



## wwPDB EM Validation Summary Report ⓘ

Nov 2, 2022 – 07:43 AM EDT

PDB ID : 5TB1  
EMDB ID : EMD-8392  
Title : Structure of rabbit RyR1 (EGTA-only dataset, class 1)  
Authors : Clarke, O.B.; des Georges, A.; Zalk, R.; Marks, A.R.; Hendrickson, W.A.;  
Frank, J.  
Deposited on : 2016-09-10  
Resolution : 4.60 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

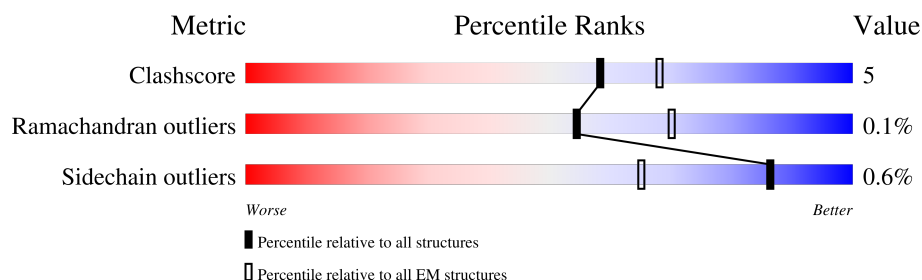
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.60 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	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  $\geq 3$ , 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	108	<div> <div>82%</div> <div>74%</div> <div>25%</div> <div>.</div> </div>
1	F	108	<div> <div>83%</div> <div>73%</div> <div>26%</div> <div>.</div> </div>
1	H	108	<div> <div>81%</div> <div>76%</div> <div>23%</div> <div>.</div> </div>
1	J	108	<div> <div>82%</div> <div>77%</div> <div>22%</div> <div>.</div> </div>
2	B	4416	<div> <div>70%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>
2	E	4416	<div> <div>71%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>
2	G	4416	<div> <div>70%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>
2	I	4416	<div> <div>70%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 121272 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	F	107	Total	C	N	O	S	0	0
			818	516	144	154	4		
1	A	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 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	I	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	E	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		
2	G	4194	Total	C	N	O	S	0	0
			29499	18686	5228	5428	157		

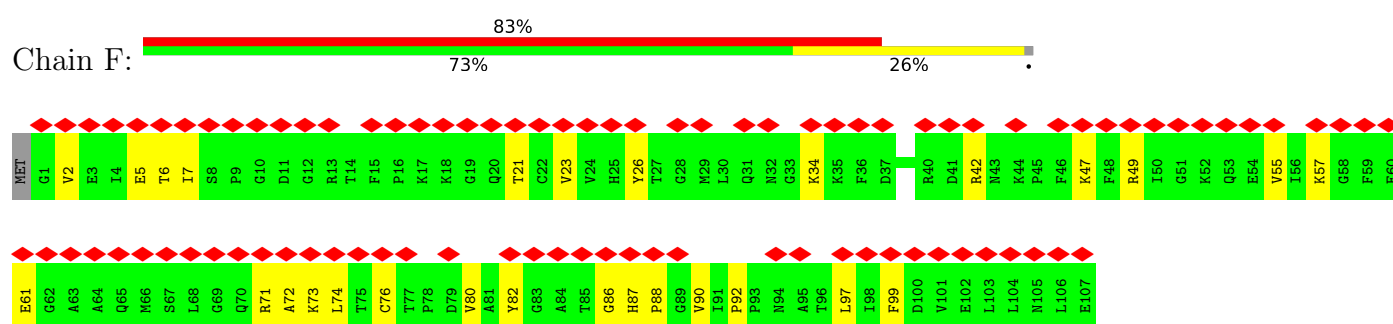
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

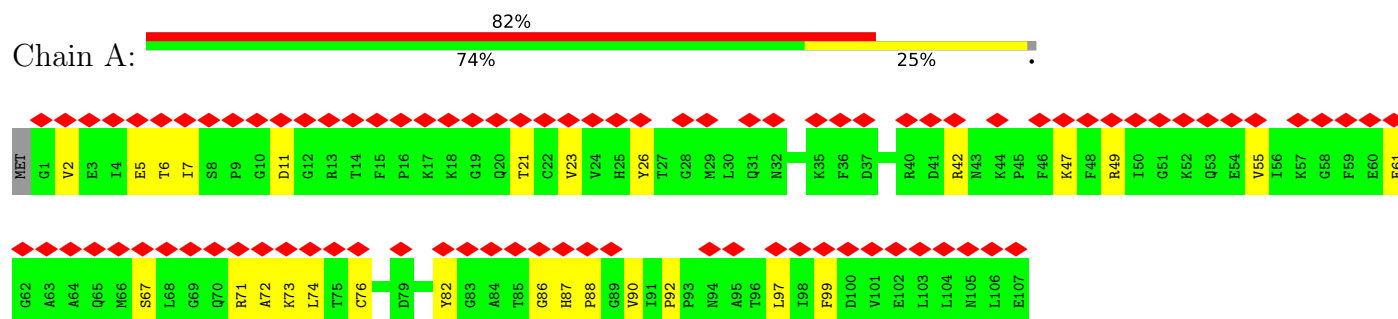
### 3 Residue-property plots [i](#)

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.

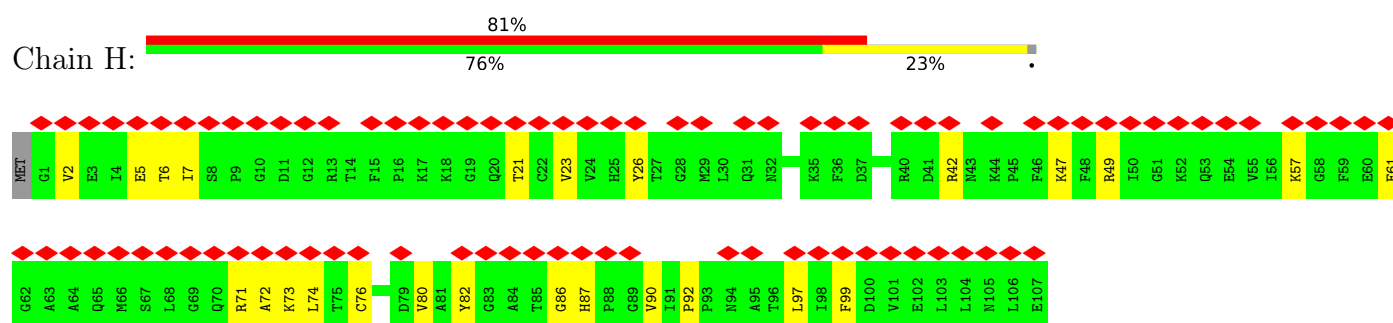
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B



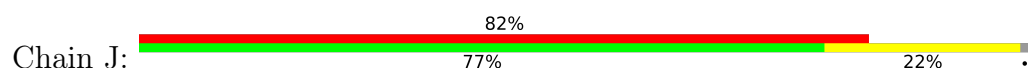
- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

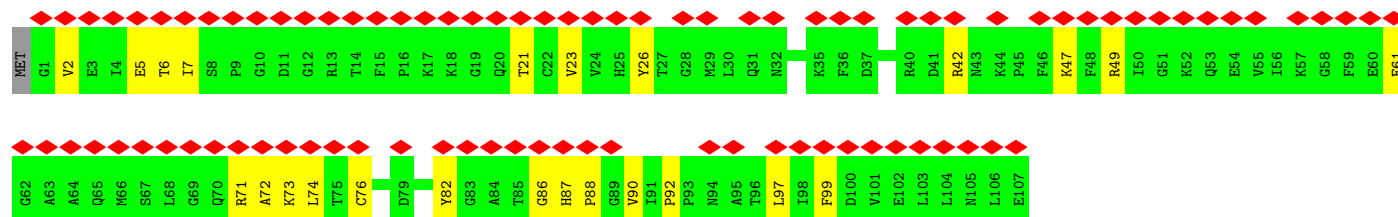


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B

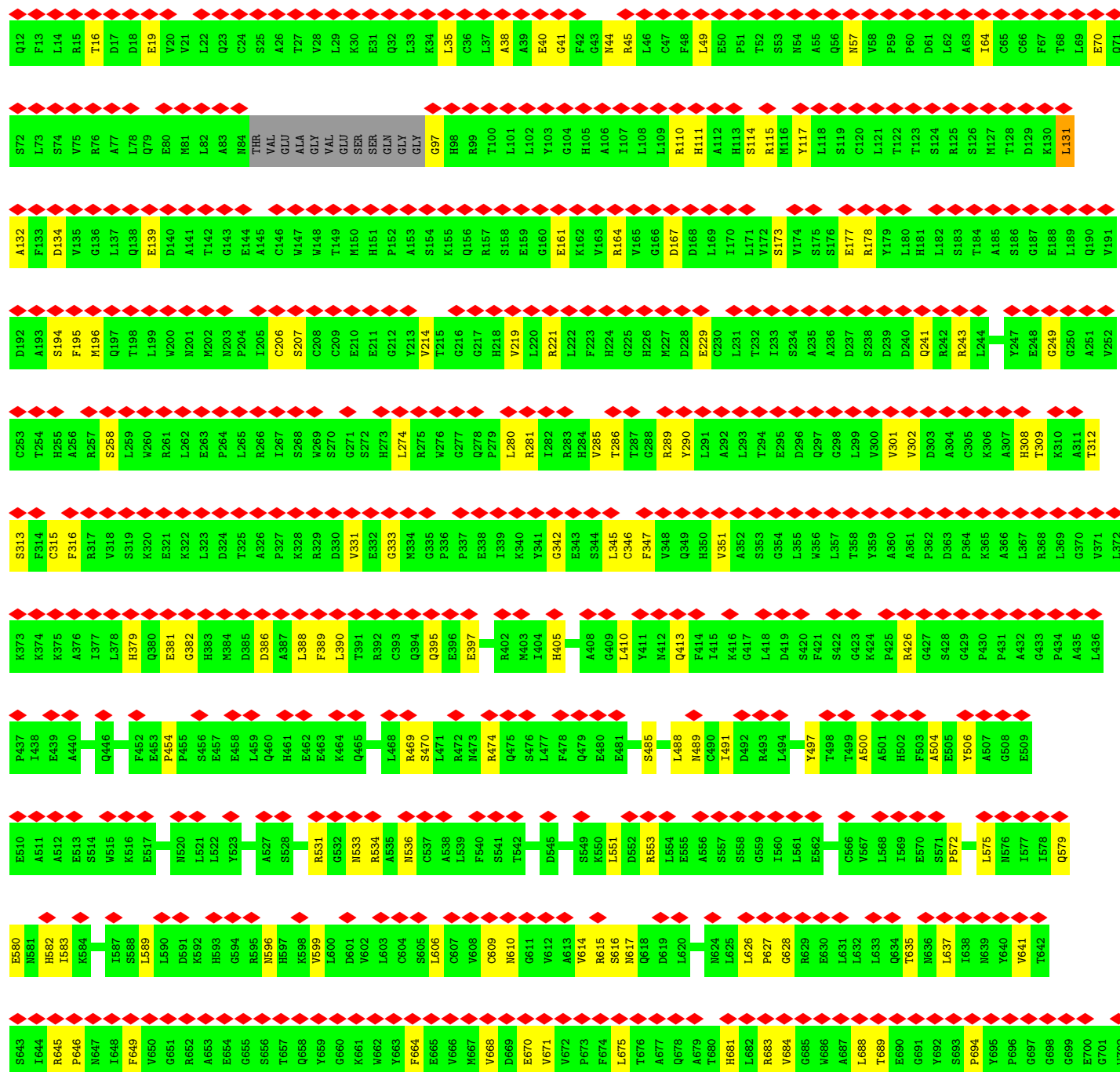
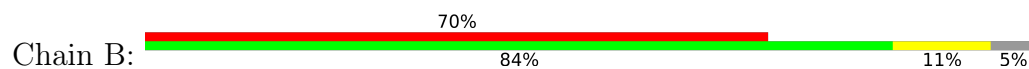


- Molecule 1: Peptidyl-prolyl cis-trans isomerase FKBP1B





• Molecule 2: Ryanodine receptor 1



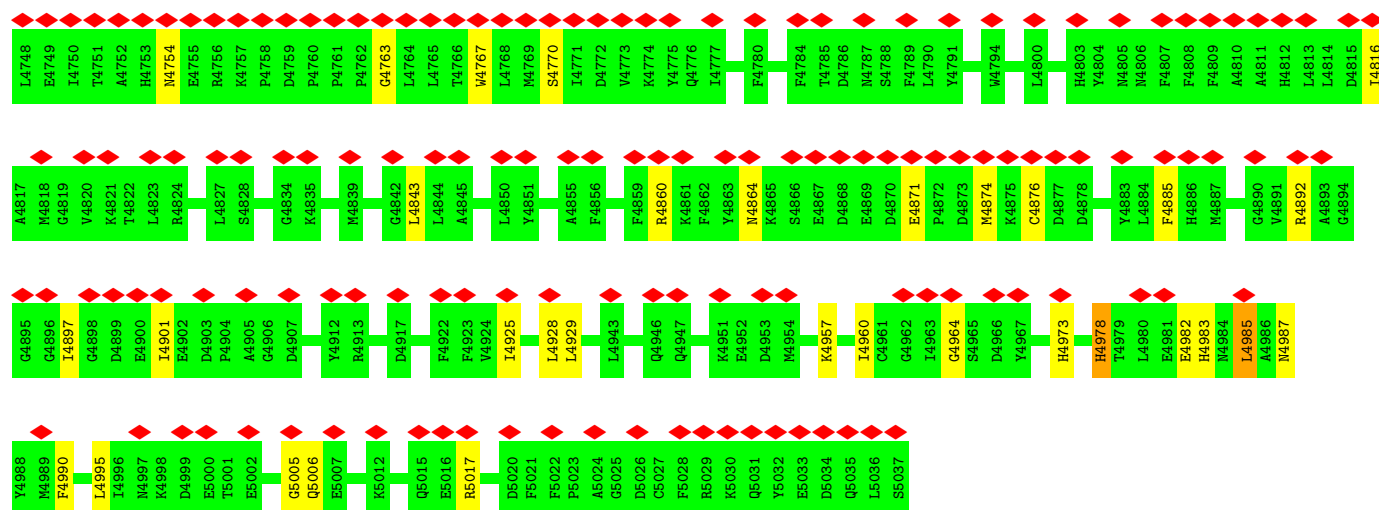
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L1600	X1525	X1526	X1527	X1528	X1529	X1530	X1531	X1532	X1533	X1534	X1535	X1536	X1537	X1538	X1539	X1540	X1541	X1542	X1543	X1544	X1545	X1546	X1547	X1548	X1549																																



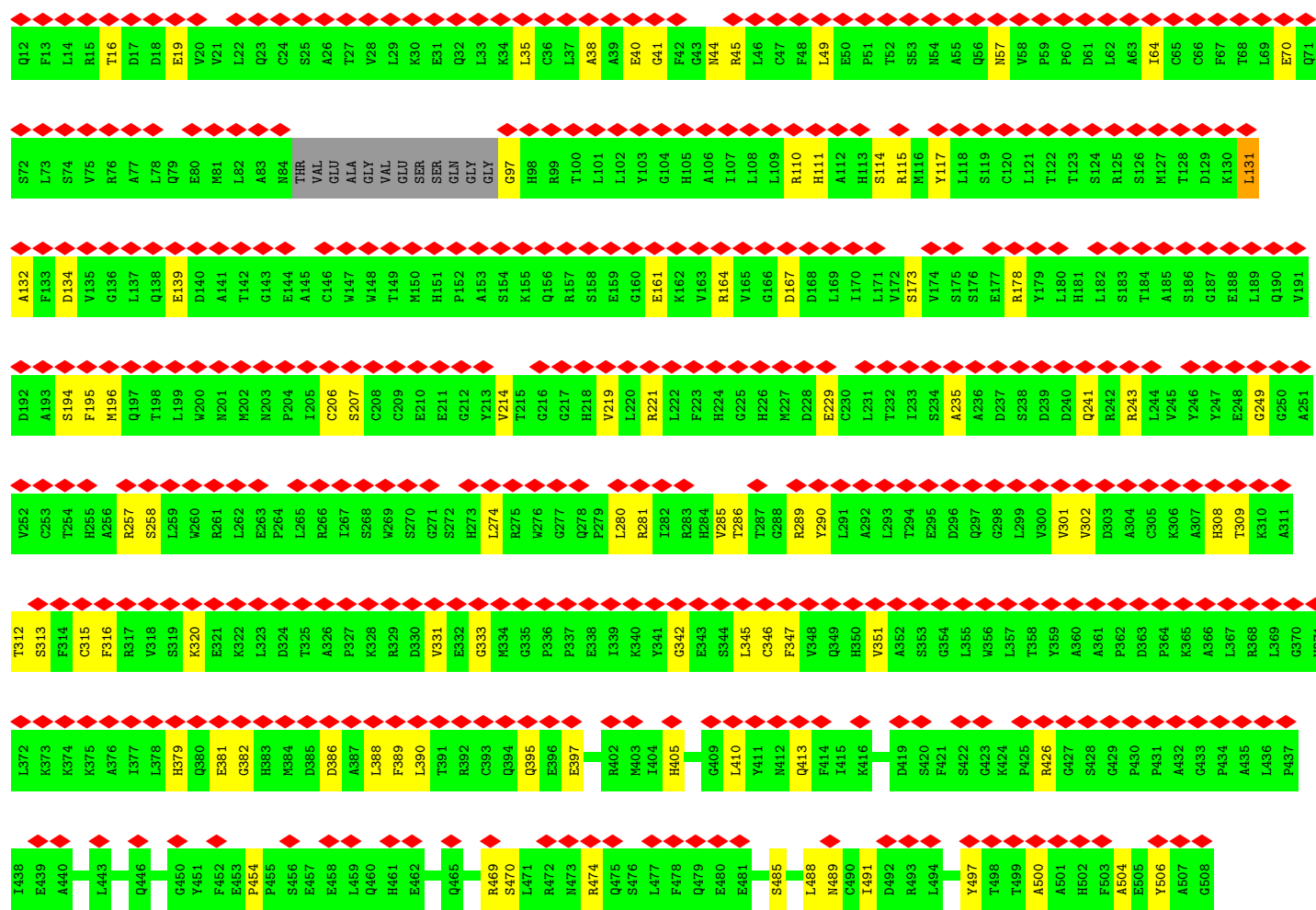
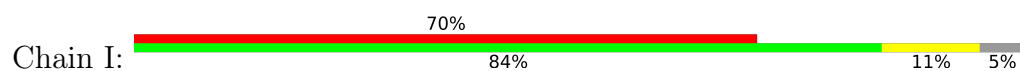
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X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363	X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3371	X3372	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412	X3413	X3414	X3415																		
X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295																		
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E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	T2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889																			
K2770	L2771	Q2772	N2773	N2774	N2775	S2776	G2777	G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	E2801	L2802	E2803	L2804	Y2805	R2806	L2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	N2819	E2820	E2821	T2822	L2823	E2824	K2825	R2826	R2827	E2828	G2829																		
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X2556	X2557	X2558	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2569	X2570	X2574	X2575	X2576	X2577	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2587	X2588	X2589	X2590	X2591	X2592	X2593	X2594	X2595	X2596	X2597	X2598	X2599	X2600	X2601	X2602	X2603	X2604	X2605	X2606	X2607	X2608	X2609	X2610	X2611	X2612	X2613	X2614	X2615	X2616	X2617	X2618	X2619																					







• Molecule 2: Ryanodine receptor 1



G1262	T1263	V1264	D1265	T1266	P1267	P1268	C1269	L1270	L1271	L1272	A1273	H1274	R1275	X1276	X1277	X1278	X1279	X1280	X1281	X1282	X1283	X1284	X1285	X1286	X1287	X1290	X1291	X1292	X1293	X1294	X1295	X1296	X1297	X1430	X1431	X1432	X1433	X1434	X1435	X1436	X1437	X1438	X1439	X1440	X1441	X1442	X1443	X1444	X1445	X1446	X1447	X1448	X1449	X1450	X1451	X1452	X1453	X1454
P1196	Q1197	Q1198	V1199	G1200	H1201	L1202	N1203	L1204	G1205	Q1206	D1207	V1208	S1209	S1210	L1211	R1212	F1213	F1214	A1215	I1216	C1217	G1218	L1219	Q1220	E1221	G1222	F1223	F1226	A1227	Q1231	R1232	T1235	T1236	W1237	S1238	S1239	K1240	P1243	Q1244	F1245	F1246	P1247	P1250	E1251	H1252	P1253	H1254	V1255	E1256	V1257	A1258	R1259	M1260	D1261				
G1135	S1136	E1137	P1138	F1139	G1140	R1141	P1142	W1143	Q1144	S1145	G1146	D1147	V1148	V1149	G1150	C1151	M1152	T1153	D1154	L1155	T1156	E1157	I1160	I1161	F1162	L1163	L1164	N1165	G1166	E1167	V1168	L1169	M1170	S1171	D1172	S1173	G1174	S1175	E1176	T1177	A1178	F1179	R1180	E1181	I1182	E1183	I1184	G1185	D1186	G1187	F1188	L1189	P1190	V1191	C1192	S1193	L1194	G1195
V1072	R1073	T1074	F1075	R1076	A1077	E1078	K1079	Q1084	S1085	G1086	R1087	W1088	Y1089	F1090	E1091	F1092	E1093	A1094	V1095	T1096	T1097	G1098	E1099	M1100	R1101	V1102	G1103	W1104	A1105	R1106	L1107	E1108	L1109	R1110	P1111	D1112	W1113	E1114	L1115	G1116	A1117	D1118	E1119	L1120	A1121	Y1122	V1123	F1124	N1125	G1126	H1127	H1128	G1129	Q1130	R1131	W1132	H1133	L1134
ASP	ILE	PRO	ALA	ARG	ARG	ASN	PRO	R1020	L1021	L1022	P1023	Y1024	R1025	L1026	D1028	E1029	A1030	T1031	K1032	R1033	S1034	M1035	R1036	D1037	S1038	L1039	C1040	Q1041	A1042	V1043	R1044	T1045	L1046	L1047	G1048	Y1049	G1050	Y1051	N1052	I1053	PRO	ASP	GLN	GLU	PRO	SER	GLN	VAL	GLU	ASN	GLN	SER	TRP	D1070	E1071			
D948	N949	L950	K951	K952	T953	K954	L955	P956	K957	T958	Y959	M960	N961	S962	N963	G964	Y965	K966	P967	A968	P969	L970	D971	L972	S973	H974	V975	R976	L977	T978	P979	A980	Q981	T982	T983	L984	V985	D986	R987	L988	A989	E990	N991	A997	R998	D999	V1000	V1001	A1002	Q1003	G1004	W1005	S1006	Y1007	S1008	VAL	GLN	
E888	Q889	G890	W891	T892	Y893	G894	P895	W896	R897	D898	N900	K901	R902	L903	H904	P905	C906	L907	V908	N909	F910	H911	S912	L913	P914	E915	P916	E917	R918	N919	Y920	N921	L922	Q923	M924	S925	G926	E927	T928	L929	K930	T931	L932	L933	A934	L935	G936	C937	H938	W939	G940	M941	A942	D943	E944	K945	A946	
E828	Y829	R830	R831	E832	Q833	P834	R835	G836	P837	H838	L839	W840	G841	S842	R844	C845	L846	S847	H848	T849	D850	F851	W852	P853	C854	P855	R856	D857	THR	VAL	GLN	I861	V862	L863	P864	P865	H866	L867	E868	R869	I870	R871	E872	K873	L874	A875	E876	N877	I878	H879	E880	L881	W882	A883	L884	T885	R886	L887
V767	F768	E769	A770	F771	N772	L773	D774	G775	L776	F777	F778	P779	W780	Y781	S782	F783	S784	A785	G786	H787	K788	V789	R790	F791	L792	L793	G794	G795	R796	H797	G798	F799	F800	K801	F802	L803	P804	P805	P806	G807	Y808	A809	H812	E813	A814	V815	L816	P817	R818	E819	R820	L821	R822	L823	E824	P825	I826	K827
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R645	P646	N647	I648	F649	V650	G651	R652	A653	E654	G655	S656	T657	Q658	Y659	G660	K661	W662	Y663	F664	E665	V666	M667	V668	D669	E670	V671	V672	G673	A674	R675	T676	Q677	Q678	A679	H681	L682	R683	V684	G685	W686	A687	L688	T689	E690	G691	Y692	S693	P694	Y695	P696	G697	G698	G699	E700	G703	G704	Y705	
E580	N581	H582	I583	I586	I587	S588	L589	L590	H593	G594	R595	N596	H597	K598	V599	L600	D601	C604	S605	L606	C607	V608	C609	N610	G611	V612	A613	V614	R615	S616	N617	Q618	D619	L620	N624	L625	L626	P627	G628	R629	E630	L631	L632	L633	Q634	T635	N636	L637	I638	N639	Y640	V641	T642	S643	I644			
E509	E510	A511	A512	E513	W514	W515	K516	E517	N520	L521	L522	Y523	E524	A527	S528	R531	G532	N533	R534	A535	N536	C537	A538	L539	F540	S541	T542	S549	K550	L551	D552	R553	L554	E555	A556	S557	S558	G559	I560	L561	E562	C566	V567	L568	I569	E570	S571	P572	L575	N576	I577	I578	Q579					

K2297	R2224	A2141	ARG	P2002	K1930	V1870	ALA	S1726	R1661	E1596	X1522	X1455
F2225	P2226	Y2142	SER	Q2003	L1931	F1871	GLY	R1727	F1662	V1597	X1523	X1456
K2227	K2227	T2143	LEU	E2004	P1932	T1872	VAL	R1728	Q1598	X1524	X1524	X1457
M2228	M2228	I2144	LEU	Q2005	V1935	E1873	ALA	S1729	M1599	X1525	X1525	X1458
Y2229	Y2229	S2147	THR	I2006	I1935	E1874	ALA	M1730	L1600	X1526	X1526	X1459
R2234	R2234	E2150	ARG	N2007	N1941	GLU	E1793	L1731	V1603	X1527	X1527	X1460
F2235	F2235	E2150	LEU	L2010	L1942	GLU	A1794	L1731	S1604	X1528	X1528	X1461
Y2238	Y2238	M2153	LYS	H2011	L1943	GLU	P1795	S1732	W1605	X1529	X1529	X1462
F2239	F2239	S2154	LYS	E1944	E1944	GLU	R1797	E1733	S1606	X1530	X1530	X1463
S2309	S2309	L2155	LYS	F1945	Y1945	GLU	L1798	Y1734	R1607	X1531	X1531	X1464
C2310	C2310	L2156	GLU	F1946	F1946	GLU	I1802	V1735	A1672	X1532	X1532	X1468
P2311	P2311	R2163	LYS	D2014	D1948	GLU	R1808	P1737	A1675	X1533	X1533	X1471
M2312	M2312	E2166	PRG	A2016	A2016	GLU	L1812	L1738	L1676	X1534	X1534	X1472
L2313	R2244	L2166	GLU	D2017	H1953	GLU	H1813	T1739	G1677	X1535	X1535	X1473
L2314	R2248	T2167	GLU	E2018	R1954	GLU	M1814	E1741	M1678	X1536	X1536	X1474
A2315	R2248	V2168	LEU	E2019	A1959	GLU	L1815	T1742	V1615	X1537	X1537	X1475
K2316	F2251	M2169	PRG	D2020	A1960	GLU	G1816	R1743	THR	X1538	X1538	X1476
G2317	D2252	Q2169	ALA	C2021	A1960	ASP	E1817	A1744	ARG	X1539	X1539	X1477
Y2318	H2253	G2171	GLU	P2022	F1961	GLU	D1828	I1745	ALA	X1540	X1540	X1478
P2319	Y2256	P2172	GLU	L2023	A1962	GLU	G1821	L1745	ARG	X1541	X1541	X1479
D2320	L2257	Q2173	GLU	P2024	E1963	LYS	G1822	F1748	GLY	X1542	X1542	X1480
L2321	L2257	Q2173	GLU	E2025	R1964	GLU	G1823	P1749	E1622	X1543	X1543	X1481
G2322	N2260	I2179	LEU	D2026	Y1965	GLU	Q1824	S1687	L1623	X1544	X1544	X1482
N2323	S2261	T2184	GLU	R2028	K1968	GLU	H1825	H1688	L1624	X1545	X1545	X1483
K2324	G2262	T2185	GLU	Q2029	L1969	GLU	A1826	V1689	G1625	X1546	X1546	X1484
P2325	L2263	L2185	GLU	D2030	Q1970	GLU	R1827	K1753	W1626	X1547	X1547	X1485
C2326	G2264	M2186	GLU	L2031	A1971	LYS	D1828	G1754	A1627	X1548	X1548	X1486
G2327	L2265	N2187	LYS	L2031	N1972	GLU	G1831	G1755	V1628	X1549	X1549	X1487
G2328	L2265	N2188	GLU	F2034	Q1973	ASP	G1832	M1756	Q1629	X1550	X1550	X1488
E2329	G2266	K2189	ALA	H2035	R1974	ALA	S1833	A1757	C1630	X1551	X1551	X1488
R2330	L2267	A2106	GLU	Q2036	S1975	GLU	F1836	R1758	Q1631	X1552	X1552	X1492
Y2331	Q2268	Q2107	LYS	D2037	R1976	GLU	Q1837	R1759	D1632	X1553	X1553	X1493
L2332	G2269	Y2110	GLU	L2038	Y1977	GLU	F1838	H1760	P1633	X1554	X1554	X1494
D2333	G2269	S2113	GLU	L2039	A1978	GLU	L1836	G1761	L1634	X1555	X1555	X1495
F2334	P2272	P2114	GLU	A2040	L1978	ALA	Q1839	D1700	T1635	X1556	X1556	X1496
L2273	L2273	P2114	GLU	C2042	R1980	PRO	P1840	P1763	M1636	X1557	X1557	X1496
D2274	D2274	E2115	GLU	G2043	L1980	ALA	P1840	G1764	M1637	X1558	X1558	X1497
A2276	A2276	R2118	GLU	I2044	M1981	GLU	L1848	G1765	A1638	X1561	X1561	X1501
A2277	A2277	R2118	GLU	Q2045	R1982	GLU	L1849	P1767	L1639	X1502	X1502	X1502
A2278	A2278	F2121	LYS	L2046	A1983	LYS	G1852	G1768	H1640	X1503	X1503	X1503
S2279	S2279	F2121	GLU	E2047	F1984	ASP	I1853	T1769	G1705	X1504	X1504	X1504
N2283	N2283	R2126	GLU	Q2048	T1985	L1922	I1854	S1770	P1706	X1505	X1505	X1505
N2284	N2284	M2211	GLU	GLU	M1986	E1923	G1855	L1771	R1708	X1506	X1506	X1506
S2345	S2345	Q2127	GLU	GLU	S1987	E1924	G1855	A1709	A1577	X1507	X1507	X1507
V2346	E2285	Y2128	GLU	GLU	A1988	G1925	D1856	G1710	R1645	X1508	X1508	X1508
L2286	L2286	D2129	GLU	PRG	A1989	L1926	E1857	Y1711	R1646	X1509	X1509	X1509
A2287	A2287	G2130	GLU	GLU	E1990	L1927	D1858	Y1712	D1649	X1510	X1510	X1510
L2288	L2288	L2215	GLU	GLU	T1991	Q1928	V1859	D1713	I1650	X1511	X1511	X1511
A2289	A2289	G2216	GLU	GLU	A1992	Q1928	K1860	I1718	L1653	X1512	X1512	X1512
L2290	L2290	R2136	THR	THR	A1992	Q1928	Q1861	H1719	S1654	X1513	X1513	X1513
Q2291	Q2291	A2137	SER	SER	R1993	M1929	I1862	L1720	E1655	X1514	X1514	X1514
E2292	E2292	E2219	LEU	SER	R1994	L1994	L1863	C1721	R1656	X1515	X1515	X1515
D2293	D2293	T2220	SER	SER	T1995	K1864	K1864	S1722	L1657	X1516	X1516	X1516
D2294	D2294	K2221	ARG	ARG	R1996	M1865	M1865	A1723	D1658	X1519	X1519	X1519
L2295	L2295	E2222	LEU	LEU	E1997	F1998	E1869	C1724	L1659	X1520	X1520	X1520
E2296	E2296	L2223	LEU	LEU	F1998	S2000	E1869	R1725	Q1660	X1521	X1521	X1521
K2360	K2360	P2361			P2001			L1786	P1787	L1595	L1595	L1595

X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3255	X3256	X3257	X3258	X3259	X3260	X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293	X3294	X3295	X3296	X3297	X3298	X3299	X3300	X3301	X3302	X3303
X3038	X3039	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3054	X3055	X3056	X3057	X3058	X3059	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3144	X3145	X3146	X3147	X3148	X3149	X3150	X3151	X3152	X3153	X3154	X3155	X3156	X3157	X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173						
X2960	X2961	X2962	X2963	X2964	X2965	X2966	X2967	X2968	X2969	X2970	X2971	X2972	X2973	X2974	X2975	X2976	X2996	X2997	X2998	X2999	X3000	X3001	X3002	X3003	X3004	X3005	X3006	X3007	X3008	X3009	X3010	X3011	X3012	X3013	X3014	X3015	X3016	X3017	X3018	X3019	X3020	X3021	X3022	X3023	X3024	X3025	X3026	X3027	X3028	X3029	X3030	X3031	X3032	X3033	X3034	X3035	X3036	X3037							
G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	L2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	A2914	E2915	K2916	A2917	D2918	R2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	P2929	L2930	Q2931	M2932	N2933	G2934	Y2935	A2936	V2937	T2938	R2939	X2942	X2943	X2944	X2945	X2946	X2947	X2948	X2949	Y2950	X2951	X2952	X2953	Y2954	X2955	X2956	X2957	X2958							
LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	TYR	ASP	PRO	ARG	ARG	GLU	GLY	Y2855	T2856	P2857	Q2858	P2859	P2860	D2861	L2862	G2863	G2864	V2865	T2866	L2867	G2868	R2869	E2870	L2871	Q2872	A2873	M2874	A2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	Q2887	R2888	K2889	R2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897						
G2778	E2779	N2780	V2781	D2782	E2783	E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	N2794	K2795	T2796	F2797	T2798	E2799	K2800	D2801	K2802	E2803	L2804	R2805	R2806	T2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	E2828	Q2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS						
X2688	X2689	X2690	X2691	X2692	X2693	X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	N2734	F2735	D2736	P2737	E2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	L2746	T2747	P2748	E2749	K2750	L2751	D2752	S2753	L2754	T2755	N2756	K2757	F2758	A2759	E2760	V2761	T2762	H2763	E2764	K2765	W2766	A2767	F2768	D2769	K2770	L2771	Q2772	N2773	W2774	T2775	S2776	V2777						
X2628	X2629	X2630	X2631	X2632	X2633	X2634	X2635	X2636	X2637	X2638	X2639	X2640	X2641	X2642	X2643	X2644	X2645	X2646	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2663	X2664	X2665	X2666	X2667	X2668	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2679	X2680	X2681	X2682	X2683	X2684	X2685	X2686	X2687						
X2566	X2567	X2568	X2569	X2570	X2571	X2572	X2573	X2574	X2575	X2576	X2577	X2580	X2581	X2582	X2583	X2584	X2585	X2586	X2587	X2588	X2589	X2590	X2591	X2592	X2593	X2594	X2595	X2596	X2597	X2598	X2599	X2600	X2601	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						
X2497	X2498	X2499	X2499	X2500	X2501	X2502	X2506	X2511	X2512	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2524	X2525	X2526	X2527	X2528	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2540	X2541	X2542	X2543	X2544	X2550	X2551	X2552	X2555	X2556	X2557	X2558	X2559	X2560	X2561	X2562	X2563	X2564	X2565										
M2423	S2424	F2425	Y2426	A2427	A2428	L2429	L2430	D2431	L2432	L2433	G2434	R2435	C2436	A2437	P2438	H2441	L2442	G2446	K2447	G2448	E2449	A2450	L2451	R2452	L2453	R2454	A2455	I2456	L2457	S2458	S2459	L2460	L2463	D2464	D2465	L2466	V2467	G2468	I2469	I2470	S2471	L2472	P2473	L2474	Q2475	L2476	P2477	T2478	L2479	X2487	X2488	X2489	X2490	X2493	X2494										
E2362	C2363	F2364	G2365	P2366	A2367	L2368	R2369	G2370	E2371	G2372	G2373	S2374	G2375	L2376	L2377	A2378	A2379	I2380	E2381	E2382	A2383	L2384	R2385	I2386	S2387	E2388	I2389	P2390	A2391	R2392	I2393	G2394	P2395	GLY	VAL	ARG	ARG	ASP	ARG	ARG	GLU	HIS	PHE	GLY	GLU	GLU	PRO	PRO	GLU	GLU	N2414	R2415	W2416	H2417	L2418	G2419	I2422								

R4188	R4189	I4190	E4191	R4192	I4193	Y4194	F4195	E4196	E4199	R4202	A4203	Q4204	W4205	E4206	M4207	R4215	Q4216	F4219	D4220	M4223	E4224	Q4225	G4226	E4227	A4228	E4229	D4230	M4231	E4232	E4239	D4240	I4247	I4251	S4252	E4253	X4320	X4321	X4322	X4330	X4336	X4337	X4338	X4339	X4340	X4341	X4342	X4343	X4344	X4345	F4540	W4541								
D4118	E4119	N4120	E4121	M4122	I4123	M4124	F4125	E4126	E4127	F4128	A4129	M4130	R4131	F4132	Q4133	E4134	P4135	A4136	R4137	D4138	I4139	F4140	F4141	N4142	L4147	E4152	H4156	R4159	L4160	R4161	M4162	F4163	L4164	E4165	L4166	A4167	E4168	S4169	Q4170	X4321	L4171	L4172	Y4173	F4174	F4175	P4176	Y4177	R4180	I4181	E4182	I4183	M4184	A4185	A4186	S4187				
L4059	K4060	F4061	F4062	D4063	M4064	F4065	L4066	K4067	L4068	K4069	D4070	I4071	V4072	Q4073	S4074	E4075	A4076	F4077	Q4078	D4079	Y4080	V4081	T4082	D4083	P4084	R4085	G4086	L4087	I4088	S4089	K4090	K4091	D4092	F4093	Q4094	K4095	A4096	M4097	D4098	S4099	Q4100	K4101	Q4102	F4103	T4104	G4105	F4106	I4107	I4108	Q4109	F4110	L4111	L4112	S4113	C4114	S4115	E4116	A4117	
R3984	L3985	W3986	F3992	L3993	H3994	V3995	F3996	A3997	H3998	M3999	M4000	M4001	K4002	L4003	A4004	Q4005	D4006	S4007	S4008	Q4009	I4010	E4011	L4012	L4013	K4014	E4015	L4016	L4017	D4018	L4019	Q4020	K4021	D4022	L4027	L4030	L4031	E4032	G4033	M4034	V4035	V4036	M4037	G4038	M4039	I4040	A4041	R4042	M4047	L4048	V4049	E4050	M4054	V4055	E4056					
L3903	R3904	T3907	G3908	N3909	T3910	T3911	V3922	L3923	L3924	R3925	S3928	I3930	S3931	D3932	F3933	Y3934	V3935	Y3936	S3937	G3938	G3939	K3940	V3941	V3942	I3943	E3944	E3945	Q3946	Q3947	K3948	R3949	N3950	A3954	M3955	K3959	Q3960	V3961	F3962	N3963	E3967	Q3970	G3971	F3972	C3973	N3976	Q3977	A3981	H3982	S3983										
K3824	E3825	F3828	F3829	Q3830	Q3833	H3836	L3842	D3843	F3847	E3848	R3849	Q3850	N3851	K3852	A3853	E3854	G3855	L3856	G3857	H3858	V3859	V3860	M3861	D3862	G3863	T3864	V3865	L3866	R3867	R3868	Q3869	N3870	G3871	E3872	K3873	V3874	M3875	D3877	D3878	E3879	F3880	D3883	L3888	Q3889	N3896	H3897	D3898	F3899	Y3902										
E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	M3758	E3759	K3760	R3762	L3763	L3764	Y3765	Q3766	S3768	R3769	H3771	T3772	R3773	G3774	A3775	A3776	E3777	M3778	Y3779	L3780	Q3781	C3786	K3787	Q3788	E3789	A3792	K3799	S3803	I3804	L3805	N3806	G3807	G3808	N3809	A3810	K3815	M3816	L3817	D3818	Y3819	L3820	K3821	D3822	K3823								
I3674	D3675	D3676	K3679	A3680	Q3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	Q3691	E3692	K3693	K3694	F3705	S3706	R3707	L3710	T3711	E3712	K3713	S3714	K3715	L3716	D3717	E3718	D3719	Y3720	L3721	Y3722	K3723	A3724	Y3725	A3726	C3733	H3734	L3735	F3736	E3737	G3738	G3739	E3740	H3741	GLY	GLU	ALA	D3666	H3667	S3668	F3669	E3670	D3671	V3749		
X3526	X3527	X3528	X3529	X3530	X3531	X3532	X3533	X3534	X3535	X3536	X3537	X3538	X3539	X3540	X3541	X3542	X3543	X3544	X3545	X3546	X3547	X3548	X3549	X3550	X3551	X3552	X3553	X3554	X3555	X3556	X3557	X3558	X3559	X3560	X3561	X3562	X3563	X3564	X3565	X3566	X3567	X3568	X3569	X3570	X3571	X3572	X3573	X3574	X3575	X3576	X3577	X3578	X3579	X3580	X3581	X3582	X3583	X3584	X3585
X3686	X3687	X3688	X3689	X3690	X3691	X3692	X3693	X3694	X3695	X3696	X3697	X3698	X3699	X3700	X3701	X3702	X3703	X3704	X3705	X3706	X3707	X3708	X3709	X3710	X3711	E3712	K3713	S3714	K3715	L3716	D3717	E3718	D3719	Y3720	L3721	Y3722	K3723	A3724	Y3725	A3726	C3733	H3734	L3735	F3736	E3737	G3738	G3739	E3740	H3741	GLY	GLU	ALA	D3666	H3667	S3668	F3669	E3670	D3671	V3749
X3364	X3365	X3366	X3367	X3368	X3369	X3370	X3371	X3372	X3373	X3374	X3375	X3376	X3377	X3378	X3379	X3380	X3381	X3382	X3383	X3384	X3385	X3386	X3387	X3388	X3389	X3390	X3391	X3392	X3393	X3394	X3395	X3396	X3397	X3398	X3399	X3400	X3401	X3402	X3403	X3404	X3405	X3406	X3407	X3408	X3409	X3410	X3411	X3412	X3413	X3414	X3415	X3416	X3417	X3418	X3419	X3420	X3421	X3422	X3423
X3424	X3425	X3426	X3427	X3428	X3429	X3430	X3431	X3432	X3433	X3434	X3435	X3436	X3437	X3438	X3439	X3440	X3441	X3442	X3443	X3444	X3445	X3446	X3447	X3448	X3449	X3450	X3451	X3452	X3453	X3454	X3455	X3456	X3457	X3458	X3459	X3460	X3461	X3462	X3463	X3464	X3465	X3466	X3467	X3468	X3511	X3512	X3513	X3514	X3515	X3516	X3517	X3518	X3519	X3520	X3521	X3522	X3523	X3524	X3525
X3304	X3305	X3306	X3307	X3308	X3309	X3310	X3311	X3312	X3313	X3314	X3315	X3316	X3317	X3318	X3319	X3320	X3321	X3322	X3323	X3324	X3325	X3326	X3327	X3328	X3329	X3330	X3331	X3332	X3333	X3334	X3335	X3336	X3337	X3338	X3339	X3340	X3341	X3342	X3343	X3344	X3345	X3346	X3347	X3348	X3349	X3350	X3351	X3352	X3353	X3354	X3355	X3356	X3357	X3358	X3359	X3360	X3361	X3362	X3363



C253	D192	A132	S72	Q12
T254	A193	F133	L73	F13
H255	S194	D134	S74	L14
A256	F195	V135	V75	R15
R257	M196	G136	R76	T16
S258	Q197	L137	A77	D17
L259	T198	Q138	L78	D18
D260	L199	E139	Q79	E19
R261	W200	D140	E80	V20
L262	N201	A141	M81	V21
E263	M202	T142	L82	L22
P264	N203	G143	A83	Q23
L265	P204	E144	M84	C24
R266	I205	A145	THR	S25
L267	C206	C146	VAL	A26
S268	S207	M147	GLJ	T27
W269	C208	W148	ALA	T27
S270	C209	T149	GLY	V28
G271	E210	M150	VAL	L29
S272	E211	M151	GLJ	R30
H273	G212	P152	SER	R30
L274	Y213	A153	GLN	E31
R275	V214	S154	GLY	Q32
W276	T215	K155	G97	L33
G277	G216	Q156	H98	R34
Q278	G217	R157	R99	L35
P279	H218	S158	T100	L37
L280	V219	E159	L101	A38
R281	L220	G160	L102	A39
T282	R221	E161	Y103	E40
R283	L222	K162	G104	C41
H284	F223	Q163	H105	F42
V285	H224	R164	A106	Q43
T286	G225	V165	I107	N44
T287	H226	G166	L108	R45
G288	M227	D167	L109	L46
R289	D228	D168	R110	C47
Y290	E229	L169	H111	F48
L291	C230	L170	A112	L49
A292	L231	L171	H113	E50
L293	T232	L172	S114	S51
T294	I233	V173	R115	T52
E295	S234	S174	M116	S53
D296	A235	V175	Y117	M54
Q297	A236	S176	L118	A55
G298	D237	E177	S119	Q56
L299	S238	R178	C120	N57
V300	D239	Y179	L121	M58
V301	D240	L180	T122	P59
V302	Q241	H181	T123	P60
D303	R242	L182	S124	D61
A304	R243	S183	R125	L62
C305	L244	L184	S126	A63
K306		A185	M127	L64
A307	Y247	S186	T128	C65
H308	E248	G187	D129	C66
T309	G249	E188	K130	F67
K310	C250	L189	L131	T68
A311	A251	Q190		L69
T312	V252	V191		E70
				O71

TRP	D1070	D1071	R1072	R1073	I1074	F1075	R1076	A1077	K1078	K1079	Q1084	S1085	G1086	R1087	W1088	Y1089	F1090	F1091	F1092	E1093	A1094	V1095	T1096	T1097	G1098	E1099	M1100	R1101	V1102	G1103	W1104	A1105	R1106	P1107	E1108	L1109	R1110	P1111	D1112	V1113	E1114	L1115	G1116	A1117	D1118	E1119	L1120	A1121	R1122	V1123	F1124	M1125	G1126	H1127	R1128	G1129	Q1130	R1131							
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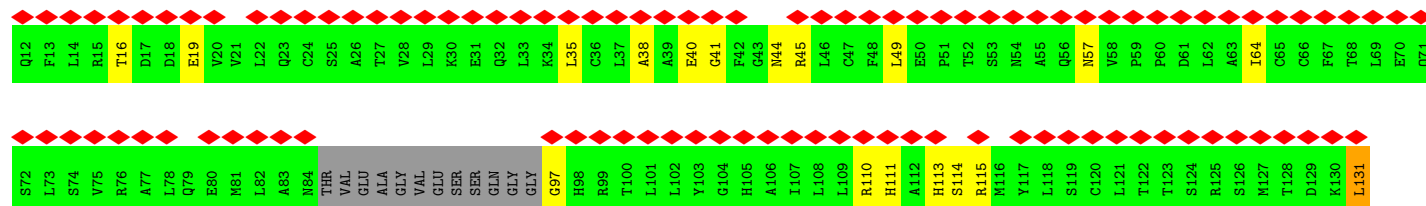
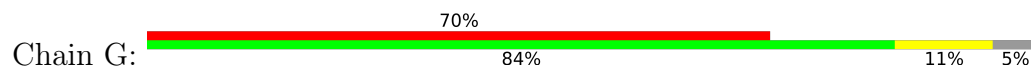




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F3962	N3963	E3967	Q3970	G3971	F3972	C3973	N3976	Q3977	A3981	H3982	S3983	L3984	N3985	W3986	F3992	L3993	H3994	S3995	F3996	A3997	H3998	N3999	M4000	N4001	L4002	S3928	S3929	I3930	S3931	D3932	F3933	S3934	W3935	Y3936	Y3937	S3938	C3939	K3940	D3941	V3942	I3943	E3944	E3945	Q3946	G3947	K3948	R3949	N3950	A3954	N3955	K3959	Q3960	N4034	V4035																																																			
N3741	GLY	GLU	ALA	GLU	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	F3758	E3759	K3760	Q3761	R3762	L3763	L3764	Q3765	Q3766	S3767	R3768	R3769	L3770	H3771	T3772	R3773	Q3774	E3777	K3778	V3779	L3780	Q3781	C3786	K3787	G3788	E3789	A3792	K3799	S3803	I3804	L3805	N3806	G3807	G3808	N3809	A3810	K3815	F3816	L3817	Y3818	L3820	K3821	D3822	K3823	K3824	E3825	F3828	F3829	Q3830	Q3833	Q3836	L3842	D3843	F3847	E3848	R3849	Q3850	N3851	Q3852	A3853	E3854	G3855	L3856	G3857	M3858	V3859	N3860	E3861	D3862	G3863	T3864	V3865	T3866	N3867	R3868	Q3869	N3870	G3871	E3872	K3873	V3874	N3875	A3876	D3877	D3878	E3879	F3880	L3884	F3885
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T3664	E3665	D3666	H3667	S3668	F3669	D3674	D3675	D3676	K3679	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	K3694	H3704	F3705	S3706	R3707	L3710	T3711	E3712	K3713	S3714	T3715	L3716	D3717	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	Y3725	A3726	K3731	H3734	L3735	E3736	E3737	G3738	G3739	E3740																																																				
N3741	GLY	GLU	ALA	GLU	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	F3758	E3759	K3760	Q3761	R3762	L3763	L3764	Q3765	Q3766	S3767	R3768	R3769	L3770	H3771	T3772	R3773	Q3774	E3777	K3778	V3779	L3780	Q3781	C3786	K3787	G3788	E3789	A3792	K3799	S3803	I3804	L3805	N3806	G3807	G3808	N3809	A3810	K3815	F3816	L3817	Y3818	L3820	K3821	D3822	K3823	K3824	E3825	F3828	F3829	Q3830	Q3833	Q3836	L3842	D3843	F3847	E3848	R3849	Q3850	N3851	Q3852	A3853	E3854	G3855	L3856	G3857	M3858	V3859	N3860	E3861	D3862	G3863	T3864	V3865	T3866	N3867	R3868	Q3869	N3870	G3871	E3872	K3873	V3874	N3875	A3876	D3877	D3878	E3879	F3880	L3884	F3885
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X3028	X3029	X3030	X3031	X3032	X3033	X3034	X3035	X3036	X3037	X3038	X3039	X3040	X3041	X3042	X3043	X3044	X3045	X3046	X3047	X3048	X3049	X3050	X3051	X3052	X3053	X3054	X3055	X3056	X3057	X3058	X3059	X3060	X3061	X3062	X3063	X3134	X3135	X3136	X3137	X3138	X3139	X3140	X3141	X3142	X3143	X3144	X3145	X3146	X3147	X3148	X3149	X3150	X3151	X3152	X3153	X3154	X3155	X3156	X3157																																														
X3158	X3159	X3160	X3161	X3162	X3163	X3170	X3171	X3172	X3173	X3174	X3175	X3176	X3177	X3178	X3179	X3180	X3181	X3182	X3183	X3184	X3185	X3186	X3187	X3188	X3189	X3190	X3191	X3192	X3193	X3194	X3195	X3196	X3197	X3198	X3199	X3200	X3201	X3202	X3203	X3204	X3205	X3206	X3207	X3208	X3209	X3210	X3211	X3212	X3213	X3214	X3215	X3216	X3217	X3218	X3219	X3220	X3221	X3222	X3223																																														
X3224	X3225	X3226	X3227	X3228	X3229	X3230	X3231	X3232	X3233	X3234	X3235	X3236	X3241	X3242	X3243	X3244	X3245	X3246	X3247	X3248	X3249	X3250	X3251	X3252	X3253	X3254	X3256	X3261	X3262	X3263	X3264	X3265	X3266	X3267	X3268	X3269	X3270	X3271	X3272	X3273	X3274	X3275	X3276	X3277	X3278	X3279	X3280	X3281	X3282	X3283	X3284	X3285	X3286	X3287	X3288	X3289	X3290	X3291	X3292	X3293																																													
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T3664	E3665	D3666	H3667	S3668	F3669	D3674	D3675	D3676	K3679	A3680	G3681	E3682	Q3683	E3684	E3685	E3686	E3687	E3688	E3689	V3690	E3691	E3692	K3693	K3694	H3704	F3705	S3706	R3707	L3710	T3711	E3712	K3713	S3714	T3715	L3716	D3717	E3718	D3719	Y3720	L3721	Y3722	M3723	A3724	Y3725	A3726	K3731	H3734	L3735	E3736	E3737	G3738	G3739	E3740																																																				
N3741	GLY	GLU	ALA	GLU	GLU	E3747	E3748	V3749	E3750	V3751	S3752	F3753	E3754	E3755	K3756	E3757	F3758	E3759	K3760	Q3761	R3762	L3763	L3764	Q3765	Q3766	S3767	R3768	R3769	L3770	H3771	T3772	R3773	Q3774	E3777	K3778	V3779	L3780	Q3781	C3786	K3787	G3788	E3789	A3792	K3799	S3803	I3804	L3805	N3806	G3807	G3808	N3809	A3810	K3815	F3816	L3817	Y3818	L3820	K3821	D3822	K3823	K3824	E3825	F3828	F3829	Q3830	Q3833	Q3836	L3842	D3843	F3847	E3848	R3849	Q3850	N3851	Q3852	A3853	E3854	G3855	L3856	G3857	M3858	V3859	N3860	E3861	D3862	G3863	T3864	V3865	T3866	N3867	R3868	Q3869	N3870	G3871	E3872	K3873	V3874	N3875	A3876	D3877	D3878	E3879	F3880	L3884	F3885
R3886	F3887	L3888	Q3889	E3893	N3896	N3897	D3898	F3899	Y3902	L3903	R3904	T3905	Q3906	T3907	G3908	N3909	T3910	T3911	T3912	I3913	Y3922	L3923	L3924	R3925	E3928	S3929	I3930	S3931	D3932	F3933	S3934	W3935	Y3936	Y3937	S3938	C3939	K3940	D3941	V3942	I3943	E3944	E3945	Q3946	G3947	K3948	R3949	N3950	A3954	N3955	K3959	Q3960	N4034	V4035																																																				
F3962	N3963	E3967	Q3970	G3971	F3972	C3973	N39																																																																																																		

- Molecule 2: Ryanodine receptor 1



E947	D948	N949	L950	K951	K952	T953	K954	L955	P956	K957	T958	Y959	N960	M961	S962	N963	G964	Y965	K966	P967	A968	P969	L970	D971	L972	S973	H974	Y975	K976	L977	T978	P979	A980	Q981	T982	T983	L984	Y985	D986	L987	L988	A989	E990	N991	A997	A998	R1000	Y1001	A1002	Q1003	G1004	Y1005	S1006	Y1007	S1008	A1009	VAL					
I887	E888	Q889	G890	W891	T892	G893	G894	P895	V896	R897	D898	D899	N900	K901	P902	N903	H904	P905	C906	S907	H908	T909	D910	F911	H911	S912	P913	C914	P915	V916	D817	THR	VAL	GLN	T961	V862	L863	P864	P865	H866	L867	E868	R869	I870	R871	E872	K873	L874	A875	E876	N877	I878	R879	E880	V939	G940	W941	L823	A883	D943	E944	K945
G766	V767	F768	E769	A770	F771	W772	L773	D774	G775	L776	F777	F778	V779	V780	S781	F782	F783	S784	A785	G786	V787	K788	V789	R790	F791	V792	L793	G794	G795	R796	H797	G798	E799	F800	K801	F802	L803	P804	P805	P806	C807	Y808	A809	H812	E813	A814	L816	P817	R818	E819	R820	L821	R822	W882	A883	P825	I826					
N705	G706	V707	G708	D709	D710	L711	Y712	S713	G714	G715	F716	D717	G718	L719	H720	L721	W722	G723	G724	H725	V726	A727	R728	P729	V730	T731	S732	P733	G734	Q735	H736	L737	L738	P740	E741	D742	V743	V744	S745	C746	C747	L748	L749	S751	V752	F753	S754	T755	S756	P757	R758	T759	W760	G761	C762	P763						
R645	P646	N647	T648	F649	V650	G651	R652	A653	G655	S656	T657	Q658	V659	G660	R661	W662	W663	F664	E665	P666	V667	D668	D669	E670	V671	V672	P673	F674	L675	T676	A677	Q618	D619	L620	N624	L625	L626	P627	C628	R629	E630	L631	L632	L633	Q634	T635	N636	L637	I638	V640	V641	T642	S643	I644								
M581	H582	I583	K584	I587	S588	L589	L590	H593	G594	R595	N596	H597	K598	V599	L600	D601	V602	L603	C604	S605	L606	C607	V608	C609	N610	G611	V612	A613	R615	S616	N617	Q618	D619	L620	N624	L625	L626	P627	C628	R629	E630	L631	L632	L633	Q634	T635	N636	L637	I638	V640	V641	T642	S643	I644								
A512	E513	S514	N515	K516	E517	N520	L521	L522	Y523	A527	S528	R531	G532	N533	R534	A535	N536	C537	A538	L539	F540	S541	T542	D545	S549	K550	L551	D552	R553	L554	E555	A556	S557	S558	G559	I560	L561	E562	C566	V567	L568	I569	E570	S571	P572	E573	V574	L575	N576	I577	Q579	E580										
T438	E439	A440	Q446	F452	E453	P454	P455	S456	E457	E458	L459	Q460	H461	E462	Q465	L466	R469	S470	L471	R472	N473	R474	Q475	S476	L477	F478	Q479	E480	E481	S485	L488	N489	C490	Q491	D492	R493	L494	Y497	T498	T499	A500	A501	H502	F503	A504	E505	Y506	A507	G508	E509	E510	A511										
K373	K374	K375	A376	L377	L378	H379	Q380	E381	G382	H383	M384	D385	D386	A387	L388	F389	L390	T391	R392	C393	Q394	Q395	E396	E397	R402	M403	I404	H405	A408	G409	L410	Y411	N412	Q413	F414	I415	K416	L418	D419	S420	F421	S422	G423	R426	G427	S428	G429	P430	P431	A432	G433	A435	L436	P437								
S313	F314	C315	F316	R317	V318	S319	K320	E321	K322	L323	D324	T325	A326	P327	K328	R329	D330	V331	E332	G333	M334	G335	P336	P337	E338	I339	K340	Y341	C342	E343	S344	C346	F347	V348	Q349	H350	V351	A352	S353	G354	L355	W356	L357	T358	Y359	A360	A361	P362	D363	P364	K365	A366	L367	T368	L369	G370	V371	L372				
C253	T254	H255	A256	R257	S258	L259	W260	R261	L262	E263	P264	L265	R266	I267	S268	W269	T270	G271	S272	E273	L274	R275	W276	G277	Q278	P279	L280	R281	I282	R283	H284	V285	T286	G288	R289	Y290	L291	A292	L293	T294	E295	D296	Q297	G298	L299	V300	V301	Y302	D303	A304	C305	K306	A307	H308	T309	K310	A311	T312				
D192	A193	S194	F195	M196	Q197	T198	L199	W200	N201	M202	P203	P204	I205	C206	S207	W208	C208	C209	E210	E211	G212	Y213	V214	T215	G216	G217	H218	V219	L220	R221	L222	F223	H224	G225	H226	M227	D228	E229	C230	L231	T232	V233	I234	S234	A235	A236	S237	D238	D239	D240	Q241	R242	A243	L244	Y247	E248	C249	G250	A251	V252		



GLN	THR	ALA	GLN	THR	TYR	ASP	PRD	ARG	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	S2798	D2861	L2862	S2863	G2864	V2865	T2866	L2867	S2868	R2869	E2870	L2871	Q2872	M2873	A2874	L2875	E2876	Q2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	Q2887	R2888	K2889	L2890	K2891	Q2892	E2893	L2894	E2895	A2896	T2897	G2898	G2899	G2778	T2901	H2902	P2903
E2784	L2785	K2786	T2787	H2788	P2789	M2790	L2791	R2792	P2793	Y2794	K2795	L2796	D2736	P2737	R2738	E2739	V2740	E2741	K2802	E2803	L2804	R2805	R2806	V2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	K2818	A2819	N2820	E2821	T2822	I2823	E2824	R2825	A2826	R2827	E2828	Q2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER		
X2694	X2695	X2696	X2697	X2698	X2699	X2700	X2701	X2702	X2703	X2704	X2705	X2706	X2647	X2648	X2649	X2650	X2651	X2652	X2653	X2654	X2655	X2656	X2657	X2658	X2659	X2660	X2661	X2662	X2663	X2664	X2665	X2666	X2667	X2668	X2669	X2670	X2671	X2672	X2673	X2674	X2675	X2676	X2677	X2678	X2679	X2680	X2681	X2682	X2683	X2684	X2685	X2686	X2687	X2688	X2689	X2690	X2691	X2692	X2693		
K2634	K2635	K2636	K2637	K2638	K2639	K2640	K2641	K2642	K2643	K2644	K2645	K2646	K2587	K2588	K2589	K2590	K2591	K2592	K2593	K2594	K2595	K2596	K2597	K2598	K2599	K2600	K2601	K2602	K2603	K2604	K2605	K2606	K2607	K2608	K2609	K2610	K2611	K2612	K2613	K2614	K2615	K2616	K2617	K2618	K2619	K2620	K2621	K2622	K2623	K2624	K2625	K2626	K2627	K2628	K2629	K2630	K2631	K2632	K2633		
X2500	X2501	X2502	X2506	X2511	X2512	X2513	X2514	X2515	X2516	X2517	X2518	X2519	X2520	X2521	X2522	X2523	X2524	X2525	X2526	X2527	X2528	X2529	X2530	X2531	X2532	X2533	X2534	X2535	X2536	X2537	X2538	X2539	X2540	X2541	X2542	X2543	X2544	X2550	X2551	X2552	X2555	X2556	X2557	X2558	X2561	X2562	X2563	X2564	X2565	X2566	X2567	X2568	X2569	X2570							
F2425	Y2426	A2427	A2428	L2429	I2430	G2434	R2435	P2438	H2441	L2442	G2446	K2447	G2448	E2449	A2450	L2451	R2452	L2453	R2454	A2455	I2456	L2457	R2458	S2459	L2460	L2463	D2464	D2465	L2466	V2467	G2468	I2469	I2470	S2471	L2472	P2473	L2474	Q2475	L2476	P2477	T2478	L2479	Q2487	X2488	X2489	X2490	X2493	X2494	X2495	X2496	X2497	X2498	X2499								
F2364	Q2365	F2366	A2367	L2368	R2369	Q2370	E2371	Q2372	Q2373	S2374	Q2375	L2376	L2377	A2378	A2379	L2380	E2381	E2382	A2383	I2384	R2385	L2386	S2387	E2388	D2389	P2390	A2391	R2392	D2393	Q2394	F2395	GLY	VAL	ARG	ASP	ARG	ARG	ARG	GLU	HIS	PHE	GLY	GLU	PRO	PRO	GLU	N2414	R2415	V2416	H2417	L2418	Q2419	I2422	M2423	S2424						
Y2301	L2302	A2303	G2304	C2305	G2306	L2307	Q2308	S2309	C2310	P2311	M2312	L2313	L2314	A2315	K2316	G2317	Y2318	P2319	D2320	I2321	G2322	W2323	N2324	P2325	C2326	G2327	G2328	E2329	R2330	Y2331	L2332	D2333	F2334	F2337	A2338	V2339	F2340	N2341	N2342	Q2343	E2344	S2345	V2346	E2347	E2348	N2349	A2350	N2351	R2355	L2356	L2357	I2358	R2359	K2360	P2361	E2362	C2363				
F2225	P2226	K2227	M2228	V2229	R2234	F2235	Y2238	F2239	I2242	S2243	R2244	R2248	F2251	D2252	H2253	Y2256	L2257	M2260	S2261	Q2262	I2263	G2264	L2265	G2266	M2267	Q2268	G2269	P2272	L2273	D2274	V2275	A2276	A2277	A2278	N2283	M2284	V2285	L2286	A2287	M2289	L2290	Q2291	E2292	Q2293	D2294	L2295	E2296	K2297													
I2144	S2147	E2150	M2153	S2154	L2155	L2156	Q2161	I2162	R2163	L2166	Q2169	M2170	G2171	P2172	Q2173	I2179	Q2183	N2184	I2185	M2186	N2187	N2188	K2189	Y2192	Q2193	M2196	R2199	A2200	H2204	M2208	E2209	V2210	M2211	V2212	N2213	V2214	L2215	G2216	G2217	G2218	E2219	T2220	K2221	E2222	I2223	R2224															
LEU	LEU	GLU	THR	VAL	ARG	LEU	VAL	LYS	LYS	GLU	GLU	LYS	H2011	F2012	K2013	D2014	E2015	A2016	D2017	E2018	E2019	D2020	C2021	F2022	L2023	P2024	E2025	D2026	I2027	R2028	Q2029	F2034	H2035	Q2036	A2040	H2041	C2042	G2043	I2044	Q2045	L2046	E2047	GLU	GLU	GLU	GLU	PRO	GLU	GLU	THR	SER	LEU	ARG	SER							

L3942	E3759	E3686	E3595	K3534	X3430	X3370	X3310	X3244	X3180	X3044	X2966	L2904
D3943	K3760	E3687	X3596	E3537	X3431	X3371	X3311	X3245	X3181	X3045	X2967	L2905
F3947	Q3761	E3688	X3597	K3538	X3432	X3372	X3312	X3246	X3182	X3046	X2968	V2906
E3948	L3762	E3689	X3598	X3539	X3433	X3373	X3313	X3247	X3183	X3047	X2969	P2907
R3949	L3763	V3690	X3599	X3540	X3434	X3374	X3314	X3248	X3184	X3048	X2970	Y2908
Q3950	L3764	E3691	X3600	X3541	X3435	X3375	X3315	X3249	X3185	X3049	X2971	D2909
N3951	Q3765	E3692	X3601	X3542	X3436	X3376	X3316	X3250	X3186	X3050	X2972	T2910
K3952	Q3766	K3693	X3602	X3543	X3437	X3377	X3317	X3251	X3187	X3051	X2973	L2911
A3953	S3768	K3694	X3603	X3544	X3440	X3378	X3318	X3252	X3188	X3052	X2974	T2912
E3954	R3769	H3704	X3604	X3545	X3441	X3379	X3319	X3253	X3189	X3053	X2975	A2913
E3955	L3770	E3854	X3605	X3546	X3442	X3380	X3320	X3254	X3190	X3054	X2976	K2914
G3956	H3771	F3705	X3606	X3547	X3443	X3381	X3321	X3255	X3191	X3055	X2977	E2915
L3957	T3772	S3706	X3607	X3548	X3444	X3382	X3322	X3256	X3192	X3056	X2978	K2916
G3957	R3773	R3707	X3608	X3549	X3445	X3383	X3323	X3257	X3193	X3057	X2979	A2917
M3958	K3774	L3710	X3609	X3548	X3446	X3384	X3324	X3258	X3194	X3058	X2980	R2918
V3959	E3777	T3711	X3610	X3550	X3447	X3385	X3325	X3259	X3195	X3059	X2981	D2919
N3960	M3778	E3712	X3611	X3551	X3448	X3386	X3326	X3260	X3196	X3060	X2982	R2920
E3961	Q3779	K3713	X3612	X3552	X3449	X3387	X3327	X3261	X3197	X3061	X2983	E2921
D3962	L3780	S3714	X3613	X3553	X3450	X3388	X3328	X3262	X3198	X3062	X2984	K2922
G3963	Q3781	K3715	T3639	X3554	X3451	X3389	X3329	X3263	X3199	X3063	X2985	A2923
T3964	R3964	L3716	P3640	X3555	X3452	X3390	X3330	X3264	X3200	X3134	X3004	Q2924
V3965	G3766	D3717	L3641	X3556	X3453	X3391	X3331	X3265	X3201	X3135	X3005	E2925
L3966	K3767	E3718	Y3642	X3557	X3454	X3392	X3332	X3266	X3202	X3136	X3006	L2926
N3967	G3788	D3719	N3643	X3558	X3455	X3393	X3333	X3267	X3203	X3137	X3007	L2927
R3968	E3789	Y3720	L3644	X3559	X3456	X3394	X3334	X3268	X3204	X3138	X3008	K2928
Q3969	A3792	L3721	H3647	X3560	X3457	X3395	X3335	X3269	X3205	X3139	X3009	P2929
N3970	K3799	Y3722	R3648	X3561	X3458	X3396	X3336	X3270	X3206	X3140	X3010	L2930
G3971	G3971	M3723	A3649	X3562	X3459	X3397	X3337	X3271	X3207	X3141	X3011	Q2931
E3972	S3803	A3724	C3650	X3563	X3460	X3398	X3338	X3272	X3208	X3142	X3012	K2932
K3973	T3804	Y3725	N3651	X3564	X3461	X3399	X3339	X3273	X3209	X3143	X3013	H2933
L3974	L3805	A3726	H3652	X3565	X3462	X3400	X3340	X3274	X3210	X3144	X3014	G2934
M3975	N3806	K3731	F3653	X3566	X3463	X3401	X3341	X3275	X3211	X3145	X3015	V2935
R3976	G3976	E3976	S3656	X3567	X3464	X3402	X3342	X3276	X3212	X3146	X3016	A2936
D3977	G3977	K3568	X3657	X3568	X3465	X3403	X3343	X3277	X3213	X3147	X3017	V2937
L3978	N3809	L3735	X3658	X3569	X3466	X3404	X3344	X3278	X3214	X3148	X3018	T2938
E3979	A3810	E3736	K3659	X3570	X3467	X3405	X3345	X3279	X3215	X3149	X3019	R2939
F3980	K3815	E3737	A3660	X3571	X3468	X3406	X3346	X3280	X3216	X3150	X3020	X2942
D3983	M3816	G3738	L3661	X3572	X3511	X3407	X3347	X3281	X3217	X3151	X3021	L2943
L3984	L3817	K3739	T3662	X3573	X3512	X3408	X3348	X3282	X3218	X3152	X3022	K2944
F3985	D3818	X3574	L3663	X3574	X3513	X3409	X3349	X3283	X3219	X3153	X3023	X2945
R3986	Y3819	N3741	T3664	X3575	X3514	X3410	X3350	X3284	X3220	X3154	X3024	X2946
F3987	L3820	GLY	E3665	X3576	X3515	X3411	X3351	X3285	X3221	X3155	X3025	X2947
L3988	K3821	GLU	D3666	X3577	X3516	X3412	X3352	X3286	X3222	X3156	X3026	X2948
Q3989	X3824	ALA	H3667	X3578	X3517	X3413	X3353	X3287	X3223	X3157	X3027	L2949
E3993	E3825	GLU	S3668	X3579	X3518	X3414	X3354	X3288	X3224	X3158	X3028	X2950
		E3747	F3669	X3580	X3519	X3415	X3355	X3289	X3225	X3159	X3029	X2951
N3996	F3828	E3748	I3674	X3581	X3520	X3416	X3356	X3290	X3226	X3160	X3030	K2952
N3997	F3829	V3749	D3675	X3582	X3521	X3417	X3357	X3291	X3227	X3161	X3031	X2953
D3998	Q3830	E3750	D3676	X3583	X3522	X3418	X3358	X3292	X3228	X3162	X3032	Y2954
F3999		V3751	K3679	X3584	X3523	X3419	X3359	X3293	X3229	X3163	X3033	X2955
	Q3833	S3752	K3679	X3585	X3524	X3420	X3360	X3294	X3230	X3170	X3034	X2956
Y3902	Y3902	F3753	A3680	X3586	X3525	X3421	X3361	X3295	X3231	X3171	X3035	X2957
L3903	L3903	E3754	G3681	X3587	X3526	X3422	X3362	X3296	X3232	X3172	X3036	K2958
T3905	T3905	E3755	G3681	X3588	X3527	X3423	X3363	X3297	X3233	X3173	X3037	X2959
Q3906	Q3906	K3756	E3682	X3589	X3528	X3424	X3364	X3298	X3234	X3174	X3038	X2960
T3907	T3907	E3757	Q3683	X3590	X3529	X3425	X3365	X3299	X3235	X3175	X3039	X2961
G3908	G3908	E3757	E3684	X3591	X3530	X3426	X3366	X3300	X3236	X3176	X3040	X2962
		M3758	E3685	X3592	X3531	X3427	X3367	X3294	X3237	X3177	X3041	X2963
				X3593	X3532	X3428	X3368	X3295	X3238	X3178	X3042	X2964
				X3594	X3533	X3429	X3369	X3296	X3239	X3179	X3043	V2965





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	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	0.058	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.025	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

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	0.30	0/834	0.52	0/1123
1	F	0.30	0/834	0.52	0/1123
1	H	0.30	0/834	0.53	0/1123
1	J	0.30	0/834	0.52	0/1123
2	B	0.29	0/25428	0.54	6/34534 (0.0%)
2	E	0.30	0/25428	0.54	6/34534 (0.0%)
2	G	0.29	0/25428	0.54	6/34534 (0.0%)
2	I	0.30	0/25428	0.54	6/34534 (0.0%)
All	All	0.30	0/105048	0.54	24/142628 (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	16
2	E	0	16
2	G	0	16
2	I	0	16
All	All	0	64

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	131	LEU	CA-CB-CG	8.01	133.72	115.30
2	B	131	LEU	CA-CB-CG	8.00	133.69	115.30
2	E	131	LEU	CA-CB-CG	7.99	133.68	115.30
2	I	131	LEU	CA-CB-CG	7.99	133.66	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4985	LEU	CA-CB-CG	7.25	131.97	115.30

There are no chirality outliers.

5 of 64 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	139	GLU	Peptide
2	B	1676	LEU	Peptide
2	B	312	THR	Peptide
2	B	694	PRO	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	16	0
1	F	818	0	824	18	0
1	H	818	0	824	15	0
1	J	818	0	824	14	0
2	B	29499	0	24746	268	0
2	E	29499	0	24746	273	0
2	G	29499	0	24746	261	0
2	I	29499	0	24746	262	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
All	All	121272	0	102280	1100	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 5.

The worst 5 of 1100 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:I:379:HIS:HD2	2:I:382:GLY:H	1.40	0.68
2:E:379:HIS:HD2	2:E:382:GLY:H	1.40	0.67
2:B:379:HIS:HD2	2:B:382:GLY:H	1.40	0.67
2:G:379:HIS:HD2	2:G:382:GLY:H	1.40	0.66
2:B:3773:ARG:HG3	2:B:3815:LYS:HZ3	1.61	0.65

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	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	F	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	H	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
1	J	105/108 (97%)	92 (88%)	13 (12%)	0	100	100
2	B	3235/4416 (73%)	2888 (89%)	343 (11%)	4 (0%)	51	85
2	E	3235/4416 (73%)	2888 (89%)	343 (11%)	4 (0%)	51	85
2	G	3235/4416 (73%)	2887 (89%)	344 (11%)	4 (0%)	51	85
2	I	3235/4416 (73%)	2888 (89%)	343 (11%)	4 (0%)	51	85
All	All	13360/18096 (74%)	11919 (89%)	1425 (11%)	16 (0%)	54	85

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1708	ARG
2	I	1708	ARG
2	E	1708	ARG
2	G	1708	ARG
2	B	1932	PRO

### 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	88/89 (99%)	88 (100%)	0	100	100
1	F	88/89 (99%)	88 (100%)	0	100	100
1	H	88/89 (99%)	88 (100%)	0	100	100
1	J	88/89 (99%)	88 (100%)	0	100	100
2	B	2493/3022 (82%)	2477 (99%)	16 (1%)	86	92
2	E	2493/3022 (82%)	2477 (99%)	16 (1%)	86	92
2	G	2493/3022 (82%)	2477 (99%)	16 (1%)	86	92
2	I	2493/3022 (82%)	2477 (99%)	16 (1%)	86	92
All	All	10324/12444 (83%)	10260 (99%)	64 (1%)	86	92

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

Mol	Chain	Res	Type
2	G	3896	ASN
2	G	4085	ARG
2	I	3787	LYS
2	I	1964	ARG
2	G	4120	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 152 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	57	ASN
2	G	3963	ASN
2	G	273	HIS
2	G	1760	HIS
2	G	4133	GLN

### 5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 4 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	B	14
2	I	14
2	E	14
2	G	14

The worst 5 of 56 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	4345:UNK	C	4540:PHE	N	73.36
1	I	4345:UNK	C	4540:PHE	N	73.36
1	E	4345:UNK	C	4540:PHE	N	73.36
1	G	4345:UNK	C	4540:PHE	N	73.36

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	3613:UNK	C	3639:THR	N	46.46



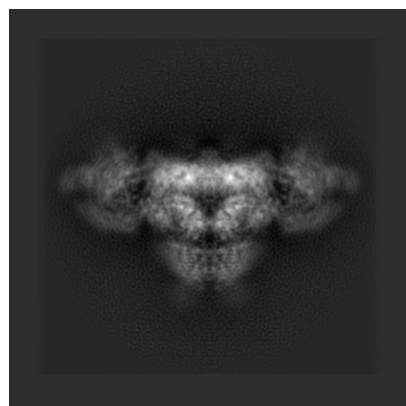
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8392. These allow visual inspection of the internal detail of the map and identification of artifacts.

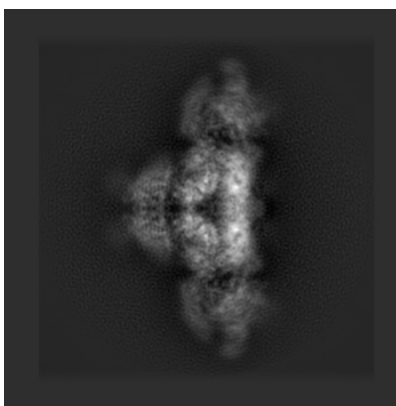
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

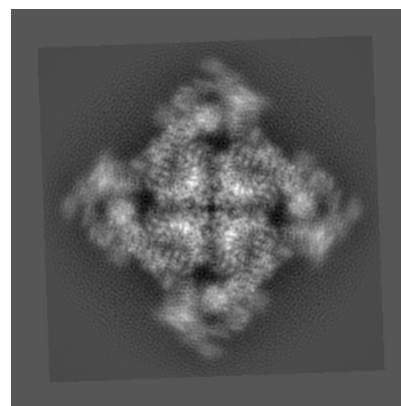
#### 6.1.1 Primary map



X

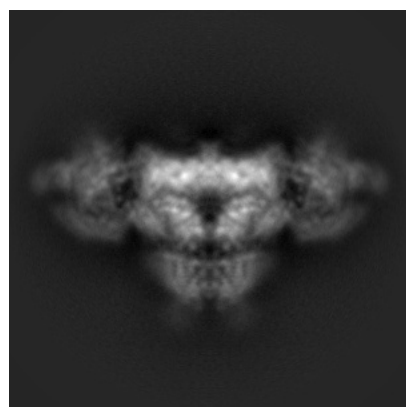


Y

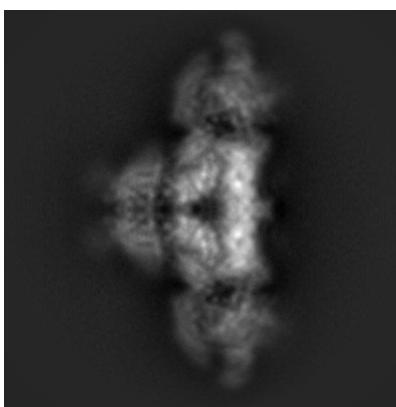


Z

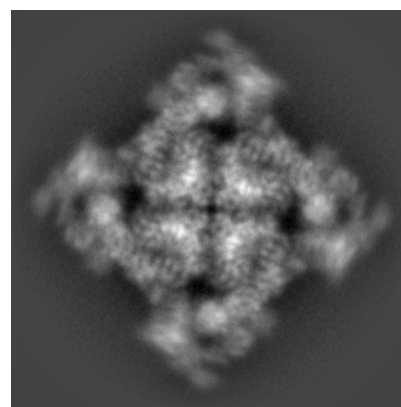
#### 6.1.2 Raw map



X



Y

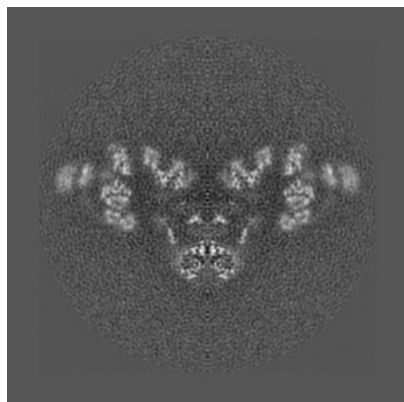


Z

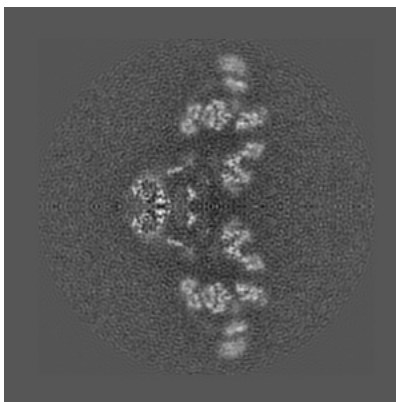
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

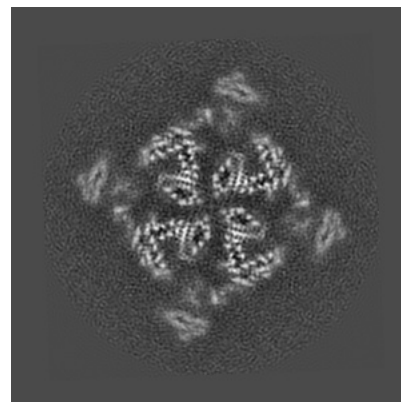
### 6.2.1 Primary map



X Index: 200

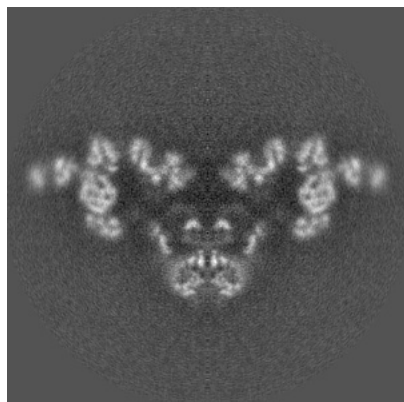


Y Index: 200

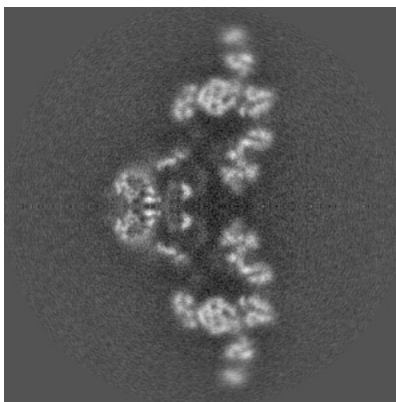


Z Index: 200

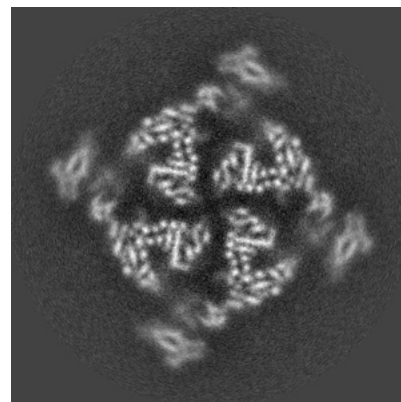
### 6.2.2 Raw map



X Index: 168



Y Index: 168

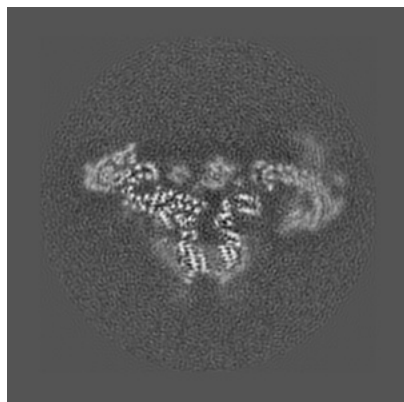


Z Index: 168

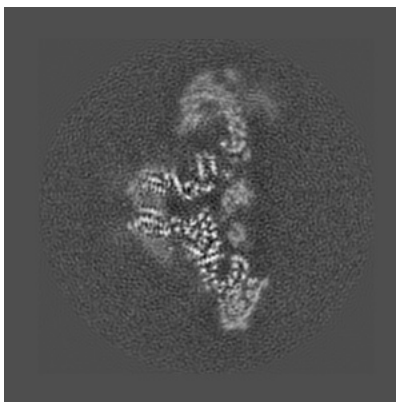
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

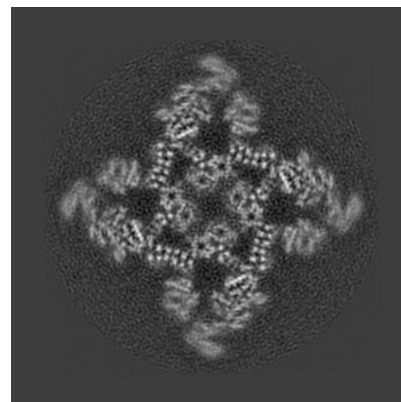
### 6.3.1 Primary map



X Index: 224

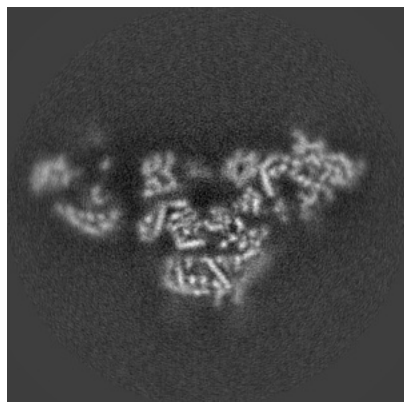


Y Index: 177

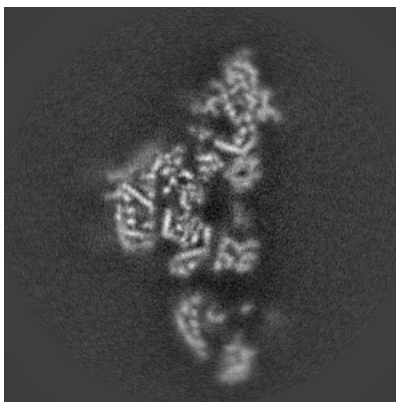


Z Index: 227

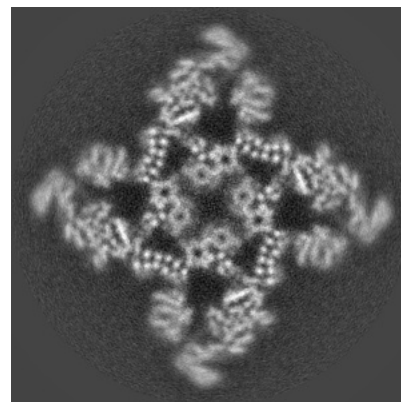
### 6.3.2 Raw map



X Index: 154



Y Index: 182

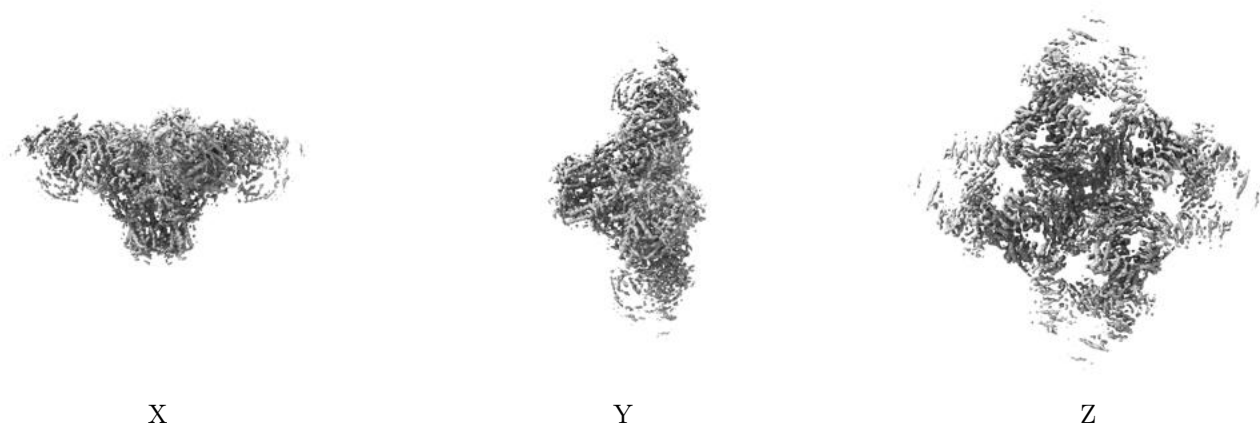


Z Index: 192

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.025. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.4.2 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.

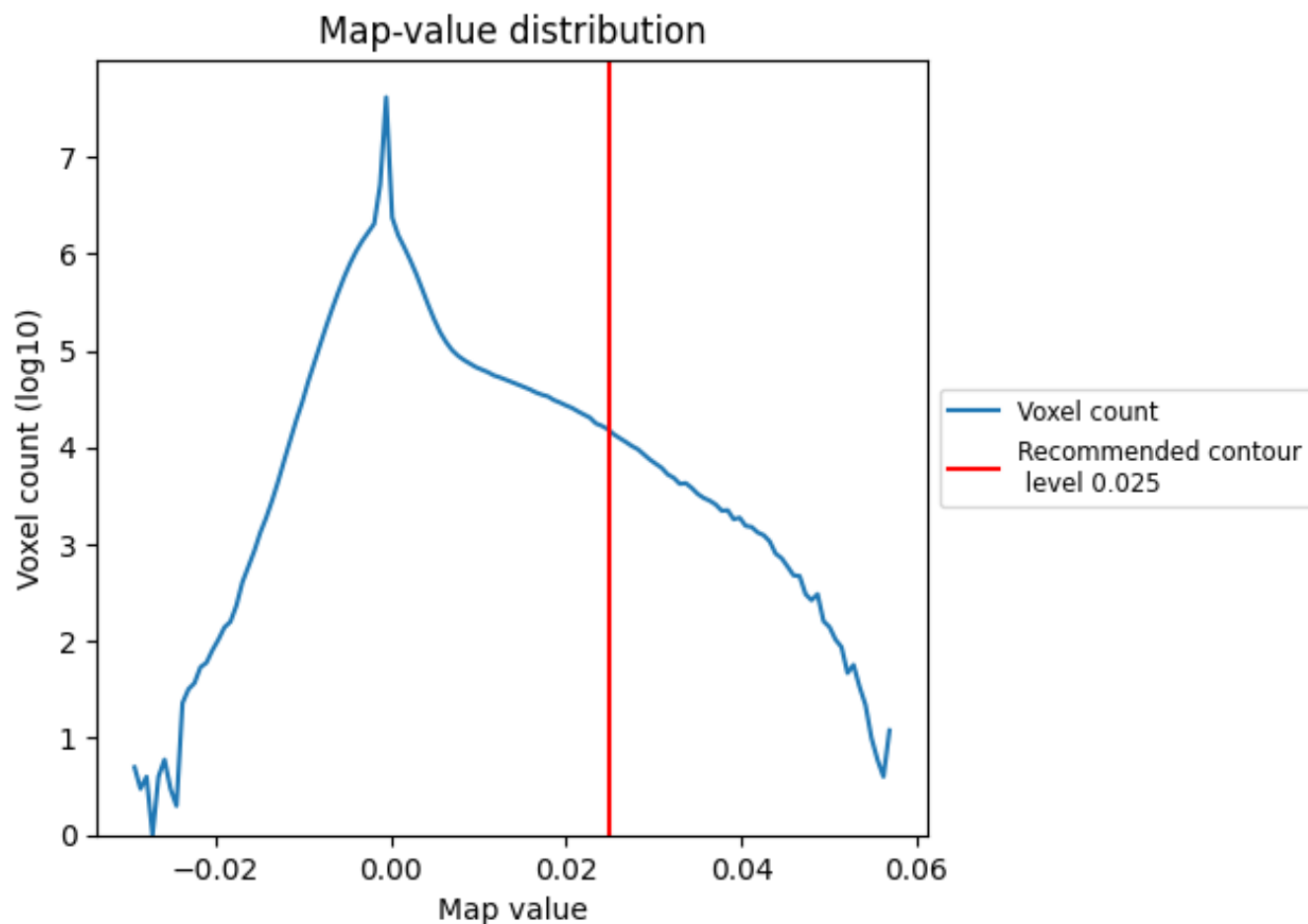
## 6.5 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

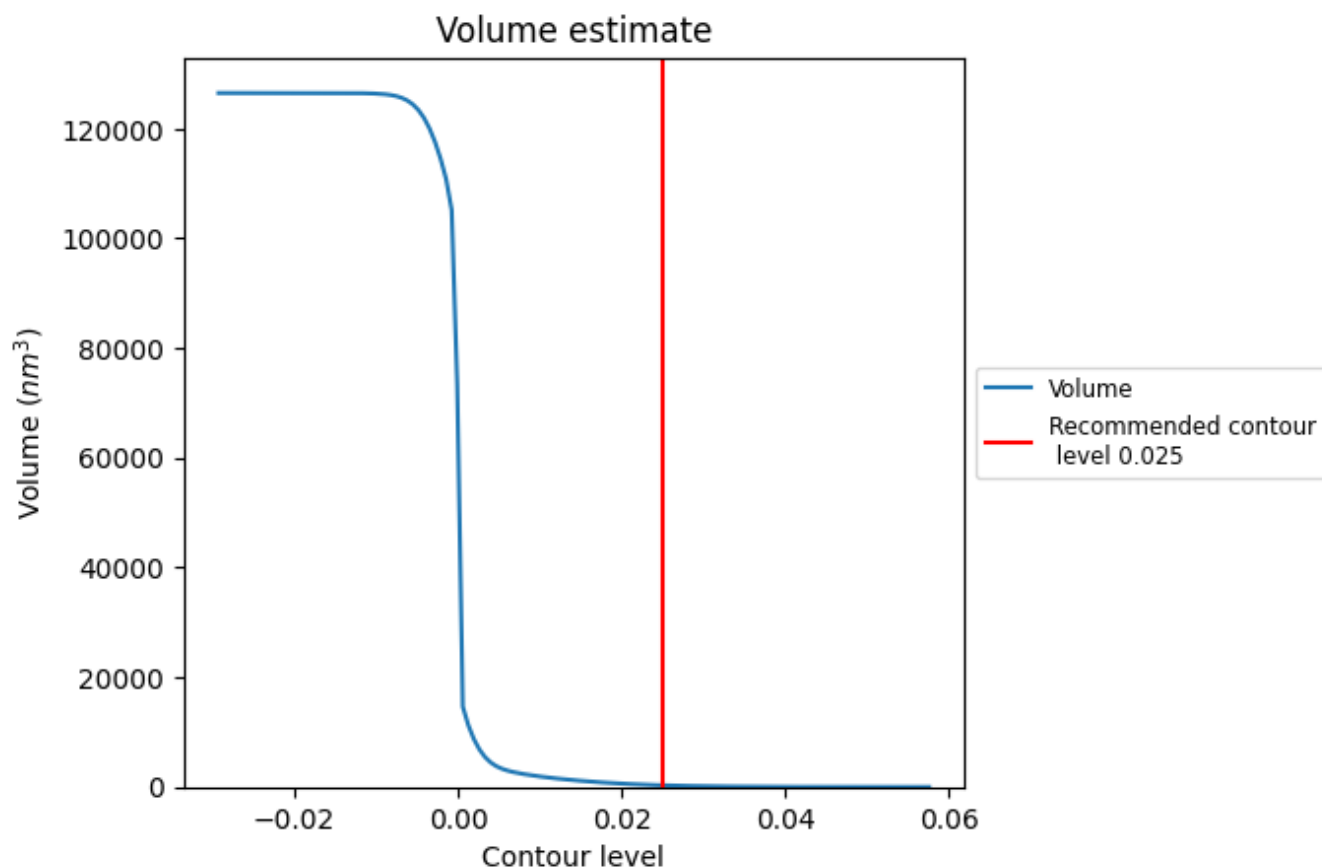
This section contains the results of statistical analysis of the map.

### 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.

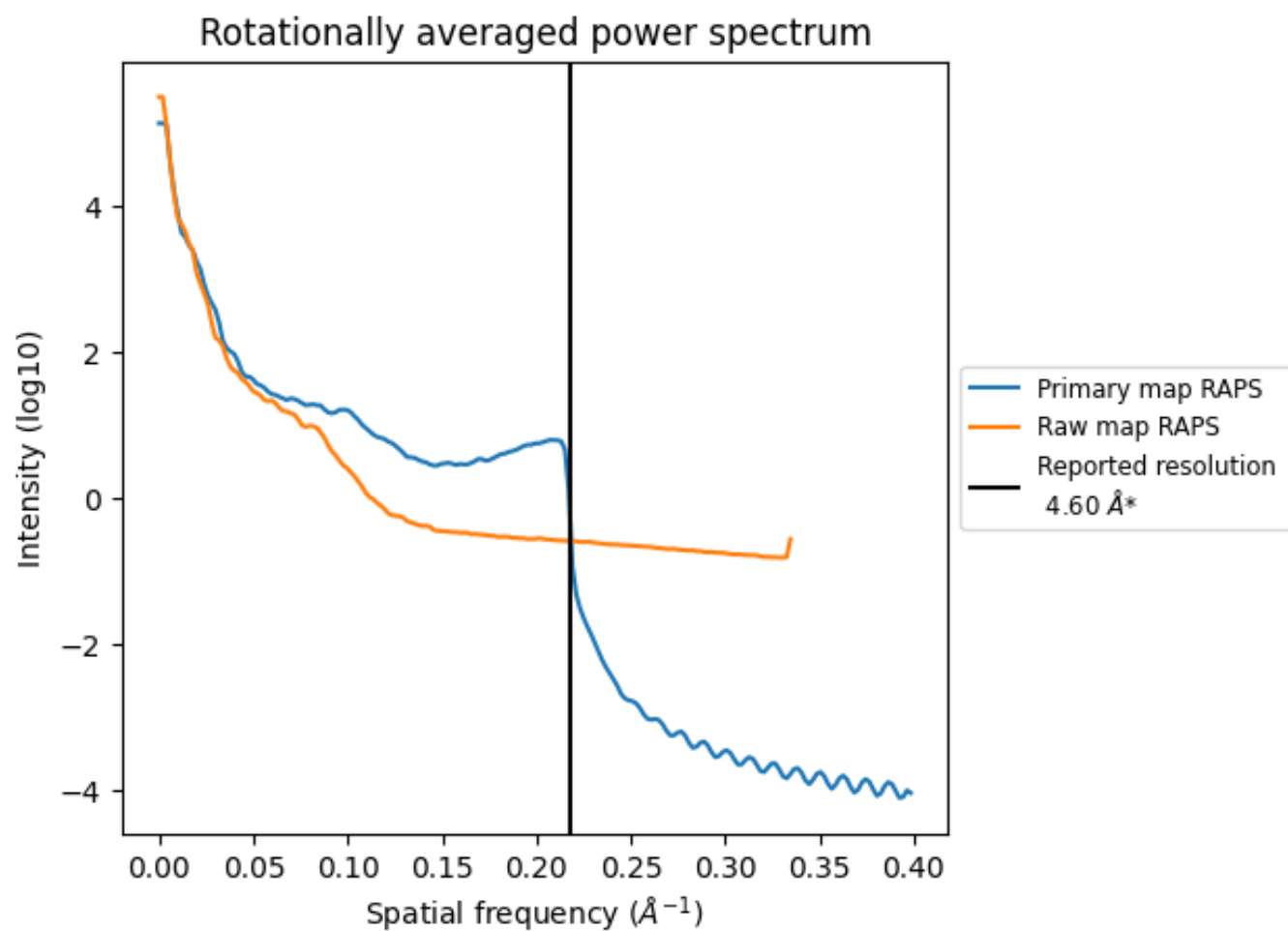
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 298 nm<sup>3</sup>; this corresponds to an approximate mass of 269 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 ⓘ

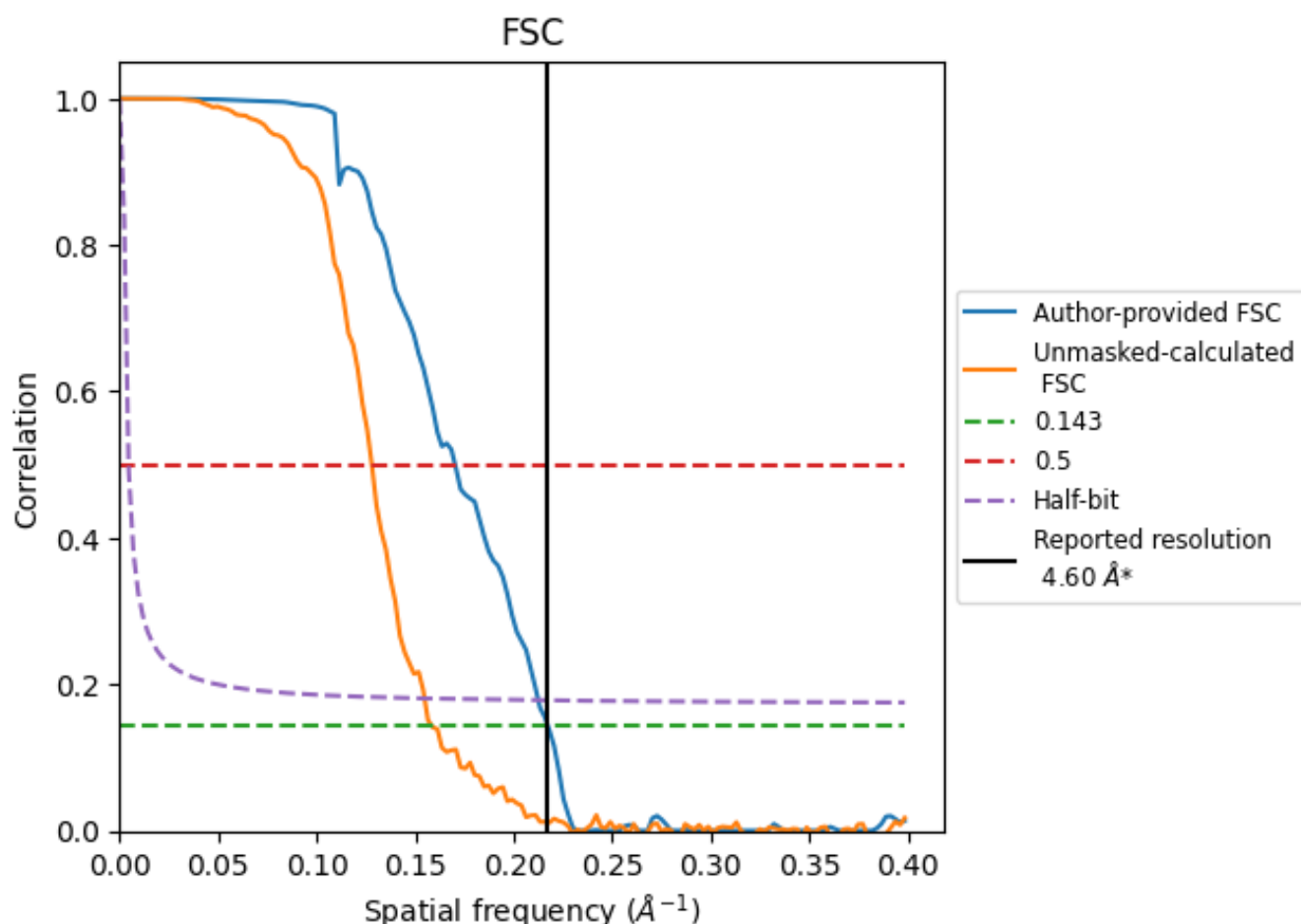


\*Reported resolution corresponds to spatial frequency of 0.217  $\text{\AA}^{-1}$

## 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 0.217 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

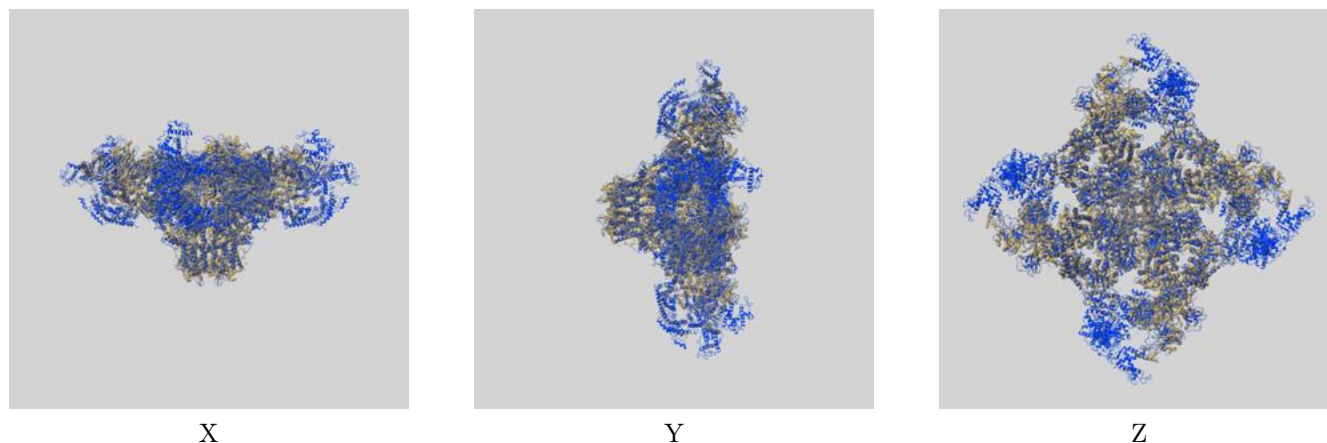
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.60	-	-
Author-provided FSC curve	4.60	5.87	4.71
Unmasked-calculated*	6.31	7.81	6.46

\*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 6.31 differs from the reported value 4.6 by more than 10 %

## 9 Map-model fit [i](#)

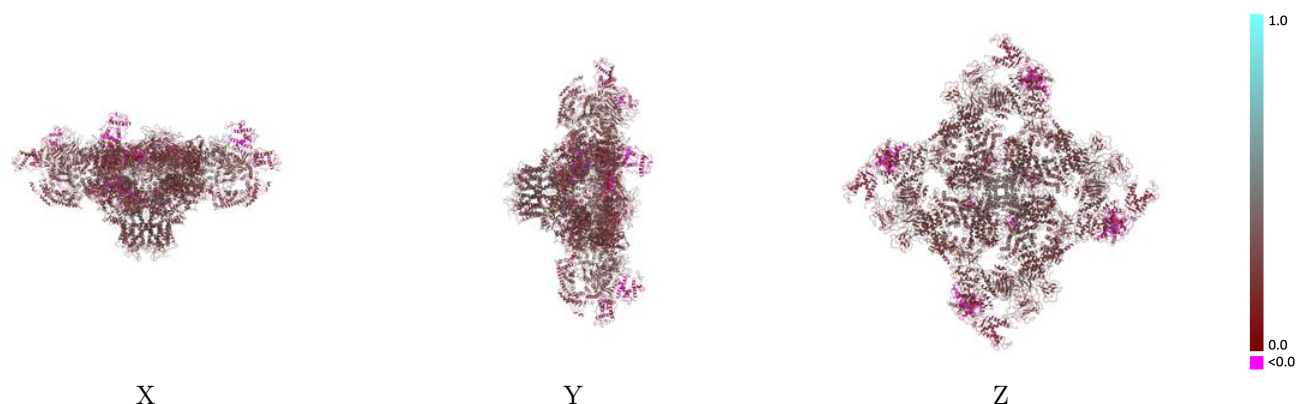
This section contains information regarding the fit between EMDB map EMD-8392 and PDB model 5TB1. Per-residue inclusion information can be found in section [3](#) on page [4](#).

### 9.1 Map-model overlay [i](#)



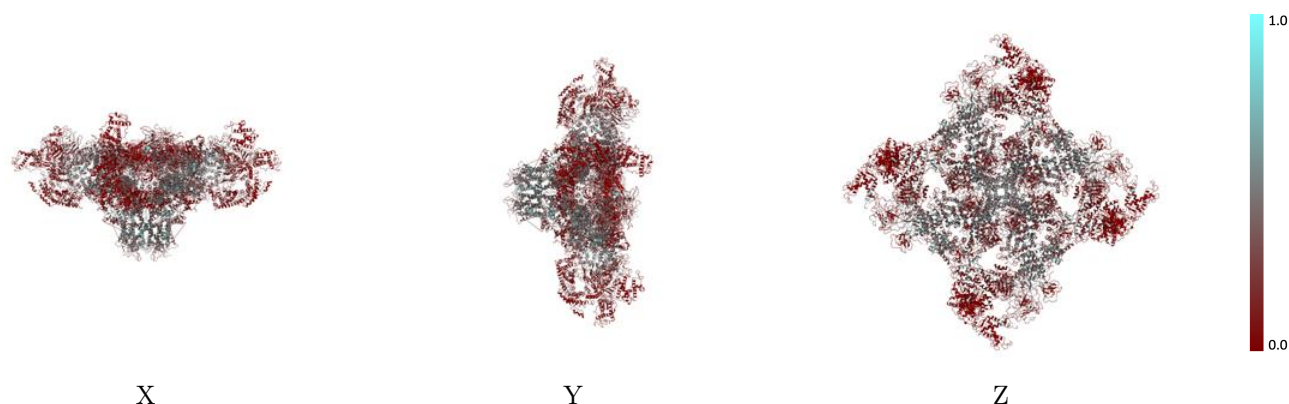
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



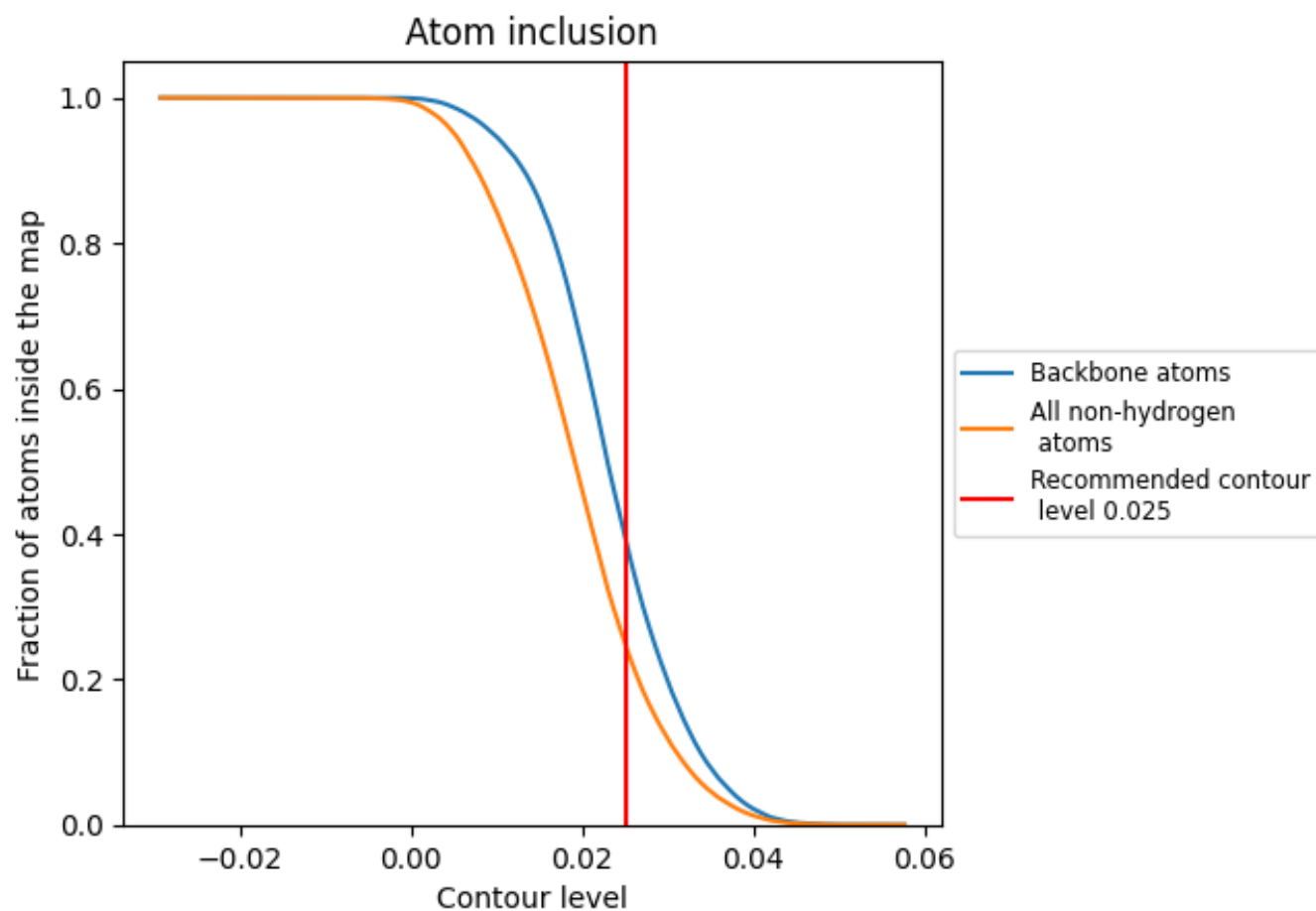
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 40% of all backbone atoms, 25% 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 (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.2492</div>	<div><div></div>0.2600</div>
A	<div><div></div>0.1886</div>	<div><div></div>0.2650</div>
B	<div><div></div>0.2509</div>	<div><div></div>0.2600</div>
E	<div><div></div>0.2505</div>	<div><div></div>0.2600</div>
F	<div><div></div>0.1836</div>	<div><div></div>0.2700</div>
G	<div><div></div>0.2513</div>	<div><div></div>0.2600</div>
H	<div><div></div>0.1886</div>	<div><div></div>0.2670</div>
I	<div><div></div>0.2512</div>	<div><div></div>0.2590</div>
J	<div><div></div>0.1886</div>	<div><div></div>0.2640</div>

1.0

0.0

<0.0