



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 08:57 PM UTC

PDB ID : 8E6T / pdb_00008e6t
EMDB ID : EMD-27925
Title : Human TRPM2 ion channel in 1 mM BR-ADPR
Authors : Wang, L.; Fu, T.M.; Xia, S.; Wu, H.
Deposited on : 2022-08-23
Resolution : 3.70 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

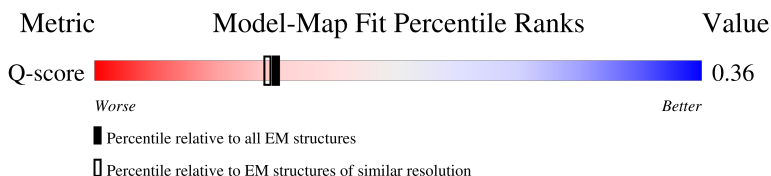
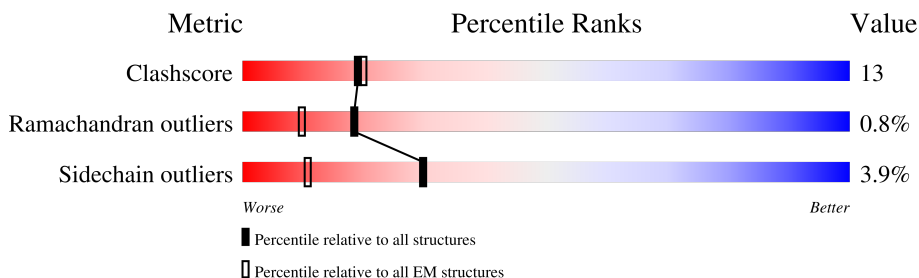
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	1503	
1	B	1503	
1	C	1503	
1	D	1503	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 38612 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 Transient receptor potential cation channel subfamily M member 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1290	Total	C	N	O	S	0	0
			9579	6158	1680	1702	39		
1	B	1290	Total	C	N	O	S	0	0
			9579	6158	1680	1702	39		
1	C	1290	Total	C	N	O	S	0	0
			9579	6158	1680	1702	39		
1	D	1290	Total	C	N	O	S	0	0
			9579	6158	1680	1702	39		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	369	ILE	LEU	conflict	UNP O94759
B	369	ILE	LEU	conflict	UNP O94759
C	369	ILE	LEU	conflict	UNP O94759
D	369	ILE	LEU	conflict	UNP O94759

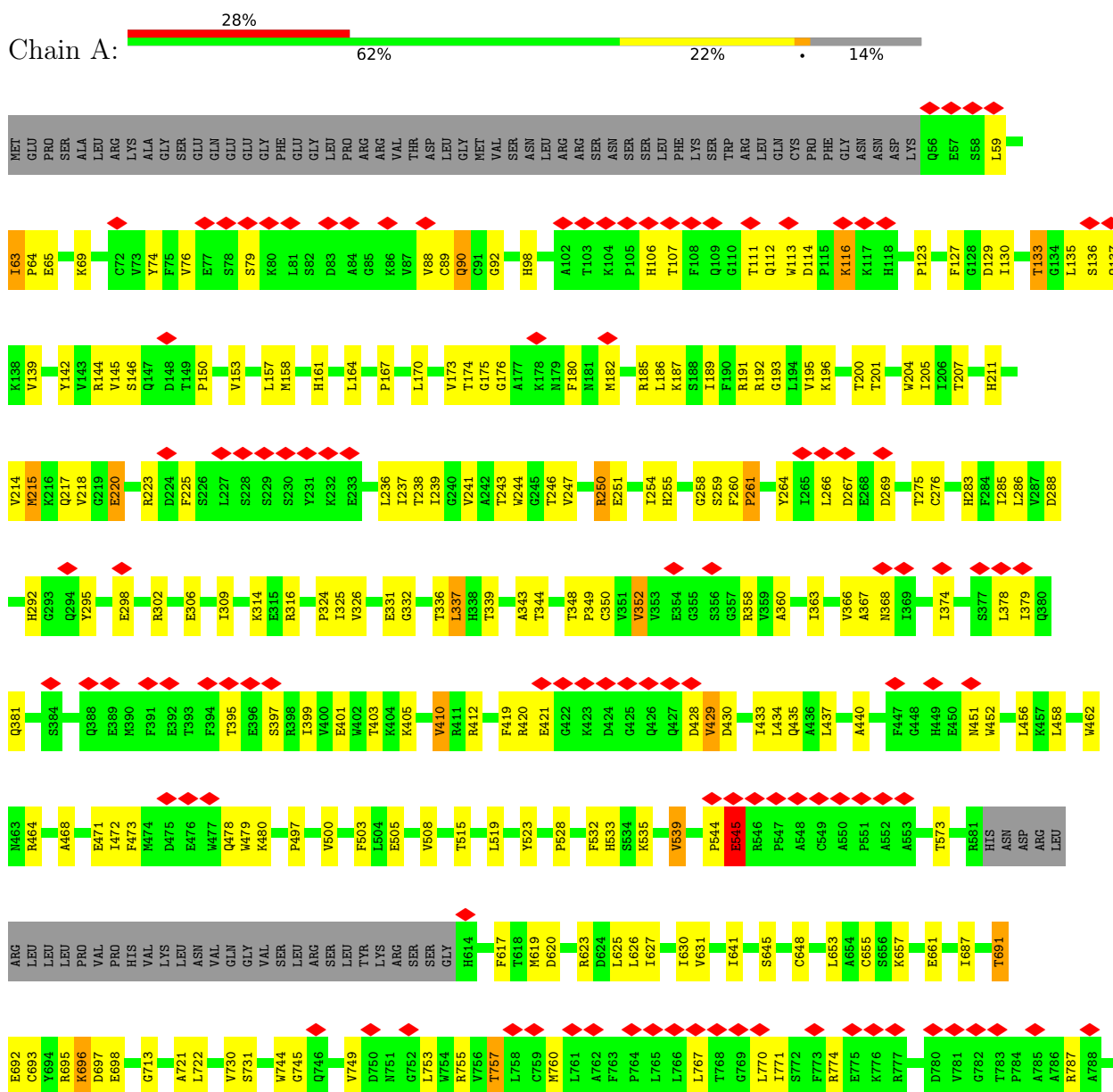
- Molecule 2 is (3R,4R,5R)-5-(6-amino-8-bromo-9H-purin-9-yl)-3,4,5-trihydroxypentyl [(2S,3S,4S,5R)-3,4,5-trihydroxyoxolan-2-yl]methyl dihydrogen diphosphate (non-preferred name) (CCD ID: UOO) (formula: C₁₅H₂₄BrN₅O₁₄P₂).

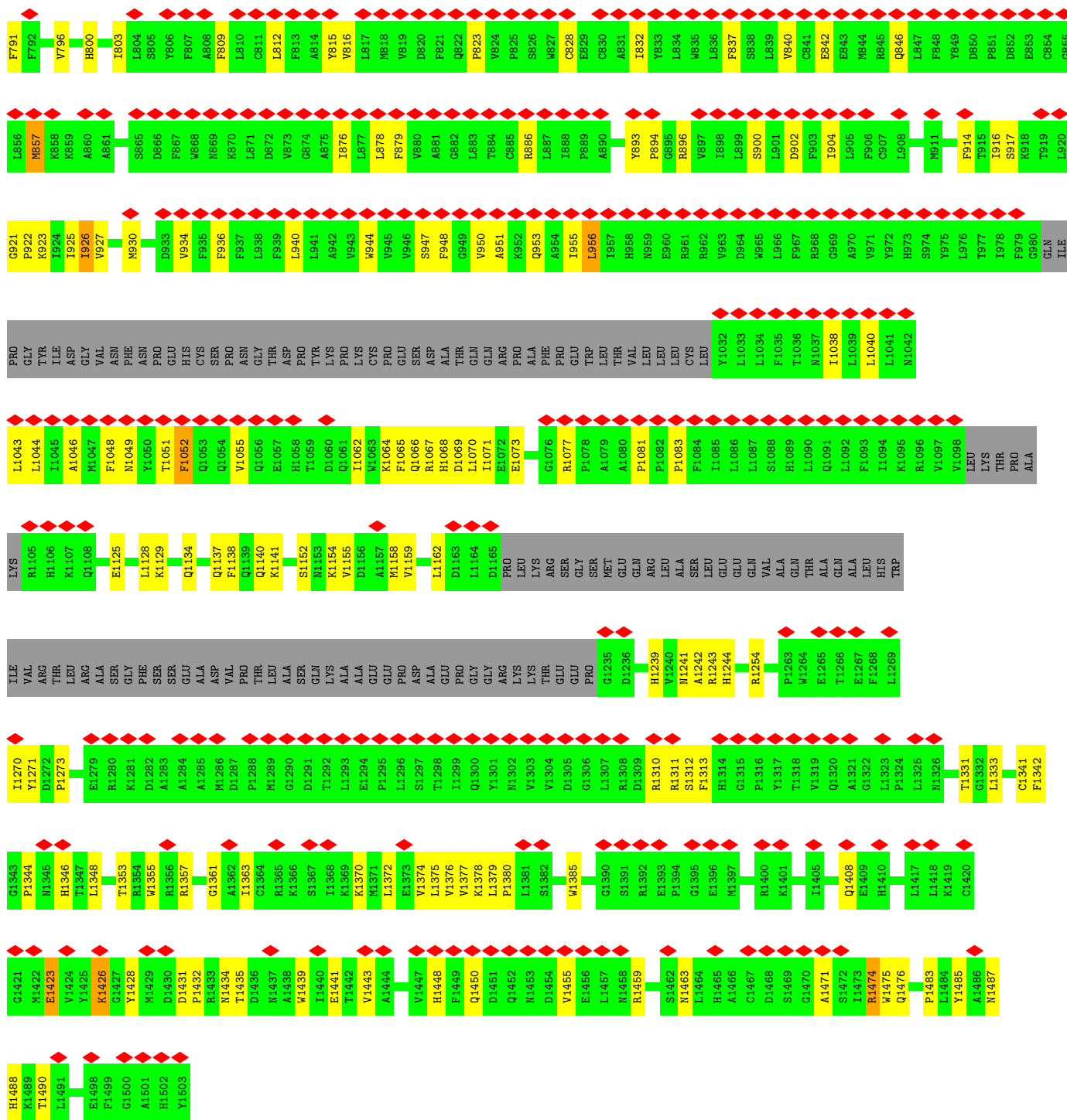


3 Residue-property plots

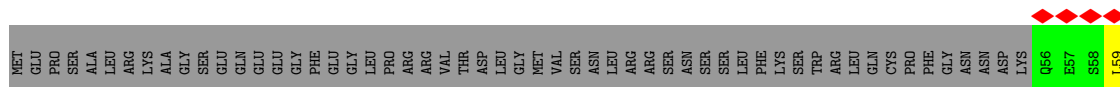
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Transient receptor potential cation channel subfamily M member 2

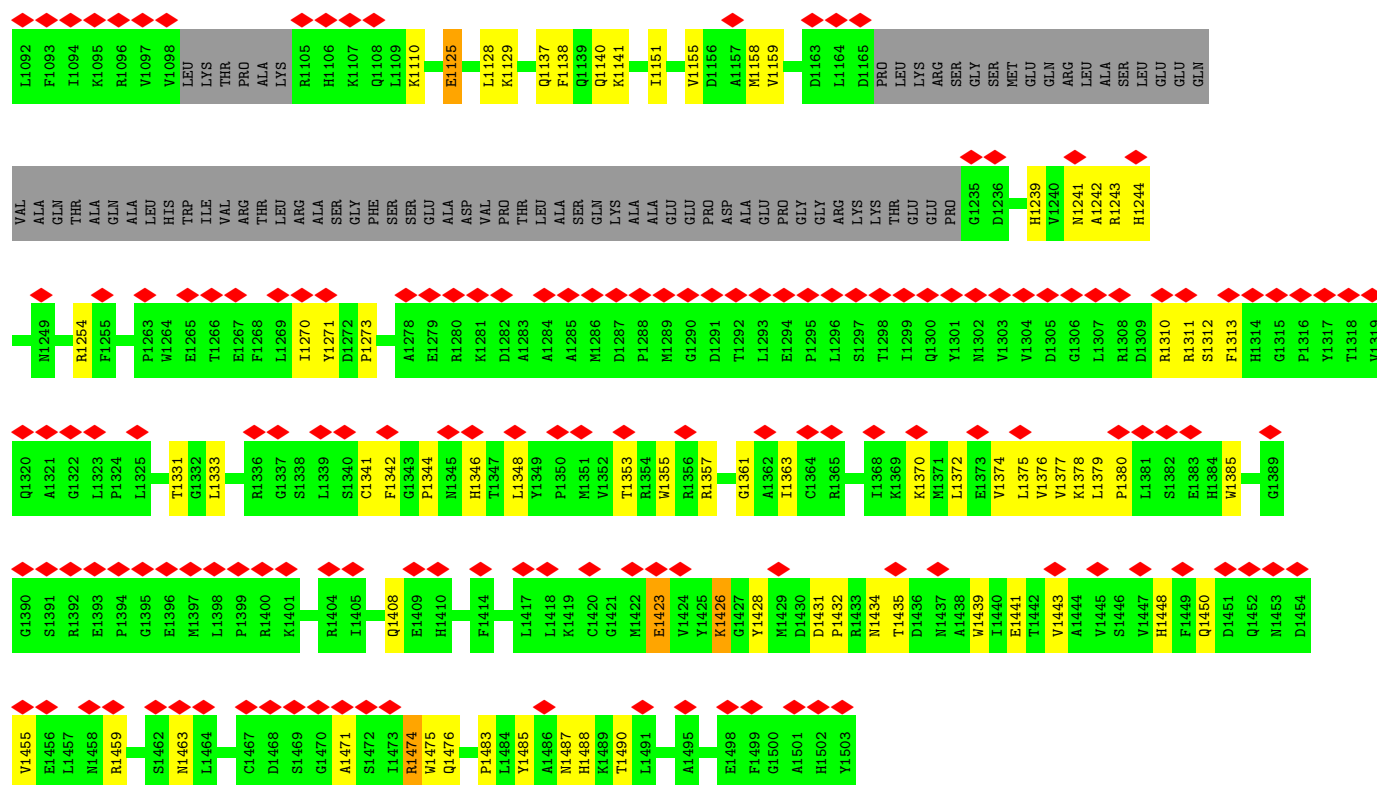




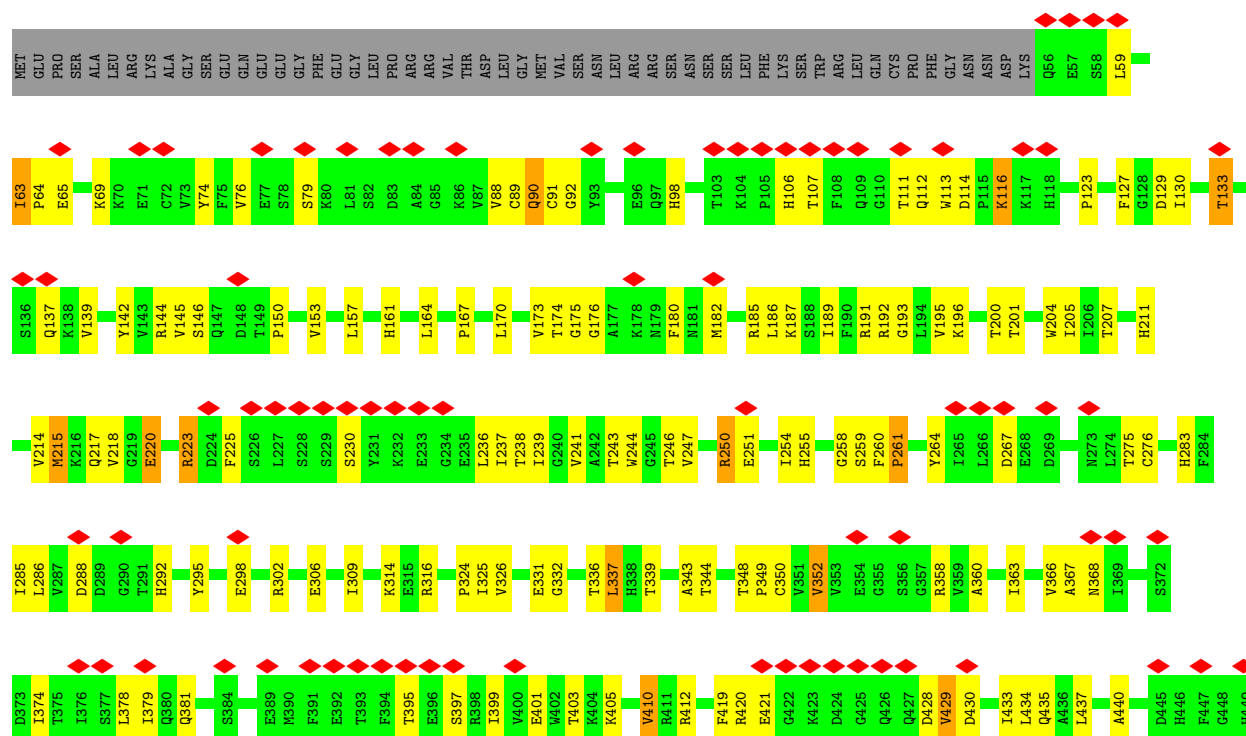
• Molecule 1: Transient receptor potential cation channel subfamily M member 2

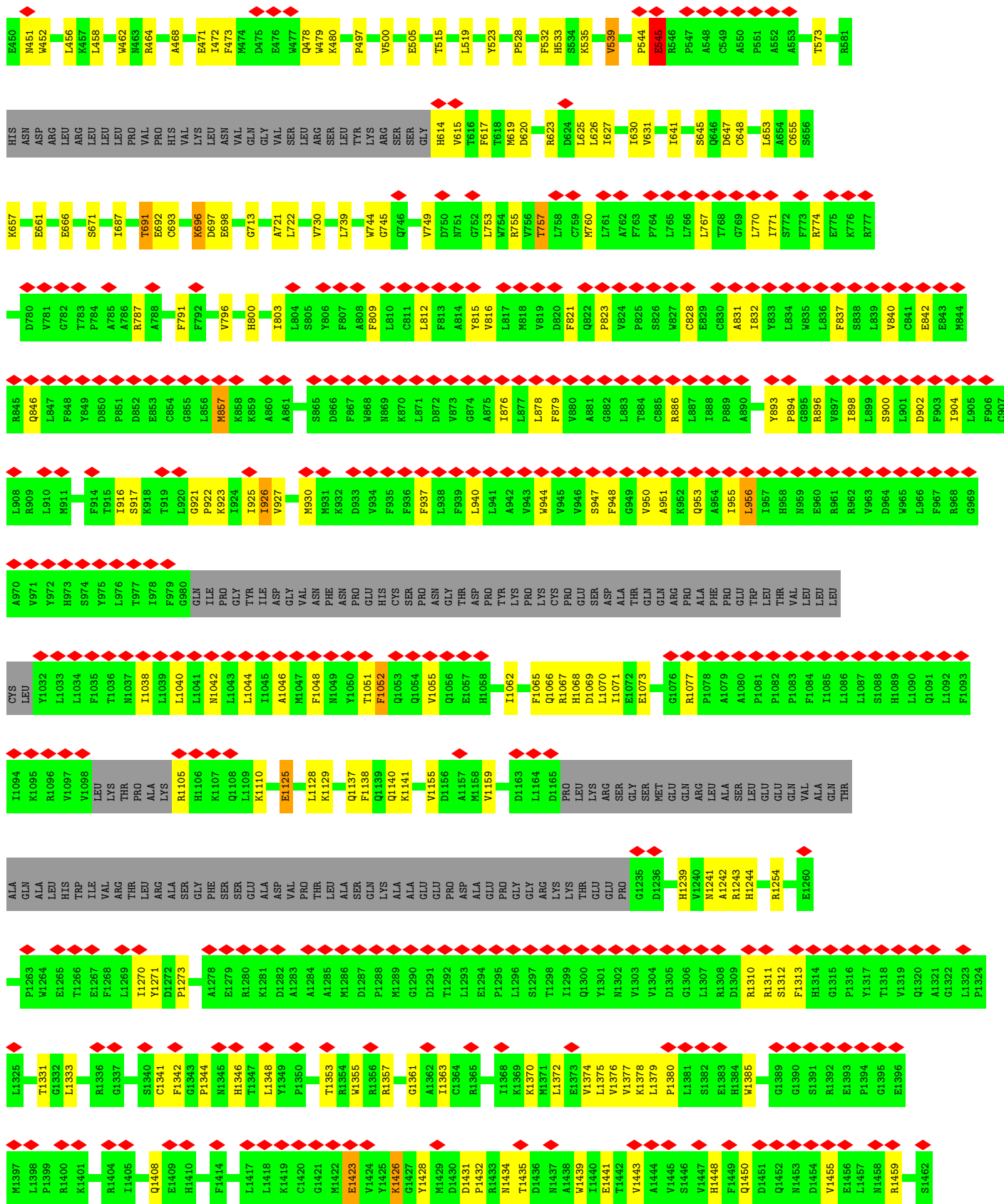


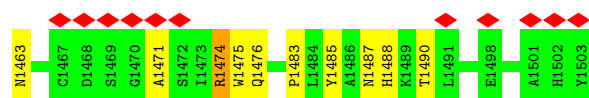
LEU	Y1032	L1033	L1034	F1035	T1036	T1037	I1038	L1039	L1040	L1041	N1042	L1043	L1044	A1045	A1046	M1047	F1048	N1049	Y1050	T1051	F1052	Q1053	Q1054	Y1055	E1057	H1058		I1062	F1065	Q1066	R1067	H1068	D1069	L1070	I1071	E1072	E1073		R1077	P1078	A1079	A1080	P1081	P1082	P1083	F1084	I1085	L1086	L1087	S1088	H1089	L1090	Q1091						
F967	Y971	Y972	H973	S974	Y975	L976	T977	F978	F979	G980	GLN	ILE	GLY	TYR	ASP	GLY	VAL	ASN	PHE	ASN	PRO	GLU	HIS	CYS	SER	PRO	ASN	GLY	THR	ASP	PRO	TYR	LYS	PRO	LYS	CYS	PRO	GLU	SER	ASP	ALA	THR	GLN	GLN	ARG	PRO	ALA	PHE	PRO	GLU	TRP	THR	VAL						
L905	F906	C907	L908	R909	L910		I913	F914	T915	T916	S917	R918	T919	L920	G921	P922	K923	T924		M930	M931	K932	D933	V934	F935	F936	F937	L938	F939	L940	L941	L942	V943	W944	V945	V946	S947	F948	G949	V950	A951	K952	Q953	A954	I955	L956	I957	H958	G959	E960	R961	R962	L963	S900	L901	D902	F903	I904	
E842	E843	M844	R845	Q846	L847	F848	Y849	D850	P851	D852	E853	C854	C855	L856	M857	R858	R859	A860	A861		S865	D866	F867	W868	M869	R870	L871	D872	W873	G874	A875	L876	L877	L878	F879	V880	A881	C882	L883	T884	C885	R886	L887	T888	P889	A890		Y893	P894	L895	R896	Y897	I898	L899	S900	L901	D902	F903	I904
E775	K776	R777		D780	V781	G782	T783	F784	A785	A786	A788		F791	F792		V796	H800	I803	L804	S805	Y806	F807	A808	F809	L810	C811	L812	F813	A814	Y815	R816	L817	M818	V819	D820	D822	P823	W824	P825	S826	W827	C828	E829	C830	A831	I832	Y833	L834	W835	F837	L838	L839	W840	C841					
S856	K857	E861		E866	S871	I867	T869	E892	C893		K896	D897	E898		G713	T716	A721	L722		V730	L739	W744	G745	Q746		V749	D750	W751	G752	L753	W754	R755	T757	L758	G759	W760	L761	A762	F763	L765	L766	L767	T768	G769	L770	I771	S772	F773	R774										
R881	HIS	ASN	ARG	LEU	ARG	LEU	LEU	PRO	VAL	PRD	HIS	VAL	LYS	LEU	ASN	VAL	GLN	GLY	VAL	SER	LEU	ARG	TYR	LYS	ARG	SER	GLY	H614	V615	F617	T618	W619	D620	R623	D624	L625	L626	I627	L630	V631	T641	S645	Q646	D647	C648	L653	A654	C655		T573									
H449	E450	W451	W452	L456	K457	L458	W462	W463	R464	A468	E471	L472	F473	W474	D475	E476	W477	Q478	W479	K480	P497	V500	E505	T515	L519	Y523	P528	F532	H533	S534	K535		V539	P544	R546	P547	A548	C549	A550	P551	A552	A553		T573															
I376	S377	L378	I379	Q380	Q381	S384	E389	M390	F391	E392	T393	F394	T395	E396	R397	I399	Y400	E401	W402	T403	K404	K405	D408	I409	V410	R412	R413	Q414	F419	R420	V421	G422	K423	D424	G425	Q426	Q427	D428	Y429	D430	I433	L434	Q435	A436	L437	A440	D445	H446	F447	G448									
V287	D288	D289	G290	H292	G293	Q294	Y295	E298	R302	E306	I309	K314	E315	R316	P324	I325	T326	P328	V329	E331	G332	T336	L337	H338	T339	A343	T344	T348	P349	C350	V351	V352	V353	E354	S355	G357	R358	V359	A360	I363	V366	A367	N368	I369	I374	T375													
M215	K216	Q217	V218	G219	E220	R223	D224	F225	S226	L227	S228	S229	S230	Y231	K232	E233	G234	L236	T237	T238	L239	G240	V241	A242	T243	W244	G245	T246	V247	R250	E251	T254	H255	G258	S259	F260	P261	Y264	L265	L266	D267	E268	D269	N273	L274	T275	C276	H283	F284	L286									
I63	P64	E65		K69	R70	E71	C72	V73	Y74	V76	E77	S78	S79	K80	L81	S82	D83	A84	G85	K86	V87	C89	Q90	C91	G92	Y93	E96	A97	H98	T103	K104	P105	H106	T107	F108	Q109	G110	T111	Q112	W113	K116	K117	H118	P123	F127	G128	D129	I130	T133	G134	L135								



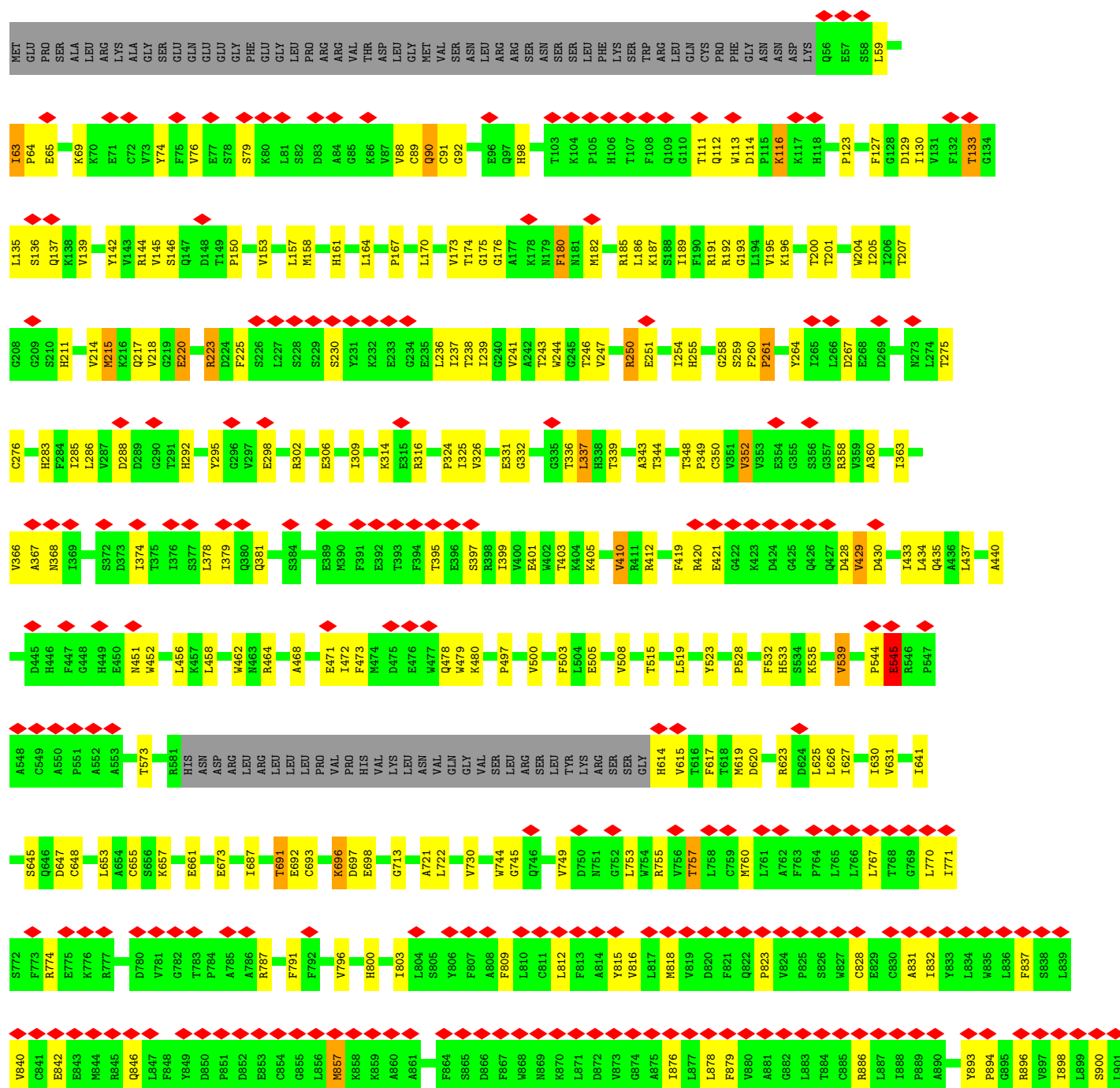
- Molecule 1: Transient receptor potential cation channel subfamily M member 2

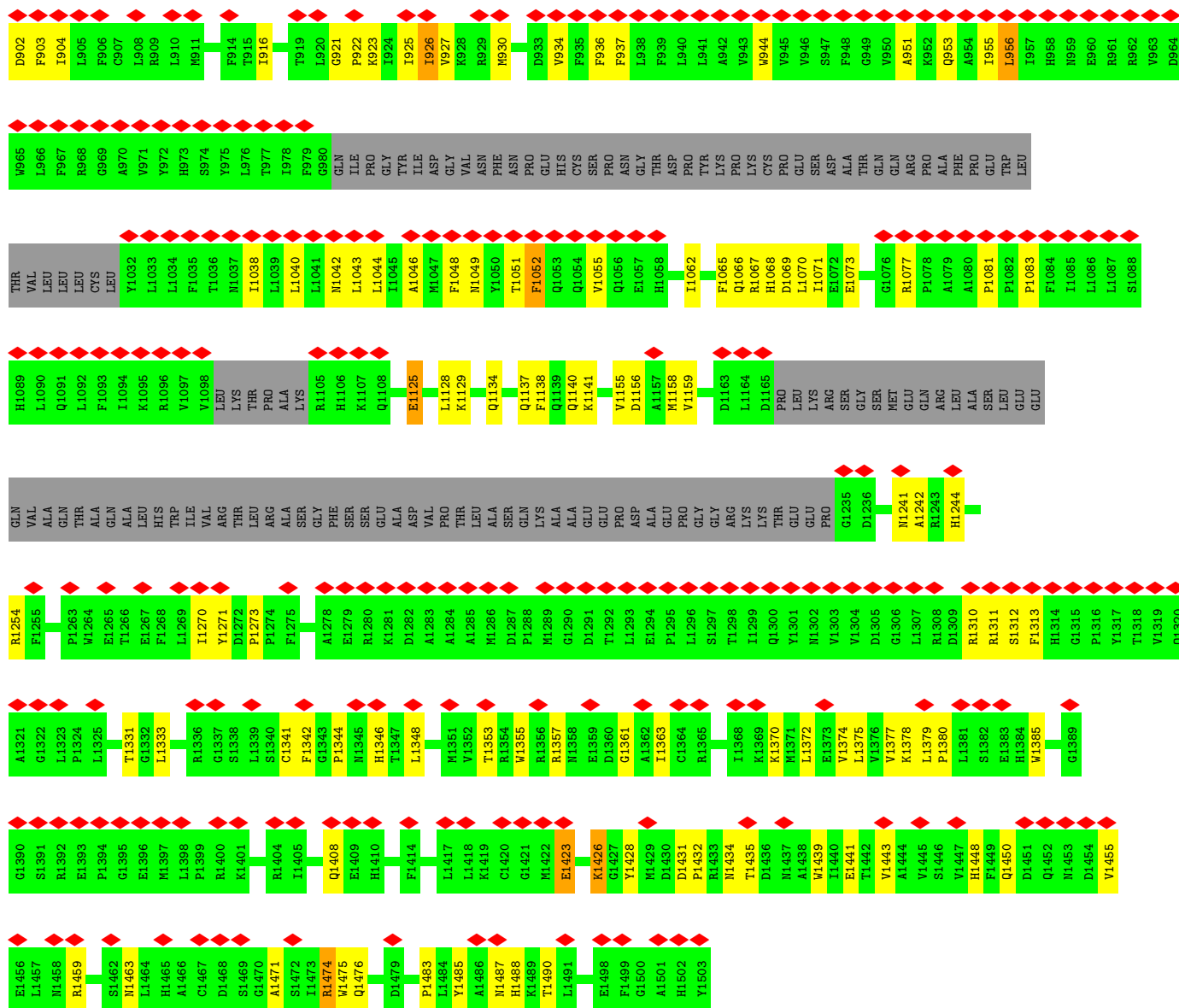






• Molecule 1: Transient receptor potential cation channel subfamily M member 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	68766	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 ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.063	Depositor
Minimum map value	-0.043	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0102	Depositor
Map size (Å)	272.0, 272.0, 272.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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: UOO

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	0.19	0/9809	0.52	1/13392 (0.0%)
1	B	0.19	0/9809	0.52	1/13392 (0.0%)
1	C	0.19	0/9809	0.52	1/13392 (0.0%)
1	D	0.19	0/9809	0.52	1/13392 (0.0%)
All	All	0.19	0/39236	0.52	4/53568 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	545	GLU	CA-CB-CG	6.17	126.45	114.10
1	D	545	GLU	CA-CB-CG	6.16	126.41	114.10
1	A	545	GLU	CA-CB-CG	6.15	126.41	114.10
1	B	545	GLU	CA-CB-CG	6.15	126.40	114.10

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	9579	0	8968	255	0
1	B	9579	0	8968	247	0
1	C	9579	0	8968	245	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	9579	0	8968	250	0
2	A	74	0	0	5	0
2	B	74	0	0	5	0
2	C	74	0	0	5	0
2	D	74	0	0	5	0
All	All	38612	0	35872	950	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 13.

The worst 5 of 950 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)
2:C:1602:UOO:C17	2:C:1602:UOO:O37	1.69	1.18
2:B:1601:UOO:C17	2:B:1601:UOO:O37	1.69	1.17
2:D:1602:UOO:C17	2:D:1602:UOO:O37	1.69	1.17
2:B:1602:UOO:O37	2:B:1602:UOO:C17	1.69	1.17
2:A:1602:UOO:C17	2:A:1602:UOO:O37	1.69	1.14

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	1280/1503 (85%)	1196 (93%)	74 (6%)	10 (1%)	16	48
1	B	1280/1503 (85%)	1196 (93%)	75 (6%)	9 (1%)	18	50
1	C	1280/1503 (85%)	1196 (93%)	74 (6%)	10 (1%)	16	48
1	D	1280/1503 (85%)	1196 (93%)	74 (6%)	10 (1%)	16	48
All	All	5120/6012 (85%)	4784 (93%)	297 (6%)	39 (1%)	18	48

5 of 39 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	261	PRO
1	A	956	LEU
1	A	1408	GLN
1	B	261	PRO
1	B	956	LEU

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	914/1318 (69%)	878 (96%)	36 (4%)	28	53
1	B	914/1318 (69%)	878 (96%)	36 (4%)	28	53
1	C	914/1318 (69%)	879 (96%)	35 (4%)	29	53
1	D	914/1318 (69%)	878 (96%)	36 (4%)	28	53
All	All	3656/5272 (69%)	3513 (96%)	143 (4%)	30	53

5 of 143 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	250	ARG
1	D	350	CYS
1	D	696	LYS
1	B	350	CYS
1	B	337	LEU

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

Mol	Chain	Res	Type
1	C	736	GLN
1	D	156	HIS
1	D	736	GLN
1	D	161	HIS
1	B	557	GLN

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](#)

8 ligands are modelled in this entry.

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	$\# Z > 2$
2	UOO	C	1601	-	38,39,39	5.56	19 (50%)	48,59,59	2.59	11 (22%)
2	UOO	B	1602	-	38,39,39	5.53	19 (50%)	48,59,59	2.66	13 (27%)
2	UOO	C	1602	-	38,39,39	5.53	19 (50%)	48,59,59	2.66	13 (27%)
2	UOO	D	1601	-	38,39,39	5.58	19 (50%)	48,59,59	2.59	11 (22%)
2	UOO	A	1602	-	38,39,39	5.54	18 (47%)	48,59,59	2.65	13 (27%)
2	UOO	A	1601	-	38,39,39	5.57	20 (52%)	48,59,59	2.59	11 (22%)
2	UOO	B	1601	-	38,39,39	5.57	20 (52%)	48,59,59	2.58	11 (22%)
2	UOO	D	1602	-	38,39,39	5.54	19 (50%)	48,59,59	2.64	13 (27%)

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
2	UOO	C	1601	-	-	16/27/47/47	0/3/3/3
2	UOO	B	1602	-	-	17/27/47/47	0/3/3/3
2	UOO	C	1602	-	-	17/27/47/47	0/3/3/3
2	UOO	D	1601	-	-	16/27/47/47	0/3/3/3
2	UOO	A	1602	-	-	17/27/47/47	0/3/3/3
2	UOO	A	1601	-	-	16/27/47/47	0/3/3/3
2	UOO	B	1601	-	-	16/27/47/47	0/3/3/3
2	UOO	D	1602	-	-	17/27/47/47	0/3/3/3

The worst 5 of 153 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1601	UOO	C28-C30	-18.90	1.31	1.52
2	A	1601	UOO	C28-C30	-18.83	1.31	1.52
2	C	1601	UOO	C28-C30	-18.83	1.31	1.52
2	B	1601	UOO	C28-C30	-18.83	1.31	1.52
2	A	1602	UOO	C28-C30	-18.34	1.31	1.52

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1602	UOO	N11-C09-N08	-8.46	108.47	115.04
2	A	1602	UOO	N11-C09-N08	-8.43	108.48	115.04
2	D	1602	UOO	N11-C09-N08	-8.43	108.49	115.04
2	B	1602	UOO	N11-C09-N08	-8.42	108.50	115.04
2	D	1601	UOO	N11-C09-N08	-8.30	108.58	115.04

There are no chirality outliers.

5 of 132 torsion outliers are listed below:

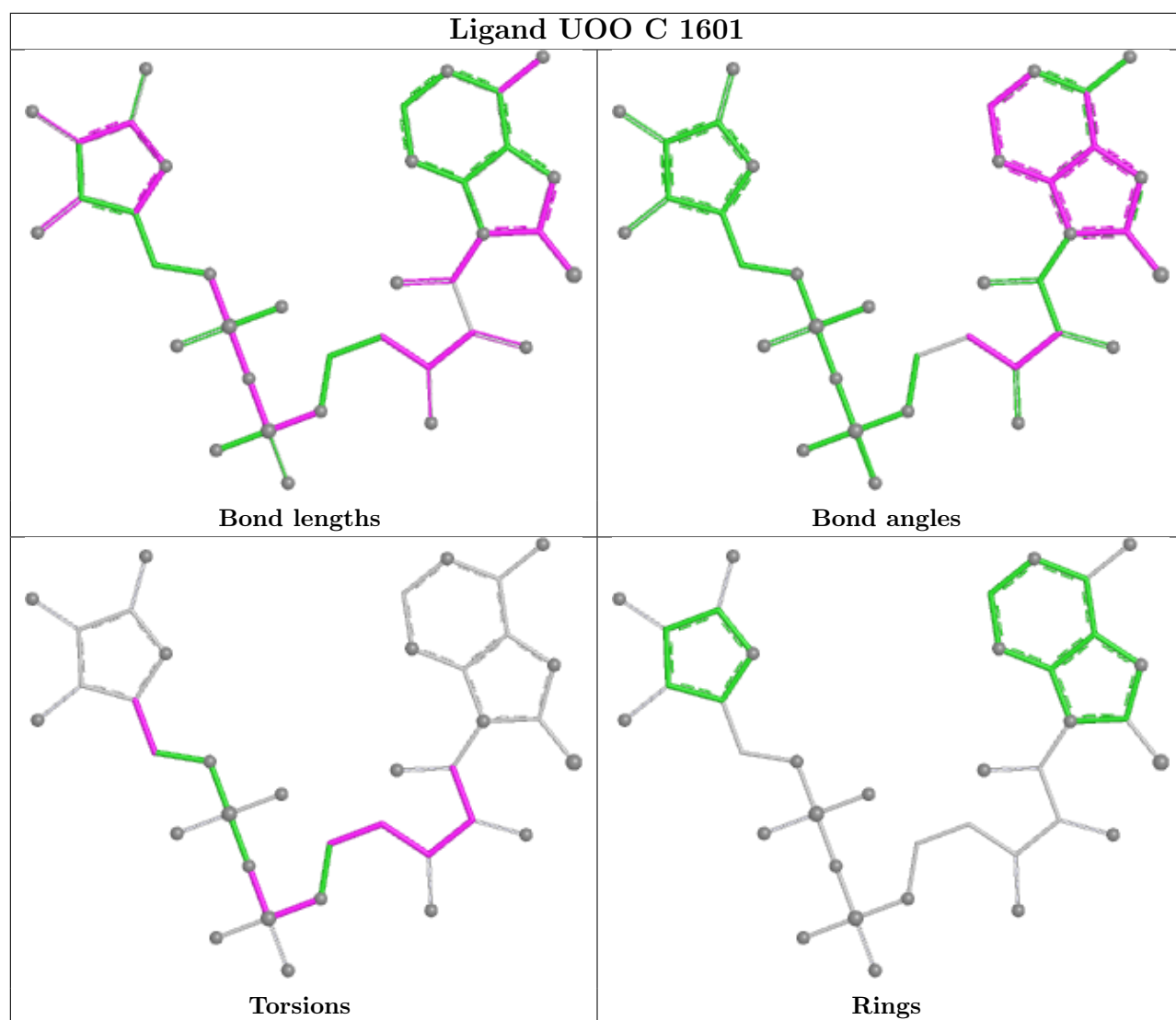
Mol	Chain	Res	Type	Atoms
2	A	1601	UOO	N11-C12-C13-C15
2	A	1601	UOO	N11-C12-C13-O14
2	A	1601	UOO	O37-C12-C13-C15
2	A	1601	UOO	O37-C12-C13-O14
2	A	1601	UOO	C12-C13-C15-C17

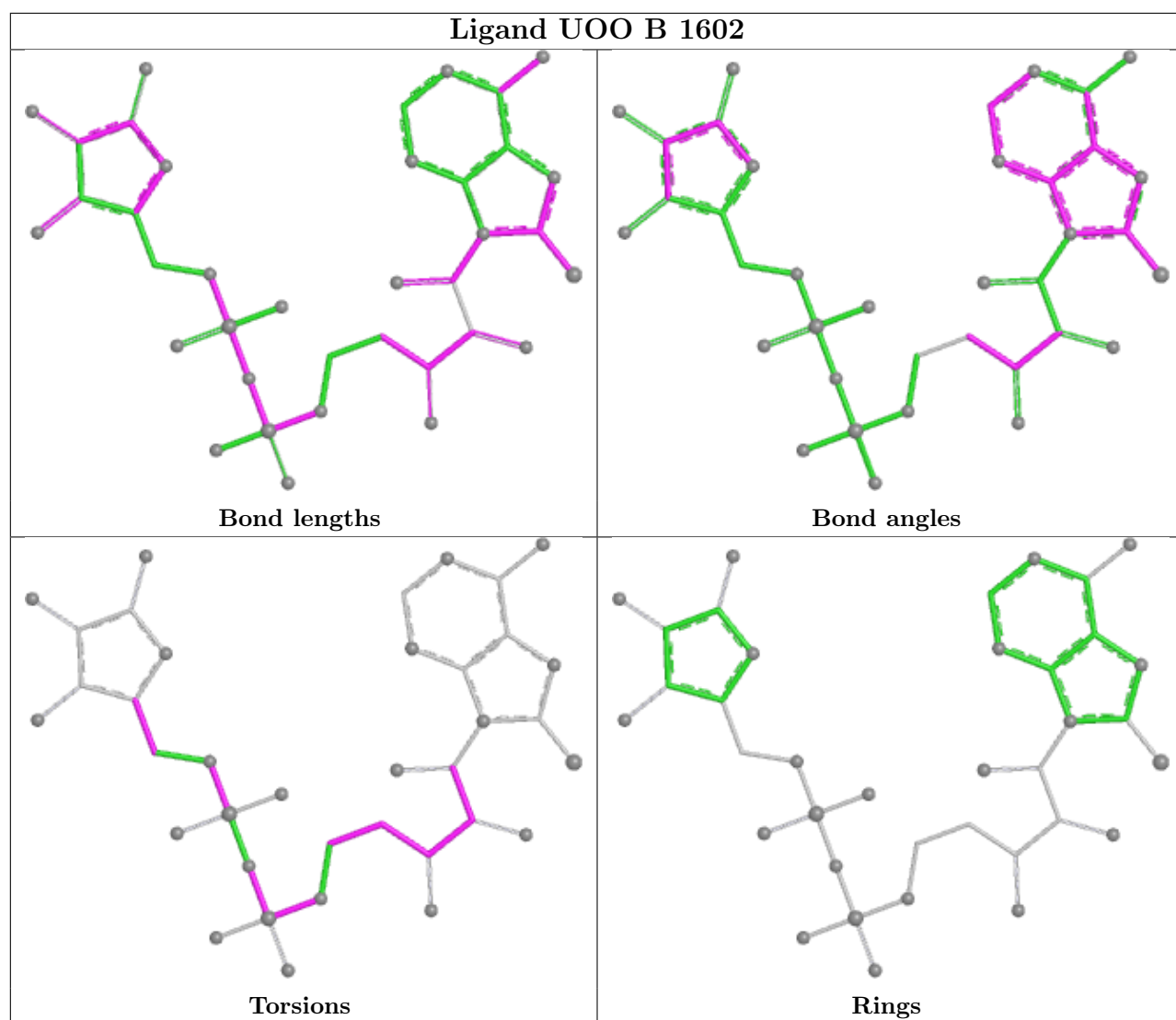
There are no ring outliers.

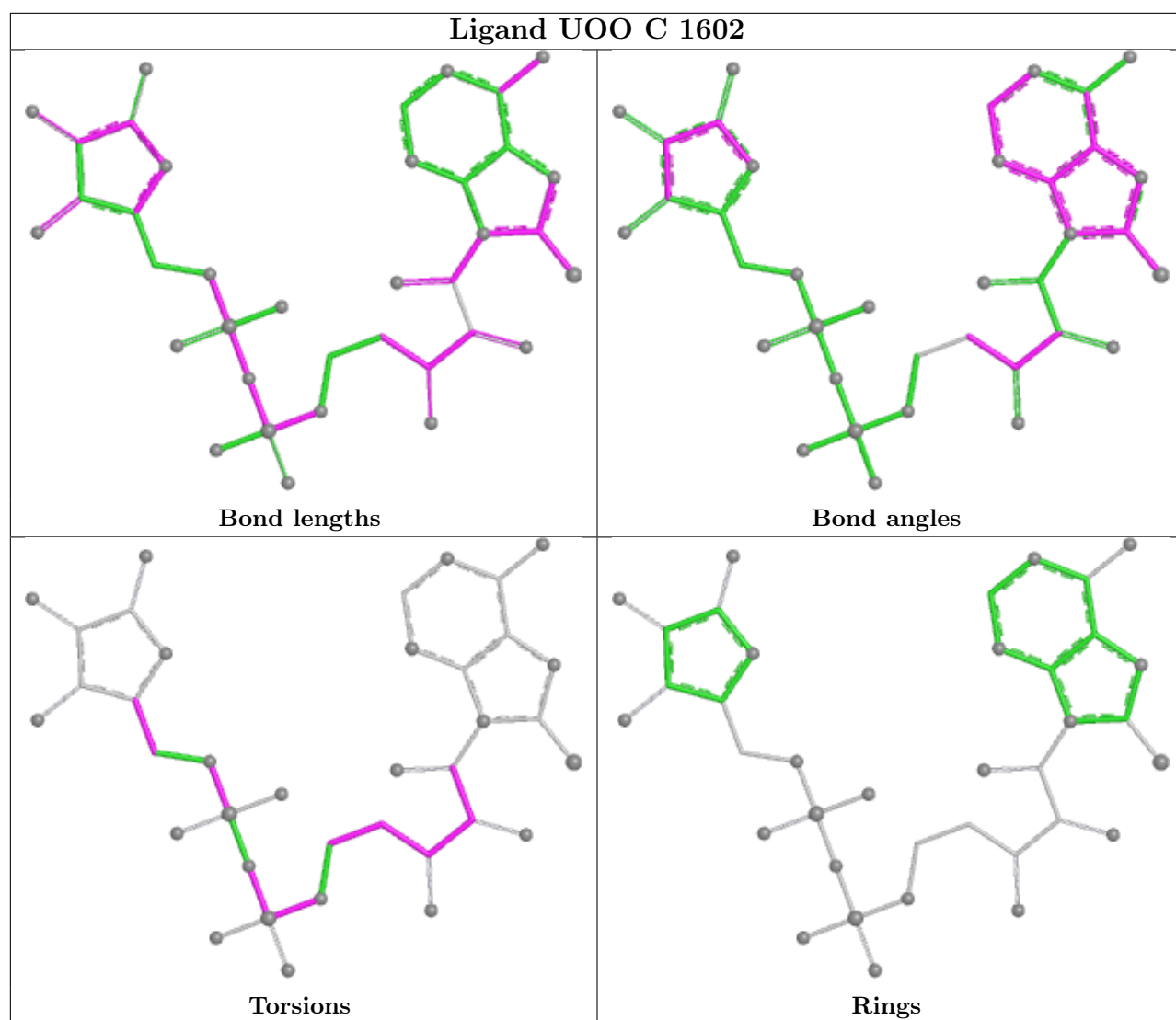
8 monomers are involved in 20 short contacts:

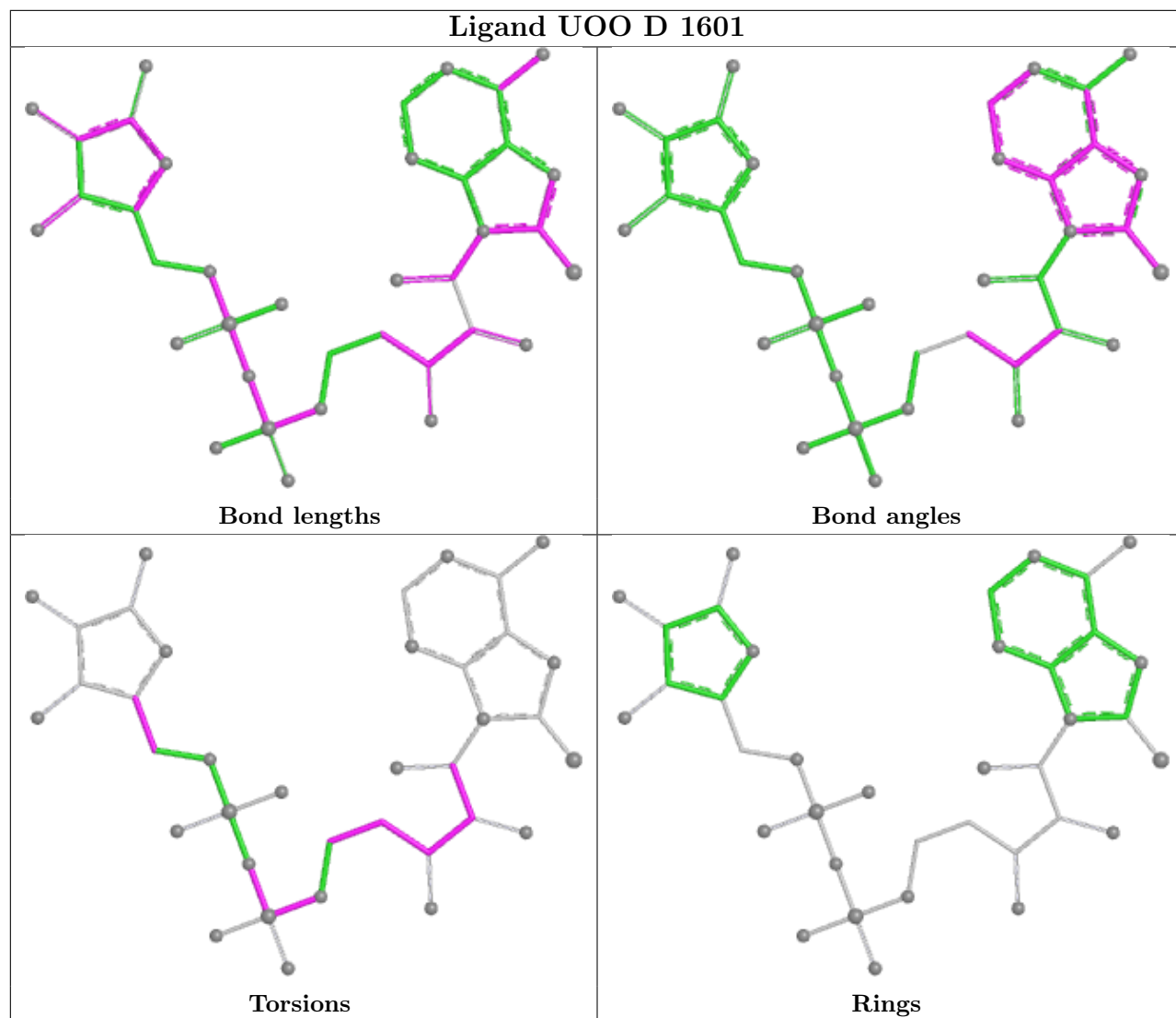
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1601	UOO	3	0
2	B	1602	UOO	2	0
2	C	1602	UOO	2	0
2	D	1601	UOO	3	0
2	A	1602	UOO	2	0
2	A	1601	UOO	3	0
2	B	1601	UOO	3	0
2	D	1602	UOO	2	0

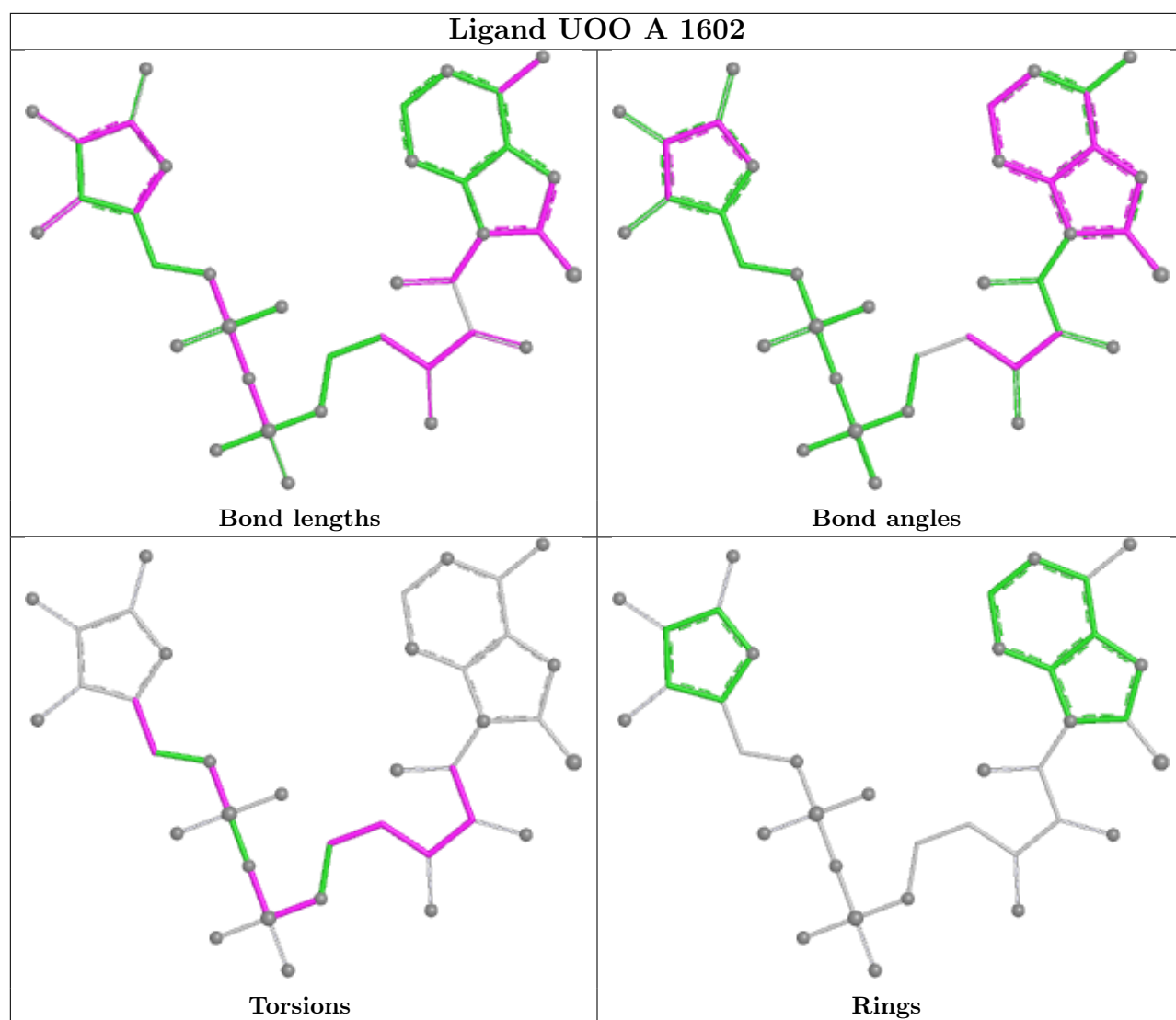
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

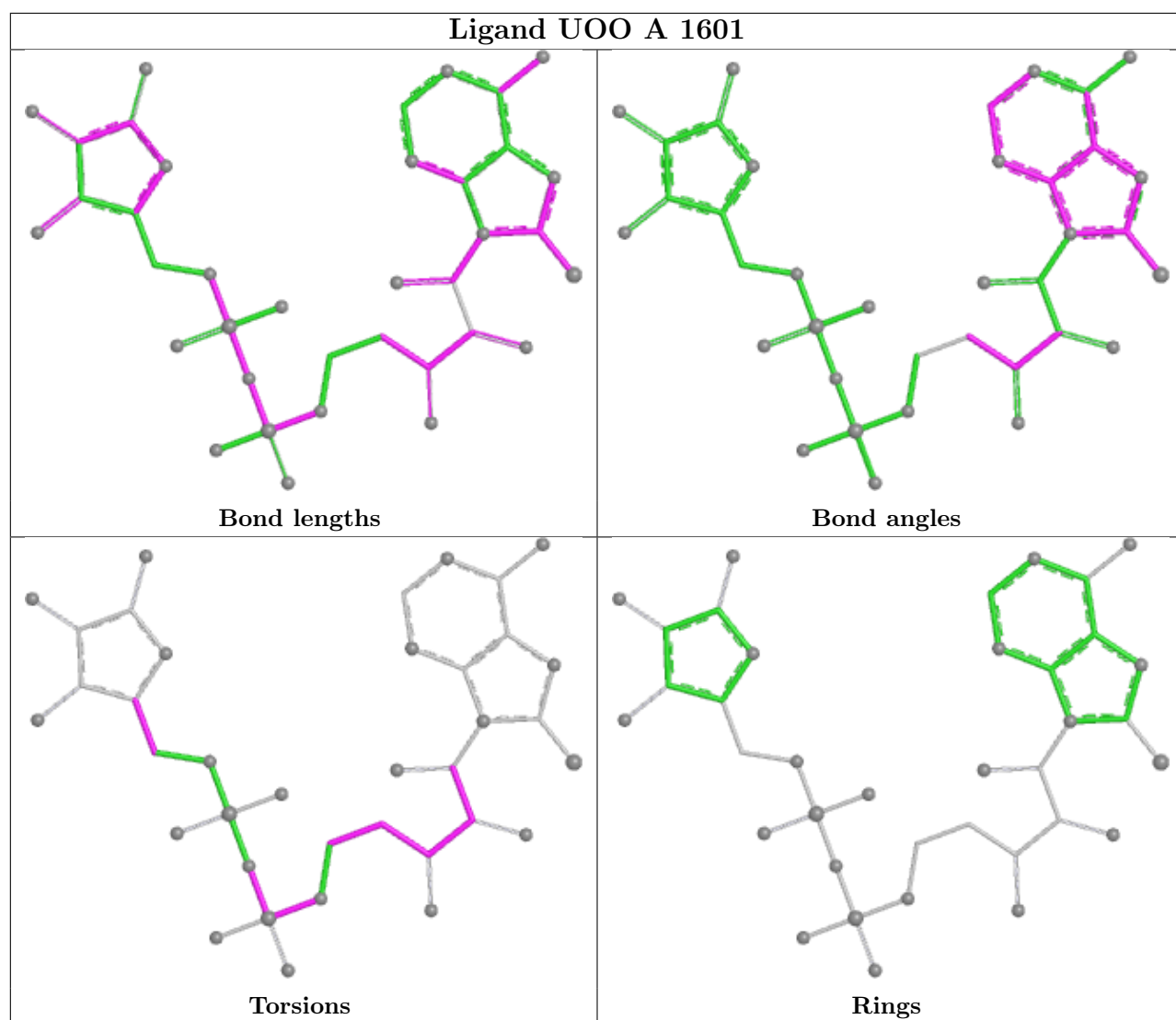


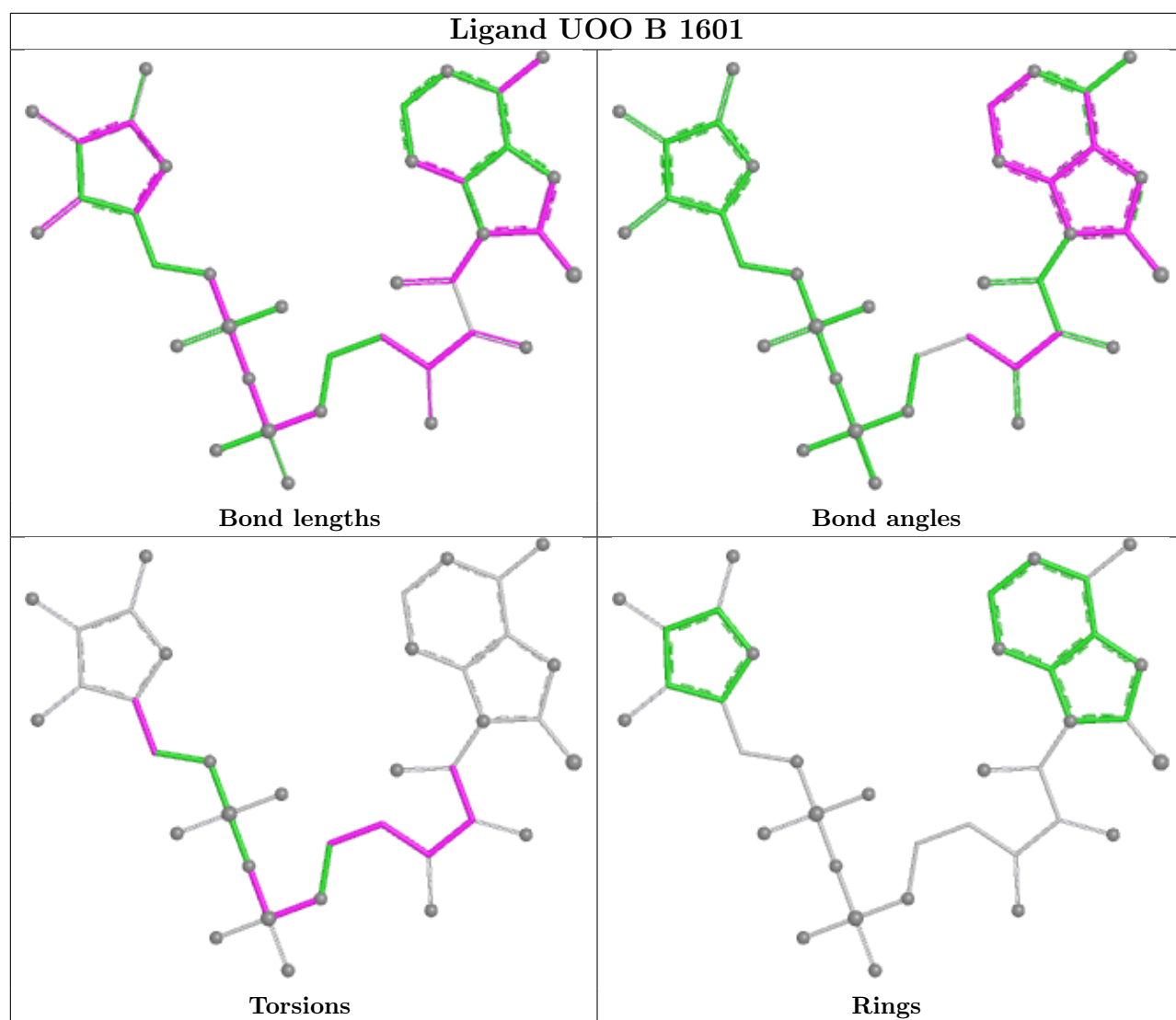


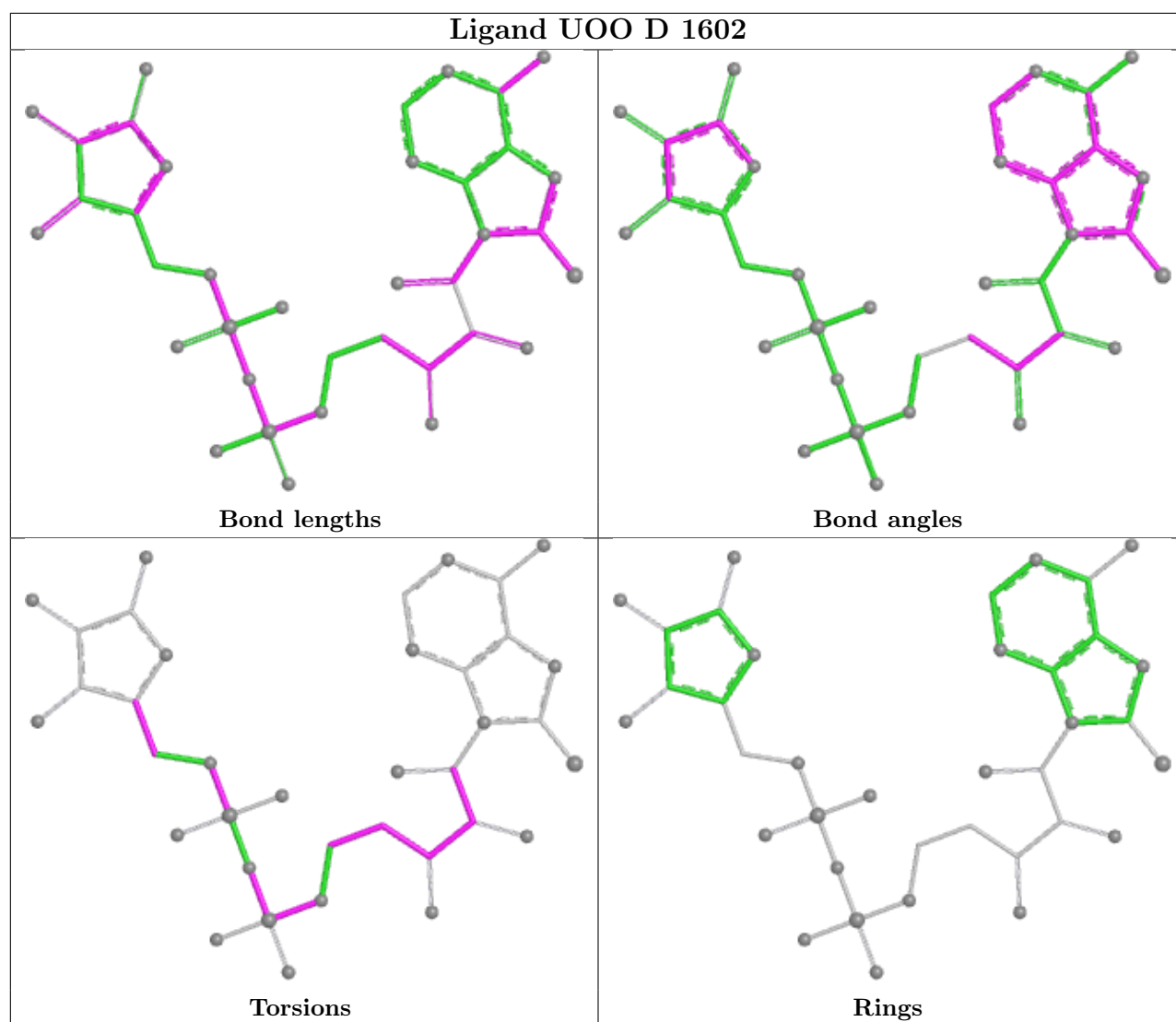












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

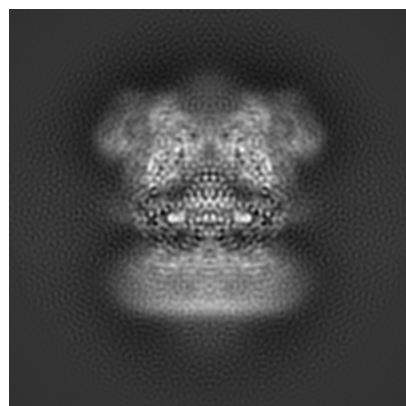
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27925. These allow visual inspection of the internal detail of the map and identification of artifacts.

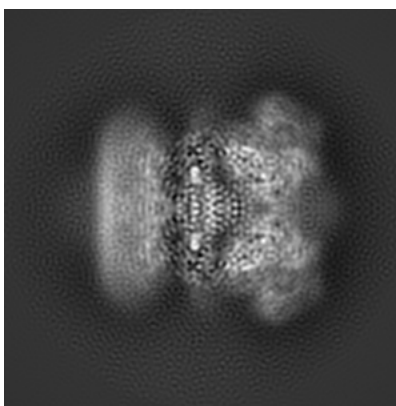
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

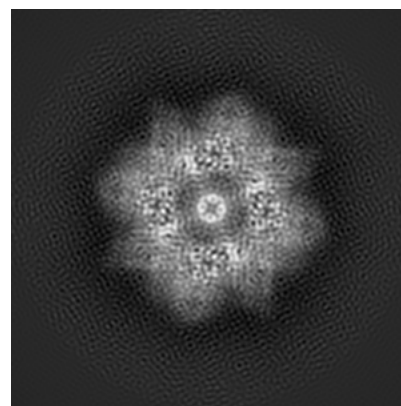
6.1.1 Primary map



X

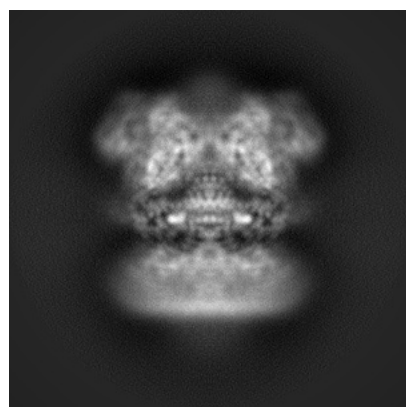


Y

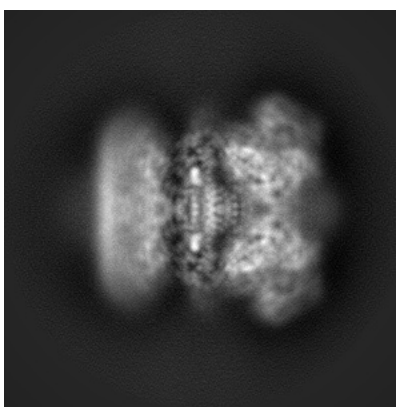


Z

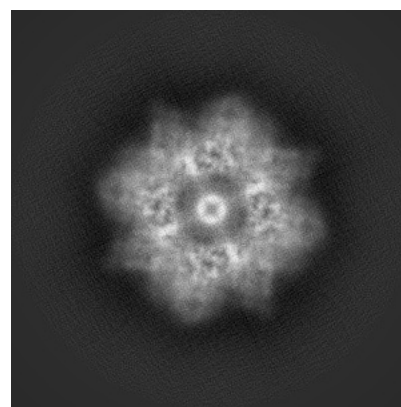
6.1.2 Raw map



X



Y

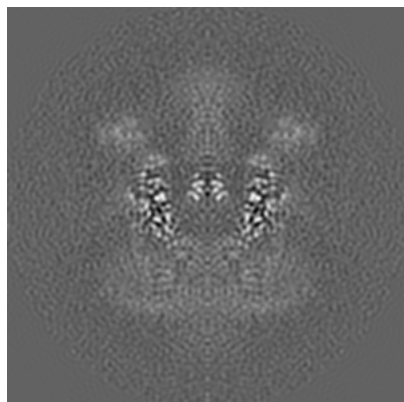


Z

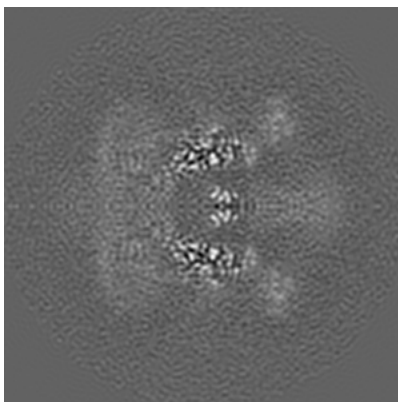
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

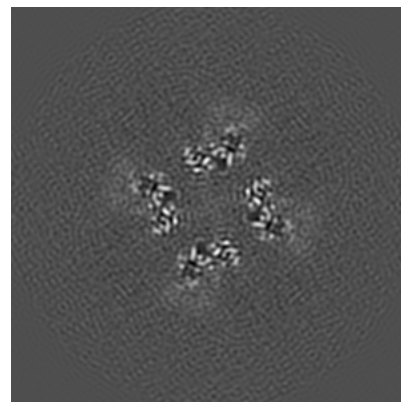
6.2.1 Primary map



X Index: 160

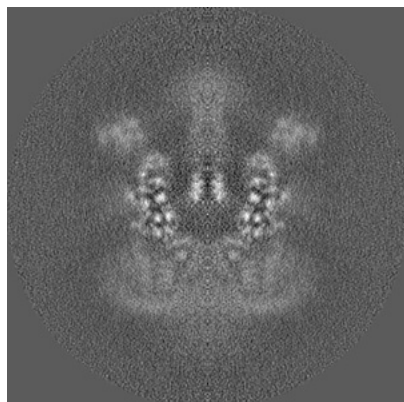


Y Index: 160

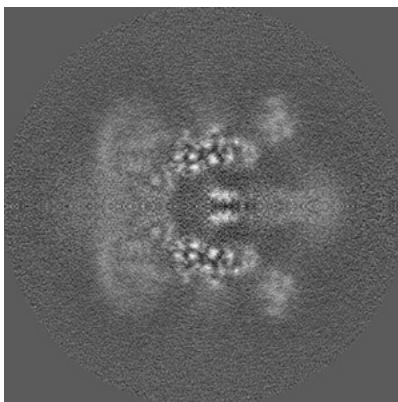


Z Index: 160

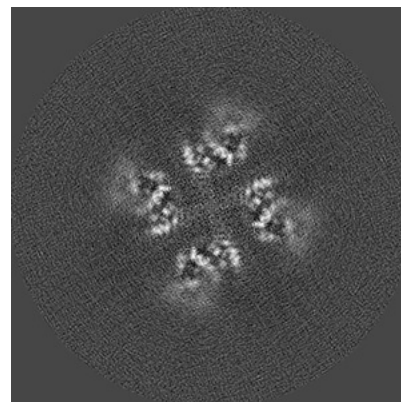
6.2.2 Raw map



X Index: 160



Y Index: 160

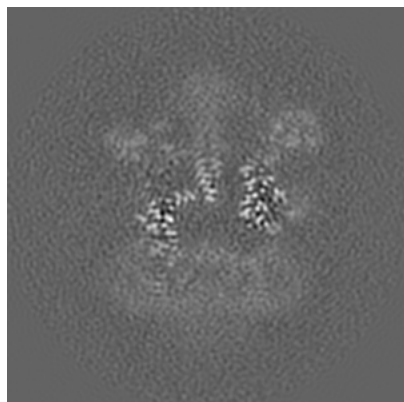


Z Index: 160

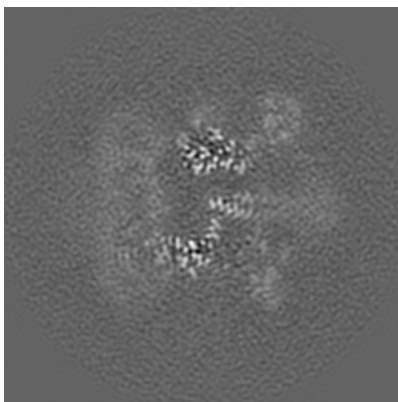
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

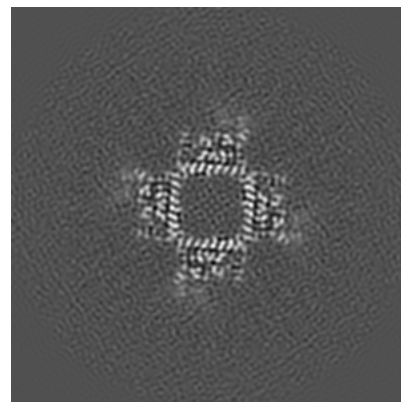
6.3.1 Primary map



X Index: 168

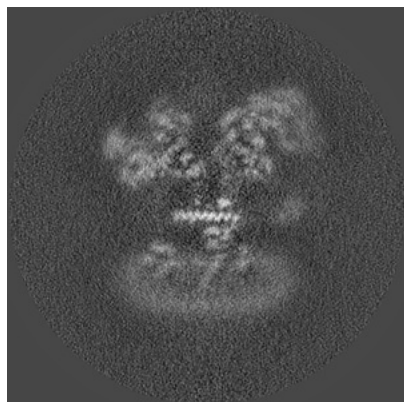


Y Index: 152

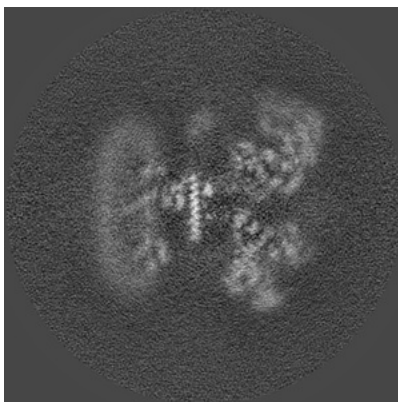


Z Index: 151

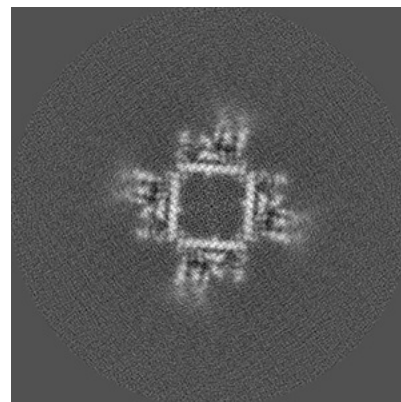
6.3.2 Raw map



X Index: 190



Y Index: 130

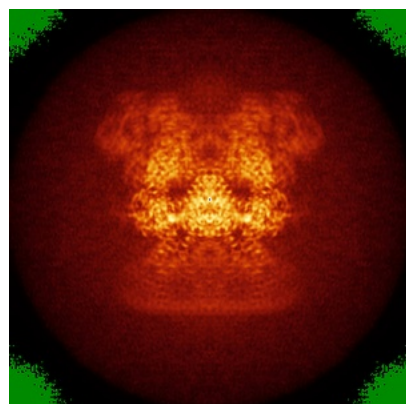


Z Index: 152

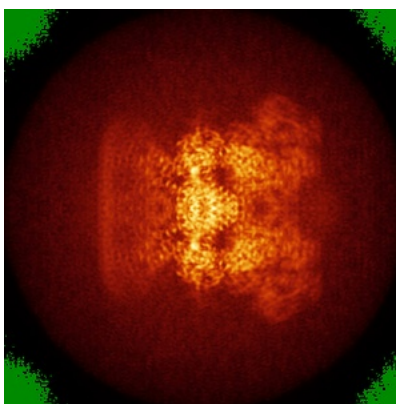
The images above show the largest variance slices of the map in three orthogonal directions.

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

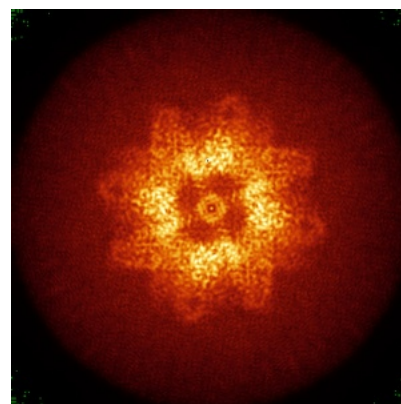
6.4.1 Primary map



X

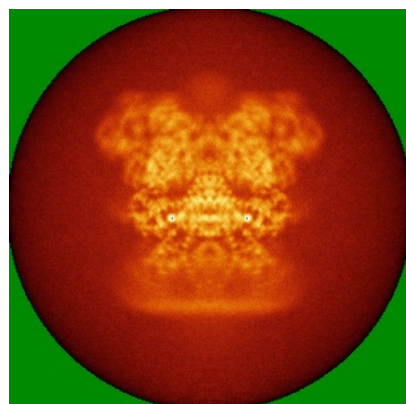


Y

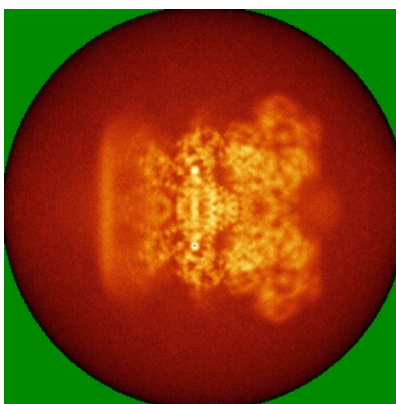


Z

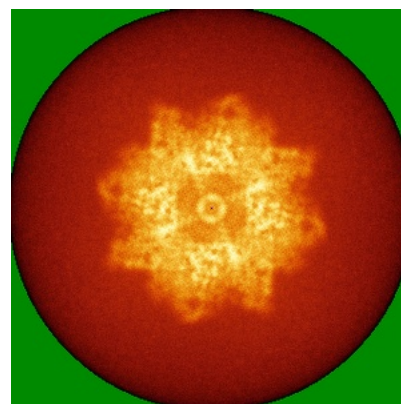
6.4.2 Raw map



X



Y

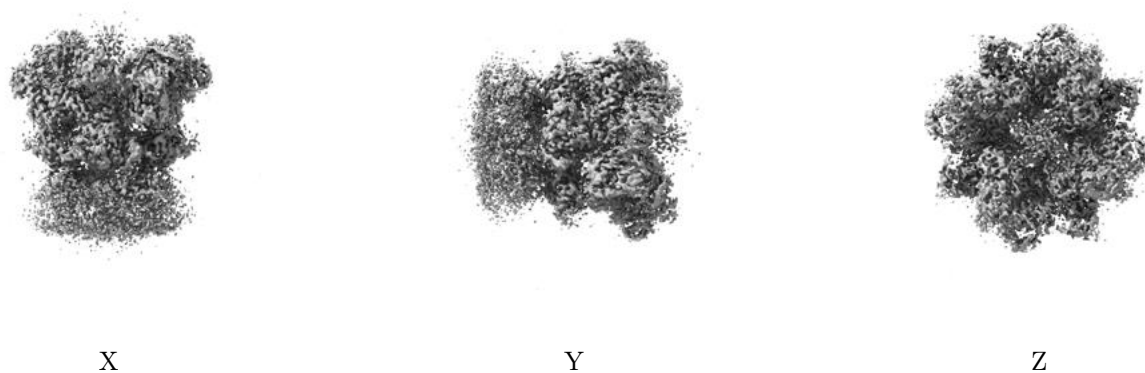


Z

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.

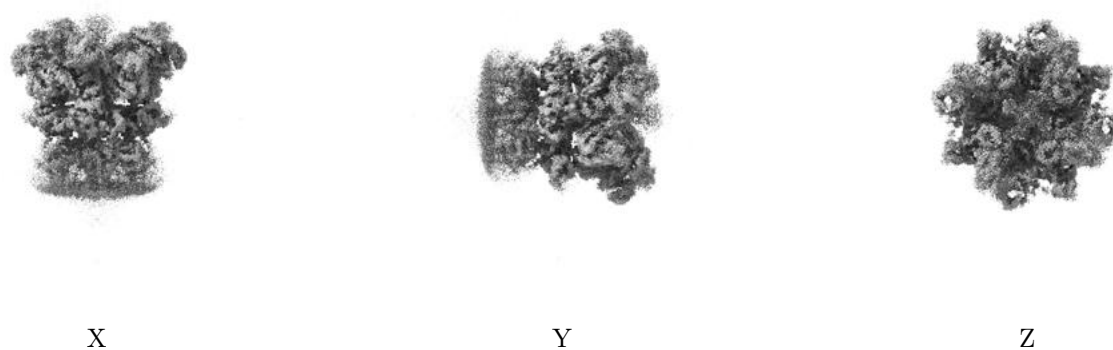
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0102. 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.

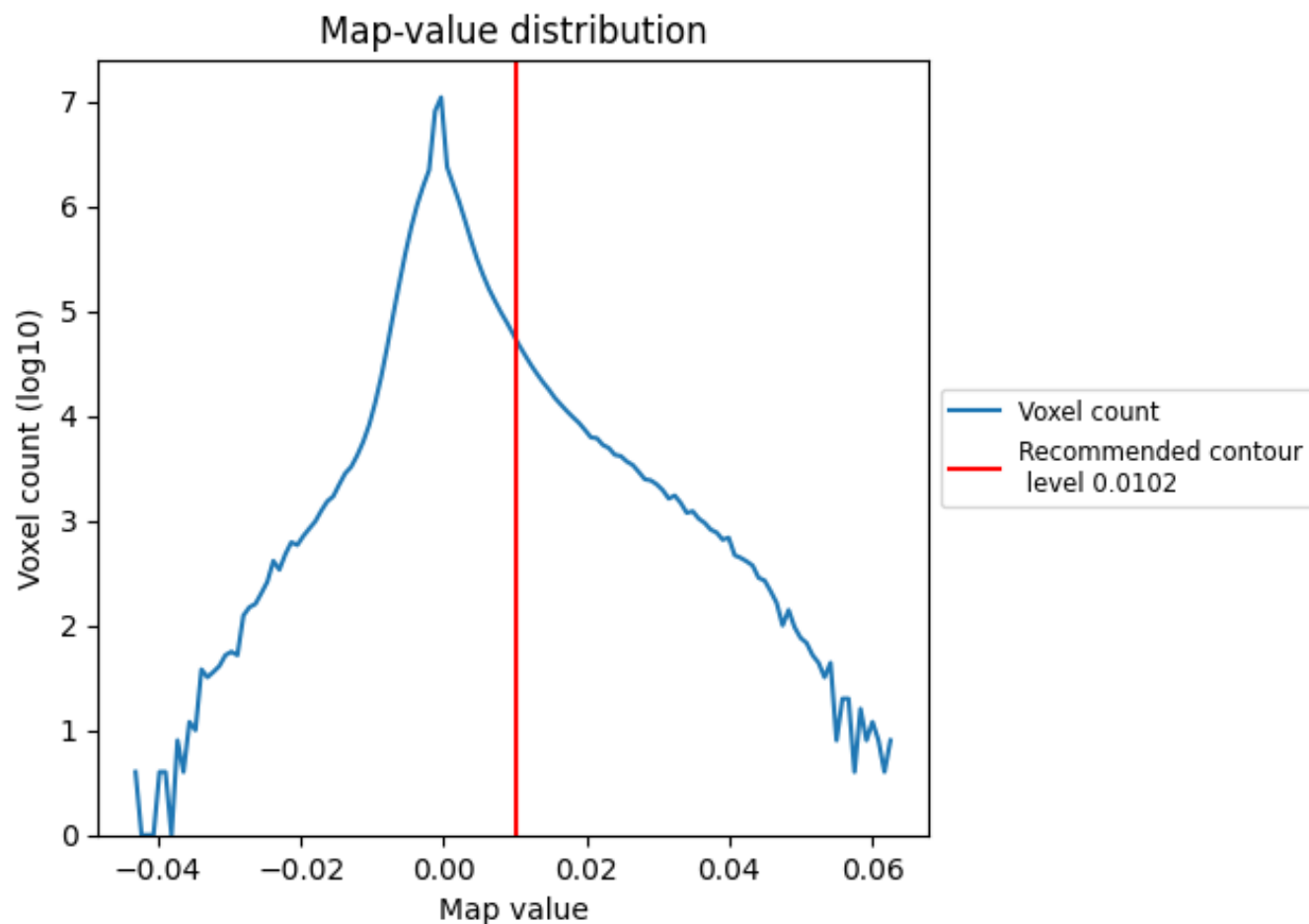
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

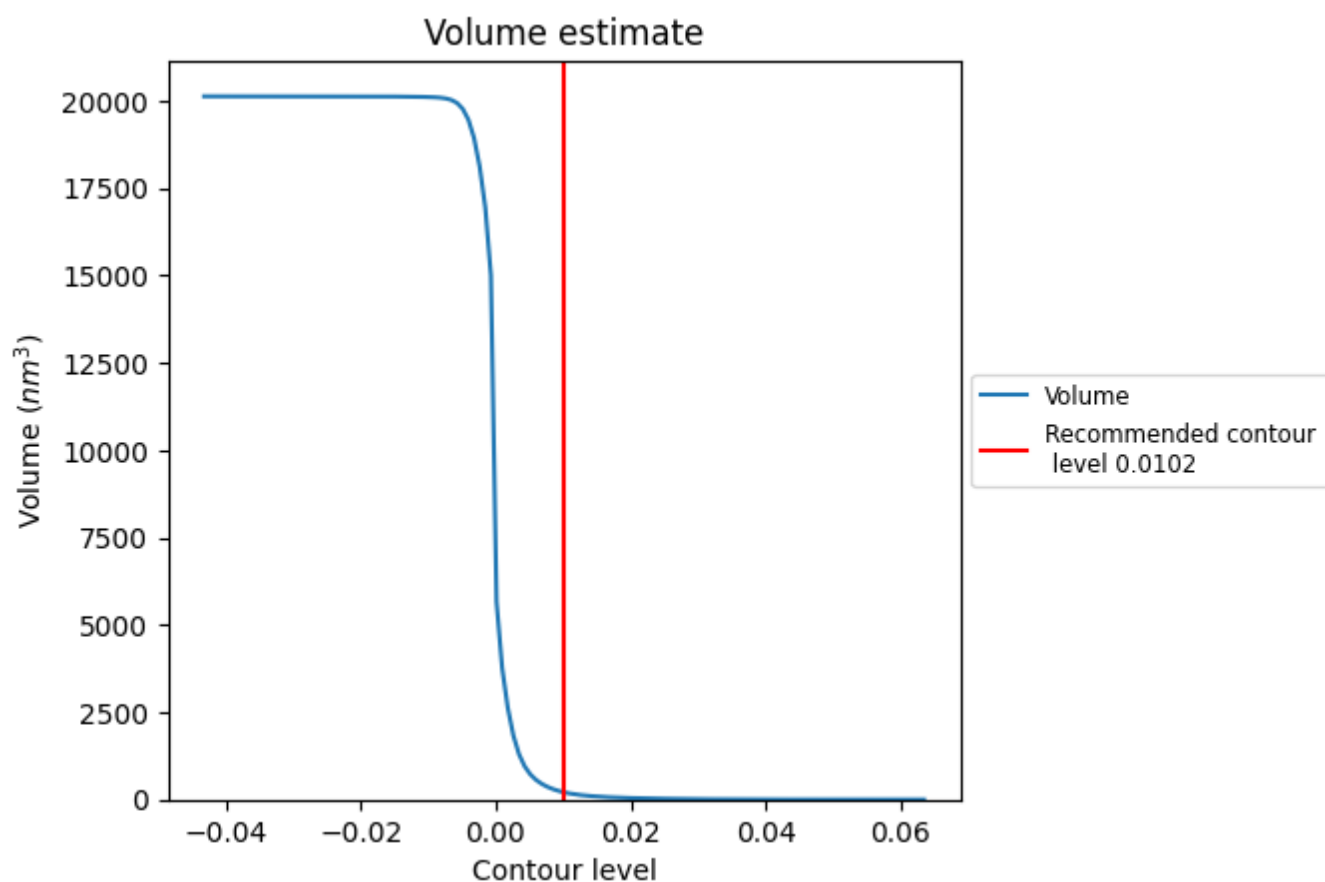
This section contains the results of statistical analysis of the map.

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.

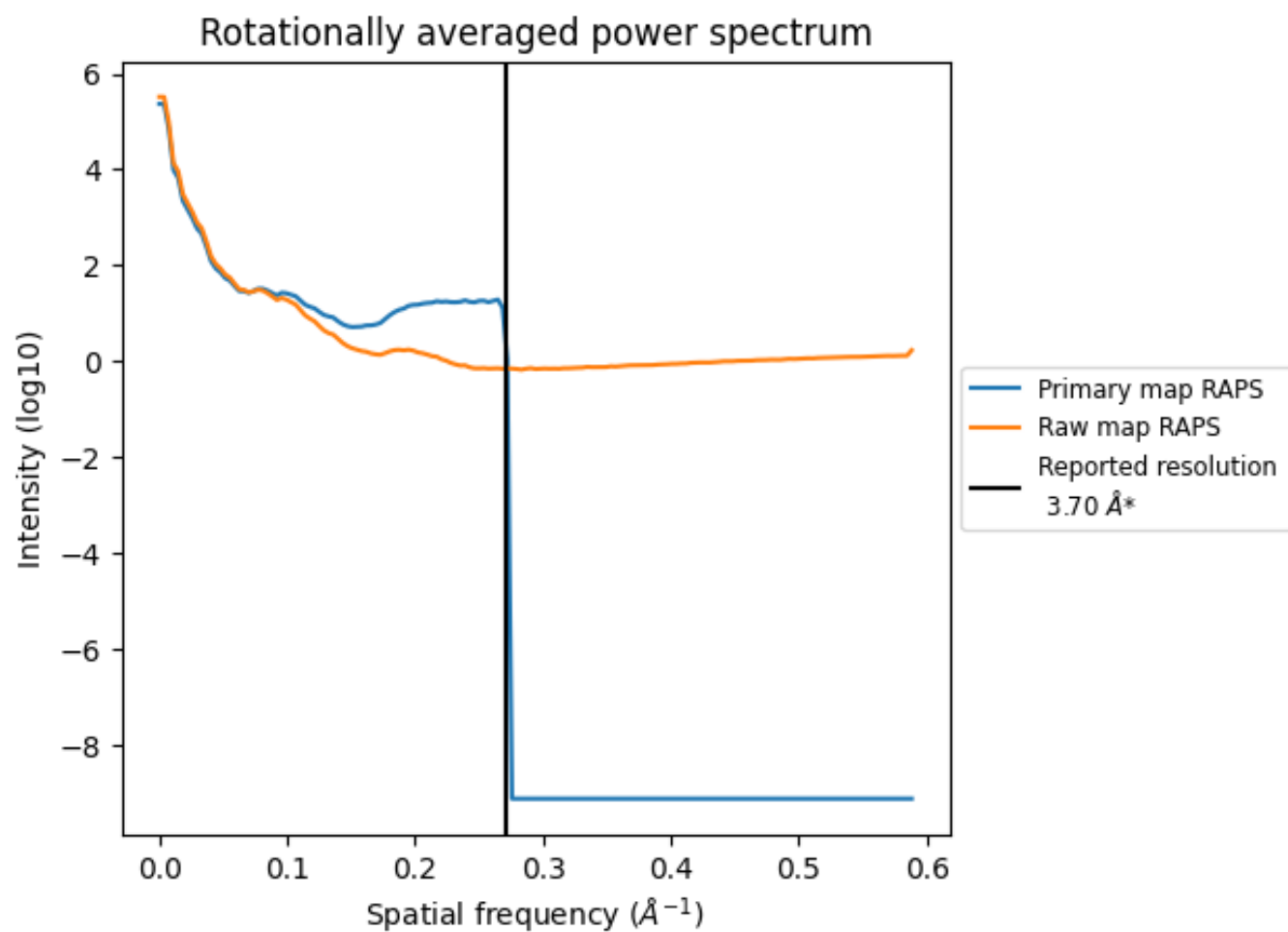
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 205 nm³; this corresponds to an approximate mass of 185 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 ⓘ

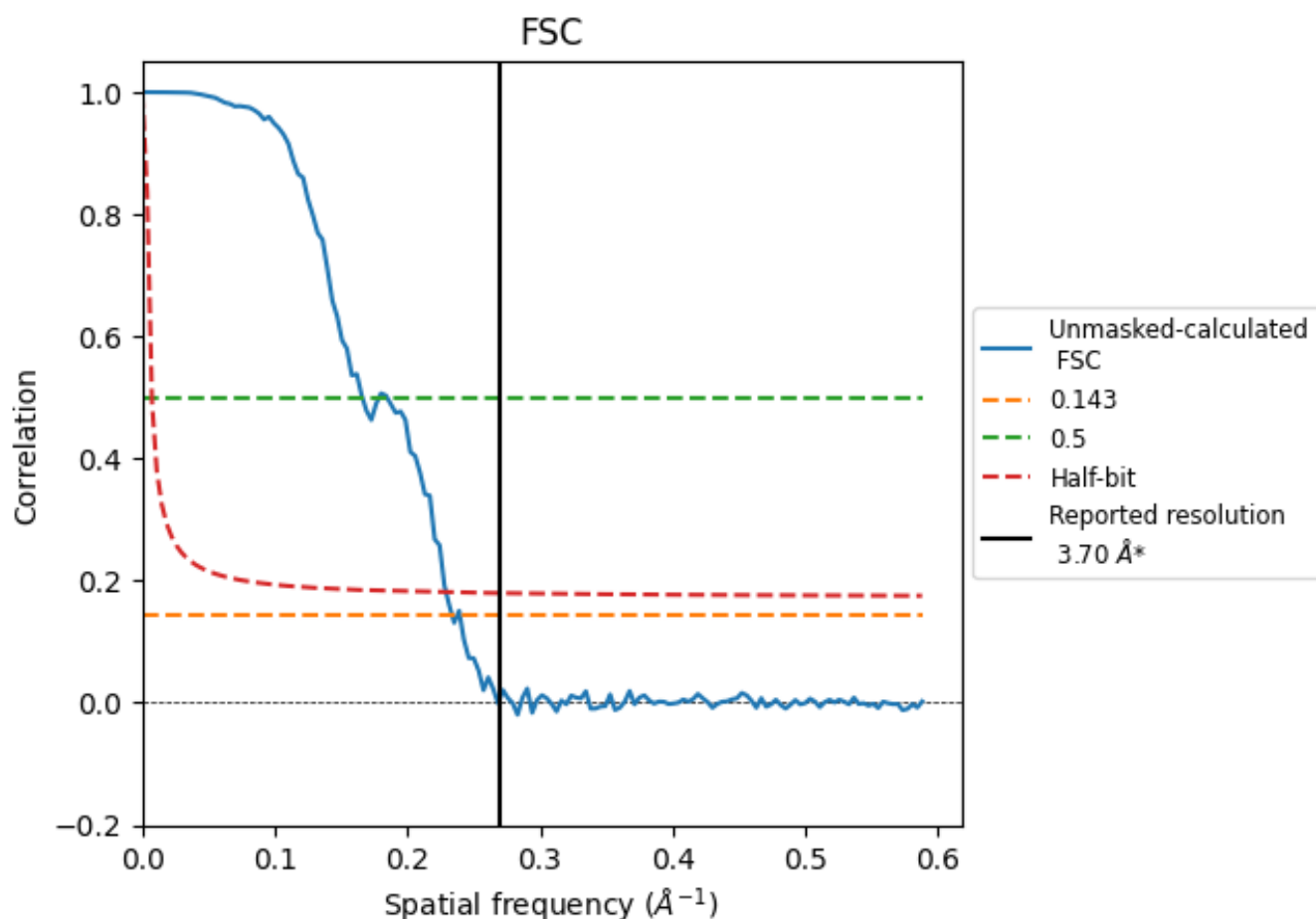


*Reported resolution corresponds to spatial frequency of 0.270 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.270 Å⁻¹

8.2 Resolution estimates [i](#)

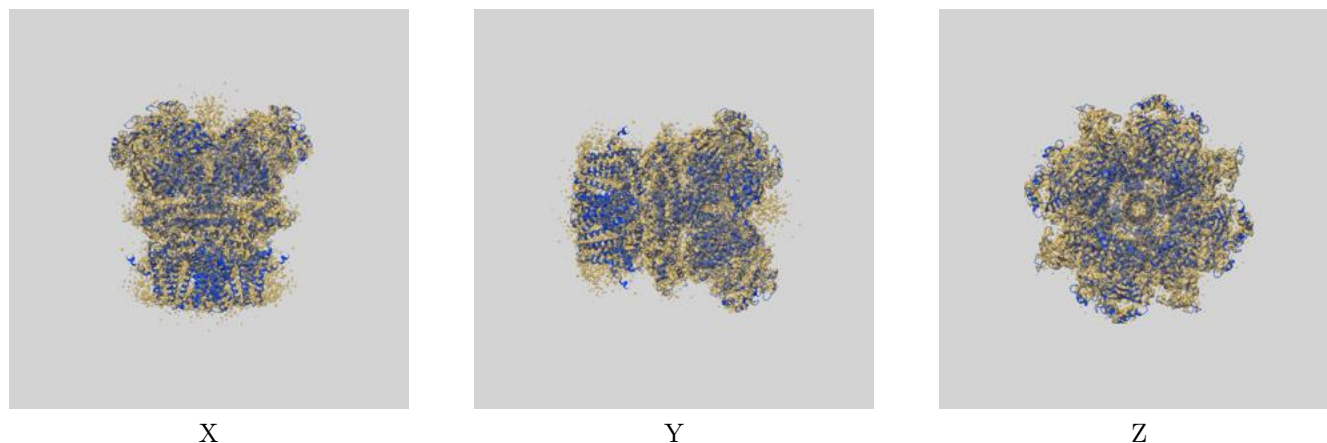
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.70	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.28	6.02	4.36

*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 4.28 differs from the reported value 3.7 by more than 10 %

9 Map-model fit [i](#)

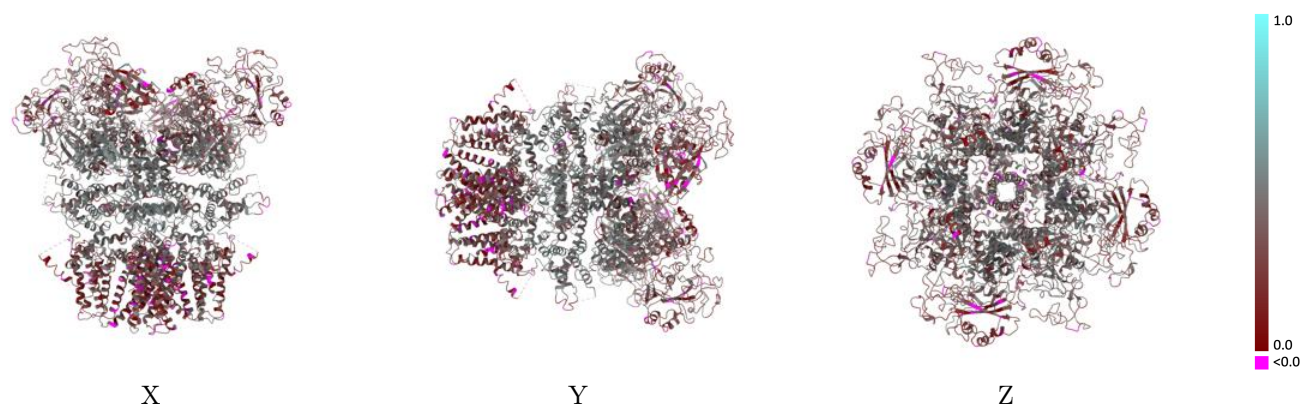
This section contains information regarding the fit between EMDB map EMD-27925 and PDB model 8E6T. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



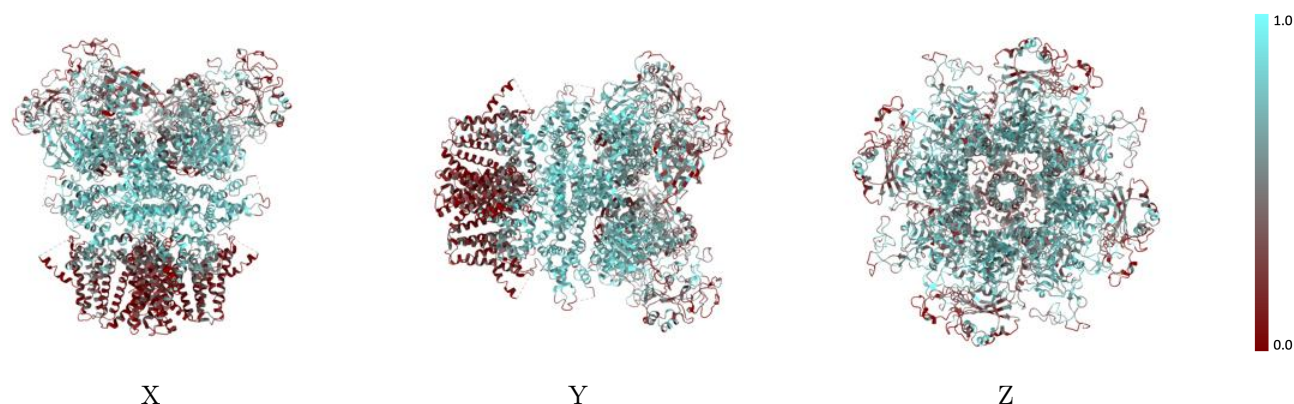
The images above show the 3D surface view of the map at the recommended contour level 0.0102 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



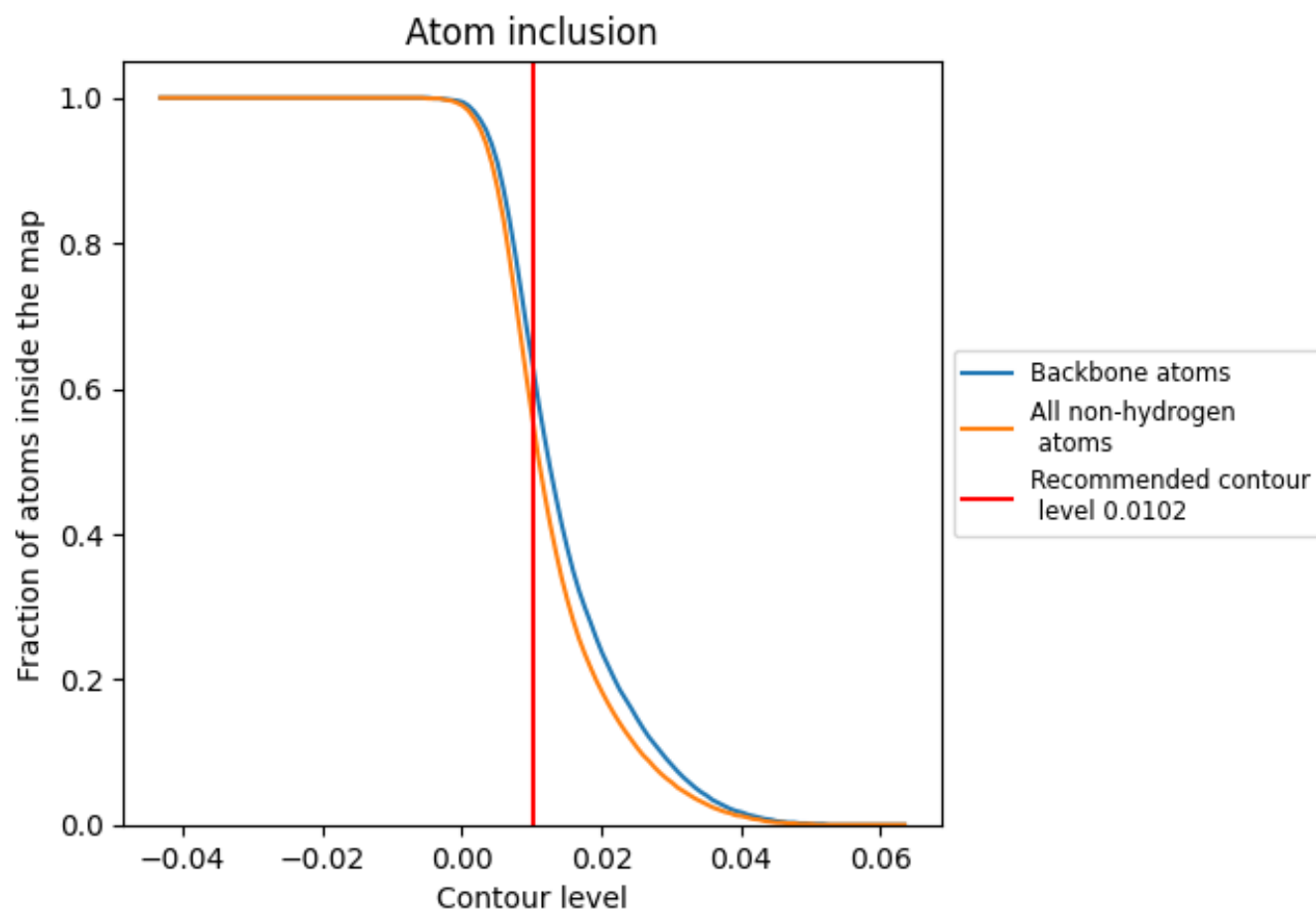
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0102).

9.4 Atom inclusion [i](#)



At the recommended contour level, 63% of all backbone atoms, 56% 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 (0.0102) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5550	0.3600
A	0.5670	0.3740
B	0.5480	0.3520
C	0.5570	0.3630
D	0.5460	0.3510

