



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 11:37 AM UTC

PDB ID : 8SEO / pdb_00008seo
EMDB ID : EMD-40423
Title : Cryo-EM Structure of RyR1 + ATP-gamma-S
Authors : Cholak, S.; Saville, J.W.; Zhu, X.; Berezuk, A.M.; Tuttle, K.S.; Haji-Ghassemi, O.; Van Petegem, F.; Subramaniam, S.
Deposited on : 2023-04-10
Resolution : 3.92 Å(reported)

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

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

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:

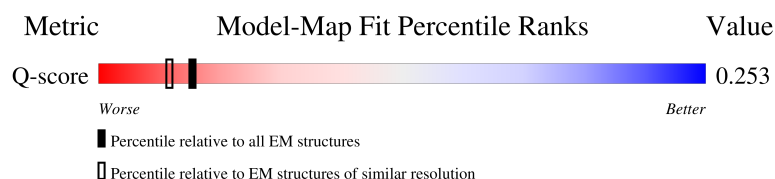
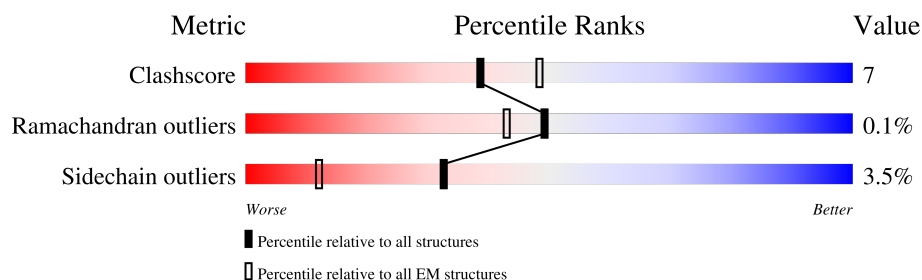
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.92 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	7862 (3.42 - 4.42)

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	
1	B	5037	
1	C	5037	
1	D	5037	

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Mol	Chain	Length	Quality of chain
2	E	350	 27% 69%
2	F	350	 27% 69%
2	G	350	 26% 69%
2	H	350	 27% 69%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 143016 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	4376	Total	C	N	O	S	9	0
			34904	22206	6023	6439	236		
1	B	4376	Total	C	N	O	S	9	0
			34904	22206	6023	6439	236		
1	C	4376	Total	C	N	O	S	9	0
			34904	22206	6023	6439	236		
1	D	4376	Total	C	N	O	S	9	0
			34904	22206	6023	6439	236		

- Molecule 2 is a protein called Glutathione S-transferase class-mu 26 kDa isozyme,Peptidyl-prolyl cis-trans isomerase FKBP1B.

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

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	-242	MET	-	expression tag	UNP P08515
E	-241	LYS	-	expression tag	UNP P08515
E	-240	SER	-	expression tag	UNP P08515
E	-239	SER	-	expression tag	UNP P08515
E	-238	HIS	-	expression tag	UNP P08515
E	-237	HIS	-	expression tag	UNP P08515
E	-236	HIS	-	expression tag	UNP P08515
E	-235	HIS	-	expression tag	UNP P08515

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-234	HIS	-	expression tag	UNP P08515
E	-233	HIS	-	expression tag	UNP P08515
E	-232	GLY	-	expression tag	UNP P08515
E	-231	SER	-	expression tag	UNP P08515
E	-230	SER	-	expression tag	UNP P08515
E	-11	GLY	-	linker	UNP P08515
E	-10	ILE	-	linker	UNP P08515
E	-9	GLU	-	linker	UNP P08515
E	-8	GLU	-	linker	UNP P08515
E	-7	ASN	-	linker	UNP P08515
E	-6	LEU	-	linker	UNP P08515
E	-5	TYR	-	linker	UNP P08515
E	-4	PHE	-	linker	UNP P08515
E	-3	GLN	-	linker	UNP P08515
E	-2	SER	-	linker	UNP P08515
E	-1	ASN	-	linker	UNP P08515
E	0	ALA	-	linker	UNP P08515
F	-242	MET	-	expression tag	UNP P08515
F	-241	LYS	-	expression tag	UNP P08515
F	-240	SER	-	expression tag	UNP P08515
F	-239	SER	-	expression tag	UNP P08515
F	-238	HIS	-	expression tag	UNP P08515
F	-237	HIS	-	expression tag	UNP P08515
F	-236	HIS	-	expression tag	UNP P08515
F	-235	HIS	-	expression tag	UNP P08515
F	-234	HIS	-	expression tag	UNP P08515
F	-233	HIS	-	expression tag	UNP P08515
F	-232	GLY	-	expression tag	UNP P08515
F	-231	SER	-	expression tag	UNP P08515
F	-230	SER	-	expression tag	UNP P08515
F	-11	GLY	-	linker	UNP P08515
F	-10	ILE	-	linker	UNP P08515
F	-9	GLU	-	linker	UNP P08515
F	-8	GLU	-	linker	UNP P08515
F	-7	ASN	-	linker	UNP P08515
F	-6	LEU	-	linker	UNP P08515
F	-5	TYR	-	linker	UNP P08515
F	-4	PHE	-	linker	UNP P08515
F	-3	GLN	-	linker	UNP P08515
F	-2	SER	-	linker	UNP P08515
F	-1	ASN	-	linker	UNP P08515
F	0	ALA	-	linker	UNP P08515

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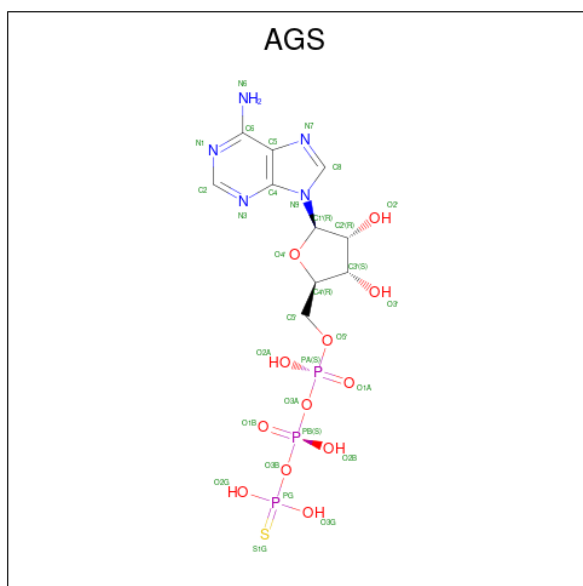
Chain	Residue	Modelled	Actual	Comment	Reference
G	-242	MET	-	expression tag	UNP P08515
G	-241	LYS	-	expression tag	UNP P08515
G	-240	SER	-	expression tag	UNP P08515
G	-239	SER	-	expression tag	UNP P08515
G	-238	HIS	-	expression tag	UNP P08515
G	-237	HIS	-	expression tag	UNP P08515
G	-236	HIS	-	expression tag	UNP P08515
G	-235	HIS	-	expression tag	UNP P08515
G	-234	HIS	-	expression tag	UNP P08515
G	-233	HIS	-	expression tag	UNP P08515
G	-232	GLY	-	expression tag	UNP P08515
G	-231	SER	-	expression tag	UNP P08515
G	-230	SER	-	expression tag	UNP P08515
G	-11	GLY	-	linker	UNP P08515
G	-10	ILE	-	linker	UNP P08515
G	-9	GLU	-	linker	UNP P08515
G	-8	GLU	-	linker	UNP P08515
G	-7	ASN	-	linker	UNP P08515
G	-6	LEU	-	linker	UNP P08515
G	-5	TYR	-	linker	UNP P08515
G	-4	PHE	-	linker	UNP P08515
G	-3	GLN	-	linker	UNP P08515
G	-2	SER	-	linker	UNP P08515
G	-1	ASN	-	linker	UNP P08515
G	0	ALA	-	linker	UNP P08515
H	-242	MET	-	expression tag	UNP P08515
H	-241	LYS	-	expression tag	UNP P08515
H	-240	SER	-	expression tag	UNP P08515
H	-239	SER	-	expression tag	UNP P08515
H	-238	HIS	-	expression tag	UNP P08515
H	-237	HIS	-	expression tag	UNP P08515
H	-236	HIS	-	expression tag	UNP P08515
H	-235	HIS	-	expression tag	UNP P08515
H	-234	HIS	-	expression tag	UNP P08515
H	-233	HIS	-	expression tag	UNP P08515
H	-232	GLY	-	expression tag	UNP P08515
H	-231	SER	-	expression tag	UNP P08515
H	-230	SER	-	expression tag	UNP P08515
H	-11	GLY	-	linker	UNP P08515
H	-10	ILE	-	linker	UNP P08515
H	-9	GLU	-	linker	UNP P08515
H	-8	GLU	-	linker	UNP P08515

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-7	ASN	-	linker	UNP P08515
H	-6	LEU	-	linker	UNP P08515
H	-5	TYR	-	linker	UNP P08515
H	-4	PHE	-	linker	UNP P08515
H	-3	GLN	-	linker	UNP P08515
H	-2	SER	-	linker	UNP P08515
H	-1	ASN	-	linker	UNP P08515
H	0	ALA	-	linker	UNP P08515

- Molecule 3 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
3	B	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
3	C	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	
3	D	1	Total	C	N	O	P	S	0
			31	10	5	12	3	1	

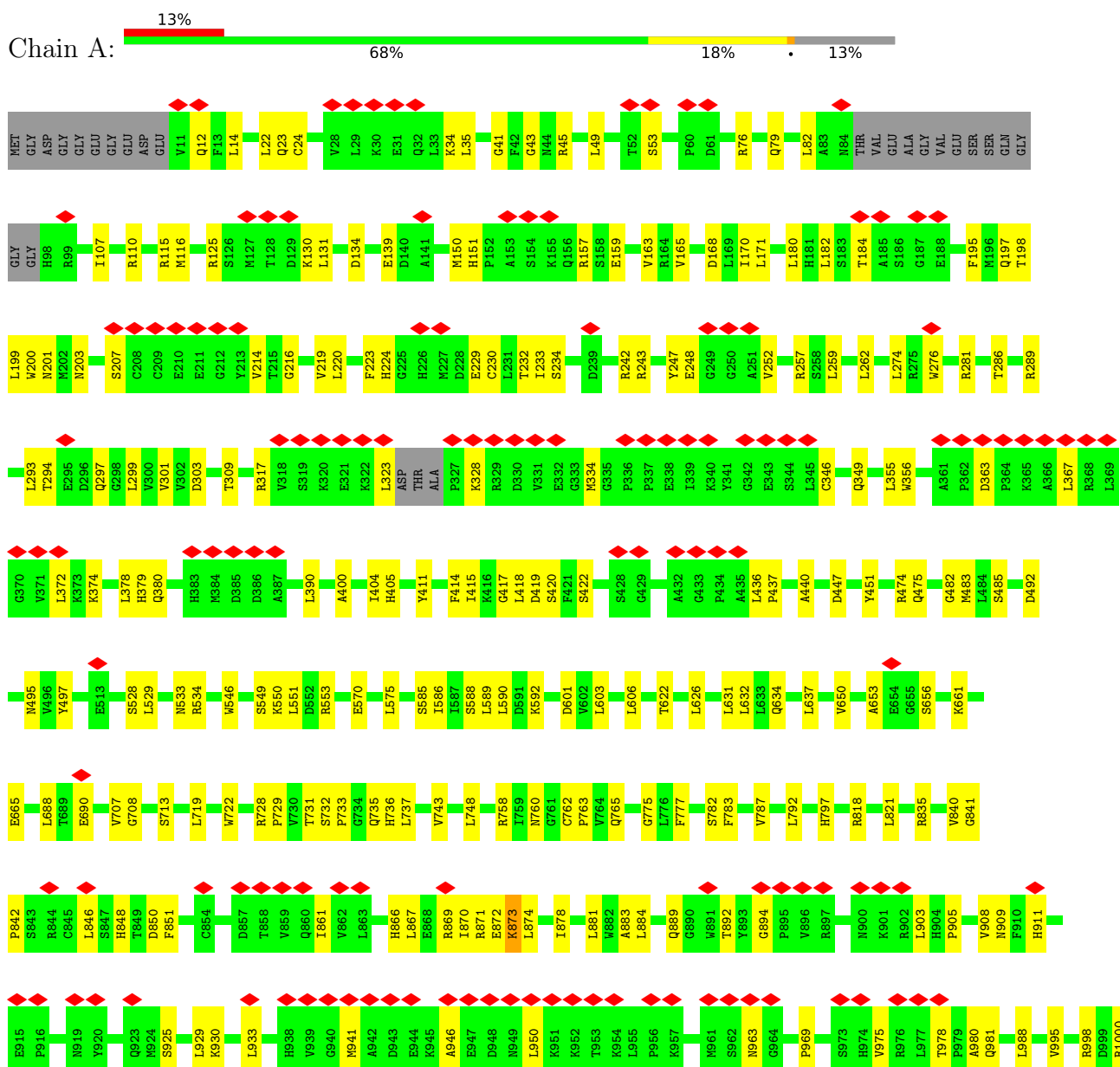
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

3 Residue-property plots

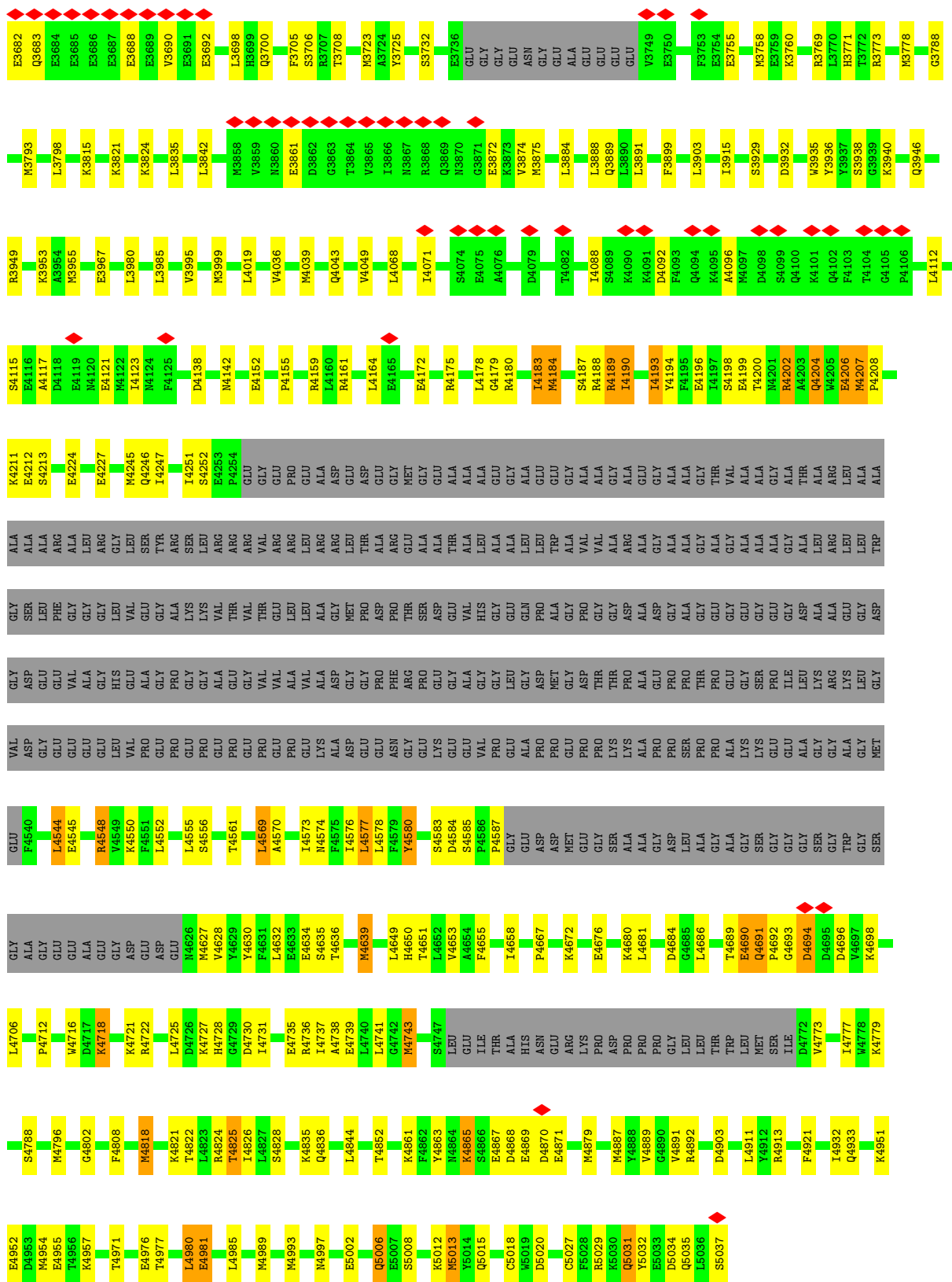
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





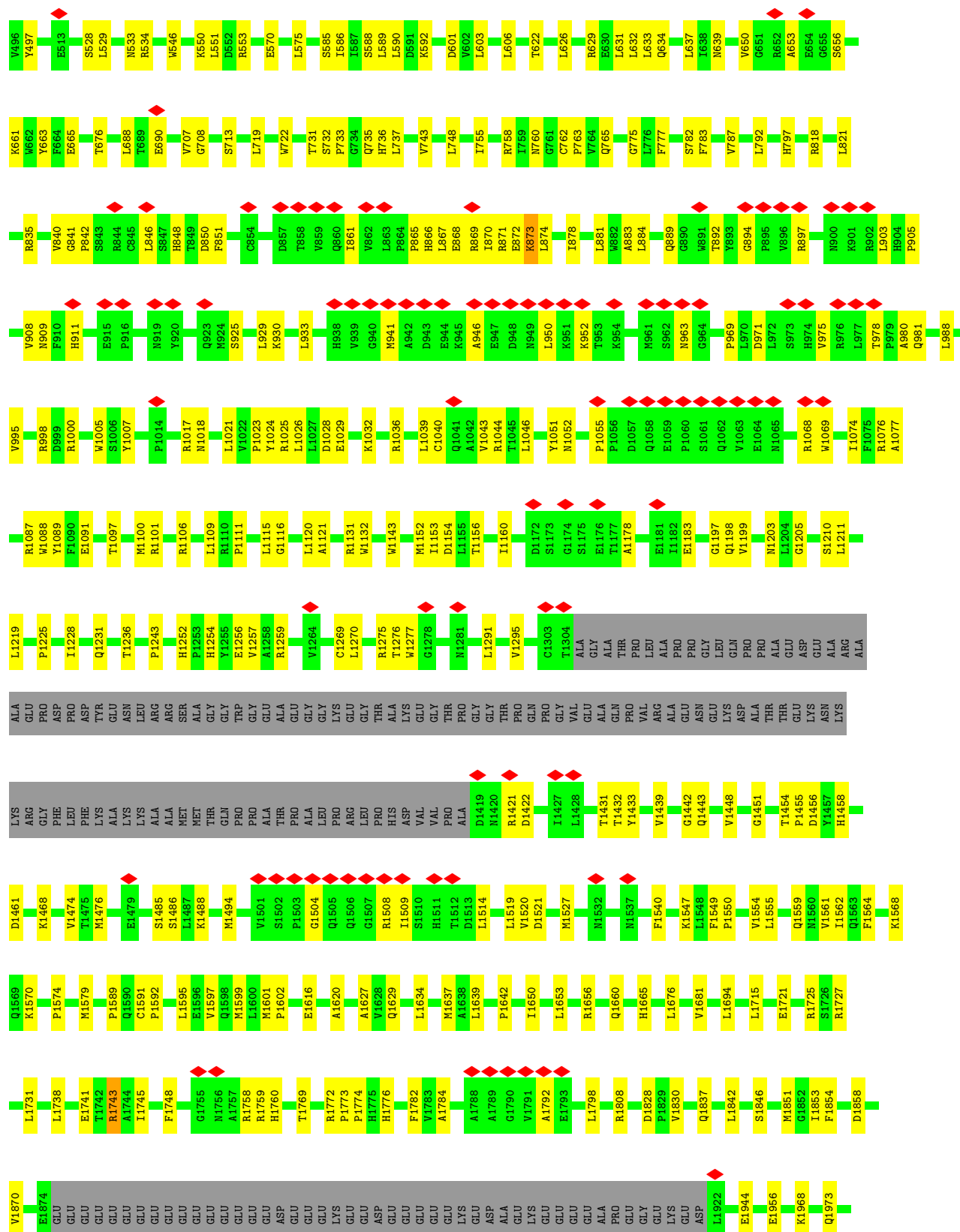
D3587	D3588	P3589	I3592	R3593	R3594	R3595	R3596	A3601	V3604	E3607	E3610	R3611	P3612	Y3613	S3614	S3615	K3616	L3617	A3618	V3619	W3620	H3621	K3622	L3623	L3624	S3625	K3626	Q3627	R3628	R3629	R3630	A3631	V3632	V3633	A3634	P3635	P3636	P3637	P3640	K3652	A3659	V3660	V3661	L3662	L3663	E3670	D3675	V3676	L3677																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
R3499	G3500	D3501	R3502	Y3503	S3504	V3505	Q3506	T3507	S3508	L3510	V3511	K3515	K3516	M3517	N3523	M3524	D3531	L3532	I3533	M3534	K3537	T3538	A3541	L3542	K3543	D3544	N3555	N3556	L3557	H3558	L3559	Q3560	G3561	V3563	E3564	G3565	S3566	L3569	L3575	V3576	K3577	P3580	G3581	E3583	E3584	D3585	A3586																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
V3415	V3416	R3420	W3423	L3424	F3435	R3436	K3437	T3443	Y3444	W3445	F3451	E3454	N3457	F3458	V3459	V3460	Q3461	N3465	N3466	M3467	S3468	F3469	L3470	T3471	A3472	D3473	S3474	K3475	S3476	K3477	N3478	A3479	L3480	G3481	A3482	G3483	S3484	G3485	G3486	G3487	G3488	G3489	G3490	F3491	L3492	R3493	R3494	R3495	R3496	R3497	R3498																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
P3293	P3294	A3295	L3296	P3297	A3298	G3299	A3300	P3301	P3302	P3303	C3304	T3305	A3306	V3324	I3329	D3330	E3331	A3332	V3340	A3341	F3342	I3343	V3344	V3345	S3346	S3347	L3354	F3358	T3361	I3362	G3363	R3364	E3377	R3380	L3381	E3382	A3383	K3384	A3385	E3386	A3387	E3388	E3389	G3390	F3391	L3392	R3403	Y3409	E3414																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
L3206	E3207	P3208	Q3209	L3210	N3214	A3215	C3216	S3217	V3218	T3219	T3220	T3221	S3222	S3223	P3224	R3225	R3226	R3227	A3228	L3229	G3231	P3232	P3233	N3234	S3235	V3236	L3246	P3247	R3248	L3253	L3256	S3259	G3260	A3261	T3264	E3265	M3266	T3273	W3284	G3288	P3289	F3292																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
E3103	E3104	V3107	L3110	R3111	L3112	G3113	K3114	V3115	S3116	G3117	A3118	A3119	T3120	V3121	K3122	G3123	G3124	T3130	Y3131	T3132	T3133	L3136	H3146	I3147	Q3151	F3152	G3153	D3154	D3155	V3156	H3157	L3158	V3163	S3171	T3172	S3174	L3175	N3180	T3181	V3182	V3183	E3184	K3185	L3190	K3201	P3202	V3203																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
F2997	F2998	I3001	L3002	L3003	F3004	L3005	N3007	T3011	L3015	S3019	A3022	K3023	V3024	L3025	G3026	S3027	G3028	N3033	K3034	E3035	K3036	E3037	L3038	L3039	L3040	L3041	L3042	L3043	L3044	L3045	L3046	L3047	L3048	L3049	L3050	L3051	L3052	L3053	L3054	L3055	L3056	F3057	G3058	T3059	P3062	V3065	L3076	D3077	A3078	R3079	V3080	M3081	K3082	V3088	D3102																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
K2914	E2915	K2916	A2917	D2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	K2927	K2928	F2929	L2930	Q2931	M2932	N2933	G2934	A2935	A2936	V2937	T2938	L2939	L3000	L3001	L3002	L3003	L3004	L3005	L3006	L3007	L3008	L3009	L3010	L3011	L3012	L3013	L3014	L3015	L3016	L3017	L3018	L3019	L3020	L3021	L3022	L3023	L3024	L3025	L3026	L3027	L3028	L3029	L3030	L3031	L3032	L3033	L3034	L3035	L3036	L3037	L3038	L3039	L3040	L3041	L3042	L3043	L3044	L3045	L3046	L3047	L3048	L3049	L3050	L3051	L3052	L3053	L3054	L3055	L3056	L3057	L3058	L3059	L3060	L3061	L3062	L3063	L3064	L3065	L3066	L3067	L3068	L3069	L3070	L3071	L3072	L3073	L3074	L3075	L3076	L3077	L3078	L3079	L3080	L3081	L3082	L3083	L3084	L3085	L3086	L3087	L3088	L3089	L3090	L3091	L3092	L3093	L3094	L3095	L3096	L3097	L3098	L3099	L3100	L3101	L3102	L3103	L3104	L3105	L3106	L3107	L3108	L3109	L3110	L3111	L3112	L3113	L3114	L3115	L3116	L3117	L3118	L3119	L3120	L3121	L3122	L3123	L3124	L3125	L3126	L3127	L3128	L3129	L3130	L3131	L3132	L3133	L3134	L3135	L3136	L3137	L3138	L3139	L3140	L3141	L3142	L3143	L3144	L3145	L3146	L3147	L3148	L3149	L3150	L3151	L3152	L3153	L3154	L3155	L3156	L3157	L3158	L3159	L3160	L3161	L3162	L3163	L3164	L3165	L3166	L3167	L3168	L3169	L3170	L3171	L3172	L3173	L3174	L3175	L3176	L3177	L3178	L3179	L3180	L3181	L3182	L3183	L3184	L3185	L3186	L3187	L3188	L3189	L3190	L3191	L3192	L3193	L3194	L3195	L3196	L3197	L3198	L3199	L3200	L3201	L3202	L3203	L3204	L3205	L3206	L3207	L3208	L3209	L3210	L3211	L3212	L3213	L3214	L3215	L3216	L3217	L3218	L3219	L3220	L3221	L3222	L3223	L3224	L3225	L3226	L3227	L3228	L3229	L3230	L3231	L3232	L3233	L3234	L3235	L3236	L3237	L3238	L3239	L3240	L3241	L3242	L3243	L3244	L3245	L3246	L3247	L3248	L3249	L3250	L3251	L3252	L3253	L3254	L3255	L3256	L3257	L3258	L3259	L3260	L3261	L3262	L3263	L3264	L3265	L3266	L3267	L3268	L3269	L3270	L3271	L3272	L3273	L3274	L3275	L3276	L3277	L3278	L3279	L3280	L3281	L3282	L3283	L3284	L3285	L3286	L3287	L3288	L3289	L3290	L3291	L3292	L3293	L3294	L3295	L3296	L3297	L3298	L3299	L3300	L3301	L3302	L3303	L3304	L3305	L3306	L3307	L3308	L3309	L3310	L3311	L3312	L3313	L3314	L3315	L3316	L3317	L3318	L3319	L3320	L3321	L3322	L3323	L3324	L3325	L3326	L3327	L3328	L3329	L3330	L3331	L3332	L3333	L3334	L3335	L3336	L3337	L3338	L3339	L3340	L3341	L3342	L3343	L3344	L3345	L3346	L3347	L3348	L3349	L3350	L3351	L3352	L3353	L3354	L3355	L3356	L3357	L3358	L3359	L3360	L3361	L3362	L3363	L3364	L3365	L3366	L3367	L3368	L3369	L3370	L3371	L3372	L3373	L3374	L3375	L3376	L3377	L3378	L3379	L3380	L3381	L3382	L3383	L3384	L3385	L3386	L3387	L3388	L3389	L3390	L3391	L3392	L3393	L3394	L3395	L3396	L3397	L3398	L3399	L3400	L3401	L3402	L3403	L3404	L3405	L3406	L3407	L3408	L3409	L3410	L3411	L3412	L3413	L3414	L3415	L3416	L3417	L3418	L3419	L3420	L3421	L3422	L3423	L3424	L3425	L3426	L3427	L3428	L3429	L3430	L3431	L3432	L3433	L3434	L3435	L3436	L3437	L3438	L3439	L3440	L3441	L3442	L3443	L3444	L3445	L3446	L3447	L3448	L3449	L3450	L3451	L3452	L3453	L3454	L3455	L3456	L3457	L3458	L3459	L3460	L3461	L3462	L3463	L3464	L3465	L3466	L3467	L3468	L3469	L3470	L3471	L3472	L3473	L3474	L3475	L3476	L3477	L3478	L3479	L3480	L3481	L3482	L3483	L3484	L3485	L3486	L3487	L3488	L3489	L3490	L3491	L3492	L3493	L3494	L3495	L3496	L3497	L3498	L3499	L3500	L3501	L3502	L3503	L3504	L3505	L3506	L3507	L3508	L3509	L3510	L3511	L3512	L3513	L3514	L3515	L3516	L3517	L3518	L3519	L3520	L3521	L3522	L3523	L3524	L3525	L3526	L3527	L3528	L3529	L3530	L3531	L3532	L3533	L3534	L3535	L3536	L3537	L3538	L3539	L3540	L3541	L3542	L3543	L3544	L3545	L3546	L3547	L3548	L3549	L3550	L3551	L3552	L3553	L3554	L3555	L3556	L3557	L3558	L3559	L3560	L3561	L3562	L3563	L3564	L3565	L3566	L3567	L3568	L3569	L3570	L3571	L3572	L3573	L3574	L3575	L3576	L3577	L3578	L3579	L3580	L3581	L3582	L3583	L3584	L3585	L3586	L3587	L3588	L3589	L3590	L3591	L3592	L3593	L3594	L3595	L3596	L3597	L3598	L3599	L3600	L3601	L3602	L3603	L3604	L3605	L3606	L3607	L3608	L3609	L3610	L3611	L3612	L3613	L3614	L3615	L3616	L3617	L3618	L3619	L3620	L3621	L3622	L3623	L3624	L3625	L3626	L3627	L3628	L3629	L3630	L3631	L3632	L3633	L3634	L3635	L3636	L3637	L3638	L3639	L3640	L3641	L3642	L3643	L3644	L3645	L3646	L3647	L3648	L3649	L3650	L3651	L3652	L3653	L3654	L3655	L3656	L3657	L3658	L3659	L3660	L3661	L3662	L3663	L3664	L3665	L3666	L3667	L3668	L3669	L3670	L3671	L3672	L3673	L3674	L3675	L3676	L3677	L3678	L3679	L3680	L3681	L3682	L3683	L3684	L3685	L3686	L3687	L3688	L3689	L3690	L3691	L3692	L3693	L3694	L3695	L3696	L3697	L3698	L3699	L3700	L3701	L3702	L3703	L3704	L3705	L3706	L3707	L3708	L3709	L3710	L3711	L3712	L3713	L3714	L3715	L3716	L3717	L3718	L3719	L3720	L3721	L3722	L3723	L3724	L3725	L3726	L3727	L3728	L3729	L3730	L3731	L3732	L3733	L3734	L3735	L3736	L3737	L3738	L3739	L3740	L3741	L3742	L3743	L3744	L3745	L3746	L3747	L3748	L3749	L3750	L3751	L3752	L3753	L3754	L3755	L3756	L3757	L3758	L3759	L3760	L3761	L3762	L3763	L3764	L3765	L3766	L3767	L3768	L3769	L3770	L3771	L3772	L3773	L3774	L3775	L3776	L3777	L3778	L3779	L3780	L3781	L3782	L3783	L3784	L3785	L3786	L3787	L3788	L3789	L3790	L3791	L3792	L3793	L3794	L3795	L3796	L3797	L3798	L3799	L3800	L3801	L3802	L3803	L3804	L3805	L3806	L3807	L3808	L3809	L3810	L3811	L3812	L3813	L3814	L3815	L3816	L3817	L3818	L3819	L3820	L3821	L3822	L3823	L3824	L3825	L3826	L3827	L3828	L3829	L3830	L3831	L3832	L3833	L3834	L3835	L3836	L3837	L3838	L3839	L3840	L3841	L3842	L3843	L3844	L3845	L3846	L3847	L3848	L3849	L3850	L3851	L3852	L3853	L3854	L3855	L3856	L3857	L3858	L3859	L3860	L3861	L3862	L3863	L3864	L3865	L3866	L3867	L3868	L3869	L3870	L3871	L3872	L3873	L3874	L3875	L3876	L3877	L3878	L3879	L3880	L3881	L3882	L3883	L3884	L3885	L3886	L3887	L3888	L3889	L3890	L3891	L3892	L3893	L3894	L3895	L3896	L3897	L3898	L3899	L3900	L3901	L3902	L3903	L3904	L3905	L3906	L3907	L3908	L3909	L3910	L3911	L3912	L3913	L3914	L3915	L3916	L3917	L3918	L3919	L3920	L3921	L3922	L3923	L3924	L3925	L3926	L3927	L3928	L3929	L3930	L3931	L3932	L3933	L3934	L3935	L3936	L3937	L3938	L3939	L3940	L3941	L3942	L3943	L3944	L3945	L3946	L3947	L3948	L3949	L3950	L3951	L3952	L3953	L3954	L3955	L3956	L3957	L3958	L3959	L3960	L3961	L3962	L3963	L3964	L3965	L3966	L3967	L3968	L3969	L3970	L3971	L3972	L3973	L3974	L3975	L3976	L3977	L3978	L3979	L3980	L3981	L3982</





E2870	L2871	Q2872	A2873	K2874	A2875	E2876	D2877	L2878	A2879	E2880	N2881	Y2882	H2883	N2884	T2885	W2886	G2887	R2888	K2889	K2890	K2891	Q2892	E2893	L2894	E2895	A2896	K2897	G2898	G2899	G2900	T2901	H2902	P2903	L2904	L2905	V2906	P2907	V2908	D2909	T2910	L2911	T2912	A2913	K2914	E2915	K2916	A2917	R2918	D2919	R2920	E2921	K2922	A2923	Q2924	E2925	L2926	L2927	K2928	F2929																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
K2810	E2811	S2812	L2813	K2814	A2815	M2816	L2817	A2818	Y2819	E2820	W2821	L2822	L2823	E2824	K2825	A2826	R2827	E2828	G2829	E2830	GLU	GLU	ARG	THR	GLU	LYS	LYS	THR	ARG	LYS	ILE	SER	GLN	THR	ALA	GLN	THR	TYR	ASP	PRO	ARG	GLU	GLY	Y2855	N2856	P2857	Q2858	P2859	P2860	D2861	L2862	S2863	G2864	V2865	T2866	Y2867	S2868	R2869																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
R2624	V2627	F2628	L2643	P2658	V2666	T2667	S2668	L2674	K2677	L2678	H2688	L2695	A2699	L2703	V2715	D2716	Y2719	S2720	S2721	K2722	A2723	E2724	K2725	LYS	ALA	THR	VAL	ASP	ALA	GLU	GLY	N2734	F2735	D2736	P2737	R2738	P2739	V2740	E2741	T2742	L2743	N2744	V2745	I2746	I2747	P2748	E2749																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
V2521	L2522	D2523	V2524	G2525	F2526	D2529	M2530	R2531	S2535	A2539	M2546	Y2553	L2559	T2562	T2563	K2564	C2565	G2571	T2572	E2573	H2574	D2575	A2576	L2577	M2578	M2582	L2583	H2584	T2585	V2586	Y2587	R2588	R2593	S2594	L2595	R2600	M2608	C2611	T2614	R2615	M2618	L2619	Q2620																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
G2419	H2420	M2423	I2430	D2431	R2435	C2436	A2437	I2443	R2454	L2457	R2458	S2459	L2460	D2464	D2465	L2466	V2467	G2468	L2469	I2470	S2471	L2472	P2473	T2478	L2479	G2480	K2481	D2482	Q2483	A2484	L2485	P2488	K2499	A2500	S2501	M2502	R2508	V2509	Y2510	G2511	T2512	E2513	D2516	F2517	L2518	L2519	H2520																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
V2299	L2307	Q2308	L2313	L2314	D2320	I2321	R2336	V2339	V2353	R2359	G2365	P2366	A2367	L2368	R2369	G2370	E2371	G2372	A2383	S2387	E2388	D2389	P2390	A2391	P2395	G2396	V2397	ARG	ASP	ARG	ARG	ARG	GLU	PHE	GLY	GLU	GLU	P2410	P2411	E2412	E2413	N2414	R2415	V2416																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
K2089	L2097	Q2107	Y2110	L2123	P2146	E2157	Q2161	T2167	Q2173	V2190	Q2193	G2202	K2203	H2204	K2208	K2211	V2214	L2215	G2216	G2217	G2218	E2219	T2220	K2221	R2244	Q2245	R2248	L2254	L2258	T2263	N2283	L2286	A2287	L2290	E2296																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
E2015	E2018	E2019	D2020	C2021	R2028	Q2029	D2030	L2031	Q2032	L2039	I2044	Q2045	L2046	GLU	GLY	GLU	GLU	GLU	GLU	PRO	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLU	E2088																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
GLU	ASP	GLU	GLU	GLU	GLU	LYS	GLU	ALA	PRO	GLU	GLU	GLU	GLU	GLU	GLY	GLU	LYS	GLU	GLU	ASP	L1922	E1944	E1956	M1951	K1968	SER	ARG	LEU	ARG	SER	LEU	LEU	A1983	F1984	T1985	M1986	S1987	A1988	E1990	R1994	T1995	R1996	S2000	Q2003	E2004	Q2005	I2006	N2007	K2013	D2014																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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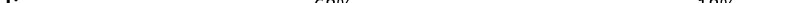
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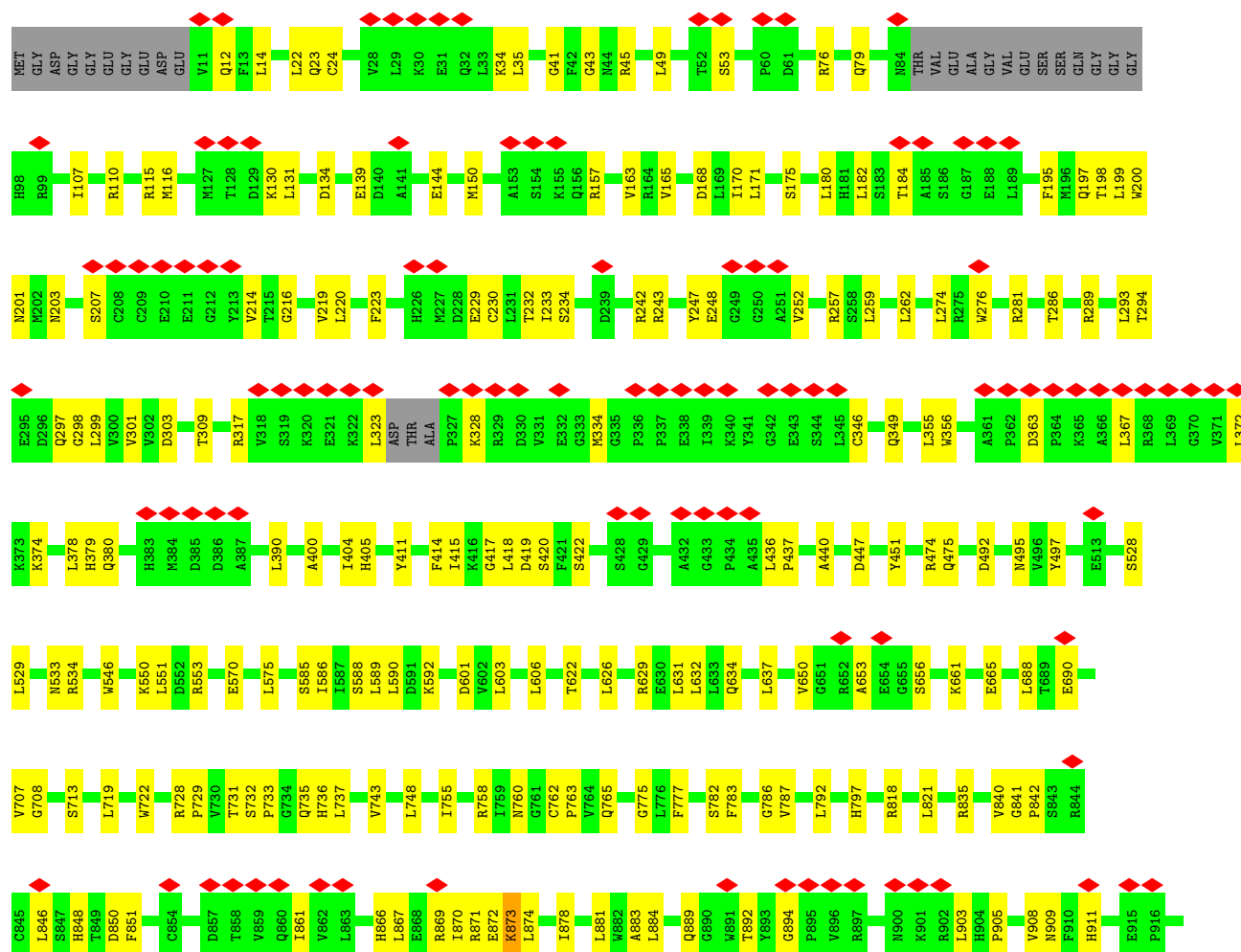


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K3222	GLN	A3022	R2806	E2870	W2807	P2748	V2666	V2522	L2307	P2146	GLU	Q2029
P3224	VAL	K3023	E2871	Q2872	P2808	E2749	T2667	L2524	Q2308	E2157	GLU	I2030
S3225		L3024	Q2873	Q2872	L2809	K2760	S2668	F2526	L2313	Q2161	GLU	Q2032
		L3025	M2874	M2874	K2810	L2751	L2674	D2529	L2314	R2163	GLU	L2039
L3229		L3026	A2875	A2875	E2811	D2752	K2677	M2530	D2320	L2166	GLU	I2044
L3230		G3027	E2876	E2876	S2812	S2753	L2678	R2531	I2321	I2167	GLU	K2045
G3231		G3028	Q2877	Q2877	S2813	F2754	H2688	S2535	R2336	Q2173	GLU	L2046
L3232		N3033	L2878	L2878	K2814	I2755	L2695	A2539	V2339	Q2193	GLU	GLU
P3233		K3034	A2879	A2815	A2815	K2756	A2699	M2546	M2349	G2202	PRO	GLU
N3234		E3035	E2880	M2816	M2816	F2757	K2699	Y2553	V2353	M2203	GLU	GLU
S3235		L3036	M2881	L2817	L2817	F2758	L2703	L2562	R2359	H2204	GLU	GLU
E3237		K3037	Y2882	A2818	A2818	A2759	V2715	I2562	G2365	M2208	THR	THR
E3238		M3038	H2883	W2819	W2819	E2760	D2716	C2565	P2366	M2211	LEU	SER
N3239		L3048	N2884	E2820	E2820	Y2761	S2720	G2571	A2367	L2368	SER	ARG
		R3051	T2885	W2821	W2821	T2762		T2572	L2467	R2369	LEU	LEU
		H3052	W2886	T2822	T2822	E2764		E2574	L2466		ARG	ARG
		R3053	G2887	L2823	L2823	K2765		I2574				
		L3056	R2888	E2824	E2824	W2766		H2574				
		F3057	K2889	K2825	K2825	A2767						
		G3058	K2890	A2826	A2826	F2768						
		T3059	Q2891	R2827	R2827	D2769						
		P3062	E2892	E2828	E2828	K2770						
			L2860	G2830	G2830	I2771						
			Q2971	GLU	GLU	N2773						
			I2974	ARG	ARG	N2774						
			L2977	THR	THR	W2775						
			E2978	GLU	GLU	S2776						
			A2979	LYS	LYS	T2777						
				THR	THR	G2778						
				ARG	ARG	N2779						



- Molecule 1: Ryanodine receptor 1

Chain D:  13% 68% 18% 1%





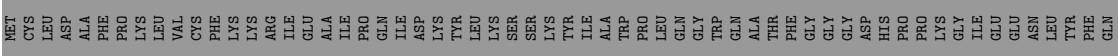
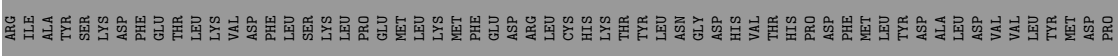
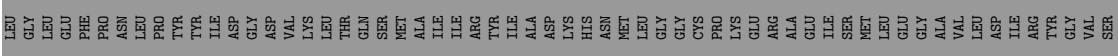
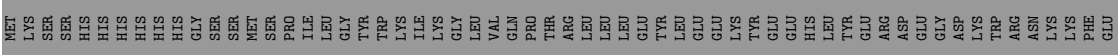
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K3517	F3451	V3329	T3220	ALA	K2928	K2928	S2868	P2748	Q2620	E2413	R2414
N3523	E3454	D3330	T3221	THR	F2929	F2929	E2870	E2749	R2624	R2415	V2416
D3531	N3457	K3332	K3222	G1N	S3019	L2930	E2870	K2750	R2624	L2518	L2519
L3532	F3458	E3331	S3223	VAL	A3022	Q2931	L2871	L2751	V2627	L2519	H2520
L3533	F3459	A3332	P3224	G3123	K3023	M2932	Q2872	D2752	F2628	H2521	H2420
N3534	V3460	V3340	R3225	G3124	V3024	N2933	E2873	E2753	L2643	L2522	M2423
K3537	Q3461	F3341	E3226	T3130	L3025	Y2935	A2875	S2755	P2658	V2524	I2430
T3538	N3465	A3342	R3227	Y3131	G3026	A2936	E2876	N2756	V2666	G2525	I2431
A3541	M3466	T3345	A3228	T3132	S3027	T2937	Q2877	K2757	T2667	F2526	D2431
L3542	S3467	V3346	I3229	T3133	G3028	V2938	L2878	F2758	S2668	M2530	R2435
K3543	S3468	S3347	L3230	L3136	N3033	R2939	K2879	A2759	L2674	R2531	A2437
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N3555	F3471	F3358	L3232	I3147	F3035	LEU	E2880	K2765	L2457	A2539	R2454
L3556	A3472	T3361	P3233	F3152	K3036	ASP	W2881	W2766	R2458	M2546	L2457
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G3561	M3478	L3381	I3248	V3163	F3057	Q2971	E2890	I2771	Y2719	E2573	I2470
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V3563	ALA	A3382	L3256	I3172	T3059	I2974	E2893	N2773	S2721	R2574	P2473
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E3584	LYS	R3403	P3289	M3201	K3082	E2988	V2906	K2786	N2734	R2593	P2488
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D3588	G3500	T3415	P3294	L3207	E3104	P2998	V2908	L2791	D2736	R2600	S2501
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			C3304	L3006			R2918	E2799			
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							K2922	K2802			
							A2923	E2803			
							Q2924	I2804			

T4956	K4779	Y4697	TRP	GLY	MET	GLY	LEU	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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| Met | Cys | Arg | Leu | Met |
| Lys | Ile | Ile | Gly | Lys |
| Ser | Ala | Ala | Leu | Ser |
| Asp | Tyr | Tyr | Glut | Asp |
| Phe | Ala | Ser | Phe | His |
| Pro | Asp | Lys | Pro | His |
| Lys | Phe | Lys | Asn | His |
| Leu | Glu | Phe | Leu | His |
| Val | Glu | Glu | Pro | His |
| Cys | Leu | Thr | Tyr | His |
| Phe | Leu | Lys | Tyr | Gly |
| Lys | Val | Lys | Ile | Ser |
| Lys | Val | Val | Asp | Ser |
| Lys | Arg | Asp | Gly | Met |
| Ile | Leu | Phe | Asp | Met |
| Glu | Ser | Leu | Val | Pro |
| Ala | Lys | Ser | Lys | Ile |
| Ile | Leu | Lys | Leu | Leu |
| Pro | Pro | Phe | Thr | Gly |
| Gln | Glu | Leu | Gln | Tyr |
| Ile | Met | Met | Ser | Trp |
| Asp | Leu | Lys | Met | Lys |
| Lys | Lys | Lys | Ala | Ile |
| Tyr | Met | Lys | Ile | Lys |
| Leu | Phe | Met | Ile | Gly |
| Lys | Glu | Glu | Tyr | Val |
| Ser | Glu | Asp | Ile | Gln |
| Ser | Arg | Arg | Ala | Pro |
| Lys | Leu | Leu | Asp | Thr |
| Tyr | Cys | Lys | Lys | Arg |
| Ile | His | His | Lys | Leu |
| Ala | Lys | Lys | Asn | Leu |
| Trp | Thr | Thr | Met | Leu |
| Pro | Tyr | Tyr | Leu | Glu |
| Leu | Leu | Leu | Gly | Tyr |
| Gln | Asn | Asn | Lys | Leu |
| Gly | Gly | Gly | Cys | Glu |
| Trp | Asp | Asp | Pro | Glu |
| Gln | His | Lys | Lys | Lys |
| Ala | Val | Val | Glu | Tyr |
| Thr | Thr | Thr | Arg | Glu |
| Phe | His | His | Ala | Glu |
| Gly | Gly | Pro | Glu | His |
| Gly | Asp | Asp | Ile | Leu |
| Asp | Met | Phe | Ser | Tyr |
| His | Met | Met | Met | Glu |
| Pro | Leu | Leu | Leu | Arg |
| Pro | Tyr | Tyr | Glu | Asp |
| Lys | Asp | Val | Gly | Glu |
| Lys | Ala | Ala | Ala | Gly |
| Leu | Leu | Leu | Val | Asp |
| Ile | Asp | Asp | Leu | Lys |
| Glu | Val | Val | Asp | Trp |
| Glu | Val | Val | Asp | Arg |
| Glu | Val | Val | Gly | Arg |
| Asn | Leu | Leu | Arg | Asn |
| Leu | Tyr | Tyr | Tyr | Lys |
| Tyr | Met | Met | Gly | Lys |
| Phe | Asp | Asp | Val | Phe |
| Trp | Pro | Pro | Ser | Glu |



● Molecule 2: Glutathione S-transferase class-mu 26 kDa isozyme,Peptidyl-prolyl cis-trans isomerase FKBP1B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55892	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.268	Depositor
Minimum map value	-0.637	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.064	Depositor
Recommended contour level	0.287	Depositor
Map size (Å)	515.2, 515.2, 515.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.288, 1.288, 1.288	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, AGS

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	0.26	0/35721	0.61	4/48375 (0.0%)
1	B	0.26	0/35721	0.61	4/48375 (0.0%)
1	C	0.26	0/35721	0.61	4/48375 (0.0%)
1	D	0.26	0/35721	0.61	4/48375 (0.0%)
2	E	0.23	0/834	0.58	0/1123
2	F	0.23	0/834	0.58	0/1123
2	G	0.23	0/834	0.58	0/1123
2	H	0.23	0/834	0.58	0/1123
All	All	0.26	0/146220	0.61	16/197992 (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	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	4693	GLY	CA-C-N	6.34	133.66	121.54
1	B	4693	GLY	C-N-CA	6.34	133.66	121.54
1	C	4693	GLY	CA-C-N	6.34	133.66	121.54
1	C	4693	GLY	C-N-CA	6.34	133.66	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	4693	GLY	CA-C-N	6.34	133.66	121.54

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	841	GLY	Mainchain
1	B	841	GLY	Mainchain
1	C	841	GLY	Mainchain
1	D	841	GLY	Mainchain

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	34904	0	34524	523	0
1	B	34904	0	34524	515	0
1	C	34904	0	34524	528	0
1	D	34904	0	34524	521	0
2	E	818	0	824	6	0
2	F	818	0	824	8	0
2	G	818	0	824	11	0
2	H	818	0	824	7	0
3	A	31	0	12	0	0
3	B	31	0	12	0	0
3	C	31	0	12	0	0
3	D	31	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	143016	0	141440	2085	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 7.

The worst 5 of 2085 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:2283:ASN:HD22	1:C:2286:LEU:HG	1.56	0.71
1:B:2283:ASN:HD22	1:B:2286:LEU:HG	1.56	0.70
1:D:2283:ASN:HD22	1:D:2286:LEU:HG	1.56	0.70
1:B:1561:VAL:HG12	1:B:1562:ILE:HG13	1.74	0.69
1:C:317:ARG:NH2	1:C:349:GLN:OE1	2.25	0.69

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	4353/5037 (86%)	4217 (97%)	131 (3%)	5 (0%)	48	81
1	B	4353/5037 (86%)	4216 (97%)	132 (3%)	5 (0%)	48	81
1	C	4353/5037 (86%)	4216 (97%)	132 (3%)	5 (0%)	48	81
1	D	4353/5037 (86%)	4217 (97%)	131 (3%)	5 (0%)	48	81
2	E	105/350 (30%)	100 (95%)	5 (5%)	0	100	100
2	F	105/350 (30%)	100 (95%)	5 (5%)	0	100	100
2	G	105/350 (30%)	100 (95%)	5 (5%)	0	100	100
2	H	105/350 (30%)	100 (95%)	5 (5%)	0	100	100
All	All	17832/21548 (83%)	17266 (97%)	546 (3%)	20 (0%)	49	81

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3616	LYS
1	B	3616	LYS
1	C	3616	LYS
1	D	3616	LYS
1	A	4694	ASP

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	3805/4276 (89%)	3666 (96%)	139 (4%)	30	52
1	B	3805/4276 (89%)	3665 (96%)	140 (4%)	30	52
1	C	3805/4276 (89%)	3665 (96%)	140 (4%)	30	52
1	D	3805/4276 (89%)	3666 (96%)	139 (4%)	30	52
2	E	88/304 (29%)	88 (100%)	0	100	100
2	F	88/304 (29%)	88 (100%)	0	100	100
2	G	88/304 (29%)	88 (100%)	0	100	100
2	H	88/304 (29%)	88 (100%)	0	100	100
All	All	15572/18320 (85%)	15014 (96%)	558 (4%)	32	53

5 of 558 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	4583	SER
1	D	4653	VAL
1	D	4580	TYR
1	D	4867	GLU
1	B	4639	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 185 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2283	ASN
1	D	460	GLN
1	C	2734	ASN
1	C	3814	GLN
1	D	860	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	AGS	D	5101	-	32,33,33	0.53	1 (3%)	45,52,52	1.11	2 (4%)
3	AGS	C	5101	-	32,33,33	0.53	1 (3%)	45,52,52	1.11	2 (4%)
3	AGS	A	5101	-	32,33,33	0.53	1 (3%)	45,52,52	1.11	2 (4%)
3	AGS	B	5101	-	32,33,33	0.53	1 (3%)	45,52,52	1.11	2 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AGS	D	5101	-	-	7/21/38/38	0/3/3/3
3	AGS	C	5101	-	-	7/21/38/38	0/3/3/3
3	AGS	A	5101	-	-	7/21/38/38	0/3/3/3
3	AGS	B	5101	-	-	7/21/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	5101	AGS	PG-S1G	2.09	1.95	1.90

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	5101	AGS	PG-S1G	2.09	1.95	1.90
3	B	5101	AGS	PG-S1G	2.09	1.95	1.90
3	C	5101	AGS	PG-S1G	2.09	1.95	1.90

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	5101	AGS	PB-O3B-PG	-3.64	119.86	133.17
3	A	5101	AGS	PB-O3B-PG	-3.64	119.86	133.17
3	B	5101	AGS	PB-O3B-PG	-3.64	119.86	133.17
3	C	5101	AGS	PB-O3B-PG	-3.64	119.86	133.17
3	C	5101	AGS	O5'-C5'-C4'	3.12	119.63	108.99

There are no chirality outliers.

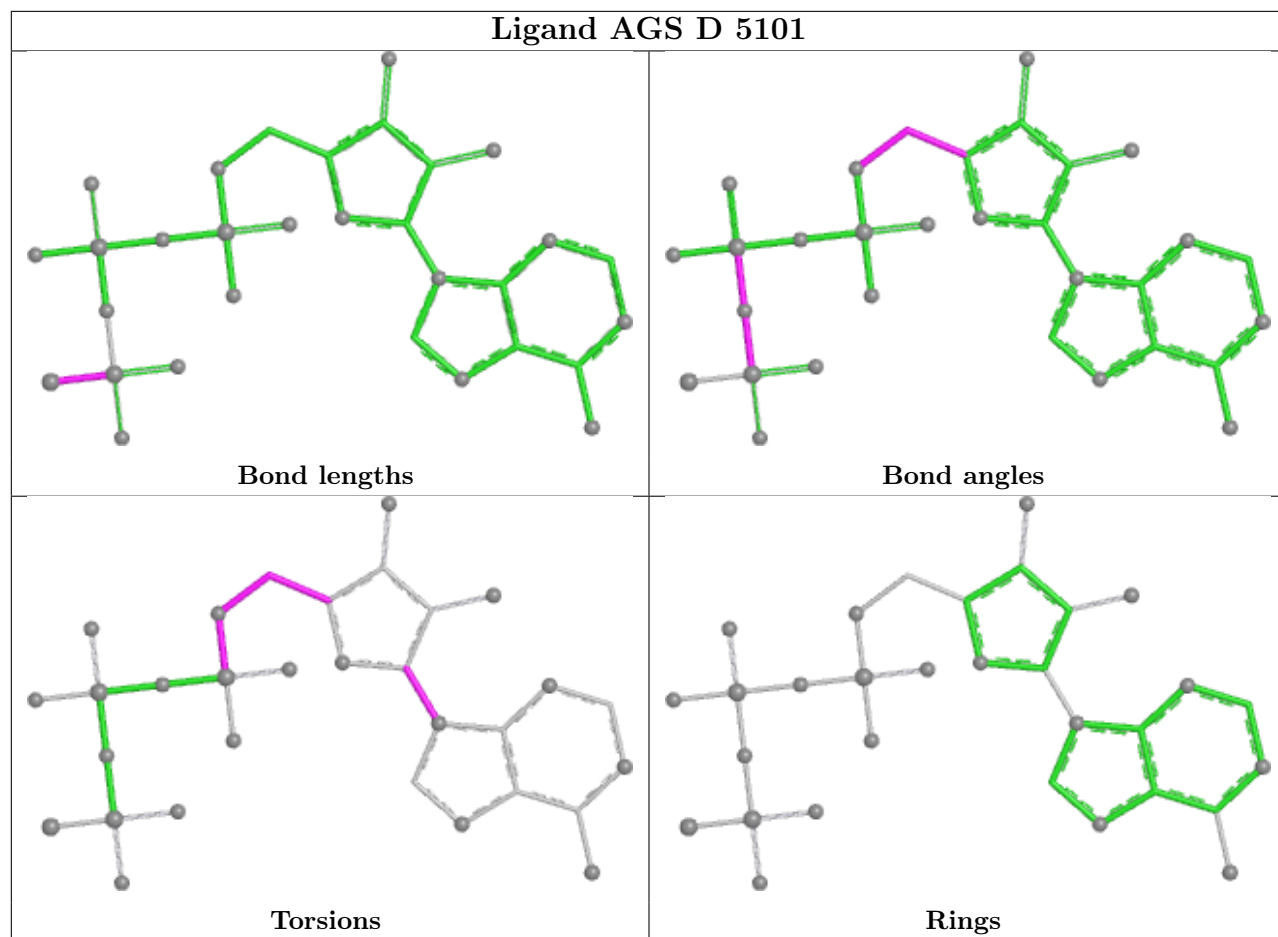
5 of 28 torsion outliers are listed below:

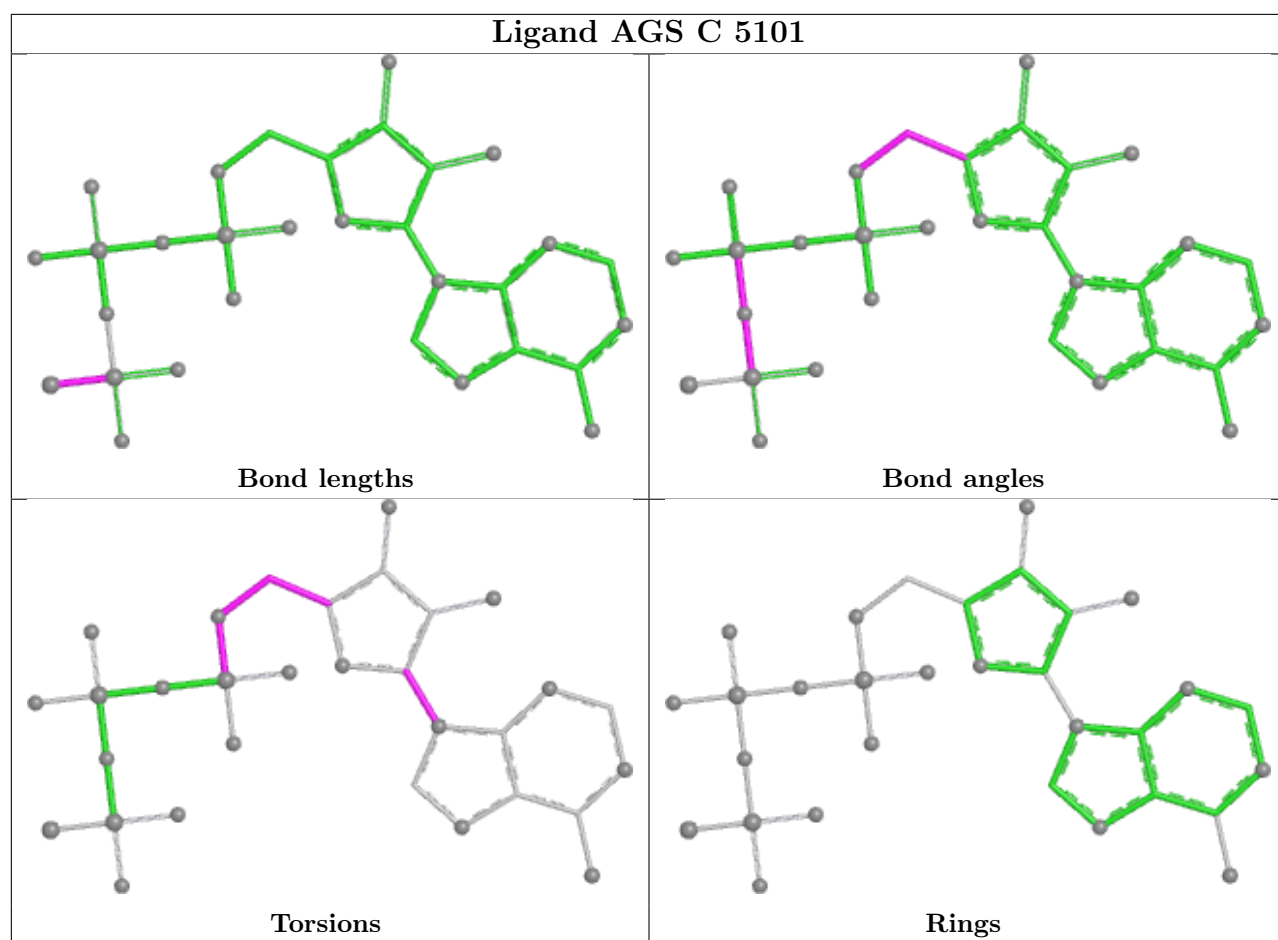
Mol	Chain	Res	Type	Atoms
3	A	5101	AGS	C5'-O5'-PA-O3A
3	A	5101	AGS	C4'-C5'-O5'-PA
3	A	5101	AGS	O4'-C4'-C5'-O5'
3	B	5101	AGS	C5'-O5'-PA-O3A
3	B	5101	AGS	C4'-C5'-O5'-PA

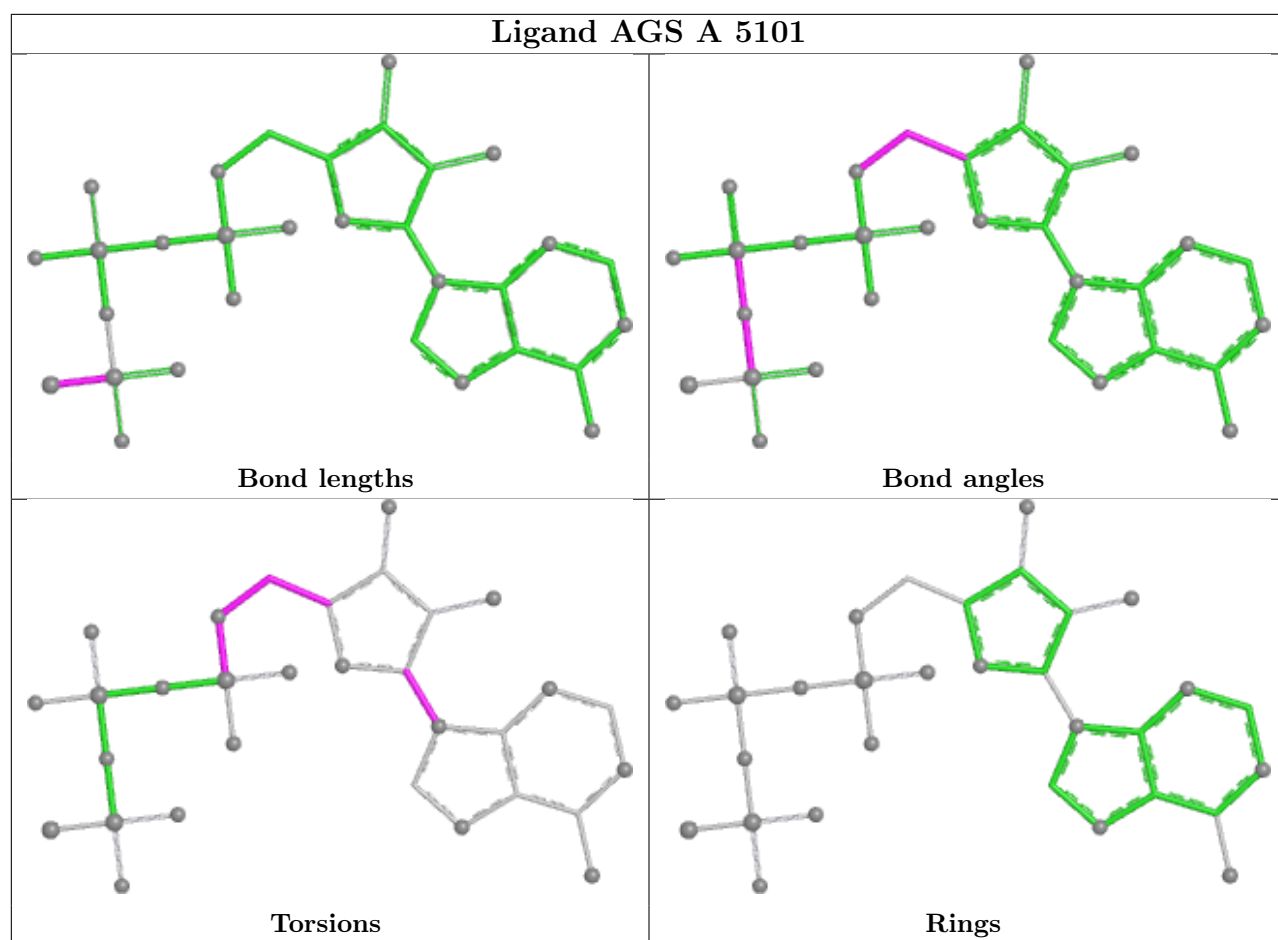
There are no ring outliers.

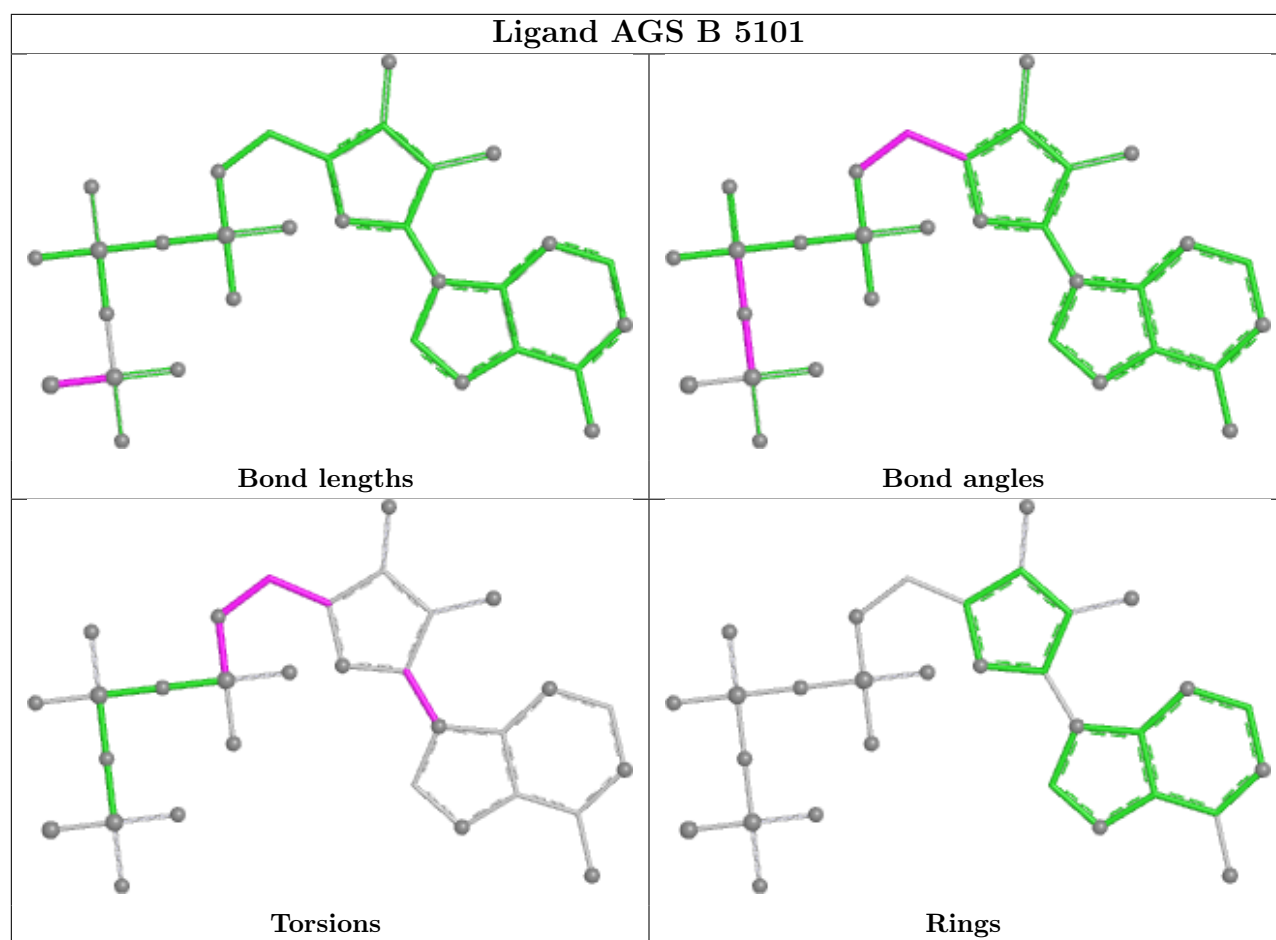
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









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.

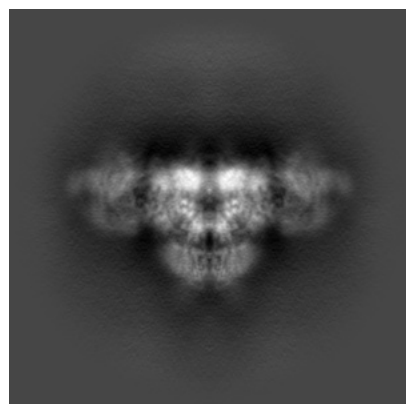
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40423. These allow visual inspection of the internal detail of the map and identification of artifacts.

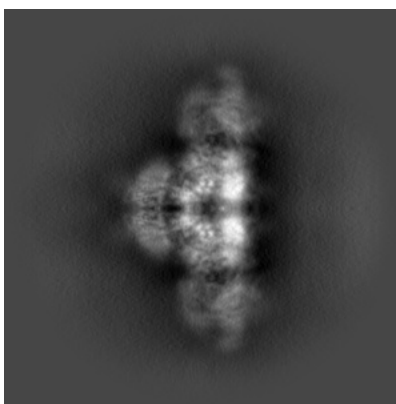
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

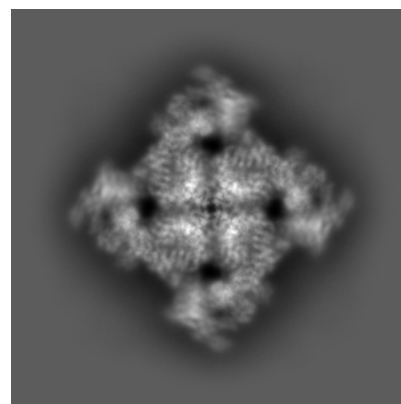
6.1.1 Primary map



X

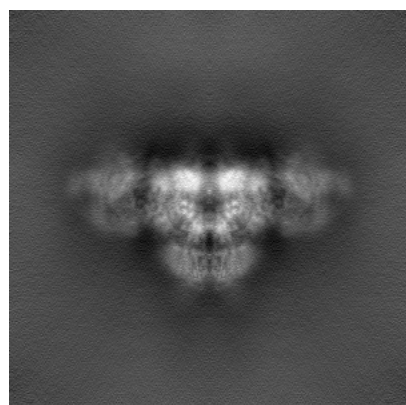


Y

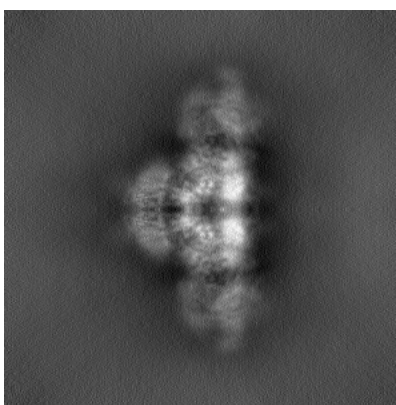


Z

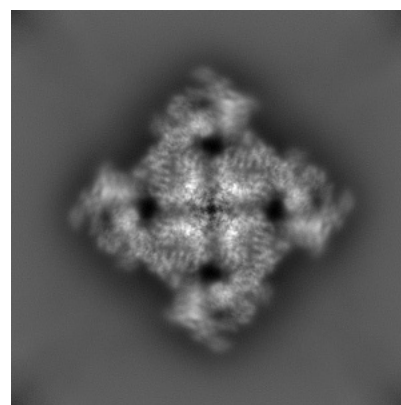
6.1.2 Raw map



X



Y

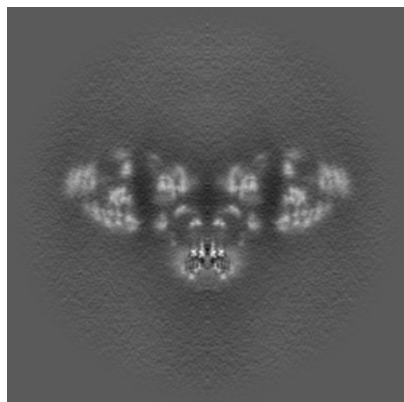


Z

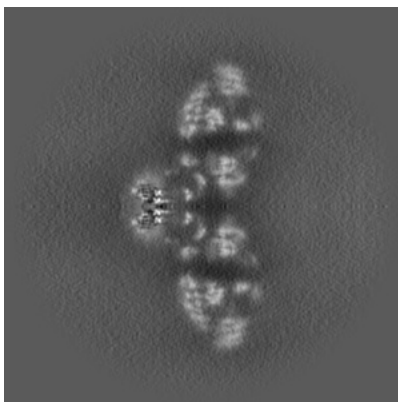
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

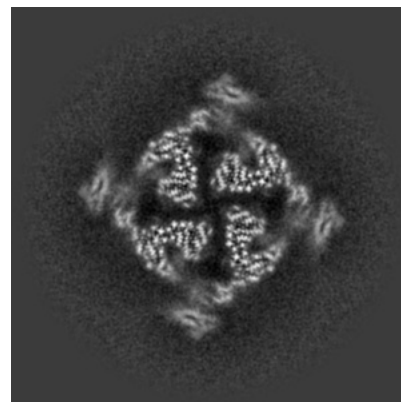
6.2.1 Primary map



X Index: 200

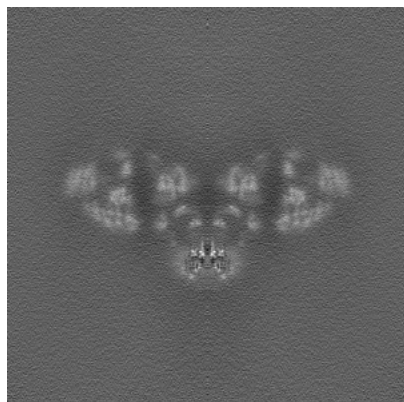


Y Index: 200

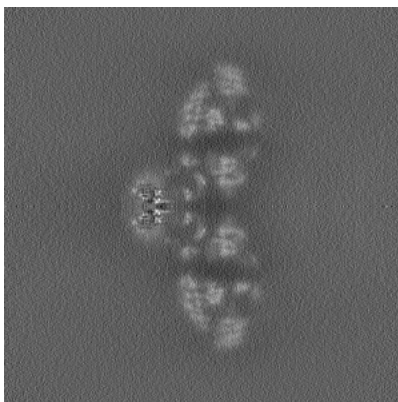


Z Index: 200

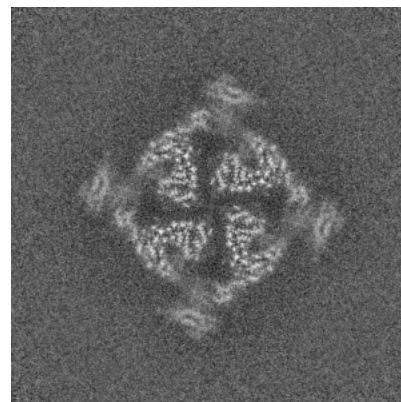
6.2.2 Raw map



X Index: 200



Y Index: 200

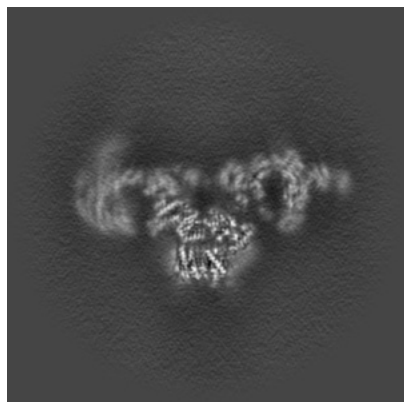


Z Index: 200

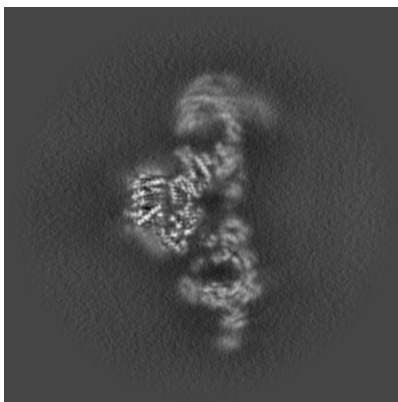
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

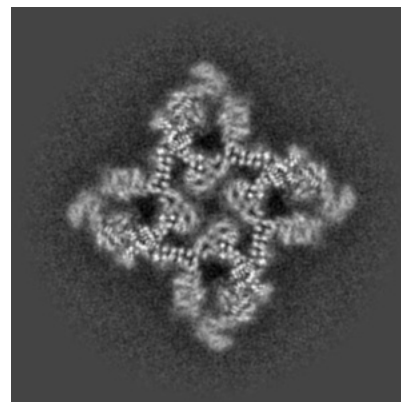
6.3.1 Primary map



X Index: 186

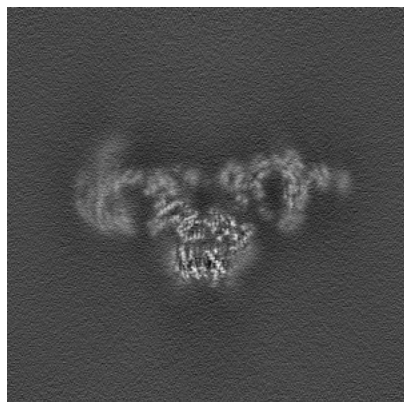


Y Index: 186

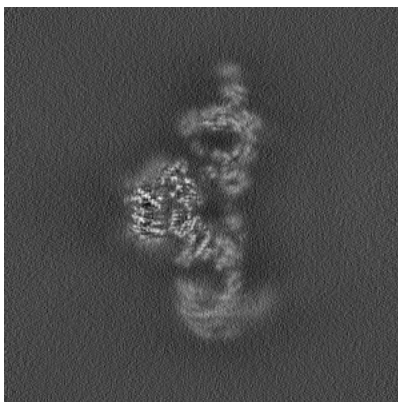


Z Index: 225

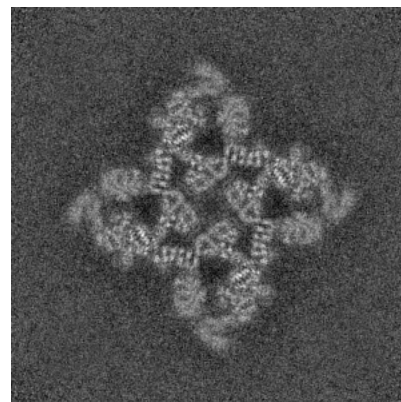
6.3.2 Raw map



X Index: 186



Y Index: 214

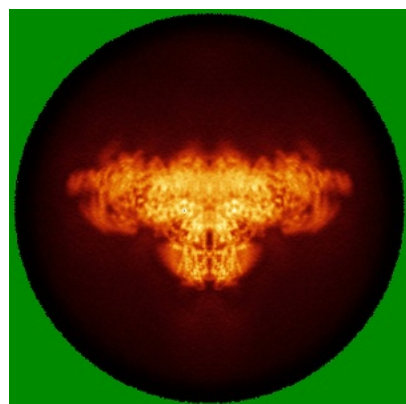


Z Index: 223

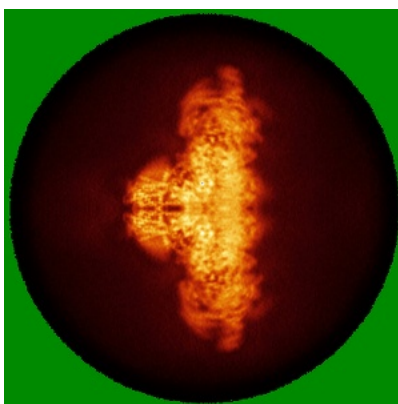
The images above show the largest variance slices of the map in three orthogonal directions.

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

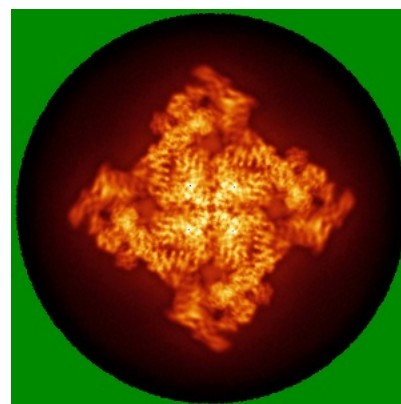
6.4.1 Primary map



X

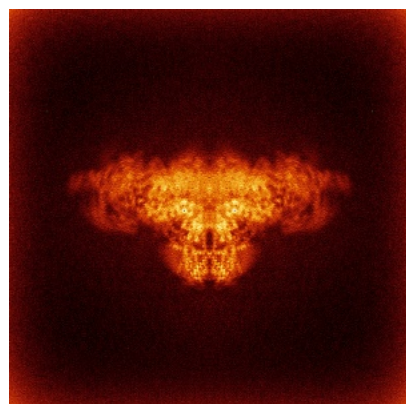


Y

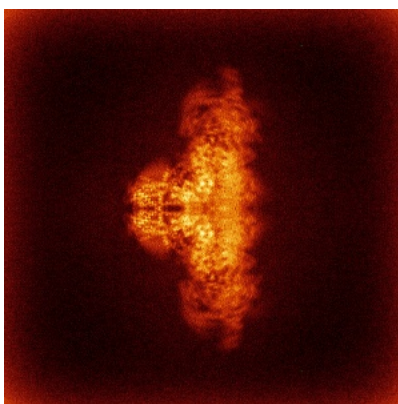


Z

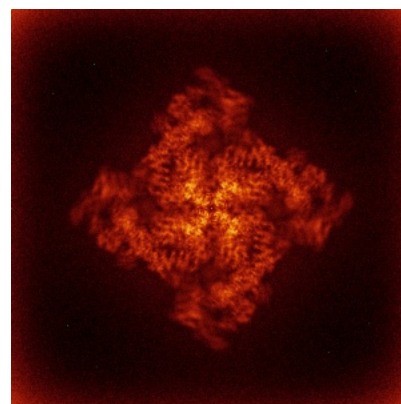
6.4.2 Raw map



X



Y

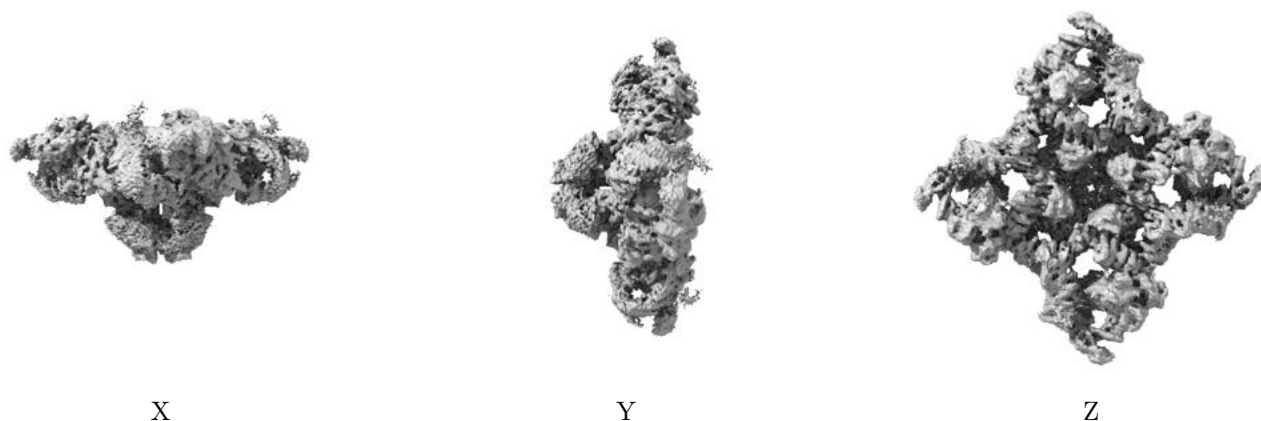


Z

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 0.287. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

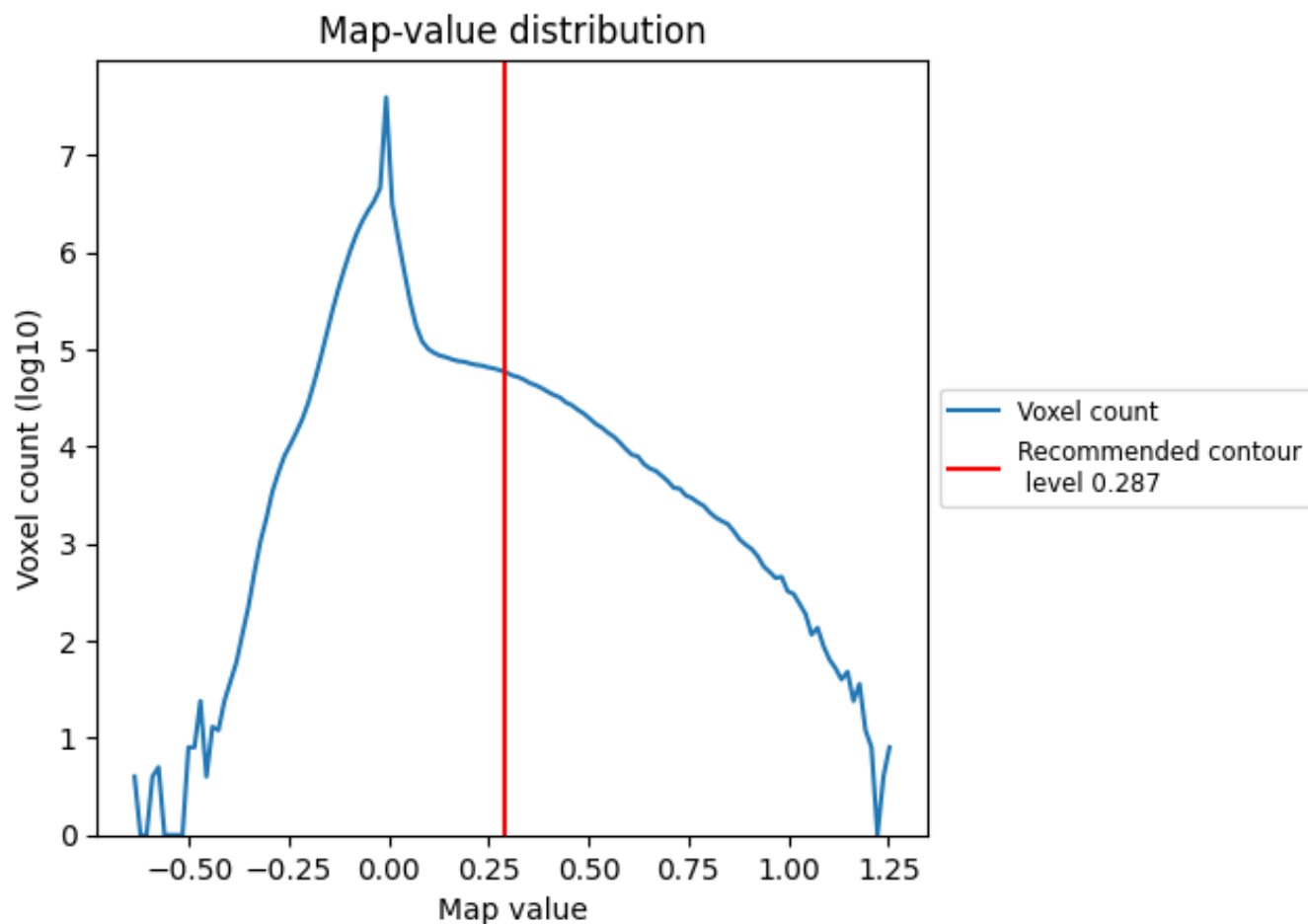
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

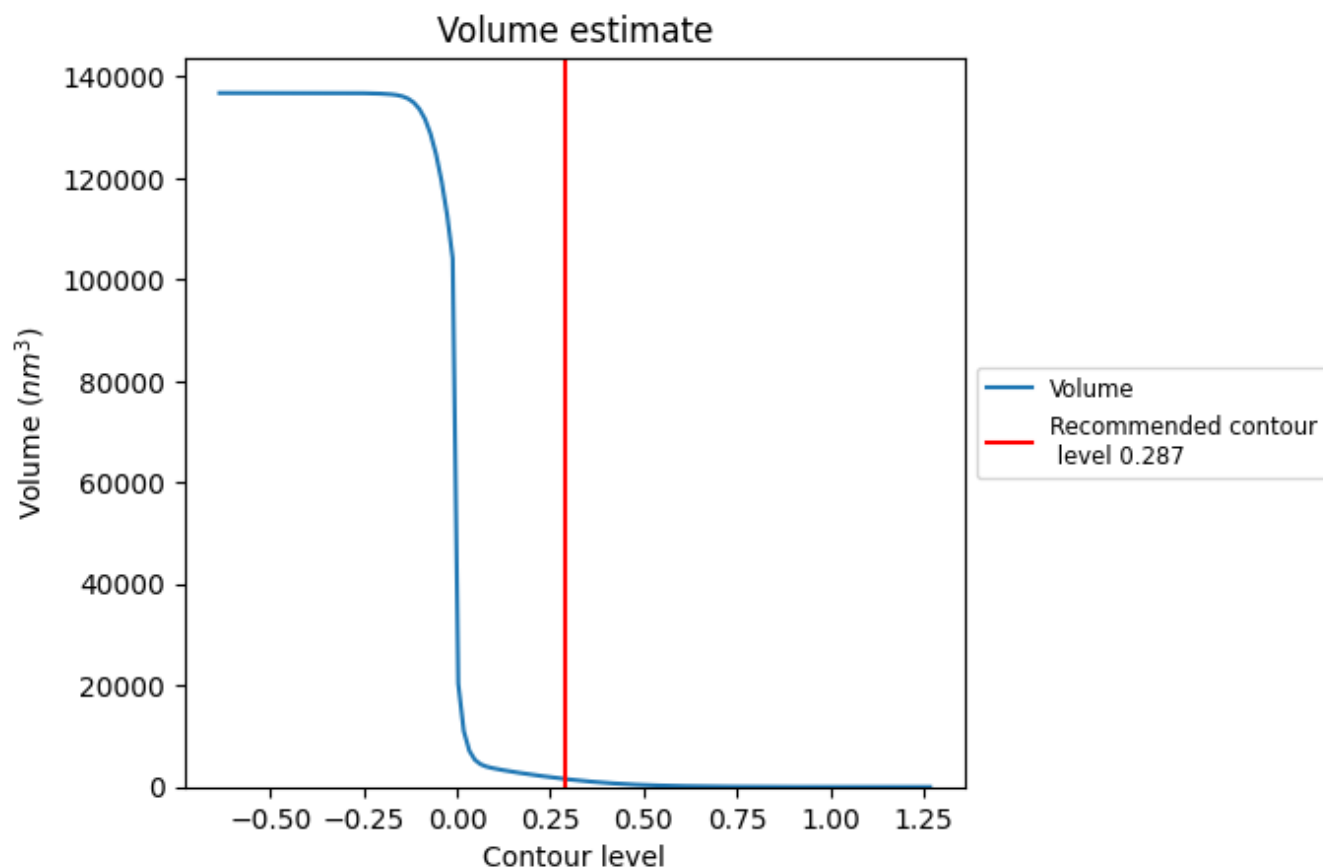
This section contains the results of statistical analysis of the map.

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.

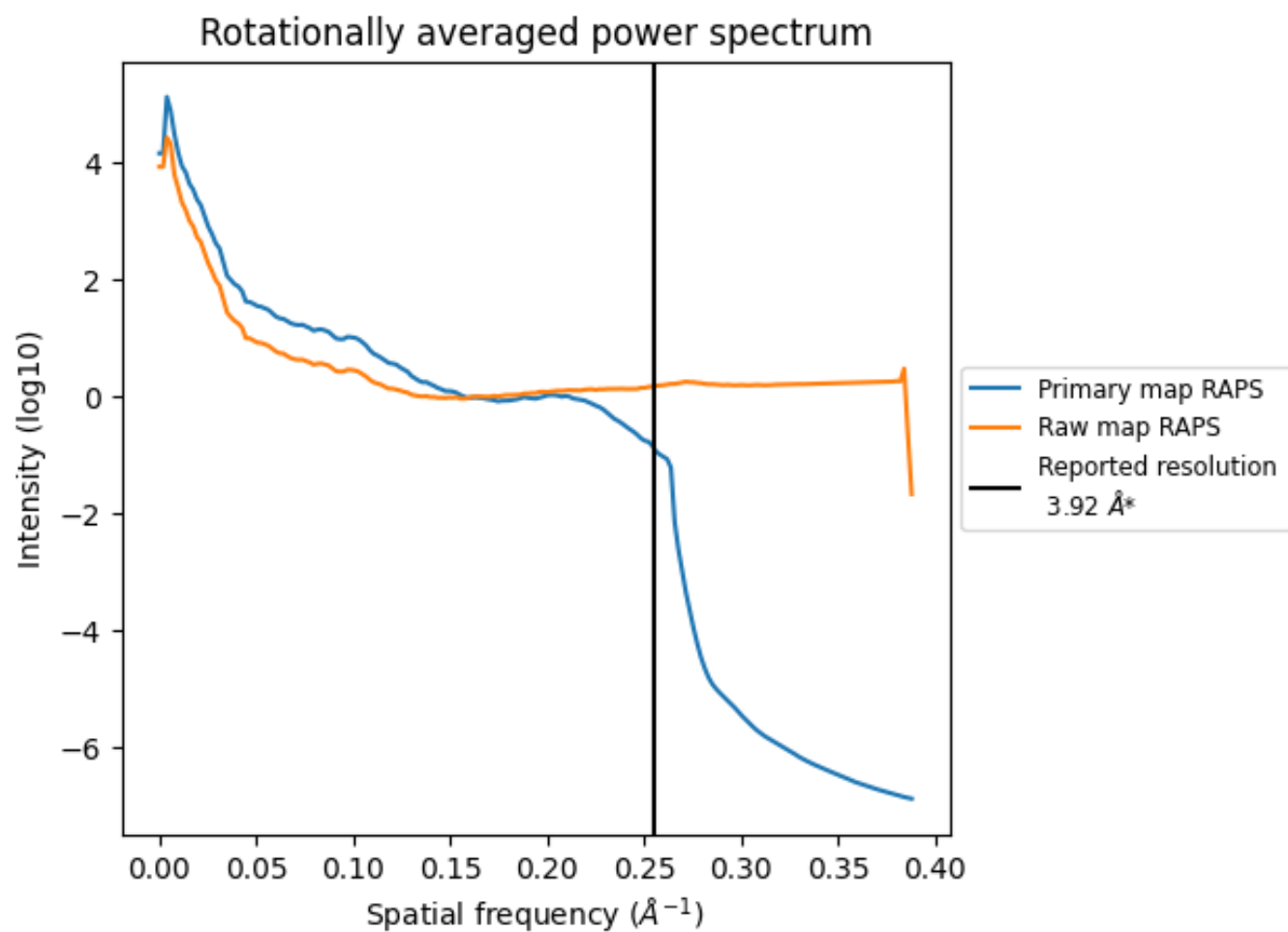
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1594 nm³; this corresponds to an approximate mass of 1440 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 ⓘ

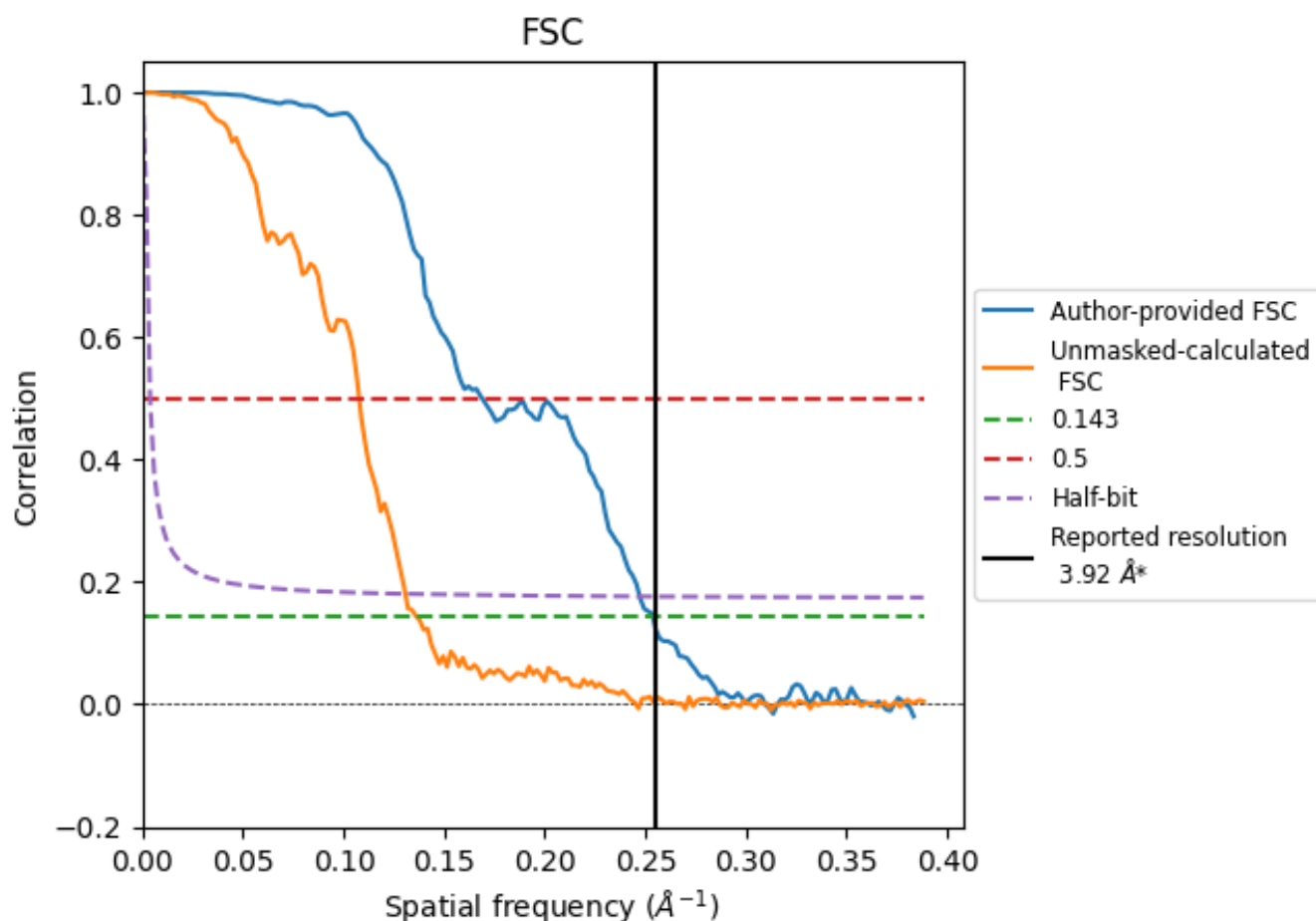


*Reported resolution corresponds to spatial frequency of 0.255 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.255 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.92	-	-
Author-provided FSC curve	3.94	5.92	4.05
Unmasked-calculated*	7.34	9.29	7.65

*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 7.34 differs from the reported value 3.92 by more than 10 %

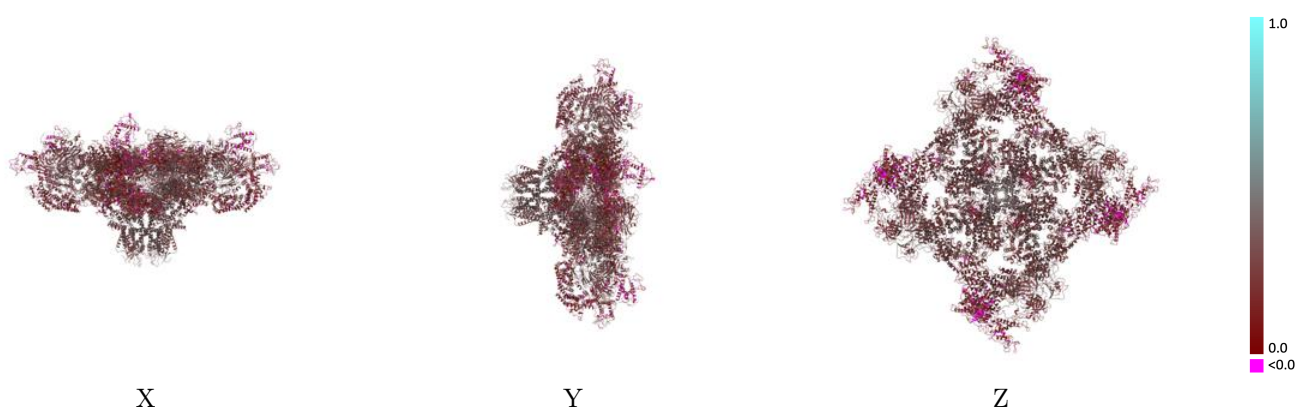
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40423 and PDB model 8SEO. Per-residue inclusion information can be found in section 3 on page 9.

9.1 Map-model overlay [i](#)

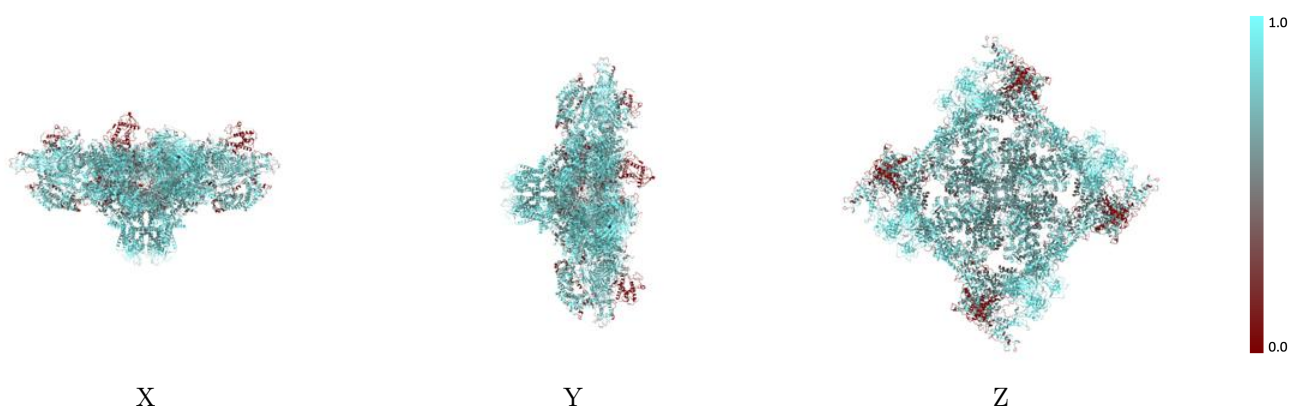
This section was not generated.

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



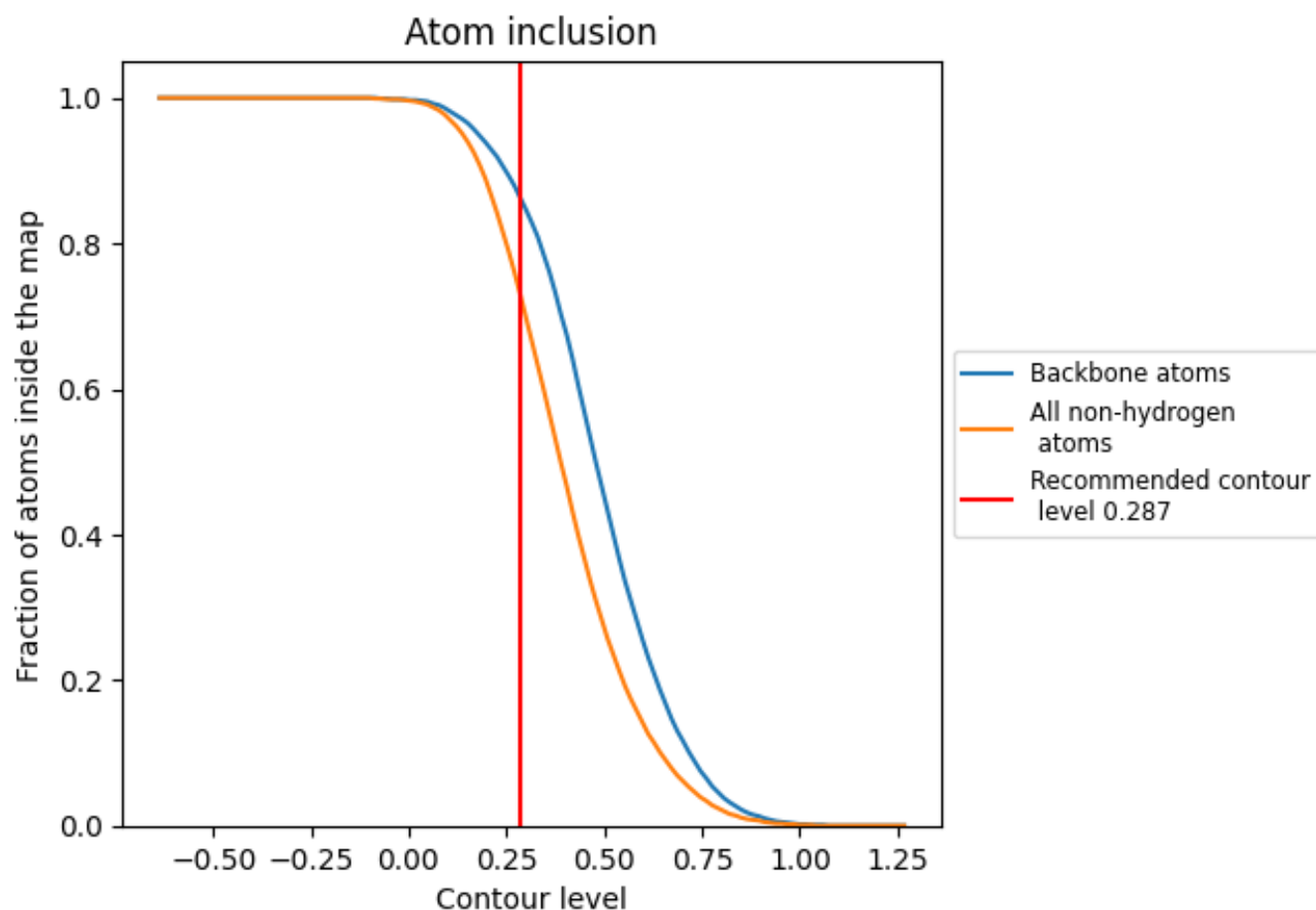
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.287).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% 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 (0.287) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7270	0.2530
A	0.7230	0.2520
B	0.7230	0.2530
C	0.7230	0.2520
D	0.7230	0.2520
E	0.8870	0.3060
F	0.8870	0.3060
G	0.8870	0.3060
H	0.8870	0.3080

1.0

0.0

<0.0