



wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 12:43 pm GMT

PDB ID : 5GL0
EMDB ID: : EMD-9520
Title : Structure of RyR1 in a closed state (C4 conformer)
Authors : Bai, X.C.; Yan, Z.; Wu, J.P.; Yan, N.
Deposited on : 2016-07-07
Resolution : 4.20 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : recalc29047

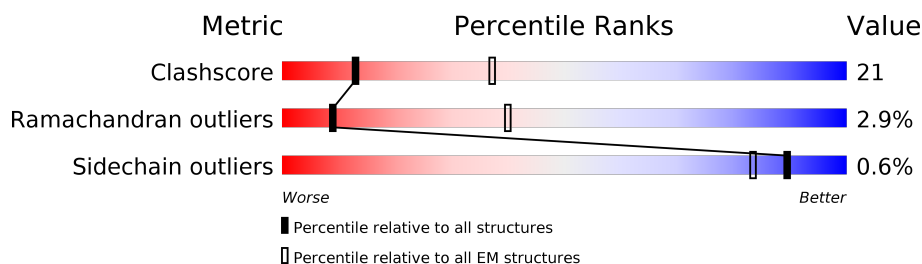
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	5037	44% 26% • 27%
1	C	5037	44% 26% • 27%
1	E	5037	44% 26% • 27%
1	G	5037	44% 27% • 27%
2	B	108	60% 38% ..
2	D	108	61% 37% ..
2	F	108	63% 35% ..
2	H	108	64% 34% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 111000 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 Ryanodine receptor 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	C	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	E	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		
1	G	3660	Total	C	N	O	S	0	0
			26917	17107	4682	4971	157		

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	D	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	F	107	Total	C	N	O	S	0	0
			832	527	146	155	4		
2	H	107	Total	C	N	O	S	0	0
			832	527	146	155	4		

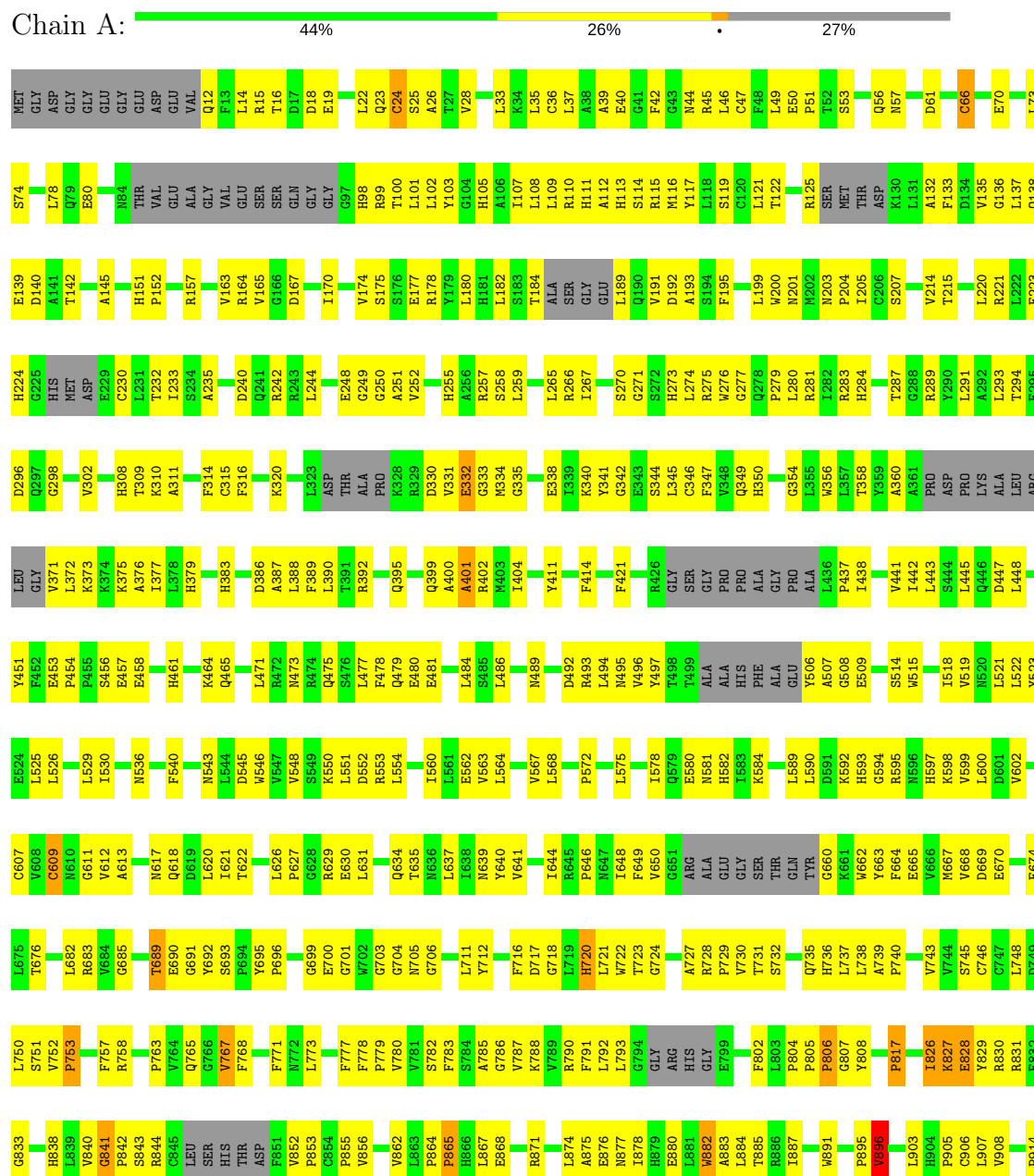
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	G	1	Total	Zn	0
			1	1	
3	A	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	E	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

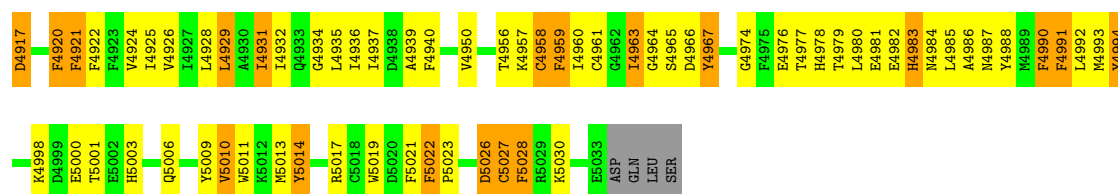
- Molecule 1: Ryanodine receptor 1



V2070	GLU	S1846	H1776	D1700	A1620	A1551	ALA	GLN	GLY	Q1280	D1207	H1127	D1028	E915
R2071	GLU	I1847	F1777	L1703	G1621	A1555	V1472	PRO	TRP	N1281	D1210	Q1130	E1029	P916
L2072	ALA	L1848	P1778	P1704	G1625	L1555	T1473	PRO	GLY	L1282	S1210	R1131	E1032	L922
VAL	PRO	L1849	P1779	P1704	G1626	P1556	T1473	THR	ALA	L1283	L1211	W1132	K1032	L922
LYS	PRO	M1851	P1780	L1707	A1627	Q1559	D1478	PRO	GLY	F1212	F1213	E1137	I1053	L929
LYS	GLU	G1852	V1783	R1708	V1628	Q1559	D1478	ALA	GLY	L1287	F1214	E1137	I1053	L929
GLU	LYS	I1853	A1784	A1709	Q1629	M1560	Q1480	LEU	LYS	F1288	G1218	F1136	P1055	A946
GLU	GLY	F1854	ALA	G1710	Q1630	V1561	G1481	PRO	GLY	L1289	L1219	F1139	ASP	GLU
PRO	ASP	G1855	LEU	Y1711	Q1631	I1562	N1482	ARG	GLY	R1290	L1219	G1140	ASP	ASN
LEU	LEU		PRO	Y1712	Q1631	I1562	N1482	LEU	GLY	L1291	F1223	R1141	GLN	ASN
GLU	GLU	D1858	ALA	D1713	L1634	E1565	L1487	PRO	THR	S1292	F1223	W1143	PRO	LYS
GLU	GLU		ALA	L1714	T1635	LEU	K1488	HIS	ALA	L1293	F1226	Q1144	THR	LYS
GLU	GLY	M1865	GLY	L1715	T1635	GLY	C1488	ASP	LYS	F1294	A1227	D1147	GLN	THR
VAL	VAL	I1866	VAL	I1716	M1636	LEU	C1488	VAL	GLY	V1295	I1228	V1148	VAL	LYS
GLU	ALA	I1867	ALA		A1638	L1639	N1491	VAL	THR	CYS	M1230	M1152	ASN	PRO
GLU	GLU	P1868	GLU	L1720	A1640	L1641	Y1493	ALA	PRO	HIS	T1235	T1156	GLN	PRO
VAL	VAL	E1869	PRO	S1722	I1641	I1641	Y1493	ASP	GLY	GLN	T1236	T1156	THR	THR
THR	PHE		ALA	A1723	P1642	P1642	G1497	ASN	GLY	HIS	T1236	T1156	ARG	Y959
THR	THR		ARG	C1724	E1643	E1643	G1497	ARG	THR	PHE	T1236	T1156	ARG	Y959
GLU	GLU	L1798	ARG	S1725	E1644	LEU	G1497	ASP	PRO	CYS	F1238	I1160	TRP	
GLU	GLU	S1799	GLU	S1726	E1644	LEU	G1497	ASP	GLN	GLN	F1238	I1160	ASP	P967
GLU	GLU	P1800	GLU	R1727	R1646	A1577	VAL	PRO	PRO	THR	S1239	I1161	ASP	
GLU	GLU	A1801	GLU	R1728	C1647	A1577	VAL	GLY	VAL	ALA	K1240	E1167	V1072	L970
GLU	GLU	I1802	GLU		M1648		PRO	ILE	VAL	GLY	S1241	E1167	R1073	
GLU	GLU	P1803	GLU	L1731	D1649	L1581	GLY	ILE	GLU	ALA	L1242	V1169	R1076	P979
GLU	GLU	L1804	GLU	I1735	I1650	L1582	GLY	ILE	GLU	ALA	P1243	L1169	R1076	
GLU	GLU	E1805	GLU	V1736	L1653	E1583	GLN	ASN	GLU	THR	Q1244	MET	A1077	L984
GLU	GLU	A1806	GLU	P1737	L1653	E1583	GLY	THR	PRO	GLN	F1245	ASP	A1078	
GLU	GLU	L1807	GLU	P1738	S1654	K1585	GLY	THR	VAL	ALA	E1246	ASP	K1079	L988
GLU	GLU	L1808	GLU	I1739	E1655	M1586	ILE	THR	ARG	PRO	P1247	ASP	K1079	A989
GLU	GLU	D1809	GLU	T1739	E1656	P1587	S1510	ALA	ALA	PRO		ASP	S1085	E990
GLU	GLU	K1810	GLU		Q1660	A1588	S1510	GLY	ALA	PRO	E1251	GLY	G1086	N991
GLU	GLU	R1813	GLU	T1742	R1661	P1589	D1513	GLU	GLU	GLY	H1252	GLU	G1087	N991
GLU	GLU	M1814	GLU	I1745	F1662	P1589	L1514	GLN	ASN	GLY	E1252	GLU	W1088	N991
GLU	GLU	L1815	GLU		H1663		V1515	GLY	GLY	GLN	H1253	THR	W1088	N991
GLU	GLU		GLU	P1750	H1663	L1595	I1516	ASP	ASP	PRO	H1254		Y1089	N994
ASP	ASP		GLY	GLY	S1664	E1596	G1517	F1440	ALA	ALA	Y1255		F1090	Q1003
GLU	GLU	D1821	GLY	ARG	H1665	V1597	C1518	A1441	THR	GLU	R1259	D1186	F1092	GLY
GLU	GLU	G1822	LYS	LYS	T1666	Q1598	L1519	GLY	THR	ASP	M1260	G1187	E1093	TRP
GLU	GLU	L1825	GLY	GLY	L1667	M1599	V1520	GLN	GLY	ALA	D1261	F1188	A1094	SER
LYS	LYS	H1825	GLY	GLY	L1676	M1600	ASP	GLY	LYS	ALA	GLY	F1188	V1095	TYR
GLU	GLU	A1826	ASN	ASN	G1677	M1601	LEU	PRO	ASN	ARG	THR	L1189	ALA	ALA
GLU	GLU	R1827	ALA	ALA	M1678	P1602	ALA	SER	LYS	ALA	VAL	P1190	VAL	VAL
GLU	GLU	D1828	ALA	ARG			G1525	C1447	LYS	ALA	VAL	V1191	GLN	GLN
ASP	ASP	P1829	ARG	ARG	A1682	S1606	L1526	P1455	ARG	GLY	ASP	C1192	ASP	ASP
GLU	GLU	V1830	ARG	ARG	A1682	M1607	L1527	D1456	PHE	PRO	PRO	S1193	ILE	ILE
GLU	GLU		HIS	HIS	H1688	M1609	M1527	Q1469	LEU	ASP	PRO	L1194	PRO	PRO
GLU	GLU	S1833	G1761	G1761	H1688	M1610	G1533	H1457	LEU	PRO	CYS		ALA	ALA
GLU	GLU		L1762	L1762	V1689	M1610	K1534	H1458	PHE	ASP	LEU	G1197	R1016	R1016
GLU	GLU	F1836	L1767	L1767	D1690	H1611	K1534	Q1469	LYS	THR	ARG	Q1198	R1017	R1017
LYS	LYS		T1768	T1768	Q1691	F1612	H1460	H1460	ALA	GLU	L1272	Q1198	R1017	R1017
GLU	GLU	V1839	T1769	T1769	A1692	L1613	V1542	F1464	LYS	ASN	A1273	G1200	P1111	N1018
ASP	ASP	P1840	T1770	T1770	Q1693	Q1614	E1543	F1464	LYS	GLY	H1274	H1201	D1112	L1021
ALA	ALA	V1841	S1770	S1770	L1694	V1615	E1544		ALA	LEU	R1275	L1202	V1113	L1021
GLU	GLU	L1842	L1771	L1771	L1695	E1616	M1545	S1467	ALA	ARG	T1276	N1203	L1115	V1022
LYS	LYS	K1843	R1772	R1772	H1696	T1617	T1546	VAL	ALA	ARG	T1277	G1204	L1115	P1023
GLU	GLU	L1844			E1699	R1618	K1547	ARG	MET	SER	G1278	G1204	N1125	Y1024
GLU	GLU	V1845	H1775	H1775	E1699	R1619	L1548	ARG	THR	GLY	S1279	Q1206	G1126	L1027

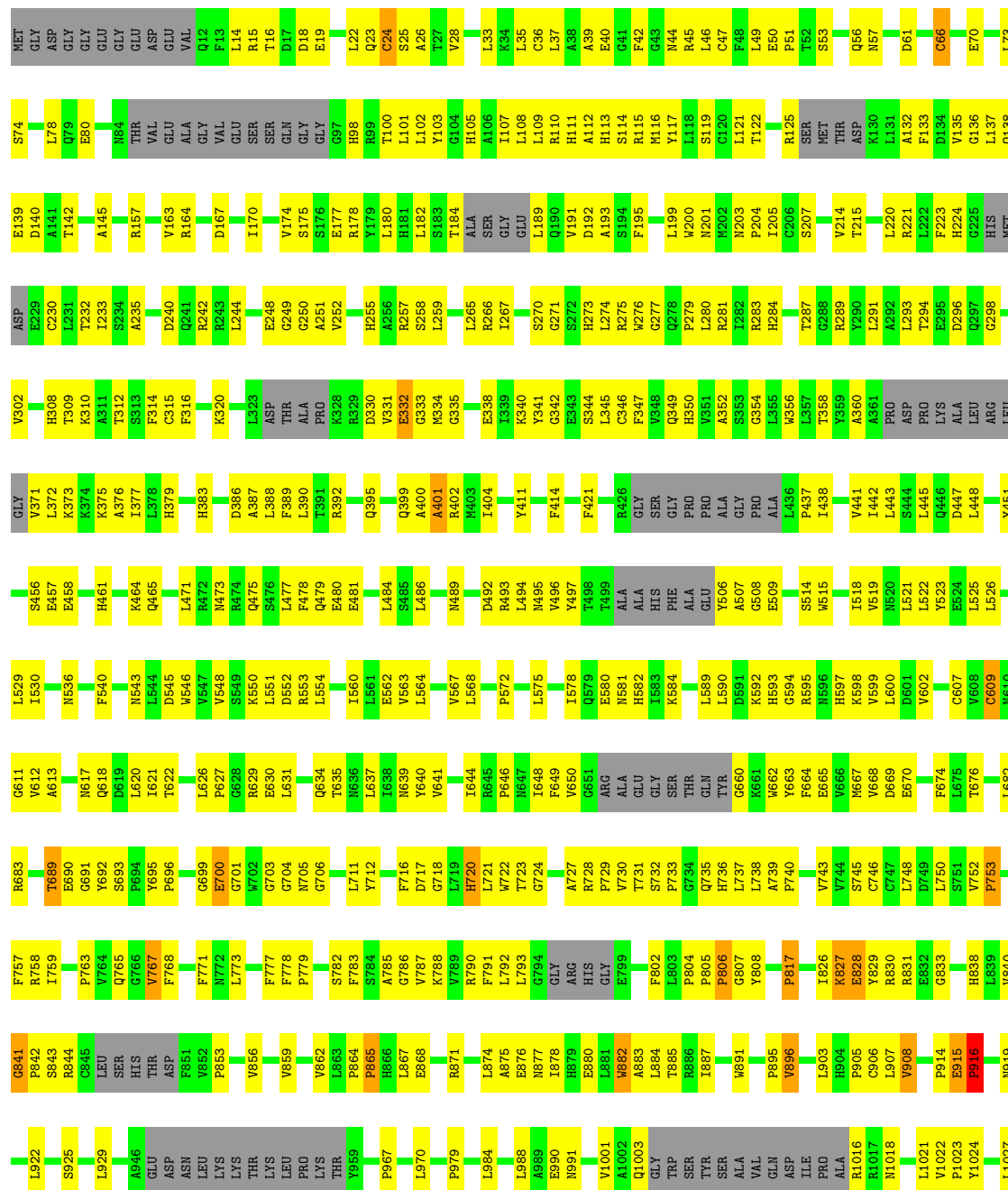



L4944	L4947	V4948	V4949	L4950	T4951	A4955	A4956	M4957	F4958	F4959	R4960	F4961	A4962	F4963	F4964	F4965	F4966	F4967	F4968	F4969	F4970	F4971	F4972	F4973	F4974	F4975	F4976	F4977	F4978	F4979	F4980	F4981	F4982	F4983	F4984	F4985	F4986	F4987	F4988	F4989	F4990	F4991	F4992	F4993	F4994	F4995	F4996	F4997	F4998	F4999	F5000	F5001	F5002	F5003	F5004	F5005	F5006	F5007	F5008	F5009	F5010	F5011	F5012	F5013	F5014	F5015	F5016	F5017	F5018	F5019	F5020	F5021	F5022	F5023	F5024	F5025	F5026	F5027	F5028	F5029	F5030	F5031	F5032	F5033	F5034	F5035	F5036	F5037	F5038	F5039	F5040	F5041	F5042	F5043	F5044	F5045	F5046	F5047	F5048	F5049	F5050	F5051	F5052	F5053	F5054	F5055	F5056	F5057	F5058	F5059	F5060	F5061	F5062	F5063	F5064	F5065	F5066	F5067	F5068	F5069	F5070	F5071	F5072	F5073	F5074	F5075	F5076	F5077	F5078	F5079	F5080	F5081	F5082	F5083	F5084	F5085	F5086	F5087	F5088	F5089	F5090	F5091	F5092	F5093	F5094	F5095	F5096	F5097	F5098	F5099	F5100	F5101	F5102	F5103	F5104	F5105	F5106	F5107	F5108	F5109	F5110	F5111	F5112	F5113	F5114	F5115	F5116	F5117	F5118	F5119	F5120	F5121	F5122	F5123	F5124	F5125	F5126	F5127	F5128	F5129	F5130	F5131	F5132	F5133	F5134	F5135	F5136	F5137	F5138	F5139	F5140	F5141	F5142	F5143	F5144	F5145	F5146	F5147	F5148	F5149	F5150	F5151	F5152	F5153	F5154	F5155	F5156	F5157	F5158	F5159	F5160	F5161	F5162	F5163	F5164	F5165	F5166	F5167	F5168	F5169	F5170	F5171	F5172	F5173	F5174	F5175	F5176	F5177	F5178	F5179	F5180	F5181	F5182	F5183	F5184	F5185	F5186	F5187	F5188	F5189	F5190	F5191	F5192	F5193	F5194	F5195	F5196	F5197	F5198	F5199	F5200	F5201	F5202	F5203	F5204	F5205	F5206	F5207	F5208	F5209	F5210	F5211	F5212	F5213	F5214	F5215	F5216	F5217	F5218	F5219	F5220	F5221	F5222	F5223	F5224	F5225	F5226	F5227	F5228	F5229	F5230	F5231	F5232	F5233	F5234	F5235	F5236	F5237	F5238	F5239	F5240	F5241	F5242	F5243	F5244	F5245	F5246	F5247	F5248	F5249	F5250	F5251	F5252	F5253	F5254	F5255	F5256	F5257	F5258	F5259	F5260	F5261	F5262	F5263	F5264	F5265	F5266	F5267	F5268	F5269	F5270	F5271	F5272	F5273	F5274	F5275	F5276	F5277	F5278	F5279	F5280	F5281	F5282	F5283	F5284	F5285	F5286	F5287	F5288	F5289	F5290	F5291	F5292	F5293	F5294	F5295	F5296	F5297	F5298	F5299	F5300	F5301	F5302	F5303	F5304	F5305	F5306	F5307	F5308	F5309	F5310	F5311	F5312	F5313	F5314	F5315	F5316	F5317	F5318	F5319	F5320	F5321	F5322	F5323	F5324	F5325	F5326	F5327	F5328	F5329	F5330	F5331	F5332	F5333	F5334	F5335	F5336	F5337	F5338	F5339	F5340	F5341	F5342	F5343	F5344	F5345	F5346	F5347	F5348	F5349	F5350	F5351	F5352	F5353	F5354	F5355	F5356	F5357	F5358	F5359	F5360	F5361	F5362	F5363	F5364	F5365	F5366	F5367	F5368	F5369	F5370	F5371	F5372	F5373	F5374	F5375	F5376	F5377	F5378	F5379	F5380	F5381	F5382	F5383	F5384	F5385	F5386	F5387	F5388	F5389	F5390	F5391	F5392	F5393	F5394	F5395	F5396	F5397	F5398	F5399	F5400	F5401	F5402	F5403																																																																																																													
E4682	F4683	L4686	L4687	L4688	L4689	L4690	L4691	L4692	L4699	Q4700	Q4701	V4705	T4708	F4709	S4710	F4711	P4712	F4715	W4716	F4717	F4718	F4719	F4720	K4721	F4722	K4723	V4724	K4727	W4728	M4806	F4807	F4808	F4809	H4812	G4819	G4894	G4895	T4822	L4823	R4824	T4825	L4826	S4828	V4830	T4831	N4833	M4839	D4873	M4874	K4875	C4876	D4877	D4878	M4879	M4880	Y4883	H4886	M4887	Y4888	C4890	V4891	R4892	G4893	G4894	G4895	I4897	C4898	E4899	E4900	I4901	P4904	E4910	R4913	V4914	F4915	Y4916	Y4917	Y4918	Y4919	Y4920	Y4921	Y4922	Y4923	Y4924	Y4925	Y4926	Y4927	Y4928	Y4929	Y4930	Y4931	Y4932	Y4933	Y4934	Y4935	Y4936	Y4937	Y4938	Y4939	Y4940	Y4941	Y4942	Y4943	Y4944	Y4945	Y4946	Y4947	Y4948	Y4949	Y4950	Y4951	Y4952	Y4953	Y4954	Y4955	Y4956	Y4957	Y4958	Y4959	Y4960	Y4961	Y4962	Y4963	Y4964	Y4965	Y4966	Y4967	Y4968	Y4969	Y4970	Y4971	Y4972	Y4973	Y4974	Y4975	Y4976	Y4977	Y4978	Y4979	Y4980	Y4981	Y4982	Y4983	Y4984	Y4985	Y4986	Y4987	Y4988	Y4989	Y4990	Y4991	Y4992	Y4993	Y4994	Y4995	Y4996	Y4997	Y4998	Y4999	Y5000	Y5001	Y5002	Y5003	Y5004	Y5005	Y5006	Y5007	Y5008	Y5009	Y5010	Y5011	Y5012	Y5013	Y5014	Y5015	Y5016	Y5017	Y5018	Y5019	Y5020	Y5021	Y5022	Y5023	Y5024	Y5025	Y5026	Y5027	Y5028	Y5029	Y5030	Y5031	Y5032	Y5033	Y5034	Y5035	Y5036	Y5037	Y5038	Y5039	Y5040	Y5041	Y5042	Y5043	Y5044	Y5045	Y5046	Y5047	Y5048	Y5049	Y5050	Y5051	Y5052	Y5053	Y5054	Y5055	Y5056	Y5057	Y5058	Y5059	Y5060	Y5061	Y5062	Y5063	Y5064	Y5065	Y5066	Y5067	Y5068	Y5069	Y5070	Y5071	Y5072	Y5073	Y5074	Y5075	Y5076	Y5077	Y5078	Y5079	Y5080	Y5081	Y5082	Y5083	Y5084	Y5085	Y5086	Y5087	Y5088	Y5089	Y5090	Y5091	Y5092	Y5093	Y5094	Y5095	Y5096	Y5097	Y5098	Y5099	Y5100	Y5101	Y5102	Y5103	Y5104	Y5105	Y5106	Y5107	Y5108	Y5109	Y5110	Y5111	Y5112	Y5113	Y5114	Y5115	Y5116	Y5117	Y5118	Y5119	Y5120	Y5121	Y5122	Y5123	Y5124	Y5125	Y5126	Y5127	Y5128	Y5129	Y5130	Y5131	Y5132	Y5133	Y5134	Y5135	Y5136	Y5137	Y5138	Y5139	Y5140	Y5141	Y5142	Y5143	Y5144	Y5145	Y5146	Y5147	Y5148	Y5149	Y5150	Y5151	Y5152	Y5153	Y5154	Y5155	Y5156	Y5157	Y5158	Y5159	Y5160	Y5161	Y5162	Y5163	Y5164	Y5165	Y5166	Y5167	Y5168	Y5169	Y5170	Y5171	Y5172	Y5173	Y5174	Y5175	Y5176	Y5177	Y5178	Y5179	Y5180	Y5181	Y5182	Y5183	Y5184	Y5185	Y5186	Y5187	Y5188	Y5189	Y5190	Y5191	Y5192	Y5193	Y5194	Y5195	Y5196	Y5197	Y5198	Y5199	Y5200	Y5201	Y5202	Y5203	Y5204	Y5205	Y5206	Y5207	Y5208	Y5209	Y5210	Y5211	Y5212	Y5213	Y5214	Y5215	Y5216	Y5217	Y5218	Y5219	Y5220	Y5221	Y5222	Y5223	Y5224	Y5225	Y5226	Y5227	Y5228	Y5229	Y5230	Y5231	Y5232	Y5233	Y5234	Y5235	Y5236	Y5237	Y5238	Y5239	Y5240	Y5241	Y5242	Y5243	Y5244	Y5245	Y5246	Y5247	Y5248	Y5249	Y5250	Y5251	Y5252	Y5253	Y5254	Y5255	Y5256	Y5257	Y5258	Y5259	Y5260	Y5261	Y5262	Y5263	Y5264	Y5265	Y5266	Y5267	Y5268	Y5269	Y5270	Y5271	Y5272	Y5273	Y5274	Y5275	Y5276	Y5277	Y5278	Y5279	Y5280	Y5281	Y5282	Y5283	Y5284	Y5285	Y5286	Y5287	Y5288	Y5289	Y5290	Y5291	Y5292	Y5293	Y5294	Y5295	Y5296	Y5297	Y5298	Y5299	Y5300	Y5301	Y5302	Y5303	Y5304	Y5305	Y5306	Y5307	Y5308	Y5309	Y5310	Y5311	Y5312	Y5313	Y5314	Y5315	Y5316	Y5317	Y5318	Y5319	Y5320	Y5321	Y5322	Y5323	Y5324	Y5325	Y5326	Y5327	Y5328	Y5329	Y5330	Y5331	Y5332	Y5333	Y5334	Y5335	Y5336	Y5337	Y5338	Y5339	Y5340	Y5341	Y5342	Y5343	Y5344	Y5345	Y5346	Y5347	Y5348	Y5349	Y5350	Y5351	Y5352	Y5353	Y5354	Y5355	Y5356	Y5357	Y5358	Y5359	Y5360	Y5361	Y5362	Y5363	Y5364	Y5365	Y5366	Y5367	Y5368	Y5369	Y5370	Y5371	Y5372	Y5373	Y5374	Y5375	Y5376	Y5377	Y5378	Y5379	Y5380	Y5381	Y5382	Y5383	Y5384	Y5385	Y5386	Y5387	Y5388	Y5389	Y5390	Y5391	Y5392	Y5393	Y5394	Y5395	Y5396	Y5397	Y5398	Y5399	Y5400	Y5401	Y5402	Y5403
ALA	GLY	PRO	GLY	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY																																																																																																																																																																																	



• Molecule 1: Ryanodine receptor 1

Chain C: 44% 26% 27%







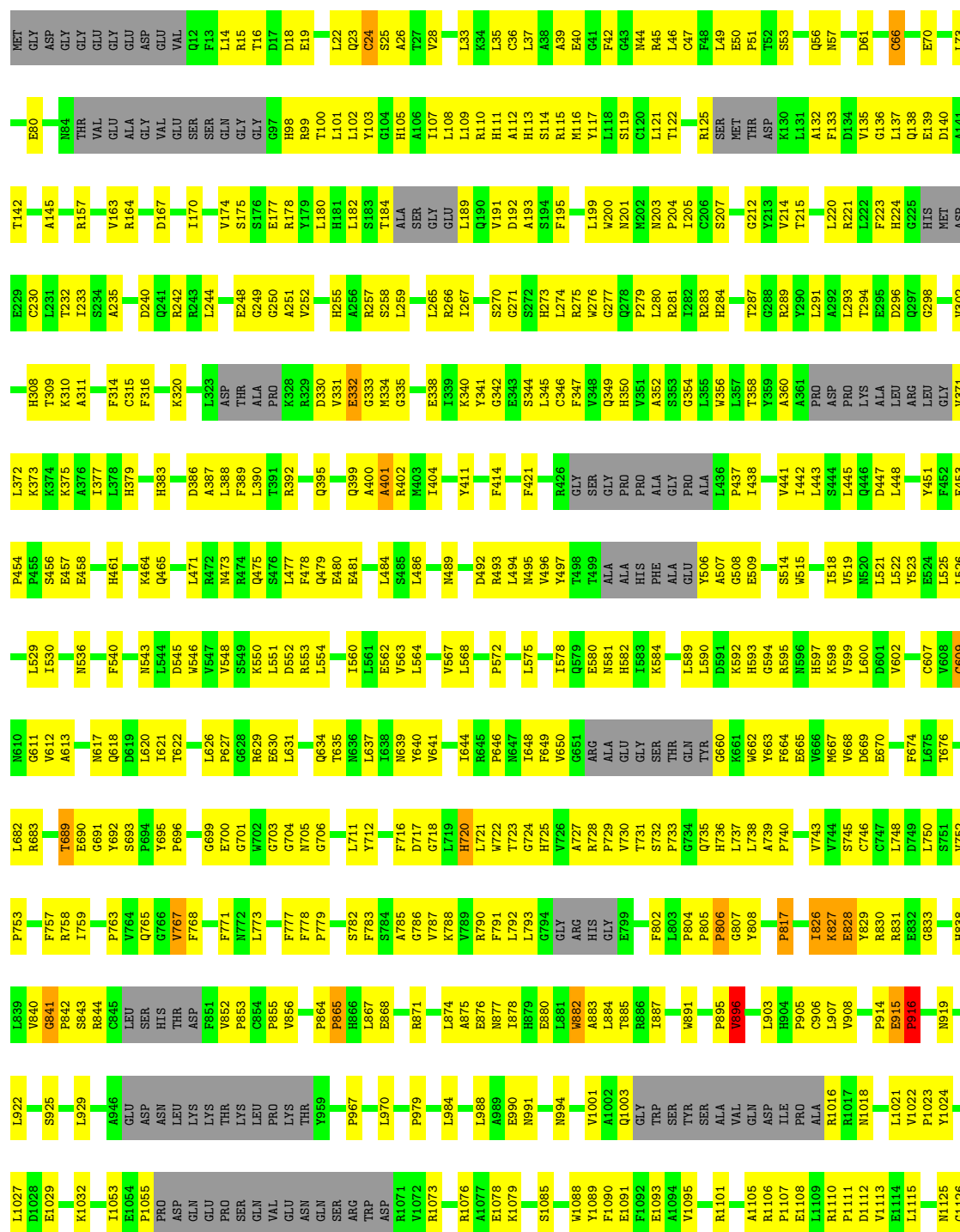


P4804	S4829	ILE	L4677	GLU	GLU	VAL	ALA	ALA	Y4177	Q4100	K4002	T3919	R3849	M3778
V4830	V4830	THR	A4678	VAL	GLY	HIS	LEU	ALA	L4178	LYS	L4003	V3920	R3850	V3779
T4831	T4831	ALA	R4679	PRO	GLY	GLY	ALA	GLY	G4179	GLY	L4013	D3921	N3851	L3780
N4832	N4832	ASN	ALA	ALA	GLY	GLY	LEU	ALA	I4181	F4103	L4017	L3924	K3852	Q3781
N4833	N4833	GLY	PRO	PRO	ASP	PRO	LEU	GLY	M4184	I4108	L4021	L3924	ALA	M3782
Q4836	Q4836	ARG	F4683	PRO	MET	GLY	TRP	ALA	M4184	I4108	L4021	L3924	GLY	I3783
Q4836	Q4836	LYS	L4886	GLY	GLY	GLY	ALA	GLY	R4188	S4115	D4022	Q3927	LEU	S3784
M4839	M4839	PRO	Y4687	PRO	ASP	PRO	VAL	VAL	R4188	S4115	D4022	Q3927	GLY	A3785
L4844	L4844	ASP	T4688	THR	THR	GLY	VAL	VAL	I4190	N4120	M4023	S3929	GLY	C3786
V4847	V4847	PRO	T4689	ALA	LYS	LYS	ALA	ARG	I4190	N4120	M4023	S3929	MET	
V4848	V4848	PRO	E4690	LYS	PRO	PRO	ARG	ALA	E4191	F4125	L4027	F3933	VAL	E3789
Y4849	Y4849	GLY	Q4691	ALA	ALA	ALA	GLY	GLY	R4192	F4125	L4027	F3933	ASN	T3790
F4822	F4822	GLY	P4692	PRO	GLY	ASP	GLY	GLY	E4191	F4125	L4027	F3933	GLU	G3791
F4923	F4923	GLY	Q4699	PRO	PRO	PRO	ALA	ALA	F4195	F4125	L4027	F3933	ASP	A3792
V4924	V4924	THR	Q4700	PRO	PRO	GLY	ALA	ALA	N4201	F4128	L4028	F3933	GLY	M3793
I4925	I4925	GLY	W4701	THR	THR	GLY	GLY	GLY	N4201	F4128	L4028	F3933	THR	V3794
V4926	V4926	GLY	Q4701	GLY	GLY	GLY	ALA	ALA	N4201	F4128	L4028	F3933	VAL	S3795
T4927	T4927	TRP	W4701	GLY	GLY	GLY	GLY	THR	N4201	F4128	L4028	F3933	ILE	S3796
L4928	L4928	GLY	W4705	ALA	ALA	GLY	GLY	VAL	W4205	R4131	E4032	K3953	ASN	T3797
L4928	L4928	LYS	W4705	LYS	GLY	GLY	ALA	ALA	W4205	R4131	E4032	K3953	ARG	L3798
F4856	F4856	SER	T4708	GLY	SER	GLY	ALA	ALA	E4206	PHE	V4036	K3953	ASN	T3802
N4857	N4857	GLY	T4708	GLY	PRO	GLY	ALA	GLY	M4207	GLY	V4036	K3953	GLY	S3803
F4858	F4858	ALA	Q4709	GLY	PRO	GLY	GLY	GLY	P4208	GLY	A4041	K3953	LYS	I3804
I4931	I4931	ALA	S4710	ILE	ILE	GLY	GLY	GLY	P4208	GLY	A4041	K3953	VAL	L3805
I4932	I4932	GLY	S4710	ALA	ALA	GLY	GLY	GLY	K4214	A4136	R4042	K3953	MET	N3806
Q4933	Q4933	GLY	F4711	LYS	LYS	ALA	LEU	ALA	K4214	A4136	R4042	K3953	ALA	G3807
Q4934	Q4934	GLY	P4712	ARG	ARG	ALA	LEU	ALA	F4219	A4136	R4042	K3953	ALA	G3807
L4935	L4935	ALA	S4713	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
F4936	F4936	ALA	W4714	TRP	TRP	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
I4936	I4936	GLY	W4715	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
I4937	I4937	ASP	W4716	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
D4938	D4938	GLY	W4717	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
A4939	A4939	GLY	D4717	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
F4940	F4940	ASP	K4718	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
D4968	D4968	TRP	K4718	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
D4873	D4873	GLY	F4719	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
N4874	N4874	ASN	W4720	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
K4875	K4875	GLY	K4721	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
C4876	C4876	GLY	R4722	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
D4877	D4877	GLY	W4723	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
N4879	N4879	GLY	W4724	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
I4963	I4963	GLY	K4727	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
G4964	G4964	GLY	H4728	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
S4965	S4965	GLY	I4731	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
D4966	D4966	GLY	F4732	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
Y4967	Y4967	GLY	Q4733	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
G4974	G4974	GLY	R4736	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
F4975	F4975	GLY	I4737	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
E4976	E4976	GLY	I4738	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
T4977	T4977	GLY	A4739	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
H4978	H4978	GLY	E4739	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
T4979	T4979	GLY	L4740	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
L4980	L4980	GLY	L4741	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
G4981	G4981	GLY	Q4742	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
I4982	I4982	GLY	MET	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
E4983	E4983	GLY	ASP	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
N4984	N4984	GLY	LEU	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
L4985	L4985	GLY	ALA	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
A4986	A4986	GLY	LEU	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808
		THR	GLU	GLY	GLY	GLY	LEU	ALA	F4219	A4136	R4042	K3953	GLY	G3808



• Molecule 1: Ryanodine receptor 1

Chain E: 44% 26% 27%



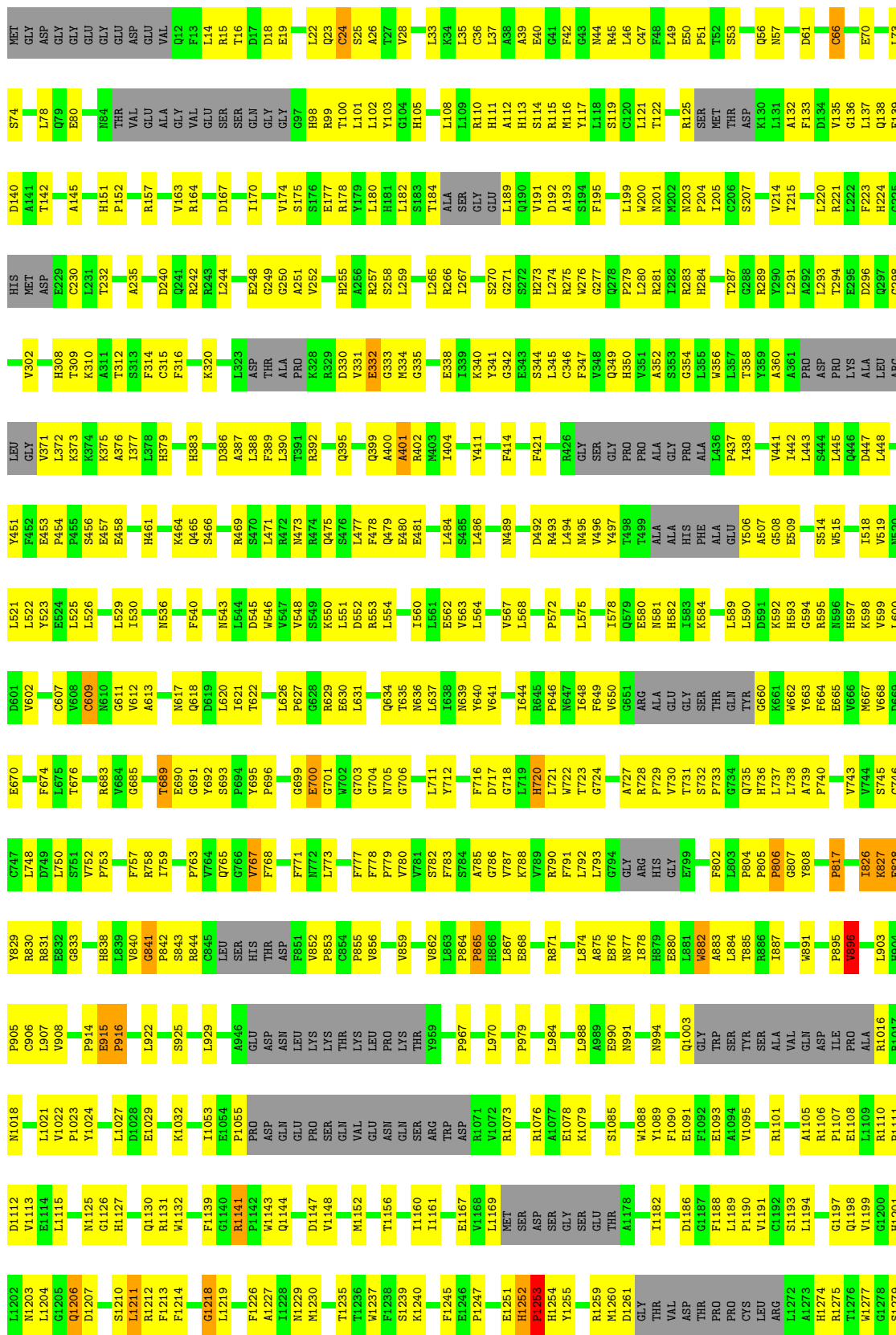
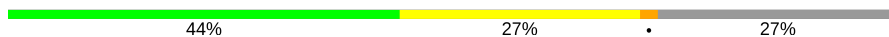
[illegible]

M3778	L3779	L3780	Q3781	M3782	L3783	L3784	A3785	C3786	E3789	T3790	G3791	A3792	M3793	L3794	S3795	S3796	T3797	L3798	L3799	L3802	S3803	L3804	L3805	N3806	G3807	G3808	N3809	A3810	G3811	V3812	Q3813	M3816	L3817	D3818	L3819	L3820	K3821	D3822	K3823	K3824	V3826	G3827	F3828	L3835	T3838	C3839	S3840	V3841	L3842	D3843	A3846																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
GLU	LEU	LYS	LYS	LYS	LYS	LYS	LYS	LYS	GLN	ARG	ARG	ARG	ALA	VAL	VAL	ALA	ALA	TYR	GLY	GLY	PRO	LEU	LEU	TYR	ASN	LEU	ASP	ALA	ASP	GLU	GLY	ILE	VAL	ASN	GLY	ARG	GLU	VAL	VAL	GLN	VAL	VAL	GLN	VAL	GLN	GLY	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU

F4375	E4976	H4812	A4738	N4662	S4583	GLU	ALA	F4174	S4089	K4002	T3919	F3849
E4977	A4892	G4819	E4739	C4863	ASP	ASN	ARG	R4175	M4097	L4003	V3920	R3850
H4978	A4893	G4820	L4740	L4664	SER	GLY	GLU	Y4177	M4097	L4013	D3921	N3851
T4979	G4894	T4822	L4741	K4665	PRO	GLY	ALA	L4178	L4013	L4013	D3922	K3852
L4980	G4895	T4823	C4742	V4666	PRO	LYS	ALA	G4179	L4013	L4017	L3923	ALA
E4981	L4897	L4824	ASP	P4667	GLY	GLU	ALA	R4180	Q4100	L4017	L3924	GLU
E4982	G4898	T4825	LEU	I4670	GLY	VAL	ALA	I4181	Q4102	K4021	Q3927	GLY
L4983	D4899	L4826	ALA	P4671	ASP	PRO	LEU	M4184	F4103	D4022	E3928	LEU
M4984	E4900	L4827	SER	K4675	GLY	GLU	ALA	M4184	I4108	M4023	S3929	GLY
L4985	L4901	S4828	LEU	L4676	GLY	ALA	LEU	I4190	S4115	V4024	F3933	VAL
A4986	S4829	T4829	GLU	E4677	SER	PRO	TRP	I4191	M4120	M4026	Y3934	ASN
M4987	T4830	T4831	ILE	A4678	ALA	PRO	ALA	R4192	M4121	L4027	W3935	GLU
Y4988	T4832	T4833	THR	L4679	ALA	GLU	ALA	E4191	E4122	L4028	Y3936	ASP
M4989	H4832	H4833	ALA	P4679	PRO	PRO	VAL	F4195	I4123	L4031	Y3937	GLY
F4990	H4833	H4834	ASN	E4682	ASP	LYS	ARG	F4195	I4124	E4032	G3938	THR
L4991	H4834	H4835	GLU	F4683	ALA	ALA	ALA	M4201	F4125	V4036	K3940	ILE
V4992	H4835	H4836	ARG	F4683	ALA	ALA	GLY	N4201	F4125	V4036	D3941	ASN
V4993	H4836	H4837	LYS	L4686	PRO	PRO	GLY	M4201	F4125	V4036	V3942	ARG
Y4994	H4837	H4838	PRO	L4687	ALA	PRO	ALA	W4205	F4128	A4041	I3943	GLN
K4998	L4844	L4845	PRO	Y4687	ALA	PRO	ALA	E4206	R4131	R4042	I3943	ASN
D4999	L4845	L4846	ASP	T4688	SER	SER	GLY	E4206	PHE	M4043	K3953	GLY
F4999	L4846	L4847	PRO	T4688	GLY	GLY	ALA	M4207	R4131	M4044	K3953	GLY
L4999	L4847	L4848	PRO	T4689	PRO	PRO	GLY	P4208	GLN	V4045	S3956	LYS
M4999	L4848	L4849	PRO	Q4691	GLY	ALA	ALA	Q4209	GLU	D4046	V3957	VAL
Y4999	L4849	L4850	GLY	P4692	GLY	LYS	ALA	K4214	F4135	D4046	A3958	ALA
K4999	L4850	L4851	SER	Q4699	SER	LYS	ALA	K4214	A4136	L4048	V3961	ALA
D4999	L4851	L4852	TRP	Q4700	TRP	GLU	GLY	F4219	R4137	L4048	F3962	D3877
F4999	L4852	L4853	LEU	W4701	GLY	ALA	LEU	F4219	D4138	V4049	F3962	D3878
Y5000	L4853	L4854	GLY	W4701	SER	GLY	ALA	V4222	I4139	S4052	N3963	E3879
W5001	L4854	L4855	GLY	V4705	GLY	GLY	ARG	V4222	I4140	S4053	N3963	E3880
E5002	L4855	L4856	ALA	L4706	ALA	ALA	LEU	E4229	F4141	M4054	T3966	T3881
H5003	L4856	L4857	ALA	L4707	GLY	GLY	LEU	E4229	M4142	V4055	E3967	Q3882
Q5006	L4857	L4858	GLY	W4708	GLY	MET	TRP	E4232	V4143	E4056	Y3968	D3883
Y5009	L4858	L4859	GLU	P4709	GLU	GLU	VAL	E4233	V4145	M4057	I3969	L3884
W5010	L4859	L4860	ALA	S4710	ALA	PHE	ASP	E4234	V4146	L4058	Q3970	F3885
E5012	L4860	L4861	ALA	F4711	GLY	TRP	LEU	V4235	L4147	L4059	G3971	R3886
Y5014	L4861	L4862	GLY	P4712	GLY	GLY	PHE	V4235	T4148	L4059	P3972	R3887
B5017	L4862	L4863	GLY	W4715	ASP	GLU	VAL	C4238	L4149	M4064	C3973	L3888
G5018	L4863	L4864	GLU	W4716	GLU	GLU	ALA	E4239	L4150	PHE	L3980	L3889
W5019	L4864	L4865	GLU	W4717	GLU	GLU	GLY	E4239	L4150	LEU	L3891	L3890
D5020	L4865	L4866	GLU	D4718	LEU	VAL	LEU	I4242	H4153	LYS	G3892	L3891
F5021	L4866	L4867	LEU	K4718	VAL	PRO	GLU	I4242	V4154	LEU	S3983	G3894
F5022	L4867	L4868	VAL	F4719	PRO	GLU	GLY	Q4246	P4155	LYS	R3984	G3894
P5023	L4868	L4869	PRO	K4720	GLU	GLY	TYR	Q4246	H4156	ASP	E3985	G3894
D5026	L4869	L4870	GLY	K4721	GLY	PRO	ALA	I4251	D4157	I4071	W3986	N3897
C5027	L4870	L4871	GLY	R4722	GLY	GLY	ALA	SER	P4158	V4072	V3989	D3898
F5028	L4871	L4872	GLY	K4723	PRO	GLY	LEU	GLU	R4159	A4076	V3990	F3899
E5029	L4872	L4873	GLY	W4724	GLU	ALA	VAL	GLU	L4160	F4077	G3991	Q3900
K5030	L4873	L4874	GLY	K4725	PRO	GLY	THR	GLY	L4164	V4081	F3992	N3901
Q5031	L4874	L4875	GLY	K4726	GLU	VAL	GLY	GLY	L4164	V4081	Y3902	Y3902
G5032	L4875	L4876	GLY	K4727	PRO	GLY	ARG	GLU	E4168	P4084	V3995	T3905
E5033	L4876	L4877	GLY	H4728	PRO	GLY	LEU	PRO	S4169	R4085	H3998	Q3906
ASP	L4877	L4878	GLY	L4731	PRO	GLY	LEU	GLY	I4170	G4086	M3999	Q3906
GLN	L4878	L4879	GLY	C4732	GLY	VAL	LEU	GLY	L4172	I4087	M4000	I3913
LEU	L4879	L4880	GLY	C4733	LYS	VAL	ALA	ALA	E4172	I4088	M4001	I3913
SER	L4880	L4881	GLY	C4734	ALA	ASP	GLY	ASP	Y4173	I4088	M4001	I3913
	L4881	L4882	GLY	R4736	ASP	GLY	MET	GLU				
	L4882	L4883	GLY	I4737	GLU	GLY	PRO	ASP				

- Molecule 1: Ryanodine receptor 1

Chain G:






D3878 F3879 F3880 T3881 L3884 F3887 Q3889 L3890 L3891 C3892 E3893 V3896 G3897 G3894 N3897 D3898 F3899 Q3900 N3901 Y3902 T3905 Q3906 I3913 I3916 T3919 V3920 D3921 Y3922 L3926 Q3927 E3928 S3929 F3933 Y3934 W3935 Y3936 Y3937 S3938 G3939 K3940 D3941 R3949 F3951 S3952 K3953 V3957 F3962 Y3963	E3811 Q3812 Q3813 L3817 D3818 Y3819 K3731 S3732 C3733 HIS LEU GLU GLU GLU GLY
--	--

S3964	E4056	N4142	E4239	ARG	GLY	GLY	GLY	GLU	LEU	ASP	E4545	Y4715	K4861	I4937
L3965	E4061	V4145	I4242	GLY	VAL	HIS	LEU	VAL	ASP	GLU	D4786	W4716	F4862	D4938
T3966	F4061	L4146	Q4246	LEU	GLU	GLU	LEU	PRO	ASN	MET	W4787	D4717	N4787	A4939
E3967	F4061	L4146	Q4246	GLY	GLY	ALA	GLU	PRO	GLU	GLU	S4788	Y4720	N4864	F4940
Y3968	M4064	V4154	Q4246	TYR	ALA	PRO	PRO	PRO	Y4554	Y4628	L4789	K4721	K4865	V4950
I3969	PHE	V4154	L4251	ARG	LYS	GLY	GLY	GLY	Y4555	Y4630	L4790	R4722	S4866	V4950
Q3970	LEU	P4158	SER	SER	LEU	GLY	GLY	PRO	S4556	Y4630	L4791	K4723	E4867	T4956
G3971	LEU	R4159	GLU	LEU	ARG	GLY	GLY	GLU	R4557	C4645	L4792	W4724	D4868	K4957
P3972	LEU	R4159	PRO	ARG	THR	GLY	GLY	PRO	F4559	L4648	W4725	L4726	L4874	C4958
L3980	LYS	N4162	GLU	ARG	VAL	GLY	GLY	GLU	L4563	L4649	L4726	K4727	K4875	F4959
L3985	ASP	E4165	GLY	VAL	THR	VAL	VAL	PRO	R4563	L4656	L4726	W4728	W4797	C4961
W3986	ASP	E4165	GLU	ARG	GLU	ALA	ALA	PRO	L4567	L4656	L4726	W4728	W4797	C4961
D3987	V4072	E4168	PRO	ARG	LEU	VAL	VAL	PRO	L4578	Y4661	G4733	G4733	M4879	G4963
A3988	G4073	S4169	GLU	LEU	LEU	GLY	GLY	GLU	L4578	C4662	R4736	R4736	M4887	T4963
V3989	A4076	I4170	ASP	ARG	ALA	ASP	ALA	LYS	K4581	L4664	L4737	L4737	V4888	C4964
V3990	F4077	L4171	GLU	LEU	GLY	GLY	GLY	GLU	V4582	K4583	A4738	A4738	V4889	S4965
F3991	F4077	A4076	ASP	THR	MET	PRO	PRO	LYS	S4583	P4667	L4740	L4740	F4890	D4966
F3992	V4081	Y4172	ASP	THR	ASP	GLY	GLY	GLY	ASP	L4670	G4742	G4742	M4891	Y4967
L3993	GLY	Y4173	GLY	ALA	PRO	GLY	GLY	GLY	GLY	E4674	MET	ASP	A4832	G4974
H3994	P4084	F4174	GLY	ALA	PRO	PHE	GLY	VAL	ASP	K4675	LEU	LEU	D4815	F4975
V3995	R4085	R4175	MET	ALA	THR	THR	GLY	GLY	E4676	E4676	ALA	ALA	T4816	E4976
F3996	G4086	P4176	ALA	ALA	SER	PRO	PRO	GLY	L4677	A4678	SER	SER	A4817	T4977
A3997	L4087	Y4177	GLU	THR	ASP	GLY	GLY	LYS	A4678	L4679	LEU	LEU	A4817	H4978
H3998	I4088	G4178	ALA	THR	GLY	GLY	GLY	GLY	GLY	R4679	GLY	GLY	H4812	A4979
M3999	S4089	C4179	ALA	ALA	VAL	ALA	ALA	GLY	GLY	K4680	ILE	ILE	T4832	A4980
K4002	F4093	R4180	ALA	LEU	HIS	GLY	GLY	PRO	ASP	L4681	THR	THR	L4823	I4901
L4003	M4097	I4181	GLY	LEU	GLY	GLY	GLY	PRO	GLY	E4682	ALA	ALA	T4825	P4904
I4010	Q4100	R4188	GLY	TRP	ALA	MET	GLY	PRO	SER	E4683	ALA	ALA	L4826	Y4909
L4013	LYS	R4189	ALA	ALA	PRO	GLY	ALA	GLY	ASP	F4683	ALA	ALA	L4827	R4913
K4021	Q4102	I4190	ALA	VAL	VAL	THR	THR	PRO	GLY	D4684	ASN	ASN	L4827	V4914
D4022	F4103	R4192	GLY	ARG	ARG	THR	THR	LYS	LEU	G4685	GLY	GLY	S4828	F4915
M4023	I4108	F4195	ALA	ALA	ALA	PRO	PRO	ALA	ALA	L4686	ARG	ARG	S4829	F4916
V4024	S4115	E4196	GLY	GLY	ASP	GLY	GLY	PRO	GLY	Y4687	LYS	LYS	V4830	D4917
M4026	N4120	I4197	ALA	ALA	ASP	PRO	PRO	PRO	ALA	T4688	PRO	PRO	T4831	M4993
L4027	N4120	R4202	GLY	GLY	GLY	THR	THR	THR	SER	E4690	ASP	ASP	H4832	Y4994
L4028	E4121	M4205	THR	ALA	GLY	GLY	GLY	PRO	GLY	V4697	PRO	PRO	N4833	K4998
L4031	M4122	W4205	VAL	ALA	VAL	GLY	GLY	ALA	GLY	K4698	GLY	GLY	Q4836	D4999
E4032	I4123	E4206	ALA	ALA	ALA	GLY	GLY	LYS	GLY	G4699	LEU	LEU	L4837	E5000
V4036	F4125	M4207	ALA	ALA	ALA	GLY	GLY	LYS	SER	Q4700	L4765	L4765	W4839	T5001
A4041	F4128	F4208	ALA	ALA	ALA	GLY	GLY	ILE	TRP	W4701	T4766	T4766	M4839	E5002
R4042	F4131	K4214	THR	ALA	THR	ALA	ALA	LYS	GLY	D4702	S4770	S4770	V4847	H5003
Q4043	PHE	F4219	ARG	ARG	ARG	ALA	ALA	GLY	GLY	V4705	K4774	K4774	W4848	Y5009
M4044	GLN	D4220	LEU	LEU	LEU	LYS	LYS	ARG	ALA	L4706	Y4775	Y4775	Y4849	V5010
V4045	GLU	V4221	ALA	ALA	ALA	GLY	GLY	GLY	GLY	W4707	Y4776	Y4776	L4850	W5011
M4046	P4135	M4231	ALA	ALA	ALA	TRP	TRP	GLY	GLY	T4708	Q4776	Q4776	Y4851	R5012
M4047	A4136	M4232	ALA	SER	SER	VAL	VAL	ASP	GLY	F4709	W4777	W4777	T4852	M5013
L4048	R4137	L4233	ALA	LEU	LEU	ASP	ASP	GLY	ALA	S4710	W4778	W4778	A4855	Y5014
V4049	D4139	L4233	ALA	PHE	PHE	GLY	GLY	TRP	GLY	F4711	K4779	K4779	F4856	R5017
S4052	F4141	V4235	LEU	GLY	GLY	VAL	VAL	ALA	ASP	P4712	V4782	V4782	F4859	G5018
				GLY	GLY	ALA	ALA	LEU	GLU	N4714	I4783	I4783	R4860	W5019

● Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain B:  60%  38%



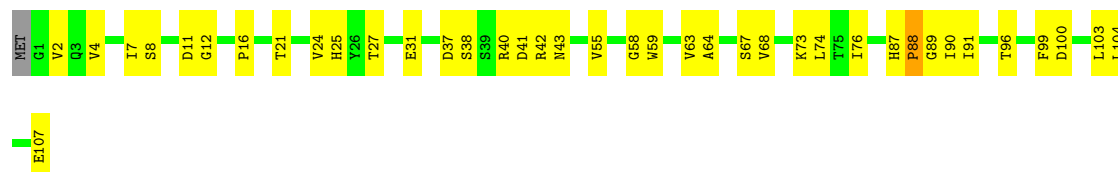
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain D: 61% 37% ..



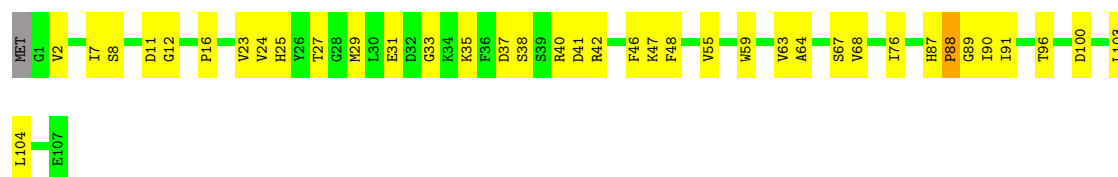
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain F: 63% 35% ..



• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H: 64% 34% ..



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	47000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	Not provided	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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.93	55/27385 (0.2%)	0.86	90/37104 (0.2%)
1	C	0.93	56/27385 (0.2%)	0.87	92/37104 (0.2%)
1	E	0.93	53/27385 (0.2%)	0.86	91/37104 (0.2%)
1	G	0.93	55/27385 (0.2%)	0.85	90/37104 (0.2%)
2	B	0.58	0/851	0.67	0/1146
2	D	0.58	0/851	0.67	0/1146
2	F	0.58	0/851	0.67	0/1146
2	H	0.60	0/851	0.67	0/1146
All	All	0.92	219/112944 (0.2%)	0.86	363/153000 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	19
1	C	0	19
1	E	0	19
1	G	0	19
All	All	0	76

The worst 5 of 219 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	4988	TYR	CG-CD2	-12.12	1.23	1.39
1	A	5014	TYR	CG-CD1	-11.55	1.24	1.39
1	E	5014	TYR	CG-CD1	-11.43	1.24	1.39
1	C	3922	TYR	CE1-CZ	-11.19	1.24	1.38
1	E	3922	TYR	CE1-CZ	-11.12	1.24	1.38

The worst 5 of 363 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	G	4128	PHE	CB-CG-CD2	-10.00	113.80	120.80
1	E	4128	PHE	CB-CG-CD2	-9.73	113.99	120.80
1	C	4128	PHE	CB-CG-CD2	-9.69	114.02	120.80
1	A	4128	PHE	CB-CG-CD2	-9.62	114.07	120.80
1	E	4064	MET	CG-SD-CE	8.87	114.39	100.20

There are no chirality outliers.

5 of 76 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1252	HIS	Peptide
1	A	1253	PRO	Peptide
1	A	1464	PHE	Mainchain
1	A	332	GLU	Mainchain,Peptide
1	A	841	GLY	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	26917	0	24461	1094	0
1	C	26917	0	24461	1105	0
1	E	26917	0	24461	1108	0
1	G	26917	0	24461	1100	0
2	B	832	0	831	38	0
2	D	832	0	831	37	0
2	F	832	0	831	36	0
2	H	832	0	831	34	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
All	All	111000	0	101168	4395	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 21.

The worst 5 of 4395 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4826:ILE:CG2	1:G:4931:ILE:HD11	1.79	1.10
1:A:4879:MET:SD	1:G:4578:LEU:HA	1.92	1.10
1:A:4826:ILE:CG2	1:C:4931:ILE:HD11	1.86	1.05
1:E:4578:LEU:HA	1:G:4879:MET:SD	1.99	1.03
1:C:4826:ILE:CG2	1:E:4931:ILE:HD11	1.91	1.00

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	3496/5037 (69%)	3173 (91%)	220 (6%)	103 (3%)	5	40
1	C	3496/5037 (69%)	3169 (91%)	223 (6%)	104 (3%)	5	39
1	E	3496/5037 (69%)	3169 (91%)	223 (6%)	104 (3%)	5	39
1	G	3496/5037 (69%)	3169 (91%)	226 (6%)	101 (3%)	5	40
2	B	105/108 (97%)	92 (88%)	12 (11%)	1 (1%)	18	61
2	D	105/108 (97%)	92 (88%)	12 (11%)	1 (1%)	18	61
2	F	105/108 (97%)	92 (88%)	12 (11%)	1 (1%)	18	61
2	H	105/108 (97%)	89 (85%)	15 (14%)	1 (1%)	18	61
All	All	14404/20580 (70%)	13045 (91%)	943 (6%)	416 (3%)	9	40

5 of 416 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	689	THR
1	A	720	HIS
1	A	806	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	916	PRO
1	A	1253	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	2500/4276 (58%)	2486 (99%)	14 (1%)	89	94
1	C	2501/4276 (58%)	2487 (99%)	14 (1%)	89	94
1	E	2502/4276 (58%)	2486 (99%)	16 (1%)	89	94
1	G	2501/4276 (58%)	2482 (99%)	19 (1%)	85	92
2	B	89/90 (99%)	89 (100%)	0	100	100
2	D	89/90 (99%)	89 (100%)	0	100	100
2	F	89/90 (99%)	89 (100%)	0	100	100
2	H	89/90 (99%)	89 (100%)	0	100	100
All	All	10360/17464 (59%)	10297 (99%)	63 (1%)	89	94

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	806	PRO
1	E	979	PRO
1	G	1934	SER
1	E	852	VAL
1	E	885	THR

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

Mol	Chain	Res	Type
1	C	3700	GLN
1	E	1127	HIS
1	G	2247	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	3813	GLN
1	E	203	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.