



wwPDB EM Validation Summary Report ⓘ

Nov 28, 2022 – 11:12 AM EST

PDB ID : 7T64
EMDB ID : EMD-25709
Title : Rabbit RyR1 disease mutant Y523S in complex with FKBP12.6 embedded in lipidic nanodisc in the closed state
Authors : Iyer, K.A.; Hu, Y.; Murayama, T.; Samso, M.
Deposited on : 2021-12-13
Resolution : 4.00 Å(reported)
Based on initial model : 6WOT

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

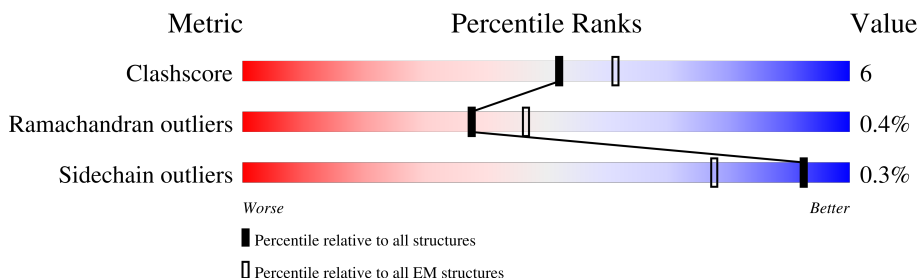
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 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	<div> <div>15%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
1	B	5037	<div> <div>15%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
1	C	5037	<div> <div>15%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
1	D	5037	<div> <div>15%</div> <div>72%</div> <div>12%</div> <div>16%</div> </div>
2	E	107	<div> <div>7%</div> <div>82%</div> <div>18%</div> </div>
2	F	107	<div> <div>7%</div> <div>83%</div> <div>17%</div> </div>
2	G	107	<div> <div>7%</div> <div>82%</div> <div>18%</div> </div>
2	H	107	<div> <div>7%</div> <div>80%</div> <div>20%</div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 134196 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	4247	Total 32730	C 20849	N 5597	O 6079	S 205	0	0
1	B	4247	Total 32730	C 20849	N 5597	O 6079	S 205	0	0
1	C	4247	Total 32730	C 20849	N 5597	O 6079	S 205	0	0
1	D	4247	Total 32730	C 20849	N 5597	O 6079	S 205	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	523	SER	TYR	engineered mutation	UNP P11716
B	523	SER	TYR	engineered mutation	UNP P11716
C	523	SER	TYR	engineered mutation	UNP P11716
D	523	SER	TYR	engineered mutation	UNP P11716

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	107	Total 818	C 516	N 144	O 154	S 4	0	0
2	F	107	Total 818	C 516	N 144	O 154	S 4	0	0
2	G	107	Total 818	C 516	N 144	O 154	S 4	0	0
2	H	107	Total 818	C 516	N 144	O 154	S 4	0	0

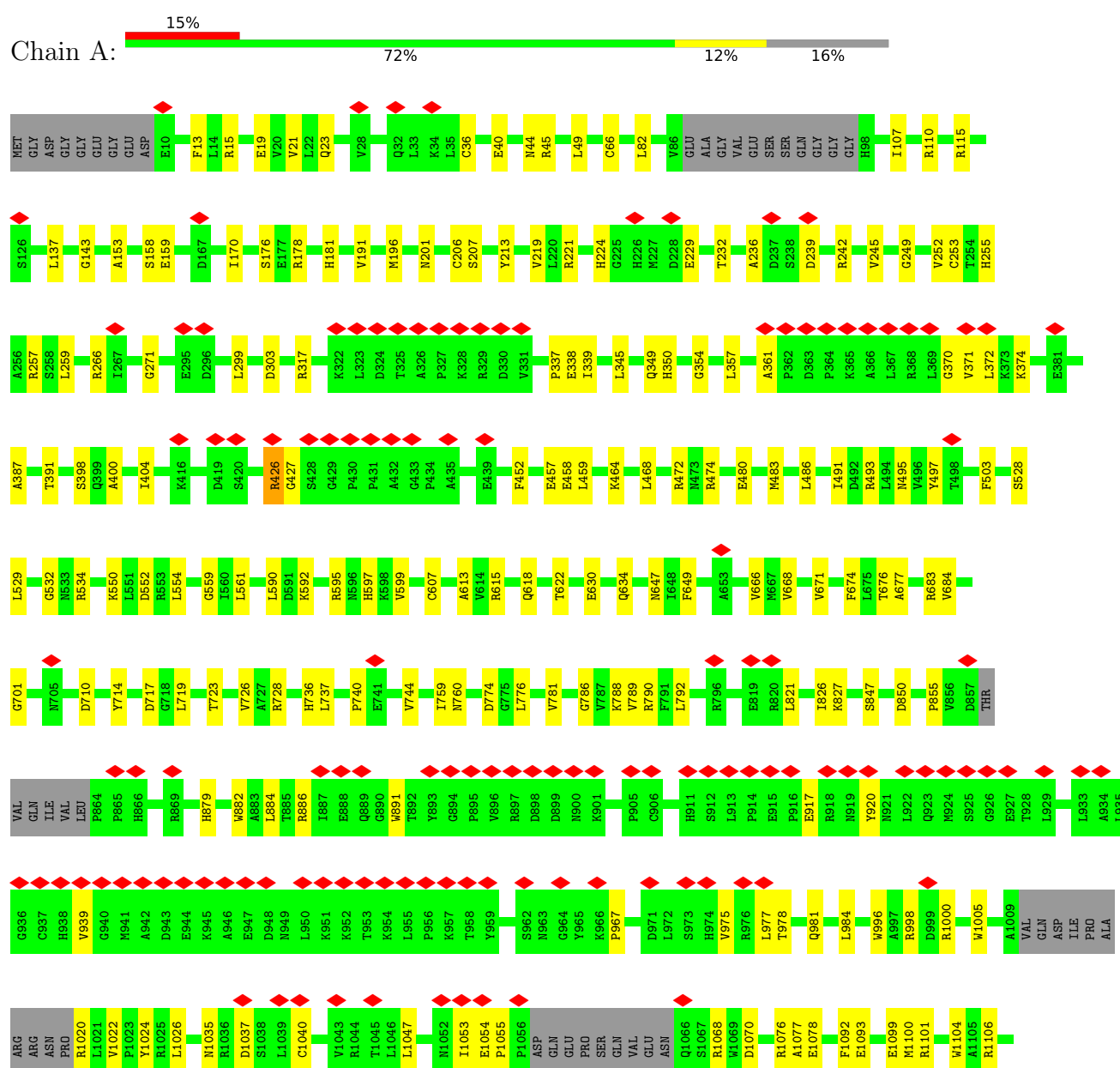
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total 1	Zn 1	0
3	B	1	Total 1	Zn 1	0
3	C	1	Total 1	Zn 1	0
3	D	1	Total 1	Zn 1	0

3 Residue-property plots

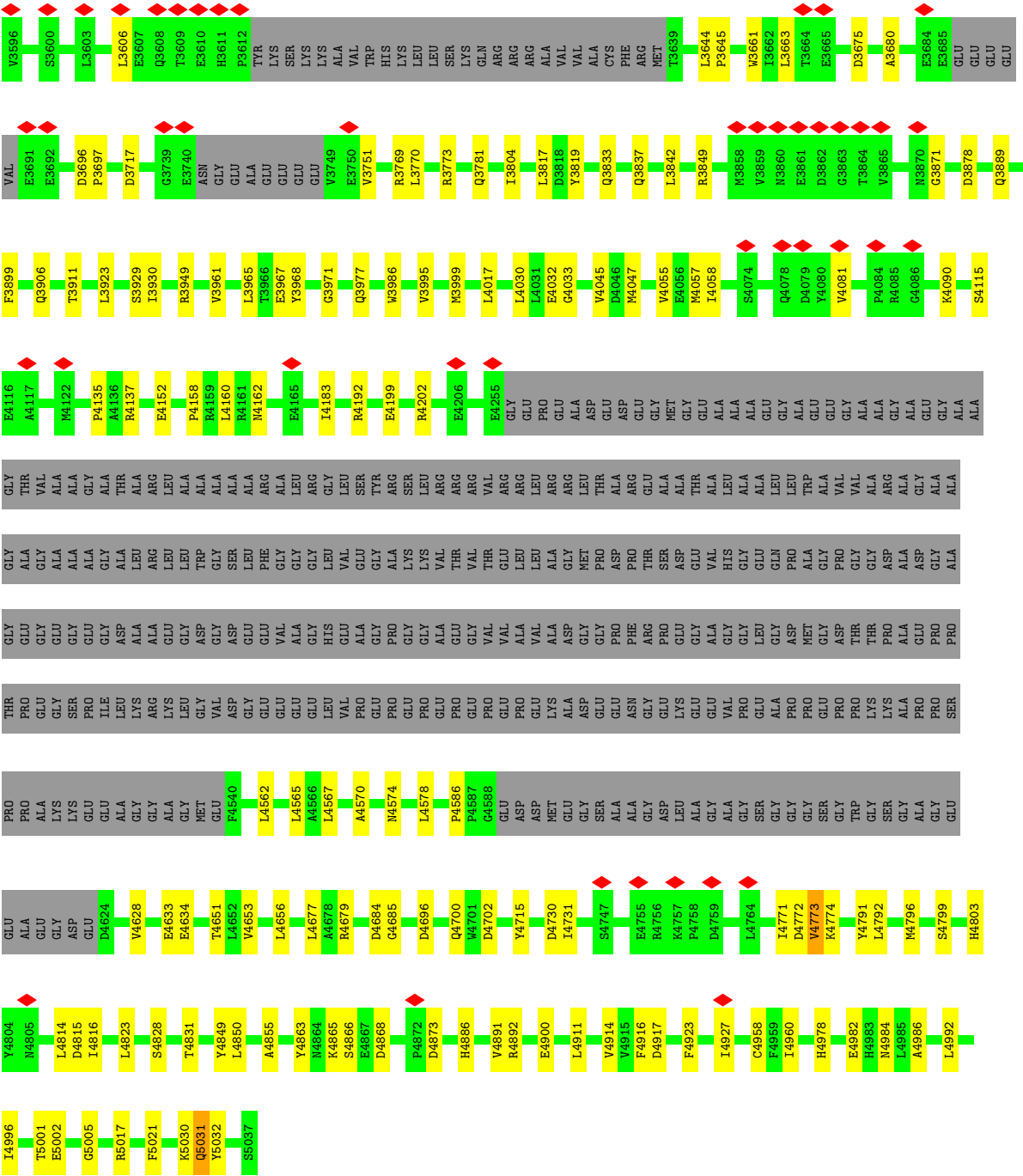
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Ryanodine receptor 1

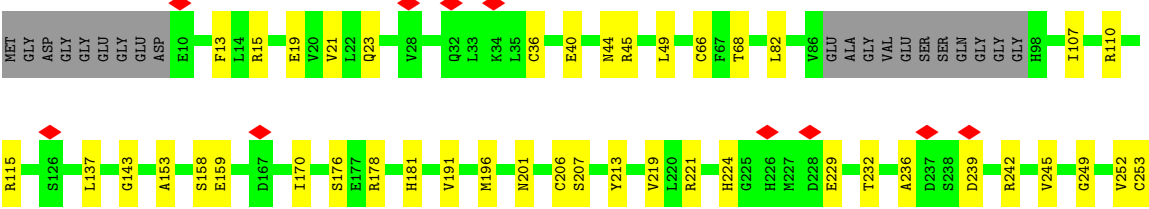


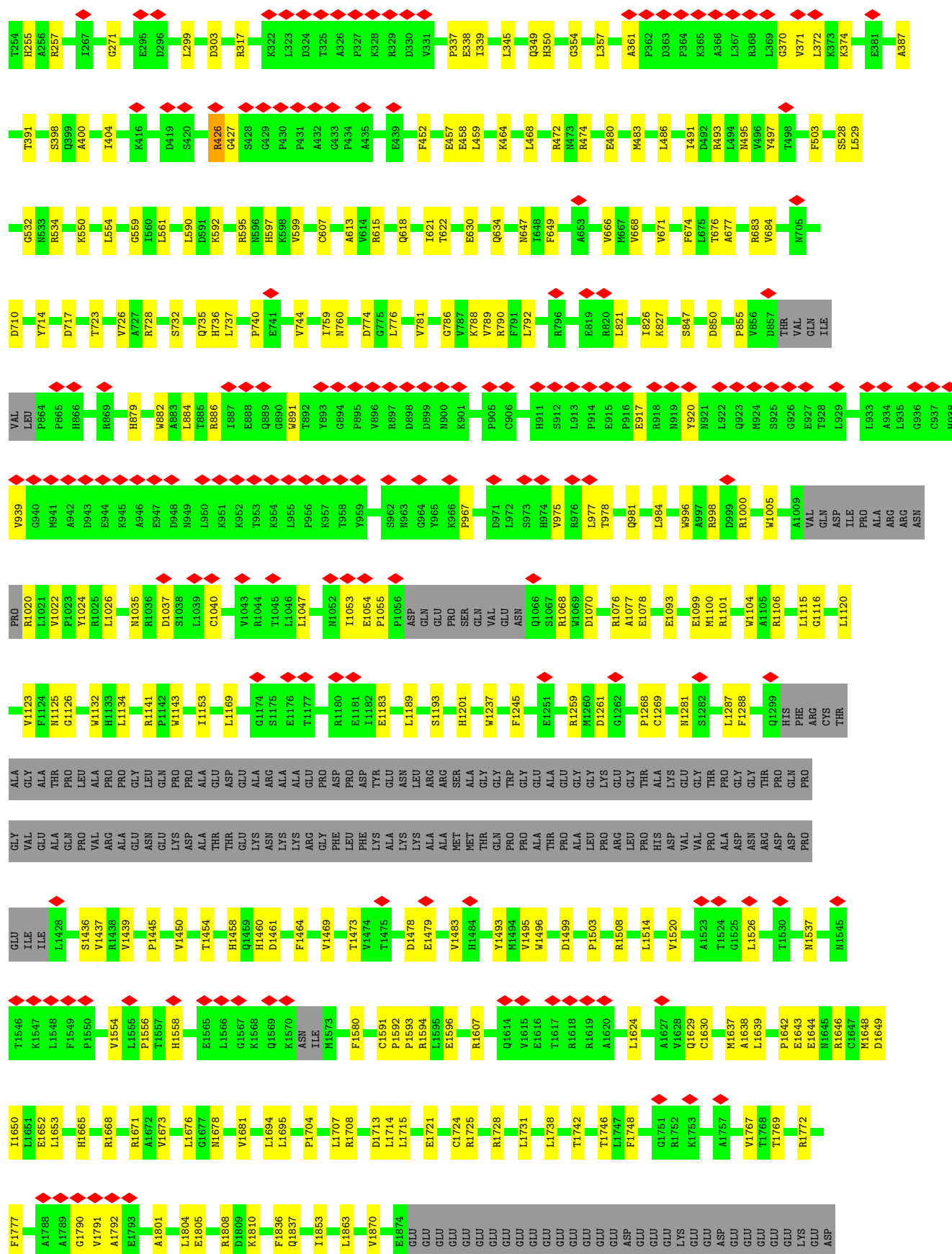


K2653	Y2654	Z2655	C2656	L2657	K2660	Z2661	Z2662	Z2663	Z2666	Z2667	Z2668	Z2669	Z2670	L2671	Z2672	Z2673	L2674	Z2675	Z2676	Z2677	Z2678	Z2679	Z2680	Z2681	Z2690	TYR	ASP	GLN	GLU	LEU	TYR	ARG	MET	ALA	MET	PRO	CYS	CYS	LEU	CYS	ALA	ILE	ALA	GLY	ALA	LEU	PRO	PRO	ASP	TYR	VAL	ASP	ALA	SER	TYR	SER	SER			
L2782	E2783	E2784	L2785	L2786	T2787	H2788	P2789	M2790	L2791	Z2792	P2793	Y2794	K2795	T2796	F2797	S2798	E2799	K2800	D2801	K2802	E2803	L2804	Y2805	K2806	W2807	P2808	L2809	K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	W2819	E2820	W2821	T2822	L2823	E2824	K2825	A2826	R2827	K2828	Z2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	LYS	LYS	LYS	ARG	LYS
H2902	P2903	L2904	L2905	P2906	P2907	Y2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	D2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	P2929	L2930	Q2931	M2932	N2933	Q2934	Y2935	A2936	V2937	T2938	R2939	G2940	L2941	K2942	D2943	M2944	E2945	L2946	D2947	T2948	S2949	K2953	F2959	W2966	E2972	F2973	L2974	A2975	H2976					
L2977	E2978	ALA	VAL	VAL	SER	GLY	ARG	GLU	LYS	SER	PRO	HIS	Q2993	I3001	P3021	A3022	K3023	V3024	L3025	GLY	SER	GLY	G3029	H3030	A3031	S3032	N3033	K3034	T3040	H3052	N3053	V3054	S3055	L3056	F3057	G3058	T3059	Q3060	H3061	R3073	A3077	R3078	T3079	V3080	ASP	K3081	K3082	S3083	G3084	P3085	E3086									
I3087	V3088	K3089	A3090	G3091	S3094	D3102	I3103	E3104	K3105	M3106	V3107	E3108	N3109	L3110	R3111	LEU	GLY	LYS	VAL	SER	GLN	ALA	ARG	THR	GLN	VAL	LYS	GLY	VAL	GLY	Q3127	T3130	Y3131	T3132	T3133	V3134	A3135	L3136	T3142	L3143	F3144	Q3145	H3146	I3147	A3148	R3149	H3150	Q3151	PHE	GLY	ASP	VAL	I3157	L3158						
D3159	L3169	C3170	S3171	I3172	Y3173	S3174	L3175	G3176	T3177	T3178	K3179	ASN	THR	TYR	VAL	E3184	K3185	L3186	R3187	L3190	L3194	A3195	R3196	L3197	A3200	M3201	P3202	V3203	A3204	F3205	L3206	E3207	P3208	Q3209	LEU	ASN	GLU	TYR	ASN	ALA	CYS	SER	VAL	Y3219	T3220	T3221	P3224	R3225	E3226	R3227	A3228	I3229	L3230	G3231						
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P3302	P3303	C3304	T3305	A3306	V3307	T3308	S3309	D3310	H3311	L3312	N3313	S3314	I3319	T3323	V3324	N3325	N3326	L3327	G3328	I3329	D3330	E3331	M3335	L3338	A3339	V3340	F3341	A3342	Q3343	P3344	I3345	V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358	I3362	R3366	K3367	R3368	K3371	A3374	E3375									
E3376	E3377	Q3378	L3379	R3380	L3381	E3382	A3383	K3384	A3385	E3386	A3387	E3388	E3389	G3390	E3391	L3392	L3393	V3394	R3395	D3396	E3397	F3398	S3399	R3403	D3404	L3405	Y3406	A3407	L3408	Y3409	P3410	L3411	H3422	V3423	L3424	T3425	E3426	P3427	N3428	A3429	F3435	R3436	M3437	V3438	G3439	F3442	T3443	Y3444	K3447	S3448	H3449	E3454	E3455							
Q3456	V3460	Q3461	N3462	E3463	L3464	N3465	N3466	L3470	T3471	A3472	ASP	SER	LYS	SER	LYS	MET	ALA	LYS	ALA	GLY	ASP	GLN	SER	GLY	SER	ASP	GLU	THR	ARG	LYS	LYS	LYS	ARG	GLY	R3502	Y3503	S3504	V3505	Q3506	T3507	S3508	L3509	I3510	V3511	A3512	T3513	L3514	K3515	K3516	M3517	L3518	P3519								
L3522	N3523	N3524	C3525	D3529	Q3530	I3533	A3536	K3537	A3541	L3542	K3543	T3544	D3545	D3546	E3547	E3548	E3551	F3552	L3553	K3554	N3555	N3556	L3557	L3558	L3559	Q3560	C3561	K3562	V3563	E3564	C3565	S3566	P3567	S3568	L3569	Q3578	L3579	P3580	G3581	L3582	E3583	E3584	D3585	A3586	D3587	D3588	P3589	E3590	K3591	R3594	R3595									



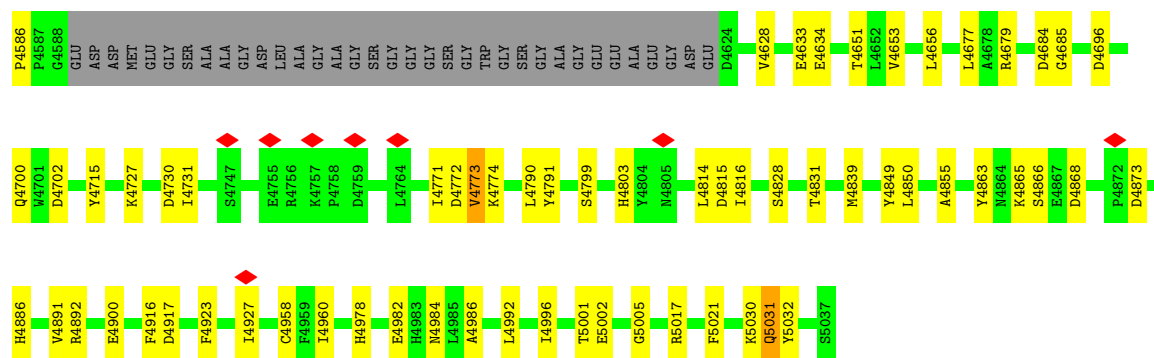
• Molecule 1: Ryanodine receptor 1



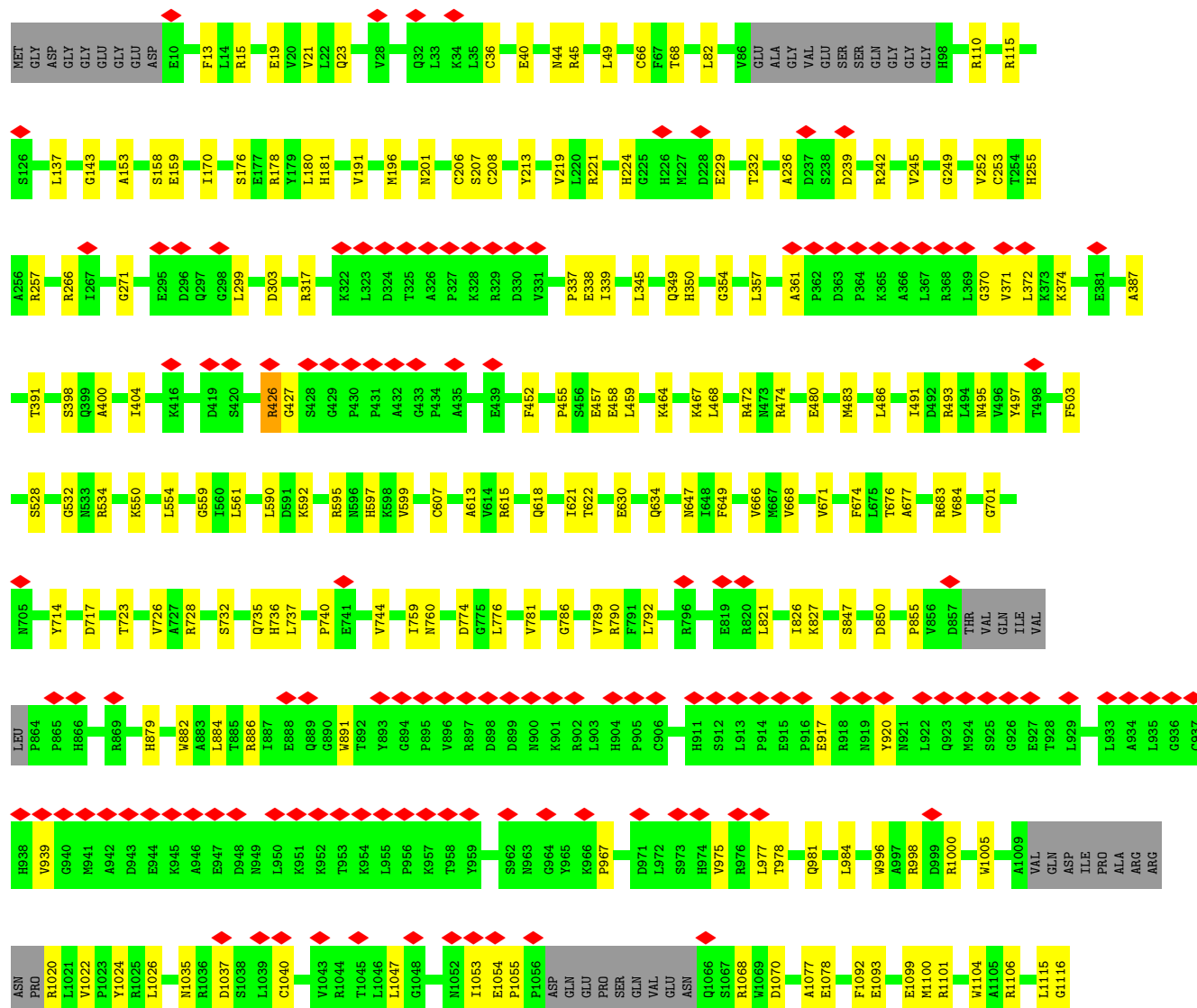






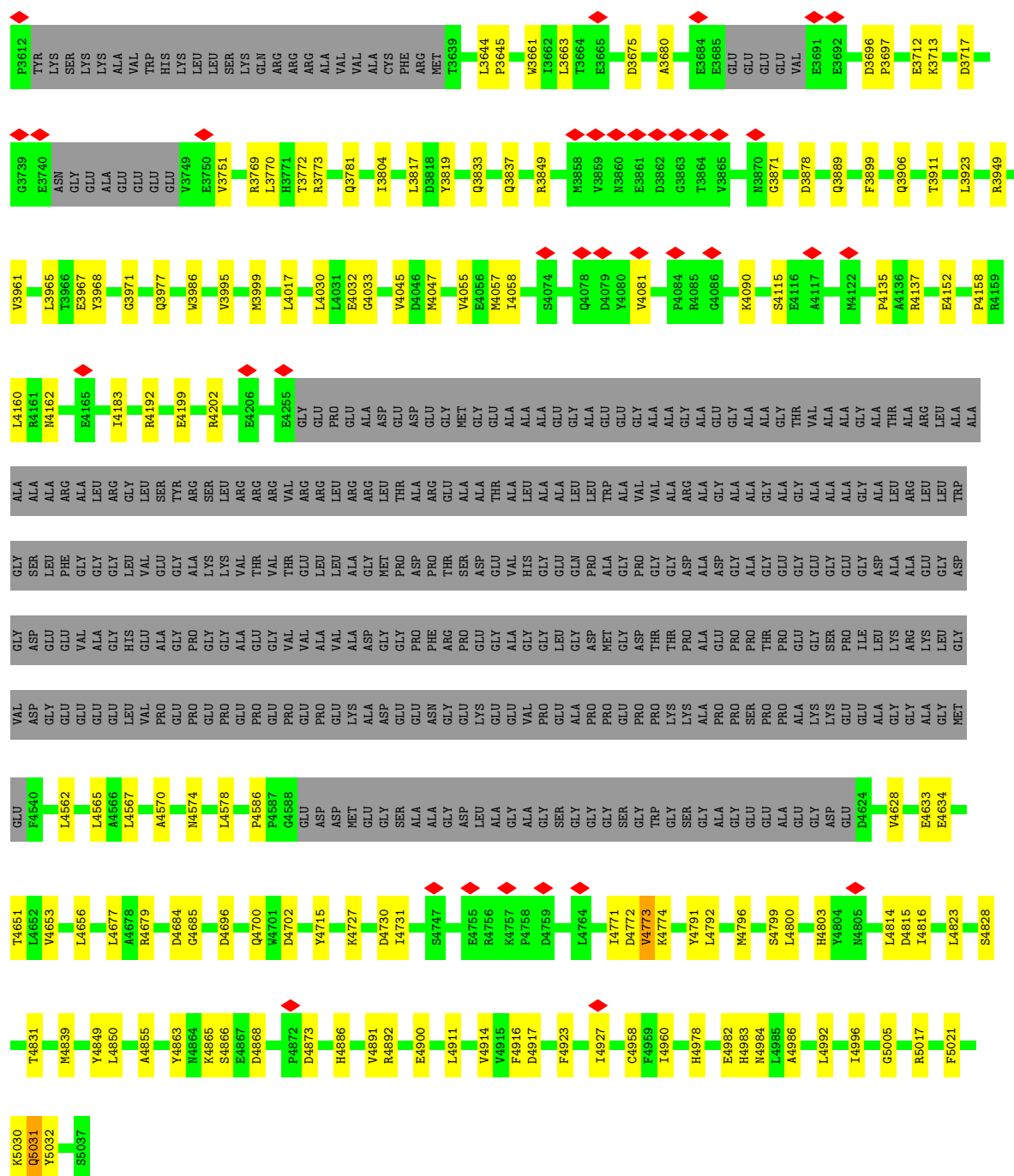


• Molecule 1: Ryanodine receptor 1

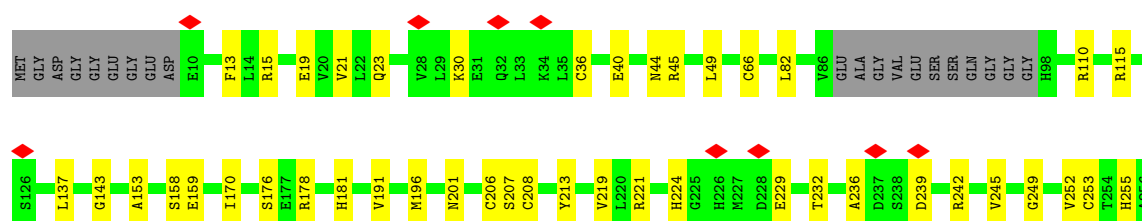
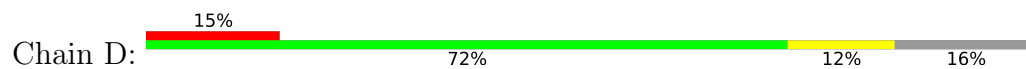




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T3471	A3472	ASP	SER	LYS	SER	LYS	ASP	ALA	ALA	GLY	ASP	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ASP	R3502	R3503	S3504	V3505	Q3506	T3507	S3508	L3509	V3510	V3511	V3512	T3513	L3514	K3515	K3516	L3517	P3518	P3519	L3522	N3523	K3524	C3525	D3529	Q3530	I3533	L3536	L3606	E3607	Q3608	T3609	E3610	H3611		
A3387	E3388	E3389	G3390	E3391	L3392	L3393	V3394	R3395	D3396	E3397	F3398	S3399	R3403	D3404	L3405	Y3406	A3407	L3408	Y3409	P3410	L3411	H3422	V3423	L3424	T3425	E3426	P3427	N3428	A3429	F3435	R3436	M3437	V3438	G3439	F3442	L3443	Y3444	K3447	S3448	H3449	E3454	E3455	Q3456	V3460	Q3461	N3462	I3463	N3464	N3465	L3470						
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C3240	P3241	D3242	I3243	P3244	V3245	L3246	D3247	R3248	L3249	M3250	A3251	D3252	I3253	G3254	G3255	L3256	A3257	E3258	S3259	G3260	A3261	R3262	P3263	T3264	E3265	M3266	P3267	H3268	V3269	E3271	I3270	I3272	L3281	E3286	P3289	E3290	A3291	P3292	P3293	P3294	A3295	L3296	P3297	A3298	G3299	A3300	P3301	P3302	P3303	C3304	T3305	A3306	V3307	T3308	S3309	D3310
H3311	L3312	N3313	S3314	L3319	I3323	V3324	N3325	N3326	L3327	G3328	I3329	D3330	E3331	M3335	L3338	A3339	V3340	F3341	A3342	Q3343	P3344	I3345	V3346	S3347	R3348	A3349	R3350	P3351	E3352	L3353	L3354	H3355	S3356	H3357	F3358	I3362	R3366	K3371	A3374	E3375	E3376	E3377	Q3378	L3379	R3380	L3381	E3382	K3383	A3384	E3386						
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T3471	A3472	ASP	SER	LYS	SER	LYS	ASP	ALA	ALA	GLY	ASP	GLN	GLN	SER	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ASP	R3502	R3503	S3504	V3505	Q3506	T3507	S3508	L3509	V3510	V3511	V3512	T3513	L3514	K3515	K3516	L3517	P3518	P3519	L3522	N3523	K3524	C3525	D3529	Q3530	I3533	L3536	L3606	E3607	Q3608	T3609	E3610	H3611		



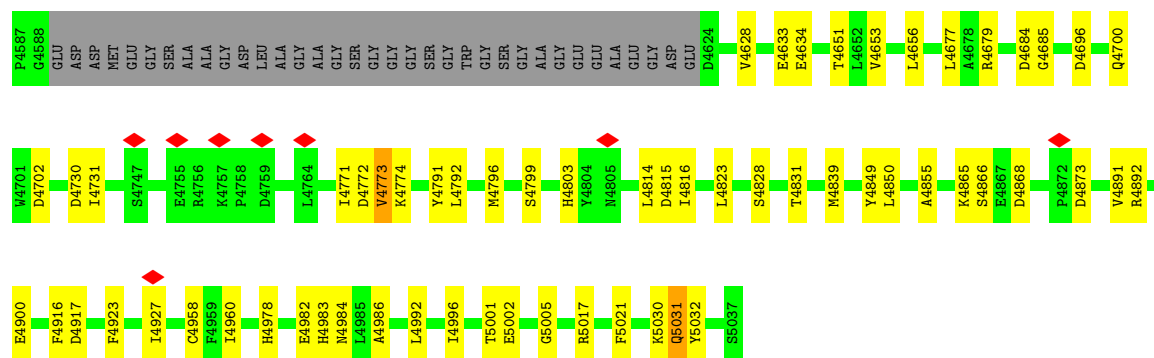
• Molecule 1: Ryanodine receptor 1



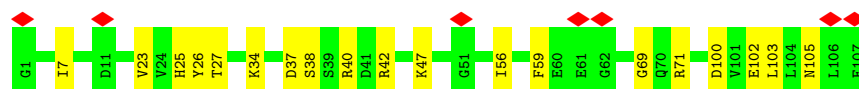
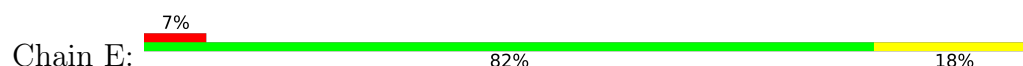




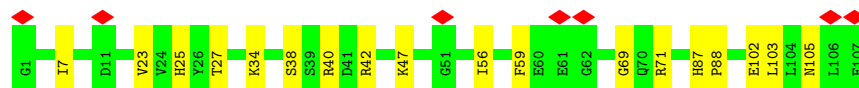
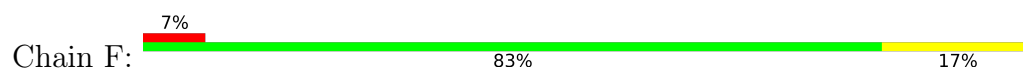




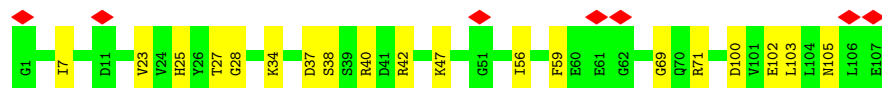
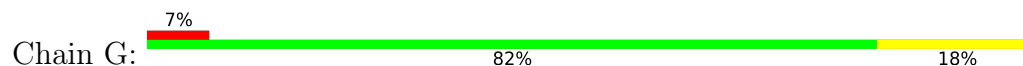
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



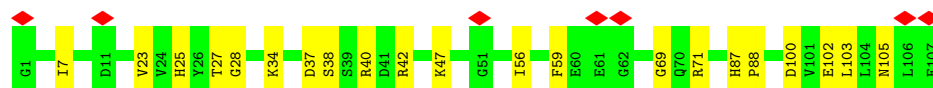
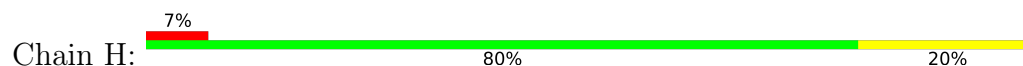
• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



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• Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	141098	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 ($e^-/\text{\AA}^2$)	53.69	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.247	Depositor
Minimum map value	-0.732	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.038	Depositor
Recommended contour level	0.155	Depositor
Map size (\AA)	464.40002, 464.40002, 464.40002	wwPDB
Map dimensions	430, 430, 430	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.08, 1.08, 1.08	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:
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	0.25	0/33461	0.50	3/45464 (0.0%)
1	B	0.25	0/33461	0.50	3/45464 (0.0%)
1	C	0.25	0/33461	0.50	3/45464 (0.0%)
1	D	0.25	0/33461	0.50	3/45464 (0.0%)
2	E	0.27	0/834	0.58	0/1123
2	F	0.27	0/834	0.58	0/1123
2	G	0.27	0/834	0.58	0/1123
2	H	0.27	0/834	0.58	0/1123
All	All	0.25	0/137180	0.50	12/186348 (0.0%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3663	LEU	CA-CB-CG	6.82	130.99	115.30
1	C	3663	LEU	CA-CB-CG	6.82	130.98	115.30
1	B	3663	LEU	CA-CB-CG	6.82	130.97	115.30
1	D	3663	LEU	CA-CB-CG	6.82	130.97	115.30
1	B	2644	LEU	CA-CB-CG	5.18	127.21	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	32730	0	31483	370	0
1	B	32730	0	31483	364	0
1	C	32730	0	31483	370	0
1	D	32730	0	31483	361	0
2	E	818	0	824	14	0
2	F	818	0	824	13	0
2	G	818	0	824	14	0
2	H	818	0	824	15	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	134196	0	129228	1495	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 6.

The worst 5 of 1495 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:C:2211:MET:HE1	1:C:2257:LEU:HD13	1.72	0.70
1:B:4045:VAL:HG22	1:B:4160:LEU:HD11	1.75	0.69
1:D:4045:VAL:HG22	1:D:4160:LEU:HD11	1.75	0.68
1:A:3144:PHE:HA	1:A:3196:ARG:HG3	1.75	0.68
1:B:3144:PHE:HA	1:B:3196:ARG:HG3	1.75	0.67

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	4197/5037 (83%)	3926 (94%)	254 (6%)	17 (0%)	34 71

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	4197/5037 (83%)	3927 (94%)	253 (6%)	17 (0%)	34	71
1	C	4197/5037 (83%)	3924 (94%)	257 (6%)	16 (0%)	34	71
1	D	4197/5037 (83%)	3922 (93%)	258 (6%)	17 (0%)	34	71
2	E	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
2	F	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
2	G	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
2	H	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
All	All	17208/20576 (84%)	16091 (94%)	1050 (6%)	67 (0%)	38	71

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4773	VAL
1	A	5031	GLN
1	B	4773	VAL
1	B	5031	GLN
1	C	4773	VAL

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	3419/4276 (80%)	3409 (100%)	10 (0%)	92	95
1	B	3419/4276 (80%)	3409 (100%)	10 (0%)	92	95
1	C	3419/4276 (80%)	3409 (100%)	10 (0%)	92	95
1	D	3419/4276 (80%)	3409 (100%)	10 (0%)	92	95
2	E	88/88 (100%)	88 (100%)	0	100	100
2	F	88/88 (100%)	88 (100%)	0	100	100
2	G	88/88 (100%)	88 (100%)	0	100	100
2	H	88/88 (100%)	88 (100%)	0	100	100
All	All	14028/17456 (80%)	13988 (100%)	40 (0%)	92	95

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3371	LYS
1	D	2336	ARG
1	C	3773	ARG
1	D	493	ARG
1	D	2564	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	618	GLN
1	C	4162	ASN
1	D	4162	ASN
1	D	495	ASN
1	B	495	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 monosaccharides 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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

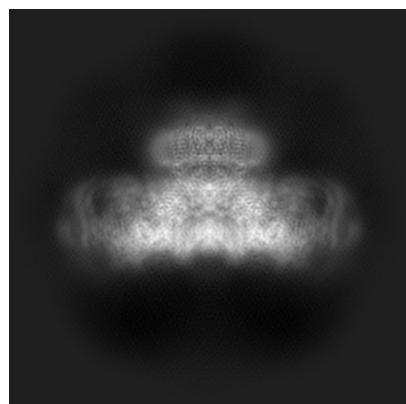
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25709. These allow visual inspection of the internal detail of the map and identification of artifacts.

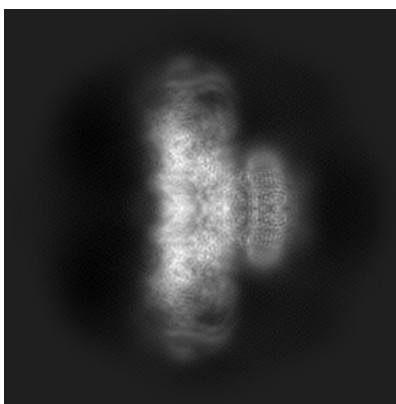
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

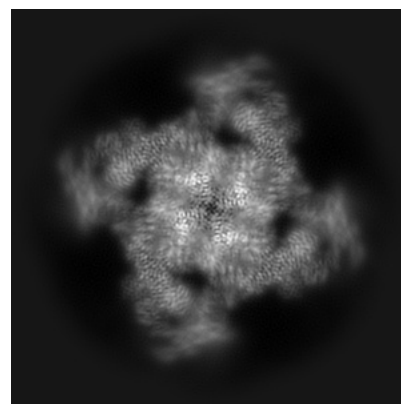
6.1.1 Primary map



X

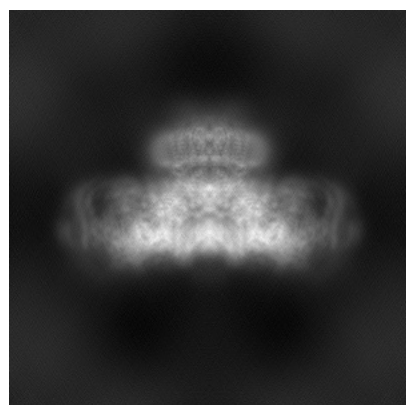


Y

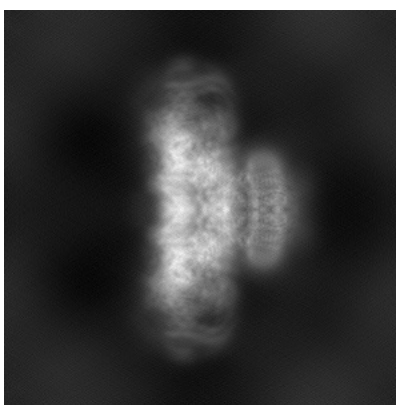


Z

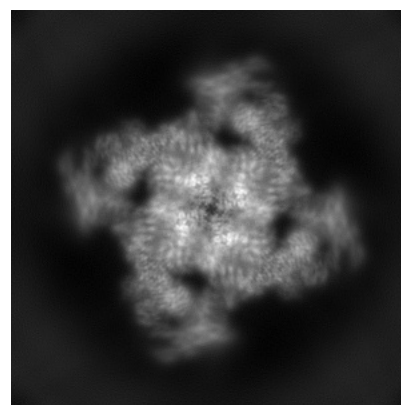
6.1.2 Raw map



X



Y

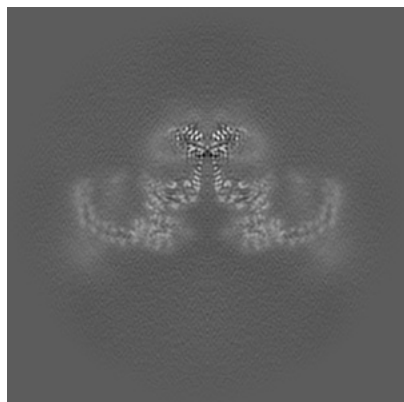


Z

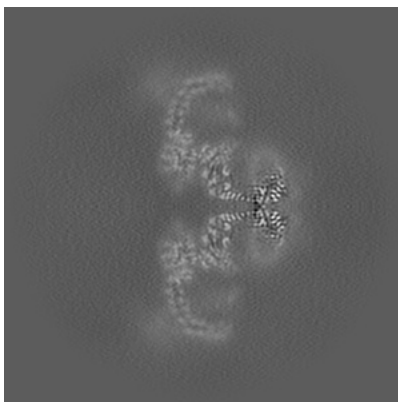
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

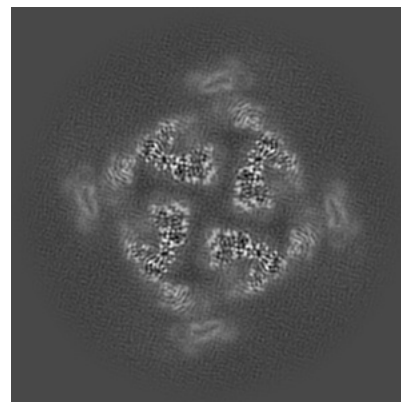
6.2.1 Primary map



X Index: 215

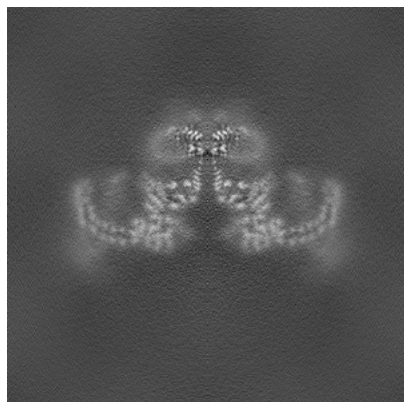


Y Index: 215

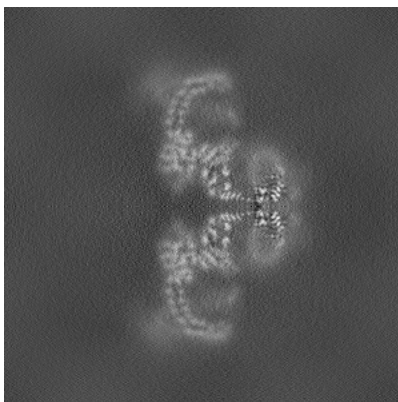


Z Index: 215

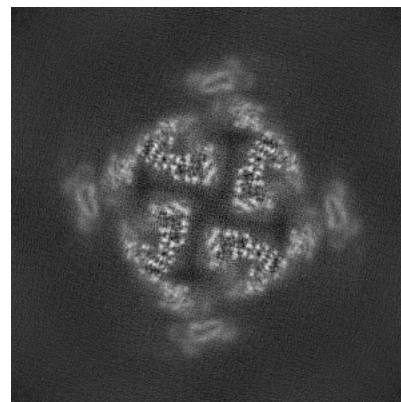
6.2.2 Raw map



X Index: 215



Y Index: 215

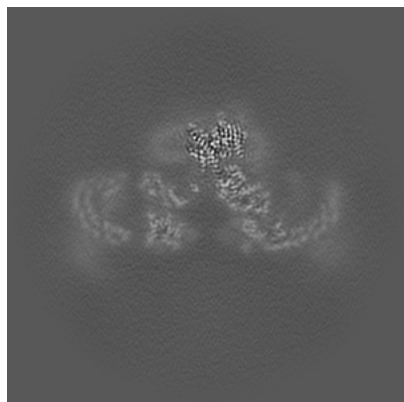


Z Index: 215

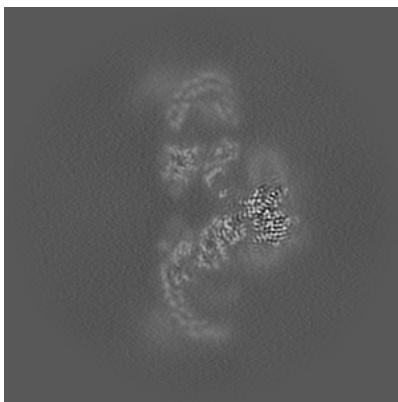
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

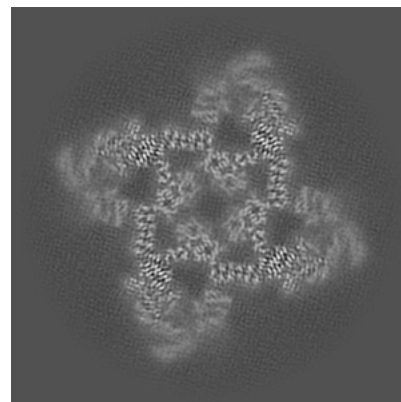
6.3.1 Primary map



X Index: 209

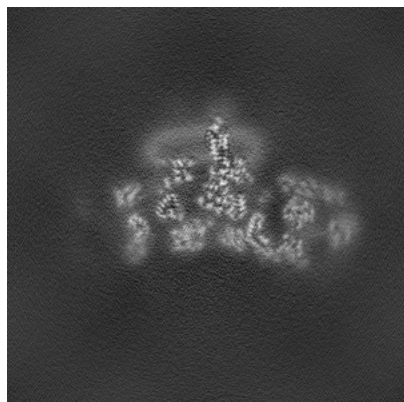


Y Index: 209

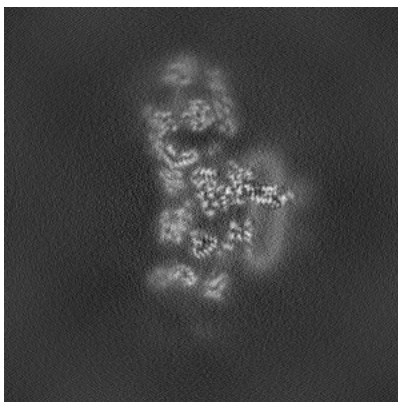


Z Index: 190

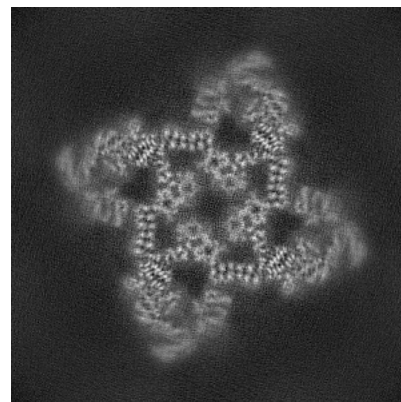
6.3.2 Raw map



X Index: 248



Y Index: 182

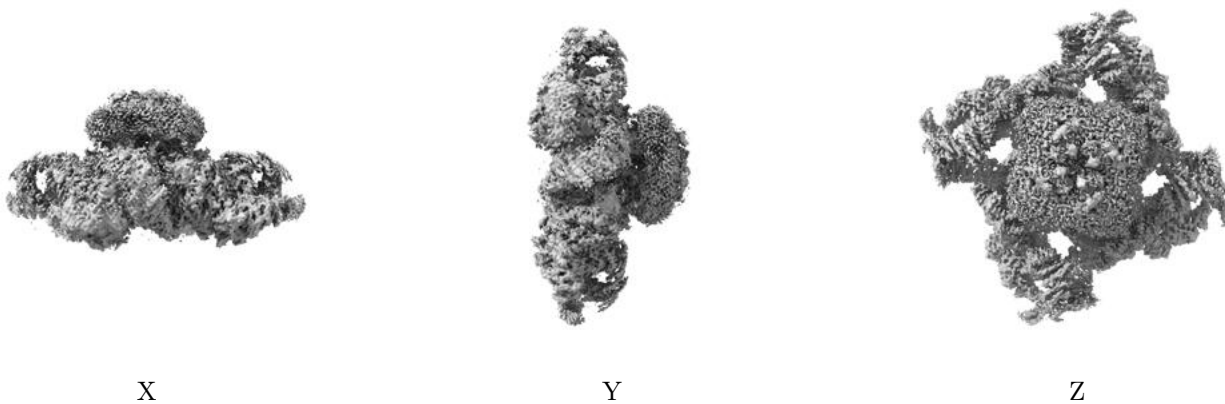


Z Index: 190

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

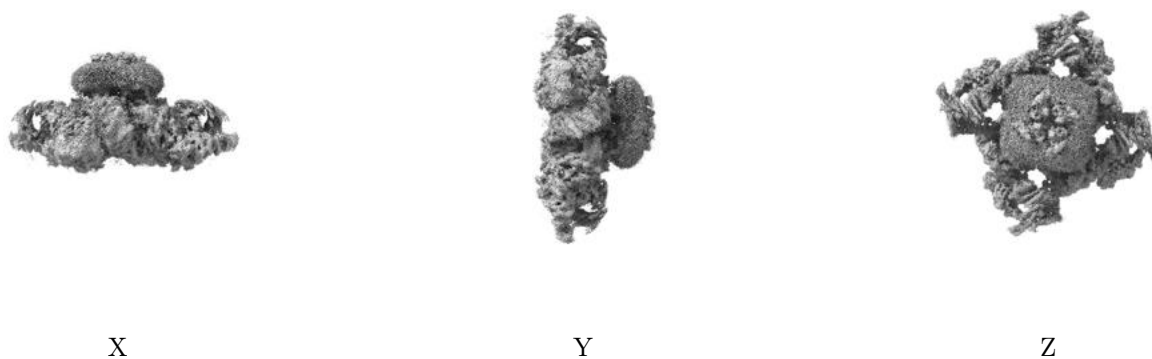
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.155. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

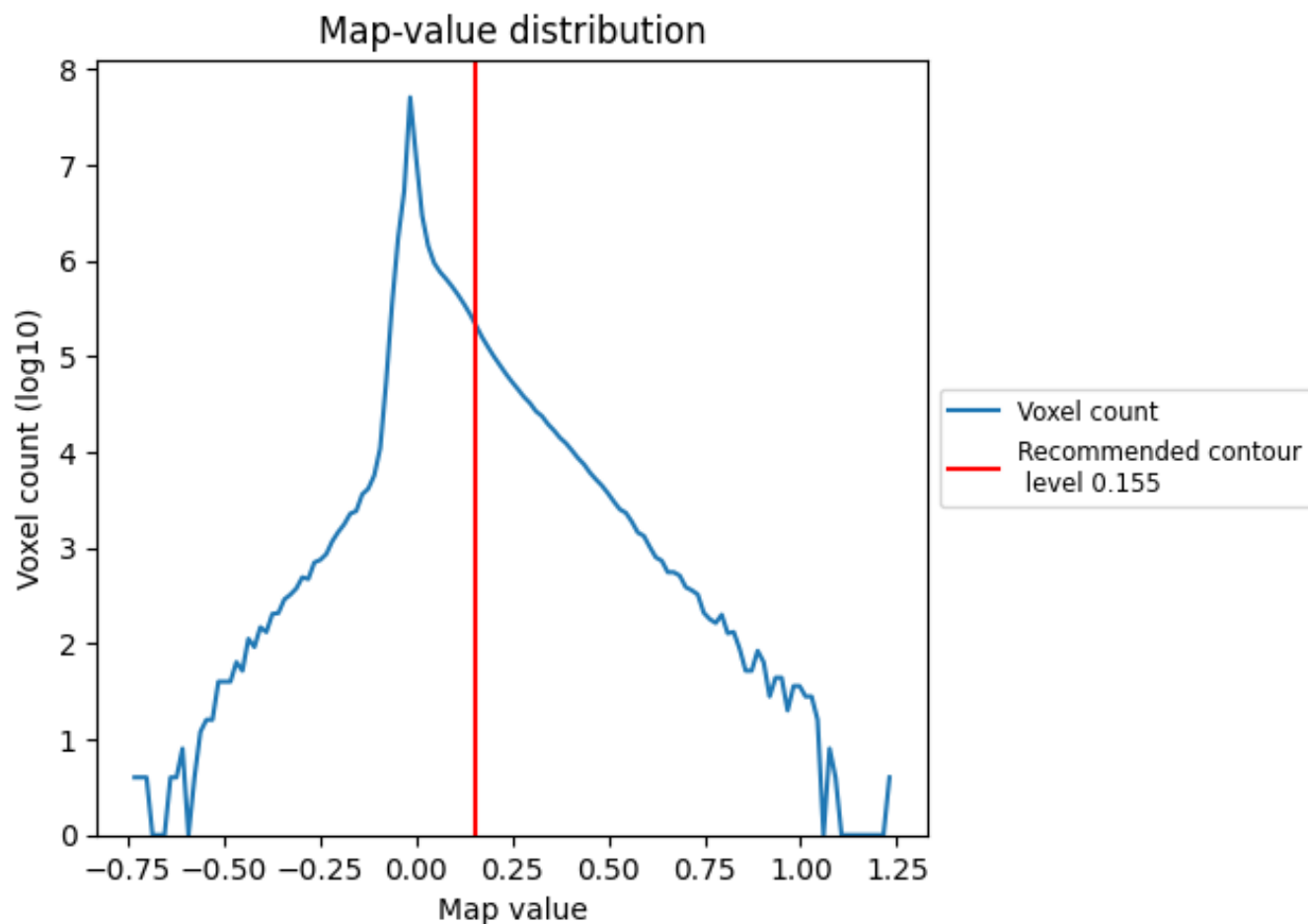
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

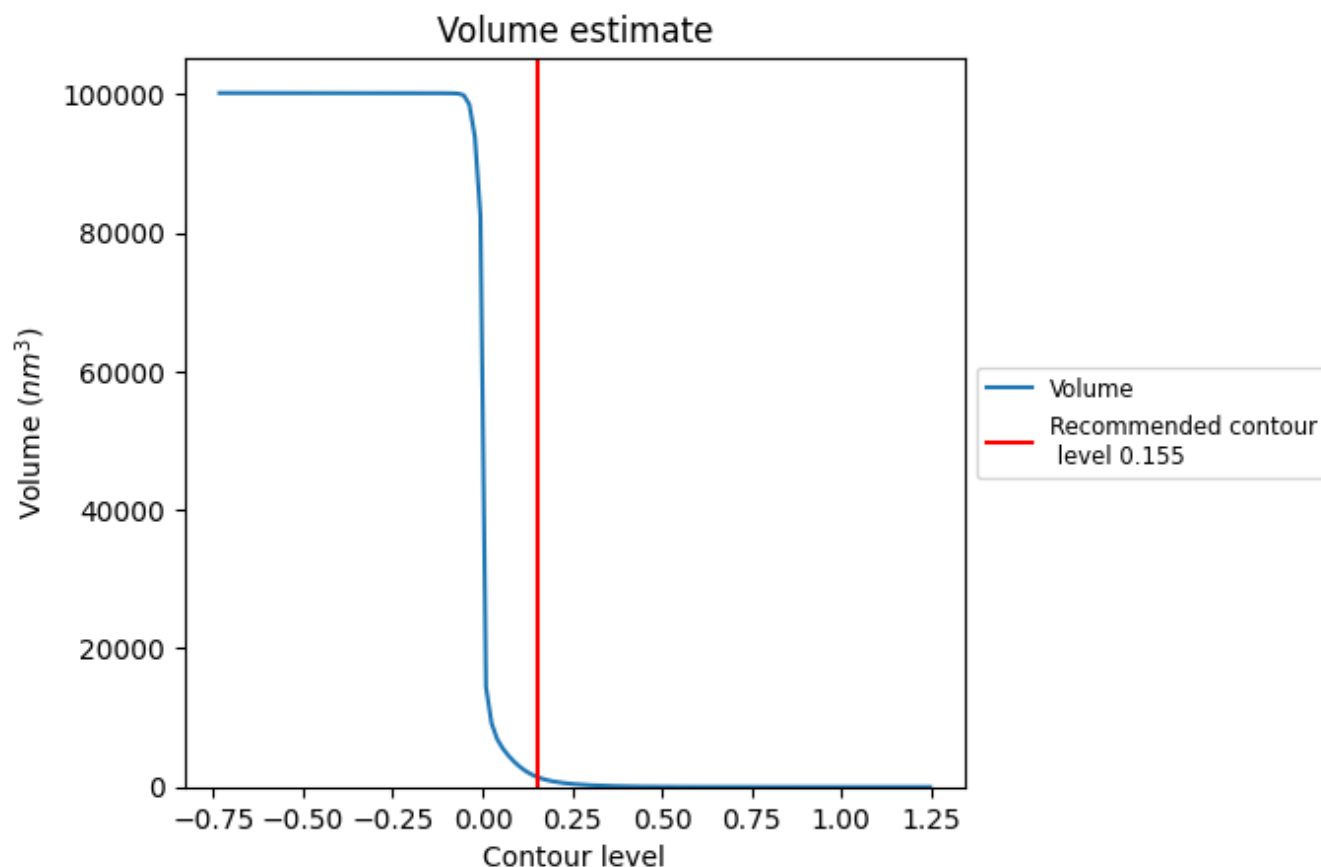
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

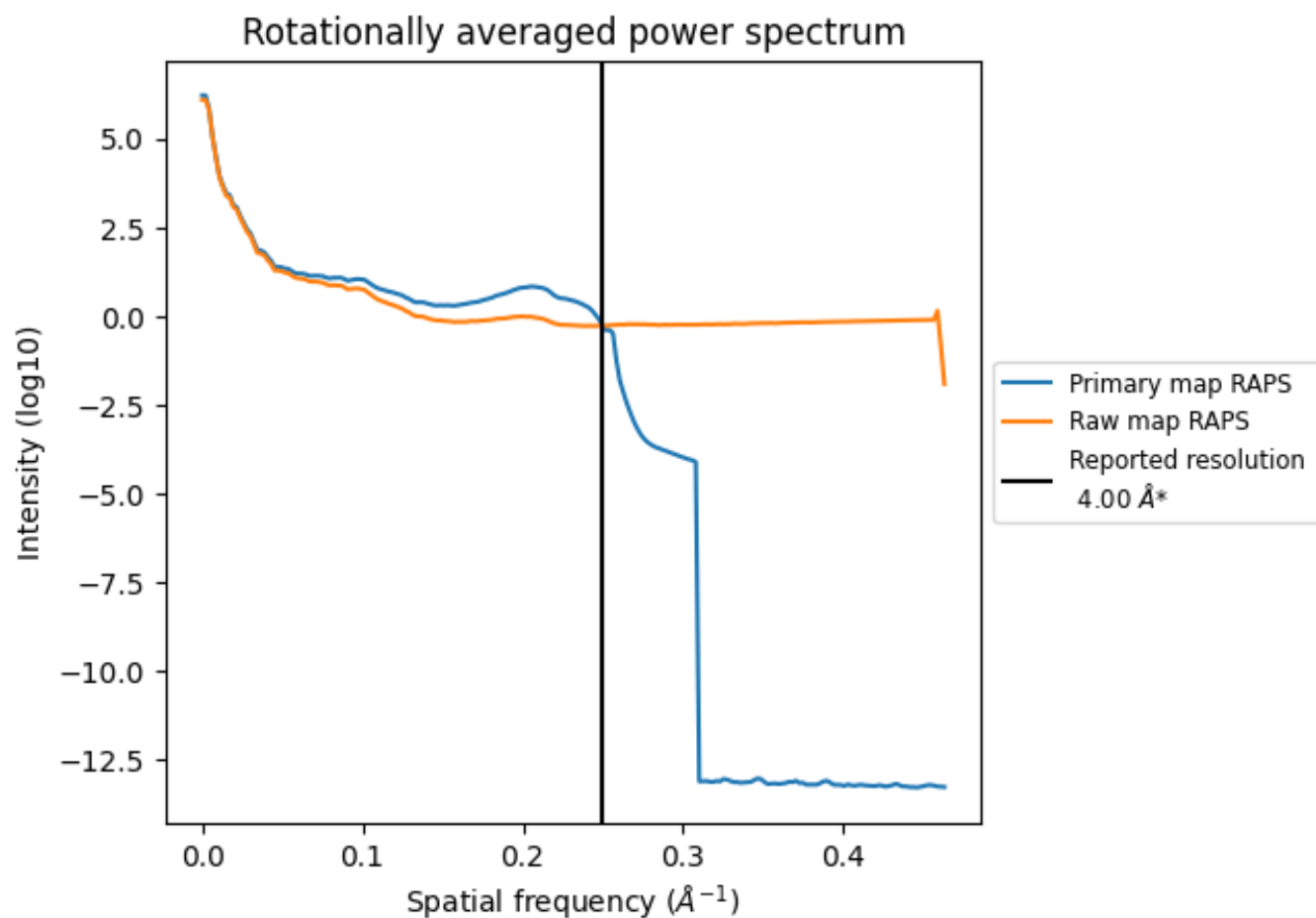
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1397 nm³; this corresponds to an approximate mass of 1262 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 ⓘ

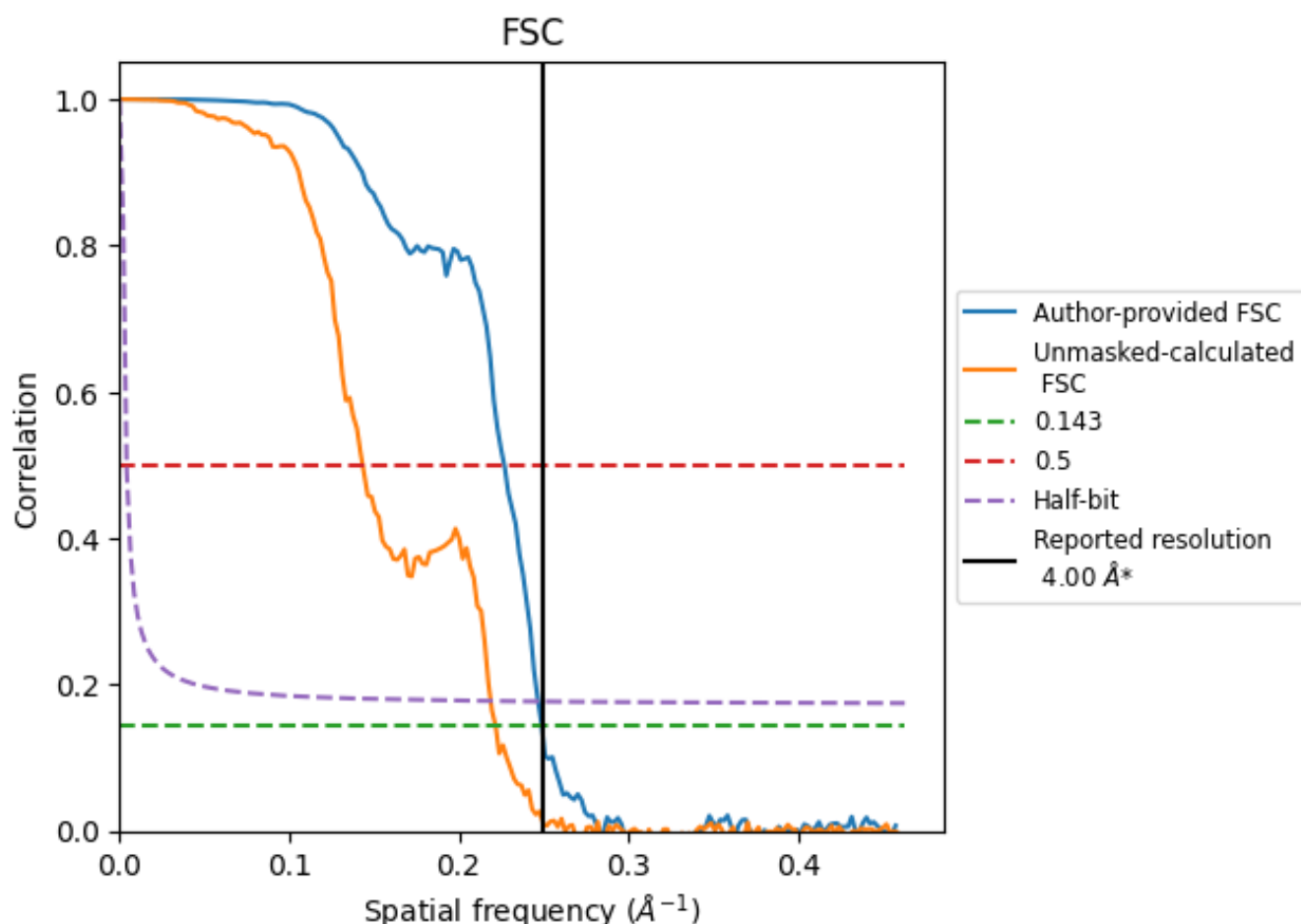


*Reported resolution corresponds to spatial frequency of 0.250 Å⁻¹

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 0.250 Å⁻¹

8.2 Resolution estimates [i](#)

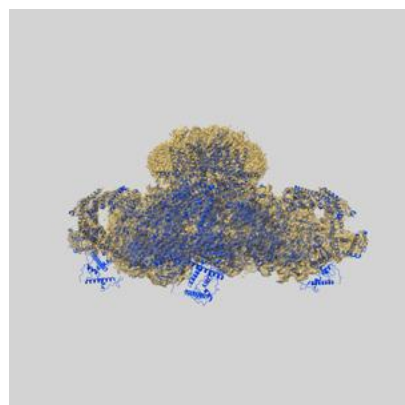
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.02	4.41	4.05
Unmasked-calculated*	4.51	6.97	4.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.51 differs from the reported value 4.0 by more than 10 %

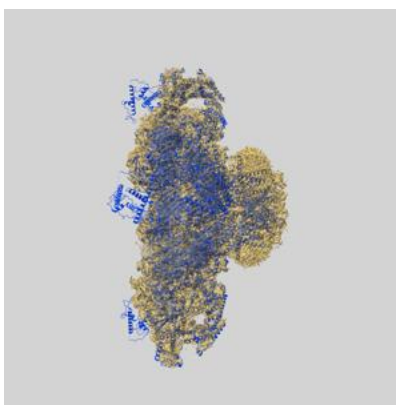
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25709 and PDB model 7T64. Per-residue inclusion information can be found in section [3](#) on page [5](#).

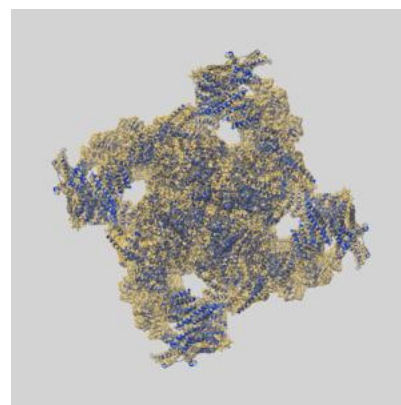
9.1 Map-model overlay [i](#)



X



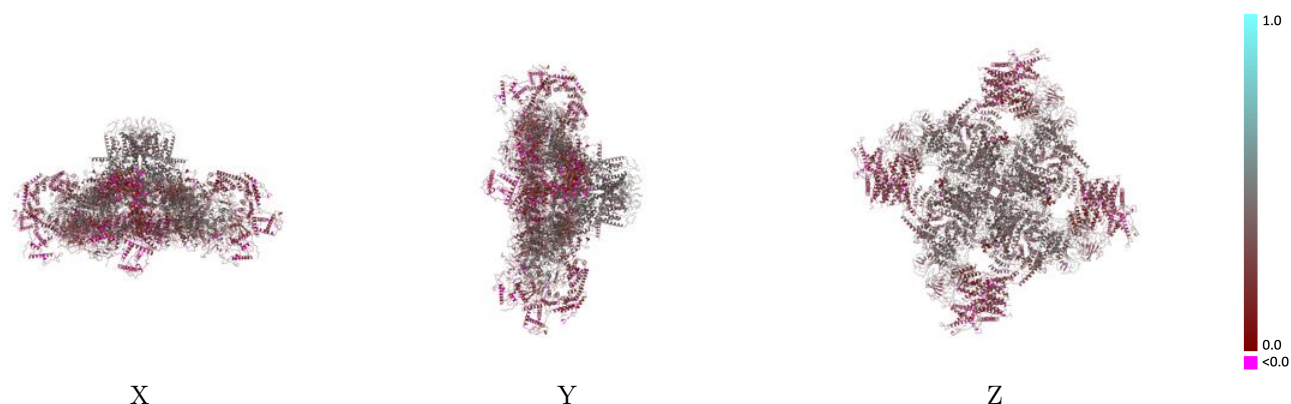
Y



Z

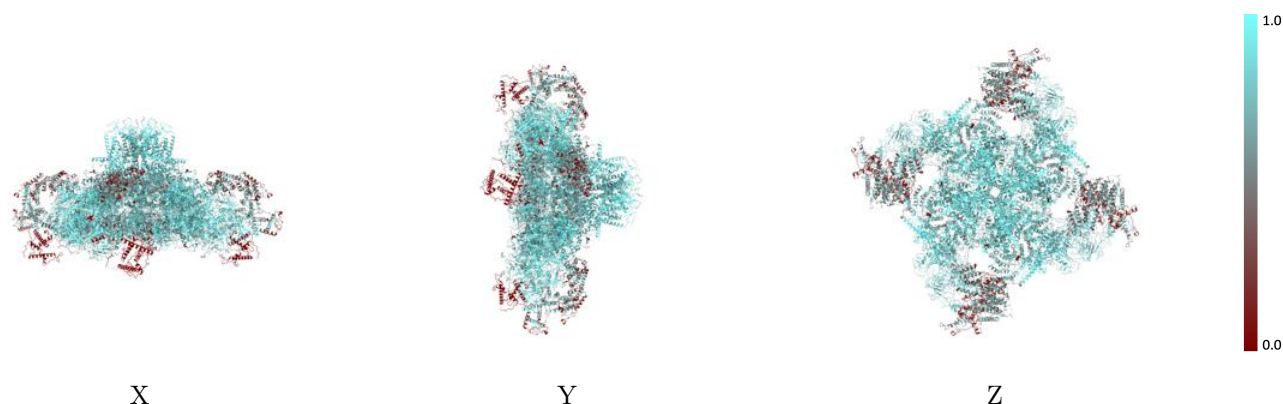
The images above show the 3D surface view of the map at the recommended contour level 0.155 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



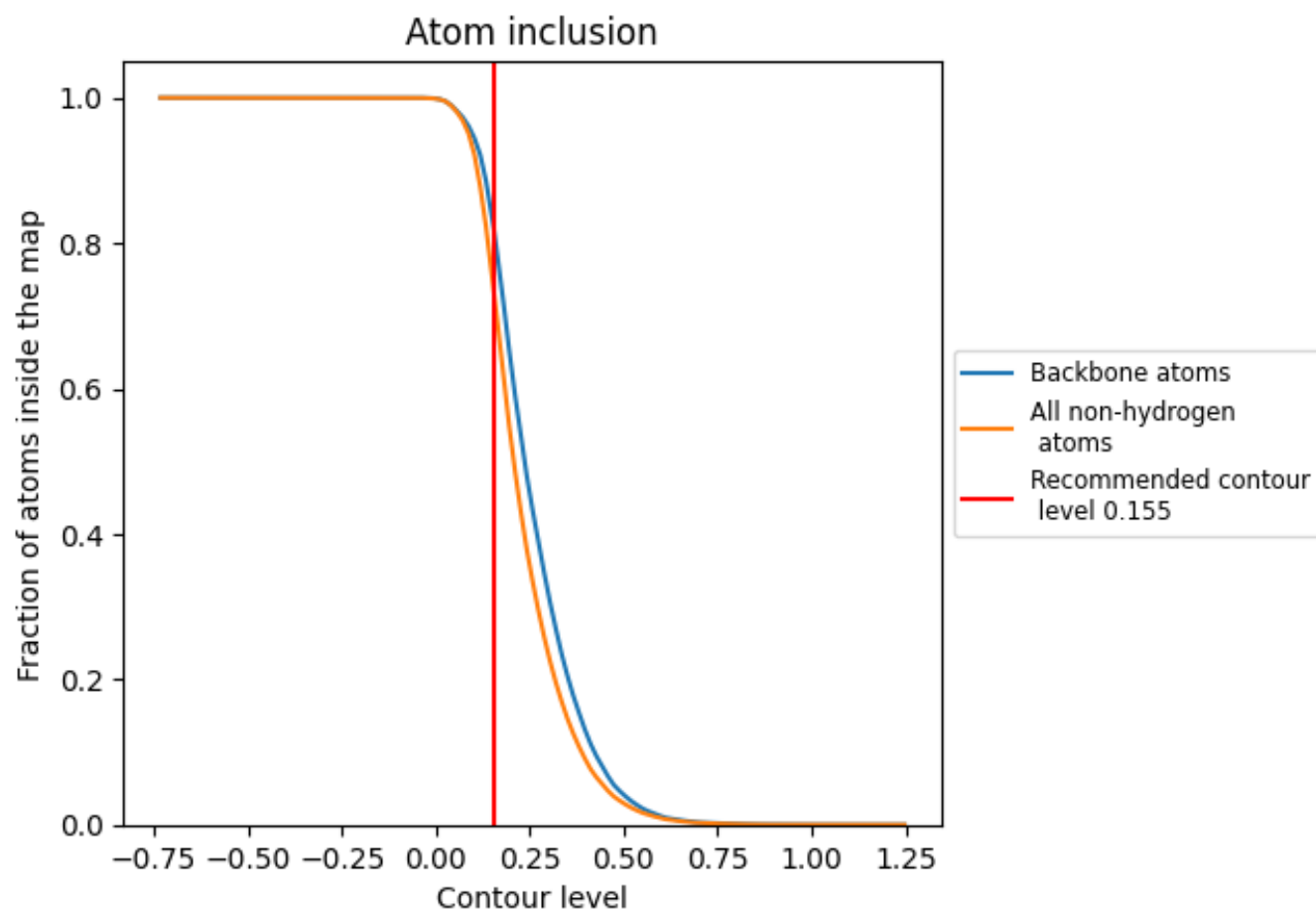
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.155).

9.4 Atom inclusion ⓘ



At the recommended contour level, 82% of all backbone atoms, 73% 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 (0.155) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.7310	<div></div> 0.3060
A	<div></div> 0.7285	<div></div> 0.3040
B	<div></div> 0.7286	<div></div> 0.3040
C	<div></div> 0.7287	<div></div> 0.3040
D	<div></div> 0.7288	<div></div> 0.3040
E	<div></div> 0.8238	<div></div> 0.3630
F	<div></div> 0.8238	<div></div> 0.3670
G	<div></div> 0.8226	<div></div> 0.3670
H	<div></div> 0.8251	<div></div> 0.3660

1.0

0.0

<0.0