065:HIS:HA	2.22	0.40
1:C:2242:LYS:C	1:C:2245:TRP:HB3	2.47	0.40
1:C:2432:LYS:HA	1:C:2444:LEU:HD12	2.02	0.40
2:D:249:HIS:C	2:D:250:GLN:N	2.80	0.40
3:E:500:UNK:CB	3:E:702:UNK:HA	2.51	0.40
3:F:803:UNK:C	3:F:805:UNK:N	2.85	0.40
5:J:730:VAL:HG21	5:J:790:PRO:N	2.36	0.40
1:A:138:HIS:HB3	1:A:145:LYS:HE2	2.03	0.40
1:A:600:ILE:HA	1:A:602:HIS:HB2	2.03	0.40
1:A:699:ILE:HD12	1:A:717:THR:HG22	2.03	0.40
1:A:1164:LYS:CB	1:A:1170:ARG:HG3	2.52	0.40
1:A:1359:LEU:HA	1:A:1362:PRO:HD3	2.03	0.40
1:A:2458:VAL:HG13	1:A:2459:GLU:H	1.87	0.40
1:C:157:ILE:CG1	1:C:172:ARG:HH22	2.31	0.40
1:C:309:LEU:HA	1:C:346:LYS:NZ	2.35	0.40
1:C:577:PHE:CG	1:C:592:PHE:HB2	2.57	0.40
1:C:750:ASP:CG	1:C:751:GLU:H	2.30	0.40
1:C:818:ARG:HB2	1:C:818:ARG:NH1	2.37	0.40
1:C:1431:VAL:HG13	1:C:1466:ALA:CB	2.52	0.40
1:C:1682:ALA:HB2	1:C:1717:ARG:HH22	1.87	0.40
1:C:1742:LEU:O	1:C:1746:LEU:HD13	2.21	0.40
1:C:1762:TRP:CE3	1:C:1763:ALA:HA	2.56	0.40
1:C:1913:VAL:O	1:C:1917:MET:N	2.52	0.40
1:C:2023:GLU:HA	1:C:2026:MET:HG2	2.02	0.40
3:E:371:UNK:C	3:E:373:UNK:N	2.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1309/2474 (53%)	872 (67%)	313 (24%)	124 (10%)	0	8
1	C	1267/2474 (51%)	849 (67%)	290 (23%)	128 (10%)	0	7
2	B	178/303 (59%)	122 (68%)	45 (25%)	11 (6%)	1	13
2	D	173/303 (57%)	113 (65%)	44 (25%)	16 (9%)	0	8
4	G	75/426 (18%)	57 (76%)	12 (16%)	6 (8%)	1	9
4	H	80/426 (19%)	43 (54%)	22 (28%)	15 (19%)	0	2
5	I	95/1176 (8%)	52 (55%)	29 (30%)	14 (15%)	0	3
5	J	88/1176 (8%)	52 (59%)	23 (26%)	13 (15%)	0	3
All	All	3265/8758 (37%)	2160 (66%)	778 (24%)	327 (10%)	1	7

All (327) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	ASP
1	A	112	SER
1	A	224	THR
1	A	257	TYR
1	A	342	LEU
1	A	348	ASP
1	A	402	ILE
1	A	490	PRO
1	A	582	ILE
1	A	583	HIS
1	A	586	TYR
1	A	650	ASP
1	A	767	CYS
1	A	769	ASP
1	A	771	SER
1	A	791	LYS
1	A	854	THR
1	A	1083	MET
1	A	1135	GLU
1	A	1192	ASN
1	A	1342	GLN
1	A	1428	GLU
1	A	1447	SER
1	A	1477	GLU
1	A	1583	GLN
1	A	1732	ARG
1	A	1750	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1753	TRP
1	A	1871	GLY
1	A	1977	PHE
1	A	1978	GLY
1	A	2089	ILE
1	A	2247	ARG
1	A	2248	SER
1	A	2288	ILE
1	A	2328	VAL
1	A	2334	SER
1	A	2391	ASN
1	A	2392	GLU
1	A	2426	ARG
1	A	2436	ILE
1	A	2440	ASN
1	A	2441	ASP
1	A	2442	LEU
1	A	2453	GLN
2	B	106	SER
2	B	107	PRO
2	B	213	ILE
1	C	167	PRO
1	C	233	SER
1	C	273	ARG
1	C	409	ASN
1	C	425	PHE
1	C	473	PRO
1	C	490	CYS
1	C	491	PRO
1	C	530	LYS
1	C	534	SER
1	C	673	ALA
1	C	838	PRO
1	C	861	ILE
1	C	1085	PRO
1	C	1152	LEU
1	C	1193	ASN
1	C	1286	VAL
1	C	1287	GLU
1	C	1293	GLN
1	C	1585	GLN
1	C	1586	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1588	ILE
1	C	1750	HIS
1	C	1857	PRO
1	C	1878	VAL
1	C	1985	GLU
1	C	1997	MET
1	C	2090	PRO
1	C	2241	TYR
1	C	2330	VAL
1	C	2355	LEU
1	C	2378	LYS
1	C	2394	GLU
2	D	5	LEU
2	D	33	SER
2	D	56	ARG
2	D	298	VAL
4	H	121	TYR
4	H	140	THR
4	H	141	ASN
5	I	687	LYS
5	I	764	ILE
5	J	692	SER
5	J	741	LEU
5	J	764	ILE
1	A	178	VAL
1	A	261	ASN
1	A	341	TYR
1	A	359	TYR
1	A	395	TYR
1	A	493	ASP
1	A	539	ASN
1	A	600	ILE
1	A	669	PRO
1	A	743	THR
1	A	751	VAL
1	A	838	LEU
1	A	1022	SER
1	A	1091	GLU
1	A	1590	GLN
1	A	1628	VAL
1	A	1731	TRP
1	A	1733	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1868	ILE
1	A	1942	VAL
1	A	1979	GLU
1	A	2298	GLY
1	A	2390	ALA
2	B	245	THR
2	B	296	VAL
1	C	97	PRO
1	C	177	LEU
1	C	184	SER
1	C	234	LYS
1	C	235	LEU
1	C	324	SER
1	C	338	LEU
1	C	416	ILE
1	C	601	ILE
1	C	603	HIS
1	C	656	ILE
1	C	748	SER
1	C	925	LEU
1	C	1176	VAL
1	C	1477	GLY
1	C	1519	ILE
1	C	1541	ALA
1	C	1602	ILE
1	C	1612	ILE
1	C	1873	GLY
1	C	1913	VAL
1	C	2087	GLY
1	C	2091	ILE
1	C	2146	VAL
1	C	2184	SER
1	C	2185	ASP
1	C	2279	ASP
1	C	2308	LEU
1	C	2332	GLY
2	D	6	VAL
4	G	66	LYS
4	G	77	THR
4	H	72	THR
4	H	77	THR
4	H	78	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	H	131	VAL
5	I	686	LYS
5	I	716	THR
5	J	653	THR
5	J	702	THR
5	J	730	VAL
5	J	747	ASP
5	J	755	PHE
5	J	790	PRO
1	A	304	TRP
1	A	377	ALA
1	A	450	LYS
1	A	555	PHE
1	A	568	ASP
1	A	602	HIS
1	A	766	LYS
1	A	778	ALA
1	A	1233	LYS
1	A	1523	LEU
1	A	1593	LEU
1	A	1736	PRO
1	A	1813	ASN
1	A	2083	ALA
1	A	2122	LYS
1	A	2326	MET
1	A	2382	GLY
1	A	2443	ASP
2	B	177	ALA
1	C	122	GLN
1	C	176	TYR
1	C	224	LEU
1	C	259	PRO
1	C	267	ASN
1	C	275	ALA
1	C	341	PRO
1	C	683	MET
1	C	712	VAL
1	C	772	SER
1	C	1013	PRO
1	C	1197	ASP
1	C	1839	SER
1	C	2063	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	2097	PHE
1	C	2116	LYS
1	C	2154	ALA
1	C	2302	CYS
1	C	2374	LEU
2	D	193	ASP
2	D	195	SER
2	D	238	ASP
4	G	131	VAL
4	H	112	PRO
4	H	120	ASP
4	H	177	GLY
4	H	183	ASP
5	I	663	SER
5	I	668	ASP
1	A	519	ASN
1	A	717	THR
1	A	720	GLU
1	A	1076	GLU
1	A	1248	GLN
1	A	1333	PRO
1	A	1539	ALA
1	A	1597	SER
1	A	1602	PRO
1	A	1711	LYS
1	A	1751	ASN
1	A	1870	ILE
1	A	2304	ALA
2	B	73	GLY
2	B	277	TRP
1	C	116	ARG
1	C	139	HIS
1	C	339	LYS
1	C	340	ALA
1	C	370	TYR
1	C	493	SER
1	C	592	PHE
1	C	1084	MET
1	C	1216	LYS
1	C	1733	TRP
1	C	2111	ARG
2	D	206	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	242	LEU
4	G	145	PRO
4	H	44	LEU
4	H	74	LYS
5	I	698	ARG
5	I	708	GLY
5	I	730	VAL
1	A	269	VAL
1	A	580	GLN
1	A	1584	LYS
1	A	1599	VAL
1	A	1820	ILE
1	A	2085	GLY
2	B	219	VAL
1	C	96	VAL
1	C	995	GLN
1	C	1510	ASN
1	C	1599	SER
1	C	1611	ARG
1	C	1848	THR
1	C	2083	THR
1	C	2110	PRO
1	C	2419	ASN
2	D	272	HIS
4	G	137	VAL
4	G	149	CYS
5	I	670	VAL
5	I	715	SER
5	I	736	PRO
5	J	736	PRO
1	A	122	PHE
1	A	842	PRO
1	A	994	GLN
1	A	1106	GLY
1	A	1205	LYS
1	A	1348	ALA
1	A	2470	PRO
2	B	183	CYS
1	C	143	SER
1	C	298	ASP
1	C	1248	ILE
1	C	1388	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	2379	ILE
2	D	22	GLY
2	D	91	VAL
2	D	277	TRP
4	H	145	PRO
5	J	699	LYS
1	A	1242	ILE
1	A	1890	ILE
1	A	1940	SER
1	A	2305	ILE
1	C	299	PRO
1	C	528	GLY
1	C	561	GLY
1	C	1019	ILE
1	C	1563	LEU
1	C	1601	VAL
1	C	2300	GLY
1	C	2312	PHE
1	C	2347	VAL
1	C	2469	GLY
2	D	219	VAL
4	H	130	GLY
5	I	749	GLU
1	A	707	PRO
1	A	1334	ILE
1	A	1458	LYS
1	A	2013	GLY
1	C	166	LEU
1	C	508	PRO
1	C	752	VAL
1	C	1630	VAL
1	C	2446	VAL
5	I	682	ILE
1	A	930	ASP
1	C	1364	PRO
1	C	1727	VAL
1	C	1942	SER
1	C	2115	ILE
2	D	23	VAL
1	A	1517	ILE
1	A	2265	VAL
2	B	65	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1468	ALA
1	C	2082	GLY
1	C	2333	ILE
5	J	703	ILE
5	J	756	GLY
1	A	2310	PHE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	2029/2219 (91%)	1689 (83%)	340 (17%)	2	10
1	C	2029/2219 (91%)	1675 (83%)	354 (17%)	2	9
2	B	264/267 (99%)	223 (84%)	41 (16%)	2	12
2	D	264/267 (99%)	230 (87%)	34 (13%)	4	15
5	I	137/1066 (13%)	113 (82%)	24 (18%)	2	9
5	J	137/1066 (13%)	109 (80%)	28 (20%)	1	7
All	All	4860/7104 (68%)	4039 (83%)	821 (17%)	4	10

All (821) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	LEU
1	A	89	ASP
1	A	90	LYS
1	A	92	LYS
1	A	93	SER
1	A	110	LEU
1	A	111	THR
1	A	112	SER
1	A	115	ARG
1	A	120	GLU
1	A	121	GLN
1	A	127	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	128	SER
1	A	133	ILE
1	A	150	LEU
1	A	152	VAL
1	A	153	ASP
1	A	179	LEU
1	A	180	ILE
1	A	187	VAL
1	A	205	LEU
1	A	210	VAL
1	A	216	THR
1	A	218	ILE
1	A	222	THR
1	A	224	THR
1	A	228	ASN
1	A	229	SER
1	A	234	LEU
1	A	238	ARG
1	A	243	LEU
1	A	244	ILE
1	A	245	ILE
1	A	252	SER
1	A	255	LEU
1	A	256	LEU
1	A	257	TYR
1	A	265	ASP
1	A	269	VAL
1	A	273	ASP
1	A	276	LEU
1	A	290	LEU
1	A	302	LYS
1	A	304	TRP
1	A	307	ARG
1	A	320	THR
1	A	321	ASN
1	A	324	VAL
1	A	329	LEU
1	A	330	VAL
1	A	334	LEU
1	A	341	TYR
1	A	342	LEU
1	A	343	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	354	MET
1	A	364	ILE
1	A	378	PHE
1	A	384	THR
1	A	386	LYS
1	A	388	LEU
1	A	395	TYR
1	A	396	LEU
1	A	401	ASN
1	A	402	ILE
1	A	409	ASN
1	A	419	ILE
1	A	421	ASP
1	A	422	ILE
1	A	431	SER
1	A	437	ILE
1	A	439	ASP
1	A	441	ILE
1	A	447	THR
1	A	449	PHE
1	A	453	LYS
1	A	466	LEU
1	A	474	PHE
1	A	480	LYS
1	A	482	LEU
1	A	487	LEU
1	A	489	CYS
1	A	493	ASP
1	A	511	SER
1	A	512	THR
1	A	520	LEU
1	A	534	ASN
1	A	549	LYS
1	A	554	SER
1	A	562	SER
1	A	571	ILE
1	A	583	HIS
1	A	592	VAL
1	A	597	ILE
1	A	600	ILE
1	A	607	VAL
1	A	616	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	622	ASP
1	A	630	VAL
1	A	633	LEU
1	A	636	VAL
1	A	654	GLU
1	A	655	ILE
1	A	660	LEU
1	A	662	HIS
1	A	670	GLN
1	A	677	LEU
1	A	680	LEU
1	A	685	ASN
1	A	698	ILE
1	A	699	ILE
1	A	701	ARG
1	A	703	SER
1	A	719	LEU
1	A	723	THR
1	A	725	LEU
1	A	739	THR
1	A	743	THR
1	A	751	VAL
1	A	756	ILE
1	A	759	ILE
1	A	760	LEU
1	A	761	ASP
1	A	764	LEU
1	A	772	SER
1	A	774	VAL
1	A	777	THR
1	A	779	LEU
1	A	793	MET
1	A	805	ILE
1	A	817	ARG
1	A	824	LEU
1	A	827	LEU
1	A	848	LEU
1	A	849	ILE
1	A	860	ILE
1	A	921	ILE
1	A	927	ILE
1	A	944	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	951	LEU
1	A	954	ARG
1	A	957	SER
1	A	958	PHE
1	A	962	ILE
1	A	968	LEU
1	A	985	LEU
1	A	996	ILE
1	A	997	ARG
1	A	1003	ILE
1	A	1006	VAL
1	A	1013	ILE
1	A	1015	LYS
1	A	1019	THR
1	A	1020	ILE
1	A	1027	ILE
1	A	1043	LEU
1	A	1049	ILE
1	A	1050	LEU
1	A	1054	GLN
1	A	1067	SER
1	A	1068	LEU
1	A	1069	VAL
1	A	1082	ILE
1	A	1083	MET
1	A	1086	VAL
1	A	1087	VAL
1	A	1090	THR
1	A	1102	ILE
1	A	1111	ASN
1	A	1116	GLU
1	A	1117	MET
1	A	1121	ILE
1	A	1127	ARG
1	A	1137	THR
1	A	1140	THR
1	A	1144	LEU
1	A	1150	GLN
1	A	1153	THR
1	A	1161	VAL
1	A	1170	ARG
1	A	1173	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1175	VAL
1	A	1182	LYS
1	A	1201	VAL
1	A	1207	TYR
1	A	1209	ASP
1	A	1212	GLN
1	A	1214	THR
1	A	1229	CYS
1	A	1230	SER
1	A	1233	LYS
1	A	1236	GLU
1	A	1243	ARG
1	A	1244	ARG
1	A	1262	SER
1	A	1265	VAL
1	A	1267	VAL
1	A	1285	VAL
1	A	1287	LEU
1	A	1290	SER
1	A	1326	ASP
1	A	1332	ILE
1	A	1353	TYR
1	A	1354	LYS
1	A	1356	VAL
1	A	1357	GLU
1	A	1366	THR
1	A	1370	LEU
1	A	1373	ILE
1	A	1379	GLN
1	A	1380	THR
1	A	1384	ILE
1	A	1401	THR
1	A	1402	TRP
1	A	1404	GLU
1	A	1408	ARG
1	A	1425	ASP
1	A	1430	MET
1	A	1433	LYS
1	A	1434	LEU
1	A	1476	LEU
1	A	1480	ASP
1	A	1491	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1493	SER
1	A	1504	CYS
1	A	1515	VAL
1	A	1523	LEU
1	A	1524	LEU
1	A	1527	GLU
1	A	1534	GLU
1	A	1555	ILE
1	A	1556	ILE
1	A	1557	LYS
1	A	1569	LEU
1	A	1570	THR
1	A	1579	LEU
1	A	1585	ASN
1	A	1587	ASP
1	A	1612	PHE
1	A	1626	LYS
1	A	1659	LEU
1	A	1669	LEU
1	A	1682	ASP
1	A	1713	LEU
1	A	1723	TRP
1	A	1731	TRP
1	A	1742	SER
1	A	1745	LEU
1	A	1747	THR
1	A	1811	SER
1	A	1820	ILE
1	A	1823	ILE
1	A	1824	LYS
1	A	1830	ILE
1	A	1832	LEU
1	A	1837	SER
1	A	1839	GLN
1	A	1844	LEU
1	A	1856	GLU
1	A	1868	ILE
1	A	1870	ILE
1	A	1875	GLU
1	A	1876	VAL
1	A	1884	ILE
1	A	1911	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1918	ILE
1	A	1921	GLU
1	A	1930	LEU
1	A	1948	GLU
1	A	1949	LEU
1	A	1955	ILE
1	A	1956	ARG
1	A	1969	LEU
1	A	1976	PHE
1	A	1979	GLU
1	A	1995	MET
1	A	1998	ARG
1	A	2003	LEU
1	A	2004	ARG
1	A	2017	ASN
1	A	2035	LEU
1	A	2041	ILE
1	A	2049	ILE
1	A	2081	THR
1	A	2090	VAL
1	A	2092	ILE
1	A	2093	SER
1	A	2095	PHE
1	A	2105	LYS
1	A	2109	ARG
1	A	2111	PHE
1	A	2122	LYS
1	A	2124	VAL
1	A	2125	LEU
1	A	2131	ILE
1	A	2134	ASP
1	A	2148	LEU
1	A	2151	ASP
1	A	2159	LEU
1	A	2191	GLU
1	A	2202	ILE
1	A	2219	LEU
1	A	2230	LEU
1	A	2231	ASN
1	A	2234	GLU
1	A	2250	GLU
1	A	2253	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2263	LEU
1	A	2272	ILE
1	A	2275	LEU
1	A	2283	LEU
1	A	2285	LEU
1	A	2288	ILE
1	A	2291	LYS
1	A	2292	VAL
1	A	2295	ILE
1	A	2299	ASP
1	A	2308	GLU
1	A	2322	LEU
1	A	2331	ILE
1	A	2335	PHE
1	A	2336	ARG
1	A	2338	THR
1	A	2353	LEU
1	A	2357	LEU
1	A	2360	PHE
1	A	2367	ASN
1	A	2372	LEU
1	A	2385	LEU
1	A	2387	VAL
1	A	2389	ASN
1	A	2416	ARG
1	A	2424	LEU
1	A	2425	LYS
1	A	2426	ARG
1	A	2427	ILE
1	A	2428	THR
1	A	2431	LEU
1	A	2437	ARG
1	A	2438	ARG
1	A	2450	LYS
2	B	4	ILE
2	B	10	TYR
2	B	20	LEU
2	B	28	ILE
2	B	38	LEU
2	B	39	GLU
2	B	40	ILE
2	B	53	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	55	VAL
2	B	56	ARG
2	B	68	VAL
2	B	78	VAL
2	B	79	THR
2	B	80	SER
2	B	85	GLN
2	B	99	ILE
2	B	103	ASP
2	B	119	VAL
2	B	122	VAL
2	B	142	ILE
2	B	155	THR
2	B	162	LEU
2	B	170	ASP
2	B	182	ASN
2	B	200	VAL
2	B	203	PHE
2	B	213	ILE
2	B	215	LEU
2	B	219	VAL
2	B	230	THR
2	B	233	VAL
2	B	244	THR
2	B	255	ASP
2	B	256	CYS
2	B	259	SER
2	B	270	SER
2	B	281	THR
2	B	286	ARG
2	B	292	HIS
2	B	301	ASN
2	B	302	ASP
1	C	82	PHE
1	C	87	LEU
1	C	91	LYS
1	C	96	VAL
1	C	99	GLU
1	C	110	THR
1	C	123	PHE
1	C	129	SER
1	C	150	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	151	LEU
1	C	153	VAL
1	C	156	LEU
1	C	157	ILE
1	C	161	LEU
1	C	176	TYR
1	C	179	VAL
1	C	181	ILE
1	C	188	VAL
1	C	191	LEU
1	C	196	LEU
1	C	199	LEU
1	C	206	LEU
1	C	207	THR
1	C	210	PHE
1	C	216	ARG
1	C	219	ILE
1	C	223	THR
1	C	225	THR
1	C	231	SER
1	C	234	LYS
1	C	235	LEU
1	C	236	GLU
1	C	237	TYR
1	C	243	LEU
1	C	260	TYR
1	C	264	ILE
1	C	268	ILE
1	C	273	ARG
1	C	278	ILE
1	C	287	LEU
1	C	298	ASP
1	C	301	LEU
1	C	304	GLN
1	C	305	TRP
1	C	314	THR
1	C	317	LEU
1	C	321	THR
1	C	323	ASP
1	C	330	LEU
1	C	331	VAL
1	C	339	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	342	TYR
1	C	349	ASP
1	C	355	MET
1	C	366	ARG
1	C	375	LEU
1	C	379	PHE
1	C	380	ASP
1	C	385	THR
1	C	387	LYS
1	C	389	LEU
1	C	392	ILE
1	C	397	LEU
1	C	412	ASP
1	C	419	SER
1	C	423	ILE
1	C	427	VAL
1	C	437	LEU
1	C	438	ILE
1	C	440	ASP
1	C	450	PHE
1	C	467	LEU
1	C	471	LEU
1	C	483	LEU
1	C	500	LEU
1	C	507	ILE
1	C	517	ARG
1	C	523	SER
1	C	526	LEU
1	C	532	ILE
1	C	541	ASN
1	C	545	ILE
1	C	566	ASP
1	C	568	THR
1	C	572	ILE
1	C	586	GLN
1	C	593	VAL
1	C	596	ILE
1	C	601	ILE
1	C	616	SER
1	C	617	CYS
1	C	630	SER
1	C	637	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	641	LEU
1	C	644	LEU
1	C	651	ASP
1	C	653	VAL
1	C	658	LEU
1	C	664	LEU
1	C	676	ASP
1	C	678	LEU
1	C	712	VAL
1	C	720	LEU
1	C	722	LEU
1	C	724	THR
1	C	730	ASN
1	C	757	ILE
1	C	762	ASP
1	C	764	ILE
1	C	765	LEU
1	C	767	LYS
1	C	768	CYS
1	C	775	VAL
1	C	785	GLU
1	C	794	MET
1	C	795	THR
1	C	801	LEU
1	C	806	ILE
1	C	816	PHE
1	C	818	ARG
1	C	822	LEU
1	C	827	GLN
1	C	828	LEU
1	C	849	LEU
1	C	850	ILE
1	C	852	ILE
1	C	854	LYS
1	C	856	GLU
1	C	860	HIS
1	C	861	ILE
1	C	862	ARG
1	C	865	THR
1	C	866	VAL
1	C	922	ILE
1	C	934	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	946	MET
1	C	948	ILE
1	C	950	GLN
1	C	964	ILE
1	C	967	ILE
1	C	971	MET
1	C	986	LEU
1	C	990	ILE
1	C	992	ILE
1	C	1004	ILE
1	C	1007	VAL
1	C	1010	GLU
1	C	1014	ILE
1	C	1017	LEU
1	C	1019	ILE
1	C	1029	SER
1	C	1048	LEU
1	C	1051	LEU
1	C	1060	ILE
1	C	1063	ILE
1	C	1066	LEU
1	C	1068	SER
1	C	1069	LEU
1	C	1080	SER
1	C	1087	VAL
1	C	1088	VAL
1	C	1094	SER
1	C	1101	ILE
1	C	1103	ILE
1	C	1108	ARG
1	C	1117	GLU
1	C	1118	MET
1	C	1122	ILE
1	C	1128	ARG
1	C	1130	LEU
1	C	1134	ASP
1	C	1141	THR
1	C	1147	LEU
1	C	1151	GLN
1	C	1154	THR
1	C	1162	VAL
1	C	1173	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1174	HIS
1	C	1175	SER
1	C	1176	VAL
1	C	1219	VAL
1	C	1220	ASN
1	C	1230	CYS
1	C	1231	SER
1	C	1240	GLN
1	C	1241	GLU
1	C	1244	ARG
1	C	1245	ARG
1	C	1266	VAL
1	C	1268	VAL
1	C	1291	SER
1	C	1334	ILE
1	C	1359	GLU
1	C	1368	THR
1	C	1372	LEU
1	C	1382	THR
1	C	1386	ILE
1	C	1398	LEU
1	C	1399	GLN
1	C	1401	LYS
1	C	1403	THR
1	C	1406	GLU
1	C	1427	ASP
1	C	1432	MET
1	C	1435	LYS
1	C	1449	SER
1	C	1451	LEU
1	C	1460	LYS
1	C	1463	VAL
1	C	1478	LEU
1	C	1484	ILE
1	C	1491	MET
1	C	1498	LYS
1	C	1499	GLU
1	C	1504	ILE
1	C	1505	LEU
1	C	1506	CYS
1	C	1517	VAL
1	C	1530	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1533	LEU
1	C	1536	GLU
1	C	1540	ARG
1	C	1557	ILE
1	C	1572	THR
1	C	1587	ASN
1	C	1588	ILE
1	C	1598	ARG
1	C	1600	LEU
1	C	1602	ILE
1	C	1603	LYS
1	C	1605	LYS
1	C	1611	ARG
1	C	1619	ARG
1	C	1626	LEU
1	C	1633	THR
1	C	1635	LEU
1	C	1650	SER
1	C	1658	LEU
1	C	1678	THR
1	C	1709	GLU
1	C	1710	ASP
1	C	1714	LEU
1	C	1725	TRP
1	C	1728	CYS
1	C	1730	GLN
1	C	1741	ILE
1	C	1746	LEU
1	C	1747	LEU
1	C	1753	ASN
1	C	1757	LYS
1	C	1816	LEU
1	C	1822	ILE
1	C	1825	ILE
1	C	1832	ILE
1	C	1834	LEU
1	C	1844	LEU
1	C	1846	LEU
1	C	1849	LEU
1	C	1870	ILE
1	C	1872	ILE
1	C	1881	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1900	LEU
1	C	1913	VAL
1	C	1920	ILE
1	C	1927	ARG
1	C	1928	GLN
1	C	1934	ILE
1	C	1936	GLU
1	C	1946	VAL
1	C	1965	GLU
1	C	1967	TRP
1	C	1971	LEU
1	C	1981	GLU
1	C	1996	GLU
1	C	1997	MET
1	C	2005	LEU
1	C	2007	GLU
1	C	2022	TYR
1	C	2027	ASN
1	C	2041	TRP
1	C	2051	ILE
1	C	2059	GLN
1	C	2063	LEU
1	C	2066	VAL
1	C	2078	LEU
1	C	2080	VAL
1	C	2097	PHE
1	C	2102	SER
1	C	2103	VAL
1	C	2104	ILE
1	C	2105	SER
1	C	2113	PHE
1	C	2121	LYS
1	C	2127	LEU
1	C	2136	ASP
1	C	2141	GLN
1	C	2145	LEU
1	C	2150	LEU
1	C	2153	ASP
1	C	2161	LEU
1	C	2163	ILE
1	C	2169	ILE
1	C	2171	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	2178	LEU
1	C	2184	SER
1	C	2190	LEU
1	C	2193	GLU
1	C	2198	LYS
1	C	2206	HIS
1	C	2209	MET
1	C	2220	THR
1	C	2221	LEU
1	C	2240	LEU
1	C	2244	LEU
1	C	2245	TRP
1	C	2256	GLU
1	C	2262	THR
1	C	2265	LEU
1	C	2274	ILE
1	C	2286	MET
1	C	2293	LYS
1	C	2294	VAL
1	C	2295	ILE
1	C	2297	ILE
1	C	2301	ASP
1	C	2308	LEU
1	C	2336	SER
1	C	2343	ASN
1	C	2355	LEU
1	C	2356	MET
1	C	2359	LEU
1	C	2362	PHE
1	C	2364	PHE
1	C	2368	ILE
1	C	2370	TRP
1	C	2374	LEU
1	C	2382	GLU
1	C	2383	THR
1	C	2386	GLN
1	C	2387	LEU
1	C	2396	LEU
1	C	2398	ASN
1	C	2402	THR
1	C	2406	VAL
1	C	2410	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	2417	ILE
1	C	2425	VAL
1	C	2430	THR
1	C	2433	LEU
1	C	2442	ASN
1	C	2443	ASP
1	C	2448	GLU
1	C	2450	VAL
1	C	2468	ILE
2	D	3	VAL
2	D	5	LEU
2	D	6	VAL
2	D	10	TYR
2	D	20	LEU
2	D	21	THR
2	D	28	ILE
2	D	31	SER
2	D	40	ILE
2	D	45	LYS
2	D	55	VAL
2	D	66	ASN
2	D	90	MET
2	D	99	ILE
2	D	101	VAL
2	D	106	SER
2	D	119	VAL
2	D	122	VAL
2	D	133	SER
2	D	135	ASP
2	D	155	THR
2	D	167	MET
2	D	174	LEU
2	D	201	THR
2	D	210	ILE
2	D	219	VAL
2	D	230	THR
2	D	236	ILE
2	D	242	LEU
2	D	256	CYS
2	D	273	TYR
2	D	286	ARG
2	D	298	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	302	ASP
5	I	658	VAL
5	I	666	CYS
5	I	672	ASN
5	I	680	ILE
5	I	682	ILE
5	I	692	SER
5	I	694	THR
5	I	695	THR
5	I	697	VAL
5	I	703	ILE
5	I	707	ILE
5	I	711	LEU
5	I	716	THR
5	I	728	LEU
5	I	730	VAL
5	I	731	GLU
5	I	741	LEU
5	I	744	VAL
5	I	758	LEU
5	I	759	ASP
5	I	760	ARG
5	I	768	SER
5	I	770	SER
5	I	775	CYS
5	J	660	GLU
5	J	675	SER
5	J	680	ILE
5	J	681	TYR
5	J	690	ARG
5	J	692	SER
5	J	697	VAL
5	J	702	THR
5	J	709	PHE
5	J	711	LEU
5	J	713	LEU
5	J	716	THR
5	J	721	ASP
5	J	728	LEU
5	J	729	THR
5	J	730	VAL
5	J	731	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	J	740	SER
5	J	743	ILE
5	J	758	LEU
5	J	759	ASP
5	J	760	ARG
5	J	764	ILE
5	J	768	SER
5	J	770	SER
5	J	775	CYS
5	J	783	SER
5	J	787	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (162) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	ASN
1	A	130	ASN
1	A	228	ASN
1	A	251	ASN
1	A	303	GLN
1	A	310	GLN
1	A	319	ASN
1	A	405	ASN
1	A	454	GLN
1	A	484	ASN
1	A	539	ASN
1	A	540	ASN
1	A	574	GLN
1	A	583	HIS
1	A	584	HIS
1	A	661	GLN
1	A	676	ASN
1	A	706	ASN
1	A	811	GLN
1	A	813	ASN
1	A	859	HIS
1	A	923	ASN
1	A	950	ASN
1	A	961	GLN
1	A	977	GLN
1	A	983	GLN
1	A	994	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1017	GLN
1	A	1054	GLN
1	A	1123	GLN
1	A	1131	ASN
1	A	1169	ASN
1	A	1206	ASN
1	A	1220	GLN
1	A	1277	ASN
1	A	1292	GLN
1	A	1364	ASN
1	A	1378	HIS
1	A	1379	GLN
1	A	1393	HIS
1	A	1509	ASN
1	A	1547	GLN
1	A	1643	ASN
1	A	1735	ASN
1	A	1839	GLN
1	A	1888	ASN
1	A	1981	ASN
1	A	2009	GLN
1	A	2010	ASN
1	A	2017	ASN
1	A	2025	ASN
1	A	2036	ASN
1	A	2037	GLN
1	A	2044	ASN
1	A	2052	GLN
1	A	2057	GLN
1	A	2145	ASN
1	A	2204	HIS
1	A	2209	GLN
1	A	2279	HIS
1	A	2282	ASN
1	A	2341	ASN
1	A	2411	HIS
1	A	2447	GLN
2	B	12	HIS
2	B	29	GLN
2	B	36	ASN
2	B	53	GLN
2	B	149	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	152	HIS
2	B	229	HIS
2	B	249	HIS
1	C	86	ASN
1	C	124	GLN
1	C	131	ASN
1	C	168	ASN
1	C	228	ASN
1	C	252	ASN
1	C	262	ASN
1	C	307	GLN
1	C	311	GLN
1	C	320	ASN
1	C	395	HIS
1	C	402	ASN
1	C	455	GLN
1	C	485	ASN
1	C	515	ASN
1	C	540	ASN
1	C	541	ASN
1	C	553	ASN
1	C	575	GLN
1	C	585	HIS
1	C	586	GLN
1	C	662	GLN
1	C	671	GLN
1	C	693	GLN
1	C	725	GLN
1	C	807	ASN
1	C	814	ASN
1	C	827	GLN
1	C	858	ASN
1	C	860	HIS
1	C	924	ASN
1	C	938	HIS
1	C	943	GLN
1	C	950	GLN
1	C	1000	HIS
1	C	1075	ASN
1	C	1112	ASN
1	C	1174	HIS
1	C	1179	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	1200	ASN
1	C	1226	ASN
1	C	1232	GLN
1	C	1233	GLN
1	C	1249	GLN
1	C	1381	GLN
1	C	1393	GLN
1	C	1395	HIS
1	C	1399	GLN
1	C	1480	GLN
1	C	1510	ASN
1	C	1521	ASN
1	C	1539	ASN
1	C	1578	ASN
1	C	1592	GLN
1	C	1676	ASN
1	C	1722	GLN
1	C	1761	ASN
1	C	1841	GLN
1	C	1871	GLN
1	C	1954	HIS
1	C	1977	GLN
1	C	1983	ASN
1	C	2012	ASN
1	C	2027	ASN
1	C	2054	GLN
1	C	2064	GLN
1	C	2065	HIS
1	C	2135	GLN
1	C	2194	HIS
1	C	2238	GLN
1	C	2284	ASN
1	C	2343	ASN
1	C	2407	GLN
1	C	2411	ASN
1	C	2415	ASN
1	C	2449	GLN
1	C	2466	HIS
2	D	12	HIS
2	D	36	ASN
2	D	53	GLN
2	D	120	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	191	HIS
2	D	249	HIS
5	I	691	ASN
5	I	735	ASN
5	I	738	ASN
5	J	737	ASN
5	J	738	ASN
5	J	754	ASN
5	J	785	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	567
1	A	534
3	E	90

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
3	F	87
2	D	75
2	B	66
4	G	45
4	H	42
5	J	31
5	I	26

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	416:UNK	C	450:UNK	N	40.12
1	F	416:UNK	C	450:UNK	N	39.07
1	E	512:UNK	C	550:UNK	N	33.98
1	F	717:UNK	C	750:UNK	N	33.97
1	E	717:UNK	C	750:UNK	N	33.43
1	F	512:UNK	C	550:UNK	N	33.24
1	F	118:UNK	C	150:UNK	N	32.46
1	E	118:UNK	C	150:UNK	N	32.20
1	F	867:UNK	C	900:UNK	N	31.99
1	E	867:UNK	C	900:UNK	N	30.60
1	F	318:UNK	C	350:UNK	N	27.65
1	E	318:UNK	C	350:UNK	N	27.26
1	E	381:UNK	C	400:UNK	N	25.02
1	F	381:UNK	C	400:UNK	N	24.83
1	E	468:UNK	C	500:UNK	N	24.07
1	F	468:UNK	C	500:UNK	N	23.91
1	F	567:UNK	C	600:UNK	N	23.32
1	E	567:UNK	C	600:UNK	N	22.55
1	F	169:UNK	C	200:UNK	N	22.46
1	E	169:UNK	C	200:UNK	N	22.15
1	F	665:UNK	C	700:UNK	N	17.20
1	E	665:UNK	C	700:UNK	N	16.83
1	E	813:UNK	C	850:UNK	N	13.94
1	F	218:UNK	C	250:UNK	N	13.04
1	F	813:UNK	C	850:UNK	N	13.02
1	E	218:UNK	C	250:UNK	N	12.00
1	A	1811:SER	C	1812:SER	N	10.40
1	E	761:UNK	C	800:UNK	N	10.32
1	A	1637:ASP	C	1638:ASP	N	9.38
1	F	761:UNK	C	800:UNK	N	9.33
1	C	1639:ASP	C	1640:ASP	N	9.18
1	F	612:UNK	C	650:UNK	N	8.93

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	668:PHE	C	669:ASP	N	8.41
1	E	612:UNK	C	650:UNK	N	8.32
1	A	667:PHE	C	668:ASP	N	8.25
1	A	225:ALA	C	226:ASP	N	7.67
1	A	1422:ALA	C	1423:GLY	N	7.39
1	C	226:ALA	C	227:ASP	N	7.36
1	J	721:ASP	C	722:ASN	N	7.31
1	I	779:ASP	C	780:ALA	N	6.42
1	C	123:PHE	C	124:GLN	N	6.40
1	C	1202:VAL	C	1203:PRO	N	6.36
1	A	1018:ILE	C	1019:THR	N	6.23
1	A	1202:PRO	C	1203:GLU	N	6.23
1	J	791:LEU	C	792:PRO	N	6.20
1	C	814:ASN	C	815:SER	N	6.18
1	A	2400:THR	C	2401:GLU	N	6.14
1	I	720:PRO	C	721:ASP	N	6.09
1	A	710:VAL	C	711:VAL	N	6.07
1	I	653:THR	C	654:ASN	N	6.02
1	C	242:ALA	C	243:LEU	N	5.89
1	C	1472:ALA	C	1473:GLY	N	5.86
1	C	2386:GLN	C	2387:LEU	N	5.84
1	A	2376:LYS	C	2377:ILE	N	5.81
1	C	118:VAL	C	119:SER	N	5.81
1	A	813:ASN	C	814:SER	N	5.77
1	C	209:ASP	C	210:PHE	N	5.76
1	A	1633:LEU	C	1634:GLU	N	5.74
1	J	733:ILE	C	734:SER	N	5.73
1	A	84:LEU	C	85:ASN	N	5.67
1	C	2375:PRO	C	2376:THR	N	5.65
1	B	3:VAL	C	4:ILE	N	5.55
1	C	1017:LEU	C	1018:GLN	N	5.55
1	A	1014:ILE	C	1015:LYS	N	5.49
1	A	116:GLU	C	117:VAL	N	5.48
1	E	808:UNK	C	809:UNK	N	5.48
1	D	165:LEU	C	166:SER	N	5.44
1	C	2243:VAL	C	2244:LEU	N	5.43
1	A	2377:ILE	C	2378:GLU	N	5.42
1	C	265:LEU	C	266:ASP	N	5.40
1	A	1169:ASN	C	1170:ARG	N	5.39
1	C	104:ALA	C	105:ASN	N	5.34
1	A	1133:ASP	C	1134:ARG	N	5.32
1	C	294:ILE	C	295:GLN	N	5.31

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	468:ALA	C	469:CYS	N	5.31
1	A	315:GLY	C	316:LEU	N	5.29
1	A	106:LEU	C	107:SER	N	5.28
1	I	787:ILE	C	788:GLU	N	5.27
1	A	219:ASP	C	220:TRP	N	5.26
1	I	747:ASP	C	748:GLY	N	5.26
1	C	2388:PRO	C	2389:VAL	N	5.24
1	A	1144:LEU	C	1145:SER	N	5.22
1	C	2395:LEU	C	2396:LEU	N	5.22
1	A	408:ASN	C	409:ASN	N	5.21
1	A	2387:VAL	C	2388:MET	N	5.18
1	C	287:LEU	C	288:GLY	N	5.18
1	J	708:GLY	C	709:PHE	N	5.17
1	A	307:ARG	C	308:LEU	N	5.15
1	A	318:LEU	C	319:ASN	N	5.15
1	C	1911:ALA	C	1912:LEU	N	5.12
1	A	1201:VAL	C	1202:PRO	N	5.11
1	A	508:SER	C	509:LEU	N	5.08
1	A	117:VAL	C	118:SER	N	5.07
1	C	1764:LEU	C	1765:ALA	N	5.05
1	A	1531:LEU	C	1532:VAL	N	5.02
1	C	1132:ASN	C	1133:GLY	N	5.02
1	J	668:ASP	C	669:LYS	N	5.02
1	J	775:CYS	C	776:LYS	N	5.02
1	A	120:GLU	C	121:GLN	N	5.00
1	A	2396:ASN	C	2397:GLY	N	5.00
1	A	286:LEU	C	287:GLY	N	4.99
1	D	59:ASP	C	60:ILE	N	4.97
1	C	430:SER	C	431:ILE	N	4.95
1	J	766:SER	C	767:ILE	N	4.91
1	A	521:LEU	C	522:SER	N	4.90
1	A	2095:PHE	C	2096:GLU	N	4.90
1	G	155:ILE	C	156:SER	N	4.89
1	A	590:GLU	C	591:PHE	N	4.87
1	G	197:VAL	C	198:LEU	N	4.87
1	A	1016:LEU	C	1017:GLN	N	4.86
1	J	648:LYS	C	649:LYS	N	4.85
1	C	130:LEU	C	131:ASN	N	4.84
1	C	703:LEU	C	704:SER	N	4.83
1	D	58:TYR	C	59:ASP	N	4.82
1	A	2205:TRP	C	2206:VAL	N	4.81
1	A	2450:LYS	C	2451:LEU	N	4.81

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1497:ASP	C	1498:LYS	N	4.80
1	C	241:ALA	C	242:ALA	N	4.79
1	C	309:LEU	C	310:PHE	N	4.78
1	J	723:PHE	C	724:GLU	N	4.77
1	C	222:LEU	C	223:THR	N	4.75
1	A	2434:ASN	C	2435:ASP	N	4.74
1	C	1819:ARG	C	1820:HIS	N	4.72
1	B	38:LEU	C	39:GLU	N	4.71
1	C	1206:LYS	C	1207:ASN	N	4.71
1	C	1671:LEU	C	1672:LYS	N	4.69
1	A	95:VAL	C	96:PRO	N	4.68
1	A	1216:LEU	C	1217:PRO	N	4.68
1	B	69:ALA	C	70:SER	N	4.68
1	C	229:ASN	C	230:SER	N	4.68
1	C	869:ILE	C	870:GLY	N	4.68
1	A	772:SER	C	773:ALA	N	4.67
1	C	89:PHE	C	90:ASP	N	4.65
1	A	126:SER	C	127:ASN	N	4.64
1	C	216:ARG	C	217:THR	N	4.64
1	A	429:SER	C	430:ILE	N	4.62
1	C	817:LYS	C	818:ARG	N	4.62
1	D	38:LEU	C	39:GLU	N	4.62
1	I	743:ILE	C	744:VAL	N	4.62
1	C	467:LEU	C	468:ALA	N	4.60
1	C	1115:LEU	C	1116:SER	N	4.60
1	C	2309:ARG	C	2310:GLU	N	4.60
1	C	2408:ARG	C	2409:VAL	N	4.60
1	A	949:GLN	C	950:ASN	N	4.59
1	A	1970:ASP	C	1971:ASP	N	4.59
1	C	127:SER	C	128:ASN	N	4.59
1	E	465:UNK	C	466:UNK	N	4.57
1	I	775:CYS	C	776:LYS	N	4.57
1	G	51:GLY	C	52:ARG	N	4.56
1	F	913:UNK	C	914:UNK	N	4.55
1	A	230:SER	C	231:SER	N	4.54
1	A	1212:GLN	C	1213:VAL	N	4.54
1	C	194:ASN	C	195:THR	N	4.54
1	C	385:THR	C	386:LYS	N	4.54
1	C	1542:TYR	C	1543:ASN	N	4.54
1	A	2036:ASN	C	2037:GLN	N	4.53
1	H	63:GLY	C	64:HIS	N	4.53
1	A	193:ASN	C	194:THR	N	4.52

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	480:LYS	C	481:ASP	N	4.51
1	C	334:GLU	C	335:LEU	N	4.51
1	H	91:LEU	C	92:HIS	N	4.51
1	C	2249:ARG	C	2250:SER	N	4.50
1	A	168:GLN	C	169:THR	N	4.49
1	C	1516:GLU	C	1517:VAL	N	4.48
1	D	48:ALA	C	49:THR	N	4.48
1	A	417:VAL	C	418:SER	N	4.47
1	C	1534:VAL	C	1535:ASN	N	4.47
1	C	1961:VAL	C	1962:LEU	N	4.47
1	I	672:ASN	C	673:TYR	N	4.47
1	A	292:ILE	C	293:ILE	N	4.46
1	F	371:UNK	C	372:UNK	N	4.45
1	A	427:GLY	C	428:SER	N	4.44
1	A	1743:TYR	C	1744:LEU	N	4.44
1	C	307:GLN	C	308:ARG	N	4.43
1	C	150:ILE	C	151:LEU	N	4.41
1	A	1455:GLY	C	1456:THR	N	4.40
1	A	1514:GLU	C	1515:VAL	N	4.40
1	A	142:SER	C	143:SER	N	4.39
1	A	335:LEU	C	336:SER	N	4.39
1	A	526:SER	C	527:GLY	N	4.39
1	C	1200:ASN	C	1201:GLU	N	4.39
1	E	711:UNK	C	712:UNK	N	4.39
1	I	651:THR	C	652:ASN	N	4.39
1	A	91:LEU	C	92:LYS	N	4.38
1	C	823:THR	C	824:THR	N	4.37
1	C	1919:ALA	C	1920:ILE	N	4.37
1	A	1524:LEU	C	1525:VAL	N	4.36
1	A	1581:GLY	C	1582:CYS	N	4.36
1	A	2126:LYS	C	2127:GLY	N	4.36
1	C	957:VAL	C	958:SER	N	4.36
1	A	1206:ASN	C	1207:TYR	N	4.35
1	C	2207:TRP	C	2208:VAL	N	4.35
1	A	404:MET	C	405:ASN	N	4.34
1	A	819:ALA	C	820:ALA	N	4.34
1	A	1114:LEU	C	1115:SER	N	4.34
1	D	199:PRO	C	200:VAL	N	4.34
1	A	1397:GLN	C	1398:LEU	N	4.33
1	C	2460:VAL	C	2461:GLU	N	4.33
1	I	680:ILE	C	681:TYR	N	4.33
1	A	502:LEU	C	503:ASN	N	4.32

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1172:ILE	C	1173:GLN	N	4.32
1	C	1213:GLN	C	1214:VAL	N	4.31
1	A	1726:CYS	C	1727:LEU	N	4.30
1	A	2111:PHE	C	2112:CYS	N	4.30
1	B	290:GLY	C	291:HIS	N	4.30
1	C	1294:GLU	C	1295:ASP	N	4.30
1	C	2434:THR	C	2435:GLY	N	4.30
1	A	816:LYS	C	817:ARG	N	4.29
1	C	250:ALA	C	251:ASP	N	4.29
1	C	990:ILE	C	991:SER	N	4.29
1	F	710:UNK	C	711:UNK	N	4.29
1	I	732:ASP	C	733:ILE	N	4.29
1	B	88:ARG	C	89:TRP	N	4.28
1	C	767:LYS	C	768:CYS	N	4.28
1	C	950:GLN	C	951:ASN	N	4.28
1	D	83:PHE	C	84:GLN	N	4.28
1	G	133:ALA	C	134:ASP	N	4.28
1	I	700:SER	C	701:SER	N	4.28
1	A	203:GLY	C	204:THR	N	4.27
1	A	277:ILE	C	278:ILE	N	4.27
1	A	1851:PHE	C	1852:GLY	N	4.26
1	B	55:VAL	C	56:ARG	N	4.26
1	C	181:ILE	C	182:PRO	N	4.26
1	C	706:VAL	C	707:ASN	N	4.26
1	C	1607:ASP	C	1608:ALA	N	4.25
1	A	2116:SER	C	2117:ASP	N	4.24
1	A	1957:MET	C	1958:ALA	N	4.23
1	A	2401:GLU	C	2402:GLU	N	4.22
1	A	1960:LEU	C	1961:TRP	N	4.21
1	A	1343:LYS	C	1344:CYS	N	4.20
1	B	54:ASN	C	55:VAL	N	4.20
1	C	151:LEU	C	152:ALA	N	4.20
1	C	205:THR	C	206:LEU	N	4.20
1	E	458:UNK	C	459:UNK	N	4.20
1	C	1221:GLN	C	1222:ASN	N	4.19
1	C	845:LEU	C	846:LEU	N	4.18
1	G	113:ILE	C	114:HIS	N	4.18
1	A	467:ALA	C	468:CYS	N	4.17
1	A	2008:PHE	C	2009:GLN	N	4.17
1	B	59:ASP	C	60:ILE	N	4.17
1	C	1405:TYR	C	1406:GLU	N	4.17
1	A	200:VAL	C	201:PRO	N	4.16

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	256:CYS	C	257:ALA	N	4.16
1	B	293:LYS	C	294:GLY	N	4.15
1	D	80:SER	C	81:VAL	N	4.15
1	G	70:ILE	C	71:LYS	N	4.15
1	C	293:ILE	C	294:ILE	N	4.14
1	C	1350:ALA	C	1351:LYS	N	4.14
1	E	552:UNK	C	553:UNK	N	4.13
1	A	1575:TRP	C	1576:ASN	N	4.12
1	C	454:LYS	C	455:GLN	N	4.12
1	C	1713:LYS	C	1714:LEU	N	4.12
1	C	2404:GLU	C	2405:GLU	N	4.12
1	F	309:UNK	C	310:UNK	N	4.12
1	J	649:LYS	C	650:ARG	N	4.12
1	A	810:ASP	C	811:GLN	N	4.11
1	A	2151:ASP	C	2152:ALA	N	4.11
1	A	2330:GLY	C	2331:ILE	N	4.11
1	C	709:ALA	C	710:TYR	N	4.11
1	C	1051:LEU	C	1052:GLU	N	4.11
1	G	91:LEU	C	92:HIS	N	4.11
1	A	2332:GLU	C	2333:GLY	N	4.10
1	C	295:GLN	C	296:ASP	N	4.10
1	C	317:LEU	C	318:SER	N	4.10
1	J	718:LYS	C	719:LYS	N	4.10
1	A	1030:ALA	C	1031:LEU	N	4.09
1	C	811:ASP	C	812:GLN	N	4.09
1	C	2181:VAL	C	2182:PRO	N	4.09
1	D	81:VAL	C	82:SER	N	4.08
1	D	269:SER	C	270:SER	N	4.08
1	H	93:LEU	C	94:LEU	N	4.08
1	B	256:CYS	C	257:ALA	N	4.07
1	C	382:ALA	C	383:ILE	N	4.07
1	A	1553:GLU	C	1554:GLU	N	4.06
1	C	1282:SER	C	1283:SER	N	4.06
1	D	87:ASN	C	88:ARG	N	4.06
1	E	268:UNK	C	300:UNK	N	4.06
1	H	79:VAL	C	80:HIS	N	4.06
1	C	1846:LEU	C	1847:LEU	N	4.05
1	F	557:UNK	C	558:UNK	N	4.05
1	H	97:GLN	C	98:PHE	N	4.05
1	A	171:ARG	C	172:LEU	N	4.04
1	C	84:THR	C	85:LEU	N	4.04
1	C	332:PHE	C	333:ARG	N	4.04

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	301:GLY	C	302:LYS	N	4.03
1	A	2054:PRO	C	2055:GLN	N	4.03
1	C	243:LEU	C	244:LEU	N	4.03
1	C	617:CYS	C	618:ASP	N	4.03
1	I	758:LEU	C	759:ASP	N	4.03
1	J	655:SER	C	656:VAL	N	4.03
1	A	1966:TYR	C	1967:GLU	N	4.02
1	D	121:GLU	C	122:VAL	N	4.02
1	D	183:CYS	C	184:TYR	N	4.01
1	A	1997:LYS	C	1998:ARG	N	4.00
1	C	568:THR	C	569:ASP	N	4.00
1	C	2135:GLN	C	2136:ASP	N	4.00
1	A	2004:ARG	C	2005:GLU	N	3.99
1	B	145:LEU	C	146:GLY	N	3.99
1	F	466:UNK	C	467:UNK	N	3.99
1	A	664:GLY	C	665:SER	N	3.98
1	C	414:PRO	C	415:PHE	N	3.98
1	C	991:SER	C	992:ILE	N	3.98
1	A	703:SER	C	704:SER	N	3.97
1	A	954:ARG	C	955:CYS	N	3.97
1	C	1755:TRP	C	1756:TYR	N	3.97
1	J	682:ILE	C	683:GLN	N	3.97
1	A	262:SER	C	263:ILE	N	3.96
1	A	1339:LYS	C	1340:TYR	N	3.96
1	E	262:UNK	C	263:UNK	N	3.96
1	A	505:LYS	C	506:ILE	N	3.95
1	A	2460:ASN	C	2461:LEU	N	3.95
1	F	611:UNK	C	612:UNK	N	3.95
1	H	134:ASP	C	135:LEU	N	3.95
1	J	732:ASP	C	733:ILE	N	3.95
1	A	166:PRO	C	167:ASN	N	3.94
1	A	594:LEU	C	595:ILE	N	3.94
1	A	645:MET	C	646:ILE	N	3.94
1	B	257:ALA	C	258:PHE	N	3.94
1	C	2049:ARG	C	2050:LYS	N	3.94
1	C	2433:LEU	C	2434:THR	N	3.94
1	D	66:ASN	C	67:PRO	N	3.94
1	E	466:UNK	C	467:UNK	N	3.94
1	C	667:ASN	C	668:PHE	N	3.93
1	A	687:GLU	C	688:ILE	N	3.92
1	C	2088:GLY	C	2089:LYS	N	3.92
1	H	157:CYS	C	158:MET	N	3.92

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	178:ASN	C	179:TRP	N	3.92
1	J	715:SER	C	716:THR	N	3.92
1	A	857:ASN	C	858:PRO	N	3.91
1	A	2105:LYS	C	2106:GLN	N	3.91
1	A	2466:ILE	C	2467:GLY	N	3.91
1	C	1427:ASP	C	1428:SER	N	3.91
1	D	65:PRO	C	66:ASN	N	3.91
1	A	1551:GLU	C	1552:LEU	N	3.90
1	C	1444:GLU	C	1445:TRP	N	3.90
1	C	1545:VAL	C	1546:VAL	N	3.90
1	C	1623:ARG	C	1624:MET	N	3.90
1	E	156:UNK	C	157:UNK	N	3.90
1	A	2324:TYR	C	2325:ALA	N	3.89
1	C	2428:ARG	C	2429:ILE	N	3.89
1	G	67:HIS	C	68:GLU	N	3.89
1	A	2130:ASP	C	2131:ILE	N	3.88
1	B	221:HIS	C	222:LEU	N	3.88
1	C	2410:GLU	C	2411:ASN	N	3.88
1	C	984:GLN	C	985:GLN	N	3.87
1	C	1583:GLY	C	1584:CYS	N	3.87
1	J	739:PHE	C	740:SER	N	3.87
1	C	989:LEU	C	990:ILE	N	3.86
1	A	811:GLN	C	812:SER	N	3.85
1	A	1566:ASP	C	1567:LYS	N	3.85
1	C	81:THR	C	82:PHE	N	3.85
1	C	371:ALA	C	372:ILE	N	3.85
1	C	952:LEU	C	953:GLY	N	3.85
1	C	1341:LYS	C	1342:TYR	N	3.85
1	C	1442:LEU	C	1443:GLY	N	3.85
1	E	709:UNK	C	710:UNK	N	3.85
1	E	753:UNK	C	754:UNK	N	3.85
1	G	99:PRO	C	100:ARG	N	3.85
1	I	765:GLN	C	766:SER	N	3.85
1	C	1889:PRO	C	1890:ASN	N	3.84
1	C	1959:MET	C	1960:ALA	N	3.84
1	C	2422:ALA	C	2423:MET	N	3.84
1	E	603:UNK	C	604:UNK	N	3.84
1	G	110:ARG	C	111:ALA	N	3.84
1	A	622:ASP	C	623:ASP	N	3.83
1	A	1965:TRP	C	1966:TYR	N	3.83
1	A	2444:VAL	C	2445:PRO	N	3.83
1	C	840:LEU	C	841:ASP	N	3.83

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	563:UNK	C	564:UNK	N	3.83
1	C	1114:ASN	C	1115:LEU	N	3.82
1	C	1119:SER	C	1120:SER	N	3.82
1	C	1833:SER	C	1834:LEU	N	3.82
1	F	313:UNK	C	314:UNK	N	3.82
1	F	910:UNK	C	911:UNK	N	3.82
1	J	706:VAL	C	707:ILE	N	3.82
1	A	302:LYS	C	303:GLN	N	3.81
1	A	589:THR	C	590:GLU	N	3.81
1	C	1073:GLY	C	1074:PRO	N	3.81
1	A	1504:CYS	C	1505:LEU	N	3.80
1	C	1182:ASN	C	1183:LYS	N	3.80
1	E	150:UNK	C	151:UNK	N	3.80
1	F	250:UNK	C	251:UNK	N	3.80
1	G	87:HIS	C	88:GLU	N	3.80
1	J	781:GLU	C	782:LYS	N	3.80
1	C	366:ARG	C	367:ARG	N	3.79
1	C	402:ASN	C	403:ILE	N	3.79
1	C	1178:ASP	C	1179:GLN	N	3.79
1	C	1684:ASP	C	1685:LEU	N	3.79
1	D	132:ILE	C	133:SER	N	3.79
1	A	143:SER	C	144:GLU	N	3.78
1	A	852:LEU	C	853:LYS	N	3.78
1	C	729:SER	C	730:ASN	N	3.78
1	C	851:ASN	C	852:ILE	N	3.78
1	C	1075:ASN	C	1076:LEU	N	3.78
1	G	63:GLY	C	64:HIS	N	3.78
1	H	115:ILE	C	116:ALA	N	3.78
1	A	1625:ALA	C	1626:LYS	N	3.77
1	B	89:TRP	C	90:MET	N	3.77
1	C	276:LYS	C	277:LEU	N	3.77
1	C	364:VAL	C	365:ILE	N	3.77
1	E	554:UNK	C	555:UNK	N	3.77
1	A	279:ARG	C	280:LEU	N	3.76
1	A	1032:GLU	C	1033:GLY	N	3.76
1	A	1638:ASP	C	1639:PRO	N	3.76
1	A	2421:MET	C	2422:LEU	N	3.76
1	A	324:VAL	C	325:HIS	N	3.75
1	A	973:CYS	C	974:PRO	N	3.75
1	C	1531:SER	C	1532:ALA	N	3.75
1	C	2113:PHE	C	2114:CYS	N	3.75
1	C	2380:GLU	C	2381:GLU	N	3.75

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	310:UNK	C	311:UNK	N	3.75
1	C	1822:ILE	C	1823:PRO	N	3.74
1	C	2383:THR	C	2384:GLY	N	3.74
1	H	149:CYS	C	150:LEU	N	3.74
1	J	670:VAL	C	671:PRO	N	3.74
1	A	1045:PHE	C	1046:PHE	N	3.73
1	A	2081:THR	C	2082:ARG	N	3.73
1	C	256:LEU	C	257:LEU	N	3.73
1	C	1647:ALA	C	1648:LYS	N	3.73
1	C	2208:VAL	C	2209:MET	N	3.73
1	D	166:SER	C	167:MET	N	3.73
1	A	856:ASN	C	857:ASN	N	3.72
1	A	1903:GLY	C	1904:LYS	N	3.72
1	C	113:SER	C	114:LEU	N	3.72
1	C	135:PHE	C	136:GLU	N	3.72
1	C	710:TYR	C	711:VAL	N	3.72
1	C	1171:ARG	C	1172:ILE	N	3.72
1	C	1460:LYS	C	1461:PRO	N	3.72
1	D	101:VAL	C	102:TRP	N	3.72
1	A	757:ASP	C	758:PRO	N	3.71
1	A	2341:ASN	C	2342:VAL	N	3.71
1	C	134:ILE	C	135:PHE	N	3.71
1	C	2360:GLU	C	2361:ALA	N	3.71
1	E	809:UNK	C	810:UNK	N	3.71
1	A	2077:ALA	C	2078:VAL	N	3.70
1	C	1256:SER	C	1257:ALA	N	3.70
1	E	464:UNK	C	465:UNK	N	3.70
1	E	502:UNK	C	503:UNK	N	3.70
1	F	859:UNK	C	860:UNK	N	3.70
1	A	1430:MET	C	1431:MET	N	3.69
1	A	2010:ASN	C	2011:SER	N	3.69
1	A	2312:GLU	C	2313:LYS	N	3.69
1	C	103:GLY	C	104:ALA	N	3.69
1	C	632:HIS	C	633:ALA	N	3.69
1	C	2072:SER	C	2073:ALA	N	3.69
1	C	2224:LYS	C	2225:VAL	N	3.69
1	D	273:TYR	C	274:VAL	N	3.69
1	H	80:HIS	C	81:LEU	N	3.69
1	I	780:ALA	C	781:GLU	N	3.69
1	J	711:LEU	C	712:PHE	N	3.69
1	A	1902:LEU	C	1903:GLY	N	3.68
1	A	2217:LEU	C	2218:THR	N	3.68

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1077:ASP	C	1078:TYR	N	3.67
1	A	1488:VAL	C	1489:MET	N	3.67
1	A	1619:SER	C	1620:GLY	N	3.67
1	A	2339:CYS	C	2340:GLU	N	3.67
1	D	128:GLN	C	129:GLY	N	3.67
1	H	90:THR	C	91:LEU	N	3.67
1	A	280:LEU	C	281:ASP	N	3.66
1	A	1892:SER	C	1893:ARG	N	3.66
1	B	181:GLY	C	182:ASN	N	3.66
1	C	1235:THR	C	1236:LYS	N	3.66
1	C	1392:ALA	C	1393:GLN	N	3.66
1	A	297:ASP	C	298:PRO	N	3.65
1	A	944:ILE	C	945:MET	N	3.65
1	C	547:LYS	C	548:ALA	N	3.65
1	C	642:SER	C	643:LYS	N	3.65
1	C	2314:GLU	C	2315:LYS	N	3.65
1	D	127:ASN	C	128:GLN	N	3.65
1	E	151:UNK	C	152:UNK	N	3.65
1	E	905:UNK	C	906:UNK	N	3.65
1	A	560:GLY	C	561:GLU	N	3.64
1	A	1050:LEU	C	1051:GLU	N	3.64
1	A	1891:VAL	C	1892:SER	N	3.64
1	C	659:GLU	C	660:ILE	N	3.64
1	C	698:LYS	C	699:ILE	N	3.64
1	D	45:LYS	C	46:LEU	N	3.64
1	F	900:UNK	C	901:UNK	N	3.64
1	H	100:ARG	C	101:PHE	N	3.64
1	A	167:ASN	C	168:GLN	N	3.63
1	A	963:ILE	C	964:PRO	N	3.63
1	A	1915:MET	C	1916:VAL	N	3.63
1	A	2313:LYS	C	2314:VAL	N	3.63
1	C	1447:GLU	C	1448:LEU	N	3.63
1	C	2119:ASP	C	2120:GLY	N	3.63
1	E	754:UNK	C	755:UNK	N	3.63
1	F	107:UNK	C	108:UNK	N	3.63
1	G	43:SER	C	44:LEU	N	3.63
1	G	157:CYS	C	158:MET	N	3.63
1	A	231:SER	C	232:SER	N	3.62
1	A	293:ILE	C	294:GLN	N	3.62
1	B	130:GLU	C	131:LEU	N	3.62
1	C	236:GLU	C	237:TYR	N	3.62
1	C	570:ALA	C	571:GLN	N	3.62

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	939:THR	C	940:ALA	N	3.62
1	C	2131:GLU	C	2132:ASP	N	3.62
1	D	253:VAL	C	254:TRP	N	3.62
1	A	1285:VAL	C	1286:GLU	N	3.61
1	A	1860:ALA	C	1861:MET	N	3.61
1	A	1907:PRO	C	1908:GLN	N	3.61
1	C	423:ILE	C	424:ALA	N	3.61
1	C	736:GLU	C	737:GLU	N	3.61
1	C	1348:ALA	C	1349:PHE	N	3.60
1	C	2084:ARG	C	2085:ALA	N	3.60
1	E	909:UNK	C	910:UNK	N	3.60
1	A	623:ASP	C	624:ILE	N	3.59
1	A	2242:LEU	C	2243:TRP	N	3.59
1	C	442:ILE	C	443:ARG	N	3.59
1	C	1222:ASN	C	1223:ILE	N	3.59
1	C	1330:LYS	C	1331:PRO	N	3.59
1	C	1432:MET	C	1433:MET	N	3.59
1	D	69:ALA	C	70:SER	N	3.59
1	E	716:UNK	C	717:UNK	N	3.59
1	A	2256:ARG	C	2257:THR	N	3.58
1	A	2368:TRP	C	2369:GLY	N	3.58
1	B	175:ALA	C	176:ALA	N	3.58
1	C	1473:GLY	C	1474:ALA	N	3.58
1	E	451:UNK	C	452:UNK	N	3.58
1	F	511:UNK	C	512:UNK	N	3.58
1	F	564:UNK	C	565:UNK	N	3.58
1	A	271:LEU	C	272:ARG	N	3.57
1	A	435:THR	C	436:LEU	N	3.57
1	A	1094:ALA	C	1095:GLY	N	3.57
1	A	1132:GLY	C	1133:ASP	N	3.57
1	A	1486:THR	C	1487:SER	N	3.57
1	C	618:ASP	C	619:LEU	N	3.57
1	C	1254:SER	C	1255:PRO	N	3.57
1	C	1625:ALA	C	1626:LEU	N	3.57
1	C	1905:GLY	C	1906:LYS	N	3.57
1	A	1434:LEU	C	1435:ARG	N	3.56
1	A	1565:SER	C	1566:ASP	N	3.56
1	D	118:PRO	C	119:VAL	N	3.56
1	E	112:UNK	C	113:UNK	N	3.56
1	G	196:LYS	C	197:VAL	N	3.56
1	A	779:LEU	C	780:LYS	N	3.55
1	A	2372:LEU	C	2373:PRO	N	3.55

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	499:THR	C	500:LEU	N	3.55
1	C	1924:SER	C	1925:LEU	N	3.55
1	C	2213:ALA	C	2214:PRO	N	3.55
1	D	125:HIS	C	126:PRO	N	3.55
1	D	188:MET	C	189:PRO	N	3.55
1	F	102:UNK	C	103:UNK	N	3.55
1	H	70:ILE	C	71:LYS	N	3.55
1	A	234:LEU	C	235:GLU	N	3.54
1	A	345:LYS	C	346:TYR	N	3.54
1	A	1765:PHE	C	1766:GLU	N	3.54
1	A	1917:ALA	C	1918:ILE	N	3.54
1	B	80:SER	C	81:VAL	N	3.54
1	B	189:PRO	C	190:ASN	N	3.54
1	C	161:LEU	C	162:SER	N	3.54
1	C	604:GLU	C	605:ASP	N	3.54
1	C	1344:GLN	C	1345:LYS	N	3.54
1	C	1413:ASP	C	1414:ALA	N	3.54
1	C	1978:PHE	C	1979:PHE	N	3.54
1	D	196:HIS	C	197:LEU	N	3.54
1	E	702:UNK	C	703:UNK	N	3.54
1	J	704:PHE	C	705:GLU	N	3.54
1	A	1034:GLU	C	1035:PHE	N	3.53
1	A	1508:ASN	C	1509:ASN	N	3.53
1	C	178:ARG	C	179:VAL	N	3.53
1	C	206:LEU	C	207:THR	N	3.53
1	C	2262:THR	C	2263:ARG	N	3.53
1	E	812:UNK	C	813:UNK	N	3.53
1	I	659:LEU	C	660:GLU	N	3.53
1	A	598:SER	C	599:TYR	N	3.52
1	A	1728:GLN	C	1729:PRO	N	3.52
1	A	1967:GLU	C	1968:GLY	N	3.52
1	C	418:VAL	C	419:SER	N	3.52
1	C	1963:TRP	C	1964:HIS	N	3.52
1	C	2318:PHE	C	2319:ARG	N	3.52
1	D	114:LYS	C	115:HIS	N	3.52
1	F	862:UNK	C	863:UNK	N	3.52
1	A	1532:VAL	C	1533:ASN	N	3.51
1	A	2302:GLU	C	2303:ALA	N	3.51
1	A	2438:ARG	C	2439:PHE	N	3.51
1	C	536:GLN	C	537:TYR	N	3.51
1	C	688:GLU	C	689:ILE	N	3.51
1	C	956:CYS	C	957:VAL	N	3.51

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1217:LEU	C	1218:PRO	N	3.51
1	E	165:UNK	C	166:UNK	N	3.51
1	A	1006:VAL	C	1007:ILE	N	3.50
1	A	1956:ARG	C	1957:MET	N	3.50
1	C	707:ASN	C	708:PRO	N	3.50
1	C	2150:LEU	C	2151:GLN	N	3.50
1	C	2411:ASN	C	2412:GLU	N	3.50
1	F	610:UNK	C	611:UNK	N	3.50
1	G	183:ASP	C	184:VAL	N	3.50
1	I	648:LYS	C	649:LYS	N	3.50
1	A	104:ASN	C	105:GLU	N	3.49
1	A	609:LYS	C	610:LEU	N	3.49
1	A	1000:VAL	C	1001:GLU	N	3.49
1	A	1194:ILE	C	1195:PHE	N	3.49
1	A	1755:LYS	C	1756:ALA	N	3.49
1	A	2364:PRO	C	2365:LEU	N	3.49
1	C	1836:GLU	C	1837:SER	N	3.49
1	C	2033:ASP	C	2034:VAL	N	3.49
1	F	350:UNK	C	351:UNK	N	3.49
1	F	414:UNK	C	415:UNK	N	3.49
1	A	249:ALA	C	250:ASP	N	3.48
1	A	346:TYR	C	347:ASP	N	3.48
1	A	441:ILE	C	442:ARG	N	3.48
1	A	485:LEU	C	486:MET	N	3.48
1	C	1212:MET	C	1213:GLN	N	3.48
1	C	1524:ASP	C	1525:LEU	N	3.48
1	C	2437:ASP	C	2438:ILE	N	3.48
1	E	202:UNK	C	203:UNK	N	3.48
1	E	258:UNK	C	259:UNK	N	3.48
1	H	135:LEU	C	136:TRP	N	3.48
1	A	1326:ASP	C	1327:ASP	N	3.47
1	A	1496:LYS	C	1497:GLU	N	3.47
1	A	1629:LEU	C	1630:ASN	N	3.47
1	C	1737:ASN	C	1738:PRO	N	3.47
1	D	102:TRP	C	103:ASP	N	3.47
1	F	658:UNK	C	659:UNK	N	3.47
1	G	94:LEU	C	95:LEU	N	3.47
1	H	196:LYS	C	197:VAL	N	3.47
1	I	756:GLY	C	757:LYS	N	3.47
1	A	499:LEU	C	500:MET	N	3.46
1	A	1762:LEU	C	1763:ALA	N	3.46
1	A	1182:LYS	C	1183:LEU	N	3.45

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1591:ARG	C	1592:ILE	N	3.45
1	C	2457:ALA	C	2458:THR	N	3.45
1	E	306:UNK	C	307:UNK	N	3.45
1	E	309:UNK	C	310:UNK	N	3.45
1	G	186:GLN	C	187:THR	N	3.45
1	H	175:ASP	C	176:LYS	N	3.45
1	A	185:ILE	C	186:GLU	N	3.44
1	A	282:ALA	C	283:ALA	N	3.44
1	A	1586:ILE	C	1587:ASP	N	3.44
1	C	329:LEU	C	330:LEU	N	3.44
1	C	692:ILE	C	693:GLN	N	3.44
1	C	2001:GLY	C	2002:PRO	N	3.44
1	C	2321:THR	C	2322:ARG	N	3.44
1	E	560:UNK	C	561:UNK	N	3.44
1	F	914:UNK	C	915:UNK	N	3.44
1	A	975:PRO	C	976:SER	N	3.43
1	A	2041:ILE	C	2042:TYR	N	3.43
1	C	365:ILE	C	366:ARG	N	3.43
1	C	569:ASP	C	570:ALA	N	3.43
1	C	608:VAL	C	609:ARG	N	3.43
1	C	850:ILE	C	851:ASN	N	3.43
1	C	1081:HIS	C	1082:LEU	N	3.43
1	C	1338:THR	C	1339:LEU	N	3.43
1	C	1491:MET	C	1492:LYS	N	3.43
1	D	151:THR	C	152:HIS	N	3.43
1	A	1157:VAL	C	1158:PHE	N	3.42
1	A	1363:LYS	C	1364:ASN	N	3.42
1	A	1622:MET	C	1623:ALA	N	3.42
1	C	697:ILE	C	698:LYS	N	3.42
1	E	406:UNK	C	407:UNK	N	3.42
1	E	904:UNK	C	905:UNK	N	3.42
1	F	214:UNK	C	215:UNK	N	3.42
1	A	1546:ALA	C	1547:GLN	N	3.41
1	B	155:THR	C	156:PRO	N	3.41
1	C	88:ILE	C	89:PHE	N	3.41
1	C	335:LEU	C	336:LEU	N	3.41
1	C	1057:ASN	C	1058:LYS	N	3.41
1	A	1130:ASN	C	1131:ASN	N	3.40
1	A	1152:GLY	C	1153:THR	N	3.40
1	B	200:VAL	C	201:THR	N	3.40
1	C	2223:GLN	C	2224:LYS	N	3.40
1	C	2473:PHE	C	2474:TRP	N	3.40

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	203:UNK	C	204:UNK	N	3.40
1	F	909:UNK	C	910:UNK	N	3.40
1	A	666:ASN	C	667:PHE	N	3.39
1	C	2365:ASP	C	2366:PRO	N	3.39
1	D	19:ALA	C	20:LEU	N	3.39
1	A	500:MET	C	501:ILE	N	3.38
1	A	2144:VAL	C	2145:ASN	N	3.38
1	A	2260:THR	C	2261:ARG	N	3.38
1	C	1054:ASP	C	1055:GLN	N	3.38
1	A	1848:TRP	C	1849:PHE	N	3.37
1	A	2048:LYS	C	2049:ILE	N	3.37
1	C	270:VAL	C	271:PRO	N	3.37
1	C	1104:ILE	C	1105:THR	N	3.37
1	C	1849:LEU	C	1850:TRP	N	3.37
1	C	2219:LEU	C	2220:THR	N	3.37
1	D	12:HIS	C	13:THR	N	3.37
1	H	127:LEU	C	128:LEU	N	3.37
1	A	164:GLU	C	165:LEU	N	3.36
1	A	691:ILE	C	692:GLN	N	3.36
1	A	731:PRO	C	732:LYS	N	3.36
1	A	1950:VAL	C	1951:SER	N	3.36
1	A	2047:ARG	C	2048:LYS	N	3.36
1	A	2379:GLU	C	2380:GLU	N	3.36
1	C	815:SER	C	816:PHE	N	3.36
1	C	853:LEU	C	854:LYS	N	3.36
1	C	936:ILE	C	937:HIS	N	3.36
1	C	1489:SER	C	1490:VAL	N	3.36
1	C	1525:LEU	C	1526:LEU	N	3.36
1	C	2231:ALA	C	2232:LEU	N	3.36
1	D	42:ASN	C	43:ASP	N	3.36
1	D	189:PRO	C	190:ASN	N	3.36
1	D	288:TYR	C	289:GLY	N	3.36
1	D	300:LEU	C	301:ASN	N	3.36
1	F	655:UNK	C	656:UNK	N	3.36
1	A	80:THR	C	81:PHE	N	3.35
1	A	337:LEU	C	338:LYS	N	3.35
1	A	507:PRO	C	508:SER	N	3.35
1	A	517:ILE	C	518:LEU	N	3.35
1	A	569:ALA	C	570:GLN	N	3.35
1	A	629:SER	C	630:VAL	N	3.35
1	A	679:LEU	C	680:LEU	N	3.35
1	A	1344:CYS	C	1345:HIS	N	3.35

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1723:TRP	C	1724:ARG	N	3.35
1	A	1885:HIS	C	1886:GLN	N	3.35
1	A	1923:LEU	C	1924:SER	N	3.35
1	A	1999:GLY	C	2000:PRO	N	3.35
1	A	2080:GLY	C	2081:THR	N	3.35
1	A	2192:HIS	C	2193:ARG	N	3.35
1	B	300:LEU	C	301:ASN	N	3.35
1	C	1091:THR	C	1092:GLU	N	3.35
1	C	1130:LEU	C	1131:ASN	N	3.35
1	C	1533:LEU	C	1534:VAL	N	3.35
1	C	1606:GLU	C	1607:ASP	N	3.35
1	C	1753:ASN	C	1754:THR	N	3.35
1	C	2412:GLU	C	2413:HIS	N	3.35
1	E	503:UNK	C	504:UNK	N	3.35
1	H	101:PHE	C	102:ILE	N	3.35
1	H	113:ILE	C	114:HIS	N	3.35
1	H	133:ALA	C	134:ASP	N	3.35
1	H	162:LEU	C	163:ASN	N	3.35
1	A	715:ARG	C	716:LYS	N	3.34
1	A	935:ILE	C	936:HIS	N	3.34
1	A	1763:ALA	C	1764:ASN	N	3.34
1	A	1859:GLN	C	1860:ALA	N	3.34
1	A	1872:THR	C	1873:TRP	N	3.34
1	A	2212:PRO	C	2213:ASP	N	3.34
1	A	2416:ARG	C	2417:ASN	N	3.34
1	B	167:MET	C	168:ALA	N	3.34
1	C	1380:HIS	C	1381:GLN	N	3.34
1	C	1414:ALA	C	1415:LEU	N	3.34
1	C	1430:GLU	C	1431:VAL	N	3.34
1	C	1530:LEU	C	1531:SER	N	3.34
1	C	1709:GLU	C	1710:ASP	N	3.34
1	C	2242:LYS	C	2243:VAL	N	3.34
1	C	2452:LYS	C	2453:LEU	N	3.34
1	E	380:UNK	C	381:UNK	N	3.34
1	E	450:UNK	C	451:UNK	N	3.34
1	E	601:UNK	C	602:UNK	N	3.34
1	E	864:UNK	C	865:UNK	N	3.34
1	F	268:UNK	C	300:UNK	N	3.34
1	F	453:UNK	C	454:UNK	N	3.34
1	F	903:UNK	C	904:UNK	N	3.34
1	G	53:TYR	C	54:LEU	N	3.34
1	H	124:CYS	C	125:LEU	N	3.34

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	161:LEU	C	162:LEU	N	3.34
1	A	834:VAL	C	835:VAL	N	3.33
1	A	1084:PRO	C	1085:ILE	N	3.33
1	A	1117:MET	C	1118:SER	N	3.33
1	A	1350:ALA	C	1351:LEU	N	3.33
1	A	1734:SER	C	1735:ASN	N	3.33
1	A	2067:LYS	C	2068:LEU	N	3.33
1	A	2091:LYS	C	2092:ILE	N	3.33
1	A	2181:ASN	C	2182:SER	N	3.33
1	A	2237:ASP	C	2238:LEU	N	3.33
1	A	2412:LYS	C	2413:ASN	N	3.33
1	B	195:SER	C	196:HIS	N	3.33
1	C	495:HIS	C	496:MET	N	3.33
1	C	541:ASN	C	542:GLN	N	3.33
1	C	639:GLU	C	640:VAL	N	3.33
1	C	760:ILE	C	761:LEU	N	3.33
1	C	1393:GLN	C	1394:GLN	N	3.33
1	C	1526:LEU	C	1527:VAL	N	3.33
1	C	1708:VAL	C	1709:GLU	N	3.33
1	C	2148:THR	C	2149:LEU	N	3.33
1	D	163:GLN	C	164:SER	N	3.33
1	F	560:UNK	C	561:UNK	N	3.33
1	F	908:UNK	C	909:UNK	N	3.33
1	G	81:LEU	C	82:ALA	N	3.33
1	G	151:GLU	C	152:TYR	N	3.33
1	G	198:LEU	C	199:LYS	N	3.33
1	H	57:VAL	C	58:TYR	N	3.33
1	H	191:GLY	C	192:ASN	N	3.33
1	A	343:ARG	C	344:ASP	N	3.32
1	A	472:PRO	C	473:ALA	N	3.32
1	A	850:ASN	C	851:ILE	N	3.32
1	A	1277:ASN	C	1278:ALA	N	3.32
1	A	1910:LEU	C	1911:VAL	N	3.32
1	A	2058:THR	C	2059:LEU	N	3.32
1	A	2399:ILE	C	2400:THR	N	3.32
1	A	2423:VAL	C	2424:LEU	N	3.32
1	C	318:SER	C	319:LEU	N	3.32
1	C	496:MET	C	497:GLN	N	3.32
1	C	865:THR	C	866:VAL	N	3.32
1	C	1232:GLN	C	1233:GLN	N	3.32
1	C	1557:ILE	C	1558:ILE	N	3.32
1	C	1664:THR	C	1665:GLY	N	3.32

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1680:ARG	C	1681:MET	N	3.32
1	C	1748:ALA	C	1749:THR	N	3.32
1	C	1766:ASN	C	1767:PHE	N	3.32
1	C	1888:GLN	C	1889:PRO	N	3.32
1	E	462:UNK	C	463:UNK	N	3.32
1	E	756:UNK	C	757:UNK	N	3.32
1	F	902:UNK	C	903:UNK	N	3.32
1	G	88:GLU	C	89:GLN	N	3.32
1	G	184:VAL	C	185:ALA	N	3.32
1	H	106:GLY	C	107:GLU	N	3.32
1	J	687:LYS	C	688:TYR	N	3.32
1	A	471:GLY	C	472:PRO	N	3.31
1	A	725:LEU	C	726:LYS	N	3.31
1	A	860:ILE	C	861:ARG	N	3.31
1	A	1215:LYS	C	1216:LEU	N	3.31
1	A	1558:TYR	C	1559:LYS	N	3.31
1	A	1574:THR	C	1575:TRP	N	3.31
1	A	1655:GLN	C	1656:LEU	N	3.31
1	A	1721:GLY	C	1722:GLU	N	3.31
1	A	1930:LEU	C	1931:SER	N	3.31
1	A	1962:HIS	C	1963:GLU	N	3.31
1	A	1990:GLU	C	1991:PRO	N	3.31
1	A	2187:VAL	C	2188:LEU	N	3.31
1	A	2457:SER	C	2458:VAL	N	3.31
1	B	216:SER	C	217:SER	N	3.31
1	C	326:HIS	C	327:ALA	N	3.31
1	C	406:ASN	C	407:ALA	N	3.31
1	C	695:GLU	C	696:ALA	N	3.31
1	C	940:ALA	C	941:ALA	N	3.31
1	C	1056:SER	C	1057:ASN	N	3.31
1	C	1281:PHE	C	1282:SER	N	3.31
1	C	1440:TYR	C	1441:ALA	N	3.31
1	C	1944:VAL	C	1945:LEU	N	3.31
1	C	2239:ASP	C	2240:LEU	N	3.31
1	D	96:ASP	C	97:GLY	N	3.31
1	E	163:UNK	C	164:UNK	N	3.31
1	F	114:UNK	C	115:UNK	N	3.31
1	F	166:UNK	C	167:UNK	N	3.31
1	F	701:UNK	C	702:UNK	N	3.31
1	G	59:LEU	C	60:ILE	N	3.31
1	G	72:THR	C	73:PHE	N	3.31
1	G	97:GLN	C	98:PHE	N	3.31

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	173:VAL	C	174:ARG	N	3.31
1	A	351:LYS	C	352:SER	N	3.30
1	A	1540:TYR	C	1541:ASN	N	3.30
1	A	1669:LEU	C	1670:LYS	N	3.30
1	A	1764:ASN	C	1765:PHE	N	3.30
1	A	2179:VAL	C	2180:PRO	N	3.30
1	A	2210:MET	C	2211:ALA	N	3.30
1	C	91:LYS	C	92:LEU	N	3.30
1	C	147:ILE	C	148:GLY	N	3.30
1	C	498:GLU	C	499:THR	N	3.30
1	C	574:ILE	C	575:GLN	N	3.30
1	C	663:HIS	C	664:LEU	N	3.30
1	C	1080:SER	C	1081:HIS	N	3.30
1	C	1146:SER	C	1147:LEU	N	3.30
1	C	1667:GLN	C	1668:ASP	N	3.30
1	C	1716:ALA	C	1717:ARG	N	3.30
1	C	2182:PRO	C	2183:ASN	N	3.30
1	C	2432:LYS	C	2433:LEU	N	3.30
1	D	88:ARG	C	89:TRP	N	3.30
1	D	117:ALA	C	118:PRO	N	3.30
1	E	256:UNK	C	257:UNK	N	3.30
1	E	308:UNK	C	309:UNK	N	3.30
1	E	559:UNK	C	560:UNK	N	3.30
1	F	304:UNK	C	305:UNK	N	3.30
1	F	375:UNK	C	376:UNK	N	3.30
1	F	410:UNK	C	411:UNK	N	3.30
1	G	90:THR	C	91:LEU	N	3.30
1	G	172:ASN	C	173:VAL	N	3.30
1	H	85:LYS	C	86:GLY	N	3.30
1	J	694:THR	C	695:THR	N	3.30
1	J	750:PRO	C	751:PHE	N	3.30
1	J	767:ILE	C	768:SER	N	3.30
1	A	762:VAL	C	763:ILE	N	3.29
1	A	1438:TYR	C	1439:ALA	N	3.29
1	A	1460:GLU	C	1461:VAL	N	3.29
1	A	1816:HIS	C	1817:ARG	N	3.29
1	A	2006:ILE	C	2007:SER	N	3.29
1	A	2043:TYR	C	2044:ASN	N	3.29
1	B	217:SER	C	218:ASP	N	3.29
1	C	159:PHE	C	160:TYR	N	3.29
1	C	204:GLY	C	205:THR	N	3.29
1	C	554:GLN	C	555:SER	N	3.29

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	614:LEU	C	615:THR	N	3.29
1	C	774:ALA	C	775:VAL	N	3.29
1	C	780:LEU	C	781:LYS	N	3.29
1	C	856:GLU	C	857:ASN	N	3.29
1	C	1869:LEU	C	1870:ILE	N	3.29
1	C	1967:TRP	C	1968:TYR	N	3.29
1	C	2187:PHE	C	2188:HIS	N	3.29
1	C	2369:ASN	C	2370:TRP	N	3.29
1	C	2385:ILE	C	2386:GLN	N	3.29
1	D	73:GLY	C	74:HIS	N	3.29
1	F	707:UNK	C	708:UNK	N	3.29
1	F	864:UNK	C	865:UNK	N	3.29
1	G	71:LYS	C	72:THR	N	3.29
1	H	92:HIS	C	93:LEU	N	3.29
1	I	701:SER	C	702:THR	N	3.29
1	A	155:LEU	C	156:ILE	N	3.28
1	A	528:GLU	C	529:LYS	N	3.28
1	A	749:ASP	C	750:GLU	N	3.28
1	A	943:ALA	C	944:ILE	N	3.28
1	A	1253:SER	C	1254:PRO	N	3.28
1	A	1360:GLU	C	1361:GLU	N	3.28
1	A	1972:ALA	C	1973:SER	N	3.28
1	A	2128:HIS	C	2129:GLU	N	3.28
1	A	2459:GLU	C	2460:ASN	N	3.28
1	B	234:TRP	C	235:SER	N	3.28
1	C	93:LYS	C	94:SER	N	3.28
1	C	735:LYS	C	736:GLU	N	3.28
1	C	980:ASP	C	981:PHE	N	3.28
1	C	1211:GLU	C	1212:MET	N	3.28
1	C	2067:SER	C	2068:PRO	N	3.28
1	C	2216:TYR	C	2217:ASP	N	3.28
1	C	2264:SER	C	2265:LEU	N	3.28
1	C	2282:PRO	C	2283:SER	N	3.28
1	C	2363:ALA	C	2364:PHE	N	3.28
1	C	2424:LEU	C	2425:VAL	N	3.28
1	D	13:THR	C	14:ILE	N	3.28
1	E	369:UNK	C	370:UNK	N	3.28
1	E	911:UNK	C	912:UNK	N	3.28
1	F	756:UNK	C	757:UNK	N	3.28
1	H	54:LEU	C	55:ILE	N	3.28
1	H	143:ASP	C	144:THR	N	3.28
1	A	156:ILE	C	157:SER	N	3.27

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	197:ARG	C	198:LEU	N	3.27
1	A	291:THR	C	292:ILE	N	3.27
1	A	818:ASP	C	819:ALA	N	3.27
1	A	1373:ILE	C	1374:ASN	N	3.27
1	A	1876:VAL	C	1877:LEU	N	3.27
1	A	2160:ASP	C	2161:ILE	N	3.27
1	A	2395:SER	C	2396:ASN	N	3.27
1	B	237:ASP	C	238:ASP	N	3.27
1	C	531:PHE	C	532:ILE	N	3.27
1	C	803:PRO	C	804:LEU	N	3.27
1	C	1065:ILE	C	1066:LEU	N	3.27
1	C	1125:ALA	C	1126:LEU	N	3.27
1	C	1335:PRO	C	1336:ILE	N	3.27
1	C	1412:GLU	C	1413:ASP	N	3.27
1	C	1744:SER	C	1745:TYR	N	3.27
1	C	2095:SER	C	2096:LYS	N	3.27
1	C	2141:GLN	C	2142:LEU	N	3.27
1	C	2366:PRO	C	2367:LEU	N	3.27
1	D	84:GLN	C	85:GLN	N	3.27
1	E	155:UNK	C	156:UNK	N	3.27
1	E	206:UNK	C	207:UNK	N	3.27
1	E	317:UNK	C	318:UNK	N	3.27
1	F	558:UNK	C	559:UNK	N	3.27
1	F	850:UNK	C	851:UNK	N	3.27
1	G	103:ASN	C	104:HIS	N	3.27
1	I	654:ASN	C	655:SER	N	3.27
1	A	332:ARG	C	333:GLU	N	3.26
1	A	985:LEU	C	986:GLY	N	3.26
1	A	1007:ILE	C	1008:ARG	N	3.26
1	A	1178:GLN	C	1179:LEU	N	3.26
1	A	1328:LYS	C	1329:PRO	N	3.26
1	A	1844:LEU	C	1845:LEU	N	3.26
1	A	2079:PRO	C	2080:GLY	N	3.26
1	A	2224:GLU	C	2225:VAL	N	3.26
1	A	2295:ILE	C	2296:ASP	N	3.26
1	A	2420:ALA	C	2421:MET	N	3.26
1	C	581:GLN	C	582:LEU	N	3.26
1	C	586:GLN	C	587:TYR	N	3.26
1	C	689:ILE	C	690:PHE	N	3.26
1	C	733:LYS	C	734:LYS	N	3.26
1	C	744:THR	C	745:LEU	N	3.26
1	C	812:GLN	C	813:SER	N	3.26

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	816:PHE	C	817:LYS	N	3.26
1	C	852:ILE	C	853:LEU	N	3.26
1	C	1376:ASN	C	1377:ASN	N	3.26
1	C	1830:HIS	C	1831:SER	N	3.26
1	C	1892:ILE	C	1893:VAL	N	3.26
1	C	2007:GLU	C	2008:ILE	N	3.26
1	C	2290:ILE	C	2291:THR	N	3.26
1	F	255:UNK	C	256:UNK	N	3.26
1	F	316:UNK	C	317:UNK	N	3.26
1	G	62:LEU	C	63:GLY	N	3.26
1	G	106:GLY	C	107:GLU	N	3.26
1	H	45:HIS	C	46:TYR	N	3.26
1	I	693:PHE	C	694:THR	N	3.26
1	I	741:LEU	C	742:LYS	N	3.26
1	J	765:GLN	C	766:SER	N	3.26
1	A	822:THR	C	823:THR	N	3.25
1	A	825:GLY	C	826:GLN	N	3.25
1	A	914:GLU	C	915:TYR	N	3.25
1	A	924:LEU	C	925:MET	N	3.25
1	A	1028:SER	C	1029:LYS	N	3.25
1	A	1053:ASP	C	1054:GLN	N	3.25
1	A	1207:TYR	C	1208:GLU	N	3.25
1	A	1542:VAL	C	1543:VAL	N	3.25
1	A	1719:LYS	C	1720:GLN	N	3.25
1	A	1742:SER	C	1743:TYR	N	3.25
1	A	1964:GLN	C	1965:TRP	N	3.25
1	A	2314:VAL	C	2315:PRO	N	3.25
1	B	193:ASP	C	194:ALA	N	3.25
1	C	654:ALA	C	655:GLU	N	3.25
1	C	970:VAL	C	971:MET	N	3.25
1	C	972:ARG	C	973:SER	N	3.25
1	C	1262:CYS	C	1263:SER	N	3.25
1	C	1366:ASN	C	1367:SER	N	3.25
1	C	1950:GLU	C	1951:LEU	N	3.25
1	C	2030:LYS	C	2031:SER	N	3.25
1	C	2055:LEU	C	2056:PRO	N	3.25
1	C	2277:LEU	C	2278:GLY	N	3.25
1	D	41:THR	C	42:ASN	N	3.25
1	D	49:THR	C	50:ALA	N	3.25
1	D	82:SER	C	83:PHE	N	3.25
1	E	310:UNK	C	311:UNK	N	3.25
1	E	566:UNK	C	567:UNK	N	3.25

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	858:UNK	C	859:UNK	N	3.25
1	F	262:UNK	C	263:UNK	N	3.25
1	F	303:UNK	C	304:UNK	N	3.25
1	F	463:UNK	C	464:UNK	N	3.25
1	F	805:UNK	C	806:UNK	N	3.25
1	H	171:ASP	C	172:ASN	N	3.25
1	A	162:THR	C	163:GLU	N	3.24
1	A	744:LEU	C	745:ILE	N	3.24
1	A	754:PRO	C	755:TYR	N	3.24
1	A	824:LEU	C	825:GLY	N	3.24
1	A	849:ILE	C	850:ASN	N	3.24
1	A	940:ALA	C	941:ILE	N	3.24
1	A	1138:LYS	C	1139:ALA	N	3.24
1	A	1527:GLU	C	1528:LEU	N	3.24
1	A	1580:LEU	C	1581:GLY	N	3.24
1	A	1959:VAL	C	1960:LEU	N	3.24
1	A	2204:HIS	C	2205:TRP	N	3.24
1	A	2383:ILE	C	2384:GLN	N	3.24
1	B	22:GLY	C	23:VAL	N	3.24
1	C	846:LEU	C	847:GLY	N	3.24
1	C	981:PHE	C	982:TYR	N	3.24
1	C	1106:LEU	C	1107:GLY	N	3.24
1	C	1112:ASN	C	1113:ILE	N	3.24
1	C	1156:PHE	C	1157:VAL	N	3.24
1	C	1236:LYS	C	1237:GLU	N	3.24
1	C	1661:LEU	C	1662:TRP	N	3.24
1	C	1665:GLY	C	1666:LEU	N	3.24
1	C	1908:HIS	C	1909:PRO	N	3.24
1	D	37:ARG	C	38:LEU	N	3.24
1	F	159:UNK	C	160:UNK	N	3.24
1	A	383:PHE	C	384:THR	N	3.23
1	A	532:GLN	C	533:SER	N	3.23
1	A	1042:THR	C	1043:LEU	N	3.23
1	A	1056:ASN	C	1057:LYS	N	3.23
1	A	1131:ASN	C	1132:GLY	N	3.23
1	A	1352:HIS	C	1353:TYR	N	3.23
1	A	1612:PHE	C	1613:ALA	N	3.23
1	A	2203:GLU	C	2204:HIS	N	3.23
1	A	2234:GLU	C	2235:GLY	N	3.23
1	C	422:ASP	C	423:ILE	N	3.23
1	C	643:LYS	C	644:LEU	N	3.23
1	C	1043:THR	C	1044:LEU	N	3.23

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1214:VAL	C	1215:THR	N	3.23
1	C	1492:LYS	C	1493:SER	N	3.23
1	C	1852:THR	C	1853:PHE	N	3.23
1	C	1894:SER	C	1895:ARG	N	3.23
1	C	1952:VAL	C	1953:SER	N	3.23
1	C	1970:GLY	C	1971:LEU	N	3.23
1	C	2031:SER	C	2032:LYS	N	3.23
1	C	2149:LEU	C	2150:LEU	N	3.23
1	D	149:GLN	C	150:CYS	N	3.23
1	G	49:TYR	C	50:HIS	N	3.23
1	G	82:ALA	C	83:LEU	N	3.23
1	G	182:ILE	C	183:ASP	N	3.23
1	H	88:GLU	C	89:GLN	N	3.23
1	H	159:LYS	C	160:MET	N	3.23
1	A	181:PRO	C	182:SER	N	3.22
1	A	245:ILE	C	246:LYS	N	3.22
1	A	728:SER	C	729:ASN	N	3.22
1	A	729:ASN	C	730:MET	N	3.22
1	A	836:GLY	C	837:PRO	N	3.22
1	A	1070:THR	C	1071:PHE	N	3.22
1	A	1530:ALA	C	1531:LEU	N	3.22
1	A	1550:ALA	C	1551:GLU	N	3.22
1	A	1838:LEU	C	1839:GLN	N	3.22
1	A	2206:VAL	C	2207:MET	N	3.22
1	A	2259:TYR	C	2260:THR	N	3.22
1	A	2300:CYS	C	2301:PHE	N	3.22
1	B	5:LEU	C	6:VAL	N	3.22
1	B	82:SER	C	83:PHE	N	3.22
1	C	153:VAL	C	154:ASP	N	3.22
1	C	1025:ILE	C	1026:GLU	N	3.22
1	C	1186:ASN	C	1187:ASN	N	3.22
1	C	1715:LEU	C	1716:ALA	N	3.22
1	C	1767:PHE	C	1768:GLU	N	3.22
1	C	2075:ASP	C	2076:LEU	N	3.22
1	C	2454:ILE	C	2455:GLN	N	3.22
1	D	86:ASP	C	87:ASN	N	3.22
1	D	281:THR	C	282:ARG	N	3.22
1	E	859:UNK	C	860:UNK	N	3.22
1	F	264:UNK	C	265:UNK	N	3.22
1	F	806:UNK	C	807:UNK	N	3.22
1	G	195:SER	C	196:LYS	N	3.22
1	H	102:ILE	C	103:ASN	N	3.22

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	726:ASP	C	727:GLY	N	3.22
1	A	1003:ILE	C	1004:TYR	N	3.21
1	A	1026:SER	C	1027:ILE	N	3.21
1	A	1494:PRO	C	1495:ASP	N	3.21
1	A	2149:GLN	C	2150:ASN	N	3.21
1	A	2350:LYS	C	2351:GLY	N	3.21
1	A	2397:GLY	C	2398:ALA	N	3.21
1	B	41:THR	C	42:ASN	N	3.21
1	B	90:MET	C	91:VAL	N	3.21
1	B	172:SER	C	173:MET	N	3.21
1	B	273:TYR	C	274:VAL	N	3.21
1	C	635:HIS	C	636:SER	N	3.21
1	C	699:ILE	C	700:ILE	N	3.21
1	C	1038:ARG	C	1039:PHE	N	3.21
1	C	1155:ASP	C	1156:PHE	N	3.21
1	C	1160:VAL	C	1161:PRO	N	3.21
1	C	1843:ALA	C	1844:LEU	N	3.21
1	C	2164:GLN	C	2165:GLN	N	3.21
1	C	2295:ILE	C	2296:HIS	N	3.21
1	C	2342:GLU	C	2343:ASN	N	3.21
1	C	2467:TYR	C	2468:ILE	N	3.21
1	D	74:HIS	C	75:ARG	N	3.21
1	D	135:ASP	C	136:ARG	N	3.21
1	F	153:UNK	C	154:UNK	N	3.21
1	F	307:UNK	C	308:UNK	N	3.21
1	A	148:GLY	C	149:ILE	N	3.20
1	A	1604:GLU	C	1605:ASP	N	3.20
1	A	1829:SER	C	1830:ILE	N	3.20
1	A	2227:THR	C	2228:TYR	N	3.20
1	B	39:GLU	C	40:ILE	N	3.20
1	B	169:SER	C	170:ASP	N	3.20
1	C	257:LEU	C	258:TYR	N	3.20
1	C	1064:ARG	C	1065:ILE	N	3.20
1	C	1245:ARG	C	1246:LEU	N	3.20
1	C	1508:HIS	C	1509:ARG	N	3.20
1	C	1826:LYS	C	1827:GLY	N	3.20
1	C	1831:SER	C	1832:ILE	N	3.20
1	E	215:UNK	C	216:UNK	N	3.20
1	E	217:UNK	C	218:UNK	N	3.20
1	H	151:GLU	C	152:TYR	N	3.20
1	A	683:ALA	C	684:LEU	N	3.19
1	A	782:LEU	C	783:GLY	N	3.19

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1107:ARG	C	1108:LEU	N	3.19
1	A	2343:MET	C	2344:LYS	N	3.19
1	B	68:VAL	C	69:ALA	N	3.19
1	B	94:SER	C	95:GLU	N	3.19
1	C	1110:ALA	C	1111:LYS	N	3.19
1	C	1251:LEU	C	1252:LYS	N	3.19
1	C	1645:ASN	C	1646:THR	N	3.19
1	C	1762:TRP	C	1763:ALA	N	3.19
1	C	2204:ILE	C	2205:GLU	N	3.19
1	D	234:TRP	C	235:SER	N	3.19
1	D	260:ALA	C	261:ASP	N	3.19
1	D	287:GLN	C	288:TYR	N	3.19
1	E	856:UNK	C	857:UNK	N	3.19
1	E	866:UNK	C	867:UNK	N	3.19
1	F	377:UNK	C	378:UNK	N	3.19
1	F	412:UNK	C	413:UNK	N	3.19
1	F	608:UNK	C	609:UNK	N	3.19
1	J	675:SER	C	676:MET	N	3.19
1	J	714:TYR	C	715:SER	N	3.19
1	A	497:GLU	C	498:THR	N	3.18
1	A	611:ALA	C	612:ALA	N	3.18
1	A	948:PHE	C	949:GLN	N	3.18
1	A	1059:ILE	C	1060:VAL	N	3.18
1	A	1284:TRP	C	1285:VAL	N	3.18
1	A	1981:ASN	C	1982:THR	N	3.18
1	A	2101:VAL	C	2102:ILE	N	3.18
1	A	2369:GLY	C	2370:PHE	N	3.18
1	A	2429:ASP	C	2430:LYS	N	3.18
1	B	188:MET	C	189:PRO	N	3.18
1	B	211:THR	C	212:ARG	N	3.18
1	C	268:ILE	C	269:TRP	N	3.18
1	C	717:LYS	C	718:THR	N	3.18
1	C	1163:ILE	C	1164:ASN	N	3.18
1	C	1180:LEU	C	1181:VAL	N	3.18
1	C	1231:SER	C	1232:GLN	N	3.18
1	C	1765:ALA	C	1766:ASN	N	3.18
1	C	1885:ARG	C	1886:ILE	N	3.18
1	C	1886:ILE	C	1887:HIS	N	3.18
1	C	1955:GLU	C	1956:LEU	N	3.18
1	E	608:UNK	C	609:UNK	N	3.18
1	F	252:UNK	C	253:UNK	N	3.18
1	F	364:UNK	C	365:UNK	N	3.18

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	510:UNK	C	511:UNK	N	3.18
1	F	758:UNK	C	759:UNK	N	3.18
1	H	49:TYR	C	50:HIS	N	3.18
1	H	107:GLU	C	108:ASN	N	3.18
1	A	566:ILE	C	567:THR	N	3.17
1	A	662:HIS	C	663:LEU	N	3.17
1	A	738:ALA	C	739:THR	N	3.17
1	A	798:LYS	C	799:GLU	N	3.17
1	A	814:SER	C	815:PHE	N	3.17
1	A	971:ARG	C	972:SER	N	3.17
1	A	1020:ILE	C	1021:ILE	N	3.17
1	A	1642:PRO	C	1643:ASN	N	3.17
1	A	2195:ALA	C	2196:LYS	N	3.17
1	A	2340:GLU	C	2341:ASN	N	3.17
1	C	480:ASN	C	481:LYS	N	3.17
1	C	670:PRO	C	671:GLN	N	3.17
1	C	719:LEU	C	720:LEU	N	3.17
1	C	834:TYR	C	835:VAL	N	3.17
1	C	1124:GLN	C	1125:ALA	N	3.17
1	C	1475:ALA	C	1476:TRP	N	3.17
1	C	2179:GLY	C	2180:TRP	N	3.17
1	C	2349:ARG	C	2350:ASP	N	3.17
1	E	109:UNK	C	110:UNK	N	3.17
1	E	204:UNK	C	205:UNK	N	3.17
1	E	401:UNK	C	402:UNK	N	3.17
1	E	706:UNK	C	707:UNK	N	3.17
1	G	96:GLN	C	97:GLN	N	3.17
1	I	674:GLU	C	675:SER	N	3.17
1	J	727:GLY	C	728:LEU	N	3.17
1	A	457:LYS	C	458:ASP	N	3.16
1	A	545:GLU	C	546:LYS	N	3.16
1	A	596:THR	C	597:ILE	N	3.16
1	A	639:VAL	C	640:LEU	N	3.16
1	A	711:VAL	C	712:PRO	N	3.16
1	A	1569:LEU	C	1570:THR	N	3.16
1	A	2039:TRP	C	2040:ASP	N	3.16
1	A	2145:ASN	C	2146:THR	N	3.16
1	A	2156:ARG	C	2157:ARG	N	3.16
1	C	179:VAL	C	180:LEU	N	3.16
1	C	239:ARG	C	240:HIS	N	3.16
1	C	513:THR	C	514:VAL	N	3.16
1	C	716:ARG	C	717:LYS	N	3.16

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	758:ASP	C	759:PRO	N	3.16
1	C	765:LEU	C	766:PRO	N	3.16
1	C	769:GLN	C	770:ASP	N	3.16
1	C	1161:PRO	C	1162:VAL	N	3.16
1	C	1331:PRO	C	1332:LEU	N	3.16
1	C	1428:SER	C	1429:VAL	N	3.16
1	C	1494:GLN	C	1495:SER	N	3.16
1	C	1622:GLY	C	1623:ARG	N	3.16
1	C	2168:ALA	C	2169:ILE	N	3.16
1	C	2180:TRP	C	2181:VAL	N	3.16
1	C	2429:ILE	C	2430:THR	N	3.16
1	C	2439:ARG	C	2440:ARG	N	3.16
1	C	2456:GLN	C	2457:ALA	N	3.16
1	D	78:VAL	C	79:THR	N	3.16
1	F	551:UNK	C	552:UNK	N	3.16
1	I	690:ARG	C	691:ASN	N	3.16
1	A	397:ARG	C	398:TYR	N	3.15
1	A	1469:ALA	C	1470:ALA	N	3.15
1	A	1492:GLN	C	1493:SER	N	3.15
1	A	1552:LEU	C	1553:GLU	N	3.15
1	A	1656:LEU	C	1657:LYS	N	3.15
1	A	1831:SER	C	1832:LEU	N	3.15
1	A	1858:THR	C	1859:GLN	N	3.15
1	A	2215:ASP	C	2216:ASN	N	3.15
1	A	2220:LEU	C	2221:GLN	N	3.15
1	A	2352:SER	C	2353:LEU	N	3.15
1	A	2465:TYR	C	2466:ILE	N	3.15
1	B	228:ASP	C	229:HIS	N	3.15
1	B	236:ILE	C	237:ASP	N	3.15
1	C	200:THR	C	201:VAL	N	3.15
1	C	360:TYR	C	361:LYS	N	3.15
1	C	713:PRO	C	714:SER	N	3.15
1	C	915:GLU	C	916:TYR	N	3.15
1	C	1567:SER	C	1568:ASP	N	3.15
1	C	2465:GLN	C	2466:HIS	N	3.15
1	D	142:ILE	C	143:TRP	N	3.15
1	E	208:UNK	C	209:UNK	N	3.15
1	F	507:UNK	C	508:UNK	N	3.15
1	H	186:GLN	C	187:THR	N	3.15
1	A	1727:LEU	C	1728:GLN	N	3.14
1	A	2106:GLN	C	2107:ARG	N	3.14
1	A	2447:GLN	C	2448:VAL	N	3.14

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	140:ILE	C	141:ARG	N	3.14
1	B	192:THR	C	193:ASP	N	3.14
1	C	510:LEU	C	511:GLU	N	3.14
1	C	1226:ASN	C	1227:ALA	N	3.14
1	C	1410:ARG	C	1411:TRP	N	3.14
1	C	1832:ILE	C	1833:SER	N	3.14
1	C	2019:ASN	C	2020:ASP	N	3.14
1	C	2259:THR	C	2260:THR	N	3.14
1	D	246:LEU	C	247:ASP	N	3.14
1	A	459:LEU	C	460:PHE	N	3.13
1	A	678:ARG	C	679:LEU	N	3.13
1	A	1266:SER	C	1267:VAL	N	3.13
1	A	1709:TYR	C	1710:THR	N	3.13
1	A	1747:THR	C	1748:HIS	N	3.13
1	A	2049:ILE	C	2050:GLY	N	3.13
1	B	220:LYS	C	221:HIS	N	3.13
1	C	458:LYS	C	459:ASP	N	3.13
1	C	476:ALA	C	477:LYS	N	3.13
1	C	775:VAL	C	776:ALA	N	3.13
1	C	790:GLY	C	791:GLY	N	3.13
1	C	1060:ILE	C	1061:VAL	N	3.13
1	C	1188:GLU	C	1189:CYS	N	3.13
1	C	1228:TRP	C	1229:TYR	N	3.13
1	C	1964:HIS	C	1965:GLU	N	3.13
1	D	129:GLY	C	130:GLU	N	3.13
1	D	201:THR	C	202:LYS	N	3.13
1	E	565:UNK	C	566:UNK	N	3.13
1	G	101:PHE	C	102:ILE	N	3.13
1	A	709:TYR	C	710:VAL	N	3.12
1	A	806:ASN	C	807:THR	N	3.12
1	A	1568:ARG	C	1569:LEU	N	3.12
1	A	1946:GLN	C	1947:ALA	N	3.12
1	A	2059:LEU	C	2060:GLU	N	3.12
1	A	2097:PRO	C	2098:VAL	N	3.12
1	A	2226:PHE	C	2227:THR	N	3.12
1	A	2331:ILE	C	2332:GLU	N	3.12
1	C	352:LYS	C	353:SER	N	3.12
1	C	802:MET	C	803:PRO	N	3.12
1	C	926:MET	C	927:LYS	N	3.12
1	C	932:PRO	C	933:SER	N	3.12
1	C	1027:SER	C	1028:ILE	N	3.12
1	C	1321:LEU	C	1322:VAL	N	3.12

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	1983:ASN	C	1984:THR	N	3.12
1	C	2173:PRO	C	2174:LYS	N	3.12
1	C	2350:ASP	C	2351:ASN	N	3.12
1	D	220:LYS	C	221:HIS	N	3.12
1	E	758:UNK	C	759:UNK	N	3.12
1	F	704:UNK	C	705:UNK	N	3.12
1	H	150:LEU	C	151:GLU	N	3.12
1	A	398:TYR	C	399:LEU	N	3.11
1	A	477:HIS	C	478:LEU	N	3.11
1	A	688:ILE	C	689:PHE	N	3.11
1	A	1980:HIS	C	1981:ASN	N	3.11
1	A	2197:LYS	C	2198:ILE	N	3.11
1	B	246:LEU	C	247:ASP	N	3.11
1	C	245:ILE	C	246:ILE	N	3.11
1	C	700:ILE	C	701:GLY	N	3.11
1	C	1347:HIS	C	1348:ALA	N	3.11
1	C	1966:GLN	C	1967:TRP	N	3.11
1	C	2002:PRO	C	2003:GLU	N	3.11
1	D	223:ALA	C	224:THR	N	3.11
1	A	760:LEU	C	761:ASP	N	3.10
1	A	785:LEU	C	786:SER	N	3.10
1	A	1754:TYR	C	1755:LYS	N	3.10
1	A	2344:LYS	C	2345:VAL	N	3.10
1	B	127:ASN	C	128:GLN	N	3.10
1	C	946:MET	C	947:HIS	N	3.10
1	C	1093:TYR	C	1094:SER	N	3.10
1	C	1646:THR	C	1647:ALA	N	3.10
1	D	252:TRP	C	253:VAL	N	3.10
1	G	181:PRO	C	182:ILE	N	3.10
1	A	440:ASN	C	441:ILE	N	3.09
1	A	549:LYS	C	550:SER	N	3.09
1	A	807:THR	C	808:PHE	N	3.09
1	A	1184:LEU	C	1185:ASN	N	3.09
1	A	2271:TYR	C	2272:ILE	N	3.09
1	A	2419:ARG	C	2420:ALA	N	3.09
1	B	185:VAL	C	186:TRP	N	3.09
1	B	284:ILE	C	285:VAL	N	3.09
1	C	315:HIS	C	316:GLY	N	3.09
1	C	1723:GLY	C	1724:GLU	N	3.09
1	C	2008:ILE	C	2009:SER	N	3.09
1	C	2036:ASN	C	2037:LEU	N	3.09
1	C	2316:VAL	C	2317:PRO	N	3.09

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	274:VAL	C	275:ARG	N	3.09
1	F	105:UNK	C	106:UNK	N	3.09
1	F	211:UNK	C	212:UNK	N	3.09
1	G	159:LYS	C	160:MET	N	3.09
1	J	672:ASN	C	673:TYR	N	3.09
1	A	559:THR	C	560:GLY	N	3.08
1	A	722:LEU	C	723:THR	N	3.08
1	B	33:SER	C	34:GLN	N	3.08
1	C	384:PHE	C	385:THR	N	3.08
1	C	1042:GLU	C	1043:THR	N	3.08
1	C	1225:LYS	C	1226:ASN	N	3.08
1	C	1603:LYS	C	1604:PRO	N	3.08
1	C	1658:LEU	C	1659:LYS	N	3.08
1	C	2048:PHE	C	2049:ARG	N	3.08
1	C	2186:THR	C	2187:PHE	N	3.08
1	D	286:ARG	C	287:GLN	N	3.08
1	E	357:UNK	C	358:UNK	N	3.08
1	E	407:UNK	C	408:UNK	N	3.08
1	F	216:UNK	C	217:UNK	N	3.08
1	A	980:PHE	C	981:TYR	N	3.07
1	A	1213:VAL	C	1214:THR	N	3.07
1	A	1706:VAL	C	1707:GLU	N	3.07
1	A	2273:LEU	C	2274:GLY	N	3.07
1	C	1063:ILE	C	1064:ARG	N	3.07
1	C	1107:GLY	C	1108:ARG	N	3.07
1	C	2054:GLN	C	2055:LEU	N	3.07
1	C	2117:GLY	C	2118:SER	N	3.07
1	E	505:UNK	C	506:UNK	N	3.07
1	G	147:HIS	C	148:VAL	N	3.07
1	A	1064:ILE	C	1065:LEU	N	3.06
1	A	1240:GLU	C	1241:TRP	N	3.06
1	A	1286:GLU	C	1287:LEU	N	3.06
1	A	1464:ALA	C	1465:MET	N	3.06
1	A	1614:ASN	C	1615:LEU	N	3.06
1	A	1938:ILE	C	1939:HIS	N	3.06
1	A	2462:CYS	C	2463:GLN	N	3.06
1	B	13:THR	C	14:ILE	N	3.06
1	B	118:PRO	C	119:VAL	N	3.06
1	B	214:LEU	C	215:LEU	N	3.06
1	C	732:PRO	C	733:LYS	N	3.06
1	C	1039:PHE	C	1040:VAL	N	3.06
1	C	2221:LEU	C	2222:LEU	N	3.06

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	77:ASN	C	78:VAL	N	3.06
1	J	660:GLU	C	661:TYR	N	3.06
1	A	1576:ASN	C	1577:THR	N	3.05
1	A	2094:LYS	C	2095:PHE	N	3.05
1	A	2154:CYS	C	2155:PHE	N	3.05
1	B	252:TRP	C	253:VAL	N	3.05
1	C	469:CYS	C	470:ALA	N	3.05
1	C	801:LEU	C	802:MET	N	3.05
1	C	923:HIS	C	924:ASN	N	3.05
1	C	1482:ASP	C	1483:GLU	N	3.05
1	C	1736:SER	C	1737:ASN	N	3.05
1	E	403:UNK	C	404:UNK	N	3.05
1	F	116:UNK	C	117:UNK	N	3.05
1	A	543:SER	C	544:ILE	N	3.04
1	A	642:LYS	C	643:LEU	N	3.04
1	A	1567:LYS	C	1568:ARG	N	3.04
1	A	1651:VAL	C	1652:VAL	N	3.04
1	A	1818:HIS	C	1819:VAL	N	3.04
1	A	1899:LEU	C	1900:SER	N	3.04
1	A	2042:TYR	C	2043:TYR	N	3.04
1	B	85:GLN	C	86:ASP	N	3.04
1	C	1267:SER	C	1268:VAL	N	3.04
1	C	1383:ASP	C	1384:SER	N	3.04
1	C	1815:ASN	C	1816:LEU	N	3.04
1	C	2053:LYS	C	2054:GLN	N	3.04
1	C	2291:THR	C	2292:GLY	N	3.04
1	E	113:UNK	C	114:UNK	N	3.04
1	F	208:UNK	C	209:UNK	N	3.04
1	G	56:CYS	C	57:VAL	N	3.04
1	A	922:HIS	C	923:ASN	N	3.03
1	A	1281:SER	C	1282:SER	N	3.03
1	A	1519:ASN	C	1520:ALA	N	3.03
1	A	1988:ALA	C	1989:LEU	N	3.03
1	C	1580:ARG	C	1581:LEU	N	3.03
1	C	2043:ILE	C	2044:TYR	N	3.03
1	H	181:PRO	C	182:ILE	N	3.03
1	I	767:ILE	C	768:SER	N	3.03
1	C	1517:VAL	C	1518:HIS	N	3.02
1	C	1881:GLN	C	1882:LEU	N	3.02
1	D	213:ILE	C	214:LEU	N	3.02
1	A	221:LEU	C	222:THR	N	3.01
1	A	756:ILE	C	757:ASP	N	3.01

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	967:ILE	C	968:LEU	N	3.01
1	A	1380:THR	C	1381:ASP	N	3.01
1	C	938:HIS	C	939:THR	N	3.01
1	C	1486:GLN	C	1487:TYR	N	3.01
1	E	604:UNK	C	605:UNK	N	3.01
1	B	148:ASN	C	149:GLN	N	3.00
1	C	1224:LEU	C	1225:LYS	N	3.00
1	C	1561:LYS	C	1562:LYS	N	3.00
1	D	216:SER	C	217:SER	N	3.00
1	D	265:LEU	C	266:VAL	N	3.00
1	A	364:ILE	C	365:ARG	N	2.99
1	A	968:LEU	C	969:VAL	N	2.99
1	A	1526:THR	C	1527:GLU	N	2.99
1	A	2315:PRO	C	2316:PHE	N	2.99
1	C	462:TYR	C	463:CYS	N	2.99
1	C	494:ASP	C	495:HIS	N	2.99
1	C	1014:ILE	C	1015:ILE	N	2.99
1	C	1677:PHE	C	1678:THR	N	2.99
1	C	2126:VAL	C	2127:LEU	N	2.99
1	C	2229:THR	C	2230:TYR	N	2.99
1	C	2413:HIS	C	2414:LYS	N	2.99
1	F	407:UNK	C	408:UNK	N	2.99
1	G	142:GLY	C	143:ASP	N	2.99
1	A	253:PRO	C	254:TYR	N	2.98
1	A	718:LEU	C	719:LEU	N	2.98
1	A	2014:ARG	C	2015:ASP	N	2.98
1	A	2045:VAL	C	2046:PHE	N	2.98
1	A	2184:THR	C	2185:PHE	N	2.98
1	B	16:PHE	C	17:TRP	N	2.98
1	C	1158:VAL	C	1159:PHE	N	2.98
1	C	2233:ASN	C	2234:ASN	N	2.98
1	D	28:ILE	C	29:GLN	N	2.98
1	D	89:TRP	C	90:MET	N	2.98
1	A	797:LEU	C	798:LYS	N	2.97
1	A	1219:ASN	C	1220:GLN	N	2.97
1	C	516:SER	C	517:ARG	N	2.97
1	C	974:CYS	C	975:PRO	N	2.97
1	C	1514:LYS	C	1515:ALA	N	2.97
1	C	1641:PRO	C	1642:ASP	N	2.97
1	C	1747:LEU	C	1748:ALA	N	2.97
1	C	1871:GLN	C	1872:ILE	N	2.97
1	C	2069:LYS	C	2070:LEU	N	2.97

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	25:SER	C	26:ARG	N	2.97
1	E	361:UNK	C	362:UNK	N	2.97
1	A	928:LEU	C	929:ASN	N	2.96
1	A	1061:PRO	C	1062:ILE	N	2.96
1	A	1265:VAL	C	1266:SER	N	2.96
1	A	1537:ASN	C	1538:ARG	N	2.96
1	A	1933:ILE	C	1934:GLU	N	2.96
1	C	778:THR	C	779:ALA	N	2.96
1	C	969:LEU	C	970:VAL	N	2.96
1	C	2108:GLN	C	2109:ARG	N	2.96
1	C	2471:CYS	C	2472:PRO	N	2.96
1	B	43:ASP	C	44:LYS	N	2.95
1	B	164:SER	C	165:LEU	N	2.95
1	C	550:LYS	C	551:SER	N	2.95
1	C	661:LEU	C	662:GLN	N	2.95
1	F	353:UNK	C	354:UNK	N	2.95
1	A	1069:VAL	C	1070:THR	N	2.94
1	A	2284:MET	C	2285:LEU	N	2.94
1	A	326:ALA	C	327:THR	N	2.93
1	A	371:ILE	C	372:LEU	N	2.93
1	A	414:PHE	C	415:ILE	N	2.93
1	A	1228:TYR	C	1229:CYS	N	2.93
1	B	260:ALA	C	261:ASP	N	2.93
1	B	275:ARG	C	276:LEU	N	2.93
1	C	1993:PRO	C	1994:LEU	N	2.93
1	A	1346:ALA	C	1347:PHE	N	2.92
1	A	1947:ALA	C	1948:GLU	N	2.92
1	C	455:GLN	C	456:PHE	N	2.92
1	C	847:GLY	C	848:ILE	N	2.92
1	C	2251:SER	C	2252:GLU	N	2.92
1	A	1119:SER	C	1120:ARG	N	2.91
1	C	1277:PHE	C	1278:ASN	N	2.91
1	C	1591:TRP	C	1592:GLN	N	2.91
1	A	780:LYS	C	781:VAL	N	2.90
1	A	1062:ILE	C	1063:ARG	N	2.90
1	A	1680:ALA	C	1681:HIS	N	2.90
1	C	378:ALA	C	379:PHE	N	2.90
1	C	793:GLU	C	794:MET	N	2.90
1	C	948:ILE	C	949:PHE	N	2.90
1	C	1483:GLU	C	1484:ILE	N	2.90
1	A	218:ILE	C	219:ASP	N	2.89
1	A	1855:PRO	C	1856:GLU	N	2.89

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	66:ASN	C	67:PRO	N	2.89
1	C	1618:CYS	C	1619:ARG	N	2.89
1	C	1840:LEU	C	1841:GLN	N	2.89
1	C	2123:TYR	C	2124:LYS	N	2.89
1	C	2133:ILE	C	2134:ARG	N	2.89
1	A	270:PRO	C	271:LEU	N	2.88
1	A	1079:SER	C	1080:HIS	N	2.88
1	B	241:LYS	C	242:LEU	N	2.88
1	C	1469:PRO	C	1470:LEU	N	2.88
1	C	1943:PRO	C	1944:VAL	N	2.88
1	A	424:PHE	C	425:GLU	N	2.86
1	A	1001:GLU	C	1002:LYS	N	2.86
1	C	1122:ILE	C	1123:VAL	N	2.86
1	C	1520:PHE	C	1521:ASN	N	2.86
1	C	2100:VAL	C	2101:PHE	N	2.86
1	A	1291:TYR	C	1292:GLN	N	2.85
1	A	2291:LYS	C	2292:VAL	N	2.85
1	C	753:ALA	C	754:LYS	N	2.85
1	C	1446:GLU	C	1447:GLU	N	2.85
1	C	556:PHE	C	557:MET	N	2.84
1	C	966:GLY	C	967:ILE	N	2.84
1	C	1898:LEU	C	1899:SER	N	2.84
1	C	2156:CYS	C	2157:PHE	N	2.84
1	C	2337:PHE	C	2338:ARG	N	2.84
1	E	214:UNK	C	215:UNK	N	2.84
1	A	723:THR	C	724:GLN	N	2.83
1	A	957:SER	C	958:PHE	N	2.83
1	A	1824:LYS	C	1825:GLY	N	2.83
1	C	566:ASP	C	567:ILE	N	2.83
1	C	1240:GLN	C	1241:GLU	N	2.83
1	C	2098:GLU	C	2099:PRO	N	2.83
1	A	2137:VAL	C	2138:MET	N	2.82
1	A	2320:ARG	C	2321:MET	N	2.82
1	A	2322:LEU	C	2323:THR	N	2.82
1	C	2139:VAL	C	2140:MET	N	2.82
1	C	804:LEU	C	805:ILE	N	2.81
1	C	2287:LEU	C	2288:ASP	N	2.81
1	C	392:ILE	C	393:MET	N	2.80
1	D	249:HIS	C	250:GLN	N	2.80
1	C	1097:SER	C	1098:LEU	N	2.79
1	C	1652:PRO	C	1653:VAL	N	2.79
1	A	671:LEU	C	672:ALA	N	2.78

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	2021:ALA	C	2022:TYR	N	2.78
1	B	136:ARG	C	137:ASP	N	2.77
1	C	964:ILE	C	965:PRO	N	2.77
1	A	2019:ALA	C	2020:TYR	N	2.76
1	A	673:GLN	C	674:PRO	N	2.75
1	A	946:HIS	C	947:ILE	N	2.73
1	C	1478:LEU	C	1479:GLU	N	2.73
1	C	1574:ARG	C	1575:GLU	N	2.73
1	C	2112:LYS	C	2113:PHE	N	2.73
1	A	461:TYR	C	462:CYS	N	2.72
1	A	534:ASN	C	535:GLN	N	2.71
1	C	2227:VAL	C	2228:PHE	N	2.71
1	C	799:LYS	C	800:GLU	N	2.70
1	C	998:ARG	C	999:PRO	N	2.68
1	A	1609:ARG	C	1610:ILE	N	2.65
1	A	960:ASP	C	961:GLN	N	2.61
1	C	542:GLN	C	543:PHE	N	2.61
1	C	2448:GLU	C	2449:GLN	N	2.59
1	C	1578:ASN	C	1579:THR	N	2.55

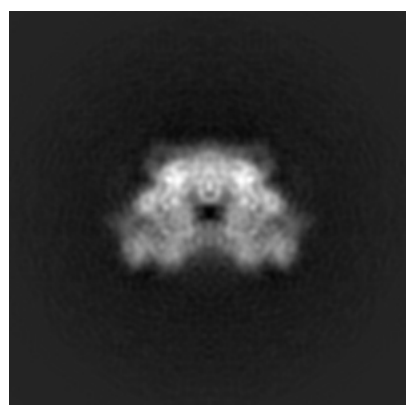
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3896. These allow visual inspection of the internal detail of the map and identification of artifacts.

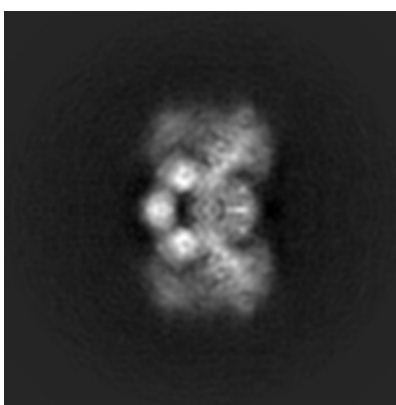
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

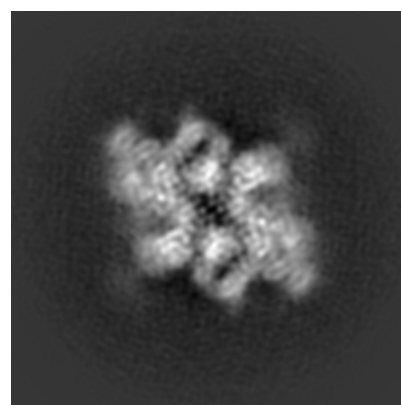
6.1.1 Primary map



X



Y

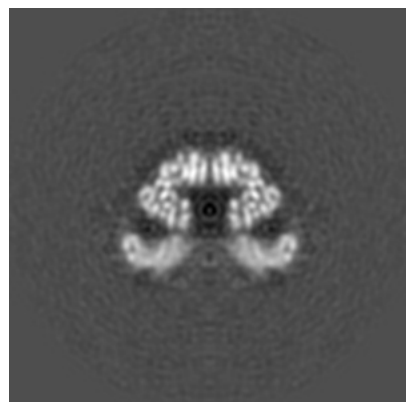


Z

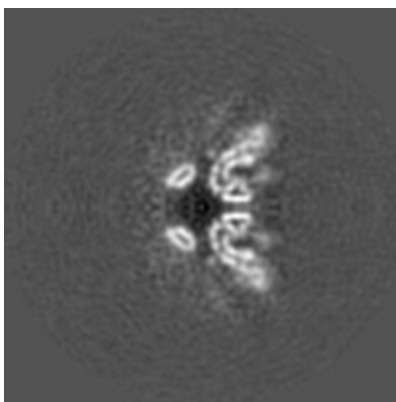
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

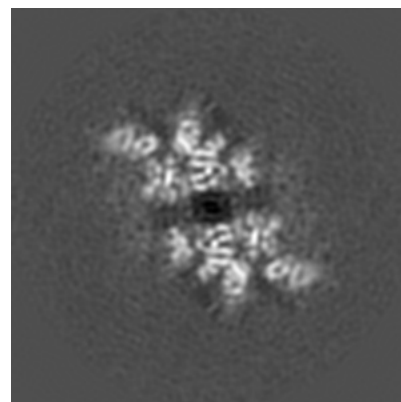
6.2.1 Primary map



X Index: 160



Y Index: 160

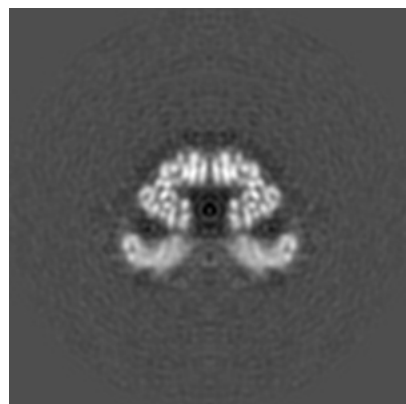


Z Index: 160

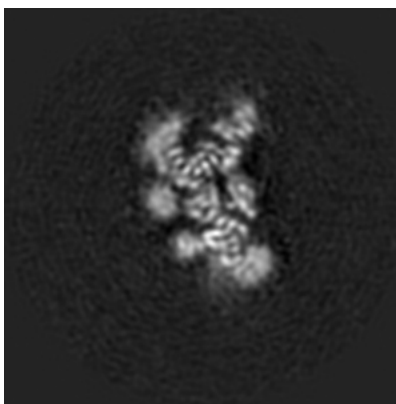
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

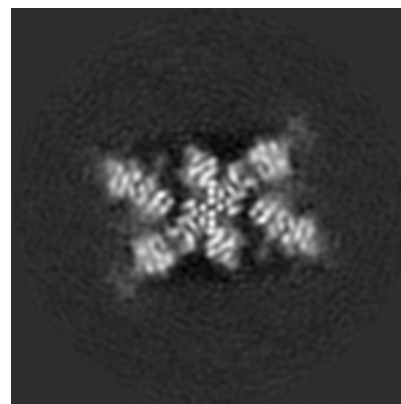
6.3.1 Primary map



X Index: 160



Y Index: 133

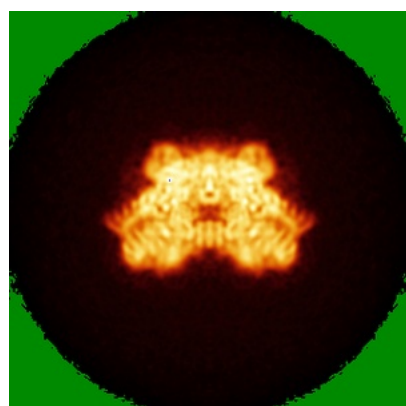


Z Index: 190

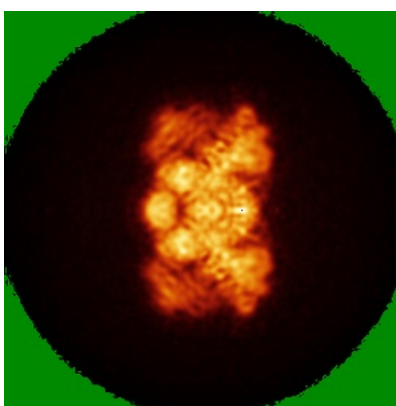
The images above show the largest variance slices of the map in three orthogonal directions.

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

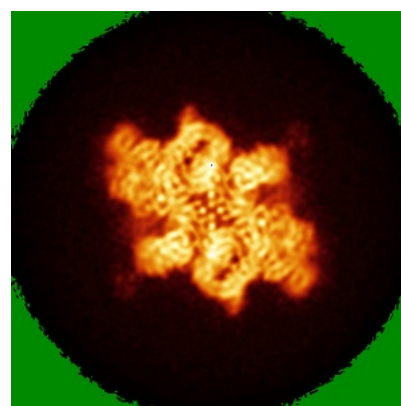
6.4.1 Primary map



X



Y

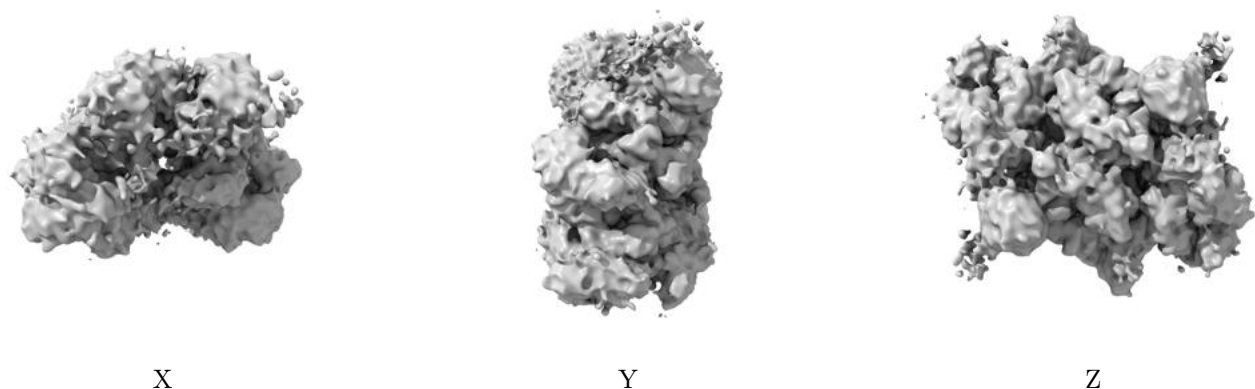


Z

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



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

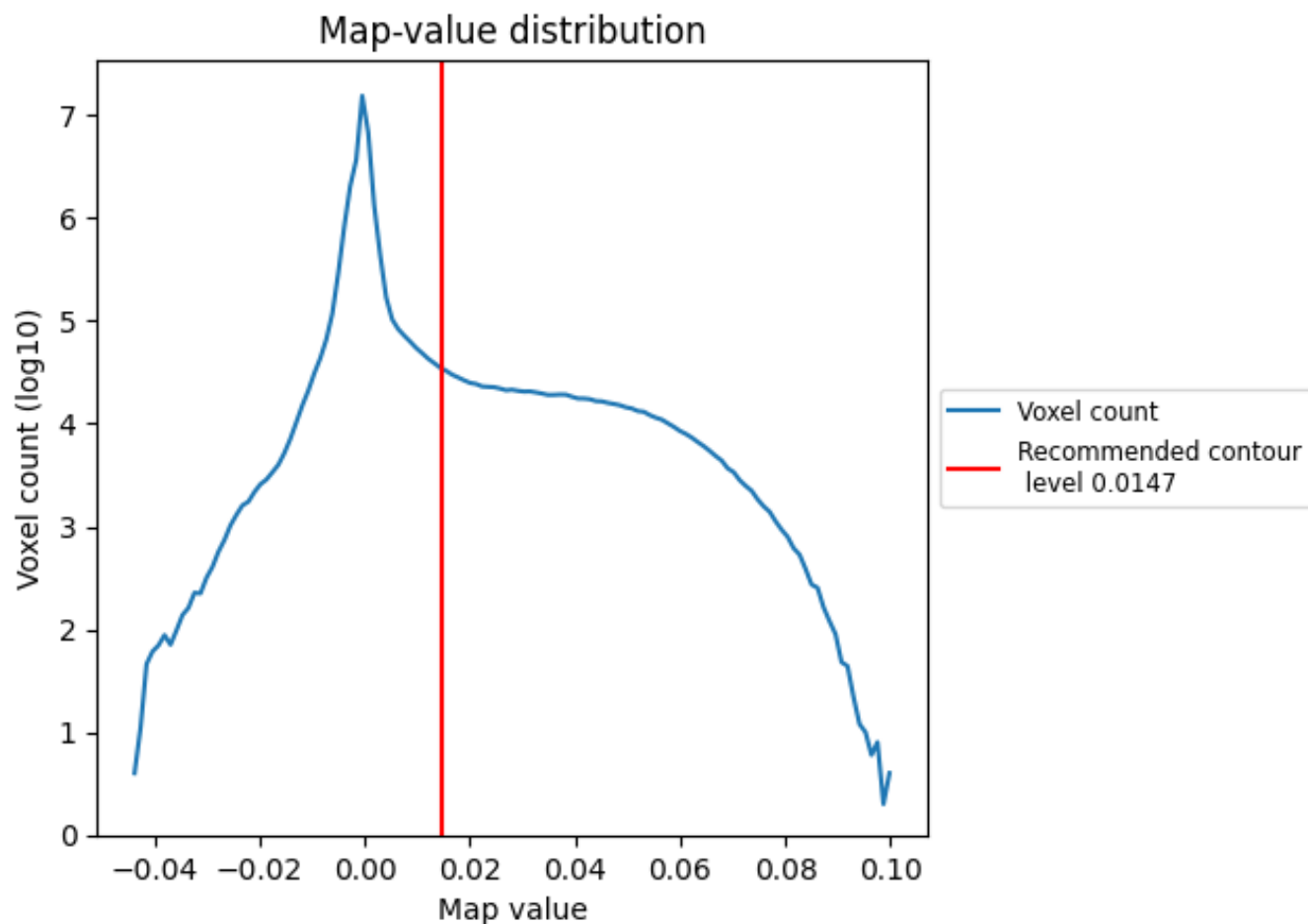
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

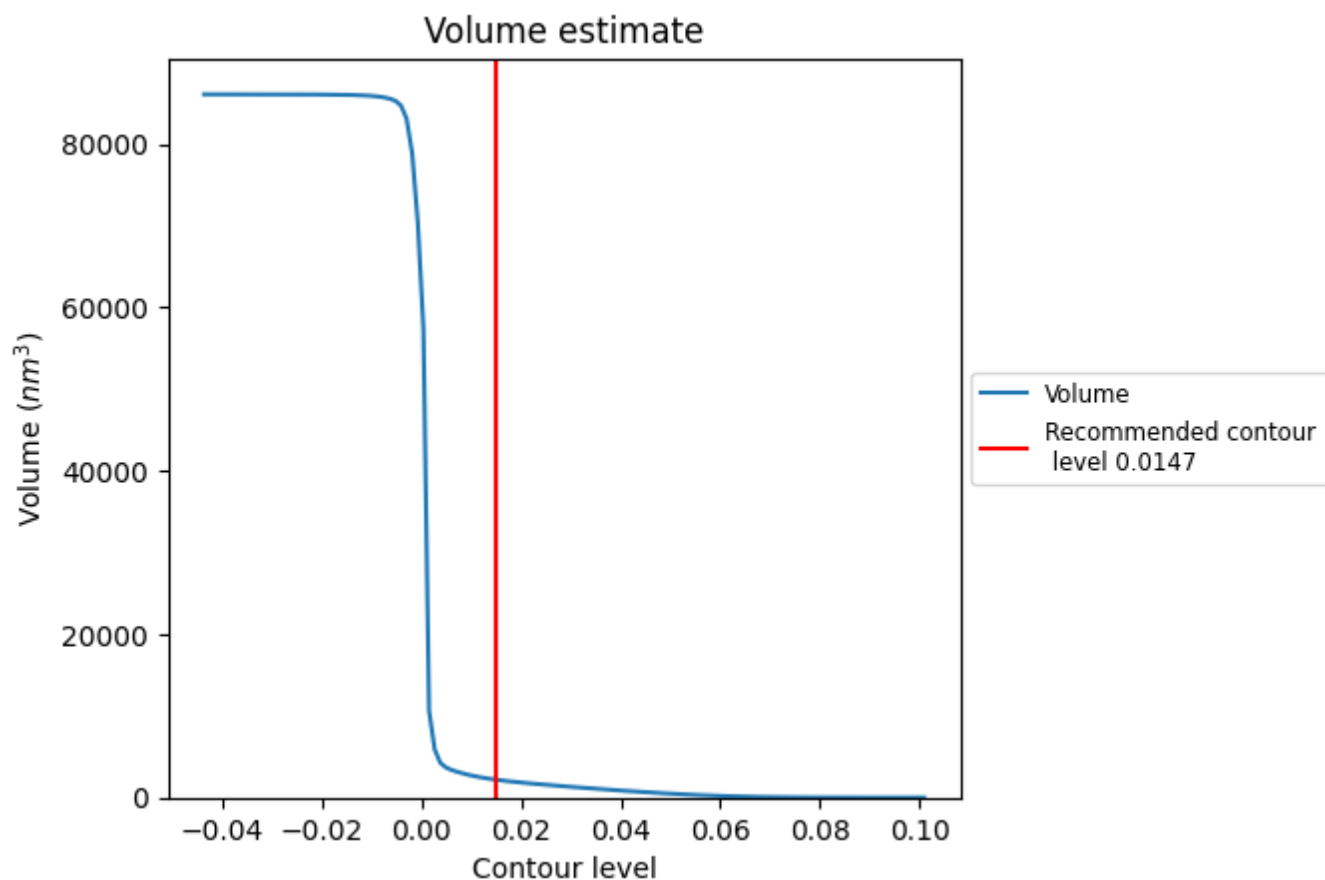
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

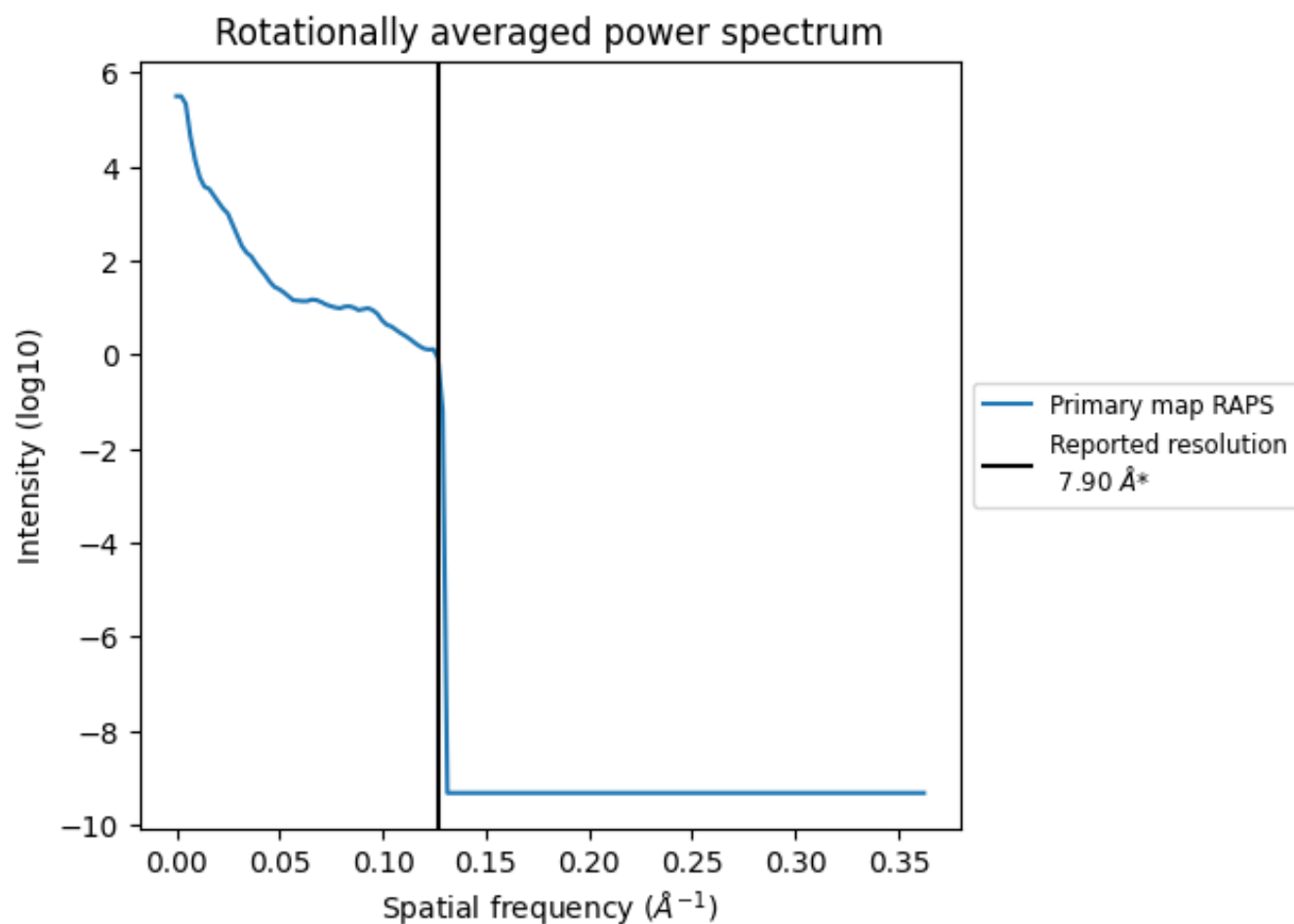
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2205 nm^3 ; this corresponds to an approximate mass of 1992 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.127 Å⁻¹

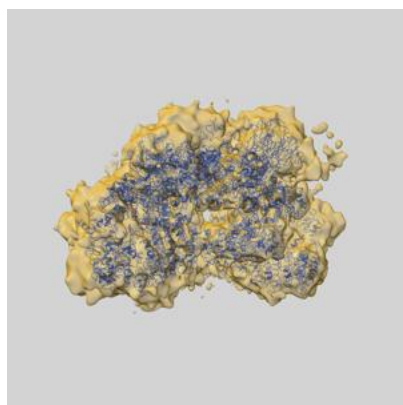
8 Fourier-Shell correlation ⓘ

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

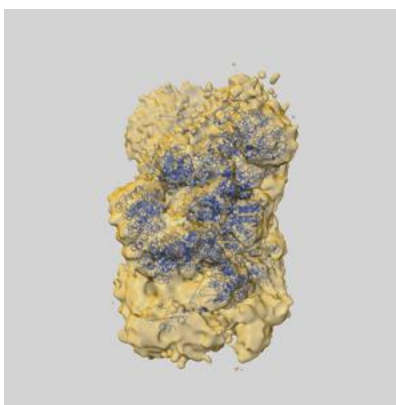
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3896 and PDB model 6EMK. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

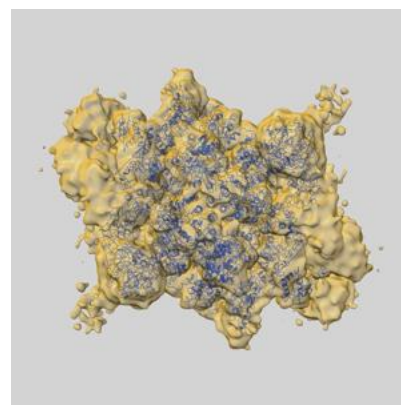
9.1 Map-model overlay [i](#)



X



Y



Z

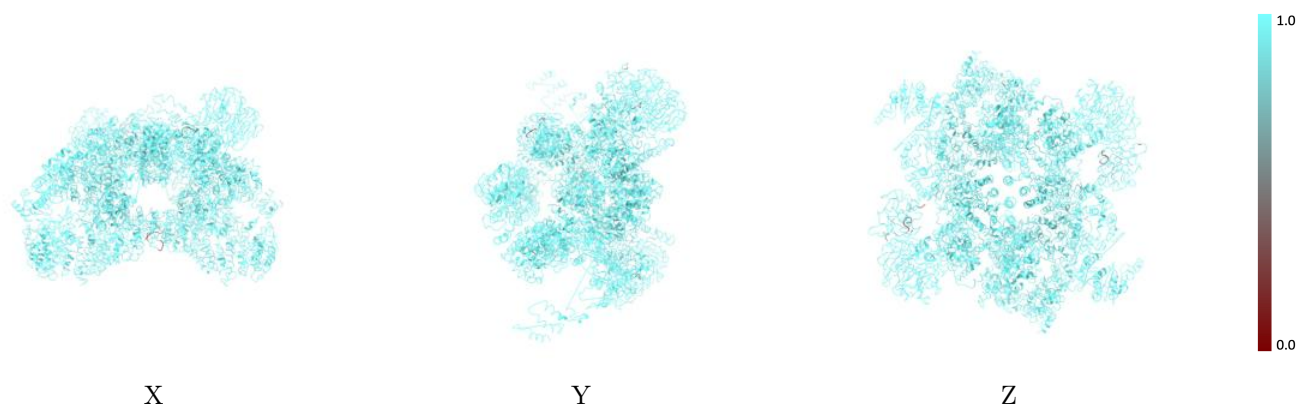
The images above show the 3D surface view of the map at the recommended contour level 0.0147 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



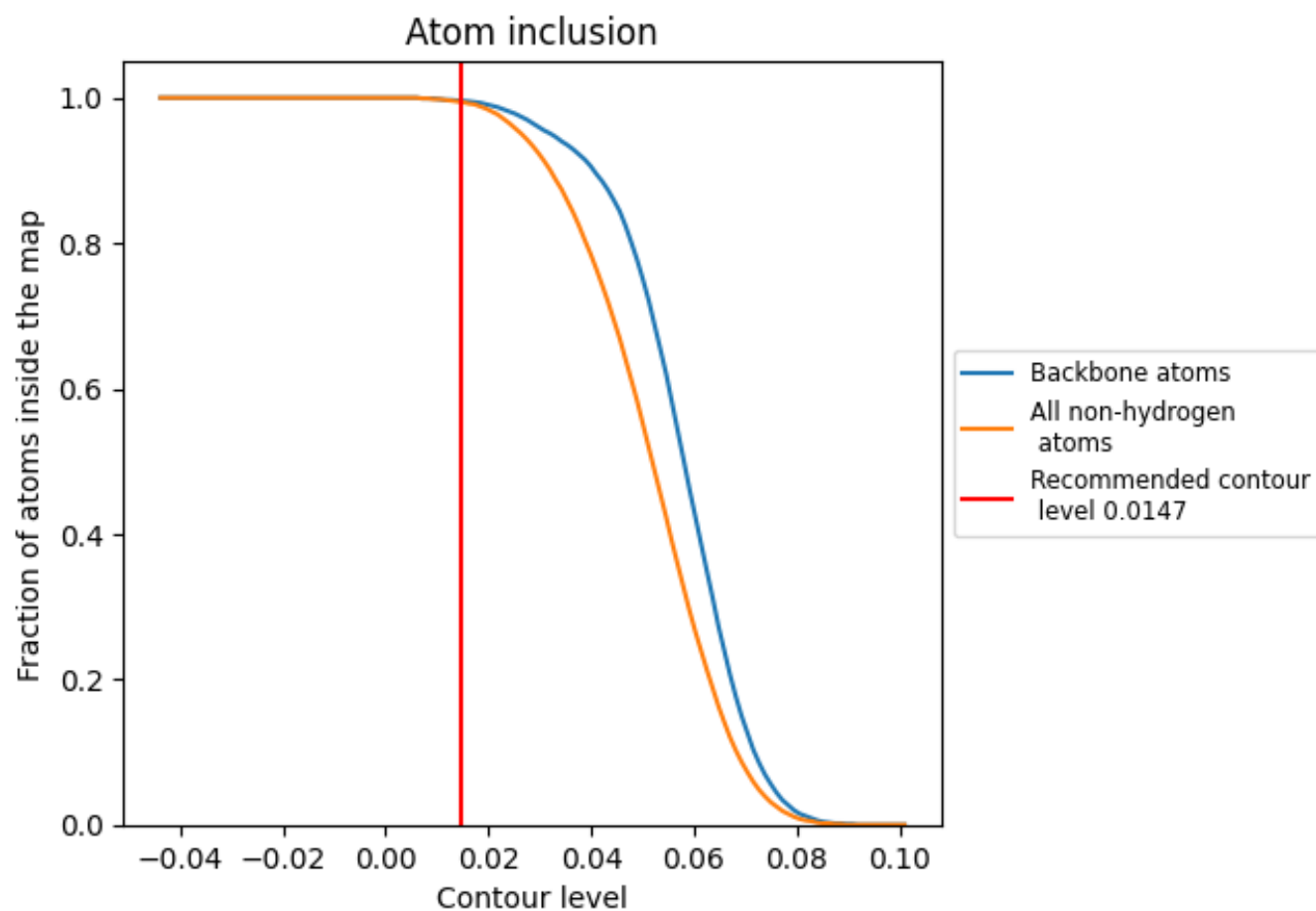
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0147).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0147) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9940	0.1450
A	0.9950	0.1430
B	1.0000	0.1080
C	0.9960	0.1410
D	1.0000	0.1070
E	1.0000	0.2680
F	1.0000	0.2690
G	1.0000	0.2330
H	1.0000	0.2340
I	0.9340	0.0480
J	0.9570	0.0550

1.0

0.0

<0.0