



wwPDB EM Validation Summary Report ⓘ

Jul 16, 2025 – 12:57 AM JST

PDB ID : 8IMZ / pdb_00008imz
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)

This is a wwPDB EM Validation Summary 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 : **FAILED**
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

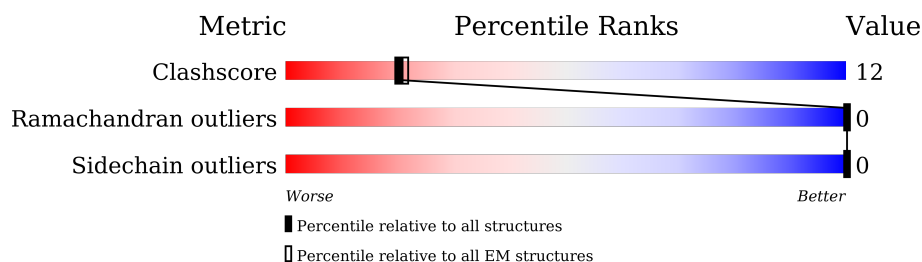
1 Overall quality at a glance

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	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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	2547	
1	B	2547	
1	C	2547	
2	D	247	
2	E	247	
2	F	247	

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
1	A	1223	Total	C	N	O	S	0	0
			9653	6324	1626	1652	51		
1	C	1223	Total	C	N	O	S	0	0
			9653	6324	1626	1652	51		
1	B	1223	Total	C	N	O	S	0	0
			9653	6324	1626	1652	51		

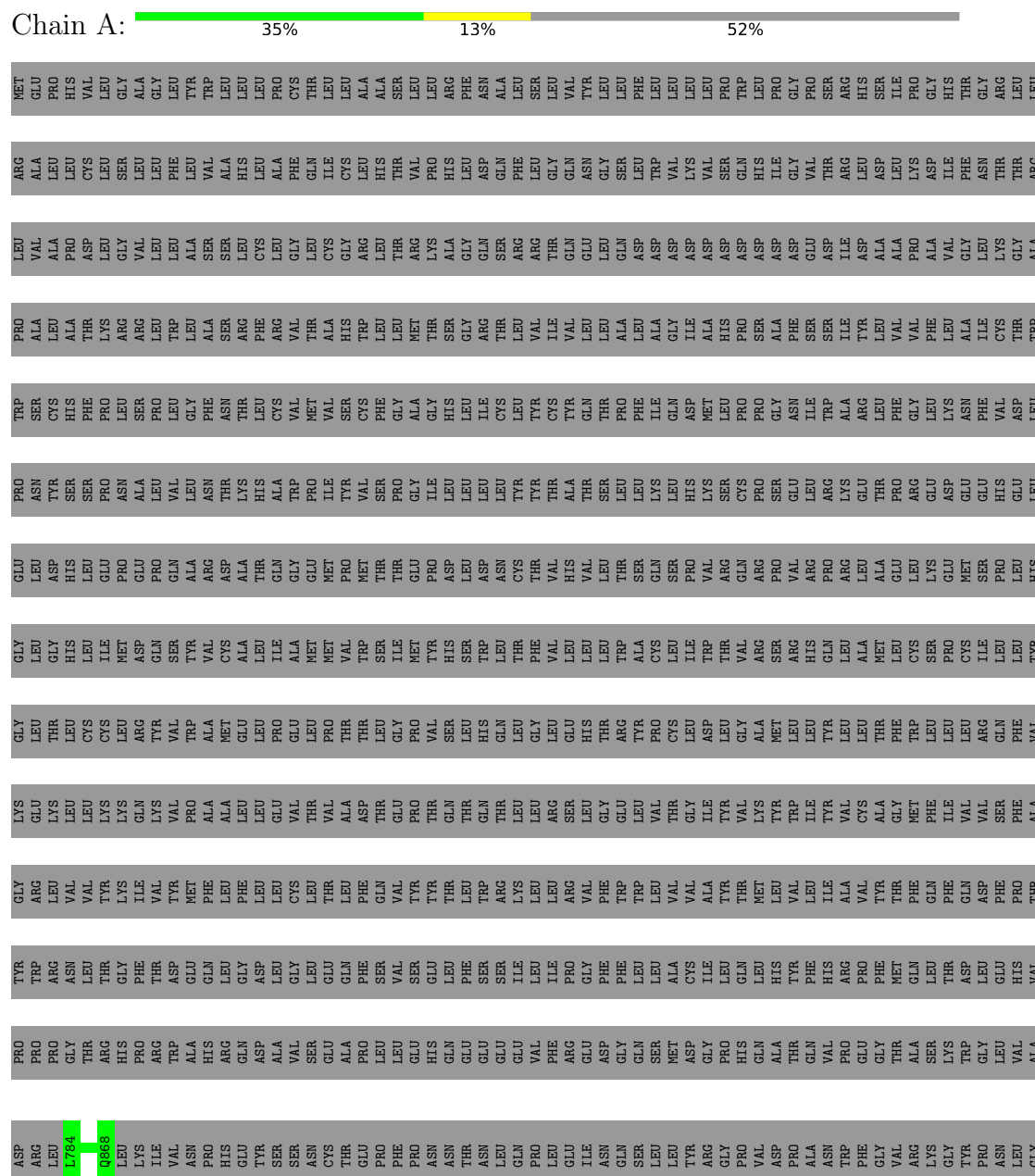
- Molecule 2 is a protein called MyoD family inhibitor domain-containing protein.

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

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. 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. 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.

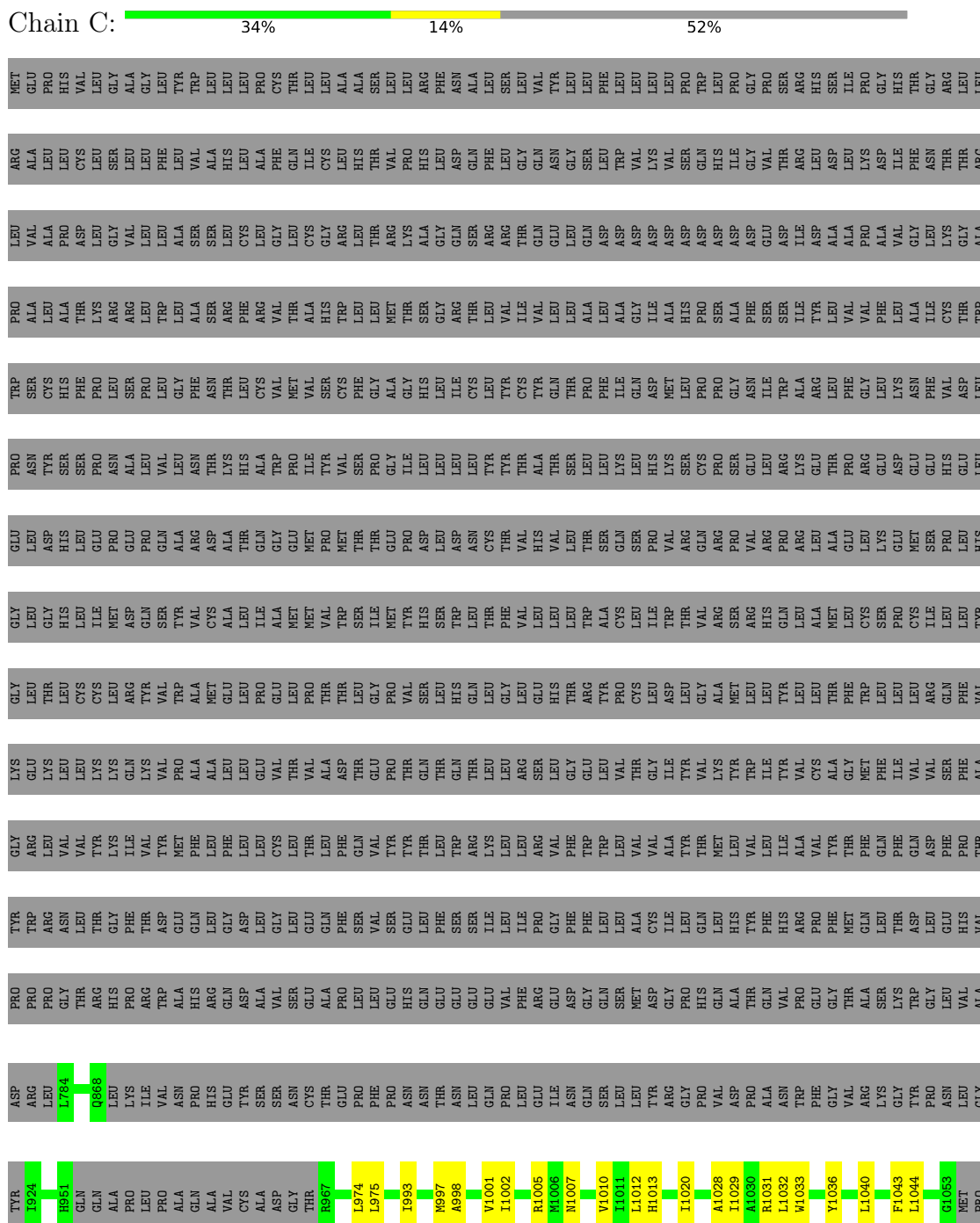
- Molecule 1: Piezo-type mechanosensitive ion channel component 1







- Molecule 1: Piezo-type mechanosensitive ion channel component 1



E2359	G2360	R2361	Q2362	P2363	S2260	M2153	L2047	ARG	HIS	VAL	F1751	ALA	PRO	GLU	PRO	L1345	VAL	L1150	PRO
G2360	F2263	D2264	P2265	Y2266	F2267	M2153	L2047	LEU	THR	LYS	F1752	ARG	THR	GLU	ALA	K1346	CYS	D1151	ALA
R2361	D2264	V2051	K2162	P2267	K2166	P1753	V2051	GLN	ARG	ASP	P1753	THR	THR	ASP	THR	R1347	THR	M1152	LEU
Q2364	Y2266	H2058	K2166	P2267	K2166	ASP	H2058	PHE	ILE	GLU	ASN	MET	SER	ARG	VAL	R1353	LYS	K1154	CYS
S2365	Y2266	H2058	K2166	P2267	K2166	THR	H2058	GLY	ALA	ALA	THR	THR	GLY	PRO	GLY	Y1359	TYR	V1165	ASP
I2368	L2268	M2061	P2178	L2268	P2178	VAL	M2061	ASN	ILE	GLU	VAL	ALA	ALA	ALA	TYR	S1365	TRP	L1166	TRP
P2369	A2269	M2061	P2178	L2268	P2178	GLN	M2061	LYS	THR	GLU	VAL	THR	GLY	GLN	ASP	S1365	ASP	F1170	TRP
H2370	M2270	E2070	K2181	L2268	P2178	PRO	E2070	PRO	PHE	GLU	ARG	ALA	ALA	ALA	GLY	GLY	TRP	I1177	TRP
L2371	Q2271	E2070	K2181	L2268	P2178	GLN	E2070	GLN	ARG	GLU	ARG	ALA	ALA	ALA	GLY	GLY	TRP	I1178	TRP
F2372	K2182	Q2075	K2182	L2268	P2178	ALA	Q2075	ALA	ARG	GLU	THR	D1651	PRO	GLU	LEU	GLN	GLY	I1179	LYS
P2373	K2183	Q2075	K2183	L2268	P2178	LEU	Q2075	LEU	LYS	LEU	THR	R1652	GLU	LEU	SER	GLN	GLY	F1180	ALA
K2374	K2184	Q2075	K2184	L2268	P2178	LEU	Q2075	LEU	GLY	LEU	THR	R1652	GLU	LEU	THR	GLN	GLY	G1181	PRO
R2377	L2186	V2078	K2186	L2268	P2178	GLN	V2078	GLN	THR	GLU	ASN	F1665	LEU	LEU	THR	GLN	GLY	G1182	PRO
E2379	E2279	A2079	K2187	L2268	P2178	PRO	A2079	PRO	GLY	GLU	LYS	F1665	LEU	LEU	THR	GLN	GLY	G1183	PRO
D2280	K2188	Q2080	K2187	L2268	P2178	GLY	Q2080	GLY	THR	GLU	THR	G1670	LEU	LEU	THR	GLN	GLY	G1184	PRO
I2281	V2189	W2082	K2188	L2268	P2178	PRO	W2082	PRO	GLY	GLU	THR	R1671	LEU	LEU	THR	GLN	GLY	Y1184	PRO
V2282	V2189	W2082	K2188	L2268	P2178	LYS	W2082	LYS	THR	GLU	THR	L1672	LEU	LEU	THR	GLN	GLY	Y1184	PRO
V2283	V2189	W2082	K2188	L2268	P2178	THR	W2082	THR	GLY	GLU	THR	L1672	LEU	LEU	THR	GLN	GLY	Y1184	PRO
E2287	E2287	A2094	K2189	L2268	P2178	ALA	A2094	ALA	VAL	GLY	THR	R1674	LEU	LEU	THR	GLN	GLY	Y1184	PRO
K2388	K2388	A2094	K2189	L2268	P2178	THR	A2094	THR	GLY	GLU	THR	R1674	LEU	LEU	THR	GLN	GLY	Y1184	PRO
L2390	L2390	A2094	K2189	L2268	P2178	GLY	A2094	GLY	THR	GLU	THR	R1674	LEU	LEU	THR	GLN	GLY	Y1184	PRO
D2393	E2394	G2291	F2209	F2209	G2291	LYS	F2209	LYS	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
E2395	A2292	F2209	F2209	F2209	G2291	THR	F2209	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
Y2398	R2295	L2296	S2211	L2210	F1988	GLY	L2296	GLY	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
L2399	I2296	S2211	L2210	F1988	G1984	THR	I2296	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
S2297	P2298	K2113	D2225	L2210	F1988	ASP	K2113	ASP	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
G2400	P2299	S2301	D2225	L2210	F1988	THR	P2299	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
V2401	S2301	R2301	D2225	L2210	F1988	ALA	S2301	ALA	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
R2402	Q2404	R2301	D2225	L2210	F1988	THR	Q2404	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
Q2404	R2405	R2301	D2225	L2210	F1988	ALA	R2405	ALA	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
R2406	R2407	R2301	D2225	L2210	F1988	THR	R2406	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
E2408	Q2409	R2301	D2225	L2210	F1988	ALA	Q2409	ALA	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
V2410	Q2411	R2301	D2225	L2210	F1988	THR	V2410	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
Q2411	Q2411	R2301	D2225	L2210	F1988	ALA	Q2411	ALA	THR	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
THR	GLY	ALA	Q2411	R2301	D2225	THR	THR	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
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GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
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GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
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GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
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GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
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GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
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GLY	ALA	Q2411	R2301	D2225	L2210	THR	GLY	THR	GLY	GLU	THR	S1687	LEU	LEU	THR	GLN	GLY	Y1184	PRO
GLY	ALA	Q2411	R																



V2447	Q2364	D2264	M2153	V2061	SER	HIS	ARG	TRP	LEU	ARG	GLU	PRO	L1345	S1250	P1141
I2448	S2365	F2265	I2162	H2058	PHE	ILE	GLU	ASN	ALA	ASP	MET	GLU	R1346	L1251	N1142
F2449	F2266	Y2267	I2162	H2058	CYS	ILE	ALA	TYR	ALA	GLY	ALA	ASP	R1347	VAL	F1143
S2450	F2267	P2267	I2162	H2058	SER	ILE	LYS	VAL	ALA	PRO	GLY	PRO	R1347	CYS	F1143
D2451	L2268	L2268	P2178	W2061	LEU	PHE	GLU	VAL	ARG	GLU	SER	ARG	R1353	THR	D1150
K2452	A2269	A2269	K2179	T2069	SER	ARG	GLU	VAL	THR	THR	HIS	PRO	R1353	VAL	D1151
V2453	W2270	W2270	G2180	E2070	ALA	ARG	PRO	LEU	ARG	ALA	ALA	ALA	Y1359	LYS	M1152
S2454	Q2271	Q2271	Q2181	Q2075	GLN	ARG	GLU	ARG	MET	SER	MET	GLN	S1365	GLY	M1153
P2373	F2272	F2272	K2182	Q2075	SER	LYS	ALA	ARG	THR	GLY	MET	ALA	S1365	TYR	K1154
K2374	L2273	L2273	K2184	Q2075	PHE	LYS	ALA	TYR	THR	GLY	GLY	SER	ARG	TYR	F1165
S2457	S2274	S2274	K2185	Q2075	TYR	GLU	LEU	GLU	ALA	LEU	ARG	ALA	GLY	ASP	F1165
R2377	P2278	P2278	K2185	Q2075	GLN	THR	GLU	ASN	GLY	GLY	VAL	PHE	GLN	PRO	F1170
A2462	E2279	E2279	I2186	Q2080	P1957	PRO	SER	LYS	L1649	ALA	LEU	GLN	LEU	LYS	F1170
P2382	D2280	D2280	V2187	Q2080	GLY	PRO	GLN	PRO	L1650	GLU	SER	MET	GLN	GLU	I1177
P2386	L2281	L2281	K2188	W2081	Y1970	LYS	GLU	TYR	D1651	GLU	THR	ALA	SER	MET	S1178
V2477	Y2189	Y2189	W2081	W2081	L1971	PRO	SER	PHE	R1652	PRO	MET	TYR	LYS	THR	I1179
F2485	W2191	W2191	G2190	Y2083	D1987	GLY	THR	F1770	F1665	LEU	PHE	GLN	ASP	THR	F1180
Q2388	T2283	T2283	M2191	Y2083	I1988	THR	GLY	L1774	F1665	SER	SER	ALA	PRO	ARG	G1181
Q2389	G2291	G2291	G2192	L2092	I1988	THR	THR	L1774	F1665	SER	THR	TRP	GLN	ASP	G1181
L2390	E2287	E2287	G2192	L2092	I1988	THR	THR	L1774	F1665	SER	THR	TRP	GLN	ASP	G1181
D2393	G2288	G2288	I2195	T2097	I1991	THR	GLY	G1775	G1670	MET	THR	VAL	ASP	ARG	L1182
E2394	S2289	S2289	I2195	T2097	I1991	THR	HIS	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2395	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
Y2398	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2403	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
Q2404	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2405	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2522	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2523	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2524	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
Q2409	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2525	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2530	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
R2534	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
S2535	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
P2536	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2537	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
T2538	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
N2539	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
I2540	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
T2543	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
R2544	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2547	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
Q2364	S2365	D2264	M2153	V2061	SER	HIS	ARG	TRP	LEU	ARG	GLU	PRO	L1345	S1250	P1141
I2368	S2365	F2265	I2162	H2058	PHE	ILE	GLU	ASN	ALA	ASP	MET	GLU	R1346	L1251	N1142
K2452	L2268	L2268	P2178	W2061	LEU	PHE	GLU	VAL	ARG	GLU	SER	ARG	R1353	THR	D1150
V2453	W2270	W2270	G2180	E2070	ALA	ARG	PRO	LEU	ARG	ALA	ALA	ALA	Y1359	LYS	M1152
S2454	Q2271	Q2271	Q2181	Q2075	GLN	ARG	GLU	ARG	MET	SER	MET	GLN	S1365	GLY	M1153
P2373	F2272	F2272	K2182	Q2075	SER	LYS	ALA	ARG	THR	GLY	MET	ALA	S1365	TYR	K1154
K2374	L2273	L2273	K2184	Q2075	PHE	LYS	ALA	TYR	THR	GLY	GLY	SER	ARG	TYR	F1165
R2377	S2274	S2274	K2185	Q2075	TYR	GLU	LEU	GLU	ALA	LEU	ARG	ALA	GLY	ASP	F1165
L2461	P2278	P2278	K2185	Q2075	GLN	THR	GLU	ASN	GLY	GLY	VAL	PHE	GLN	PRO	F1170
A2462	E2279	E2279	I2186	Q2080	P1957	PRO	SER	LYS	L1649	ALA	LEU	GLN	LEU	LYS	F1170
P2382	D2280	D2280	V2187	Q2080	GLY	PRO	GLN	PRO	L1650	GLU	SER	MET	GLN	GLU	I1177
P2386	L2281	L2281	K2188	W2081	Y1970	LYS	GLU	TYR	D1651	GLU	THR	ALA	SER	MET	S1178
V2477	Y2189	Y2189	W2081	W2081	L1971	PRO	SER	PHE	R1652	PRO	MET	TYR	LYS	THR	I1179
F2485	W2191	W2191	G2190	Y2083	D1987	GLY	THR	F1770	F1665	LEU	PHE	GLN	ASP	THR	F1180
H2490	T2283	T2283	M2191	Y2083	I1988	THR	GLY	L1774	F1665	SER	SER	ALA	PRO	ARG	G1181
S2491	G2291	G2291	G2192	L2092	I1988	THR	THR	L1774	F1665	SER	THR	TRP	GLN	ASP	G1181
L2497	E2287	E2287	G2192	L2092	I1988	THR	THR	L1774	F1665	SER	THR	TRP	GLN	ASP	G1181
L2504	G2288	G2288	I2195	T2097	I1991	THR	GLY	G1775	G1670	MET	THR	VAL	ASP	ARG	L1182
L2504	S2289	S2289	I2195	T2097	I1991	THR	HIS	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
T2516	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2519	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2520	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2521	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2522	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2523	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2524	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
Q2409	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2525	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
L2530	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
R2534	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
S2535	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
P2536	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2537	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
T2538	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
N2539	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
I2540	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
T2543	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
R2544	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
E2547	S2289	S2289	I2195	T2097	I1991	THR	GLU	G1775	R1671	THR	VAL	THR	PRO	ASP	G1183
Q2364	S2365	D2264	M2153	V2061	SER	HIS	ARG	TRP	LEU	ARG	GLU	PRO	L1345	S1250	P1141
I2368	S2365	F2265	I2162	H2058	PHE	ILE	GLU	ASN	ALA	ASP	MET	GLU	R1346	L1251	N1142
K2452	L2268	L2268	P2178	W2061	LEU	PHE	GLU	VAL	ARG	GLU	SER	ARG	R1353	THR	D1150
V2453	W2270	W2270	G2180	E2070	ALA	ARG	PRO	LEU	ARG	ALA	ALA	ALA	Y1359	LYS	M1152
S2454	Q2271	Q2271	Q2181	Q2075	GLN	ARG	GLU	ARG	MET	SER	MET	GLN	S1365	GLY	M1153
P2373	F2272	F2272	K2182	Q2075	SER	LYS	ALA	ARG	THR	GLY	MET	ALA	S1365	TYR	K1154
K2374	L2273	L2273	K2184	Q2075	PHE	LYS	ALA	TYR	THR	GLY	GLY	SER	ARG	TYR	F1165
R2377	S2274	S2274	K2185	Q2075	TYR	GLU	LEU	GLU	ALA	LEU	ARG	ALA	GLY	ASP	F1165
L2461	P2278	P2278	K2185	Q2075	GLN	THR	GLU	ASN	GLY	GLY	VAL	PHE	GLN	PRO	F1170
A2462	E2279	E2279	I2186	Q2080	P1957	PRO	SER	LYS	L1649	ALA	LEU	GLN	LEU	LYS	F1170
P2382	D2280	D2280	V2187	Q2080	GLY	PRO	GLN	PRO	L1650	GLU	SER	MET	GLN	GLU	I1177
P2386	L2281	L2281	K2188	W2081	Y1970	LYS	GLU	TYR	D1651	GLU	THR	ALA	SER	MET	S1178
V2477	Y2189	Y2189	W2081	W2081	L1971	PRO	SER	PHE	R1652	PRO	MET	TYR	LYS	THR	I1179
F2485	W2191	W2191	G2190	Y2083	D1987	GLY	THR	F1770	F1665	LEU	PHE	GLN	ASP	THR	F1180</

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

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	0.29	0/9877	0.45	1/13401 (0.0%)
1	B	0.29	0/9877	0.45	1/13401 (0.0%)
1	C	0.29	0/9877	0.45	1/13401 (0.0%)
2	D	0.24	0/151	0.45	0/200
2	E	0.24	0/151	0.45	0/200
2	F	0.24	0/151	0.45	0/200
All	All	0.29	0/30084	0.45	3/40803 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1180	PHE	N-CA-C	-6.65	107.04	114.62
1	B	1180	PHE	N-CA-C	-6.60	107.10	114.62
1	A	1180	PHE	N-CA-C	-6.59	107.11	114.62

There are no chirality outliers.

There are no planarity outliers.

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	9653	0	9495	247	0
1	B	9653	0	9495	255	0
1	C	9653	0	9495	254	0
2	D	150	0	132	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	150	0	132	7	0
2	F	150	0	132	5	0
All	All	29409	0	28881	706	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 706 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 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	1681	GLN
1	B	2364	GLN
1	C	2254	GLN
1	B	1681	GLN
1	C	2116	HIS

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](#)

There are no chain breaks in this entry.