



## wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 08:41 AM UTC

PDB ID : 8SER / pdb\_00008ser  
EMDB ID : EMD-40426  
Title : Cryo-EM Structure of RyR1 + Adenosine  
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 : 3.42 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

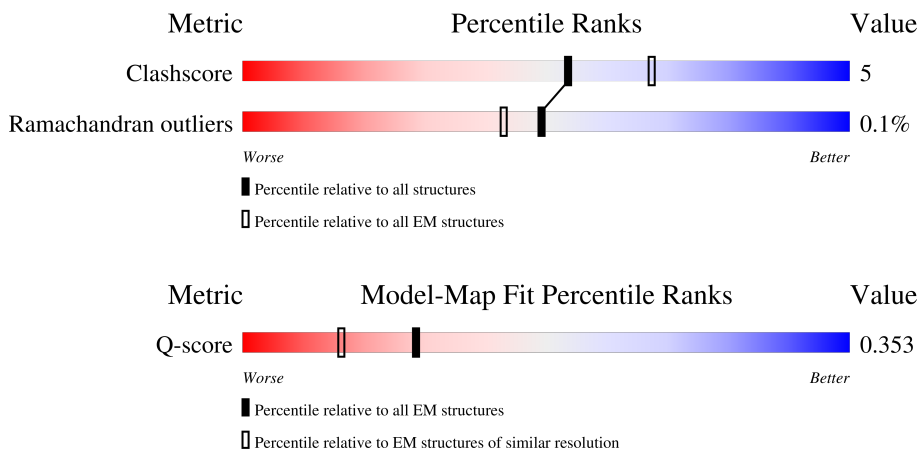
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01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

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

The reported resolution of this entry is 3.42 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	-
Q-score	-	25397	13959 ( 2.92 - 3.92 )

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

Mol	Chain	Length	Quality of chain
1	A	5037	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, red 12%, orange 12%, yellow 12%, green 75%, grey 13%);"></span> 12% 75% 12% 13%
1	B	5037	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, red 12%, orange 12%, yellow 12%, green 75%, grey 13%);"></span> 12% 75% 12% 13%
1	C	5037	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, red 13%, orange 12%, yellow 12%, green 74%, grey 13%);"></span> 13% 74% 12% 13%
1	D	5037	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, red 12%, orange 12%, yellow 12%, green 75%, grey 13%);"></span> 12% 75% 12% 13%
2	E	350	<span style="display: inline-block; width: 100%; height: 15px; background: linear-gradient(to right, green 26%, yellow 5%, grey 69%);"></span> 26% 5% 69%

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Mol	Chain	Length	Quality of chain			
2	F	350		26%	5%	69%
2	G	350		26%	5%	69%
2	H	350		26%	5%	69%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 142952 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
			Total	C	N	O	S		
1	A	4376	34900	22201	6022	6441	236	9	0
1	B	4376	34900	22201	6022	6441	236	9	0
1	C	4376	34900	22201	6022	6441	236	9	0
1	D	4376	34900	22201	6022	6441	236	9	0

- 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
			Total	C	N	O	S		
2	E	107	818	516	144	154	4	0	0
2	F	107	818	516	144	154	4	0	0
2	G	107	818	516	144	154	4	0	0
2	H	107	818	516	144	154	4	0	0

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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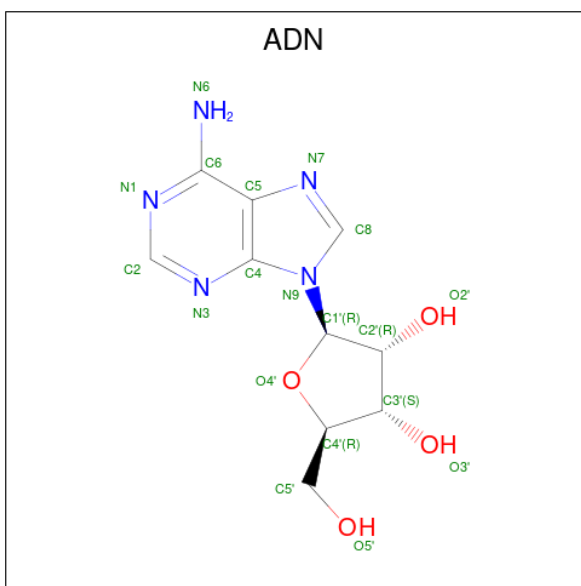
Chain	Residue	Modelled	Actual	Comment	Reference
G	-242	MET	-	expression tag	UNP P08515
G	-241	LYS	-	expression tag	UNP P08515
G	-240	SER	-	expression tag	UNP P08515
G	-239	SER	-	expression tag	UNP P08515
G	-238	HIS	-	expression tag	UNP P08515
G	-237	HIS	-	expression tag	UNP P08515
G	-236	HIS	-	expression 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 ADENOSINE (CCD ID: ADN) (formula:  $C_{10}H_{13}N_5O_4$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
3	A	1	Total	C	N	O	0
			19	10	5	4	
3	B	1	Total	C	N	O	0
			19	10	5	4	
3	C	1	Total	C	N	O	0
			19	10	5	4	
3	D	1	Total	C	N	O	0
			19	10	5	4	

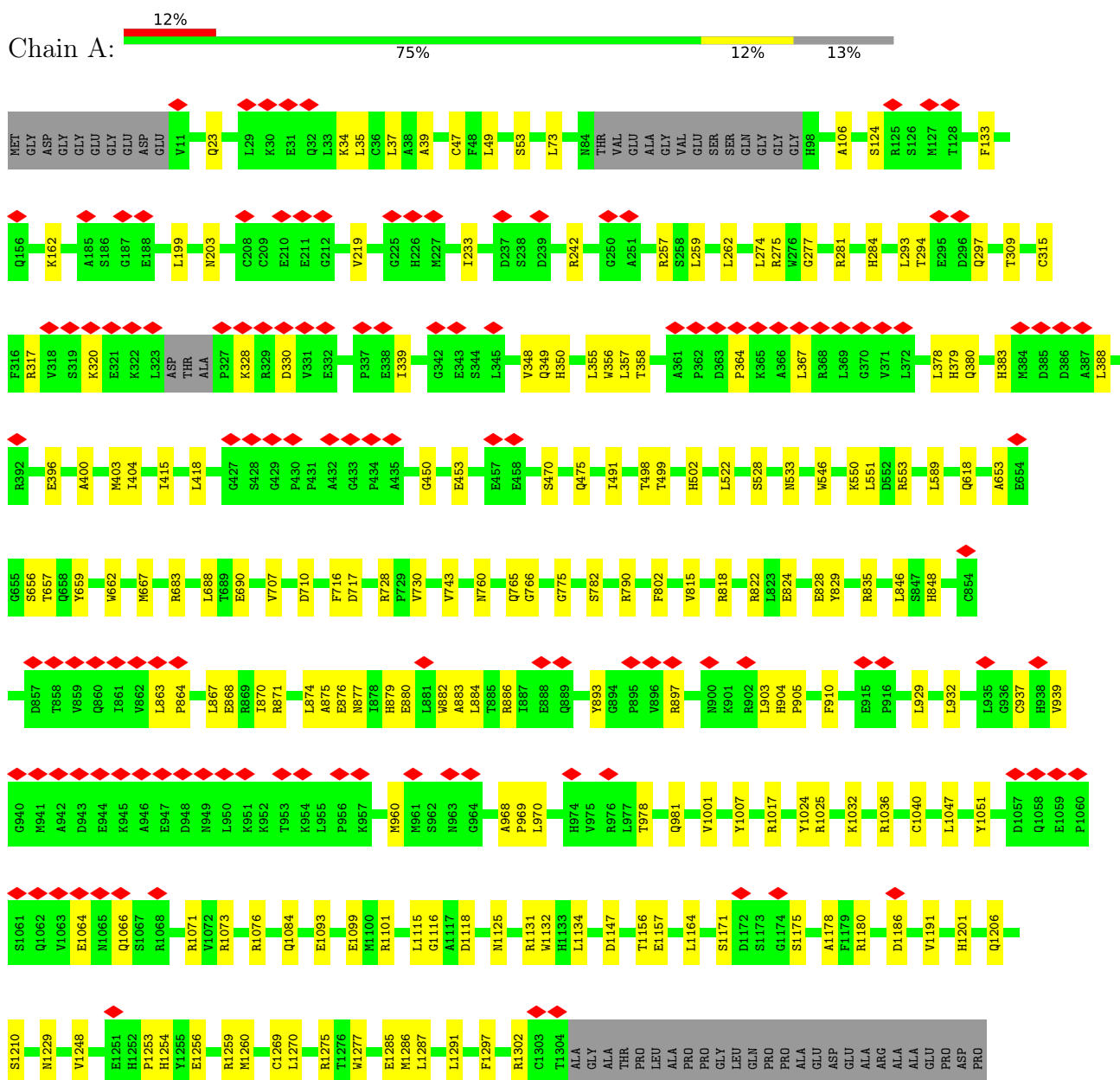
- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
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





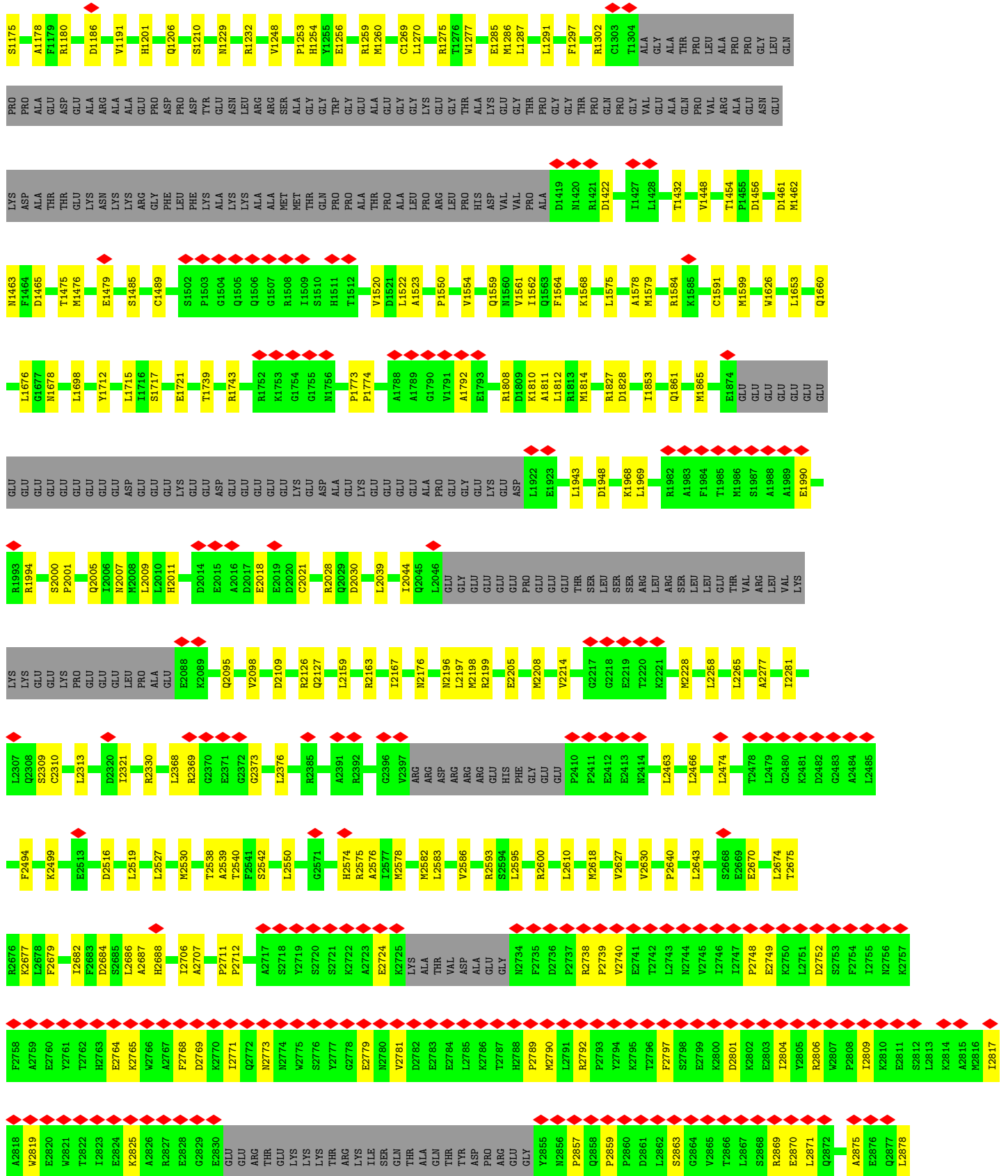






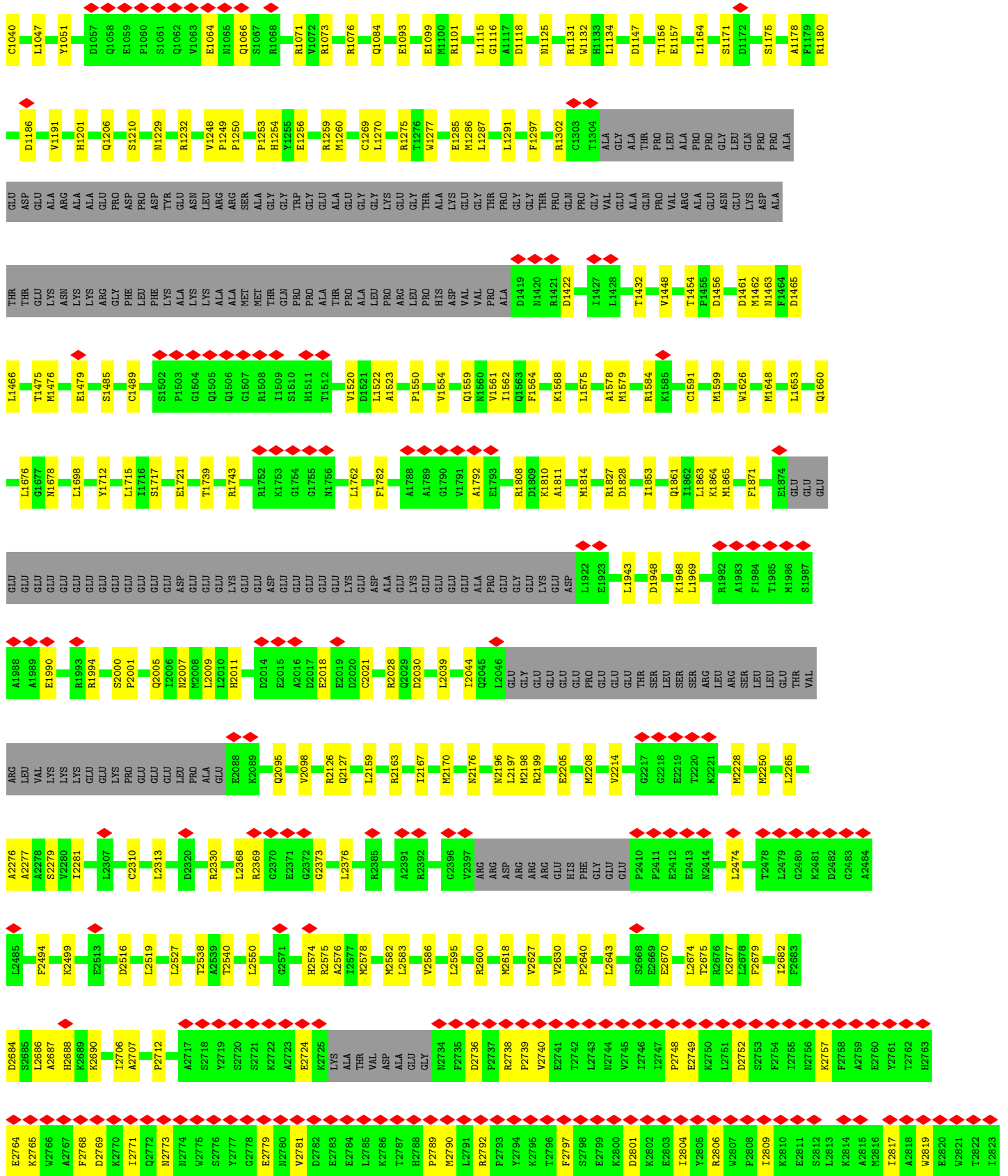
LEU	ALA	LEU	GLU	F4110	R3769	K3623	M3523	Y3409	P3292	S3171	L3075	G2889
ALA	ARG	L3622	ALA	L3770	M3524	L3623	M3524	R3414	P3293	N3180	R3078	G2900
GLY	ARG	L3624	ASP	H3771	I3533	S3625	I3533	R3450	P3294	E2978	A2979	T2901
MET	THR	S3626	ASP	R3773	T3538	K3627	T3538	M3081	A2980	V2980	V2980	H2902
ASP	ALA	K3628	ASP	G3788	A3541	Q3627	A3541	E3086	V2981	S2982	S2982	P2903
PRO	ALA	R3629	ASP	K3823	L3542	R3628	L3542	I3087	S2983	S2983	I3087	L2904
THR	ALA	R3630	ASP	L3835	K3543	R3629	K3543	V3088	G2984	G2984	V3088	L2905
SER	ALA	R3631	ASP	S3840	T3545	R3630	T3545	L3092	P2907	P2907	L3092	V2906
GLU	ALA	V3632	ASP	G3857	D3546	R3631	D3546	D3102	R2908	R2908	D3102	P2907
GLU	ALA	V3633	ASP	M3858	E3547	R3632	E3547	I3103	D2909	D2909	I3103	H2910
GLU	ALA	A3634	ASP	V3859	E3548	V3633	E3548	M3106	T2911	T2911	M3106	L2911
GLU	ALA	C3635	ASP	N3860	E3549	A3634	E3549	V3107	S2983	S2983	V3107	T2912
GLU	ALA	F3636	ASP	N3861	E3550	C3635	E3550	G3216	G2984	G2984	G3216	A2913
GLU	ALA	R3637	ASP	E3862	N3555	F3636	N3555	S3217	R2985	R2985	S3217	K2914
ALA	ALA	A3659	ASP	D3862	M3556	R3637	M3556	G3218	V2986	V2986	G3218	E2992
ALA	ALA	L3663	ASP	T3864	L3557	A3659	L3557	T3221	E2987	E2987	T3221	K2915
ALA	ALA	G3661	ASP	V3865	H3558	L3663	H3558	K3222	K2988	K2988	K3222	T2912
ALA	ALA	E3682	ASP	I3866	Q3560	L3663	Q3560	S3222	P2990	P2990	S3222	A2913
ALA	ALA	Q3683	ASP	I3867	G3561	L3663	G3561	P3224	H2991	H2991	P3224	K2914
THR	ALA	R3684	ASP	R3868	K3562	L3663	K3562	R3225	E2992	E2992	R3225	K2914
VAL	ALA	E3684	ASP	R3869	V3563	L3663	V3563	R3226	Q2992	Q2992	R3226	E2911
ALA	ALA	E3685	ASP	N3870	E3564	L3663	E3564	A3228	K2922	K2922	A3228	K2916
ALA	ALA	E3686	ASP	M3875	E3565	L3663	E3565	I3229	K2923	K2923	I3229	A2917
ALA	ALA	E3687	ASP	M3876	L3579	L3663	L3579	L3230	Q2924	Q2924	L3230	E2925
ALA	ALA	E3688	ASP	D3877	P3580	L3663	P3580	G3231	E2925	E2925	G3231	E2925
ALA	ALA	E3689	ASP	D3877	G3581	L3663	G3581	L3232	L2926	L2926	L3232	E2925
ALA	ALA	F3680	ASP	F3880	R3582	L3663	R3582	P3233	L2926	L2926	P3233	E2925
ALA	ALA	Q3689	ASP	Q3889	E3583	L3663	E3583	R3234	L2927	L2927	R3234	E2925
ALA	ALA	L3924	ASP	L3924	E3584	L3663	E3584	S2236	K2928	K2928	S2236	E2925
ALA	ALA	K3940	ASP	K3940	E3585	L3663	E3585	M3239	F2929	F2929	M3239	E2925
ALA	ALA	D3941	ASP	D3941	E3586	L3663	E3586	V3245	L2930	L2930	V3245	E2925
ALA	ALA	K3948	ASP	K3948	D3587	L3663	D3587	R3248	Q2924	Q2924	R3248	E2925
ALA	ALA	K3959	ASP	K3959	E3688	L3663	E3688	G3260	E2925	E2925	G3260	E2925
ALA	ALA	E3967	ASP	E3967	G3588	L3663	G3588	A3261	E2925	E2925	A3261	E2925
ALA	ALA	Y3968	ASP	Y3968	R3589	L3663	R3589	T3264	E2925	E2925	T3264	E2925
ALA	ALA	L3969	ASP	L3969	E3690	L3663	E3690	E3265	E2925	E2925	E3265	E2925
ALA	ALA	D4098	ASP	D4098	E3691	L3663	E3691	M3266	E2925	E2925	M3266	E2925
ALA	ALA	S4099	ASP	S4099	E3692	L3663	E3692	V3269	E2925	E2925	V3269	E2925
ALA	ALA	Q4100	ASP	Q4100	P3695	L3663	P3695	T3270	E2925	E2925	T3270	E2925
ALA	ALA	K4101	ASP	K4101	D3696	L3663	D3696	E3271	E2925	E2925	E3271	E2925
ALA	ALA	Q4102	ASP	Q4102	Q3700	L3663	Q3700	T3272	E2925	E2925	T3272	E2925
ALA	ALA	F4103	ASP	F4103	K3713	L3663	K3713	T3273	E2925	E2925	T3273	E2925
ALA	ALA	G4105	ASP	G4105	E3736	L3663	E3736	G3274	E2925	E2925	G3274	E2925
ALA	ALA	P4106	ASP	P4106	GLU	L3663	GLU	L3275	E2925	E2925	L3275	E2925
ALA	ALA	E4107	ASP	E4107	GLY	L3663	GLY	M3276	E2925	E2925	M3276	E2925
ALA	ALA	T4108	ASP	T4108	ASN	L3663	ASN	G3288	E2925	E2925	G3288	E2925
ALA	ALA	P4254	ASP	P4254	R3498	L3663	R3498	L3168	E2925	E2925	L3168	E2925
ALA	ALA	GLU	ASP	GLU	E3610	L3663	E3610	R3167	E2925	E2925	R3167	E2925
ALA	ALA	GLU	ASP	GLU	H3611	L3663	H3611	T3168	E2925	E2925	T3168	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	G3068	E2925	E2925	G3068	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	T3069	E2925	E2925	T3069	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	P3062	E2925	E2925	P3062	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	V3065	E2925	E2925	V3065	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	L3068	E2925	E2925	L3068	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	L2963	E2925	E2925	L2963	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	K2967	E2925	E2925	K2967	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	S2970	E2925	E2925	S2970	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	Q2971	E2925	E2925	Q2971	E2925
ALA	ALA	PRO	ASP	PRO	GLY	L3663	GLY	E2972	E2925	E2925	E2972	E2925



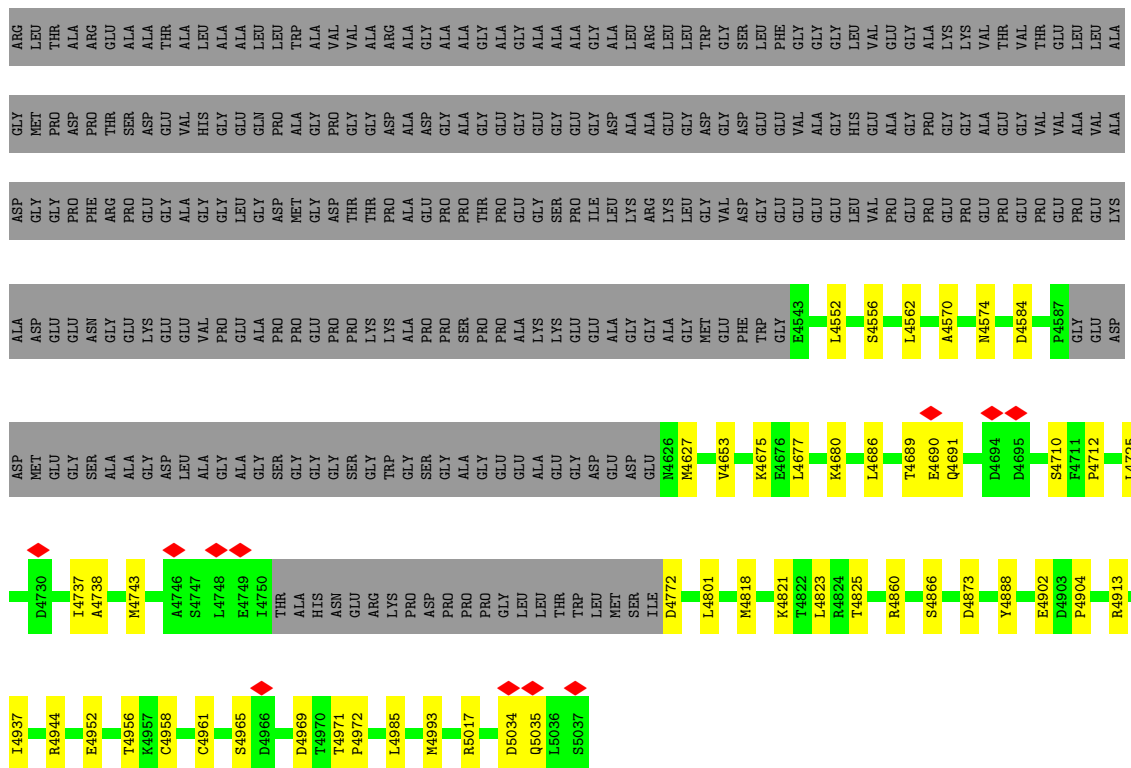


ALA	K4214	D4092	S3600	THR	E3382	E3665	H3146	K3036	GLY	E2879
ARG	E4224	F4093	A3601	LYS	A3383	M3266	D3154	LEU	LEU	E2880
LEU	G4225	Q4094	V3602	LYS	K3384	V3269	I3157	ASP	ASP	I2881
ARG	G4226	K4095	H3605	R3498	A3385	E3271	L3158	MET	MET	H2882
GLY	G4227	A4096	E3610	R3499	A3386	I3272	D3159	GLY	GLY	H2883
LEU	E4228	M4097	H3611	G3500	A3387	I3273	D3160	LEU	LEU	H2884
SER	A4228	I3968	H3612	G3501	A3388	L3274	V3161	LEU	LEU	T2885
TYR	E4232	T3974	F3613	R3502	E3389	M3276	Q3162	LEU	LEU	H2886
ARG	E4232	Q3578	K3614	Y3503	G3390	E3286	G3058	LEU	LEU	G2887
LEU	I4242	S3979	S3615	Q3506	E3391	R3287	T3059	LEU	LEU	R2888
ARG	E4253	L3980	K3616	I3510	L3392	G3288	R3167	LEU	LEU	R2889
VAL	P4254	A3617	A3618	L3514	R3403	P3292	T3168	LEU	LEU	R2890
ARG	GLY	K3618	V3619	M3524	D3404	P3293	S3171	LEU	LEU	R2891
ARG	GLY	R3620	H3621	Y3409	Y3409	P3294	V3065	LEU	LEU	Q2892
LEU	PRO	L3770	H3622	M3533	R3414	A3295	L3068	LEU	LEU	E2893
ARG	GLY	H3771	L3623	I3533	R3414	L3296	L3075	LEU	LEU	L2894
LEU	ALA	R3773	L3624	T3538	H3449	P3297	M3081	LEU	LEU	E2895
LEU	ALA	G3788	L3625	T3538	N3450	A3298	E3086	LEU	LEU	A2896
ALA	GLY	T3797	S3626	A3541	N3450	G3299	F3087	LEU	LEU	R2897
ALA	MET	L3835	K3627	K3542	E3454	A3300	V3088	LEU	LEU	G2899
THR	GLY	L3835	Q3627	K3543	N3457	P3301	V2981	LEU	LEU	G2900
ALA	GLY	D4118	R3628	D3544	Q3461	P3302	S2983	LEU	LEU	T2901
LEU	ALA	E4119	R3629	T3545	N3462	P3303	G2984	LEU	LEU	H2902
ALA	ALA	R3630	R3630	R3546	I3464	L3316	R2985	LEU	LEU	F2903
LEU	ALA	A3631	A3631	E3546	I3464	I3316	L2904	LEU	LEU	L2904
LEU	ALA	V3632	E3547	E3548	I3464	I3322	L2905	LEU	LEU	L2905
LEU	ALA	V3633	M3555	M3555	N3465	N3325	V2906	LEU	LEU	V2906
LEU	ALA	A3634	N3556	N3556	N3466	N3326	F2907	LEU	LEU	F2907
LEU	ALA	F3635	L3557	L3557	H3467	M3326	V2908	LEU	LEU	V2908
LEU	ALA	F3636	F3636	F3636	S3468	I3329	D2909	LEU	LEU	D2909
LEU	ALA	R3637	R3637	R3637	F3469	D3330	T2910	LEU	LEU	T2910
ALA	ALA	A3659	A3659	A3659	L3470	M3335	L2911	LEU	LEU	L2911
ALA	ALA	L3663	L3663	L3663	T3471	K3336	T2912	LEU	LEU	T2912
ALA	ALA	G3681	G3681	G3681	A3472	R3337	A2913	LEU	LEU	A2913
ALA	ALA	E3682	E3682	E3682	D3473	V3346	E2915	LEU	LEU	E2915
ALA	ALA	E3684	E3684	E3684	S3474	L3354	R2916	LEU	LEU	R2916
ALA	ALA	Q3683	Q3683	Q3683	K3475	L3354	A2917	LEU	LEU	A2917
ALA	ALA	E3685	E3685	E3685	K3476	F3368	R2918	LEU	LEU	R2918
ALA	ALA	E3686	E3686	E3686	K3477	R3368	D2919	LEU	LEU	D2919
ALA	ALA	E3687	E3687	E3687	A3478	R3368	R2920	LEU	LEU	R2920
ALA	ALA	E3688	E3688	E3688	L3479	K3371	E2921	LEU	LEU	E2921
ALA	ALA	E3689	E3689	E3689	LYS	E3371	K2922	LEU	LEU	K2922
ALA	ALA	V3690	V3690	V3690	ALA	E3375	A2923	LEU	LEU	A2923
ALA	ALA	E3691	E3691	E3691	GLY	E3376	Q2924	LEU	LEU	Q2924
ALA	ALA	E3692	E3692	E3692	ALA	E3377	E2925	LEU	LEU	E2925
ALA	ALA	K3940	K3940	K3940	GLN	Q3378	L2926	LEU	LEU	L2926
ALA	ALA	D3941	D3941	D3941	GLY	L3379	L2927	LEU	LEU	L2927
ALA	ALA	K4091	K4091	K4091	GLY	R3380	K2928	LEU	LEU	K2928
ALA	ALA	E4196	E4196	E4196	ASP	I3592	F2929	LEU	LEU	F2929
ALA	ALA	E4196	E4196	E4196	GLN	R3595	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	GLU	V3596	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	GLU	Q3700	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	Y3722	E2935	LEU	LEU	E2935
ALA	ALA	E4196	E4196	E4196	ALA	E3736	A2936	LEU	LEU	A2936
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E4196	E4196	E4196	ALA	E3736	E2933	LEU	LEU	E2933
ALA	ALA	E4196	E4196	E4196	ALA	E3736	G2934	LEU	LEU	G2934
ALA	ALA	E4196	E4196	E4196	ALA	E3736	R2939	LEU	LEU	R2939
ALA	ALA	E4196	E4196	E4196	ALA	E3736	L2930	LEU	LEU	L2930
ALA	ALA	E41								

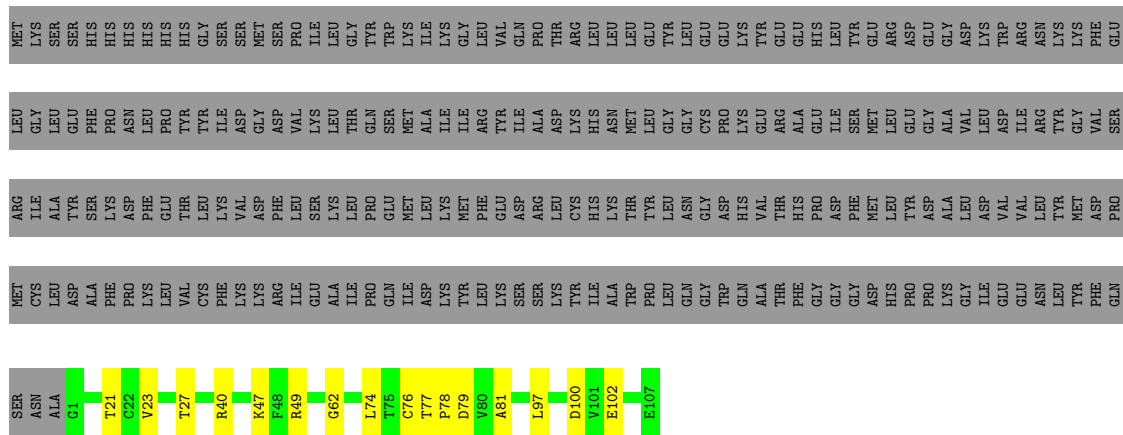




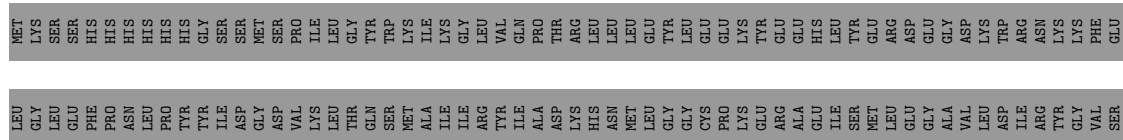




● Molecule 2: Glutathione S-transferase class-mu 26 kDa isozyme,Peptidyl-prolyl cis-trans isomerase FKBP1B



● 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	51504	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	1.346	Depositor
Minimum map value	-0.409	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.073	Depositor
Recommended contour level	0.387	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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADN, 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	0.27	0/35714	0.59	6/48365 (0.0%)
1	B	0.27	0/35714	0.59	6/48365 (0.0%)
1	C	0.27	0/35714	0.59	6/48365 (0.0%)
1	D	0.27	0/35714	0.59	6/48365 (0.0%)
2	E	0.23	0/834	0.53	0/1123
2	F	0.23	0/834	0.53	0/1123
2	G	0.23	0/834	0.53	0/1123
2	H	0.23	0/834	0.53	0/1123
All	All	0.27	0/146192	0.59	24/197952 (0.0%)

There are no bond length outliers.

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4178	LEU	CA-C-N	-8.77	116.13	122.18
1	A	4178	LEU	C-N-CA	-8.77	116.13	122.18
1	C	4178	LEU	CA-C-N	-8.75	116.14	122.18
1	C	4178	LEU	C-N-CA	-8.75	116.14	122.18
1	B	4178	LEU	CA-C-N	-8.73	116.16	122.18

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	34900	0	34530	358	0
1	B	34900	0	34530	363	0
1	C	34900	0	34530	367	0
1	D	34900	0	34530	362	0
2	E	818	0	824	8	0
2	F	818	0	824	9	0
2	G	818	0	824	8	0
2	H	818	0	824	9	0
3	A	19	0	13	0	0
3	B	19	0	13	0	0
3	C	19	0	13	0	0
3	D	19	0	13	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	142952	0	141468	1473	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 5.

The worst 5 of 1473 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:B:1810:LYS:HG2	1:B:1814:MET:HE2	1.72	0.72
1:C:1810:LYS:HG2	1:C:1814:MET:HE2	1.72	0.72
1:D:1810:LYS:HG2	1:D:1814:MET:HE2	1.72	0.72
1:A:1810:LYS:HG2	1:A:1814:MET:HE2	1.72	0.72
1:A:3335:MET:SD	1:A:3403:ARG:NH1	2.64	0.70

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	4353/5037 (86%)	4168 (96%)	182 (4%)	3 (0%)	48	78
1	B	4353/5037 (86%)	4168 (96%)	182 (4%)	3 (0%)	48	78
1	C	4353/5037 (86%)	4167 (96%)	183 (4%)	3 (0%)	48	78
1	D	4353/5037 (86%)	4167 (96%)	183 (4%)	3 (0%)	48	78
2	E	105/350 (30%)	98 (93%)	7 (7%)	0	100	100
2	F	105/350 (30%)	98 (93%)	7 (7%)	0	100	100
2	G	105/350 (30%)	98 (93%)	7 (7%)	0	100	100
2	H	105/350 (30%)	98 (93%)	7 (7%)	0	100	100
All	All	17832/21548 (83%)	17062 (96%)	758 (4%)	12 (0%)	49	78

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3616	LYS
1	A	4712	PRO
1	B	3616	LYS
1	B	4712	PRO
1	C	3616	LYS

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

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

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	ADN	A	5101	-	21,21,21	0.19	0	31,31,31	0.32	0
3	ADN	D	5101	-	21,21,21	0.19	0	31,31,31	0.32	0
3	ADN	B	5101	-	21,21,21	0.19	0	31,31,31	0.32	0
3	ADN	C	5101	-	21,21,21	0.19	0	31,31,31	0.32	0

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	ADN	A	5101	-	-	3/6/22/22	0/3/3/3
3	ADN	D	5101	-	-	3/6/22/22	0/3/3/3
3	ADN	B	5101	-	-	3/6/22/22	0/3/3/3
3	ADN	C	5101	-	-	3/6/22/22	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

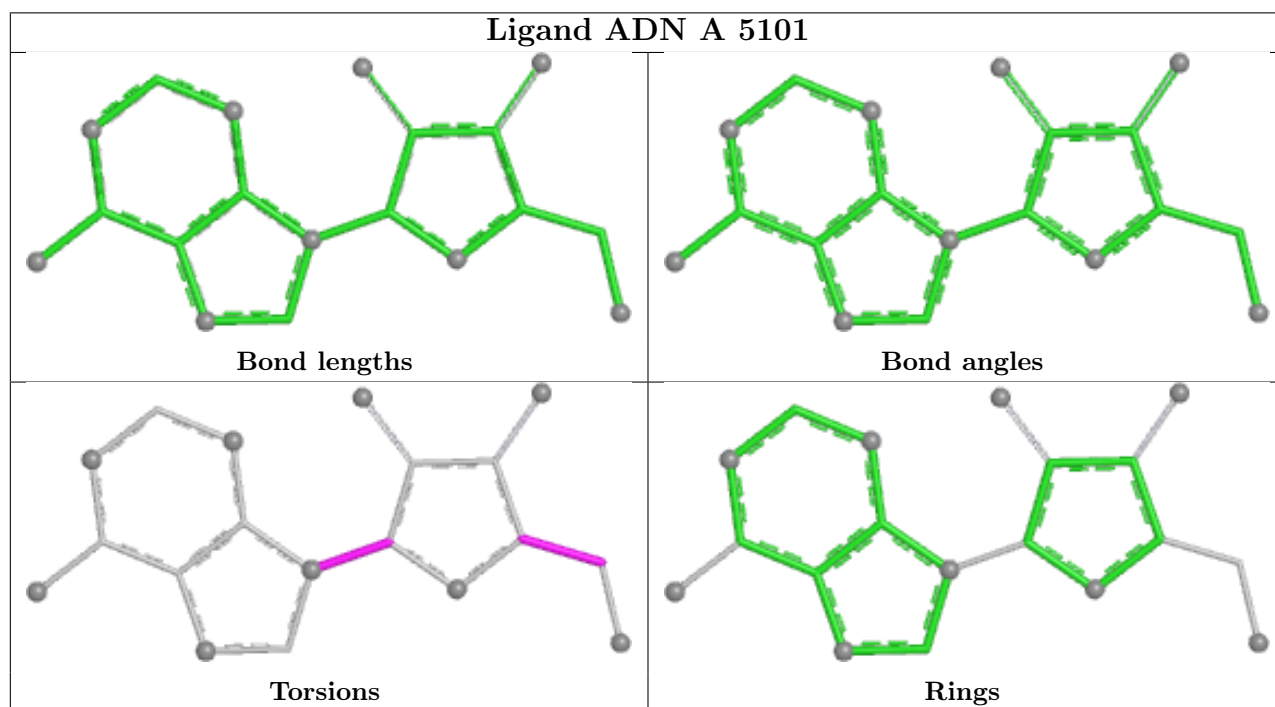
5 of 12 torsion outliers are listed below:

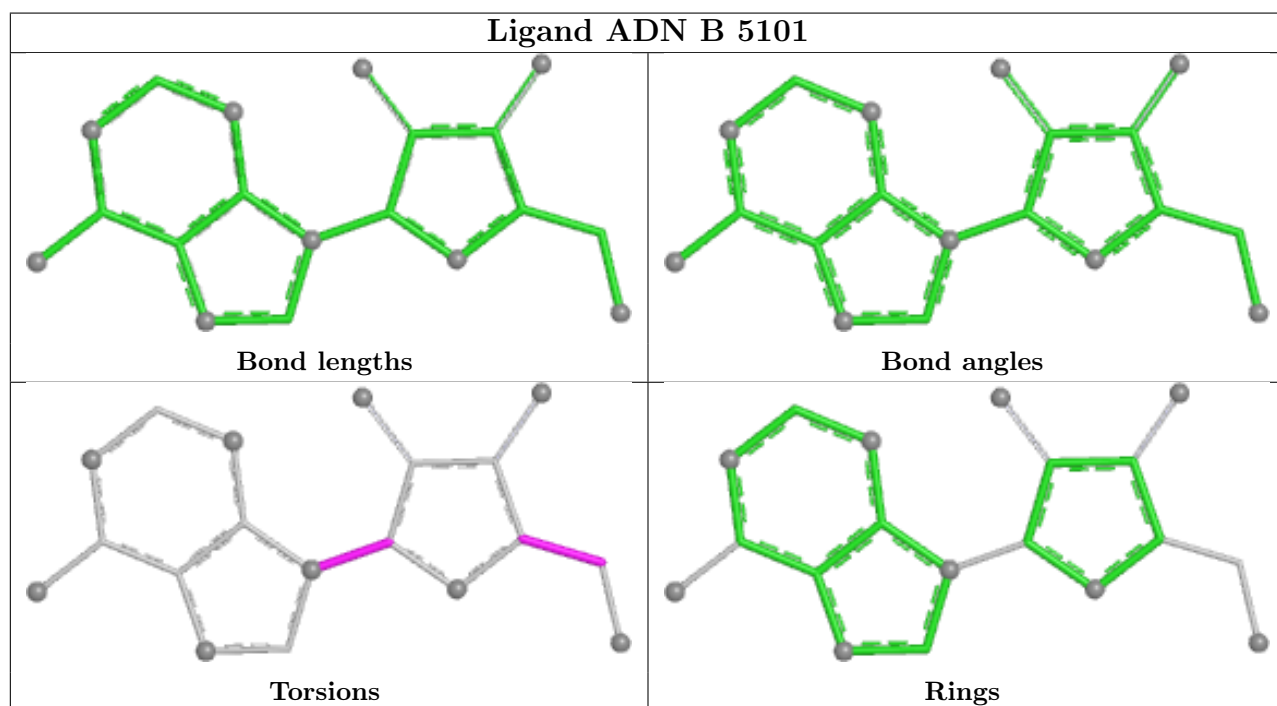
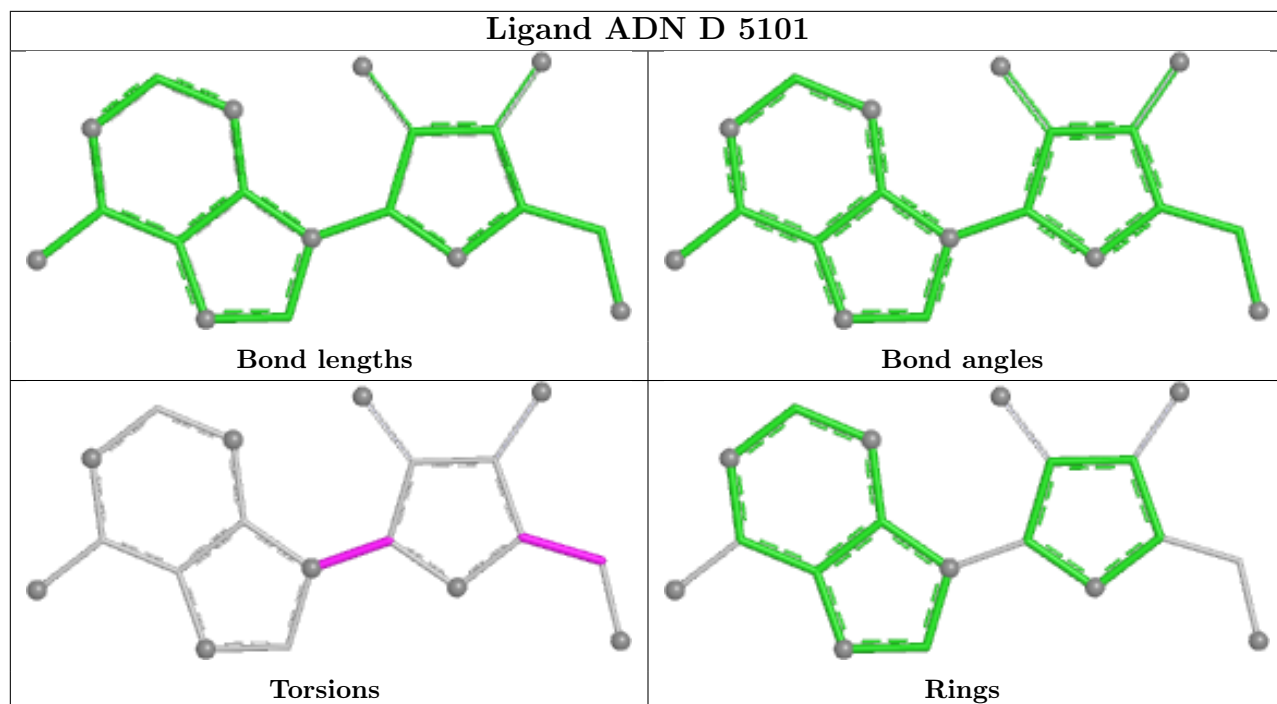
Mol	Chain	Res	Type	Atoms
3	A	5101	ADN	C3'-C4'-C5'-O5'
3	B	5101	ADN	C3'-C4'-C5'-O5'
3	C	5101	ADN	C3'-C4'-C5'-O5'
3	D	5101	ADN	C3'-C4'-C5'-O5'
3	A	5101	ADN	O4'-C4'-C5'-O5'

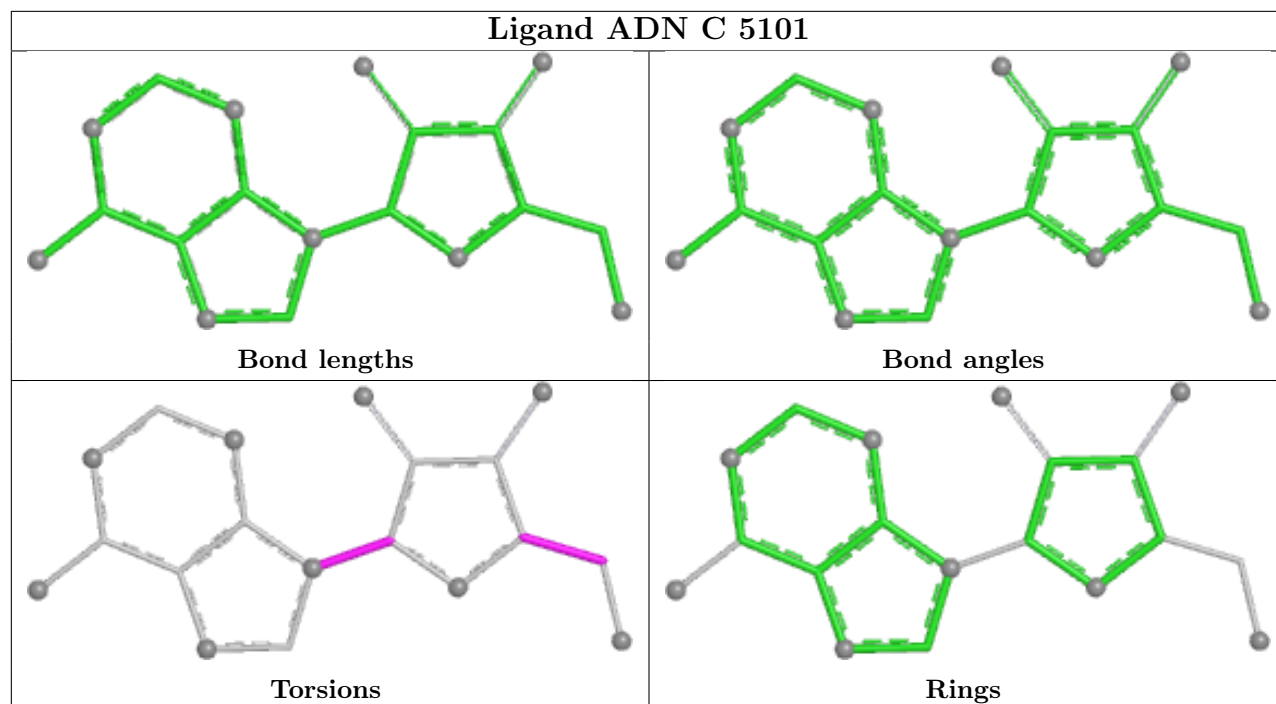
There are no ring outliers.

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.

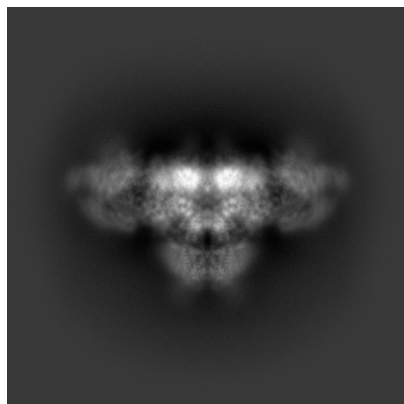
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40426. These allow visual inspection of the internal detail of the map and identification of artifacts.

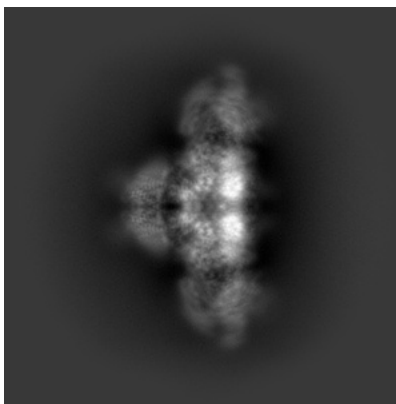
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

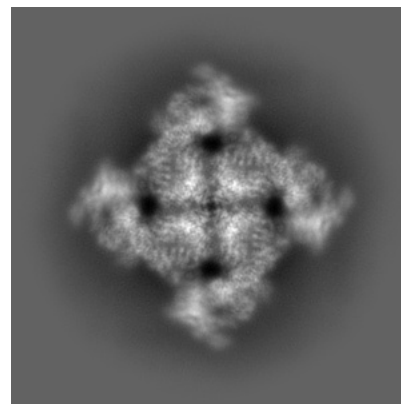
#### 6.1.1 Primary map



X

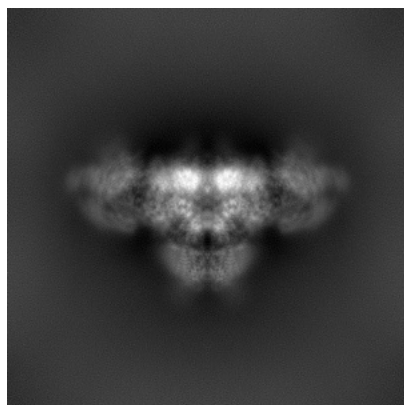


Y

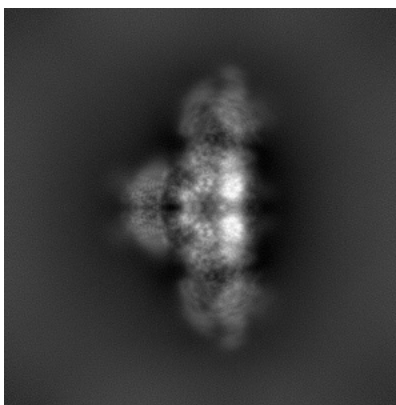


Z

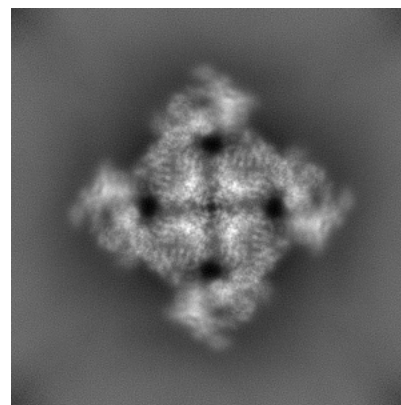
#### 6.1.2 Raw map



X



Y

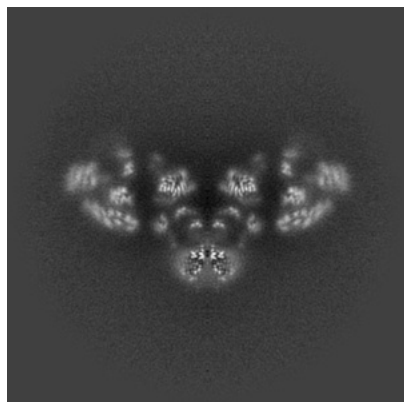


Z

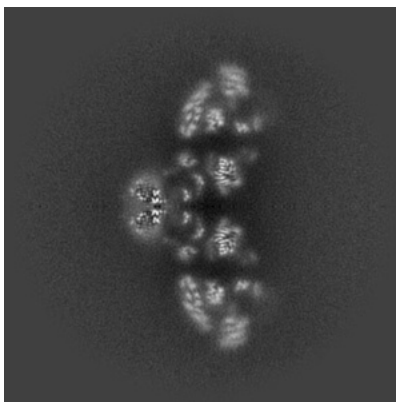
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

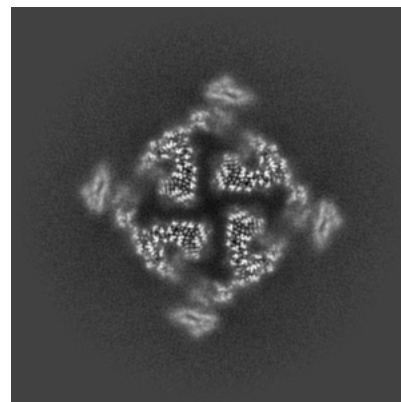
### 6.2.1 Primary map



X Index: 200

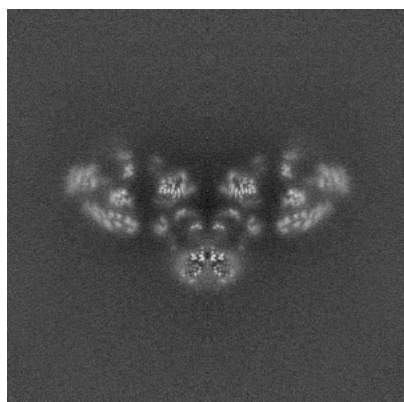


Y Index: 200

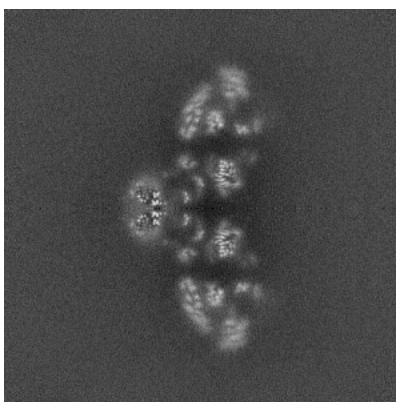


Z Index: 200

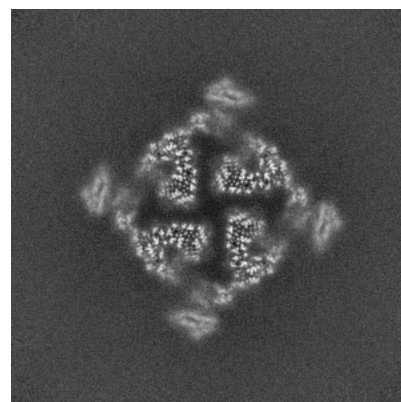
### 6.2.2 Raw map



X Index: 200



Y Index: 200

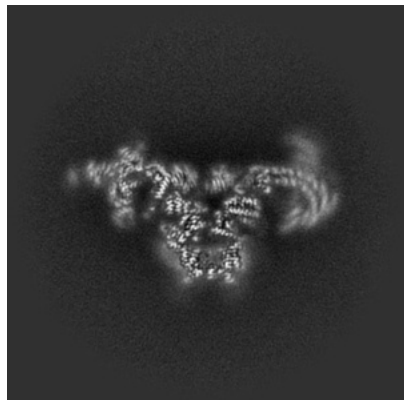


Z Index: 200

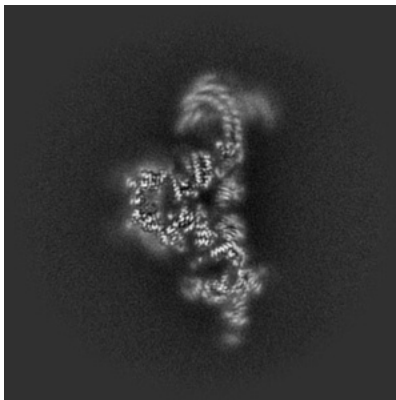
The images above show central slices of the map in three orthogonal directions.

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

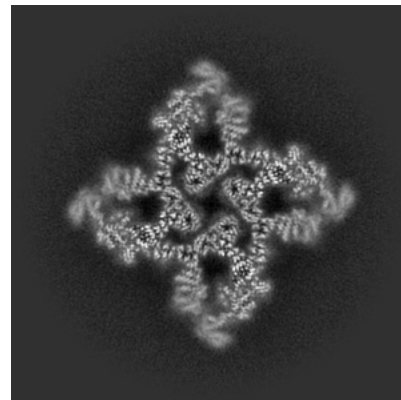
### 6.3.1 Primary map



X Index: 218

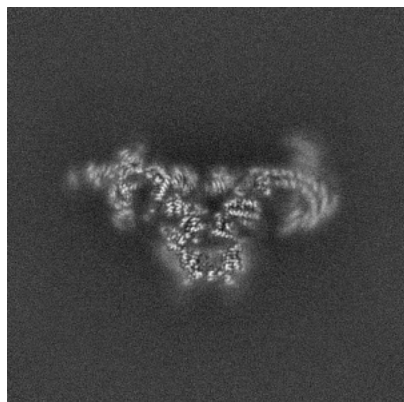


Y Index: 182

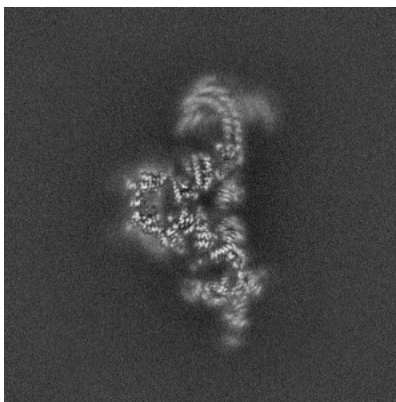


Z Index: 225

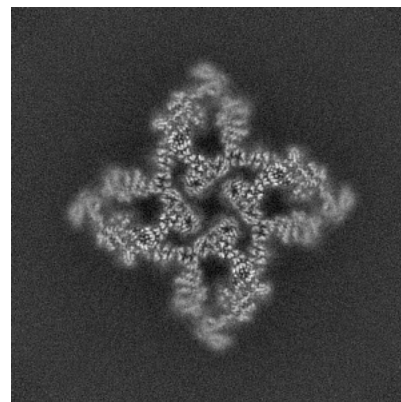
### 6.3.2 Raw map



X Index: 218



Y Index: 182

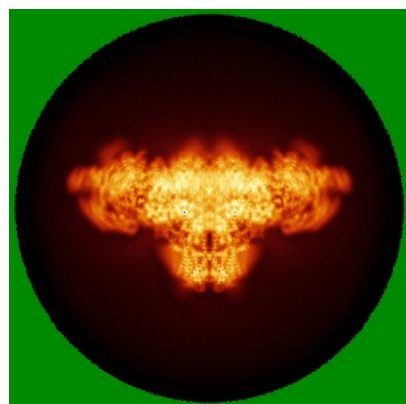


Z Index: 225

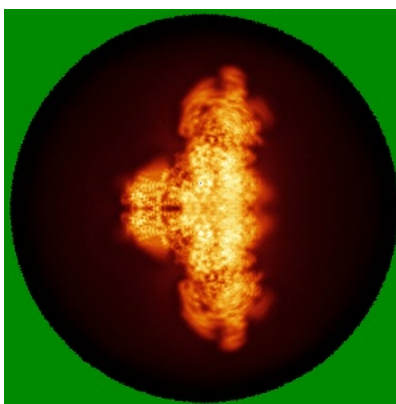
The images above show the largest variance slices of the map in three orthogonal directions.

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

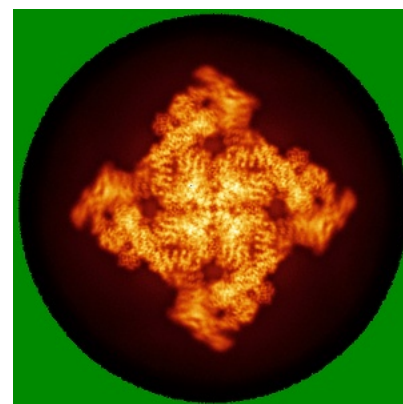
### 6.4.1 Primary map



X

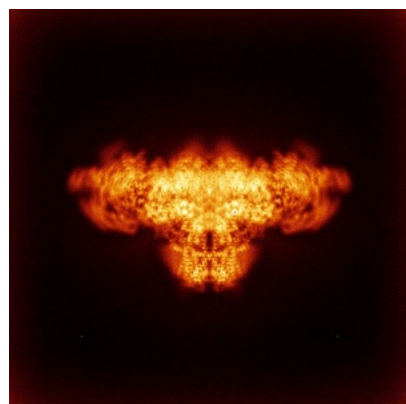


Y

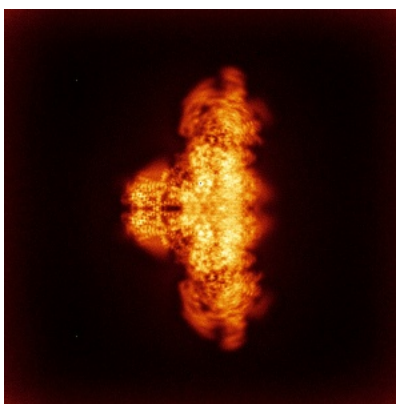


Z

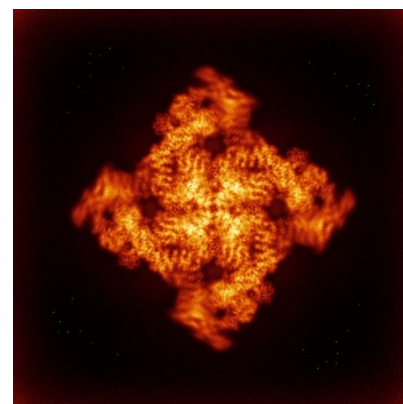
### 6.4.2 Raw map



X



Y

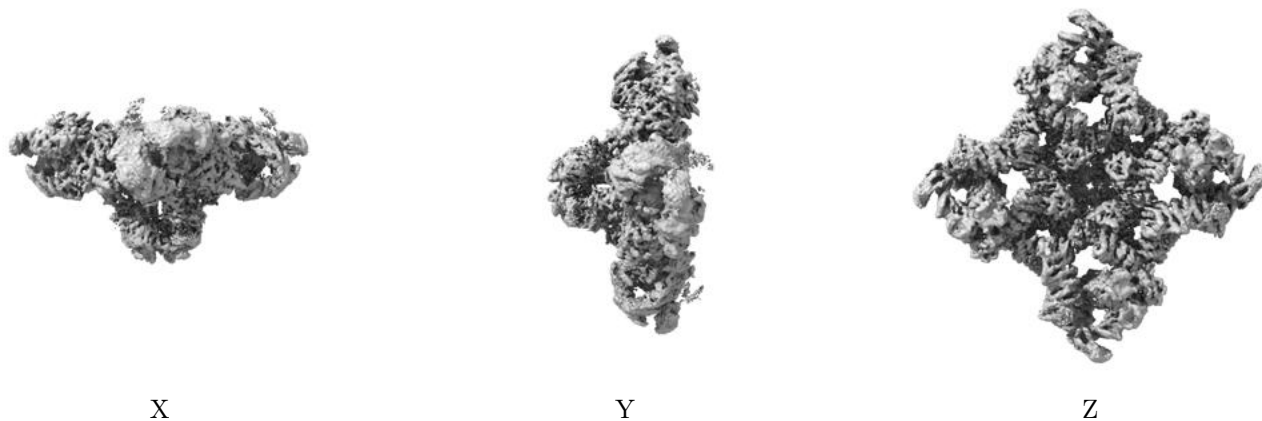


Z

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.

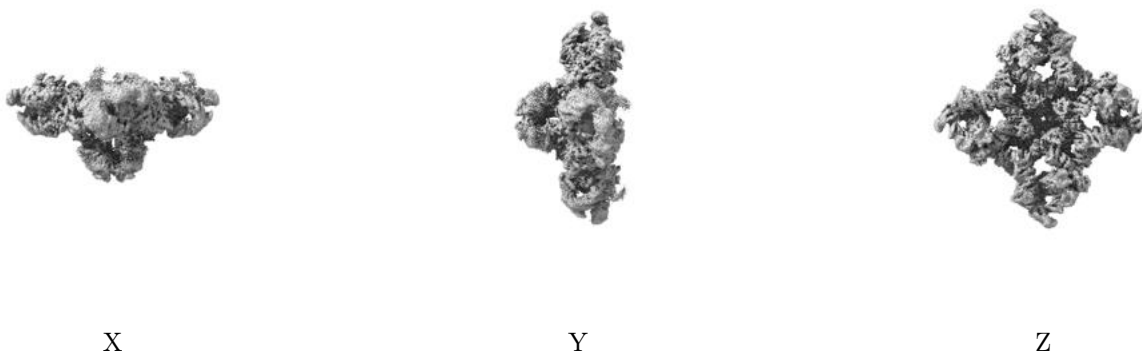
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.387. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 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.

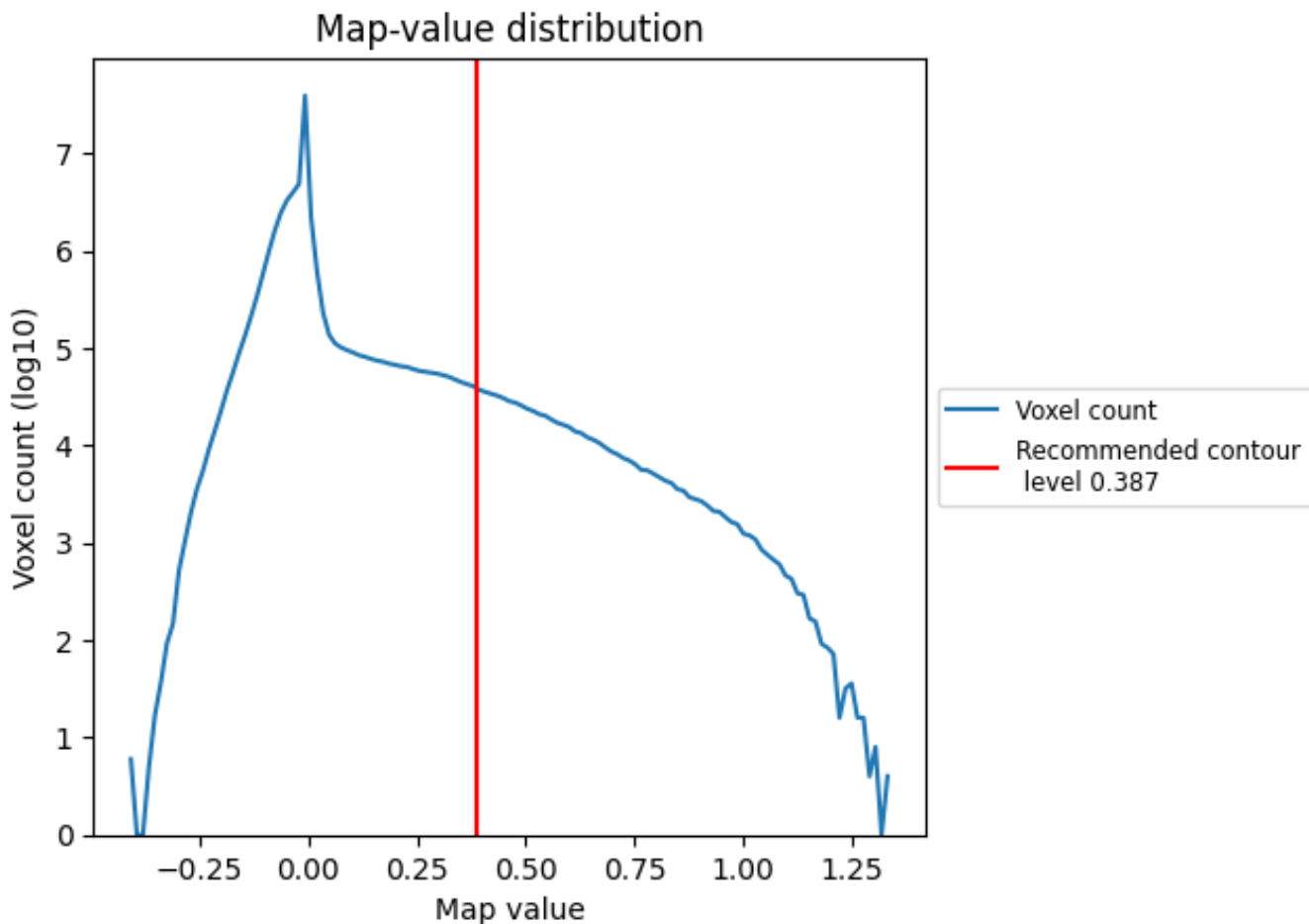
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

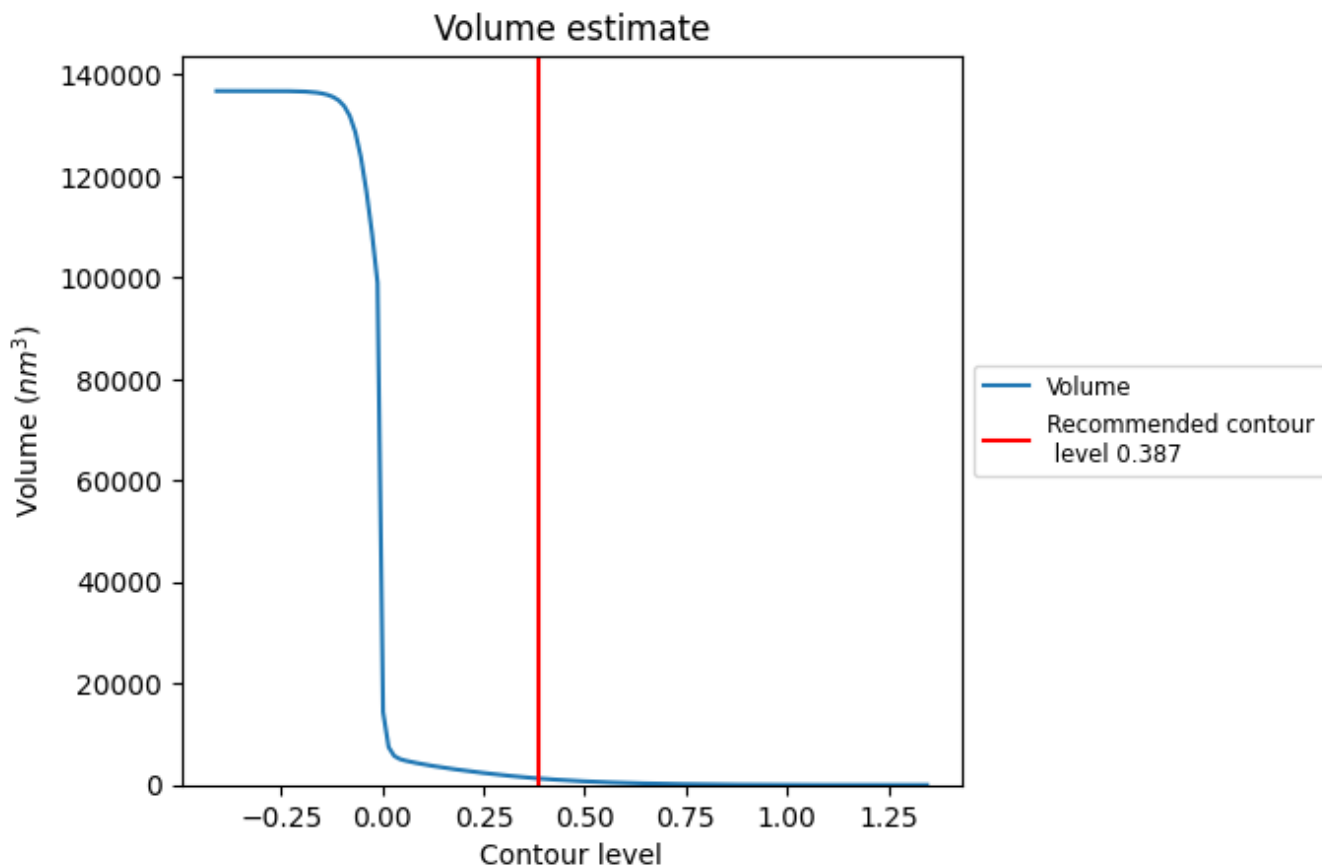
This section contains the results of statistical analysis of the map.

### 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.

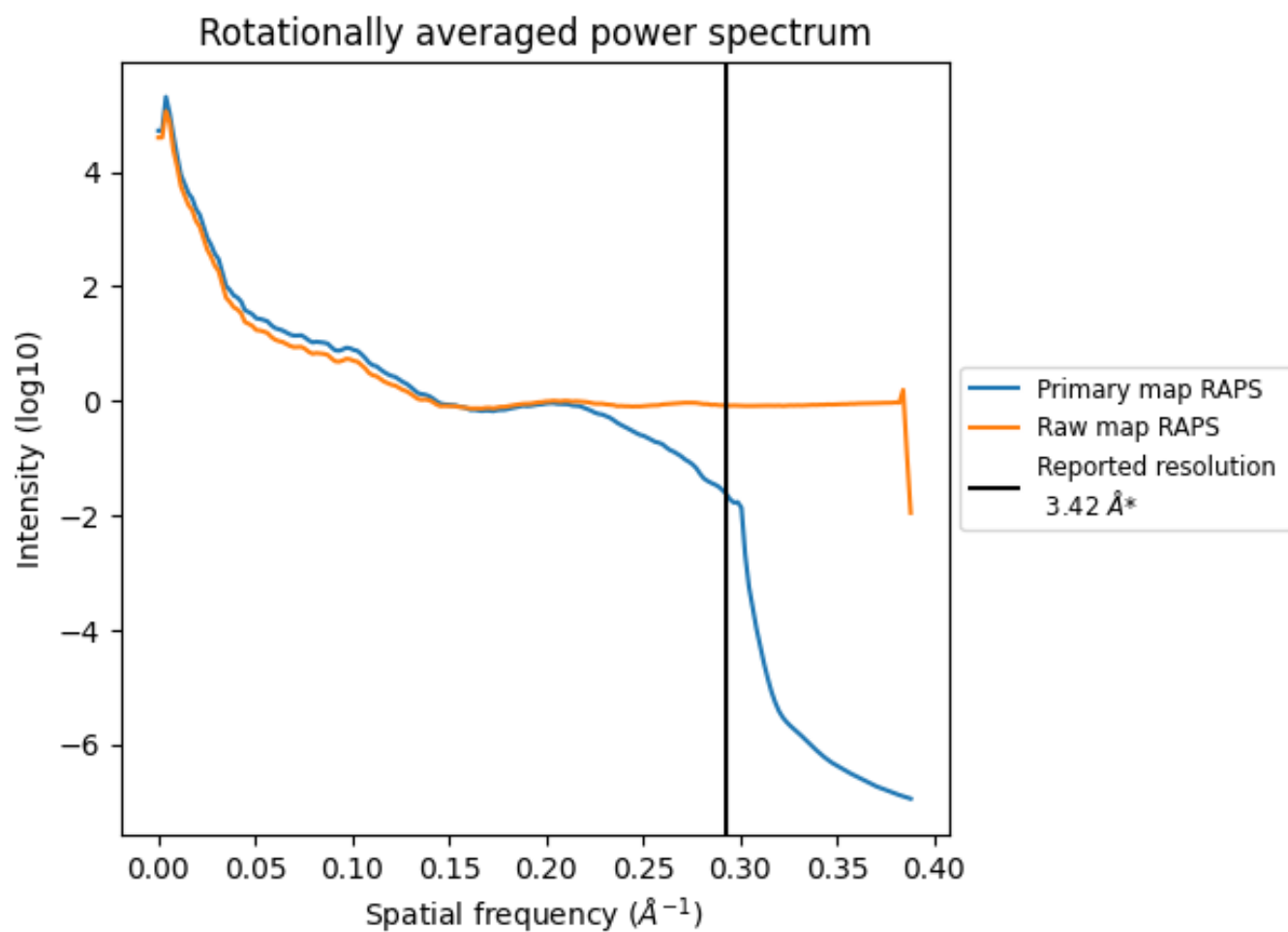
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1280  $\text{nm}^3$ ; this corresponds to an approximate mass of 1156 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 i

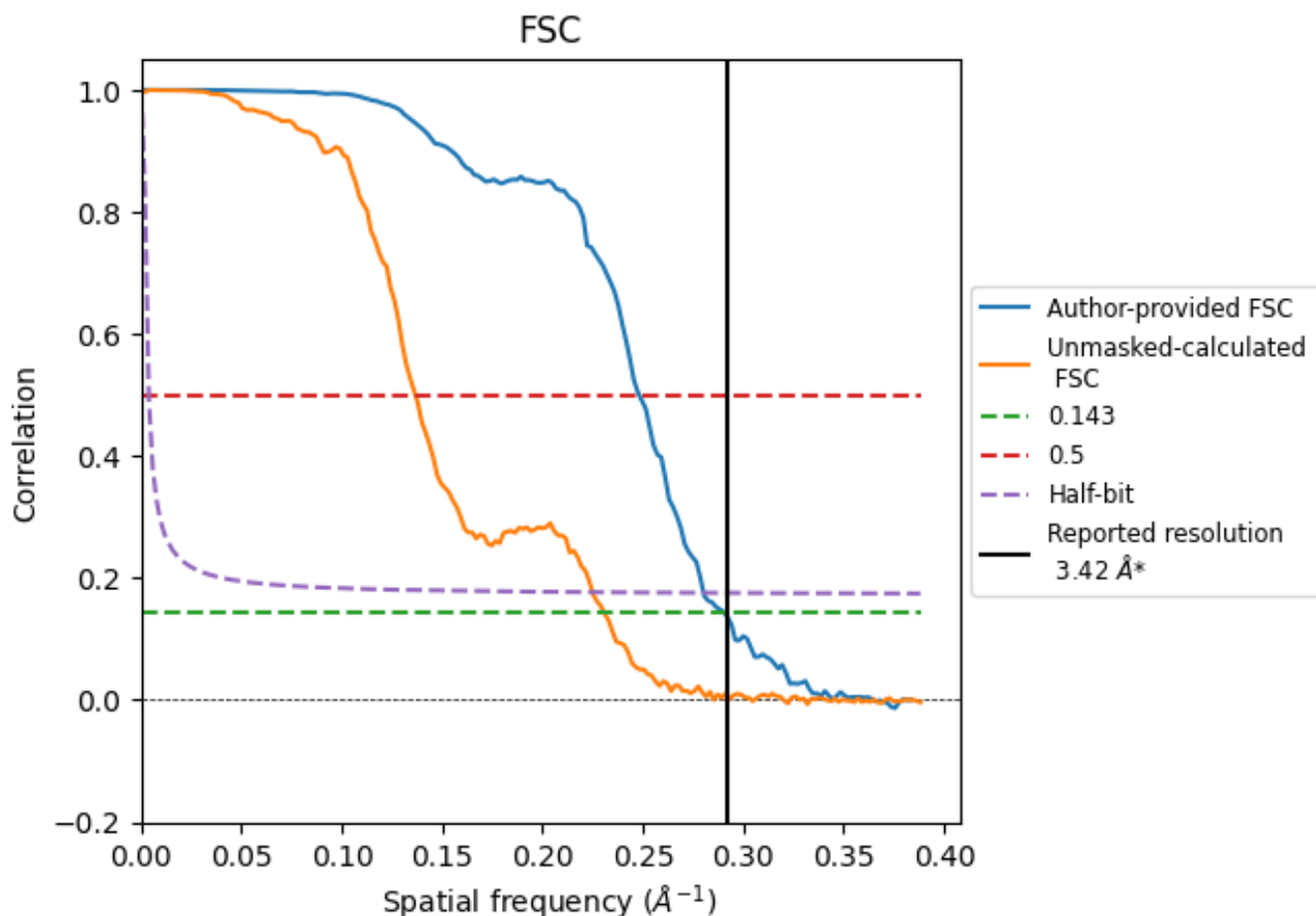


\*Reported resolution corresponds to spatial frequency of 0.292 Å<sup>-1</sup>

## 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 0.292 Å<sup>-1</sup>

## 8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.42	-	-
Author-provided FSC curve	3.44	4.03	3.57
Unmasked-calculated*	4.33	7.32	4.45

\*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 4.33 differs from the reported value 3.42 by more than 10 %

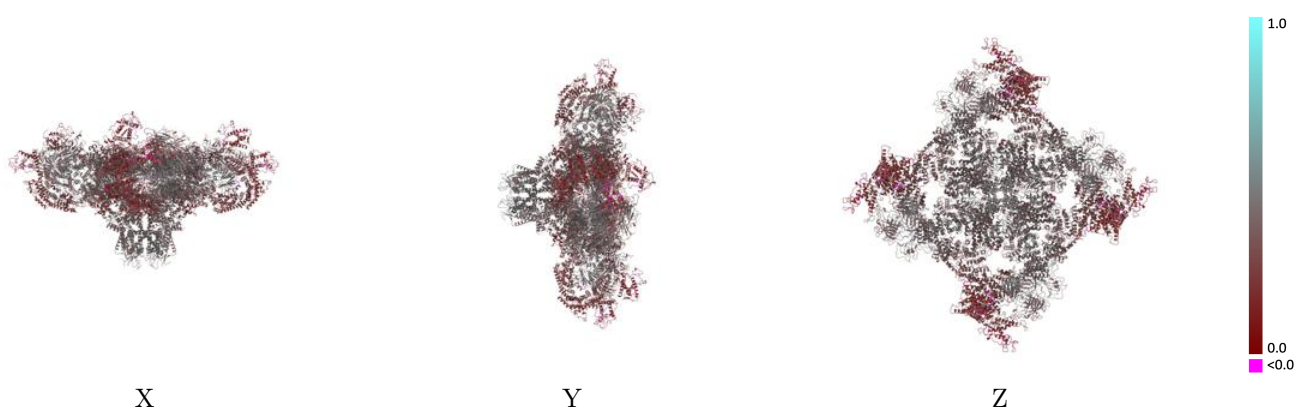
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40426 and PDB model 8SER. Per-residue inclusion information can be found in section 3 on page 9.

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

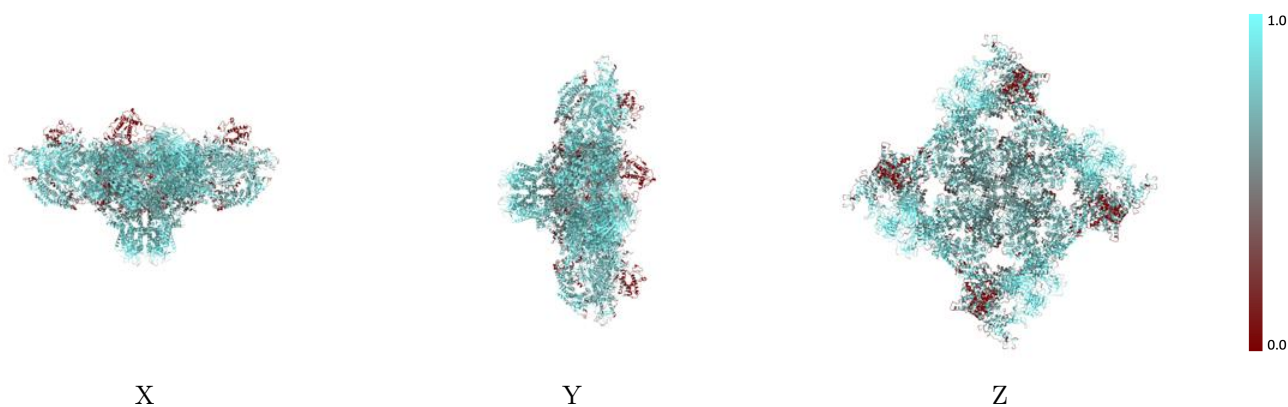
This section was not generated.

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



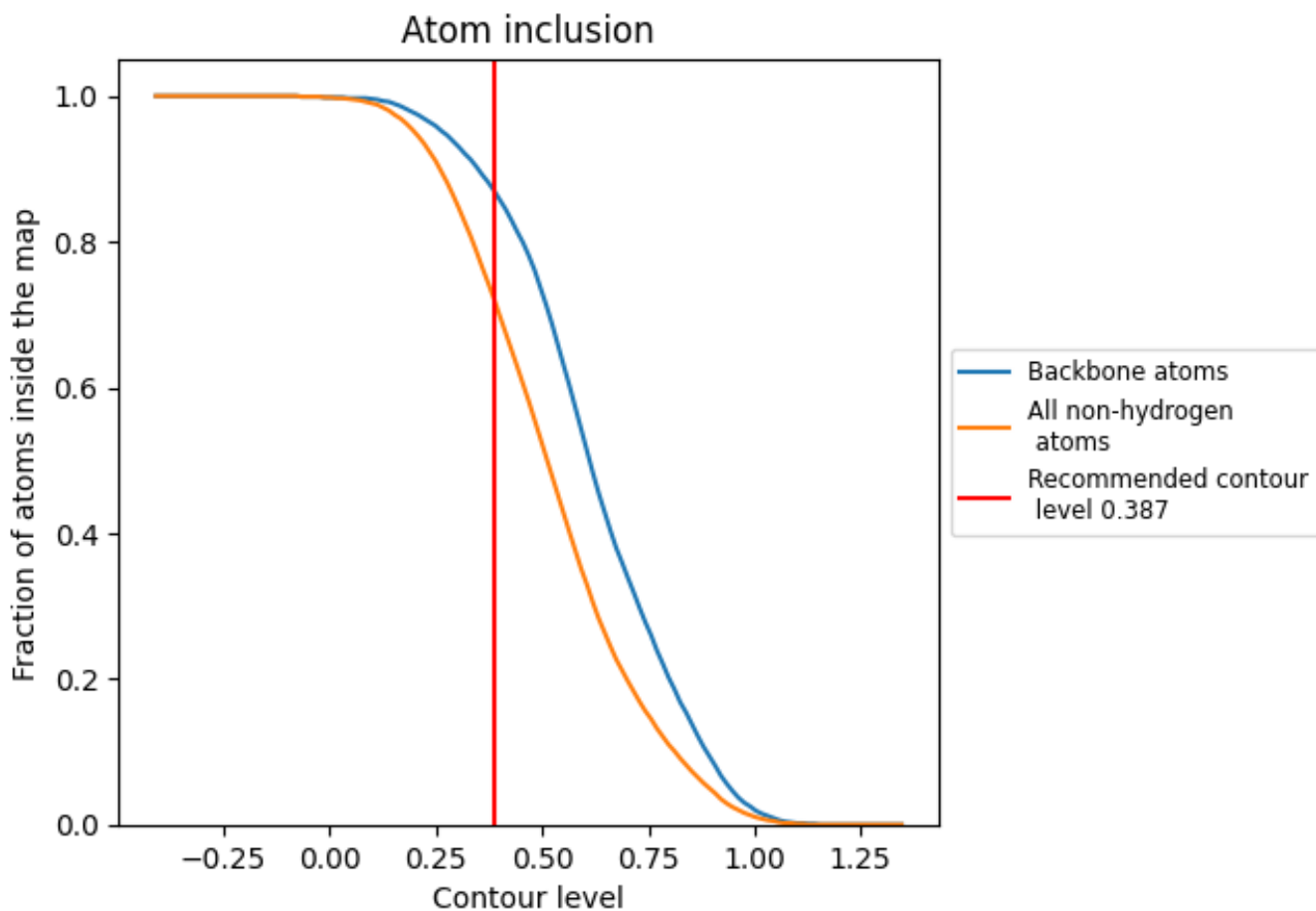
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.387).



















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 72% 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 (0.387) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7210	 0.3530
A	 0.7170	 0.3510
B	 0.7170	 0.3510
C	 0.7170	 0.3510
D	 0.7170	 0.3520
E	 0.8730	 0.4230
F	 0.8730	 0.4230
G	 0.8730	 0.4240
H	 0.8730	 0.4250

