



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 04:35 PM UTC

PDB ID : 7N84 / pdb_00007n84
EMDB ID : EMD-24231
Title : Double nuclear outer ring from the isolated yeast NPC
Authors : Akey, C.W.; Rout, M.P.; Ouch, C.; Echeverria, I.; Fernandez-Martinez, J.;
Nudelman, I.
Deposited on : 2021-06-13
Resolution : 11.60 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

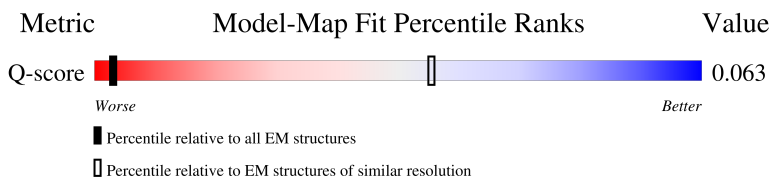
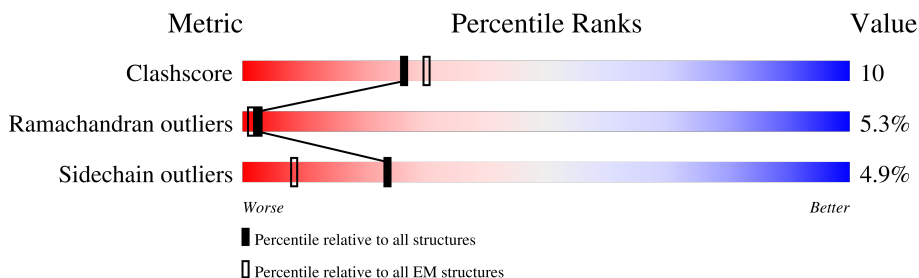
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



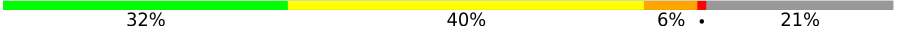
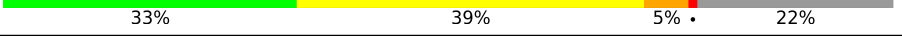
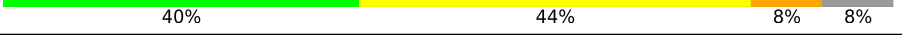
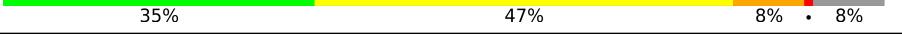
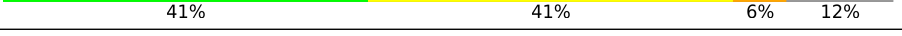
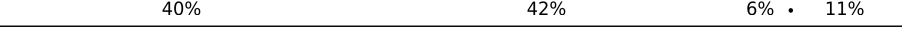
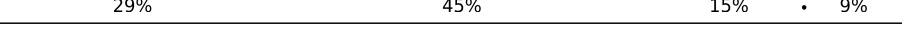
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	94 (11.10 - 12.10)

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	X	1655	 6% 26% 33% 8% 31%
2	Y	63	 100%
2	Z	63	 100%
3	a	1037	 40% 44% 11% 5%

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Mol	Chain	Length	Quality of chain
3	l	1037	
4	b	744	
4	m	744	
5	c	712	
5	n	712	
6	d	297	
6	o	297	
7	e	349	
7	p	349	
8	f	726	
8	q	726	
9	g	1157	
9	r	1157	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 83142 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 Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	1137	Total	C	N	O	S	0	0
			9208	6035	1455	1700	18		

- Molecule 2 is a protein called unknown.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	Y	63	Total	C	N	O	0	0
			315	189	63	63		
2	Z	63	Total	C	N	O	0	0
			315	189	63	63		

- Molecule 3 is a protein called Nucleoporin NUP120.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	1006	Total	C	N	O	S	0	0
			8279	5346	1334	1566	33		
3	l	1006	Total	C	N	O	S	0	0
			8279	5346	1334	1566	33		

- Molecule 4 is a protein called Nucleoporin NUP85.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	675	Total	C	N	O	S	0	0
			5424	3493	863	1038	30		
4	m	670	Total	C	N	O	S	0	0
			5384	3468	857	1031	28		

- Molecule 5 is a protein called Nucleoporin 145c.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	559	Total	C	N	O	S	0	0
			4520	2884	750	869	17		

Continued on next page...

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	n	557	Total	C	N	O	S	0	0
			4505	2873	748	867	17		

- Molecule 6 is a protein called Protein transport protein SEC13.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	d	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		
6	o	274	Total	C	N	O	S	0	0
			2160	1379	369	409	3		

- Molecule 7 is a protein called Nucleoporin SEH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	e	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		
7	p	307	Total	C	N	O	S	0	0
			2438	1543	422	462	11		

- Molecule 8 is a protein called Nucleoporin NUP84.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	f	649	Total	C	N	O	S	0	0
			5261	3370	866	1011	14		
8	q	648	Total	C	N	O	S	0	0
			5254	3365	865	1010	14		

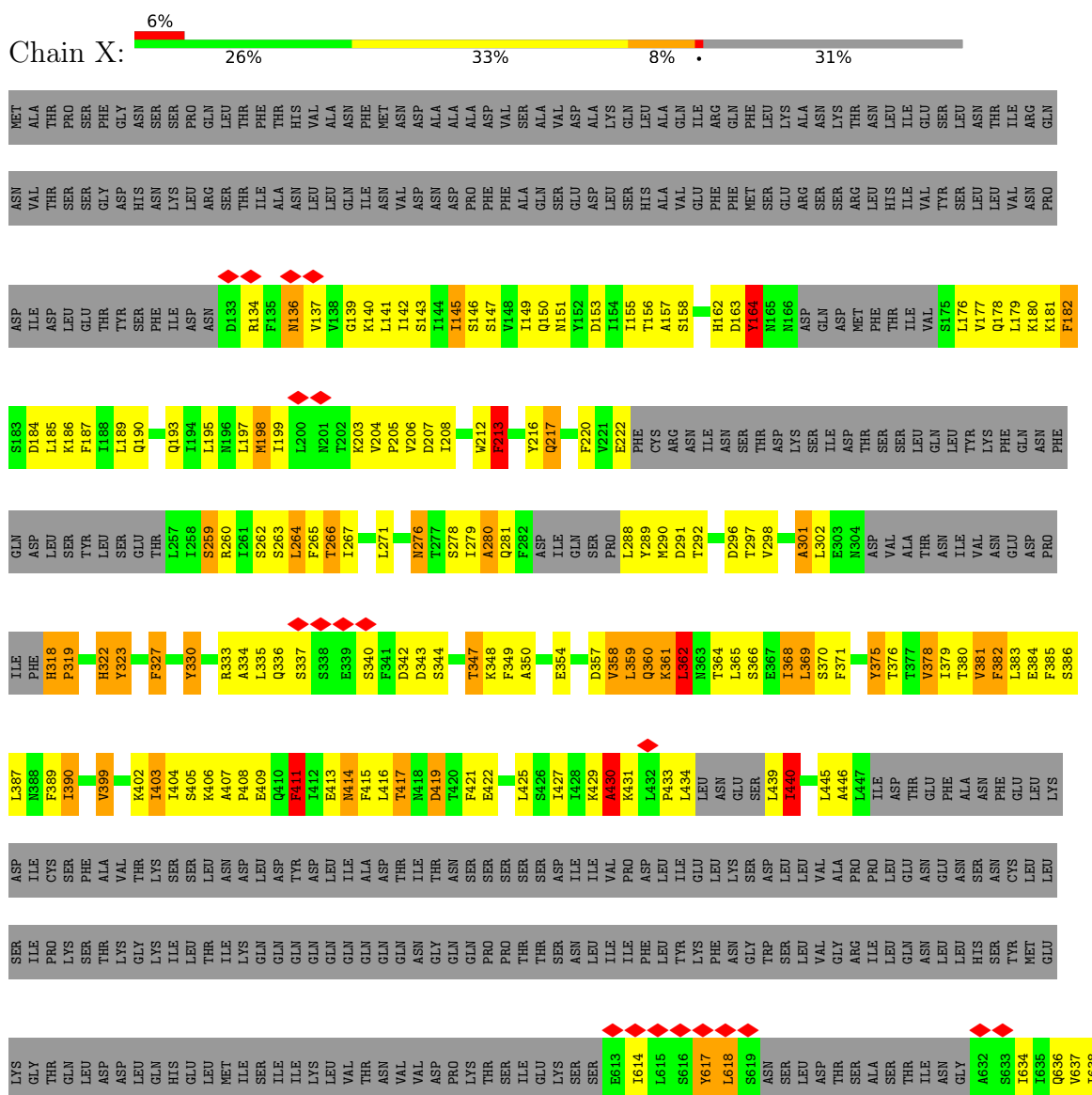
- Molecule 9 is a protein called Nucleoporin NUP133.

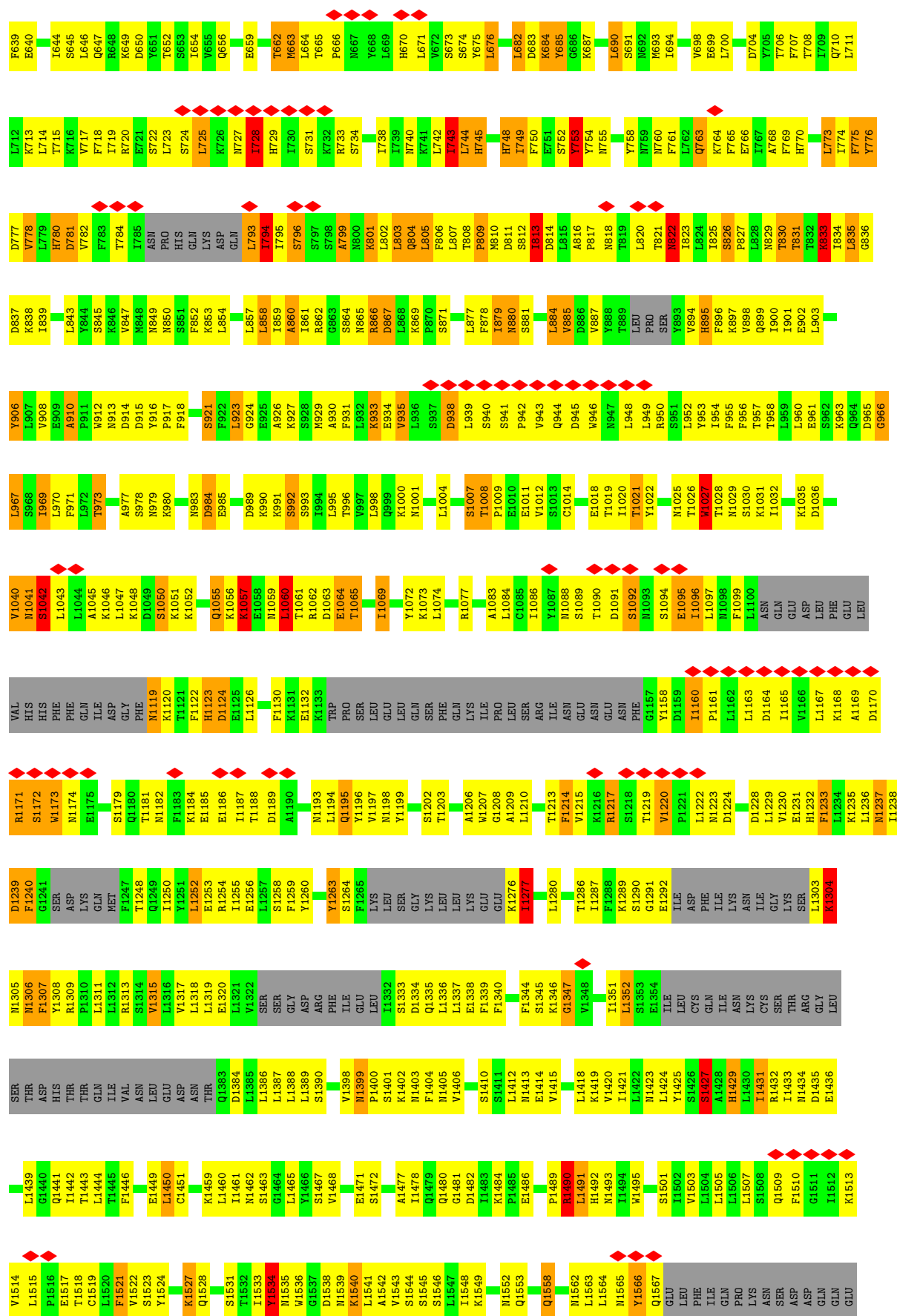
Mol	Chain	Residues	Atoms					AltConf	Trace
9	g	1062	Total	C	N	O	S	0	0
			8627	5541	1393	1664	29		
9	r	1056	Total	C	N	O	S	0	0
			8575	5511	1381	1654	29		

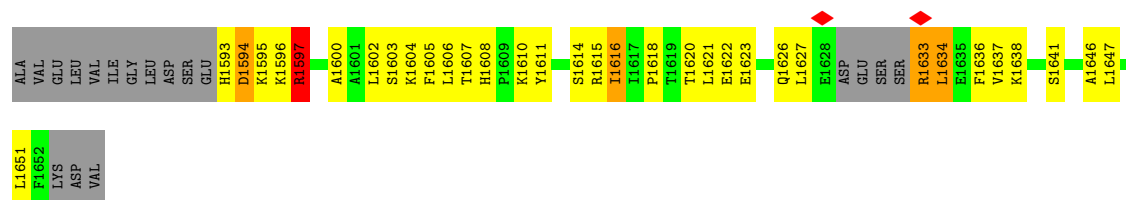
3 Residue-property plots

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: Nucleoporin NUP188







- Molecule 2: unknown

Chain Y: 100%

There are no outlier residues recorded for this chain.

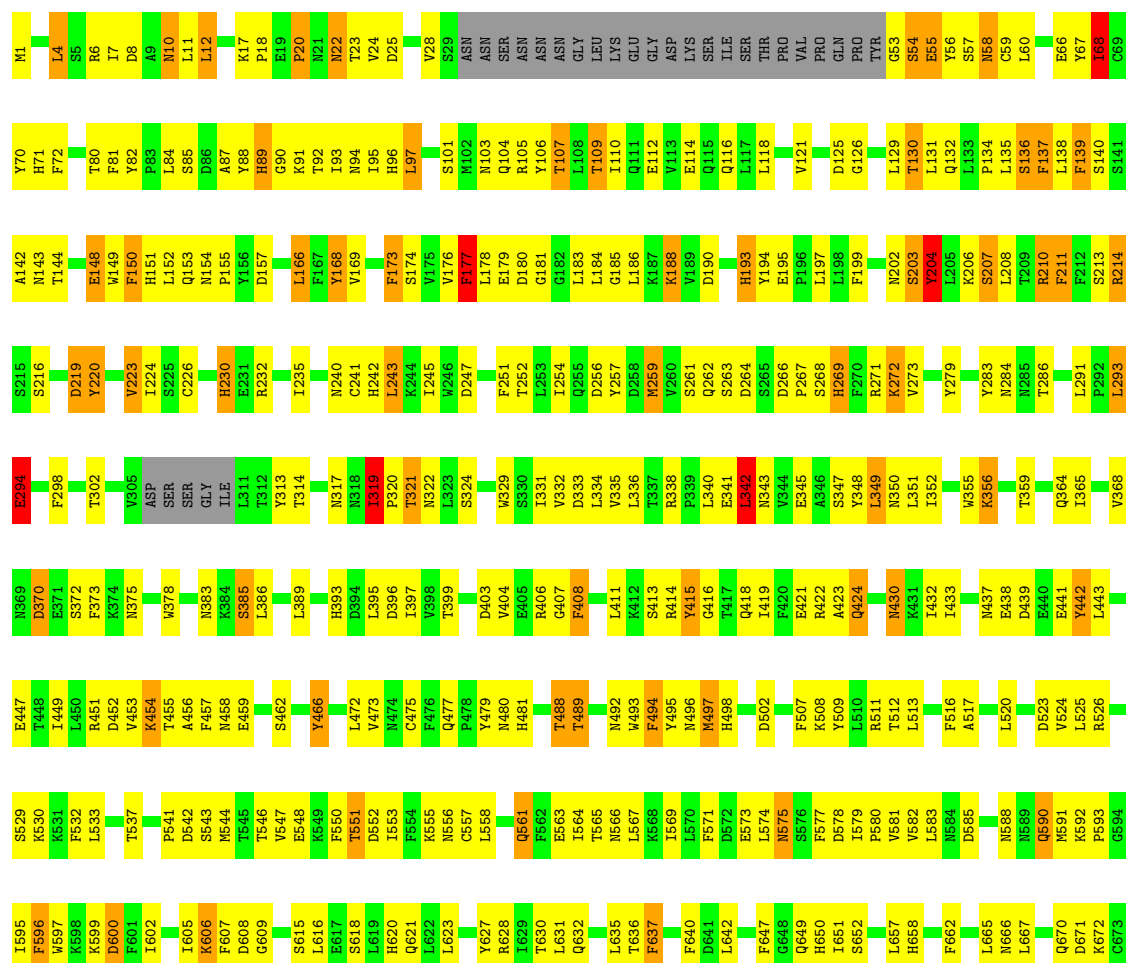
- Molecule 2: unknown

Chain Z: 100%

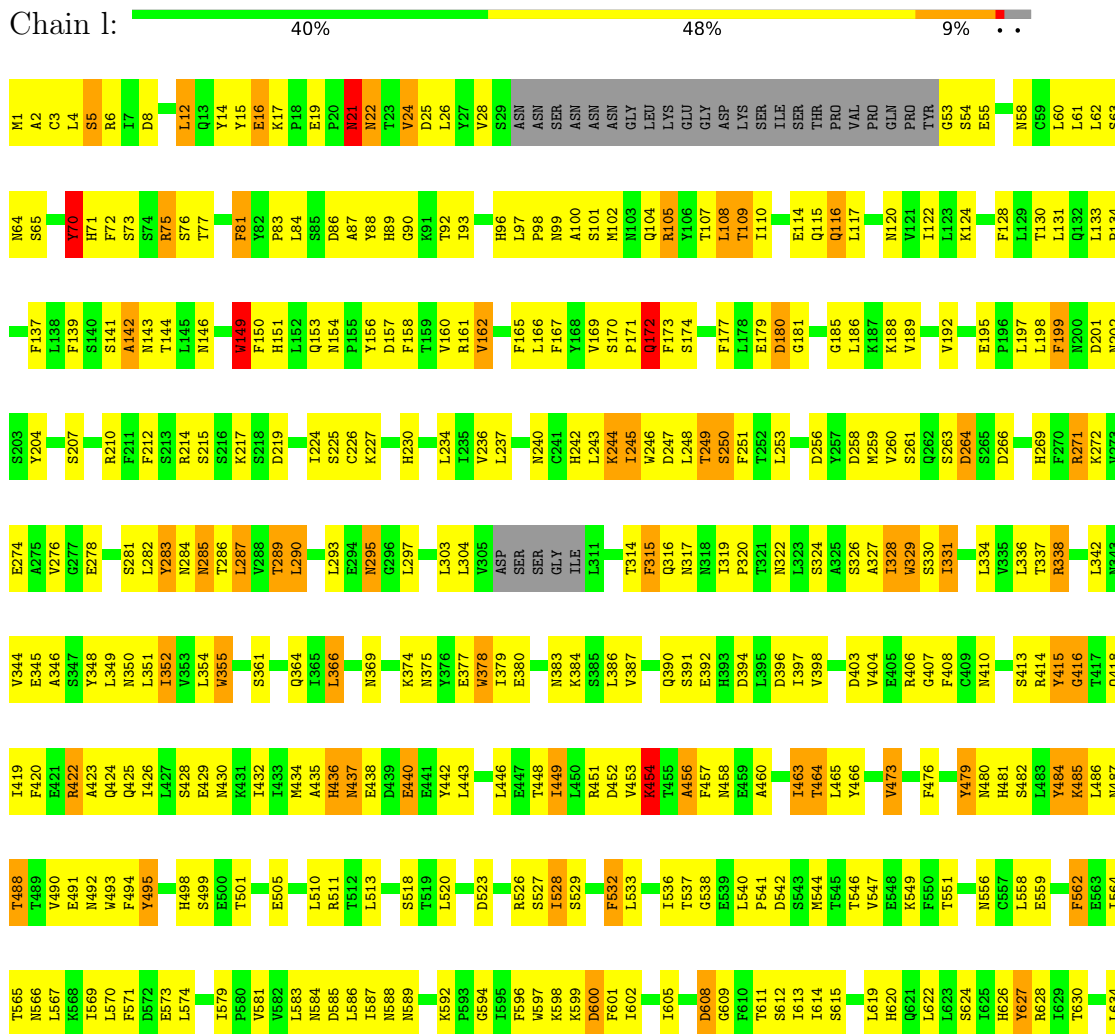
There are no outlier residues recorded for this chain.

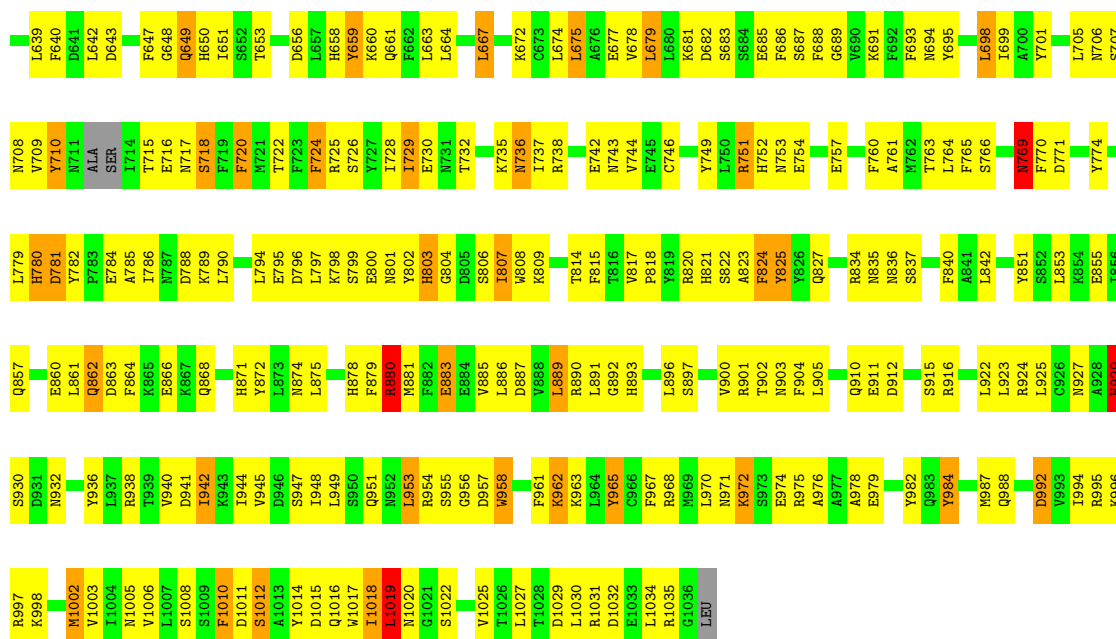
- Molecule 3: Nucleoporin NUP120

Chain a: 40% 44% 11% ..



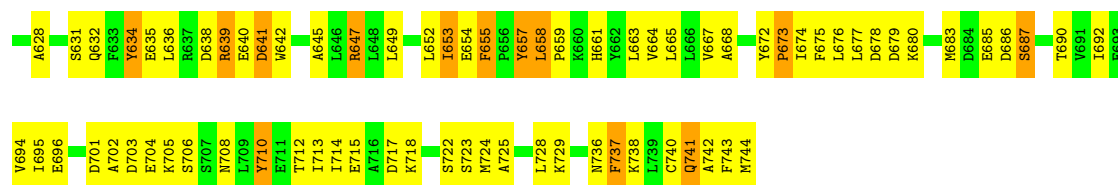
- Molecule 3: Nucleoporin NUP120





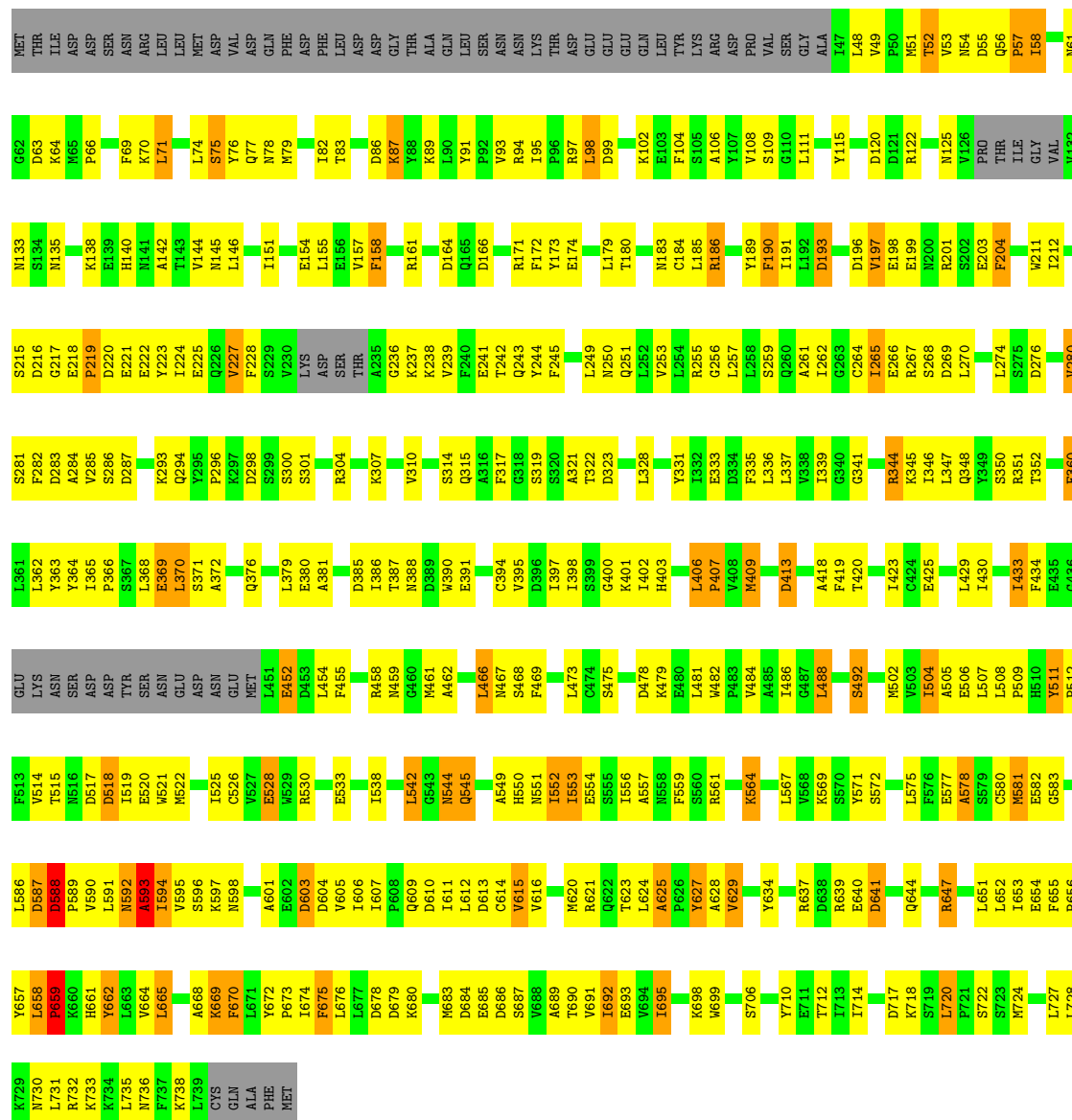
• Molecule 4: Nucleoporin NUP85





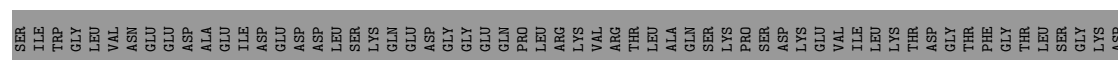
• Molecule 4: Nucleoporin NUP85

Chain m: 40% 42% 8% 10%



• Molecule 5: Nucleoporin 145c

Chain c: 32% 40% 6% 21%

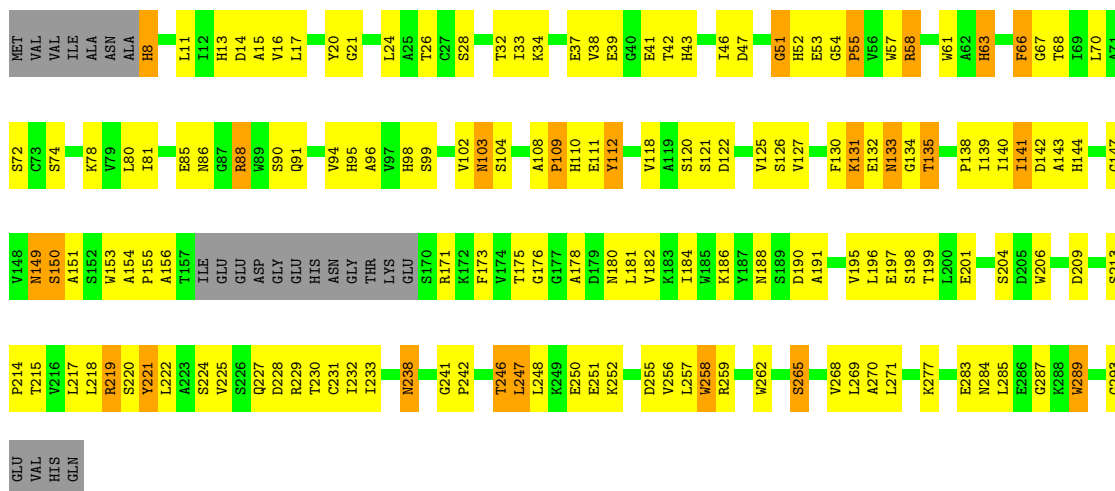
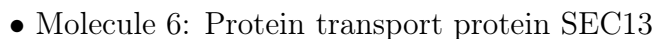


ASP	GLU	D186	Q257	S323	S398	F475	S554	E629	ALA
SER	ILE	D187	K261	Y324	Q404	A476	S554	T630	GLN
ILE	ASP	Y188	K262	L325	H406	F477	Q557	Q631	ASP
VAL	LEU	Y189	E263	G326	L407	A478	N558	E632	LEU
GLU	PHE	L190	K264	N327	T633	A479	N558	I634	MET
LYS	SER	E195	H265	N328	L408	F483	S563	I638	LYS
ALA	GLU	E196	C266	K269	K409	L486	S564	S639	CYS
TYR	CYS	E199	C267	R331	L412	L487	Y565	I638	THR
GLU	N129	E200	L268	R332	L413	H488	D566	S639	TYR
PRO	D130	A201	S270	R333	L414	H489	L567	I643	LYS
ASP	E131	E202	K271	D334	Y414	S490	A568	Y645	ILE
LEU	N134	K203	L272	A336	D416	L491	M570	Y645	
SER	A135	N205	V273	E337	V420	V493	A571	Y645	
ASP	A136	P206	S274	L338	Q423	L497	I572	Y645	
ALA	K137	Y207	S274	Q339	Q423	L497	I572	Y645	
ASP	L137	P208	G277	Q341	Y425	M498	S575	Y645	
PHE	L138	Q209	P278	T345	A426	E504	R579	Y645	
GLU	N139	K140	E279	G346	A427	D506	L580	Y645	
GLY	K142	E280	I280	G347	N428	T506	L581	Y645	
ILE	R143	E281	S214	C348	E429	I507	L582	Y645	
GLU	F144	E282	E217	S349	K433	K508	S583	Y645	
PRG	S147	E283	K218	T350	L434	L510	N584	Y645	
LYS	Y148	E284	D219	K356	Y435	V511	N585	Y645	
LEU	Y149	E285	S287	K356	K436	M512	V587	Y645	
ASP	F150	E286	N288	K356	E437	I515	K593	Y645	
VAL	A151	E287	Y223	K356	R438	I515	T594	Y645	
SER	E155	E288	W224	K356	Q440	R519	L595	Y645	
LYS	T155	E289	E225	K356	T442	A520	R596	Y645	
ASP	G156	E290	E225	K356	N443	T522	L599	Y645	
TRP	S157	E291	E225	K356	L444	D524	E601	Y645	
VAL	M158	E292	E225	K356	L445	H525	F602	Y645	
GLN	L159	E293	E225	K356	D446	I526	P603	Y645	
LEU	K162	E294	E225	K356	V447	L527	D604	Y645	
ILE	D163	E295	E225	K356	L453	S605	S605	Y645	
LEU	I164	E296	E225	K356	I454	R528	E606	Y645	
ALA	V165	E297	E225	K356	Q455	L530	R607	Y645	
GLY	G166	E298	E225	K356	T456	K631	D608	Y645	
SER	K167	E299	E225	K356	L457	L537	K609	Y645	
SER	K167	E300	E225	K356	R458	I538	W610	Y645	
LEU	V170	E301	E225	K356	F459	F539	S612	Y645	
ARG	S171	E302	E225	K356	N460	N540	S613	Y645	
SER	I172	E303	E225	K356	R463	A541	I614	Y645	
VAL	K173	E304	E225	K356	V464	Q542	F617	Y645	
PHE	R174	E305	E225	K356	F465	A543	F617	Y645	
ALA	R174	E306	E225	K356	Y391	L544	K622	Y645	
THR	L175	E307	E225	K356	G392	K345	L623	Y645	
SER	P176	E308	E225	K356	Q393	R547	V624	Y645	
LYS	T177	E309	E225	K356	I394	Y548	L625	Y645	
GLU	E178	E310	E225	K356	D395	N551	V628	Y645	
PHE	L179	E311	E225	K356	E396			Y645	
GLY	Q180	E312	E225	K356	Y397			Y645	
ASP	R181	E313	E225	K356				Y645	
PRO	K182	E314	E225	K356				Y645	
CYS	F183	E315	E225	K356				Y645	
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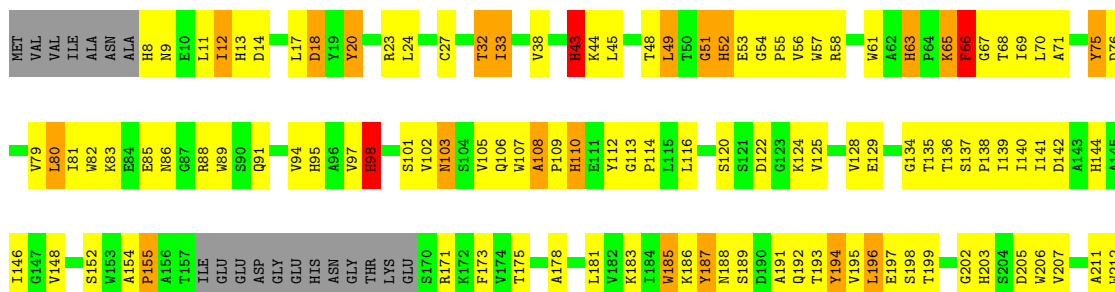
• Molecule 5: Nucleoporin 145c

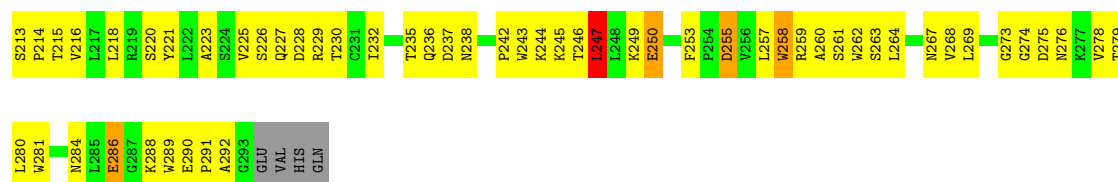
Chain n: 33% 39% 5% • 22%

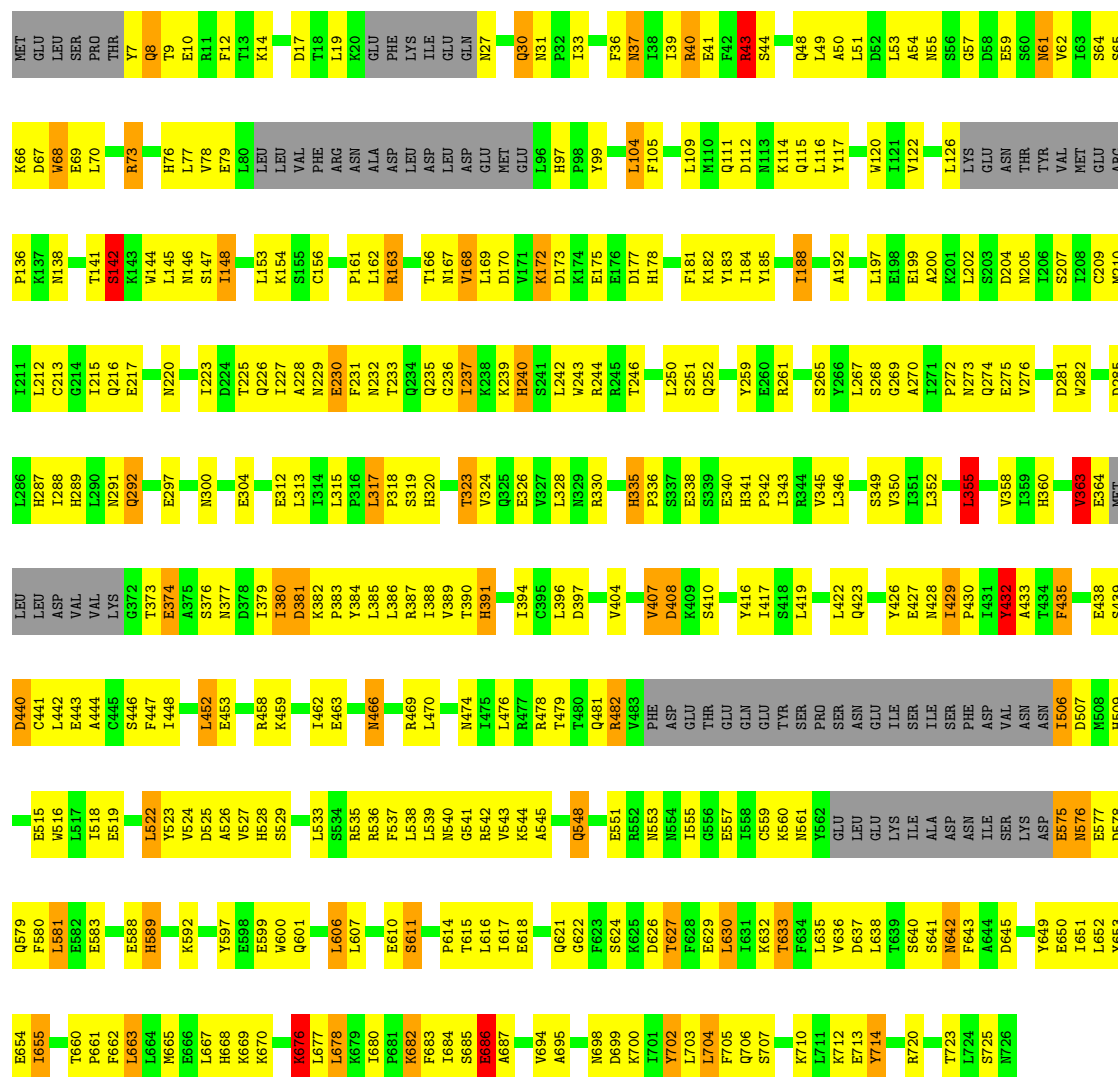
SER	GLU	K196	ASP	GLU	Q266
ILE	ILE	V197	SER	TYR	R267
TRP	ASP	L268	ILE	PRO	P206
GLY	LEU	I199	VAL	ASP	Y207
LEU	LEU	E200	GLU	ASP	P208
VAL	PHE	E201	GLU	LEU	Q209
ASN	SER	R202	LYS	SER	I210
GLU	GLU	N205	ALA	ASP	S211
GLU	CYS	P206	TYR	ALA	L137
ASP	N129	Y207	GLU	ALA	D130
ASP	E131	P208	PRO	ASP	E131
GLU	I132	Q209	LEU	ASP	I132
ASP	K136	I210	SER	ASP	K136
GLU	L137	S211	ASP	ASP	L137
ASP	I138	S213	ALA	ASP	I138
ASP	S214	R285	PHE	ASP	S214
SER	L215	N286	GLU	ASP	L215
LYS	E141	S287	GLY	GLU	E141
LYS	R142	P216	GLY	GLY	R142
GLN	S147	K218	ILE	ILE	S147
GLU	Y148	L221	GLU	GLU	Y148
ASP	T149	D222	GLU	ASP	T149
GLY	F150	Y223	SER	ASP	F150
GLU	A151	M224	PRO	LYS	A151
GLN	K152	T227	LYS	LEU	K152
LEU	S154	S228	LEU	VAL	S154
ARG	T155	S229	SER	VAL	T155
LYS	V304	R305	LYS	LYS	V304
VAL	T161	A306	ASP	ASP	T161
ARG	K162	S307	TRP	TRP	K162
THR	D163	K308	VAL	VAL	D163
GLU	I164	L233	GLU	GLU	I164
ALA	V165	W234	GLN	GLN	V165
GLN	G166	I239	LEU	LEU	G166
SER	K167	L240	ILE	ILE	K167
LYS	S168	F241	LEU	LEU	S168
LYS	G169		ALA	ALA	G169
ASP	V170		GLY	GLY	V170
LYS	K173	Y246	SER	SER	K173
GLU	R174	P247	LYS	LYS	R174
VAL	L175	Y248	GLU	GLU	L175
ILE	P176	R249	VAL	VAL	P176
LEU	T177	D251	ILE	ILE	T177
LYS	E178	N252	LYS	PHE	E178
THR	L179	D253	ALA	ALA	L179
ASP	Q180	Q254	THR	THR	Q180
GLY	R181	V255	SER	SER	R181
THR	K182	K256	LYS	LYS	K182
THR	F183	M257	THR	THR	F183
LYS	L190	A258	GLY	GLY	L190
PHE	D191	L259	PHE	PHE	D191
GLY	K192	L260	GLY	GLY	K192
PRO	E193	K261	PRO	PRO	E193
GLY	I194	K262	CYS	CYS	I194
LYS	E195	H265	GLN	GLN	E195
ASP			ASN	ASN	



- Molecule 6: Protein transport protein SEC13

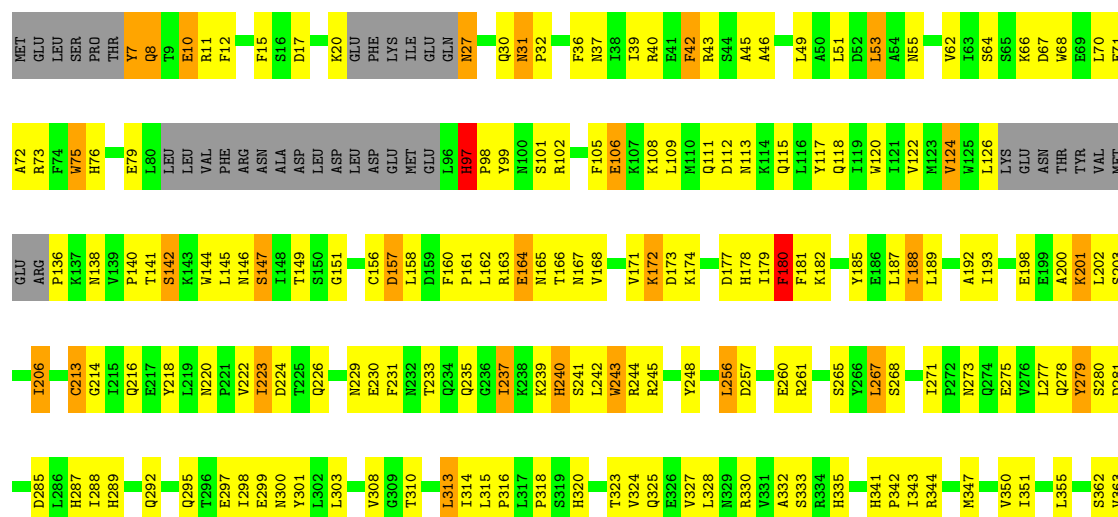


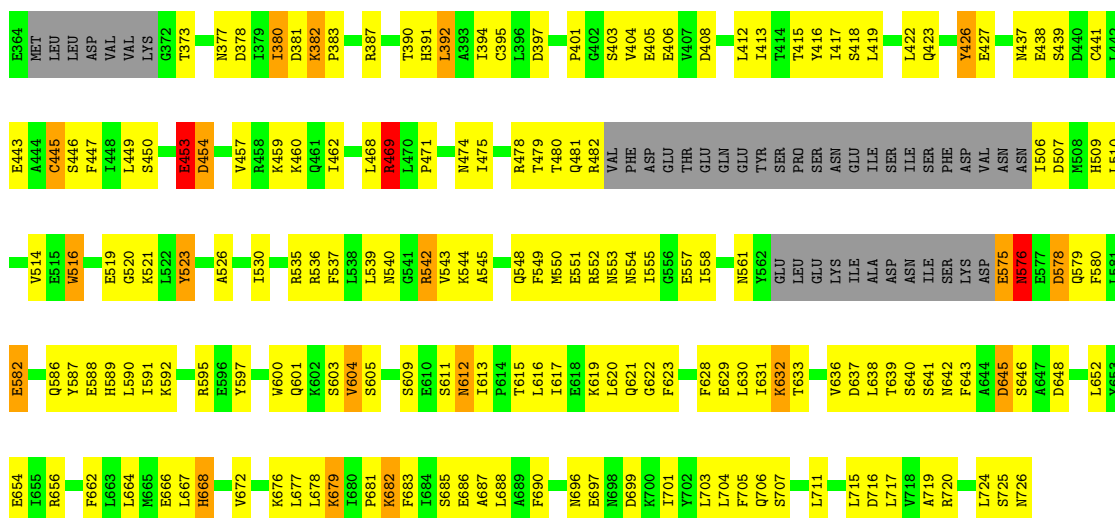




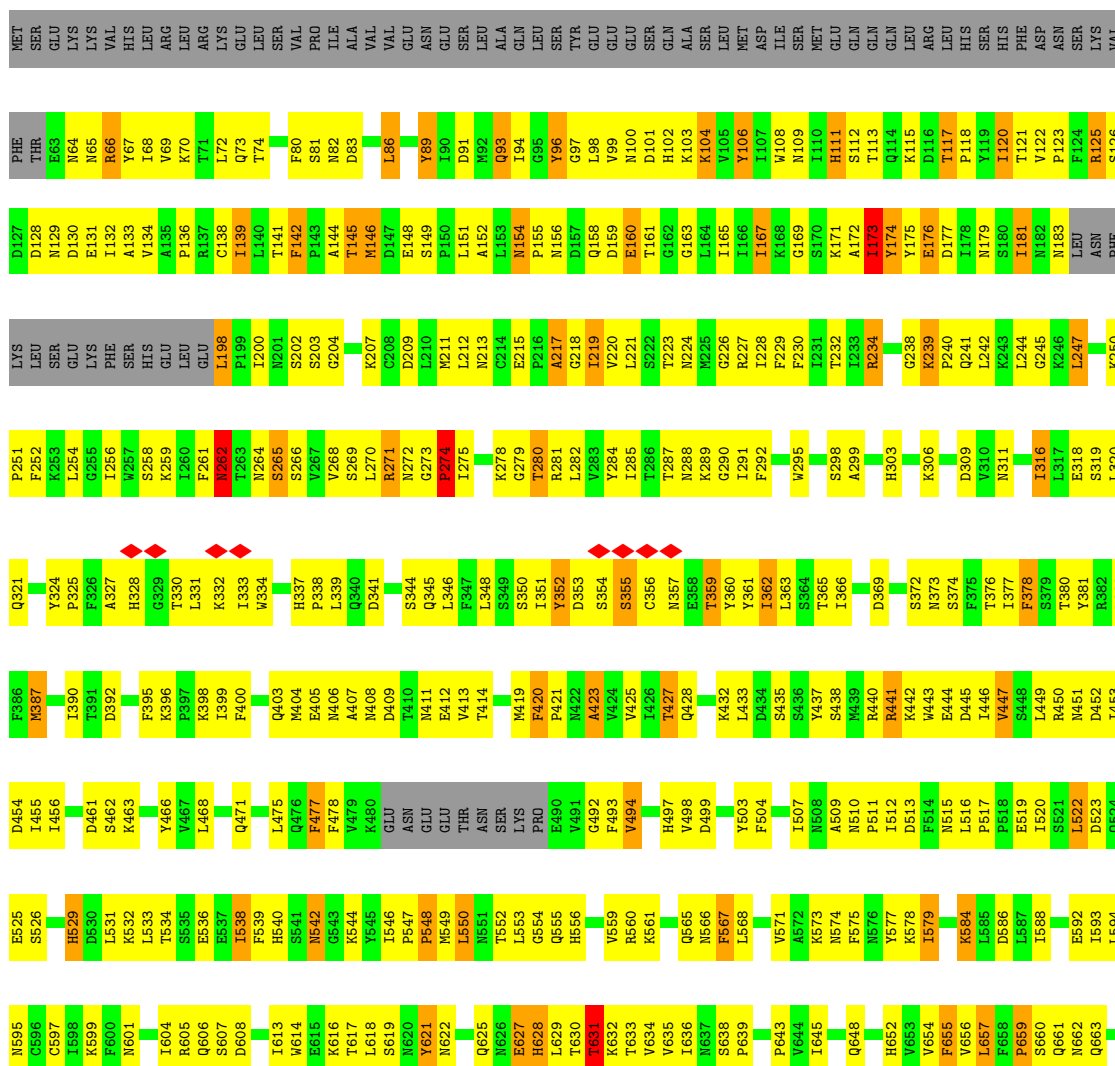
• Molecule 8: Nucleoporin NUP84

Chain q: 40% 42% 6% 11%





• Molecule 9: Nucleoporin NUP133





I1148	P1079	N998	Y850	LYS	Y691	L623	T552	THR	V425
N1149	S1080	L999	L851	SER	E992	L624	L553	ASN	I426
Y1150	Y1081	S1000	L852	VAL		Q825	L554	SER	T427
E1151	D1082	L1001	K853	ASN	L696	N826	H556	PRO	Q428
T1152	L1083	L1002	H854	ALA	D697	E627		LYS	V429
N1153	V1003	V1003		ASN	P698	H628	V559	E490	N430
T1154	G1085	E1004	L860	D772	M699	L629	K560	V491	S431
V1155	L1005	L1005	L861	N773	E700	T630	K561	G492	K432
GLU	K1087	Y1006	R862	F774	F701	T631	E562	F493	L433
TYR	S1007	S1007	R863		D702	K632	F563	V494	D434
	T1091		E935	I777		T633		S435	S436
	D1010		R864	N778	K705	V634	N566	H497	S436
	D1011		Q866			V634	F567		Y437
	E1012		Q867	H785	F709	I636	F568	Q500	S438
	E1013		H868	L766	I710	N637	L569	A501	N439
	T1098		D940	D787	N711	S638	F570	V502	R440
	G1100		V870	W788	F712	P639		Y503	R441
	R1101		L871	N789	D713	V641	K573	F504	K442
	D1024		L872	H790	W714	V641			N443
	D1025		Q873		L715	F642			I444
	G1026		F874	L797	N716	P643			I445
	I1104		F875	C801	C717	I645			V447
	D1106		S878	F807	N718	F646			S448
	Q1106		A879		Q720	K647			L449
	N1107				C721	Q648			F514
					F722	F649		N615	N451
	R1110		Y882	D810	F723	L650		L516	D452
	E1111		G883	L811		N651		P517	T453
	E1112		H884	S812		H652		P518	D454
			V885	G813	F727	V653		E519	I455
	E1116		N980	L814		V654		I520	I456
	I1117					F591		S521	G457
			L888	T817	E731	E592		L522	S458
			Q889		E732	I593		D523	G459
			Q890	L818	C733	L594		Q524	T460
			L891	Q819	S734	F658		L533	V460
				T820	L735	P659		C596	D461
			G894	L821	D736	S660		S526	S462
			S985	D822		C597		I598	K463
	S1124	D1055	E968	Q823	K739	F740		I627	S464
	S1125	K1056	Y969	H824	F740	K399		E528	L465
	D1126	L1057	A897	Q824	G741	Q663		H529	V466
	N1127			D825	L742				V467
	S1128	Q1059	R973	S826	L742				L468
	L1129	H1060	N901	T827	L743				T469
	I1061			T902		V669		L533	K470
	I1131			R903	K747	T670		Q606	D471
	L1132	L1064		L904		N671		S607	S536
	K1133	V1065		N905	Y751	L672		E536	M472
	H1134	F1066		I906	Q752	I758			G473
	S1135	D1067		E833	F753				V474
	T1137	T1136		T834	N754			F539	L475
		E1068		R835	Q755	Y678		H540	Q476
	E1069	V983		F836	F756	D679			F477
	L1070	L1070		N837	K757	G680			F478
	P1071	L1071		E915	I758				VAL
	K1072	L1072		S916					LYS
	L1073	N1073		L917	N761				I546
	D1074	L1074		E918	T762				P547
	E1143	D1075		S919	Q763				ASN
	A1141	L1141		L917	F839				GLU
	L1142	L1142		E918	P840				GLU
	E1143	D1075		S919	K841				GLU
	N1145	L1145		T994	T762				GLU
	Y1146	P1077		Y996	F848				GLU
	T1147	L1078		Y997	E849				GLU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	45000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3800	Depositor
Magnification	37651	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.130	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.01	Depositor
Map size ($\text{\AA}$)	1276.8, 1276.8, 1276.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.66, 2.66, 2.66	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	X	2.22	278/9370 (3.0%)	2.51	665/12670 (5.2%)
3	a	2.24	284/8464 (3.4%)	2.39	507/11469 (4.4%)
3	l	2.30	281/8461 (3.3%)	2.43	532/11460 (4.6%)
4	b	2.21	189/5533 (3.4%)	2.39	359/7493 (4.8%)
4	m	2.23	177/5492 (3.2%)	2.37	295/7440 (4.0%)
5	c	2.23	160/4600 (3.5%)	2.41	289/6211 (4.7%)
5	n	2.24	155/4584 (3.4%)	2.41	290/6188 (4.7%)
6	d	2.33	88/2220 (4.0%)	2.36	130/3028 (4.3%)
6	o	2.31	95/2220 (4.3%)	2.40	140/3028 (4.6%)
7	e	2.31	113/2499 (4.5%)	2.35	139/3388 (4.1%)
7	p	2.23	93/2499 (3.7%)	2.33	121/3388 (3.6%)
8	f	2.17	164/5359 (3.1%)	2.41	337/7258 (4.6%)
8	q	2.22	164/5352 (3.1%)	2.42	350/7248 (4.8%)
9	g	2.21	286/8806 (3.2%)	2.41	530/11936 (4.4%)
9	r	4.09	203/8755 (2.3%)	3.33	664/11870 (5.6%)
All	All	2.50	2730/84214 (3.2%)	2.52	5348/114075 (4.7%)

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	X	7	51
3	a	0	71
3	l	1	50
4	b	0	30
4	m	0	29
5	c	0	27
5	n	0	28
6	d	0	5
6	o	0	11
7	e	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	p	0	12
8	f	1	15
8	q	1	19
9	g	0	54
9	r	0	33
All	All	10	444

The worst 5 of 2730 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	r	251	PRO	N-CD	123.92	3.21	1.47
9	r	150	PRO	N-CD	123.39	3.20	1.47
9	r	155	PRO	N-CD	122.51	3.19	1.47
9	r	325	PRO	N-CD	121.67	3.18	1.47
9	r	304	PRO	N-CD	119.28	3.14	1.47

The worst 5 of 5348 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	r	72	LEU	O-C-N	-85.55	23.37	121.76
9	r	325	PRO	N-CA-CB	65.10	148.57	102.35
9	r	431	SER	O-C-N	-59.46	43.50	122.59
9	r	155	PRO	N-CA-CB	44.27	148.65	102.17
9	r	274	PRO	N-CA-CB	43.52	148.95	103.25

5 of 10 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	X	793	LEU	CA
1	X	794	ILE	CA
1	X	1060	LEU	CA
1	X	1276	LYS	CA
1	X	1277	ILE	CA

5 of 444 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	X	150	GLN	Peptide
1	X	164	TYR	Sidechain
1	X	182	PHE	Sidechain
1	X	213	PHE	Peptide
1	X	322	HIS	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	X	9208	0	9538	158	0
2	Y	315	0	65	0	0
2	Z	315	0	65	0	0
3	a	8279	0	8125	34	0
3	l	8279	0	8121	40	0
4	b	5424	0	5397	16	0
4	m	5384	0	5361	11	0
5	c	4520	0	4539	16	0
5	n	4505	0	4521	21	0
6	d	2160	0	2096	9	0
6	o	2160	0	2096	14	0
7	e	2438	0	2378	5	0
7	p	2438	0	2378	8	0
8	f	5261	0	5261	30	0
8	q	5254	0	5252	23	0
9	g	8627	0	8539	47	0
9	r	8575	0	8472	1256	0
All	All	83142	0	82204	1659	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 1659 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:r:334:TRP:CZ3	9:r:336:SER:HB2	1.23	1.67
9:r:284:TYR:CG	9:r:292:PHE:HZ	1.12	1.66
9:r:207:LYS:HG2	9:r:229:PHE:CD2	1.16	1.65
9:r:284:TYR:HB3	9:r:292:PHE:CZ	1.27	1.65
9:r:284:TYR:CD2	9:r:292:PHE:CZ	1.82	1.64

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	X	1099/1655 (66%)	839 (76%)	171 (16%)	89 (8%)	1	9
3	a	996/1037 (96%)	825 (83%)	114 (11%)	57 (6%)	1	14
3	l	991/1037 (96%)	809 (82%)	115 (12%)	67 (7%)	1	11
4	b	667/744 (90%)	545 (82%)	80 (12%)	42 (6%)	1	13
4	m	662/744 (89%)	531 (80%)	81 (12%)	50 (8%)	1	10
5	c	551/712 (77%)	474 (86%)	53 (10%)	24 (4%)	2	17
5	n	549/712 (77%)	488 (89%)	48 (9%)	13 (2%)	4	27
6	d	270/297 (91%)	229 (85%)	35 (13%)	6 (2%)	5	29
6	o	270/297 (91%)	231 (86%)	28 (10%)	11 (4%)	2	18
7	e	303/349 (87%)	263 (87%)	30 (10%)	10 (3%)	3	21
7	p	303/349 (87%)	265 (88%)	30 (10%)	8 (3%)	4	25
8	f	635/726 (88%)	554 (87%)	55 (9%)	26 (4%)	2	18
8	q	634/726 (87%)	546 (86%)	66 (10%)	22 (4%)	3	20
9	g	1052/1157 (91%)	847 (80%)	137 (13%)	68 (6%)	1	12
9	r	1048/1157 (91%)	917 (88%)	88 (8%)	43 (4%)	2	18
All	All	10030/11699 (86%)	8363 (83%)	1131 (11%)	536 (5%)	2	15

5 of 536 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	X	136	ASN
1	X	217	GLN
1	X	370	SER
1	X	408	PRO
1	X	430	ALA

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	X	1072/1557 (69%)	986 (92%)	86 (8%)	11	31
3	a	945/972 (97%)	894 (95%)	51 (5%)	20	41
3	l	945/972 (97%)	909 (96%)	36 (4%)	29	50
4	b	606/670 (90%)	581 (96%)	25 (4%)	27	49
4	m	602/670 (90%)	572 (95%)	30 (5%)	22	43
5	c	513/646 (79%)	491 (96%)	22 (4%)	26	47
5	n	511/646 (79%)	494 (97%)	17 (3%)	33	55
6	d	233/252 (92%)	222 (95%)	11 (5%)	23	45
6	o	233/252 (92%)	220 (94%)	13 (6%)	19	40
7	e	269/305 (88%)	258 (96%)	11 (4%)	27	49
7	p	269/305 (88%)	257 (96%)	12 (4%)	24	46
8	f	594/669 (89%)	552 (93%)	42 (7%)	13	35
8	q	593/669 (89%)	560 (94%)	33 (6%)	19	40
9	g	997/1088 (92%)	949 (95%)	48 (5%)	23	44
9	r	991/1088 (91%)	966 (98%)	25 (2%)	42	63
All	All	9373/10761 (87%)	8911 (95%)	462 (5%)	24	43

5 of 462 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	f	376	SER
9	r	585	LEU
9	g	985	ASN
9	r	104	LYS
7	p	229	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 291 such sidechains are listed below:

Mol	Chain	Res	Type
6	o	95	HIS
9	r	1027	ASN
7	p	105	ASN
9	r	100	ASN
5	c	480	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	l	4
5	c	2
5	n	2
9	r	1
3	a	1
9	g	1

The worst 5 of 11 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	r	877:GLU	C	878:SER	N	16.07
1	l	207:SER	C	208:LEU	N	14.63
1	l	206:LYS	C	207:SER	N	13.72
1	a	486:LEU	C	487:ASN	N	6.43
1	c	533:PRO	C	535:SER	N	5.54

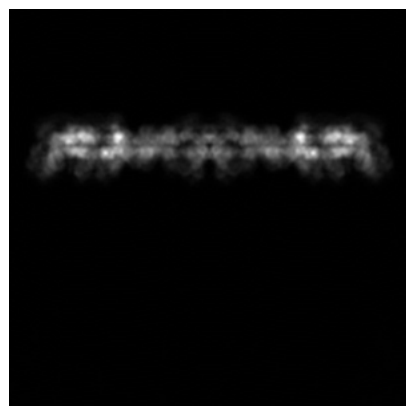
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24231. These allow visual inspection of the internal detail of the map and identification of artifacts.

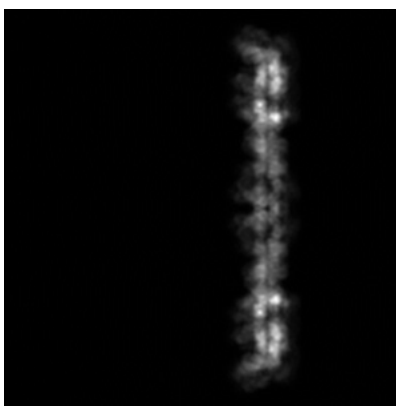
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

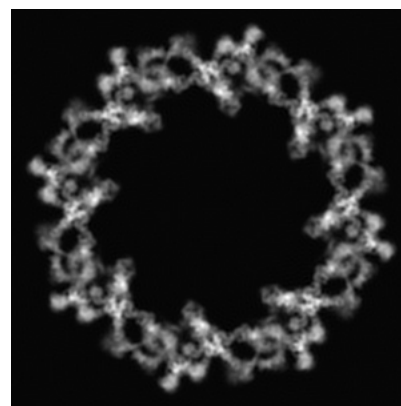
6.1.1 Primary map



X

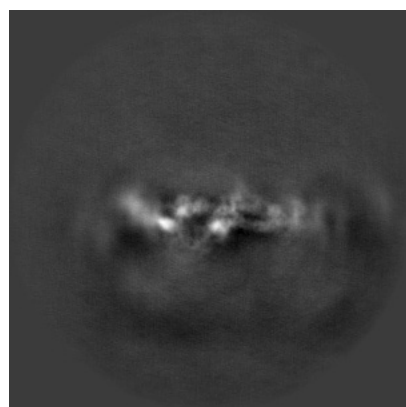


Y

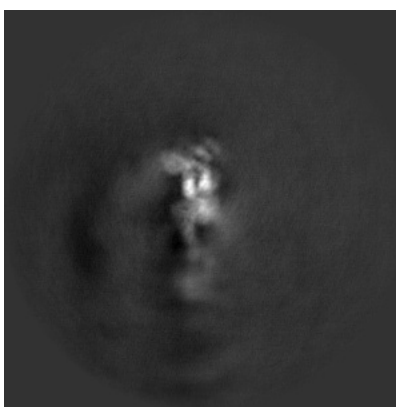


Z

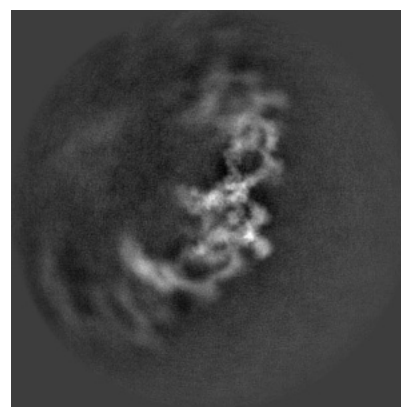
6.1.2 Raw map



X



Y

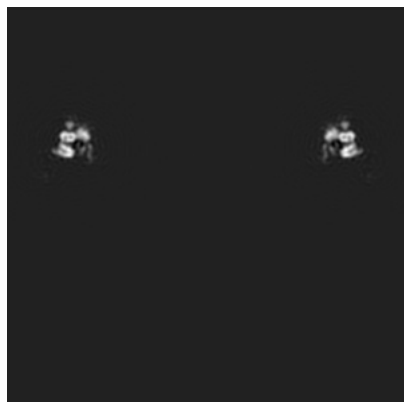


Z

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

6.2 Central slices [i](#)

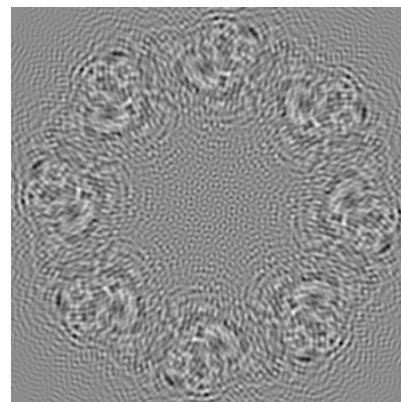
6.2.1 Primary map



X Index: 240

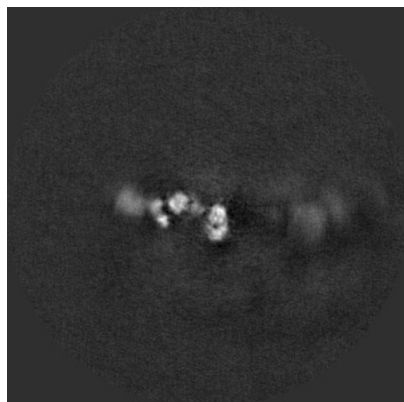


Y Index: 240

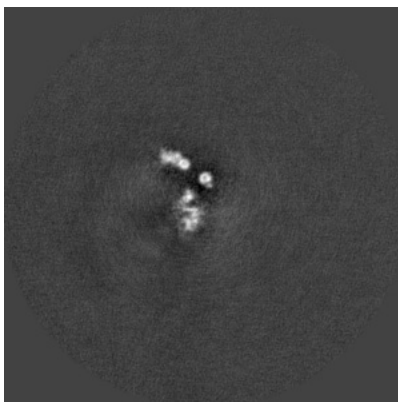


Z Index: 240

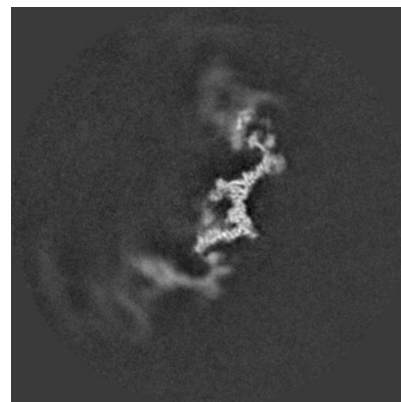
6.2.2 Raw map



X Index: 150



Y Index: 150

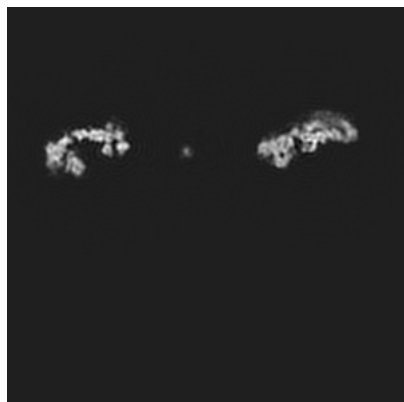


Z Index: 150

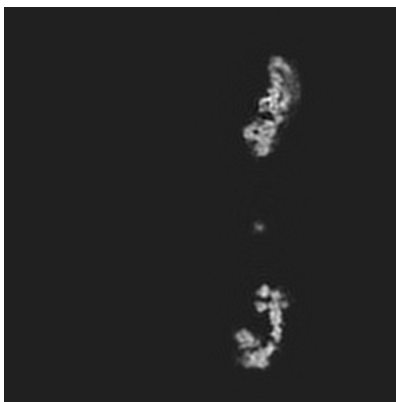
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

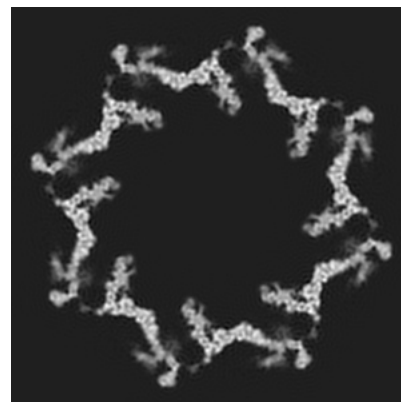
6.3.1 Primary map



X Index: 351

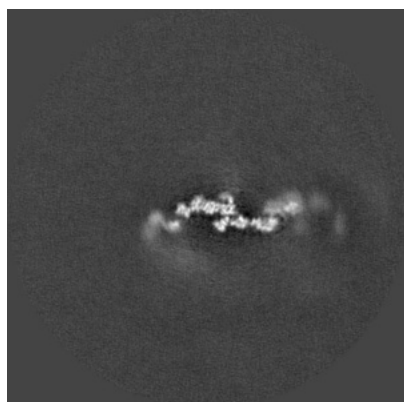


Y Index: 129

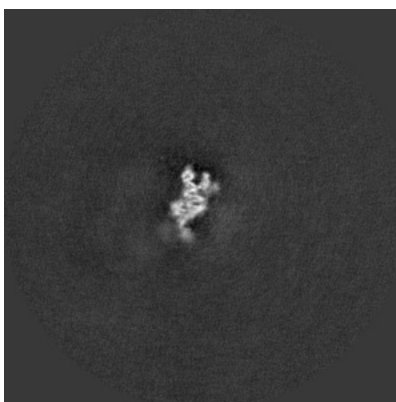


Z Index: 309

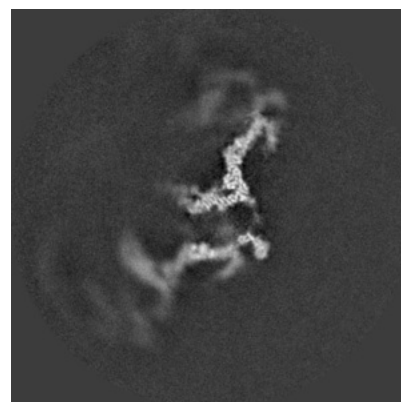
6.3.2 Raw map



X Index: 170



Y Index: 158

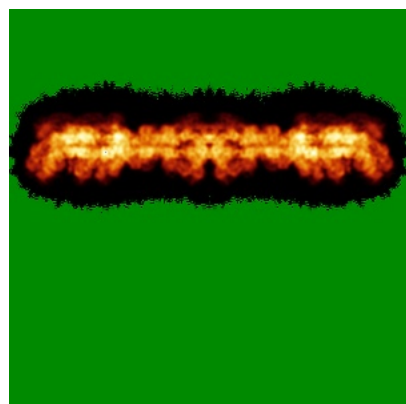


Z Index: 140

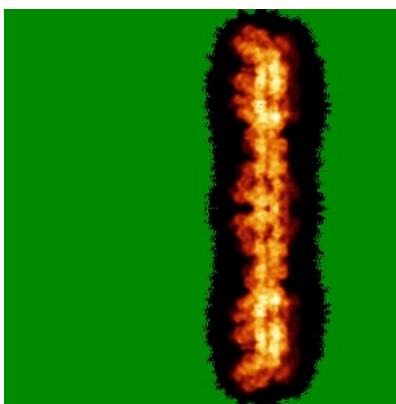
The images above show the largest variance slices of the map in three orthogonal directions.

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

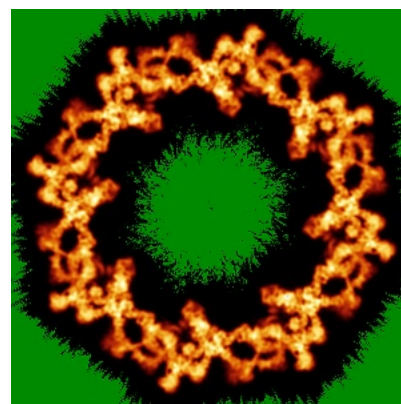
6.4.1 Primary map



X

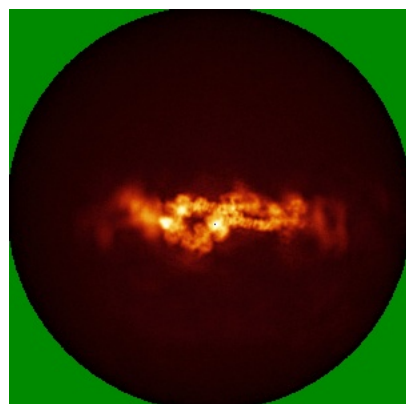


Y

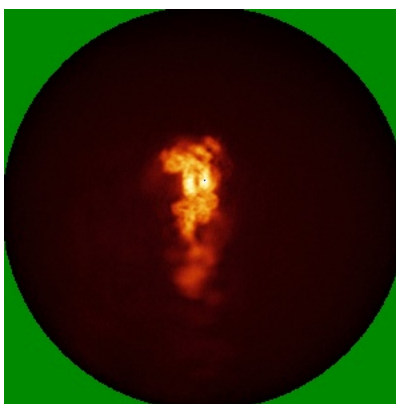


Z

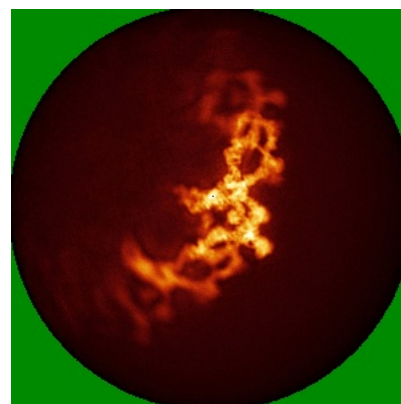
6.4.2 Raw map



X



Y

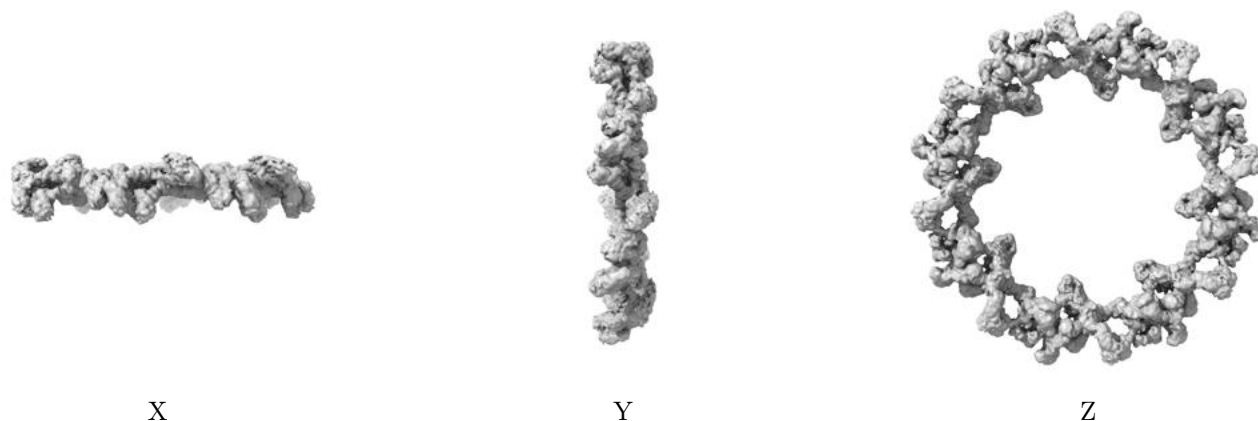


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

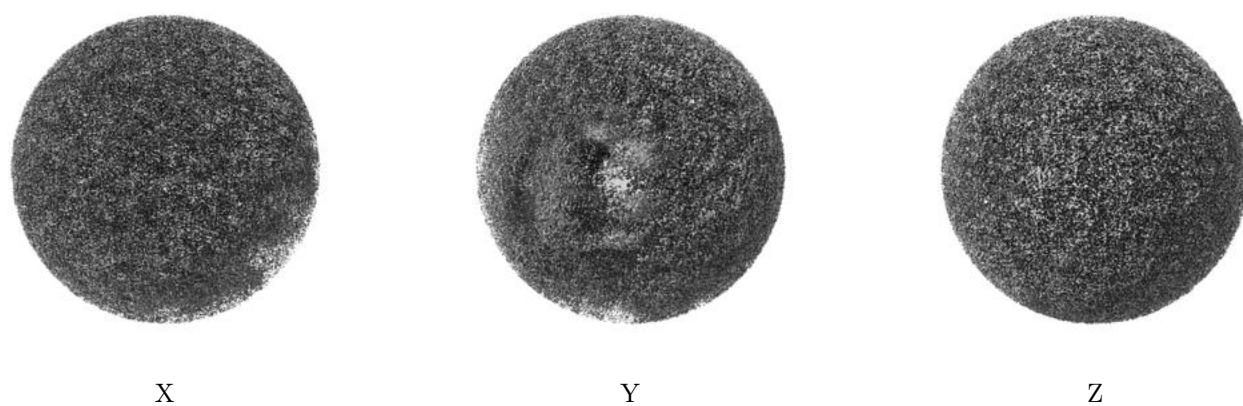
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

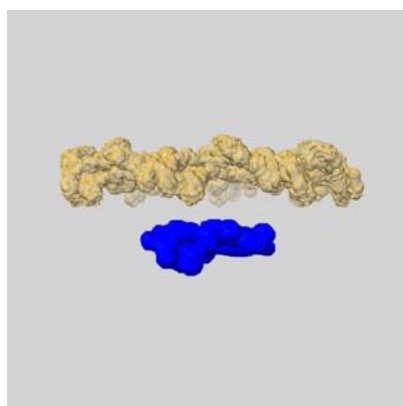
6.6 Mask visualisation [i](#)

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

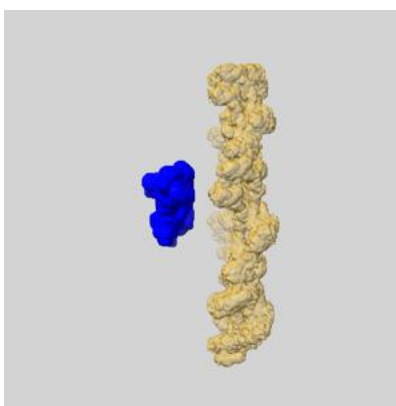
A mask typically either:

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

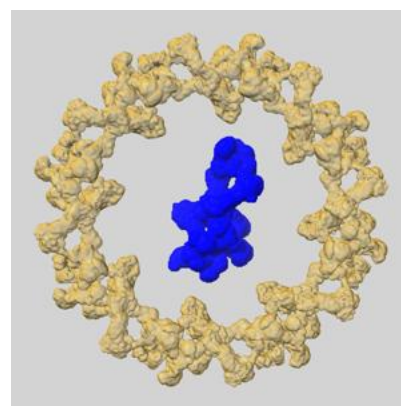
6.6.1 emd_24231_msk_1.map [i](#)



X



Y

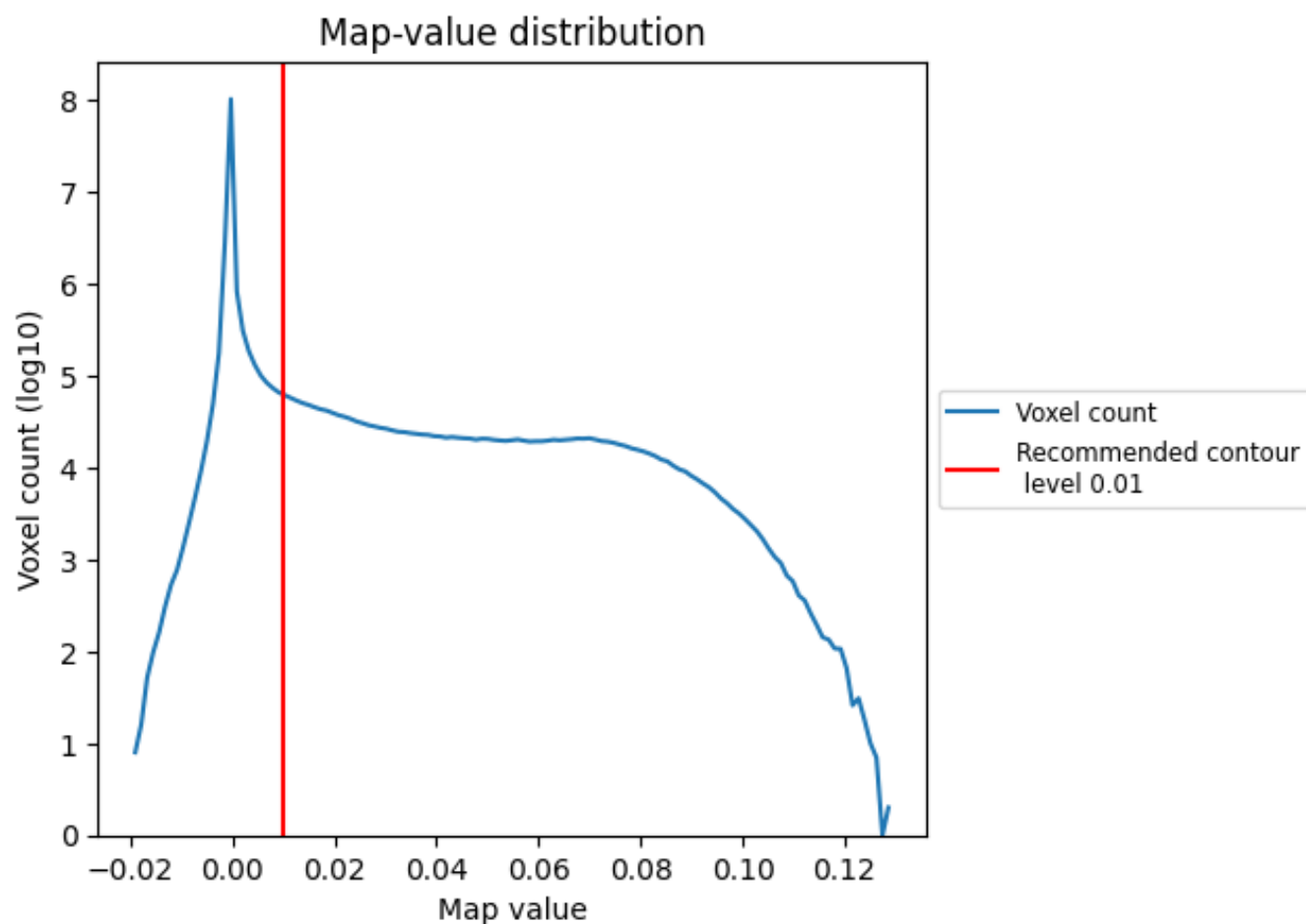


Z

7 Map analysis [i](#)

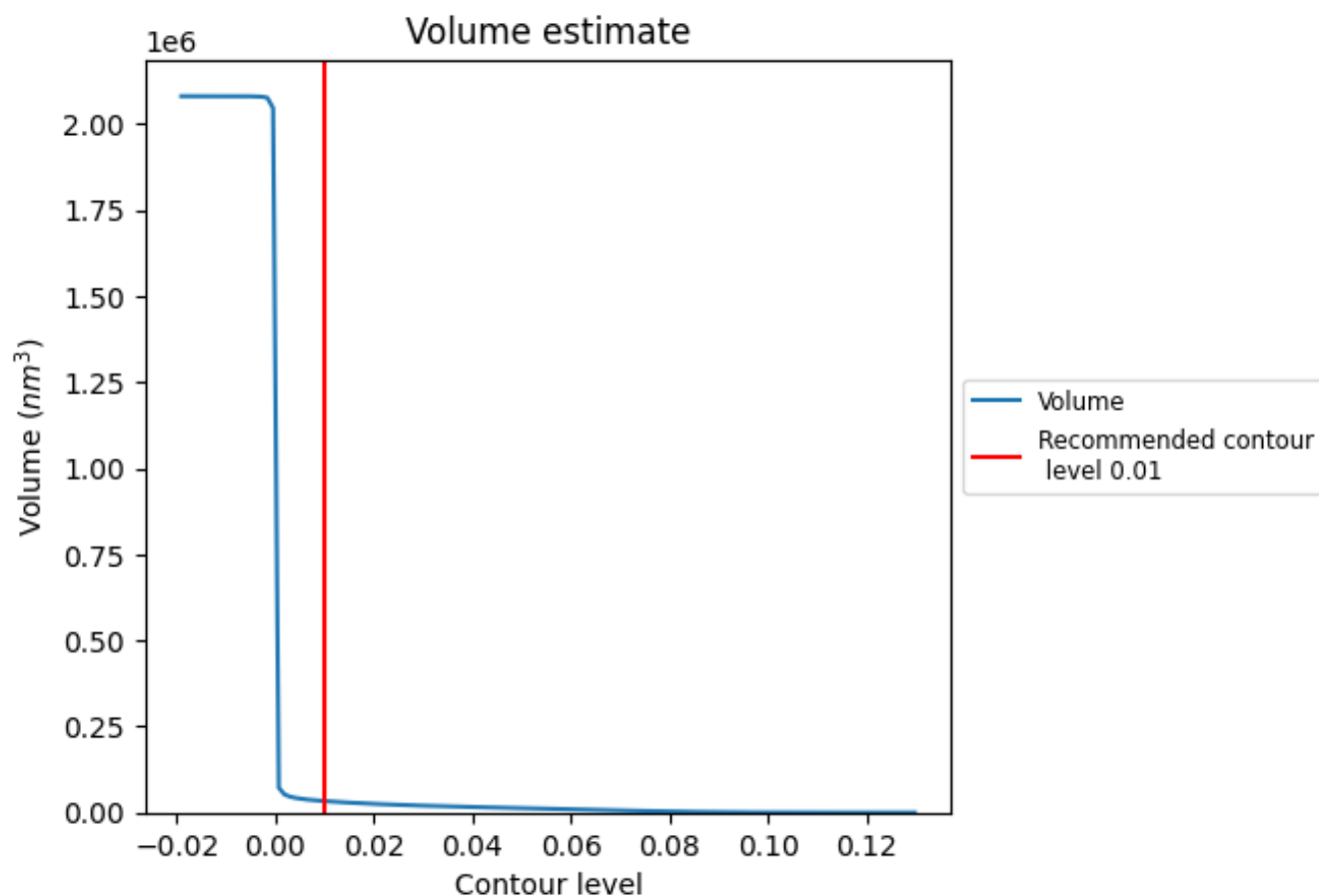
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

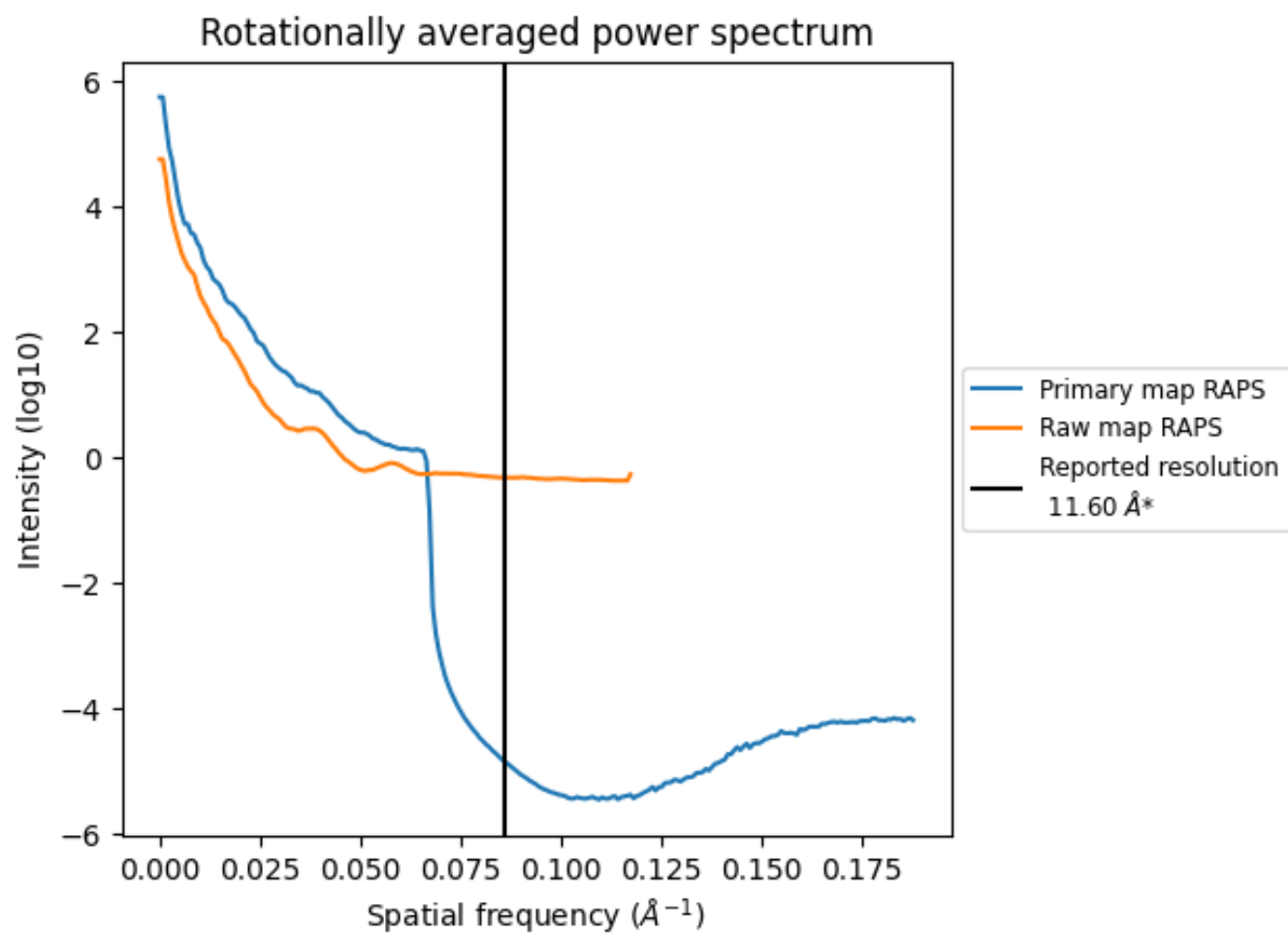
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 33303 nm³; this corresponds to an approximate mass of 30083 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 ⓘ

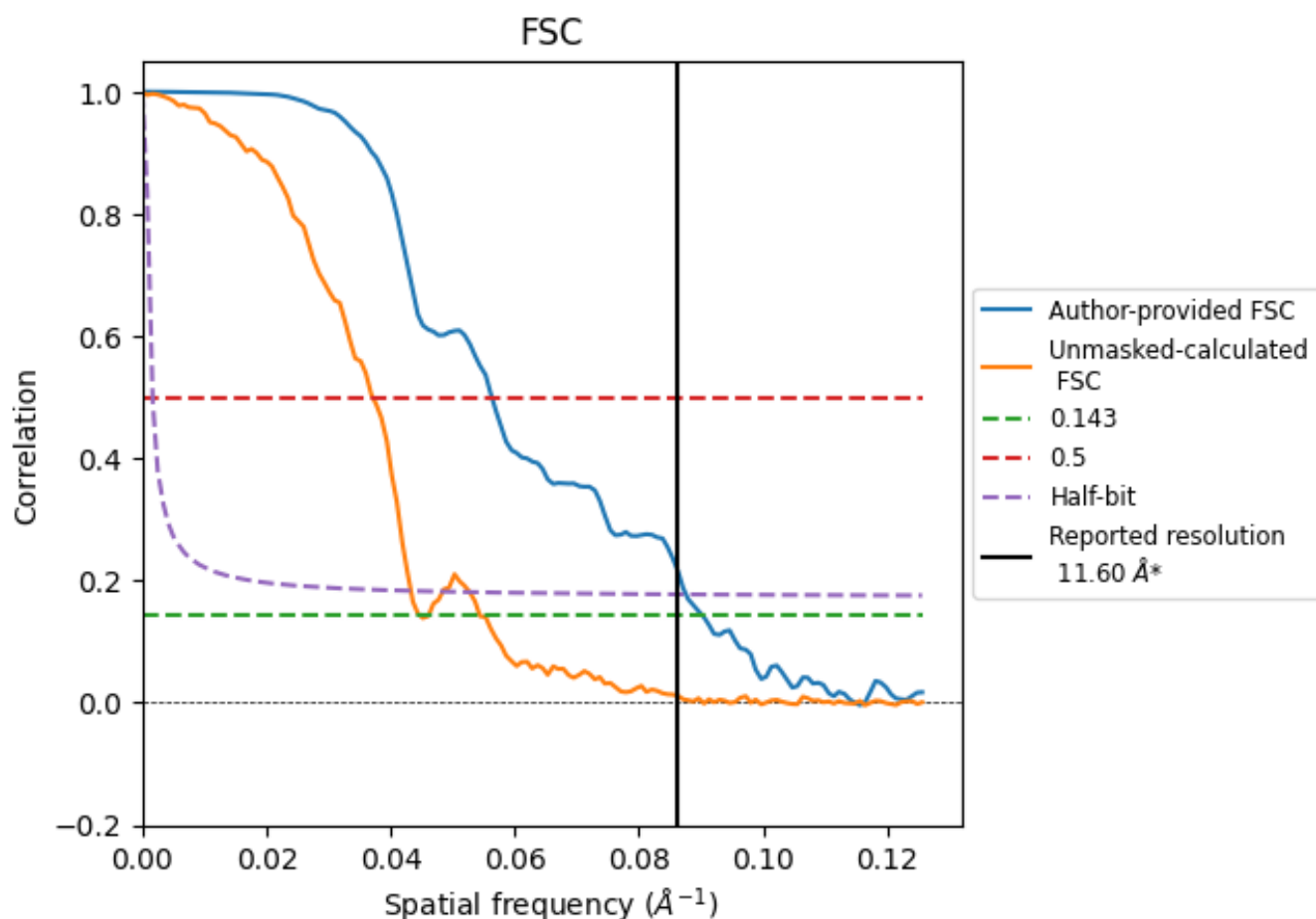


*Reported resolution corresponds to spatial frequency of 0.086 Å⁻¹

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 0.086 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	11.60	-	-
Author-provided FSC curve	11.09	17.76	11.42
Unmasked-calculated*	22.37	26.95	23.15

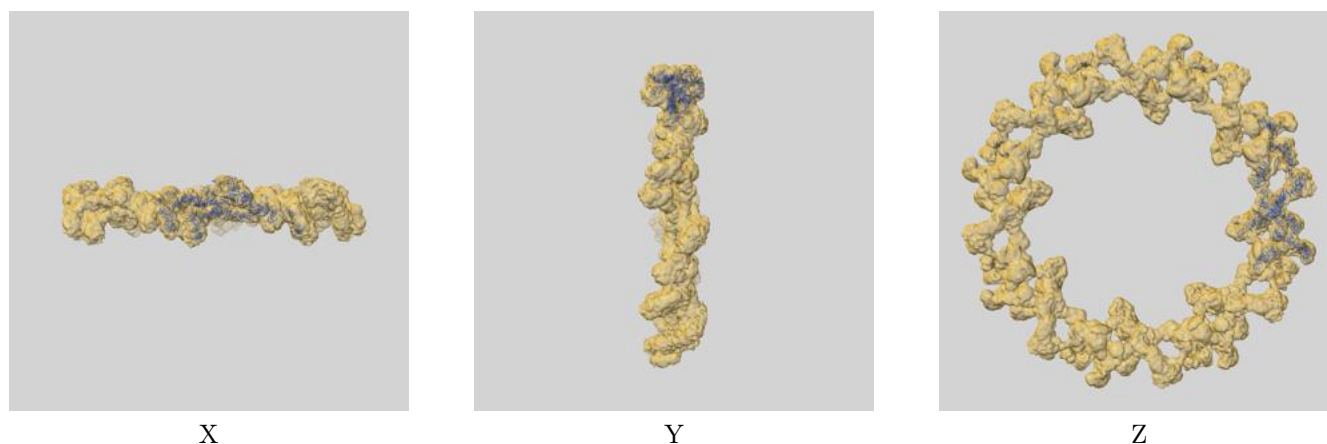
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 22.37 differs from the reported value 11.6 by more than 10 %

9 Map-model fit [i](#)

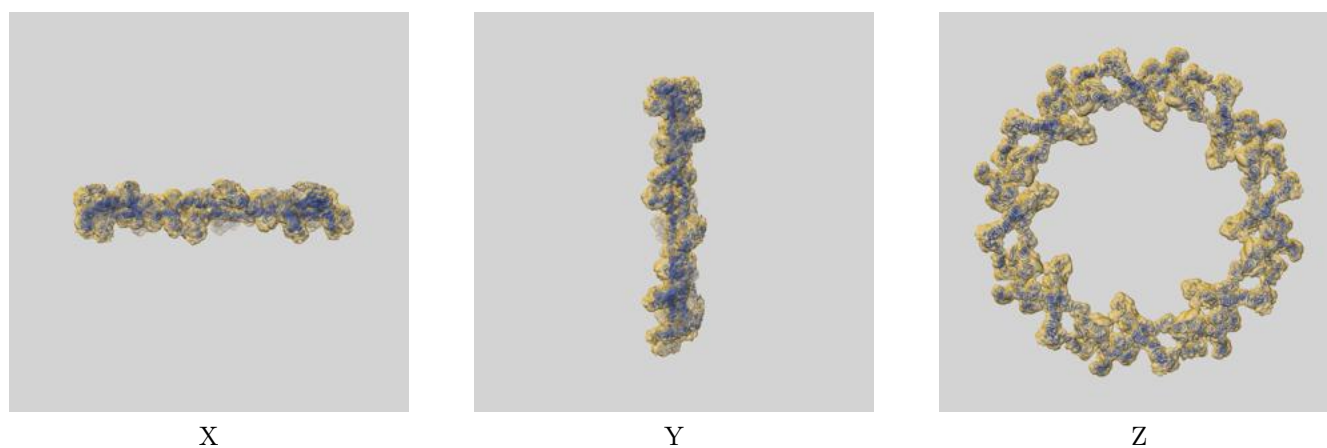
This section contains information regarding the fit between EMDB map EMD-24231 and PDB model 7N84. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay [i](#)

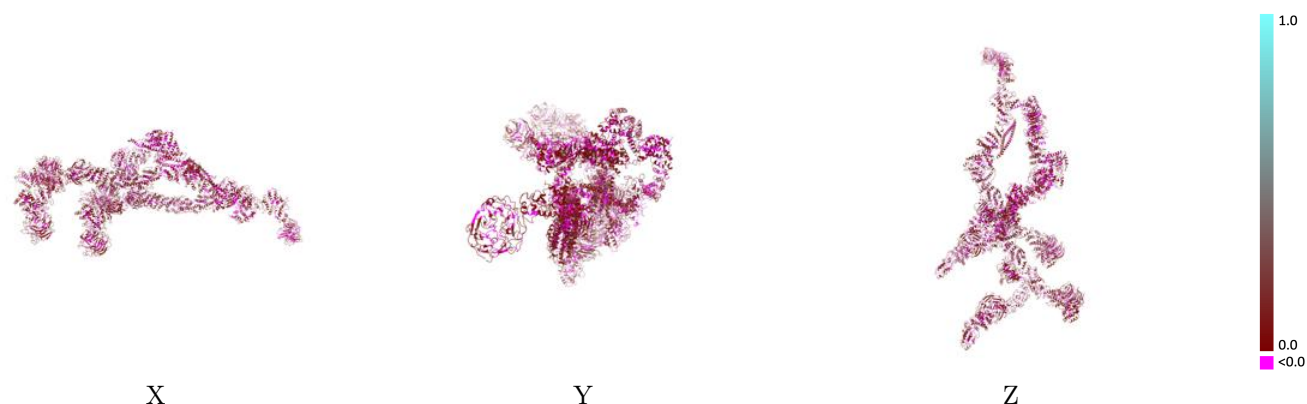


9.1.2 Map-model assembly overlay [i](#)



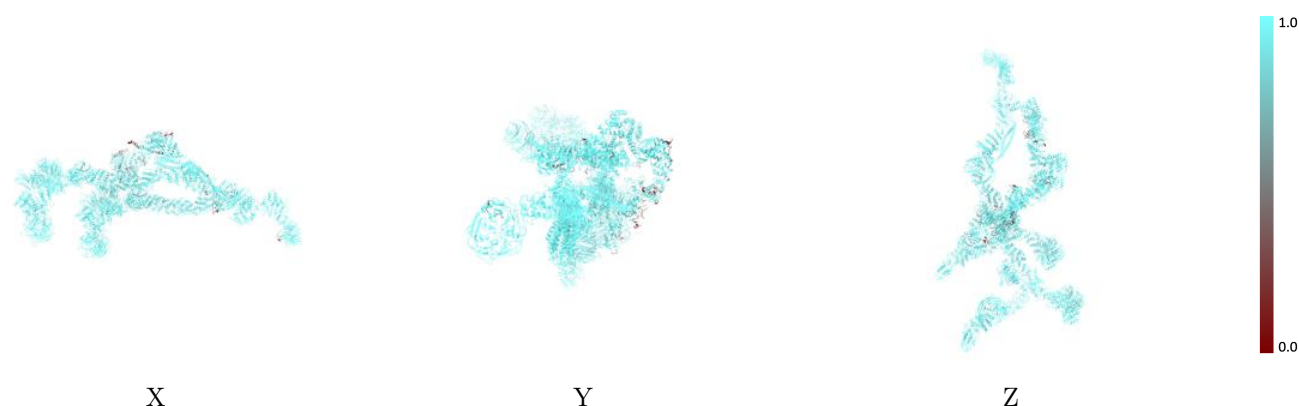
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



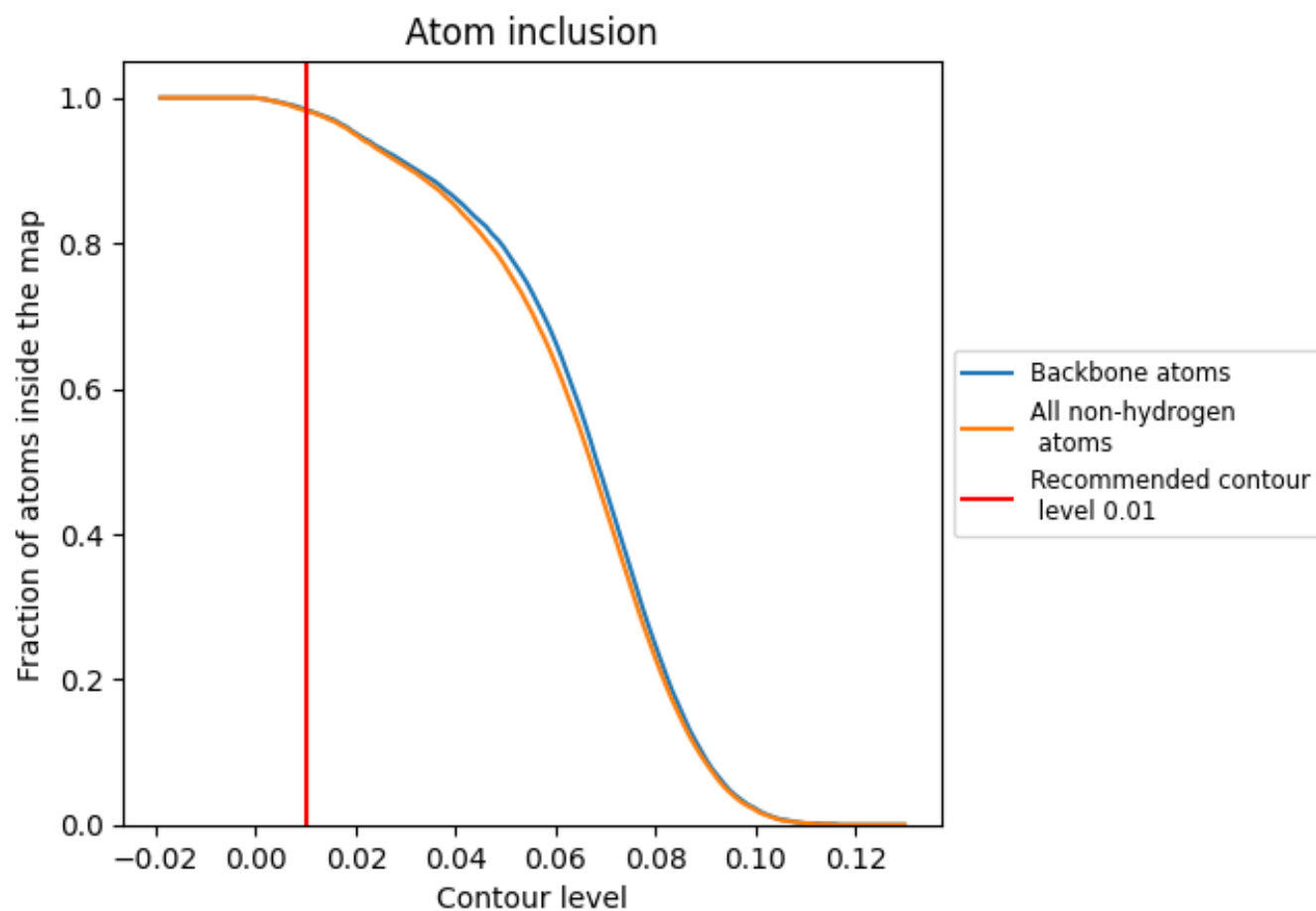
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9820	0.0630
X	0.8870	0.0340
Y	0.9870	0.0690
Z	1.0000	0.0680
a	1.0000	0.0700
b	1.0000	0.0610
c	1.0000	0.0820
d	1.0000	0.0660
e	1.0000	0.0680
f	1.0000	0.0760
g	0.9910	0.0490
l	1.0000	0.0700
m	1.0000	0.0700
n	1.0000	0.0860
o	1.0000	0.0690
p	1.0000	0.0620
q	1.0000	0.0770
r	0.9610	0.0520

1.0

0.0

<0.0