



wwPDB EM Validation Summary Report ⓘ

May 18, 2025 – 09:06 AM EDT

PDB ID : 8E6R / pdb_00008e6r
EMDB ID : EMD-27923
Title : Human TRPM2 ion channel in 1 mM dADPR
Authors : Wang, L.; Fu, T.M.; Xia, S.; Wu, H.
Deposited on : 2022-08-23
Resolution : 5.60 Å(reported)

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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.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

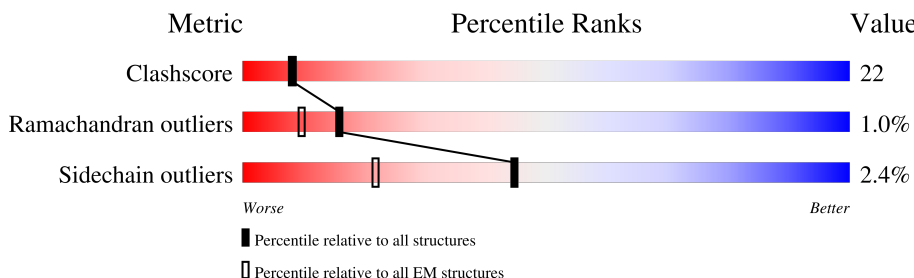
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 5.60 Å.

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



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

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	1503	
1	B	1503	
1	C	1503	
1	D	1503	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	AR6	A	1602	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	AR6	B	1602	X	-	-	-
3	AR6	C	1602	X	-	-	-
3	AR6	D	1602	X	-	-	-

2 Entry composition [i](#)

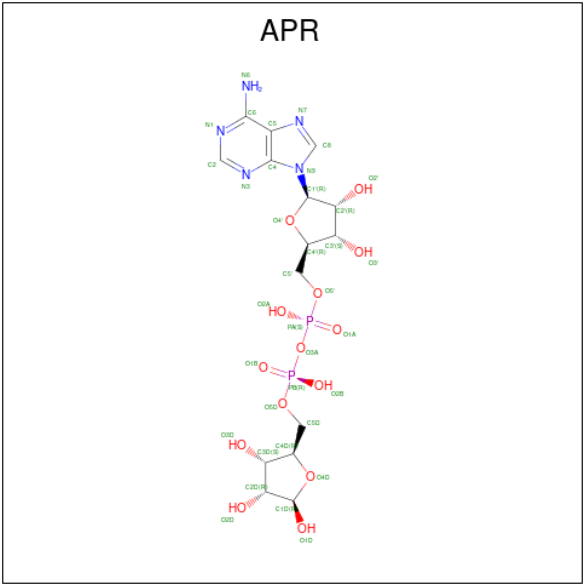
There are 3 unique types of molecules in this entry. The entry contains 42336 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Transient receptor potential cation channel subfamily M member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1323	10523	6796	1829	1848	50	0	0
1	B	1323	10523	6796	1829	1848	50	0	0
1	C	1323	10523	6796	1829	1848	50	0	0
1	D	1323	10523	6796	1829	1848	50	0	0

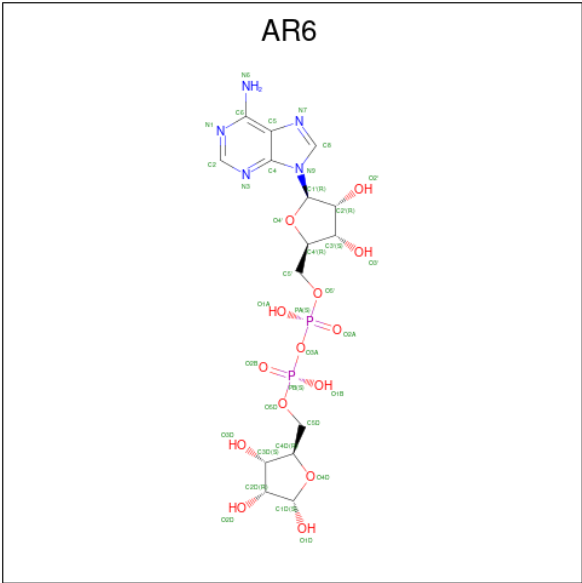
- Molecule 2 is ADENOSINE-5-DIPHOSPHORIBOSE (CCD ID: APR) (formula: C₁₅H₂₃N₅O₁₄P₂).



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Mol	Chain	Residues	Atoms					AltConf
2	C	1	Total	C	N	O	P	0
			26	10	5	9	2	
2	D	1	Total	C	N	O	P	0
			26	10	5	9	2	

- Molecule 3 is [(2R,3S,4R,5R)-5-(6-AMINOPURIN-9-YL)-3,4-DIHYDROXY-OXOLAN-2-YL]METHYL[HYDROXY-[(2R,3S,4R,5S)-3,4,5-TRIHYDROXYOXOLAN-2-YL]METHOXY]PHOSPHORYL] HYDROGEN PHOSPHATE (CCD ID: AR6) (formula: C₁₅H₂₃N₅O₁₄P₂).

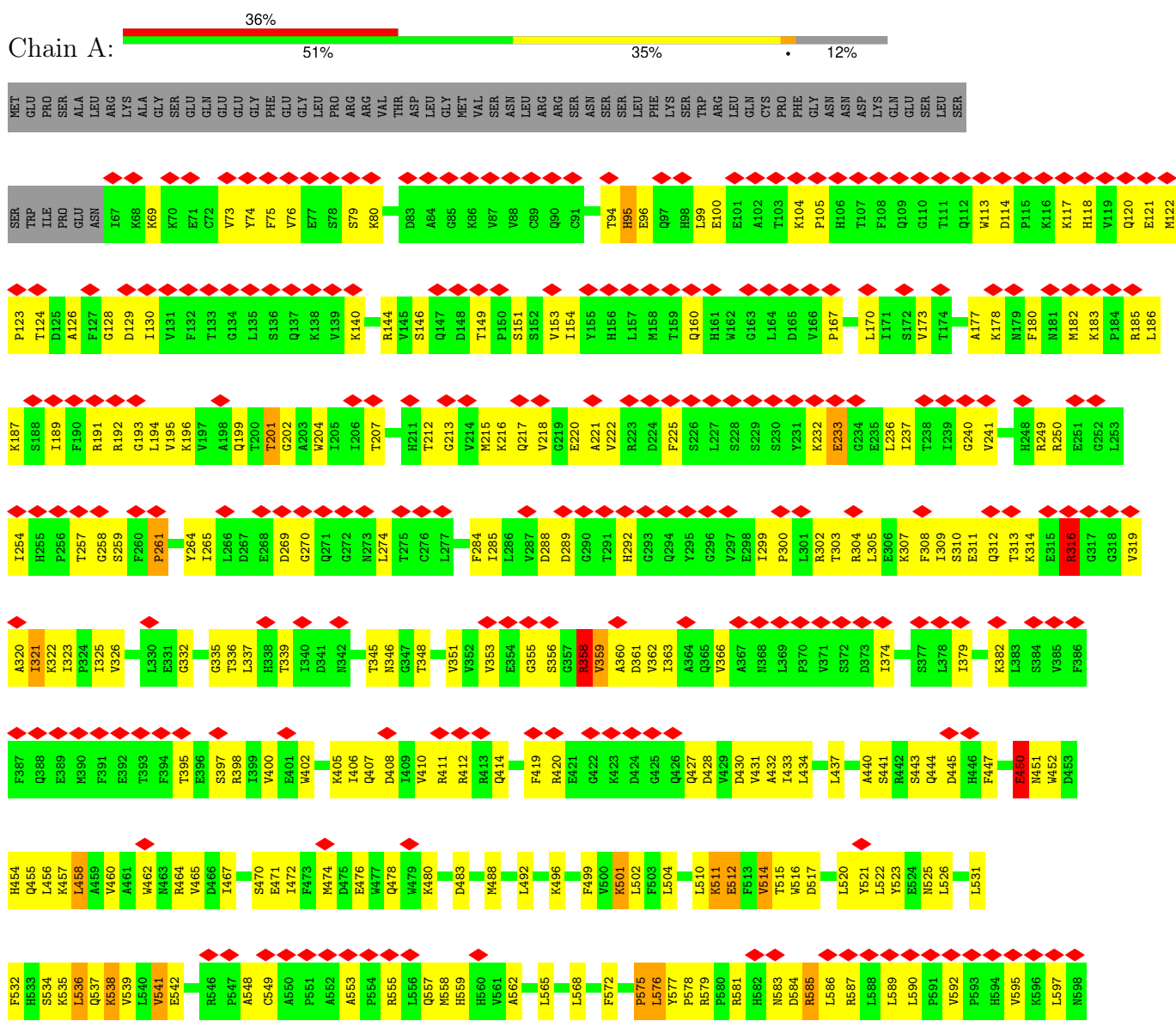


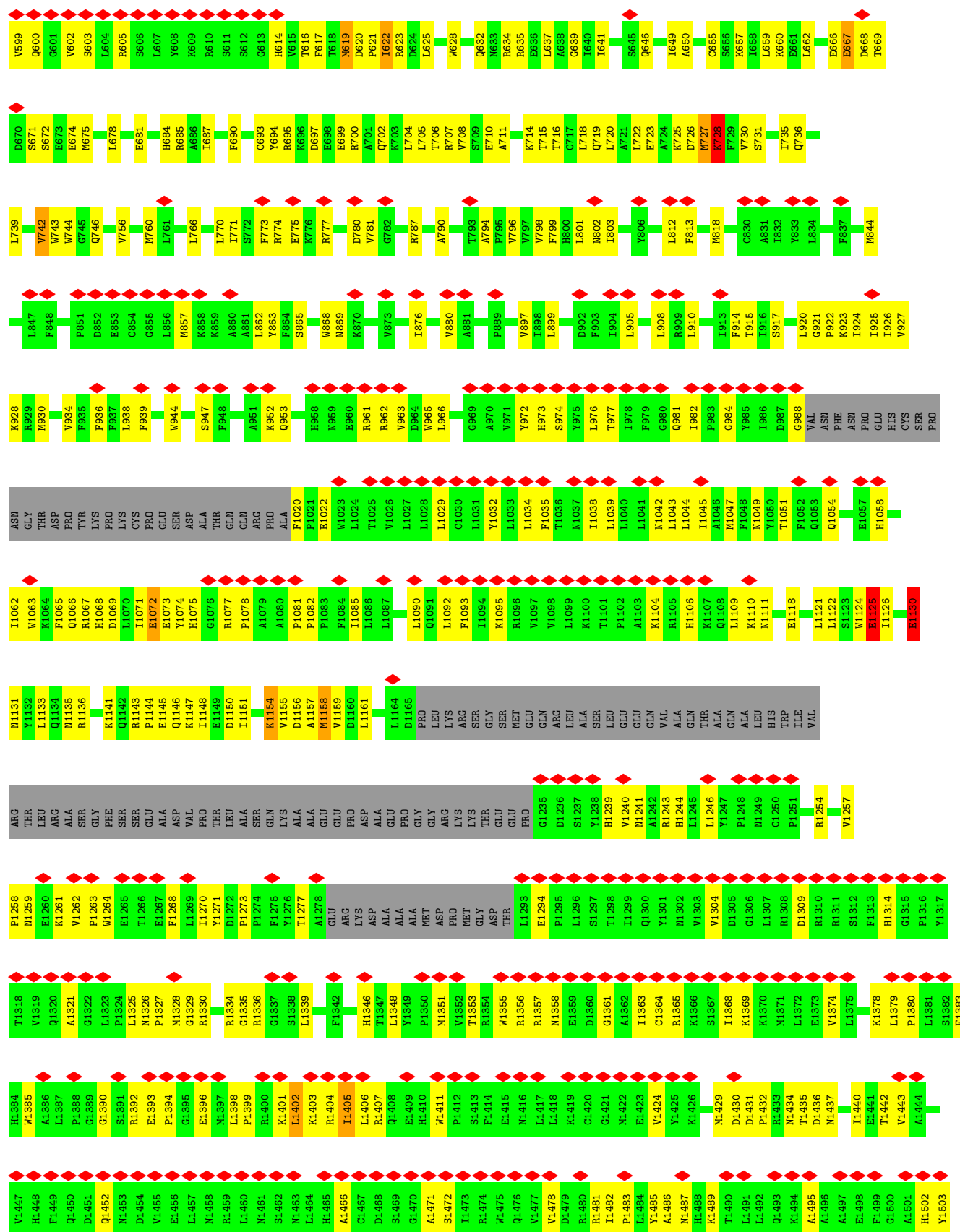
Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			35	15	5	13	2	
3	B	1	Total	C	N	O	P	0
			35	15	5	13	2	
3	C	1	Total	C	N	O	P	0
			35	15	5	13	2	
3	D	1	Total	C	N	O	P	0
			35	15	5	13	2	

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.

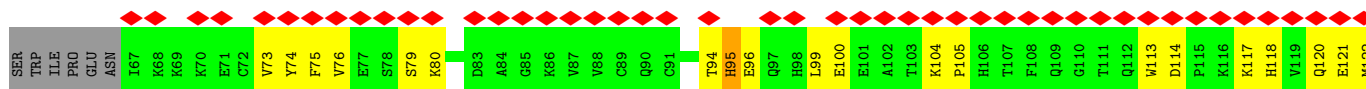
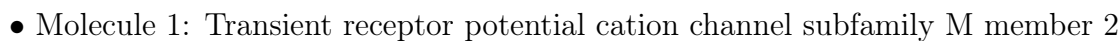
- Molecule 1: Transient receptor potential cation channel subfamily M member 2



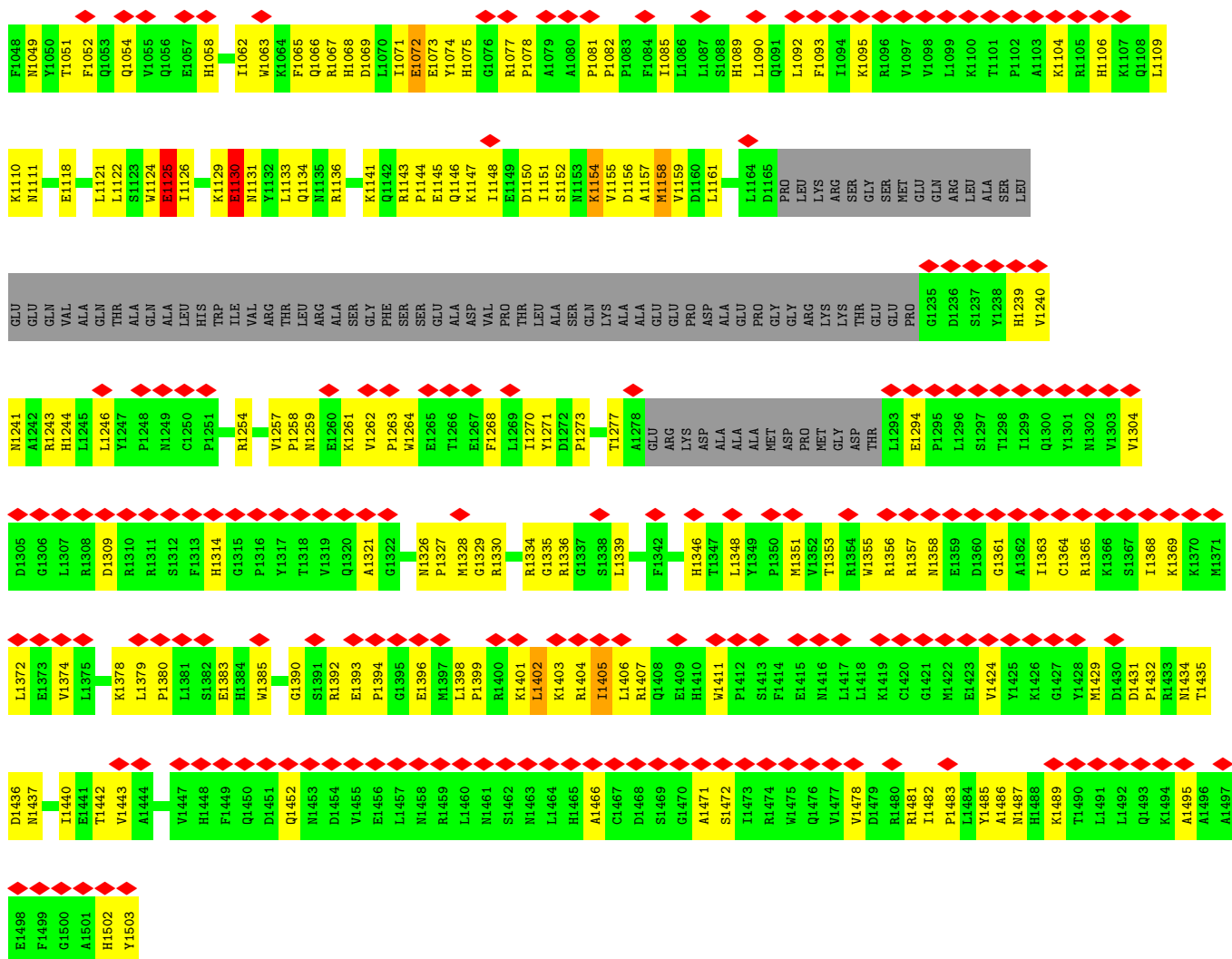


- Molecule 1: Transient receptor potential cation channel subfamily M member 2

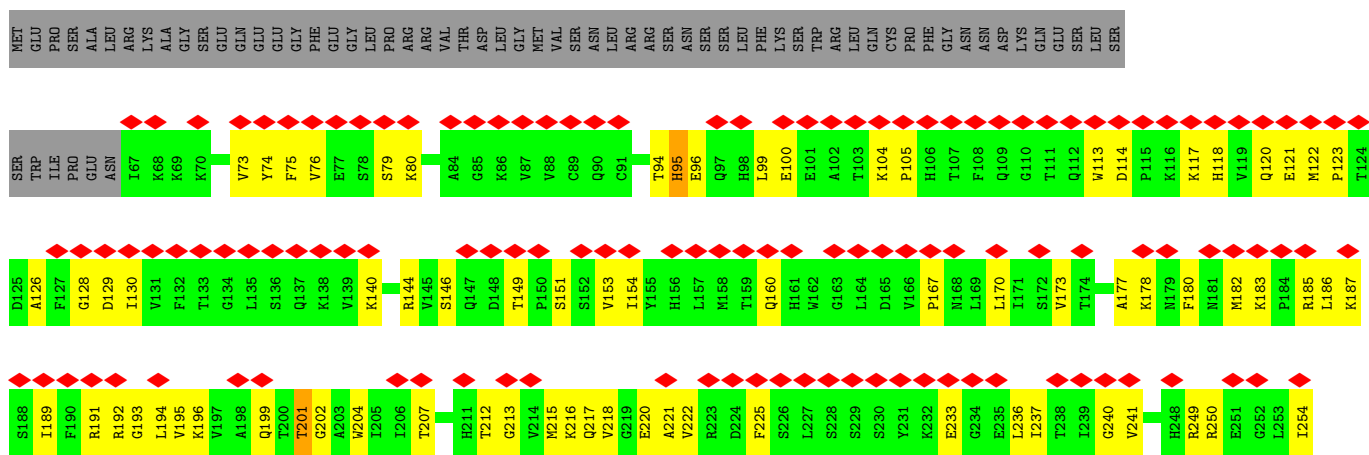
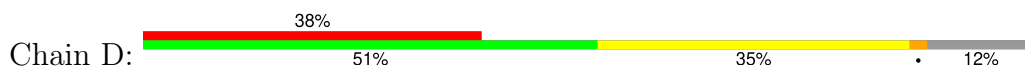




D987	G988	VAL	ASN	PHE	ASN	ASN	PRO	PRO	GLU	HIS	CYS	SER	PRO	PRO	ASN	GLY	THR	ASP	PRO	THR	GLN	GLN	ARG	PRO	ALA	F1020	V1023	L1024	T1025	V1026	L1027	L1028	V1029	C1030	L1031	Y1032	L1033	L1034	F1035	H973	S974	T975	L976	L977	T978	F979	Q980	Q981	L982	P983	G984	I985	I986																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
I924	I925	I926	I927	K928	R929	M930	M931	K932	D933	C934	C935	G936	G937	F938	L939	F940	F941	F942	F943	F944	F945	F946	F947	F948	F949	F950	A951	K952	Q953	A954	I955	H956	H957	H958	D959	E960	R961	R962	V963	D964	W965	L966	A967	V968	Y969	H970	S971	H972	H973	S974	T975	L976	L977	C978	E979	C980	E981	E982	E983	E984	E985	E986	E987	E988	E989	E990	E991	E992	E993	E994	E995	E996	E997	E998	E999	Q1000																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
E943	M944	F945	F946	F947	F948	P949	D950	D951	D952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020	C1021	C1022	C1023	C1024	C1025	C1026	C1027	C1028	C1029	C1030	C1031	C1032	C1033	C1034	C1035	C1036	C1037	C1038	C1039	C1040	C1041	C1042	C1043	C1044	C1045	C1046	C1047	C1048	C1049	C1050	C1051	C1052	C1053	C1054	C1055	C1056	C1057	C1058	C1059	C1060	C1061	C1062	C1063	C1064	C1065	C1066	C1067	C1068	C1069	C1070	C1071	C1072	C1073	C1074	C1075	C1076	C1077	C1078	C1079	C1080	C1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	C1090	C1091	C1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455	C1456	C1457	C1458	C1459	C1460	C1461	C1462	C1463	C1464	C1465	C1466	C1467	C1468	C1469	C1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	C1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515	C1516	C1517	C1518	C1519	C1520	C1521	C1522	C1523	C1524	C1525	C1526	C1527	C1528	C1529	C1530	C1531	C1532	C1533	C1534	C1535	C1536	C1537	C1538	C1539	C1540	C1541	C1542	C1543	C1544	C1545	C1546	C1547	C1548	C1549	C1550	C1551	C1552	C1553	C1554	C1555	C1556	C1557	C1558	C1559	C1560	C1561	C1562	C1563	C1564	C1565	C1566	C1567	C1568	C1569	C1570	C1571	C1572	C1573	C1574	C1575	C1576	C1577	C1578	C1579	C1580	C1581	C1582	C1583	C1584	C1585	C1586	C1587	C1588	C1589	C1590	C1591	C1592	C1593	C1594	C1595	C1596	C1597	C1598	C1599	C1600	C1601	C1602	C1603	C1604	C1605	C1606	C1607	C1608	C1609	C1610	C1611	C1612	C1613	C1614	C1615	C1616	C1617	C1618	C1619	C1620	C1621	C1622	C1623	C1624	C1625	C1626	C1627	C1628	C1629	C1630	C1631	C1632	C1633	C1634	C1635	C1636	C1637	C1638	C1639	C1640	C1641	C1642	C1643	C1644	C1645	C1646	C1647	C1648	C1649	C1650	C1651	C1652	C1653	C1654	C1655	C1656	C1657	C1658	C1659	C1660	C1661	C1662	C1663	C1664	C1665	C1666	C1667	C1668	C1669	C1670	C1671	C1672	C1673	C1674	C1675	C1676	C1677	C1678	C1679	C1680	C1681	C1682	C1683	C1684	C1685	C1686	C1687	C1688	C1689	C1690	C1691	C1692	C1693	C1694	C1695	C1696	C1697	C1698	C1699	C1700	C1701	C1702	C1703	C1704	C1705	C1706	C1707	C1708	C1709	C1710	C1711	C1712	C1713	C1714	C1715	C1716	C1717	C1718	C1719	C1720	C1721	C1722	C1723	C1724	C1725	C1726	C1727	C1728	C1729	C1730	C1731	C1732	C1733	C1734	C1735	C1736	C1737	C1738	C1739	C1740	C1741	C1742	C1743	C1744	C1745	C1746	C1747	C1748	C1749	C1750	C1751	C1752	C1753	C1754	C1755	C1756	C1757	C1758	C1759	C1760	C1761	C1762	C1763	C1764	C1765	C1766	C1767	C1768	C1769	C1770	C1771	C1772	C1773	C1774	C1775	C1776	C1777	C1778	C1779	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	C1790	C1791	C1792	C1793	C1794	C1795	C1796	C1797	C1798	C1799	C1800	C1801	C1802	C1803	C1804	C1805	C1806	C1807	C1808	C1809	C1810	C1811	C1812	C1813	C1814	C1815	C1816	C1817	C1818	C1819	C1820	C1821	C1822	C1823	C1824	C1825	C1826	C1827	C1828	C1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	C1840	C1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	C1850	C1851	C1852	C1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	C1862	C1863	C1864	C1865	C1866	C1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899	C1900	C1901	C1902	C1903	C1904	C1905	C1906	C1907	C1908	C1909	C1910	C1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920	C1921	C1922	C1923	C1924	C1925	C1926	C1927	C1928	C1929	C1930	C1931	C1932	C1933	C1934	C1935	C1936	C1937	C1938	C1939	C1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	C1980	C1981	C1982	C1983	C1984	C1985	C1986	C1987	C1988	C1989	C1990	C1991	C1992	C1993	C1994	C1995	C1996	C1997	C1998	C1999	C2000
E389	M390	F391	E392	T393	F394	T395	E396	S397	V400	E401	W402	K405	I406	Q407	D408	I409	V410	R411	R412	R413	Q414	F419	R420	E421	G422	K423	D424	G425	Q426	D427	D428	Y429	D430	V431	A432	I433	L434	L437	A440	S441	R442	S443	Q444	D445	H446	F447	E450	N451	W452	D453	H454	Q455	L456	E389	M390	F391	E392	T393	F394	T395	E396	S397	V400	E401	W402	K405	I406	Q407	D408	I409	V410	R411	R412	R413	Q414	F419	R420	E421	G422	K423	D424	G425	Q426	D427	D428	Y429	D430	V431	A432	I433	L434	L437	A440	S441	R442	S443	Q444	D445	H446	F447	E450	N451	W452	D453	H454	Q455	L456	A320	I321	K322	I323	F324	I325	V326	L330	E331	G332	G335	T336	L337	H338	T339	I340	T345	N346	G347	T348	V351	V352	V353	E354	G355	S356	G357	R358	V359	A360	D361	V362	I363	A364	Q365	V366	A367	N368	L369	P370	V371	S372	D373	I374	S377	L378	I379	K382	L383	S384	V385	F386	F387	Q388	T254	H255	P256	T257	G258	S259	F260	P261	Y264	L265	L266	D267	E268	D269	G270	Q271	G272	N273	L274	T275	C276	L277	F284	I285	L286	V287	D288	D289	G290	T291	H292	G293	Q294	S295	V296	G296	V297	S298	E298	I299	P300	L301	R302	T303	R304	L305	E306	K307	F308	I309	S310	E311	Q312	T313	K314	E315	R316	G317	G318	V319	K187	S188	I189	F190	R191	G192	G193	L194	V195	K196																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										



● Molecule 1: Transient receptor potential cation channel subfamily M member 2



Met	F102	L1039	F979	T915	L834	I735	D668	N598	L531	H454	E389	K322	H255
GLU	A1103	L1040	Q980	S917	F837	Q736	T669	V599	F532	Q455	M390	I323	P256
ARG	K1104	L1041	Q981			L739	S671	Q600	K535	L456	F391	P324	
LEU	H1105	N1042	P983	G921	V840	V742	S672	G601	L536	L458	E392	V326	G258
ALA	H1106	L1043	C841	P922	W743	W743	E673	V602	Q537	A559	T393		S259
SER	K1107	L1044	Q984	K923	E842	W744	E674	K638	V460	V460	F394	L330	F260
LEU	Q1108	I1045	Y985	K924	E843	Q745	M675	S603	V539	A461	T394	E331	
GLU	L1109	A1046	Y986	I924	M844	Q746	L678	L604	L540	W462	T395	G332	P261
GLU	N1110	N1047	I986	I925				R605	E396	N463	E396		
GLN	N1111	F1048	D987	I926				R606	E542	R464	S397	G335	I264
VAL		N1049	G988	I927	L847	V756	E681	S606		V465	S397	I265	I264
ALA				K928	F848	W760	Y682	L607	R546	R464	S398	G336	I266
GLN	E1118	F1052	VAL	K929	F849	L761	E683	Y608	P547	V466	I399	L337	L266
THR	Q1053	N930	ASN	M930	P851	L766	H684	K609	A548	I467	V400	T339	E268
THR	L1121	Q1054	ASN	M931	D852		E685	R610	C549		W402	I340	D269
GLN	L1122	V1055	PRD	K932	E853		A686	S611	A550		T403	D341	G270
ALA	S1123	V1056	GLU	D933	E854	L770	I687	S612	A551	F473	K404	N942	Q271
LEU	W1124		HIS	V934	C854	I771	F690	G613	P551	M474	K405	G272	N273
HIS	E1125	H1058	CYS	F935	G855	S772	C693	G614	A552	D475	I406	I341	L274
TRP	I1126	I1059	SER	F936	L856	W774	G694	H614	P554	W477	D408	G347	L275
ILE			PRD	F937	M857	T775	R695	T616	R555	W478	I409	C276	L277
VAL	E1130	I1062	ASN	F938	K858	K776	K696	F617	L556	W479	V109	V351	
ARG	N1131	W1063	GLY	F939	K859	R777	R697	T618	L557	K480	R411	V352	F284
THR	Y1132	K1064	THR	L938	K858		E698	M619	M568	D483	R412	V353	I285
LEU	L1133	Q1065	ASP	F940	K860		E699	D620	Q557	E354	I406	E354	L286
ARG	Q1134	Q1066	PRD	L940	A861		E699	D621	M559	G355	Q407	G355	V287
ALA	N1135	Q1067	PRD	L941	A861		E699	D622	H560	M488	R413	G356	D288
SER	L1136	L1068	LYS	W944	L862	D780	A701	R623	H561	L492	F419	G357	D289
GLY	K1141	D1069	PRD	W945	Y863	W781	Q702	R624	A562	N495	R420	R358	G290
PHE	L1142	L1070	LYS	W946	F864	G782	Q703	L625	L565	K496	E421	V359	T291
SER	L1143	L1071	CYS	S947	S865	R787	K703	L625	L568	F499	G422	A360	H292
GLU	F1144	E1072	GLU	F948	W868	A790	L704	W628		N495	K423	D361	G293
ALA	Q1145	E1073	ASP	F948	N869		L705	W628		K501	D424	V362	Q294
VAL	Y1074	Y1074	ALA	A951	K870	T793	S709	Q632	D571	L502	G425	I363	Y295
PRO	K1147	G1075	ALA	K952	V873	A794	E710	R634	F572	F503	Q426	A364	G296
THR	L1148	G1076	THR	Q953	V873	W795	A711	R635		L504	Q427	Q365	V297
LEU	D1150	R1077	GLN	Q954	V873	W796		E836	P575	L576	D428	V366	E298
ALA	I1151	P1078	GLN	Q955	I876	V997	K714	L637	L577	L504	D428	V366	V297
SER	L1152	A1079	ARG				T715	G638	P577	L510	V429	A367	E298
GLN	N1153	A1080	PRD	H958	W880	V798	T715	A638	R579	K511	D430	N368	I299
LYS	K1154	P1081	ALA	N959	A881	F799	T716	G639	P580	E512	V431	I299	P300
ALA	V1155	P1082	ALA	E960	Q882	H800	Q717	P580	F513	F513	I432	P370	L301
LEU	D1156	P1083	LEU	R961	L883	L801	L718	R581	H582	V514	V371	V371	R302
GLU	A1157	F1084	H1085	R962	L883	N802	Q719	R581	H582	V514	V371	V371	T303
GLU	M1158	I1085	ASP	R963	L883	I803	L720	Q646	H583	V514	V371	V371	R304
PRO	D1160	L1086	PRD	V963	L883		A721	Q646	H583	V514	V371	V371	
ALA	L1161	L1087	ALA	R964	L883		A721	Q646	H583	V514	V371	V371	
GLU	L1162	S1088	GLU	W965	L883		A721	Q646	H583	V514	V371	V371	
PRO	D1163	H1089	PRO	R966	L883		A721	Q646	H583	V514	V371	V371	
GLY	L1164	I1090	GLY	F967	L883		A721	Q646	H583	V514	V371	V371	
GLY	L1165	Q1091	GLY	R968	L883		A721	Q646	H583	V514	V371	V371	
ARG	P1165	L1092	ARG	G969	L883		A721	Q646	H583	V514	V371	V371	
LYS	PRD	L1093	LYS	R970	L883		A721	Q646	H583	V514	V371	V371	
LYS	LEU	F1093	LYS	A970	L883		A721	Q646	H583	V514	V371	V371	
THR	LYS	I1094	THR	V971	L883		A721	Q646	H583	V514	V371	V371	
GLU	LYS	K1095	GLU	Y972	L883		A721	Q646	H583	V514	V371	V371	
GLU	ARG	L1033	GLU	Y972	L883		A721	Q646	H583	V514	V371	V371	
GLU	SER	L1034	GLU	H973	L883		A721	Q646	H583	V514	V371	V371	
GLY	GLY	L1035	GLY	S974	L883		A721	Q646	H583	V514	V371	V371	
LYS	PRD	V1097	LYS	Y975	L883		A721	Q646	H583	V514	V371	V371	
LYS	LEU	V1098	LYS	R909	L883		A721	Q646	H583	V514	V371	V371	
THR	LYS	L1036	THR	L976	L883		A721	Q646	H583	V514	V371	V371	
GLU	SER	L1037	GLU	T977	L883		A721	Q646	H583	V514	V371	V371	
GLU	ARG	L1038	GLU	I978	L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY	K1100	GLU	I913	L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY	T1101	GLU	F914	L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	
GLU	GLY		GLU		L883		A721	Q646	H583	V514	V371	V371	

I1482	G1421	E1359	P1295	GLU
P1483	M1422	D1360	L1296	PRO
L1484	E1423	G1361	S1297	G1235
Y1485	V1424	A1362	I1298	D1236
A1486	Y1425	I1363	I1299	S1237
N1487	K1426	C1364	Q1300	Y1238
K1488	G1427	R1365	Y1301	H1239
K1489	Y1428	K1366	N1302	V1240
T1490	M1429	S1367	V1303	M1241
L1491	D1430	I1368	V1304	A1242
L1492	D1431	K1369	D1305	R1243
Q1493	P1432	K1370	G1306	H1244
K1494	R1433	M1371	L1307	L1245
A1495	T1434	L1372	R1308	Y1246
	T1435	K1373	Y1309	L1247
	M1437	V1374	D1310	P1248
		L1375	R1311	N1249
	I1440		S1312	C1250
	E1441		F1313	P1251
	T1442	K1378	H1314	
	V1443	L1379		R1254
	A1444	P1380	G1315	
	V1445	L1381	P1316	V1257
	S1446	S1382	Y1317	P1258
	V1447	E1383	T1318	N1259
	H1448	H1384	Q1319	K1261
	F1449	W1385	V1320	V1262
	Q1450		A1321	P1263
	D1451	P1388	G1322	W1264
	Q1452	G1389		E1265
	M1453	G1390		T1266
	D1454	S1391	L1325	E1267
	V1455	E1392	P1326	F1268
	E1456	E1393	P1327	L1269
	L1457	P1394	M1328	I1270
	N1458	G1395	G1329	Y1271
	R1459	E1396	R1330	D1272
	L1460	M1397		T1273
	N1461	L1398	L1333	P1274
	S1462	P1399	G1334	F1275
	N1463	R1400	G1335	Y1276
	L1464	K1401	L1336	T1277
	H1465	K1402	G1337	A1278
	A1466	R1404	S1338	GLU
	C1467	I1405	L1339	ARG
	D1468	L1406	Y1346	LYS
	G1470	Q1408	T1347	ASP
	A1471	E1409	L1348	ALA
	S1472	H1410	Y1349	ALA
	T1473	W1411	P1350	ALA
	R1474	P1412	M1351	MET
	V1475	F1413	V1352	ASP
	Q1476	F1414	T1353	PRO
	V1477	E1415	R1354	MET
	V1478	N1416	W1355	GLY
	D1479	L1417	R1356	ASP
	R1480	L1418	R1357	THR
	R1481	K1419	N1358	
		C1420		L1293
				E1294

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86858	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.070	Depositor
Minimum map value	-0.025	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0118	Depositor
Map size (Å)	324.0, 324.0, 324.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: APR, AR6

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	0.19	0/10789	0.62	11/14649 (0.1%)
1	B	0.19	0/10789	0.62	11/14649 (0.1%)
1	C	0.19	0/10789	0.62	11/14649 (0.1%)
1	D	0.19	0/10789	0.62	11/14649 (0.1%)
All	All	0.19	0/43156	0.62	44/58596 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	316	ARG	CA-CB-CG	7.37	128.84	114.10
1	B	316	ARG	CA-CB-CG	7.36	128.82	114.10
1	A	316	ARG	CA-CB-CG	7.35	128.80	114.10
1	D	316	ARG	CA-CB-CG	7.33	128.77	114.10
1	A	728	LYS	CB-CG-CD	6.43	126.10	111.30

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	160	GLN	Peptide
1	A	358	ARG	Peptide
1	B	160	GLN	Peptide
1	B	358	ARG	Peptide
1	C	160	GLN	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	10523	0	10458	475	0
1	B	10523	0	10458	467	0
1	C	10523	0	10458	467	0
1	D	10523	0	10458	468	0
2	A	26	0	10	1	0
2	B	26	0	10	1	0
2	C	26	0	10	1	0
2	D	26	0	10	1	0
3	A	35	0	19	1	0
3	B	35	0	19	1	0
3	C	35	0	19	0	0
3	D	35	0	19	0	0
All	All	42336	0	41948	1817	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 22.

The worst 5 of 1817 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:B:727:MET:H	1:B:727:MET:HE2	1.20	1.06
1:A:727:MET:H	1:A:727:MET:HE2	1.20	1.06
1:C:727:MET:H	1:C:727:MET:HE2	1.20	1.05
1:D:727:MET:HE2	1:D:727:MET:H	1.20	1.02
1:A:1429:MET:HB3	1:A:1487:ASN:HD21	1.37	0.89

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1313/1503 (87%)	1140 (87%)	160 (12%)	13 (1%)	13	49
1	B	1313/1503 (87%)	1140 (87%)	160 (12%)	13 (1%)	13	49
1	C	1313/1503 (87%)	1140 (87%)	160 (12%)	13 (1%)	13	49
1	D	1313/1503 (87%)	1140 (87%)	160 (12%)	13 (1%)	13	49
All	All	5252/6012 (87%)	4560 (87%)	640 (12%)	52 (1%)	16	49

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	HIS
1	A	261	PRO
1	A	1294	GLU
1	A	1321	ALA
1	B	95	HIS

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	1116/1318 (85%)	1089 (98%)	27 (2%)	44	62
1	B	1116/1318 (85%)	1089 (98%)	27 (2%)	44	62
1	C	1116/1318 (85%)	1088 (98%)	28 (2%)	42	61
1	D	1116/1318 (85%)	1089 (98%)	27 (2%)	44	62
All	All	4464/5272 (85%)	4355 (98%)	109 (2%)	45	62

5 of 109 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	458	LEU
1	C	812	LEU
1	D	812	LEU
1	C	511	LYS
1	C	557	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 74 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	118	HIS
1	D	1135	ASN
1	D	248	HIS
1	D	478	GLN
1	B	346	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](#)

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	APR	D	1601	-	24,28,39	1.00	1 (4%)	30,43,60	0.97	2 (6%)
2	APR	C	1601	-	24,28,39	1.01	1 (4%)	30,43,60	0.98	2 (6%)
3	AR6	B	1602	-	35,38,39	0.67	0	43,58,60	0.78	2 (4%)
2	APR	A	1601	-	24,28,39	1.01	1 (4%)	30,43,60	0.98	2 (6%)
3	AR6	A	1602	-	35,38,39	0.66	0	43,58,60	0.78	2 (4%)
3	AR6	D	1602	-	35,38,39	0.66	0	43,58,60	0.78	2 (4%)
3	AR6	C	1602	-	35,38,39	0.67	0	43,58,60	0.78	1 (2%)
2	APR	B	1601	-	24,28,39	1.01	1 (4%)	30,43,60	0.97	2 (6%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AR6	B	1602	-	1/1/9/10	5/18/50/54	0/4/4/4
2	APR	C	1601	-	-	3/12/28/54	0/3/3/4
2	APR	D	1601	-	-	3/12/28/54	0/3/3/4
2	APR	A	1601	-	-	3/12/28/54	0/3/3/4
3	AR6	A	1602	-	1/1/9/10	5/18/50/54	0/4/4/4
3	AR6	D	1602	-	1/1/9/10	5/18/50/54	0/4/4/4
3	AR6	C	1602	-	1/1/9/10	5/18/50/54	0/4/4/4
2	APR	B	1601	-	-	3/12/28/54	0/3/3/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1601	APR	PB-O1B	3.34	1.60	1.50
2	B	1601	APR	PB-O1B	3.32	1.60	1.50
2	A	1601	APR	PB-O1B	3.32	1.60	1.50
2	D	1601	APR	PB-O1B	3.32	1.60	1.50

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1601	APR	O5D-PB-O2B	2.78	118.22	107.80
2	D	1601	APR	O5D-PB-O2B	2.77	118.19	107.80
2	B	1601	APR	O5D-PB-O2B	2.77	118.18	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1601	APR	O5D-PB-O2B	2.76	118.17	107.80
3	D	1602	AR6	C5-C6-N6	2.32	123.85	120.31

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	1602	AR6	C1'
3	B	1602	AR6	C1'
3	C	1602	AR6	C1'
3	D	1602	AR6	C1'

5 of 32 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1602	AR6	C5'-O5'-PA-O3A
3	A	1602	AR6	C3'-C4'-C5'-O5'
3	A	1602	AR6	O4'-C4'-C5'-O5'
3	B	1602	AR6	C5'-O5'-PA-O3A
3	B	1602	AR6	C3'-C4'-C5'-O5'

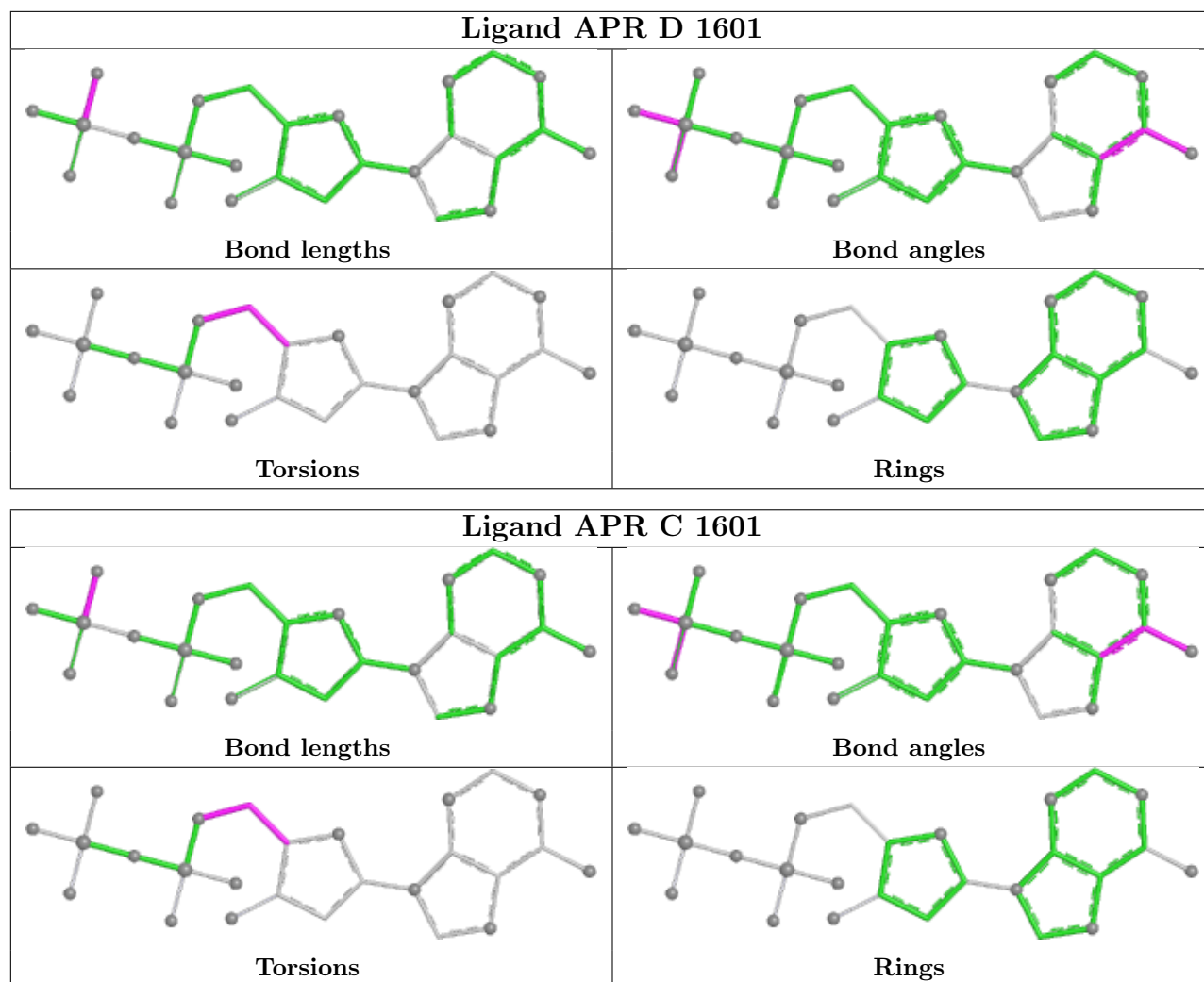
There are no ring outliers.

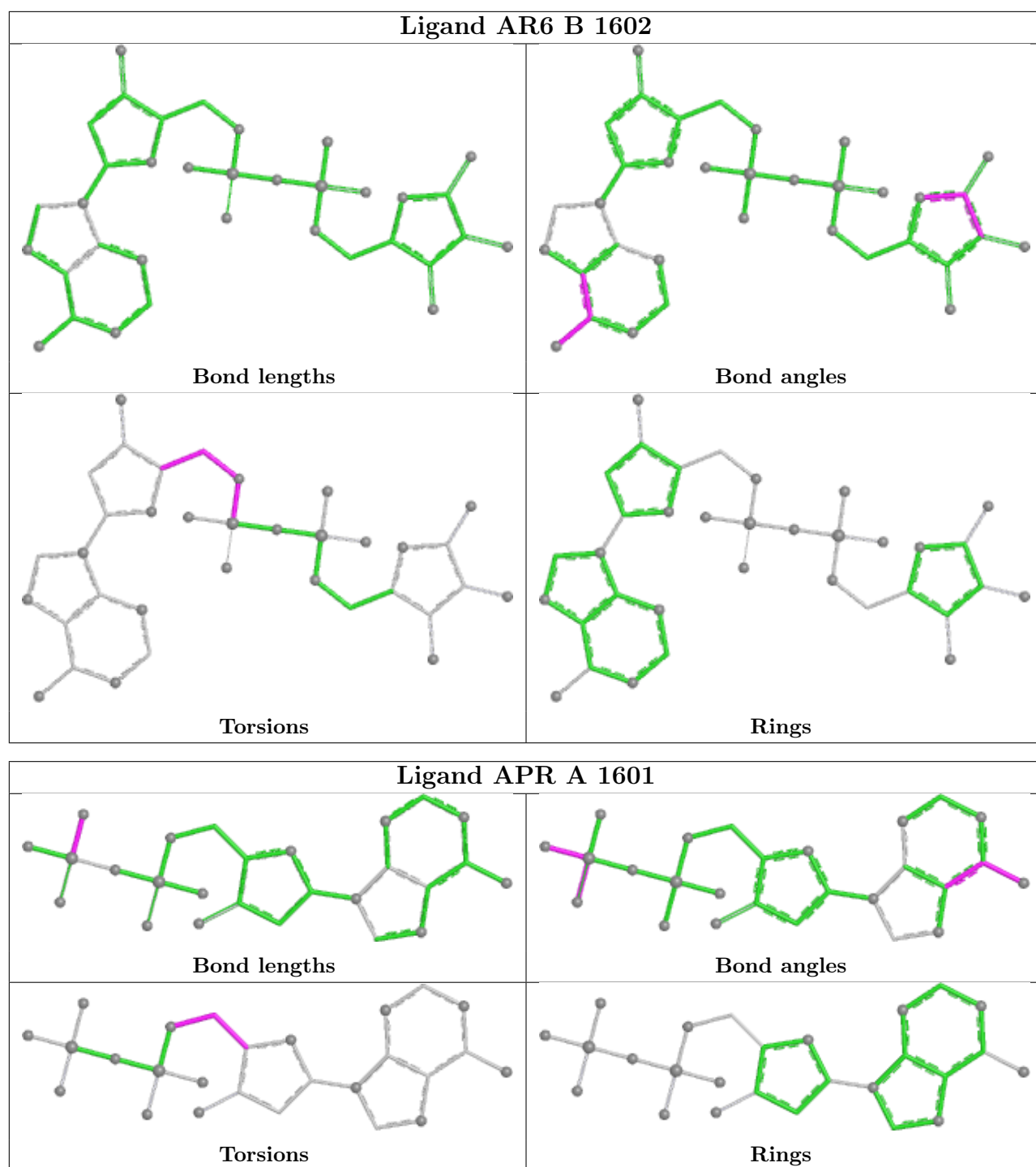
6 monomers are involved in 6 short contacts:

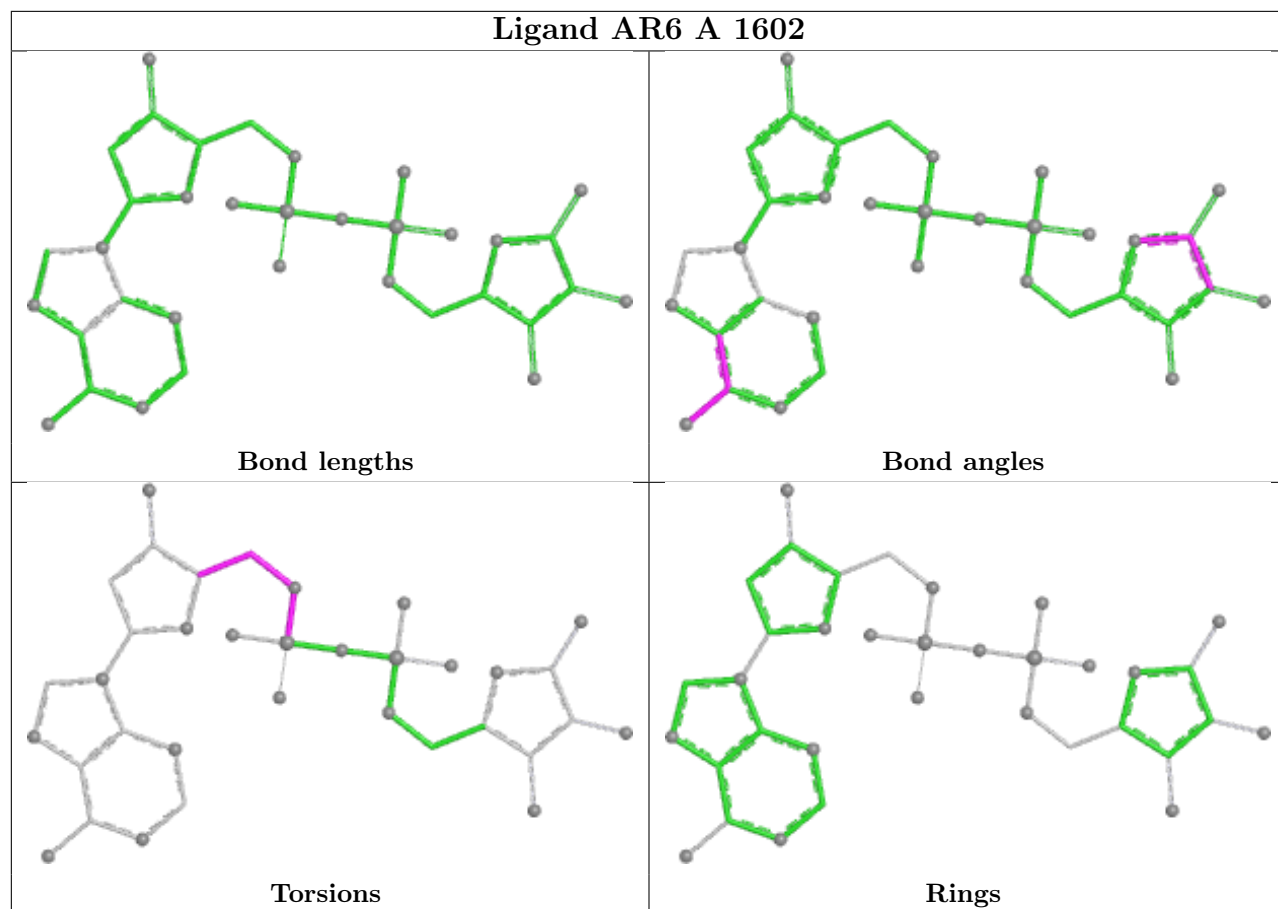
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1601	APR	1	0
2	C	1601	APR	1	0
3	B	1602	AR6	1	0
2	A	1601	APR	1	0
3	A	1602	AR6	1	0
2	B	1601	APR	1	0

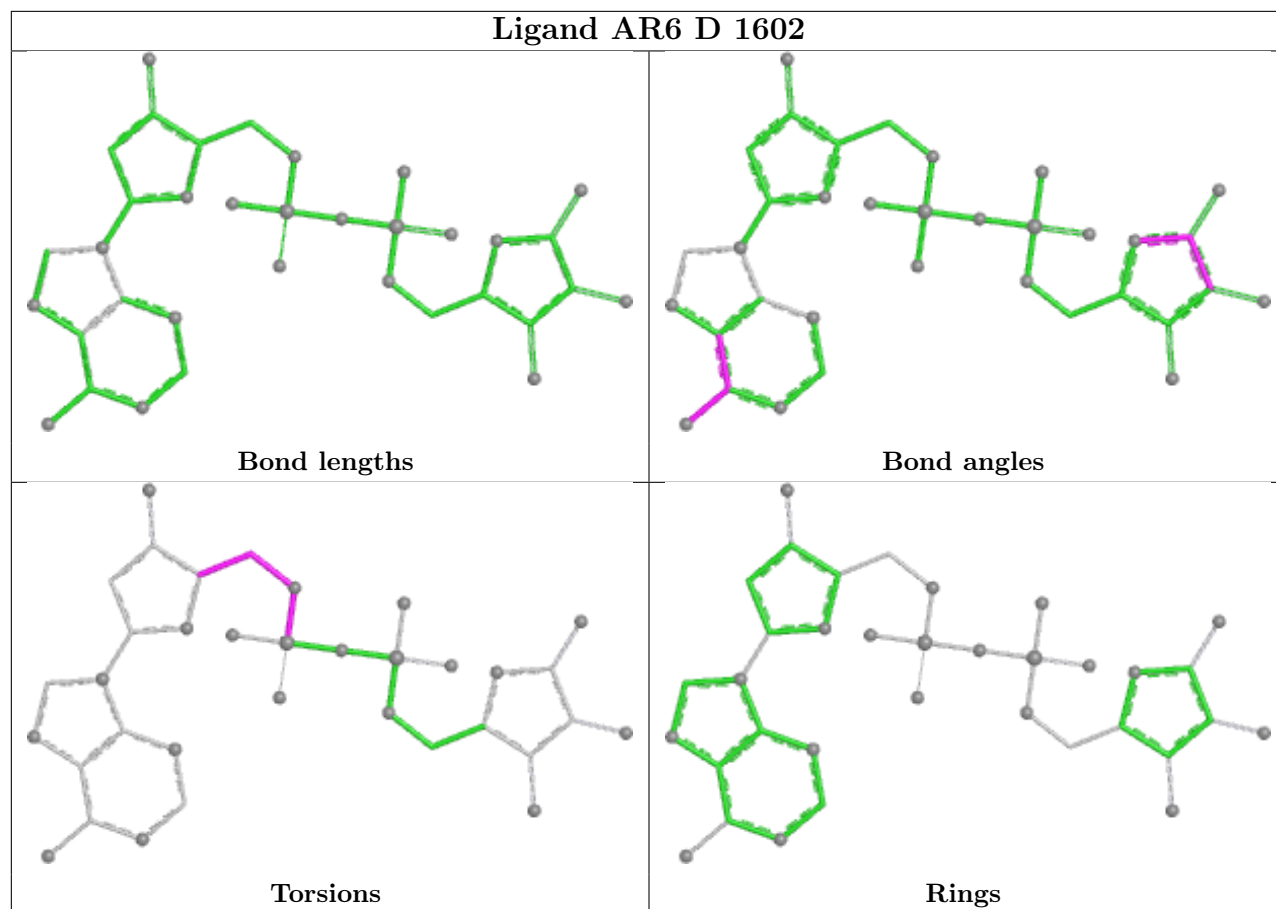
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

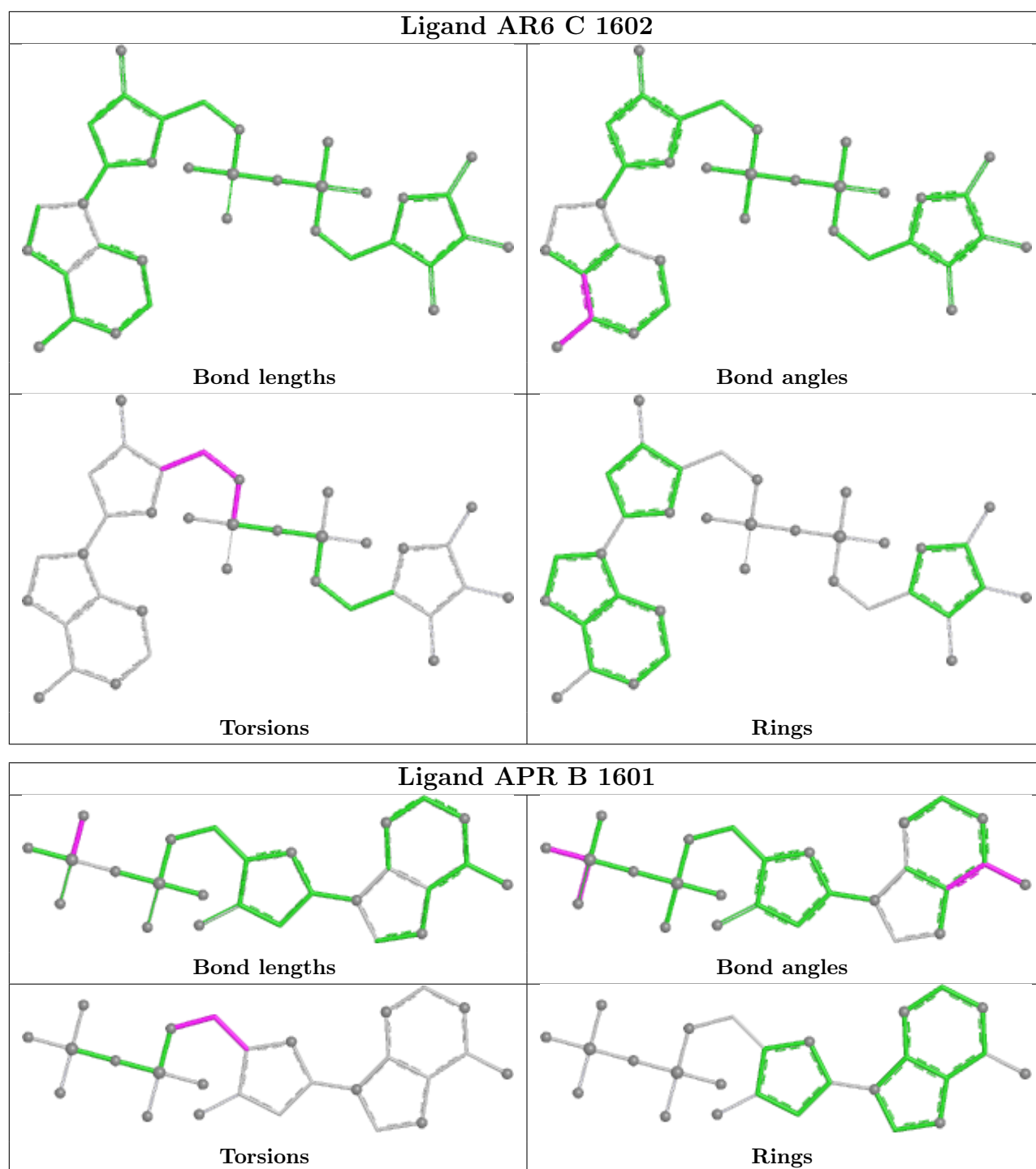
equivalents in the CSD to analyse the geometry.











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	A	1
1	B	1
1	C	1
1	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	462:TRP	C	463:ASN	N	3.00
1	B	462:TRP	C	463:ASN	N	3.00
1	C	462:TRP	C	463:ASN	N	3.00
1	D	462:TRP	C	463:ASN	N	3.00

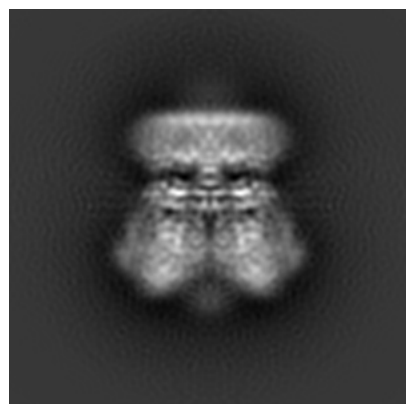
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27923. These allow visual inspection of the internal detail of the map and identification of artifacts.

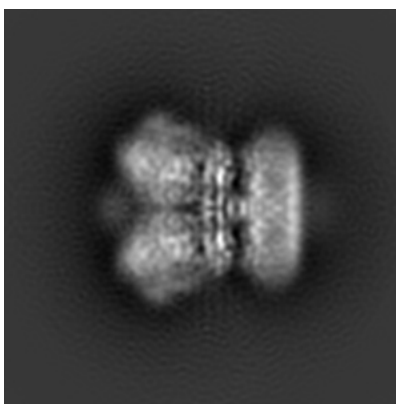
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

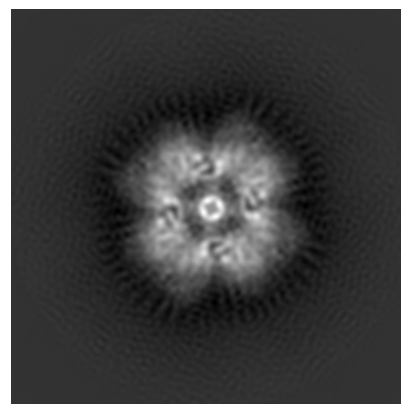
6.1.1 Primary map



X

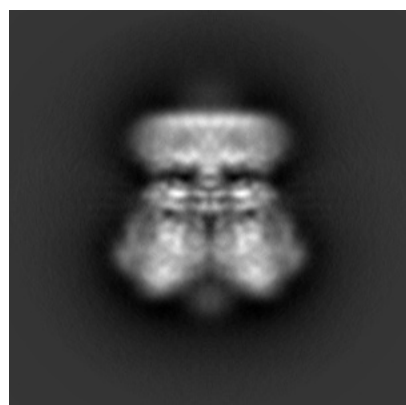


Y

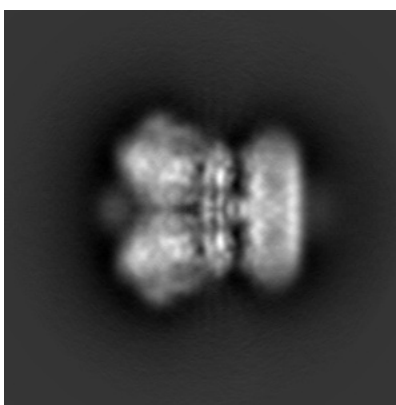


Z

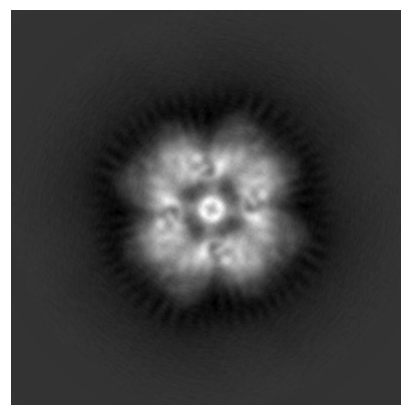
6.1.2 Raw map



X



Y



Z

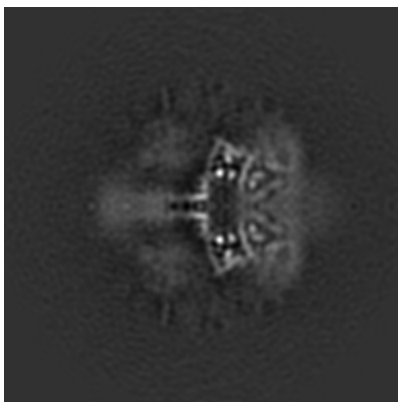
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

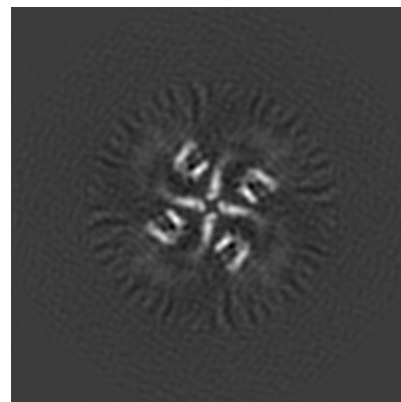
6.2.1 Primary map



X Index: 150

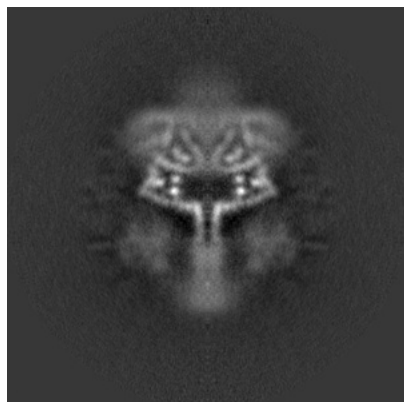


Y Index: 150

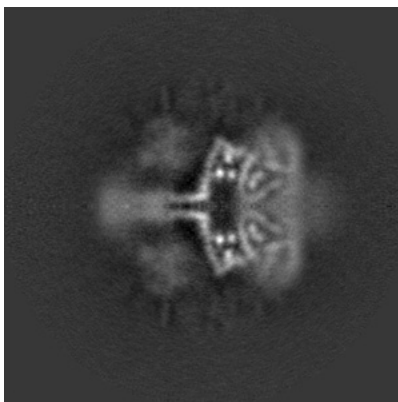


Z Index: 150

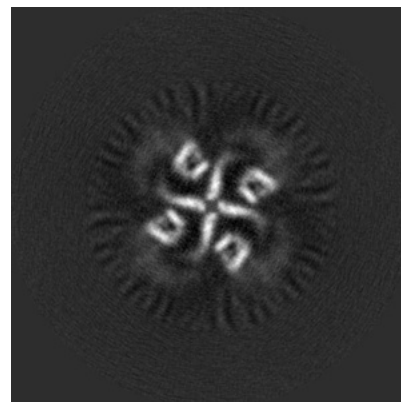
6.2.2 Raw map



X Index: 150



Y Index: 150



Z Index: 150

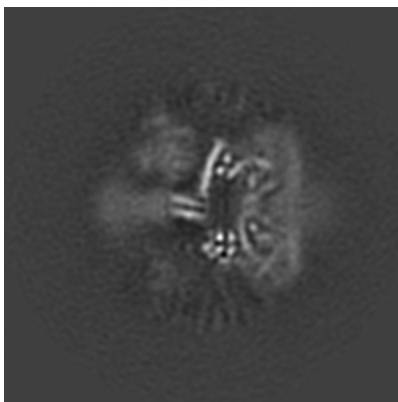
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

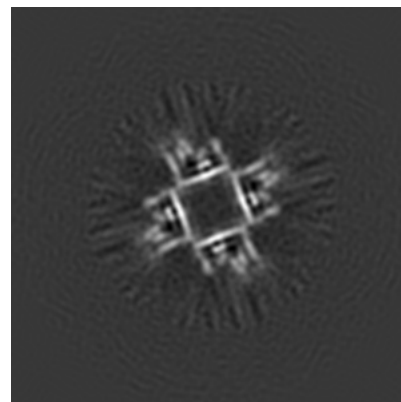
6.3.1 Primary map



X Index: 154

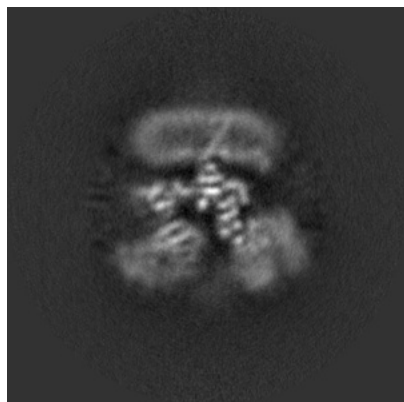


Y Index: 146

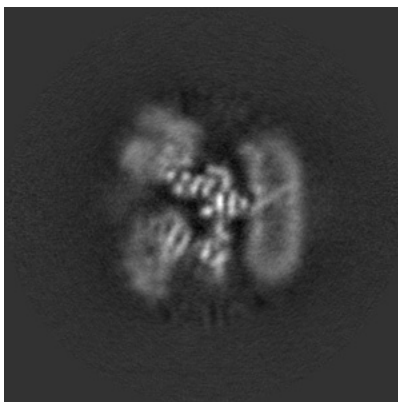


Z Index: 161

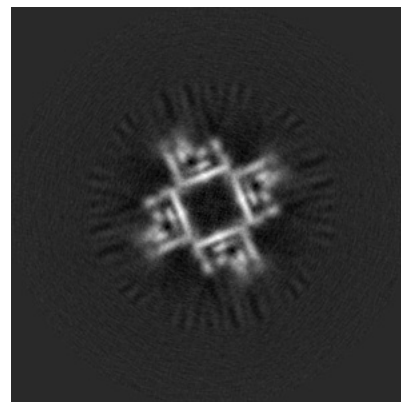
6.3.2 Raw map



X Index: 174



Y Index: 126

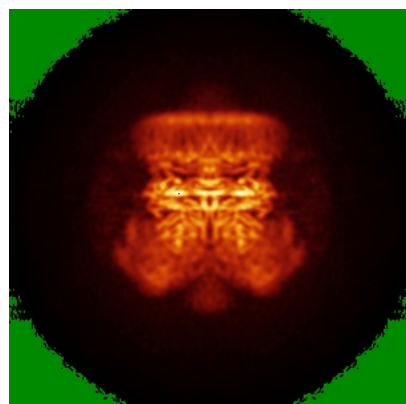


Z Index: 162

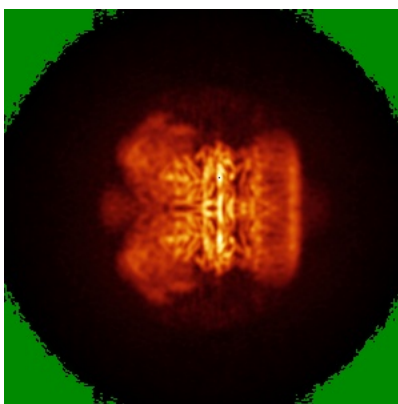
The images above show the largest variance slices of the map in three orthogonal directions.

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

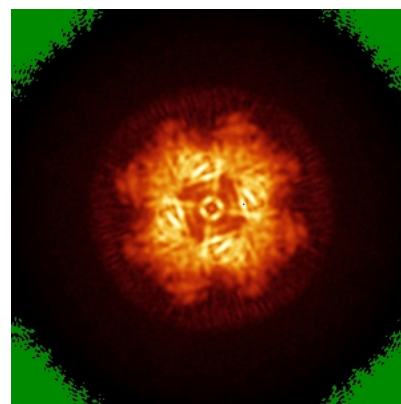
6.4.1 Primary map



X

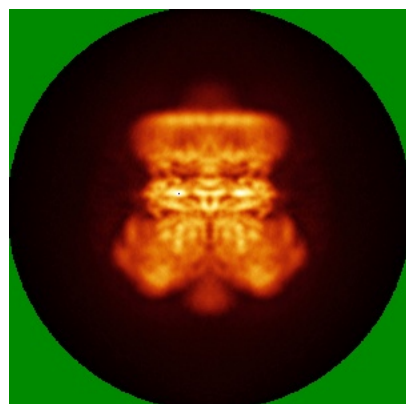


Y

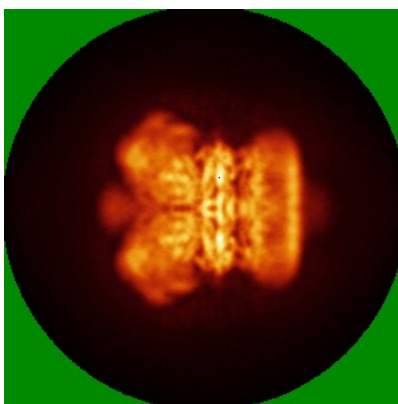


Z

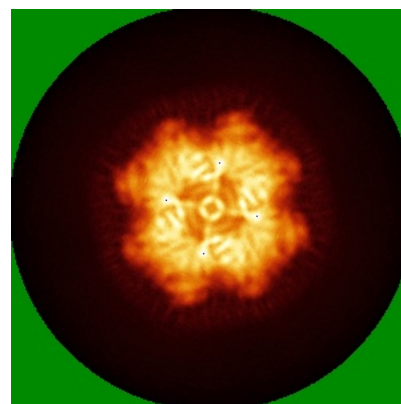
6.4.2 Raw map



X



Y

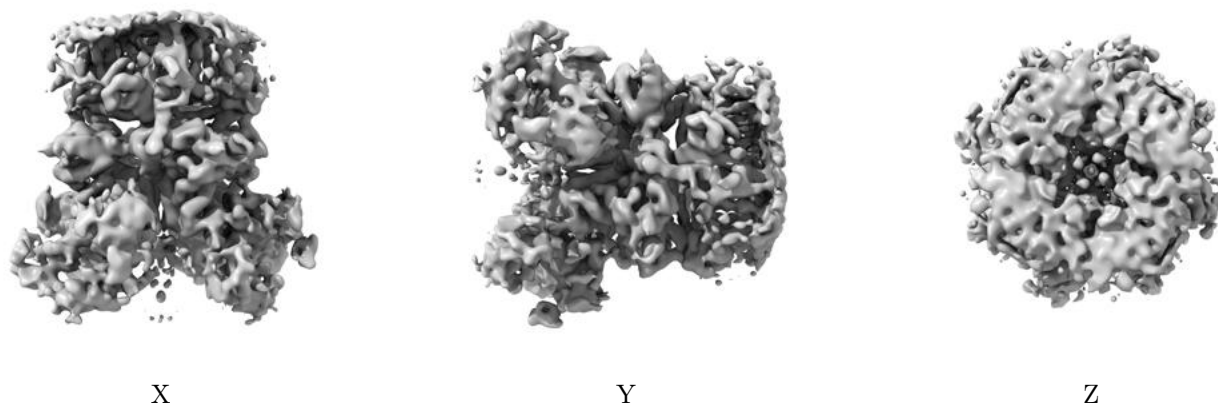


Z

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

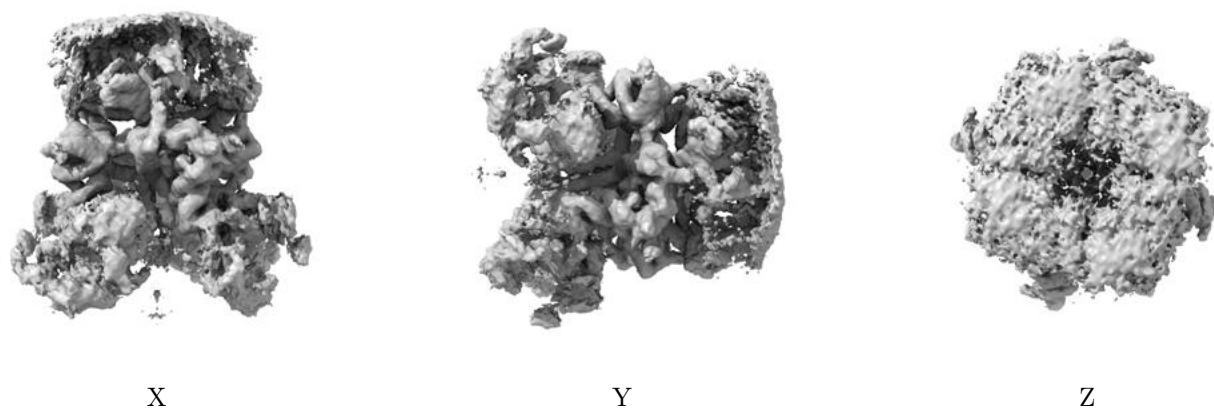
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0118. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

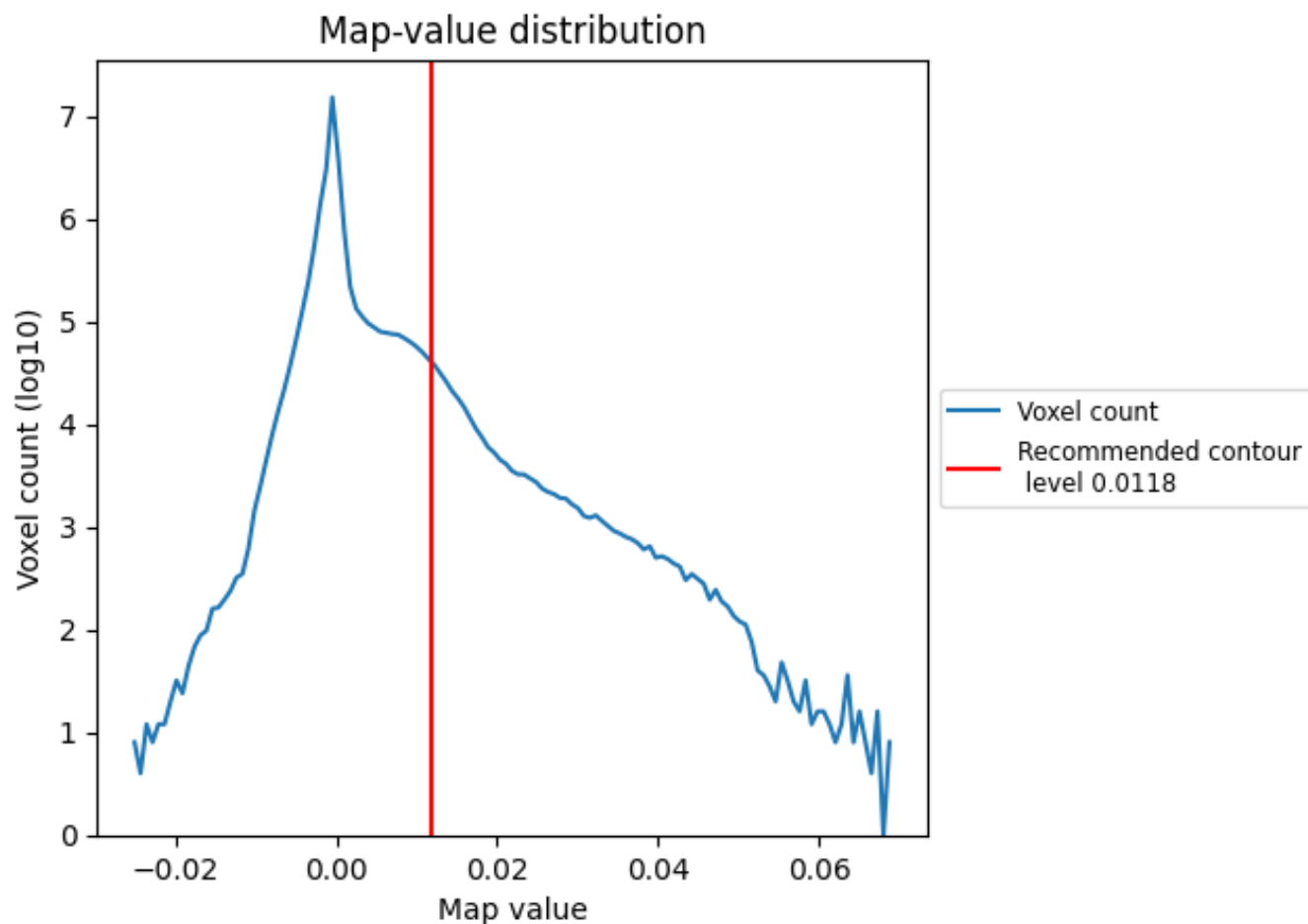
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

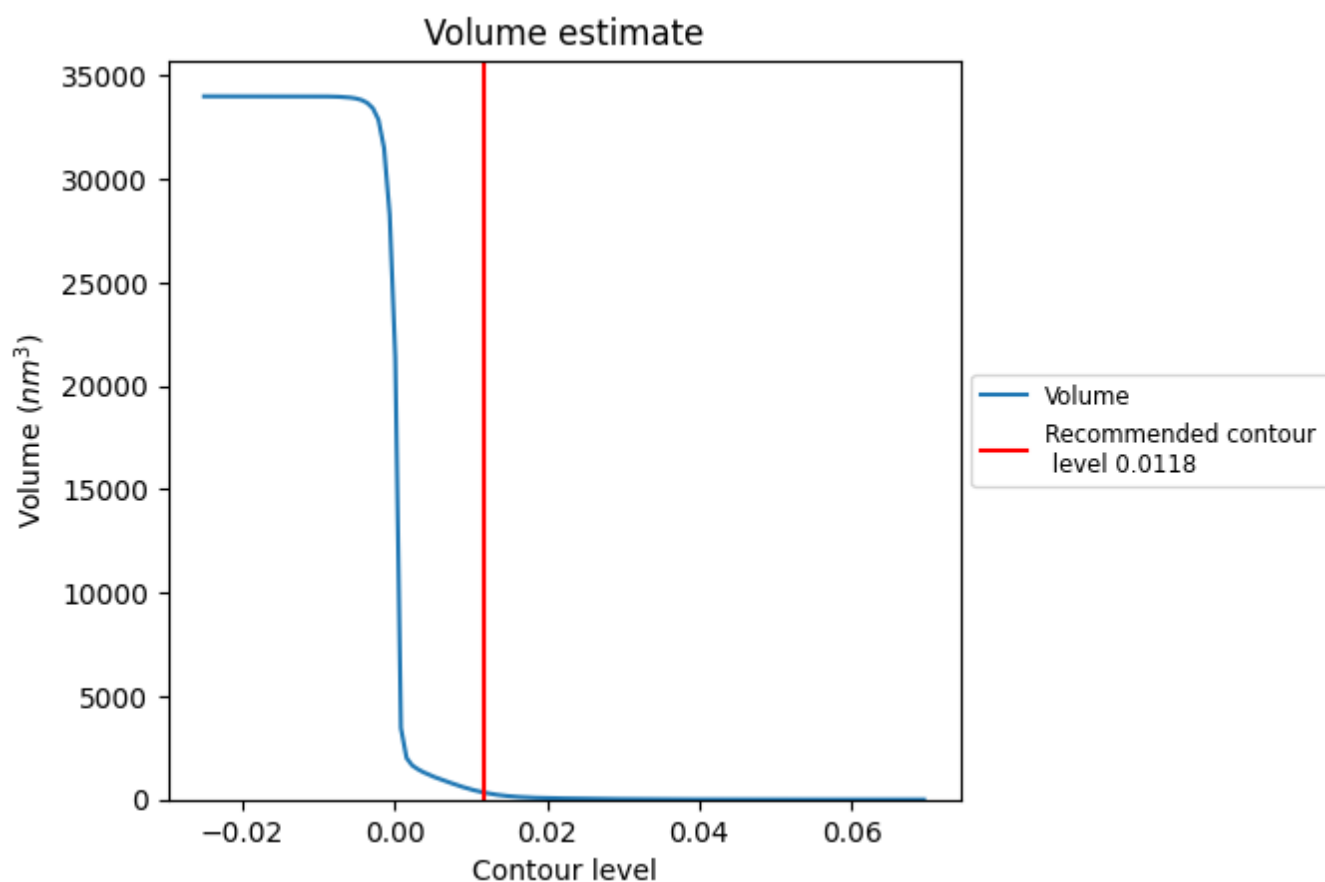
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

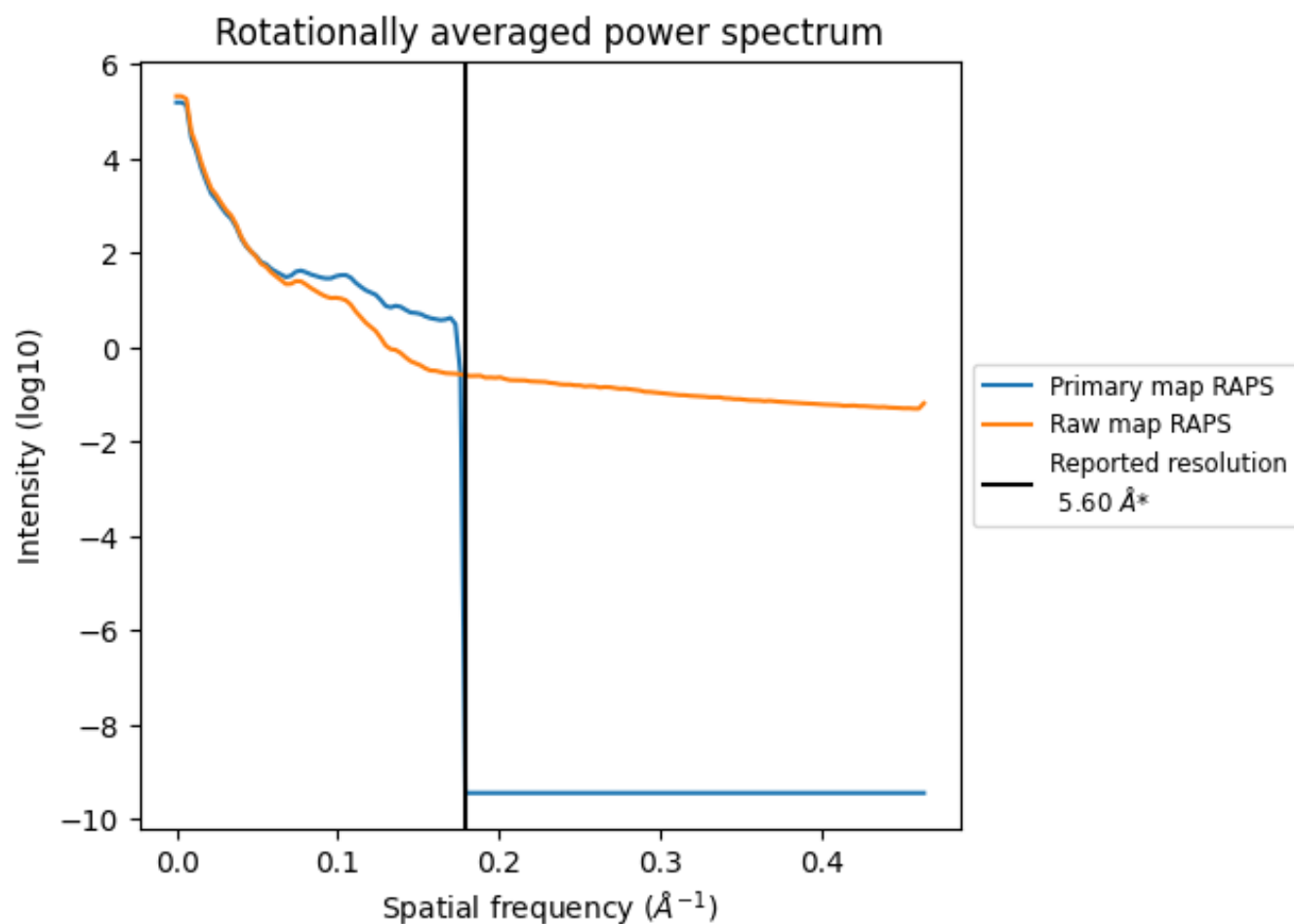
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 334 nm³; this corresponds to an approximate mass of 302 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 ⓘ

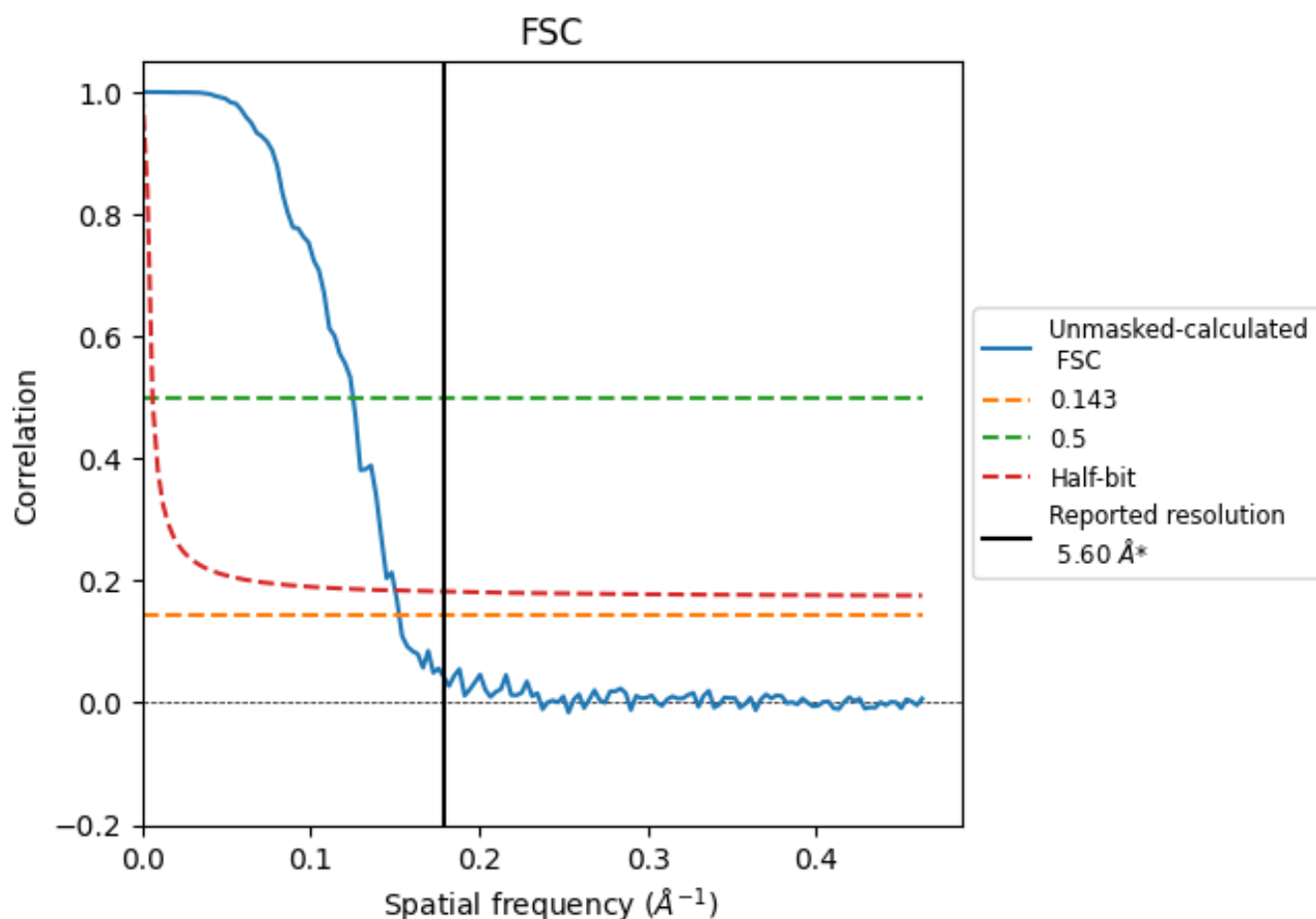


*Reported resolution corresponds to spatial frequency of 0.179 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.179 Å⁻¹

8.2 Resolution estimates [i](#)

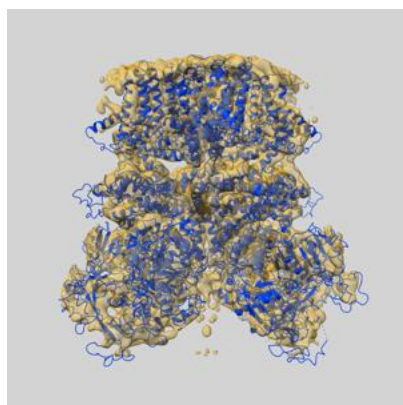
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.60	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.55	7.99	6.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.55 differs from the reported value 5.6 by more than 10 %

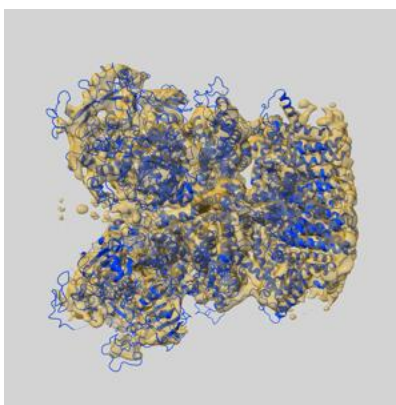
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27923 and PDB model 8E6R. Per-residue inclusion information can be found in section [3](#) on page [6](#).

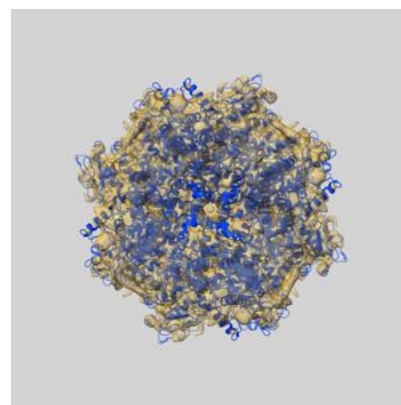
9.1 Map-model overlay [i](#)



X



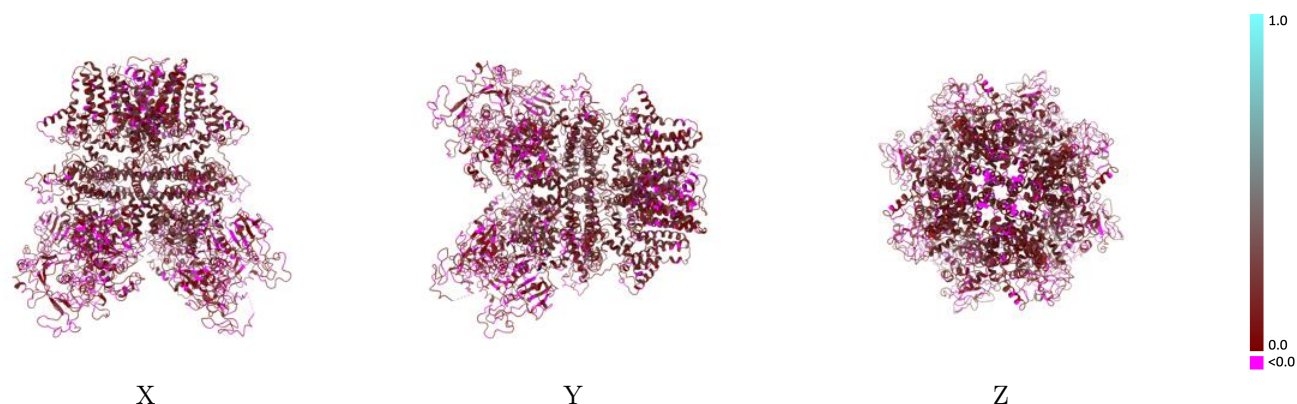
Y



Z

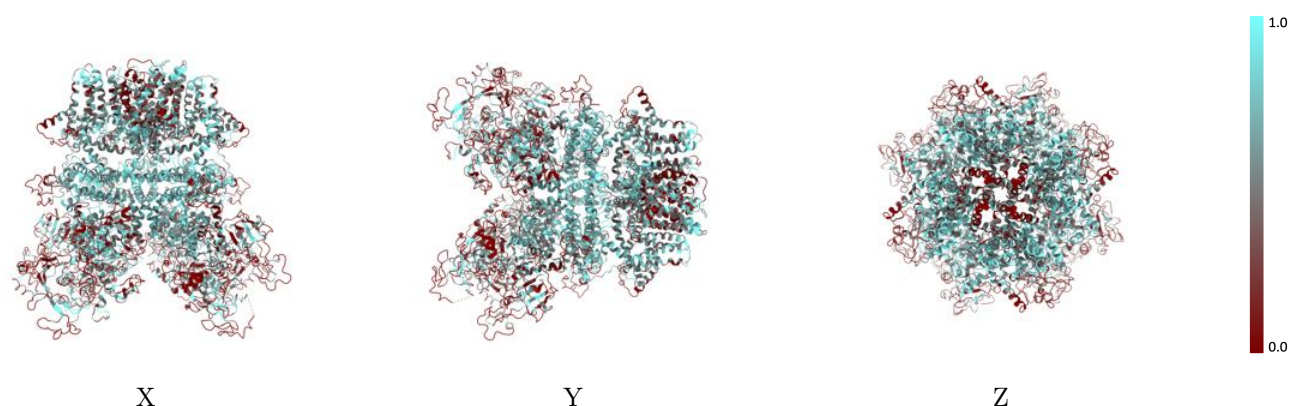
The images above show the 3D surface view of the map at the recommended contour level 0.0118 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



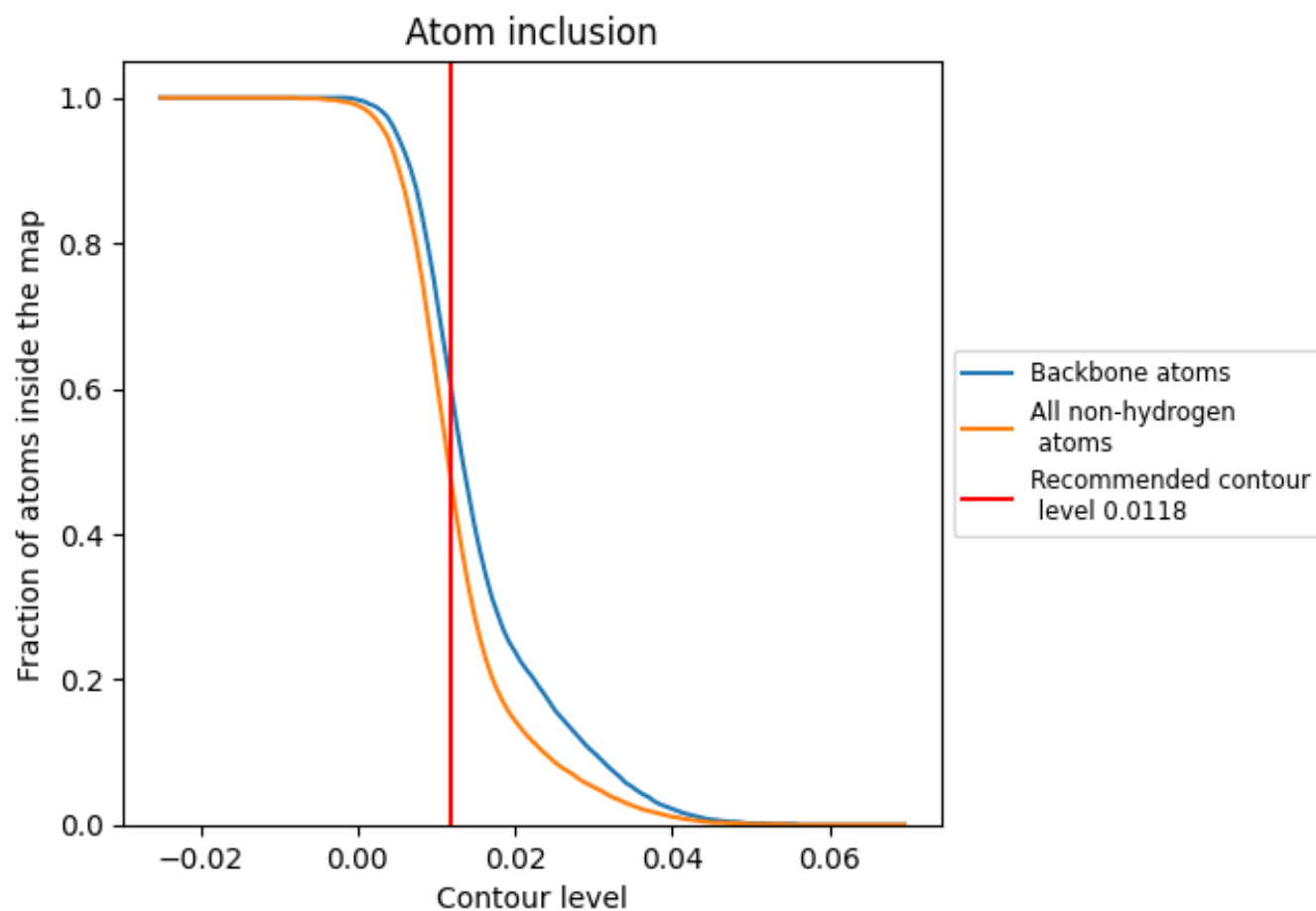
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0118).

9.4 Atom inclusion [i](#)



At the recommended contour level, 61% of all backbone atoms, 48% 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 (0.0118) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.4790	<div></div> 0.1230
A	<div></div> 0.4810	<div></div> 0.1250
B	<div></div> 0.4770	<div></div> 0.1220
C	<div></div> 0.4820	<div></div> 0.1240
D	<div></div> 0.4770	<div></div> 0.1210

