



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 04:18 AM UTC

PDB ID : 8RTS / pdb\_00008rts  
EMDB ID : EMD-19495  
Title : Structure of a homomeric human LRRC8C Volume-Regulated Anion Channel  
Authors : Rutz, S.; Quinodoz, M.; Peter, V.; Garavelli, L.; Innes, M.; Kellenberger, S.; Barone, A.; Campos-Xavier, B.; Unger, S.; Rivolta, C.; Dutzler, R.; Superti-Furga, A.  
Deposited on : 2024-01-29  
Resolution : 3.73 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

---

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

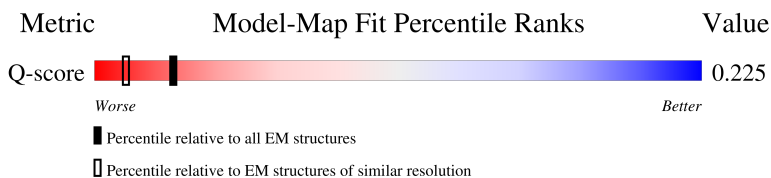
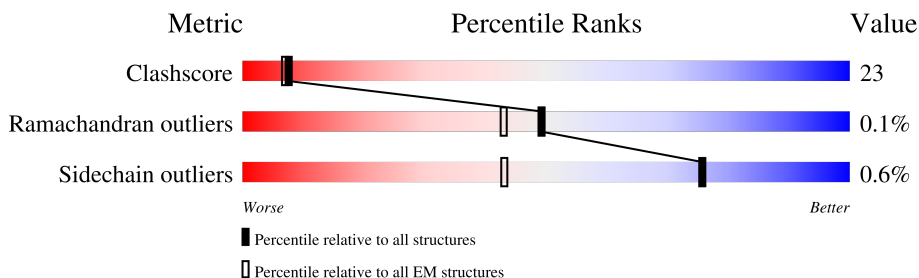
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins)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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.73 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	10415 ( 3.23 - 4.23 )

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

Mol	Chain	Length	Quality of chain
1	A	811	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>26%</p> </div> <div style="text-align: center;"> <p>45%</p> </div> <div style="text-align: center;"> <p>40%</p> </div> <div style="text-align: center;"> <p>15%</p> </div> </div>
1	B	811	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>27%</p> </div> <div style="text-align: center;"> <p>43%</p> </div> <div style="text-align: center;"> <p>41%</p> </div> <div style="text-align: center;"> <p>15%</p> </div> </div>
1	C	811	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>74%</p> </div> <div style="text-align: center;"> <p>49%</p> </div> <div style="text-align: center;"> <p>35%</p> </div> <div style="text-align: center;"> <p>15%</p> </div> </div>
1	D	811	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>77%</p> </div> <div style="text-align: center;"> <p>57%</p> </div> <div style="text-align: center;"> <p>28%</p> </div> <div style="text-align: center;"> <p>15%</p> </div> </div>

Continued on next page...

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	E	811	 <p>72% 47% 38% 15%</p>
1	F	811	 <p>67% 48% 37% 15%</p>
1	G	811	 <p>16% 18% 6% 76%</p>

## 2 Entry composition i

There is only 1 type of molecule in this entry. The entry contains 35445 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 Volume-regulated anion channel subunit LRRC8C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	692	5641	3675	926	1004	36	0	0
1	B	692	5641	3675	926	1004	36	0	0
1	C	692	5641	3675	926	1004	36	0	0
1	D	692	5641	3675	926	1004	36	0	0
1	E	692	5641	3675	926	1004	36	0	0
1	F	692	5641	3675	926	1004	36	0	0
1	G	192	1599	1070	246	265	18	0	0

There are 91 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q8TDW0
A	1	SER	-	expression tag	UNP Q8TDW0
A	205	GLY	ASP	variant	UNP Q8TDW0
A	781	ARG	GLY	conflict	UNP Q8TDW0
A	802	ALA	-	expression tag	UNP Q8TDW0
A	803	ASP	-	expression tag	UNP Q8TDW0
A	804	ALA	-	expression tag	UNP Q8TDW0
A	805	LEU	-	expression tag	UNP Q8TDW0
A	806	GLU	-	expression tag	UNP Q8TDW0
A	807	VAL	-	expression tag	UNP Q8TDW0
A	808	LEU	-	expression tag	UNP Q8TDW0
A	809	PHE	-	expression tag	UNP Q8TDW0
A	810	GLN	-	expression tag	UNP Q8TDW0
B	0	MET	-	initiating methionine	UNP Q8TDW0
B	1	SER	-	expression tag	UNP Q8TDW0
B	205	GLY	ASP	variant	UNP Q8TDW0

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	781	ARG	GLY	conflict	UNP Q8TDW0
B	802	ALA	-	expression tag	UNP Q8TDW0
B	803	ASP	-	expression tag	UNP Q8TDW0
B	804	ALA	-	expression tag	UNP Q8TDW0
B	805	LEU	-	expression tag	UNP Q8TDW0
B	806	GLU	-	expression tag	UNP Q8TDW0
B	807	VAL	-	expression tag	UNP Q8TDW0
B	808	LEU	-	expression tag	UNP Q8TDW0
B	809	PHE	-	expression tag	UNP Q8TDW0
B	810	GLN	-	expression tag	UNP Q8TDW0
C	0	MET	-	initiating methionine	UNP Q8TDW0
C	1	SER	-	expression tag	UNP Q8TDW0
C	205	GLY	ASP	variant	UNP Q8TDW0
C	781	ARG	GLY	conflict	UNP Q8TDW0
C	802	ALA	-	expression tag	UNP Q8TDW0
C	803	ASP	-	expression tag	UNP Q8TDW0
C	804	ALA	-	expression tag	UNP Q8TDW0
C	805	LEU	-	expression tag	UNP Q8TDW0
C	806	GLU	-	expression tag	UNP Q8TDW0
C	807	VAL	-	expression tag	UNP Q8TDW0
C	808	LEU	-	expression tag	UNP Q8TDW0
C	809	PHE	-	expression tag	UNP Q8TDW0
C	810	GLN	-	expression tag	UNP Q8TDW0
D	0	MET	-	initiating methionine	UNP Q8TDW0
D	1	SER	-	expression tag	UNP Q8TDW0
D	205	GLY	ASP	variant	UNP Q8TDW0
D	781	ARG	GLY	conflict	UNP Q8TDW0
D	802	ALA	-	expression tag	UNP Q8TDW0
D	803	ASP	-	expression tag	UNP Q8TDW0
D	804	ALA	-	expression tag	UNP Q8TDW0
D	805	LEU	-	expression tag	UNP Q8TDW0
D	806	GLU	-	expression tag	UNP Q8TDW0
D	807	VAL	-	expression tag	UNP Q8TDW0
D	808	LEU	-	expression tag	UNP Q8TDW0
D	809	PHE	-	expression tag	UNP Q8TDW0
D	810	GLN	-	expression tag	UNP Q8TDW0
E	0	MET	-	initiating methionine	UNP Q8TDW0
E	1	SER	-	expression tag	UNP Q8TDW0
E	205	GLY	ASP	variant	UNP Q8TDW0
E	781	ARG	GLY	conflict	UNP Q8TDW0
E	802	ALA	-	expression tag	UNP Q8TDW0
E	803	ASP	-	expression tag	UNP Q8TDW0

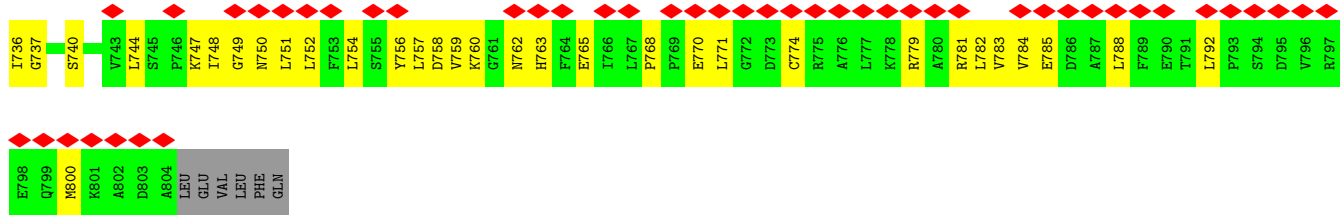
*Continued on next page...*

*Continued from previous page...*

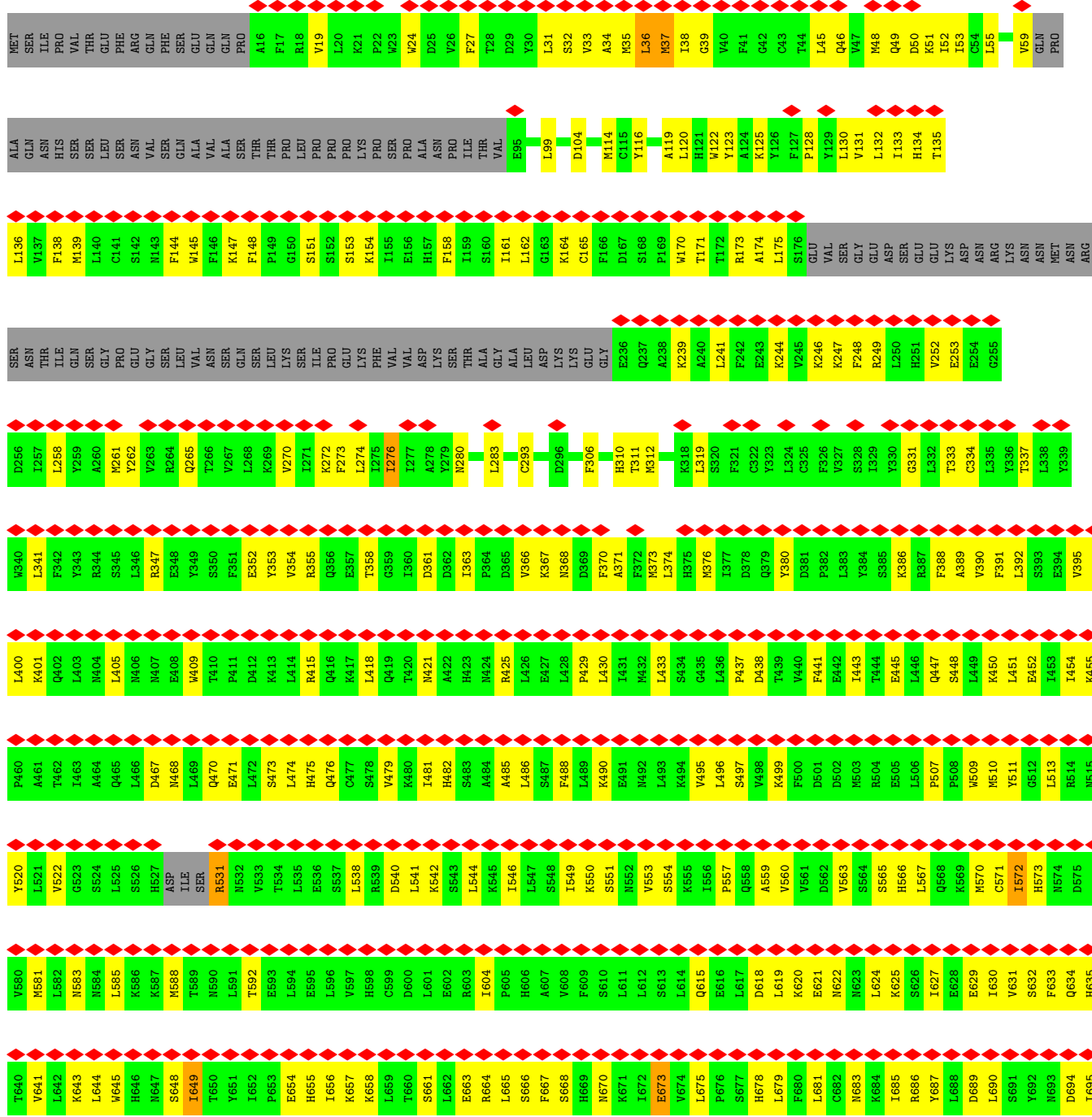
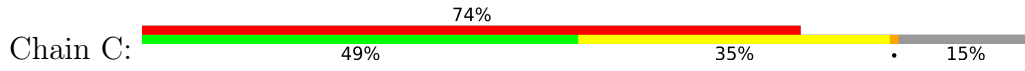
Chain	Residue	Modelled	Actual	Comment	Reference
E	804	ALA	-	expression tag	UNP Q8TDW0
E	805	LEU	-	expression tag	UNP Q8TDW0
E	806	GLU	-	expression tag	UNP Q8TDW0
E	807	VAL	-	expression tag	UNP Q8TDW0
E	808	LEU	-	expression tag	UNP Q8TDW0
E	809	PHE	-	expression tag	UNP Q8TDW0
E	810	GLN	-	expression tag	UNP Q8TDW0
F	0	MET	-	initiating methionine	UNP Q8TDW0
F	1	SER	-	expression tag	UNP Q8TDW0
F	205	GLY	ASP	variant	UNP Q8TDW0
F	781	ARG	GLY	conflict	UNP Q8TDW0
F	802	ALA	-	expression tag	UNP Q8TDW0
F	803	ASP	-	expression tag	UNP Q8TDW0
F	804	ALA	-	expression tag	UNP Q8TDW0
F	805	LEU	-	expression tag	UNP Q8TDW0
F	806	GLU	-	expression tag	UNP Q8TDW0
F	807	VAL	-	expression tag	UNP Q8TDW0
F	808	LEU	-	expression tag	UNP Q8TDW0
F	809	PHE	-	expression tag	UNP Q8TDW0
F	810	GLN	-	expression tag	UNP Q8TDW0
G	0	MET	-	initiating methionine	UNP Q8TDW0
G	1	SER	-	expression tag	UNP Q8TDW0
G	205	GLY	ASP	variant	UNP Q8TDW0
G	781	ARG	GLY	conflict	UNP Q8TDW0
G	802	ALA	-	expression tag	UNP Q8TDW0
G	803	ASP	-	expression tag	UNP Q8TDW0
G	804	ALA	-	expression tag	UNP Q8TDW0
G	805	LEU	-	expression tag	UNP Q8TDW0
G	806	GLU	-	expression tag	UNP Q8TDW0
G	807	VAL	-	expression tag	UNP Q8TDW0
G	808	LEU	-	expression tag	UNP Q8TDW0
G	809	PHE	-	expression tag	UNP Q8TDW0
G	810	GLN	-	expression tag	UNP Q8TDW0







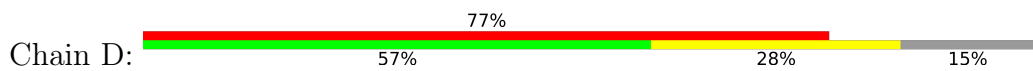
• Molecule 1: Volume-regulated anion channel subunit LRRC8C



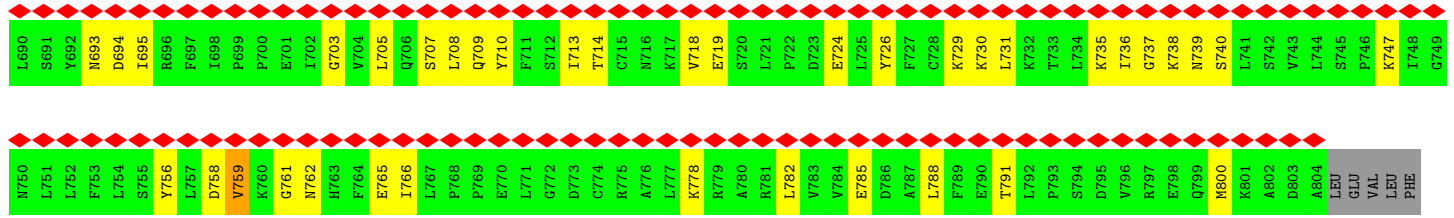
P700	E701	I702	G703	V704	L705	Q706	S707	L708	Q709	Y710	F711	S712	I713	T714	C715	N716	K717	V718	E719	S720	L721	P722	D723	E724	L725	Y726	F727	C728	K729	K730	L731	K732	T733	L734	K735	I736	G737	K738	N739	S740	L741	S742	V743	L744	S745	P746	K747	I748	G749	N750	L751	L752	F753	L754	S755	Y756	D758	V759
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

K761	G762	N763	H764	F765	E766	L767	P768	Q769	E770	L771	G772	D773	C774	R775	A776	L777	K778	R779	A780	L781	L782	V783	E784	E785	D786	A787	L788	F789	E790	T791	L792	P793	S794	D795	V796	R797	E798	Q799	M800	K801	A802	D803	L804	L805	V806	V807	L808	L809	L810	L811	L812	L813	L814	L815	L816	L817	L818	L819	L820	L821	L822	L823	L824	L825	L826	L827	L828	L829	L830	L831	L832	L833	L834	L835	L836	L837	L838	L839	L840	L841	L842	L843	L844	L845	L846	L847	L848	L849	L850	L851	L852	L853	L854	L855	L856	L857	L858	L859	L860	L861	L862	L863	L864	L865	L866	L867	L868	L869	L870	L871	L872	L873	L874	L875	L876	L877	L878	L879	L880	L881	L882	L883	L884	L885	L886	L887	L888	L889	L890	L891	L892	L893	L894	L895	L896	L897	L898	L899	L900	L901	L902	L903	L904	L905	L906	L907	L908	L909	L910	L911	L912	L913	L914	L915	L916	L917	L918	L919	L920	L921	L922	L923	L924	L925	L926	L927	L928	L929	L930	L931	L932	L933	L934	L935	L936	L937	L938	L939	L940	L941	L942	L943	L944	L945	L946	L947	L948	L949	L950	L951	L952	L953	L954	L955	L956	L957	L958	L959	L960	L961	L962	L963	L964	L965	L966	L967	L968	L969	L970	L971	L972	L973	L974	L975	L976	L977	L978	L979	L980	L981	L982	L983	L984	L985	L986	L987	L988	L989	L990	L991	L992	L993	L994	L995	L996	L997	L998	L999	L1000
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------

• Molecule 1: Volume-regulated anion channel subunit LRRC8C

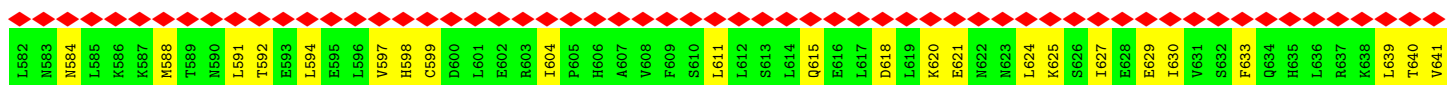
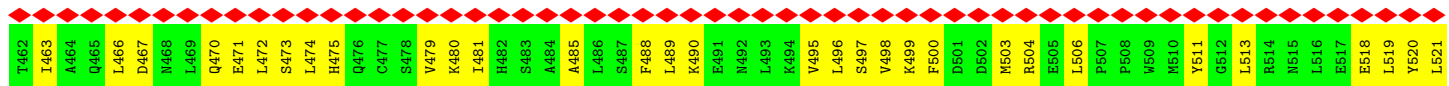
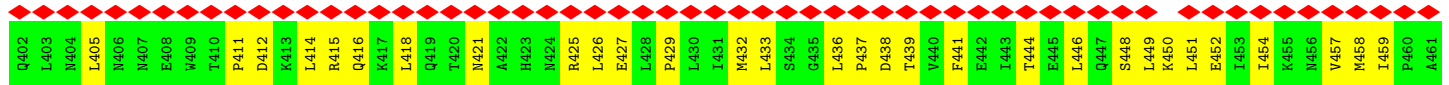
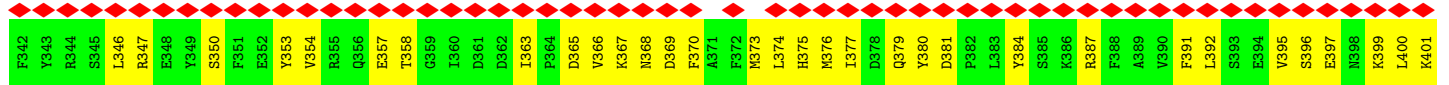
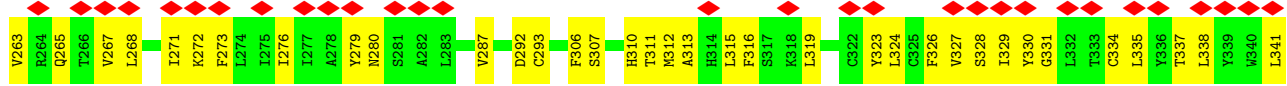
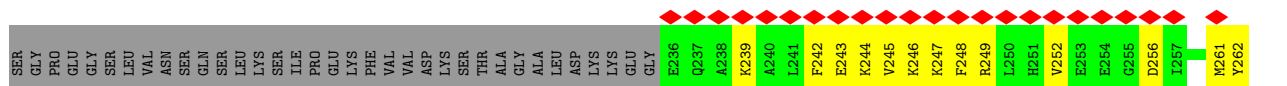
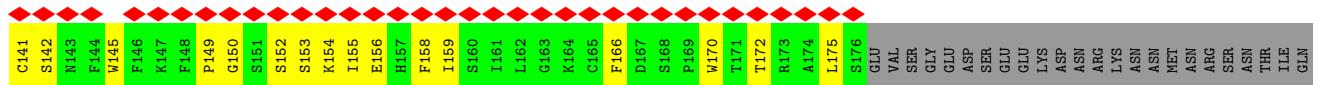
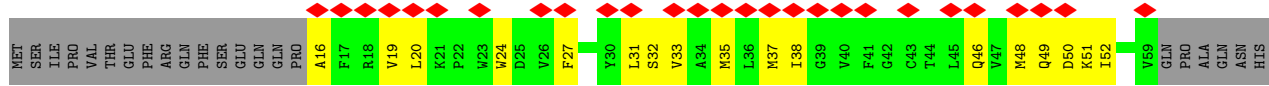


MET	SER	ILE	PRO	VAL	THR	GLU	PHE	ARG	GLN	ALA	GLN	PHE	SER	GLU	GLN	PRO	A16	F17	R18	V19	L20	K21	P22	W23	W24	D25	V26	F27	T28	Y29	X30	L31	S32	A33	V34	M35	L36	M37	I38	G39	V40	F41	C42	T44	L45	Q46	V47	M48	Q49	D50	K51	I52	V59	PRO	ALA	GLN	ASN					
HIS	SER	SER	LEU	ASN	VAL	SER	GLN	ALA	VAL	ALA	VAL	SER	THR	THR	PRO	LEU	PRO	PRO	PRO	LYS	PRO	SER	PRO	ALA	ASN	PRO	ILE	LYS	THR	VAL	E95	D102	L103	D104	L105	I111	Y116	E117	R118	A119	L120	H121	W122	Y123	A124	K125	Y126	F127	P128	Y129	L130	V131	L132	I133	H134	T135	L136	SER				
V137	F138	M139	L140	C141	S142	M143	F144	M145	F146	K147	F148	P149	G150	S151	S152	S153	K154	I155	E156	H157	F158	I159	S160	I161	L162	G163	K164	K165	F166	D167	S168	P169	W170	H171	T172	R173	A174	L175	S176	GLU	VAL	SER	GLY	GLU	ASP	SER	GLU	LYS	ASP	ASN	ARG	LYS	ASN	ASN	MET	ASN	ARG	SER				
ASN	THR	ILE	GLN	SER	GLY	PRO	GLU	GLY	SER	LEU	VAL	ASN	SER	GLN	SER	LEU	LYS	ILE	SER	ILE	PRO	GLU	LYS	PHE	VAL	VAL	ASP	LYS	THR	THR	ALA	ALA	GLY	ALA	ALA	A282	ASP	ASP	LYS	LYS	GLY	E236	Q237	A238	K239	A240	L241	F242	E243	K244	V245	K246	K247	F248	R249	L250	H251	H252	E253	E254	Q255	D256
I257	L258	Y259	A260	M261	Y262	V263	R264	Q265	T266	V267	L268	K269	V270	I271	K272	F273	L274	I275	I276	I277	A278	Y279	N280	S281	A282	L283	V284	S285	K286	V287	Q288	C293	N294	D299	M300	N305	F306	H310	T311	M312	A313	H314	K318	L319	S320	F321	C322	Y323	L324	C325	F326	V327	S328	I329								
Y330	G331	L332	T333	C334	L335	Y336	T337	L338	Y339	W340	L341	F342	Y343	R344	S345	L346	R347	E348	Y349	S350	F351	E352	Y353	V354	Q356	E357	T358	G359	I360	D361	D362	I363	P364	D365	V366	K367	N368	D369	F370	A371	F372	M373	L374	H375	M376	I377	D378	Q379	Y380	D381	F382	L383	Y384	S385	K386	F388	A389					
V390	F391	L392	S393	E394	N395	S396	E397	N398	K399	L400	K401	Q402	L403	M404	L405	N406	M407	E408	W409	T410	P411	D412	K413	L414	R415	Q416	K417	L418	Q419	T420	M421	A422	H423	S424	A425	L426	E427	L428	P429	L430	I431	M432	L433	S434	G435	L436	P437	D438	K439	V440	F441	E442	I443	T444	E445	L446	Q447	S448	L449			
K450	L451	E452	I453	I454	K455	M456	V457	M458	L459	P460	A461	T462	L463	A464	Q465	L466	D467	N468	L469	Q470	E471	L472	S473	L474	H475	Q476	C477	S478	V479	K480	I481	H482	S483	L484	A484	A485	L486	S487	F488	L489	K490	E491	M492	L493	K494	V495	L496	S497	V498	K499	F500	D501	D502	S503	R504	E505	L506	P507	S508	N509		
M510	Y511	G512	L513	R514	N515	L516	E517	E518	L519	Y520	L521	G522	G523	S524	L525	S526	H527	ASP	ILE	SER	R531	N532	L533	T534	L535	E536	S537	L538	R539	D540	L541	K542	S543	L544	L545	I546	L547	S548	I549	K550	S551	N552	V553	S554	K555	I556	P557	Q558	A559	V560	V561	D562	V563	N564	L564	S565	H566	Q567	Q568	K569		
M570	C571	I572	H573	N574	D575	G576	T577	K578	L579	V580	M581	L582	N583	N584	L585	K586	K587	M588	T589	N590	R591	L591	T592	E593	L594	E595	L596	V597	H598	C599	D600	L601	E602	S603	L604	P605	H606	A607	V608	F609	S610	L611	L612	S613	L614	Q615	E616	L617	D618	L619	K620	E621	N622	N623	L624	G625	S626	L627	Q628	E628	E629	
L630	V631	S632	F633	Q634	H635	L636	R637	L638	L639	T640	V641	L642	K643	L644	N645	H646	N647	S648	I649	T650	L651	L652	P653	E654	H655	L656	K657	L658	L659	T660	S661	L662	E663	H664	L665	S666	F667	S668	H669	N670	K671	L672	E673	L674	Q675	E676	S677	H678	L679	F680	L681	C682	N683	L684	T685	R686	S687	L688	L689			



GLN

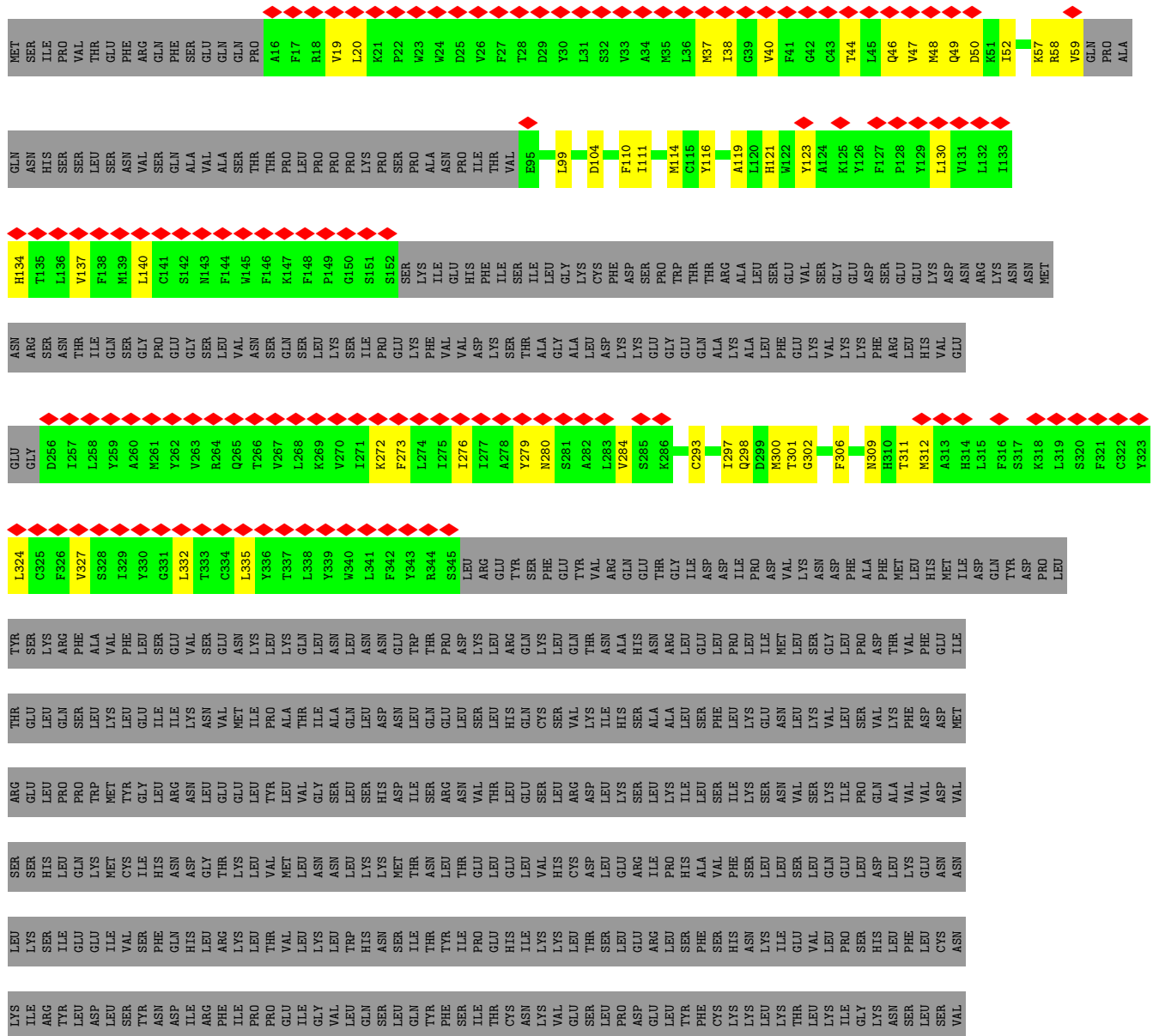
• Molecule 1: Volume-regulated anion channel subunit LRRC8C







● Molecule 1: Volume-regulated anion channel subunit LRRC8C



LEU SER  
PRO PRO  
LYS LYS  
ILE ILE  
GLY GLY  
ASN ASN  
LEU LEU  
PHE PHE  
LEU LEU  
SER SER  
TYR TYR  
LEU LEU  
ASP ASP  
VAL VAL  
LYS LYS  
GLY GLY  
ASN ASN  
HIS HIS  
PHE PHE  
GLU GLU  
ILE ILE  
LEU LEU  
PRO PRO  
PRO PRO  
GLU GLU  
LEU LEU  
GLY GLY  
ASP ASP  
CYS CYS  
ARG ARG  
ALA ALA  
LEU LEU  
LYS LYS  
ARG ARG  
ALA ALA  
ARG ARG  
LEU LEU  
VAL VAL  
VAL VAL  
GLU GLU  
ASP ASP  
ALA ALA  
LEU LEU  
PHE PHE  
GLU GLU  
THR THR  
LEU LEU  
PRO PRO  
SER SER  
ASP ASP  
VAL VAL  
ARG ARG  
GLU GLU  
GLN GLN  
MET MET  
LYS LYS  
ALA ALA  
ASP ASP

ALA  
LEU  
GLU  
VAL  
PHE  
GLN

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	216564	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 ( $e^-/\text{\AA}^2$ )	65	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.756	Depositor
Minimum map value	-0.261	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.175	Depositor
Map size ( $\text{\AA}$ )	437.47202, 437.47202, 437.47202	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.302, 1.302, 1.302	Depositor

## 5 Model quality [i](#)

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

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	0.31	0/5764	0.44	0/7790
1	B	0.32	0/5764	0.48	0/7790
1	C	0.26	0/5764	0.44	1/7790 (0.0%)
1	D	0.25	0/5764	0.37	0/7790
1	E	0.26	0/5764	0.43	0/7790
1	F	0.27	0/5764	0.41	0/7790
1	G	0.25	0/1645	0.42	0/2227
All	All	0.28	0/36229	0.43	1/48967 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	C	36	LEU	CA-CB-CG	6.03	137.39	116.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	531	ARG	Sidechain
1	B	531	ARG	Sidechain
1	C	531	ARG	Sidechain
1	D	531	ARG	Sidechain
1	E	531	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	5641	0	5764	306	0
1	B	5641	0	5764	310	0
1	C	5641	0	5764	231	0
1	D	5641	0	5764	183	0
1	E	5641	0	5764	295	0
1	F	5641	0	5764	287	0
1	G	1599	0	1601	42	0
All	All	35445	0	36185	1643	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 23.

The worst 5 of 1643 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:F:531:ARG:HH22	1:F:552:ASN:ND2	1.22	1.33
1:E:766:ILE:HD13	1:E:791:THR:CG2	1.67	1.25
1:E:673:GLU:OE1	1:E:674:VAL:CG2	1.83	1.25
1:A:507:PRO:O	1:A:510:MET:SD	1.99	1.19
1:C:763:HIS:O	1:C:765:GLU:OE2	1.62	1.18

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	684/811 (84%)	631 (92%)	53 (8%)	0	100	100
1	B	684/811 (84%)	630 (92%)	53 (8%)	1 (0%)	48	78
1	C	684/811 (84%)	648 (95%)	35 (5%)	1 (0%)	48	78
1	D	684/811 (84%)	647 (95%)	36 (5%)	1 (0%)	48	78
1	E	684/811 (84%)	646 (94%)	37 (5%)	1 (0%)	48	78
1	F	684/811 (84%)	641 (94%)	43 (6%)	0	100	100
1	G	186/811 (23%)	177 (95%)	9 (5%)	0	100	100
All	All	4290/5677 (76%)	4020 (94%)	266 (6%)	4 (0%)	49	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	649	ILE
1	B	649	ILE
1	C	649	ILE
1	D	649	ILE

### 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	642/757 (85%)	638 (99%)	4 (1%)	78	79
1	B	642/757 (85%)	637 (99%)	5 (1%)	73	76

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	642/757 (85%)	638 (99%)	4 (1%)	78	79
1	D	642/757 (85%)	638 (99%)	4 (1%)	78	79
1	E	642/757 (85%)	636 (99%)	6 (1%)	70	74
1	F	642/757 (85%)	639 (100%)	3 (0%)	81	80
1	G	178/757 (24%)	178 (100%)	0	100	100
All	All	4030/5299 (76%)	4004 (99%)	26 (1%)	76	79

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	531	ARG
1	E	27	PHE
1	F	581	MET
1	D	759	VAL
1	E	531	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	106	GLN
1	F	143	ASN
1	F	468	ASN
1	C	294	ASN
1	C	280	ASN

### 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](#)

There are no ligands in this entry.

## 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.

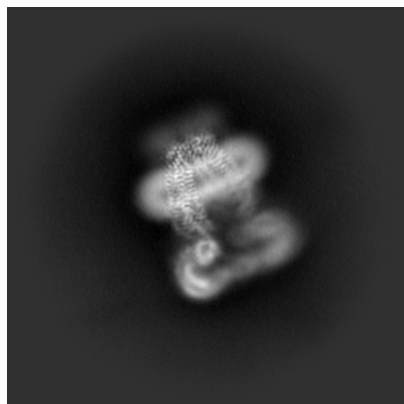
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19495. These allow visual inspection of the internal detail of the map and identification of artifacts.

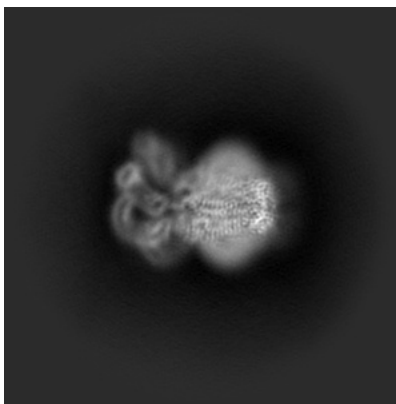
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

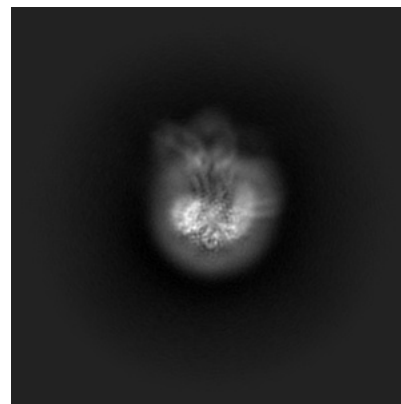
#### 6.1.1 Primary map



X

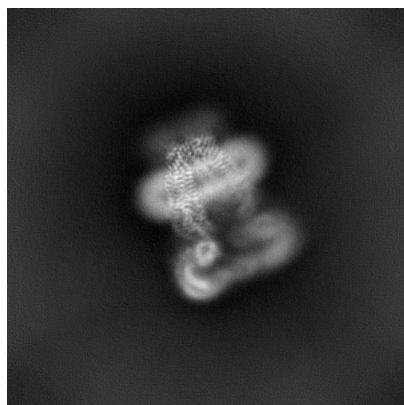


Y

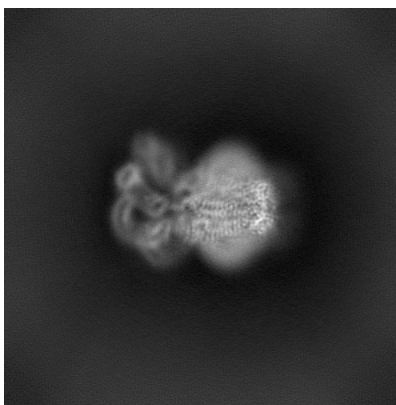


Z

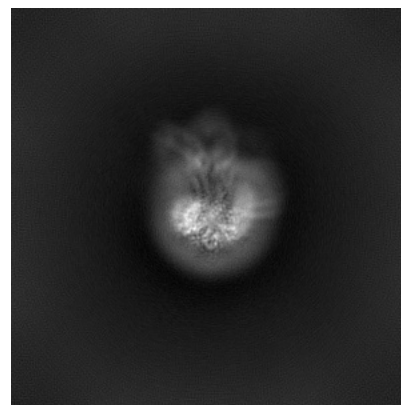
#### 6.1.2 Raw map



X



Y

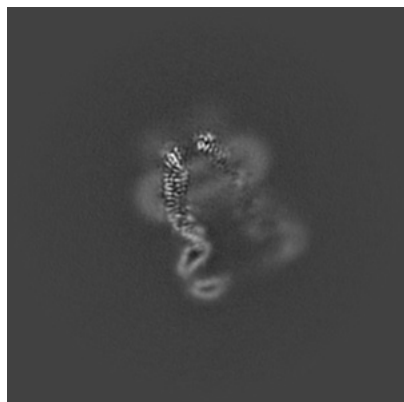


Z

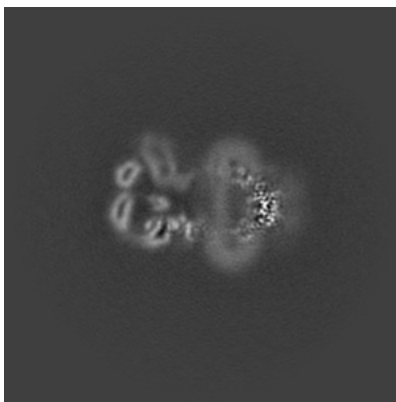
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

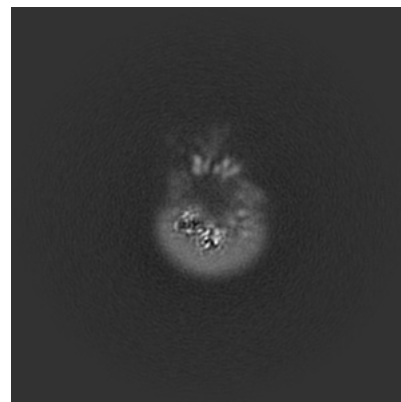
### 6.2.1 Primary map



X Index: 168

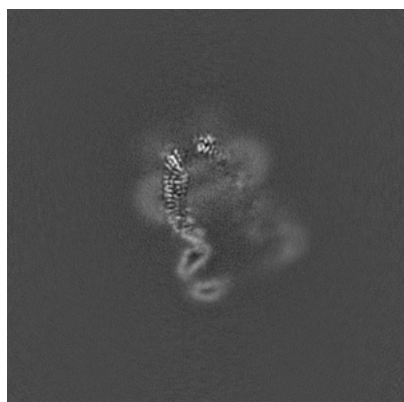


Y Index: 168

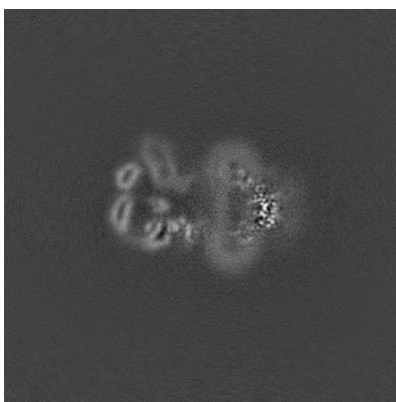


Z Index: 168

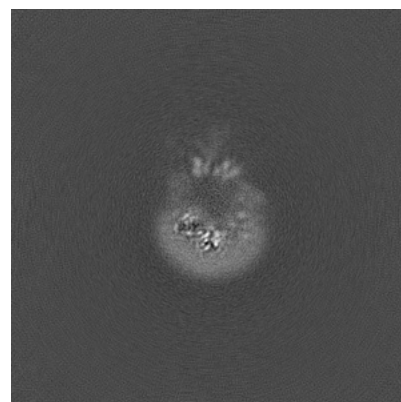
### 6.2.2 Raw map



X Index: 168



Y Index: 168

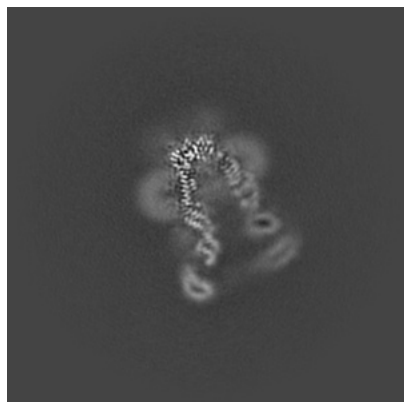


Z Index: 168

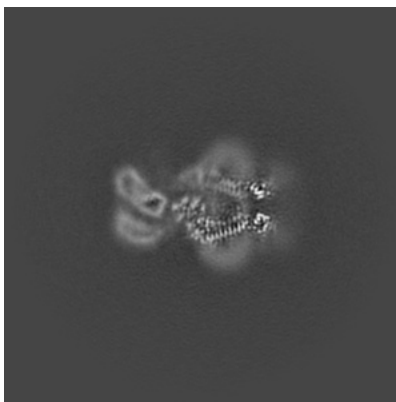
The images above show central slices of the map in three orthogonal directions.

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

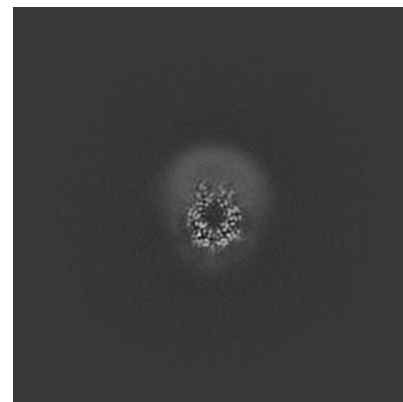
### 6.3.1 Primary map



X Index: 154

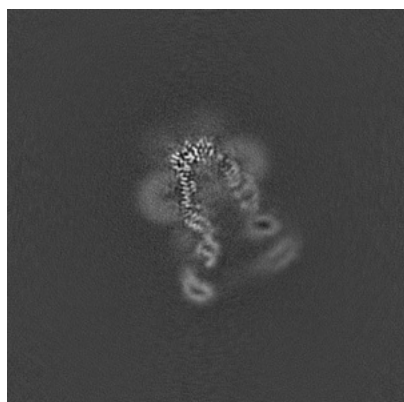


Y Index: 152

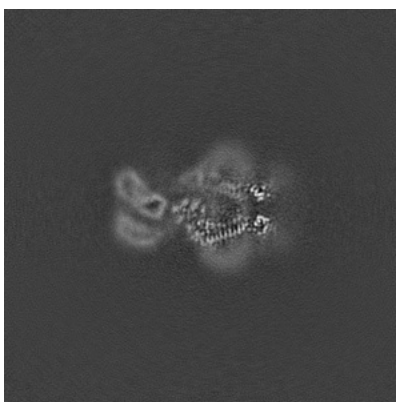


Z Index: 213

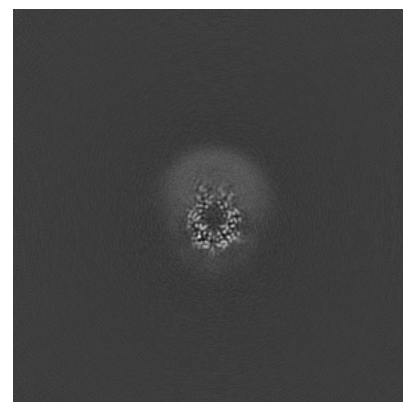
### 6.3.2 Raw map



X Index: 154



Y Index: 152

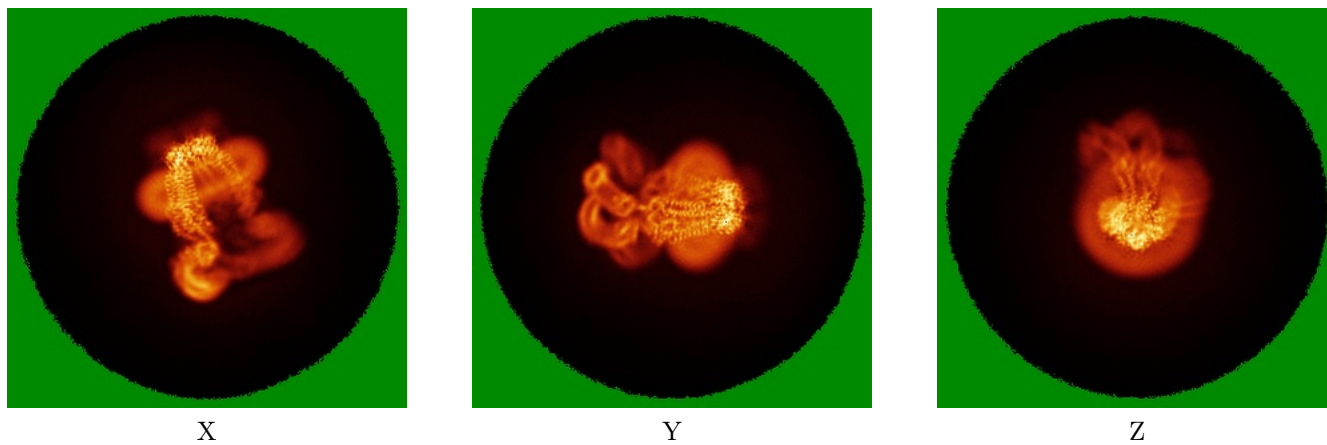


Z Index: 213

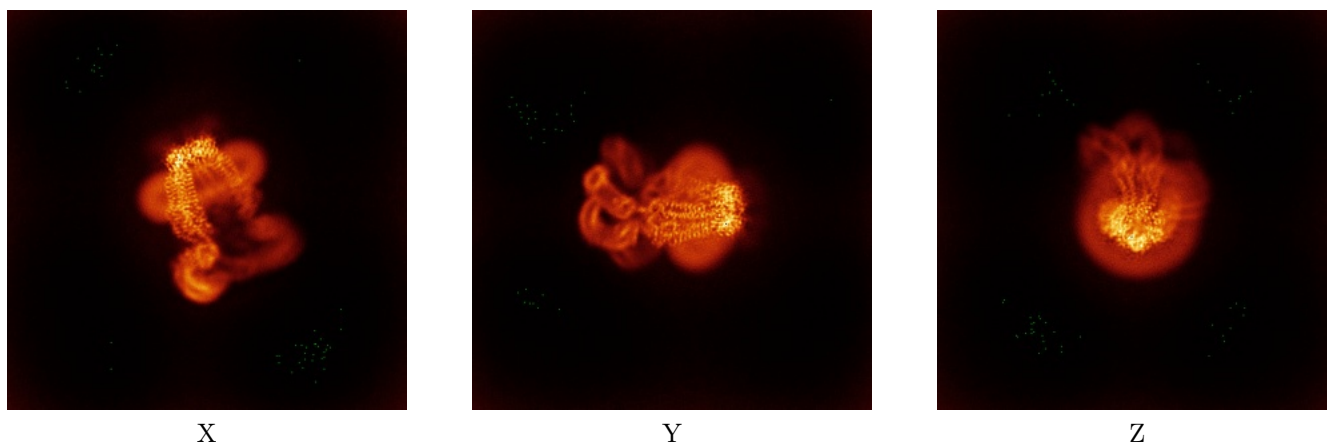
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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](#)

This section was not generated.

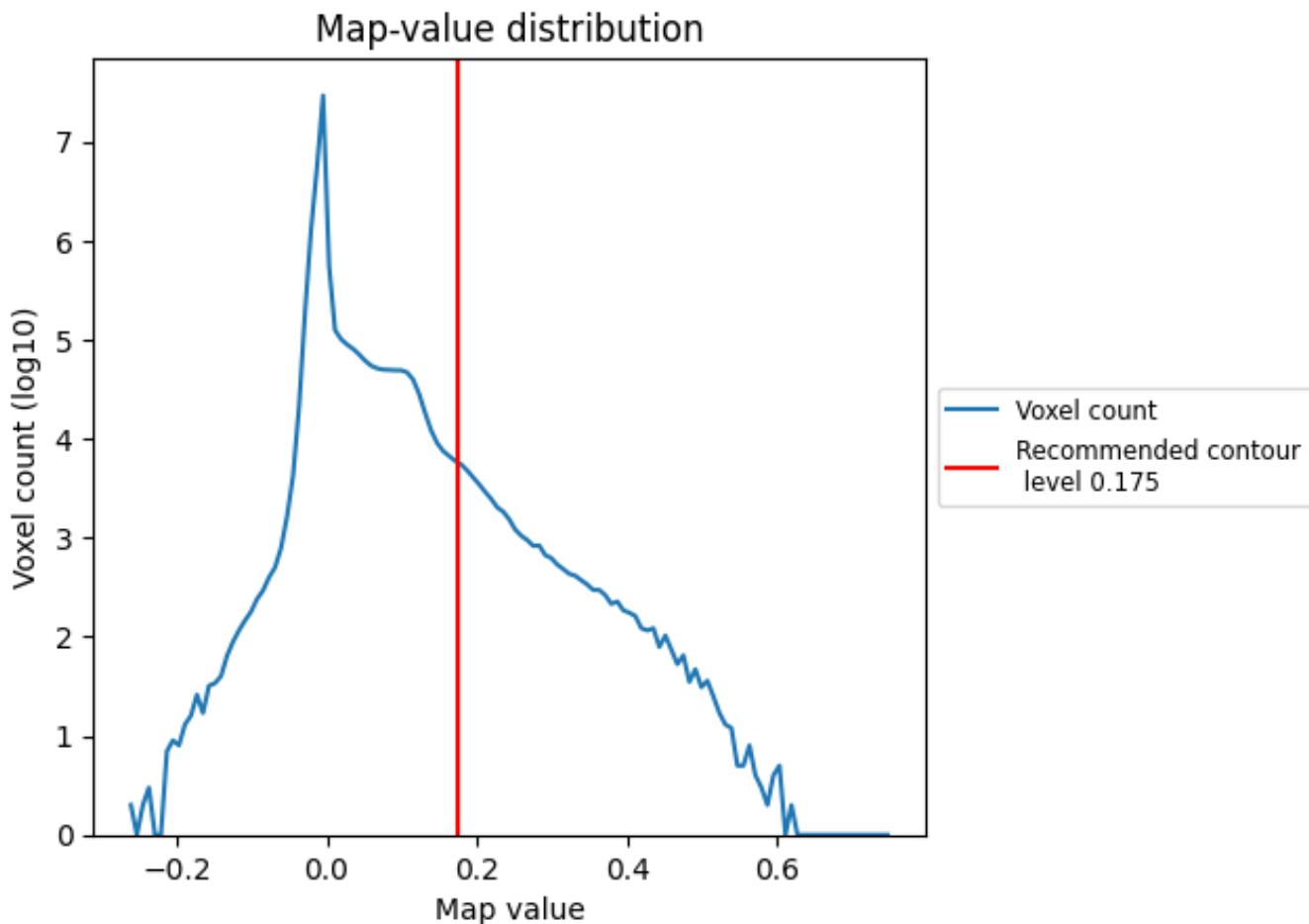
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

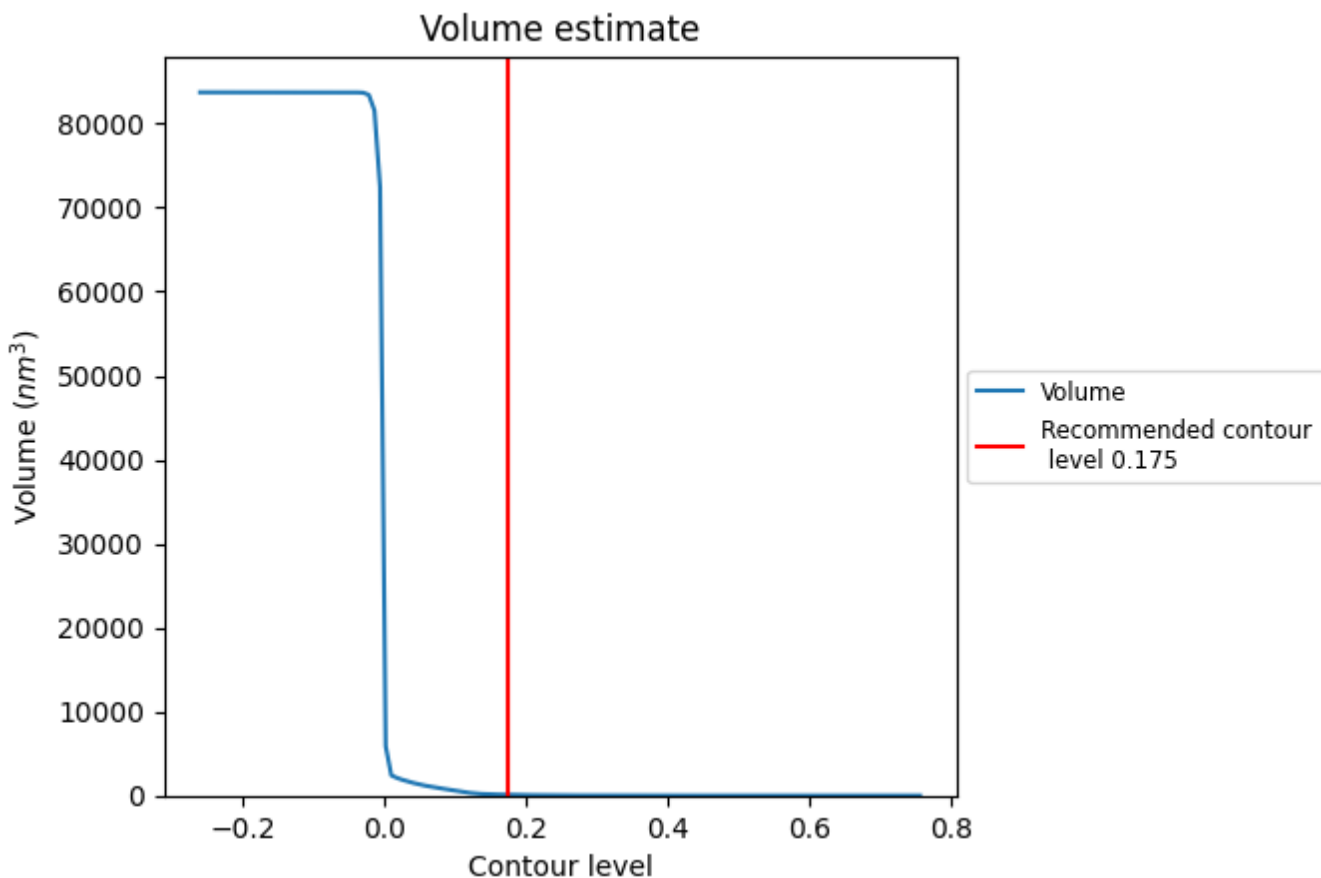
This section contains the results of statistical analysis of the map.

### 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.

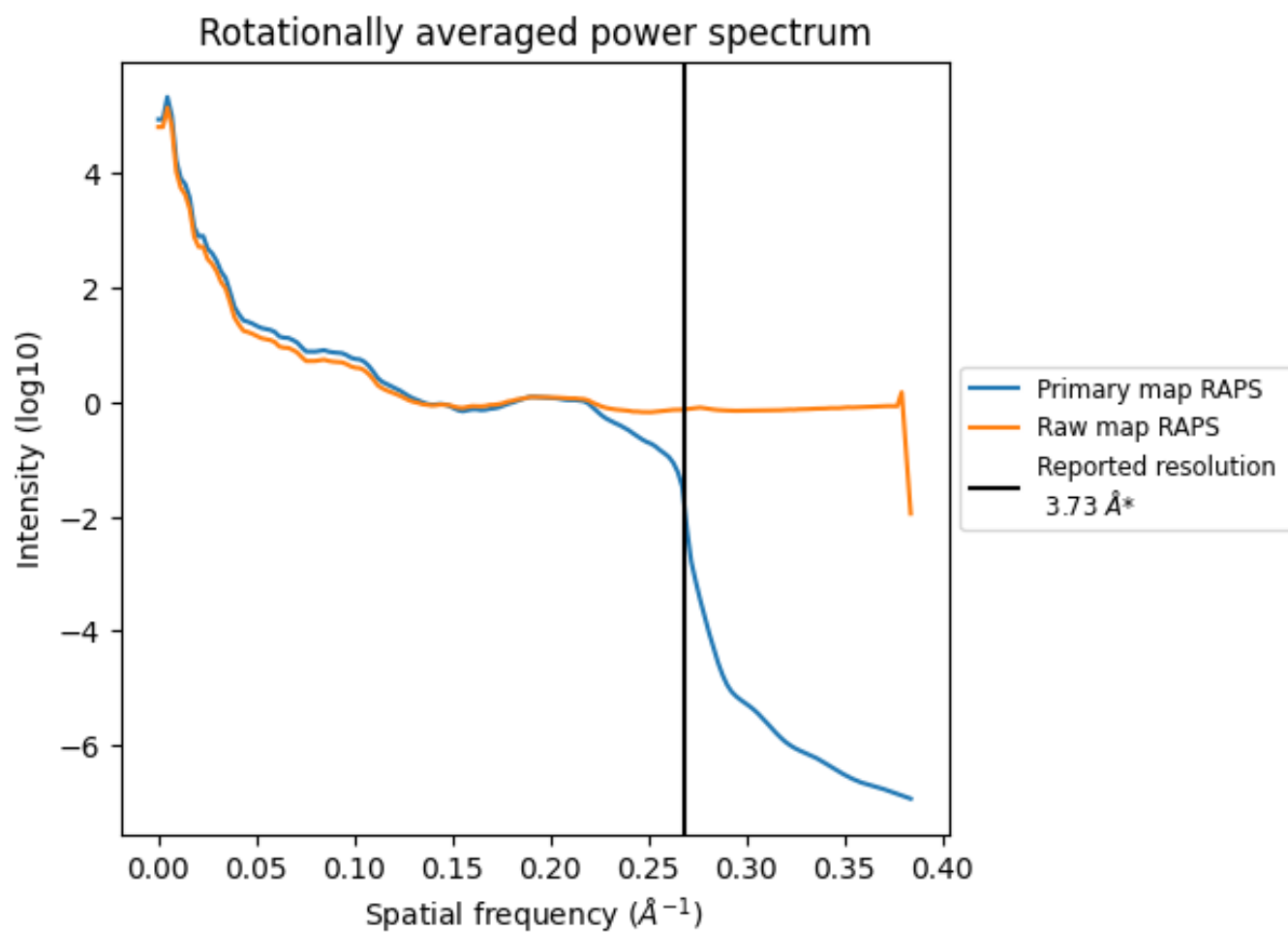
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 96 nm<sup>3</sup>; this corresponds to an approximate mass of 86 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](#)

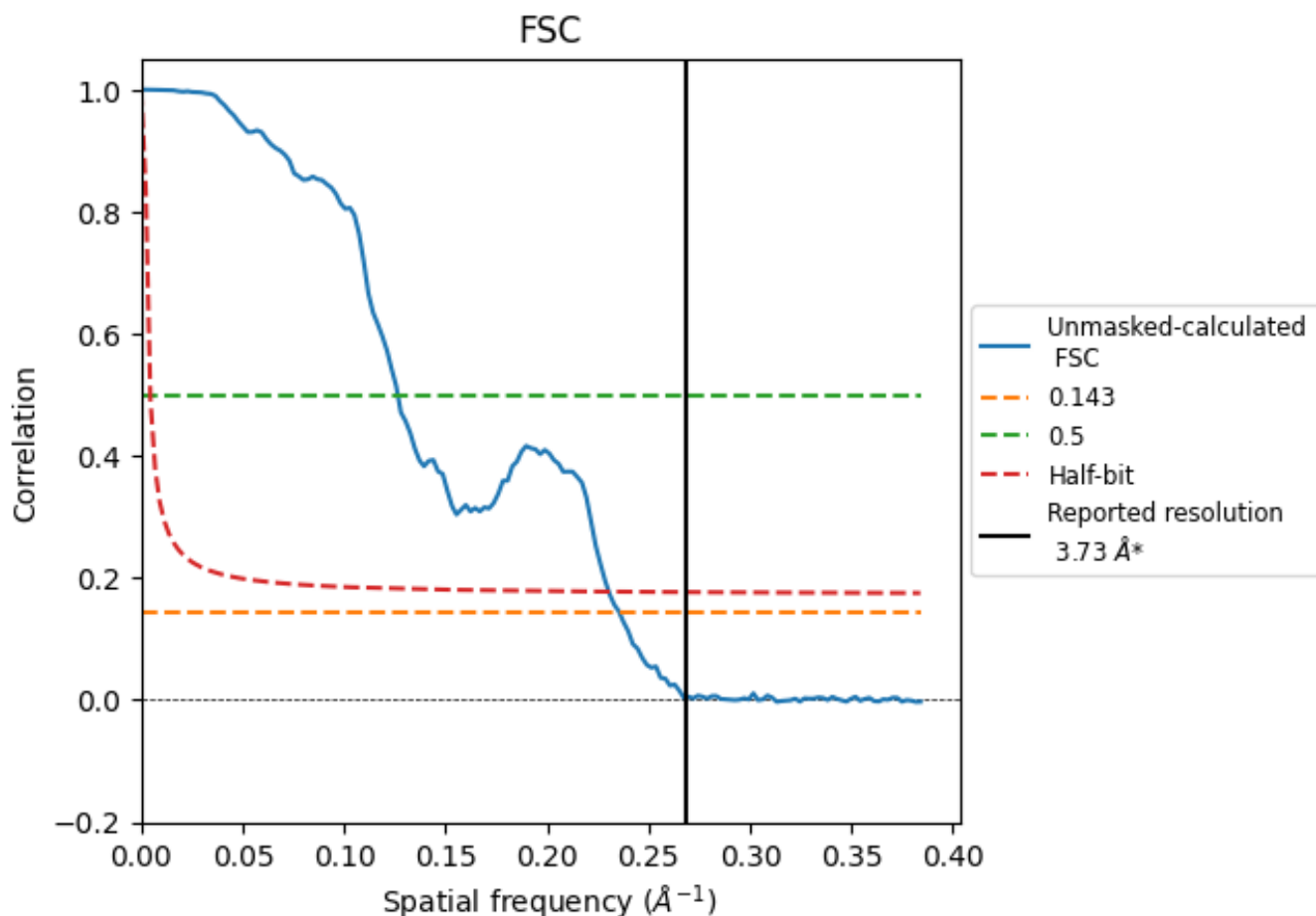


\*Reported resolution corresponds to spatial frequency of 0.268 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.268 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

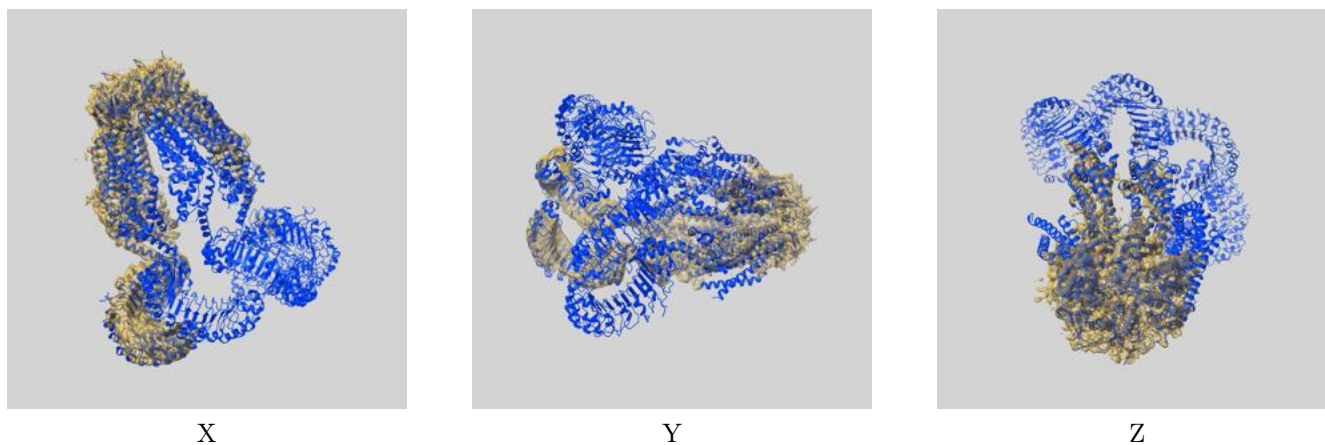
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.73	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.24	7.91	4.34

\*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 4.24 differs from the reported value 3.73 by more than 10 %

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

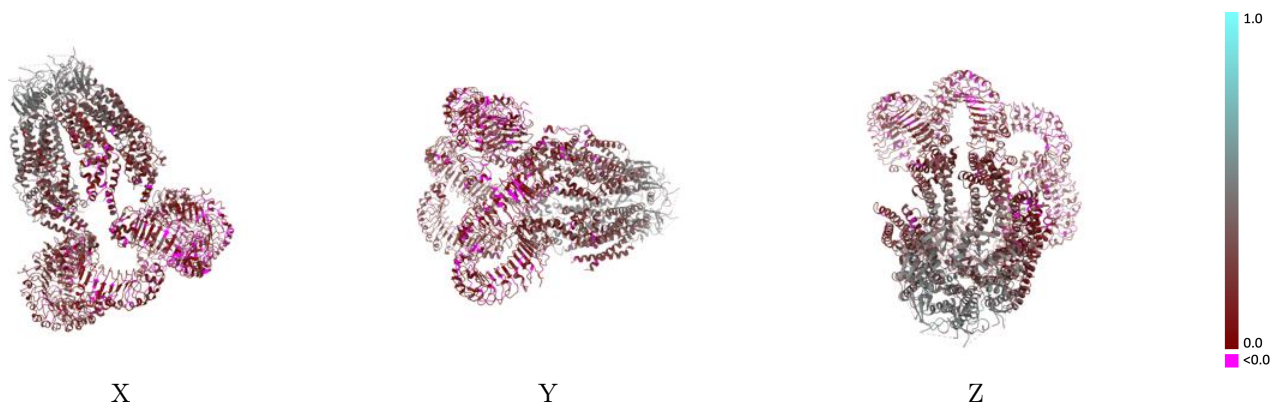
This section contains information regarding the fit between EMDB map EMD-19495 and PDB model 8RTS. Per-residue inclusion information can be found in section 3 on page 7.

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



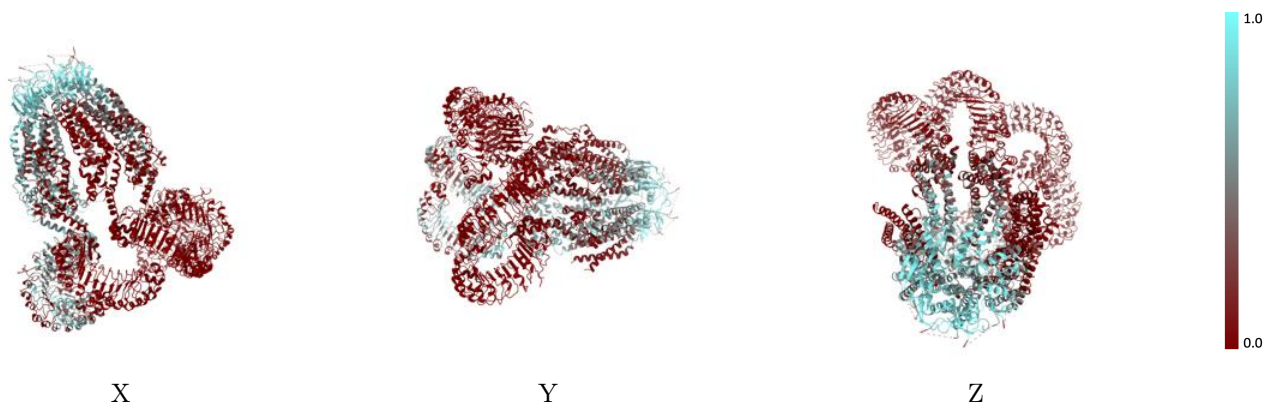
The images above show the 3D surface view of the map at the recommended contour level 0.175 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



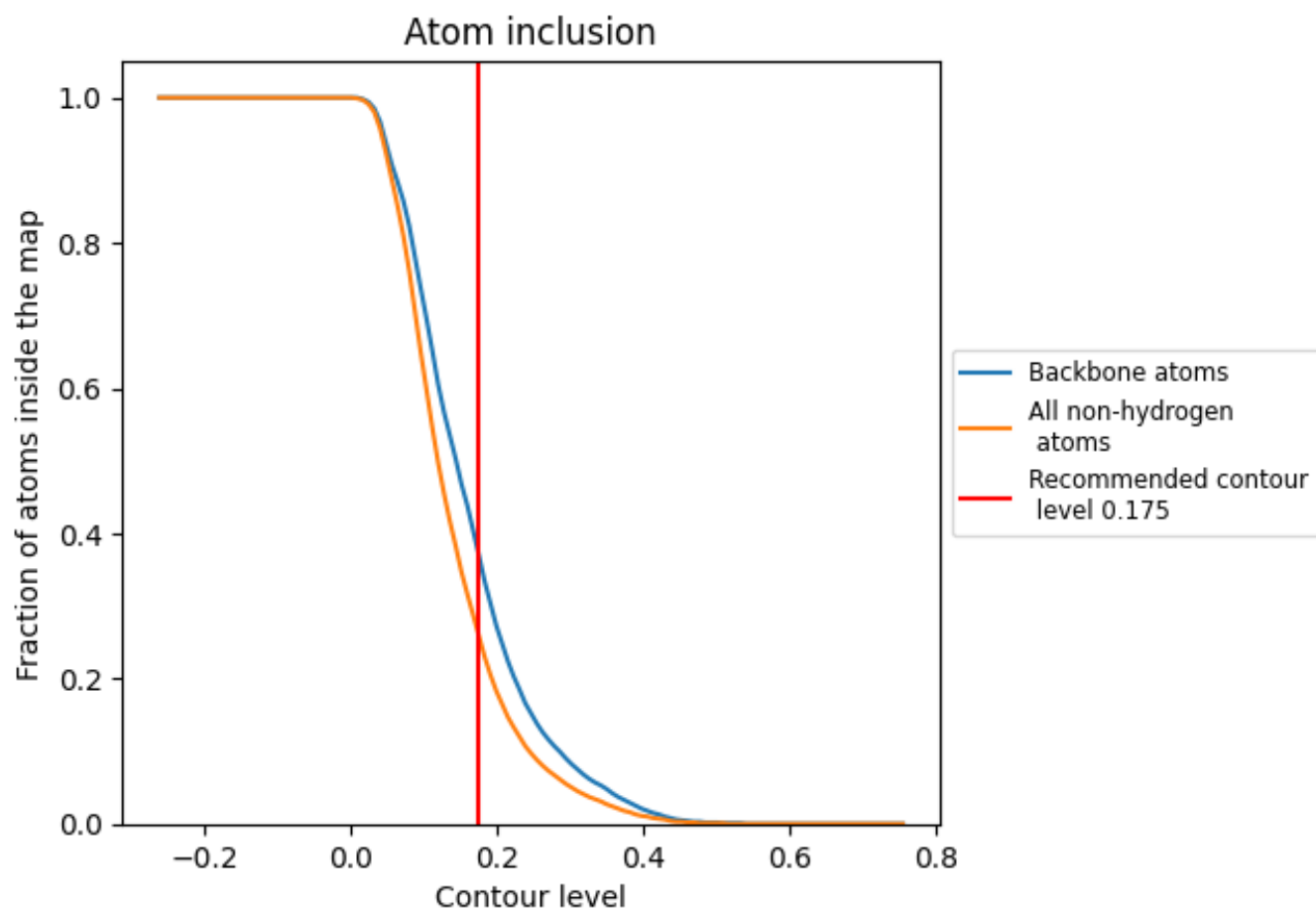
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.175).

















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 37% of all backbone atoms, 26% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.2620	 0.2250
A	 0.5320	 0.2850
B	 0.5110	 0.2810
C	 0.1200	 0.1990
D	 0.0810	 0.1600
E	 0.1410	 0.1940
F	 0.1800	 0.2150
G	 0.2770	 0.2860

