



Full wwPDB EM Validation Report ⓘ

Jun 20, 2024 – 05:46 AM JST

PDB ID : 7WKK
EMDB ID : EMD-32566
Title : Cryo-EM structure of the IR subunit from *X. laevis* NPC
Authors : Huang, G.; Zhan, X.; Shi, Y.
Deposited on : 2022-01-10
Resolution : 4.20 Å(reported)

This is a Full wwPDB EM Validation 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:

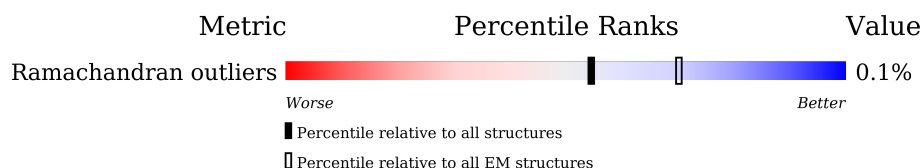
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

1 Overall quality at a glance

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


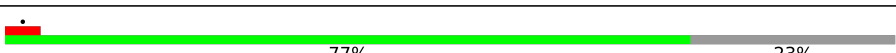

The reported resolution of this entry is 4.20 Å.

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.






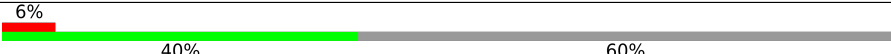

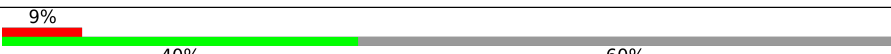
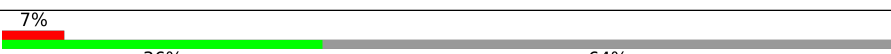


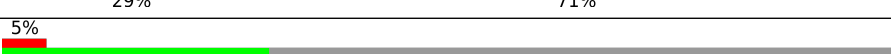

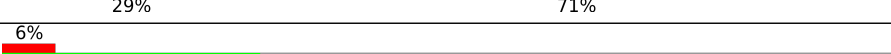
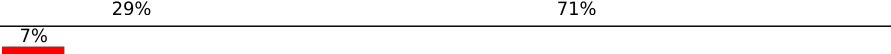






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023

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	2011	 84% 16%
1	a	2011	 83% 17%
2	B	1739	 85% 15%
2	b	1739	 85% 15%
3	C	820	 5% 77% 23%
3	E	820	 76% 24%
3	c	820	 77% 23%
3	e	820	 76% 24%
4	D	1388	 80% 20%
4	F	1388	 79% 21%
4	M	1388	 12% 62% 37%

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Mol	Chain	Length	Quality of chain
4	d	1388	
4	f	1388	
4	m	1388	
5	G	535	
5	J	535	
5	g	535	
5	j	535	
6	H	547	
6	L	547	
6	h	547	
6	l	547	
7	I	599	
7	K	599	
7	i	599	
7	k	599	
8	O	523	
8	o	523	
9	N	660	
9	n	660	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 92821 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 MGC83295 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	1684	Total	C	N	O	0	0
			8339	4971	1684	1684		
1	a	1669	Total	C	N	O	0	0
			8268	4930	1669	1669		

- Molecule 2 is a protein called Nup188 domain-containing protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	1482	Total	C	N	O	0	0
			7347	4383	1482	1482		
2	b	1482	Total	C	N	O	0	0
			7347	4383	1482	1482		

- Molecule 3 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	633	Total	C	N	O	0	0
			3144	1878	633	633		
3	E	625	Total	C	N	O	0	0
			3105	1855	625	625		
3	c	633	Total	C	N	O	0	0
			3144	1878	633	633		
3	e	625	Total	C	N	O	0	0
			3105	1855	625	625		

- Molecule 4 is a protein called Nup155-prov protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	1115	Total	C	N	O	0	0
			5524	3294	1115	1115		
4	F	1094	Total	C	N	O	0	0
			5417	3229	1094	1094		

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Mol	Chain	Residues	Atoms				AltConf	Trace
4	M	869	Total	C	N	O	0	0
			4296	2558	869	869		
4	d	1123	Total	C	N	O	0	0
			5563	3317	1123	1123		
4	f	1097	Total	C	N	O	0	0
			5432	3238	1097	1097		
4	m	869	Total	C	N	O	0	0
			4296	2558	869	869		

- Molecule 5 is a protein called Nup54.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	215	Total	C	N	O	0	0
			1063	633	215	215		
5	J	195	Total	C	N	O	0	0
			963	573	195	195		
5	g	215	Total	C	N	O	0	0
			1063	633	215	215		
5	j	195	Total	C	N	O	0	0
			963	573	195	195		

- Molecule 6 is a protein called IL4I1 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	H	163	Total	C	N	O	0	0
			813	487	163	163		
6	L	156	Total	C	N	O	0	0
			778	466	156	156		
6	h	163	Total	C	N	O	0	0
			813	487	163	163		
6	l	156	Total	C	N	O	0	0
			778	466	156	156		

- Molecule 7 is a protein called MGC84997 protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	I	171	Total	C	N	O	0	0
			853	511	171	171		
7	K	166	Total	C	N	O	0	0
			829	497	166	166		
7	i	171	Total	C	N	O	0	0
			853	511	171	171		

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Mol	Chain	Residues	Atoms				AltConf	Trace
7	k	166	Total	C	N	O	0	0
			829	497	166	166		

- Molecule 8 is a protein called Aaas-prov protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	O	367	Total	C	N	O	0	0
			1805	1071	367	367		
8	o	367	Total	C	N	O	0	0
			1805	1071	367	367		

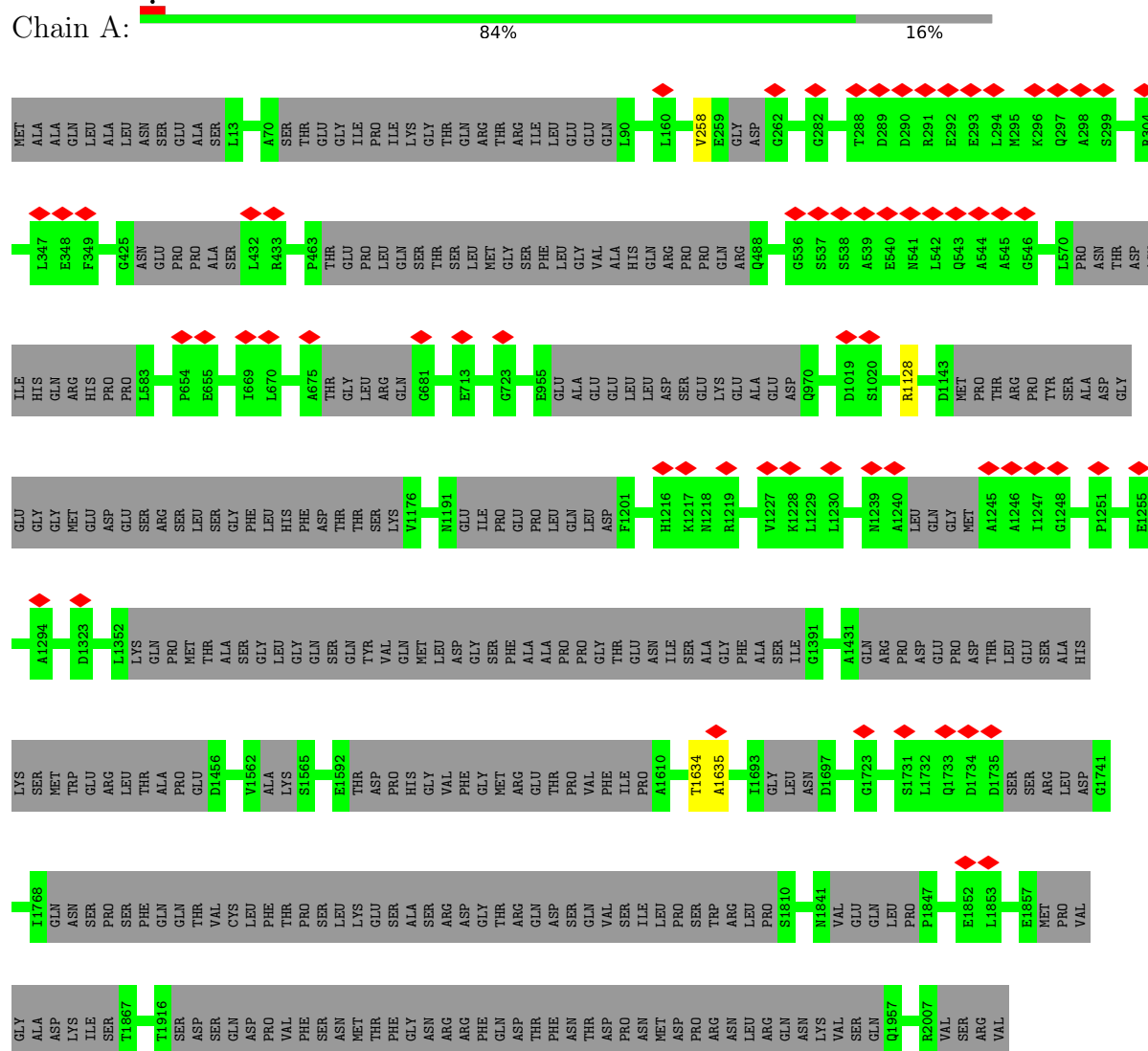
- Molecule 9 is a protein called Nucleoporin NDC1.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	N	431	Total	C	N	O	0	0
			2143	1281	431	431		
9	n	431	Total	C	N	O	0	0
			2143	1281	431	431		

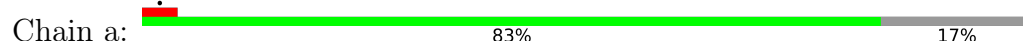
3 Residue-property plots

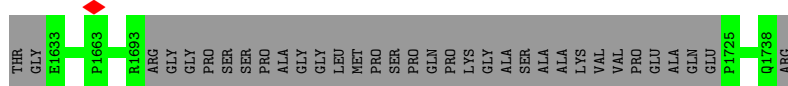
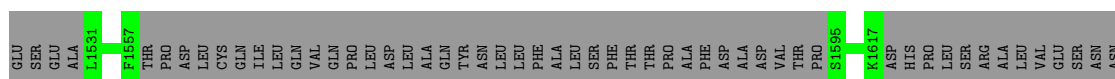
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: MGC83295 protein



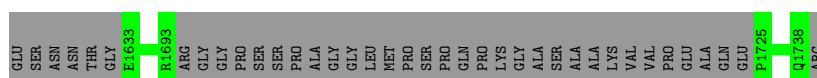
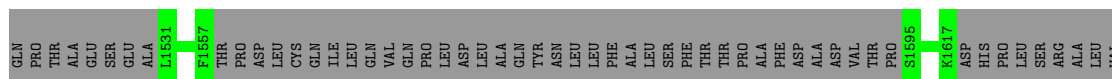
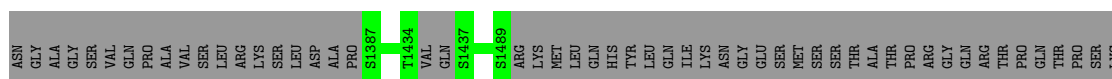
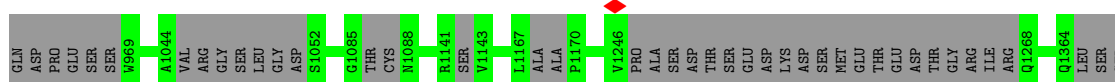
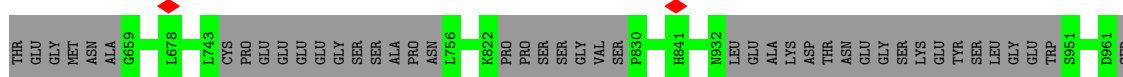
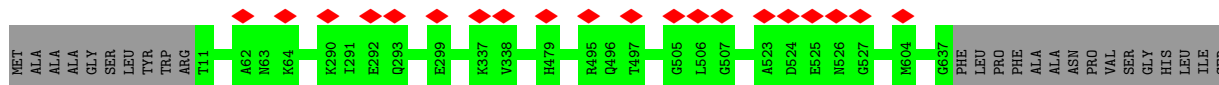
• Molecule 1: MGC83295 protein





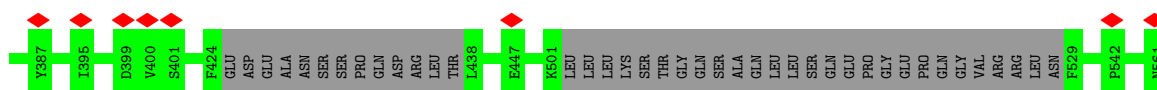
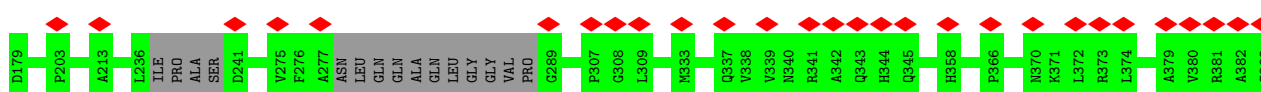
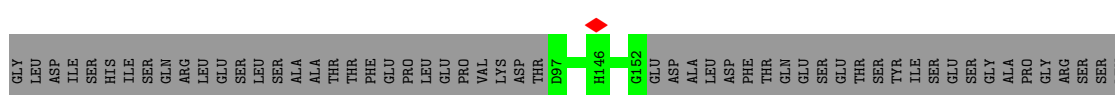
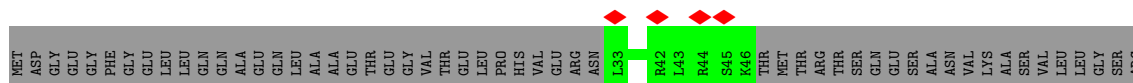
• Molecule 2: Nup188 domain-containing protein

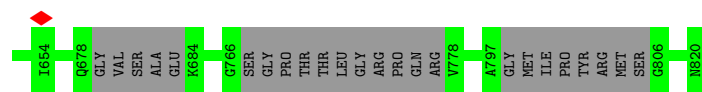
Chain b: 85% 15%



• Molecule 3: Nuclear pore complex protein Nup93

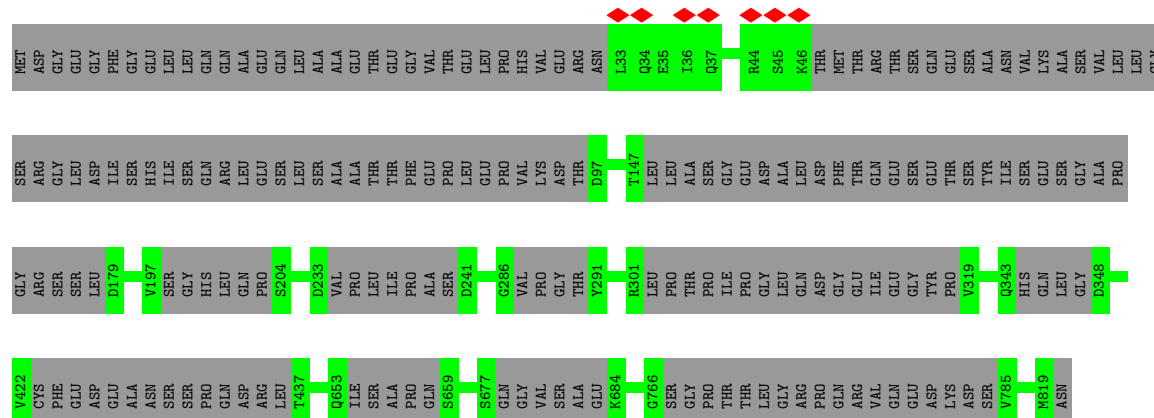
Chain C: 5% 77% 23%





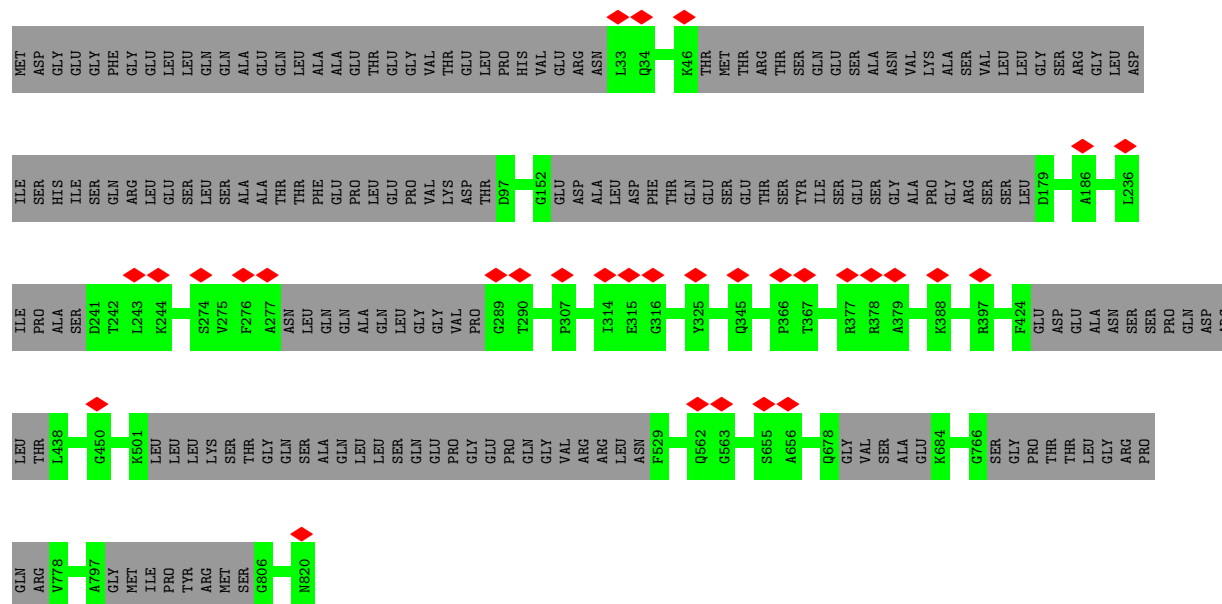
• Molecule 3: Nuclear pore complex protein Nup93

Chain E: 76% 24%



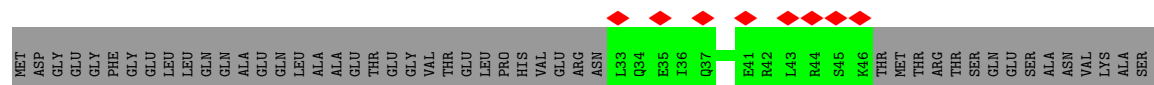
• Molecule 3: Nuclear pore complex protein Nup93

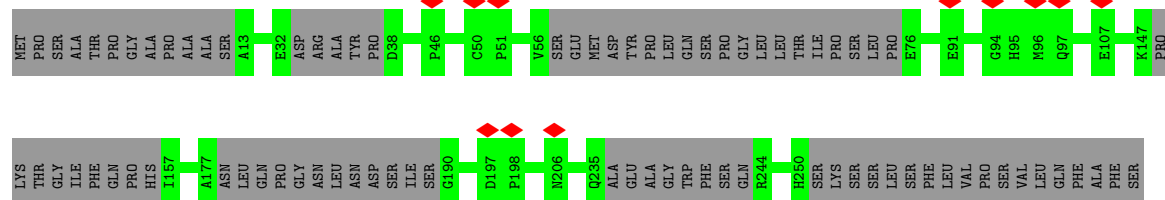
Chain c: 77% 23%

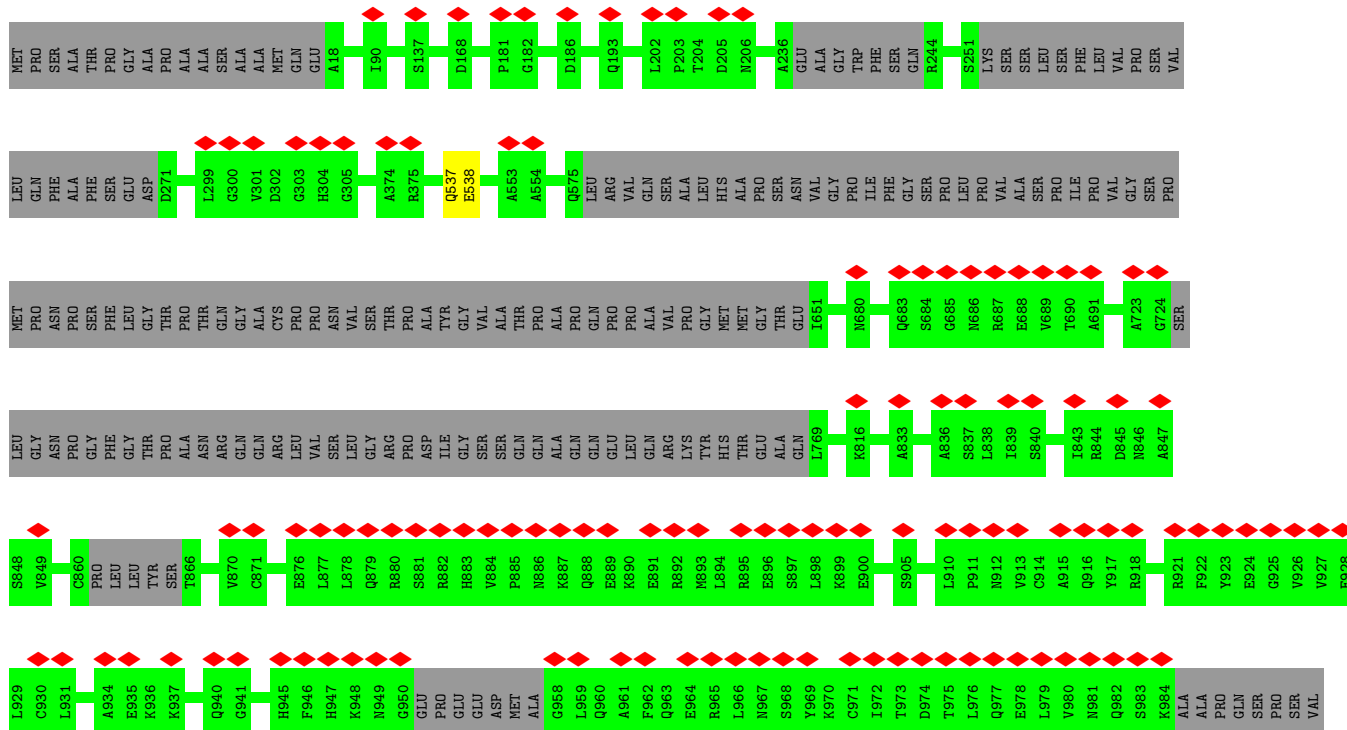


• Molecule 3: Nuclear pore complex protein Nup93

Chain e: 76% 24%







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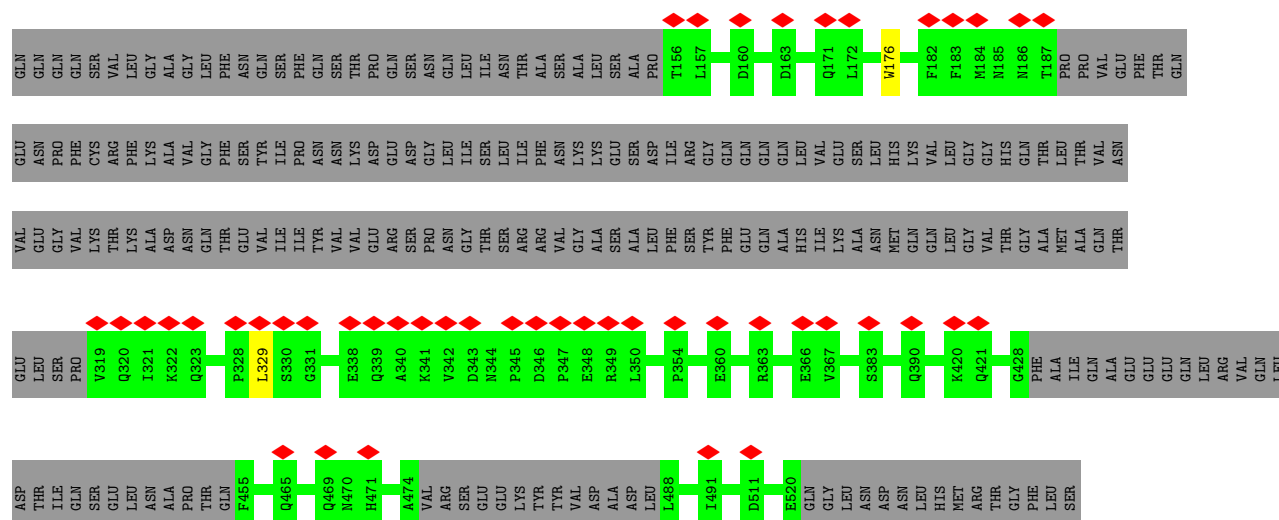
- Molecule 5: Nup54



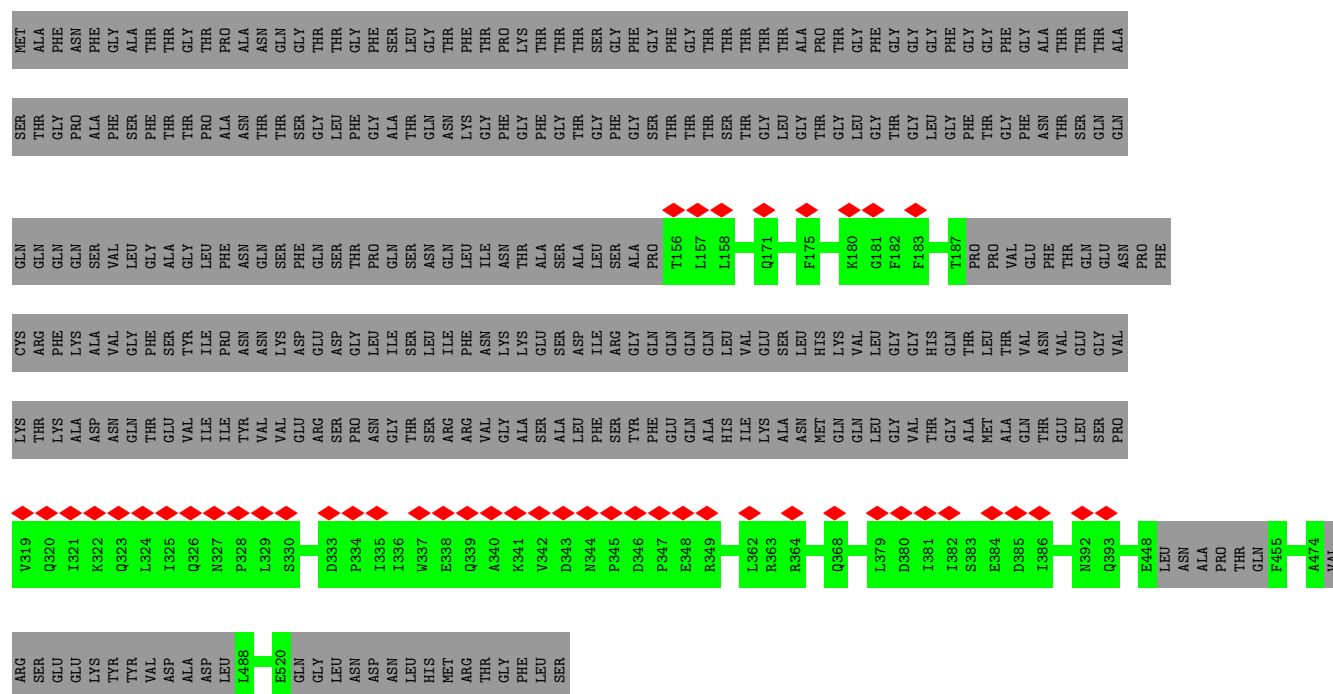
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I335	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
E338	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
Q339	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
A340	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
K341	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
V342	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
D343	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
N344	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
P345	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
D346	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
P347	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
E348	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
R349	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
L350	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
I356	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
G357	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
L365	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
D369	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
D385	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
E388	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
I400	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
S411	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
L415	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
S427	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
E448	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
LEU	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
ASN	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
ALA	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
PRO	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
THR	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
GLN	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
F455	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
A474	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
VAL	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
ARG	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
SER	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
GLU	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
Q319	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
Q320	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
I321	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
K322	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER
ASP	GLN	THR	GLU	VAL	ILE	ILE	TYR	ARG	GLU	ASP	ASP	LEU	SER

- Molecule 5: Nup54

[illegible]



- Molecule 5: Nup54



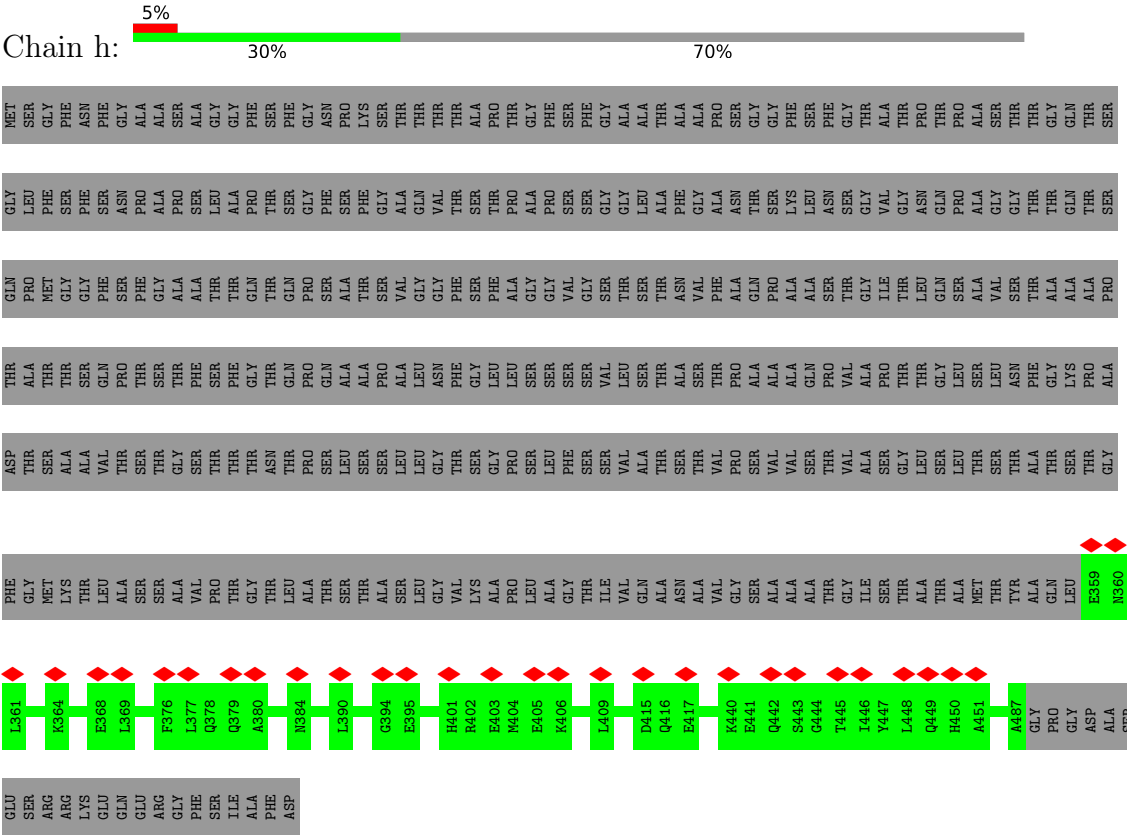
- Molecule 5: Nup54







• Molecule 6: IL4I1 protein



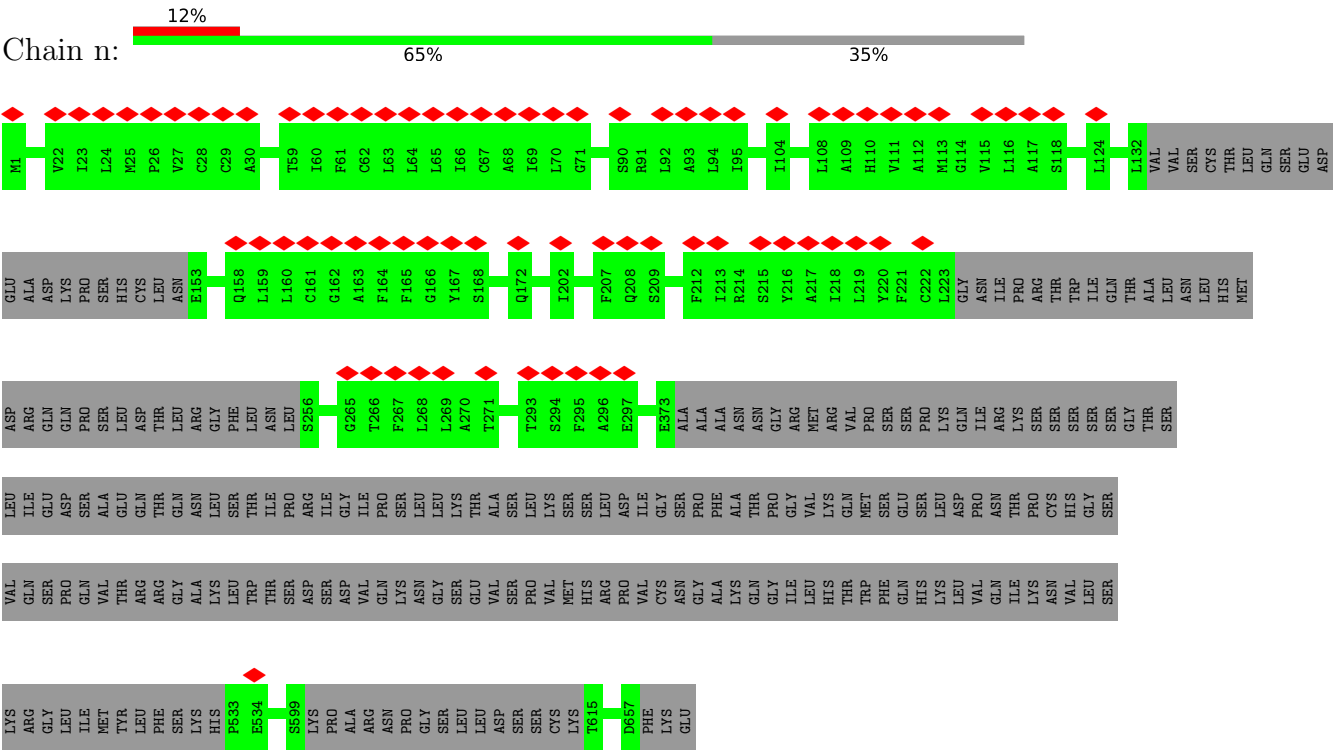
• Molecule 6: IL4I1 protein

THR	SER	ALA	+	VAL	GLN	SER	GLY	MET
THR	SER	PHE	L327	SER	SER	LEU	LEU	
SER	SER	LEU		GLN	THR	ALA	GLY	
PHE	ALA	GLY	V330	VAL	THR	SER	GLY	
GLY	PHE	ASP	A331	THR	GLY	ALA	GLY	
GLN	GLY	SER	S332	THR	SER	LEU	LEU	
ASN	ASN	THR	S332	HIS	THR	THR	PHE	
		THR			THR	SER	GLY	
LEU	THR	ASP	S333	GLU	THR	THR	SER	
LEU	SER	PHE	G334	GLY	LEU	PRO	THR	
GLN	GLY	VAL	L335	LEU	GLY	PRO	LYS	
LEU	SER	GLU		GLY	GLN	ALA	PRO	
SER	SER	ALA	Q336	GLY	SER	THR	ALA	
LYS	SER	ARG	R337	LEU	THR	GLY	ALA	
LYS	SER	ARG				ALA	SER	
PRO	PHE	ARG	L340	ASP	LEU	PRO	ALA	
PRO	GLY	ALA		PHE	GLY	THR	GLY	
ALA	PHE	GLU		THR	GLN	PRO	PHE	
GLY	GLY	ALA	R344	SER	SER	PHE	LEU	
ASN	THR	LYS		SER	LEU	THR	GLY	
LYS	ALA	LYS		SER	LEU	THR	GLY	
ARG	ASN	TRP	A350	ASP	GLY	ALA	GLY	
LYS	PRO	GLN		LYS	GLN	LEU	ASN	
	SER	ALA	K354	SER	SER	SER	ALA	
GLY	GLY	PRO	N355	ASP	LEU	THR	ALA	
SER	SER	ARG	A356	LYS	GLY	PRO	ALA	
LEU	THR	VAL	E357	ALA	SER	THR	THR	
ALA	SER	THR		GLY	GLN	THR	GLY	
GLY	GLY	GLY	A359	THR	LEU	THR	ALA	
PHE	GLY	PRO	L360	ARG	LEU	ALA	ALA	
GLY	THR	THR	R361	PRO	GLY	ALA	THR	
THR	GLY	THR		GLU	GLN	ALA	PRO	
SER	PRO	PHE		ASP	SER	ALA	SER	
THR	THR	SER	P367	GLY	SER	THR	THR	
THR	THR	ASN		LYS	LEU	GLY	PHE	
SER	THR	ILE	GLN	LEU	GLY	LEU	SER	
GLY	GLY	PRO	HIS	LYS	SER	LEU	VAL	
PHE	ASN	ASN	GLU	ASP	THR	GLY	GLY	
ALA	ALA	ALA	N373	GLU	LEU	GLY	ASN	
SER	PHE	ALA		ASN	GLY	THR	LYS	
ASN	ASN	VAL	S376	LEU	GLN	LEU	PRO	
PRO	GLY	MET	Q390	P282	SER	THR	ALA	
ILE	ASN	ALA		Q283	LEU	GLY	GLY	
ALA	ASN	ALA	E400	L284	GLY	ALA	ALA	
THR	ALA	THR		L285	GLN	GLY	THR	
SER	SER	LEU	Q406	C286	SER	SER	PRO	
THR	THR	ALA	S409	Q287	LEU	LEU	PHE	
GLY	GLY	GLN	H410	D288	LEU	PHE	SER	
THR	LEU	GLN	T411	V289	GLY	ASN	LEU	
PHE	PHE	GLN	L412	E290	GLY	THR	VAL	
GLY	GLY	PRO	H413	H291	ASN	PRO	THR	
VAL	VAL	THR	L414	F292	LEU	SER	SER	
SER	SER	THR	S415	Q293	GLY	ALA	THR	
ASN	ASN	GLY	P416	R294	VAL	GLY	SER	
PRO	PRO	PHE				THR	GLY	
SER	SER	SER	S420	E304	PRO	GLY	LEU	

Chain i:  8% 29% 71%



● Molecule 9: Nucleoporin NDC1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2093631	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.038	Depositor
Minimum map value	-0.020	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (\AA)	710.144, 710.144, 710.144	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.387, 1.387, 1.387	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	0.30	0/8318	0.40	0/11563
1	a	0.29	0/8246	0.40	0/11463
2	B	0.25	0/7330	0.38	0/10197
2	b	0.25	0/7330	0.38	0/10197
3	C	0.25	0/3134	0.37	0/4359
3	E	0.33	0/3093	0.41	0/4299
3	c	0.25	0/3134	0.38	0/4359
3	e	0.32	0/3093	0.42	0/4299
4	D	0.29	0/5506	0.43	0/7649
4	F	0.28	0/5399	0.42	0/7498
4	M	0.25	0/4288	0.43	0/5961
4	d	0.29	0/5545	0.44	0/7703
4	f	0.28	0/5414	0.42	0/7519
4	m	0.25	0/4288	0.43	0/5961
5	G	0.26	0/1059	0.41	0/1469
5	J	0.25	0/959	0.39	0/1329
5	g	0.26	0/1059	0.41	0/1469
5	j	0.26	0/959	0.40	0/1329
6	H	0.26	0/811	0.35	0/1131
6	L	0.35	0/775	0.38	0/1079
6	h	0.27	0/811	0.34	0/1131
6	l	0.34	0/775	0.37	0/1079
7	I	0.26	0/852	0.37	0/1190
7	K	0.41	1/827 (0.1%)	0.40	1/1154 (0.1%)
7	i	0.27	0/852	0.36	0/1190
7	k	0.30	0/827	0.37	0/1154
8	O	0.29	0/1799	0.49	0/2491
8	o	0.29	0/1799	0.49	0/2491
9	N	0.26	0/2138	0.36	0/2978
9	n	0.26	0/2138	0.36	0/2978
All	All	0.28	1/92558 (0.0%)	0.41	1/128669 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
4	F	0	1
4	M	0	1
4	f	0	1
4	m	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	K	415	SER	C-N	7.98	1.49	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	K	415	SER	C-N-CA	5.52	145.19	122.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1634	THR	Peptide
4	F	537	GLN	Peptide
4	M	537	GLN	Peptide
4	f	115	ILE	Peptide
4	m	537	GLN	Peptide

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	1642/2011 (82%)	1523 (93%)	116 (7%)	3 (0%)	47	80
1	a	1625/2011 (81%)	1509 (93%)	114 (7%)	2 (0%)	51	85
2	B	1448/1739 (83%)	1406 (97%)	42 (3%)	0	100	100
2	b	1448/1739 (83%)	1407 (97%)	41 (3%)	0	100	100
3	C	613/820 (75%)	593 (97%)	20 (3%)	0	100	100
3	E	601/820 (73%)	542 (90%)	59 (10%)	0	100	100
3	c	613/820 (75%)	592 (97%)	21 (3%)	0	100	100
3	e	601/820 (73%)	547 (91%)	54 (9%)	0	100	100
4	D	1079/1388 (78%)	1020 (94%)	58 (5%)	1 (0%)	51	85
4	F	1058/1388 (76%)	1018 (96%)	39 (4%)	1 (0%)	51	85
4	M	853/1388 (62%)	823 (96%)	29 (3%)	1 (0%)	51	85
4	d	1087/1388 (78%)	1029 (95%)	56 (5%)	2 (0%)	47	80
4	f	1061/1388 (76%)	1014 (96%)	46 (4%)	1 (0%)	51	85
4	m	853/1388 (62%)	823 (96%)	29 (3%)	1 (0%)	51	85
5	G	207/535 (39%)	193 (93%)	14 (7%)	0	100	100
5	J	187/535 (35%)	178 (95%)	7 (4%)	2 (1%)	14	52
5	g	207/535 (39%)	192 (93%)	15 (7%)	0	100	100
5	j	187/535 (35%)	174 (93%)	12 (6%)	1 (0%)	29	68
6	H	159/547 (29%)	154 (97%)	5 (3%)	0	100	100
6	L	150/547 (27%)	150 (100%)	0	0	100	100
6	h	159/547 (29%)	153 (96%)	6 (4%)	0	100	100
6	l	150/547 (27%)	148 (99%)	2 (1%)	0	100	100
7	I	169/599 (28%)	162 (96%)	7 (4%)	0	100	100
7	K	162/599 (27%)	154 (95%)	6 (4%)	2 (1%)	13	50
7	i	169/599 (28%)	159 (94%)	10 (6%)	0	100	100
7	k	162/599 (27%)	156 (96%)	4 (2%)	2 (1%)	13	50
8	O	355/523 (68%)	339 (96%)	16 (4%)	0	100	100
8	o	355/523 (68%)	339 (96%)	16 (4%)	0	100	100
9	N	421/660 (64%)	412 (98%)	9 (2%)	0	100	100
9	n	421/660 (64%)	412 (98%)	9 (2%)	0	100	100

Continued on next page...

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	18202/28198 (65%)	17321 (95%)	862 (5%)	19 (0%)	54	85

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1635	ALA
1	a	1635	ALA
1	A	258	VAL
4	F	538	GLU
5	J	176	TRP
4	M	538	GLU
4	m	538	GLU
1	A	1128	ARG
4	D	538	GLU
7	K	411	THR
4	d	538	GLU
4	f	538	GLU
7	k	412	LEU
7	k	413	HIS
7	K	416	PRO
1	a	1128	ARG
5	J	329	LEU
5	j	176	TRP
4	d	698	PRO

5.3.2 Protein sidechains [i](#)

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

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 monosaccharides 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.

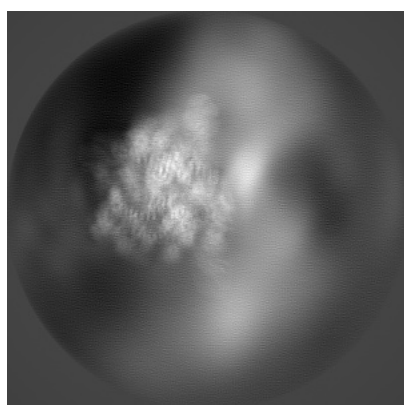
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32566. These allow visual inspection of the internal detail of the map and identification of artifacts.

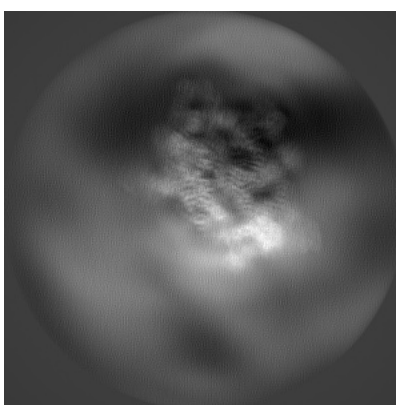
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

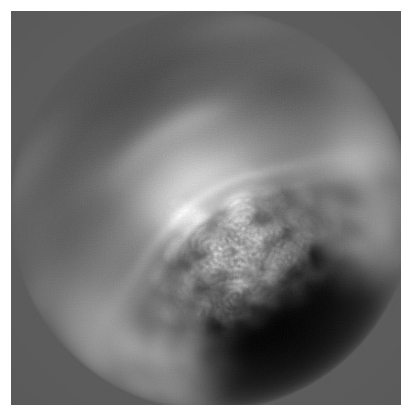
6.1.1 Primary map



X



Y

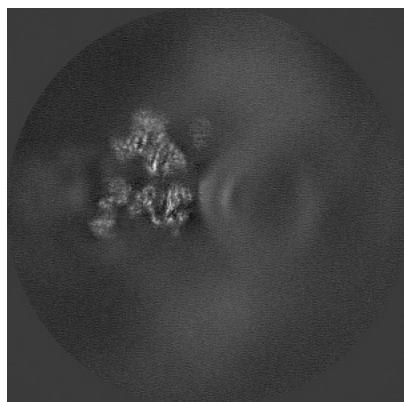


Z

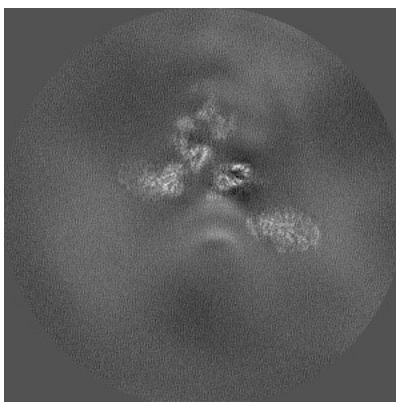
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

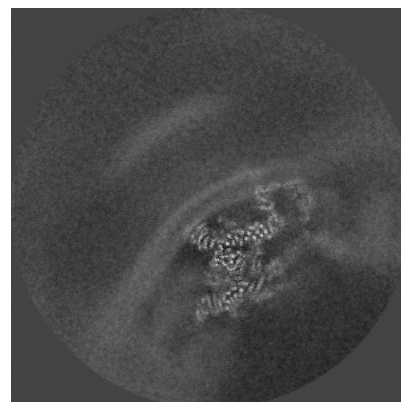
6.2.1 Primary map



X Index: 256



Y Index: 256

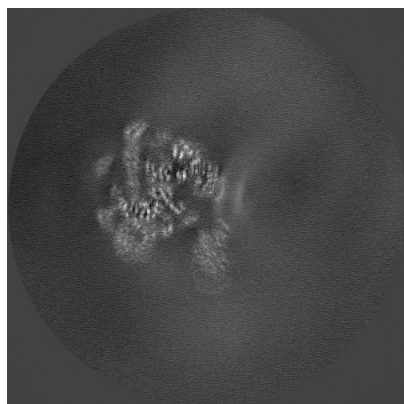


Z Index: 256

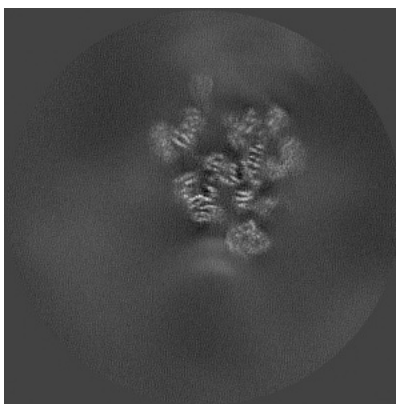
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

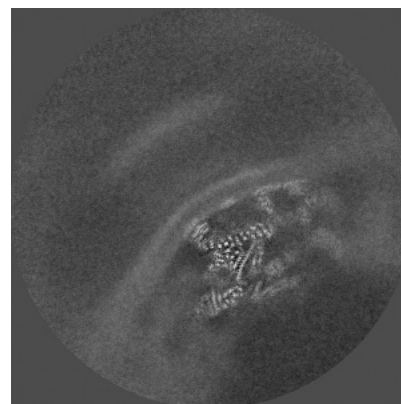
6.3.1 Primary map



X Index: 293



Y Index: 206

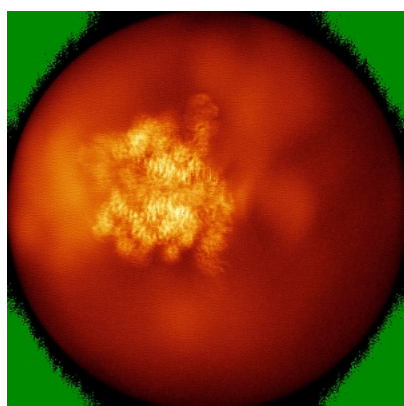


Z Index: 260

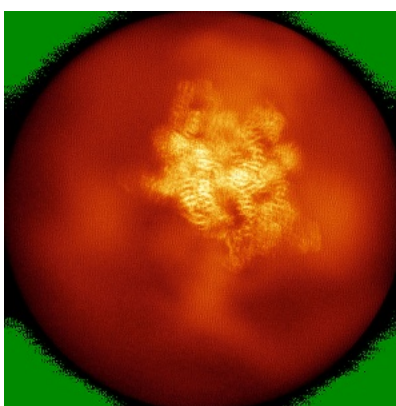
The images above show the largest variance slices of the map in three orthogonal directions.

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

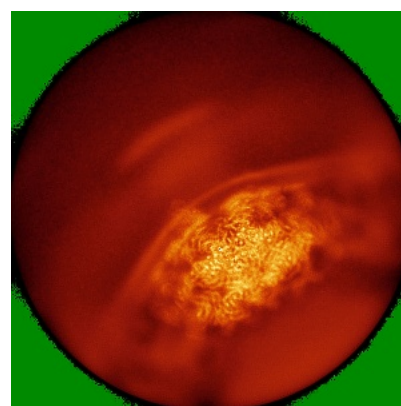
6.4.1 Primary map



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



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

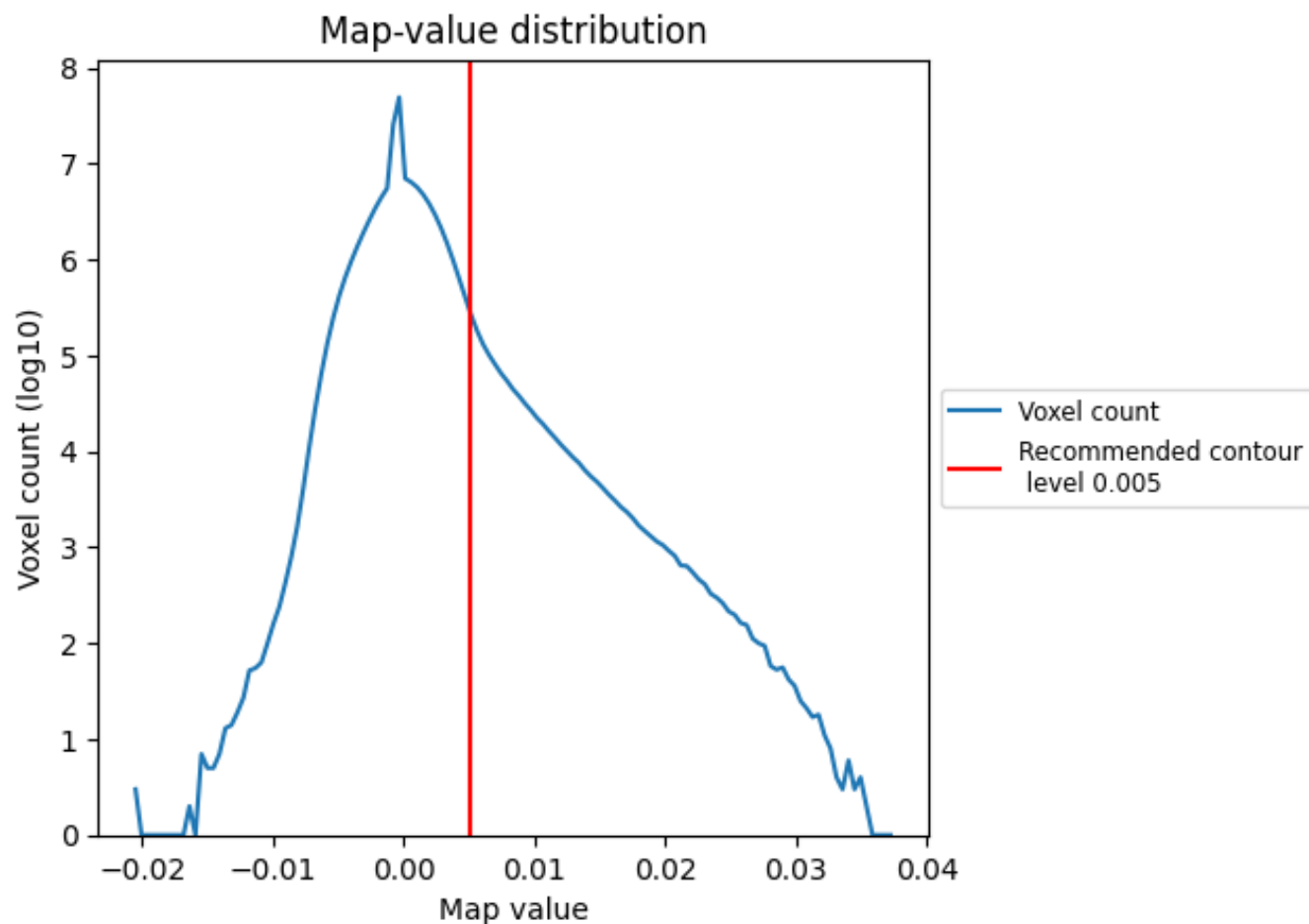
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

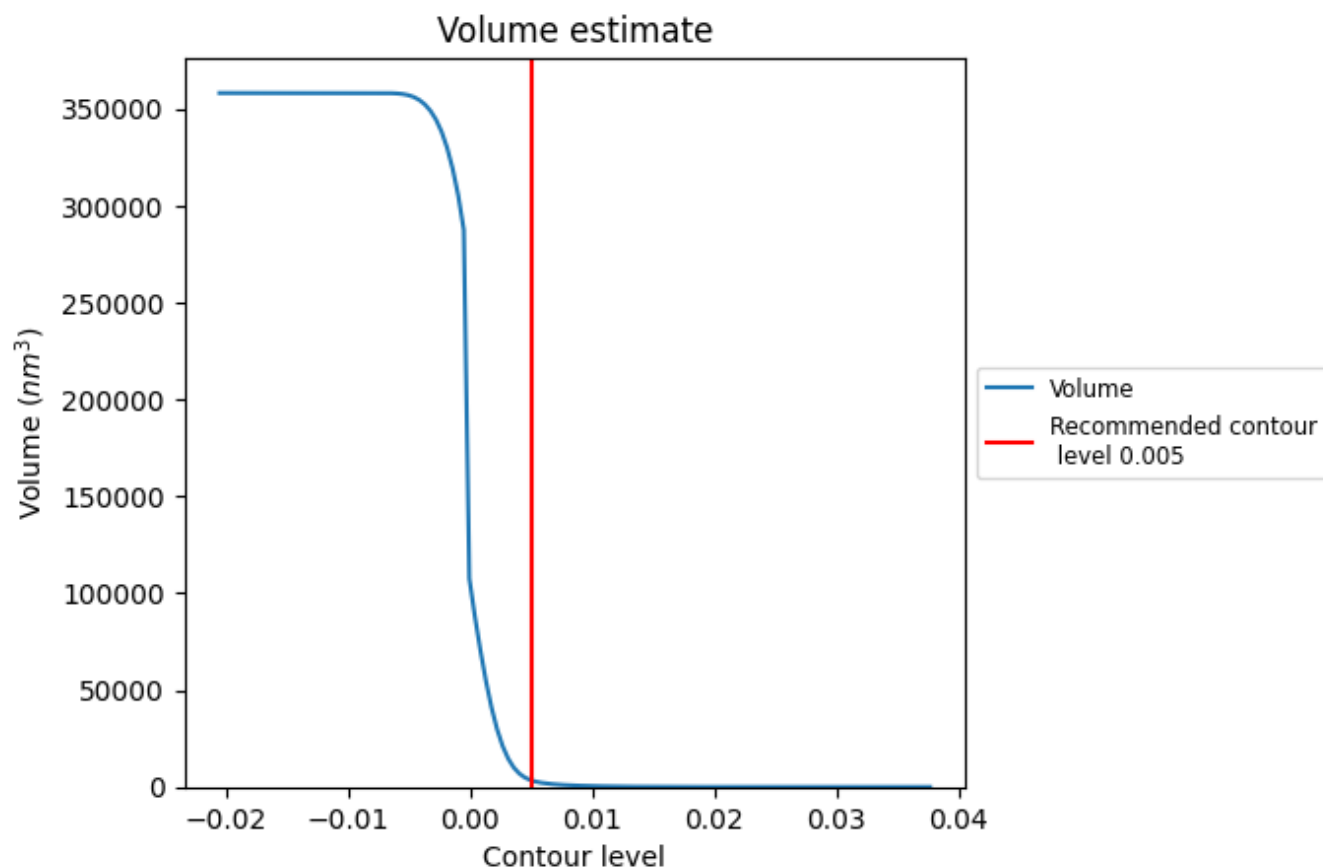
This section contains the results of statistical analysis of the map.

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.

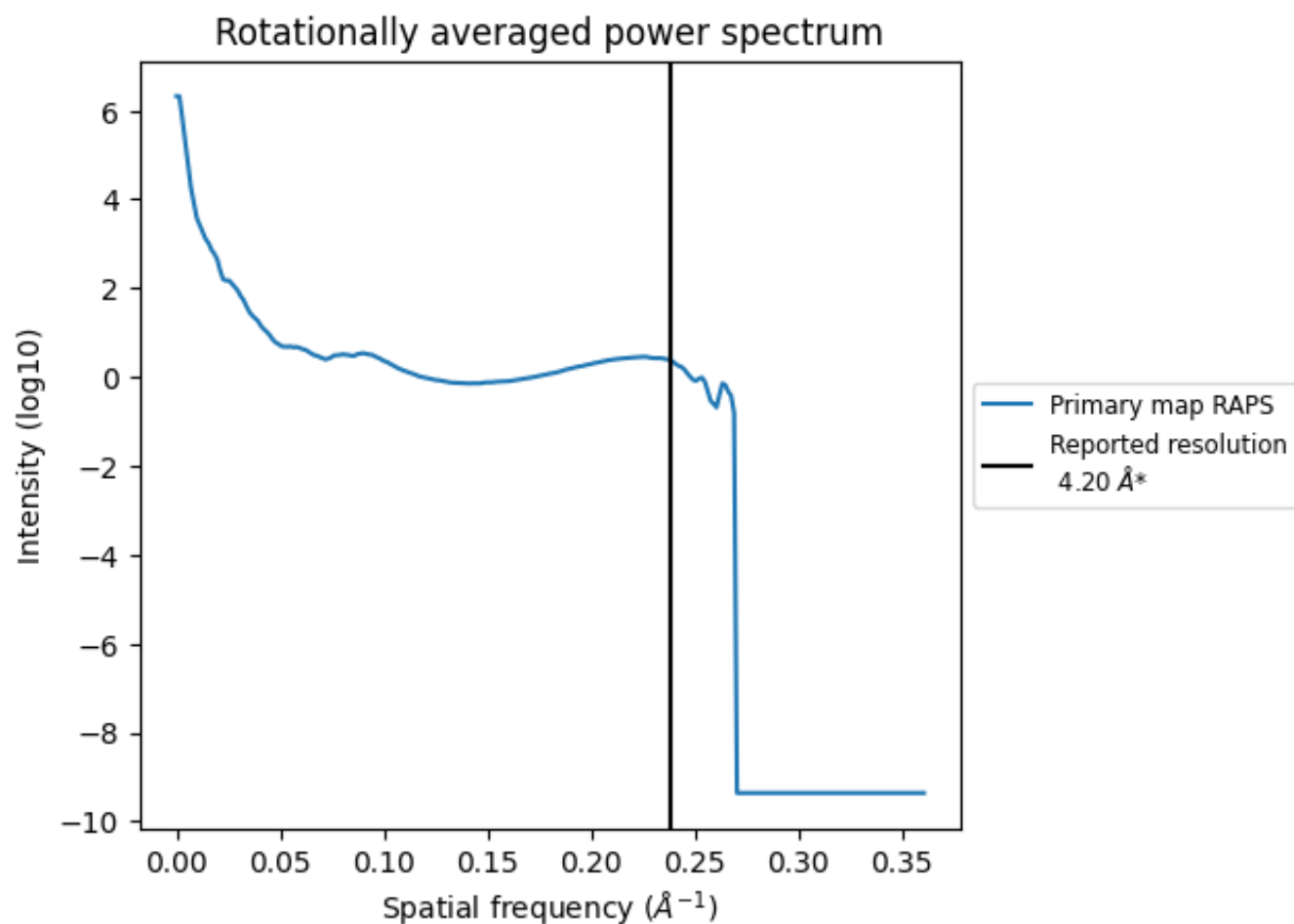
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3486 nm^3 ; this corresponds to an approximate mass of 3149 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 0.238 Å⁻¹

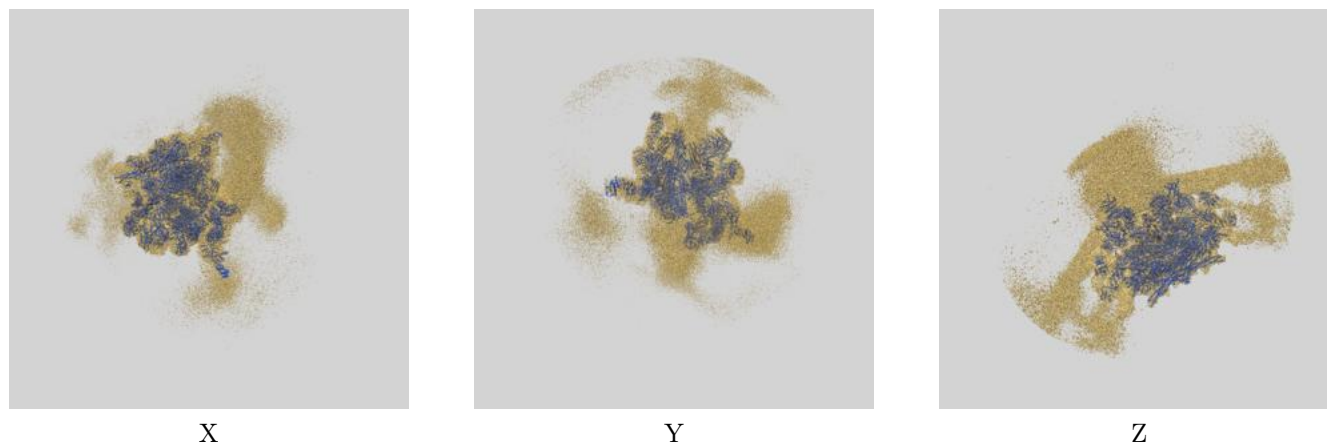
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

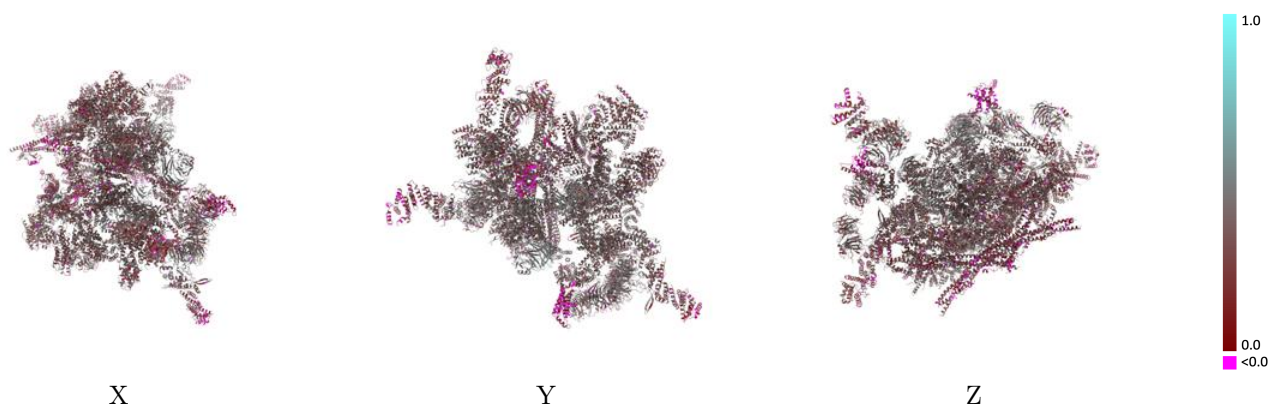
This section contains information regarding the fit between EMDB map EMD-32566 and PDB model 7WKK. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



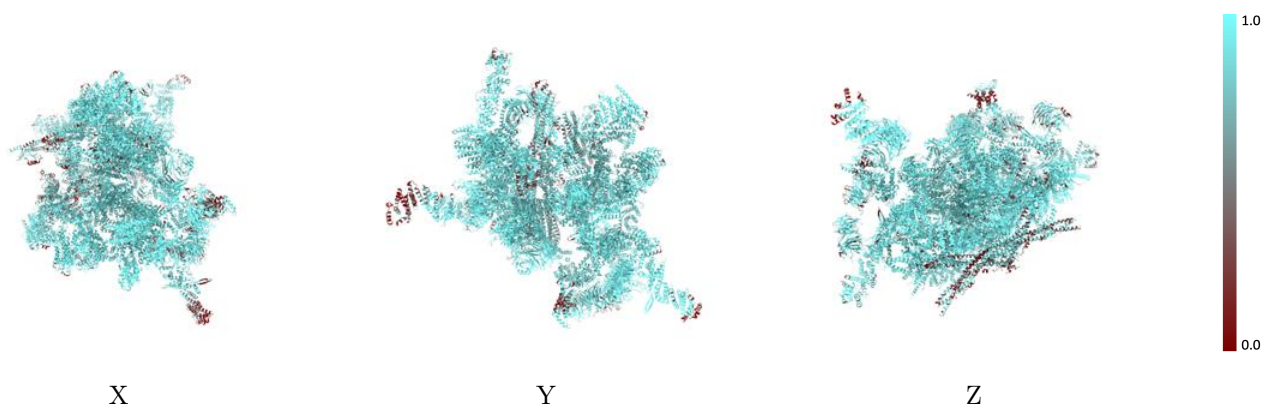
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



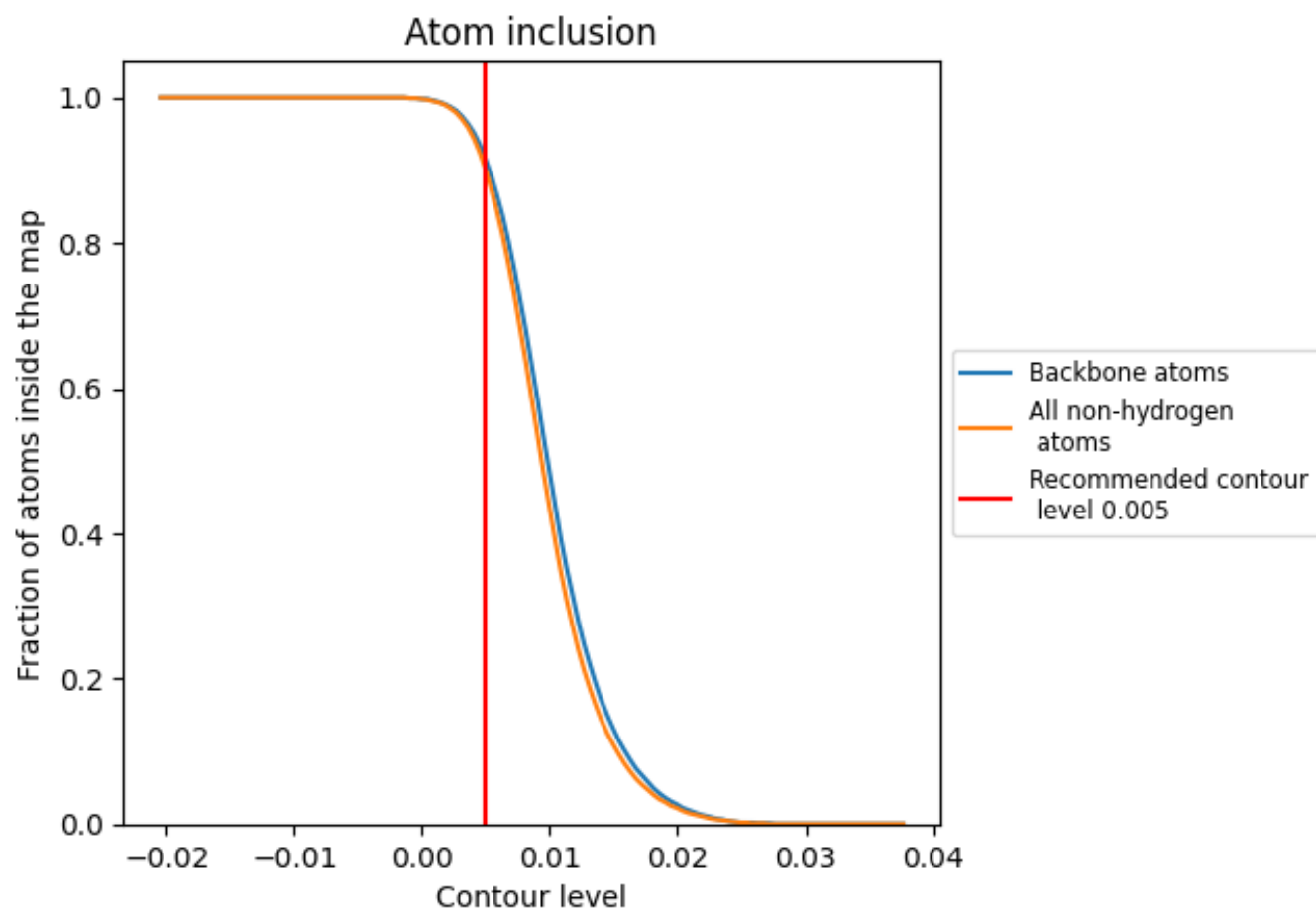
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 90% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.3490
A	 0.9400	 0.3610
B	 0.9650	 0.3500
C	 0.8980	 0.3010
D	 0.9710	 0.4130
E	 0.9760	 0.4020
F	 0.9220	 0.3760
G	 0.8070	 0.3160
H	 0.7170	 0.2640
I	 0.7690	 0.2870
J	 0.7300	 0.2680
K	 0.6790	 0.2380
L	 0.7200	 0.2520
M	 0.7910	 0.3620
N	 0.7640	 0.2400
O	 0.8340	 0.3690
a	 0.9270	 0.3590
b	 0.9640	 0.3420
c	 0.9170	 0.3040
d	 0.9540	 0.4020
e	 0.9720	 0.3950
f	 0.8950	 0.3660
g	 0.7290	 0.2720
h	 0.7470	 0.2870
i	 0.6920	 0.2760
j	 0.7590	 0.2820
k	 0.7370	 0.2500
l	 0.7760	 0.2530
m	 0.9230	 0.3720
n	 0.8090	 0.2360
o	 0.8260	 0.3550

