



# wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 01:47 PM JST

PDB ID : 5J8V  
EMDB ID : EMD-8073  
Title : Structure of rabbit ryanodine receptor RyR1 open state activated by calcium ion  
Authors : Wang, X.; Wei, R.; Yin, C.; Sun, F.  
Deposited on : 2016-04-08  
Resolution : 4.90 Å(reported)  
Based on initial model : 3J8H

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.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

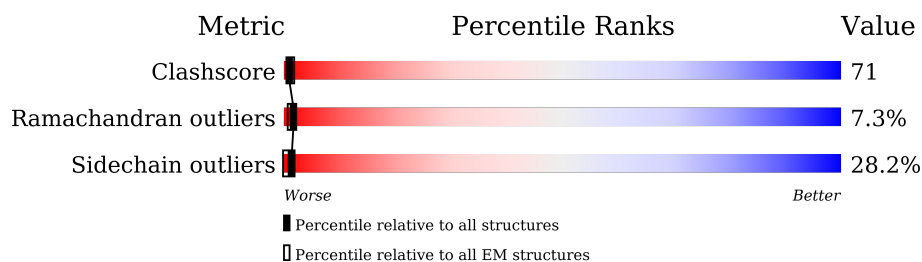
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	5037	
1	B	5037	
1	C	5037	
1	D	5037	

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 73616 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	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0
1	B	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0
1	C	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0
1	D	3453	Total 18404	C 11343	N 3553	O 3501	S 7	0	0



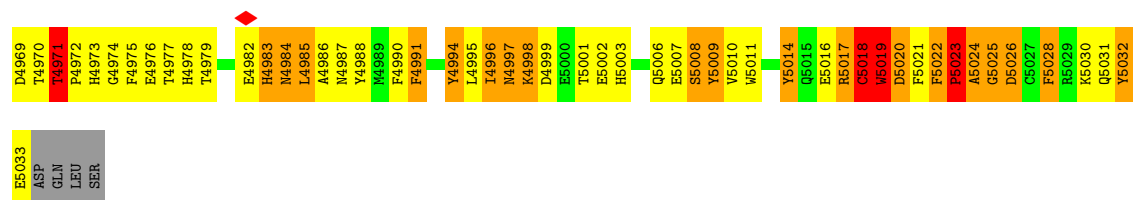




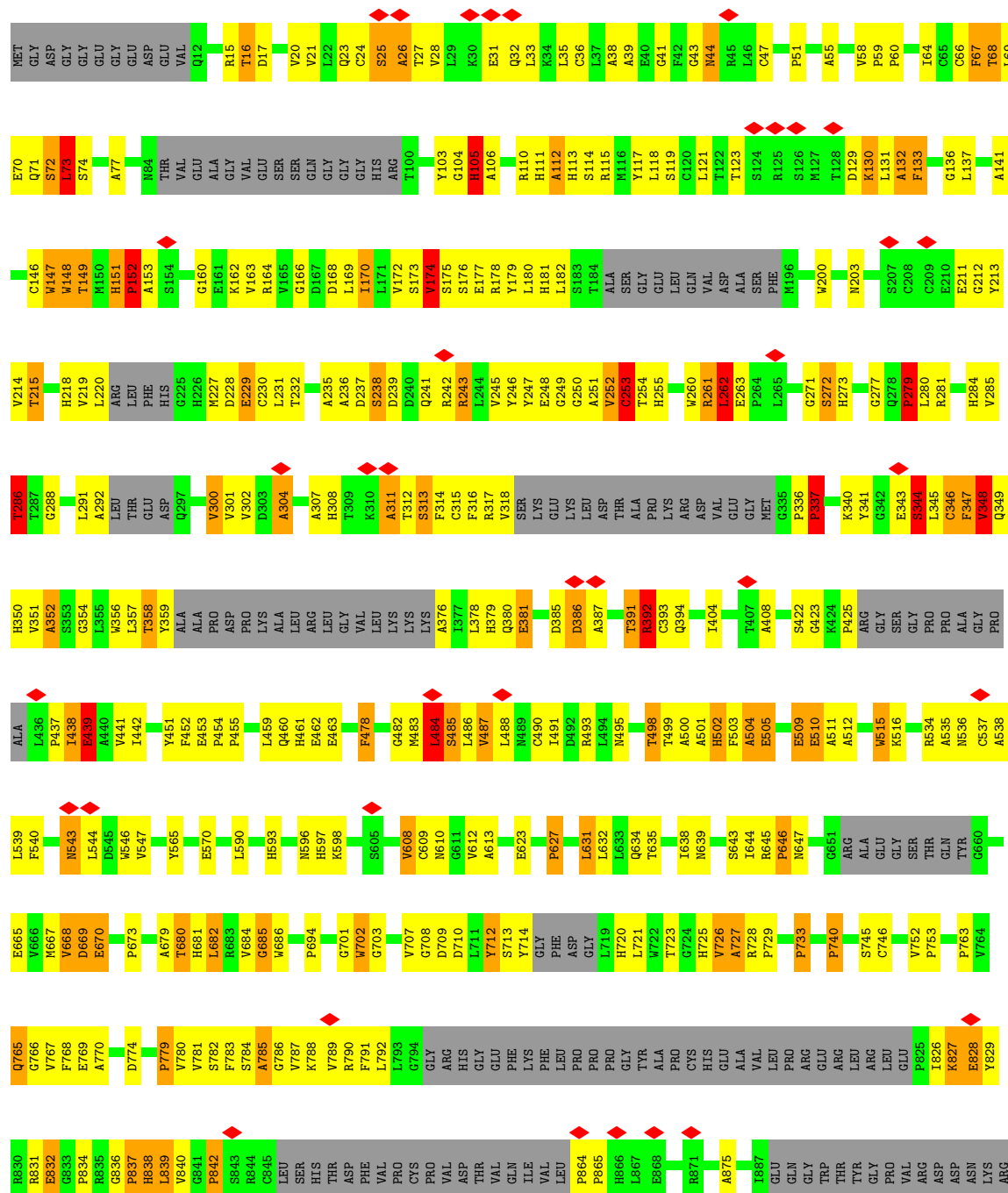
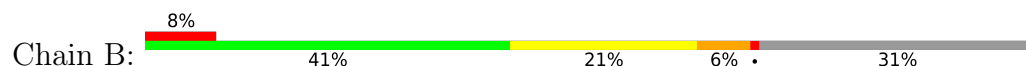
E3757	M3758	E3759	K3760	Q3761	K3762	L3763	L3764	Y3765	Q3766	R3769	R3773	A3785	C3786	K3787	A3792	M3793	V3794	S3795	S3796	L3805	N3806	G3807	G3808	N3809	A3810	E3811	Y3819	K3823	K3824	E3825	V3826	E3827	F3828	F3829	Q3830	Q3833	A3834	L3835	M3836	Q3837	T3838	C3839	S3840	Q3850	A3853	GLU	GLY	LEU									
F3669	E3670	D3671	K3679	ALA	GLY	GLU	GLN	GLU	GLU	GLU	GLU	VAL	GLU	VAL	LYS	P3695	D3696	P3697	L3698	H3699	Q3700	L3701	V3702	G3708	A3709	L3710	D3717	E3718	D3719	V3720	L3721	Y3725	H3734	LEU	GLU	GLU	GLY	ASN	P3645	R3648	K3658	W3661	I3662	E3665	D3666	H3667	S3752										
F3458	Q3461	L3470	ALA	ASP	SER	K3475	S3476	K3477	G3482	S3486	G3487	G3488	SER	ASP	GLN	GLU	ARG	GLY	ASP	GLU	THR	ARG	GLY	ASP	GLY	VAL	ARG	GLY	VAL	ALA	T3513	K3516	M3517	L3518	P3519	T3520	N3523	M3524	K3525	A3526	P3527	THR	ASP	GLN	ASP	LEU											
A3883	K3384	A3387	E3388	E3389	GLY	GLU	LEU	VAL	ARG	ASP	GLU	PHE	SER	VAL	VAL	CYS	ASP	L3405	A3407	L3408	Y3409	P3410	L3411	Y3415	V3416	D3417	N3418	N3419	H3422	W3423	P3427	N3430	A3431	E3432	E3433	L3434	PHE	ARG	M3437	V3438	G3439	F3442	S3446	K3452	E3455	Q3456	N3457										
P3302	P3303	C3304	T3305	A3306	M3313	SER	LEU	LEU	GLY	ASN	ILE	LEU	R3321	N3325	E3331	A3332	T3333	L3338	A3339	VAL	PHE	ALA	GLN	PRO	ILE	V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	H3356	H3357	P3360	T3361	I3362	G3363	ARG	LEU	ARG	K3367	A3374	E3377	Q3378	L3379	R3380	L3381	E3382					
MET	CYS	PRO	ASP	ILE	PRO	VAL	GLY	LEU	ASP	LEU	ARG	MET	GLY	ASP	ALA	GLY	GLY	ARG	VAL	ILE	ILE	VAL	VAL	ILE	T3273	L3274	E3207	P3208	Q3209	L3210	Y3213	S3217	VAL	TYR	THR	THR	LYS	SER	PRO	ARG	GLU	ALA	LEU	PRO	ASN	ASP	VAL	GLU									
E3086	I3087	K3088	K3089	A3090	GLY	LEU	ARG	SER	PHE	GLU	S3098	A3099	I3103	E3104	K3105	V3107	E3108	N3109	L3110	R3111	L3112	G3113	K3114	VAL	SER	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	GLN	ASN	LEU	THR	T3132	T3133	P3138	F3152	GLY	ASP	ASP	VAL	ILE	L3158	D3159	D3160	V3161	Q3162				
I3039	THR	SER	LEU	ARG	TRP	MET	ASP	ILE	SER	SER	GLN	VAL	V3050	D3060	A3061	P3062	A3063	V3064	VAL	ASN	CYS	LEU	HIS	T3070	L3071	A3072	R3073	D3076	L3158	D3159	D3160	V3161	Q3162																								
H2874	A2875	E2876	Q2877	L2878	R2879	E2880	H2883	N2884	T2885	W2886	G2887	R2888	K2889	T2890	K2891	Q2892	E2893	L2894	E2895	E2896	K2897	K2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	V2908	D2909	T2910	L2911	T2912	A2913	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929	L2930	Q2931	H2932	H2933	G2934
Y2935	A2936	V2937	T2938	G2940	LEU	LYS	ASP	MET	GLU	ASN	GLN	TYR	THR	SER	ASN	ILE	GLU	LYS	PHE	ALA	PHE	PHE	PHE	LEU	GLN	GLN	TRP	MET	ASP	ILE	SER	GLN	VAL	ALA	VAL	VAL	SER	SER	GLY	ARG	VAL	GLU	LYS	SER	PRO	HIS	GLU	GLN	GLU								

D4907	D4908	K4835	LEU	THR	TRP	ASN	GLY	L4562	PRO	THR	VAL	GLY	L4178	GLY	Q4102	G3939	GLY	D3877
E4907	Q4836	Q4837	THR	THR	TRP	MET	NET	L4565	GLY	GLU	VAL	GLU	G4179	GLU	F4103	G3942	NET	D3878
Y4909	Y4909	Y4838	TRP	TRP	TRP	GLY	GLY	A4570	PRO	LEU	ALA	PRO	I4180	PRO	T4104	V3942	VAL	E3879
E4910	E4910	Y4839	THR	THR	THR	GLY	GLY	F4571	GLY	LEU	ALA	GLY	I4181	GLY	C4105	I3943	ASN	E3879
L4911	L4911	T4840	THR	THR	THR	GLY	GLY	A4572	ALA	ALA	ALA	ASP	I4183	ASP	P4106	E3944	ASP	F3880
V4914	V4914	L4843	THR	THR	THR	GLY	GLY	A4573	ASP	GLY	GLY	GLY	M4184	GLY	E4107	Q3946	GLY	F3887
V4915	V4915	L4844	THR	THR	THR	GLY	GLY	I4574	GLY	PRO	GLY	ASP	R4188	ASP	I4108	G3947	THR	L3888
F4916	F4916	A4845	THR	THR	THR	GLY	GLY	F4575	GLY	ASP	ALA	ALA	R4189	GLY	Q4109	F3951	VAL	Q3970
D4917	D4917	V4846	THR	THR	THR	GLY	GLY	I4576	GLY	PRO	GLY	GLY	I4190	GLY	F4110	F3962	VAL	D3877
T4918	T4918	V4847	THR	THR	THR	GLY	GLY	L4577	GLY	PRO	GLY	GLY	E4191	GLY	S4115	ARG	ASN	L3889
V4920	V4920	V4848	THR	THR	THR	GLY	GLY	F4578	GLY	PRO	GLY	GLY	R4192	GLY	D4118	GLN	GLN	Q3987
F4921	F4921	Y4849	THR	THR	THR	GLY	GLY	F4579	GLY	PRO	GLY	GLY	I4193	ALA	E4119	S3964	ASN	L3890
F4922	F4922	L4850	THR	THR	THR	GLY	GLY	TYR	GLY	PRO	GLY	GLY	I4194	ALA	E4120	L3965	GLY	L3891
F4923	F4923	F4851	THR	THR	THR	GLY	GLY	L4579	VAL	GLY	ALA	ALA	F4195	ALA	N4120	T3966	GLY	C3892
V4924	V4924	F4852	THR	THR	THR	GLY	GLY	L4579	VAL	GLY	ALA	ALA	F4196	ALA	E4121	E3967	GLY	E3893
L4925	L4925	V4853	THR	THR	THR	GLY	GLY	L4579	GLY	GLY	ALA	ALA	I4197	GLY	F4122	LYS	LYS	C3894
V4926	V4926	V4854	THR	THR	THR	GLY	GLY	L4579	GLY	GLY	ALA	ALA	I4197	GLY	F4123	LYS	LYS	H3895
I4927	I4927	A4855	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	Q3970
L4928	L4928	F4856	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
L4929	L4929	F4857	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
A4930	A4930	F4858	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
I4931	I4931	K4860	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
I4932	I4932	K4861	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
Q4933	Q4933	K4862	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
G4934	G4934	F4863	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
L4935	L4935	Y4864	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
I4936	I4936	K4865	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
I4937	I4937	K4866	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
D4938	D4938	E4867	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
D4939	D4939	F4868	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
F4940	F4940	K4869	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
G4941	G4941	L4870	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
E4942	E4942	Y4871	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
L4943	L4943	Y4872	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
R4944	R4944	N4805	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
D4945	D4945	N4806	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
Q4946	Q4946	Y4873	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
Q4947	Q4947	L4874	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
E4948	E4948	N4810	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
Q4949	Q4949	H4811	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
V4950	V4950	H4812	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
K4951	K4951	L4813	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
E4952	E4952	T4816	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
D4953	D4953	C4882	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
N4954	N4954	Y4883	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
E4955	E4955	L4884	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
T4956	T4956	F4885	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
K4957	K4957	Y4886	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
C4958	C4958	H4887	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
F4959	F4959	V4888	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
I4960	I4960	Y4889	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
C4961	C4961	L4890	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
G4964	G4964	V4891	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
S4965	S4965	F4892	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
D4966	D4966	Y4893	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
Y4967	Y4967	G4894	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877
F4968	F4968	P4904	THR	THR	THR	GLY	GLY	L4579	PRO	PRO	ASP	GLY	W4206	GLY	N4124	D3877	GLY	D3877





• Molecule 1: Ryanodine receptor 1





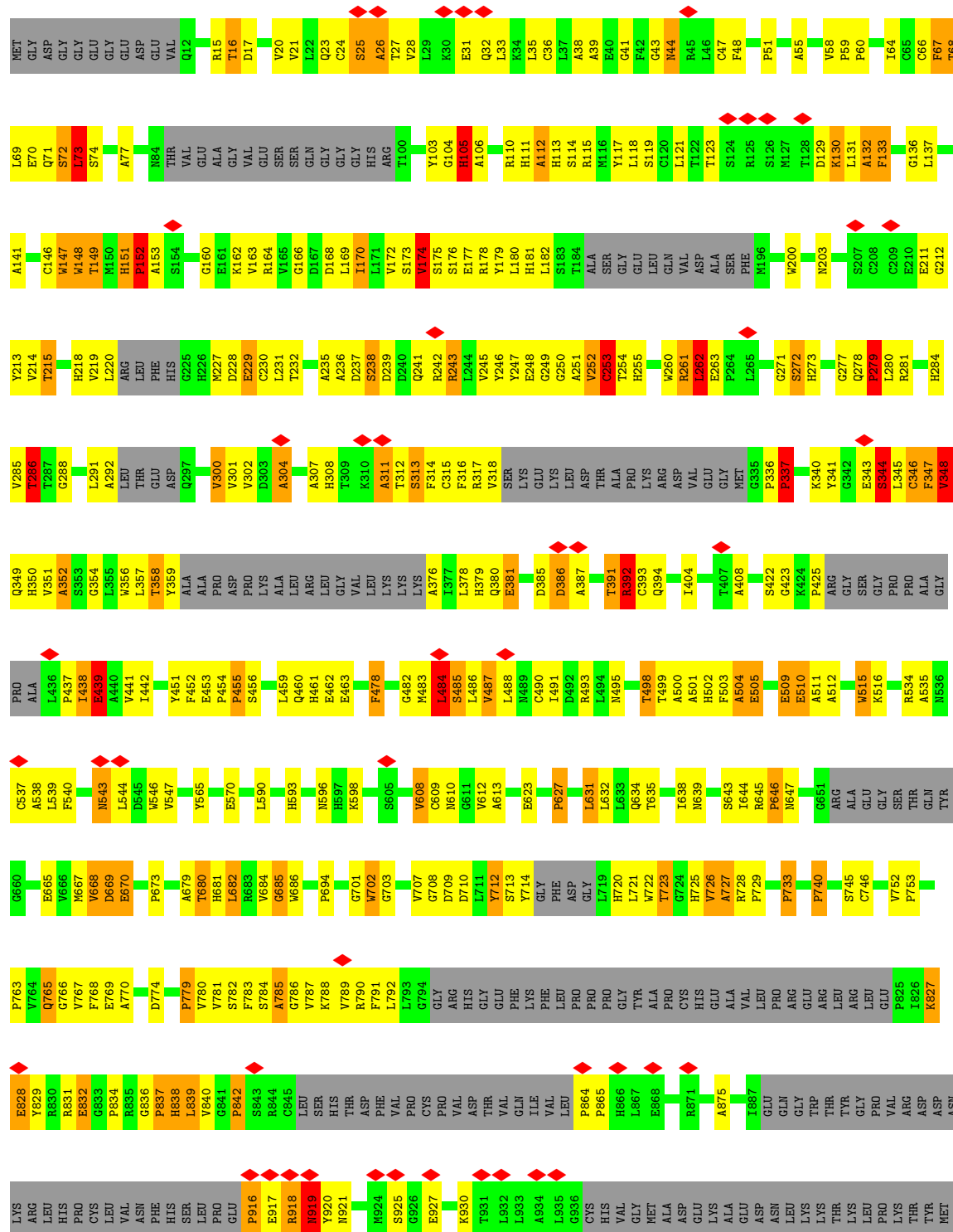




S4985	D4966	Y4967	F4968	D4969	T4970	F4971	F4972	V4914	V4915	F4916	D4917	L4918	T4919	F4920	F4921	F4922	N4984	L4985	A4986	N4987	V4926	L4927	L4928	F4989	F4990	F4991	Y4994	L4995	L4996	N4997	K4998	D4999	E5000	T5001	D4938	A4939	F4940	G4941	E4942	L4943	R4944	D4945	Q4946	Q4947	E4948	Q4949	V4950	Y5014	Q5015	R5016	R5017	C5018	D5019	E5020	F5021	F5022	P5023	A5024	F4959	T4960	G4961	G4964																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
H4832	N4833	G4834	K4835	Q4836	L4837	V4838	M4839	T4840	L4843	L4844	A4845	V4846	V4847	V4848	Y4849	F4850	Y4851	T4852	V4853	H4854	A4855	F4856	N4857	F4858	F4859	L4860	K4861	F4862	L4863	N4864	K4865	S4866	E4867	D4868	GLU	ASP	GLU	N4804	N4805	N4806	F4807	A4810	A4811	H4812	L4813	T4881	C4882	Y4883	L4884	F4885	H4886	N4887	Y4888	V4889	F4959	I4960	G4961	G4964																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
PRO	PRO	GLY	LEU	LEU	THR	TRP	L4768	M4769	S4770	V4773	K4774	Y4775	Q4776	L4777	W4778	K4779	F4780	Q4781	D4782	L4783	F4784	E4789	L4790	Y4791	W4794	Y4795	L4796	W4797	M4798	S4799	L4800	L4801	G4802	H4803	Y4804	N4805	N4806	F4807	A4810	A4811	H4812	L4813	I4816	A4817	M4818	G4819	V4820	L4821	T4822	L4823	R4824	T4825	S4829																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
Q4691	F4692	D4696	F4697	K4698	G4699	W4701	Y4705	L4706	M4707	F4711	M4714	Y4715	W4716	D4717	K4718	F4719	V4720	K4721	V4724	L4725	D4726	K4727	H4728	G4729	D4730	I4731	F4732	L4733	I4737	A4738	E4739	L4740	G4741	G4742	M4743	ASP	LEU	ALA	SER	LEU	ILE	THR	ALA	V4818	G4819	V4820	L4821	T4822	L4823	R4824	T4825	S4829																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
ASP	GLU	ASP	GLU	ASN	MET	Y4628	L4632	E4633	E4634	S4635	Y4638	F4641	A4642	L4643	V4644	C4645	L4646	L4649	H4650	T4651	L4652	V4653	A4654	F4655	C4657	L4658	L4659	G4660	Y4661	N4662	C4663	L4664	K4665	V4666	L4668	V4669	F4670	F4671	X4672	B4673	L4677	L4681	E4682	F4683	D4684	C4685	L4686	Y4687	T4689	E4690																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
S4556	R4557	N4558	F4559	Y4560	T4561	L4562	A4570	F4571	A4572	I4573	N4574	F4575	L4576	L4577	F4578	F4579	TYR	L4580	SER	ASP	SER	PRO	PRO	GLY	GLU	ASP	ASP	MET	GLY	GLU	GLY	SER	PRO	PRO	PRO	PRO	PRO	PRO	GLY	GLU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
PRO	GLU	PRO	GLU	PRO	GLU	PRO	GLU	GLY	GLY	ASP	GLU	GLU	ASN	GLY	GLY	GLY	VAL	VAL	ASP	SER	PRO	PRO	PRO	GLY	GLU	ASP	ASP	MET	LYS	LYS	ALA	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
ARG	SER	LEU	ARG	ARG	ARG	VAL	ARG	ARG	ARG	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	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























## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	41743	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	48	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	5400	Depositor
Magnification	100286	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.532	Depositor
Minimum map value	-0.339	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.0967	Depositor
Map size ( $\text{\AA}$ )	547.232, 547.232, 547.232	wwPDB
Map dimensions	392, 392, 392	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.396, 1.396, 1.396	Depositor



## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	1.17	51/18508 (0.3%)	1.21	262/25601 (1.0%)
1	B	1.17	51/18508 (0.3%)	1.21	262/25601 (1.0%)
1	C	1.17	51/18508 (0.3%)	1.21	262/25601 (1.0%)
1	D	1.17	51/18508 (0.3%)	1.21	262/25601 (1.0%)
All	All	1.17	204/74032 (0.3%)	1.21	1048/102404 (1.0%)

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	1	3
1	B	1	3
1	C	1	3
1	D	1	3
All	All	4	12

The worst 5 of 204 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4859	PHE	CA-CB	-43.48	0.58	1.53
1	B	4859	PHE	CA-CB	-43.48	0.58	1.53
1	C	4859	PHE	CA-CB	-43.48	0.58	1.53
1	D	4859	PHE	CA-CB	-43.48	0.58	1.53
1	A	4691	GLN	CA-CB	-40.95	0.63	1.53

The worst 5 of 1048 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2047	GLU	N-CA-CB	-38.23	41.78	110.60
1	C	2047	GLU	N-CA-CB	-38.23	41.78	110.60
1	D	2047	GLU	N-CA-CB	-38.23	41.78	110.60

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2047	GLU	N-CA-CB	-38.22	41.80	110.60
1	A	4168	GLU	N-CA-CB	-30.53	55.64	110.60

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	4691	GLN	CA
1	B	4691	GLN	CA
1	C	4691	GLN	CA
1	D	4691	GLN	CA

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2192	TYR	Mainchain
1	A	2586	VAL	Peptide
1	A	4091	LYS	Peptide
1	B	2192	TYR	Mainchain
1	B	2586	VAL	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	18404	0	9770	2060	0
1	B	18404	0	9770	2067	0
1	C	18404	0	9770	2068	0
1	D	18404	0	9770	2069	0
All	All	73616	0	39080	8025	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 71.

The worst 5 of 8025 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:D:4978:HIS:HE2	1:D:4983:HIS:CD2	1.11	1.67
1:A:4235:VAL:HG21	1:A:5019:TRP:CZ3	1.15	1.67
1:C:4115:SER:HA	1:C:4128:PHE:CZ	1.23	1.66
1:A:4978:HIS:HE2	1:A:4983:HIS:CD2	1.11	1.66
1:B:4978:HIS:HE2	1:B:4983:HIS:CD2	1.11	1.65

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	3311/5037 (66%)	2865 (86%)	203 (6%)	243 (7%)	1	11
1	B	3311/5037 (66%)	2865 (86%)	204 (6%)	242 (7%)	1	11
1	C	3311/5037 (66%)	2865 (86%)	203 (6%)	243 (7%)	1	11
1	D	3311/5037 (66%)	2864 (86%)	205 (6%)	242 (7%)	1	11
All	All	13244/20148 (66%)	11459 (86%)	815 (6%)	970 (7%)	2	11

5 of 970 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	25	SER
1	A	26	ALA
1	A	44	ASN
1	A	67	PHE

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	317/4276 (7%)	225 (71%)	92 (29%)	0	2
1	B	317/4276 (7%)	229 (72%)	88 (28%)	0	3
1	C	317/4276 (7%)	229 (72%)	88 (28%)	0	3
1	D	317/4276 (7%)	228 (72%)	89 (28%)	0	2
All	All	1268/17104 (7%)	911 (72%)	357 (28%)	1	2

5 of 357 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4799	SER
1	D	4061	PHE
1	C	4849	TYR
1	C	4997	ASN
1	D	4561	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 44 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	4803	HIS
1	D	3833	GLN
1	C	4806	ASN
1	C	5031	GLN
1	D	4650	HIS

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

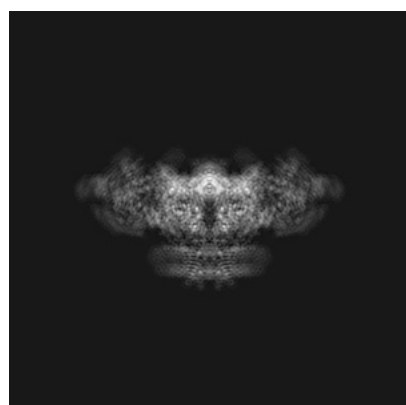
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8073. These allow visual inspection of the internal detail of the map and identification of artifacts.

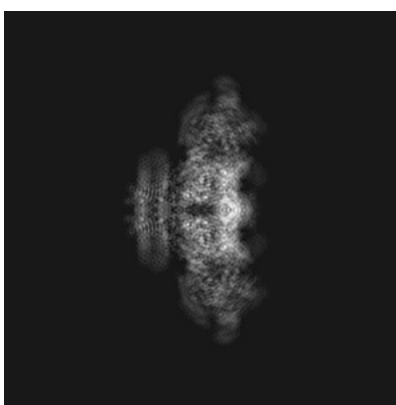
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

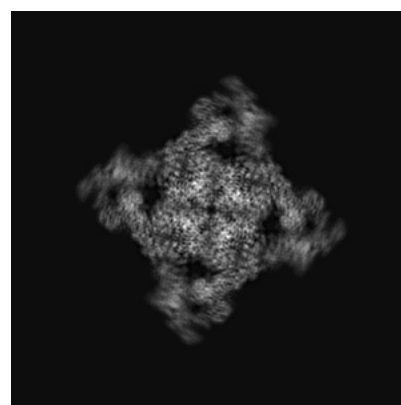
#### 6.1.1 Primary map



X



Y



Z

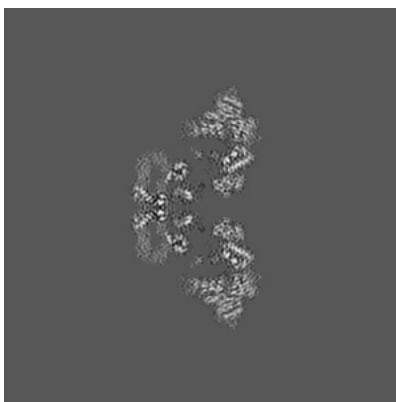
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

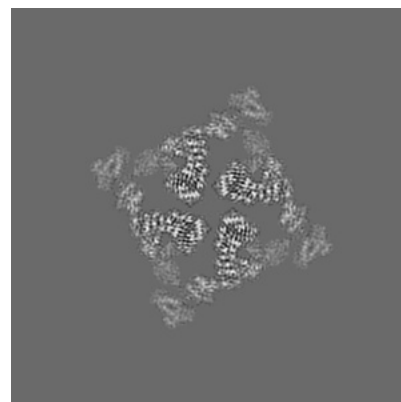
#### 6.2.1 Primary map



X Index: 196



Y Index: 196



Z Index: 196

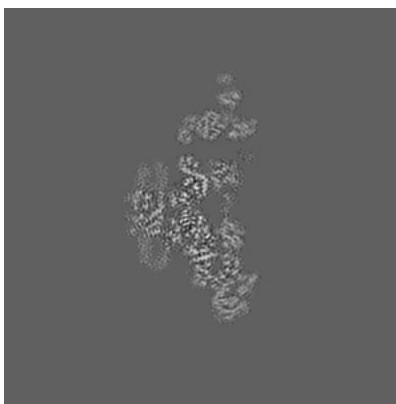
The images above show central slices of the map in three orthogonal directions.

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

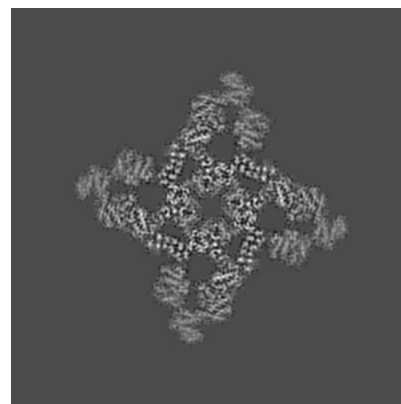
### 6.3.1 Primary map



X Index: 208



Y Index: 184

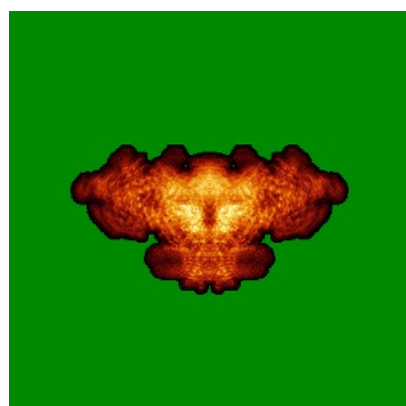


Z Index: 215

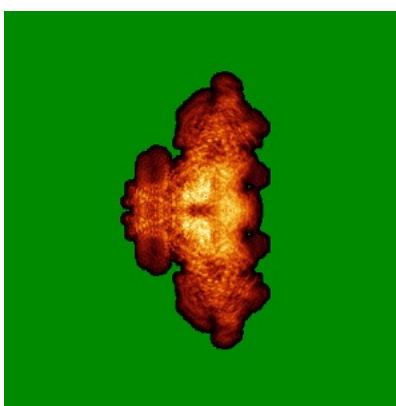
The images above show the largest variance slices of the map in three orthogonal directions.

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

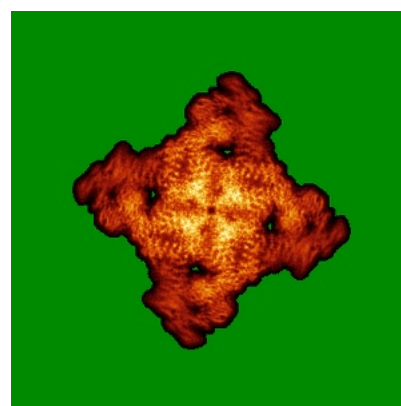
### 6.4.1 Primary map



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 0.0967. 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](#)

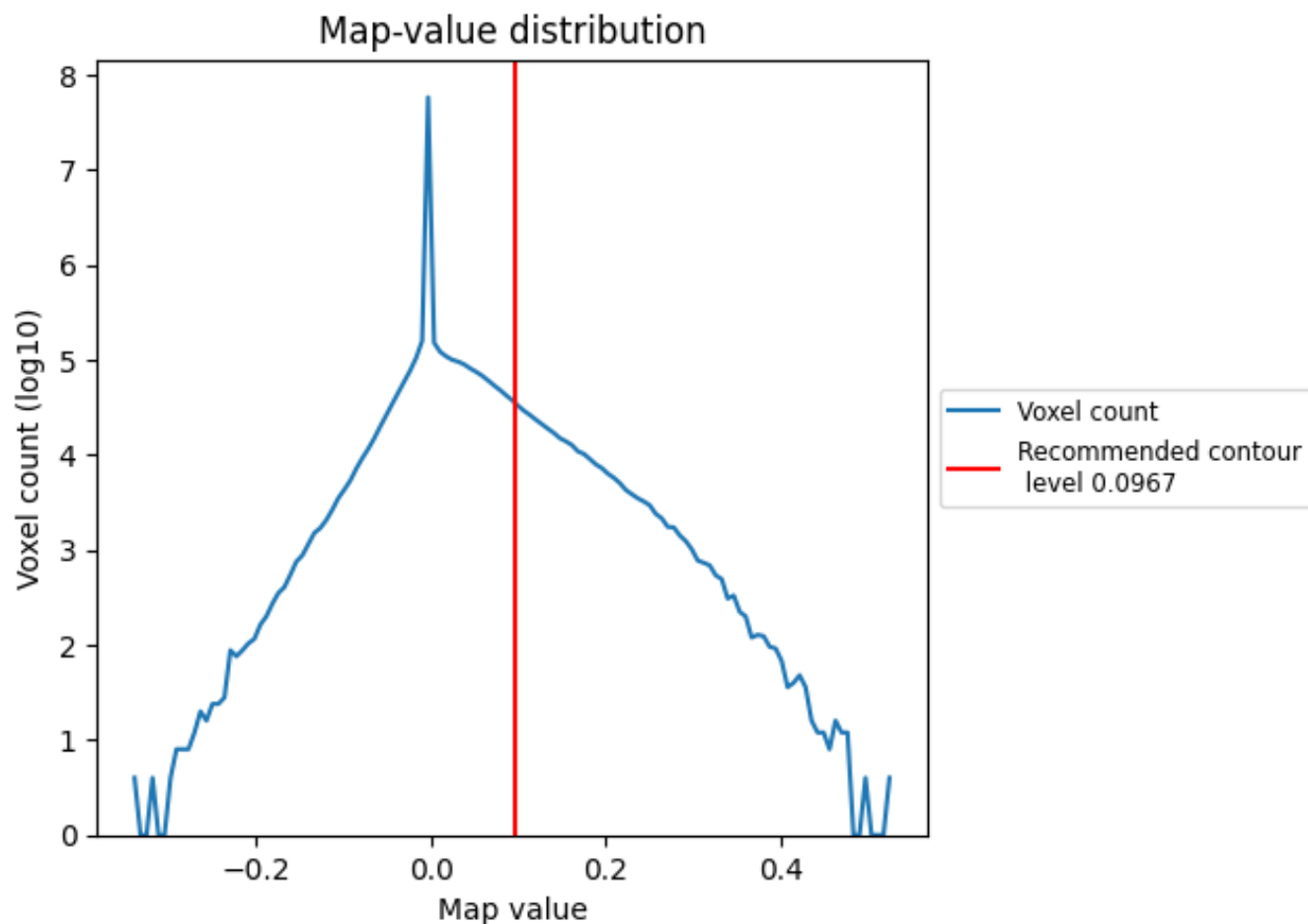
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

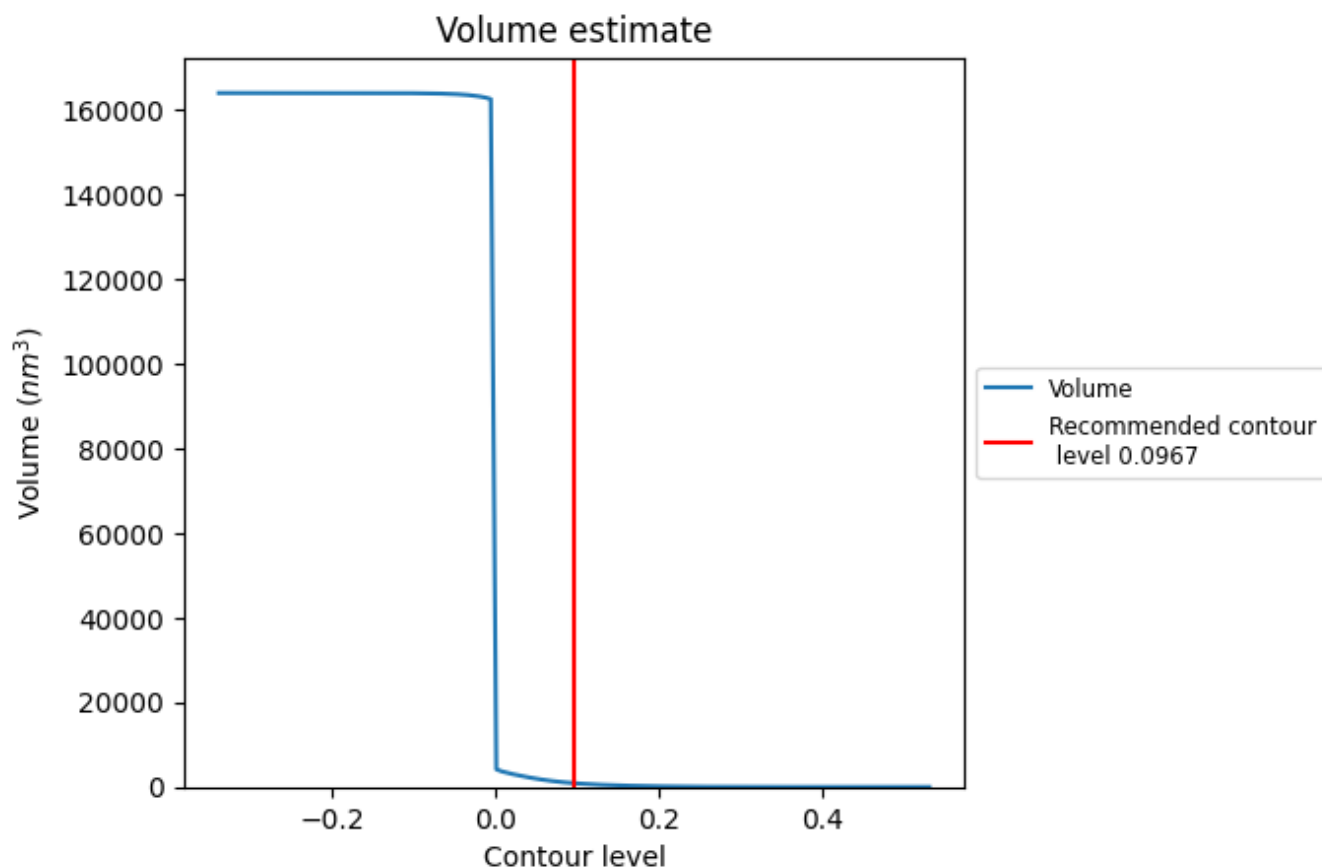
This section contains the results of statistical analysis of the map.

### 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.

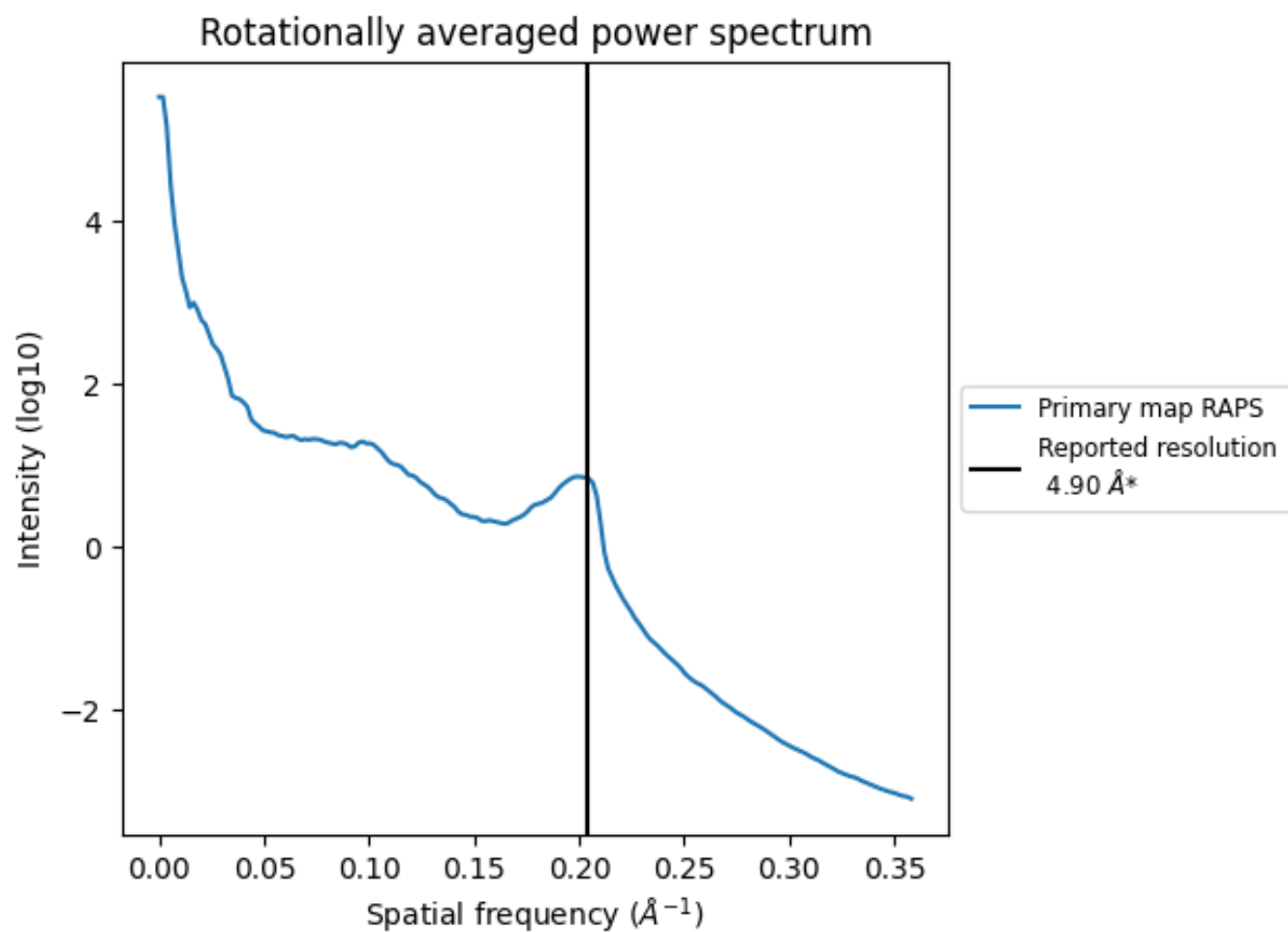
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 885 nm<sup>3</sup>; this corresponds to an approximate mass of 799 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 0.204  $\text{\AA}^{-1}$

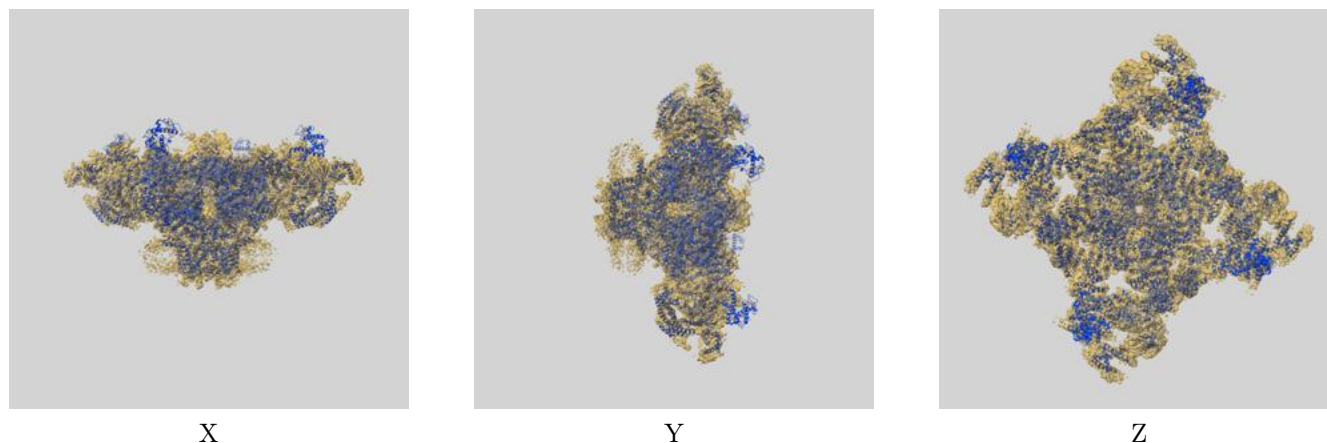
## 8 Fourier-Shell correlation ⓘ

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

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

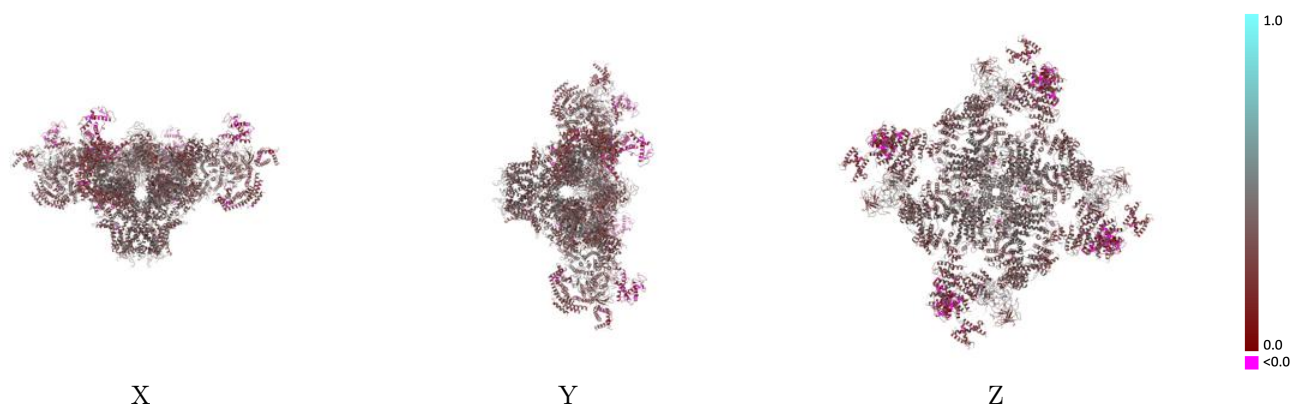
This section contains information regarding the fit between EMDB map EMD-8073 and PDB model 5J8V. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

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



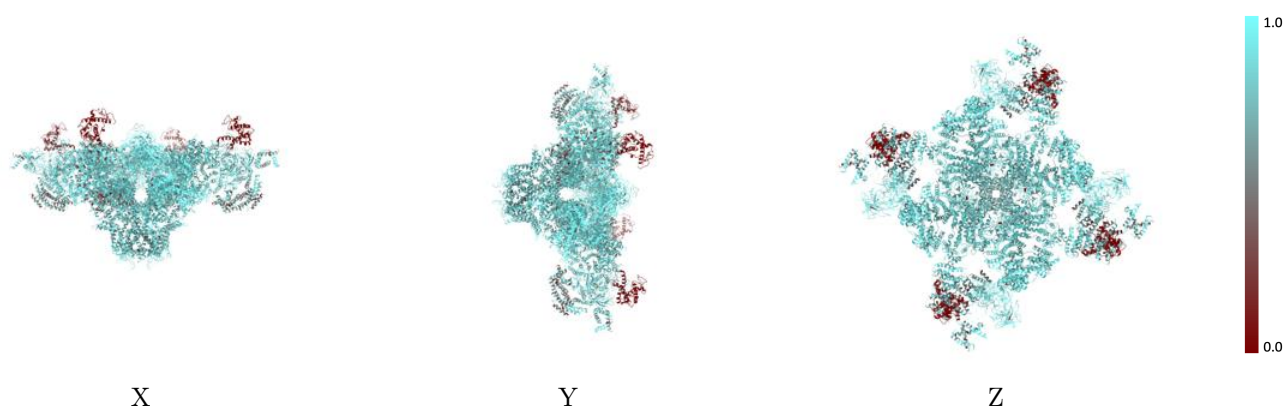
The images above show the 3D surface view of the map at the recommended contour level 0.0967 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



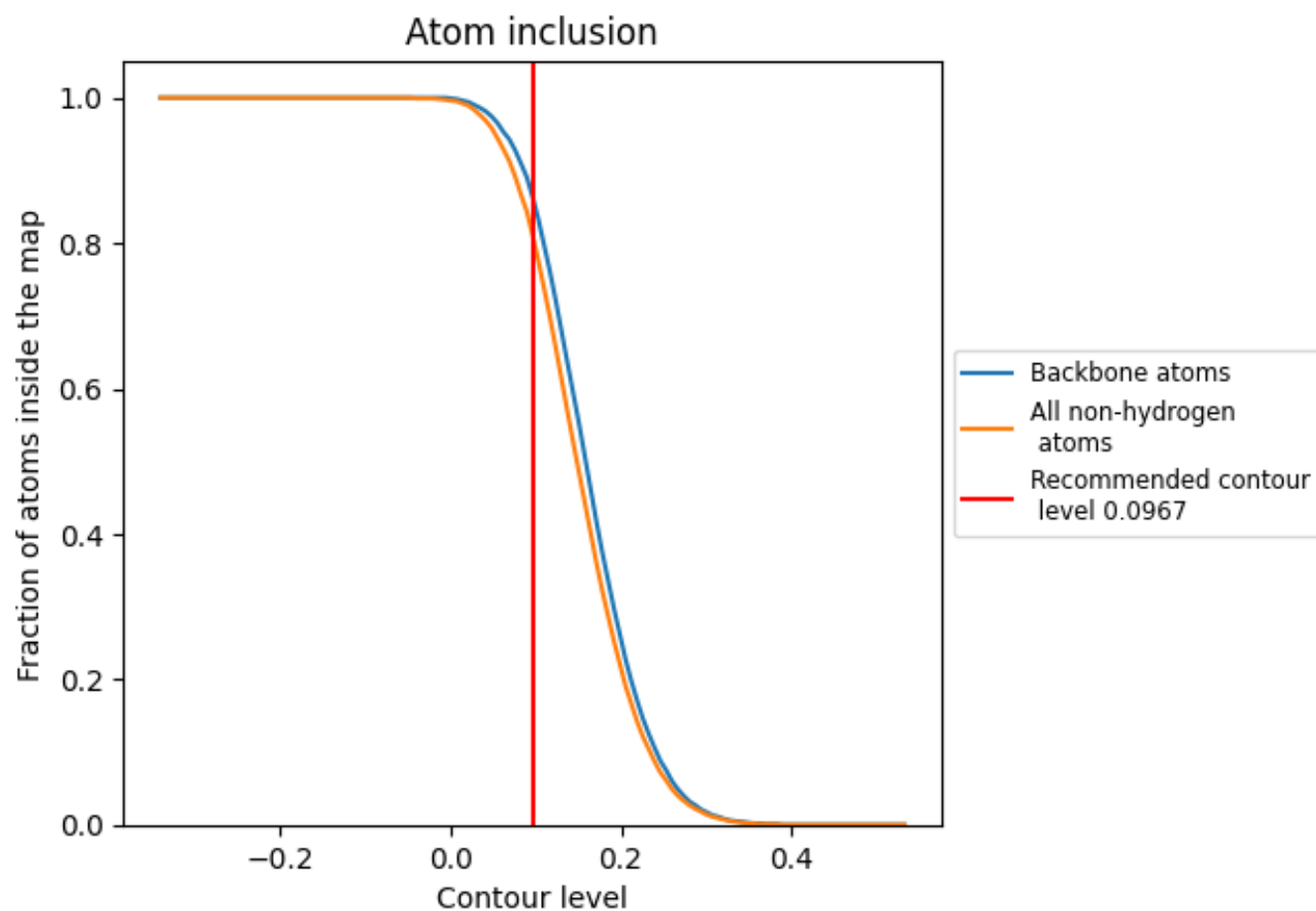
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0967).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (0.0967) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div></div> 0.8100	<div><div></div></div> 0.3470
A	<div><div></div></div> 0.8090	<div><div></div></div> 0.3470
B	<div><div></div></div> 0.8100	<div><div></div></div> 0.3470
C	<div><div></div></div> 0.8100	<div><div></div></div> 0.3470
D	<div><div></div></div> 0.8090	<div><div></div></div> 0.3470

