



wwPDB EM Validation Summary Report ⓘ

Aug 20, 2023 – 12:07 AM JST

PDB ID : 8IMZ
EMDB ID : EMD-35577
Title : Cryo-EM structure of mouse Piezo1-MDFIC complex (composite map)
Authors : Zhou, Z.; Ma, X.; Lin, Y.; Cheng, D.; Bavi, N.; Li, J.V.; Sutton, D.; Yao, M.; Harvey, N.; Corry, B.; Zhang, Y.; Cox, C.D.
Deposited on : 2023-03-07
Resolution : 3.66 Å(reported)

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<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 : **FAILED**
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

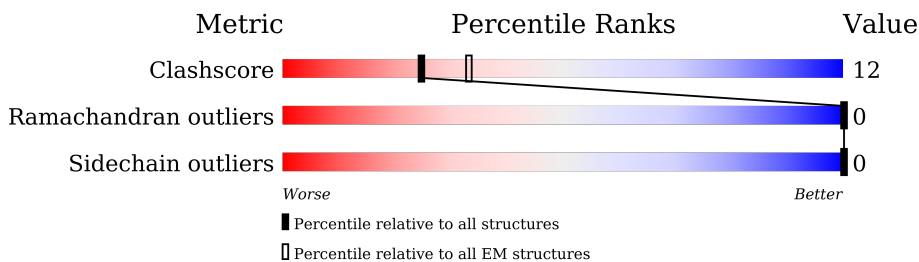
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.66 Å.

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



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

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	2547	35% 13% 52%
1	B	2547	35% 13% 52%
1	C	2547	35% 13% 52%
2	D	247	91%
2	E	247	6% 91%
2	F	247	6% 91%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 29409 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 Piezo-type mechanosensitive ion channel component 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1223	9653	6324	1626	1652	51	0	0
1	C	1223	9653	6324	1626	1652	51	0	0
1	B	1223	9653	6324	1626	1652	51	0	0

- Molecule 2 is a protein called MyoD family inhibitor domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	D	21	150	88	21	33	8	0	0
2	E	21	150	88	21	33	8	0	0
2	F	21	150	88	21	33	8	0	0

S2290	G2291	A2292	R2296	L2295	S2297	P2298	P2299	S2300	R2301	A2302	Q2303	M2304	W2321	Q2324	V2333	E2334	Y2335	E2338	T2349	Q2353	Q2356	L2357	L2358	E2359	G2360	S2361	Q2364	S2365	I2368	L2371	F2372	P2373	K2374	Y2375	I2376	R2377	P2382	P2386	D2280	I2381	Q2388	Q2389	L2390	E2394	Y2398																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
P1987	I2097	R2098	R2104	L2105	L2106	G2107	M2108	F2109	K2113	H2116	L2117	M2118	F2128	V2128	P2129	F2130	L2131	V2132	E2133	V2137	W2140	V2141	W2142	T2143	D2144	T2145	T2146	L2147	S2148	L2149	W2153	L2162	T2171	P2178	K2179	G2180	Q2181	K2182	K2183	K2184	K2185	L2186	V2187	K2188	Y2189	G2190	H2191	G2192	I2202																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
F2209	M2210	S2211	L2212	L2213	M2221	Q2222	D2225	Y2235	E2236	P2237	L2238	F2239	M2241	S2242	A2243	Q2244	Q2245	P2246	S2247	P2250	F2251	T2252	P2253	Q2254	Q2255	E2257	S2260	F2263	D2264	P2266	L2268	A2269	M2270	Q2271	I2272	I2273	S2274	P2278	E2279	D2280	I2281	V2282	T2283	E2287	G2288	S2289																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
P1987	Y1970	R1971	D1987	I1988	I1991	G1994	F1998	L2007	HIS	L2010	SER	L2011	L2012	L2013	L2014	L2015	L2016	L2021	L2024	Q2027	T2030	M2031	R2035	R2040	L2047	V2051	H2058	T2069	E2070	Q2075	V2078	W2082	Y2083	L2097	R2098	R2104	L2105	L2106	G2107	M2108	F2109	K2113	H2116	L2117	M2118	F2128	V2128	P2129	F2130	L2131	V2132	E2133	V2137	W2140	V2141	W2142	T2143	D2144	T2145	T2146	L2147	S2148	L2149	W2153	L2162	T2171	P2178	K2179	G2180	Q2181	K2182	K2183	K2184	K2185	L2186	V2187	K2188	Y2189	G2190	H2191	G2192	I2202																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
GLN	ARG	VAL	GLN	THR	GLN	THR	G1589	D1514	M1530	R1588	L1541	T1542	V1548	G1549	E1550	R1551	R1552	G1554	V1555	L1556	D1557	L1558	T1559	T1560	T1561	T1562	T1563	T1564	T1565	T1566	T1567	T1568	T1569	T1570	T1571	T1572	T1573	T1574	T1575	T1576	T1577	T1578	T1579	T1580	T1581	T1582	T1583	T1584	T1585	T1586	T1587	T1588	T1589	T1590	T1591	T1592	T1593	T1594	T1595	T1596	T1597	T1598	T1599	T1600	T1601	T1602	T1603	T1604	T1605	T1606	T1607	T1608	T1609	T1610	T1611	T1612	T1613	T1614	T1615	T1616	T1617	T1618	T1619	T1620	T1621	T1622	T1623	T1624	T1625	T1626	T1627	T1628	T1629	T1630	T1631	T1632	T1633	T1634	T1635	T1636	T1637	T1638	T1639	T1640	T1641	T1642	T1643	T1644	T1645	T1646	T1647	T1648	T1649	T1650	T1651	T1652	T1653	T1654	T1655	T1656	T1657	T1658	T1659	T1660	T1661	T1662	T1663	T1664	T1665	T1666	T1667	T1668	T1669	T1670	T1671	T1672	T1673	T1674	T1675	T1676	T1677	T1678	T1679	T1680	T1681	T1682	T1683	T1684	T1685	T1686	T1687	T1688	T1689	T1690	T1691	T1692	T1693	T1694	T1695	T1696	T1697	T1698	T1699	T1700	T1701	T1702	T1703	T1704	T1705	T1706	T1707	T1708	T1709	T1710	T1711	T1712	T1713	T1714	T1715	T1716	T1717	T1718	T1719	T1720	T1721	T1722	T1723	T1724	T1725	T1726	T1727	T1728	T1729	T1730	T1731	T1732	T1733	T1734	T1735	T1736	T1737	T1738	T1739	T1740	T1741	T1742	T1743	T1744	T1745	T1746	T1747	T1748	T1749	T1750	T1751	T1752	T1753	T1754	T1755	T1756	T1757	T1758	T1759	T1760	T1761	T1762	T1763	T1764	T1765	T1766	T1767	T1768	T1769	T1770	T1771	T1772	T1773	T1774	T1775	T1776	T1777	T1778	T1779	T1780	T1781	T1782	T1783	T1784	T1785	T1786	T1787	T1788	T1789	T1790	T1791	T1792	T1793	T1794	T1795	T1796	T1797	T1798	T1799	T1800	T1801	T1802	T1803	T1804	T1805	T1806	T1807	T1808	T1809	T1810	T1811	T1812	T1813	T1814	T1815	T1816	T1817	T1818	T1819	T1820	T1821	T1822	T1823	T1824	T1825	T1826	T1827	T1828	T1829	T1830	T1831	T1832	T1833	T1834	T1835	T1836	T1837	T1838	T1839	T1840	T1841	T1842	T1843	T1844	T1845	T1846	T1847	T1848	T1849	T1850	T1851	T1852	T1853	T1854	T1855	T1856	T1857	T1858	T1859	T1860	T1861	T1862	T1863	T1864	T1865	T1866	T1867	T1868	T1869	T1870	T1871	T1872	T1873	T1874	T1875	T1876	T1877	T1878	T1879	T1880	T1881	T1882	T1883	T1884	T1885	T1886	T1887	T1888	T1889	T1890	T1891	T1892	T1893	T1894	T1895	T1896	T1897	T1898	T1899	T1900	T1901	T1902	T1903	T1904	T1905	T1906	T1907	T1908	T1909	T1910	T1911	T1912	T1913	T1914	T1915	T1916	T1917	T1918	T1919	T1920	T1921	T1922	T1923	T1924	T1925	T1926	T1927	T1928	T1929	T1930	T1931	T1932	T1933	T1934	T1935	T1936	T1937	T1938	T1939	T1940	T1941	T1942	T1943	T1944	T1945	T1946	T1947	T1948	T1949	T1950	T1951	T1952	T1953	T1954	T1955	T1956	T1957	T1958	T1959	T1960	T1961	T1962	T1963	T1964	T1965	T1966	T1967	T1968	T1969	T1970	T1971	T1972	T1973	T1974	T1975	T1976	T1977	T1978	T1979	T1980	T1981	T1982	T1983	T1984	T1985	T1986	T1987	T1988	T1989	T1990	T1991	T1992	T1993	T1994	T1995	T1996	T1997	T1998	T1999	T2000	T2001	T2002	T2003	T2004	T2005	T2006	T2007	T2008	T2009	T2010	T2011	T2012	T2013	T2014	T2015	T2016	T2017	T2018	T2019	T2020	T2021	T2022	T2023	T2024	T2025	T2026	T2027	T2028	T2029	T2030	T2031	T2032	T2033	T2034	T2035	T2036	T2037	T2038	T2039	T2040	T2041	T2042	T2043	T2044	T2045	T2046	T2047	T2048	T2049	T2050	T2051	T2052	T2053	T2054	T2055	T2056	T2057	T2058	T2059	T2060	T2061	T2062	T2063	T2064	T2065	T2066	T2067	T2068	T2069	T2070	T2071	T2072	T2073	T2074	T2075	T2076	T2077	T2078	T2079	T2080	T2081	T2082	T2083	T2084	T2085	T2086	T2087	T2088	T2089	T2090	T2091	T2092	T2093	T2094	T2095	T2096	T2097	T2098	T2099	T2100	T2101	T2102	T2103	T2104	T2105	T2106	T2107	T2108	T2109	T2110	T2111	T2112	T2113	T2114	T2115	T2116	T2117	T2118	T2119	T2120	T2121	T2122	T2123	T2124	T2125	T2126	T2127	T2128	T2129	T2130	T2131	T2132	T2133	T2134	T2135	T2136	T2137	T2138	T2139	T2140	T2141	T2142	T2143	T2144	T2145	T2146	T2147	T2148	T2149	T2150	T2151	T2152	T2153	T2154	T2155	T2156	T2157	T2158	T2159	T2160	T2161	T2162	T2163	T2164	T2165	T2166	T2167	T2168	T2169	T2170	T2171	T2172	T2173	T2174	T2175	T2176	T2177	T2178	T2179	T2180	T2181	T2182	T2183	T2184	T2185	T2186	T2187	T2188	T2189	T2190	T2191	T2192	T2193	T2194	T2195	T2196	T2197	T2198	T2199	T2200	T2201	T2202	T2203	T2204	T2205	T2206	T2207	T2208	T2209	T2210	T2211	T2212	T2213	T2214	T2215	T2216	T2217	T2218	T2219	T2220	T2221	T2222	T2223	T2224	T2225	T2226	T2227	T2228	T2229	T2230	T2231	T2232	T2233	T2234	T2235	T2236	T2237	T2238	T2239	T2240	T2241	T2242	T2243	T2244	T2245	T2246	T2247	T2248	T2249	T2250	T2251	T2252	T2253	T2254	T2255	T2256	T2257	T2258	T2259	T2260	T2261	T2262	T2263	T2264	T2265	T2266	T2267	T2268	T2269	T2270	T2271	T2272	T2273	T2274	T2275	T2276	T2277	T2278	T2279	T2280	T2281	T2282	T2283	T2284	T2285	T2286	T2287	T2288	T2289	T2290	T2291	T2292	T2293	T2294	T2295	T2296	T2297	T2298	T2299	T2300	T2301	T2302	T2303	T2304	T2305	T2306	T2307	T2308	T2309	T2310	T2311	T2312	T2313	T2314	T2315	T2316	T2317	T2318	T2319	T2320	T2321	T2322	T2323	T2324	T2325	T2326	T2327	T2328	T2329	T2330	T2331	T2332	T2333	T2334	T2335	T2336	T2337	T2338	T2339	T2340	T2341	T2342	T2343	T2344	T2345	T2346	T2347	T2348	T2349	T2350	T2351	T2352	T2353	T2354	T2355	T2356	T2357	T2358	T2359	T2360	T2361	T2362	T2363	T2364	T2365	T2366	T2367	T2368	T2369	T2370	T237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H2490	R2377	S2274	K2184	T2069	LEU	VAL	ARG	GLU	ALA	ALA	HIS	ALA	ALA	Y1369	VAL	H1400
S2491	P2382	E2278	K2186	E2070	ALA	LEU	ARG	GLU	GLN	GLN	MET	SER	SER	P1141	CYS	P1141
L2492	P2382	E2278	I2186	Q2075	SER	ARG	THR	ALA	ARG	THR	THR	GLY	GLY	S1365	THR	F1143
M2493	K2188	D2280	V2187	Q2075	PHE	THR	ARG	LYS	TYR	TYR	A1645	TYR	ALA	GLY	VAL	F1143
F2494	Y2189	I2281	Y2189	V2078	TYR	GLY	LYS	LEU	GLN	GLN	L1649	GLY	PHE	GLY	GLY	L1150
L2497	K2388	T2283	G2190	W2082	GLN	ASN	ASN	GLU	ASN	ALA	L1650	ALA	MET	LEU	TYR	K1154
L2504	Q2389	T2283	M2191	Y2083	LYS	LYS	PRO	SER	PRO	GLU	D1651	GLU	ASP	GLN	ASP	V1165
T2516	L2390	E2287	R1971	L2092	PHE	P1770	PHE	THR	PHE	ALA	G1670	ALA	PRO	GLN	LYS	F1170
L2519	E2394	G2288	D1987	T2097	THR	L1774	L1672	THR	THR	THR	R1671	SER	GLN	GLN	MET	I1177
E2520	Y2398	A2292	I1988	R2098	ALA	L1774	L1672	THR	THR	THR	L1673	THR	VAL	ASP	THR	S1178
L2521	L2399	A2292	I1988	R2098	VAL	L1774	L1672	THR	THR	THR	L1673	THR	VAL	ASP	THR	S1178
E2522	G2400	M2210	I1991	R2104	MET	HIS	MET	HIS	HIS	THR	G1509	ALA	ASN	SER	LEU	I1179
E2523	V2401	S2211	I1991	L2105	GLU	THR	GLU	PRO	PRO	THR	D1514	GLN	ALA	GLY	ARG	L1182
E2524	R2402	L2212	G1994	L2106	THR	D1780	D1780	GLU	GLU	SER	D1514	GLN	GLN	PRO	ARG	G1183
L2525	I2403	I2213	F1998	G2107	GLU	S1781	S1781	GLU	GLU	SER	D1514	THR	THR	ASP	ASP	Y1184
Q2404	Q2404	I2213	F1998	G2107	HIS	S1781	S1781	GLU	GLU	SER	D1514	VAL	VAL	CYS	CYS	
L2405	L2405	I2213	F1998	G2107	GLU	Y1782	Y1782	VAL	VAL	PRO	M1550	LEU	LEU	LEU	LEU	
R2406	S2300	I2213	F1998	G2107	GLY	I1783	I1783	GLY	GLY	LEU	R1538	ARG	ARG	LEU	LEU	
R2407	R2301	I2213	F1998	G2107	ALA	K1784	K1784	ALA	ALA	SER	R1538	GLN	GLN	PRO	PRO	
E2408	Q2302	I2213	F1998	G2107	GLY	L1787	L1787	THR	THR	TYR	L1541	ARG	ARG	VAL	VAL	
Q2409	Q2302	I2213	F1998	G2107	ALA	Y1788	Y1788	PRO	PRO	TYR	T1542	GLY	GLY	GLU	GLU	
Y2410	H2304	I2213	F1998	G2107	ALA	Q1789	Q1789	ARG	ARG	ASN	T1542	GLY	GLY	GLU	GLU	
Q2411	H2304	I2213	F1998	G2107	THR	Q1789	Q1789	ARG	ARG	ASN	T1542	GLY	GLY	GLU	GLU	
Q2412	H2304	I2213	F1998	G2107	ASP	H1796	H1796	ASP	ASP	THR	V1548	SER	ALA	ALA	ALA	
Q2413	H2304	I2213	F1998	G2107	ALA	H1796	H1796	HIS	HIS	THR	V1548	SER	ALA	ALA	ALA	
Q2414	H2304	I2213	F1998	G2107	ALA	H1796	H1796	ILE	ILE	THR	G1549	ARG	ARG	PRO	PRO	
Q2415	H2304	I2213	F1998	G2107	SER	Q1799	Q1799	GLN	GLN	SER	E1550	GLN	GLN	ILE	ILE	
Q2416	H2304	I2213	F1998	G2107	SER	L1800	L1800	GLY	GLY	SER	V1551	ARG	ARG	PRO	PRO	
Q2417	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2418	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2419	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2420	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2421	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2422	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2423	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2424	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2425	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2426	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2427	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2428	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2429	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2430	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2431	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2432	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2433	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2434	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2435	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2436	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2437	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2438	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2439	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2440	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2441	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2442	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2443	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2444	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2445	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2446	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2447	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2448	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2449	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2450	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2451	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2452	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2453	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2454	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2455	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2456	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2457	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2458	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2459	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2460	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2461	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2462	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2463	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2464	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2465	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2466	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2467	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2468	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2469	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2470	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2471	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2472	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2473	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2474	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2475	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2476	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2477	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2478	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2479	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552	ARG	ARG	PRO	PRO	
Q2480	H2304	I2213	F1998	G2107	LEU	L1800	L1800	GLY	GLY	SER	R1552					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	102644	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 ($e^-/\text{\AA}^2$)	49.4	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.38	0/9877	0.48	0/13401
1	B	0.38	0/9877	0.48	0/13401
1	C	0.38	0/9877	0.48	0/13401
2	D	0.34	0/151	0.49	0/200
2	E	0.34	0/151	0.49	0/200
2	F	0.34	0/151	0.50	0/200
All	All	0.38	0/30084	0.48	0/40803

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	9653	0	9495	239	0
1	B	9653	0	9495	245	0
1	C	9653	0	9495	241	0
2	D	150	0	132	9	0
2	E	150	0	132	7	0
2	F	150	0	132	5	0
All	All	29409	0	28881	681	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 12.

The worst 5 of 681 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:2295:ARG:HD2	1:C:2295:ARG:HH12	1.18	1.05
1:A:2295:ARG:HH12	1:B:2295:ARG:HD2	1.19	1.04
1:C:2295:ARG:HD2	1:B:2295:ARG:HH12	1.19	1.03
1:C:1971:ARG:NE	1:C:2098:ARG:O	2.02	0.92
1:A:1971:ARG:NE	1:A:2098:ARG:O	2.02	0.91

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	1193/2547 (47%)	1107 (93%)	86 (7%)	0	100	100
1	B	1193/2547 (47%)	1108 (93%)	85 (7%)	0	100	100
1	C	1193/2547 (47%)	1107 (93%)	86 (7%)	0	100	100
2	D	19/247 (8%)	18 (95%)	1 (5%)	0	100	100
2	E	19/247 (8%)	18 (95%)	1 (5%)	0	100	100
2	F	19/247 (8%)	18 (95%)	1 (5%)	0	100	100
All	All	3636/8382 (43%)	3376 (93%)	260 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	983/2246 (44%)	983 (100%)	0	100	100
1	B	983/2246 (44%)	983 (100%)	0	100	100
1	C	983/2246 (44%)	983 (100%)	0	100	100
2	D	20/206 (10%)	20 (100%)	0	100	100
2	E	20/206 (10%)	20 (100%)	0	100	100
2	F	20/206 (10%)	20 (100%)	0	100	100
All	All	3009/7356 (41%)	3009 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2254	GLN
1	C	2364	GLN
1	B	2364	GLN
1	B	2116	HIS
1	B	2254	GLN

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 monosaccharides 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](#)

There are no chain breaks in this entry.