



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 08:55 AM UTC

PDB ID : 8VJJ / pdb_00008vjj
EMDB ID : EMD-43283
Title : Structure of mouse RyR1 (EGTA-only dataset)
Authors : Weninger, G.; Marks, A.R.
Deposited on : 2024-01-07
Resolution : 2.53 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:

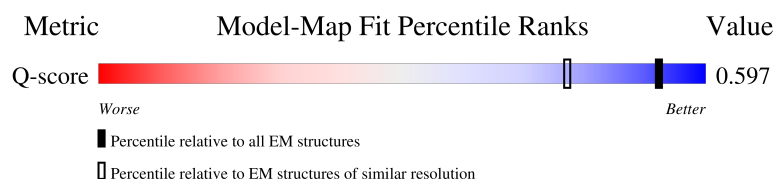
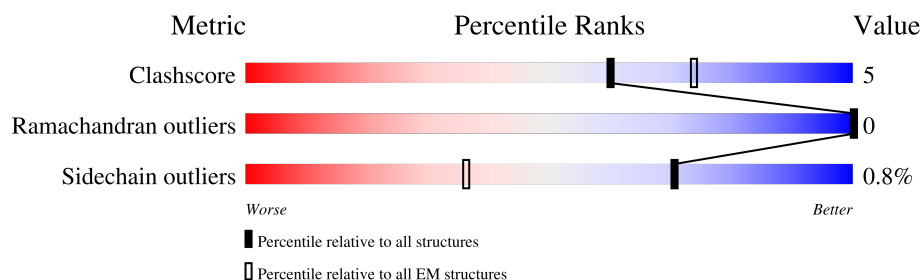
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 2.53 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	7309 (2.03 - 3.03)

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	13% 78% 9% 13%
1	B	5035	13% 78% 8% 13%
1	C	5035	13% 78% 9% 13%
1	D	5035	13% 78% 9% 13%

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Mol	Chain	Length	Quality of chain
2	E	108	95%
2	F	108	95%
2	G	108	94% 5%
2	H	108	94% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 284568 atoms, of which 141580 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	4374	Total	C	H	N	O	S	1	0
			69210	22140	34401	5985	6447	237		
1	D	4374	Total	C	H	N	O	S	1	0
			69210	22140	34401	5985	6447	237		
1	B	4374	Total	C	H	N	O	S	1	0
			69210	22140	34401	5985	6447	237		
1	C	4374	Total	C	H	N	O	S	1	0
			69210	22140	34401	5985	6447	237		

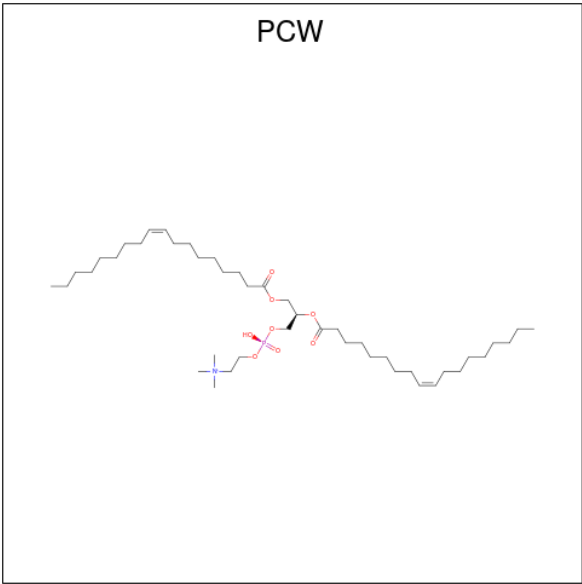
- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	E	107	Total	C	H	N	O	S	0	0
			1655	526	826	145	155	3		
2	H	107	Total	C	H	N	O	S	0	0
			1655	526	826	145	155	3		
2	F	107	Total	C	H	N	O	S	0	0
			1655	526	826	145	155	3		
2	G	107	Total	C	H	N	O	S	0	0
			1655	526	826	145	155	3		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).

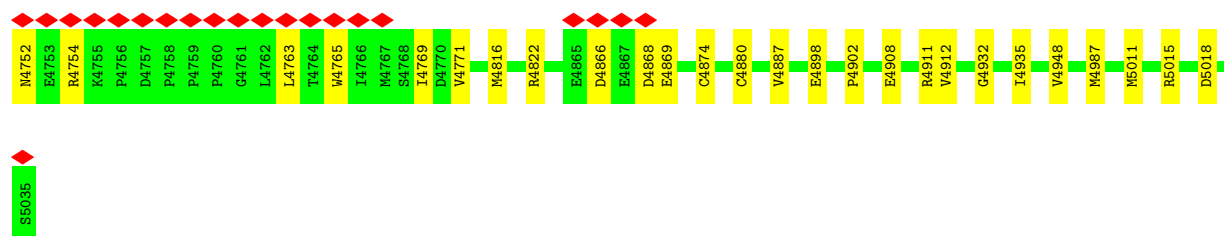


Mol	Chain	Residues	Atoms						AltConf
4	A	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	A	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	D	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	D	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	B	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	B	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	C	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	
4	C	1	Total	C	H	N	O	P	0
			138	44	84	1	8	1	

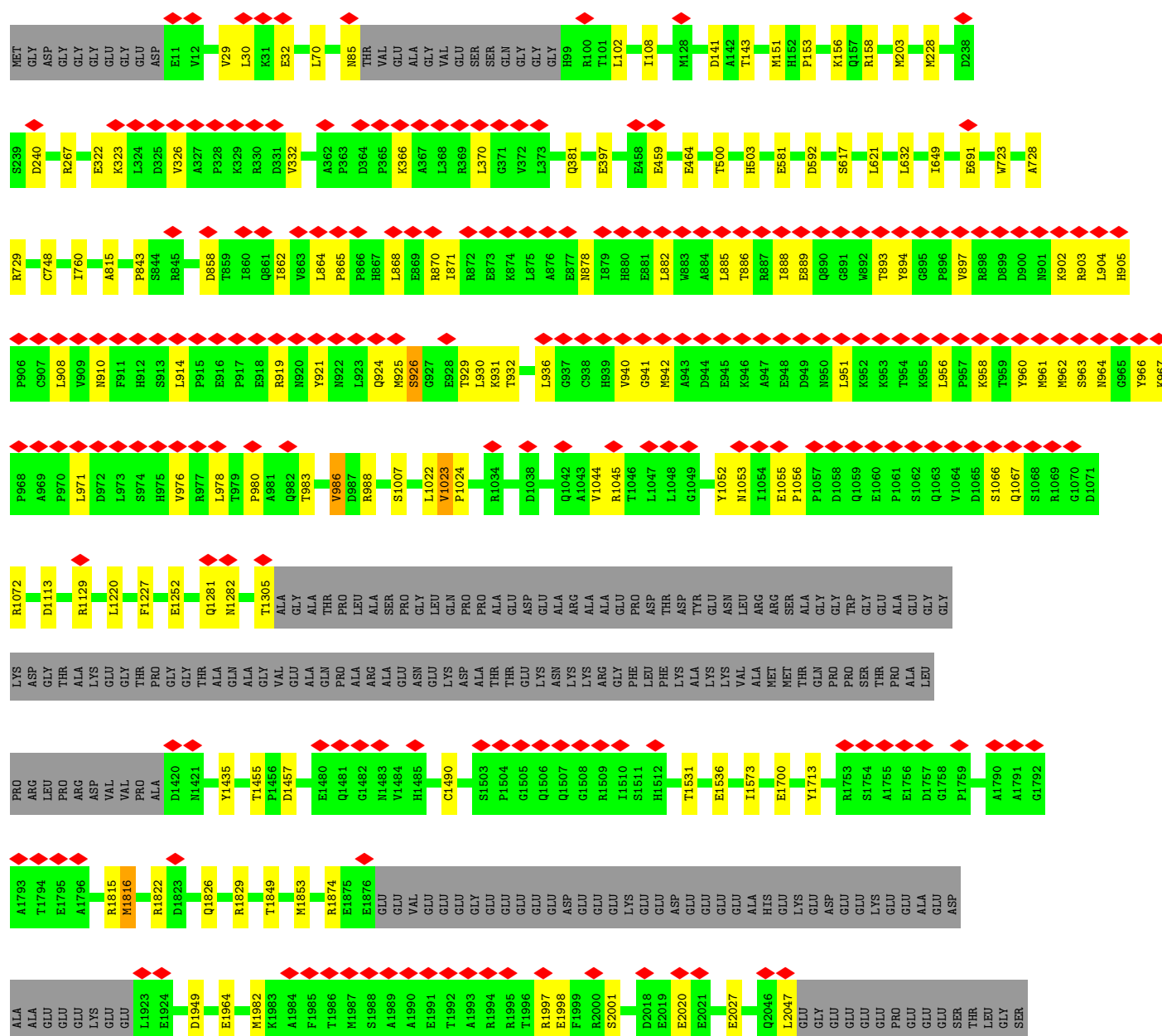
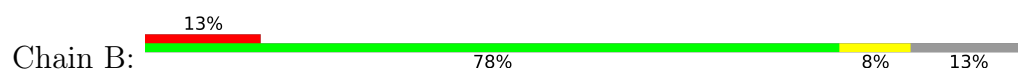






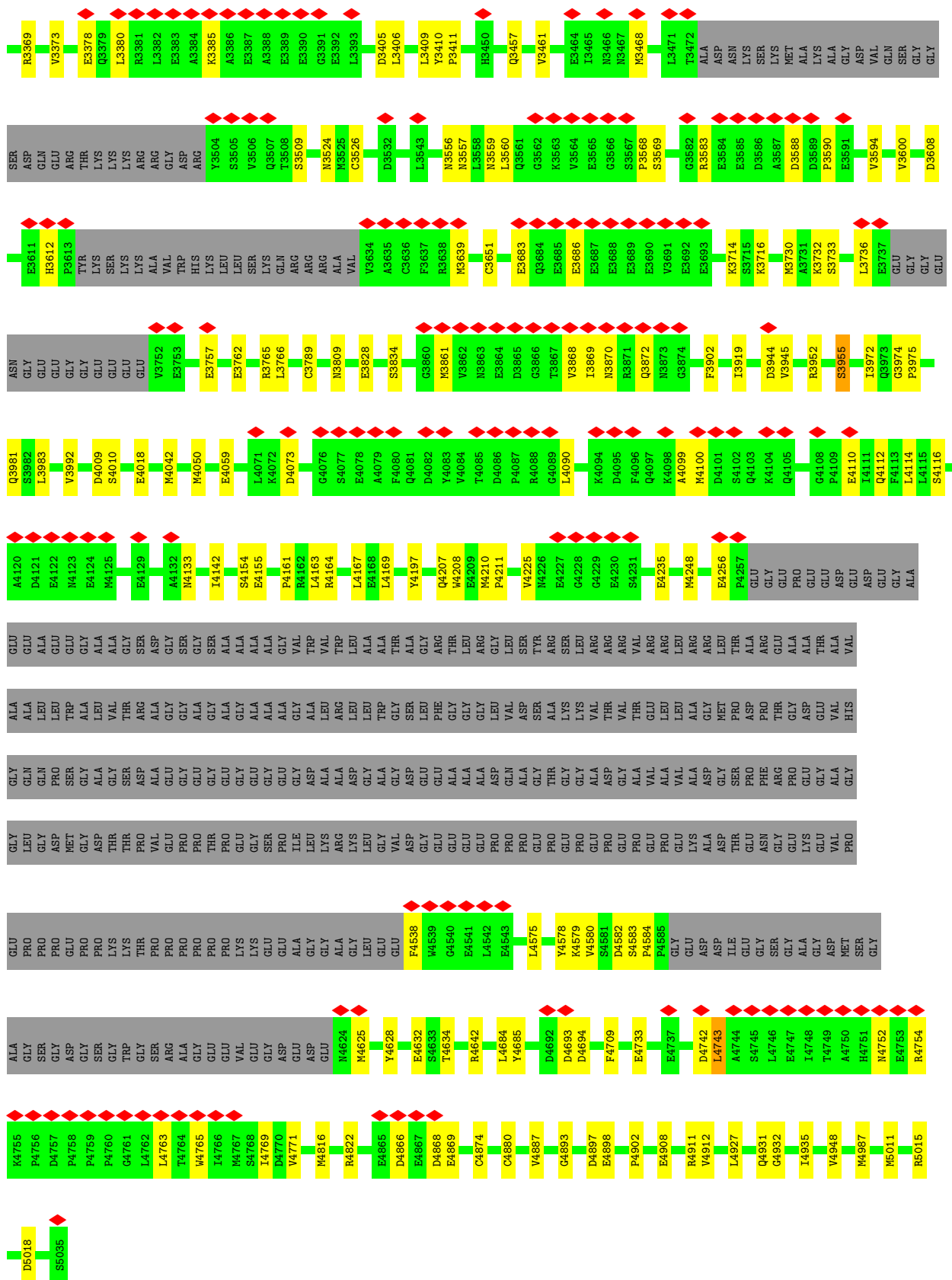


• Molecule 1: Ryanodine receptor 1

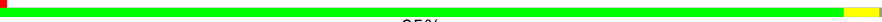


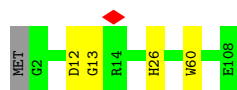
E4059	E3757	HIS	ASP	E3383	H3147	R2940	A2880	W2820	A2760	ARG
L4071	E3762	LYS	ARG	A3384	L3170	G2941	E2981	E2621	E2761	LEU
L4072	R3765	LEU	Y3504	K3385	L2942	L2942	E2882	W2822	Y2762	MET
D4073	L3766	SER	S3505	A3386	L3176	K2943	Y2883	T2823	T2763	LEU
G4076	C3789	LYS	Q3507	A3387	R3180	D2944	W2884	V2824	H2764	LEU
S4077	N3809	GLN	T3508	A3388	M2945	M2945	W2885	E2825	E2765	GLU
E4078	N3809	ARG	S3509	E3389	E2946	E2946	T2886	K2826	K2766	LYS
F4079	S3834	ARG	N3524	E3390	L2947	L2947	W2887	A2827	W2767	VAL
F4080	S3834	ALA	N3525	G3391	D2948	D2948	Q2888	R2828	F2768	LYS
Q4081	G3860	VAL	C3526	L3393	S2950	S2950	W2889	E2829	A2769	VAL
D4082	M3861	VAL	D3532	D3405	K2954	K2954	W2890	G2830	L2641	LYS
Y4083	V3862	C3636	L3543	L3406	S2971	S2971	E2891	E2831	L2645	LYS
Y4084	N3863	F3637	N3556	Y3410	F2974	F2974	W2892	GLU	L2679	THR
T4085	E3864	R3638	L3557	P3411	L2978	L2978	E2893	GLU	E2286	LYS
D4086	D3865	C3651	N3558	H3450	V2981	V2981	W2894	LYS	E2283	LYS
P4087	G3866	Q3651	L3560	Q3457	Y2982	Y2982	E2895	THR	E2297	THR
R4088	T3867	E3683	L3561	E3464	D3236	D3236	E2896	LYS	E2372	GLU
G4089	V3868	Q3684	G3562	I3465	E3239	E3239	E2897	LYS	E2372	PRO
L4090	V3869	E3685	Q3561	N3466	F2974	F2974	E2898	LYS	E2383	GLU
K4094	R3870	E3686	N3565	N3467	L2978	L2978	E2899	THR	R2386	GLU
D4095	N3871	E3687	L3566	N3468	V2981	V2981	E2900	ARG	D2394	PRO
F4096	Q3872	E3688	L3567	N3469	Y2982	Y2982	E2901	LYS	G2397	GLU
Q4097	N3873	E3689	P3567	N3470	E2988	E2988	E2902	ILE	V2398	GLU
K4098	G3874	E3690	S3568	N3471	E2989	E2989	E2903	GLN	ARG	H2090
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Q4103	V3945	K3714	E3584	LYS	P3005	P3005	E2907	GLN	ASP	K2127
K4104	R3952	S3715	A3296	SER	T3041	T3041	E2908	TYR	GLU	HIS
Q4105	S3952	K3716	L3297	LYS	L3057	L3057	E2909	ASP	GLY	PHE
G4108	S3955	N3730	P3298	MET	L3057	L3057	E2910	PRO	GLU	K2187
P4109	I3972	S3733	A3299	ALA	L3076	L3076	E2911	ARG	GLU	Y2193
E4110	Q3973	E3737	G3300	LYS	I3088	I3088	E2912	GLY	P2411	W2213
D4112	G3974	L3736	A3301	GLY	V3108	V3108	E2913	VAL	W2214	W2215
F4113	P3975	E3737	L3316	ASP	V3108	V3108	E2914	GLN	E2414	E2415
L4114	Q3981	GLY	V3325	VAL	L3111	L3111	E2915	ALA	N2419	G2218
A4120	S3982	GLY	T3362	GLN	R3112	R3112	E2916	ARG	L2419	G2219
D4121	L3983	GLY	L3366	GLY	L3113	L3113	E2917	THR	A2438	E2220
N4123	V3992	ASN	R3369	SER	GLY	GLY	E2918	GLN	T2441	K2222
E4124	D4009	GLY	E3611	ASP	VAL	VAL	E2919	ALA	Q2445	E2223
M4125	S4010	GLY	H3612	GLN	GLY	GLY	E2920	ALA	T2445	L2224
E4129	E4018	GLY	P3613	ARG	GLY	GLY	E2921	ALA	Q2445	R2225
A4132	M4042	GLY	T3379	THR	GLY	GLY	E2922	ARG	F2226	F2227
L4142	M4050	GLY	Q3379	LYS	GLY	GLY	E2923	LYS	L2480	K2228
S4154	E4155	GLY	L3380	LYS	GLY	GLY	E2924	THR	G2481	W2229
P4161	E4161	GLY	R3381	ARG	GLY	GLY	E2925	ARG	K2482	R2249
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		GLY		GLY	GLY	GLY	E3037	GLY		
		GLY		GLY	GLY	GLY	E3038	GLY		
		GLY		GLY	GLY	GLY	E3039	GLY		





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

Chain E:  95% ..



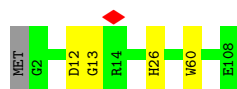
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain H:  94% 6% .



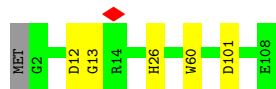
- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A

Chain F:  95% ..



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

Chain G:  94% 5% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	336237	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN 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	0.804	Depositor
Minimum map value	0.000	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.029	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	428.544, 428.544, 428.544	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.837, 0.837, 0.837	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, PCW

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	0.16	0/35601	0.31	2/48224 (0.0%)
1	B	0.16	0/35601	0.31	1/48224 (0.0%)
1	C	0.16	0/35601	0.31	1/48224 (0.0%)
1	D	0.16	0/35601	0.31	1/48224 (0.0%)
2	E	0.14	0/847	0.27	0/1142
2	F	0.13	0/847	0.26	0/1142
2	G	0.14	0/847	0.27	0/1142
2	H	0.14	0/847	0.27	0/1142
All	All	0.16	0/145792	0.31	5/197464 (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	B	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	4584	PRO	CA-N-CD	-9.53	98.66	112.00
1	C	4584	PRO	CA-N-CD	-9.46	98.76	112.00
1	B	4584	PRO	CA-N-CD	-9.35	98.91	112.00
1	A	4584	PRO	CA-N-CD	-9.29	98.99	112.00
1	A	3568	PRO	CA-N-CD	-5.55	104.22	112.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	3230	ILE	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	34809	34401	34401	325	0
1	B	34809	34401	34401	311	0
1	C	34809	34401	34401	327	0
1	D	34809	34401	34401	321	0
2	E	829	826	826	1	0
2	F	829	826	826	1	0
2	G	829	826	826	2	0
2	H	829	826	826	2	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	168	167	0	0
4	B	108	168	167	3	0
4	C	108	168	168	3	0
4	D	108	168	167	1	0
All	All	142988	141580	141577	1291	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 1291 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2828:ARG:NH1	1:D:2935:GLY:O	1.99	0.93
1:C:4110:GLU:O	1:C:4114:LEU:HD12	1.70	0.91
1:B:4110:GLU:O	1:B:4114:LEU:HD12	1.70	0.90
1:A:4110:GLU:O	1:A:4114:LEU:HD12	1.70	0.90
1:C:893:THR:HG23	1:C:904:LEU:HD23	1.50	0.89

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	4347/5035 (86%)	4240 (98%)	107 (2%)	0	100	100
1	B	4347/5035 (86%)	4238 (98%)	109 (2%)	0	100	100
1	C	4347/5035 (86%)	4236 (97%)	111 (3%)	0	100	100
1	D	4347/5035 (86%)	4241 (98%)	106 (2%)	0	100	100
2	E	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	F	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	G	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
2	H	105/108 (97%)	102 (97%)	3 (3%)	0	100	100
All	All	17808/20572 (87%)	17363 (98%)	445 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	3808/4296 (89%)	3783 (99%)	25 (1%)	76	89
1	B	3808/4296 (89%)	3780 (99%)	28 (1%)	76	89
1	C	3808/4296 (89%)	3780 (99%)	28 (1%)	76	89
1	D	3808/4296 (89%)	3781 (99%)	27 (1%)	76	89
2	E	89/90 (99%)	87 (98%)	2 (2%)	45	71
2	F	89/90 (99%)	87 (98%)	2 (2%)	45	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	G	89/90 (99%)	87 (98%)	2 (2%)	45	71
2	H	89/90 (99%)	86 (97%)	3 (3%)	32	57
All	All	15588/17544 (89%)	15471 (99%)	117 (1%)	70	88

5 of 117 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	4116	SER
1	C	3902	PHE
1	B	2297	GLU
1	C	3509	SER
1	C	2761	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1512	HIS
1	B	4226	ASN
1	B	1950	GLN
1	B	3557	ASN
1	C	114	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	A	8003	-	53,53,53	1.17	5 (9%)	59,61,61	2.27	9 (15%)
4	PCW	D	5103	-	53,53,53	1.18	6 (11%)	59,61,61	2.37	10 (16%)
4	PCW	A	8002	-	53,53,53	1.17	4 (7%)	59,61,61	2.34	9 (15%)
4	PCW	C	5103	-	53,53,53	1.17	5 (9%)	59,61,61	2.36	9 (15%)
4	PCW	C	5101	-	53,53,53	1.18	5 (9%)	59,61,61	2.27	9 (15%)
4	PCW	B	8002	-	53,53,53	1.16	5 (9%)	59,61,61	2.39	9 (15%)
4	PCW	B	8003	-	53,53,53	1.18	5 (9%)	59,61,61	2.28	9 (15%)
4	PCW	D	5101	-	53,53,53	1.18	5 (9%)	59,61,61	2.29	9 (15%)

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	A	8003	-	-	22/57/57/57	-
4	PCW	D	5103	-	-	25/57/57/57	-
4	PCW	A	8002	-	-	25/57/57/57	-
4	PCW	C	5103	-	-	24/57/57/57	-
4	PCW	C	5101	-	-	26/57/57/57	-
4	PCW	B	8002	-	-	22/57/57/57	-
4	PCW	B	8003	-	-	23/57/57/57	-
4	PCW	D	5101	-	-	20/57/57/57	-

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	5103	PCW	O3-C11	3.12	1.42	1.33
4	B	8002	PCW	O3-C11	3.10	1.42	1.33
4	C	5103	PCW	O3-C11	3.09	1.42	1.33
4	D	5101	PCW	O3-C11	3.04	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	8003	PCW	O3-C11	3.04	1.42	1.33

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	5103	PCW	C8-N-C6	12.12	140.80	108.98
4	B	8002	PCW	C8-N-C6	12.05	140.63	108.98
4	C	5103	PCW	C8-N-C6	11.88	140.18	108.98
4	A	8002	PCW	C8-N-C6	11.74	139.82	108.98
4	D	5101	PCW	C8-N-C6	10.63	136.90	108.98

There are no chirality outliers.

5 of 187 torsion outliers are listed below:

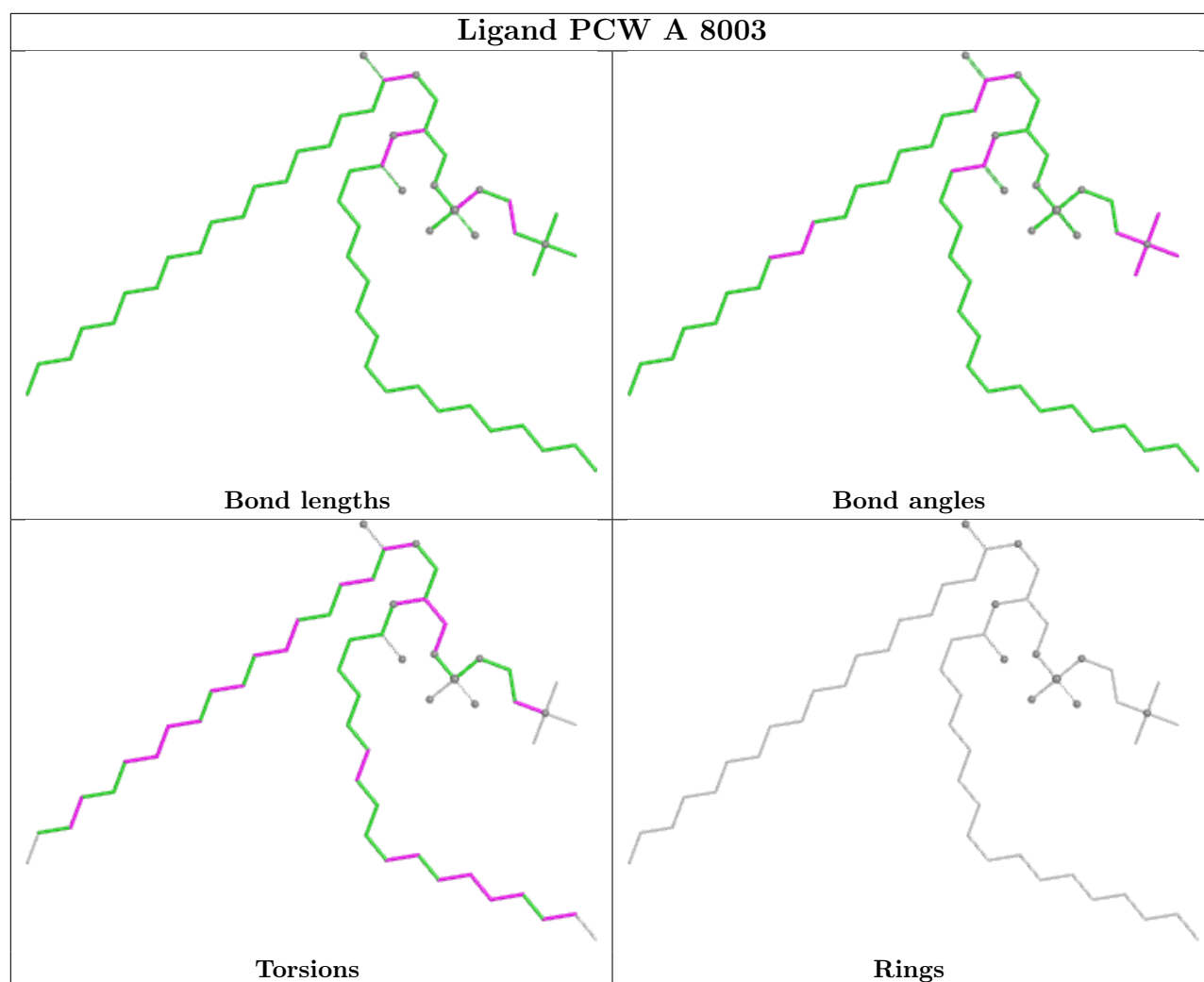
Mol	Chain	Res	Type	Atoms
4	A	8002	PCW	O4P-C4-C5-N
4	A	8002	PCW	C1-O3P-P-O4P
4	D	5101	PCW	O4P-C4-C5-N
4	D	5103	PCW	O4P-C4-C5-N
4	D	5103	PCW	C1-O3P-P-O4P

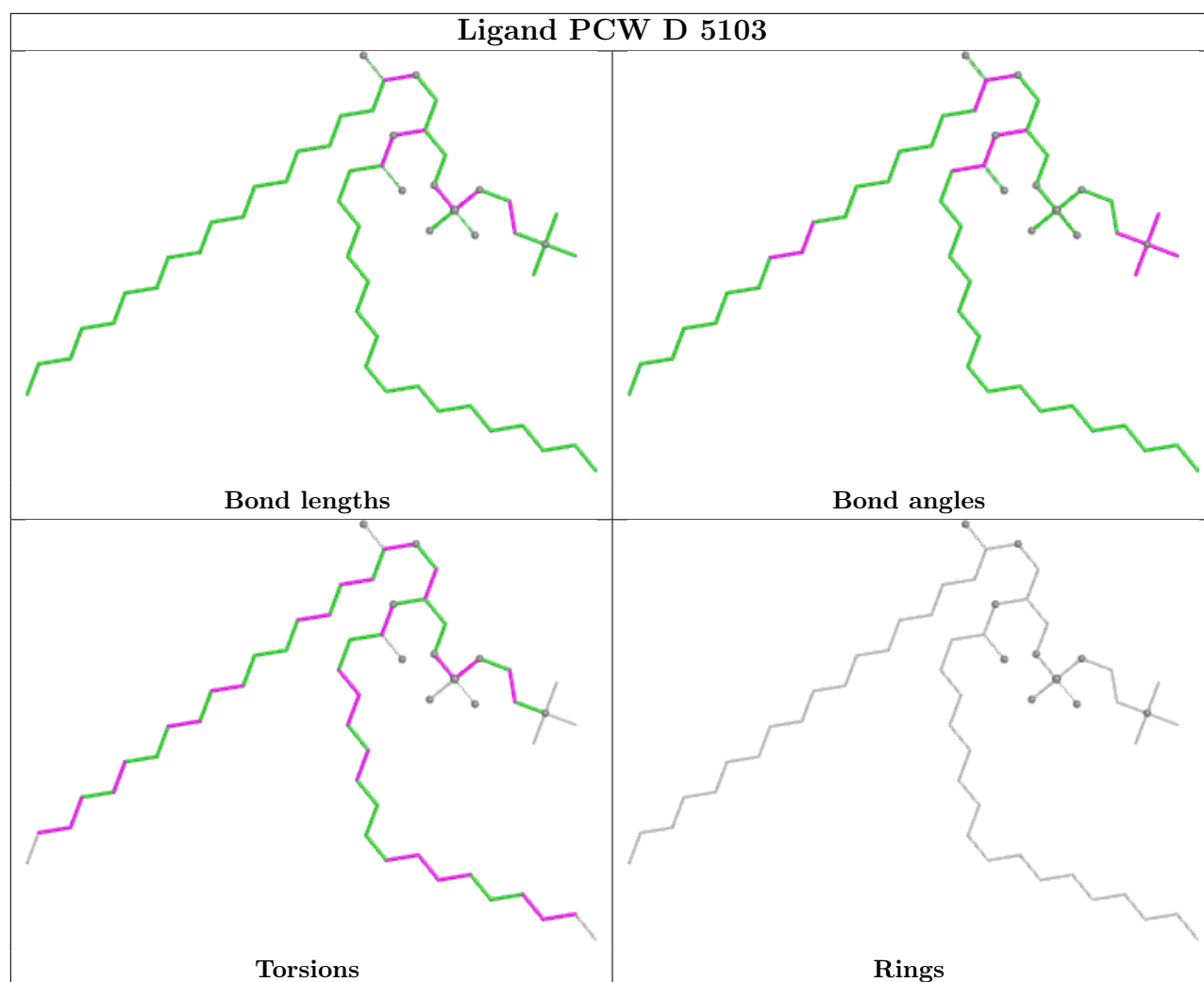
There are no ring outliers.

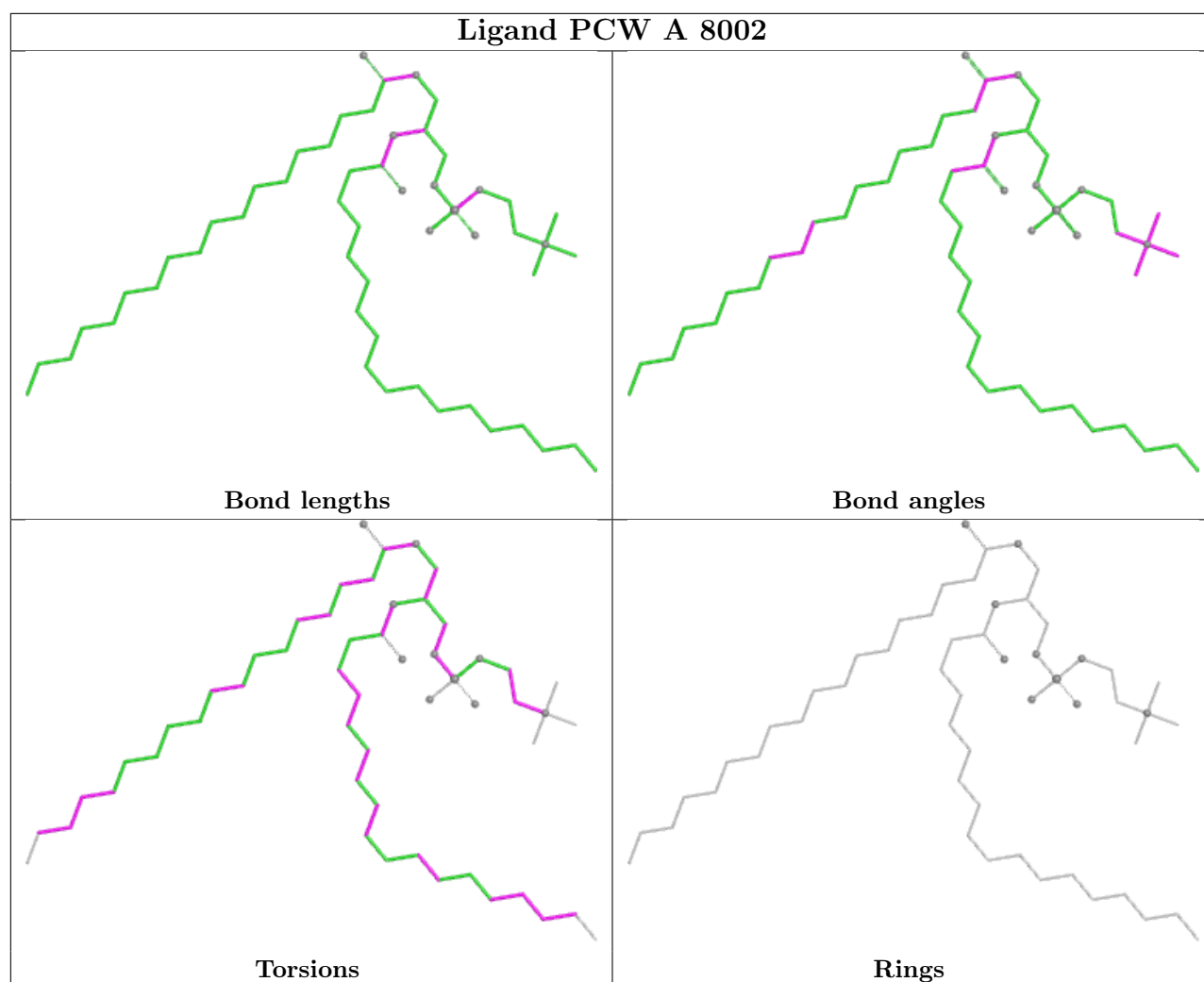
4 monomers are involved in 6 short contacts:

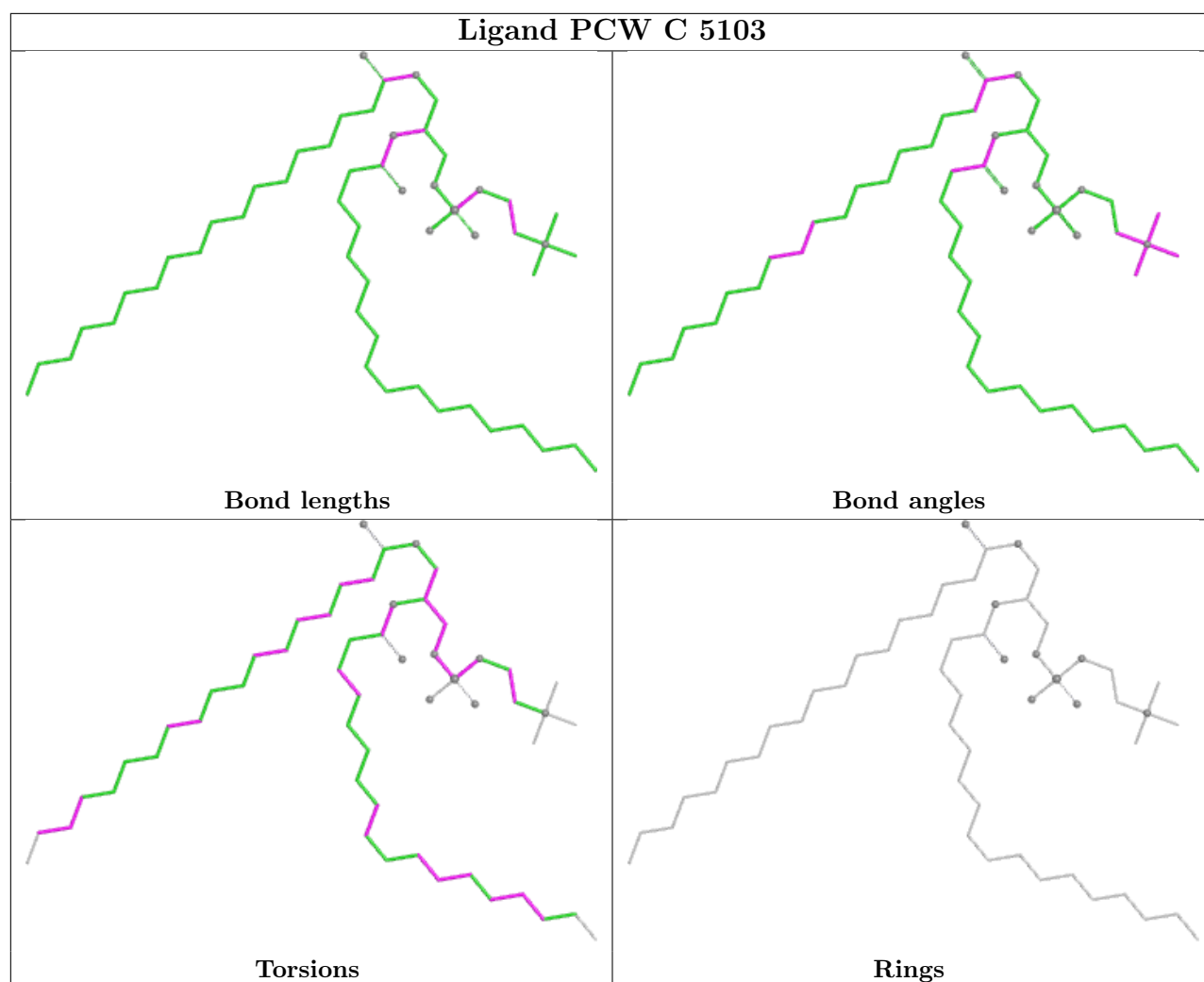
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	5103	PCW	1	0
4	C	5103	PCW	3	0
4	B	8002	PCW	2	0
4	B	8003	PCW	1	0

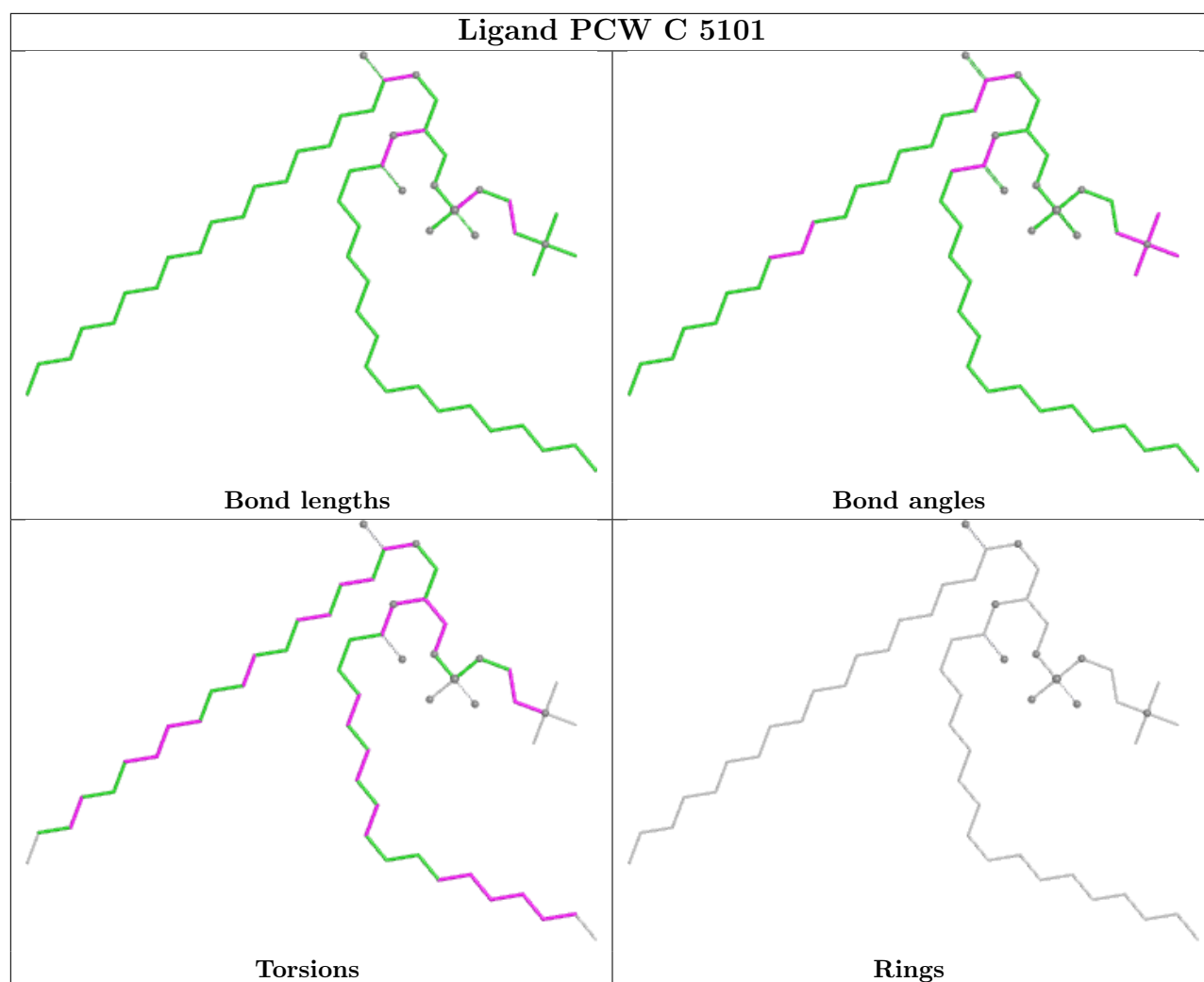
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

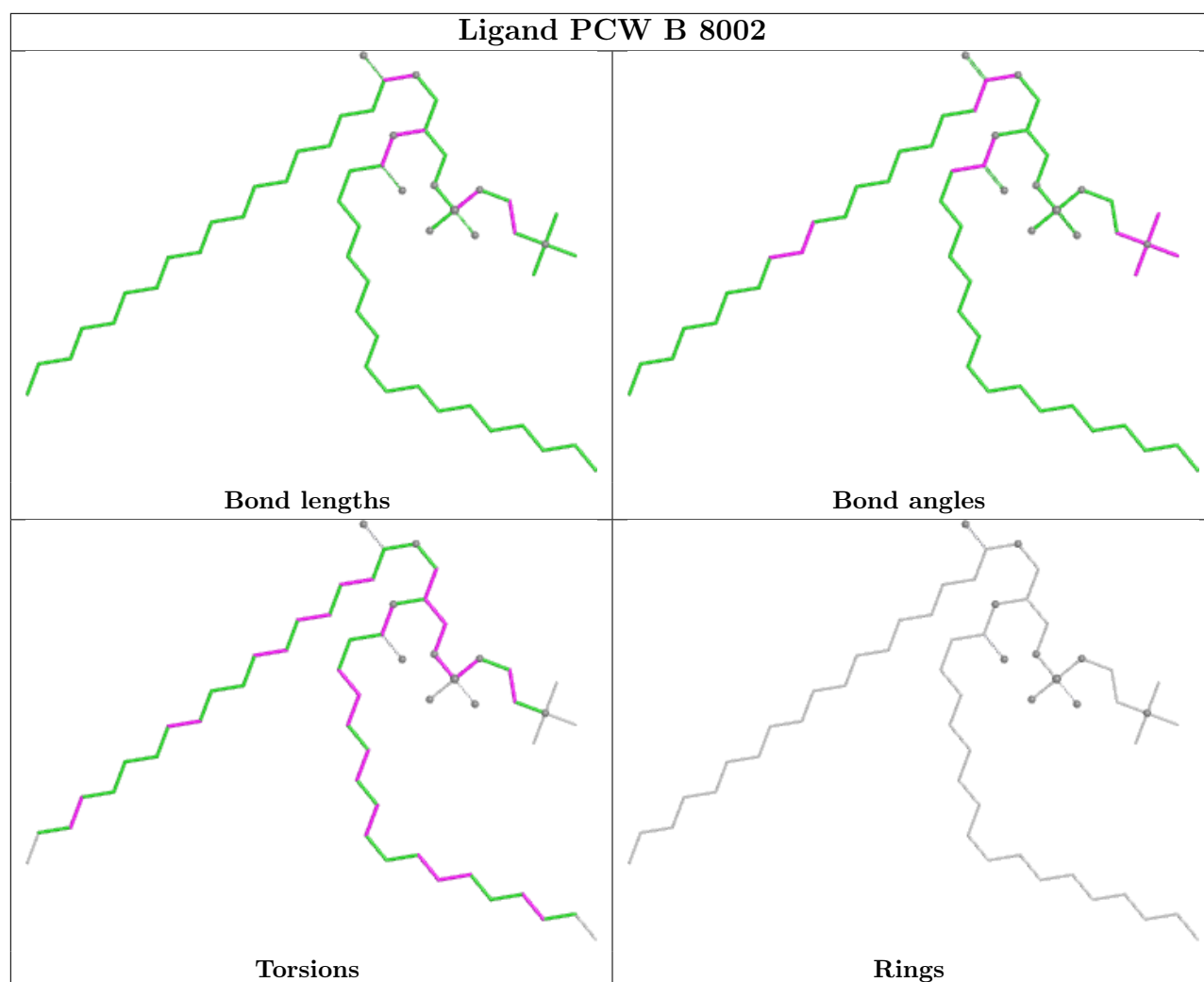


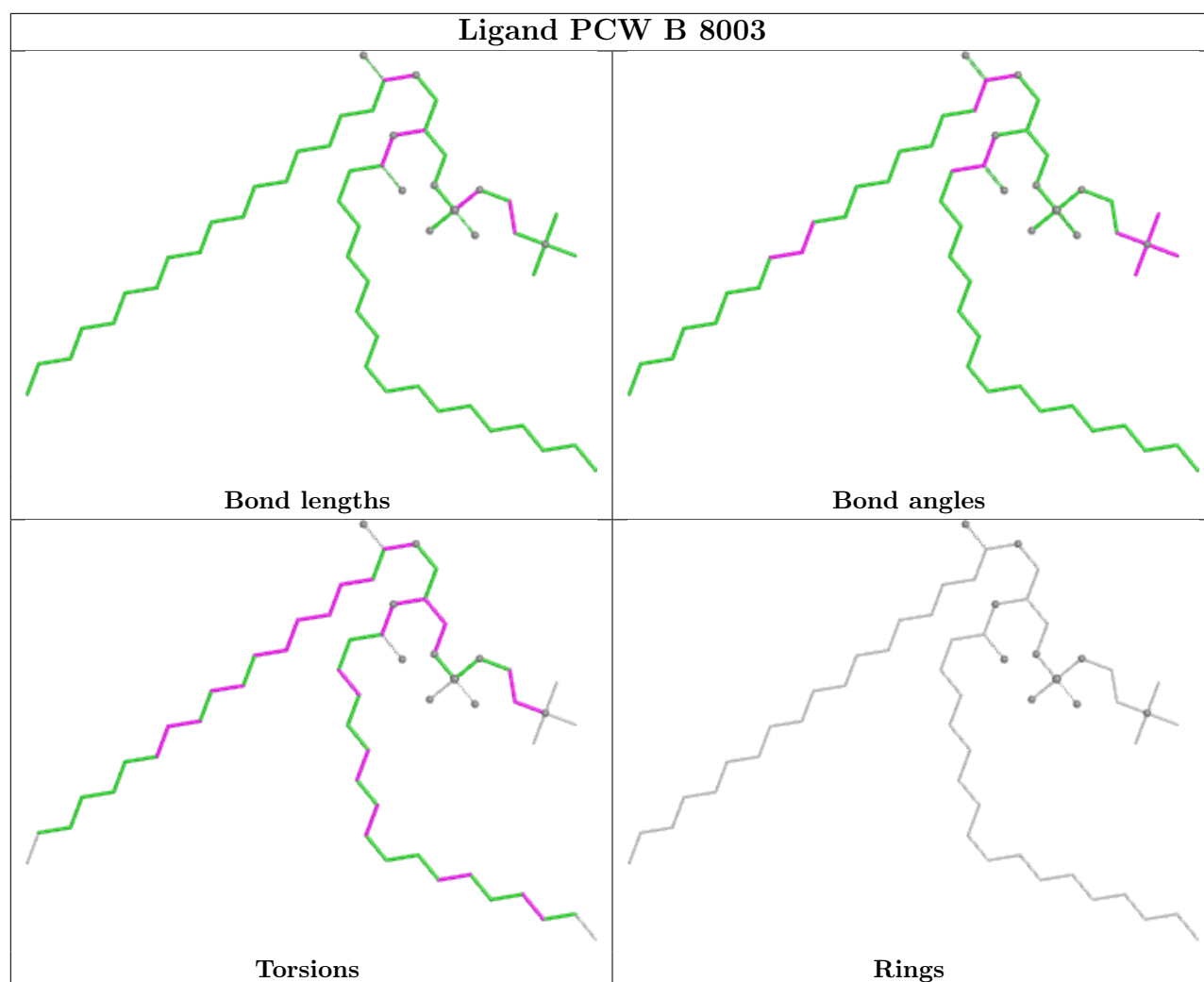


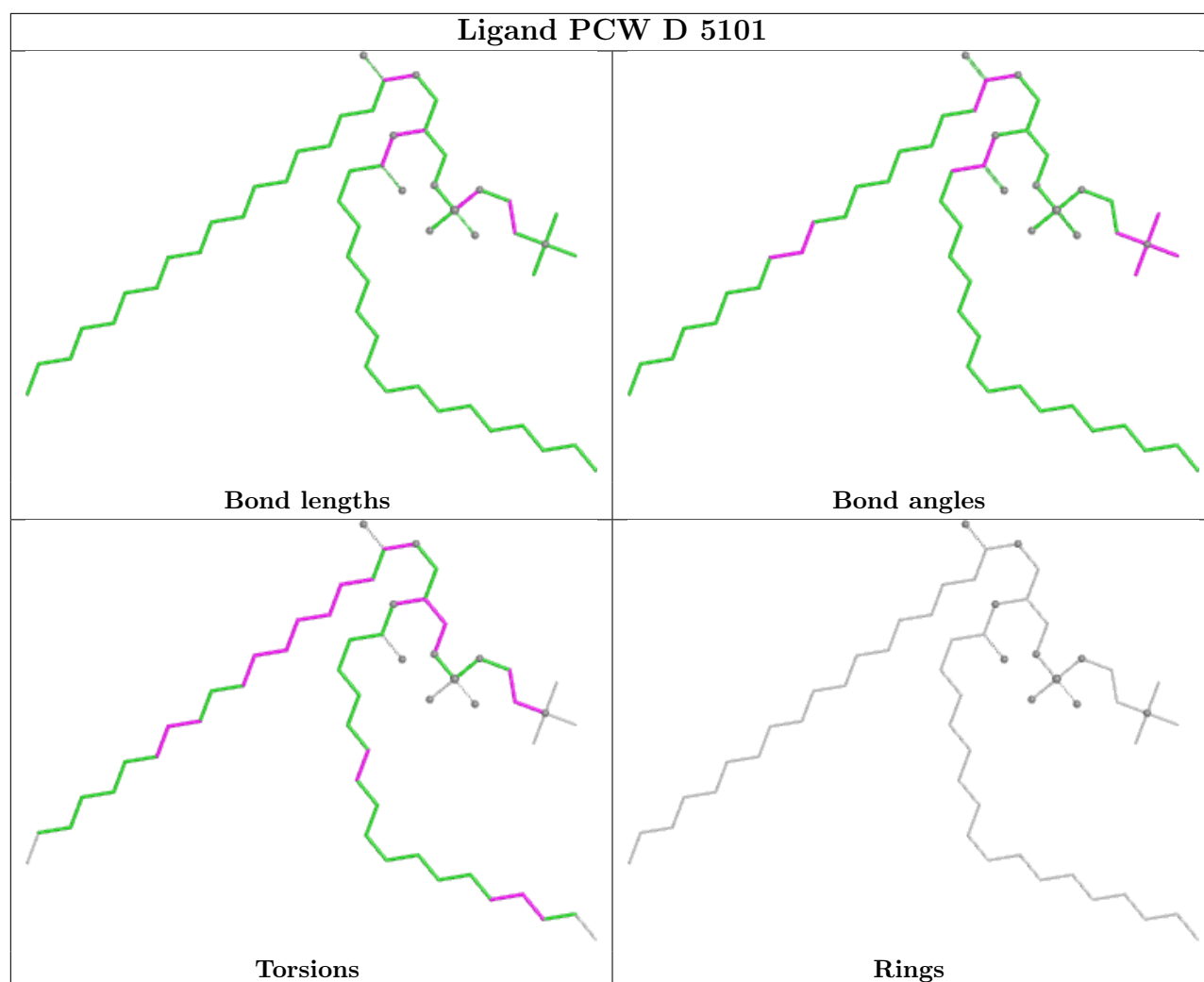












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

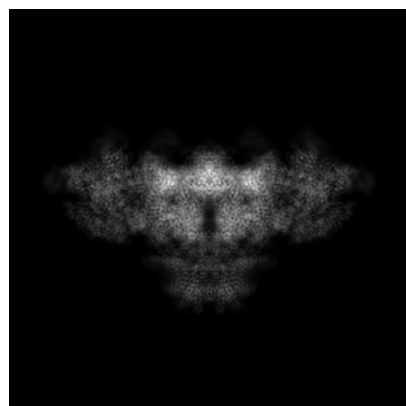
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43283. These allow visual inspection of the internal detail of the map and identification of artifacts.

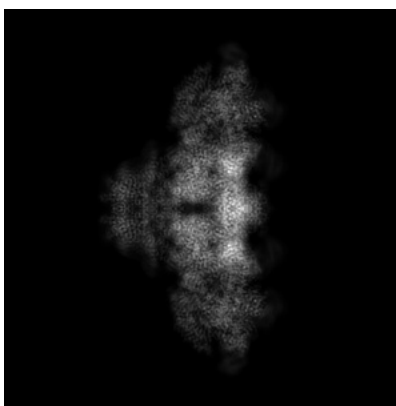
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

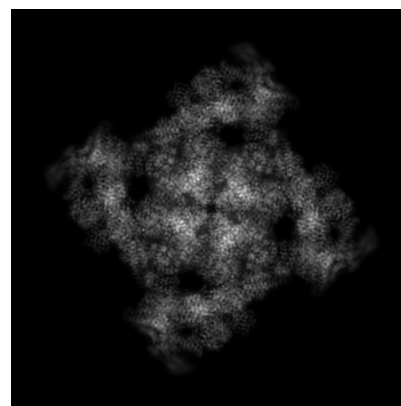
6.1.1 Primary map



X

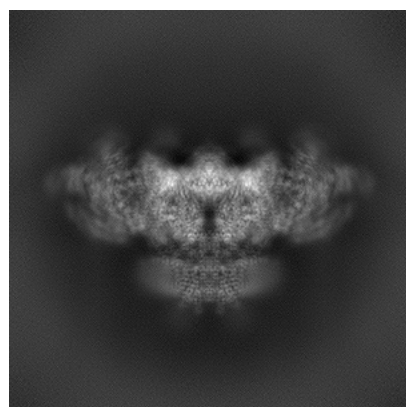


Y

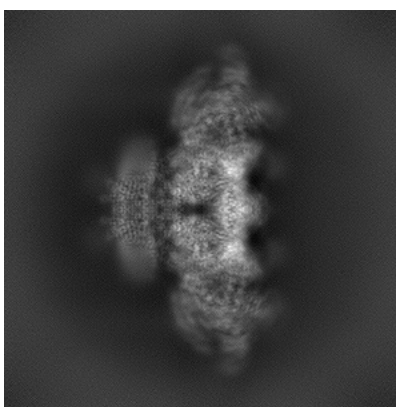


Z

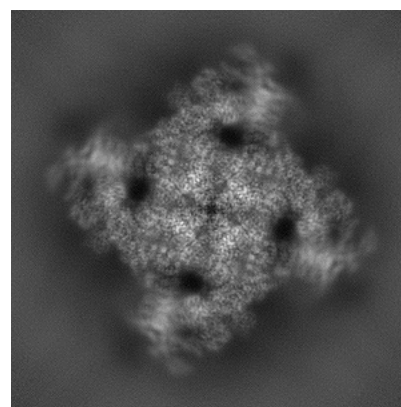
6.1.2 Raw map



X



Y



Z

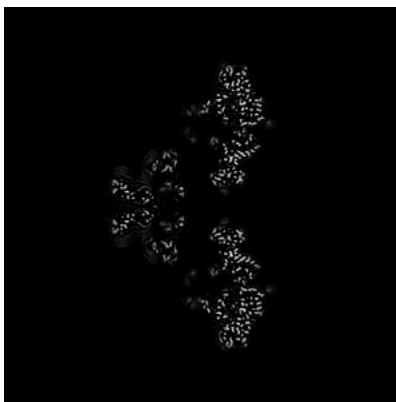
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

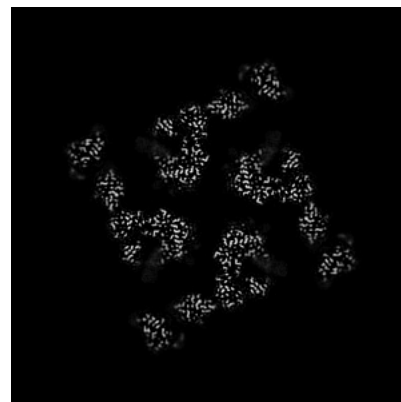
6.2.1 Primary map



X Index: 256

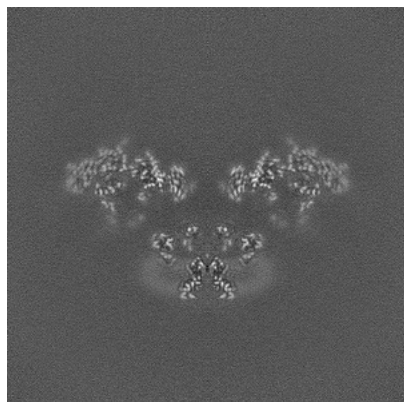


Y Index: 256

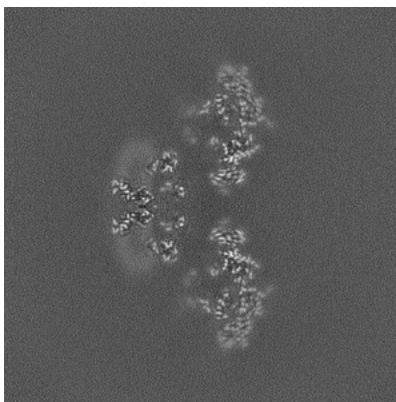


Z Index: 256

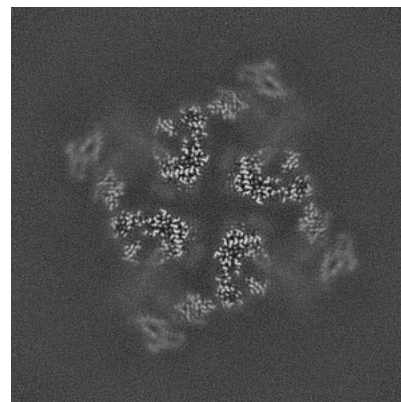
6.2.2 Raw map



X Index: 256



Y Index: 256



Z Index: 256

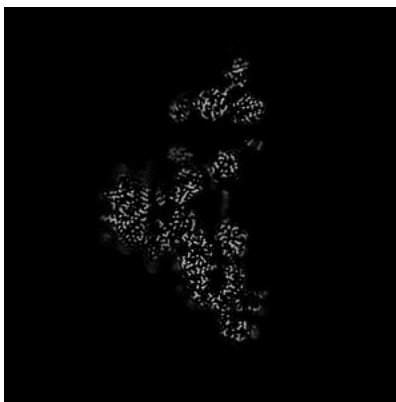
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

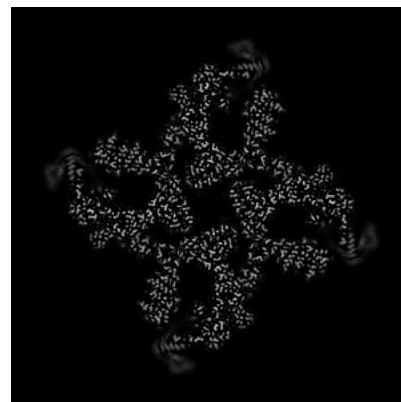
6.3.1 Primary map



X Index: 238

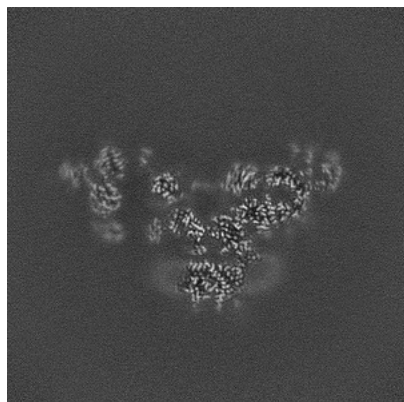


Y Index: 238

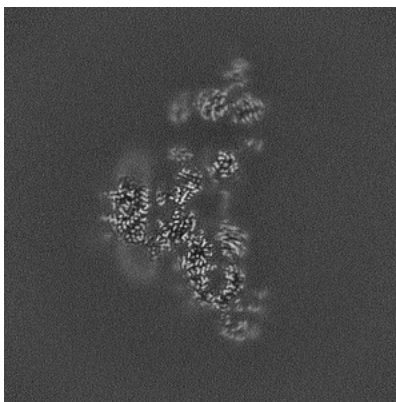


Z Index: 289

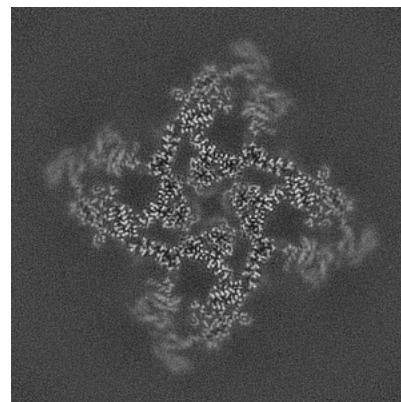
6.3.2 Raw map



X Index: 238



Y Index: 238

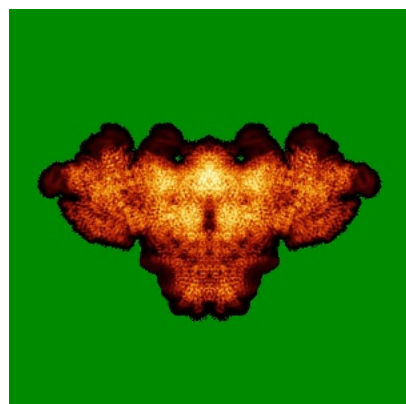


Z Index: 285

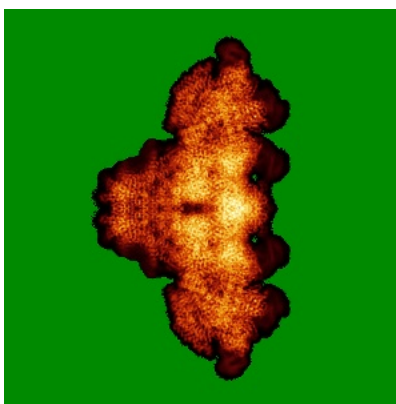
The images above show the largest variance slices of the map in three orthogonal directions.

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

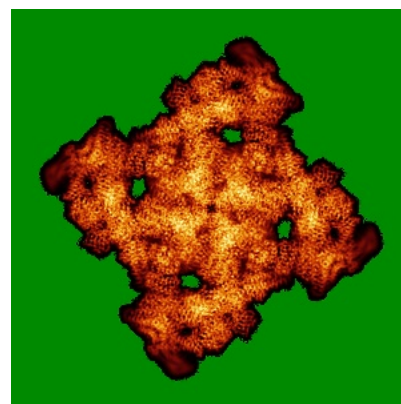
6.4.1 Primary map



X



Y

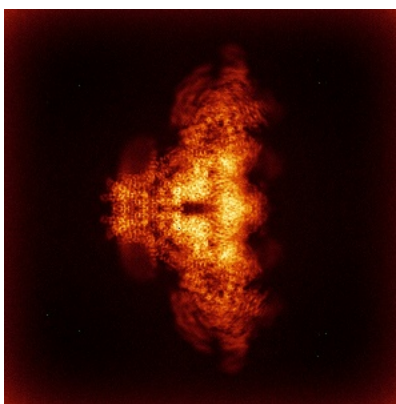


Z

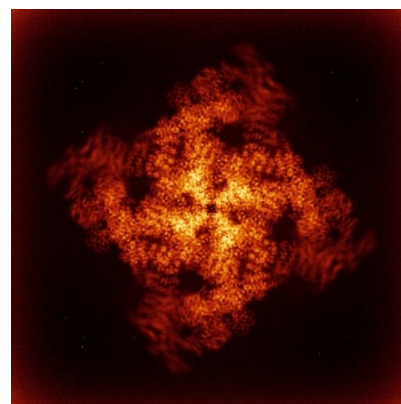
6.4.2 Raw map



X



Y

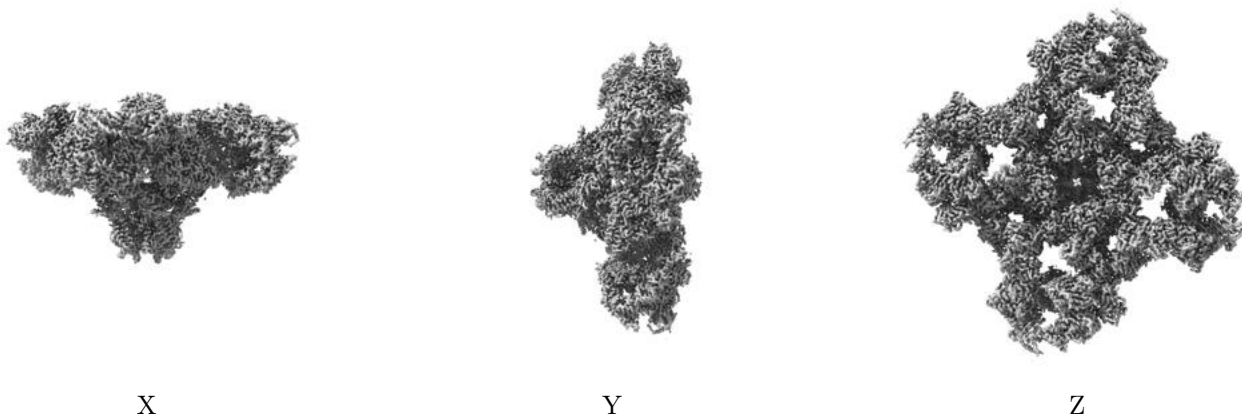


Z

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.

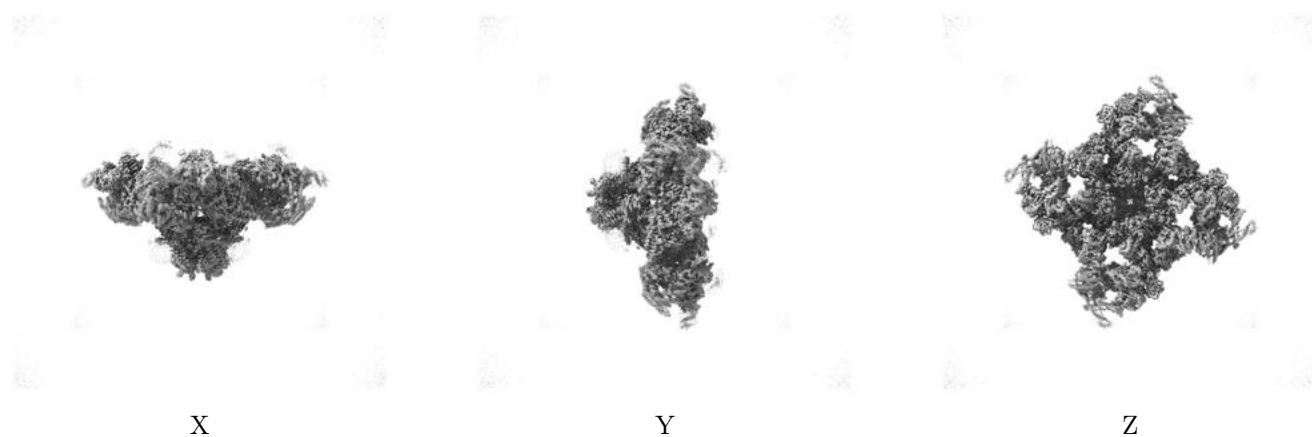
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.15. 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.

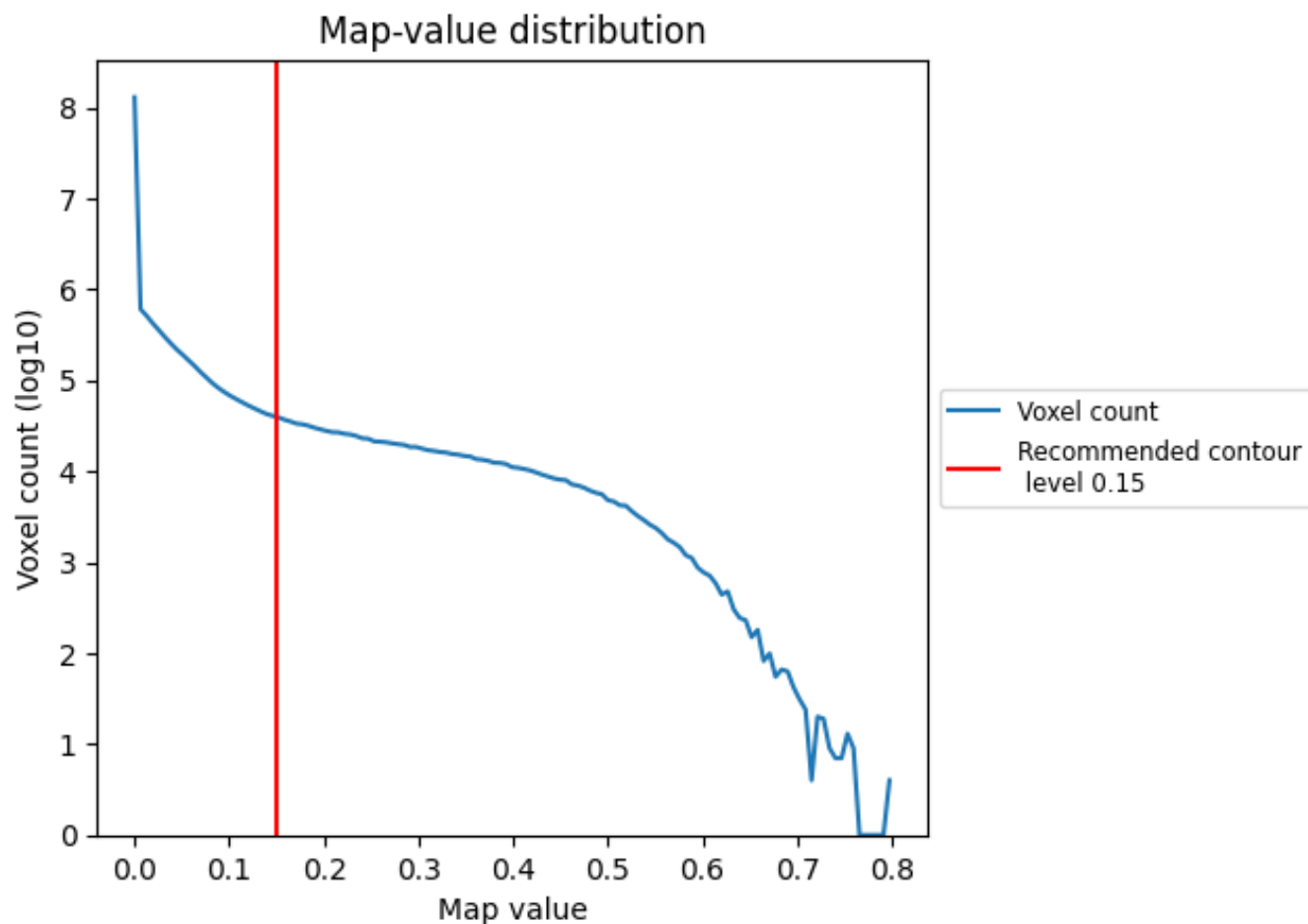
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

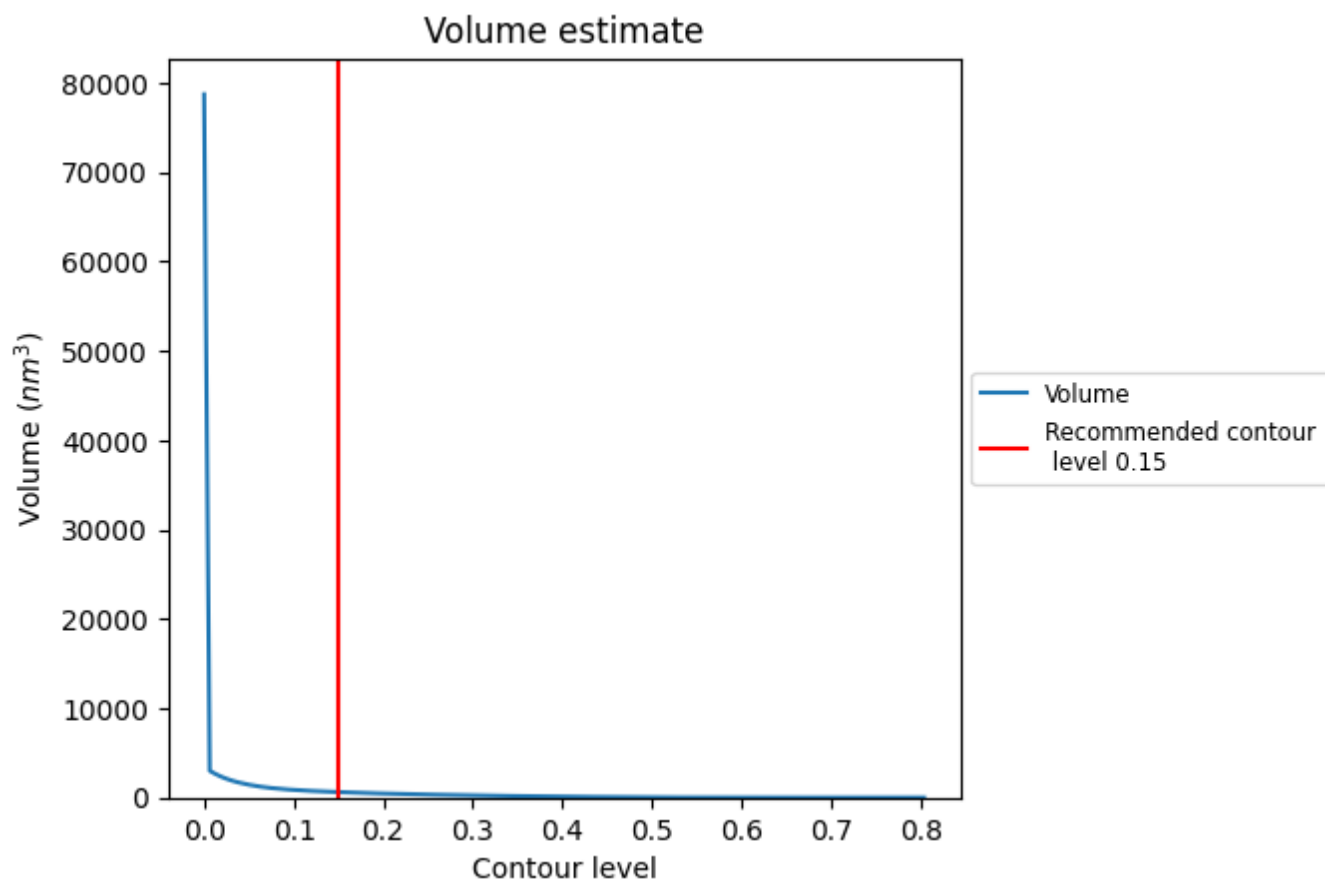
This section contains the results of statistical analysis of the map.

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.

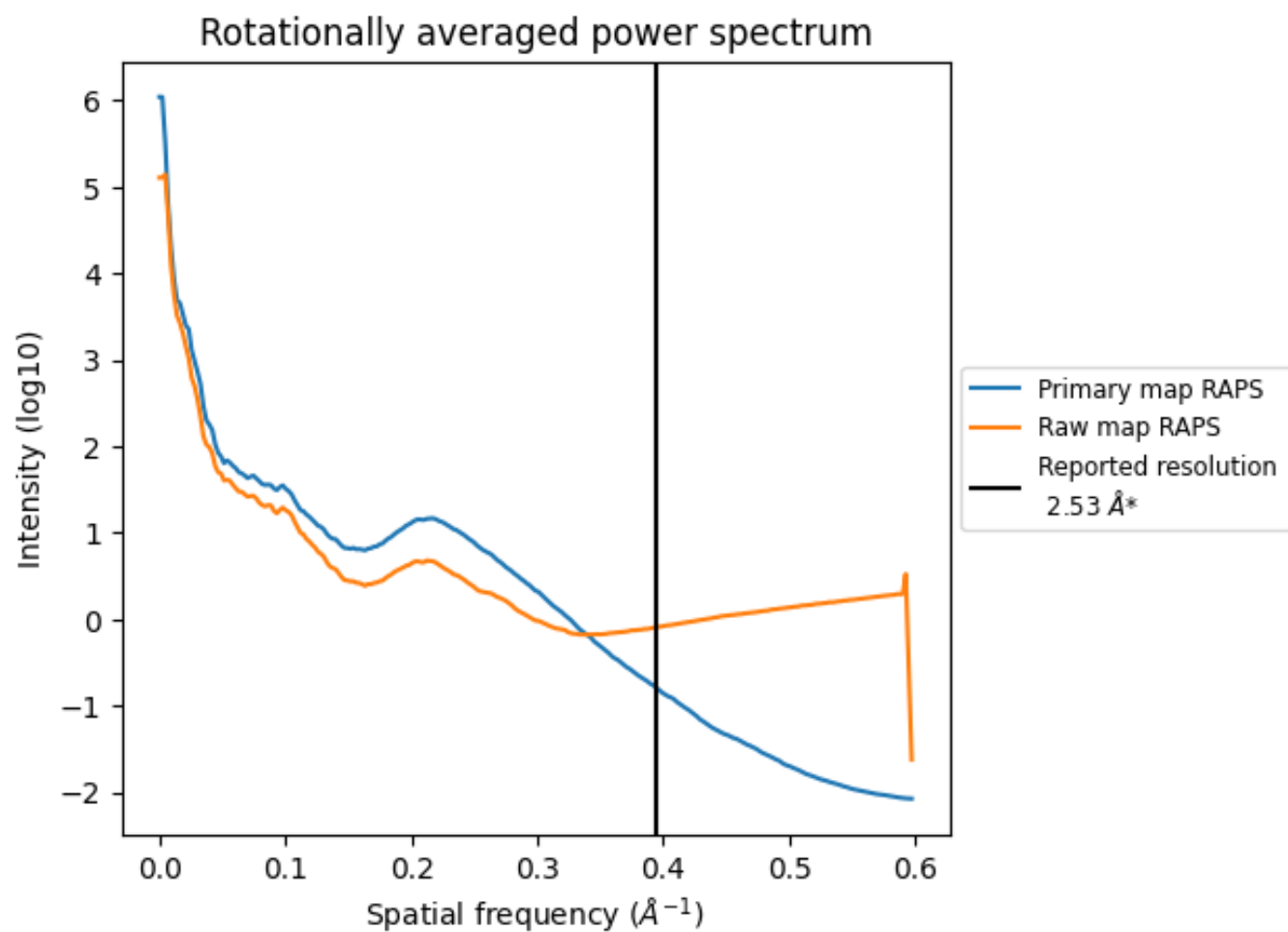
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 612 nm³; this corresponds to an approximate mass of 552 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 ⓘ

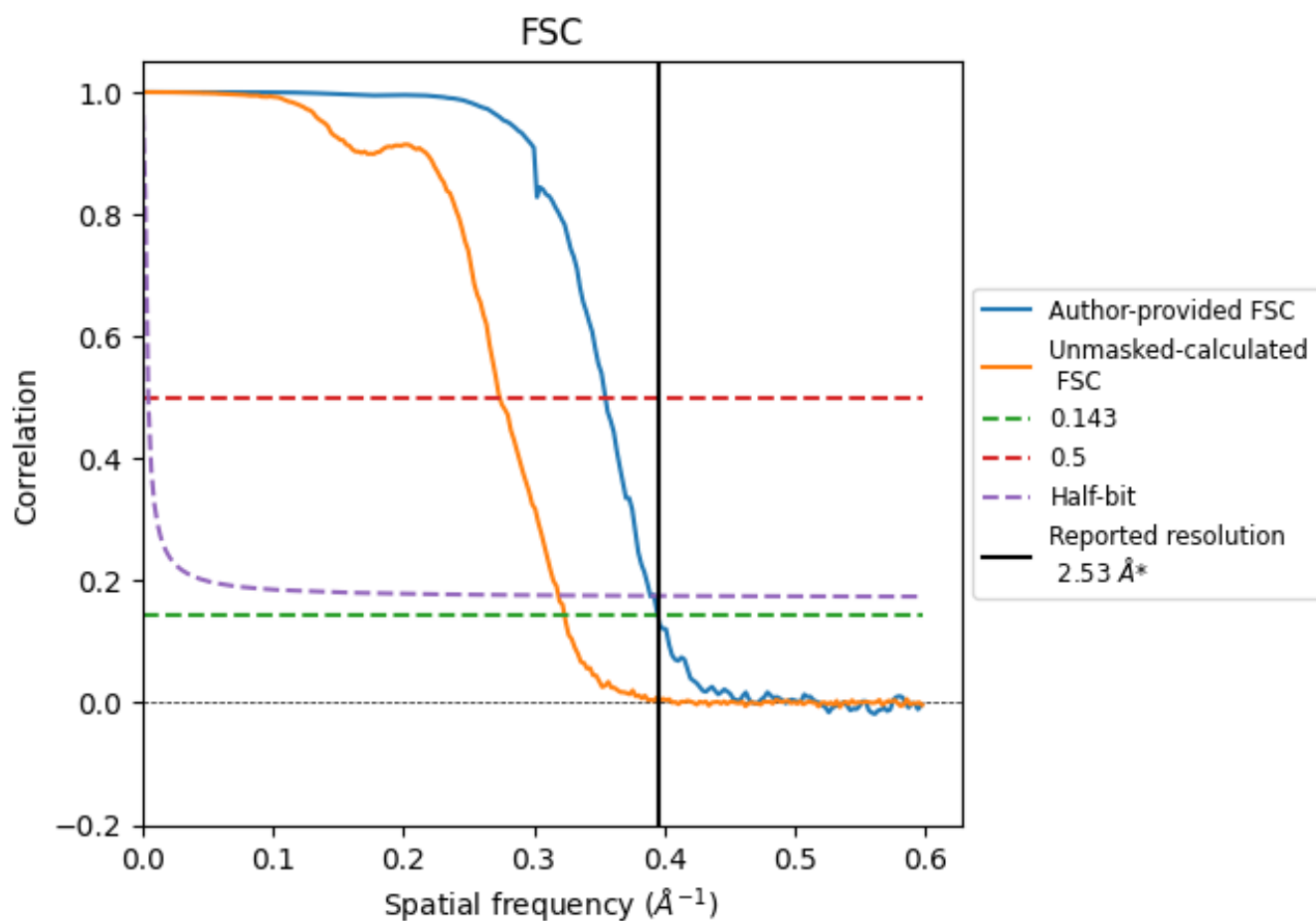


*Reported resolution corresponds to spatial frequency of 0.395 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.395 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

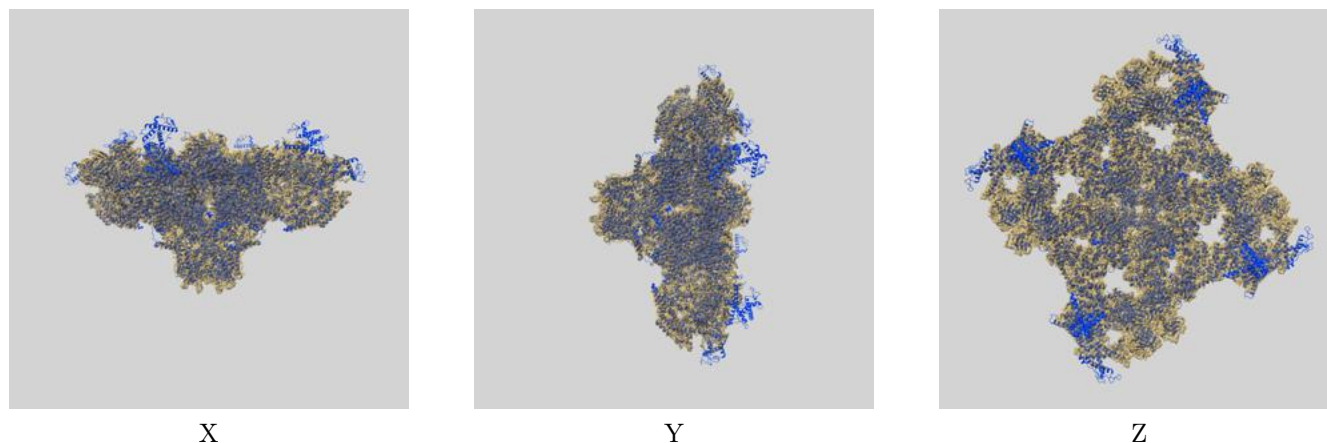
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.53	-	-
Author-provided FSC curve	2.53	2.82	2.57
Unmasked-calculated*	3.09	3.65	3.14

*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 3.09 differs from the reported value 2.53 by more than 10 %

9 Map-model fit [i](#)

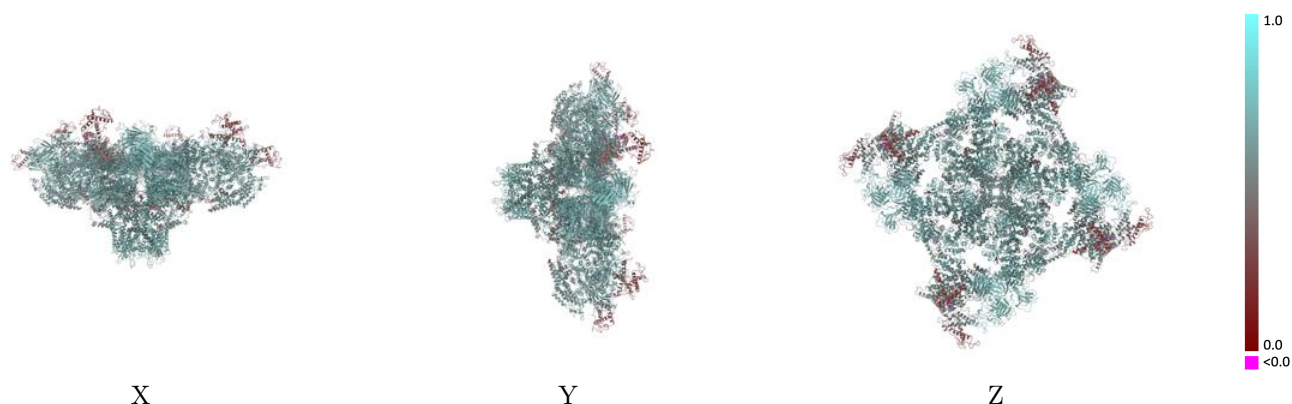
This section contains information regarding the fit between EMDB map EMD-43283 and PDB model 8VJJ. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



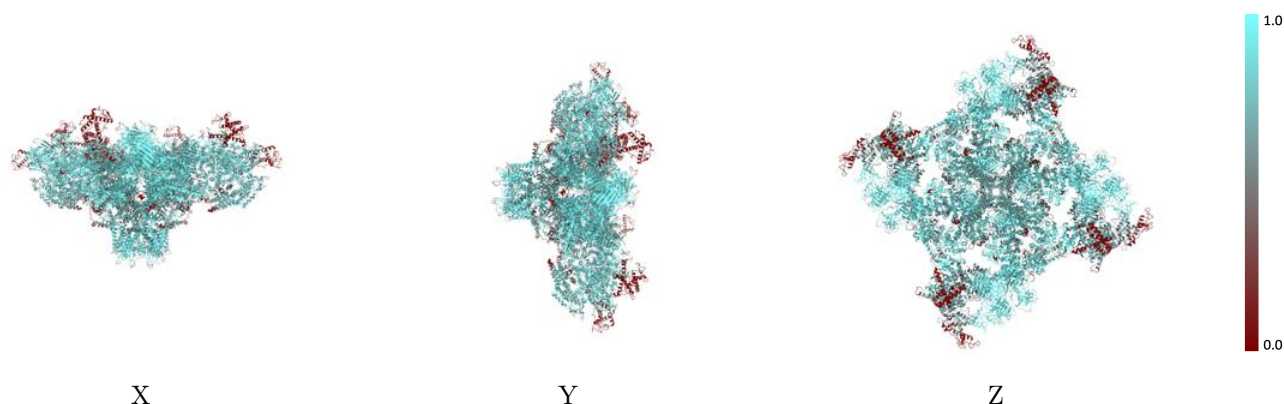
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



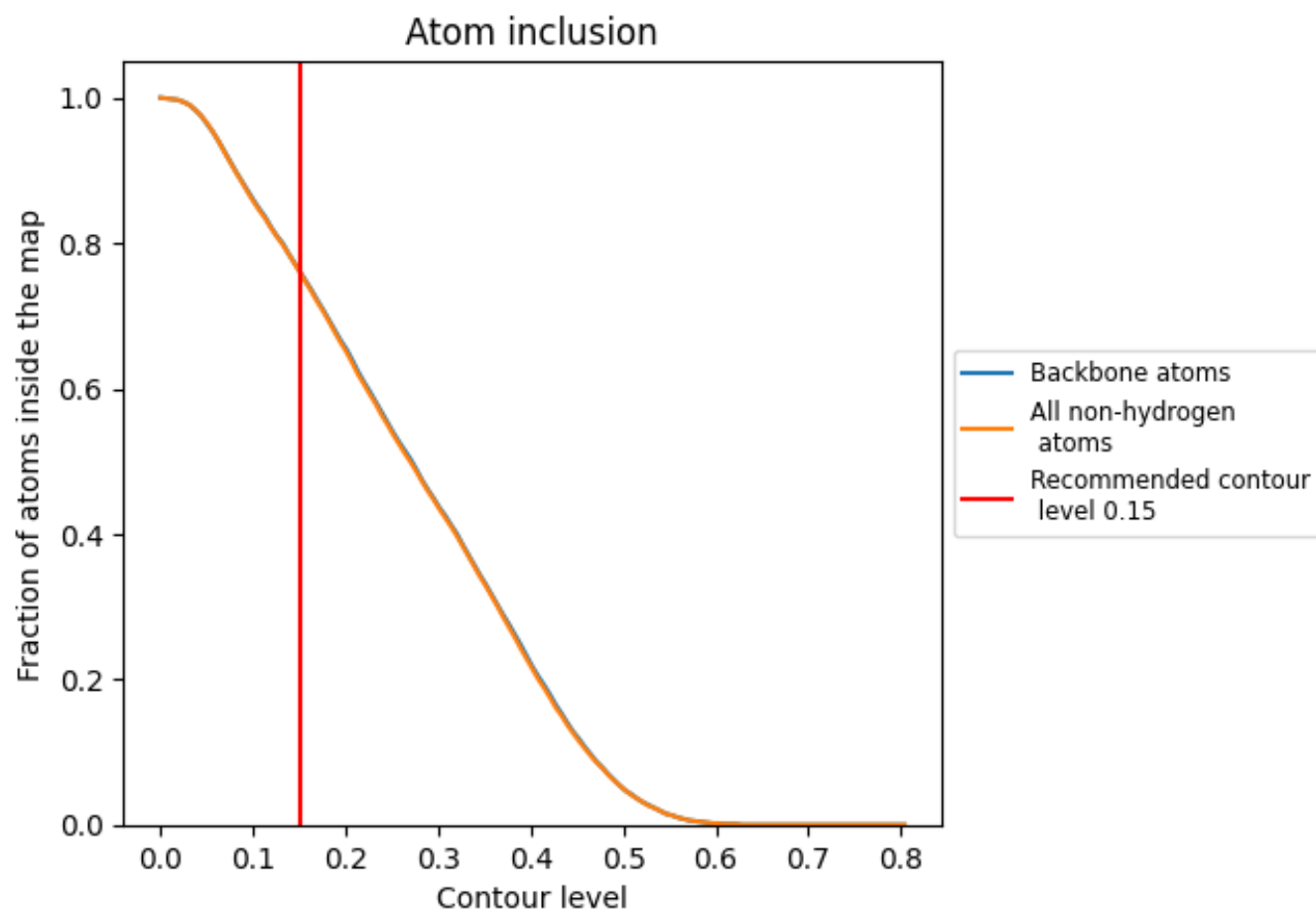
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 76% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7610	0.5970
A	0.7630	0.5960
B	0.7640	0.5950
C	0.7630	0.5960
D	0.7640	0.5960
E	0.8670	0.6550
F	0.8660	0.6530
G	0.8650	0.6530
H	0.8680	0.6540

1.0

0.0

<0.0