



wwPDB EM Validation Summary Report ⓘ

Oct 14, 2024 – 06:16 AM EDT

PDB ID : 8CT1
EMDB ID : EMD-26977
Title : CryoEM structure of human S-OPA1 assembled on lipid membrane in membrane-adjacent state
Authors : Du Pont, K.E.; Aydin, H.
Deposited on : 2022-05-13
Resolution : 4.80 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

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 4.80 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)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	960	<div> <div>13%</div> <div>73%</div> <div>27%</div> </div>
1	B	960	<div> <div>13%</div> <div>73%</div> <div>27%</div> </div>
1	C	960	<div> <div>13%</div> <div>73%</div> <div>27%</div> </div>
1	D	960	<div> <div>13%</div> <div>73%</div> <div>27%</div> </div>
1	E	960	<div> <div>14%</div> <div>73%</div> <div>27%</div> </div>
1	F	960	<div> <div>13%</div> <div>73%</div> <div>27%</div> </div>
1	G	960	<div> <div>14%</div> <div>73%</div> <div>27%</div> </div>
1	H	960	<div> <div>14%</div> <div>73%</div> <div>27%</div> </div>
1	I	960	<div> <div>13%</div> <div>73%</div> <div>27%</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain		
1	J	960	13%	73%	27%
1	K	960	14%	73%	27%
1	L	960	13%	73%	27%
1	M	960	14%	73%	27%
1	N	960	13%	73%	27%
1	O	960	13%	73%	27%
1	P	960	13%	73%	27%
1	Q	960	14%	73%	27%
1	R	960	13%	73%	27%
1	S	960	13%	73%	27%
1	T	960	14%	73%	27%
1	U	960	13%	73%	27%
1	V	960	13%	73%	27%
1	W	960	13%	73%	27%
1	X	960	14%	73%	27%
1	Y	960	13%	73%	27%
1	Z	960	13%	73%	27%
1	a	960	13%	73%	27%
1	b	960	14%	73%	27%
1	c	960	13%	73%	27%
1	d	960	13%	73%	27%
1	e	960	13%	73%	27%
1	f	960	13%	73%	27%
1	g	960	14%	73%	27%
1	h	960	13%	73%	27%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 193290 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.

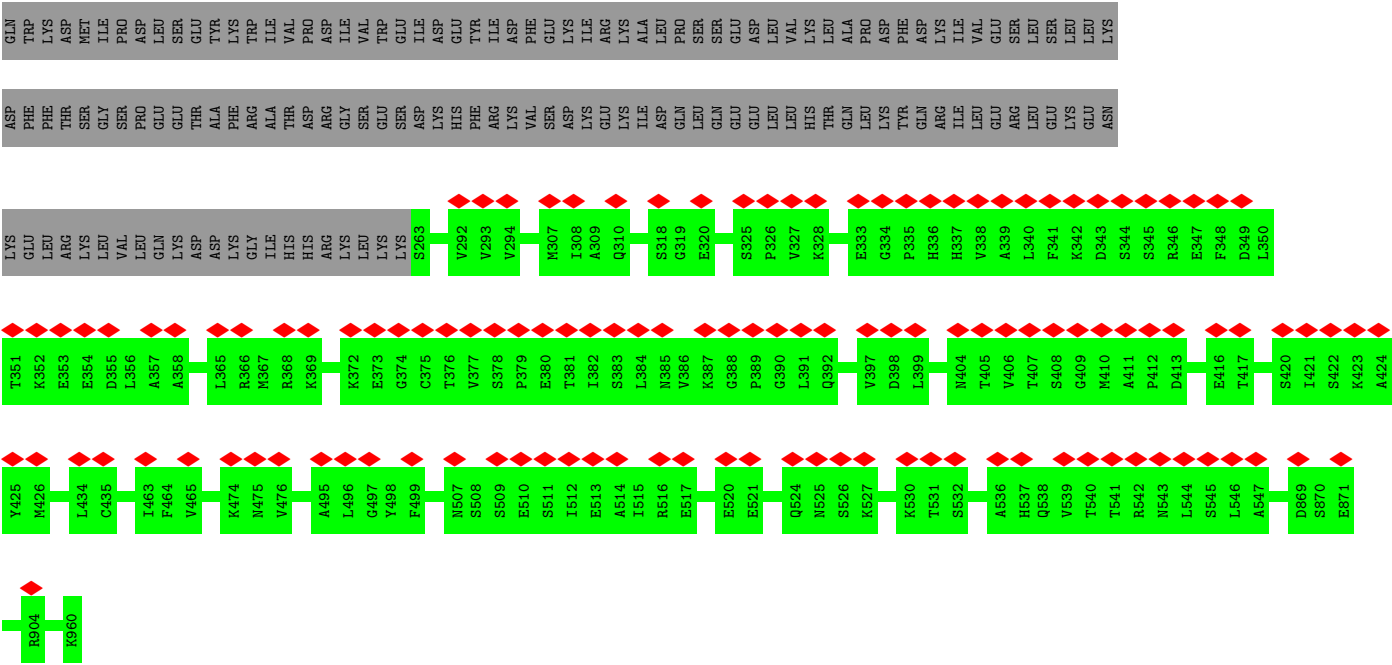
- Molecule 1 is a protein called Dynamin-like 120 kDa protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	a	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	B	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	b	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	C	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	c	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	D	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	d	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	E	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	e	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	F	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	f	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	G	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	g	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	H	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	h	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	I	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		

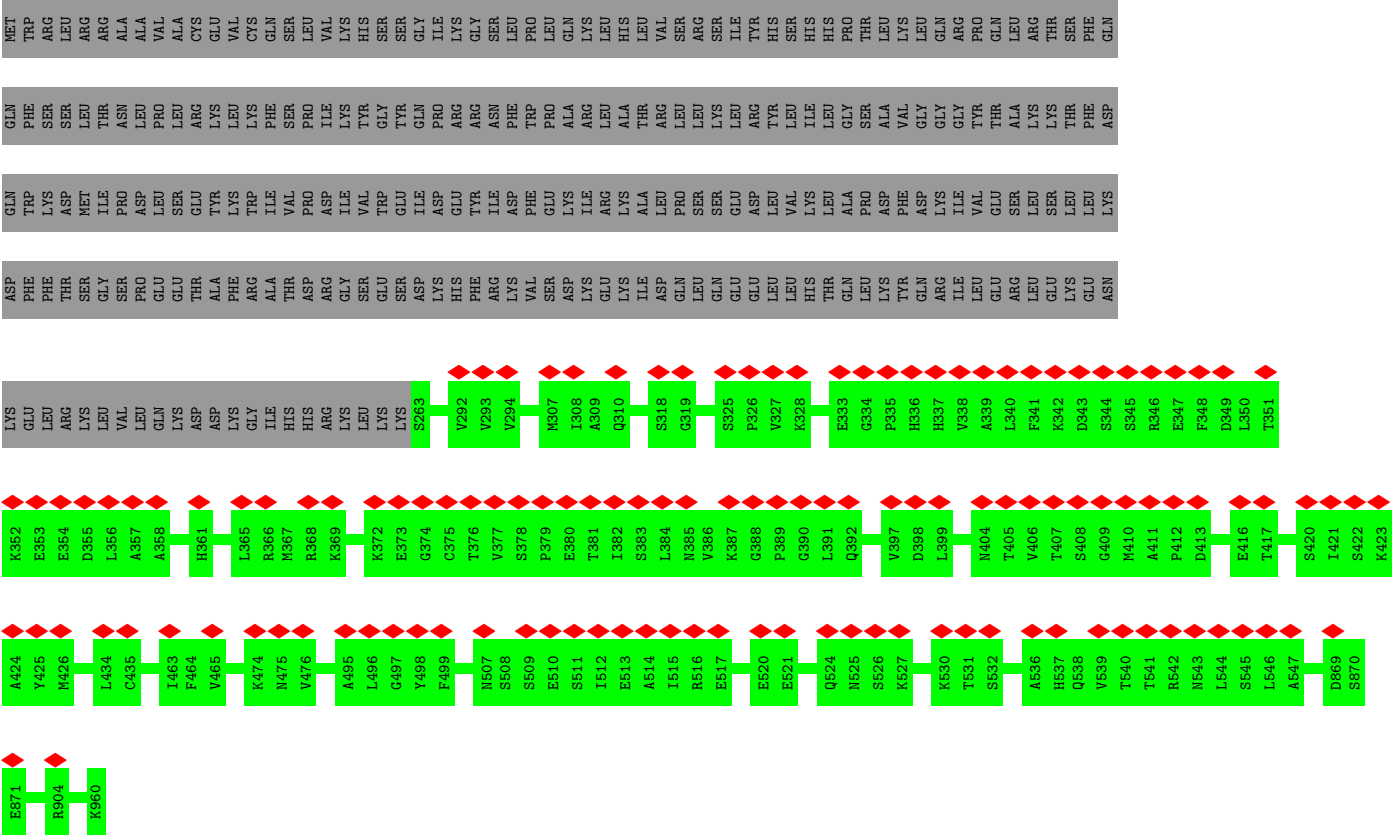
Continued on next page...

Continued from previous page...

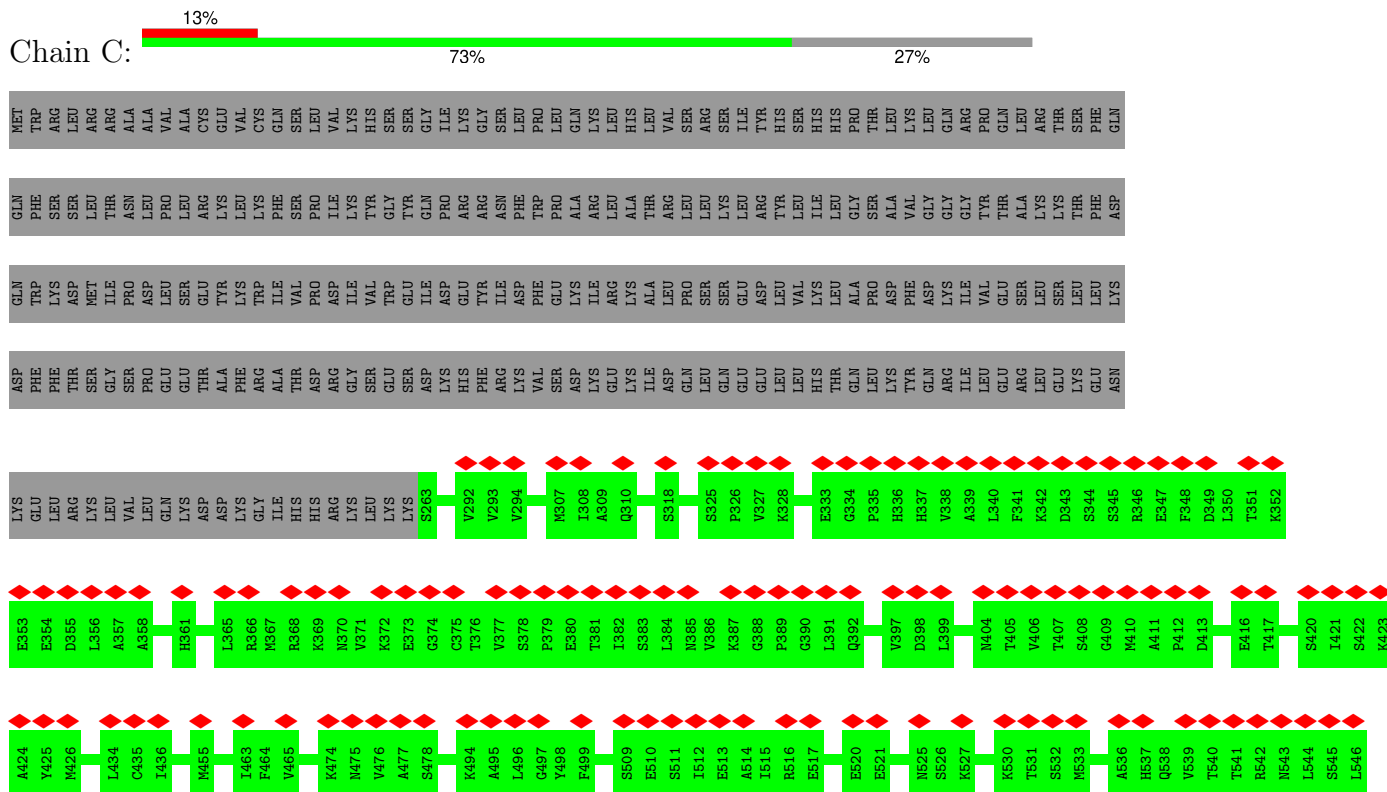
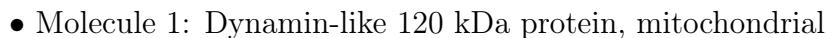
Mol	Chain	Residues	Atoms					AltConf	Trace
1	J	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	K	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	L	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	M	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	N	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	O	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	P	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	Q	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	R	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	S	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	T	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	U	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	V	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	W	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	X	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	Y	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		
1	Z	698	Total	C	N	O	S	0	0
			5685	3572	996	1091	26		

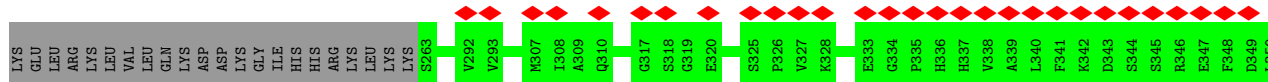


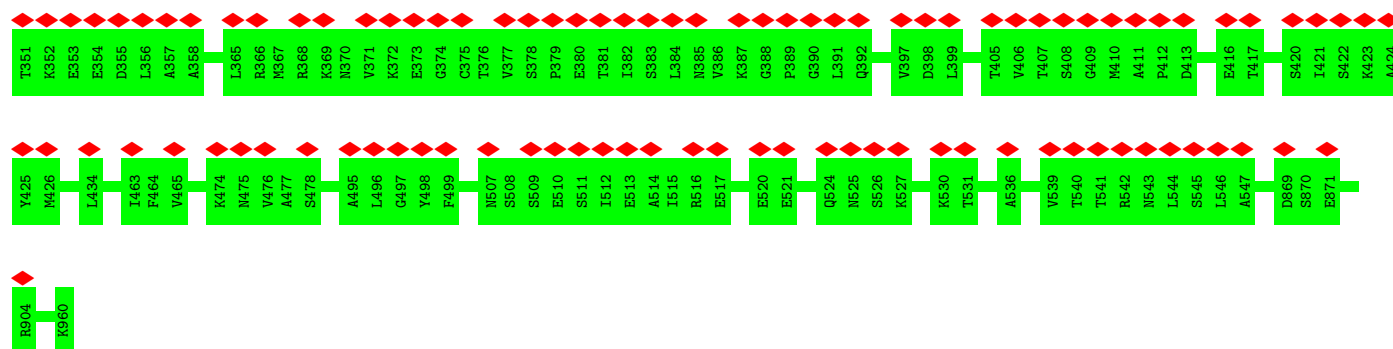
• Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



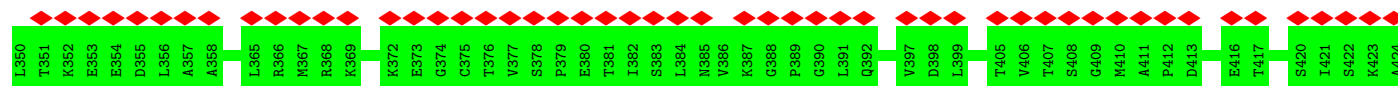
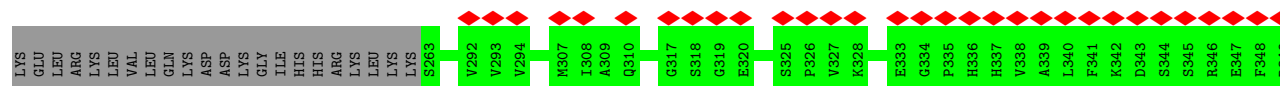
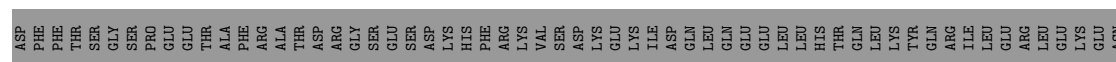
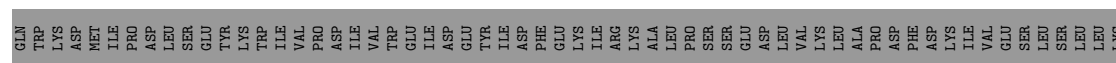
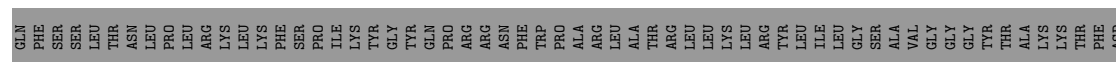
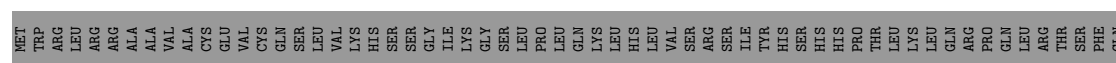
• Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



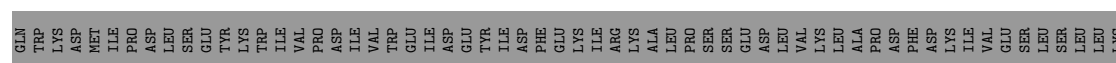
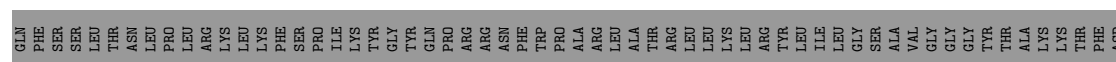
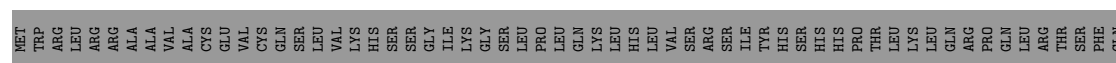
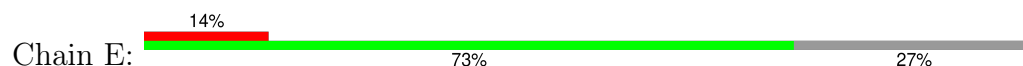


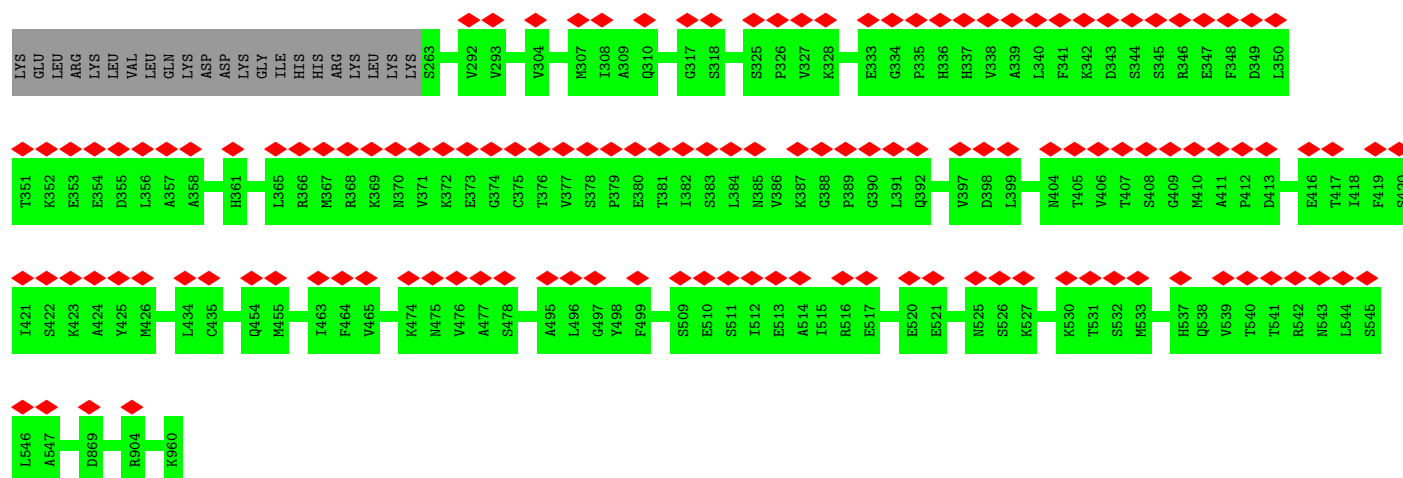


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



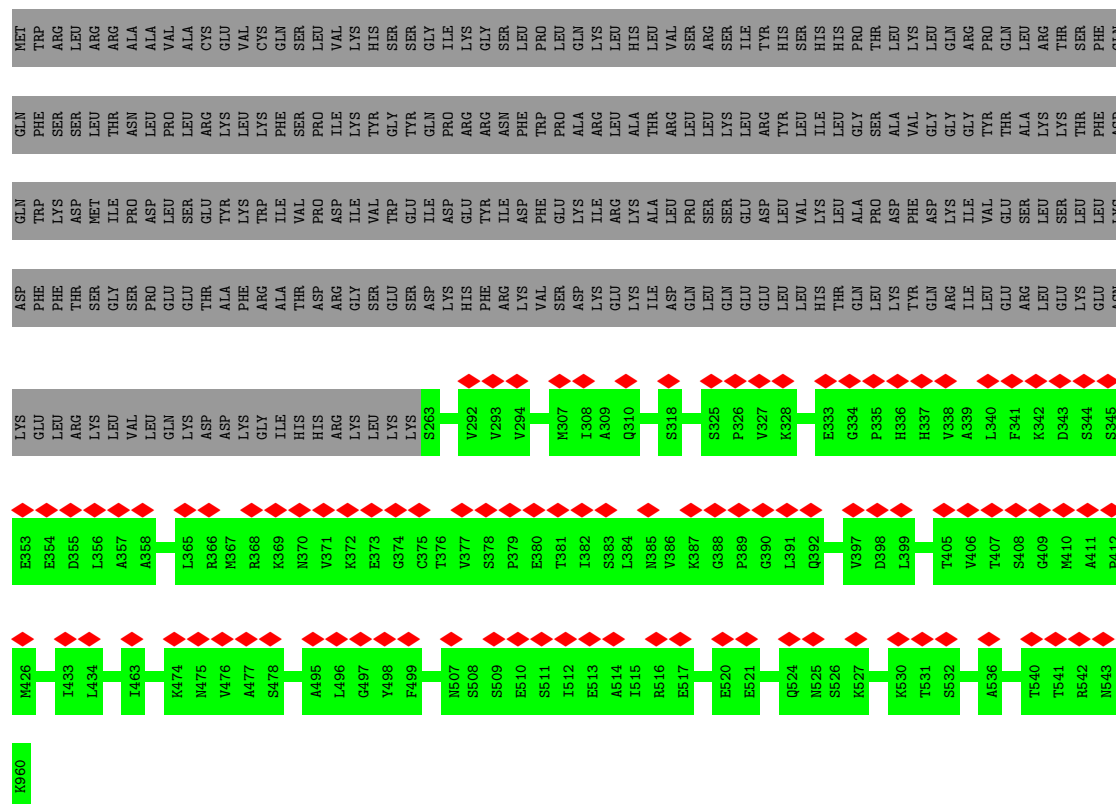
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial





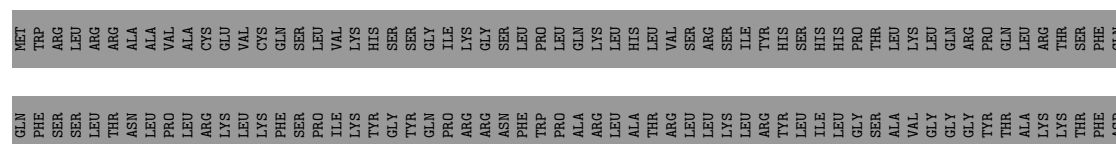
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

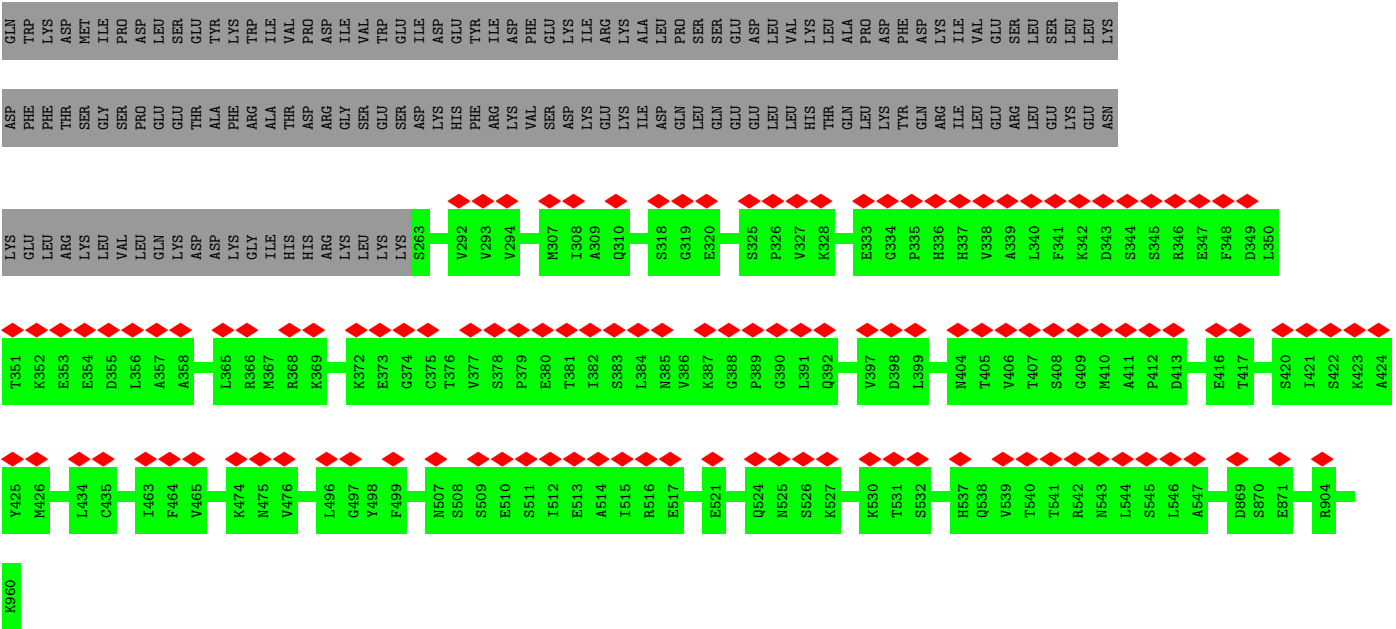
Chain e: 13% 73% 27%



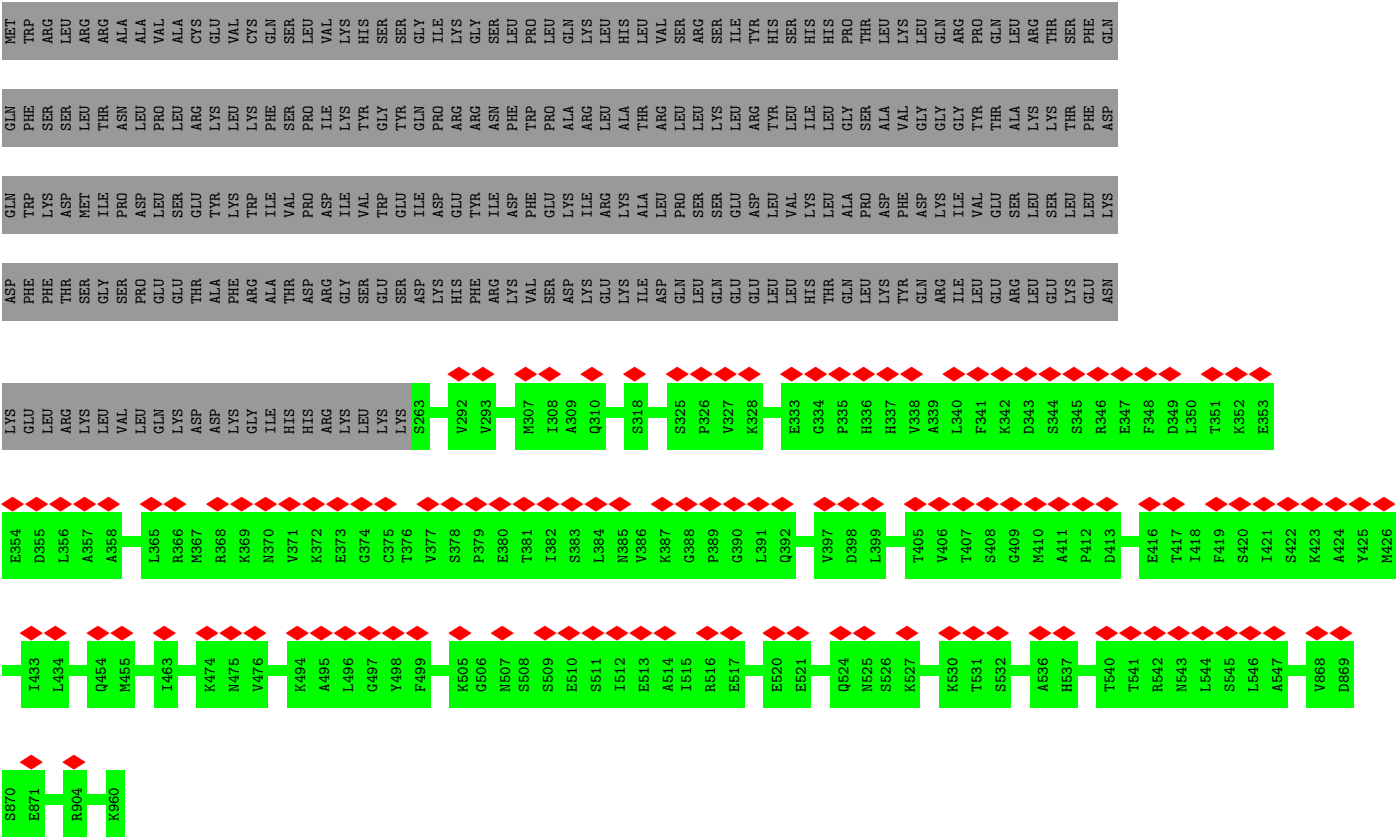
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

Chain F: 13% 73% 27%



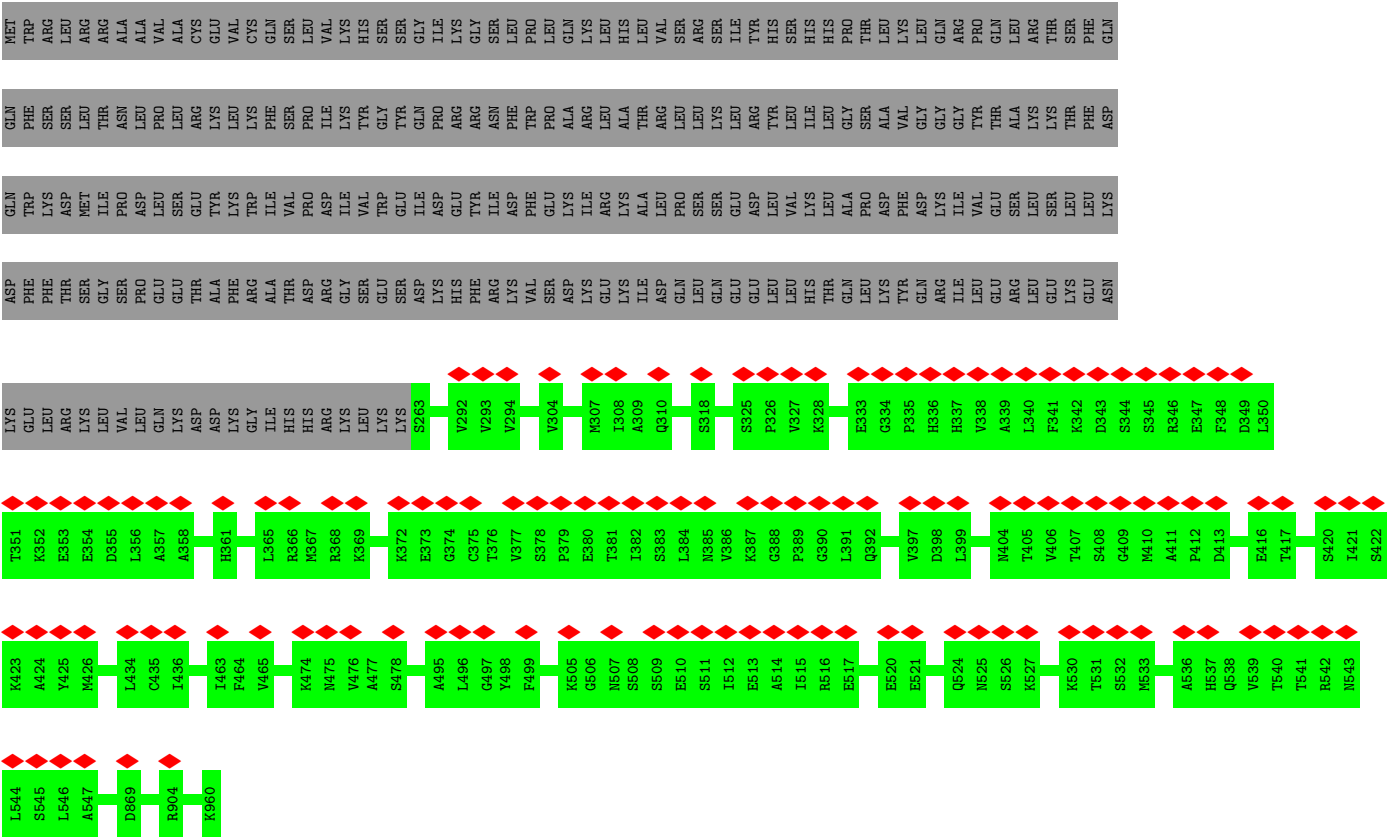


• Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



• Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

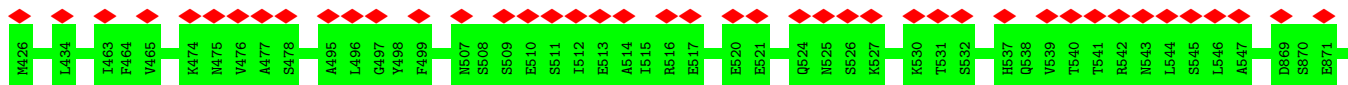
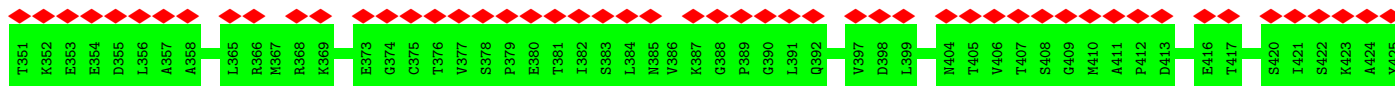
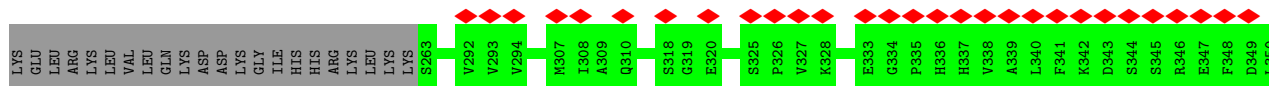
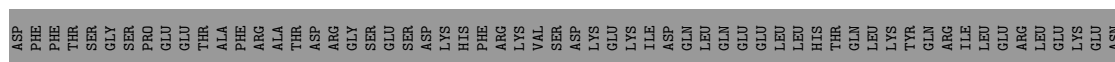
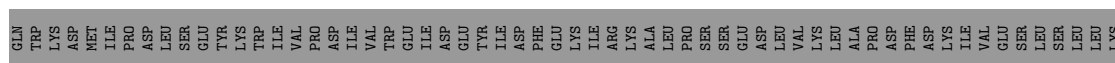
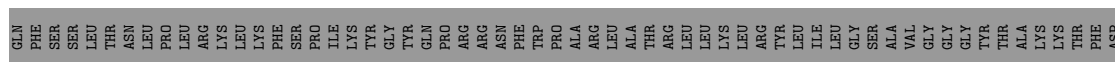
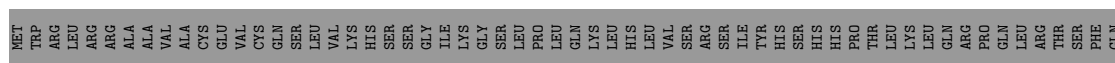




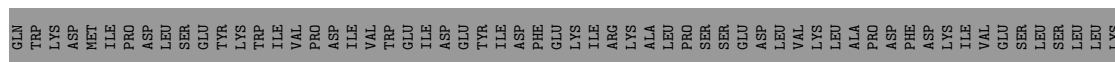
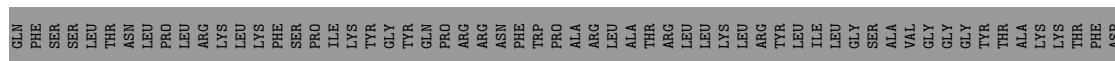
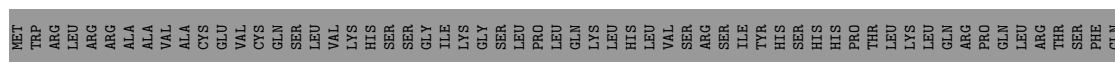
● Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

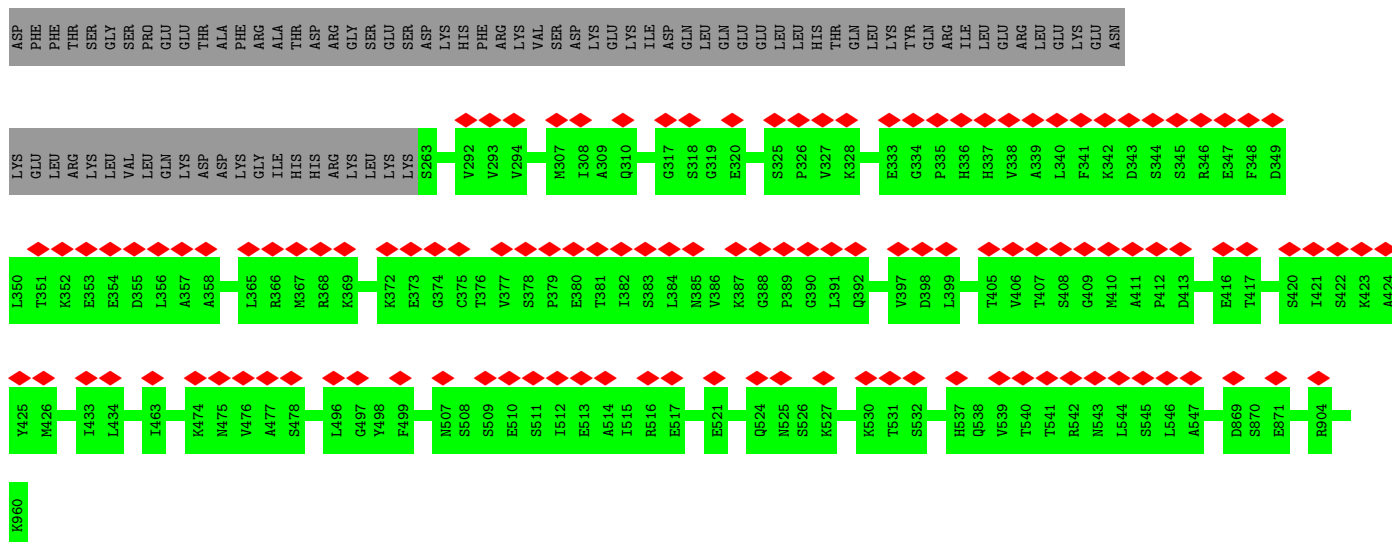


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

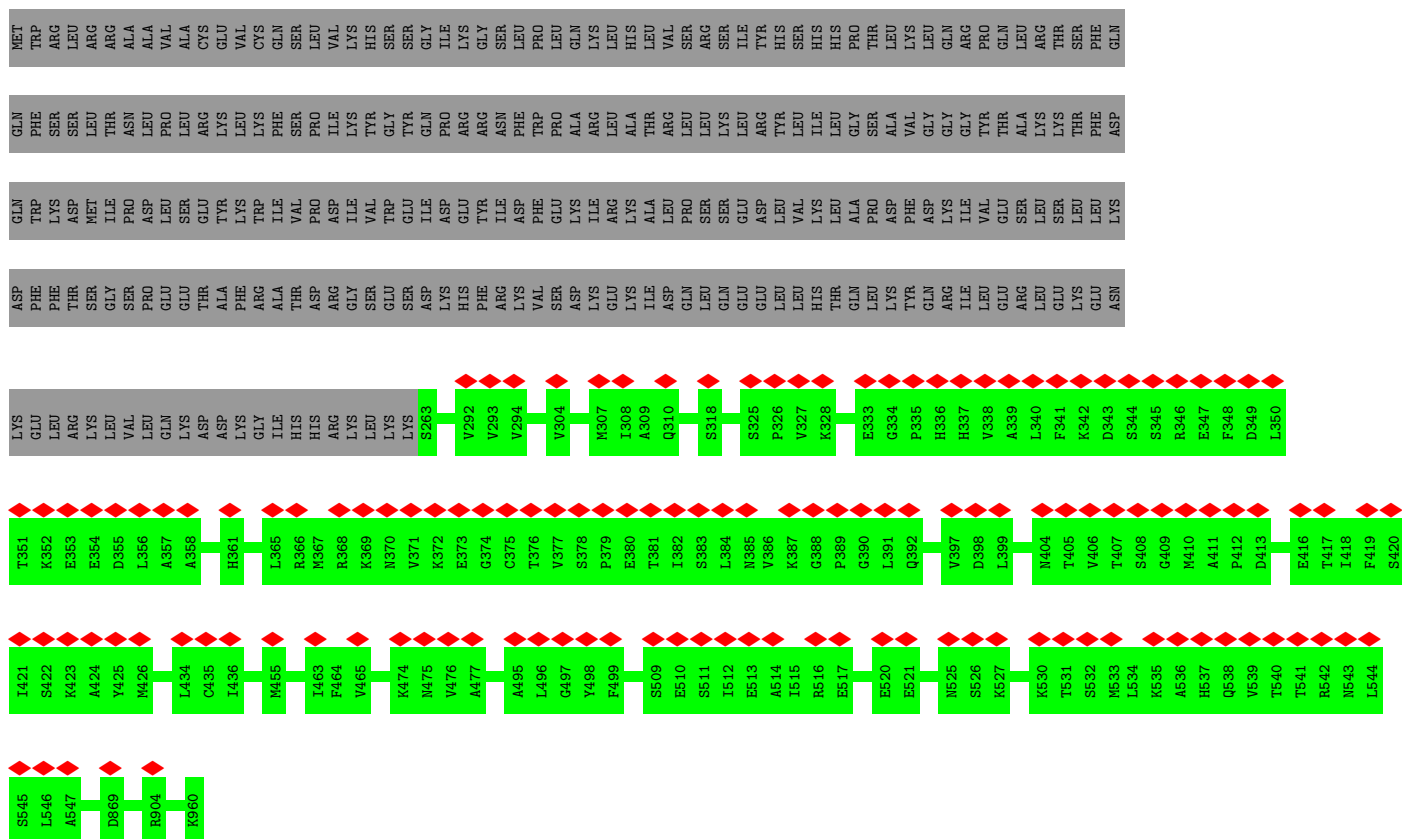


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

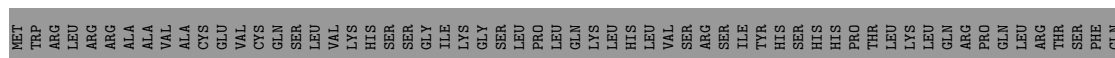


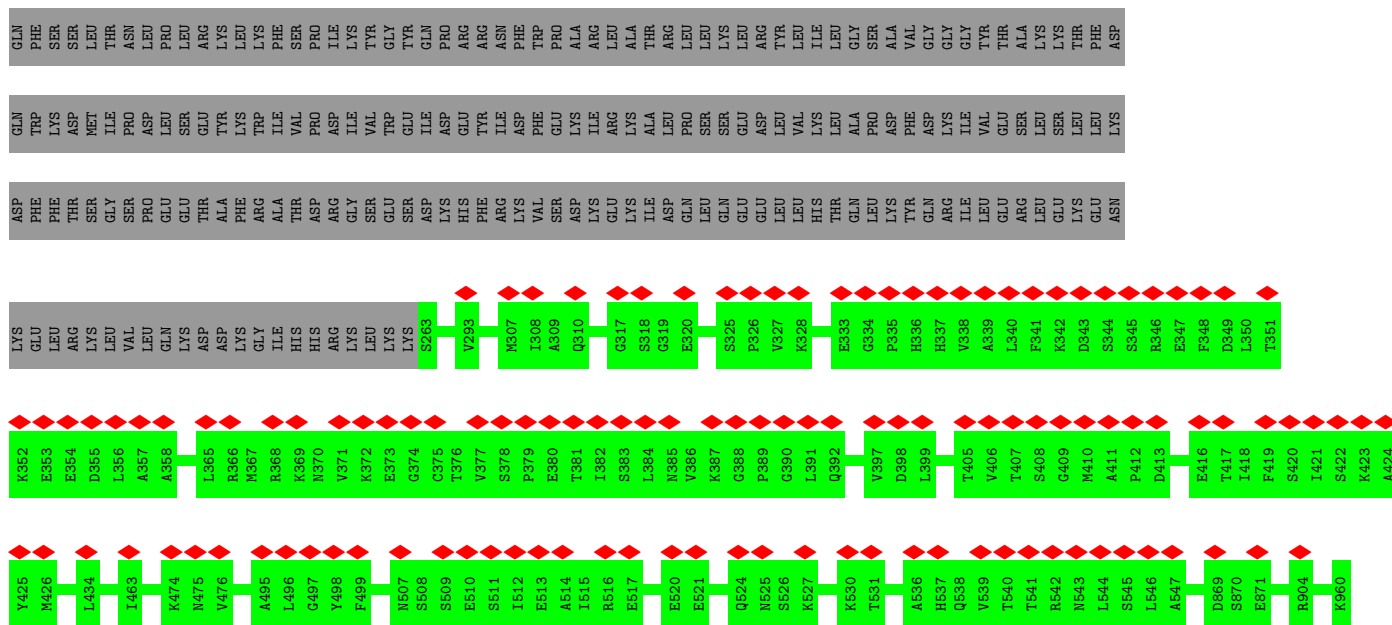


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

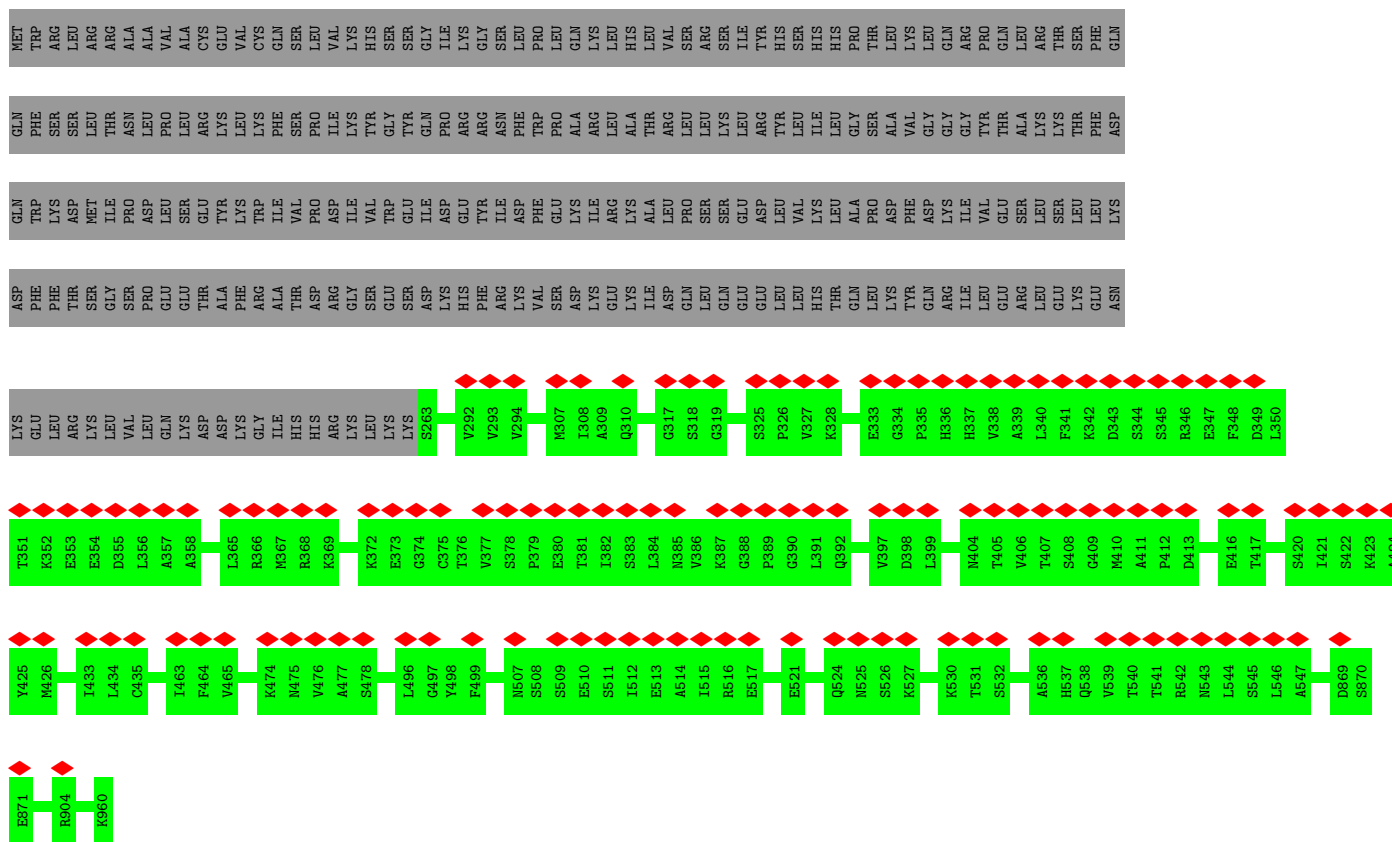


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial





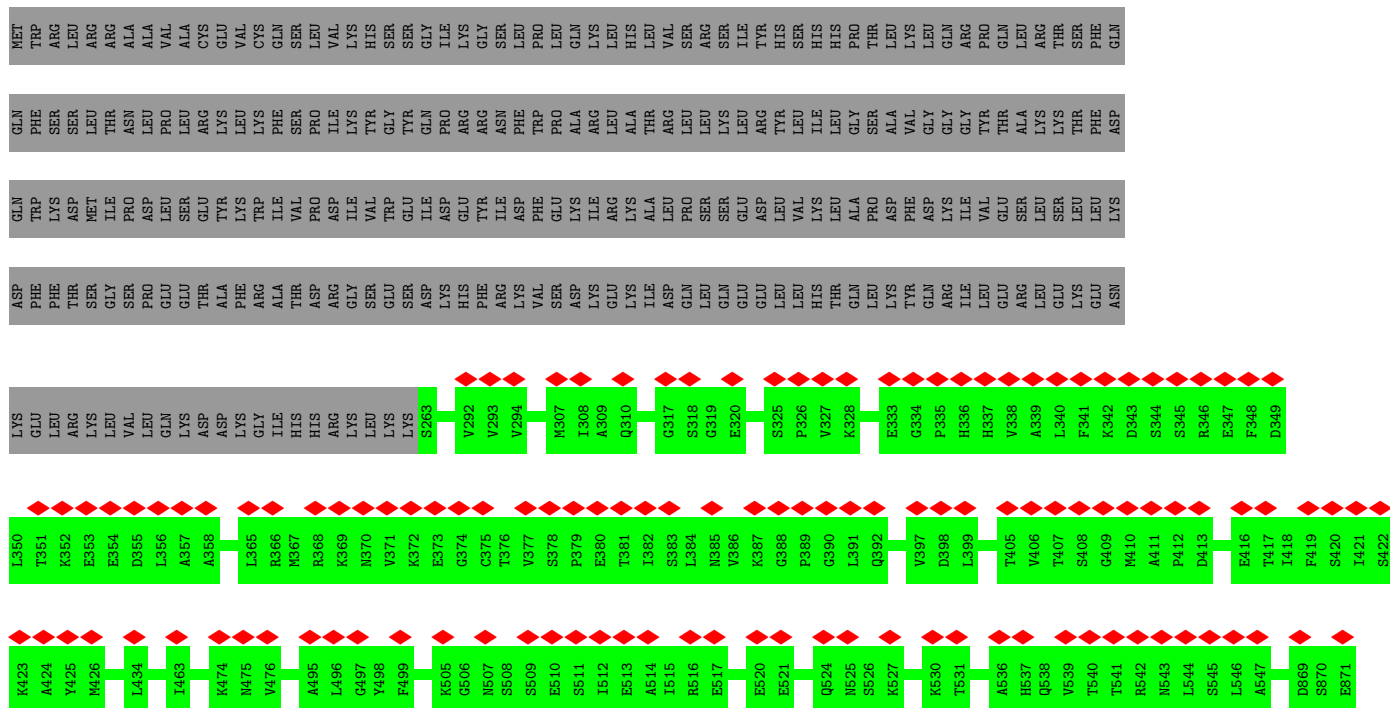
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial





- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

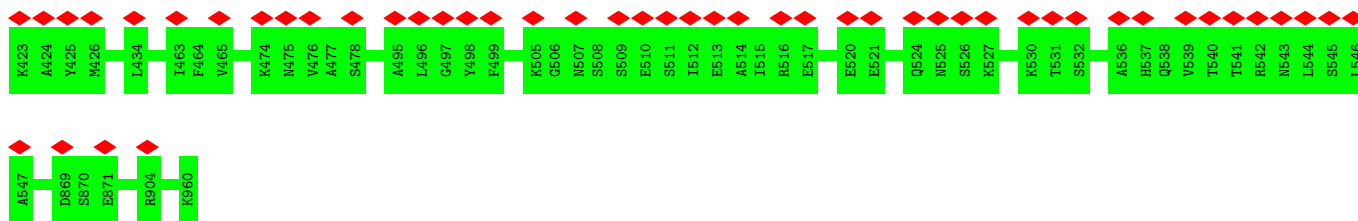
Chain P: 13% 73% 27%

MET	TRP	ARG	LEU	ARG	ARG	ALA	ALA	CYS	VAL	VAL	CYS	GLN	SER	PRO	LEU	VAL	LEU	HIS	SER	GLY	ILE	LYS	GLY	LEU	LEU	GLN	LYS	ARG	LEU	ILE	TYR	HIS	HIS	PRO	THR	LEU	VAL	LEU	GLN	PRO	ARG	THR	LEU	LEU	GLN	ASP							
GLN	PHE	SER	SER	LEU	THR	ASN	LEU	PRO	LEU	ARG	LYS	LYS	PHE	SER	PRO	ILE	LYS	TYR	ASN	PHE	TRP	GLN	ARG	ARG	PRO	ALA	ARG	LEU	LEU	LEU	TYR	ILE	LYS	LEU	GLY	SER	ALA	VAL	GLY	GLY	GLN	ARG	PRO	GLN	THR	PHE	ASP						
GLN	TRP	LYS	ASP	MET	ASP	PRO	LEU	GLU	SER	TYR	TRP	ASP	ILE	VAL	ASP	ASP	ILE	VAL	TRP	GLY	ASP	GLY	ASP	GLY	ASP	ASP	GLY	GLN	PRO	PRO	GLU	ASP	VAL	LYS	GLY	PHE	ASP	GLY	ASP	GLY	GLY	GLN	VAL	GLY	GLY	GLY	GLY	GLN					
ASP	PHE	PHE	THR	SER	GLY	SER	PRO	GLU	THR	ALA	ARG	ALA	ARG	THR	ASP	ARG	GLY	SER	GLU	GLY	ASP	LYS	HIS	PHE	VAL	VAL	GLN	GLY	ASP	LYS	ASP	GLY	LEU	HIS	THR	GLN	LEU	LEU	LYS	TYR	GLN	ARG	ILE	LEU	GLU	GLY	ASP						
LYS	GLU	ARG	LYS	LEU	LYS	VAL	LEU	GLN	LYS	ASP	ASP	ASP	LYS	HIS	ARG	ARG	LYS	LEU	LYS	LYS	S263	V292	V293	V294	M307	I308	A309	Q310	S318	G319	E320	S325	P326	V327	K328	E333	G334	P335	H336	H337	V338	A339	L340	F341	K342	D343	S344	S345	R346	E347	F348	D349	L350
T351	K352	E353	E354	D355	L356	A357	A358	L365	R366	K367	K368	K369	K372	E373	G374	C375	T376	V377	S378	P379	E380	T381	I382	S383	L384	N385	V386	K387	G388	P389	G390	L391	Q392	V397	D398	L399	T405	V406	T407	S408	G409	M410	A411	D343	S344	S345	R346	E347	F348	D349	L350		
M426	L434	C435	I463	F464	V465	K474	M475	V476	L496	C497	Y498	F499	M507	S508	S509	E510	S511	I512	E513	A514	I515	R516	E517	E521	Q524	M525	S526	K527	K530	T531	S532	H537	Q538	V539	T540	T541	R542	M543	L544	S545	L546	A547	D869	S870	E871	R904	K960						

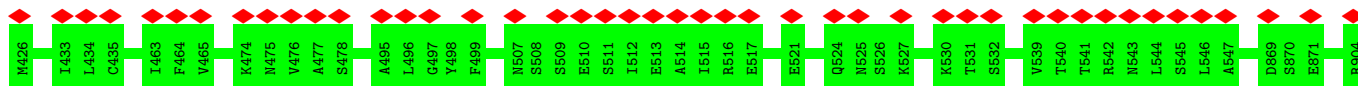
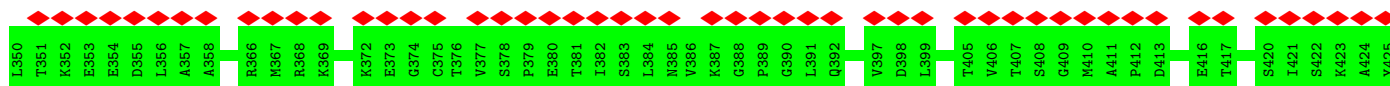
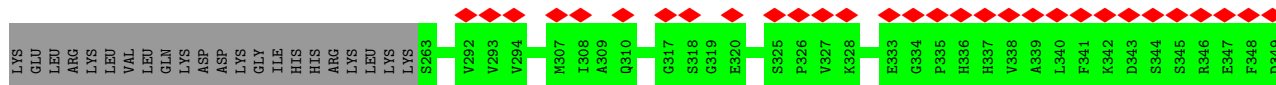
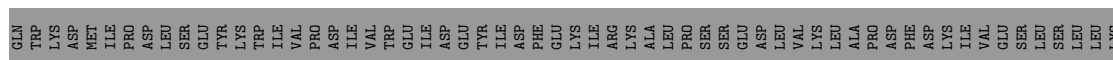
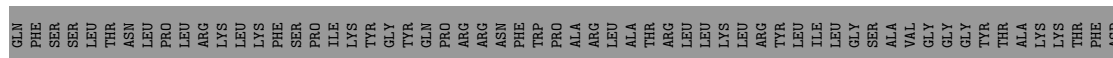
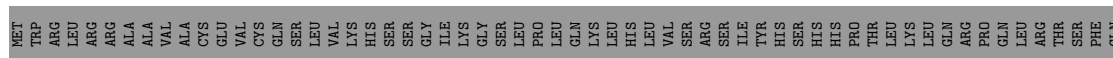
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

Chain Q: 14% 73% 27%

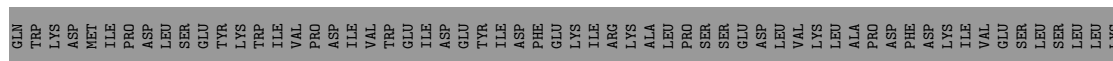
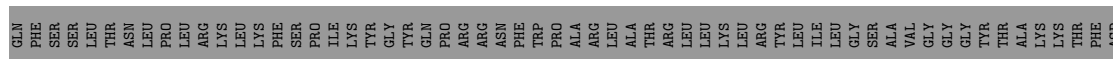
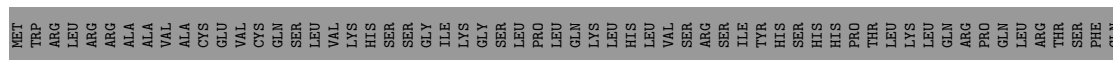
T351	K352	E353	E354	D355	L356	A357	A358	L365	R366	K367	K368	K369	N370	V371	K372	E373	G374	C375	T376	V377	S378	P379	E380	T381	I382	S383	L384	N385	V386	K387	G388	P389	G390	L391	Q392	V397	D398	L399	N404	T405	V406	T407	S408	
LYS	GLU	ARG	LYS	VAL	GLN	LYS	ASP	ASP	LYS	GLY	HIS	HIS	LYS	LEU	LYS	LYS	S263	V292	V293	V294	M307	I308	A309	Q310	S318	G319	E320	S325	P326	V327	K328	E333	G334	P335	H336	H337	V338	A339	L340	F341	K342	D343		
ASP	PHE	THR	SER	GLY	PRO	GLU	THR	ALA	PHE	ARG	THR	ASP	ARG	GLY	GLU	SER	ASP	LYS	PHE	ARG	VAL	SER	ASP	GLU	ILE	ASP	GLN	LEU	LEU	GLU	GLU	LEU	LYS	TYR	GLN	ARG	ILE	VAL	GLU	LEU	GLY	GLY	THR	PHE
GLN	TRP	ASP	MET	ILE	PRO	LEU	SER	TYR	LYS	TRP	VAL	PRO	ASP	ILE	LYS	VAL	GLU	ASP	GLY	TYR	ARG	ASN	PHE	TRP	PRO	ALA	ARG	LEU	LYS	LEU	LEU	GLY	PRO	THR	LEU	ASP	PHE	VAL	GLY	GLY	THR	GLN	PRO	
MET	TRP	ARG	LEU	ARG	ALA	VAL	ALA	CYS	GLU	VAL	LEU	VAL	GLN	HIS	SER	SER	GLY	ILE	ASP	GLU	PHE	GLU	LYS	ALA	ALA	LEU	PRO	LEU	VAL	LYS	LEU	ASP	THR	HIS	HIS	THR	PRO	ARG	GLY	GLY	THR	LEU	THR	

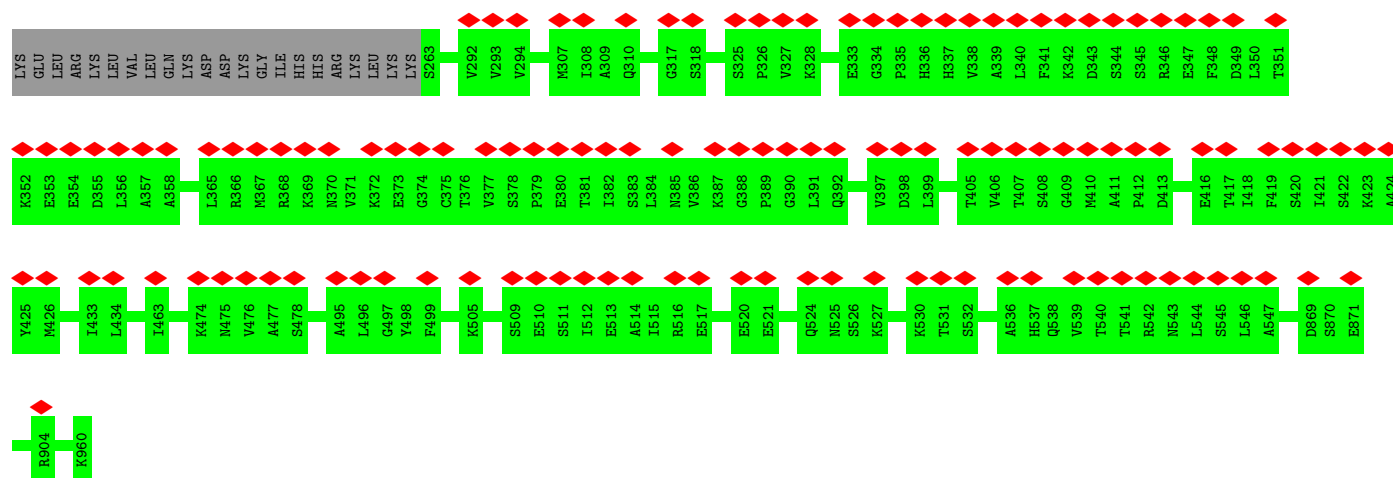


- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial



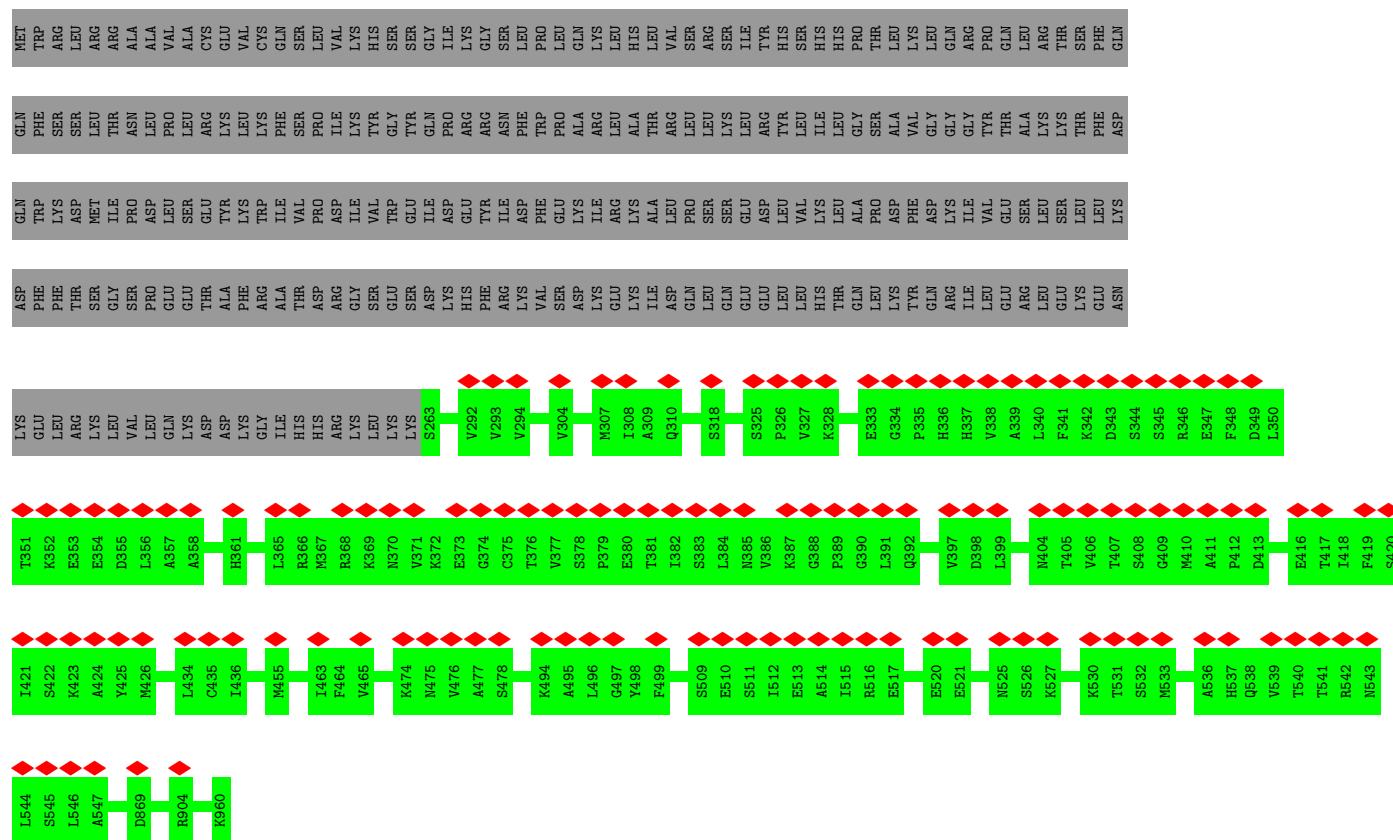
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial





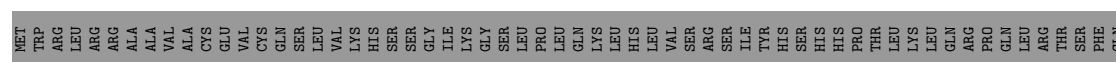
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

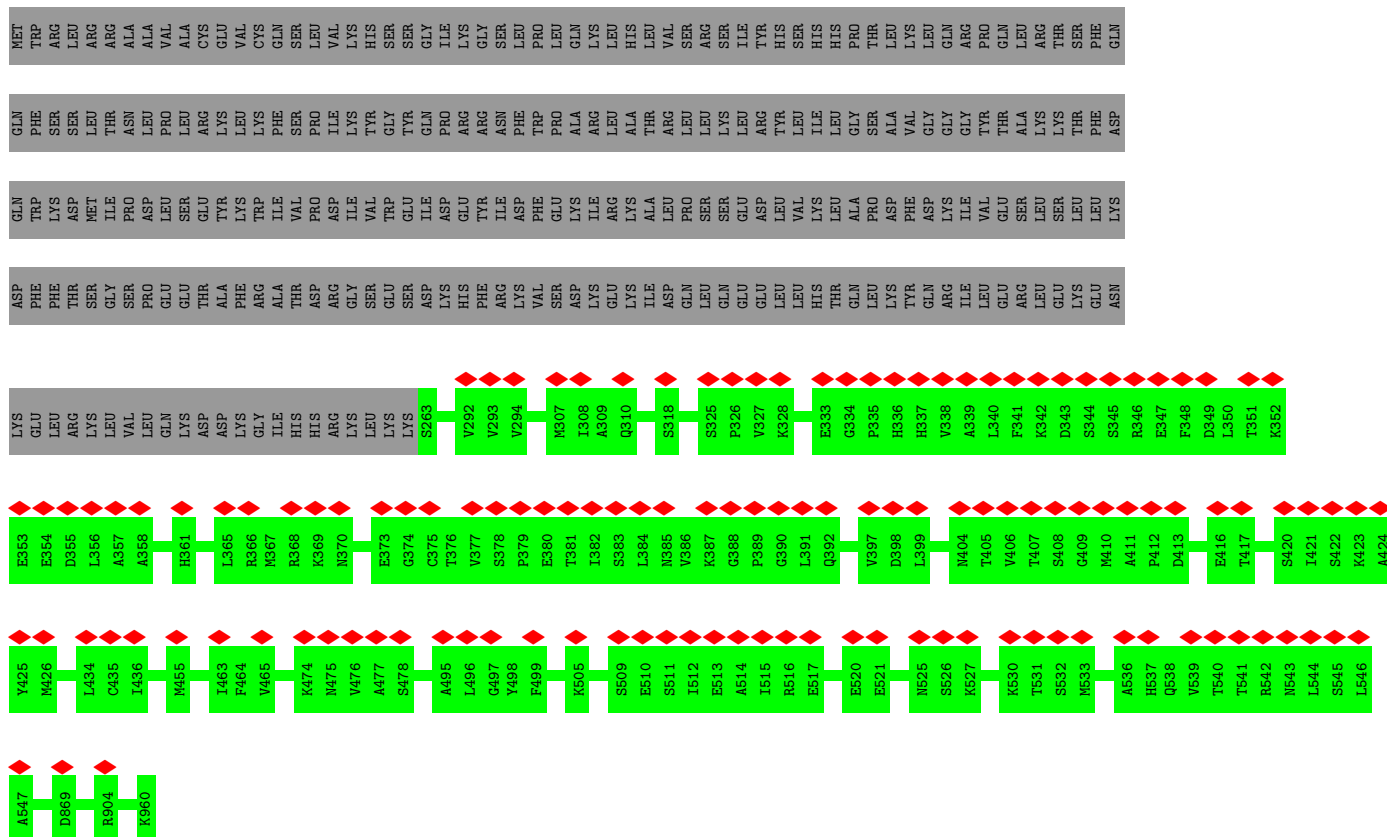
Chain T: 14% 73% 27%




- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

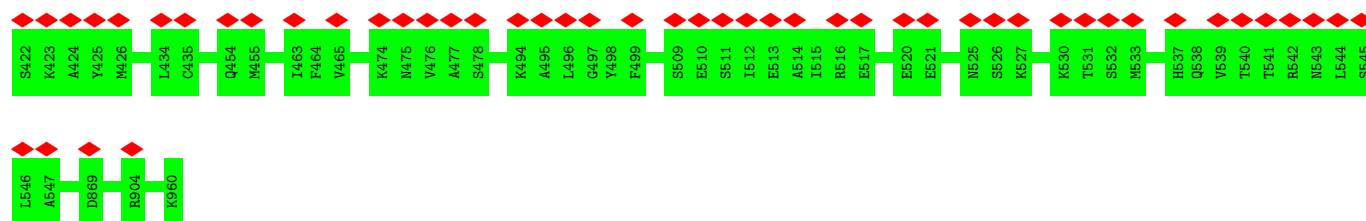
Chain U: 13% 73% 27%





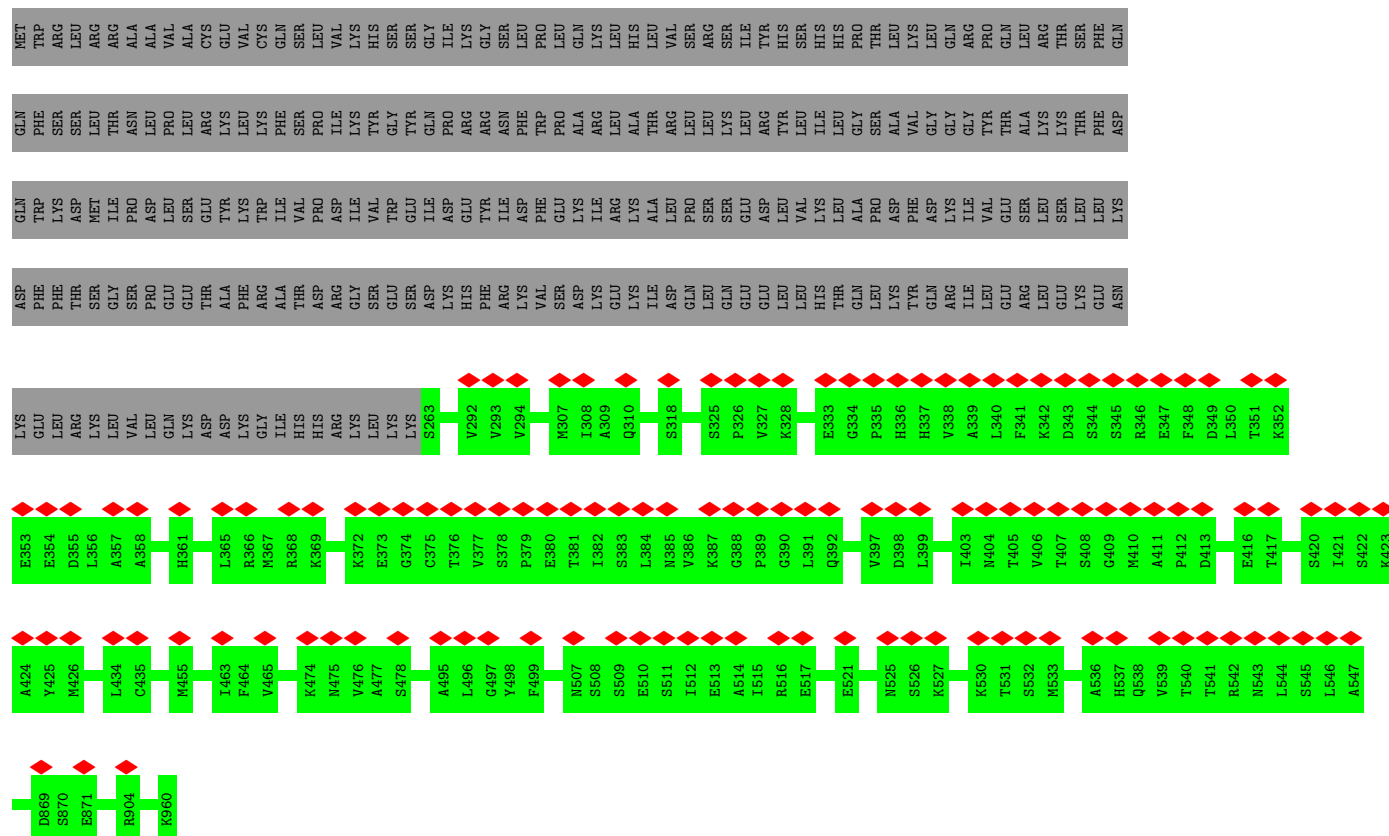
- Chain W: 





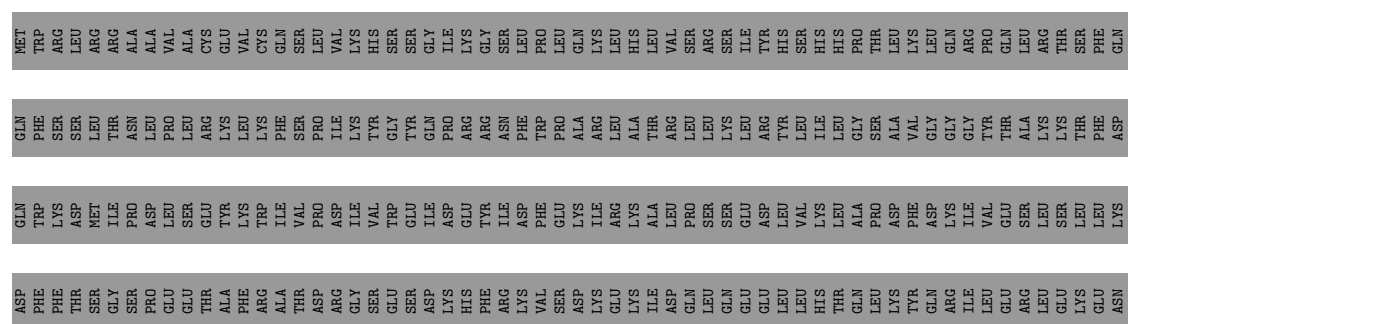
- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

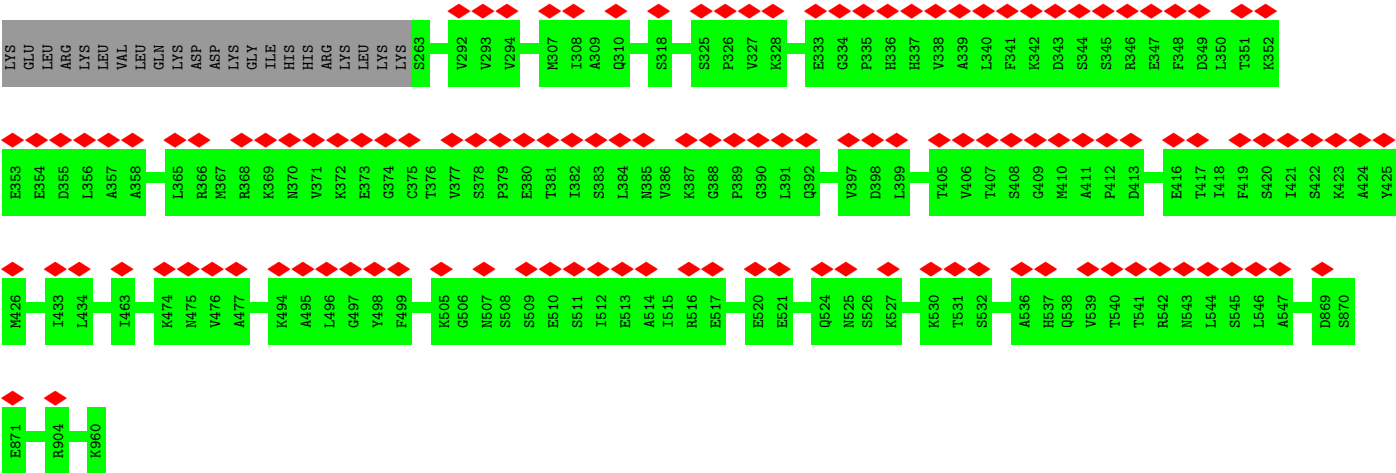
Chain Y: 13% 73% 27%



- Molecule 1: Dynamin-like 120 kDa protein, mitochondrial

Chain Z: 13% 73% 27%





4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=128.634°, rise=7.73 Å, axial sym=C1	Depositor
Number of segments used	139018	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 ($e^-/\text{Å}^2$)	82	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.023	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0025	Depositor
Map size (Å)	699.72003, 699.72003, 699.72003	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6660001, 1.6660001, 1.6660001	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.23	0/5788	0.42	0/7811
1	B	0.23	0/5788	0.42	0/7811
1	C	0.23	0/5788	0.42	0/7811
1	D	0.23	0/5788	0.42	0/7811
1	E	0.23	0/5788	0.42	0/7811
1	F	0.23	0/5788	0.42	0/7811
1	G	0.23	0/5788	0.42	0/7811
1	H	0.23	0/5788	0.42	0/7811
1	I	0.23	0/5788	0.42	0/7811
1	J	0.23	0/5788	0.42	0/7811
1	K	0.23	0/5788	0.42	0/7811
1	L	0.23	0/5788	0.42	0/7811
1	M	0.23	0/5788	0.42	0/7811
1	N	0.23	0/5788	0.42	0/7811
1	O	0.23	0/5788	0.42	0/7811
1	P	0.23	0/5788	0.42	0/7811
1	Q	0.23	0/5788	0.42	0/7811
1	R	0.23	0/5788	0.42	0/7811
1	S	0.23	0/5788	0.42	0/7811
1	T	0.23	0/5788	0.42	0/7811
1	U	0.23	0/5788	0.42	0/7811
1	V	0.23	0/5788	0.42	0/7811
1	W	0.23	0/5788	0.42	0/7811
1	X	0.23	0/5788	0.42	0/7811
1	Y	0.23	0/5788	0.42	0/7811
1	Z	0.23	0/5788	0.42	0/7811
1	a	0.23	0/5788	0.42	0/7811
1	b	0.23	0/5788	0.42	0/7811
1	c	0.23	0/5788	0.42	0/7811
1	d	0.23	0/5788	0.42	0/7811
1	e	0.23	0/5788	0.42	0/7811
1	f	0.23	0/5788	0.42	0/7811
1	g	0.23	0/5788	0.42	0/7811
1	h	0.23	0/5788	0.42	0/7811

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.23	0/196792	0.42	0/265574

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 [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	B	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	C	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	D	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	E	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	F	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	G	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	H	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	I	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	J	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	K	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	L	696/960 (72%)	693 (100%)	3 (0%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	M	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	N	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	O	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	P	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	Q	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	R	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	S	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	T	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	U	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	V	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	W	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	X	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	Y	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	Z	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	a	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	b	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	c	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	d	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	e	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	f	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	g	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
1	h	696/960 (72%)	693 (100%)	3 (0%)	0	100	100
All	All	23664/32640 (72%)	23562 (100%)	102 (0%)	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	633/874 (72%)	633 (100%)	0	100	100
1	B	633/874 (72%)	633 (100%)	0	100	100
1	C	633/874 (72%)	633 (100%)	0	100	100
1	D	633/874 (72%)	633 (100%)	0	100	100
1	E	633/874 (72%)	633 (100%)	0	100	100
1	F	633/874 (72%)	633 (100%)	0	100	100
1	G	633/874 (72%)	633 (100%)	0	100	100
1	H	633/874 (72%)	633 (100%)	0	100	100
1	I	633/874 (72%)	633 (100%)	0	100	100
1	J	633/874 (72%)	633 (100%)	0	100	100
1	K	633/874 (72%)	633 (100%)	0	100	100
1	L	633/874 (72%)	633 (100%)	0	100	100
1	M	633/874 (72%)	633 (100%)	0	100	100
1	N	633/874 (72%)	633 (100%)	0	100	100
1	O	633/874 (72%)	633 (100%)	0	100	100
1	P	633/874 (72%)	633 (100%)	0	100	100
1	Q	633/874 (72%)	633 (100%)	0	100	100
1	R	633/874 (72%)	633 (100%)	0	100	100
1	S	633/874 (72%)	633 (100%)	0	100	100
1	T	633/874 (72%)	633 (100%)	0	100	100
1	U	633/874 (72%)	633 (100%)	0	100	100
1	V	633/874 (72%)	633 (100%)	0	100	100
1	W	633/874 (72%)	633 (100%)	0	100	100
1	X	633/874 (72%)	633 (100%)	0	100	100
1	Y	633/874 (72%)	633 (100%)	0	100	100
1	Z	633/874 (72%)	633 (100%)	0	100	100
1	a	633/874 (72%)	633 (100%)	0	100	100
1	b	633/874 (72%)	633 (100%)	0	100	100
1	c	633/874 (72%)	633 (100%)	0	100	100
1	d	633/874 (72%)	633 (100%)	0	100	100
1	e	633/874 (72%)	633 (100%)	0	100	100
1	f	633/874 (72%)	633 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	g	633/874 (72%)	633 (100%)	0	100	100
1	h	633/874 (72%)	633 (100%)	0	100	100
All	All	21522/29716 (72%)	21522 (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. There are no such sidechains identified.

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.

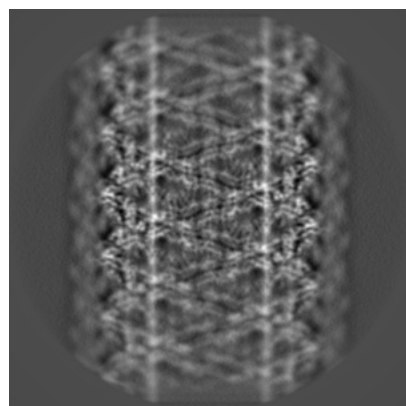
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26977. These allow visual inspection of the internal detail of the map and identification of artifacts.

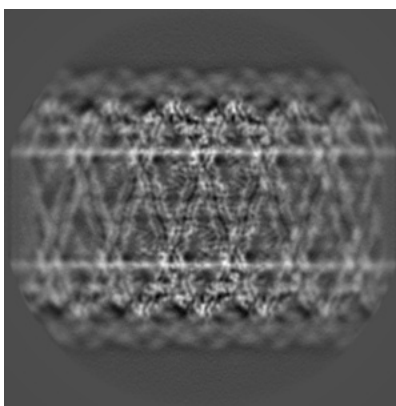
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

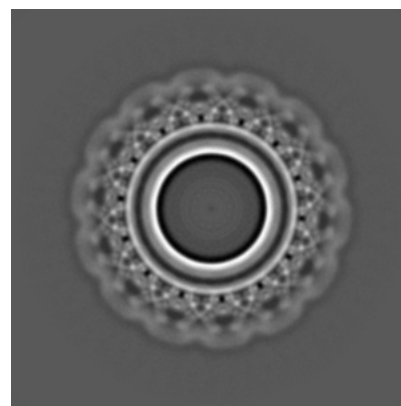
6.1.1 Primary map



X

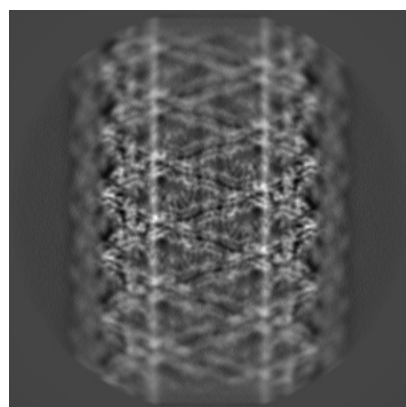


Y

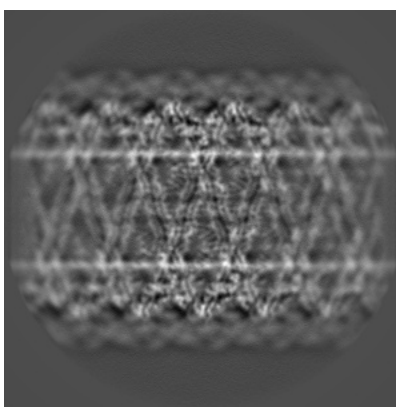


Z

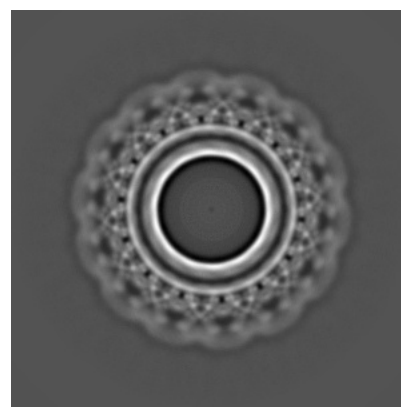
6.1.2 Raw map



X



Y

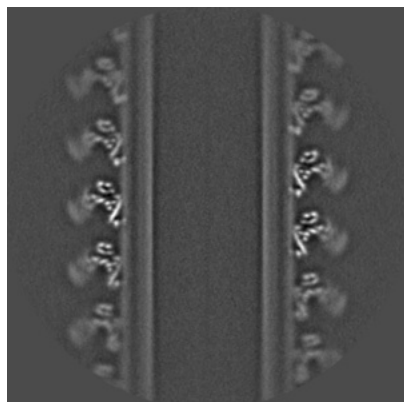


Z

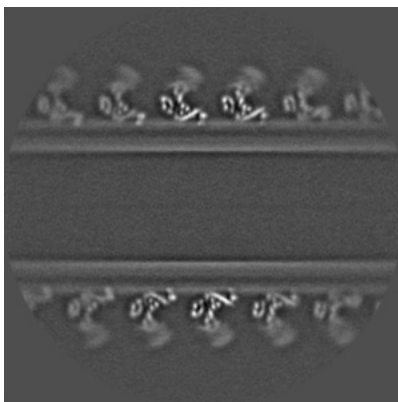
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

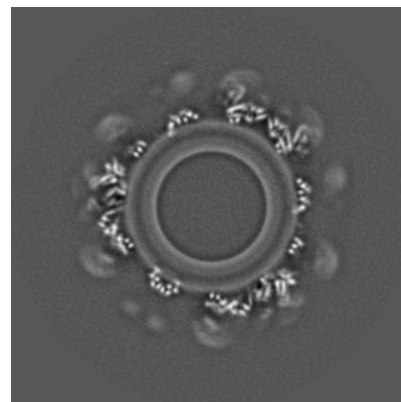
6.2.1 Primary map



X Index: 210

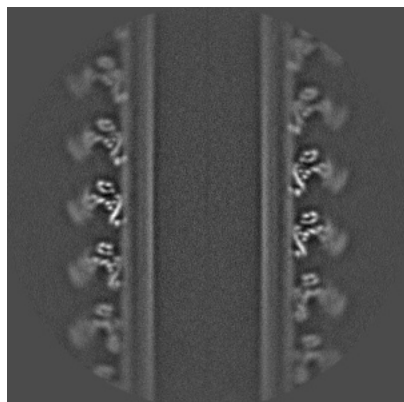


Y Index: 210

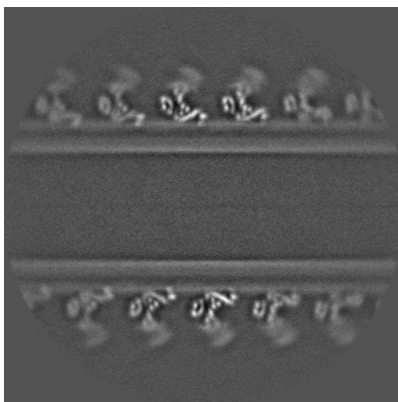


Z Index: 210

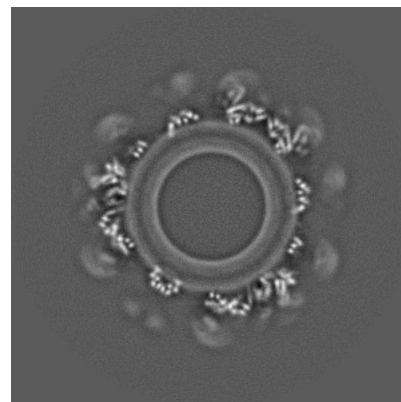
6.2.2 Raw map



X Index: 210



Y Index: 210

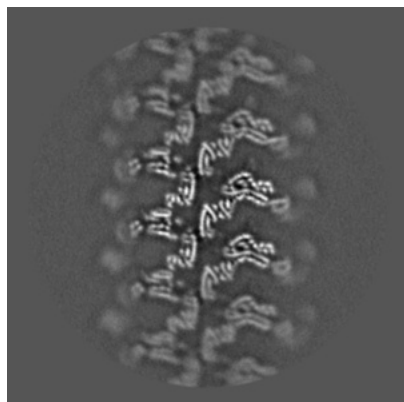


Z Index: 210

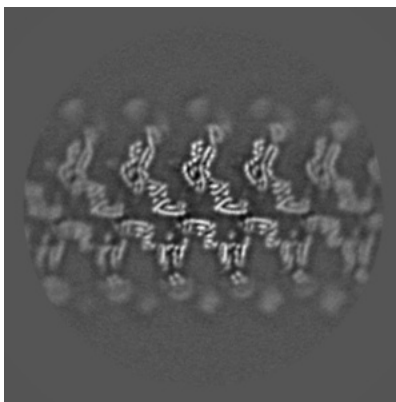
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

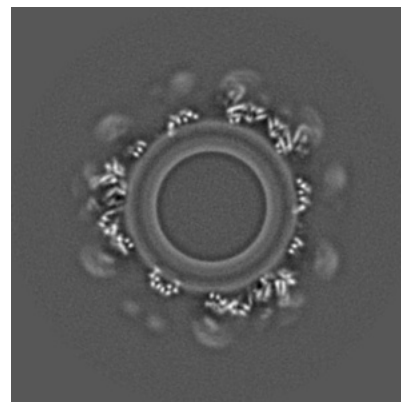
6.3.1 Primary map



X Index: 305

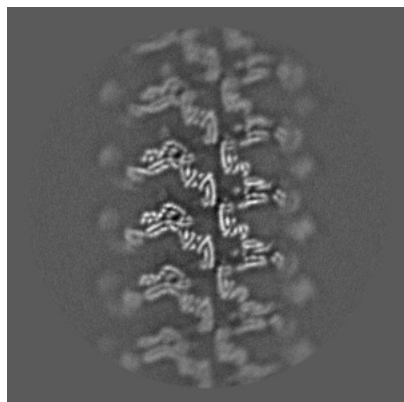


Y Index: 305

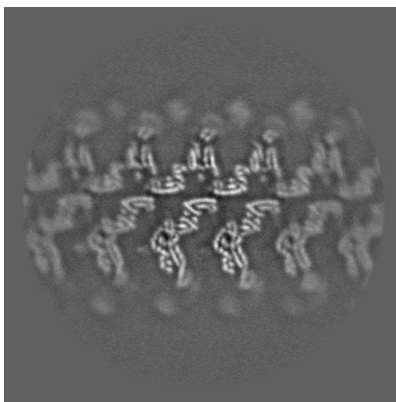


Z Index: 210

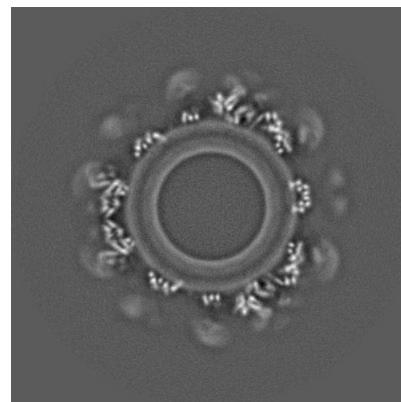
6.3.2 Raw map



X Index: 116



Y Index: 116

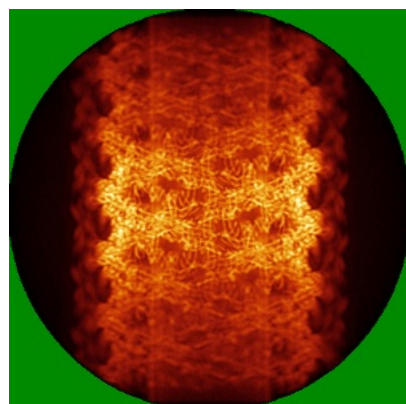


Z Index: 205

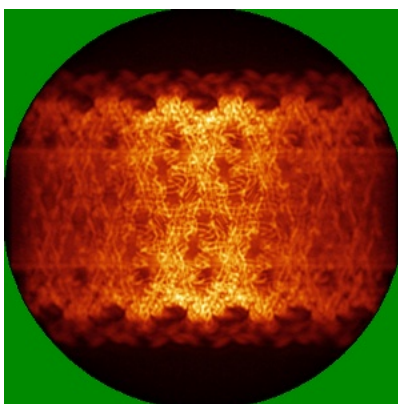
The images above show the largest variance slices of the map in three orthogonal directions.

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

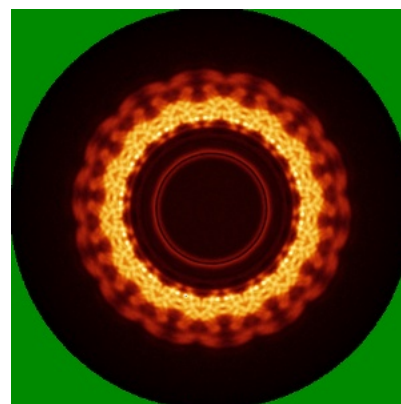
6.4.1 Primary map



X

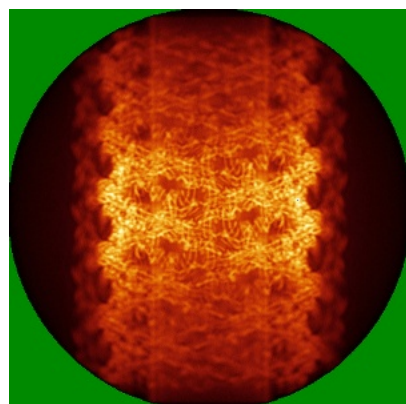


Y

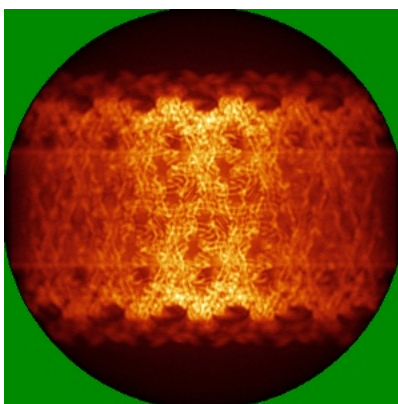


Z

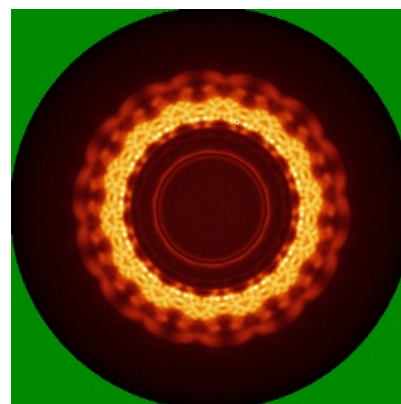
6.4.2 Raw map



X



Y

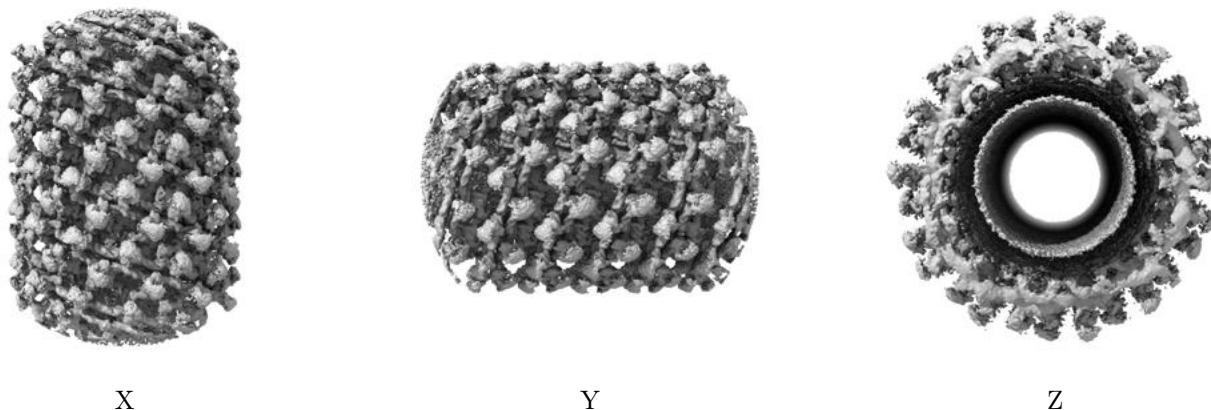


Z

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.

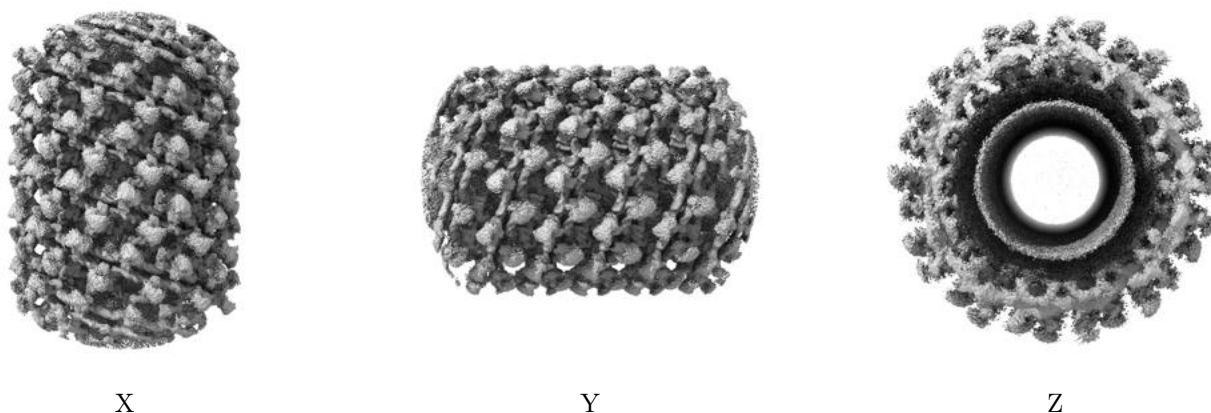
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0025. 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.

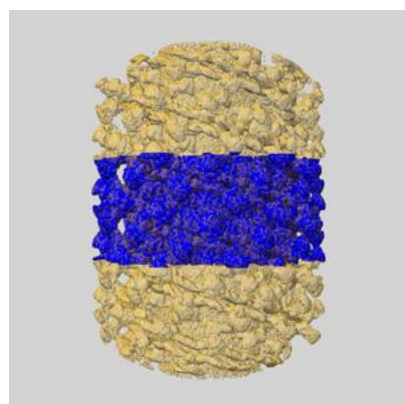
6.6 Mask visualisation [i](#)

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

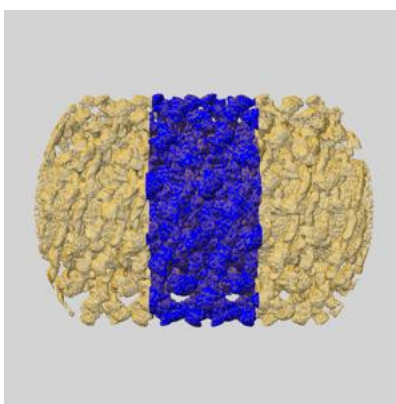
A mask typically either:

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

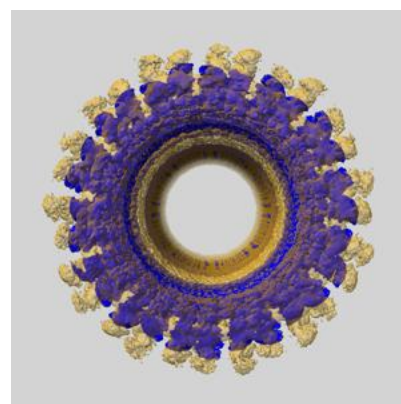
6.6.1 emd_26977_msk_1.map [i](#)



X



Y

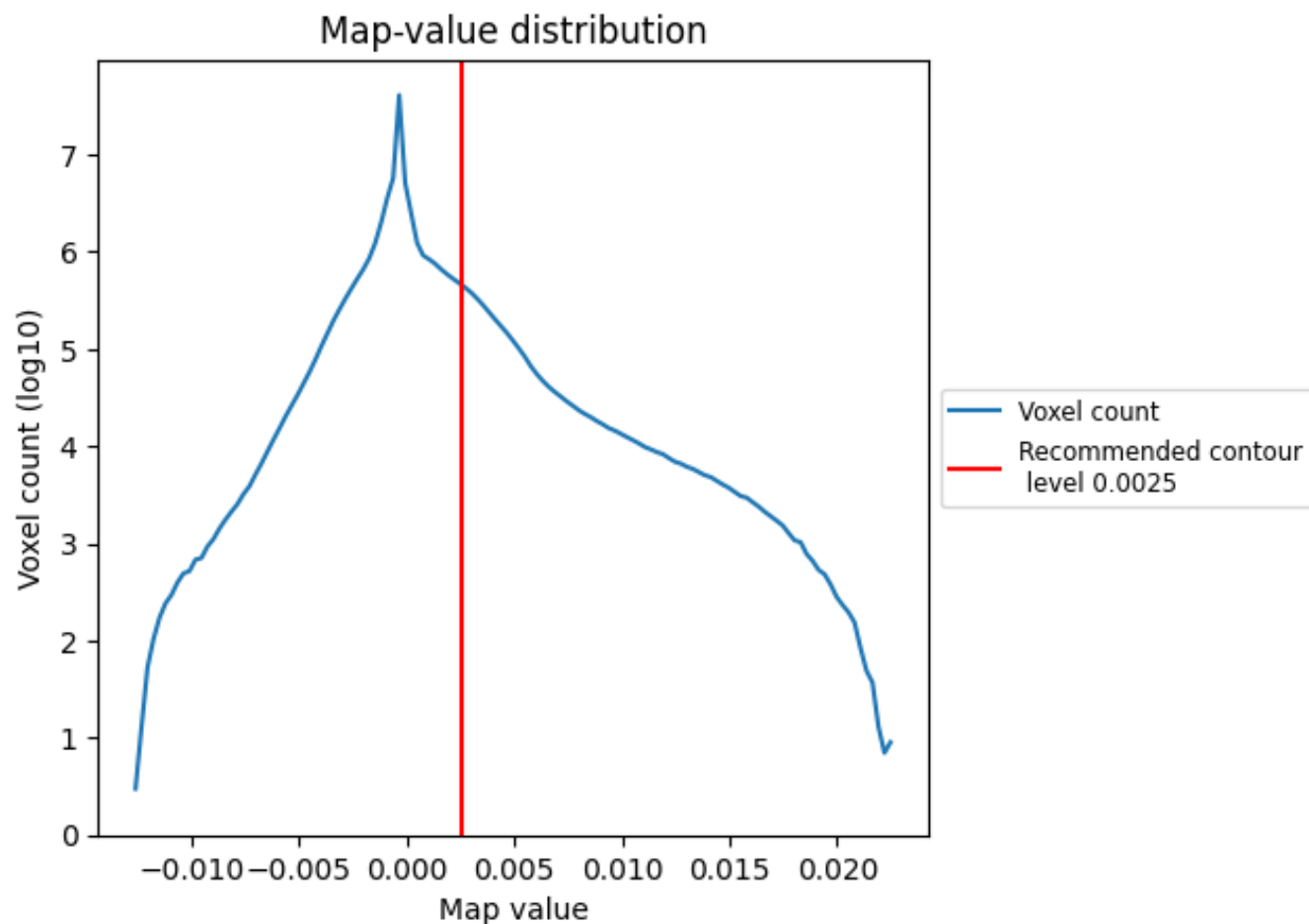


Z

7 Map analysis [i](#)

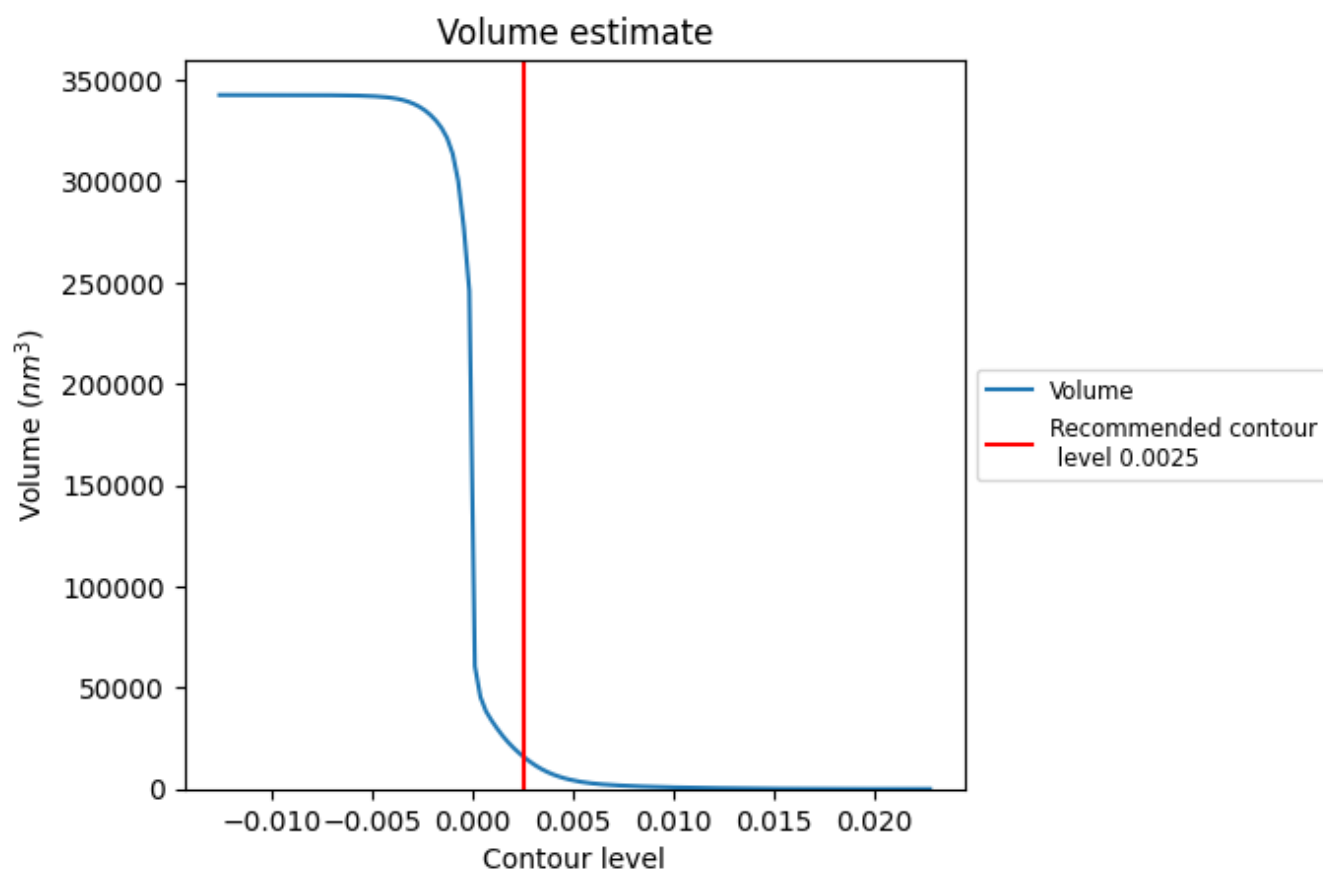
This section contains the results of statistical analysis of the map.

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.

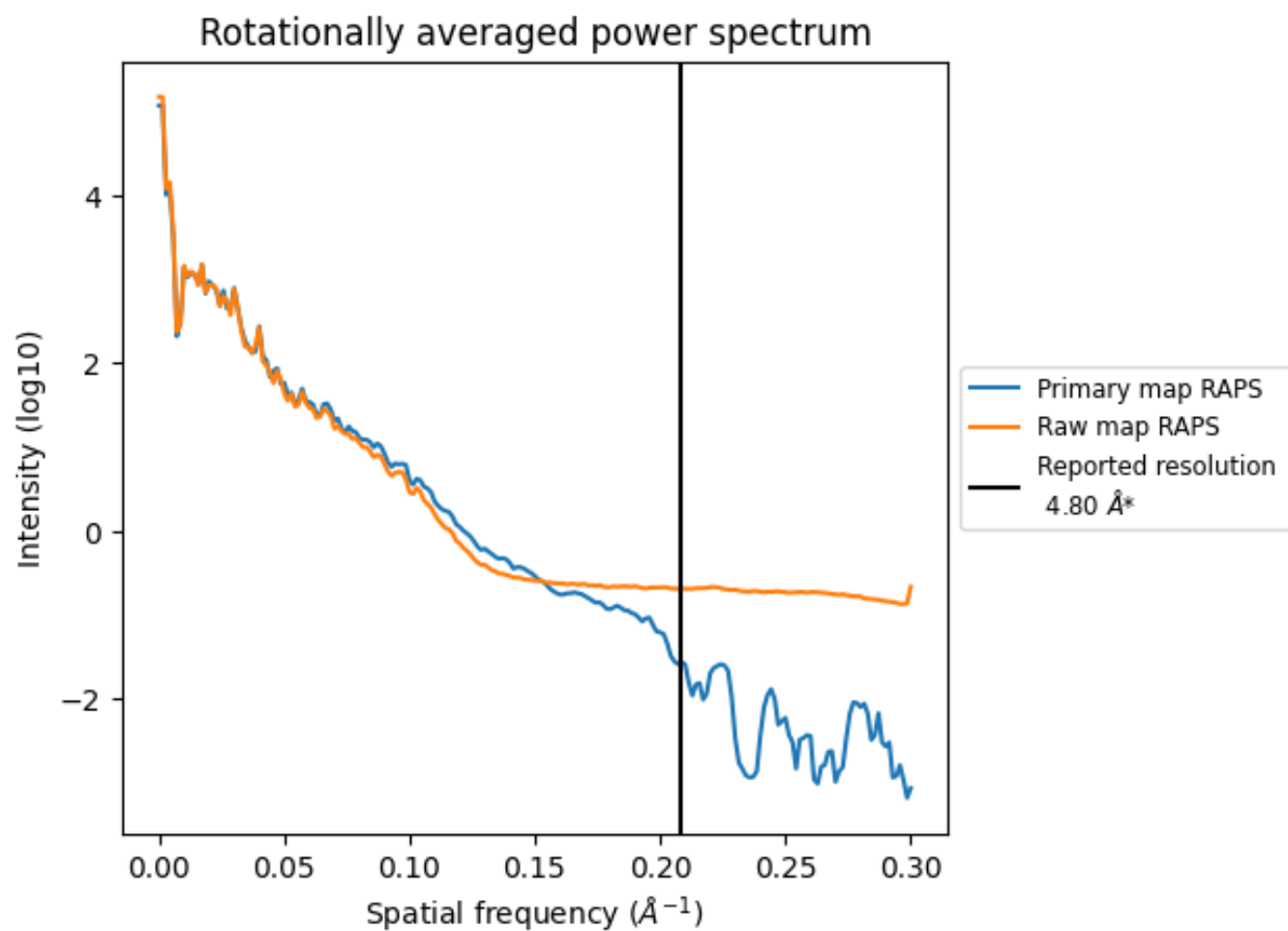
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 16099 nm^3 ; this corresponds to an approximate mass of 14542 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 ⓘ

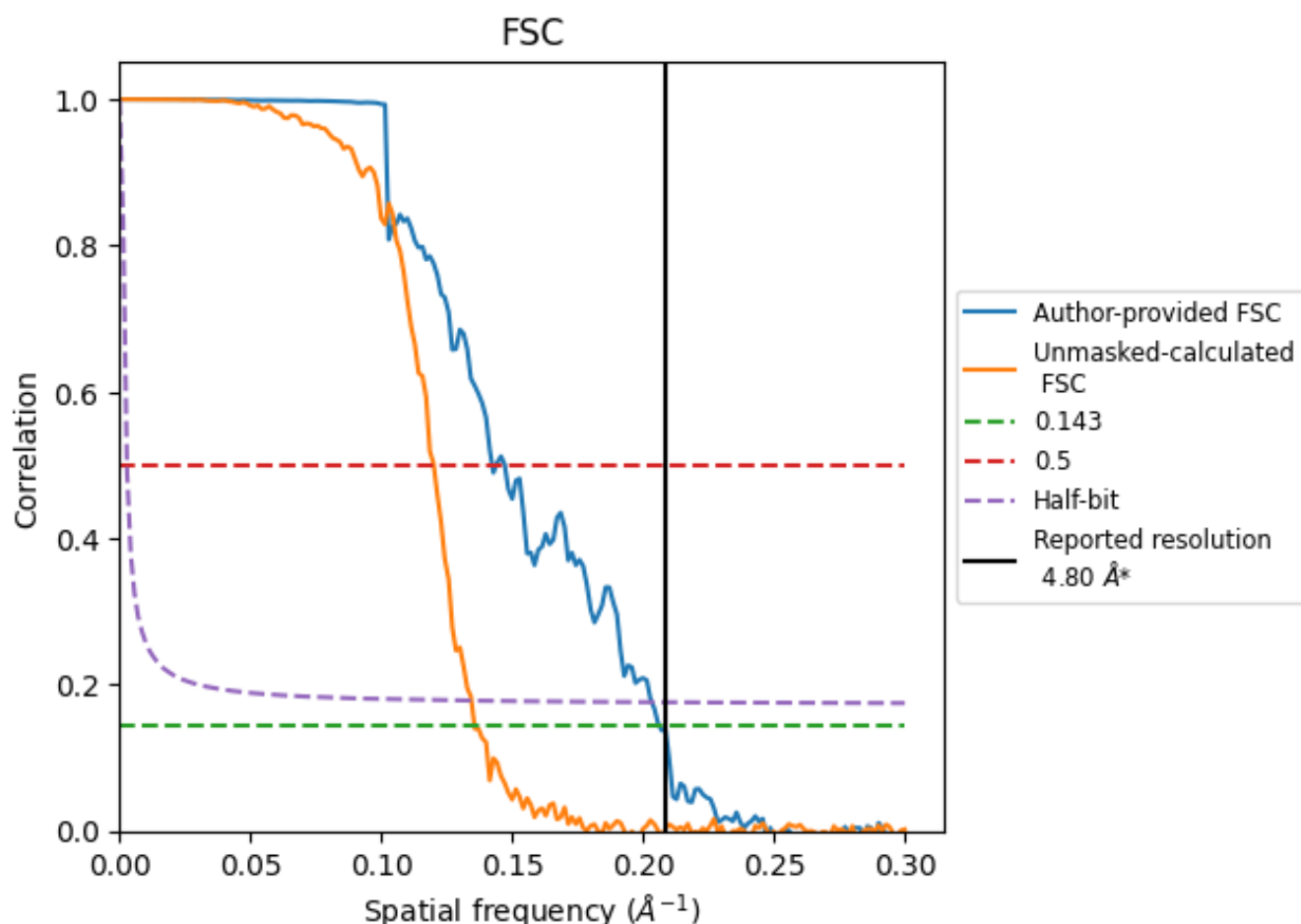


*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.208 Å⁻¹

8.2 Resolution estimates [i](#)

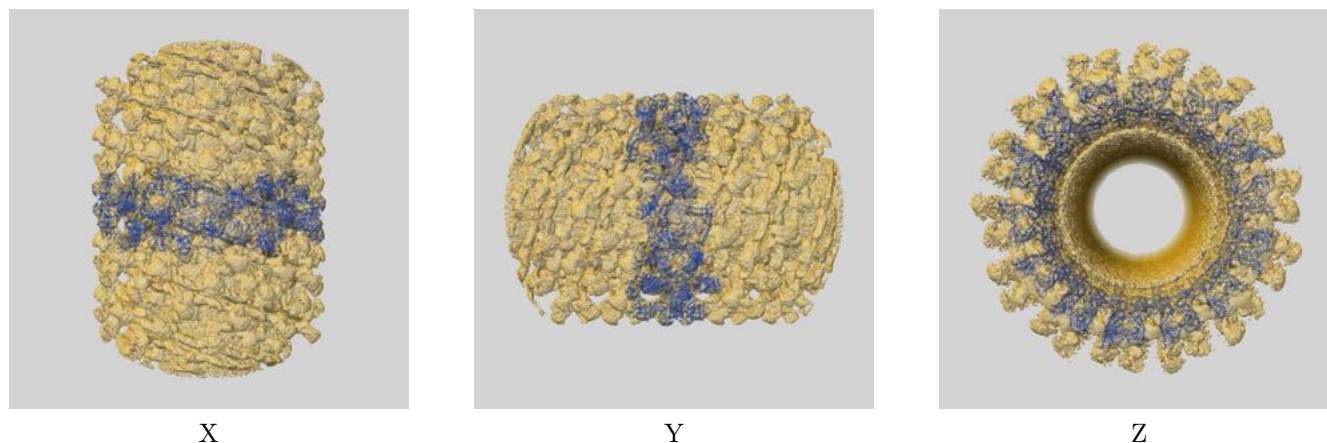
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.80	-	-
Author-provided FSC curve	4.84	7.02	4.92
Unmasked-calculated*	7.37	8.33	7.43

*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 7.37 differs from the reported value 4.8 by more than 10 %

9 Map-model fit [i](#)

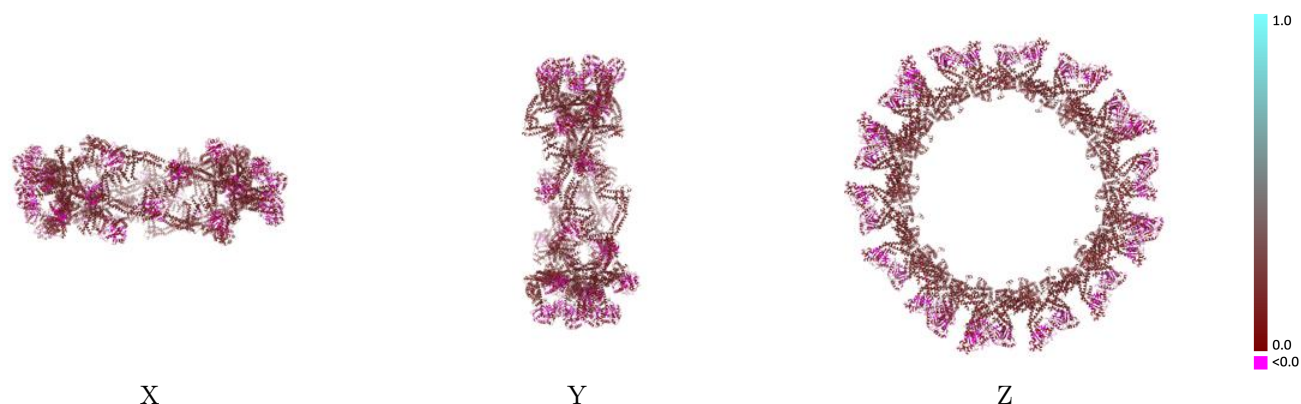
This section contains information regarding the fit between EMDB map EMD-26977 and PDB model 8CT1. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



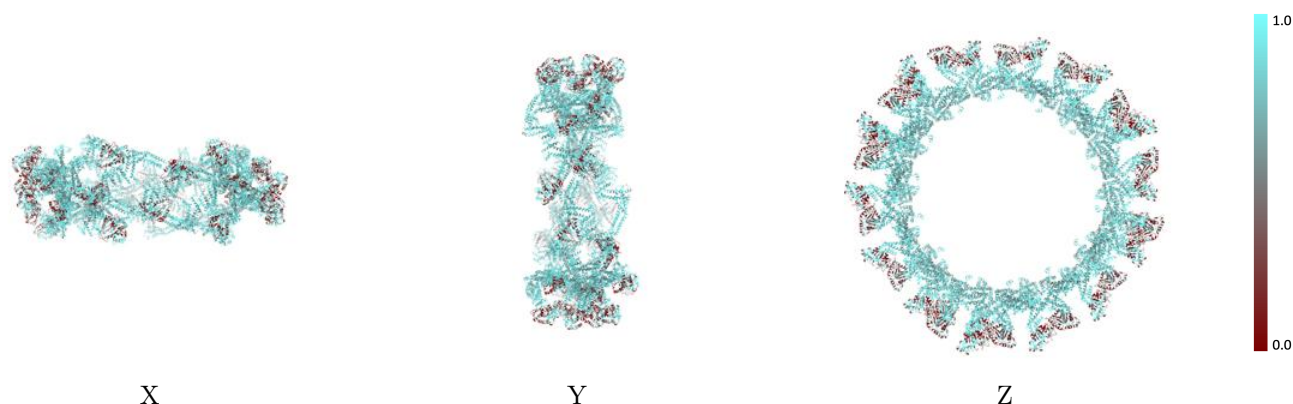
The images above show the 3D surface view of the map at the recommended contour level 0.0025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



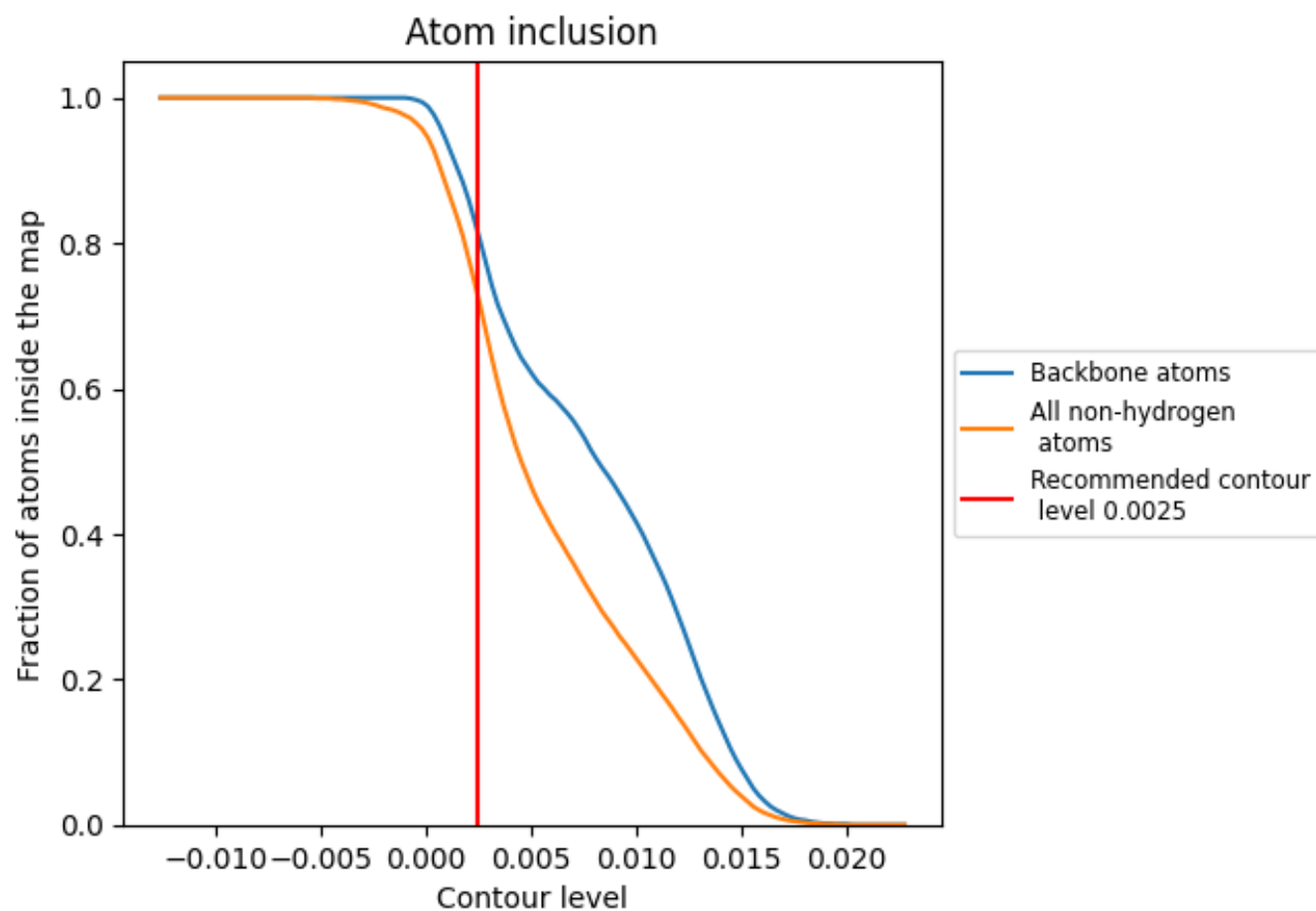
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0025).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 72% 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 (0.0025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.1440
A	 0.7220	 0.1480
B	 0.7270	 0.1450
C	 0.7210	 0.1440
D	 0.7330	 0.1460
E	 0.7170	 0.1410
F	 0.7250	 0.1440
G	 0.7240	 0.1430
H	 0.7180	 0.1420
I	 0.7310	 0.1470
J	 0.7260	 0.1420
K	 0.7150	 0.1400
L	 0.7290	 0.1450
M	 0.7240	 0.1440
N	 0.7220	 0.1410
O	 0.7280	 0.1430
P	 0.7260	 0.1450
Q	 0.7290	 0.1470
R	 0.7250	 0.1430
S	 0.7210	 0.1390
T	 0.7200	 0.1420
U	 0.7300	 0.1490
V	 0.7240	 0.1440
W	 0.7280	 0.1460
X	 0.7200	 0.1420
Y	 0.7240	 0.1470
Z	 0.7230	 0.1400
a	 0.7280	 0.1480
b	 0.7210	 0.1460
c	 0.7260	 0.1400
d	 0.7260	 0.1430
e	 0.7270	 0.1430
f	 0.7200	 0.1390
g	 0.7230	 0.1470
h	 0.7290	 0.1490

