



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:34 PM UTC

PDB ID : 8ET2 / pdb_00008et2
EMDB ID : EMD-28584
Title : CryoEM structure of the GSDMB pore
Authors : Wang, C.; Ruan, J.
Deposited on : 2022-10-15
Resolution : 4.96 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
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

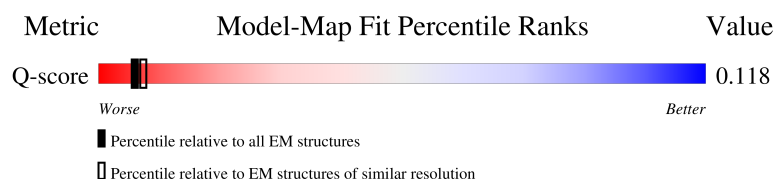
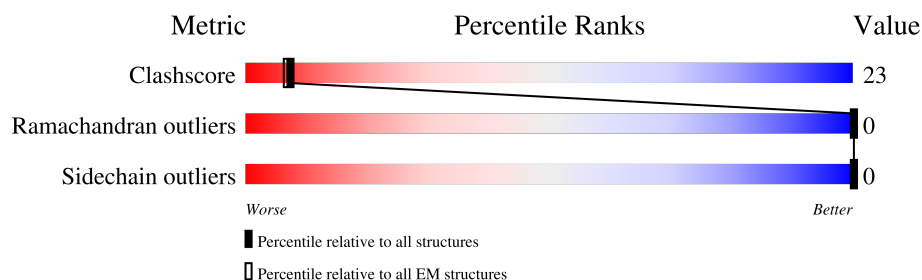
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.96 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.



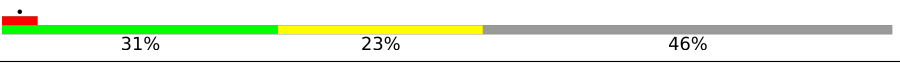
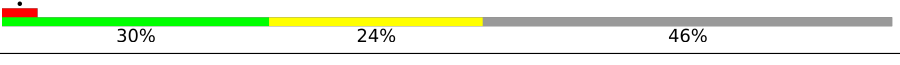
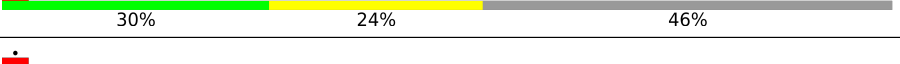
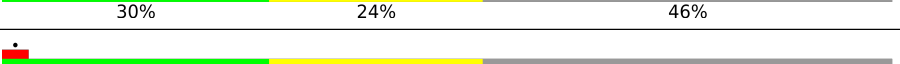
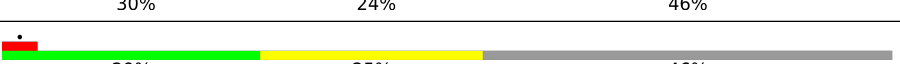
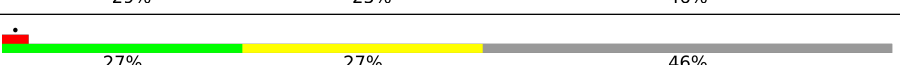
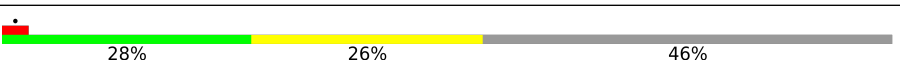
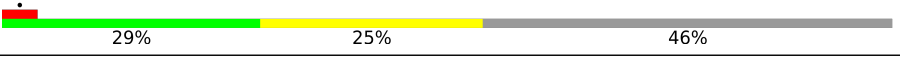
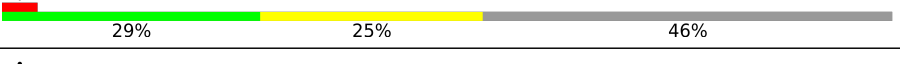
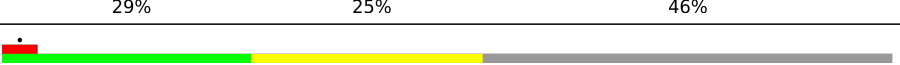
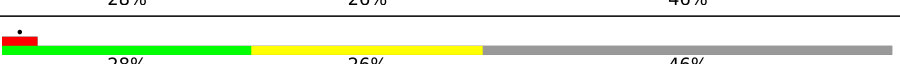
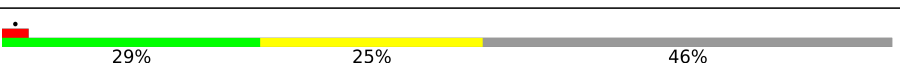
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1045 (4.46 - 5.45)

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	411	 30% 24% 46%
1	B	411	 30% 24% 46%
1	C	411	 30% 24% 46%
1	D	411	 30% 24% 46%

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Mol	Chain	Length	Quality of chain
1	E	411	 31%23%46%
1	F	411	 30%24%46%
1	G	411	 31%23%46%
1	H	411	 30%24%46%
1	I	411	 30%24%46%
1	J	411	 30%24%46%
1	K	411	 29%25%46%
1	L	411	 27%27%46%
1	M	411	 28%26%46%
1	N	411	 29%24%46%
1	O	411	 29%25%46%
1	P	411	 29%25%46%
1	Q	411	 29%24%46%
1	R	411	 29%25%46%
1	S	411	 5%29%25%46%
1	T	411	 28%26%46%
1	U	411	 28%26%46%
1	V	411	 29%25%46%
1	W	411	 29%25%46%
1	X	411	 29%24%46%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 43584 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 Isoform 1 of Gasdermin-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	B	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	C	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	D	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	E	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	F	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	G	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	H	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	I	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	J	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	K	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	L	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	M	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	N	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	O	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	P	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	Q	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		

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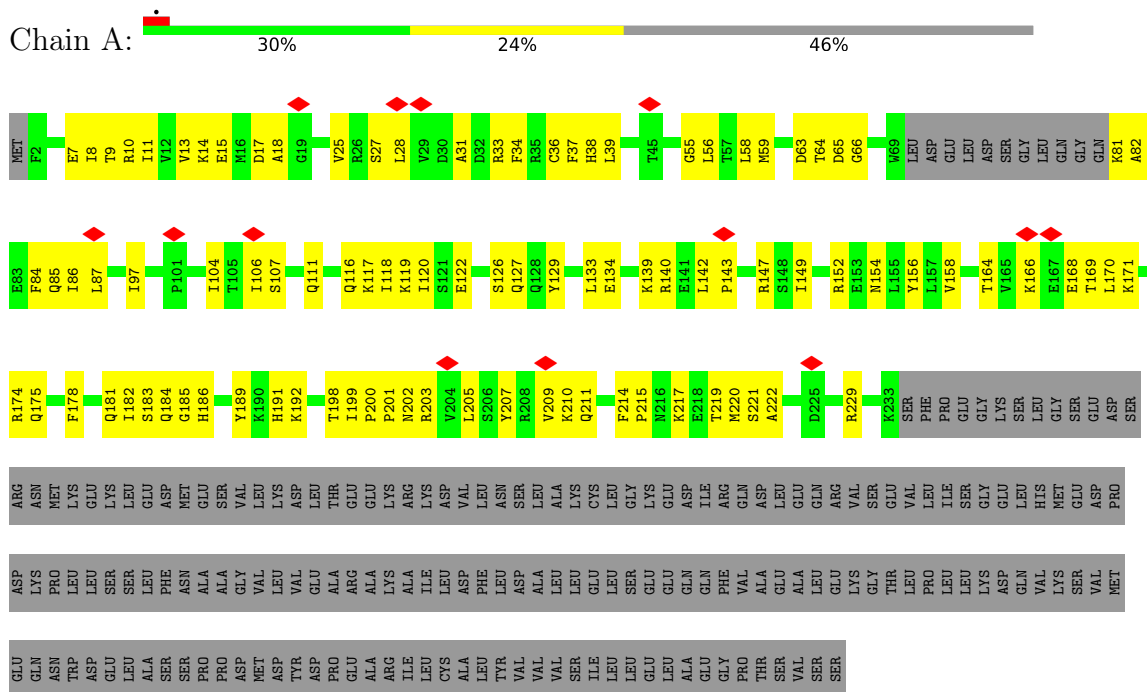
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	221	Total	C	N	O	S	0	0
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1	S	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	T	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	U	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	V	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	W	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		
1	X	221	Total	C	N	O	S	0	0
			1816	1153	323	334	6		

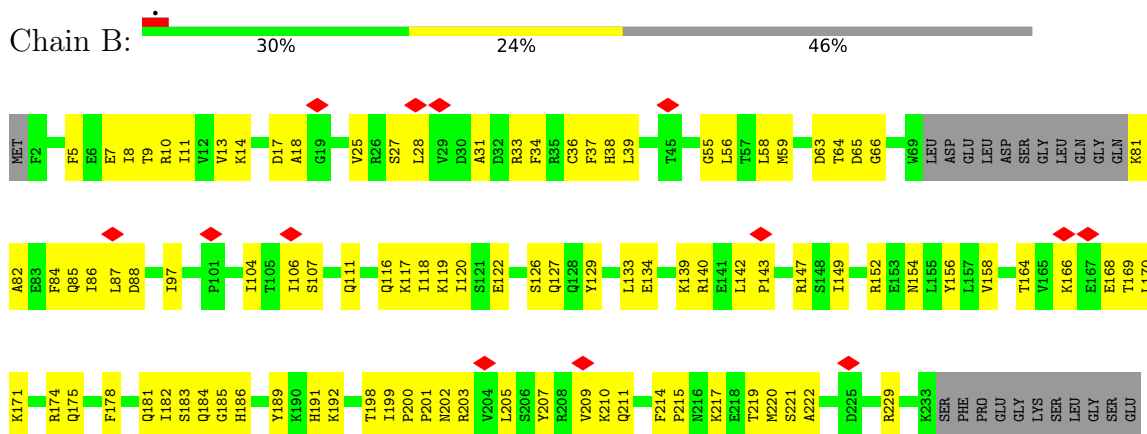
3 Residue-property plots

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.

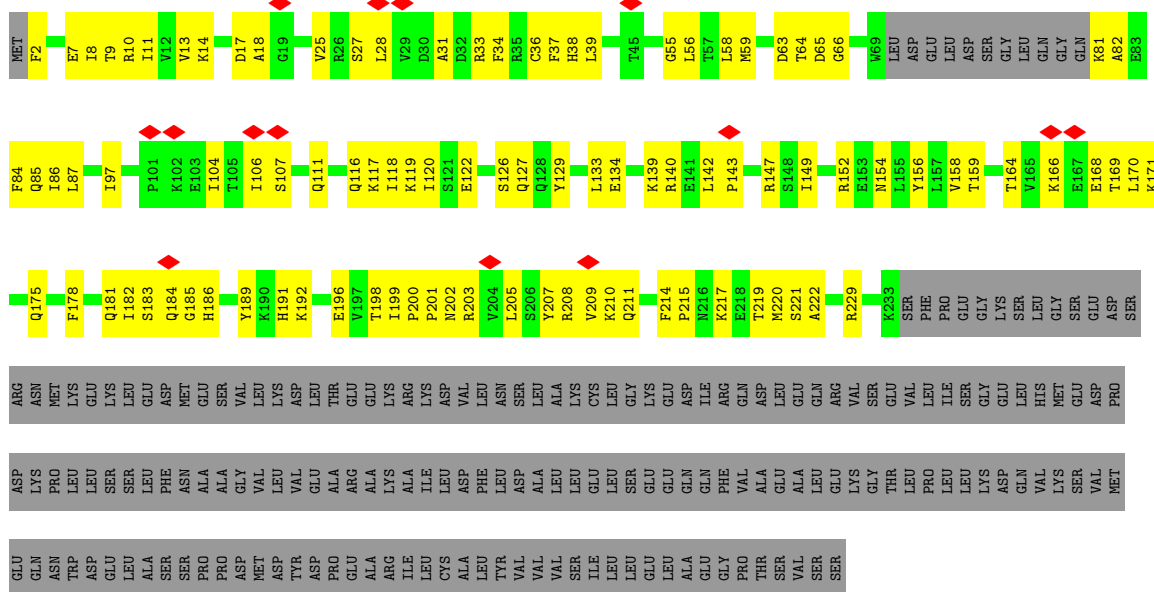
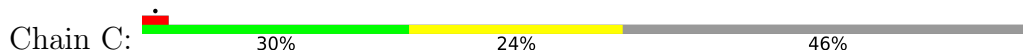
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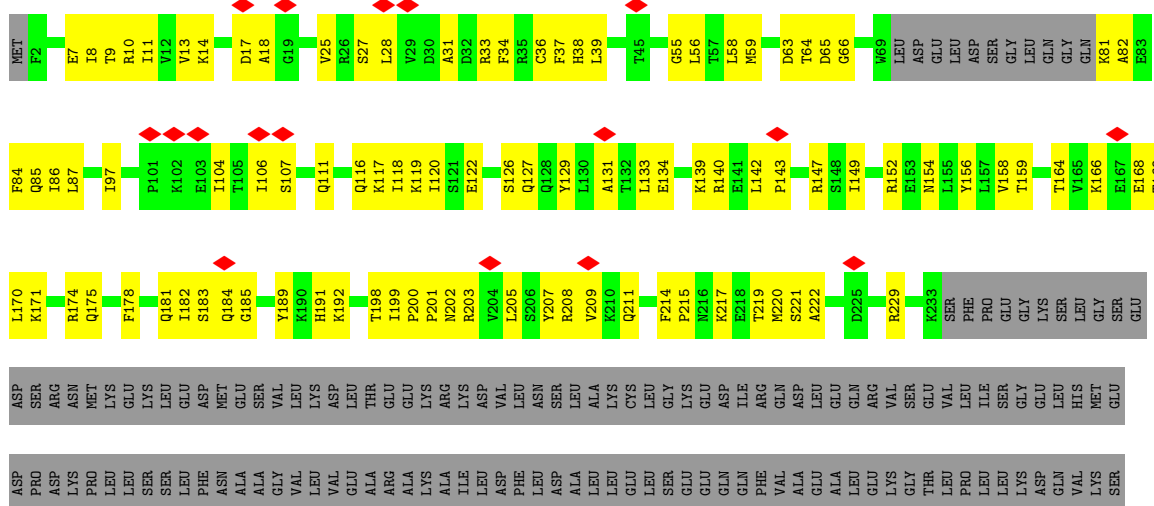
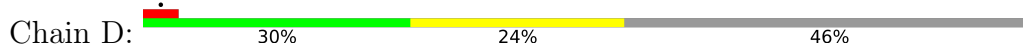
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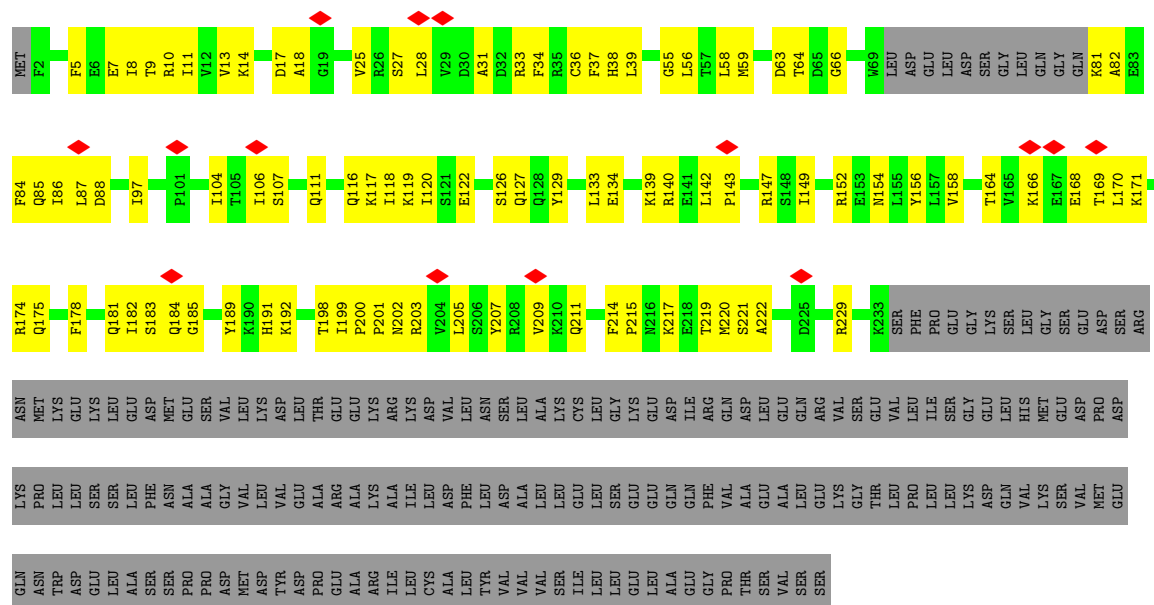
- Molecule 1: Isoform 1 of Gasdermin-B



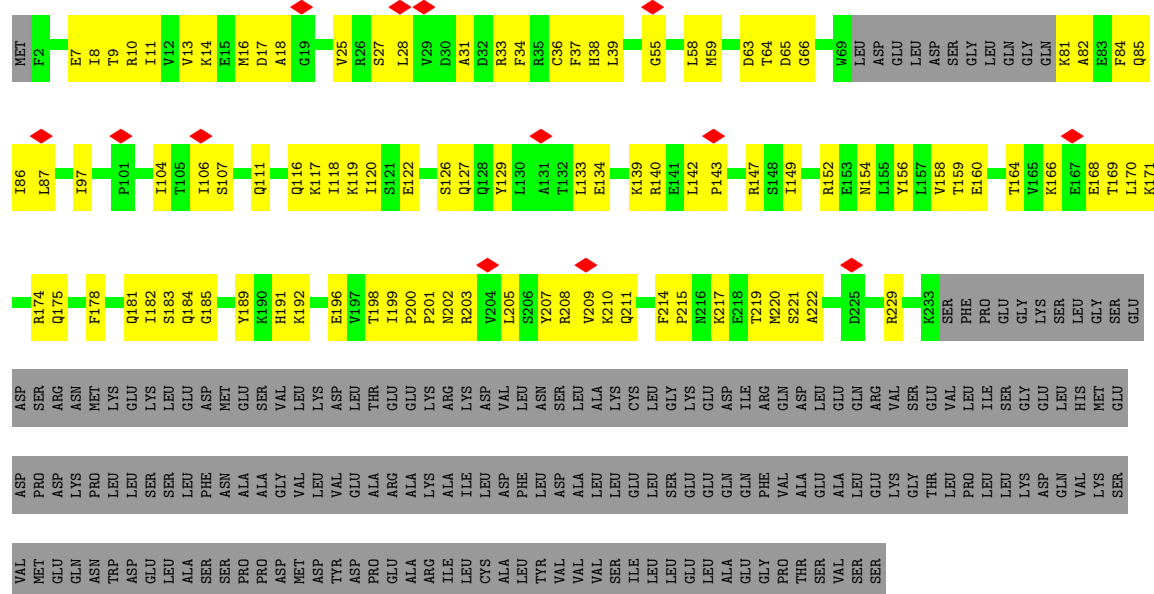
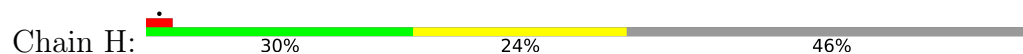
- Molecule 1: Isoform 1 of Gasdermin-B



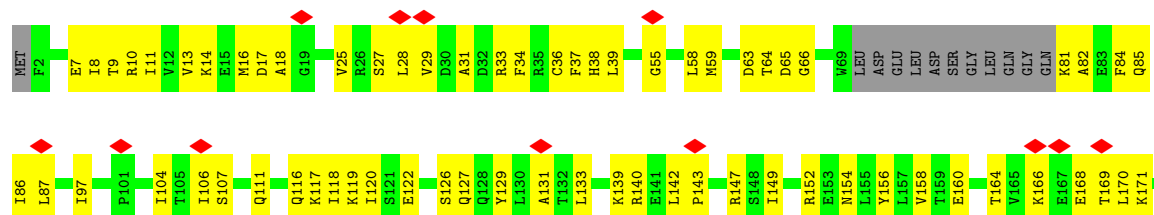
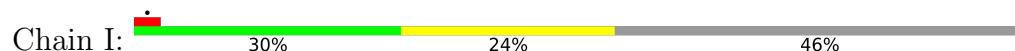
Chain G: 

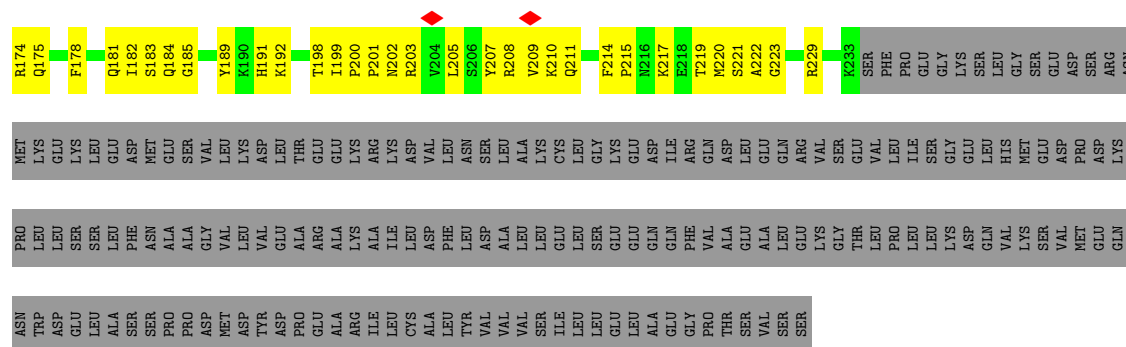


• Molecule 1: Isoform 1 of Gasdermin-B

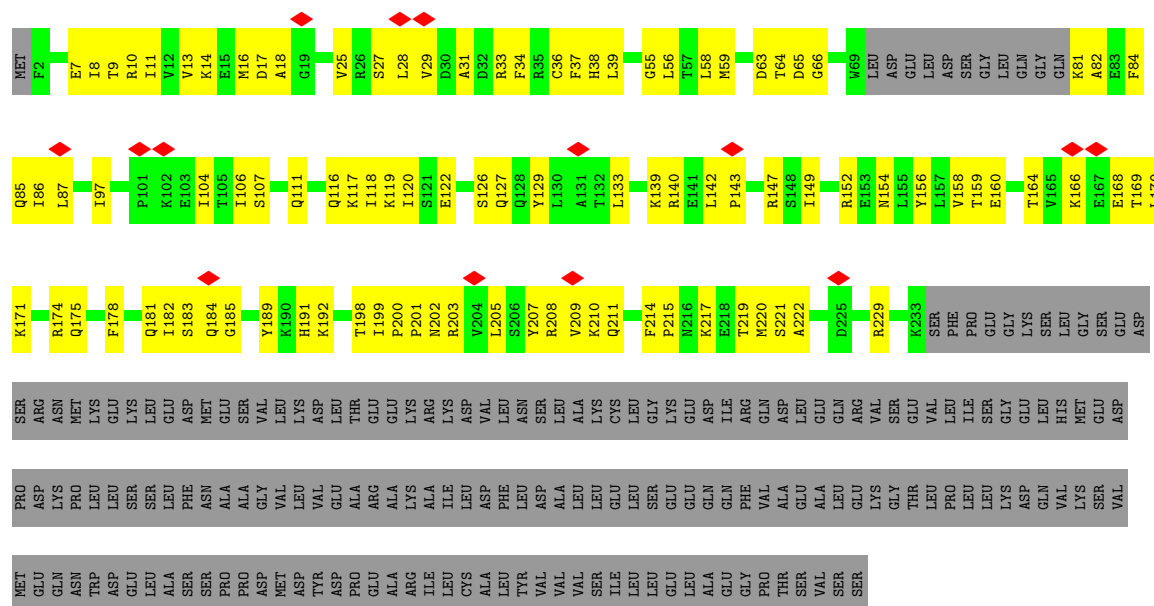
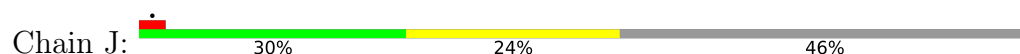


• Molecule 1: Isoform 1 of Gasdermin-B

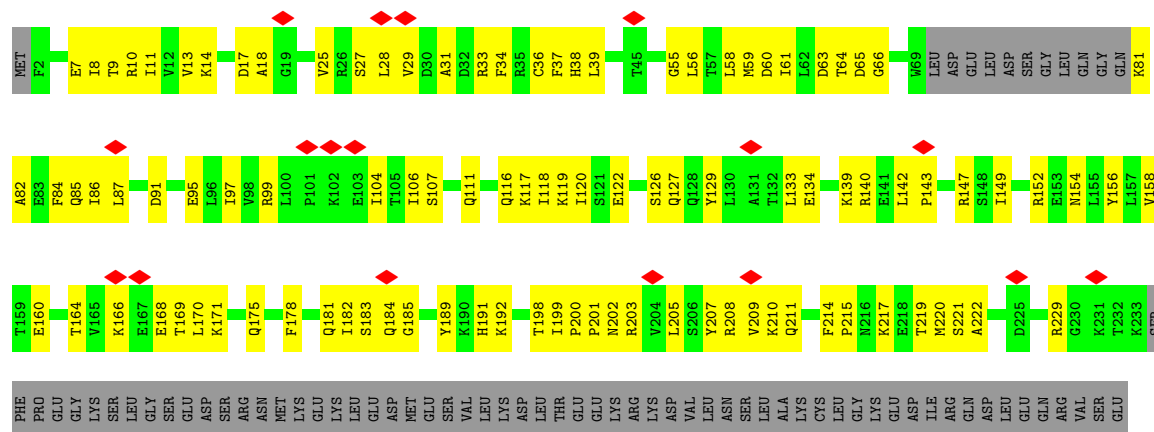
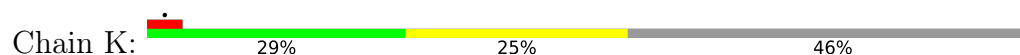




• Molecule 1: Isoform 1 of Gasdermin-B



• Molecule 1: Isoform 1 of Gasdermin-B



VAL	LEU	ILE	SER	GLY	LEU	HIS	MET	GLU	ASP	PRO	GLY	LYS	PRO	LEU	SER	GLU	ALA	LEU	SER	LEU	ALA	LEU	PHE	ASN	SER	PRO	ALA	ALA	GLY	VAL	VAL	LEU	VAL	ASP	GLU	ASP	PRO	GLY	ARG	ALA	ALA	LYS	ARG	ILE	LEU	CYS	LEU	ASP	PHE	LEU	ASP	VAL	VAL	LEU	SER	LEU	GLU	LEU	SER	GLU	GLN	GLN	PHE	VAL	ALA	SER	GLU	VAL	ALA	SER	GLY	THR
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• Molecule 1: Isoform 1 of Gasdermin-B

Chain L:  27% 27% 46%

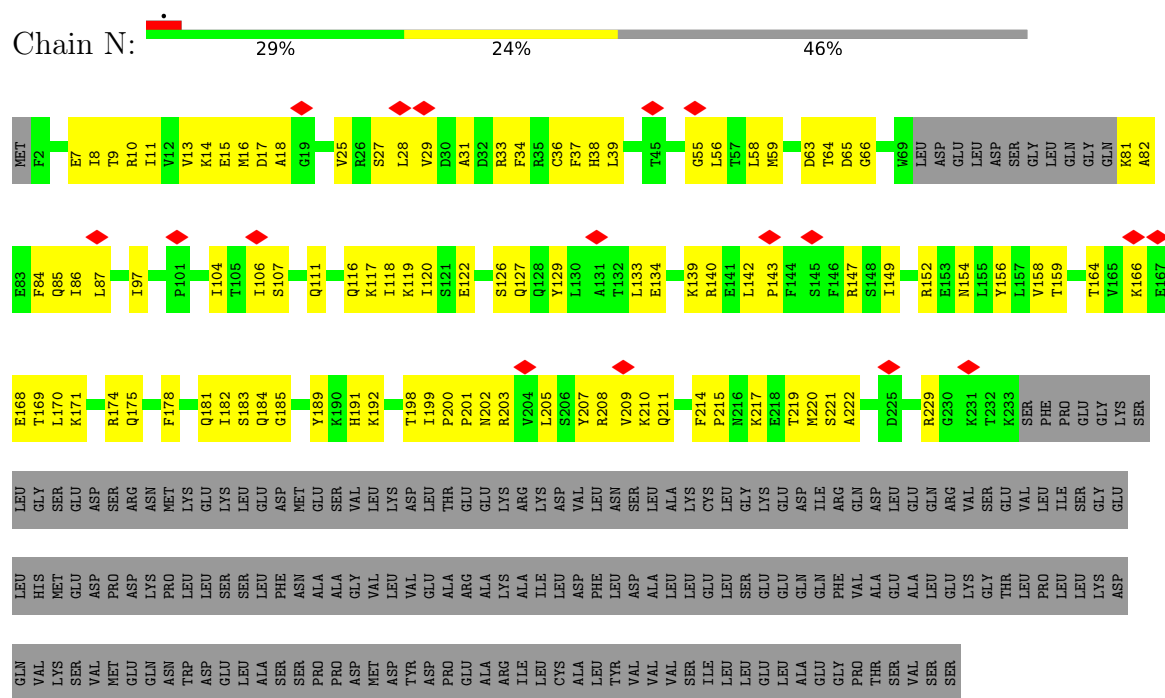
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• Molecule 1: Isoform 1 of Gasdermin-B

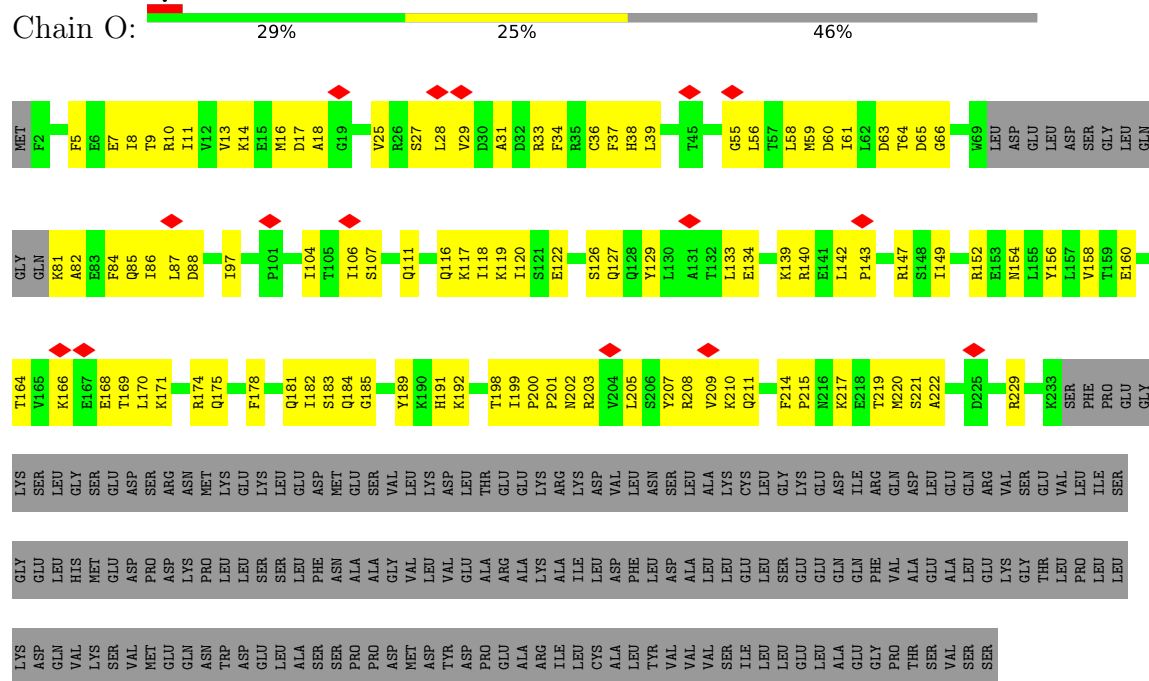
Chain M:  28% 26% 46%

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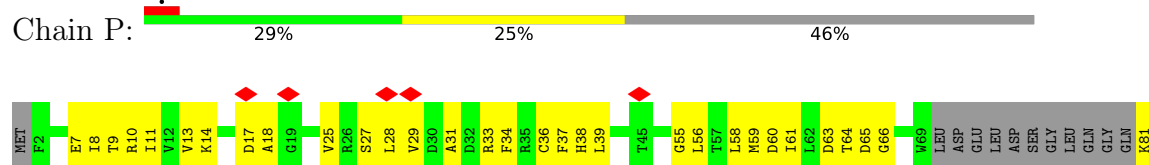
• Molecule 1: Isoform 1 of Gasdermin-B



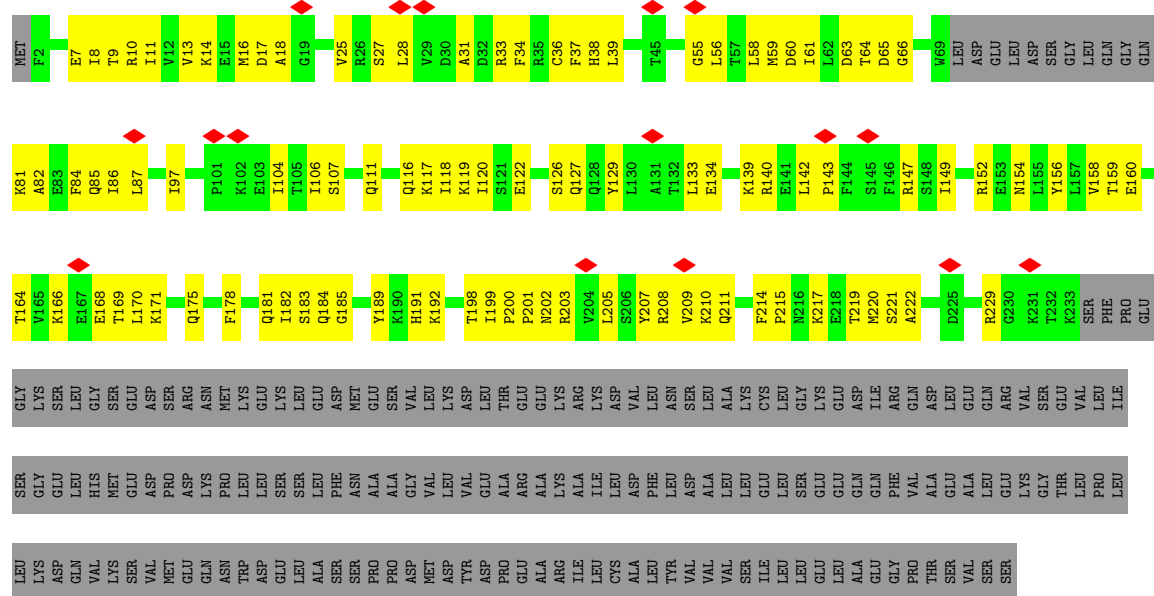
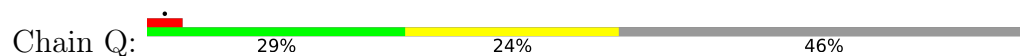
- Molecule 1: Isoform 1 of Gasdermin-B



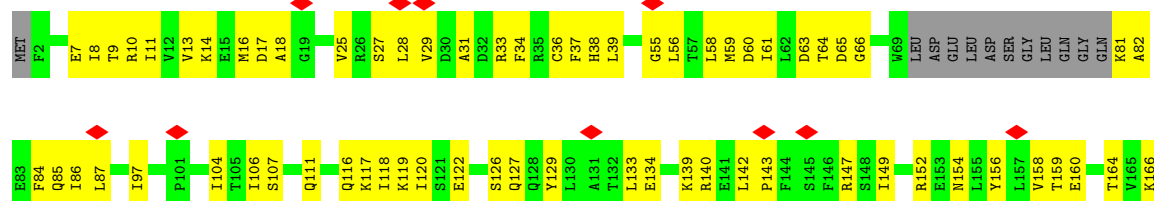
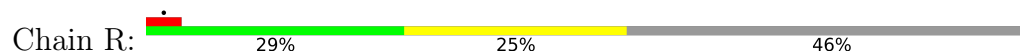
- Molecule 1: Isoform 1 of Gasdermin-B



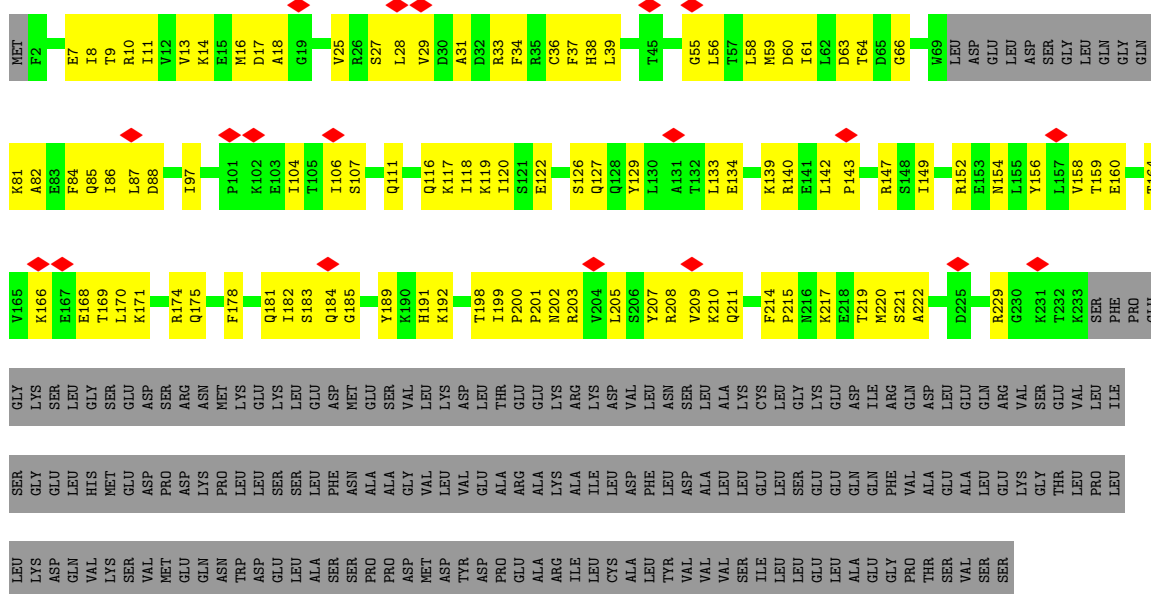
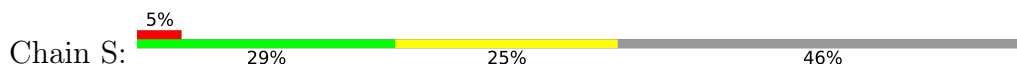
- Molecule 1: Isoform 1 of Gasdermin-B



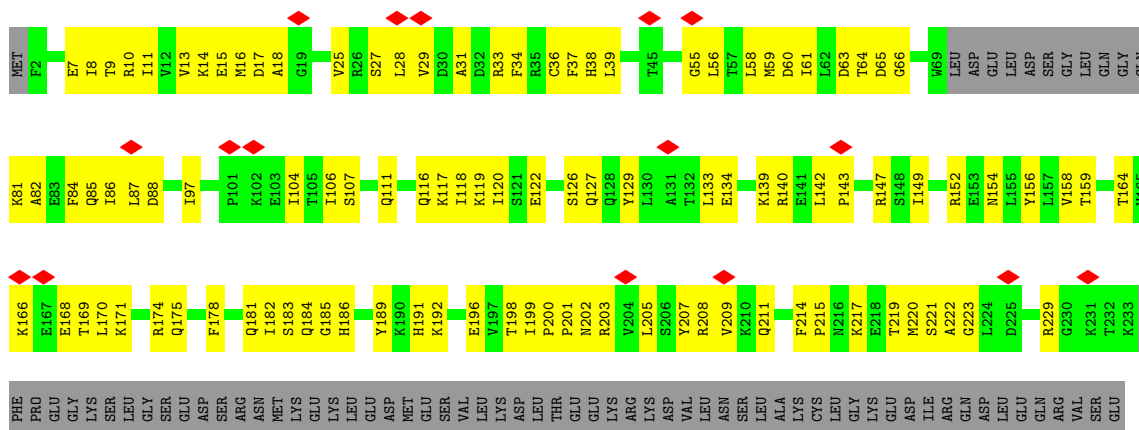
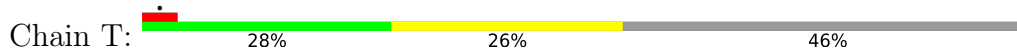
- Molecule 1: Isoform 1 of Gasdermin-B



- Molecule 1: Isoform 1 of Gasdermin-B



- Molecule 1: Isoform 1 of Gasdermin-B



VAL	LEU	ILE	SER	GLY	LEU	HIS	MET	GLU	ASP	PRO	PRO	GLY	ASP	LYS	PRO	LEU	LEU	SER	VAL	LEU	SER	ALA	LEU	PHE	SER	ASN	ALA	ALA	GLY	VAL	LEU	VAL	TYR	ASP	GLU	PRO	ALA	ALA	ARG	GLY	ALA	ALA	LYS	ILE	LEU	LEU	CYS	LEU	ASP	ALA	PHE	LEU	ASP	VAL	VAL	LEU	LEU	SER	ILE	LEU	LEU	SER	GLU	GLU	GLN	GLN	PHE	GLY	VAL	THR	SER	VAL	GLU	LEU	LYS	GLY	THR
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• Molecule 1: Isoform 1 of Gasdermin-B

Chain U: 

GLY	THR	LEU	LEU	PRO	LEU	LEU	LEU	LYS	GLY	GLU	ASP	GLN	VAL	LEU	HIS	MET	GLY	SER	LEU	GLY	GLU	ASP	VAL	LYS	GLY	THR	ASP	PRO	ALA	ALA	GLY	ASP	MET	ASP	TYR	ASP	PRO	ALA	ALA	ALA	ARG	ILE	CYS	ALA	ALA	LEU	LEU	TYR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL</
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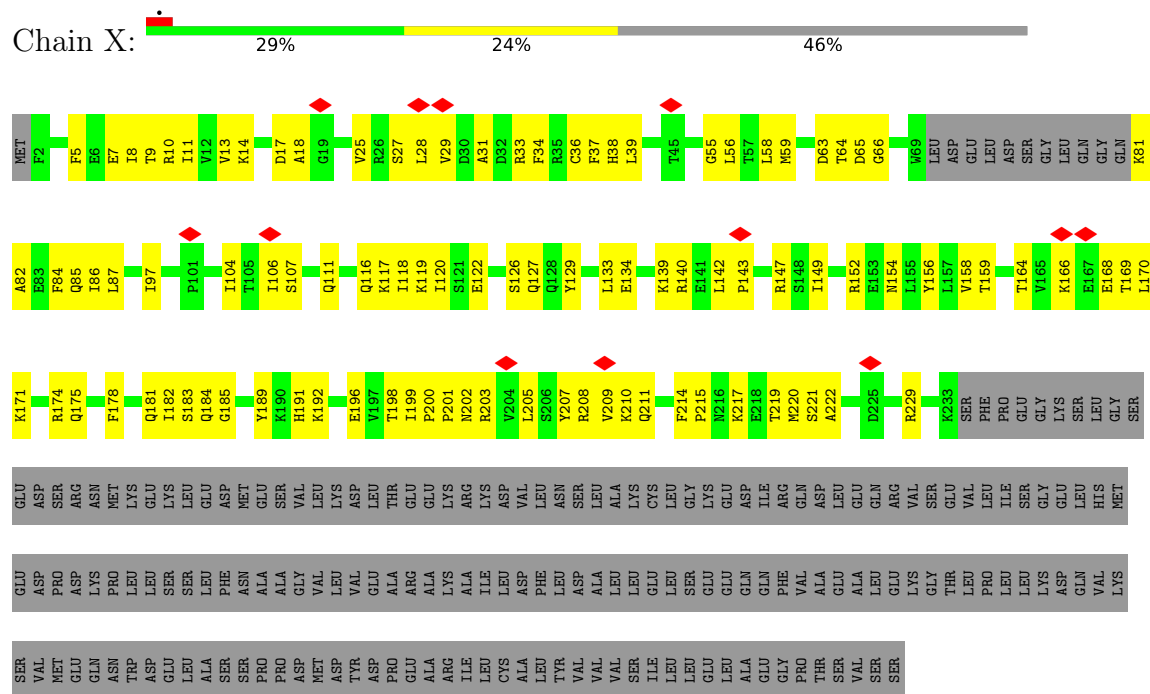
• Molecule 1: Isoform 1 of Gasdermin-B

Chain V: 

LEU	SER	GLY	LYS	E168	A82	MET
GLY	GLY	GLY	LYS	T169	E83	F2
ASP	GLU	SER	LEU	L170	F84	E7
GLN	LEU	LEU	LEU	K171	Q85	T8
VAL	HIS	GLY	GLY		T86	T9
LYS	MET	SER	SER	R174	L87	R10
SER	GLU	GLU	GLU	Q175		R11
VAL	ASP	ASP	ASP	F178	D91	V12
MET	PRO	SER	SER		I97	K14
GLY	ASP	ARG	ARG			
ASN	LYS	ASN	ASN	Q181	P101	D17
PRO	PRO	MET	MET	I182		A18
TRP	LEU	LYS	LYS	S183	I104	G19
ASP	GLU	GLU	GLU	Q184	T105	
GLY	SER	LEU	LYS	G185	I106	V25
LEU	SER	LEU	LEU	H186	S107	R26
ALA	LEU	GLU	GLU	L187		S27
SER	PHE	ASP	ASP	S188	Q111	L28
ASN	ASN	MET	MET	Y189		V29
PRO	ALA	GLU	GLU	K190		D30
PRO	ALA	SER	VAL	H191	Q116	A31
ASP	GLY	VAL	VAL	K192	K117	D32
MET	VAL	LEU	LYS	G193	I118	R33
ASP	LEU				K119	F34
TYR	VAL	ASP	ASP	E196	I120	R35
GLY	GLU	GLY	THR	V197	S121	C36
ASP	PRO	ALA	LEU	T198	E122	F37
PRO	ALA	ARG	GLU	I199		H38
GLY	ALA	ALA	GLU	P200	S126	L39
ALA	ALA	ALA	GLY	P201	Q127	
ARG	LYS	LYS	LYS	N202	Q128	
ILE	ALA	ARG	ARG	R203	Y129	
LEU	LEU	LEU	ASP	V204		T45
CYS	LEU	ASP	VAL	L205	L133	
ALA	ASP	ASP	VAL	S206	E134	
LYU	PHE	LEU	ASN	Y207		
LEU	LEU	LEU	ASN	R208	K139	G55
VAL	ASP	ALA	LEU	V209	L58	L56
VAL	LEU	ALA	LEU	K210	R140	T57
SER	LEU	LEU	LYS	Q211	E141	M59
ILE	GLY	CYS	GLY		L142	D60
LEU	LEU	LEU	LEU	F214	P143	L61
LEU	SER	GLY	GLY	P215	F144	L62
GLU	GLY	GLY	LYS	K216	S145	D63
LEU	GLU	GLU	GLU	K217	F146	T64
ALA	GLN	GLN	ASP	E218	R147	D65
GLY	GLN	ILE	ILE	T219	S148	G66
PHE	ARG	ARG	ARG	M220	I149	
VAL	GLN	GLN	GLN	S221		W69
PRO	VAL	ASP	ASP	A222	R152	LEU
THR	ALA	LEU	LEU		E153	ASP
SER	GLY	GLY	GLY	D225	N154	GLY
VAL	ALA	ALA	GLN		L155	LEU
VAL	VAL	VAL	GLN	R229	Y156	ASP
SER	GLY	VAL	ARG		L157	SER
GLY	GLY	THR	VAL	K233	V158	GLY
LYS	LYS	SER	VAL			GLY
THR	GLY	GLY	GLY		T164	LEU
SER	GLY	LEU	VAL	SER	V165	GLN
VAL	LEU	LEU	VAL	PHE	K166	GLY
VAL	LEU	PRO	ILE	PRO		GLN
SER	LEU	LEU	LEU	GLU	E167	K81

• Molecule 1: Isoform 1 of Gasdermin-B

- Molecule 1: Isoform 1 of Gasdermin-B



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	41799	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.058	Depositor
Minimum map value	-0.716	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.036	Depositor
Recommended contour level	0.15	Depositor
Map size ($\text{\AA}$)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.66, 1.66, 1.66	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	0.20	0/1850	0.58	0/2484
1	B	0.20	0/1850	0.58	0/2484
1	C	0.20	0/1850	0.58	0/2484
1	D	0.20	0/1850	0.58	0/2484
1	E	0.20	0/1850	0.58	0/2484
1	F	0.20	0/1850	0.58	0/2484
1	G	0.20	0/1850	0.58	0/2484
1	H	0.20	0/1850	0.58	0/2484
1	I	0.20	0/1850	0.58	0/2484
1	J	0.20	0/1850	0.58	0/2484
1	K	0.20	0/1850	0.58	0/2484
1	L	0.20	0/1850	0.58	0/2484
1	M	0.20	0/1850	0.58	0/2484
1	N	0.20	0/1850	0.58	0/2484
1	O	0.20	0/1850	0.58	0/2484
1	P	0.20	0/1850	0.58	0/2484
1	Q	0.20	0/1850	0.58	0/2484
1	R	0.20	0/1850	0.58	0/2484
1	S	0.20	0/1850	0.58	0/2484
1	T	0.20	0/1850	0.58	0/2484
1	U	0.20	0/1850	0.58	0/2484
1	V	0.20	0/1850	0.58	0/2484
1	W	0.20	0/1850	0.58	0/2484
1	X	0.20	0/1850	0.58	0/2484
All	All	0.20	0/44400	0.58	0/59616

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1816	0	1829	85	0
1	B	1816	0	1829	90	0
1	C	1816	0	1829	87	0
1	D	1816	0	1829	83	0
1	E	1816	0	1829	84	0
1	F	1816	0	1829	88	0
1	G	1816	0	1829	87	0
1	H	1816	0	1829	82	0
1	I	1816	0	1829	84	0
1	J	1816	0	1829	91	0
1	K	1816	0	1829	91	0
1	L	1816	0	1829	110	0
1	M	1816	0	1829	105	0
1	N	1816	0	1829	85	0
1	O	1816	0	1829	94	0
1	P	1816	0	1829	89	0
1	Q	1816	0	1829	82	0
1	R	1816	0	1829	89	0
1	S	1816	0	1829	92	0
1	T	1816	0	1829	94	0
1	U	1816	0	1829	106	0
1	V	1816	0	1829	103	0
1	W	1816	0	1829	94	0
1	X	1816	0	1829	88	0
All	All	43584	0	43896	2034	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 2034 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:I:168:GLU:HA	1:I:199:ILE:O	1.67	0.95
1:O:168:GLU:HA	1:O:199:ILE:O	1.67	0.95
1:H:168:GLU:HA	1:H:199:ILE:O	1.67	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:168:GLU:HA	1:N:199:ILE:O	1.67	0.95
1:R:168:GLU:HA	1:R:199:ILE:O	1.67	0.95

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	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	B	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	C	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	D	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	E	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	F	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	G	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	H	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	I	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	J	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	K	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	L	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	M	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	N	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	O	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	P	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	Q	217/411 (53%)	190 (88%)	27 (12%)	0	100	100
1	R	217/411 (53%)	192 (88%)	25 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	T	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	U	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	V	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
1	W	217/411 (53%)	192 (88%)	25 (12%)	0	100	100
1	X	217/411 (53%)	191 (88%)	26 (12%)	0	100	100
All	All	5208/9864 (53%)	4597 (88%)	611 (12%)	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	202/370 (55%)	202 (100%)	0	100	100
1	B	202/370 (55%)	202 (100%)	0	100	100
1	C	202/370 (55%)	202 (100%)	0	100	100
1	D	202/370 (55%)	202 (100%)	0	100	100
1	E	202/370 (55%)	202 (100%)	0	100	100
1	F	202/370 (55%)	202 (100%)	0	100	100
1	G	202/370 (55%)	202 (100%)	0	100	100
1	H	202/370 (55%)	202 (100%)	0	100	100
1	I	202/370 (55%)	202 (100%)	0	100	100
1	J	202/370 (55%)	202 (100%)	0	100	100
1	K	202/370 (55%)	202 (100%)	0	100	100
1	L	202/370 (55%)	202 (100%)	0	100	100
1	M	202/370 (55%)	202 (100%)	0	100	100
1	N	202/370 (55%)	202 (100%)	0	100	100
1	O	202/370 (55%)	202 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	202/370 (55%)	202 (100%)	0	100	100
1	Q	202/370 (55%)	202 (100%)	0	100	100
1	R	202/370 (55%)	202 (100%)	0	100	100
1	S	202/370 (55%)	202 (100%)	0	100	100
1	T	202/370 (55%)	202 (100%)	0	100	100
1	U	202/370 (55%)	202 (100%)	0	100	100
1	V	202/370 (55%)	202 (100%)	0	100	100
1	W	202/370 (55%)	202 (100%)	0	100	100
1	X	202/370 (55%)	202 (100%)	0	100	100
All	All	4848/8880 (55%)	4848 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	186	HIS
1	P	216	ASN
1	W	51	HIS
1	M	216	ASN
1	O	181	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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.

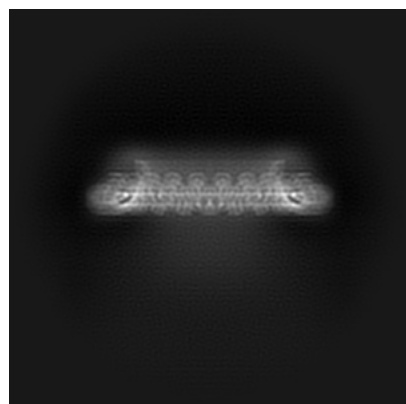
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28584. These allow visual inspection of the internal detail of the map and identification of artifacts.

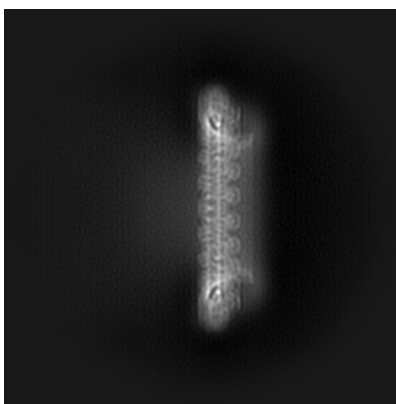
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

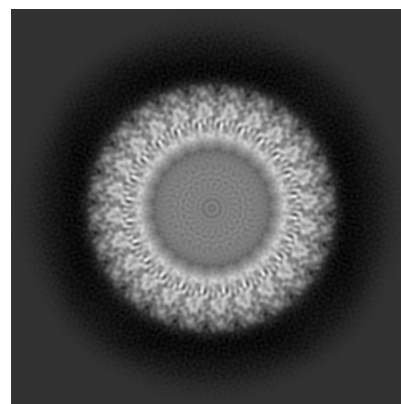
6.1.1 Primary map



X

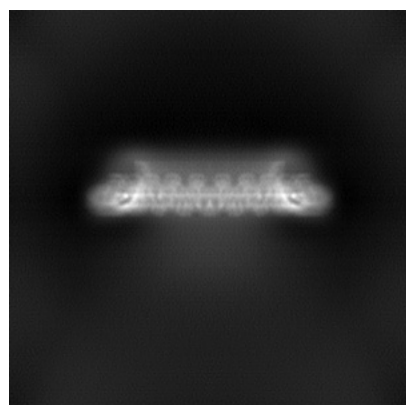


Y

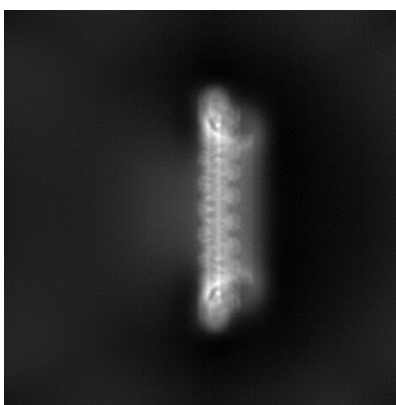


Z

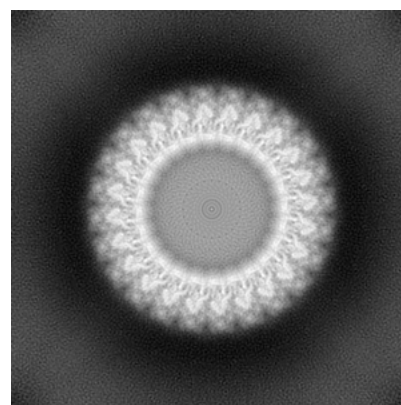
6.1.2 Raw map



X



Y

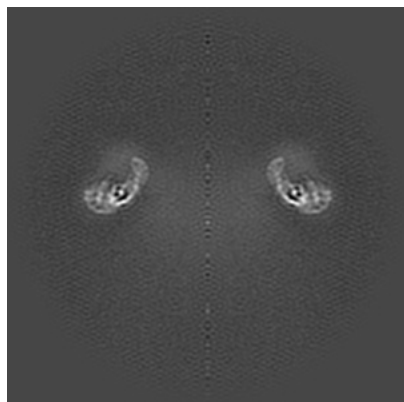


Z

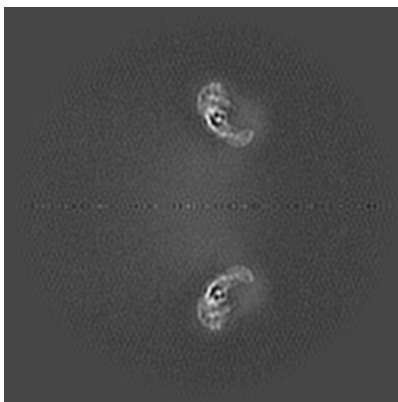
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

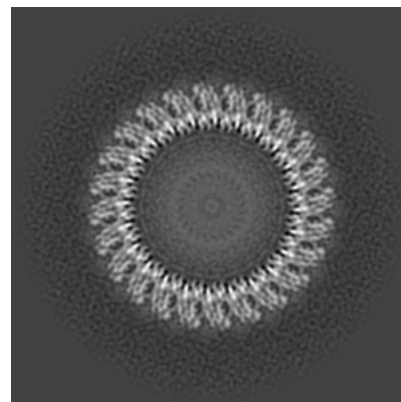
6.2.1 Primary map



X Index: 128



Y Index: 128



Z Index: 128

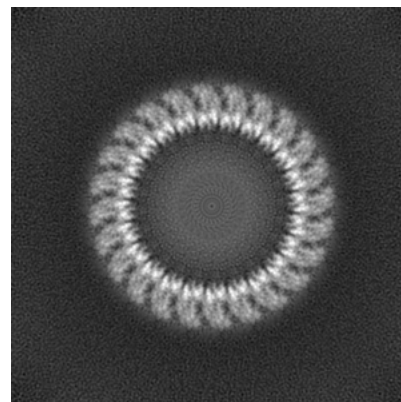
6.2.2 Raw map



X Index: 128



Y Index: 128

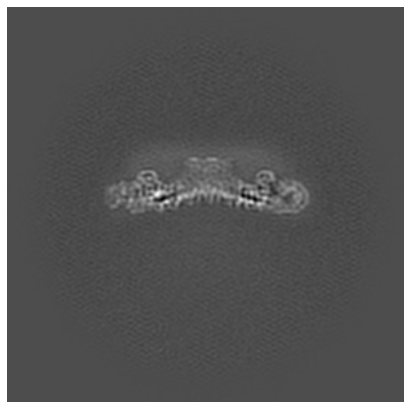


Z Index: 128

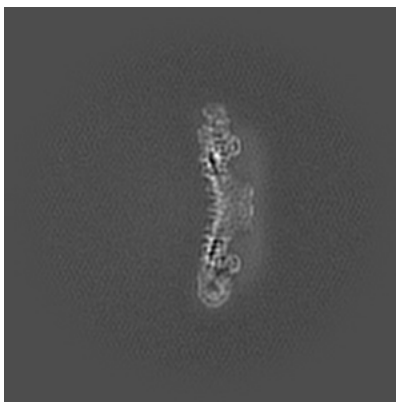
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

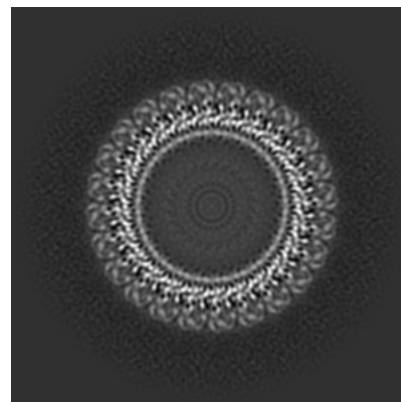
6.3.1 Primary map



X Index: 175



Y Index: 175



Z Index: 137

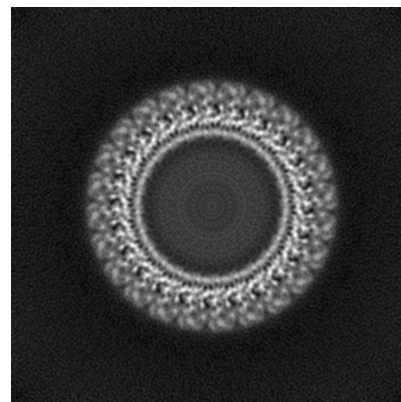
6.3.2 Raw map



X Index: 175



Y Index: 81

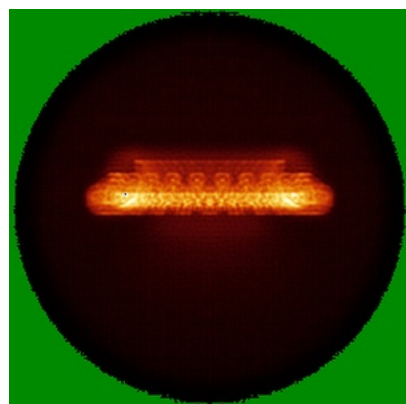


Z Index: 137

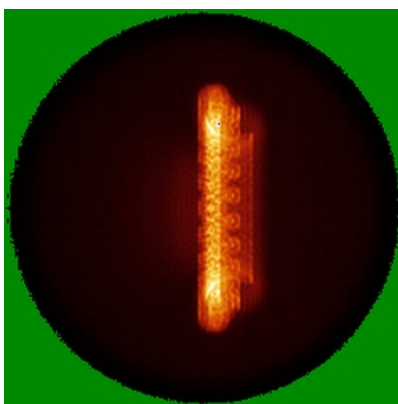
The images above show the largest variance slices of the map in three orthogonal directions.

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

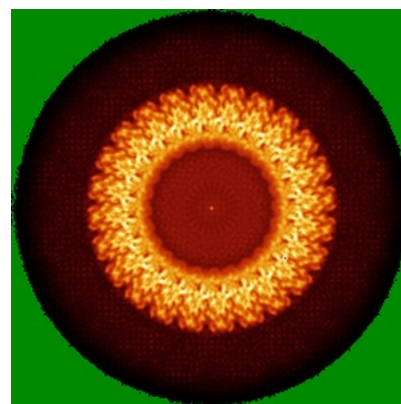
6.4.1 Primary map



X

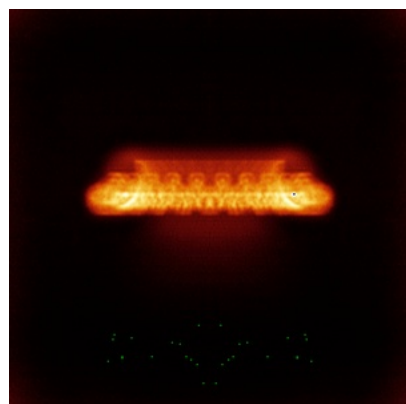


Y

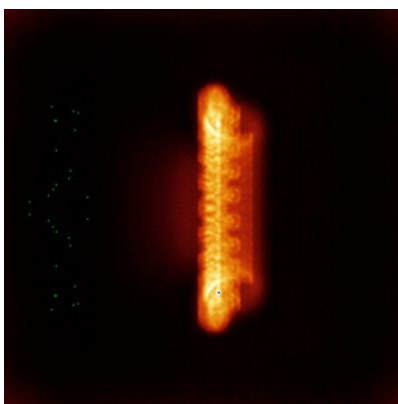


Z

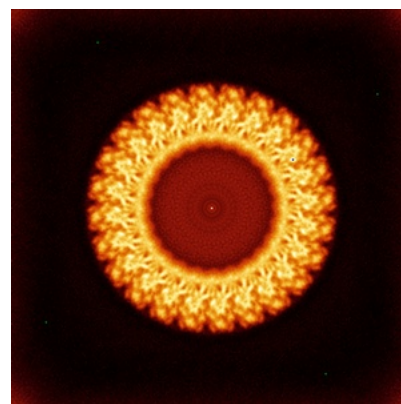
6.4.2 Raw map



X



Y

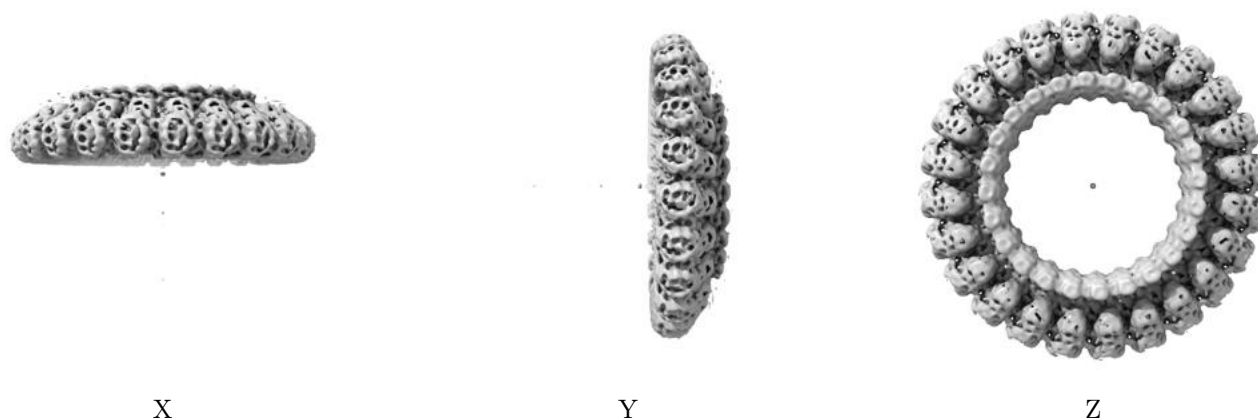


Z

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 shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

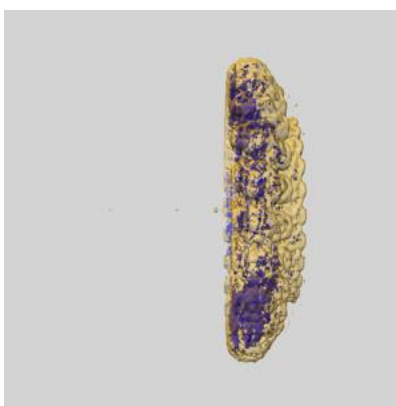
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

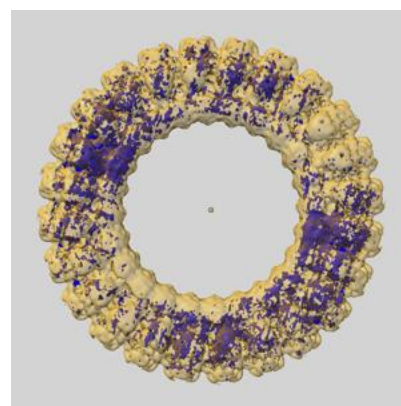
6.6.1 emd_28584_msk_1.map [i](#)



X



Y

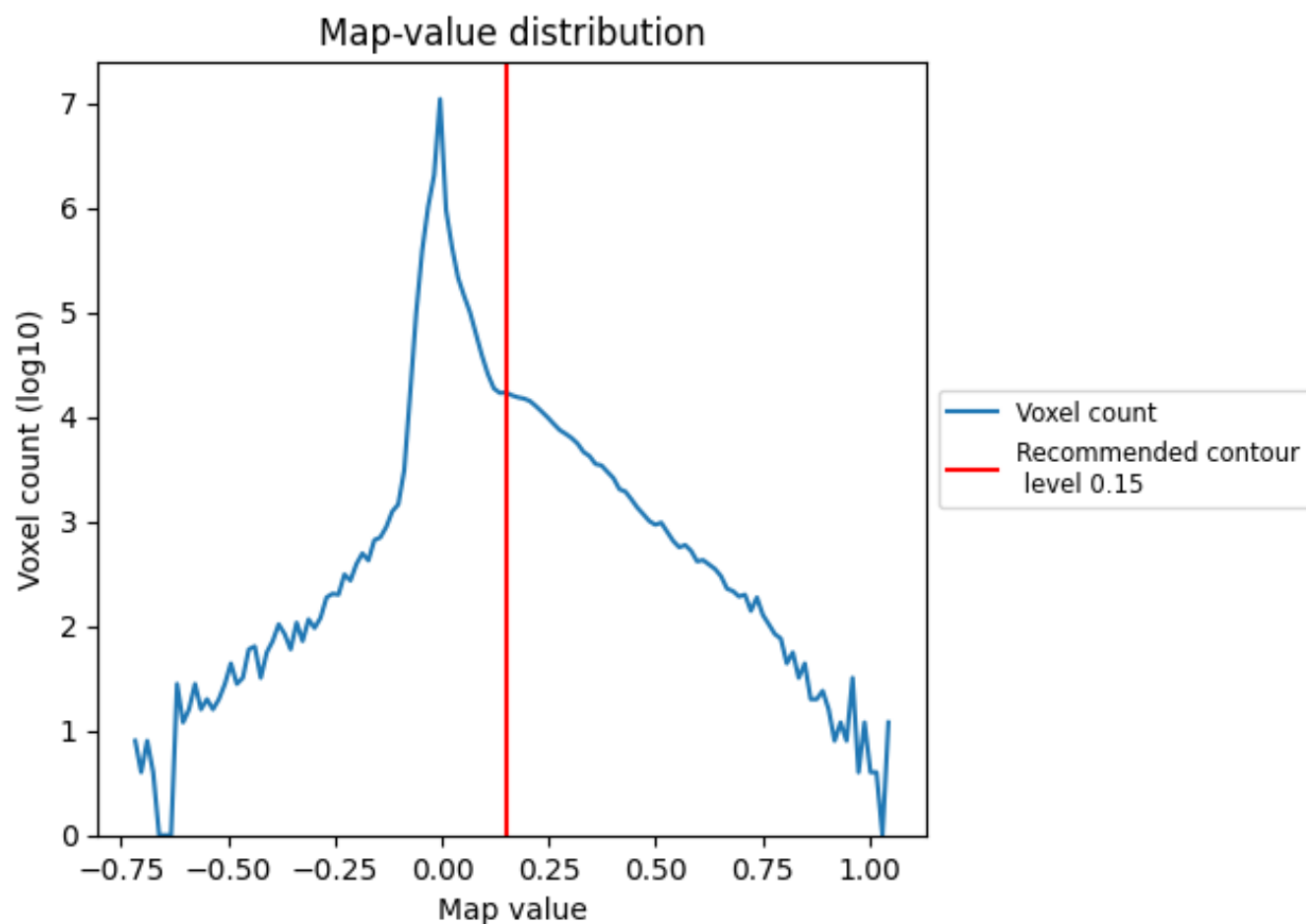


Z

7 Map analysis [i](#)

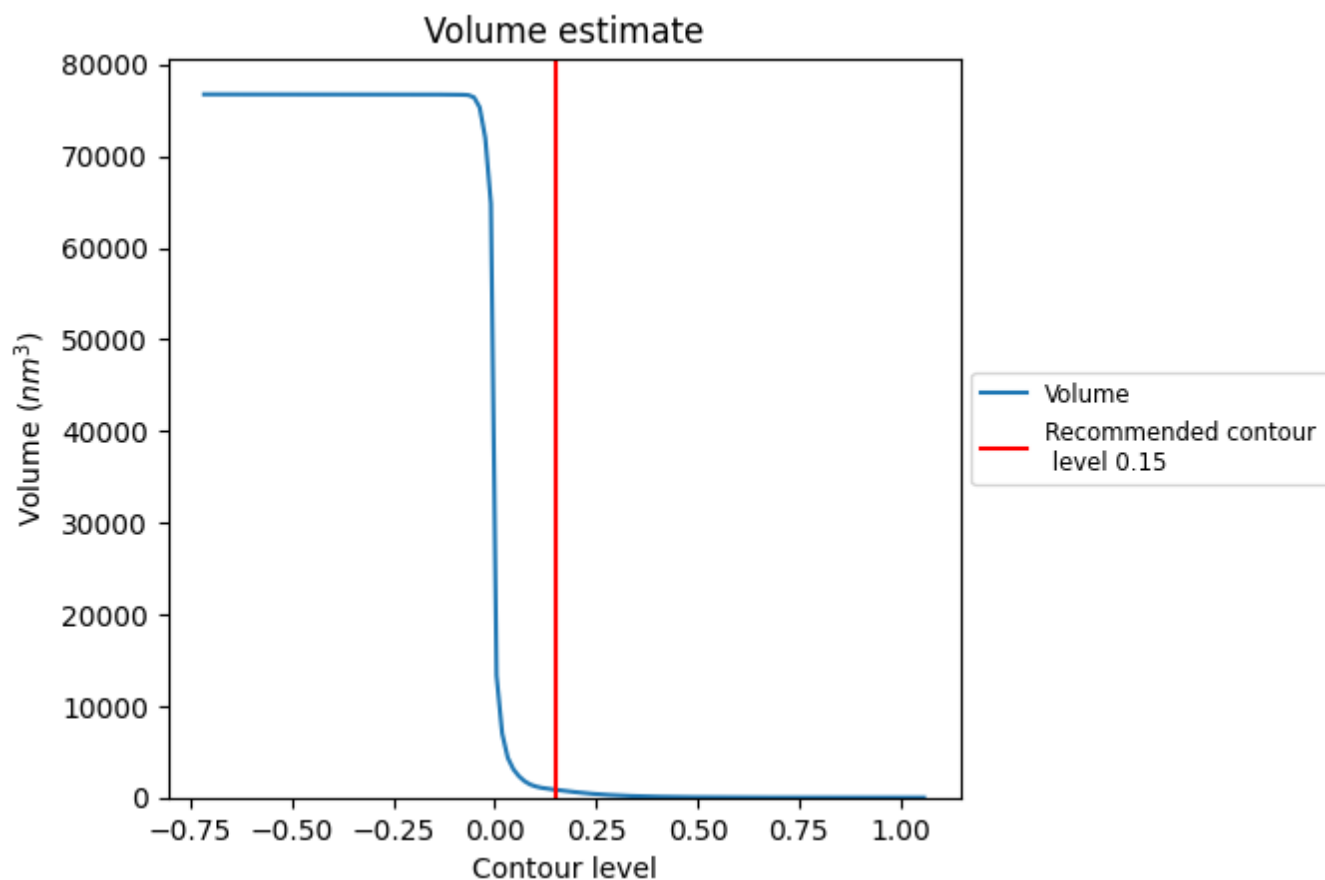
This section contains the results of statistical analysis of the map.

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.

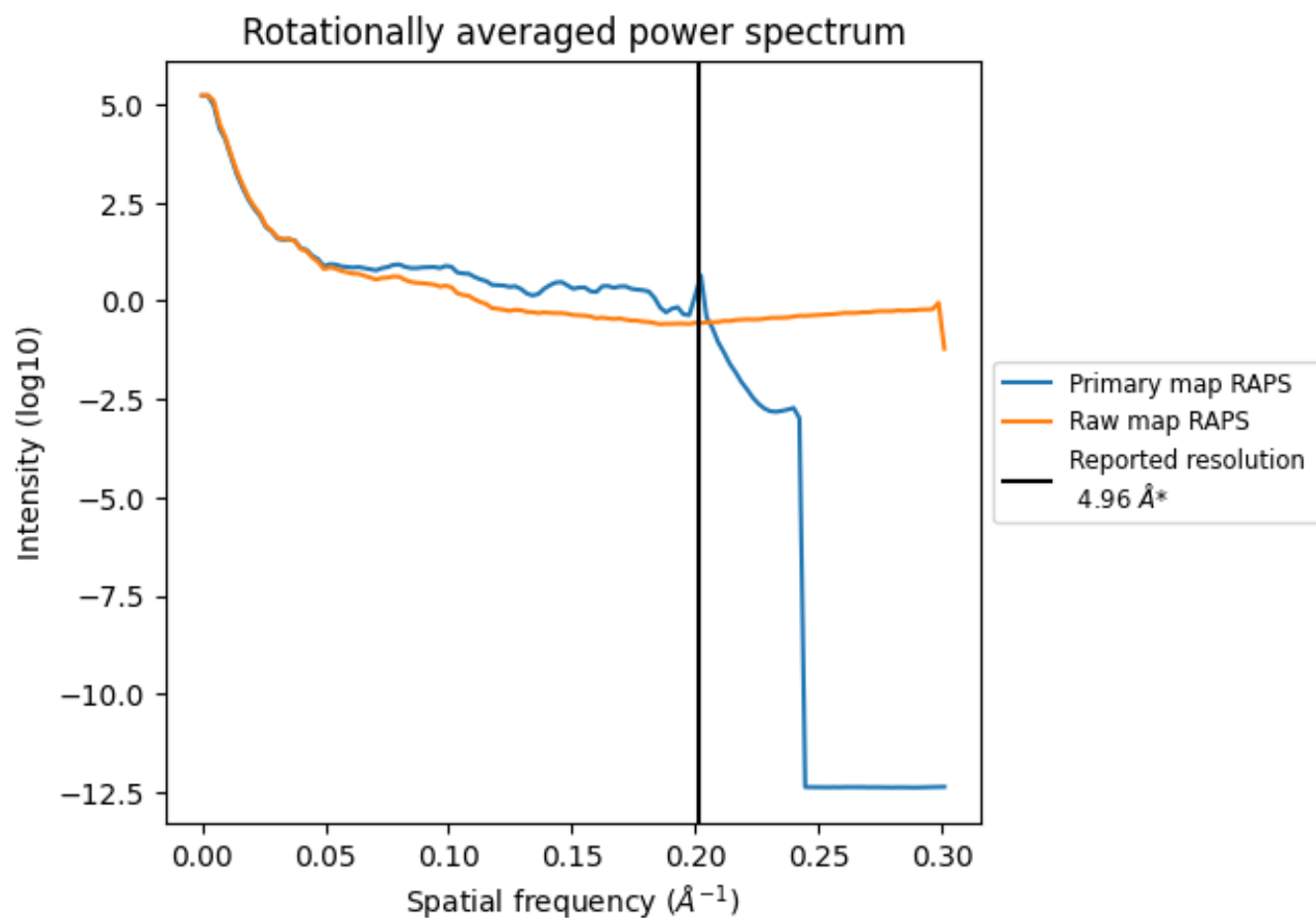
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 852 nm³; this corresponds to an approximate mass of 769 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 ⓘ

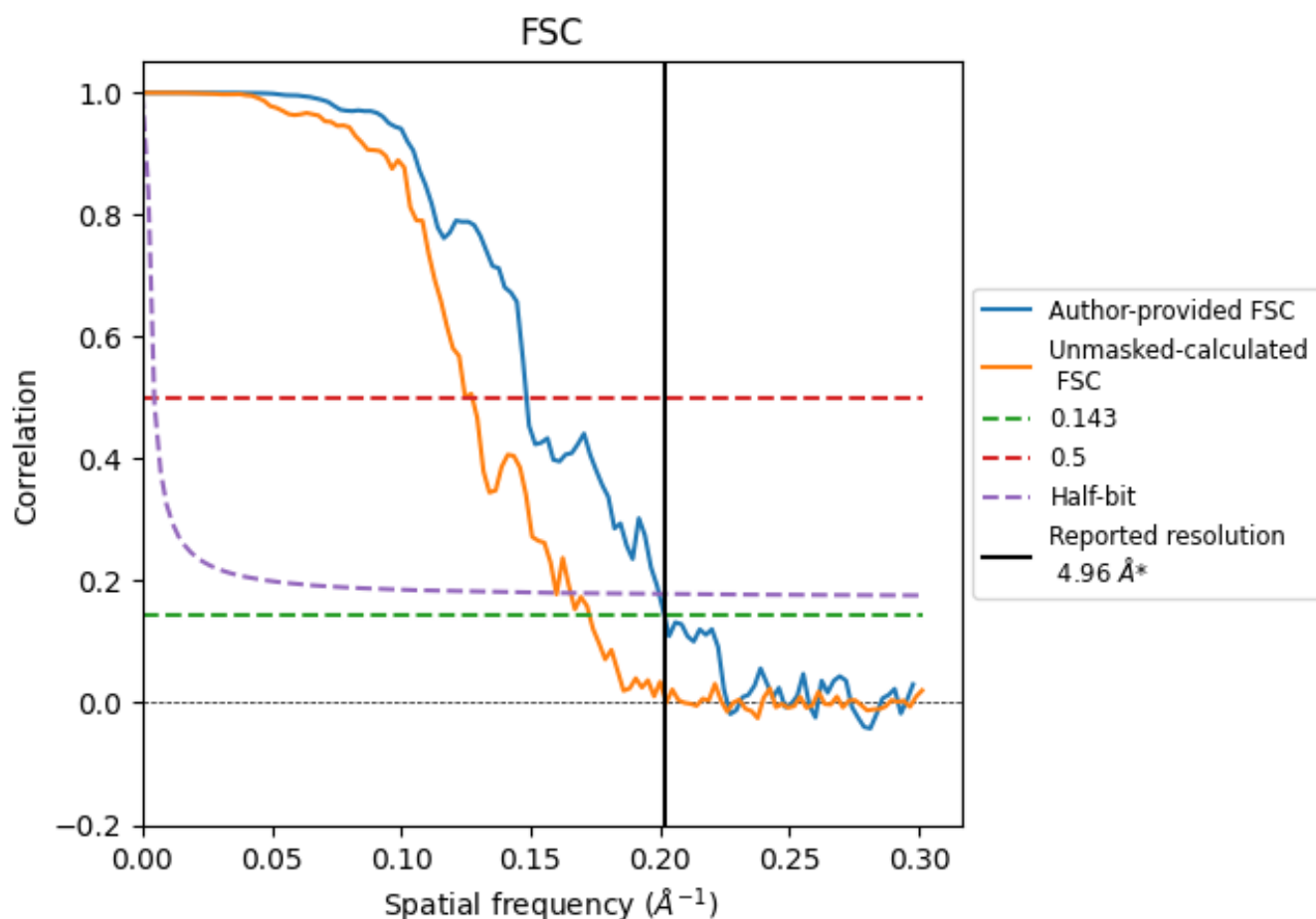


*Reported resolution corresponds to spatial frequency of 0.202 $\text{\AA}^{-1}$

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 0.202 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

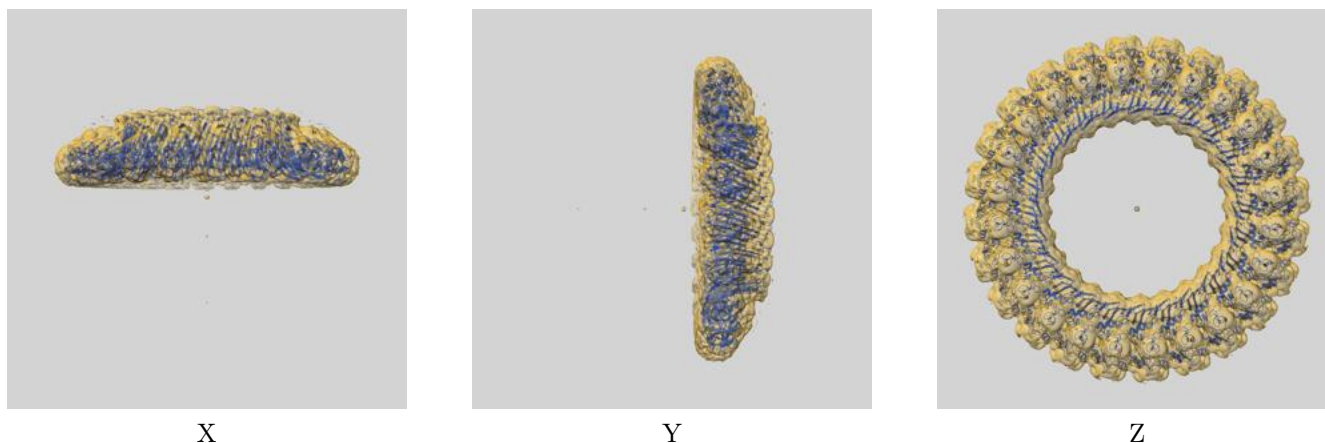
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.96	-	-
Author-provided FSC curve	4.96	6.74	5.01
Unmasked-calculated*	5.79	7.84	6.25

*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 5.79 differs from the reported value 4.96 by more than 10 %

9 Map-model fit [i](#)

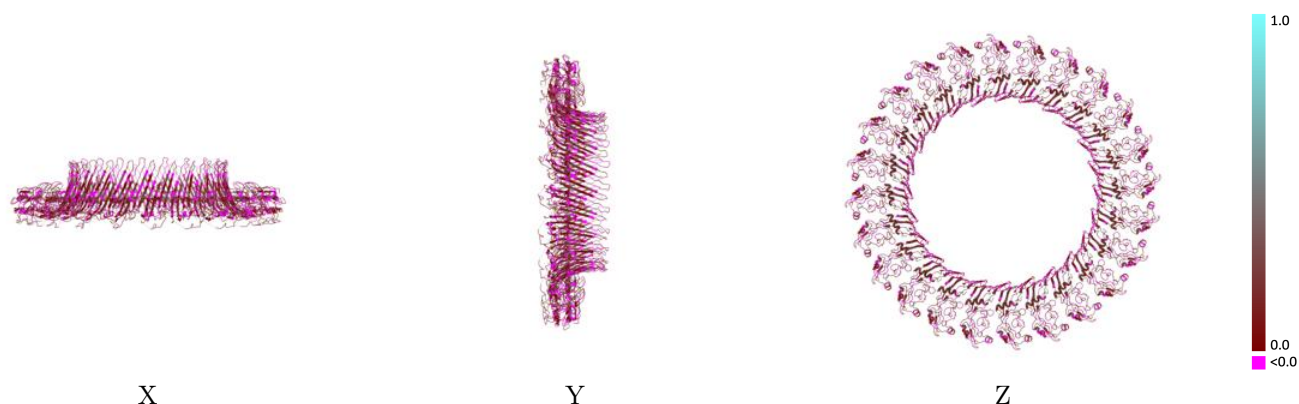
This section contains information regarding the fit between EMDB map EMD-28584 and PDB model 8ET2. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



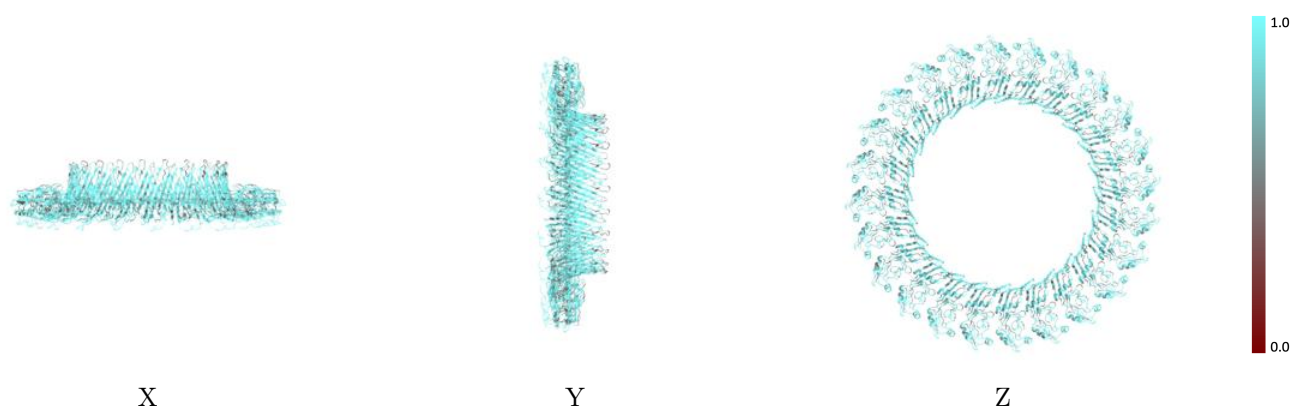
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



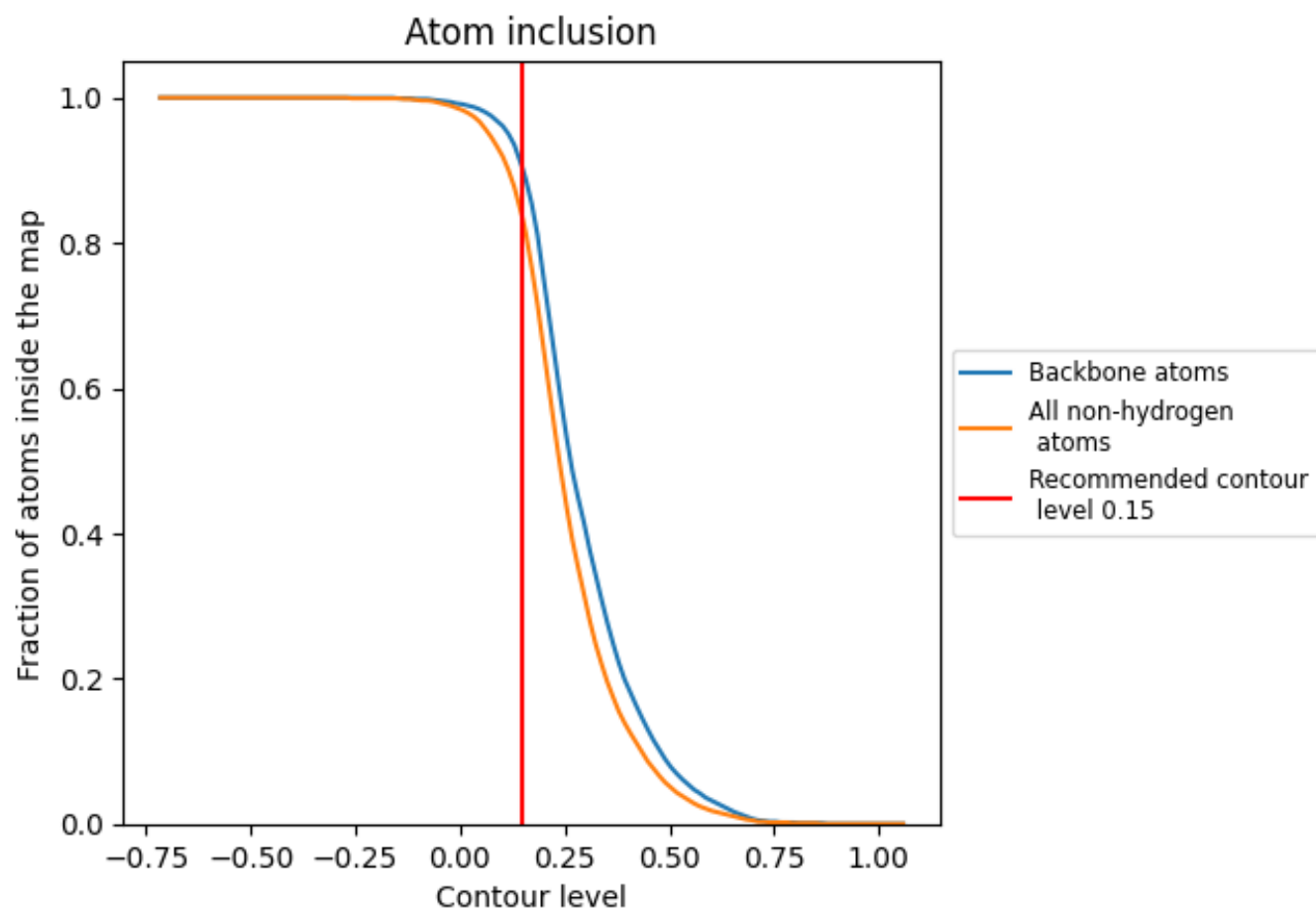
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 90% of all backbone atoms, 83% 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	 0.8320	 0.1180
A	 0.8380	 0.1200
B	 0.8350	 0.1170
C	 0.8360	 0.1180
D	 0.8300	 0.1170
E	 0.8350	 0.1200
F	 0.8310	 0.1200
G	 0.8300	 0.1190
H	 0.8300	 0.1210
I	 0.8340	 0.1200
J	 0.8300	 0.1210
K	 0.8280	 0.1170
L	 0.8320	 0.1210
M	 0.8360	 0.1180
N	 0.8350	 0.1190
O	 0.8360	 0.1200
P	 0.8350	 0.1160
Q	 0.8290	 0.1140
R	 0.8290	 0.1180
S	 0.8210	 0.1140
T	 0.8260	 0.1150
U	 0.8320	 0.1170
V	 0.8380	 0.1150
W	 0.8370	 0.1180
X	 0.8320	 0.1160

