



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 06:11 AM UTC

PDB ID : 9NMR / pdb_00009nmr
EMDB ID : EMD-49538
Title : Structure of mouse RyR1 (including auxiliary transmembrane helix TMx; EGTA-only dataset)
Authors : Weninger, G.; Marks, A.R.
Deposited on : 2025-03-04
Resolution : 2.91 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:

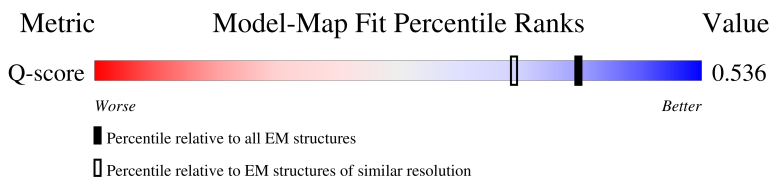
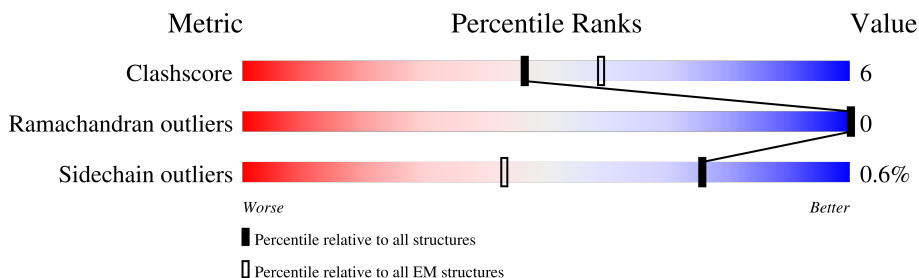
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

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

The reported resolution of this entry is 2.91 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	12972 (2.41 - 3.41)

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	5035	8% (red), 74% (green), 13% (yellow), 13% (grey)
1	B	5035	8% (red), 74% (green), 13% (yellow), 13% (grey)
1	C	5035	8% (red), 74% (green), 13% (yellow), 13% (grey)
1	D	5035	8% (red), 74% (green), 13% (yellow), 13% (grey)

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Mol	Chain	Length	Quality of chain
2	E	108	 91% 8%
2	F	108	 89% 10%
2	G	108	 90% 9%
2	H	108	 91% 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 143684 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	4397	34983	22250	6021	6475	237	1	0
1	B	4397	34983	22250	6021	6475	237	1	0
1	C	4397	34983	22250	6021	6475	237	1	0
1	D	4397	34983	22250	6021	6475	237	1	0

- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

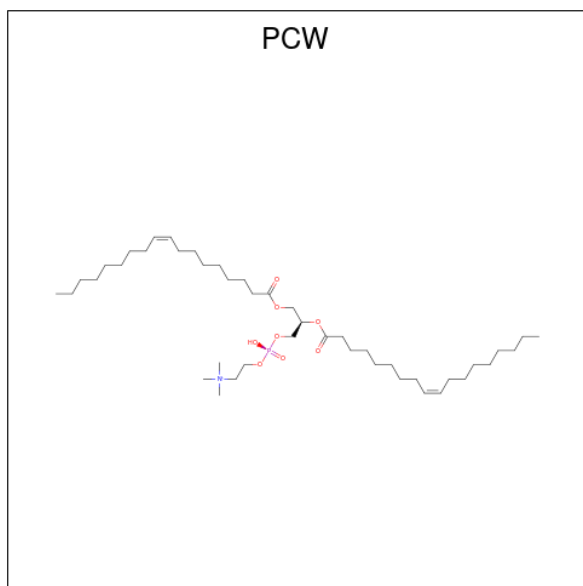
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	E	107	829	526	145	155	3	0	0
2	F	107	829	526	145	155	3	0	0
2	G	107	829	526	145	155	3	0	0
2	H	107	829	526	145	155	3	0	0

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

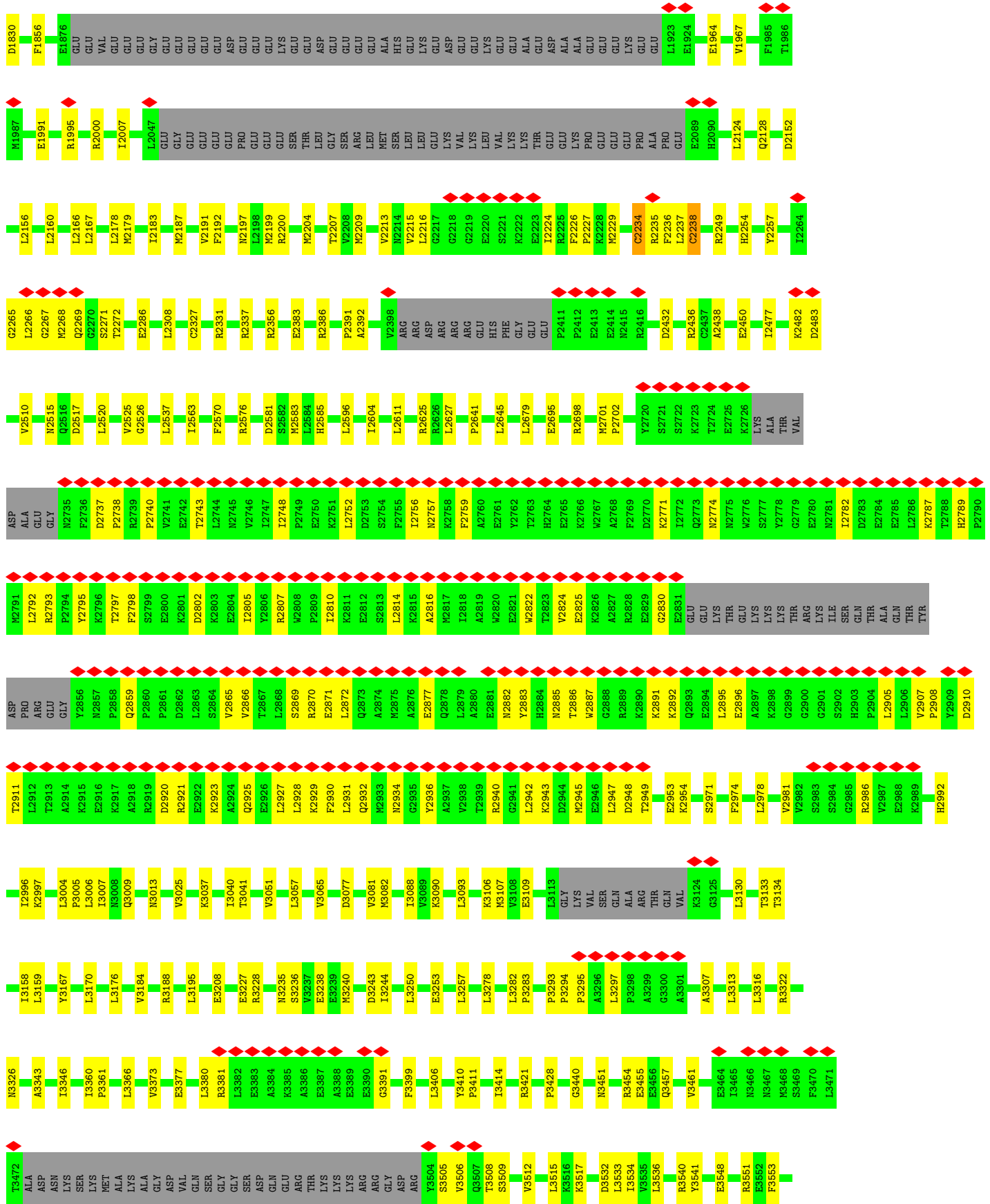
Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	
3	B	1	Total	Zn	0
			1	1	
3	C	1	Total	Zn	0
			1	1	
3	D	1	Total	Zn	0
			1	1	

- Molecule 4 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW)

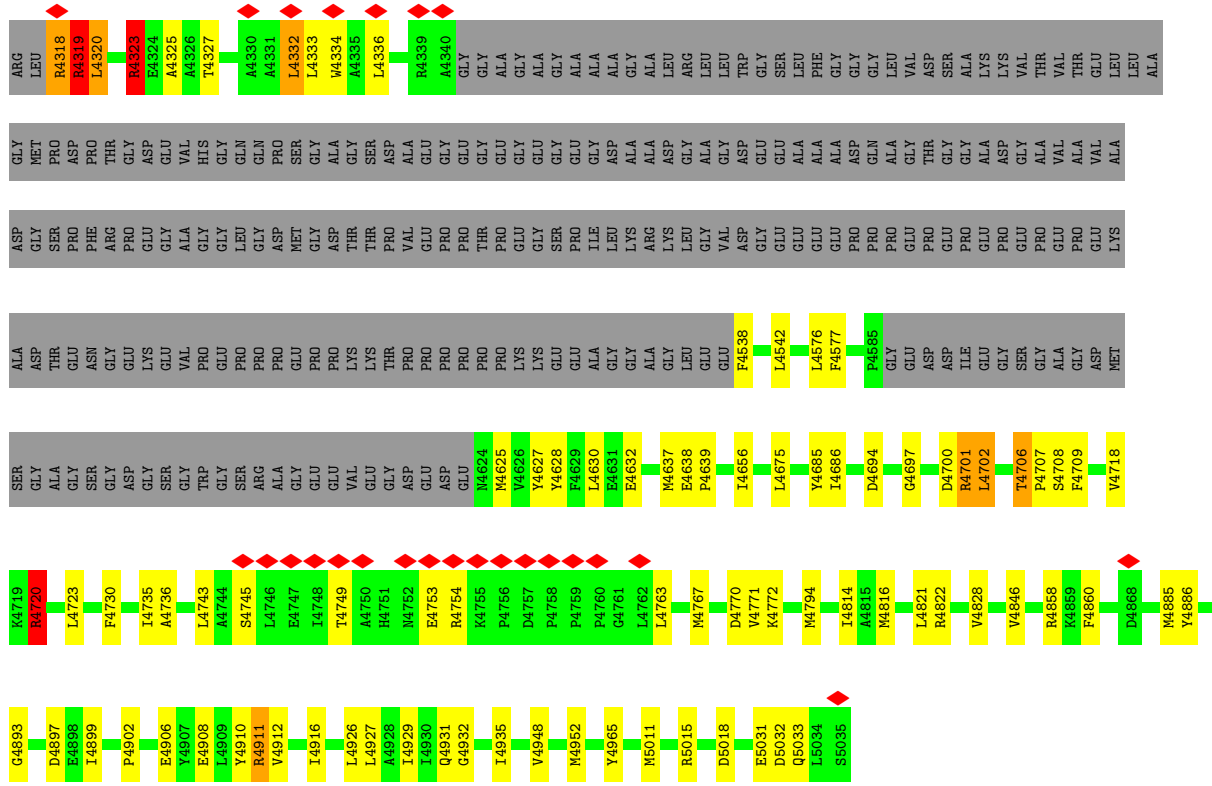
(formula: C₄₄H₈₅NO₈P).



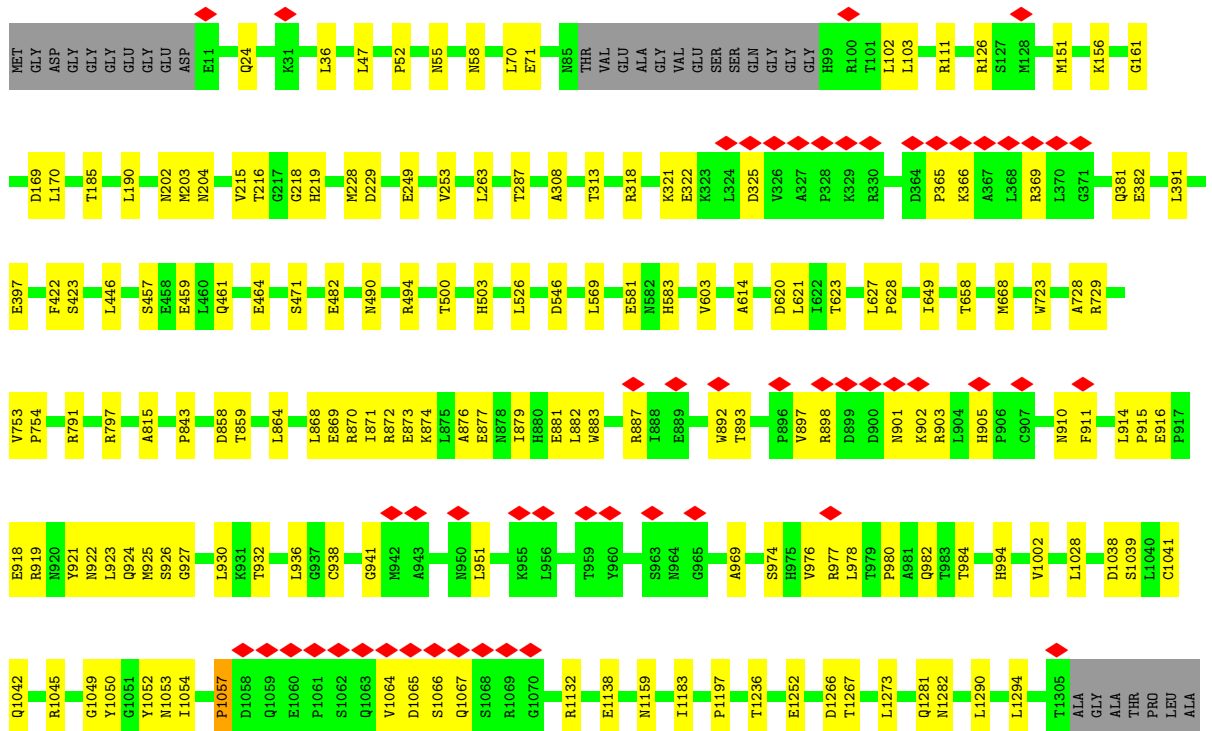
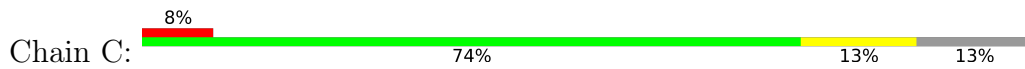
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
4	A	1	Total 54	44	1	8	1	0
4	A	1	Total 54	44	1	8	1	0
4	B	1	Total 54	44	1	8	1	0
4	B	1	Total 54	44	1	8	1	0
4	C	1	Total 54	44	1	8	1	0
4	C	1	Total 54	44	1	8	1	0
4	D	1	Total 54	44	1	8	1	0
4	D	1	Total 54	44	1	8	1	0



P4257	P4091	R3871	R3673	E3584	L3380	L3176	R3008	A2918	P2858	F2798	P2738
GLU	S4092	Q3872	M3674	E3585	R3381	Y3184	Q3009	R2919	Q2859	S2799	R2739
GLU	K4093	M3873	E3683	D3586	E3382	R3188	N3013	D2920	P2860	E2800	P2740
PRO	K4094	G3874	E3684	A3587	E3383	R3188	V3025	R2921	P2861	K2801	V2741
	D4095		E3685	D3588	E3384	L3195	K3037	E2922	D2862	D2802	E2742
	F4096		E3686	D3589	A3384	E3227	I3040	A2924	L2863	K2803	T2743
	Q4097		E3687	P3590	K3385	R3228	I3040	Q2925	S2864	E2804	L2744
	K4098		E3688	K3592	A3386	R3228	T3041	Q2925	V2865	L2805	H2745
	A4098		E3689	K3593	E3387	A3387	T3041	E2926	V2866	L2806	I2746
	M4100		E3688	V3594	A3388	I3230	V3051	L2927	T2867	R2807	I2747
	Q4103		E3689	V3594	A3388	M2335	L3057	L2928	L2868	V2808	I2748
	K4104		E3690	R3596	E3389	S2336	L3057	K2929	S2869	P2809	P2749
	T4107		E3692	V3597	V3237	E3238	V3065	F2930	E2870	I2810	E2750
	G4108		E3693	Q3598	E3239	E3239	V3065	F2930	E2871	K2811	K2751
	P4109		K3695	V3603	K3240	M3243	D3077	Q2932	L2872	E2812	L2752
	E4110			Y3604		I3244	V3081	M2933	Q2873	S2813	D2753
	D4121			Y3605		I3244	M3082	M2934	M2874	L2814	S2754
	E4122			Y3606		E3253	I3088	G2935	M2875	K2815	F2755
	M4125			T3508		L3257	V3088	Y2936	A2876	A2816	I2756
	E4129			S3509		L3282	K3090	A2937	E2877	M2817	H2757
	A4132			V3512		P3282	L3093	V2938	Q2878	L2818	K2758
	F4135			L3515		P3283	K3106	V2938	L2879	A2819	F2759
	Q4136			K3516		P3294	M3107	R2940	A2880	V2820	A2760
	A4136			K3517		P3294	M3107	G2941	E2881	E2821	E2761
	L4163			D3532		P3295	E3109	L2942	M2882	V2822	I2762
	L4167			L3533		A3296	L3113	D2944	H2884	V2824	T2763
	A4170			L3534		L3297	GLY	M2945	H2885	E2825	H2764
	I4173			V3535		P3298	LYS	E2946	T2886	K2826	E2765
	Q4046			L3536		A3299	VAL	L2947	M2887	A2827	E2766
	L4062			R3540		G3300	SER	L2948	G2888	R2828	A2768
	D4066			Y3541		A3301	GLN	T2949	R2889	E2829	F2769
	M4067			E3548		L3313	ALA	E2953	K2890	G2830	D2770
	K4072			R3551		L3316	THR	K2954	K2891	K2771	K2771
	D4073			E3552		R3322	VAL	S2971	GLU	L2772	L2772
	V4074			F3553		R3322	K3124	E2974	GLU	O2773	O2773
	V4075			N3556		M3326	G3125	L2978	THR	L2774	H2774
	E4078			M3468		A3343	L3130	V2981	L2895	L2775	H2775
	D4082			F3470		L3346	L3133	V2982	L2896	L2776	H2776
	Y4083			L3471		L3360	T3133	K2897	A2897	S2777	S2777
	T4085			T3472		P3361	T3134	K2898	K2897	L2778	L2778
	R4088			ALA		L3366	I3158	V2981	ARG	G2779	G2779
	G4089			ASP		V3373	L3159	S2983	ARG	G2779	G2779
	L4090			ASN		E3377	L3159	S2984	LYS	E2780	E2780
				LYS		L3366	Y3167	G2985	SER	I2781	I2781
				SER		E3377	L3170	R2986	GLN	L2782	L2782
				LYS		V3373		V2987	THR	D2783	D2783
				MET		E3377		E2988	ALA	E2784	E2784
				ALA		L3366		V2988	GLN	E2785	E2785
				LYS		E3377		K2989	THR	L2786	L2786
				ALA		E3377		H2992	ASP	K2787	K2787
				GLY		E3377		L2996	PRO	ARG	ARG
				ASP		E3377		L2996	ARG	GLU	GLU
						E3377		D2910	GLY	H2789	H2789
						E3377		D2910	GLY	F2790	F2790
						E3377		T2911	GLY	H2791	H2791
						E3377		L2912	GLY	L2792	L2792
						E3377		A2914	GLY	R2793	R2793
						E3377		K2915	GLY	F2794	F2794
						E3377		E2916	GLY	Y2795	Y2795
						E3377		K2917	GLY	K2796	K2796
						E3377		K2917	GLY	T2797	T2797

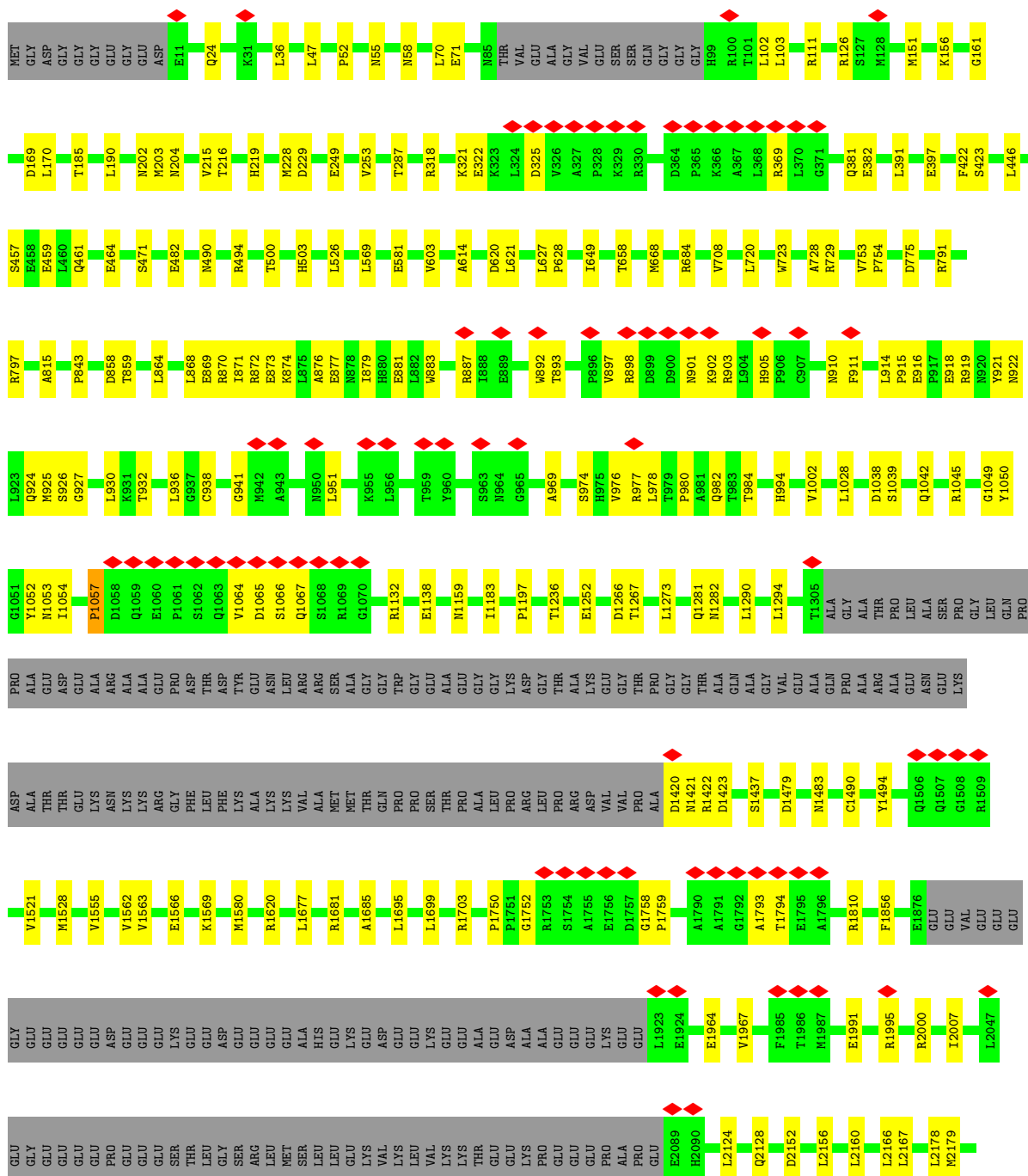
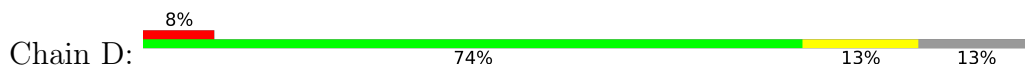


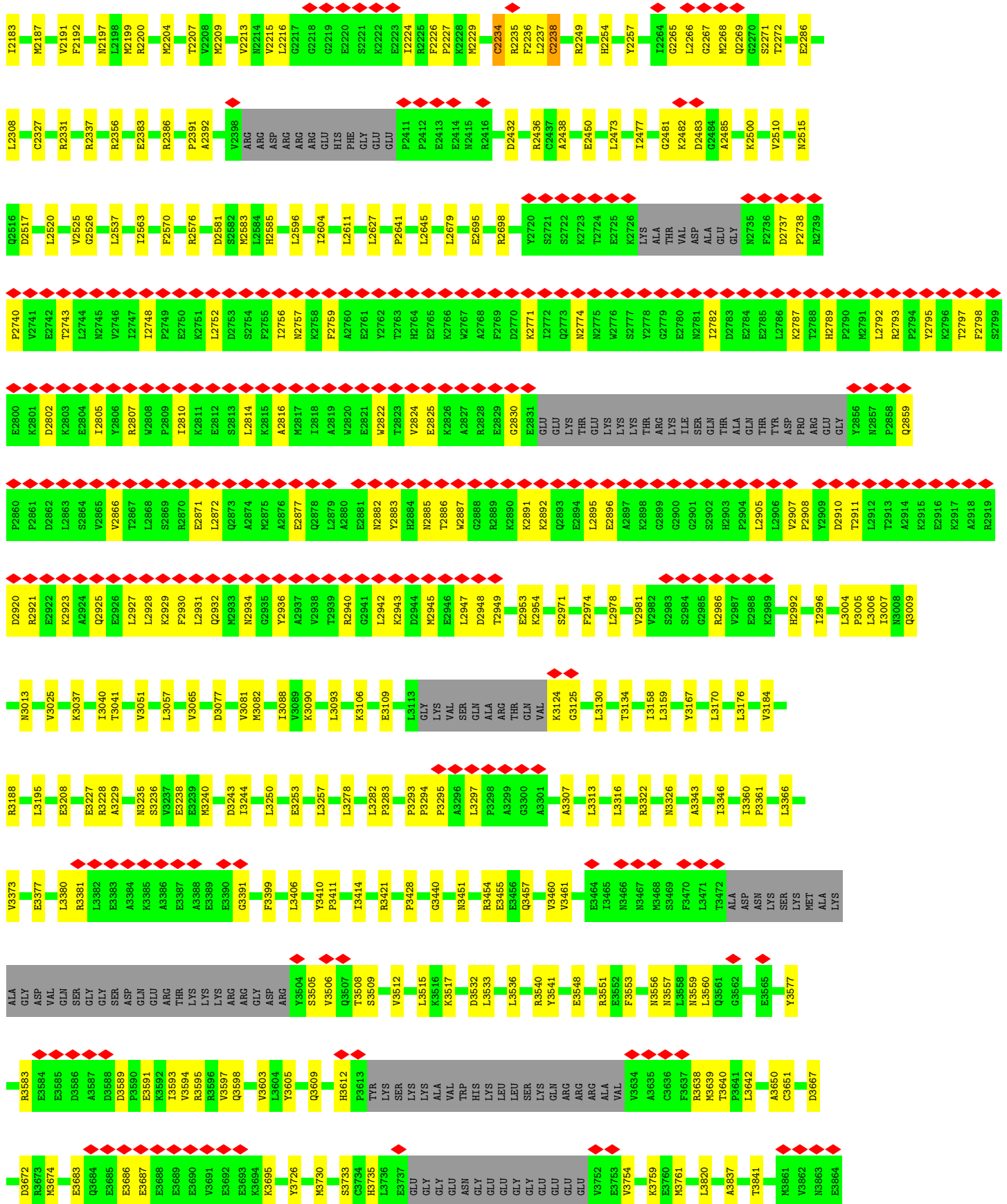
• Molecule 1: Ryanodine receptor 1






● Molecule 1: Ryanodine receptor 1






Chain G:  90% 9%



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H:  91% 8%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	129073	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 ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.613	Depositor
Minimum map value	0.000	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	427.008, 427.008, 427.008	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.834, 0.834, 0.834	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: PCW, 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	0.23	0/35776	0.41	5/48462 (0.0%)
1	B	0.23	0/35776	0.41	5/48462 (0.0%)
1	C	0.23	0/35776	0.41	5/48462 (0.0%)
1	D	0.23	0/35776	0.41	5/48462 (0.0%)
2	E	0.18	0/847	0.32	0/1142
2	F	0.18	0/847	0.32	0/1142
2	G	0.18	0/847	0.31	0/1142
2	H	0.18	0/847	0.31	0/1142
All	All	0.23	0/146492	0.40	20/198416 (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	8
1	B	0	8
1	C	0	8
1	D	0	8
All	All	0	32

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2238	CYS	CA-CB-SG	9.06	135.23	114.40
1	A	2238	CYS	CA-CB-SG	9.05	135.21	114.40
1	D	2238	CYS	CA-CB-SG	9.05	135.21	114.40
1	C	2238	CYS	CA-CB-SG	9.04	135.19	114.40

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	2238	CYS	CB-CA-C	6.19	120.63	110.17

There are no chirality outliers.

5 of 32 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2238	CYS	Peptide
1	A	4088	ARG	Sidechain
1	A	4318	ARG	Sidechain
1	A	4319	ARG	Sidechain
1	A	4323	ARG	Sidechain

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	34983	0	34589	445	0
1	B	34983	0	34589	438	0
1	C	34983	0	34589	437	0
1	D	34983	0	34589	432	0
2	E	829	0	826	8	0
2	F	829	0	826	10	0
2	G	829	0	826	9	0
2	H	829	0	826	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	108	0	168	0	0
4	B	108	0	168	0	0
4	C	108	0	168	0	0
4	D	108	0	168	0	0
All	All	143684	0	142332	1748	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1748 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:2752:LEU:HD13	1:C:2814:LEU:HD21	1.43	1.00
1:B:2752:LEU:HD13	1:B:2814:LEU:HD21	1.43	0.98
1:C:1991:GLU:OE2	1:C:1995:ARG:NH1	1.97	0.97
1:D:2752:LEU:HD13	1:D:2814:LEU:HD21	1.43	0.97
1:A:1991:GLU:OE2	1:A:1995:ARG:NH1	1.97	0.96

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	4368/5035 (87%)	4233 (97%)	135 (3%)	0	100	100
1	B	4368/5035 (87%)	4233 (97%)	135 (3%)	0	100	100
1	C	4368/5035 (87%)	4233 (97%)	135 (3%)	0	100	100
1	D	4368/5035 (87%)	4234 (97%)	134 (3%)	0	100	100
2	E	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
2	F	105/108 (97%)	100 (95%)	5 (5%)	0	100	100
2	G	105/108 (97%)	101 (96%)	4 (4%)	0	100	100
2	H	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
All	All	17892/20572 (87%)	17337 (97%)	555 (3%)	0	100	100

There are no Ramachandran outliers to report.

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

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	3823/4296 (89%)	3801 (99%)	22 (1%)	78	92
1	B	3823/4296 (89%)	3801 (99%)	22 (1%)	78	92
1	C	3823/4296 (89%)	3801 (99%)	22 (1%)	78	92
1	D	3823/4296 (89%)	3801 (99%)	22 (1%)	78	92
2	E	89/90 (99%)	89 (100%)	0	100	100
2	F	89/90 (99%)	89 (100%)	0	100	100
2	G	89/90 (99%)	89 (100%)	0	100	100
2	H	89/90 (99%)	89 (100%)	0	100	100
All	All	15648/17544 (89%)	15560 (99%)	88 (1%)	76	92

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	4332	LEU
1	D	4094	LYS
1	C	4576	LEU
1	C	4772	LYS
1	D	4129	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 169 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	2992	HIS
1	D	1939	GLN
1	C	3598	GLN
1	D	242	GLN
1	D	2499	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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
4	PCW	B	8003	-	53,53,53	1.24	7 (13%)	59,61,61	1.03	3 (5%)
4	PCW	A	8002	-	53,53,53	1.25	7 (13%)	59,61,61	1.04	3 (5%)
4	PCW	C	8003	-	53,53,53	1.24	7 (13%)	59,61,61	1.03	3 (5%)
4	PCW	C	8002	-	53,53,53	1.25	7 (13%)	59,61,61	1.04	3 (5%)
4	PCW	A	8003	-	53,53,53	1.24	7 (13%)	59,61,61	1.03	3 (5%)
4	PCW	B	8002	-	53,53,53	1.25	7 (13%)	59,61,61	1.04	3 (5%)
4	PCW	D	5103	-	53,53,53	1.25	7 (13%)	59,61,61	1.04	3 (5%)
4	PCW	D	5101	-	53,53,53	1.24	7 (13%)	59,61,61	1.03	3 (5%)

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
4	PCW	B	8003	-	-	25/57/57/57	-
4	PCW	A	8002	-	-	33/57/57/57	-
4	PCW	C	8003	-	-	25/57/57/57	-
4	PCW	C	8002	-	-	33/57/57/57	-
4	PCW	A	8003	-	-	25/57/57/57	-
4	PCW	B	8002	-	-	33/57/57/57	-
4	PCW	D	5103	-	-	33/57/57/57	-
4	PCW	D	5101	-	-	25/57/57/57	-

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	8003	PCW	O3-C11	3.02	1.42	1.33
4	C	8003	PCW	O3-C11	3.02	1.42	1.33
4	D	5101	PCW	O3-C11	3.02	1.42	1.33
4	A	8003	PCW	O3-C11	2.99	1.42	1.33
4	A	8002	PCW	O3-C11	2.96	1.42	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	8002	PCW	C21-C20-C19	3.88	153.88	124.83
4	B	8002	PCW	C21-C20-C19	3.88	153.88	124.83
4	C	8002	PCW	C21-C20-C19	3.88	153.88	124.83
4	D	5103	PCW	C21-C20-C19	3.88	153.88	124.83
4	A	8003	PCW	C21-C20-C19	3.81	153.38	124.83

There are no chirality outliers.

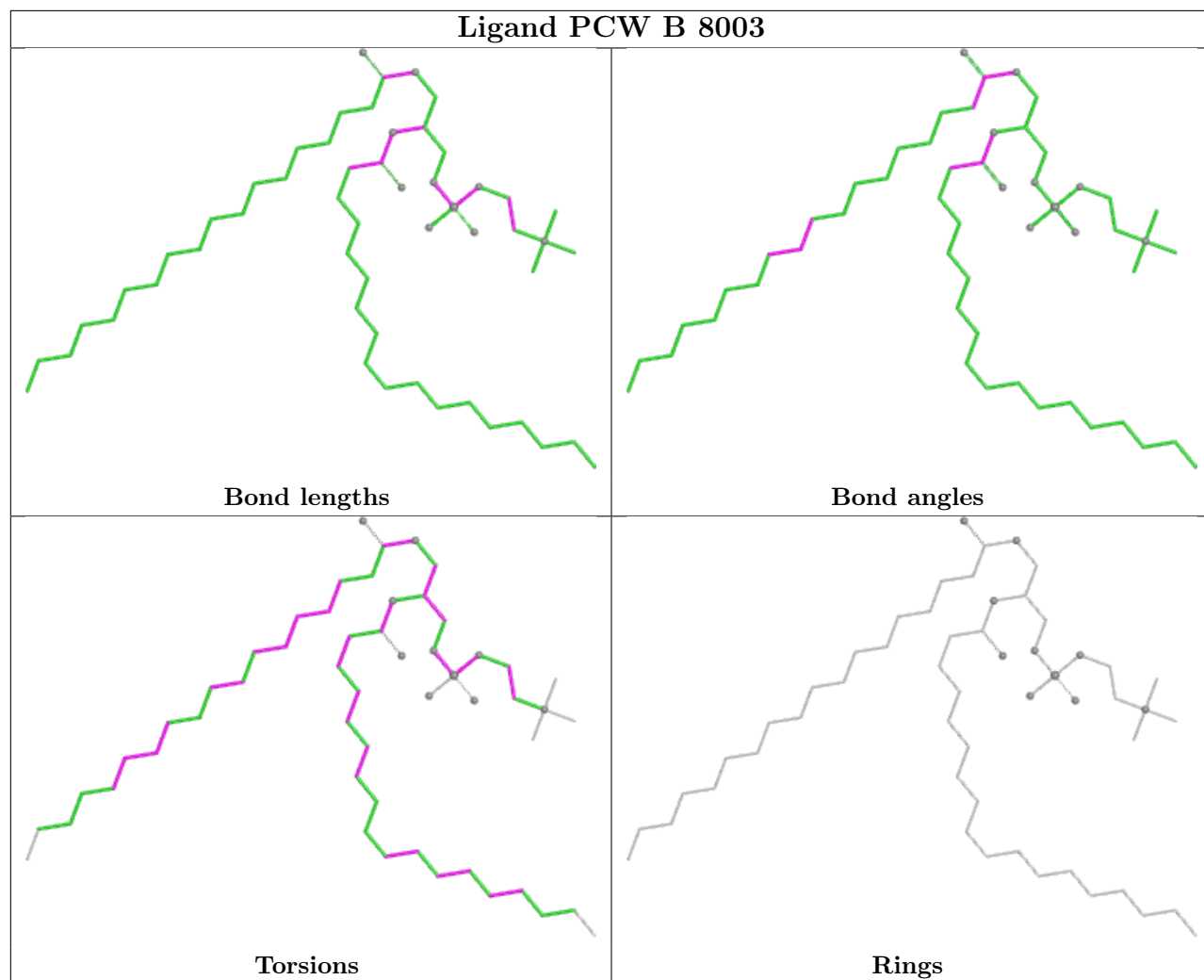
5 of 232 torsion outliers are listed below:

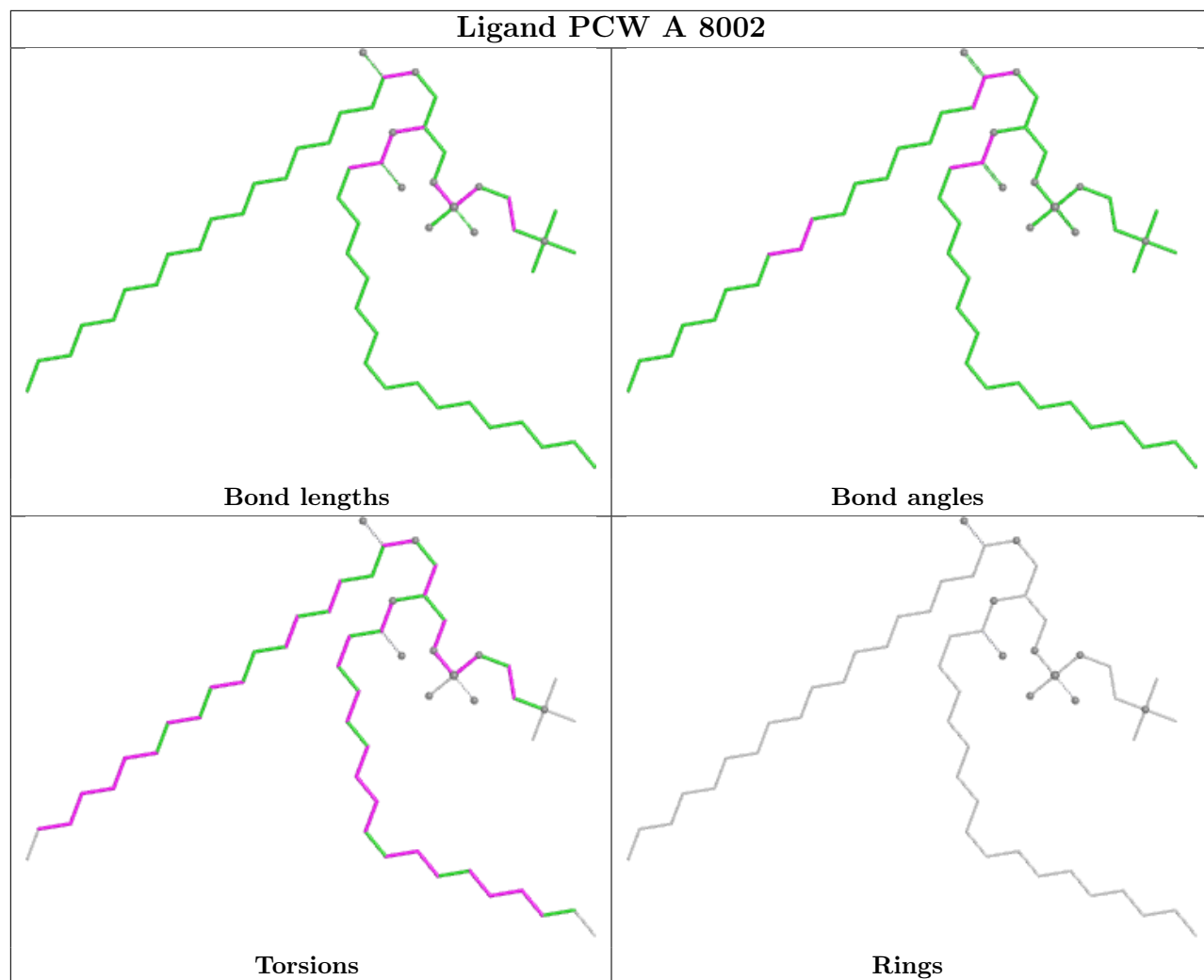
Mol	Chain	Res	Type	Atoms
4	A	8002	PCW	C32-C31-O2-C2
4	A	8002	PCW	C1-O3P-P-O1P
4	A	8002	PCW	C1-O3P-P-O2P
4	A	8002	PCW	C1-O3P-P-O4P
4	A	8002	PCW	C4-O4P-P-O1P

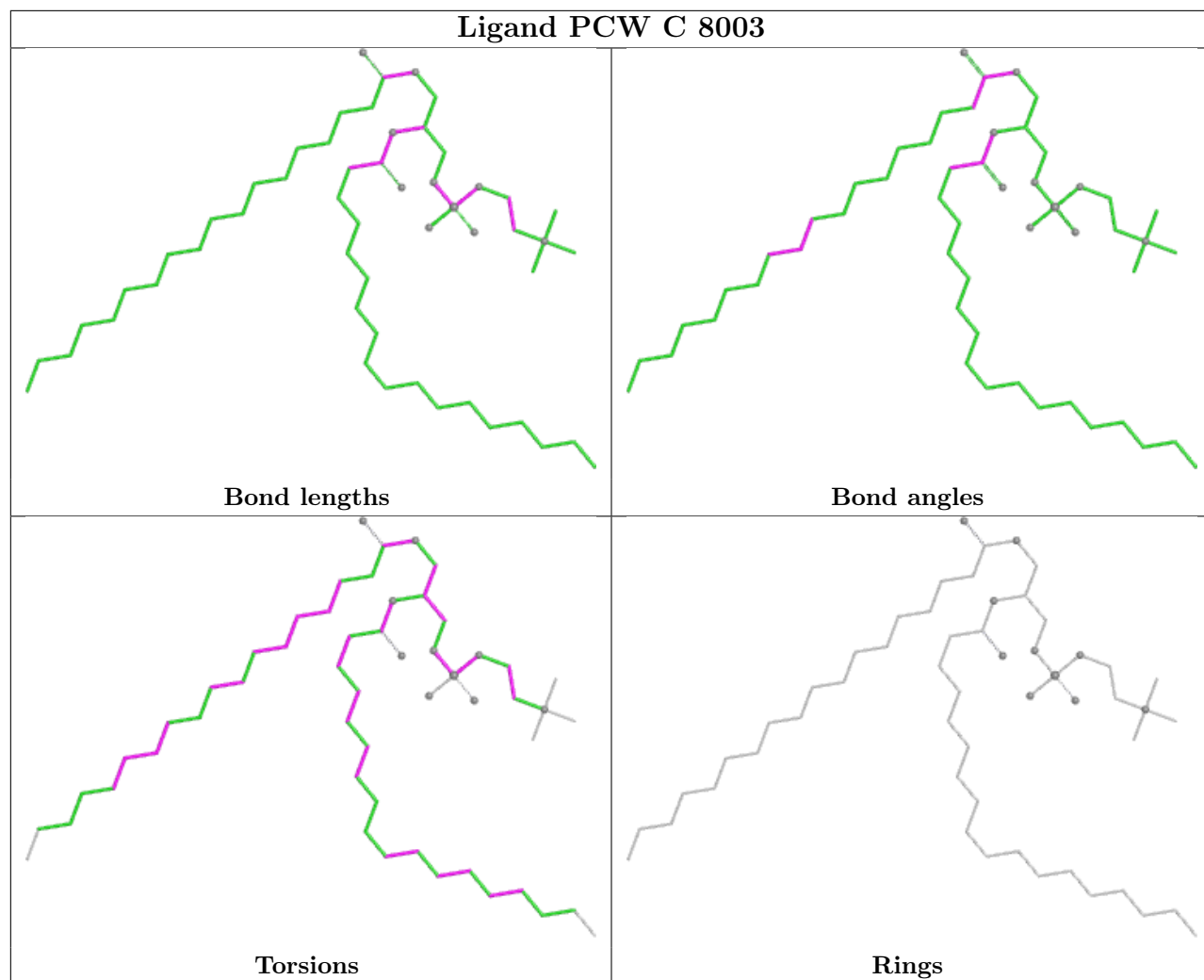
There are no ring outliers.

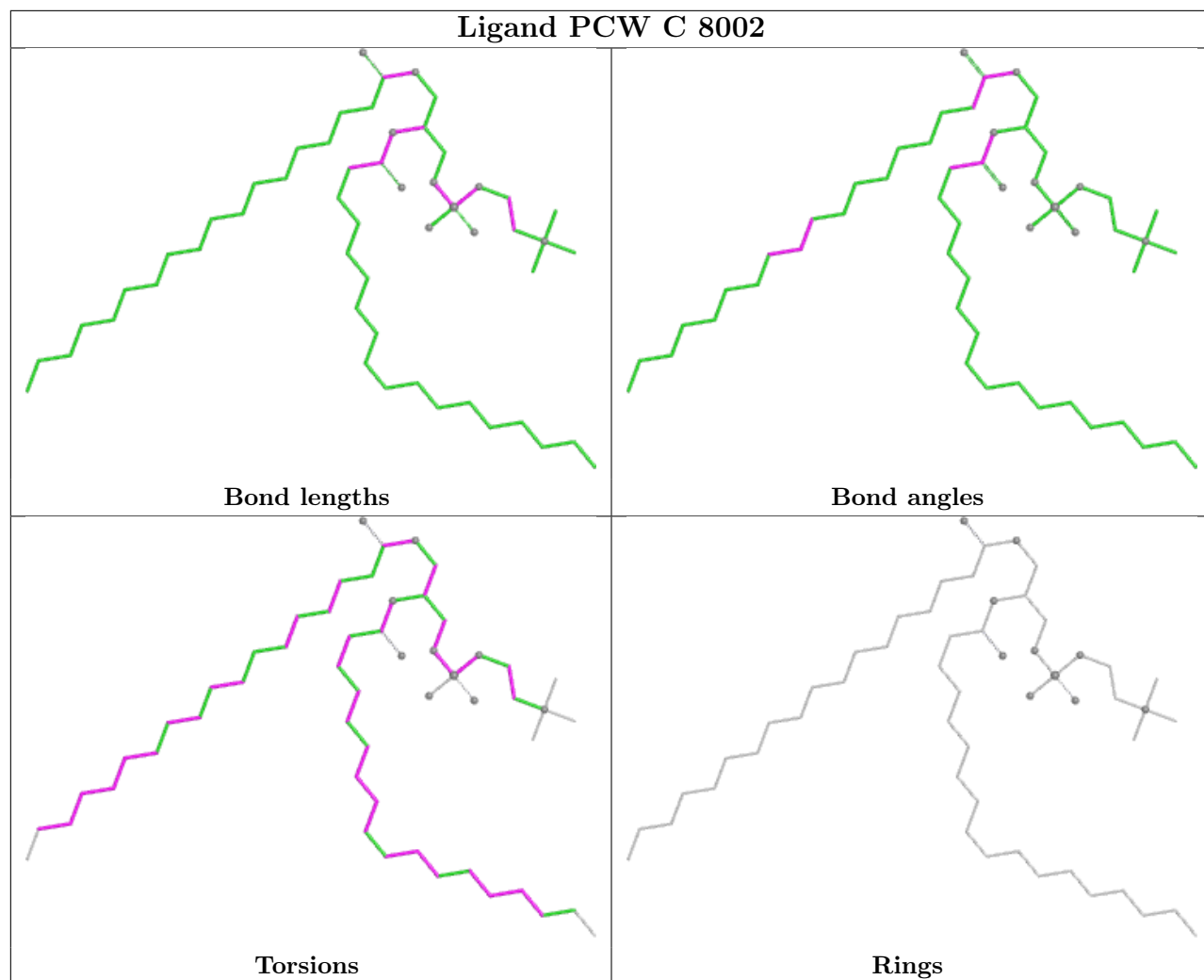
No monomer is involved in short contacts.

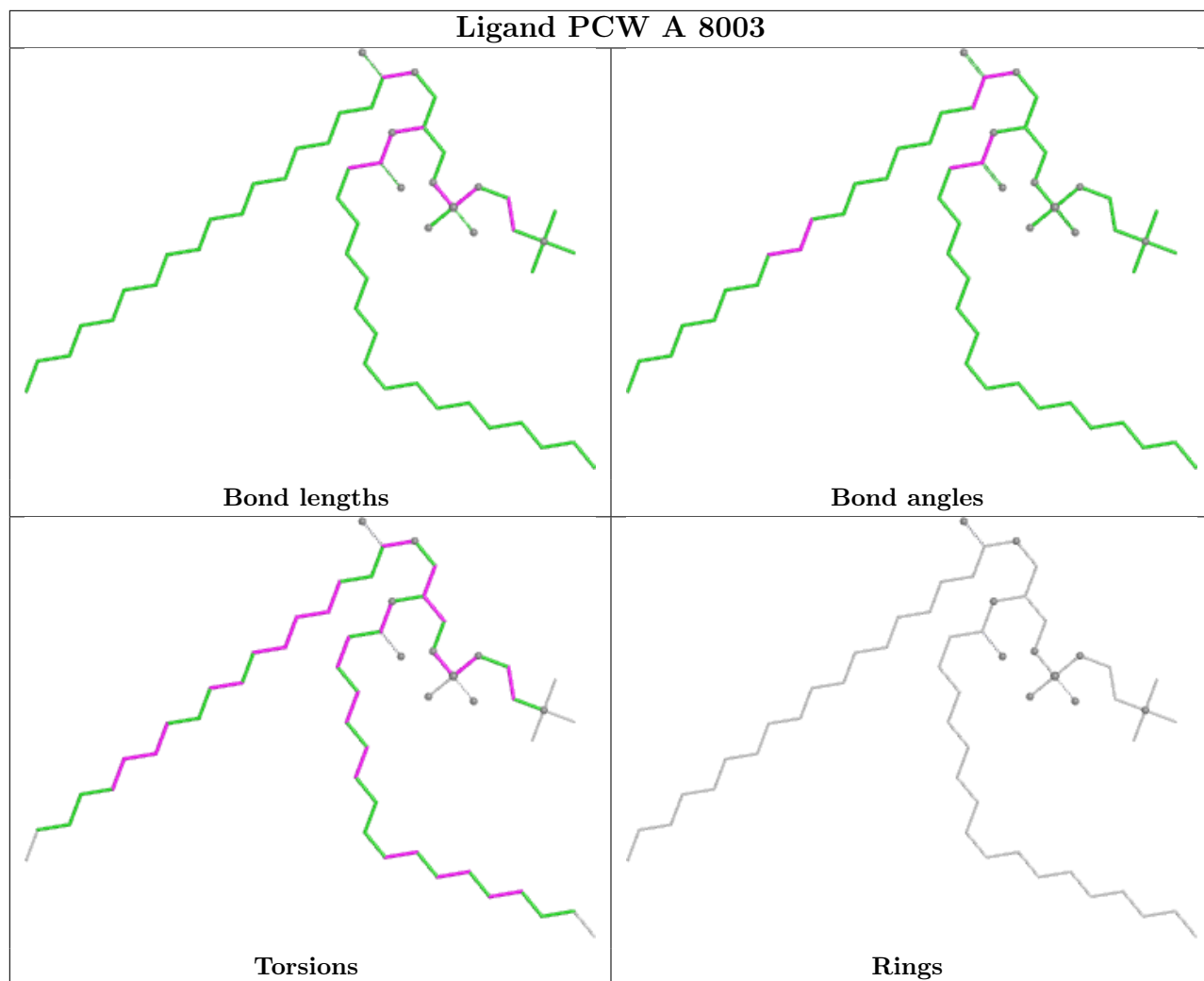
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

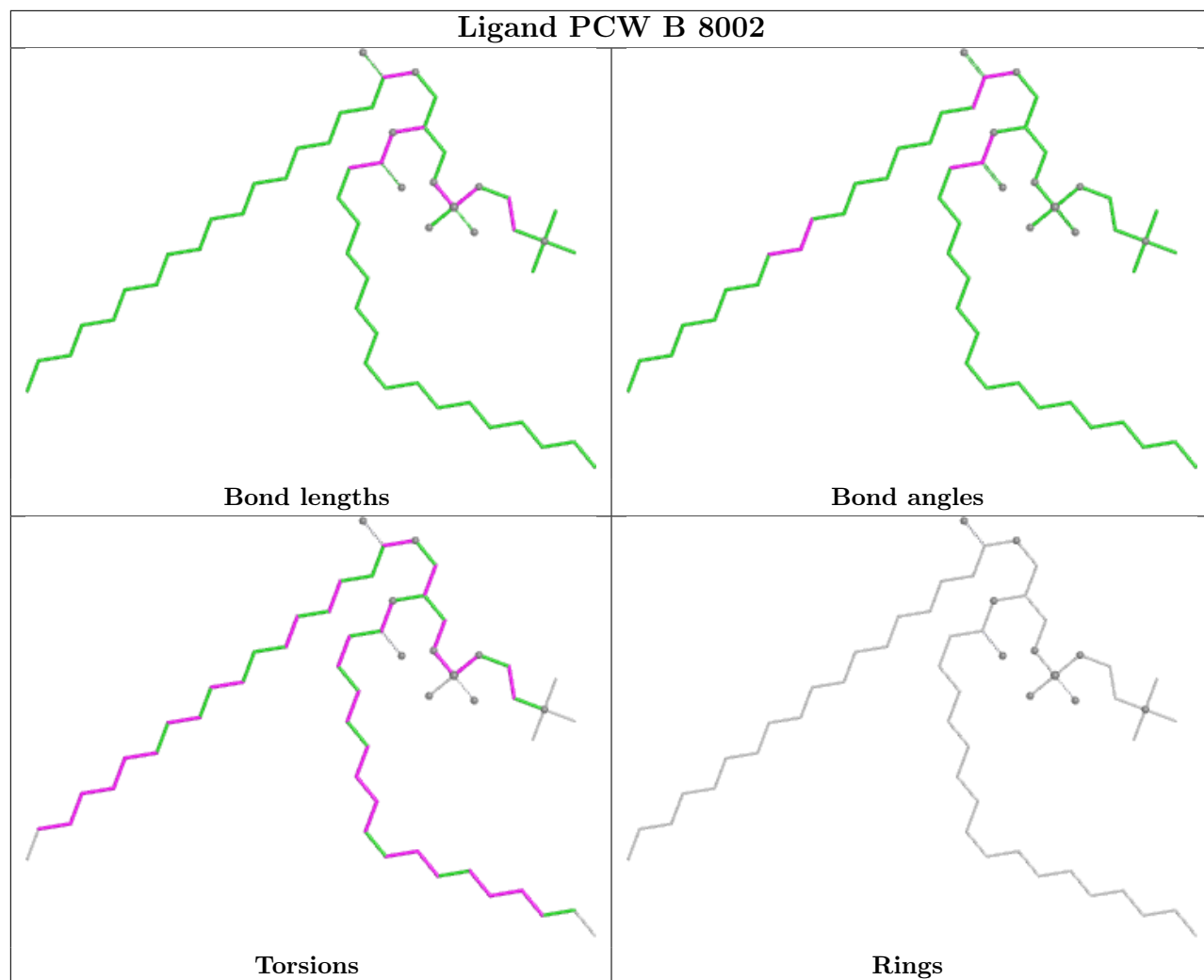


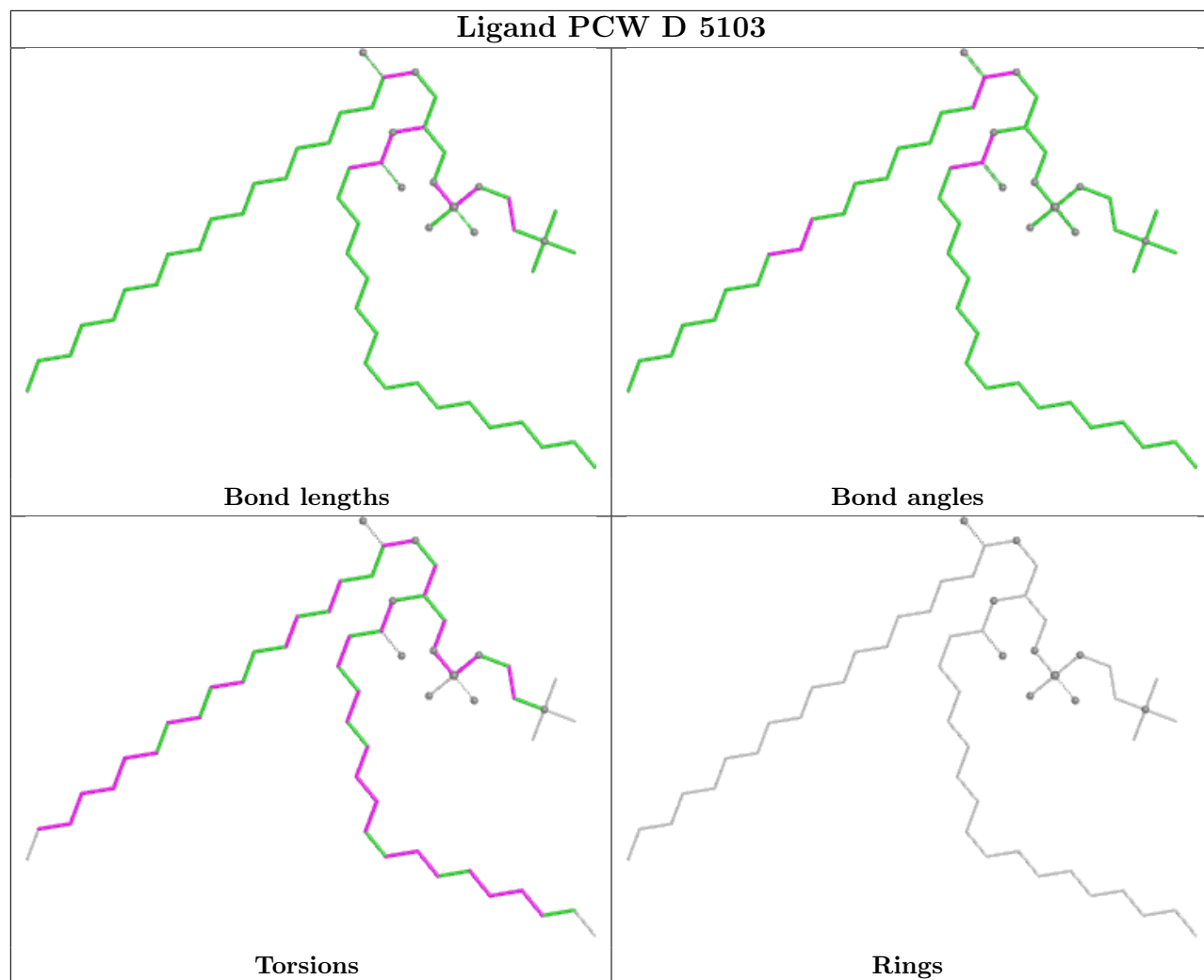


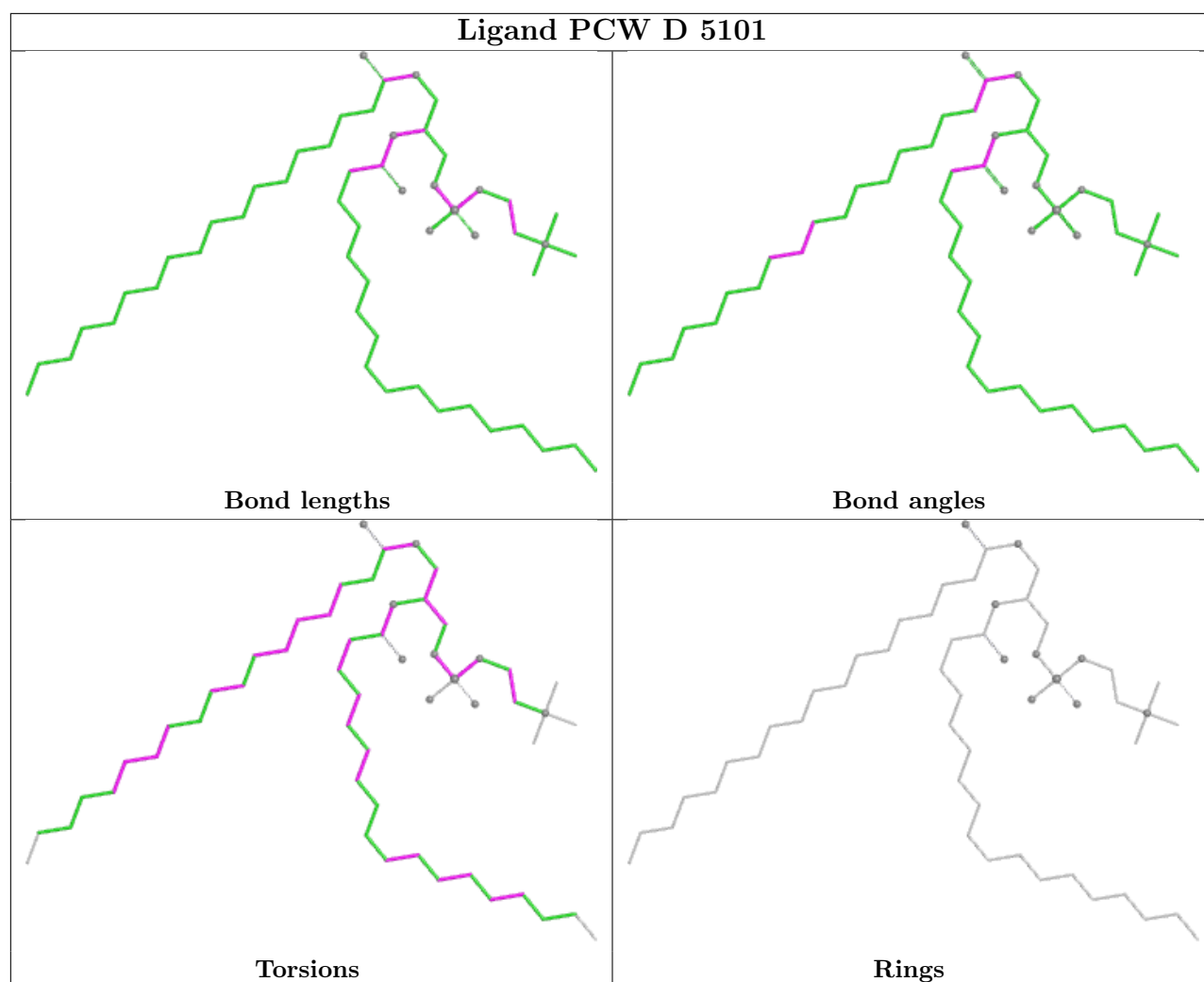












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

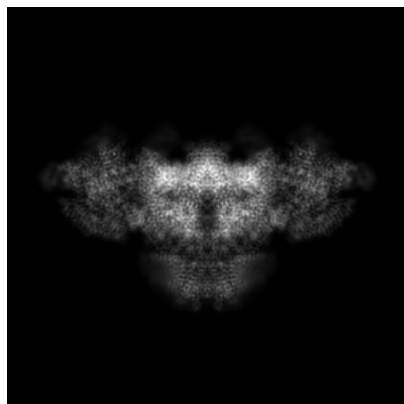
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-49538. These allow visual inspection of the internal detail of the map and identification of artifacts.

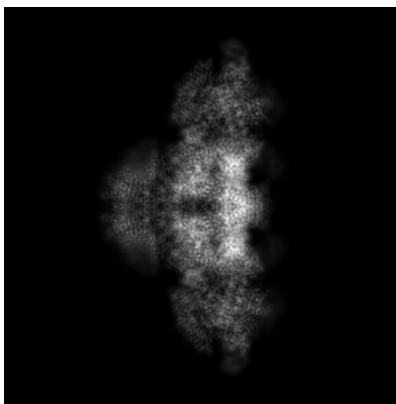
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

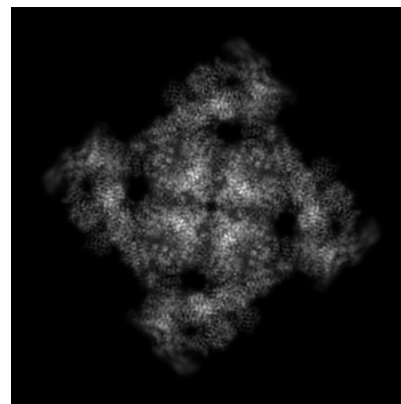
6.1.1 Primary map



X

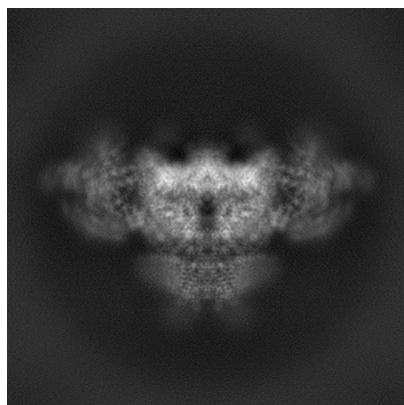


Y

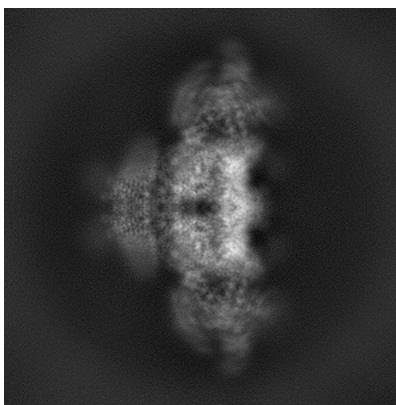


Z

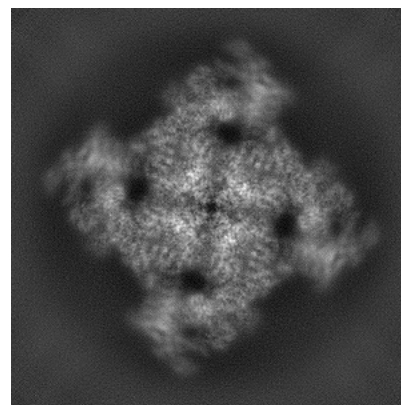
6.1.2 Raw map



X



Y



Z

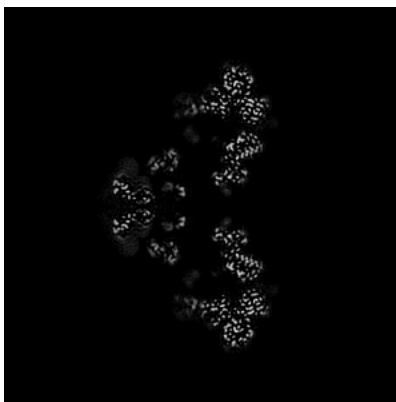
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

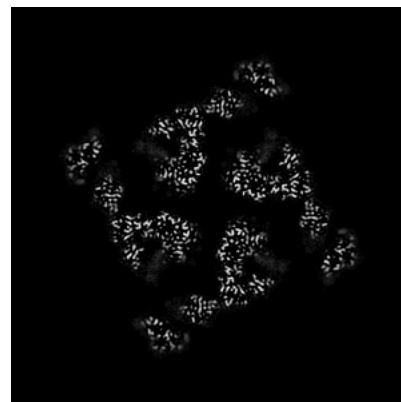
6.2.1 Primary map



X Index: 256

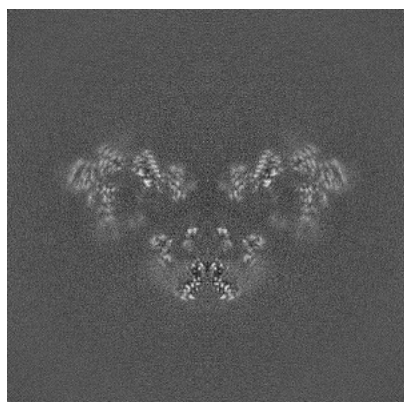


Y Index: 256

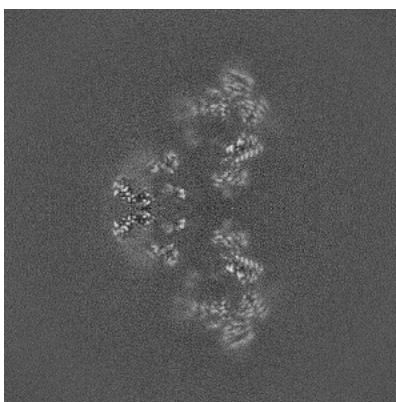


Z Index: 256

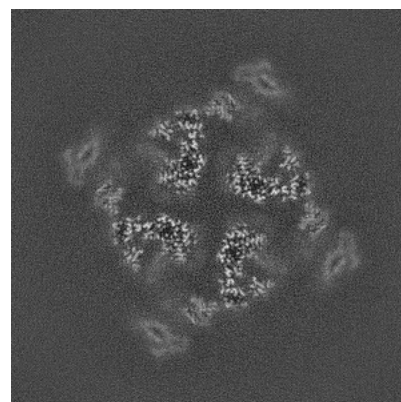
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

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

6.3 Largest variance slices [i](#)

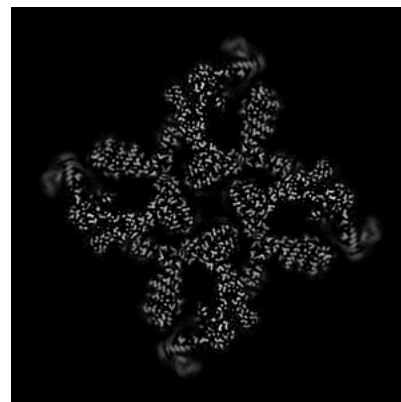
6.3.1 Primary map



X Index: 238

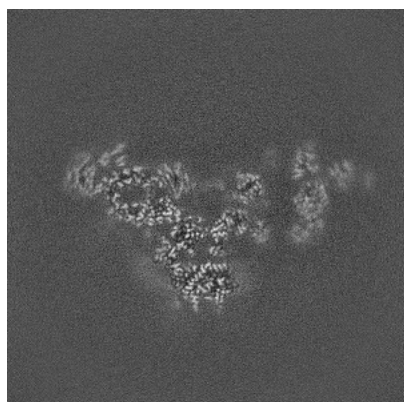


Y Index: 274

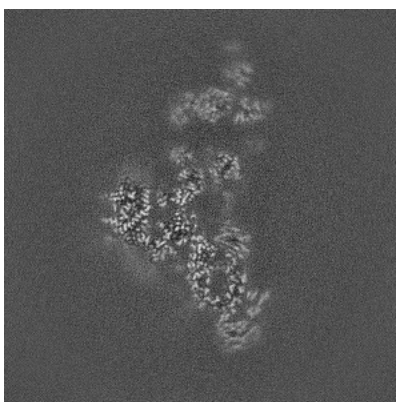


Z Index: 291

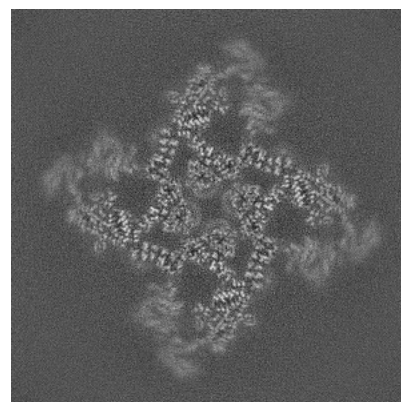
6.3.2 Raw map



X Index: 274



Y Index: 238

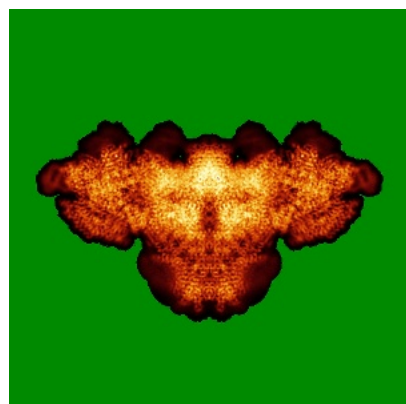


Z Index: 286

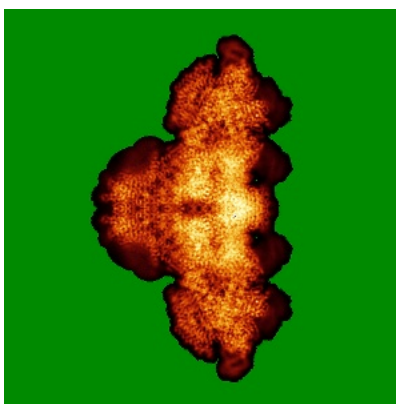
The images above show the largest variance slices of the map in three orthogonal directions.

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

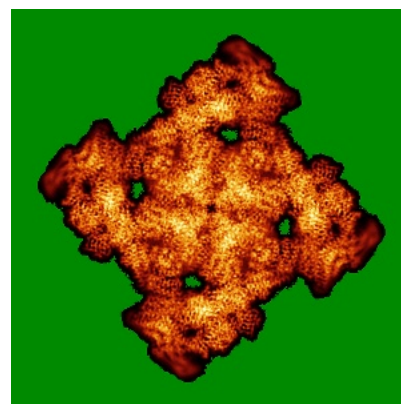
6.4.1 Primary map



X

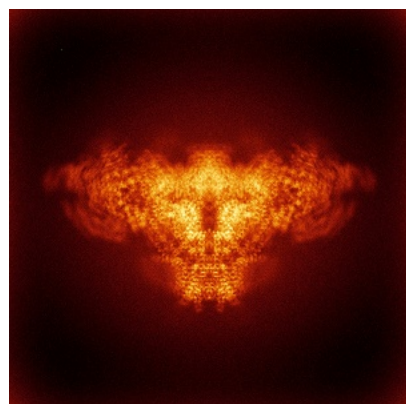


Y

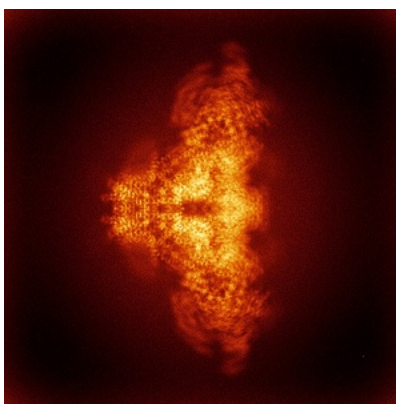


Z

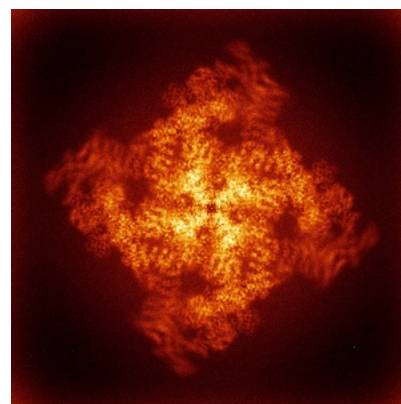
6.4.2 Raw map



X



Y

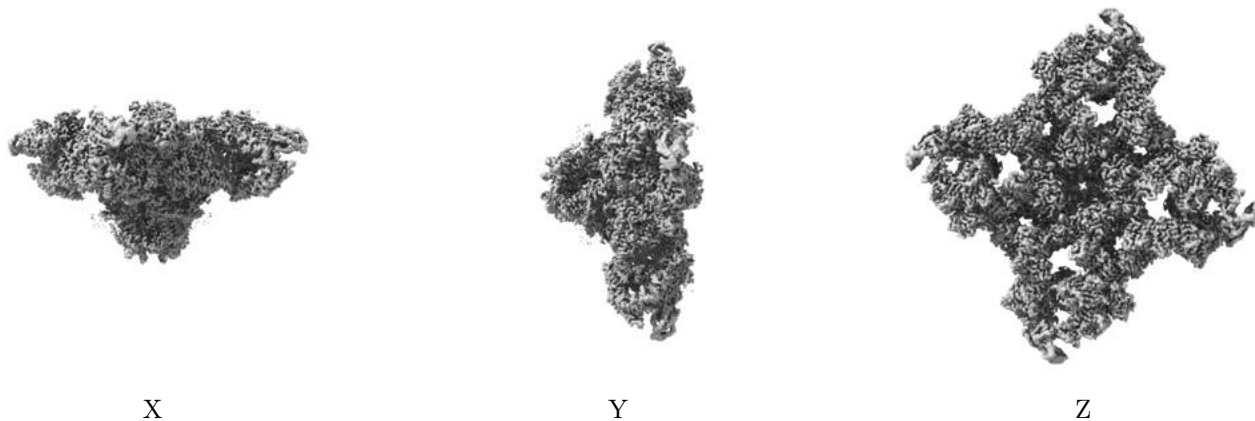


Z

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.

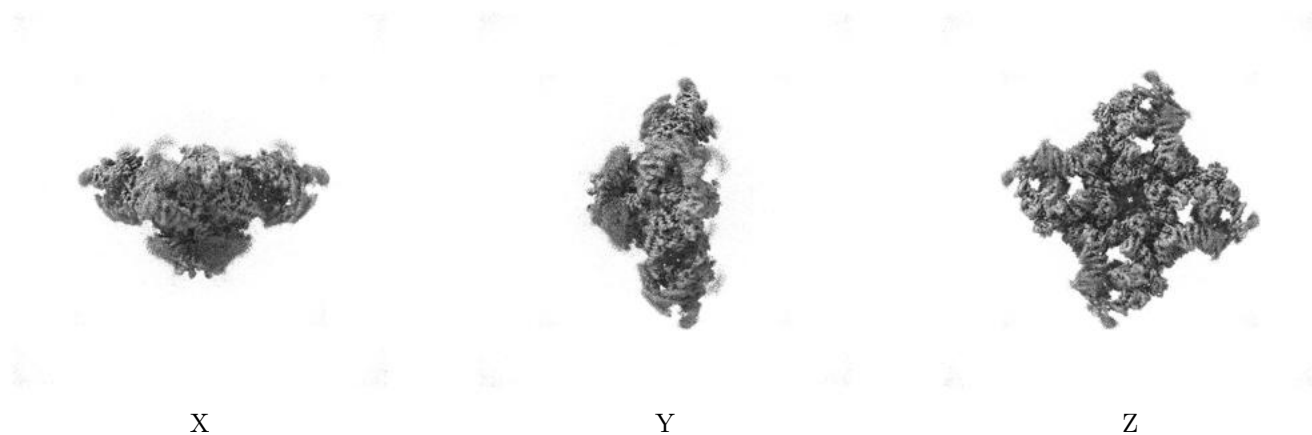
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

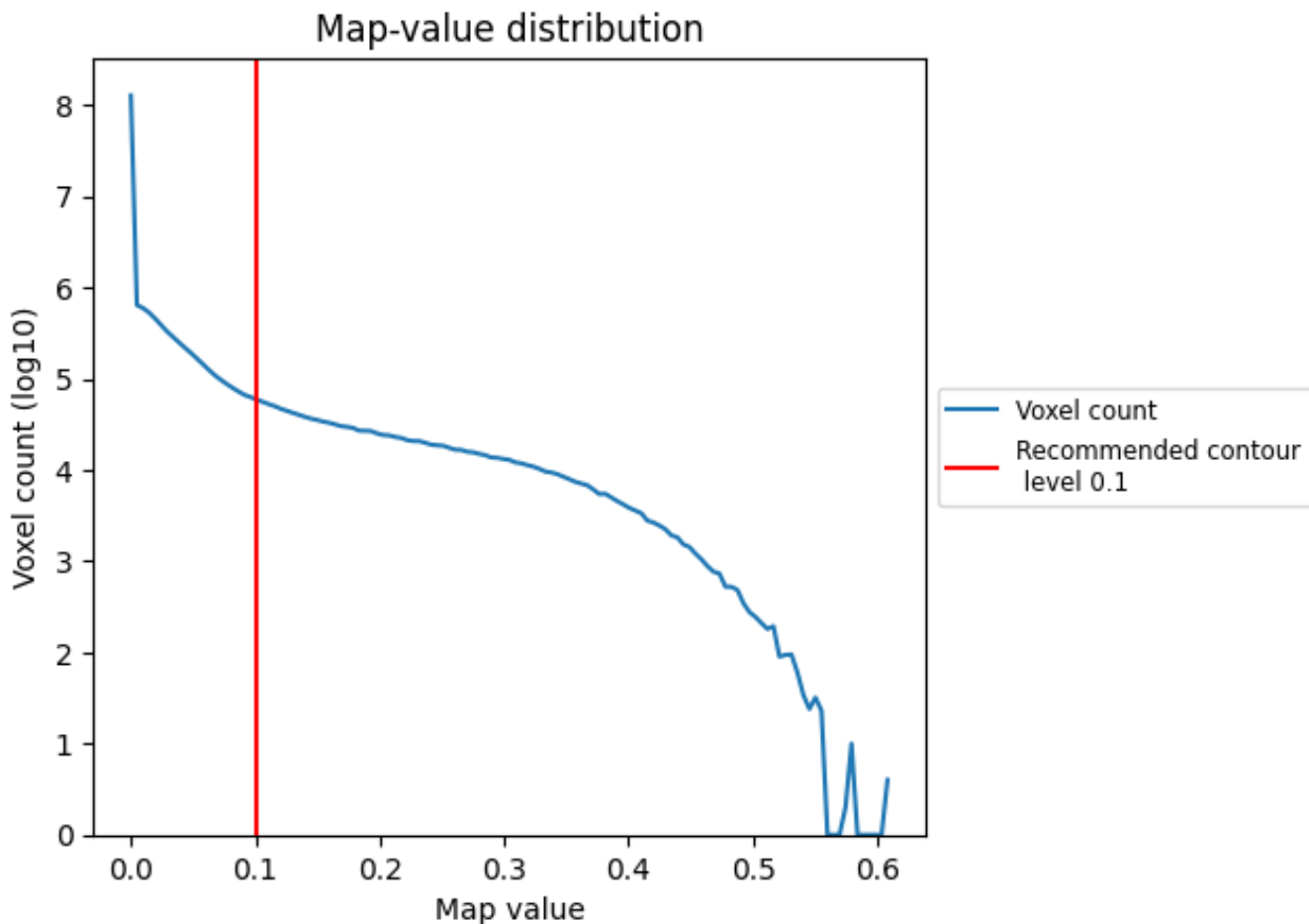
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

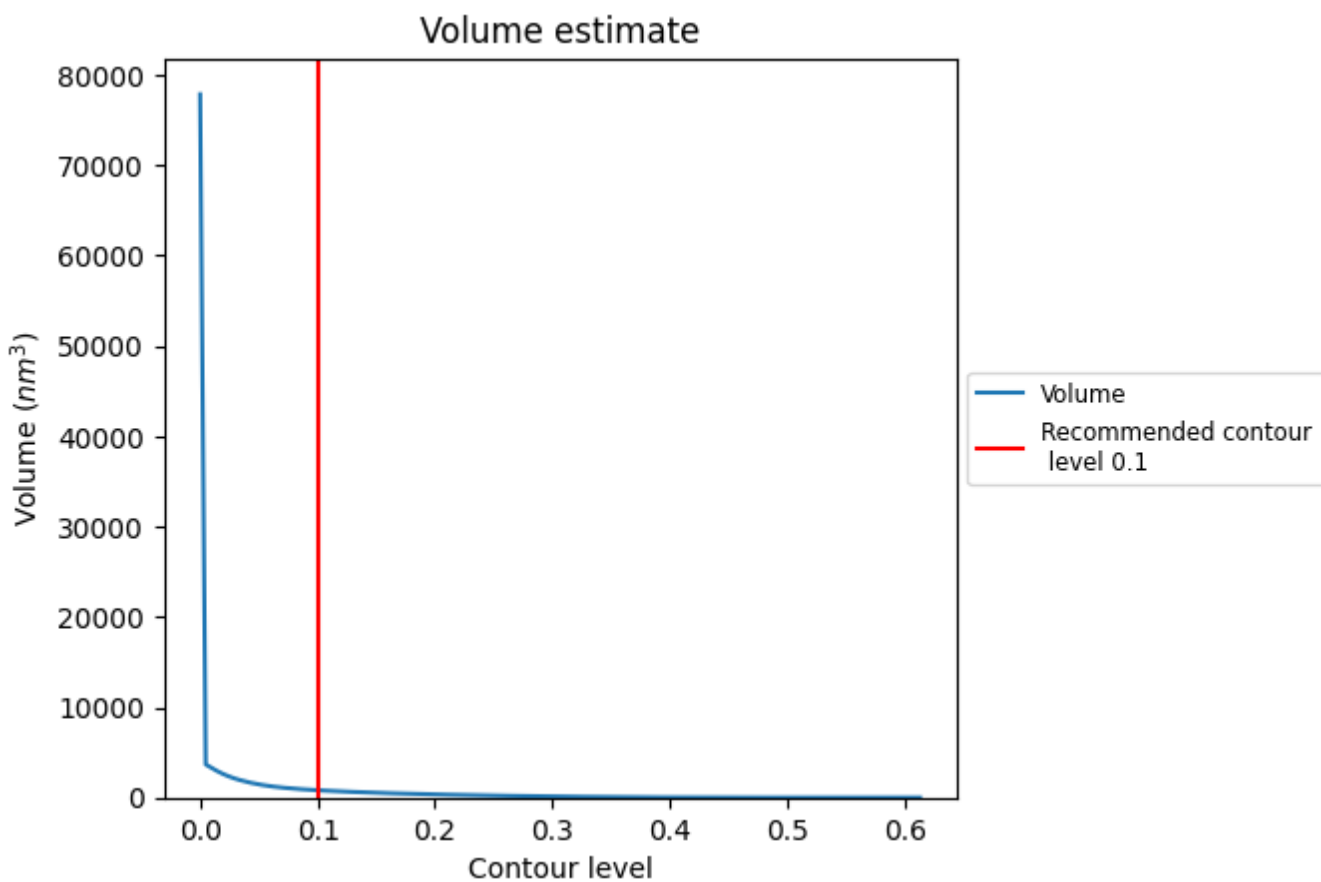
This section contains the results of statistical analysis of the map.

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.

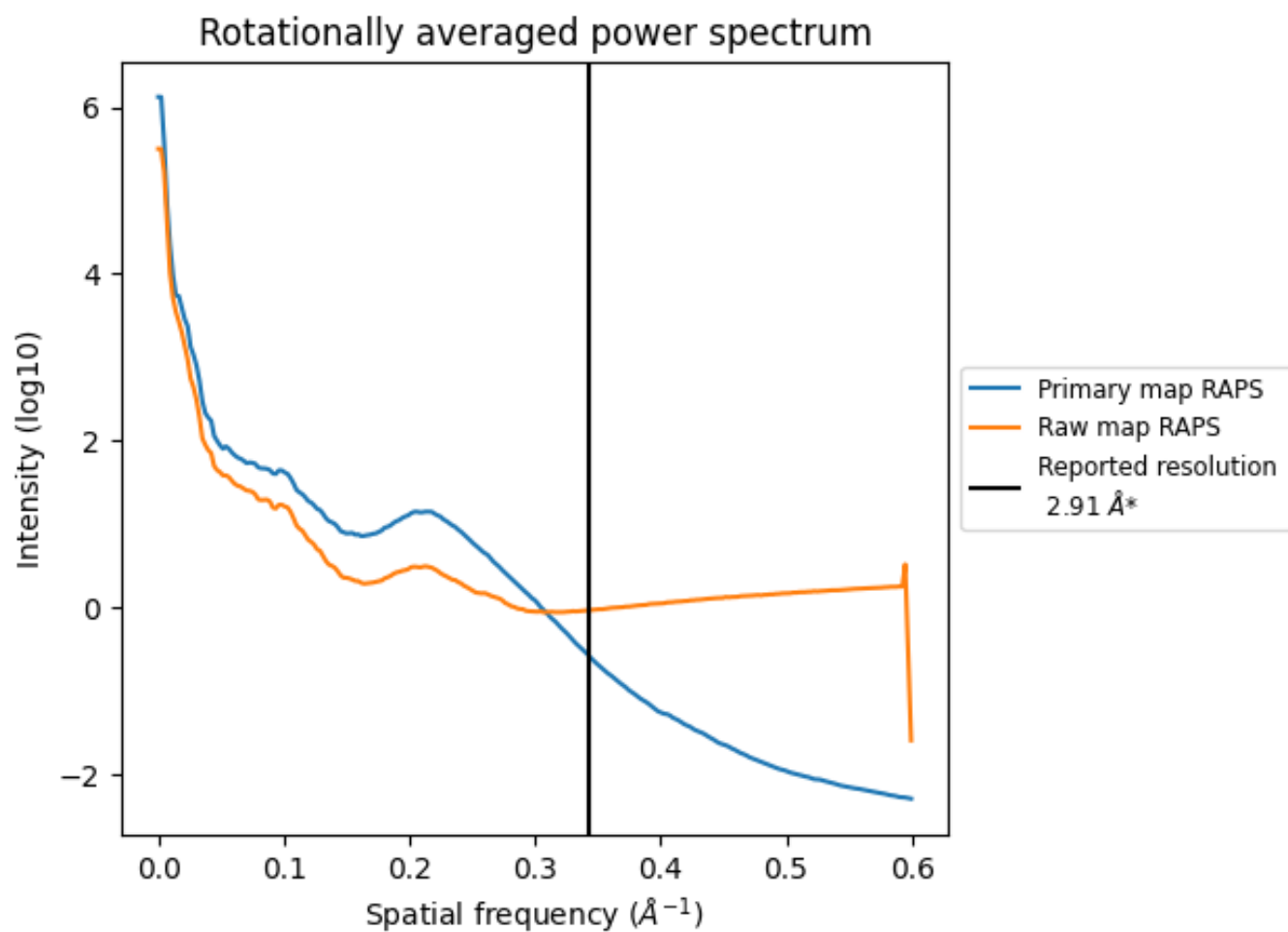
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 812 nm³; this corresponds to an approximate mass of 734 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

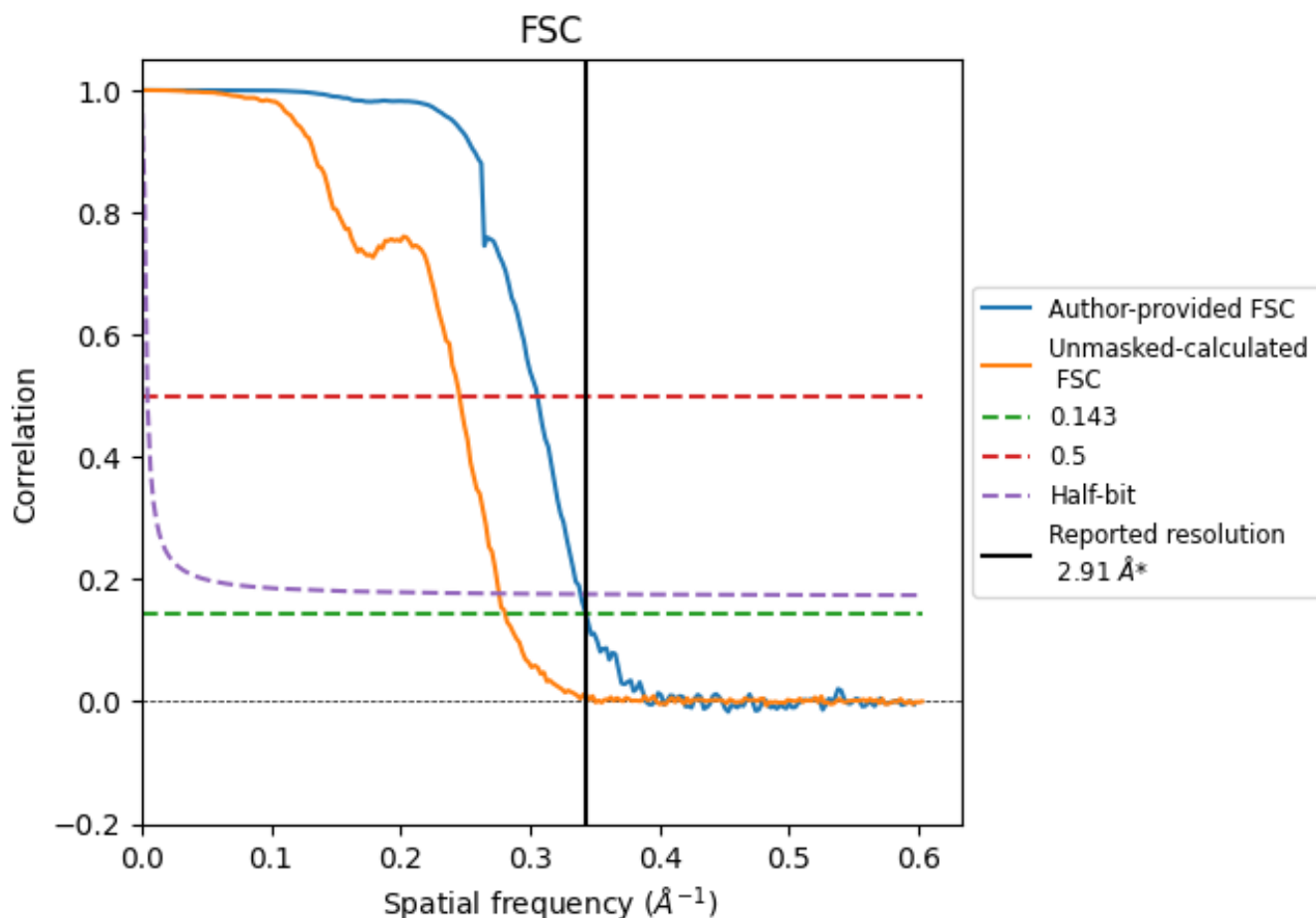


*Reported resolution corresponds to spatial frequency of 0.344 \AA^{-1}

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 0.344 Å⁻¹

8.2 Resolution estimates [i](#)

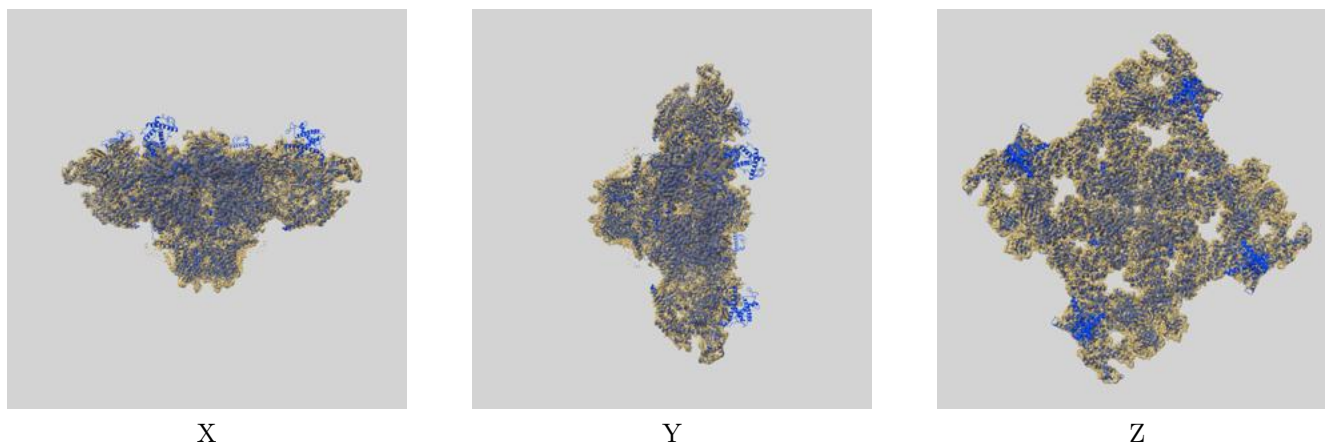
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	2.91	3.27	2.95
Unmasked-calculated*	3.56	4.07	3.62

*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 3.56 differs from the reported value 2.91 by more than 10 %

9 Map-model fit [i](#)

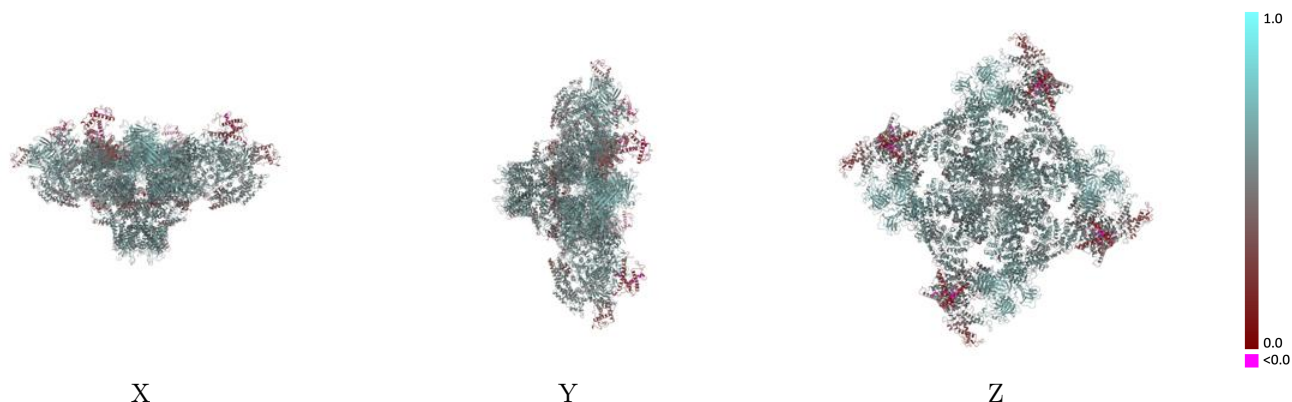
This section contains information regarding the fit between EMDB map EMD-49538 and PDB model 9NMR. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



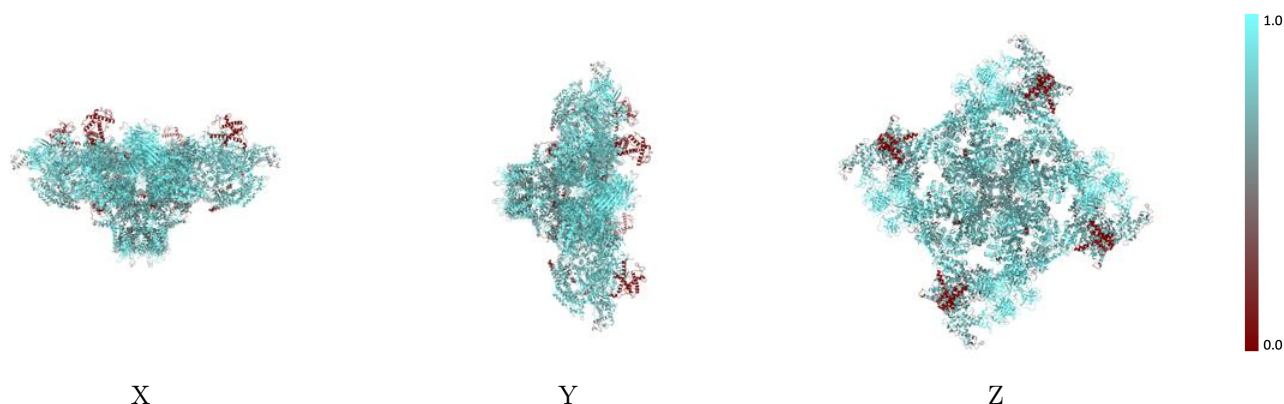
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



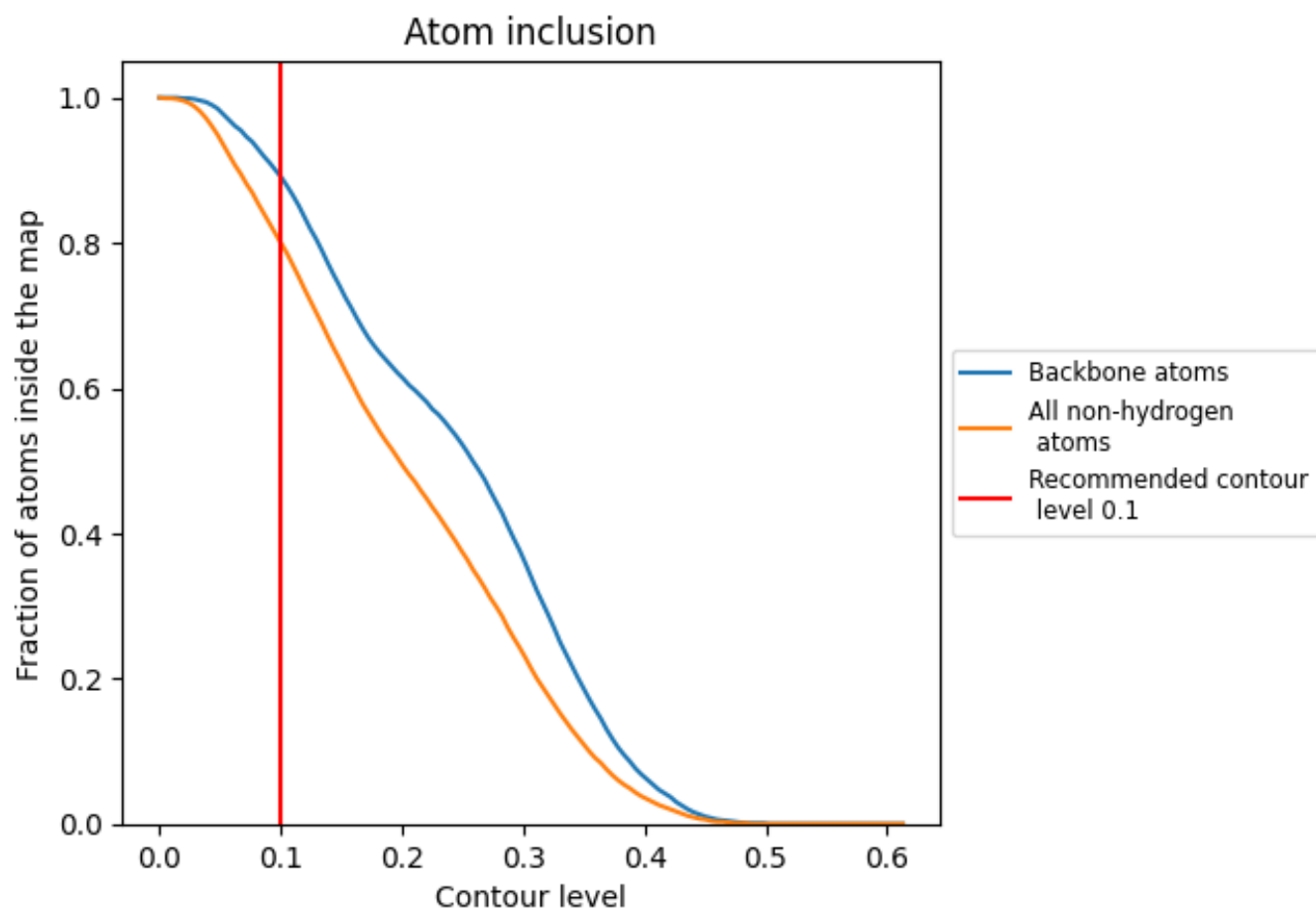
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).



















9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 80% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8000	 0.5360
A	 0.7980	 0.5340
B	 0.7980	 0.5340
C	 0.7970	 0.5340
D	 0.7980	 0.5350
E	 0.9050	 0.6020
F	 0.9000	 0.6000
G	 0.9040	 0.6040
H	 0.9020	 0.6040

