



wwPDB EM Validation Summary Report ⓘ

Mar 12, 2026 – 02:18 PM UTC

PDB ID : 7JMJ / pdb_00007jnj
EMDB ID : EMD-22396
Title : Functional Pathways of Biomolecules Retrieved from Single-particle Snapshots
- Frame 37 - State 5 (S5)
Authors : Dashti, A.; des Georges, A.; Frank, J.; Ourmazd, A.
Deposited on : 2020-07-31
Resolution : 4.50 Å(reported)
Based on initial model : 5TB4

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:

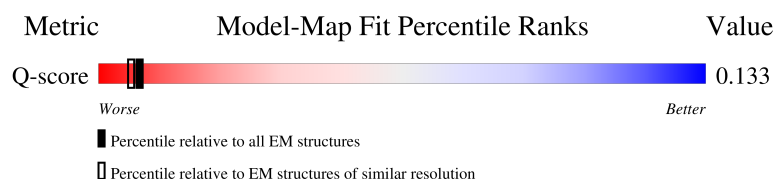
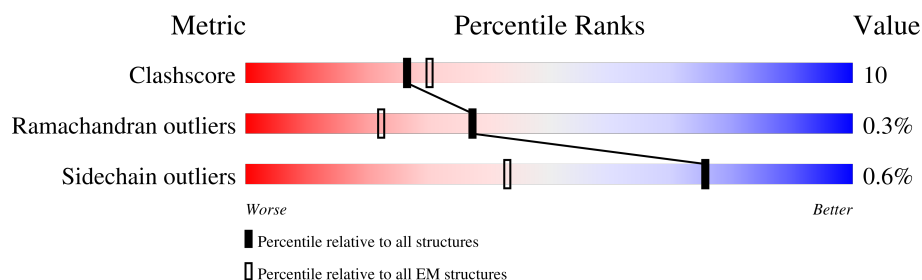
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	2937 (4.00 - 5.00)

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	107	36% 69% 30% .
1	F	107	52% 73% 26% .
1	H	107	52% 71% 28% .
1	J	107	52% 72% 26% .

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Mol	Chain	Length	Quality of chain
2	B	4687	39% 69% 19% 11%
2	E	4687	44% 70% 19% 11%
2	G	4687	49% 69% 19% 11%
2	I	4687	48% 70% 19% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 120756 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 Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	H	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	J	107	Total	C	N	O	S	0	0
			818	516	144	154	4		

- Molecule 2 is a protein called ryanodine receptor type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	E	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	G	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		
2	I	4168	Total	C	N	O	S	0	0
			29369	18608	5202	5402	157		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	B	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	
3	G	1	Total	Zn	0
			1	1	
3	I	1	Total	Zn	0
			1	1	

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest")

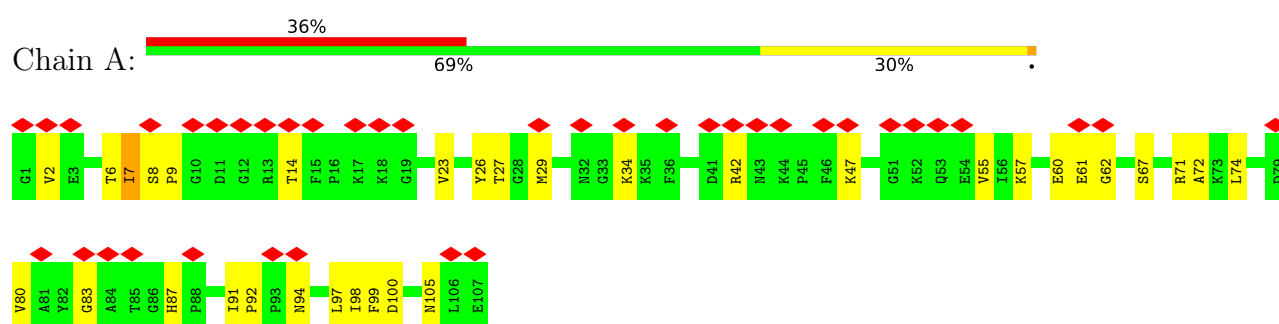
by depositor).

Mol	Chain	Residues	Atoms		AltConf
4	B	1	Total 1	Ca 1	0
4	E	1	Total 1	Ca 1	0
4	G	1	Total 1	Ca 1	0
4	I	1	Total 1	Ca 1	0

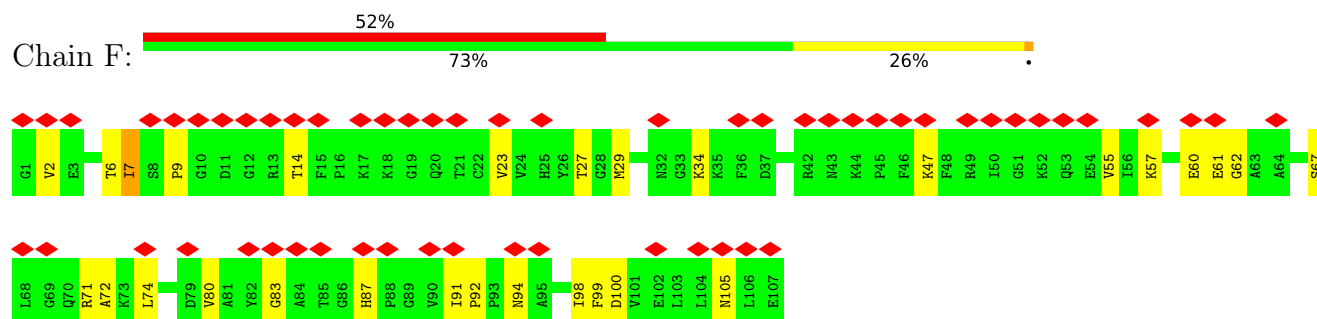
3 Residue-property plots [i](#)

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

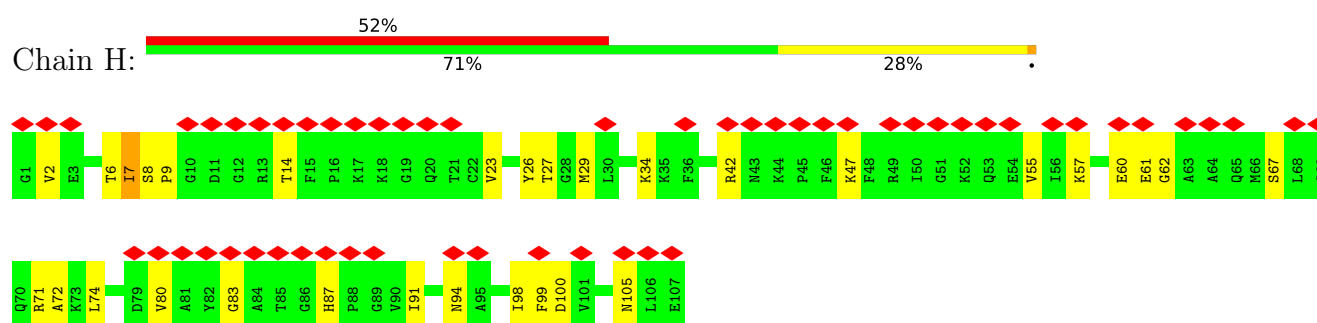
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



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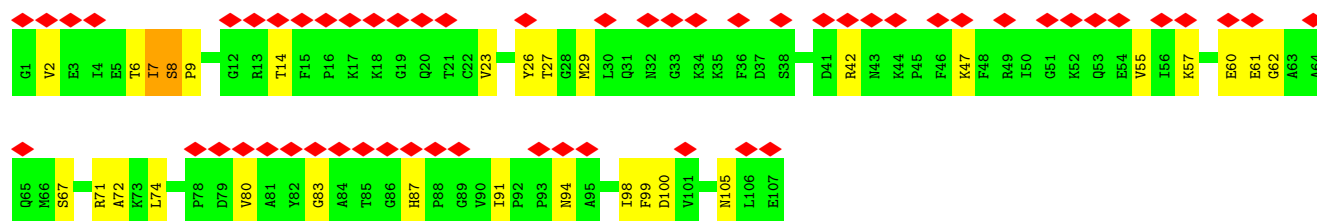


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

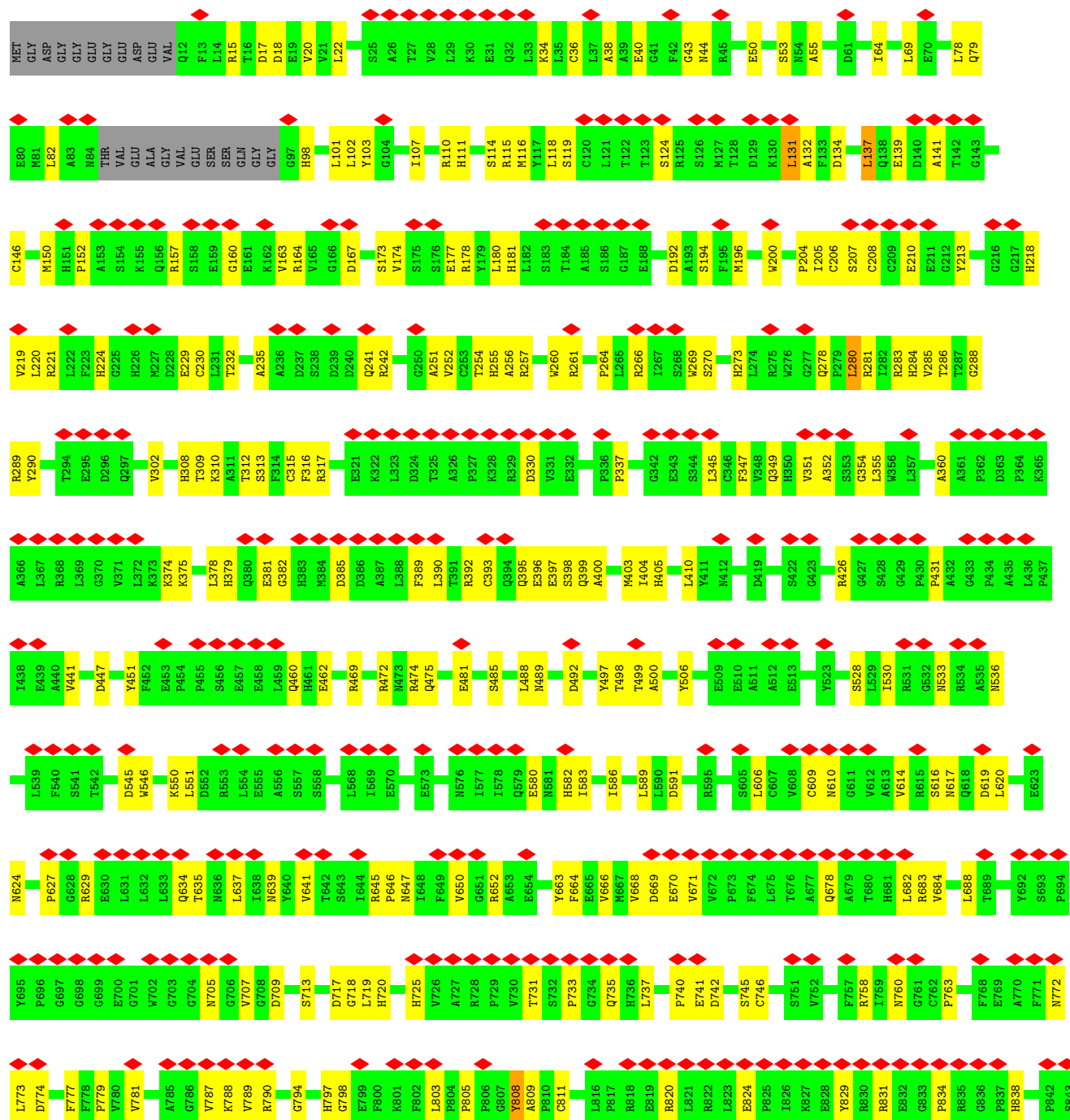
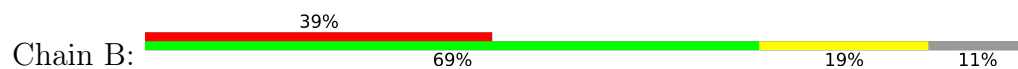


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





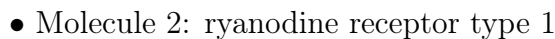
• Molecule 2: ryanodine receptor type 1



GLU	R844	R916	A980	E1054	A1117	L1202	T1263	X1514	S1606	R1671	R1743	E1817	GLU	L1922
GLU	C945	E917	Q981	PRO	D1118	N1203	V1264	X1515	R1607	L1676	F1748	D1821	GLU	E1923
GLU	L846	R918	T982	ASP	L1119	L1204	D1265	X1516	M1608	G1677	P1749	G1822	GLU	E1924
GLU	S947	N919	T983	GLN	A1121	G1205	P1268	X1519	P1609	N1678	P1750	G1823	ASP	E1925
GLU	H848	Y920	R987	PRO	V1122	Q1206	C1269	X1520	N1610	N1679	P1751	G1824	GLU	L1926
GLU	T849	Q923	R988	GLU	V1123	D1207	R1270	X1521	H1611	G1680	P1752	H1825	GLU	L1927
GLU	D850	M924	A989	GLN	F1124	V1208	L1271	X1522	F1612	N1681	R1753	A1826	GLU	L1928
GLU	F851	S925	G992	ASN	F1139	S1209	L1272	X1523	L1614	A1682	G1754	D1827	GLU	L1929
GLU	V852	G926	G992	GLU	G1140	S1210	A1273	X1524	V1615	H1683	G1755	P1829	GLU	L1930
GLU	P853	E927	A1002	GLN	R1141	L1211	X1279	X1525	GLU	D1690	M1756	V1830	GLU	L1931
GLU	D857	T928	A1003	TRP	Q1144	R1212	X1280	X1526	ARG	Q1693	L1762	G1831	GLU	L1932
GLU	THR	L929	G1004	ARG	S1145	F1213	X1281	X1527	ALA	L1694	P1763	G1832	GLU	L1933
GLU	VAL	K930	W1005	TRP	G1146	A1214	X1282	X1528	GLY	L1695	G1764	G1833	GLU	L1934
GLU	I861	L932	Y1007	D1070	D1147	F1215	X1283	X1529	E1622	H1696	P1765	E1835	GLU	L1935
GLU	V862	L933	Y1007	R1071	V1148	A1216	X1289	X1530	R1623	A1697	G1766	F1836	GLU	L1936
GLU	L863	L935	S1008	Y1073	V1149	C1217	X1290	X1531	L1624	L1698	V1767	F1837	GLU	L1937
GLU	P864	A934	A1009	I1074	V1152	G1218	X1291	X1532	G1625	L1699	G1768	F1838	GLU	L1938
GLU	P865	L935	GLN	F1075	M1152	L1219	X1292	X1533	W1626	A1701	L1771	V1839	GLU	L1939
GLU	H866	C937	ASP	R1076	I1153	Q1220	X1293	X1534	ARG	H1702	R1772	P1840	GLU	L1940
GLU	E868	H938	ILE	A1077	F1162	G1222	X1294	X1543	ALA	L1703	P1773	V1841	GLU	L1941
GLU	R869	V939	PRO	E1078	T1163	F1223	X1430	X1544	GLY	P1704	G1774	L1842	GLU	L1942
GLU	I870	G940	ALA	K1079	L1164	E1224	X1440	X1545	GLY	L1707	H1775	K1843	GLU	L1943
GLU	N877	M941	ARG	S1080	T1165	F1225	X1441	X1546	GLY	A1708	H1776	L1844	GLU	L1944
GLU	I878	A942	ASN	Y1081	V1168	A1226	X1442	X1547	GLY	G1709	G1777	L1845	GLU	L1945
GLU	H879	E944	PRO	T1082	L1169	L1228	X1443	X1548	E1643	G1710	F1778	K1852	GLU	L1946
GLU	E880	K945	Y1024	Q1084	M1170	N1229	X1444	X1549	E1644	L1712	P1779	F1853	GLU	L1947
GLU	L881	A946	R1025	S1085	S1171	Q1231	X1445	X1550	E1645	D1713	G1780	F1854	GLU	L1948
GLU	L884	E947	D1028	W1088	D1172	P1233	X1449	X1551	R1646	L1717	C1781	G1855	GLU	L1949
GLU	T885	E947	E1029	Y1089	G1174	N1234	X1450	X1552	M1648	I1718	F1782	G1856	GLU	L1950
GLU	R886	N949	A1030	E1091	S1175	T1235	X1451	X1553	D1649	H1719	A1784	D1858	GLU	L1951
GLU	I887	L950	T1031	F1092	E1176	L1238	X1452	X1554	L1650	L1720	A1785	V1859	GLU	L1952
GLU	E888	K951	K1032	E1093	R1180	F1239	X1453	X1577	R1647	E1721	L1786	I1862	GLU	L1953
GLU	Q889	K952	S1034	A1094	E1181	X1240	X1454	X1578	C1647	S1722	P1787	M1865	GLU	L1954
GLU	G890	T953	N1035	V1095	I1182	L1242	X1455	X1579	M1648	R1725	ALA	I1866	GLU	L1955
GLU	W891	K954	R1036	T1096	E1183	P1243	X1469	X1580	D1649	R1726	GLY	M1867	GLU	L1956
GLU	T892	L955	D1037	L1097	I1184	Q1244	X1470	X1581	L1651	R1727	VAL	F1867	GLU	L1957
GLU	Y893	P956	S1038	R1101	G1185	F1245	X1471	X1582	L1652	S1728	ALA	E1874	GLU	L1958
GLU	G894	K957	L1039	V1102	D1186	E1246	X1472	X1583	L1653	M1730	E1793	T1872	GLU	L1959
GLU	P895	T958	Q1041	G1103	G1187	P1247	X1473	X1584	E1654	L1731	A1794	E1873	GLU	L1960
GLU	V896	Y959	A1042	W1104	F1188	P1248	X1474	X1585	R1656	S1732	P1795	E1874	GLU	L1961
GLU	R897	M960	V1043	L1105	L1189	V1248	X1475	X1586	L1657	L1735	A1796	GLU	GLU	L1962
GLU	D898	M961	V1043	P1106	L1190	P1249	X1498	X1587	L1657	R1736	GLU	GLU	GLU	L1963
GLU	D899	S962	T1044	P1107	P1190	P1250	X1499	X1588	D1658	P1737	GLU	GLU	GLU	L1964
GLU	N900	N963	T1045	E1108	V1191	E1251	X1500	X1589	L1659	L1738	GLU	GLU	GLU	L1965
GLU	K901	G964	L1046	L1109	C1192	H1252	X1504	X1590	L1660	T1739	GLU	GLU	GLU	L1966
GLU	R902	A968	L1047	R1110	S1193	P1253	X1505	X1591	R1661	I1736	L1802	GLU	GLU	L1967
GLU	L903	D971	G1048	D1112	P1196	P1254	X1506	X1592	L1662	P1737	P1803	GLU	GLU	L1968
GLU	H904	L972	Y1049	V1113	Q1197	H1255	X1507	X1593	S1663	L1738	L1804	GLU	GLU	L1969
GLU	P905	S973	G1050	E1114	G1198	E1256	X1508	X1594	H1665	T1739	E1805	GLU	GLU	L1970
GLU	H911	H974	L1115	G1116	V1199	V1257	X1509	X1595	T1666	P1740	A1806	GLU	GLU	L1971
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GLU	E915	T978											GLU	L1975
GLU	P916	P979											GLU	L1976
GLU	E917												GLU	L1977
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GLU	Q923												GLU	L1981
GLU	M924												GLU	L1982
GLU	S925												GLU	L1983
GLU	G926												GLU	L1984
GLU	E927												GLU	L1985
GLU	T928												GLU	L1986
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GLU	T931												GLU	L1989
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GLU	T885												GLU	L2005
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GLU	S925												GLU	L2038
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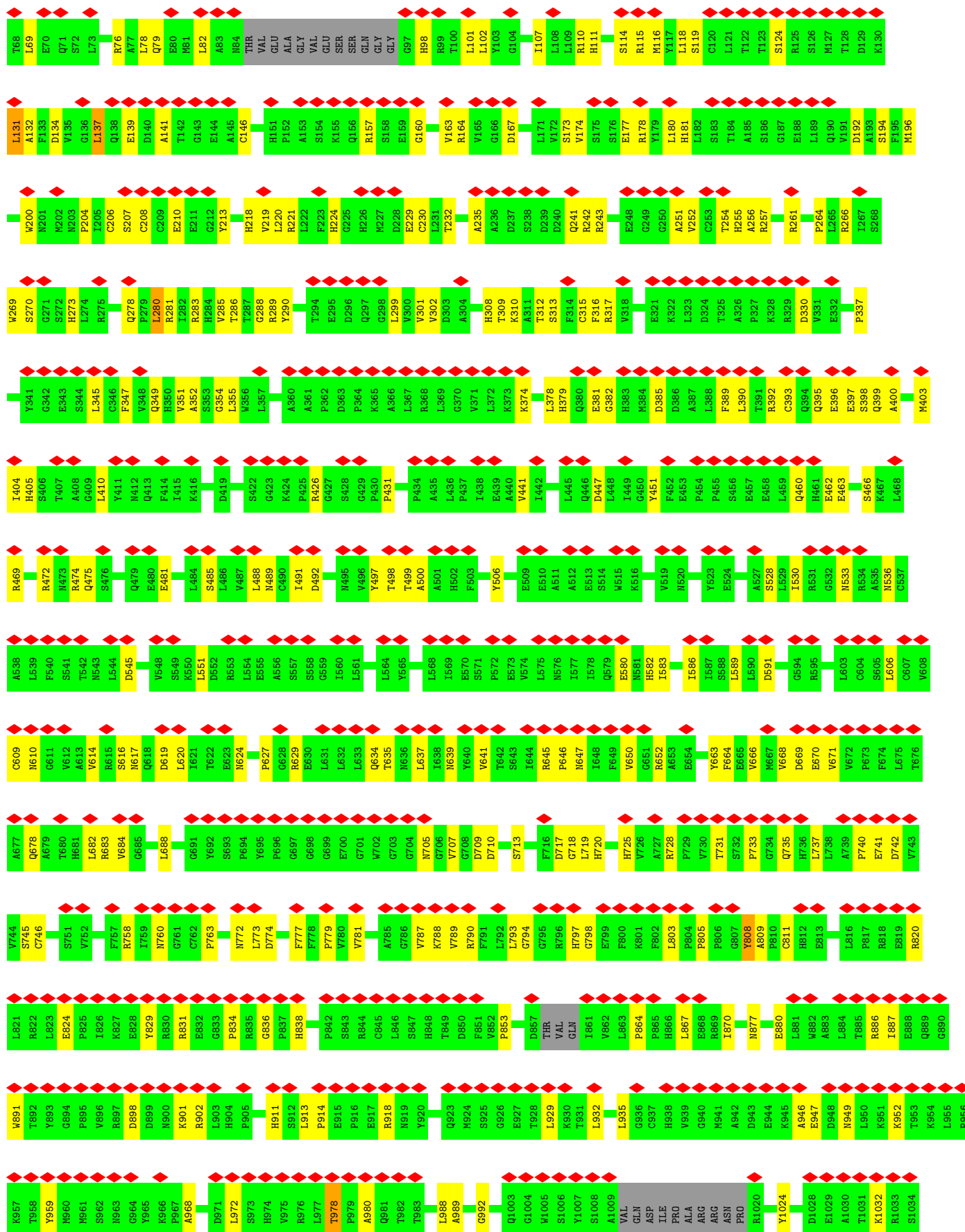






Category	Percentage
Very bad	44%
Bad	70%
Good	19%
Very good	11%







X3138	X3139	X3140	X3143	X3158	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3177	X3186	X3187	X3188	X3189	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3200	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3229	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252									
X2959	X2964	X2965	X2968	X2971	X2972	X2975	X2976	X2995	X2996	X3001	X3009	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3026	X3027	X3028	X3032	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3056	X3057	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137												
L2894	E2895	A2896	K2897	G2898	G2900	T2901	H2902	P2903	L2904	L2905	P2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	D2918	X2919	R2920	E2921	A2922	Q2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2956			
THR	GLU	LYS	LYS	THR	LYS	SER	GLN	THR	GLN	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	L2883	T2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893			
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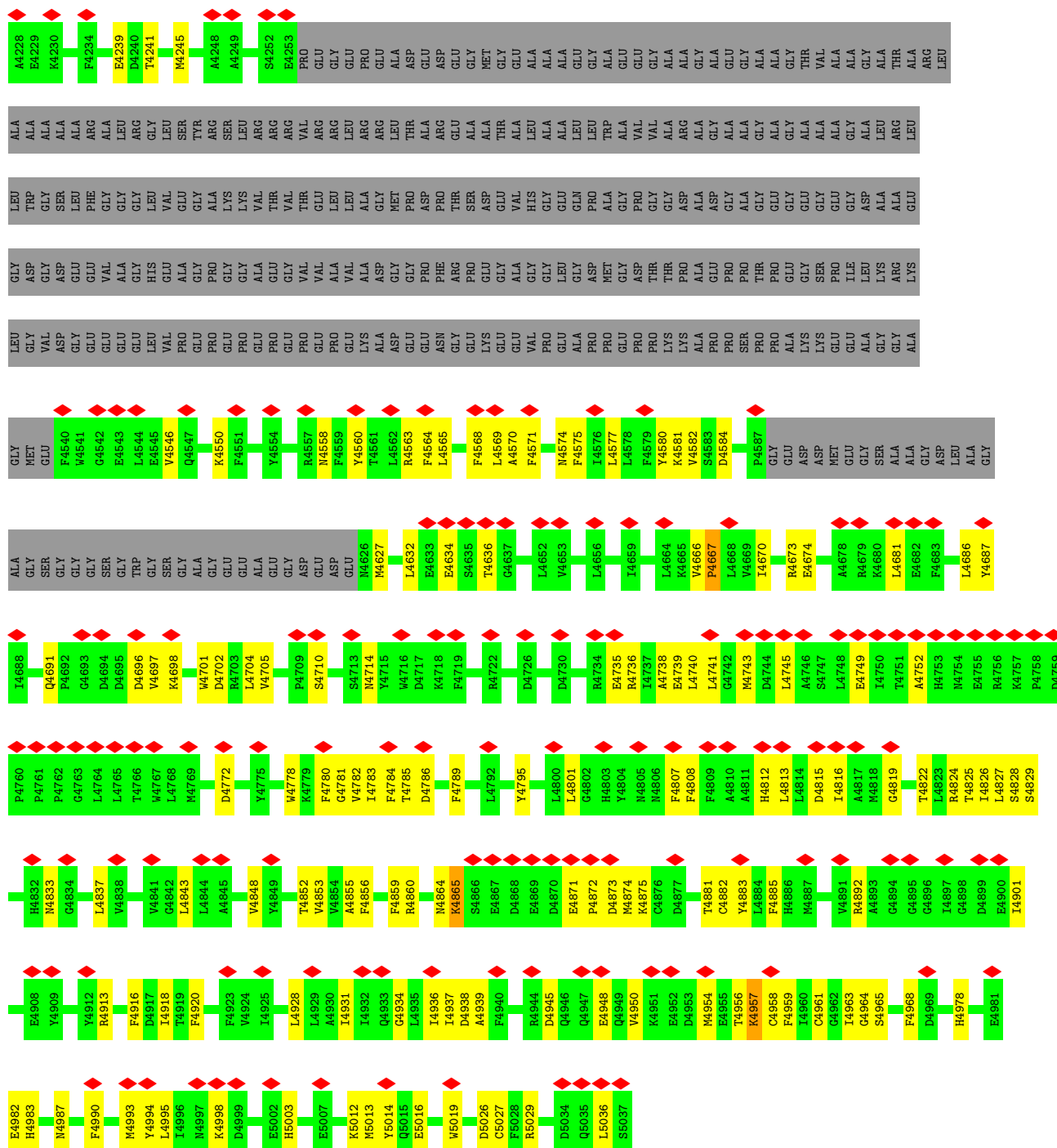
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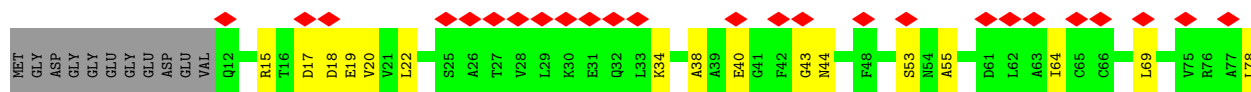
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GLU	L2009	L1804	E1873	L1804	P1740	G1677	H1611		X1447	Q1244	I1182	V1102
LEU	L2010	E1805	E1874	E1806	R1743	N1678	F1612	X1539	X1448	F1245	E1183	G1103
PRO	H2011	A1806	GLU	A1807	A1744	N1679	L1613	X1540	X1449	E1246	G1184	W1104
ALA	F2012	R1808	GLU	L1745	I1746	M1680	Q1614	X1541	X1450	P1247	G1185	A1105
GLU	K2013		GLU	T1746	T1747	V1681	V1615	X1542	X1451	V1248	D1186	A1106
GLU			GLU	L1747	F1748	A1682	THR	X1543	X1452	P1249	L1189	P1107
GLU	A2016	A1811	GLU	F1748	P1749	ARG	ARG	X1544	X1453	P1250	P1190	E1108
GLU	D2017	L1812	GLU	P1749	P1750	ALA	ALA	X1545	X1454	E1251	V1191	L1109
GLU	E2018	L1813	GLU	P1750	G1751	S1687	GLY	X1546	X1455	H1252	C1192	R1110
GLU	D2020	L1814	GLU	G1751	R1752	D1690	E1622	X1547	X1461		L1189	P1111
GLU	D2021	L1815	GLU	R1752	K1753	Q1691	R1623	X1548	X1471		P1190	D1112
GLU	C2022	E1817	GLU	K1753	G1754	G1692	L1624	X1549	X1472		V1191	W1113
GLU	L2023	A1818	GLU	G1754	G1755	Q1693	G1625	X1550	X1473		P1196	E1114
GLU	P2024	R1819	GLU	G1755	M1756	L1694	W1626	X1551			G1197	L1115
GLU	E2025	D1821	GLU	M1756	A1757	L1695	A1627	X1552	X1488		Q1198	G1116
GLU	D2026	G1822	GLU	A1757	R1758	H1696	V1628	X1553	X1489		W1199	A1117
GLU	R2028	Q1823	GLU	R1758	L1762	A1697	Q1629		X1490		H1201	E1119
GLU	C2042	H1825	GLU	L1762	P1763	L1698	C1630	X1559	X1491		L1202	L1120
GLU	G2043	A1826	GLU	P1763	G1764	E1699	Q1631	X1560	X1492		N1203	A1121
GLU	I2044	R1827	GLU	G1764	V1765	D1700	D1632	X1561	X1497		L1204	W1122
GLU	Q2045	D1828	GLU	V1765	G1766	A1701	P1633	X1562	X1498		G1205	V1123
GLU	L2046	P1829	GLU	G1766	V1767	H1702	L1634	X1563	X1499		Q1206	F1124
GLU	E2047	V1830	GLU	V1767	T1768	L1703	T1635	X1564	X1500		D1207	M1125
GLU	G2048		GLU	T1768		P1704	M1636	X1573	X1501		C1269	F1139
GLU		E1835	GLU			G1705	M1637	X1574	X1502		S1208	G1140
GLU		F1836	GLU			P1706	L1638		X1503		S1209	R1141
GLU		Q1837	GLU			L1707	L1639		X1504		L1211	
GLU		V1839	GLU			R1708	H1640		X1505		R1212	
GLU		P1840	GLU			A1709	E1643		X1506		F1213	Q1144
GLU		V1841	GLU			G1710	E1644		X1507		F1214	S1145
GLU		L1842	GLU			Y1711	M1645		X1508		A1215	G1146
GLU		K1843	GLU			Y1712	C1647		X1511		I1216	D1147
GLU		L1844	GLU			D1713	M1648		X1512		C1217	V1148
GLU			ALA				D1649		X1513		G1218	W1149
PRO			PRO				I1650		X1514		L1219	M1152
GLU			GLU				T1651		X1515		Q1220	L1153
GLU			GLU				L1652		X1516		E1221	D1154
GLU			GLU				L1653		X1517		G1222	L1155
GLU			GLU				S1654		X1518		F1223	T1156
GLU			GLU				E1655		X1519		E1224	E1157
GLU			GLU				R1656		X1520		P1225	M1158
GLU			GLU				L1657		X1521		A1227	
GLU			GLU				D1658		X1522		I1228	
GLU			GLU				L1659		X1523		N1229	
GLU			GLU				Q1660		X1524		M1230	
GLU			GLU				H1663		X1525		Q1231	
GLU			GLU				S1664		X1526		P1232	
GLU			GLU				H1665		X1527		V1234	
GLU			GLU				T1666		X1528		T1235	
GLU			GLU				L1667		X1529		F1238	
GLU			GLU				R1668		X1530		S1239	
GLU			GLU				L1669		X1531		K1240	
GLU			GLU				Y1670		X1532		S1241	
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GLU												

X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3054	X3055	X3056	X3057	X3060	X3061	X3062	X3063	X3064	X3065	X3066	X3067	X3068	X3071	X3072	X3073	X3074	X3075	X3076	X3077	X3078	X3079	X3080	X3081	X3082	X3083	X3084	X3085	X3086	X3087	X3088	X3089	X3090	X3091	X3092	X3093	X3094	X3095	X3096	X3097	X3098	X3001	X3009	X3012	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3028	X3029	X3030	X3031	X3032	X3035	X3036	X3037	X3038	X3045	X3213	X3214	X3215	X3216																															
G2148	V2149	D2150	D2151	T2152	H2153	S2154	L2155	L2156	L2159	L2162	R2163	S2164	L2165	L2166	L2167	V2168	Q2169	H2170	H2176	L2179	Q2180	G2183	H2184	L2185	H2186	L2187	H2188	K2189	V2190	F2191	V2192	Q2193	H2194	F2195	H2196	L2197	H2198	R2199	H2203	H2204	E2205	T2206	V2207	H2208	E2209	V2210	H2211	V2212	H2213	V2214	L2215	G2216	G2217	G2218	E2219	T2220	K2221	L2286	E2222	L2223	P2226	K2227	H2228	V2229	S2231	R2234	F2235	L2236	G2237	F2238	C2240	R2241	L2242	S2243	R2244	Q2245	Q2246	Q2247	F2251	L2252	H2253	L2254	S2255	L2256	L2257	L2258	E2259	N2260	S2261	G2262	L2263	G2264	L2265	G2266	M2267	Q2268	G2269	S2270	T2271	P2272	L2273	D2274	V2275	A2276	A2277	A2278	L2281	V2354	R2355
D2282	H2283	N2284	E2285	L2286	A2287	L2288	A2289	L2290	Q2291	E2292	Q2293	D2294	L2295	E2296	K2297	V2298	V2299	L2302	A2303	G2304	C2305	G2306	L2307	C2310	P2311	M2312	L2313	L2314	Y2318	P2319	D2320	L2321	G2322	E2329	R2330	L2335	R2336	V2339	F2340	V2341	N2342	G2343	E2344	S2345	V2346	E2347	E2348	N2349	A2350	N2351	V2354	R2355																																																									
L2356	L2357	L2358	R2359	K2360	F2361	E2362	C2363	F2364	G2365	L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	E2381	E2382	A2383	L2384	R2385	E2388	L2389	P2390	A2391	P2395	GLY	VAL	ARG	ARG	ASP	ARG	GLU	HIS	PHE	GLY	GLU	PRO	PRO	GLU	GLU	N2414	L2422	Y2426	A2427	A2428																																																											
L2429	L2430	D2431	L2432	L2433	G2434	R2435	C2436	A2437	M2440	H2441	L2442	L2443	Q2444	A2445	G2446	K2447	G2448	E2449	A2450	L2451	L2452	R2453	R2454	A2455	L2456	L2457	R2458	S2459	L2460	V2461	L2462	L2463	D2464	L2465	L2466	V2467	G2468	L2469	L2470	S2471	L2472	P2473	L2474	Q2475	L2476	P2477	T2478	L2479	X2487	X2488	X2499	X2500	X2501	X2502	X2503	X2506																																																					
X2507	X2508	X2509	X2510	X2511	X2512	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520	X2521	X2522	X2525	X2526	X2533	X2534	X2535	X2536	X2537	X2544	X2545	X2548	X2555	X2556	X2557	X2558	X2559	X2560	X2561	X2562	X2563	X2564	X2565	X2566	X2572	X2580	X2583	X2584	X2585	X2586	X2587	X2588	X2591	X2592	X2598	X2599																																																												
X2602	X2603	X2604	X2605	X2606	X2607	X2608	X2609	X2610	X2611	X2612	X2613	X2614	X2615	X2616	X2617	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2627	X2628	X2629	X2632	X2641	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2665	X2666	X2669	X2673																																																									
X2674	X2675	X2676	X2677	X2678	X2679	X2682	X2683	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	F2735	D2736	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	L2746	L2747	P2748	E2749	K2750	L2751	D2752	S2753	F2754	L2755	N2756	K2757	F2758	E2759	L2760	Y2761	T2762	H2763	E2764	K2765																																																					
W2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773	N2774	S2776	V2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	V2794	K2795	L2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	L2805	R2806	V2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	N2818	N2819	E2820	N2821	T2822	L2823	E2824	K2825																																																			
A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	THR	L2894	L2895	A2896	K2897	G2898	G2899	ILE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	F2860	L2861	S2862	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885																																																			
W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	L2916	A2917	D2918	R2919	R2920	E2921	L2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	Y2947																																																		
X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2961	X2964	X2965	X2966	X2967	X2968	X2971	X2972	X2973	X2974	X2975	X2976	X2977	X2978	X2979	X2980	X2981	X2982	X2983	X2984	X2985	X2986	X2987	X2988	X2989	X2990	X2991	X2992	X2993	X2994	X2995	X2996	X2997	X2998	X3001	X3009	X3012	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3028	X3029	X3030	X3031	X3032	X3035	X3036	X3037	X3038	X3045																																									
X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3054	X3055	X3056	X3057	X3060	X3061	X3062	X3063	X3064	X3065	X3066	X3067	X3068	X3071	X3072	X3073	X3074	X3075	X3076	X3077	X3078	X3079	X3080	X3081	X3082	X3083	X3084	X3085	X3086	X3087	X3088	X3089	X3090	X3091	X3092	X3093	X3094	X3095	X3096	X3097	X3098	X3001	X3009	X3012	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3028	X3029	X3030	X3031	X3032	X3035	X3036	X3037	X3038	X3045	X3213	X3214	X3215	X3216																															





• Molecule 2: ryanodine receptor type 1







X2975	X2976	X2995	X2996	X2997	X2998	X3001	X3002	X3003	X3004	X3010	X3011	X3012	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3026	X3027	X3028	X3031	X3032	X3035	X3038	X3041	X3045	X3046	X3047	X3048	X3049	X3050	X3053	X3056	X3057	X3058	X3059	X3060	X3061	X3062	X3063	X3134	X3135									
P2903	L2904	L2905	V2906	P2907	V2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	R2932	N2933	Q2934	V2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	X2950	X2951	X2952	X2953	X2954	X2955	X2956	X2961	X2964	X2965	X2968					
SER	GLN	THR	ALA	GLN	THR	TVR	ASP	PRO	ARG	GLU	GLY	N2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	A2876	Q2877	L2878	A2879	E2880	N2881	H2882	H2883	N2884	T2885	V2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	A2895	A2896	K2897	G2898	G2899	T2900	T2901	H2902
E2783	E2784	L2785	K2786	L2787	H2788	P2789	M2790	L2791	L2792	P2793	V2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	T2805	R2806	P2807	L2808	I2809	K2810	E2811	L2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	E2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS	THR	ARG	LYS	ILE
X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	N2735	D2736	P2737	R2738	V2739	E2741	T2742	L2743	N2744	V2745	L2746	I2747	T2748	E2749	K2750	L2751	D2752	S2753	F2754	L2755	N2756	K2757	F2758	A2759	E2760	Y2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	I2771	Q2772	N2773	N2774	W2775	S2776	Y2777	G2778	E2779	N2780	V2781	D2782	
X2613	X2614	X2615	X2616	X2617	X2618	X2619	X2620	X2621	X2622	X2623	X2624	X2625	X2626	X2629	X2632	X2641	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2662	X2666	X2669	X2673	X2674	X2675	X2676	X2677	X2678	X2683	X2686	X2687	X2688	X2689	X2690	X2691	X2692										
X2521	X2522	X2523	E2524	X2525	X2526	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2544	X2545	X2548	X2551	X2552	X2553	X2554	X2555	X2556	X2557	X2558	X2559	X2560	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2583	X2584	X2585	X2586	X2589	X2594	X2598	X2603	X2604	X2605	X2606	X2607	X2608	X2609	X2610	X2611	X2612							
G2446	K2447	G2448	E2449	A2450	L2451	R2452	L2453	R2454	A2455	L2456	L2457	R2458	S2459	L2460	V2461	P2462	L2463	D2464	D2465	L2466	V2467	G2468	L2469	L2470	S2471	L2472	P2473	Q2475	T2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2499	X2500	X2501	X2502	X2503	X2506	X2507	X2508	X2509	X2510	X2511	X2512	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520			
G2373	S2374	G2375	L2376	L2377	A2378	E2381	E2382	A2383	I2384	R2385	E2388	D2389	P2390	A2391	R2392	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	N2414	M2423	A2427	A2428	L2429	L2430	L2433	G2434	R2435	G2436	A2437	P2438	E2439	M2440	H2441	L2442	L2443	Q2444	A2445								
V2298	V2299	S2300	Y2301	L2302	A2303	G2304	C2305	G2306	L2307	M2312	L2313	L2314	A2315	Y2318	P2319	D2320	L2321	G2322	R2330	L2331	L2332	L2335	R2336	V2339	F2340	N2341	N2342	G2343	E2344	S2345	V2346	E2347	E2348	N2349	A2350	N2351	V2354	R2355	L2356	L2357	L2358	R2359	K2360	P2361	E2362	G2363	F2364	L2368	R2369	G2370	E2371	G2372							
L2236	G2237	Y2238	F2239	C2240	R2241	L2242	S2243	R2244	Q2245	N2246	Q2247	R2248	F2251	D2252	H2253	L2254	S2255	L2256	L2257	L2258	E2259	N2260	S2261	Q2262	L2263	Q2264	L2265	Q2266	M2267	Q2268	G2269	S2270	T2271	P2272	L2273	D2274	V2275	A2276	S2279	V2280	L2281	D2282	N2283	L2284	E2285	L2286	A2287	L2288	A2289	L2290	Q2291	F2292	Q2293	D2294	L2295	E2296	K2297		
R2104	W2105	A2106	Q2107	V2110	W2111	Q2112	S2113	P2114	E2115	L2116	W2117	R2118	A2119	M2120	F2121	S2122	L2123	L2124	H2125	R2126	Q2127	V2128	D2129	G2130	L2131	G2132	L2135	R2136	A2137	L2138	E2209	P2139	R2140	A2141	L2142	T2143	L2144	S2145	P2146	S2147	S2148	V2149	T2152	R2153	S2154	L2155	L2156	L2159	T2162	R2163	S2164	L2165	L2166	T2167	V2168				
Q2169	M2170	G2171	P2172	N2176	I2179	Q2180	N2184	I2185	M2186	N2187	N2188	K2189	F2191	Y2192	Q2193	H2194	P2195	N2196	L2197	M2198	R2199	M2203	H2204	E2205	T2206	V2207	M2208	E2209	V2210	M2211	V2212	N2213	V2214	L2215	G2216	G2217	G2218	E2219	T2220	K2221	E2222	I2223	R2224	F2225	P2226	K2227	M2228	V2229	T2230	S2231	C2232	C2233	R2234	F2235					





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	791956	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.466	Depositor
Minimum map value	-0.266	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.16	Depositor
Map size (Å)	502.0, 502.0, 502.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.255, 1.255, 1.255	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.27	0/834	0.64	3/1123 (0.3%)
1	F	0.27	0/834	0.64	2/1123 (0.2%)
1	H	0.27	0/834	0.63	3/1123 (0.3%)
1	J	0.27	0/834	0.64	3/1123 (0.3%)
2	B	0.36	0/25428	0.67	1/34534 (0.0%)
2	E	0.36	0/25428	0.67	1/34534 (0.0%)
2	G	0.36	0/25428	0.67	1/34534 (0.0%)
2	I	0.36	0/25428	0.67	1/34534 (0.0%)
All	All	0.36	0/105048	0.67	15/142628 (0.0%)

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
2	B	0	19
2	E	0	19
2	G	0	19
2	I	0	20
All	All	0	77

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	4872	PRO	N-CA-C	-6.67	104.64	113.65
2	B	4872	PRO	N-CA-C	-6.62	104.72	113.65
2	G	4872	PRO	N-CA-C	-6.46	104.55	113.53
2	I	4872	PRO	N-CA-C	-6.39	104.65	113.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	7	ILE	CA-C-N	5.92	128.40	120.58

There are no chirality outliers.

5 of 77 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	137	LEU	Peptide
2	B	1676	LEU	Peptide
2	B	1690	ASP	Peptide
2	B	1712	TYR	Peptide
2	B	808	TYR	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	818	0	824	21	0
1	F	818	0	824	19	0
1	H	818	0	824	19	0
1	J	818	0	824	20	0
2	B	29369	0	24716	551	0
2	E	29369	0	24712	538	0
2	G	29369	0	24713	551	0
2	I	29369	0	24713	546	0
3	B	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
4	B	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	I	1	0	0	0	0
All	All	120756	0	102150	2235	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 10.

The worst 5 of 2235 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)
2:G:4860:ARG:HD2	2:I:4582:VAL:HG11	1.65	0.79
2:B:853:PRO:HB3	2:B:1024:TYR:H	1.51	0.76
2:B:379:HIS:HD2	2:B:382:GLY:H	1.35	0.75
2:I:853:PRO:HB3	2:I:1024:TYR:H	1.51	0.75
2:E:853:PRO:HB3	2:E:1024:TYR:H	1.51	0.75

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	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	F	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	H	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
1	J	105/107 (98%)	95 (90%)	10 (10%)	0	100	100
2	B	3235/4687 (69%)	2859 (88%)	367 (11%)	9 (0%)	36	71
2	E	3235/4687 (69%)	2860 (88%)	367 (11%)	8 (0%)	43	77
2	G	3235/4687 (69%)	2859 (88%)	367 (11%)	9 (0%)	36	71
2	I	3235/4687 (69%)	2860 (88%)	366 (11%)	9 (0%)	36	71
All	All	13360/19176 (70%)	11818 (88%)	1507 (11%)	35 (0%)	37	71

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	3772	THR
2	B	4667	PRO
2	E	3772	THR
2	E	4667	PRO

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Mol	Chain	Res	Type
2	G	3772	THR

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	88/88 (100%)	88 (100%)	0	100	100
1	F	88/88 (100%)	88 (100%)	0	100	100
1	H	88/88 (100%)	88 (100%)	0	100	100
1	J	88/88 (100%)	88 (100%)	0	100	100
2	B	2493/3209 (78%)	2477 (99%)	16 (1%)	78	80
2	E	2493/3209 (78%)	2477 (99%)	16 (1%)	78	80
2	G	2493/3209 (78%)	2477 (99%)	16 (1%)	78	80
2	I	2493/3209 (78%)	2477 (99%)	16 (1%)	78	80
All	All	10324/13188 (78%)	10260 (99%)	64 (1%)	76	80

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	4059	LEU
2	I	4180	ARG
2	E	3896	ASN
2	E	3805	LEU
2	I	4871	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 240 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	4209	GLN
2	I	3889	GLN
2	G	1035	ASN
2	I	3814	GLN

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Mol	Chain	Res	Type
2	I	4728	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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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
2	G	12
2	I	12

Continued on next page...

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Mol	Chain	Number of breaks
2	B	12
2	E	12

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	3613:UNK	C	3639:THR	N	44.11
1	I	3613:UNK	C	3639:THR	N	44.00
1	B	3613:UNK	C	3639:THR	N	43.94
1	E	3613:UNK	C	3639:THR	N	43.92
1	B	3163:UNK	C	3170:UNK	N	16.36

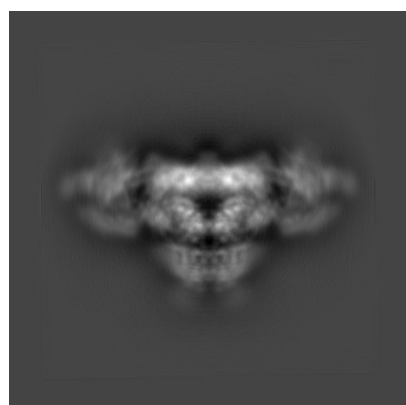
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22396. These allow visual inspection of the internal detail of the map and identification of artifacts.

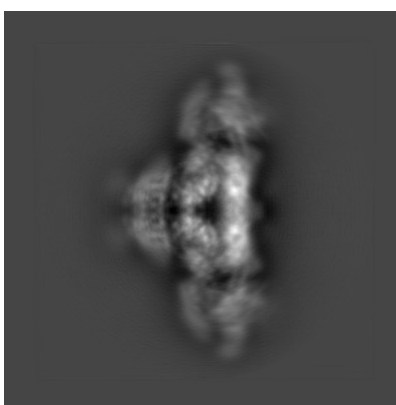
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

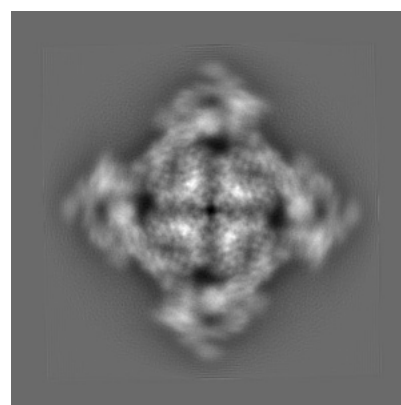
6.1.1 Primary map



X



Y

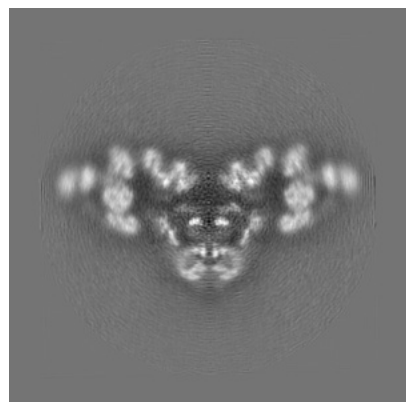


Z

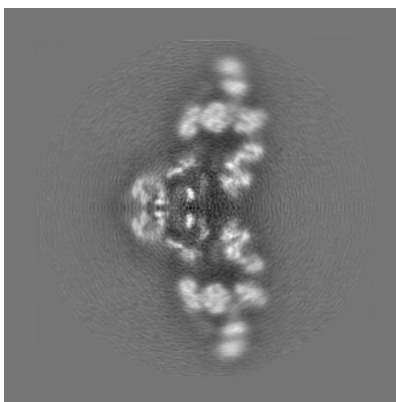
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

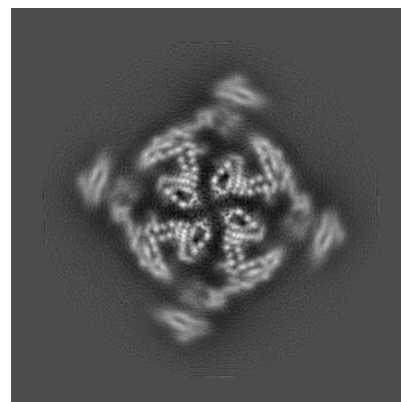
6.2.1 Primary map



X Index: 200



Y Index: 200

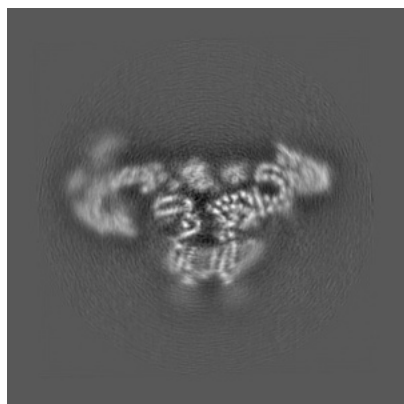


Z Index: 200

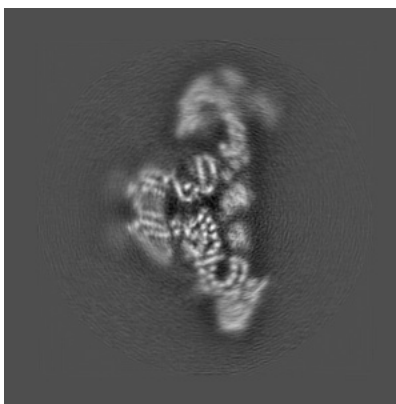
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

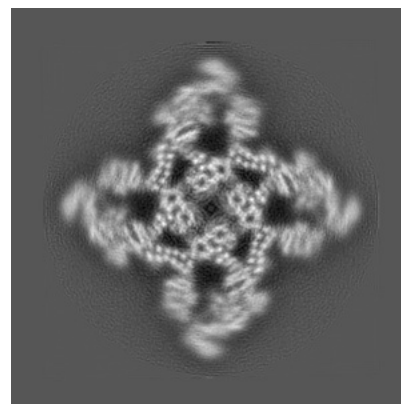
6.3.1 Primary map



X Index: 177



Y Index: 177

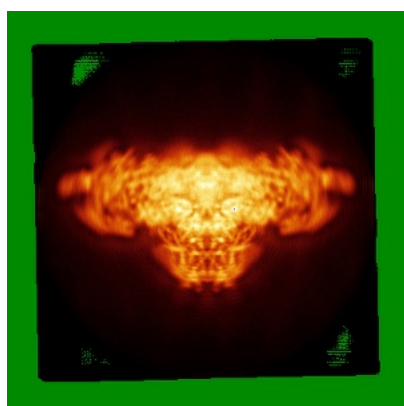


Z Index: 227

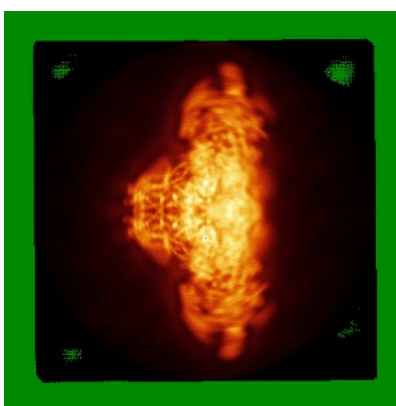
The images above show the largest variance slices of the map in three orthogonal directions.

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

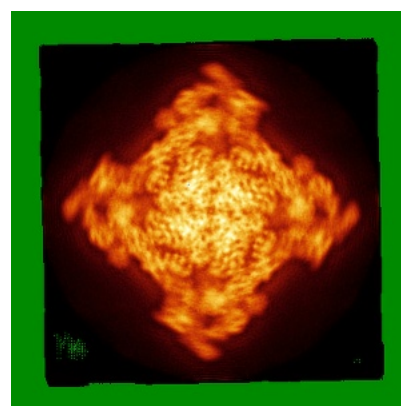
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.16. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

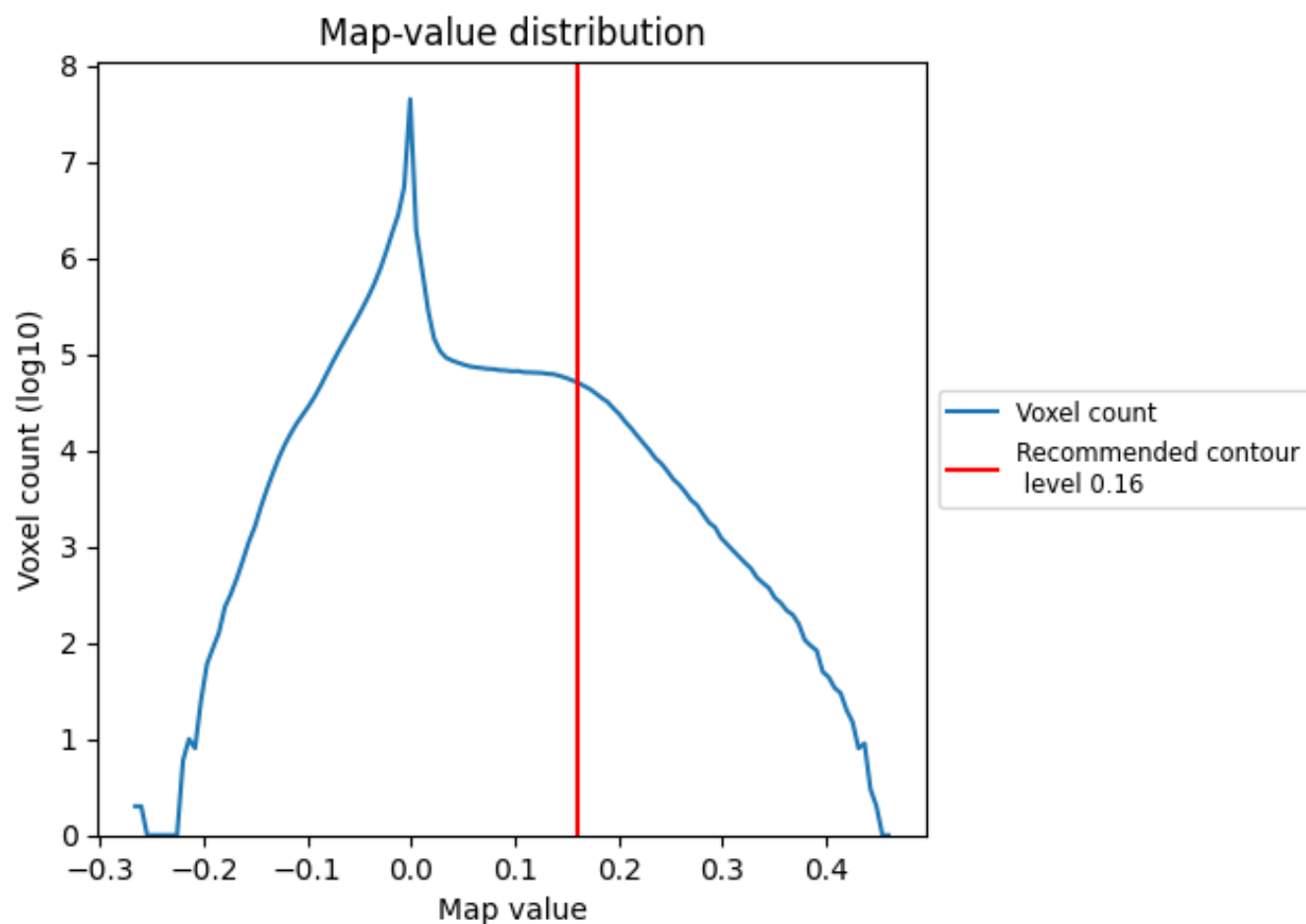
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

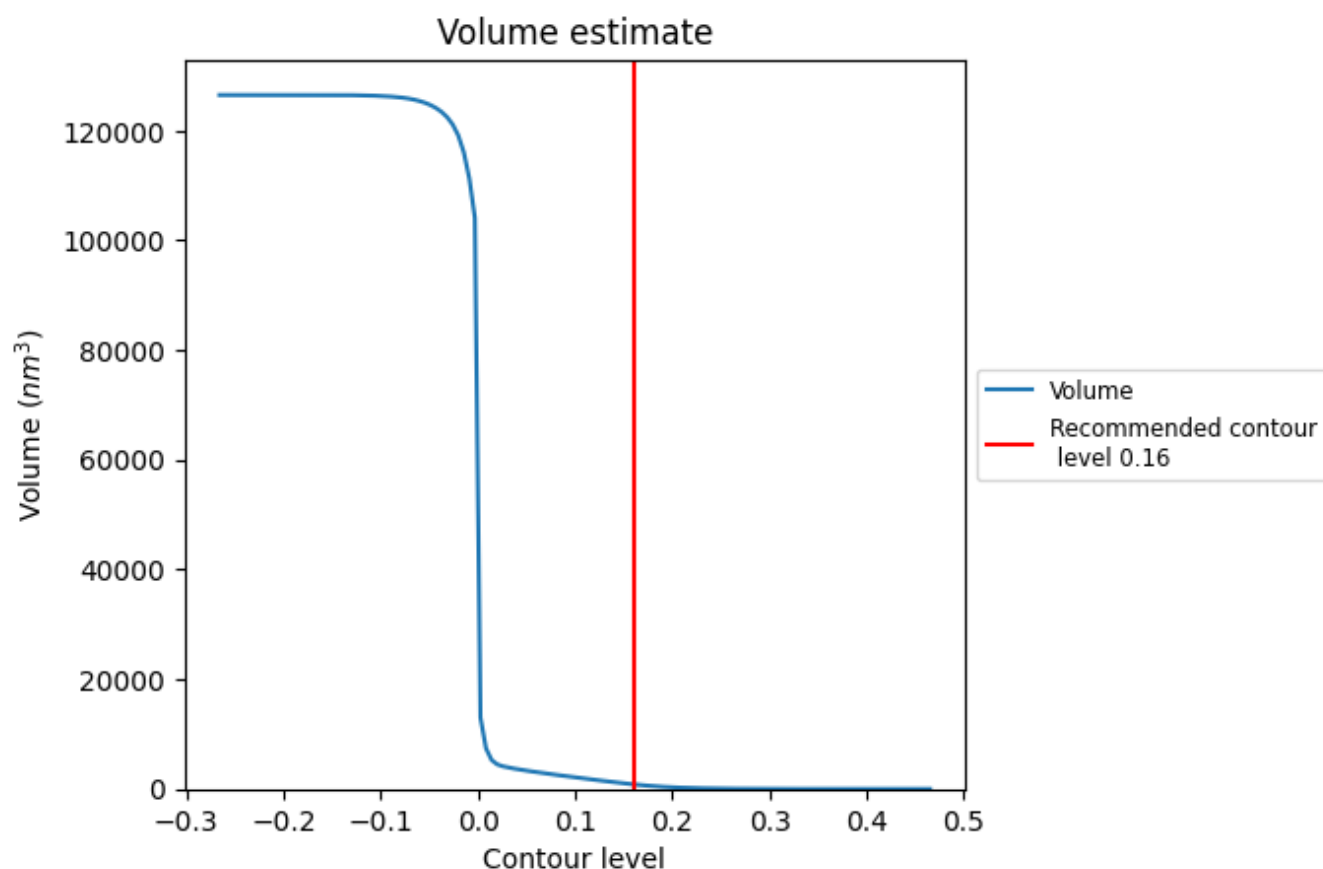
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

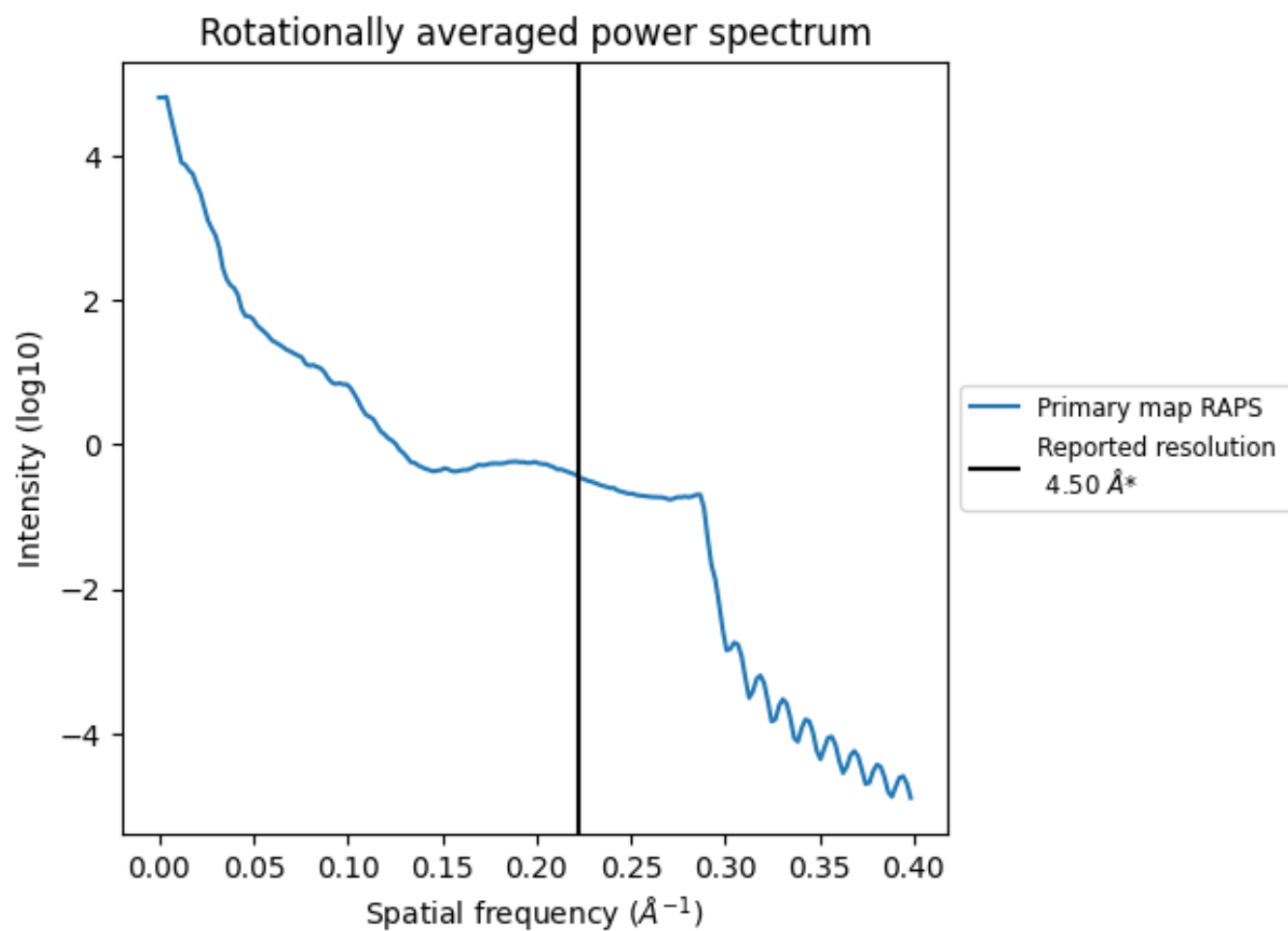
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 846 nm³; this corresponds to an approximate mass of 764 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 0.222 Å⁻¹

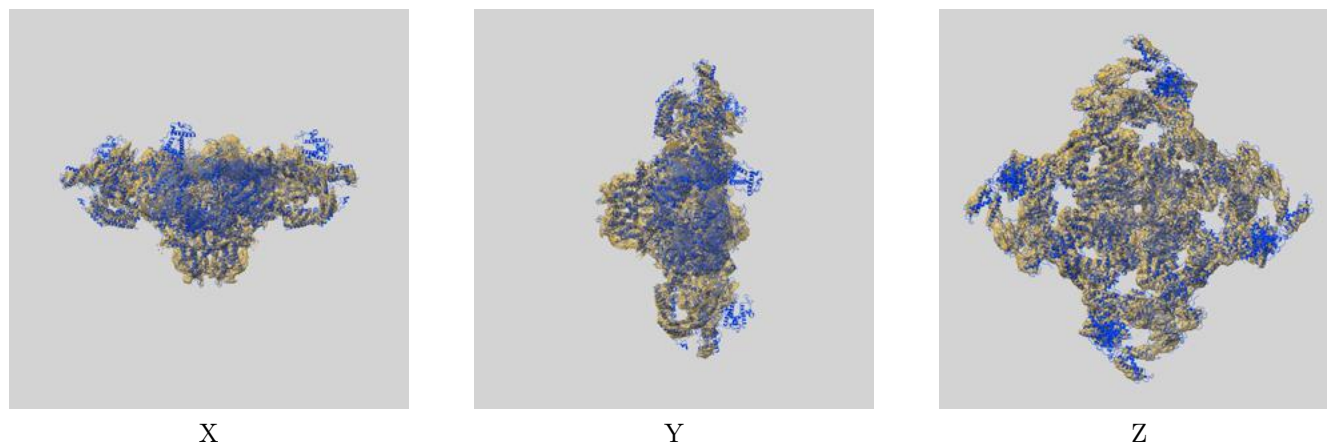
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

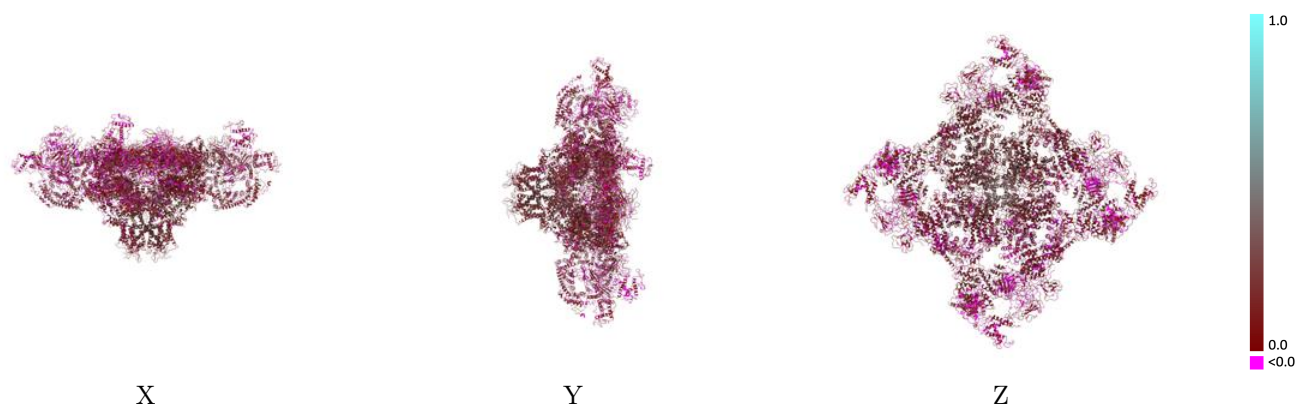
This section contains information regarding the fit between EMDB map EMD-22396 and PDB model 7JMJ. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



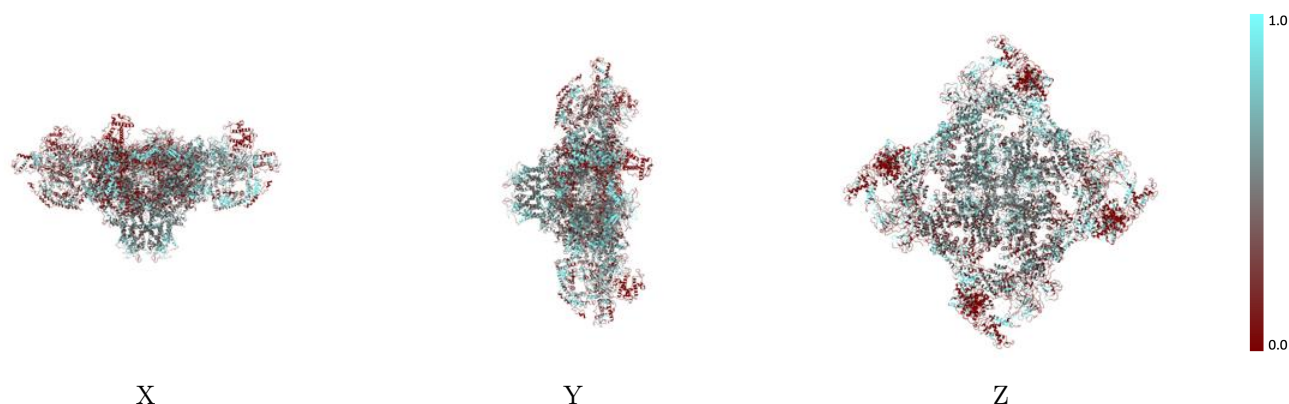
The images above show the 3D surface view of the map at the recommended contour level 0.16 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



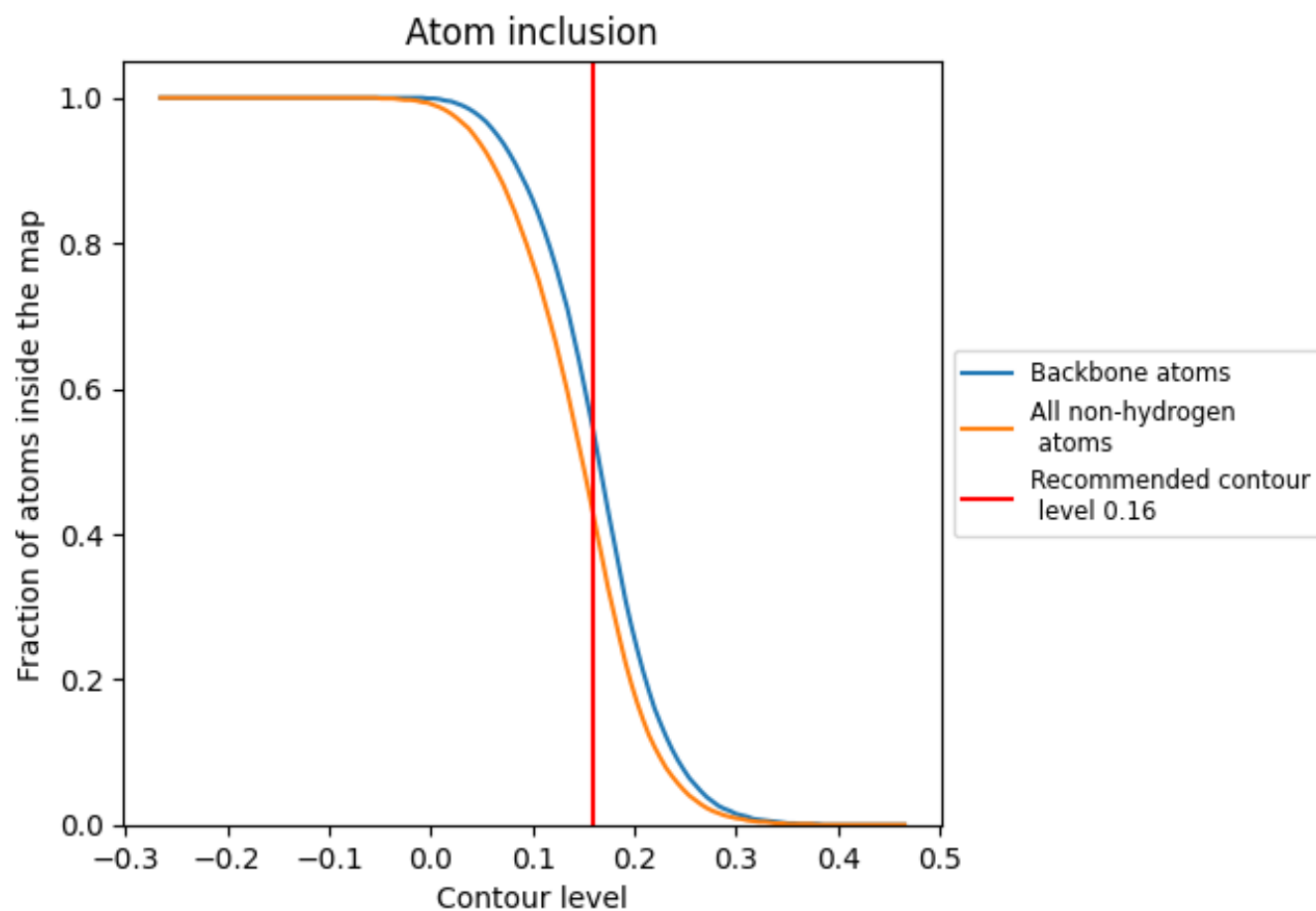
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.16).

9.4 Atom inclusion [i](#)



At the recommended contour level, 54% of all backbone atoms, 42% 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 (0.16) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4250	0.1330
A	0.4530	0.1410
B	0.4630	0.1670
E	0.4320	0.1360
F	0.4260	0.1110
G	0.3980	0.1060
H	0.3920	0.1210
I	0.4060	0.1230
J	0.4020	0.1150

1.0

0.0

<0.0