wwPDB EM Validation Summary Report (i)

Sep 28, 2024 – 07:39 AM EDT

PDB ID	:	5T0V
EMDB ID	:	EMD-8341
Title	:	Architecture of the Yeast Mitochondrial Iron-Sulfur Cluster Assembly Machinery: the Sub-Complex Formed by the Iron Donor, Yfh1, and the Scaffold, Isu1
Authors	:	Ranatunga, W.; Gakh, O.; Galeano, B.K.; Smith IV, D.Y.; Soderberg, C.A.; Al-Karadaghi, S.; Thompson, J.R.; Isaya, G.
Deposited on	:	2016-08-16
Resolution	:	17.50 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 (i) 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 (i)) were used in the production of this report:

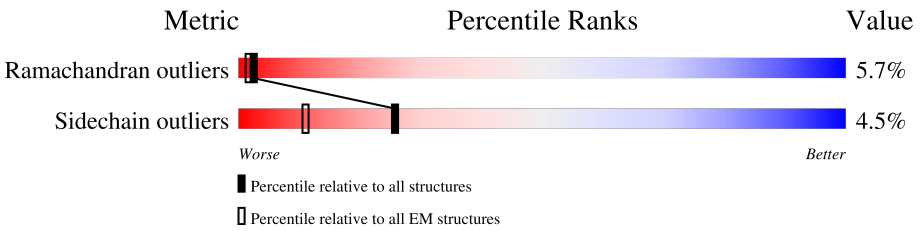
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 17.50 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 <=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	142	38% 92% 7% •
1	b	142	38% 92% 7% •
1	c	142	36% 90% 9% •
1	d	142	37% 97% •
1	e	142	38% 91% 8% •
1	f	142	37% 93% 6% •
1	g	142	36% 94% 6%
1	h	142	38% 92% 8%
1	i	142	42% 92% 8% •

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Mol	Chain	Length	Quality of chain
1	j	142	38% 92% 8%
1	k	142	37% 90% 8% •
1	l	142	35% 89% 11%
1	m	142	38% 94% 6%
1	n	142	38% 93% 6% •
1	o	142	37% 94% 6%
1	p	142	37% 88% 12%
1	q	142	42% 91% 9%
1	r	142	37% 91% 8% •
1	s	142	37% 94% 6%
1	t	142	39% 91% 6% •
1	u	142	41% 94% 6%
1	v	142	35% 94% 6%
1	w	142	37% 94% 6%
1	x	142	37% 92% 7% •
2	A	121	37% 83% 14% •
2	B	121	33% 88% 12%
2	C	121	33% 87% 12% •
2	D	121	36% 81% 17% •
2	E	121	31% 85% 14% •
2	F	121	36% 86% 14%
2	G	121	35% 81% 18% •
2	H	121	31% 83% 16% •
2	I	121	34% 89% 11%
2	J	121	36% 84% 14% ••

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Mol	Chain	Length	Quality of chain
2	K	121	31% 80% 20%
2	L	121	33% 90% 9% •
2	M	121	36% 90% 9% •
2	N	121	31% 83% 16% •
2	O	121	36% 92% 7% •
2	P	121	36% 86% 14%
2	Q	121	34% 86% 12% •
2	R	121	35% 92% 7% •
2	S	121	36% 87% 12% •
2	T	121	33% 88% 11% •
2	U	121	39% 80% 18% •
2	V	121	34% 86% 14%
2	W	121	35% 83% 16% •
2	X	121	33% 90% 9% •

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 48456 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 Iron sulfur cluster assembly protein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	a	142	1072	672	186	205	9	0	0
1	b	142	1072	672	186	205	9	0	0
1	c	142	1072	672	186	205	9	0	0
1	d	142	1072	672	186	205	9	0	0
1	e	142	1072	672	186	205	9	0	0
1	f	142	1072	672	186	205	9	0	0
1	g	142	1072	672	186	205	9	0	0
1	h	142	1072	672	186	205	9	0	0
1	i	142	1072	672	186	205	9	0	0
1	j	142	1072	672	186	205	9	0	0
1	k	142	1072	672	186	205	9	0	0
1	l	142	1072	672	186	205	9	0	0
1	m	142	1072	672	186	205	9	0	0
1	n	142	1072	672	186	205	9	0	0
1	o	142	1072	672	186	205	9	0	0
1	p	142	1072	672	186	205	9	0	0
1	q	142	1072	672	186	205	9	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	r	142	1072	672	186	205	9	0	0
1	s	142	1072	672	186	205	9	0	0
1	t	142	1072	672	186	205	9	0	0
1	u	142	1072	672	186	205	9	0	0
1	v	142	1072	672	186	205	9	0	0
1	w	142	1072	672	186	205	9	0	0
1	x	142	1072	672	186	205	9	0	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	24	GLY	-	expression tag	UNP Q03020
a	25	SER	-	expression tag	UNP Q03020
a	26	HIS	-	expression tag	UNP Q03020
a	27	MET	-	expression tag	UNP Q03020
b	24	GLY	-	expression tag	UNP Q03020
b	25	SER	-	expression tag	UNP Q03020
b	26	HIS	-	expression tag	UNP Q03020
b	27	MET	-	expression tag	UNP Q03020
c	24	GLY	-	expression tag	UNP Q03020
c	25	SER	-	expression tag	UNP Q03020
c	26	HIS	-	expression tag	UNP Q03020
c	27	MET	-	expression tag	UNP Q03020
d	24	GLY	-	expression tag	UNP Q03020
d	25	SER	-	expression tag	UNP Q03020
d	26	HIS	-	expression tag	UNP Q03020
d	27	MET	-	expression tag	UNP Q03020
e	24	GLY	-	expression tag	UNP Q03020
e	25	SER	-	expression tag	UNP Q03020
e	26	HIS	-	expression tag	UNP Q03020
e	27	MET	-	expression tag	UNP Q03020
f	24	GLY	-	expression tag	UNP Q03020
f	25	SER	-	expression tag	UNP Q03020
f	26	HIS	-	expression tag	UNP Q03020
f	27	MET	-	expression tag	UNP Q03020
g	24	GLY	-	expression tag	UNP Q03020

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Chain	Residue	Modelled	Actual	Comment	Reference
g	25	SER	-	expression tag	UNP Q03020
g	26	HIS	-	expression tag	UNP Q03020
g	27	MET	-	expression tag	UNP Q03020
h	24	GLY	-	expression tag	UNP Q03020
h	25	SER	-	expression tag	UNP Q03020
h	26	HIS	-	expression tag	UNP Q03020
h	27	MET	-	expression tag	UNP Q03020
i	24	GLY	-	expression tag	UNP Q03020
i	25	SER	-	expression tag	UNP Q03020
i	26	HIS	-	expression tag	UNP Q03020
i	27	MET	-	expression tag	UNP Q03020
j	24	GLY	-	expression tag	UNP Q03020
j	25	SER	-	expression tag	UNP Q03020
j	26	HIS	-	expression tag	UNP Q03020
j	27	MET	-	expression tag	UNP Q03020
k	24	GLY	-	expression tag	UNP Q03020
k	25	SER	-	expression tag	UNP Q03020
k	26	HIS	-	expression tag	UNP Q03020
k	27	MET	-	expression tag	UNP Q03020
l	24	GLY	-	expression tag	UNP Q03020
l	25	SER	-	expression tag	UNP Q03020
l	26	HIS	-	expression tag	UNP Q03020
l	27	MET	-	expression tag	UNP Q03020
m	24	GLY	-	expression tag	UNP Q03020
m	25	SER	-	expression tag	UNP Q03020
m	26	HIS	-	expression tag	UNP Q03020
m	27	MET	-	expression tag	UNP Q03020
n	24	GLY	-	expression tag	UNP Q03020
n	25	SER	-	expression tag	UNP Q03020
n	26	HIS	-	expression tag	UNP Q03020
n	27	MET	-	expression tag	UNP Q03020
o	24	GLY	-	expression tag	UNP Q03020
o	25	SER	-	expression tag	UNP Q03020
o	26	HIS	-	expression tag	UNP Q03020
o	27	MET	-	expression tag	UNP Q03020
p	24	GLY	-	expression tag	UNP Q03020
p	25	SER	-	expression tag	UNP Q03020
p	26	HIS	-	expression tag	UNP Q03020
p	27	MET	-	expression tag	UNP Q03020
q	24	GLY	-	expression tag	UNP Q03020
q	25	SER	-	expression tag	UNP Q03020
q	26	HIS	-	expression tag	UNP Q03020

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Chain	Residue	Modelled	Actual	Comment	Reference
q	27	MET	-	expression tag	UNP Q03020
r	24	GLY	-	expression tag	UNP Q03020
r	25	SER	-	expression tag	UNP Q03020
r	26	HIS	-	expression tag	UNP Q03020
r	27	MET	-	expression tag	UNP Q03020
s	24	GLY	-	expression tag	UNP Q03020
s	25	SER	-	expression tag	UNP Q03020
s	26	HIS	-	expression tag	UNP Q03020
s	27	MET	-	expression tag	UNP Q03020
t	24	GLY	-	expression tag	UNP Q03020
t	25	SER	-	expression tag	UNP Q03020
t	26	HIS	-	expression tag	UNP Q03020
t	27	MET	-	expression tag	UNP Q03020
u	24	GLY	-	expression tag	UNP Q03020
u	25	SER	-	expression tag	UNP Q03020
u	26	HIS	-	expression tag	UNP Q03020
u	27	MET	-	expression tag	UNP Q03020
v	24	GLY	-	expression tag	UNP Q03020
v	25	SER	-	expression tag	UNP Q03020
v	26	HIS	-	expression tag	UNP Q03020
v	27	MET	-	expression tag	UNP Q03020
w	24	GLY	-	expression tag	UNP Q03020
w	25	SER	-	expression tag	UNP Q03020
w	26	HIS	-	expression tag	UNP Q03020
w	27	MET	-	expression tag	UNP Q03020
x	24	GLY	-	expression tag	UNP Q03020
x	25	SER	-	expression tag	UNP Q03020
x	26	HIS	-	expression tag	UNP Q03020
x	27	MET	-	expression tag	UNP Q03020

- Molecule 2 is a protein called Frataxin homolog, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	A	121	947	597	153	195	2	0	0
2	B	121	947	597	153	195	2	0	0
2	C	121	947	597	153	195	2	0	0
2	D	121	947	597	153	195	2	0	0
2	E	121	947	597	153	195	2	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	F	121	947	597	153	195	2	0	0
2	G	121	947	597	153	195	2	0	0
2	H	121	947	597	153	195	2	0	0
2	I	121	947	597	153	195	2	0	0
2	J	121	947	597	153	195	2	0	0
2	K	121	947	597	153	195	2	0	0
2	L	121	947	597	153	195	2	0	0
2	M	121	947	597	153	195	2	0	0
2	N	121	947	597	153	195	2	0	0
2	O	121	947	597	153	195	2	0	0
2	P	121	947	597	153	195	2	0	0
2	Q	121	947	597	153	195	2	0	0
2	R	121	947	597	153	195	2	0	0
2	S	121	947	597	153	195	2	0	0
2	T	121	947	597	153	195	2	0	0
2	U	121	947	597	153	195	2	0	0
2	V	121	947	597	153	195	2	0	0
2	W	121	947	597	153	195	2	0	0
2	X	121	947	597	153	195	2	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	ALA	TYR	conflict	UNP Q07540

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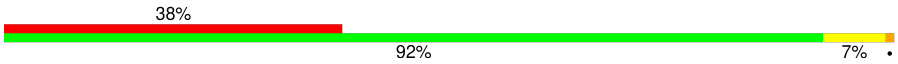
Chain	Residue	Modelled	Actual	Comment	Reference
B	73	ALA	TYR	conflict	UNP Q07540
C	73	ALA	TYR	conflict	UNP Q07540
D	73	ALA	TYR	conflict	UNP Q07540
E	73	ALA	TYR	conflict	UNP Q07540
F	73	ALA	TYR	conflict	UNP Q07540
G	73	ALA	TYR	conflict	UNP Q07540
H	73	ALA	TYR	conflict	UNP Q07540
I	73	ALA	TYR	conflict	UNP Q07540
J	73	ALA	TYR	conflict	UNP Q07540
K	73	ALA	TYR	conflict	UNP Q07540
L	73	ALA	TYR	conflict	UNP Q07540
M	73	ALA	TYR	conflict	UNP Q07540
N	73	ALA	TYR	conflict	UNP Q07540
O	73	ALA	TYR	conflict	UNP Q07540
P	73	ALA	TYR	conflict	UNP Q07540
Q	73	ALA	TYR	conflict	UNP Q07540
R	73	ALA	TYR	conflict	UNP Q07540
S	73	ALA	TYR	conflict	UNP Q07540
T	73	ALA	TYR	conflict	UNP Q07540
U	73	ALA	TYR	conflict	UNP Q07540
V	73	ALA	TYR	conflict	UNP Q07540
W	73	ALA	TYR	conflict	UNP Q07540
X	73	ALA	TYR	conflict	UNP Q07540

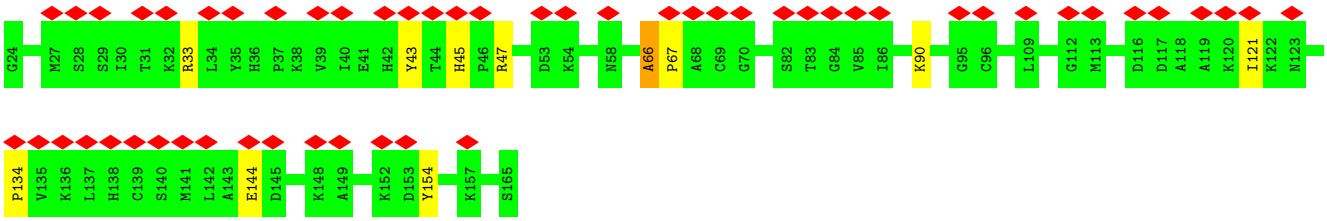
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

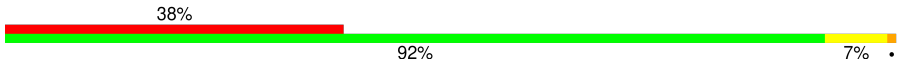
Chain a:

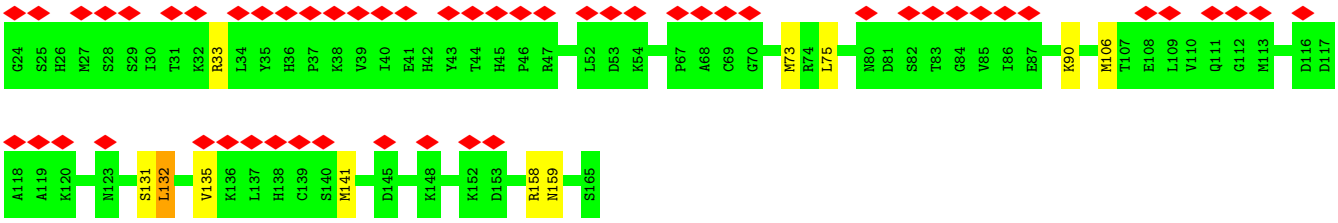




• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

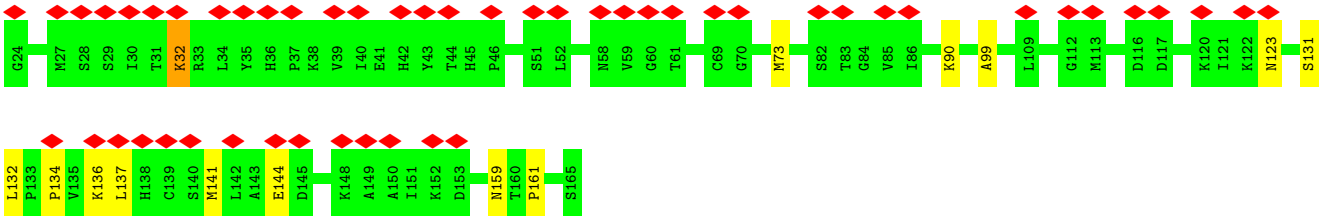
Chain b:





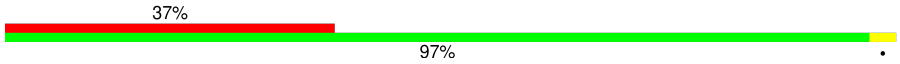
• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

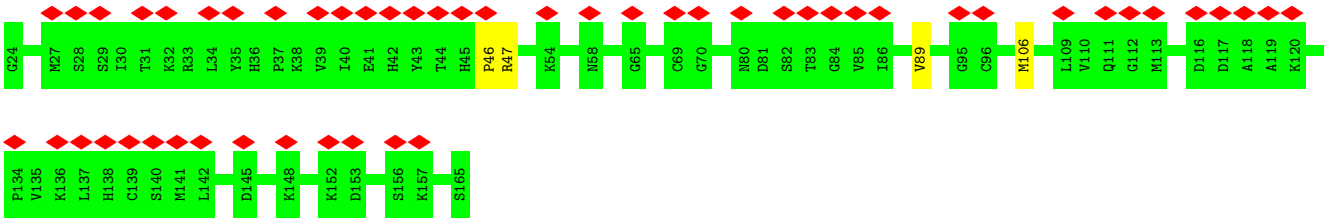
Chain c:



• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

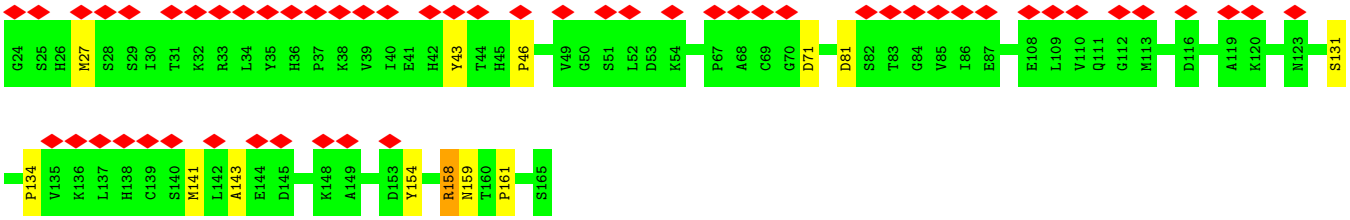
Chain d:





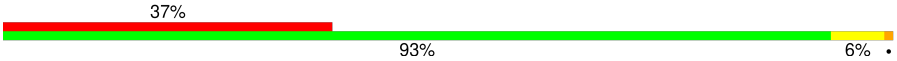
• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

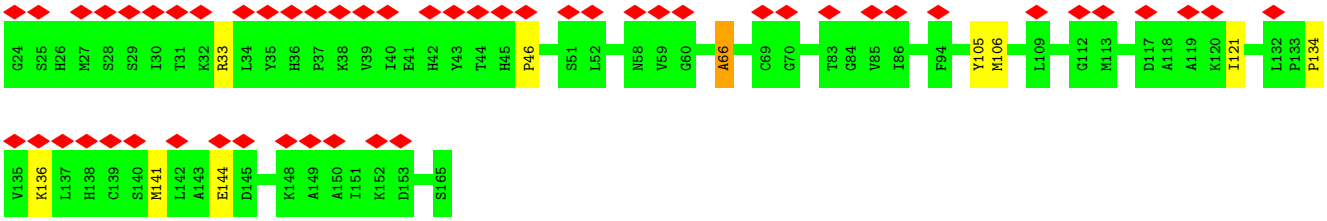
Chain e:



• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

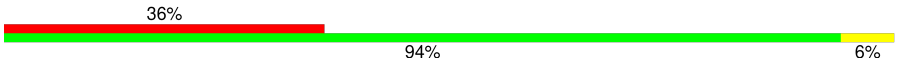
Chain f:

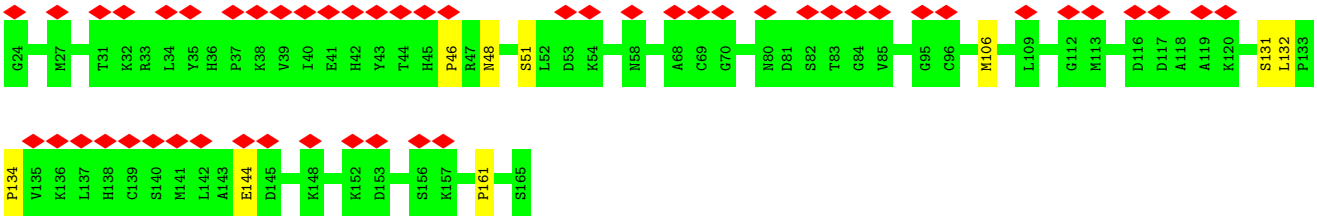




• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

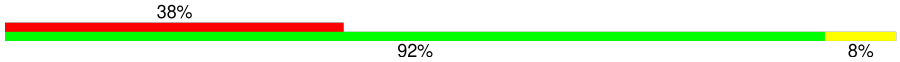
Chain g:

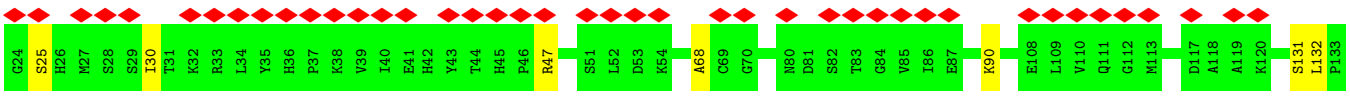


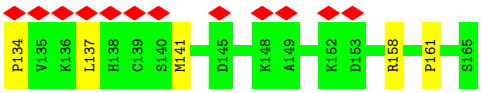


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain h:

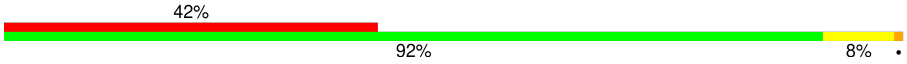


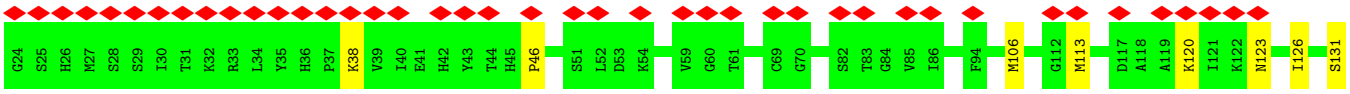


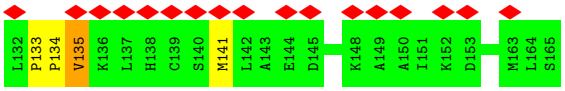


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain i:

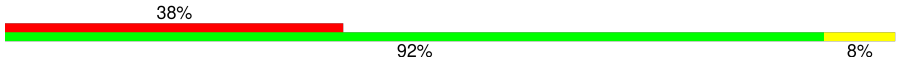


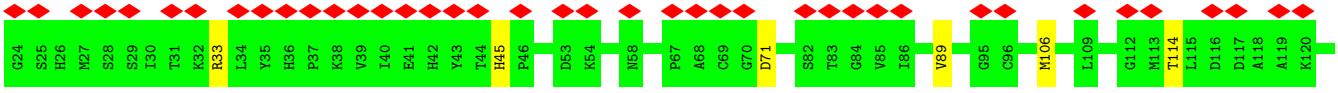


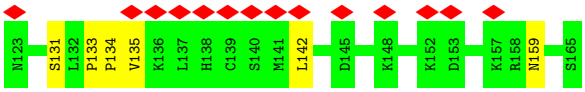


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain j:

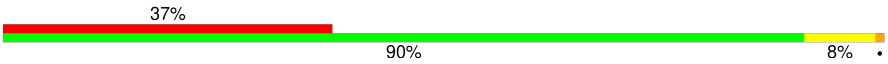


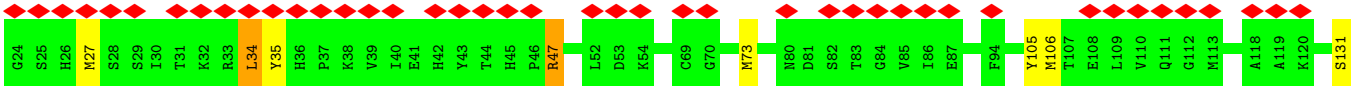


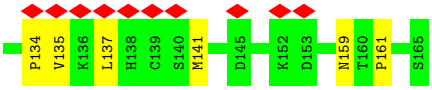


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain k:

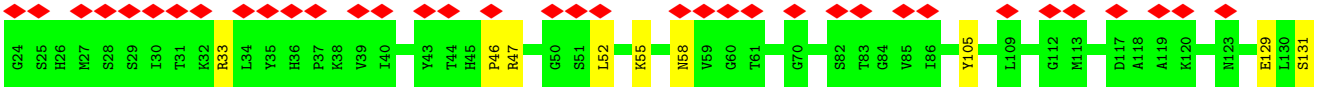


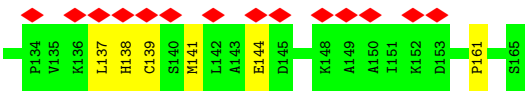




• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

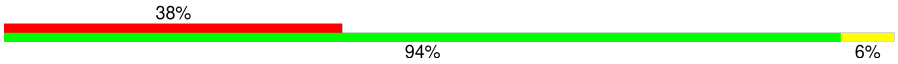
Chain l:

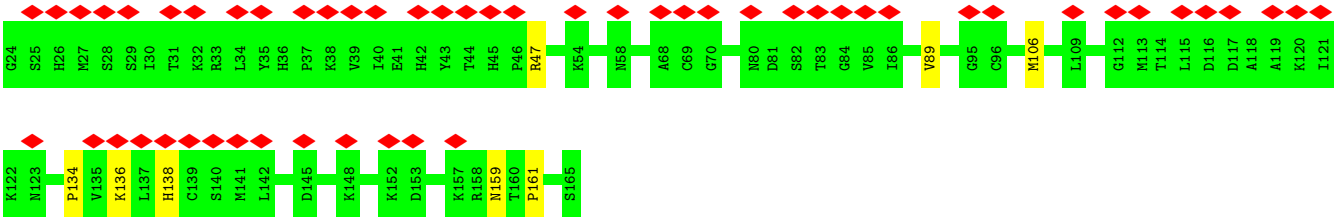




• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

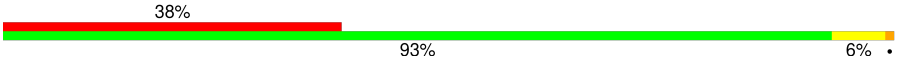
Chain m:

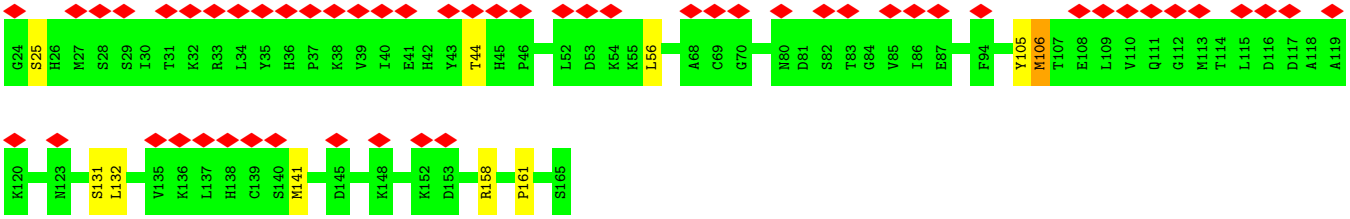




- Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

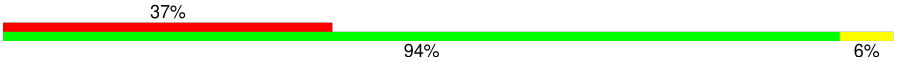
Chain n:

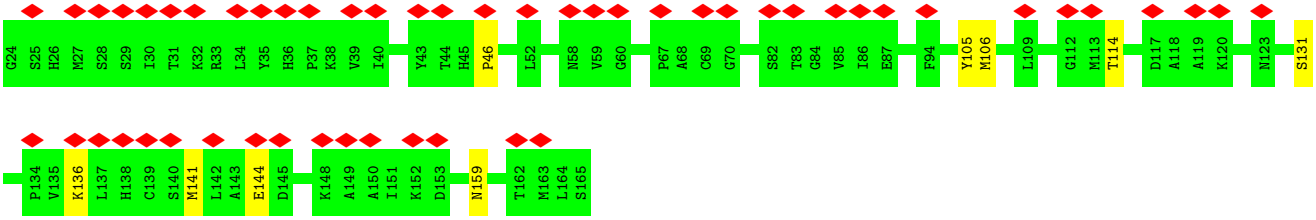




- Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

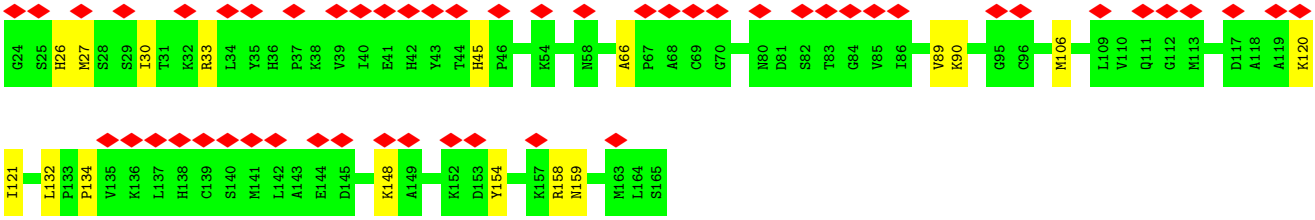
Chain o:





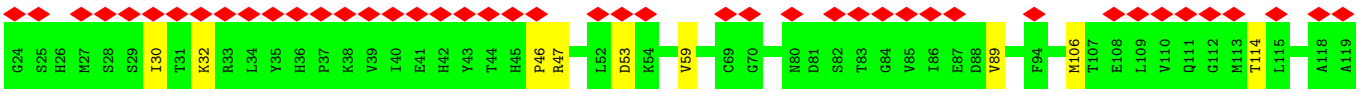
- Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

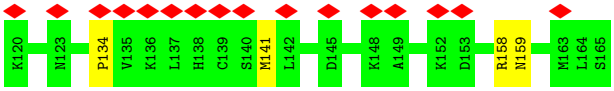
Chain p:



- Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

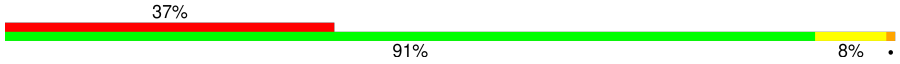
Chain q:

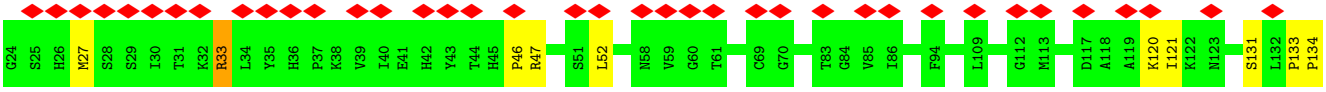


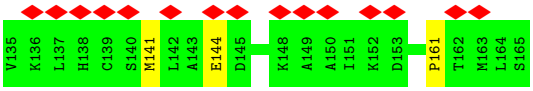


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain r:

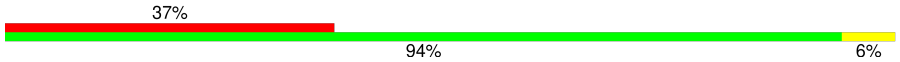


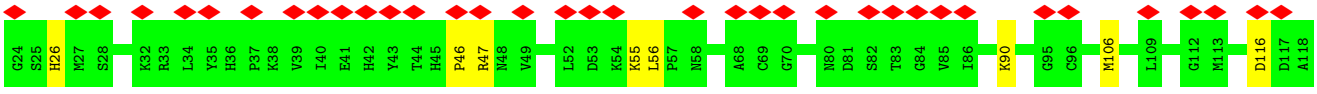


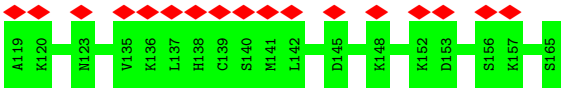


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain s:

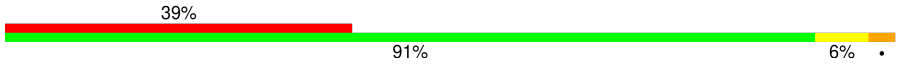


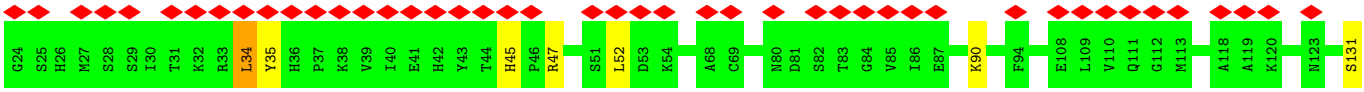


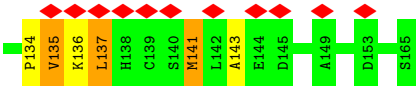


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain t:

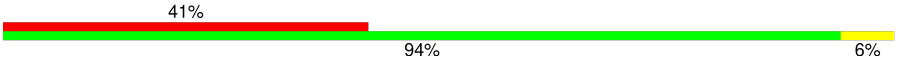


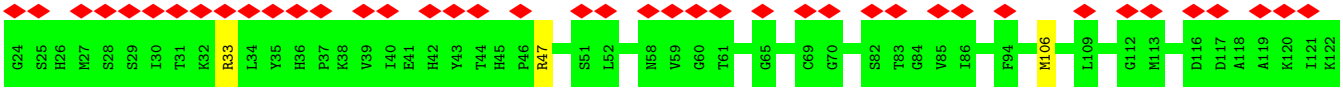


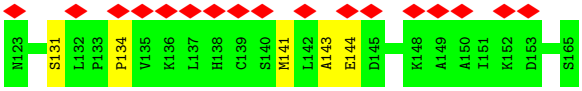


• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

Chain u:

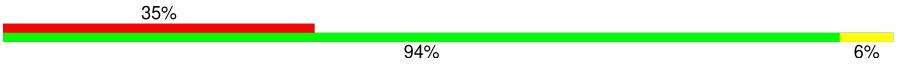


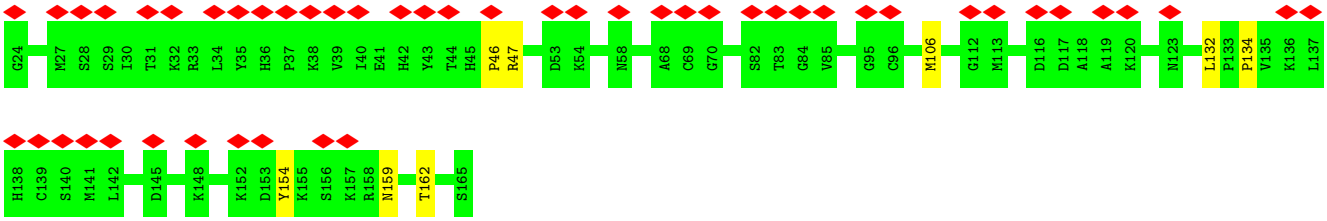




• Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

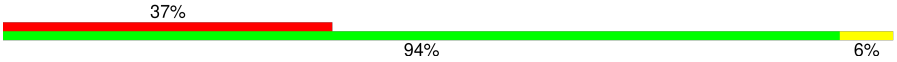
Chain v:

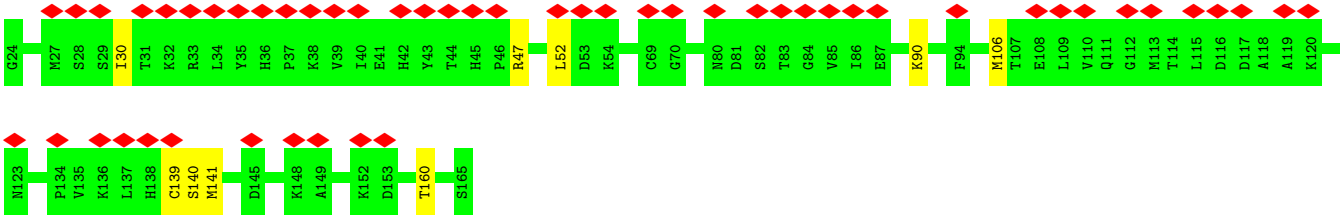




- Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

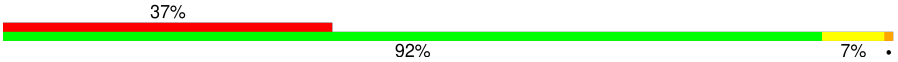
Chain w:

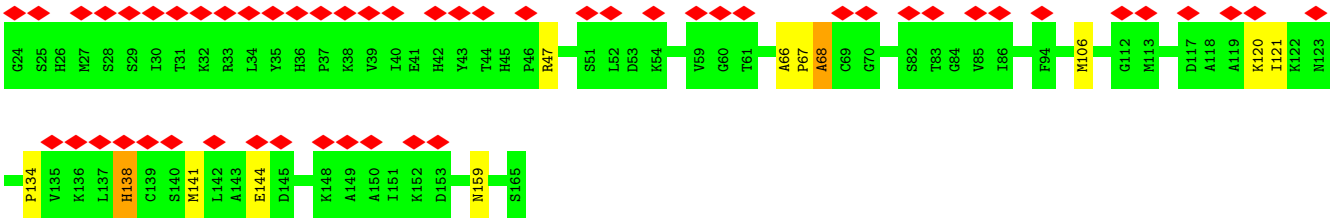




- Molecule 1: Iron sulfur cluster assembly protein 1, mitochondrial

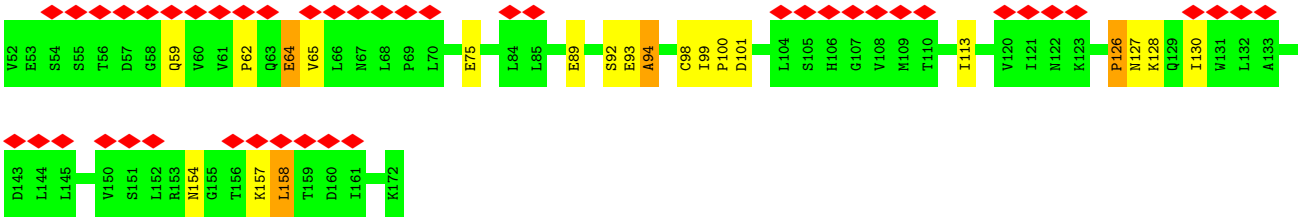
Chain x:





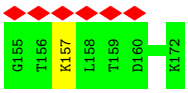
- Molecule 2: Frataxin homolog, mitochondrial

Chain A:



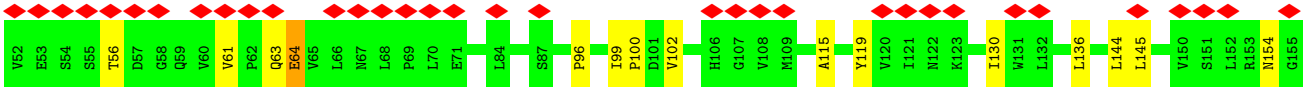
- Molecule 2: Frataxin homolog, mitochondrial

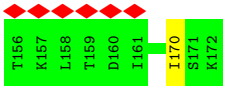
Chain B:



• Molecule 2: Frataxin homolog, mitochondrial

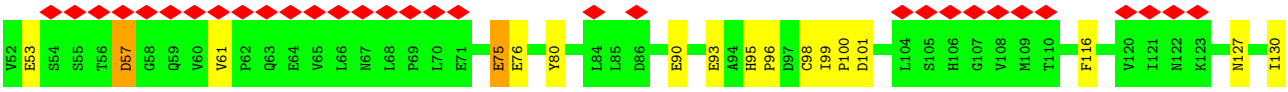
Chain C:

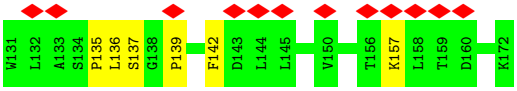




• Molecule 2: Frataxin homolog, mitochondrial

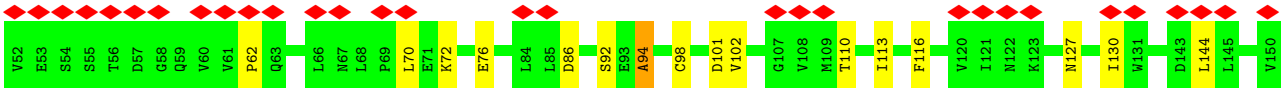
Chain D:

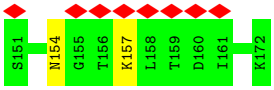




• Molecule 2: Frataxin homolog, mitochondrial

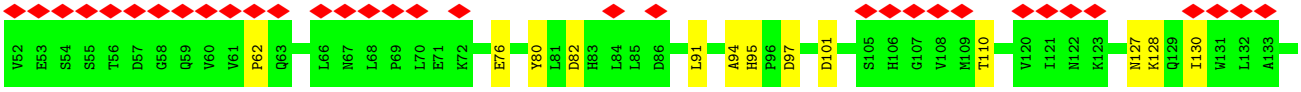
Chain E:

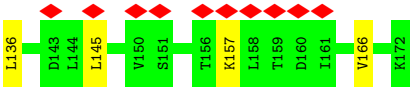




• Molecule 2: Frataxin homolog, mitochondrial

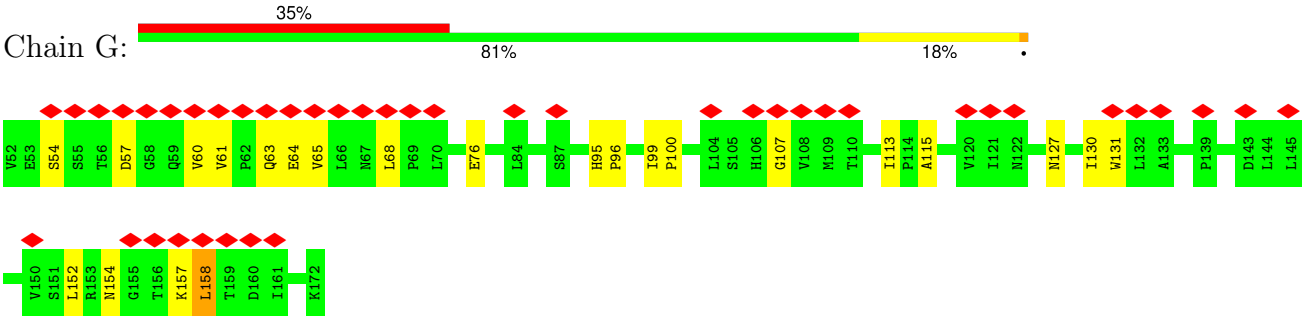
Chain F:





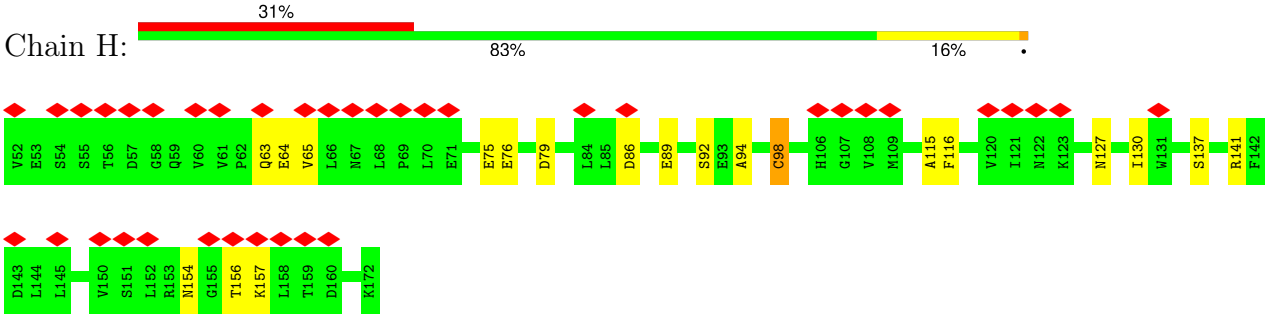
• Molecule 2: Frataxin homolog, mitochondrial

Chain G:



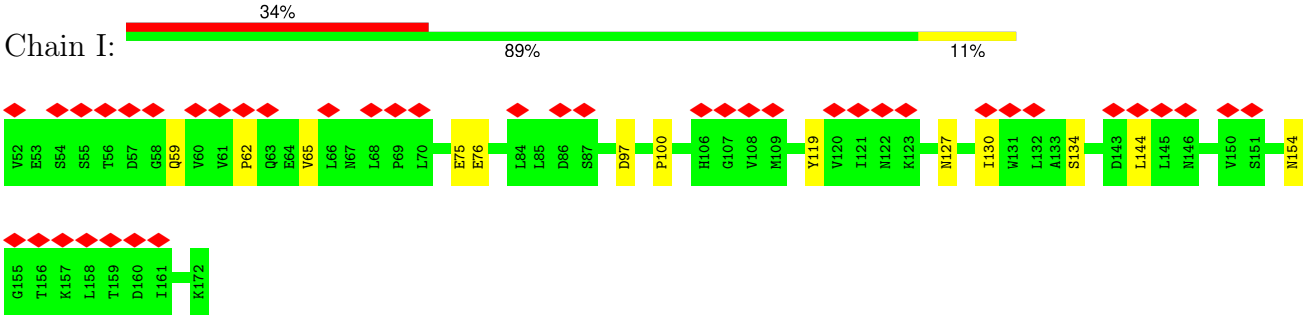
- Molecule 2: Frataxin homolog, mitochondrial

Chain H:



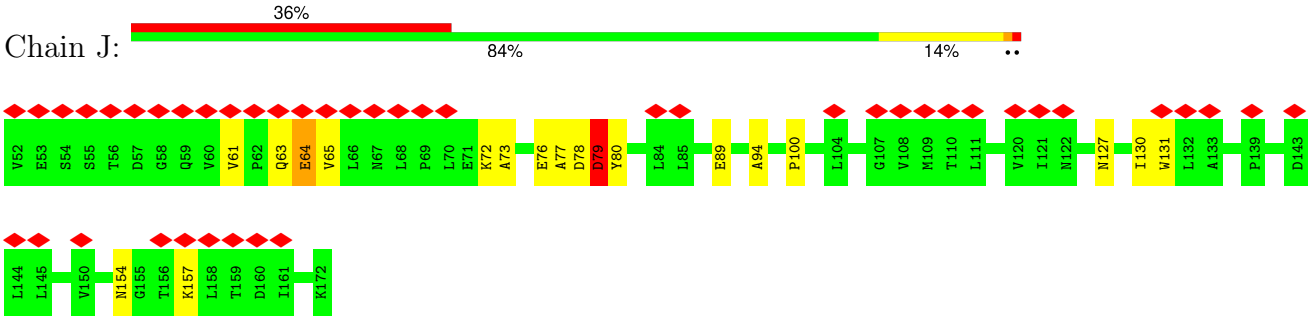
- Molecule 2: Frataxin homolog, mitochondrial

Chain I:



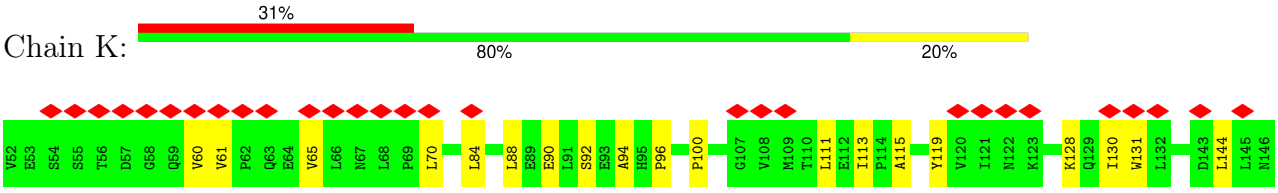
- Molecule 2: Frataxin homolog, mitochondrial

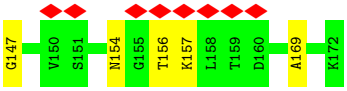
Chain J:



- Molecule 2: Frataxin homolog, mitochondrial

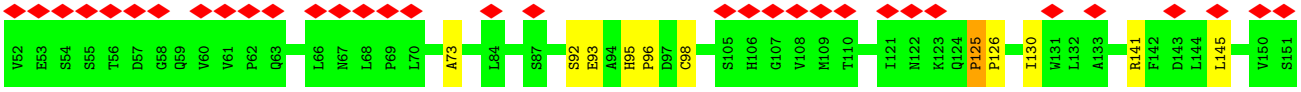
Chain K:

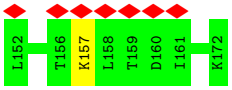




• Molecule 2: Frataxin homolog, mitochondrial

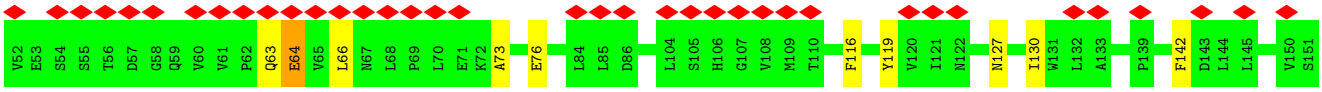
Chain L:

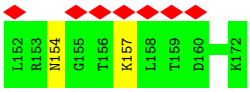




• Molecule 2: Frataxin homolog, mitochondrial

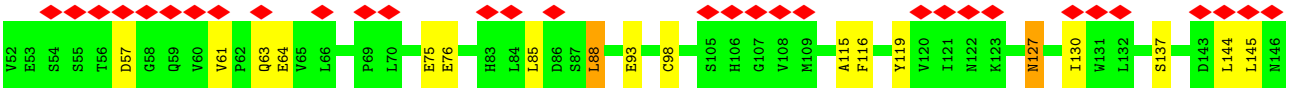
Chain M:

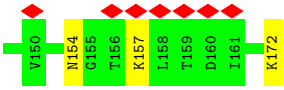




• Molecule 2: Frataxin homolog, mitochondrial

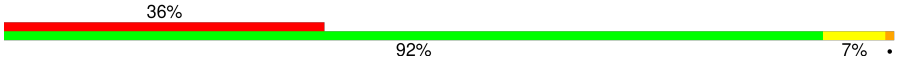
Chain N:

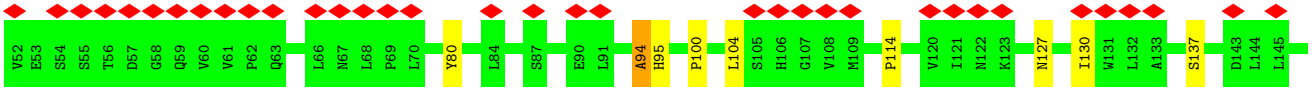


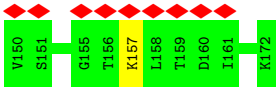


• Molecule 2: Frataxin homolog, mitochondrial

Chain O:

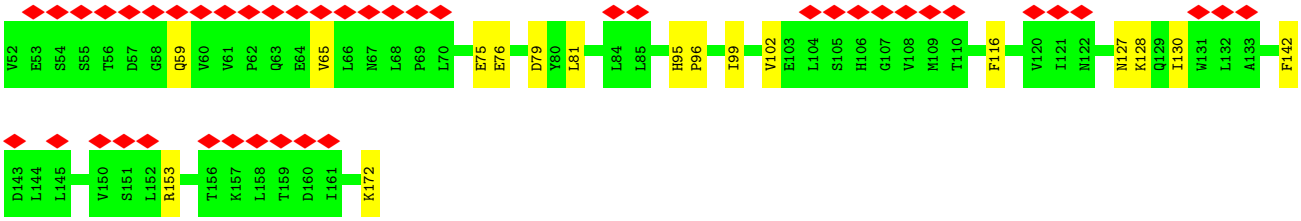






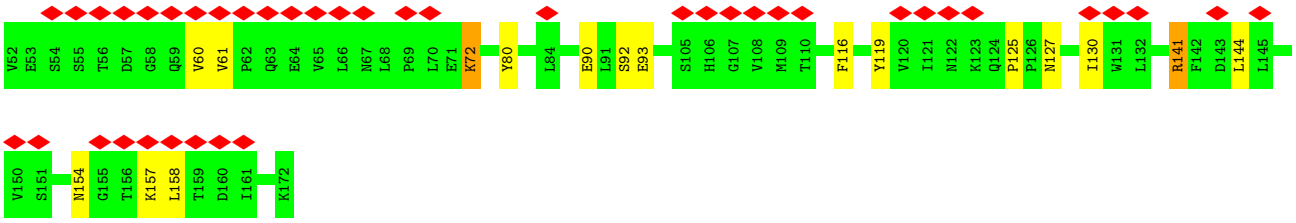
• Molecule 2: Frataxin homolog, mitochondrial

Chain P: 36% 86% 14%



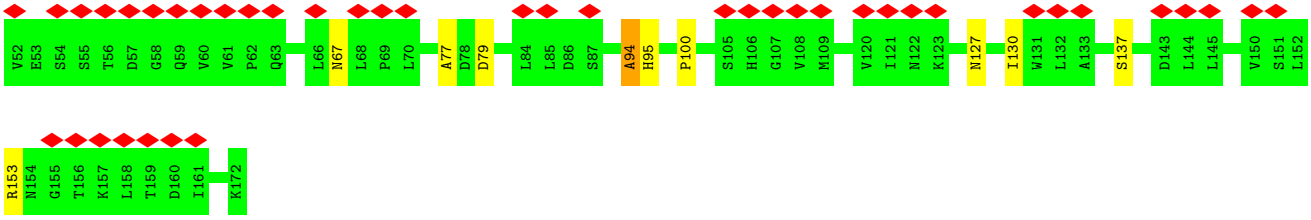
- Molecule 2: Frataxin homolog, mitochondrial

Chain Q: 34% 86% 12%



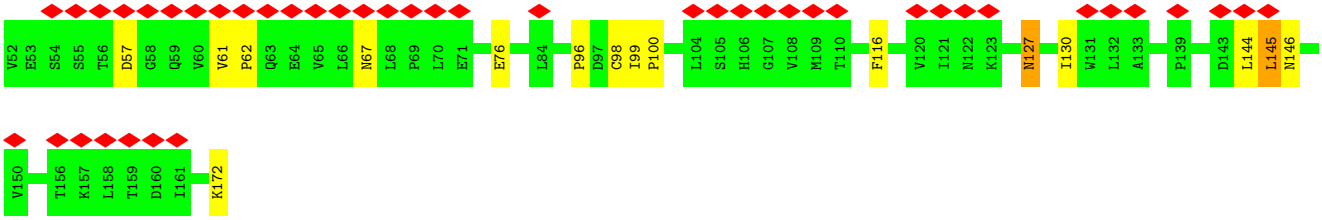
- Molecule 2: Frataxin homolog, mitochondrial

Chain R: 35% 92% 7%



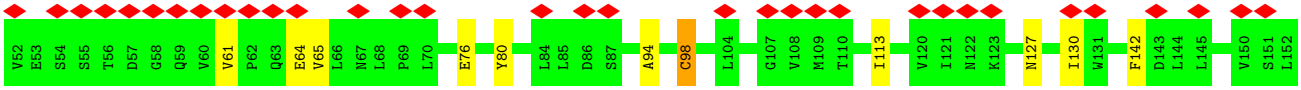
- Molecule 2: Frataxin homolog, mitochondrial

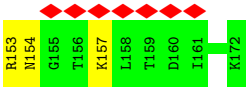
Chain S: 36% 87% 12%



- Molecule 2: Frataxin homolog, mitochondrial

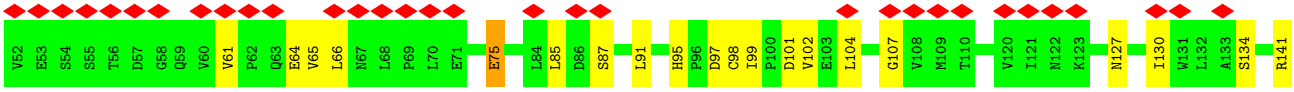
Chain T: 33% 88% 11%

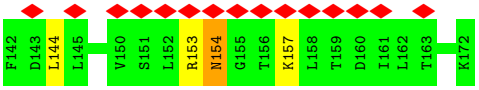




• Molecule 2: Frataxin homolog, mitochondrial

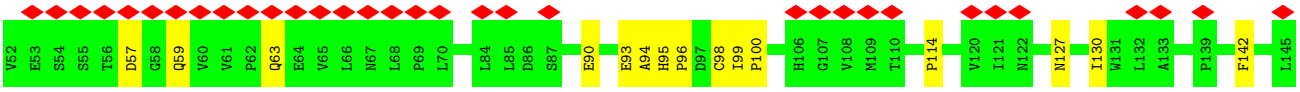
Chain U:

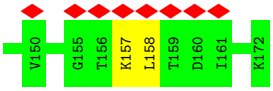




• Molecule 2: Frataxin homolog, mitochondrial

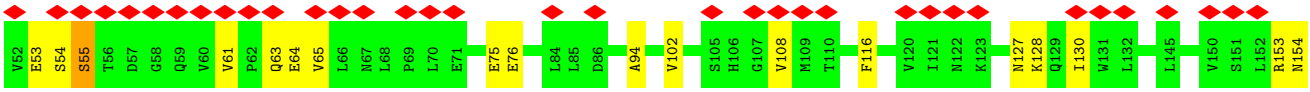
Chain V:

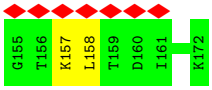




• Molecule 2: Frataxin homolog, mitochondrial

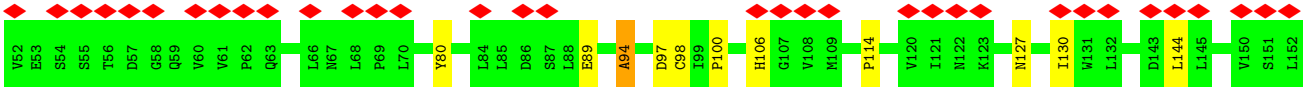
Chain W:

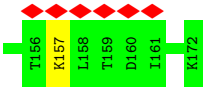




• Molecule 2: Frataxin homolog, mitochondrial

Chain X:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, O	Depositor
Number of particles used	4153	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; The ctf.auto function from EMAN2 was applied.	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	30	Depositor
Minimum defocus (nm)	210	Depositor
Maximum defocus (nm)	2800	Depositor
Magnification	115000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	12.440	Depositor
Minimum map value	-8.726	Depositor
Average map value	0.043	Depositor
Map value standard deviation	0.800	Depositor
Recommended contour level	0.8	Depositor
Map size (Å)	297.79202, 297.79202, 297.79202	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.034, 1.034, 1.034	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	1.04	0/1089	1.23	3/1466 (0.2%)
1	b	1.04	0/1089	1.28	6/1466 (0.4%)
1	c	1.02	0/1089	1.24	2/1466 (0.1%)
1	d	1.05	0/1089	1.18	0/1466
1	e	1.03	0/1089	1.29	5/1466 (0.3%)
1	f	1.06	0/1089	1.24	1/1466 (0.1%)
1	g	1.04	0/1089	1.18	1/1466 (0.1%)
1	h	1.00	0/1089	1.27	4/1466 (0.3%)
1	i	1.03	0/1089	1.19	1/1466 (0.1%)
1	j	1.02	0/1089	1.26	1/1466 (0.1%)
1	k	1.04	0/1089	1.27	6/1466 (0.4%)
1	l	1.04	0/1089	1.32	5/1466 (0.3%)
1	m	1.01	0/1089	1.17	0/1466
1	n	0.98	0/1089	1.22	3/1466 (0.2%)
1	o	0.98	0/1089	1.18	2/1466 (0.1%)
1	p	1.04	0/1089	1.27	5/1466 (0.3%)
1	q	1.04	0/1089	1.21	2/1466 (0.1%)
1	r	1.01	0/1089	1.24	1/1466 (0.1%)
1	s	1.05	0/1089	1.22	2/1466 (0.1%)
1	t	1.07	0/1089	1.24	2/1466 (0.1%)
1	u	1.05	0/1089	1.18	0/1466
1	v	1.04	0/1089	1.22	3/1466 (0.2%)
1	w	1.05	0/1089	1.22	0/1466
1	x	1.06	0/1089	1.25	3/1466 (0.2%)
2	A	0.99	0/967	1.21	2/1319 (0.2%)
2	B	1.02	0/967	1.24	0/1319
2	C	1.03	0/967	1.28	2/1319 (0.2%)
2	D	1.02	0/967	1.28	5/1319 (0.4%)
2	E	1.01	0/967	1.27	4/1319 (0.3%)
2	F	1.06	0/967	1.30	3/1319 (0.2%)
2	G	1.02	0/967	1.25	1/1319 (0.1%)
2	H	1.01	0/967	1.25	4/1319 (0.3%)
2	I	1.02	0/967	1.23	1/1319 (0.1%)
2	J	1.05	0/967	1.27	2/1319 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
2	K	0.98	0/967	1.27	3/1319 (0.2%)
2	L	1.01	0/967	1.23	1/1319 (0.1%)
2	M	1.02	0/967	1.26	3/1319 (0.2%)
2	N	1.00	0/967	1.32	7/1319 (0.5%)
2	O	1.01	0/967	1.19	1/1319 (0.1%)
2	P	1.03	0/967	1.31	4/1319 (0.3%)
2	Q	1.01	0/967	1.29	5/1319 (0.4%)
2	R	1.02	0/967	1.26	3/1319 (0.2%)
2	S	1.01	0/967	1.29	3/1319 (0.2%)
2	T	1.05	0/967	1.20	3/1319 (0.2%)
2	U	1.02	0/967	1.29	2/1319 (0.2%)
2	V	1.04	0/967	1.29	2/1319 (0.2%)
2	W	1.05	0/967	1.26	4/1319 (0.3%)
2	X	0.99	0/967	1.23	2/1319 (0.2%)
All	All	1.03	0/49344	1.25	125/66840 (0.2%)

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	n	0	1
1	r	0	2
1	t	0	1
2	I	0	1
2	M	0	1
All	All	0	7

There are no bond length outliers.

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	119	TYR	CB-CG-CD2	-10.14	114.91	121.00
2	C	119	TYR	CB-CG-CD1	10.11	127.07	121.00
1	l	105	TYR	CB-CG-CD2	-9.20	115.48	121.00
1	x	68	ALA	N-CA-CB	9.11	122.86	110.10
1	p	154	TYR	CB-CG-CD2	-8.95	115.63	121.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	I	119	TYR	Sidechain
2	M	119	TYR	Sidechain
1	a	33	ARG	Sidechain
1	n	105	TYR	Sidechain
1	r	33	ARG	Sidechain

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	140/142 (99%)	124 (89%)	11 (8%)	5 (4%)	3	20
1	b	140/142 (99%)	120 (86%)	17 (12%)	3 (2%)	5	30
1	c	140/142 (99%)	119 (85%)	15 (11%)	6 (4%)	2	17
1	d	140/142 (99%)	123 (88%)	16 (11%)	1 (1%)	19	57
1	e	140/142 (99%)	117 (84%)	18 (13%)	5 (4%)	3	20
1	f	140/142 (99%)	118 (84%)	18 (13%)	4 (3%)	3	23
1	g	140/142 (99%)	121 (86%)	13 (9%)	6 (4%)	2	17
1	h	140/142 (99%)	116 (83%)	19 (14%)	5 (4%)	3	20
1	i	140/142 (99%)	122 (87%)	12 (9%)	6 (4%)	2	17
1	j	140/142 (99%)	123 (88%)	12 (9%)	5 (4%)	3	20
1	k	140/142 (99%)	119 (85%)	14 (10%)	7 (5%)	1	16
1	l	140/142 (99%)	119 (85%)	13 (9%)	8 (6%)	1	14
1	m	140/142 (99%)	126 (90%)	10 (7%)	4 (3%)	3	23
1	n	140/142 (99%)	127 (91%)	9 (6%)	4 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	o	140/142 (99%)	121 (86%)	16 (11%)	3 (2%)	5	30
1	p	140/142 (99%)	123 (88%)	10 (7%)	7 (5%)	1	16
1	q	140/142 (99%)	121 (86%)	12 (9%)	7 (5%)	1	16
1	r	140/142 (99%)	120 (86%)	15 (11%)	5 (4%)	3	20
1	s	140/142 (99%)	124 (89%)	13 (9%)	3 (2%)	5	30
1	t	140/142 (99%)	118 (84%)	16 (11%)	6 (4%)	2	17
1	u	140/142 (99%)	127 (91%)	10 (7%)	3 (2%)	5	30
1	v	140/142 (99%)	127 (91%)	8 (6%)	5 (4%)	3	20
1	w	140/142 (99%)	127 (91%)	11 (8%)	2 (1%)	9	41
1	x	140/142 (99%)	116 (83%)	19 (14%)	5 (4%)	3	20
2	A	119/121 (98%)	89 (75%)	15 (13%)	15 (13%)	0	4
2	B	119/121 (98%)	89 (75%)	21 (18%)	9 (8%)	1	10
2	C	119/121 (98%)	96 (81%)	12 (10%)	11 (9%)	0	8
2	D	119/121 (98%)	83 (70%)	21 (18%)	15 (13%)	0	4
2	E	119/121 (98%)	95 (80%)	14 (12%)	10 (8%)	0	9
2	F	119/121 (98%)	88 (74%)	23 (19%)	8 (7%)	1	12
2	G	119/121 (98%)	87 (73%)	15 (13%)	17 (14%)	0	3
2	H	119/121 (98%)	94 (79%)	13 (11%)	12 (10%)	0	7
2	I	119/121 (98%)	87 (73%)	24 (20%)	8 (7%)	1	12
2	J	119/121 (98%)	88 (74%)	18 (15%)	13 (11%)	0	6
2	K	119/121 (98%)	93 (78%)	13 (11%)	13 (11%)	0	6
2	L	119/121 (98%)	94 (79%)	16 (13%)	9 (8%)	1	10
2	M	119/121 (98%)	99 (83%)	14 (12%)	6 (5%)	1	16
2	N	119/121 (98%)	98 (82%)	14 (12%)	7 (6%)	1	13
2	O	119/121 (98%)	97 (82%)	17 (14%)	5 (4%)	2	17
2	P	119/121 (98%)	90 (76%)	20 (17%)	9 (8%)	1	10
2	Q	119/121 (98%)	98 (82%)	15 (13%)	6 (5%)	1	16
2	R	119/121 (98%)	93 (78%)	21 (18%)	5 (4%)	2	17
2	S	119/121 (98%)	98 (82%)	9 (8%)	12 (10%)	0	7
2	T	119/121 (98%)	98 (82%)	16 (13%)	5 (4%)	2	17
2	U	119/121 (98%)	85 (71%)	18 (15%)	16 (13%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	V	119/121 (98%)	90 (76%)	19 (16%)	10 (8%)	0 9
2	W	119/121 (98%)	89 (75%)	18 (15%)	12 (10%)	0 7
2	X	119/121 (98%)	95 (80%)	16 (13%)	8 (7%)	1 12
All	All	6216/6312 (98%)	5131 (82%)	729 (12%)	356 (6%)	2 14

5 of 356 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	a	47	ARG
1	a	66	ALA
2	A	59	GLN
2	A	93	GLU
2	A	94	ALA

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	121/121 (100%)	118 (98%)	3 (2%)	42 61
1	b	121/121 (100%)	117 (97%)	4 (3%)	33 52
1	c	121/121 (100%)	114 (94%)	7 (6%)	17 38
1	d	121/121 (100%)	118 (98%)	3 (2%)	42 61
1	e	121/121 (100%)	117 (97%)	4 (3%)	33 52
1	f	121/121 (100%)	115 (95%)	6 (5%)	20 41
1	g	121/121 (100%)	119 (98%)	2 (2%)	56 72
1	h	121/121 (100%)	117 (97%)	4 (3%)	33 52
1	i	121/121 (100%)	115 (95%)	6 (5%)	20 41
1	j	121/121 (100%)	115 (95%)	6 (5%)	20 41
1	k	121/121 (100%)	118 (98%)	3 (2%)	42 61
1	l	121/121 (100%)	117 (97%)	4 (3%)	33 52
1	m	121/121 (100%)	117 (97%)	4 (3%)	33 52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	n	121/121 (100%)	118 (98%)	3 (2%)	42	61
1	o	121/121 (100%)	117 (97%)	4 (3%)	33	52
1	p	121/121 (100%)	115 (95%)	6 (5%)	20	41
1	q	121/121 (100%)	117 (97%)	4 (3%)	33	52
1	r	121/121 (100%)	115 (95%)	6 (5%)	20	41
1	s	121/121 (100%)	117 (97%)	4 (3%)	33	52
1	t	121/121 (100%)	113 (93%)	8 (7%)	14	34
1	u	121/121 (100%)	116 (96%)	5 (4%)	26	47
1	v	121/121 (100%)	120 (99%)	1 (1%)	79	85
1	w	121/121 (100%)	114 (94%)	7 (6%)	17	38
1	x	121/121 (100%)	115 (95%)	6 (5%)	20	41
2	A	109/109 (100%)	101 (93%)	8 (7%)	11	31
2	B	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	C	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	D	109/109 (100%)	103 (94%)	6 (6%)	18	39
2	E	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	F	109/109 (100%)	102 (94%)	7 (6%)	14	35
2	G	109/109 (100%)	103 (94%)	6 (6%)	18	39
2	H	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	I	109/109 (100%)	106 (97%)	3 (3%)	38	57
2	J	109/109 (100%)	102 (94%)	7 (6%)	14	35
2	K	109/109 (100%)	100 (92%)	9 (8%)	9	27
2	L	109/109 (100%)	106 (97%)	3 (3%)	38	57
2	M	109/109 (100%)	105 (96%)	4 (4%)	29	49
2	N	109/109 (100%)	98 (90%)	11 (10%)	6	20
2	O	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	P	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	Q	109/109 (100%)	99 (91%)	10 (9%)	7	23
2	R	109/109 (100%)	106 (97%)	3 (3%)	38	57
2	S	109/109 (100%)	106 (97%)	3 (3%)	38	57
2	T	109/109 (100%)	102 (94%)	7 (6%)	14	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U	109/109 (100%)	101 (93%)	8 (7%)	11	31
2	V	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	W	109/109 (100%)	104 (95%)	5 (5%)	23	44
2	X	109/109 (100%)	106 (97%)	3 (3%)	38	57
All	All	5520/5520 (100%)	5272 (96%)	248 (4%)	26	45

5 of 248 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	l	58	ASN
1	v	106	MET
1	o	106	MET
2	U	154	ASN
2	W	128	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	l	111	GLN
2	V	95	HIS
2	M	95	HIS
2	V	83	HIS
2	X	63	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

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-8341. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary 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: 144

Y Index: 144

Z Index: 144

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: 144

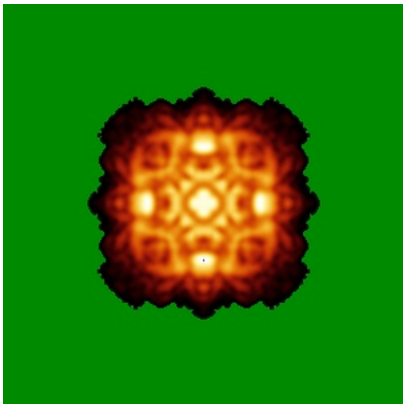
Y Index: 144

Z Index: 144

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

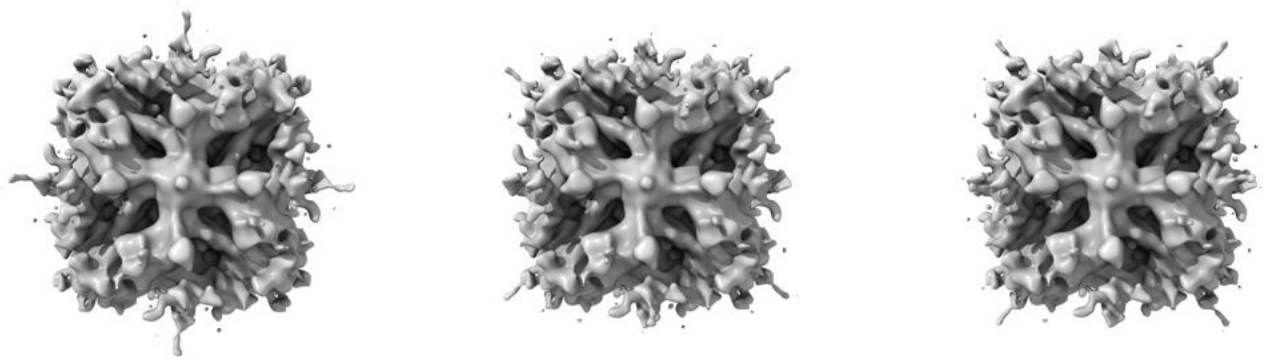
Y

Z

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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

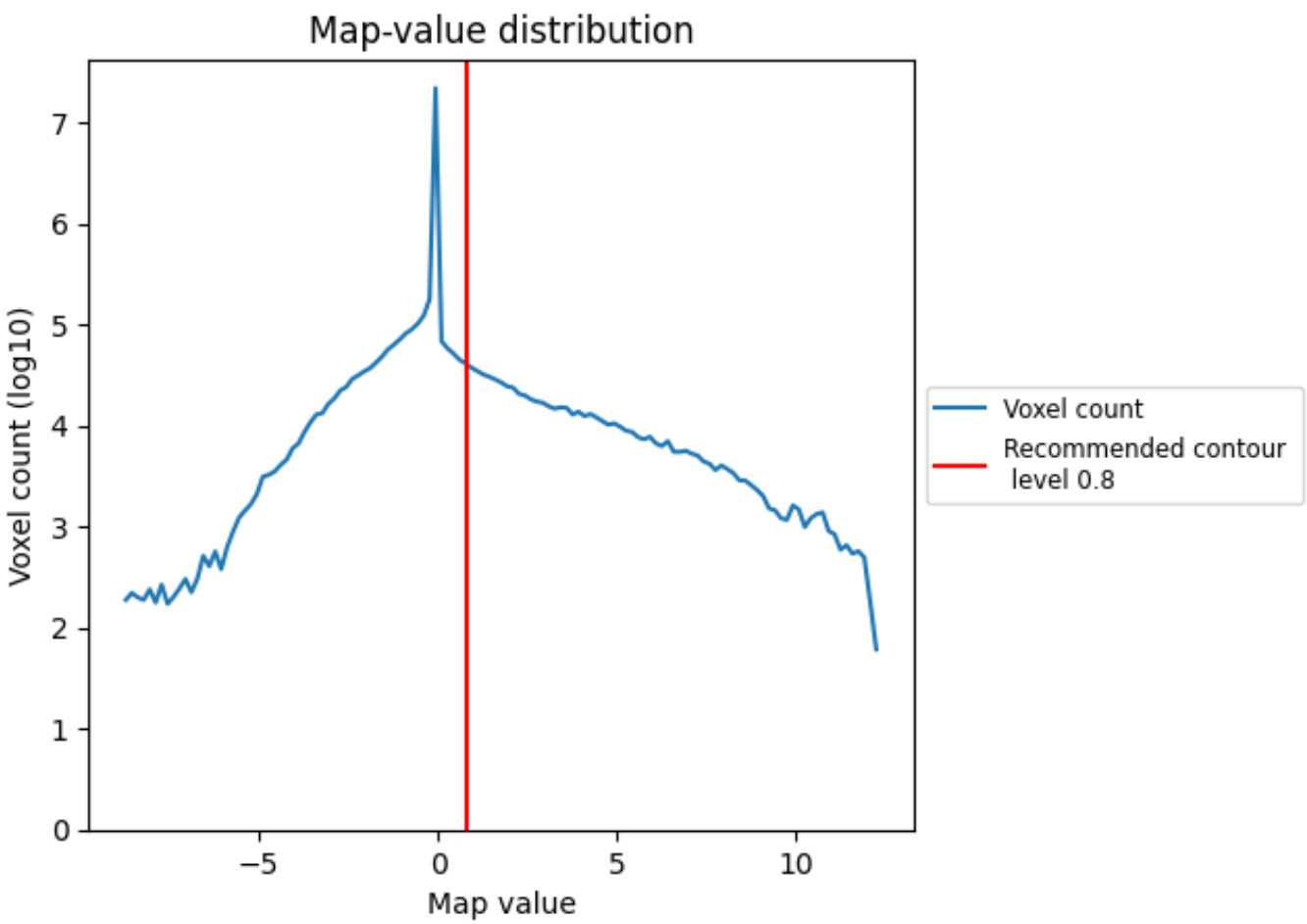
6.6 Mask visualisation (i)

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

7 Map analysis (i)

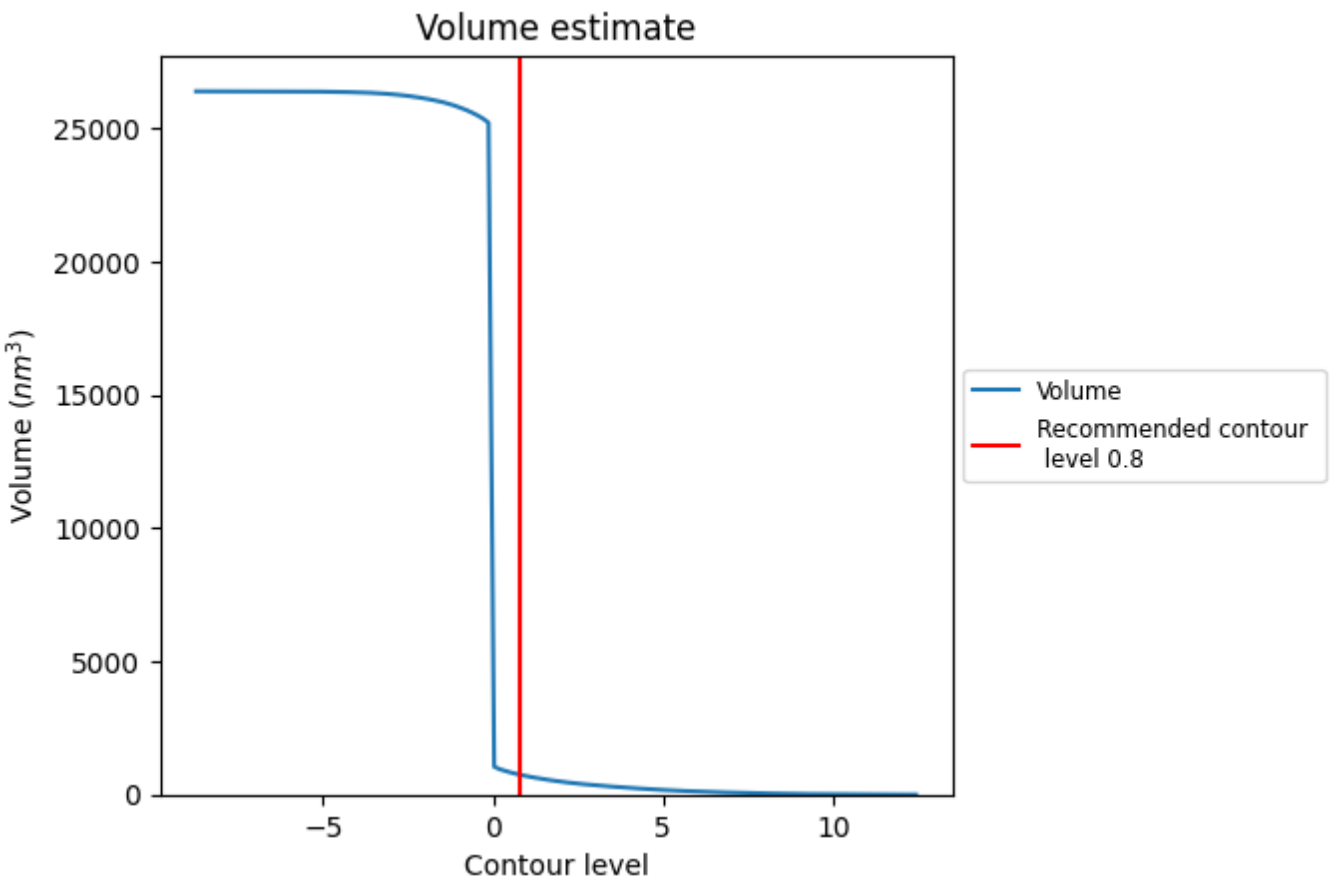
This section contains the results of statistical analysis of the map.

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.

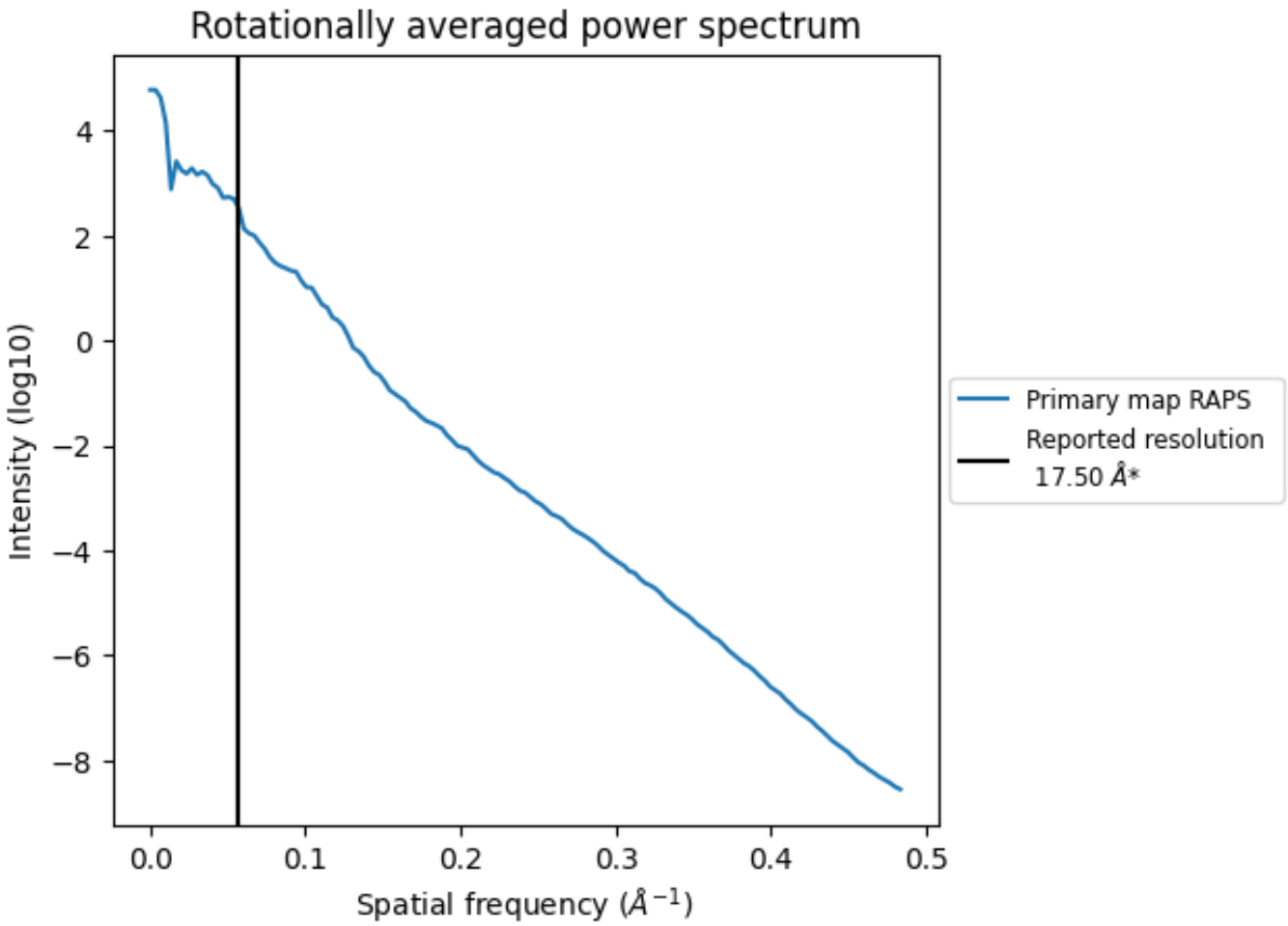
7.2 Volume estimate (i)



The volume at the recommended contour level is 743 nm^3; this corresponds to an approximate mass of 672 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)

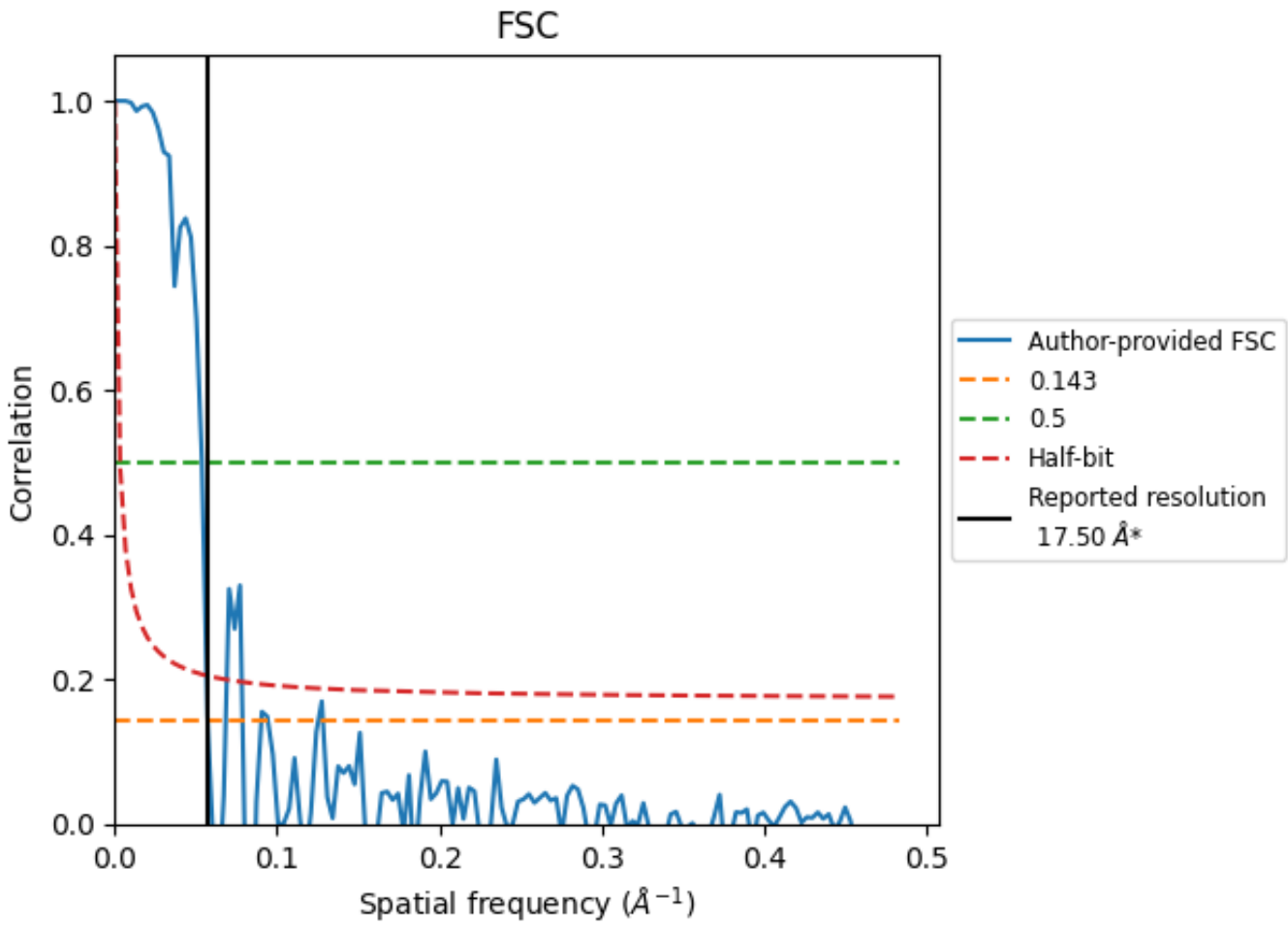


*Reported resolution corresponds to spatial frequency of 0.057 Å^{-1}

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 0.057 Å^{-1}

8.2 Resolution estimates (i)

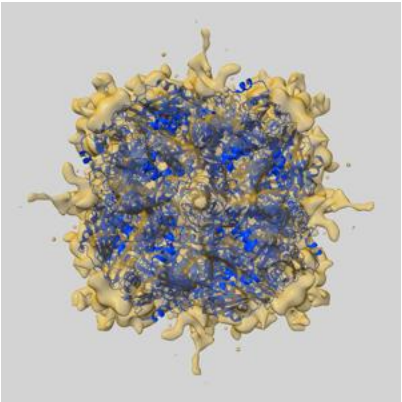
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	17.50	-	-
Author-provided FSC curve	17.45	18.59	17.67
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

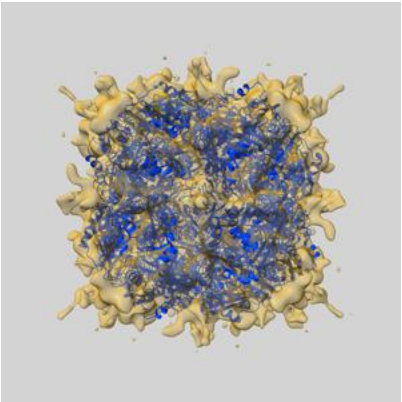
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-8341 and PDB model 5T0V. Per-residue inclusion information can be found in section 3 on page 11.

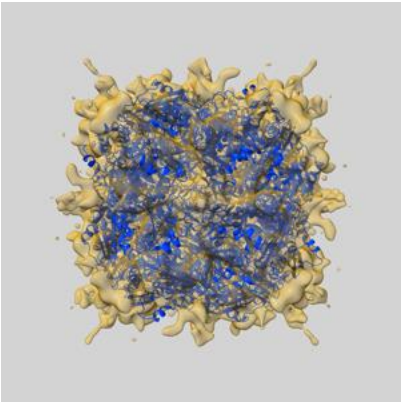
9.1 Map-model overlay (i)



X



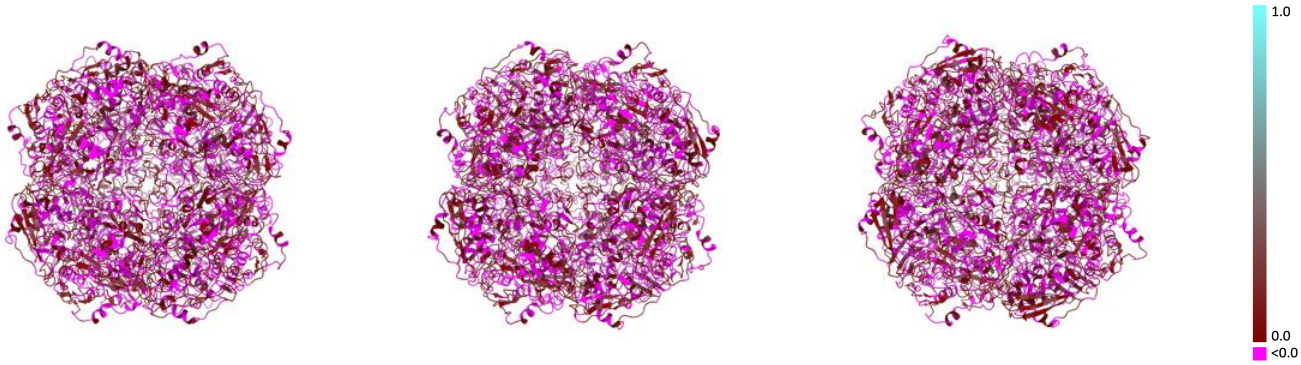
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.8 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.

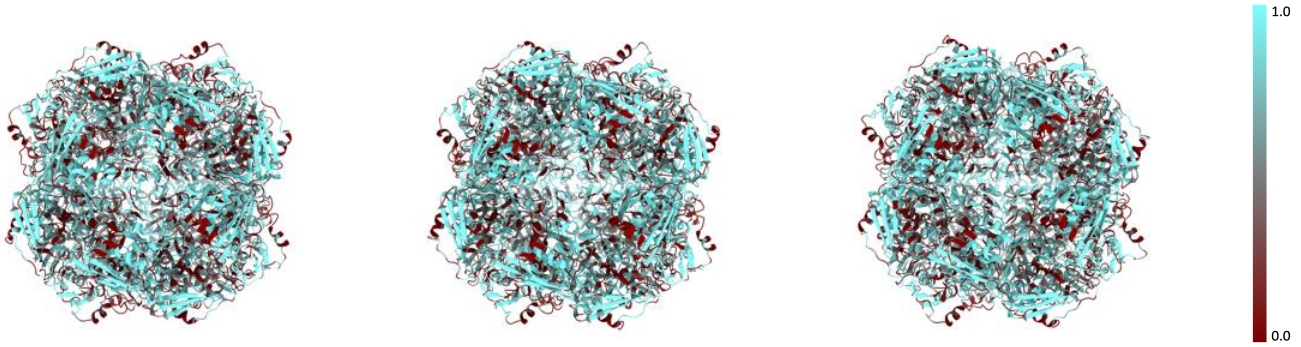
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

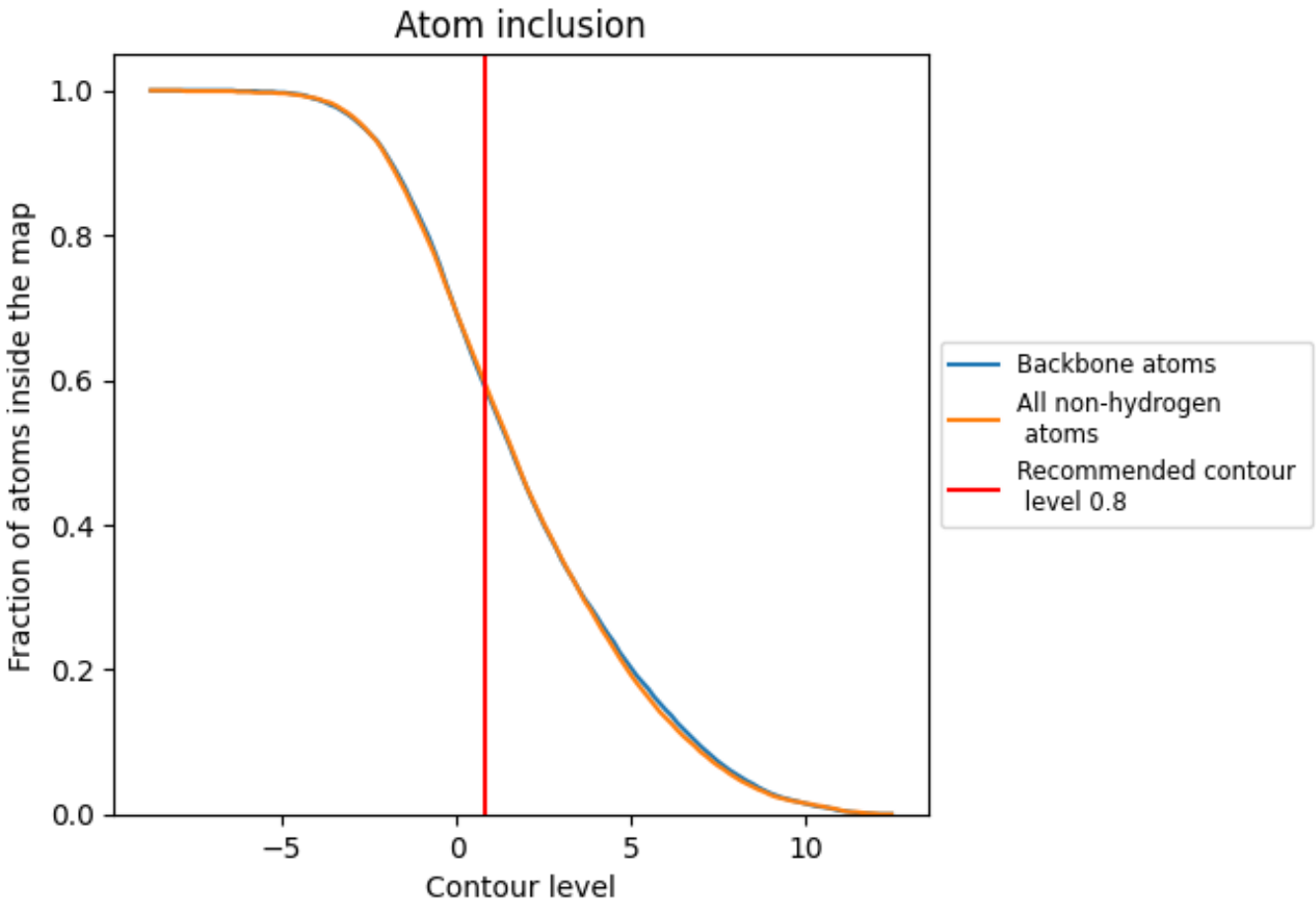
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.8).

9.4 Atom inclusion (i)



At the recommended contour level, 59% of all backbone atoms, 60% 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 (0.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5980	0.0120
A	0.6230	0.0110
B	0.6420	0.0250
C	0.6450	0.0120
D	0.6090	0.0150
E	0.6460	0.0350
F	0.6220	0.0160
G	0.6290	0.0120
H	0.6410	0.0280
I	0.6390	0.0150
J	0.6180	0.0110
K	0.6580	0.0430
L	0.6400	0.0260
M	0.6120	0.0080
N	0.6450	0.0180
O	0.6230	0.0050
P	0.6150	0.0140
Q	0.6380	0.0280
R	0.6360	0.0140
S	0.6060	0.0030
T	0.6460	0.0260
U	0.6090	0.0080
V	0.6330	0.0190
W	0.6500	0.0260
X	0.6460	0.0160
a	0.5660	0.0070
b	0.5700	0.0090
c	0.5750	0.0060
d	0.5800	0.0150
e	0.5570	0.0010
f	0.5730	0.0010
g	0.5740	0.0120
h	0.5540	0.0110
i	0.5540	0.0070
j	0.5620	0.0110

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Chain	Atom inclusion	Q-score
k	0.5500	0.0110
l	0.5710	0.0030
m	0.5470	-0.0050
n	0.5680	0.0070
o	0.5760	-0.0020
p	0.5840	0.0110
q	0.5480	-0.0020
r	0.5860	0.0120
s	0.5630	0.0140
t	0.5660	0.0170
u	0.5730	0.0090
v	0.5780	0.0050
w	0.5540	0.0070
x	0.5760	0.0110