



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 04:07 AM UTC

PDB ID : 6JV2 / pdb_00006jv2
EMDB ID : EMD-9889
Title : Structure of RyR2 (P/L-Ca²⁺/Ca²⁺-CaM dataset)
Authors : Gong, D.S.; Chi, X.M.; Zhou, G.W.; Huang, G.X.Y.; Lei, J.L.; Yan, N.
Deposited on : 2019-04-15
Resolution : 4.40 Å(reported)

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A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

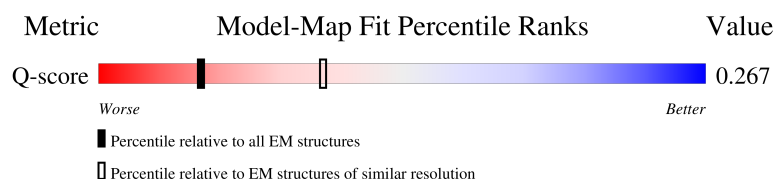
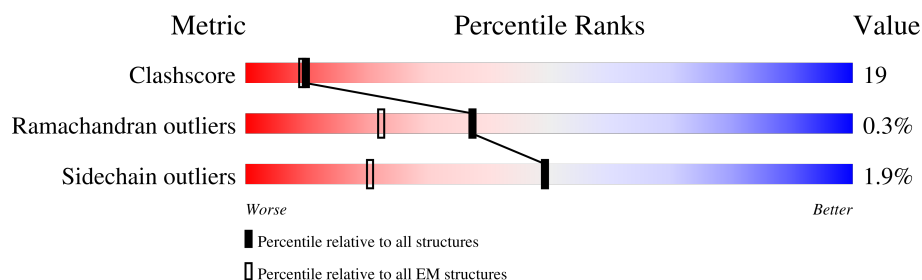
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 4.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	3132 (3.91 - 4.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	4968	7% 42% 28% 29%
1	C	4968	7% 41% 28% 29%
1	E	4968	7% 42% 28% 29%
1	G	4968	7% 41% 28% 29%

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Mol	Chain	Length	Quality of chain
2	B	149	55% 58% 30% 11%
2	D	149	55% 59% 30% 11%
2	F	149	55% 61% 28% 11%
2	H	149	55% 59% 30% 11%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 111080 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 RyR2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3509	Total	C	N	O	S	0	0
			26722	17028	4575	4961	158		
1	C	3509	Total	C	N	O	S	0	0
			26722	17028	4575	4961	158		
1	E	3509	Total	C	N	O	S	0	0
			26722	17028	4575	4961	158		
1	G	3509	Total	C	N	O	S	0	0
			26722	17028	4575	4961	158		

- Molecule 2 is a protein called Calmodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	132	Total	C	N	O	S	0	0
			1042	643	169	221	9		
2	D	132	Total	C	N	O	S	0	0
			1042	643	169	221	9		
2	F	132	Total	C	N	O	S	0	0
			1042	643	169	221	9		
2	H	132	Total	C	N	O	S	0	0
			1042	643	169	221	9		

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

Mol	Chain	Residues	Atoms		AltConf
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	G	1	Total	Zn	0
			1	1	

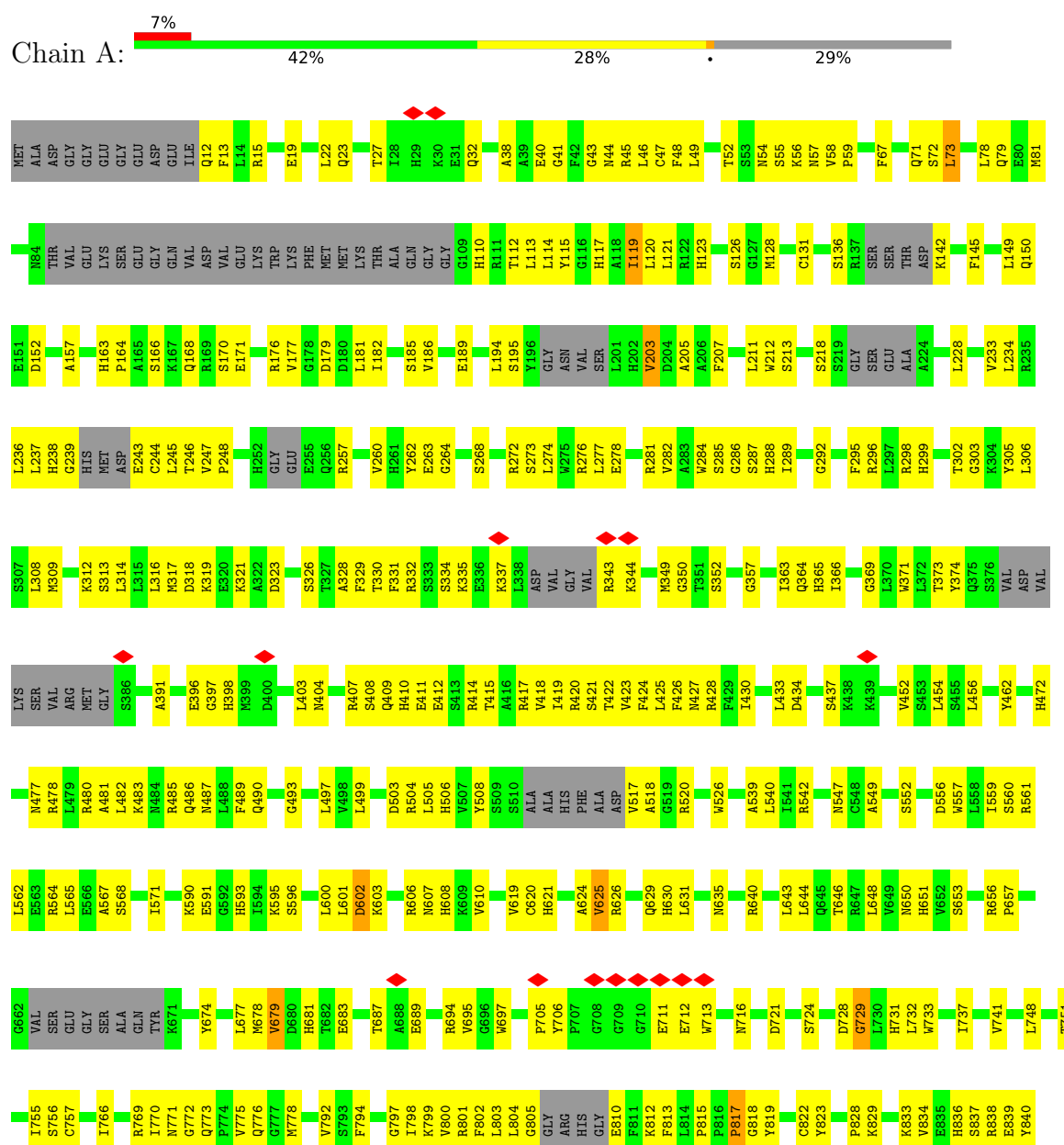
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total 1	Ca 1	0
4	B	4	Total 4	Ca 4	0
4	C	1	Total 1	Ca 1	0
4	D	4	Total 4	Ca 4	0
4	E	1	Total 1	Ca 1	0
4	F	4	Total 4	Ca 4	0
4	G	1	Total 1	Ca 1	0
4	H	4	Total 4	Ca 4	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

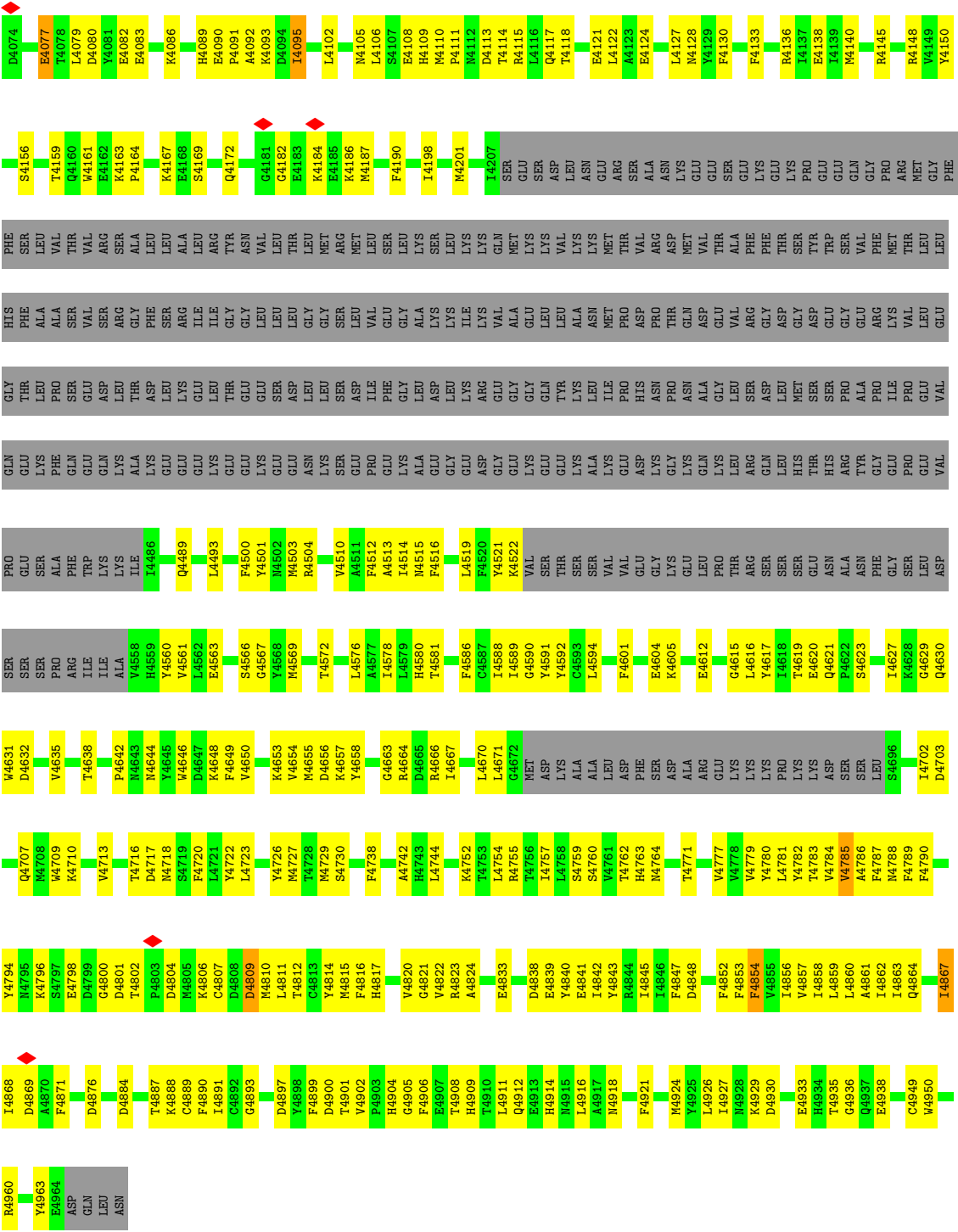
• Molecule 1: RyR2





H2850	H2851	L2852	W2853	A2854	K2855	K2856	K2857	K2858	L2859	E2860	L2861	E2862	S2863	K2864	G2865	G2866	G2867	N2868	H2869	P2870	L2871	L2872	V2873	P2874	V2875	D2876	T2877	L2878	T2879	A2880	K2881	E2882	K2883	A2884	D2885	K2886	R2887	E2888	K2889	A2890	Q2891	D2892	I2893	L2894	K2895	F2896	L2897	Q2898	E2899	N2900	G2901	Y2902	A2903	V2904	S2905	R2906	G2907	PHE	LYS
L2790	E2791	R2792	T2793	R2794	E2795	G2796	L2797	SER	MET	ALA	LEU	TYR	ASN	ARG	THR	ARG	ILE	SER	GLN	THR	SER	VAL	ALA	A2819	H2820	G2821	Y2822	S2823	P2824	R2825	A2826	L2827	D2828	N2829	S2830	T2831	V2832	L2833	S2835	L2834	R2836	D2837	L2838	L2839	A2840	N2841	A2842	E2843	N2844	N2845	A2846	E2847	N2848	S2849	R2906	G2907	PHE	LYS	
H2730	D2731	K2732	W2733	S2734	M2735	D2736	K2737	L2738	A2739	N2740	G2741	W2742	I2743	Y2744	G2745	E2746	I2747	Y2748	S2749	D2750	S2751	S2752	K2753	V2754	Q2755	P2756	L2757	M2758	K2759	P2760	Y2761	K2762	L2763	L2764	S2765	E2766	K2767	E2768	K2769	E2770	I2771	Y2772	R2773	W2774	P2775	I2776	K2777	E2778	S2779	L2780	K2781	T2782	M2783	L2784	A2785	W2786	G2787	W2788	R2789
Y2658	L2667	P2668	S2671	A2672	P2678	P2679	ASP	TYR	MET	GLU	SER	ASN	TYR	VAL	SER	MET	GLU	LYS	GLN	SER	MET	ASP	GLU	N2701	F2702	N2703	P2704	Q2705	P2706	V2707	D2708	T2709	S2710	N2711	L2712	T2713	L2714	P2715	E2716	K2717	L2718	E2719	Y2720	F2721	I2722	N2723	K2724	Y2725	A2726	E2727	H2728	S2729							
Q2559	L2562	T2563	Q2566	S2576	ILE	CYS	GLN	LEU	R2582	L2593	V2597	N2601	GLU	HIS	ALA	K2605	K2609	T2612	E2616	G2627	TRP	GLY	ASN	PHE	ALA	A2634	E2638	L2639	H2640	L2641	S2642	K2643	K2644	L2645	F2646	W2647	G2648	I2649	D2650	L2651	A2652	L2653	SER	GLN	LYS	LYS													
GLY	F2461	C2462	P2463	D2464	R2475	V2476	Y2477	GLY	ILE	GLU	V2481	Q2482	L2485	L2503	ASP	THR	ALA	ALA	SER	ALA	T2511	L2515	A2516	L2517	R2518	Y2519	L2520	L2521	L2529	G2430	G2431	D2432	L2433	V2436	Q2442	MET	PRO	THR	ILE	ALA	LYS	ASP	GLY	ASN	VAL	VAL	GLU	PRO	ASP	LEU	SER	K2558							
ILE	HIS	MET	G2386	N2387	A2388	L2389	F2392	L2399	L2400	G2401	R2402	P2405	A2406	M2407	H2408	L2409	A2413	A2417	L2418	R2419	I2420	S2422	L2423	L2424	R2425	S2426	P2429	L2430	G2431	D2432	L2433	V2436	Q2442	MET	PRO	THR	ILE	ALA	LYS	ASP	GLY	ASN	VAL	VAL	GLU	PRO	ASP	LEU	SER	K2558									
N2310	V2314	E2315	N2316	E2317	A2318	N2319	R2323	L2324	L2325	L2326	R2327	R2328	F2329	E2330	CYS	PHE	GLY	PRO	ALA	LEU	ARG	GLY	GLU	GLY	GLY	G2343	L2354	ALA	GLU	ASP	PRO	SER	GLN	ASP	LEU	VAL	SER	LYS	TYR	PRO	ASP	ILE	GLY	TRP	ASN	P2293	V2294	D2301	F2302	L2303	R2304	V2307	F2308	C2309					
SER	PRO	ALA	MET	ARG	GLY	SER	T2239	D2242	S2247	D2250	L2256	A2257	L2258	R2259	D2262	L2263	E2264	K2265	V2267	R2268	Y2269	L2270	A2271	L2275	GLN	SER	CYS	GLN	ASP	LEU	VAL	SER	LYS	TYR	PRO	ASP	ILE	GLY	TRP	ASN	P2293	V2294	D2301	F2302	L2303	R2304	V2307	F2308	C2309										
Q2060	Q2061	L2062	S2064	E2065	PHE	LYS	ASP	ASP	SER	E1986	V2075	L2076	P2079	E2080	L2081	V2082	R2083	F2086	L2087	L2088	L2089	Q2092	G2098	R2101	A2102	L2103	Y2106	Y2107	V2114	T2117	I2118	N2119	L2120	L2124	G2125	R2128	S2129	V2133	ARG	MET	GLY	LYS	E2138	K2141	L2142														
ILE	ASN	MET	LEU	LEU	ASN	PHE	LYS	ASP	SER	E1986	V2075	L2076	P2079	E2080	L2081	V2082	R2083	F2086	L2087	L2088	L2089	Q2092	G2098	R2101	A2102	L2103	Y2106	Y2107	V2114	T2117	I2118	N2119	L2120	L2124	G2125	R2128	S2129	V2133	ARG	MET	GLY	LYS	E2138	K2141	L2142														
GLU	G1893	P1900	K1904	L1905	Q1906	M1907	L1911	L1914	V1919	R1920	I1923	I1926	S1930	D1931	F1932	F1933	V1934	A1935	K1936	L1937	ASN	ASP	THR	LEU	R1942	F1943	R1944	Y1945	N1946	E1947	N1953	MET	SER	ALA	ALA	LEU	THR	ALA	GLY	PRO	LYS	PRO	GLN	GLU	GLN														
I1833	F1834	N1835	N1836	E1837	D1838	L1839	H1841	L1842	L1843	O1844	L1845	E1846	P1847	S1848	VAL	PHE	LYS	ALA	ALA	GLY	PRO	GLU	GLU	ASN	ASP	THR	LEU	LYS	GLY	PRO	CYS	ALA	SER	GLU	SER	ALA	LEU	THR	ALA	GLY	PRO	LYS	PRO	GLN	GLU	GLN													





● Molecule 1: RyR2



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GLY	GLN	GLU	LEU	LEU	THR	T4118	L4044	S3972	Y3892	K3785	K3682	R3614	ASN	LEU	THR	LYS	GLN	ASP	ILE
GLN	TYR	LEU	LEU	ALA	E4121	S4045	S4045	M3973	Y3893	K3788	L3683	R3615	ASN	TYR	ILE	THR	GLY	ASP	ILE
TYR	ALA	ALA	ASN	L4122	K4046	K4047	K4046	L3974	Y3893	V3788	E3684	R3616	MET	ALA	GLY	VAL	ILE	SER	ASN
LEU	ASN	ASN	GLY	A4123	D4048	D4048	D4048	L3976	K3896	F3790	E3685	L3617	PHE	PRO	ARG	VAL	LEU	PHE	LYS
ILE	MET	MET	THR	E4124	F4049	F4049	F4049	K3977	K3896	F3790	F3687	F3621	VAL	PRO	ARG	VAL	LEU	VAL	LYS
PRO	ASP	THR	SER	LEU	H4050	H4050	H4050	K3978	L3899	S3793	M3690	L3622	SER	LEU	LEU	VAL	ALA	PRO	GLN
HIS	ASP	VAL	ALA	L4127	K4051	K4051	K4051	M3979	D3900	S3793	A3691	L3622	ASP	LEU	GLN	ASP	ALA	PRO	GLN
ASN	ASN	ARG	ASN	N4128	E4054	E4054	E4054	V3980	E3901	S3800	A3691	L3622	ASP	LEU	GLN	ASP	ALA	PRO	GLN
PRO	ASN	ARG	ASN	N4129	E4054	E4054	E4054	V3980	E3901	S3800	A3691	L3622	ASP	LEU	GLN	ASP	ALA	PRO	GLN
ASN	ASN	MET	GLY	Y4129	S4055	S4055	S4055	M3981	Q3902	C3801	A3692	L3625	THR	ILE	ARG	ASN	ASP	ALA	PRO
ALA	ASP	VAL	THR	F4130	H4056	H4056	H4056	M3982	Q3903	S3802	A3693	L3626	PHE	THR	PHE	LYS	ASP	ALA	PRO
GLY	GLY	THR	SER	F4133	K4057	K4057	K4057	L3983	Q3904	V3803	D3694	K3627	SER	VAL	VAL	VAL	LEU	VAL	THR
LEU	LEU	ALA	GLU	F4133	H4058	H4058	H4058	L3984	R3905	V3803	D3694	K3627	SER	VAL	VAL	VAL	LEU	VAL	THR
SER	SER	ARG	GLY	R4136	H4059	H4059	H4059	S3985	K3909	A3808	A3697	L3630	MET	TYR	TYR	PHE	LYS	ASP	HIS
ASP	ASP	PHE	GLY	I4137	Y4060	Y4060	Y4060	M3986	K3909	F3809	S3698	L3630	SER	ASN	ASN	PHE	LYS	ASP	PHE
LEU	LEU	THR	LYS	E4138	Q4061	Q4061	Q4061	N3990	E3910	F3810	S3699	L3632	THR	ASN	THR	HIS	ASP	ASN	ASN
SER	SER	THR	LYS	ASP	S4062	S4062	S4062	V3991	L3911	R3811	C3700	L3633	GLU	ALA	ALA	ALA	ALA	ALA	PRO
ASP	ASP	THR	GLY	K4144	E4063	E4063	E4063	V3992	Q3912	R3811	C3700	L3633	GLU	ALA	ALA	ALA	ALA	ALA	PRO
GLY	GLY	THR	GLY	R4145	T4064	T4064	T4064	N3993	V3913	Q3812	HIS	L3634	GLN	VAL	TRP	LYS	ASP	ALA	PRO
PRO	PRO	SER	GLY	LEU	L4068	L4068	L4068	K3994	V3917	A3815	ASP	L3635	SER	VAL	TRP	LYS	ASP	ALA	PRO
ALA	ALA	GLY	GLY	R4148	L4069	L4069	L4069	G3994	V3917	A3815	ASP	L3635	SER	VAL	TRP	LYS	ASP	ALA	PRO
PRO	PRO	THR	GLY	Y4149	E4070	E4070	E4070	T3996	F3918	L3818	ASP	L3635	SER	VAL	TRP	LYS	ASP	ALA	PRO
ILE	ILE	THR	LYS	Y4150	A4071	A4071	A4071	T3997	N3919	G3819	ASP	L3635	SER	VAL	TRP	LYS	ASP	ALA	PRO
GLY	GLY	LEU	LEU	S4156	E4072	E4072	E4072	K3998	T3920	M3820	ASP	L3635	SER	VAL	TRP	LYS	ASP	ALA	PRO
VAL	VAL	LEU	LEU	S4156	T4073	T4073	T4073	Q3999	T3922	THR	GLY	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLN	GLN	GLY	GLY	T4159	D4074	D4074	D4074	L4004	E3923	GLY	GLY	L3645	MET	ALA	ALA	ALA	ALA	ALA	ALA
LEU	LEU	THR	THR	Q4160	E4077	E4077	E4077	V4005	E3924	GLY	GLY	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LEU	LEU	ALA	LEU	W4161	T4078	T4078	T4078	E4006	L3925	VAL	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
VAL	VAL	VAL	VAL	E4162	L4079	L4079	L4079	S4007	L3926	G3825	S3714	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLY	GLY	THR	THR	K4163	D4080	D4080	D4080	S4008	Q3929	F3715	F3715	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLN	GLN	VAL	VAL	P4164	Y4081	Y4081	Y4081	M4009	N3932	K3718	PRO	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	ASP	ASP	K4167	E4082	E4082	E4082	M4010	N3932	K3718	PRO	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ASP	ASP	THR	THR	S4169	E4083	E4083	E4083	L4015	S3935	Q3729	ASP	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LEU	LEU	LEU	LEU	S4169	K4086	K4086	K4086	L4018	L3936	R3785	GLY	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LEU	LEU	ALA	ALA	Q4172	H4089	H4089	H4089	F4018	L3941	L3944	THR	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLY	GLY	ILE	ILE	Q4172	E4090	E4090	E4090	L4022	W3942	Q3945	THR	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	THR	THR	G4181	P4091	P4091	P4091	K4023	D3943	H3851	LYS	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLY	GLY	GLY	GLY	E4182	A4092	A4092	A4092	L4024	A3944	N3852	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	VAL	VAL	E4183	K4093	K4093	K4093	K4025	V3945	S3853	ALA	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLY	GLY	LEU	LEU	K4184	D4094	D4094	D4094	D4026	L3949	D3854	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ASP	ASP	THR	THR	E4185	L4095	L4095	L4095	L4027	L3949	F3855	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ASN	ASN	LEU	LEU	K4186	L4095	L4095	L4095	T4028	F3952	Q3856	THR	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	GLY	GLY	M4187	L4102	L4102	L4102	S4030	F3952	Q3856	THR	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
SER	SER	THR	THR	F4190	N4105	N4105	N4105	D4031	Q3956	N3857	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ASP	ASP	VAL	VAL	F4193	L4106	L4106	L4106	T4032	Q3956	N3857	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
PHE	PHE	GLY	GLY	F4193	S4107	S4107	S4107	F4033	L3959	N3870	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	GLY	GLY	T4197	E4108	E4108	E4108	E4034	S3960	T3871	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ALA	ALA	LEU	LEU	L4198	H4109	H4109	H4109	E4035	Q3961	L3872	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
GLY	GLY	ASP	ASP	L4198	M4110	M4110	M4110	D3962	D3962	L3873	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	LYS	LYS	M4201	D4113	D4113	D4113	P4038	Q3965	T3875	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ILE	ILE	LYS	LYS	M4201	T4114	T4114	T4114	D4039	Q3965	T3875	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
LYS	LYS	VAL	VAL	L4207	R4115	R4115	R4115	G4040	L3968	Y3781	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
VAL	VAL	GLY	GLY	SER	L4116	L4116	L4116	K4041	L3968	Y3781	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA
ALA	ALA	GLY	GLY	GLY	L4117	L4117	L4117	V4043	E3971	S3885	VAL	L3645	LYS	GLY	GLY	LYS	SER	ALA	ALA

L4911	L4912	L4913	L4914	L4915	L4916	L4917	L4918	L4919	F4921	M4924	Y4925	L4926	K4929	D4930	E4933	H4934	T4935	G4936	Q4937	E4938	S4939	C4949	W4950	R4960	Y4963	E4964	ASP	GLN	LEU	ASN																													
D4838	E4839	Y4840	E4841	L4842	Y4843	R4844	I4845	F4847	D4848	F4851	F4852	F4853	F4854	V4855	I4856	V4857	I4858	L4859	I4860	I4861	I4862	I4863	Q4864	I4867	I4868	K4795	D4869	F4870	F4871	D4876	D4884	T4887	K4888	C4889	F4890	I4891	C4892	G4893	D4897	Y4898	F4899	I4810	L4811	T4812	C4813	Y4814	N4815	F4816	V4901	V4902	F4903	H4904	C4905	F4906	E4907	R4823	T4908	H4909	T4910
L4755	T4756	I4757	L4758	S4759	S4760	V4761	T4762	H4763	N4764	T4771	V4777	V4778	V4779	Y4780	L4781	Y4782	T4783	V4784	V4785	A4786	F4787	N4788	F4789	F4790	Y4794	N4795	K4796	S4797	E4798	D4799	G4800	D4801	T4802	P4803	D4804	K4805	K4806	C4807	D4808	D4809	N4810	L4811	M4729	S4730	F4738	F4739	P4740	A4741	A4742	H4743	S4668	E4669	L4670	L4671	L4754				
MET	ASP	LYS	ALA	LEU	ASP	PHE	SER	ASP	ALA	ARG	GLU	LYS	LYS	PRO	LYS	LYS	ASN	ALA	ASN	PHE	GLY	PRO	GLU	VAL	ASP	SER	SER	PRO	ARG	ILE	ILE	ALA	V4558	H4559	Y4560	V4561	L4562	E4563	S4566	G4567	Y4568	M4569	T4572	L4576	A4577	I4578	L4579	N4580	N4515	F4516	L4519	C4587	I4588	I4589					
G4590	Y4591	Y4592	C4593	L4594	F4601	K4605	E4606	K4610	L4611	E4612	G4615	L4616	Y4617	T4618	L4619	E4620	Q4621	P4622	S4623	L4627	G4628	Q4630	W4631	V4635	T4638	P4642	M4646	K4648	F4649	V4650	K4653	V4654	M4655	D4656	K4657	Y4658	G4663	K4664	D4665	L4667	S4668	E4669	L4670	L4671	G4672														
VAL	SER	THR	SER	SER	VAL	VAL	GLU	LYS	GLY	LYS	GLU	LEU	PRO	THR	ARG	SER	GLN	HIS	THR	THR	GLU	ASN	ALA	ASN	PHE	GLY	SER	LEU	ASP	SER	VAL	ASP	VAL	H4559	Y4560	V4561	L4562	E4563	S4566	G4567	Y4568	M4569	T4572	L4576	A4577	I4578	L4579	N4580	N4515	F4516	L4519	C4587	I4588	I4589					

• Molecule 1: RyR2



W371	L372	T373	Y374	Q375	S376	VAL	ASP	VAL	LYS	SER	VAL	ARG	MET	GLY	S386	A391	E396	G397	H398	M399	D400	L403	N404	R407	S408	Q409	H410	E411	E412	S413	R414	T415	A416	R417	V418	I419	R420	S421	T422	V423	F424	L425	F426	N427	R428	F429	I430	L433	D434	A435	L436	S437	K438	L439																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
H299	A224	G303	K304	Y305	L306	S307	L308	M309	K312	S313	L314	L315	L316	M317	D318	K319	E320	K321	A322	D323	S326	T327	F329	T330	F331	R332	S333	S334	K335	E336	K337	L338	ASP	VAL	GLY	VAL	R343	K344	M349	G350	T351	S352	K355	Y356	G357	I363	Q364	H365	L366	S367	K368	L370																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
ALA	F145	L228	V233	L234	R235	L236	L237	H238	G239	HIS	MET	ASP	E243	C244	L245	T246	V247	P248	H252	GLY	E255	Q256	R257	V260	H261	Y262	E263	G264	S268	R272	S273	L274	W275	R276	L277	E278	R281	V282	S285	G286	S287	H288	I289	G292	F295	R296	L297	R298																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
L78	Q79	E80	M81	L82	E83	Q84	THR	VAL	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU</



L2641	L2642	H2541	Q2442	SER	SER	LYS	F2204	T2117	T2038	SER	ASP	G1802	M1721	L1644	K1572
S2642	Q2442	H2542	Q2442	PRO	PRO	GLY	F2204	I2118	T2039	ALA	SER	R1807	N1722	T1645	K1573
K2643	Q2442	S2543	Q2442	THR	THR	TYR	T2207	L2119	T2039	LEU	ARG	D1808	M1723	E1646	H1576
L2644	Q2442	S2544	Q2442	GLY	GLY	ASP	T2207	L2120	T2039	THR	GLY	T1813	I1726	Q1647	V1579
L2645	Q2442	L2546	Q2442	ILE	ILE	ASP	Q2210	L2124	T2039	ALA	PRO	F1816	M1729	K1652	P1580
L2646	Q2442	D2547	Q2442	GLY	GLY	TRP	Q2212	Q2126	T2039	ARG	ALA	F1816	T1730	F1653	R1585
L2647	Q2442	L2550	Q2442	ASP	ASP	ASP	Q2212	Q2127	T2039	THR	GLY	F1818	E1731	L1656	L1586
G2648	Q2442	L2551	Q2442	ASP	ASP	ASP	Q2212	S2129	T2039	GLY	GLY	F1818	E1732	H1656	Q1589
D2651	Q2442	H2552	Q2442	ASP	ASP	ASP	Q2212	Q2133	T2039	ARG	GLY	L1821	T1733	T1657	F1590
L2652	Q2442	T2552	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1822	T1734	L1658	L1591
L2653	Q2442	T2553	Q2442	GLY	GLY	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	S1735	L1659	S1592
SER	Q2442	ARG	Q2442	GLY	GLY	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
GLN	Q2442	LEU	Q2442	GLY	GLY	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
LYS	Q2442	SER	Q2442	GLY	GLY	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
Y2658	Q2442	K2558	Q2442	ASP	ASP	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
L2667	Q2442	Q2559	Q2442	ALA	ALA	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
P2668	Q2442	L2662	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
S2671	Q2442	T2563	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
A2672	Q2442	Q2566	Q2442	ILE	ILE	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
P2678	Q2442	S2576	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
P2679	Q2442	ILE	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
ASP	Q2442	CYS	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
TYR	Q2442	GLY	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
MET	Q2442	GLN	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
GLU	Q2442	LEU	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
SER	Q2442	R2582	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
ASN	Q2442	L2593	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
TYR	Q2442	V2597	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
VAL	Q2442	GLY	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
SER	Q2442	ASP	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
MET	Q2442	THR	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
GLU	Q2442	GLY	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
GLY	Q2442	ALA	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
N2701	Q2442	K2605	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
F2702	Q2442	GLY	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
N2703	Q2442	ASP	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
P2704	Q2442	THR	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
Q2705	Q2442	GLY	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
P2706	Q2442	ALA	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
V2707	Q2442	ARG	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
D2708	Q2442	CYS	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
T2709	Q2442	ALA	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
S2710	Q2442	PRO	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
N2711	Q2442	L2535	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
I2712	Q2442	THR	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594
T2713	Q2442	ALA	Q2442	THR	THR	ASP	Q2212	Q2133	T2039	GLY	GLY	L1823	T1737	S1662	V1594







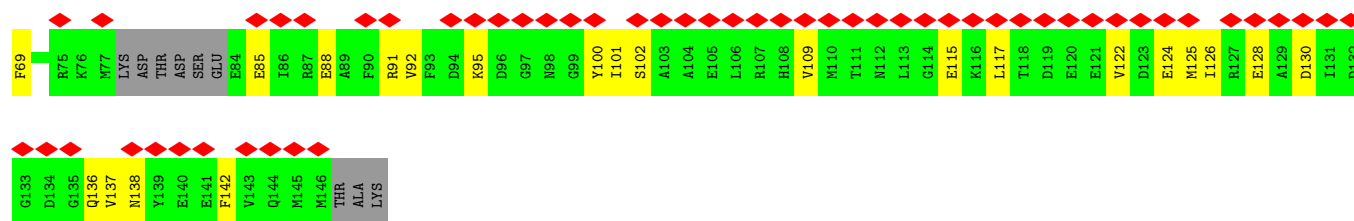




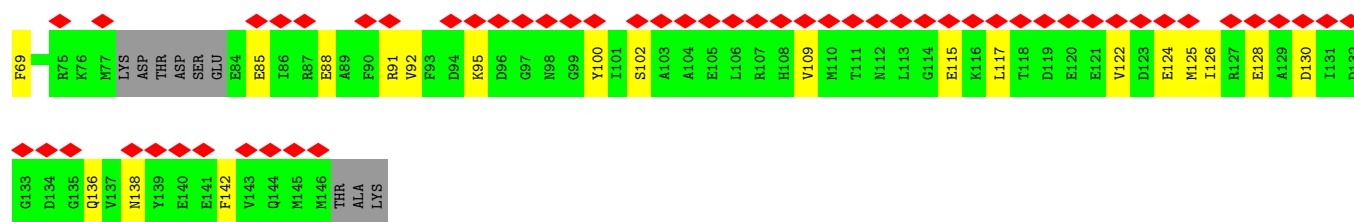


- Molecule 2: Calmodulin-1

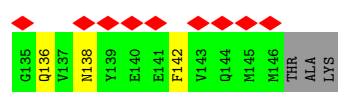
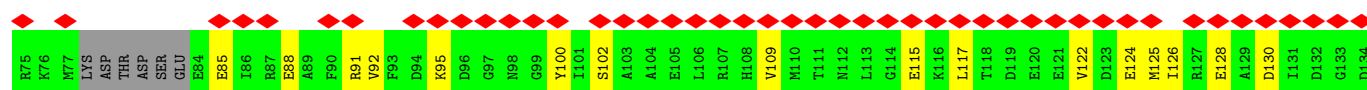




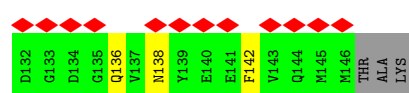
• Molecule 2: Calmodulin-1



• Molecule 2: Calmodulin-1



• Molecule 2: Calmodulin-1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	22876	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	-0.016	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (Å)	436.4, 436.4, 436.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.091, 1.091, 1.091	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, 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	0.56	1/27223 (0.0%)	0.76	7/36827 (0.0%)
1	C	0.56	1/27223 (0.0%)	0.77	10/36827 (0.0%)
1	E	0.56	1/27223 (0.0%)	0.76	7/36827 (0.0%)
1	G	0.56	1/27223 (0.0%)	0.76	7/36827 (0.0%)
2	B	0.26	0/1053	0.52	0/1411
2	D	0.26	0/1053	0.52	0/1411
2	F	0.26	0/1053	0.52	0/1411
2	H	0.26	0/1053	0.52	0/1411
All	All	0.56	4/113104 (0.0%)	0.76	31/152952 (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
1	A	0	33
1	C	0	33
1	E	0	33
1	G	0	33
All	All	0	132

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1692	LYS	CA-C	-5.40	1.45	1.52
1	C	1692	LYS	CA-C	-5.40	1.45	1.52
1	E	1692	LYS	CA-C	-5.40	1.45	1.52
1	G	1692	LYS	CA-C	-5.40	1.45	1.52

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	4519	LEU	CB-CA-C	-10.79	91.61	110.72
1	C	4520	PHE	N-CA-C	-8.11	101.44	113.61
1	C	2431	GLY	CA-C-N	5.82	131.81	120.99
1	C	2431	GLY	C-N-CA	5.82	131.81	120.99
1	A	2431	GLY	CA-C-N	5.81	131.80	120.99

There are no chirality outliers.

5 of 132 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	729	GLY	Peptide
1	A	817	PRO	Peptide
1	A	818	GLY	Peptide
1	A	819	TYR	Peptide
1	A	829	LYS	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	26722	0	25168	1062	0
1	C	26722	0	25168	1084	0
1	E	26722	0	25168	1080	0
1	G	26722	0	25168	1089	0
2	B	1042	0	979	31	0
2	D	1042	0	979	31	0
2	F	1042	0	979	31	0
2	H	1042	0	979	33	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
4	A	1	0	0	0	0
4	B	4	0	0	0	0
4	C	1	0	0	0	0
4	D	4	0	0	0	0
4	E	1	0	0	0	0
4	F	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	1	0	0	0	0
4	H	4	0	0	0	0
All	All	111080	0	104588	4204	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 19.

The worst 5 of 4204 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:4811:LEU:CD2	1:G:4519:LEU:HD13	1.75	1.15
1:A:4860:LEU:HD13	1:C:4863:ILE:HD12	1.29	1.11
1:A:4863:ILE:HD12	1:G:4860:LEU:HD13	1.29	1.11
1:E:4860:LEU:HD13	1:G:4863:ILE:HD12	1.29	1.10
1:C:4860:LEU:HD13	1:E:4863:ILE:HD12	1.29	1.09

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	3387/4968 (68%)	2919 (86%)	459 (14%)	9 (0%)	36	71
1	C	3387/4968 (68%)	2917 (86%)	460 (14%)	10 (0%)	36	71
1	E	3387/4968 (68%)	2921 (86%)	457 (14%)	9 (0%)	36	71
1	G	3387/4968 (68%)	2920 (86%)	458 (14%)	9 (0%)	36	71
2	B	128/149 (86%)	120 (94%)	8 (6%)	0	100	100
2	D	128/149 (86%)	120 (94%)	8 (6%)	0	100	100
2	F	128/149 (86%)	120 (94%)	8 (6%)	0	100	100
2	H	128/149 (86%)	120 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	14060/20468 (69%)	12157 (86%)	1866 (13%)	37 (0%)	37	71

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	4521	TYR
1	A	853	PRO
1	A	1580	PRO
1	A	2309	CYS
1	C	853	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	2675/4355 (61%)	2623 (98%)	52 (2%)	50	66
1	C	2675/4355 (61%)	2622 (98%)	53 (2%)	48	66
1	E	2676/4355 (61%)	2621 (98%)	55 (2%)	47	65
1	G	2675/4355 (61%)	2621 (98%)	54 (2%)	48	66
2	B	112/127 (88%)	112 (100%)	0	100	100
2	D	112/127 (88%)	112 (100%)	0	100	100
2	F	112/127 (88%)	112 (100%)	0	100	100
2	H	112/127 (88%)	112 (100%)	0	100	100
All	All	11149/17928 (62%)	10935 (98%)	214 (2%)	49	66

5 of 214 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	237	LEU
1	E	3840	LEU
1	G	3936	LEU
1	E	907	VAL
1	E	2198	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 260 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	2831	ASN
1	G	3792	GLN
1	C	2211	ASN
1	C	1906	GLN
1	G	3961	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 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 ⓘ

There are no chain breaks in this entry.

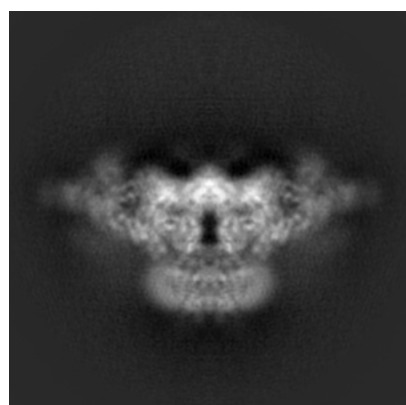
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9889. These allow visual inspection of the internal detail of the map and identification of artifacts.

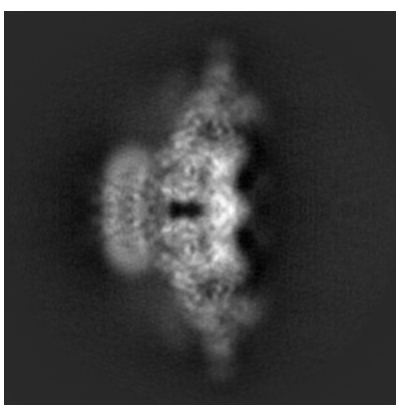
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

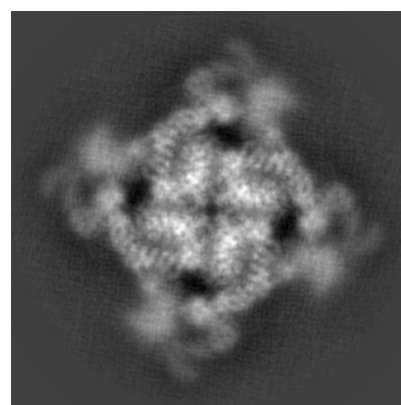
6.1.1 Primary map



X



Y

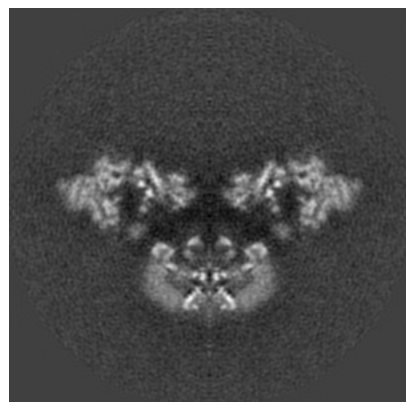


Z

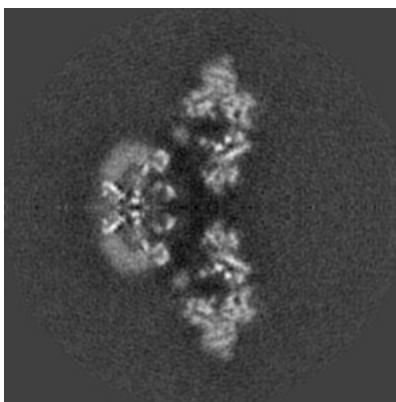
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

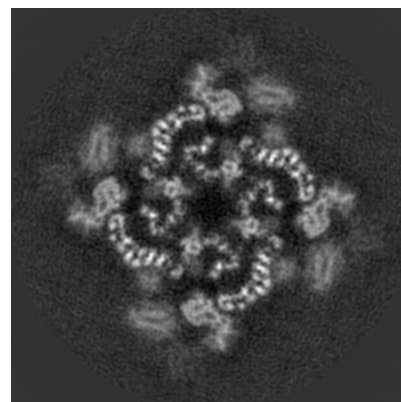
6.2.1 Primary map



X Index: 200



Y Index: 200

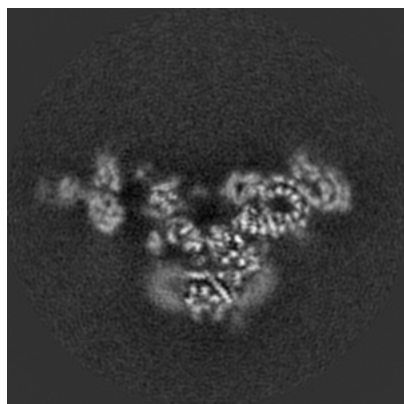


Z Index: 200

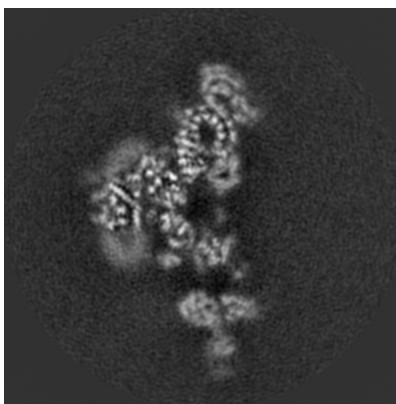
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

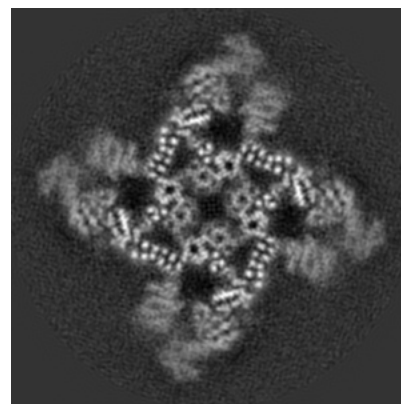
6.3.1 Primary map



X Index: 187



Y Index: 213

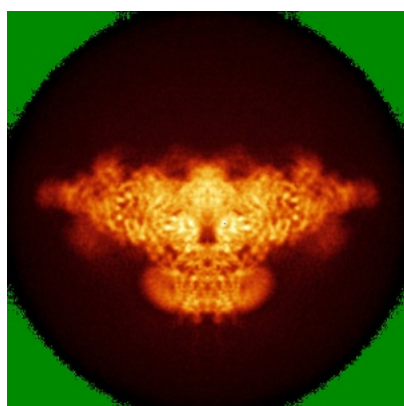


Z Index: 211

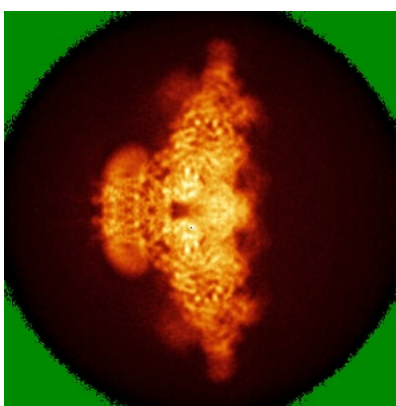
The images above show the largest variance slices of the map in three orthogonal directions.

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

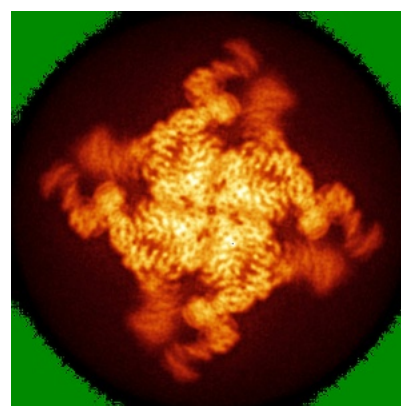
6.4.1 Primary map



X



Y

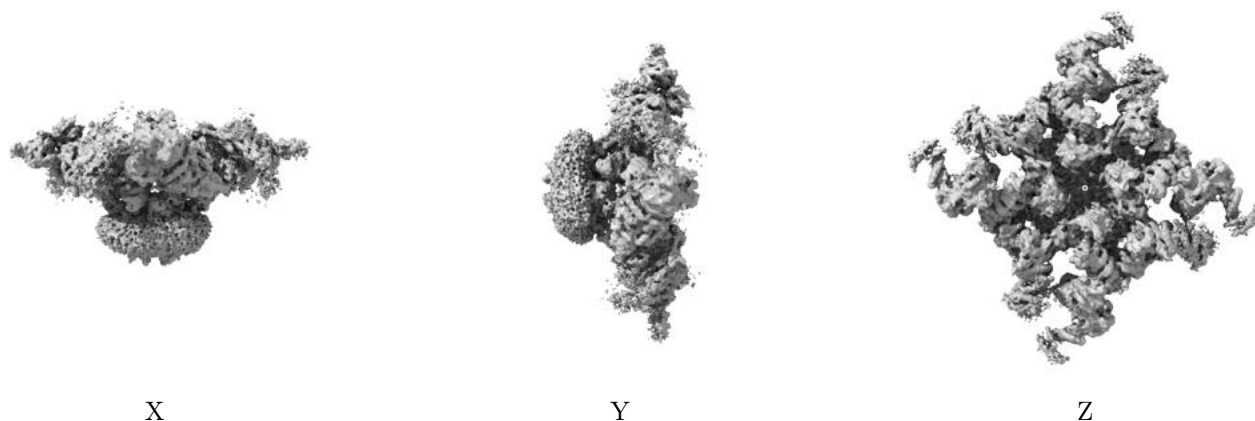


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

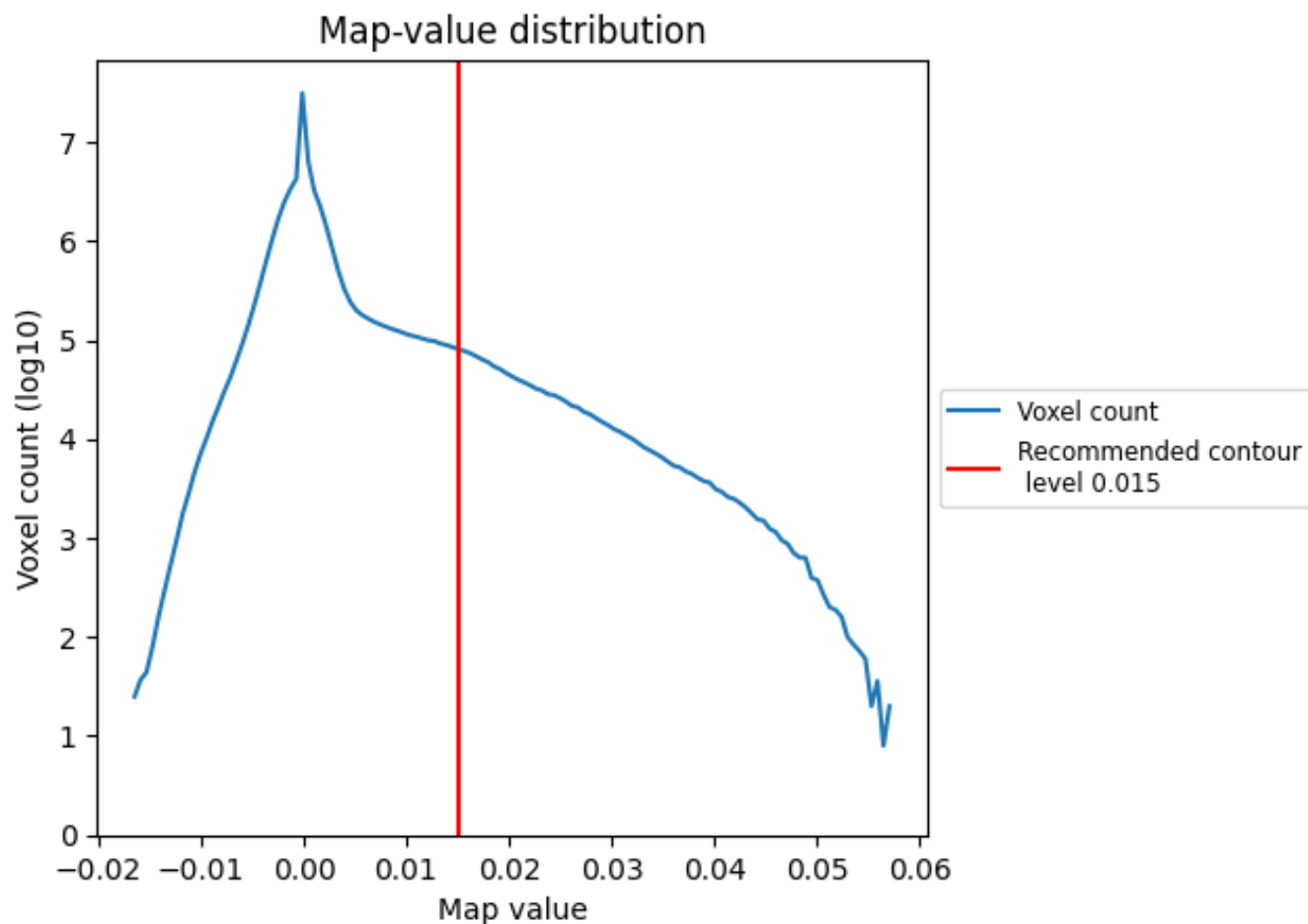
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

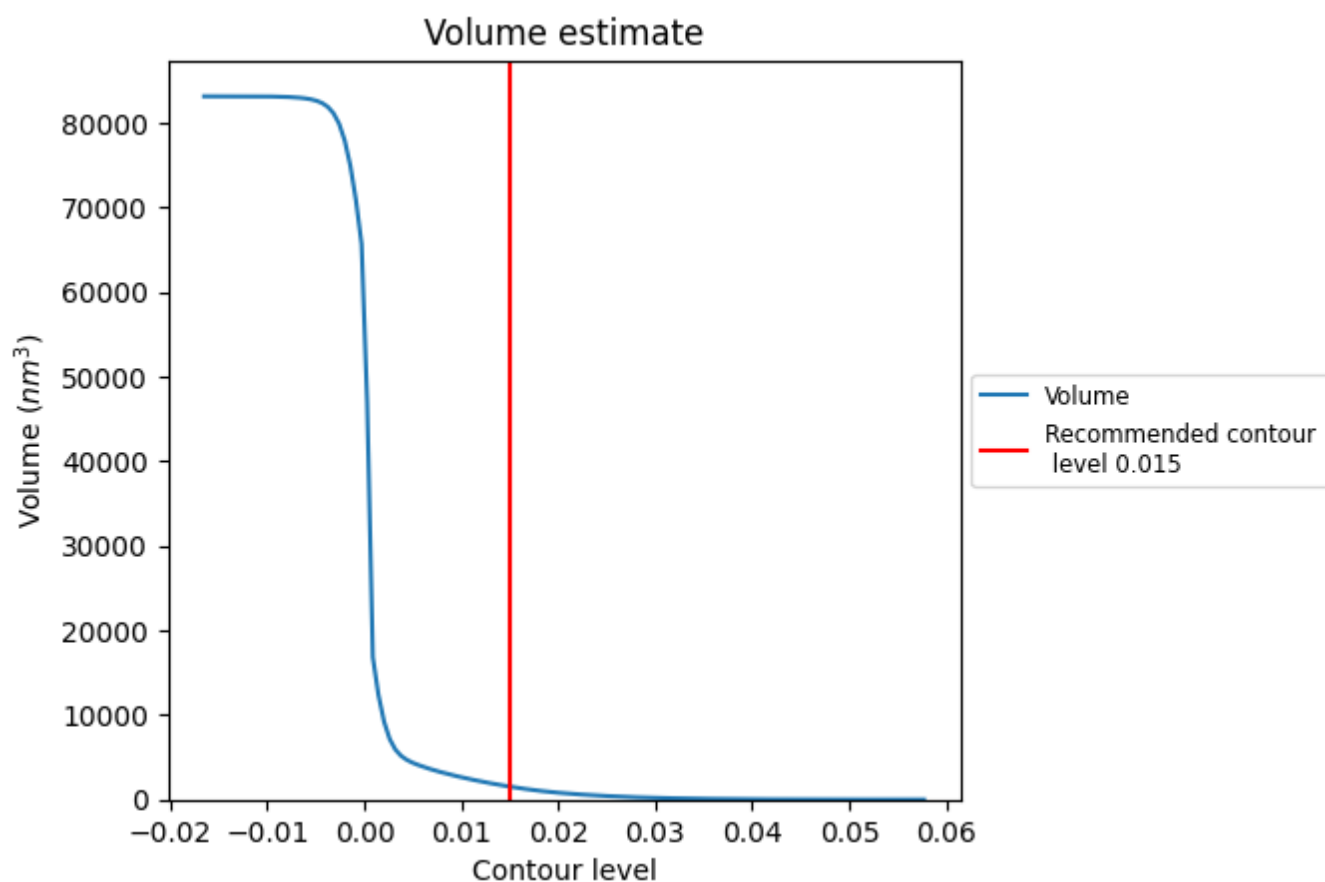
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

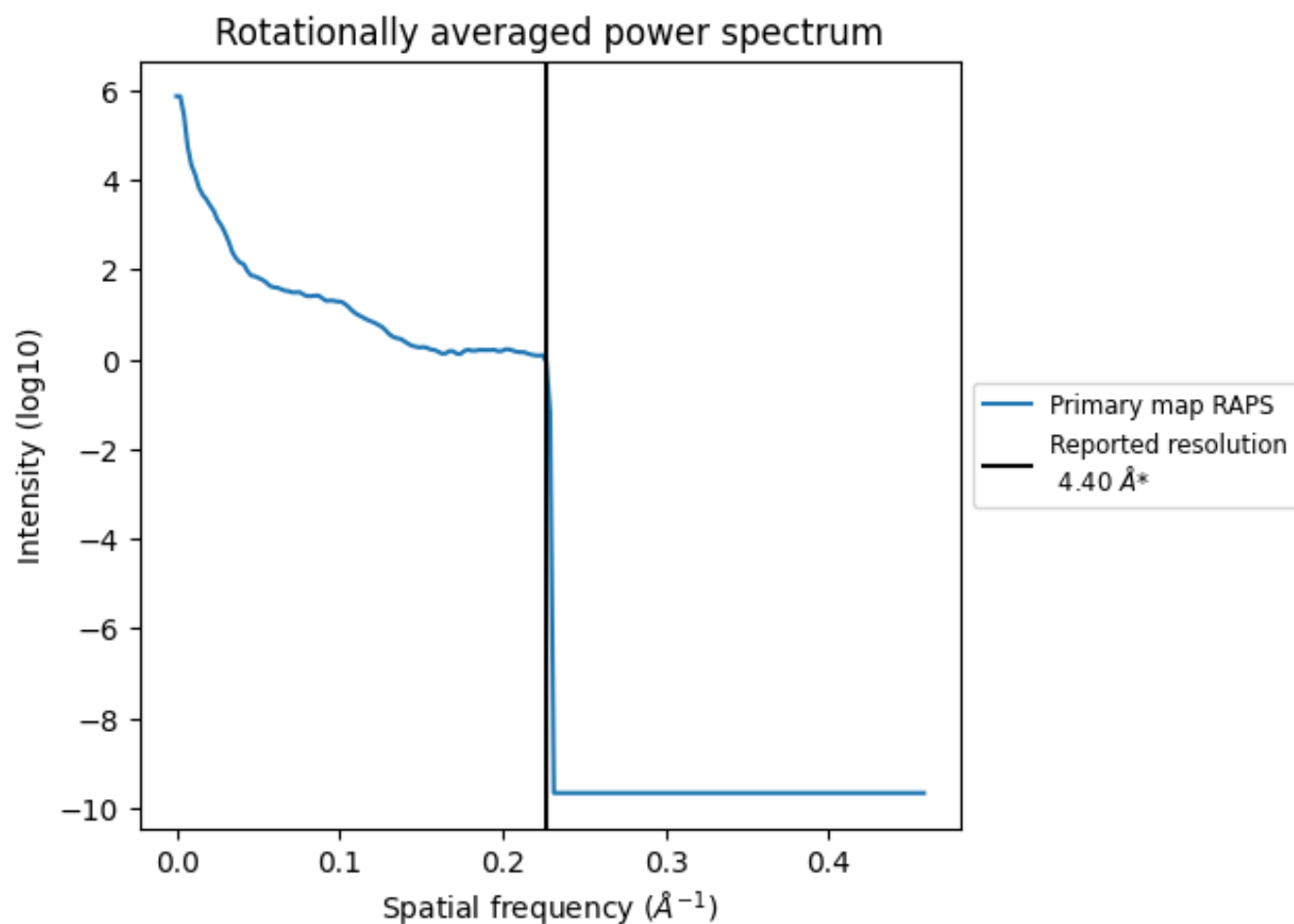
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1535 nm³; this corresponds to an approximate mass of 1386 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 ⓘ

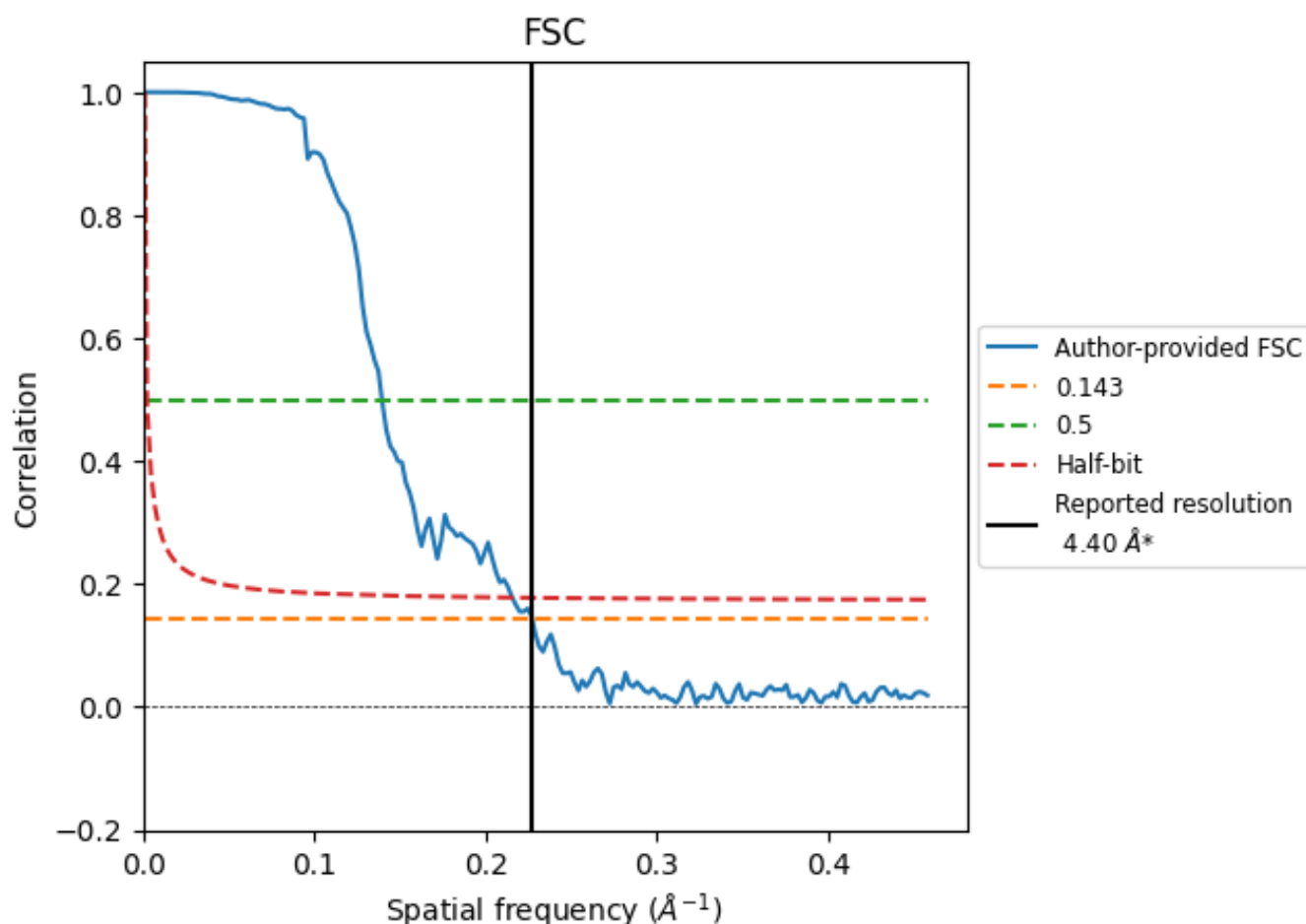


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

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 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

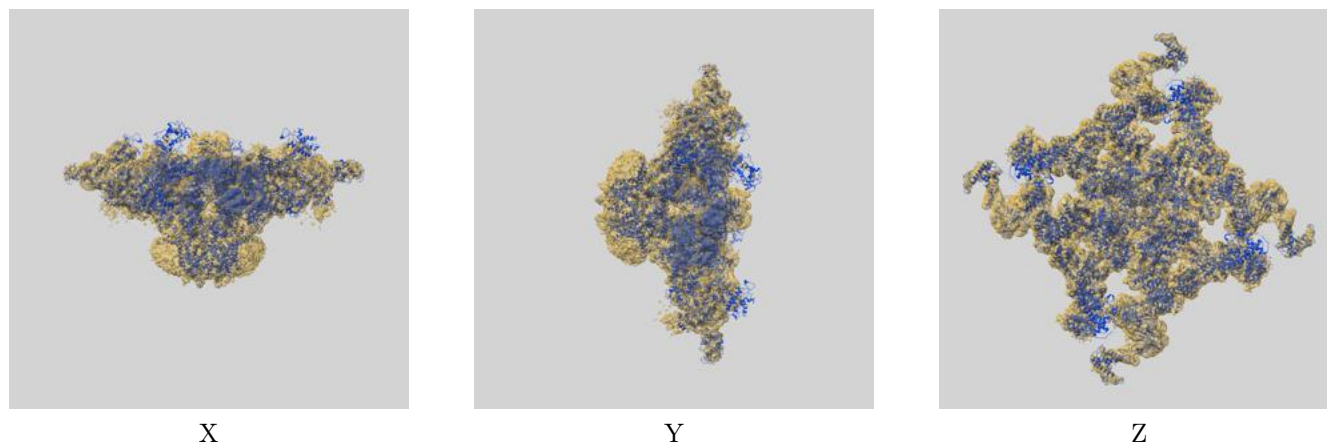
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.40	7.17	4.64
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

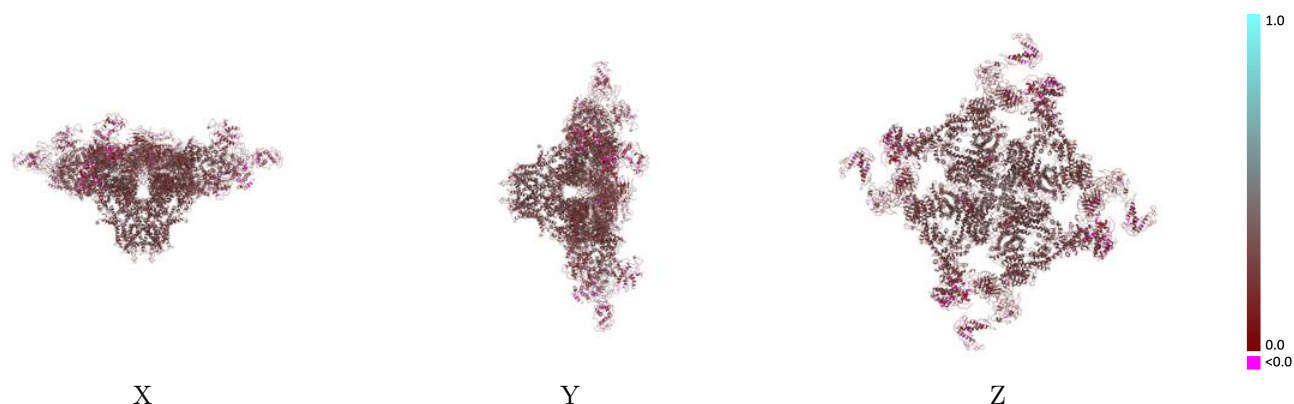
This section contains information regarding the fit between EMDB map EMD-9889 and PDB model 6JV2. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



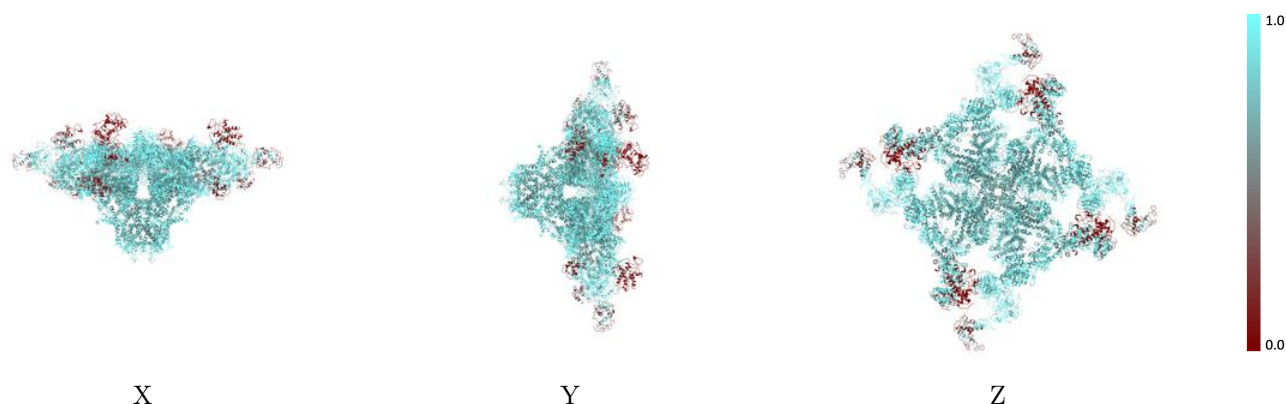
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



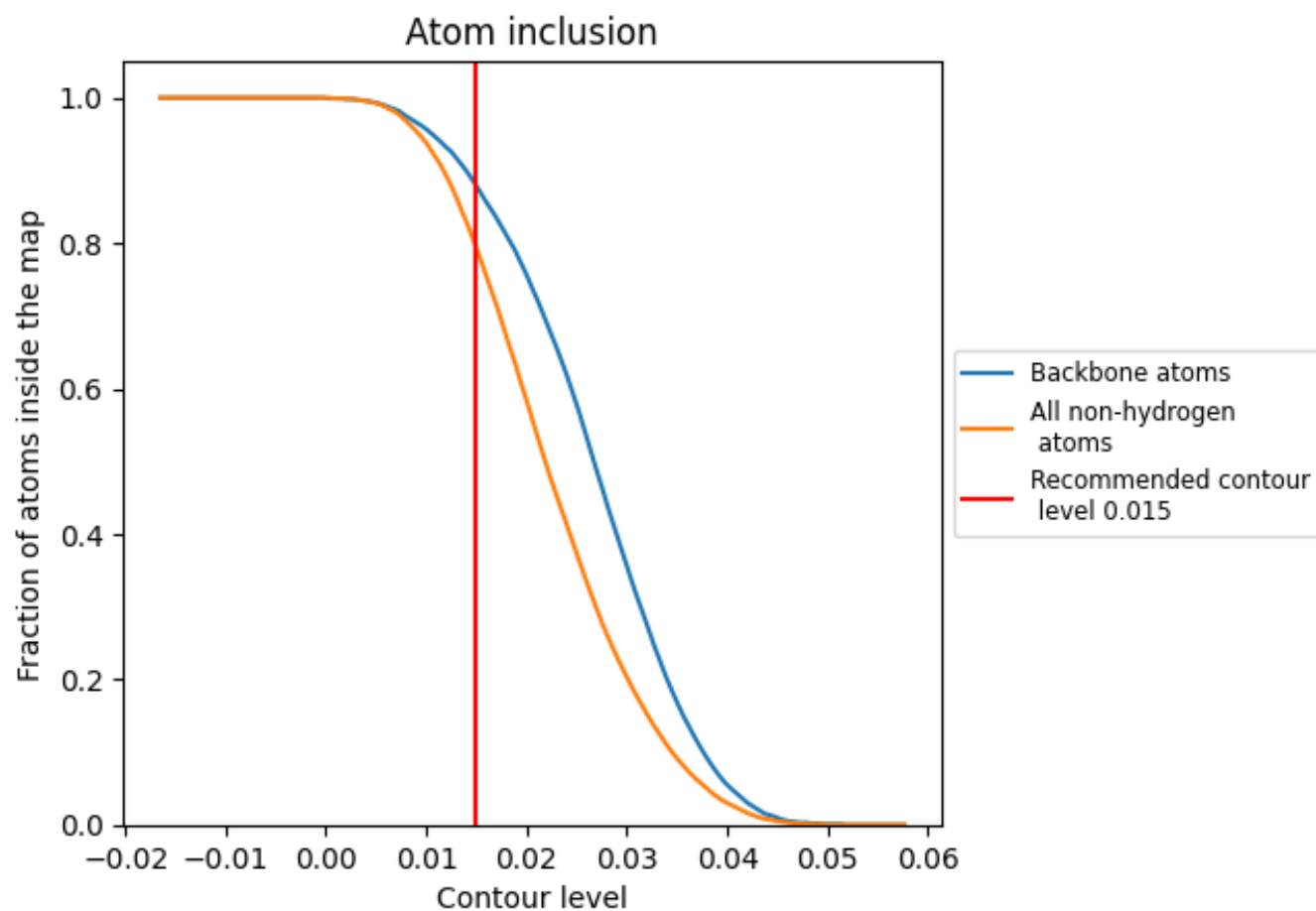
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 79% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7940	0.2670
A	0.8120	0.2680
B	0.3300	0.2230
C	0.8130	0.2690
D	0.3290	0.2250
E	0.8130	0.2680
F	0.3300	0.2220
G	0.8120	0.2680
H	0.3290	0.2210

1.0

0.0

<0.0