



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 02:35 AM UTC

PDB ID : 7TDZ / pdb_00007tdz
EMDB ID : EMD-25817
Title : Cryo-EM model of protomer of the cytoplasmic ring of the nuclear pore complex from *Xenopus laevis*
Authors : Fontana, P.; Wu, H.
Deposited on : 2022-01-03
Resolution : 6.90 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

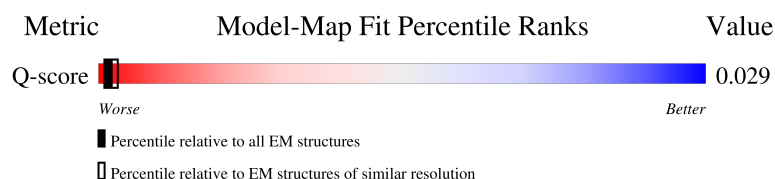
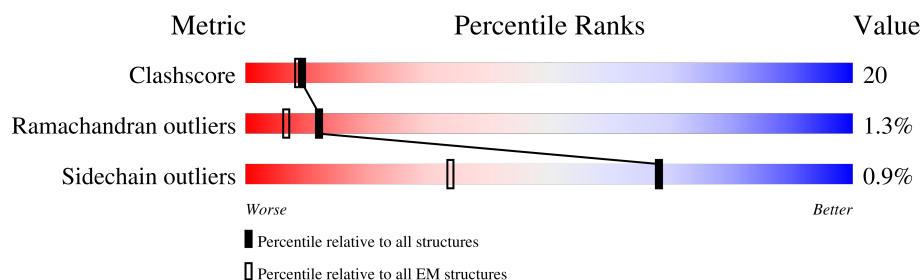
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.90 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.



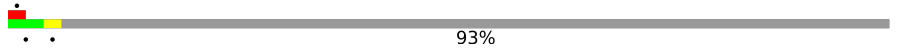
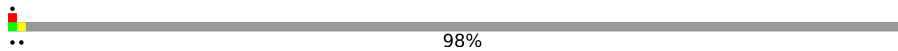
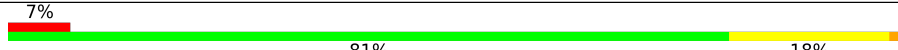
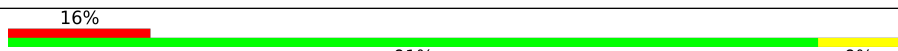
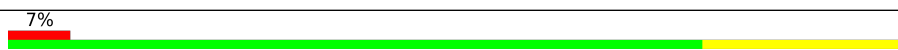
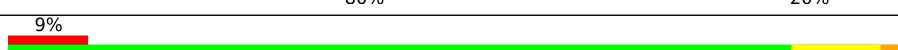
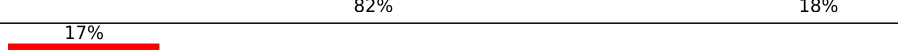
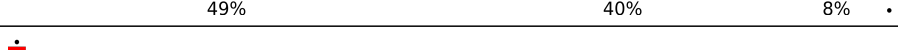
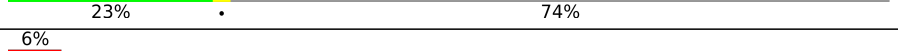
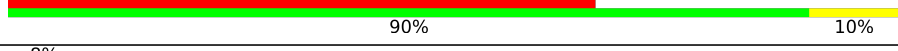
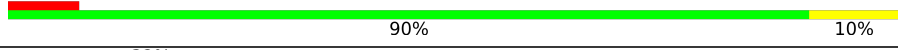
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	479 (6.40 - 7.40)

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	H	916	20% 78% 7% 14%
1	h	916	69% 81% 5% 14%
2	T	547	7% 11% 12% 76%
2	t	547	95%

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Mol	Chain	Length	Quality of chain
3	S	2037	
3	s	2037	
4	R	728	
4	r	728	
5	G	306	
5	g	306	
6	L	2011	
6	l	2011	
7	E	322	
7	e	322	
8	D	375	
8	d	375	
9	C	653	
9	c	653	
10	U	1388	
11	M	2905	
11	N	2905	
11	O	2905	
11	P	2905	
11	Q	2905	
12	B	326	
12	b	326	
13	A	1435	
13	a	1435	
14	I	1140	

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Mol	Chain	Length	Quality of chain
14	i	1140	93% 87% 5% 7%
15	F	673	19% 81% 13% 5%
15	f	673	17% 79% 15% 5%

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 331243 atoms, of which 162589 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 Nuclear pore complex protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	H	789	Total	C	H	N	O	S	0	0
			12767	4080	6346	1085	1224	32		
1	h	789	Total	C	H	N	O	S	0	0
			12767	4080	6346	1085	1224	32		

- Molecule 2 is a protein called Nup62.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	t	29	Total	C	H	N	O		0	0
			479	153	235	42	49			
2	T	130	Total	C	H	N	O	S	0	0
			2140	664	1064	189	220	3		

- Molecule 3 is a protein called Nup214.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	s	32	Total	C	H	N	O		0	0
			518	158	261	46	53			
3	S	142	Total	C	H	N	O	S	0	0
			2333	722	1164	208	236	3		

- Molecule 4 is a protein called Nup88A protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	r	470	Total	C	H	N	O	S	0	0
			7354	2349	3679	598	703	25		
4	R	680	Total	C	H	N	O	S	0	0
			10786	3395	5396	916	1048	31		

- Molecule 5 is a protein called Protein SEC13 homolog.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	g	306	Total	C	H	N	O	S	0	0
			4657	1506	2270	408	460	13		
5	G	306	Total	C	H	N	O	S	0	0
			4657	1506	2270	408	460	13		

- Molecule 6 is a protein called Nup205.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	L	2011	Total	C	H	N	O	S	0	0
			32130	10112	16156	2785	2978	99		
6	l	2011	Total	C	H	N	O	S	0	0
			32130	10112	16156	2785	2978	99		

- Molecule 7 is a protein called Nucleoporin SEH1-A.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	E	322	Total	C	H	N	O	S	0	0
			4973	1582	2445	452	476	18		
7	e	322	Total	C	H	N	O	S	0	0
			4973	1582	2445	452	476	18		

- Molecule 8 is a protein called Nup42.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	D	375	Total	C	H	N	O	S	0	0
			5727	1813	2800	524	571	19		
8	d	375	Total	C	H	N	O	S	0	0
			5727	1813	2800	524	571	19		

- Molecule 9 is a protein called Nuclear pore complex protein Nup85.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	C	653	Total	C	H	N	O	S	0	0
			10494	3341	5226	904	984	39		
9	c	653	Total	C	N	O	S		0	0
			5267	3341	904	983	39			

- Molecule 10 is a protein called Nup155-prov protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	U	358	Total	C	H	N	O	S	0	0
			5843	1868	2931	490	538	16		

- Molecule 11 is a protein called Nup358.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	P	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	O	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	Q	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	N	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		
11	M	798	Total	C	H	N	O	S	0	0
			12862	4088	6444	1096	1202	32		

- Molecule 12 is a protein called Nup37.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	B	326	Total	C	H	N	O	S	0	0
			5076	1640	2503	443	473	17		
12	b	326	Total	C	H	N	O	S	0	0
			5076	1640	2503	443	473	17		

- Molecule 13 is a protein called Nup160.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	A	1352	Total	C	H	N	O	S	0	0
			21491	6819	10745	1855	2005	67		
13	a	1352	Total	C	H	N	O	S	0	0
			21491	6819	10745	1855	2005	67		

- Molecule 14 is a protein called Nup133.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	I	671	Total	C	H	N	O	S	0	0
			10733	3406	5353	899	1048	27		
14	i	1064	Total	C	H	N	O	S	0	0
			16672	5313	8274	1394	1641	50		

- Molecule 15 is a protein called Nuclear pore complex protein Nup96.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	F	639	Total	C	H	N	O	S	0	0
			10336	3298	5128	928	954	28		

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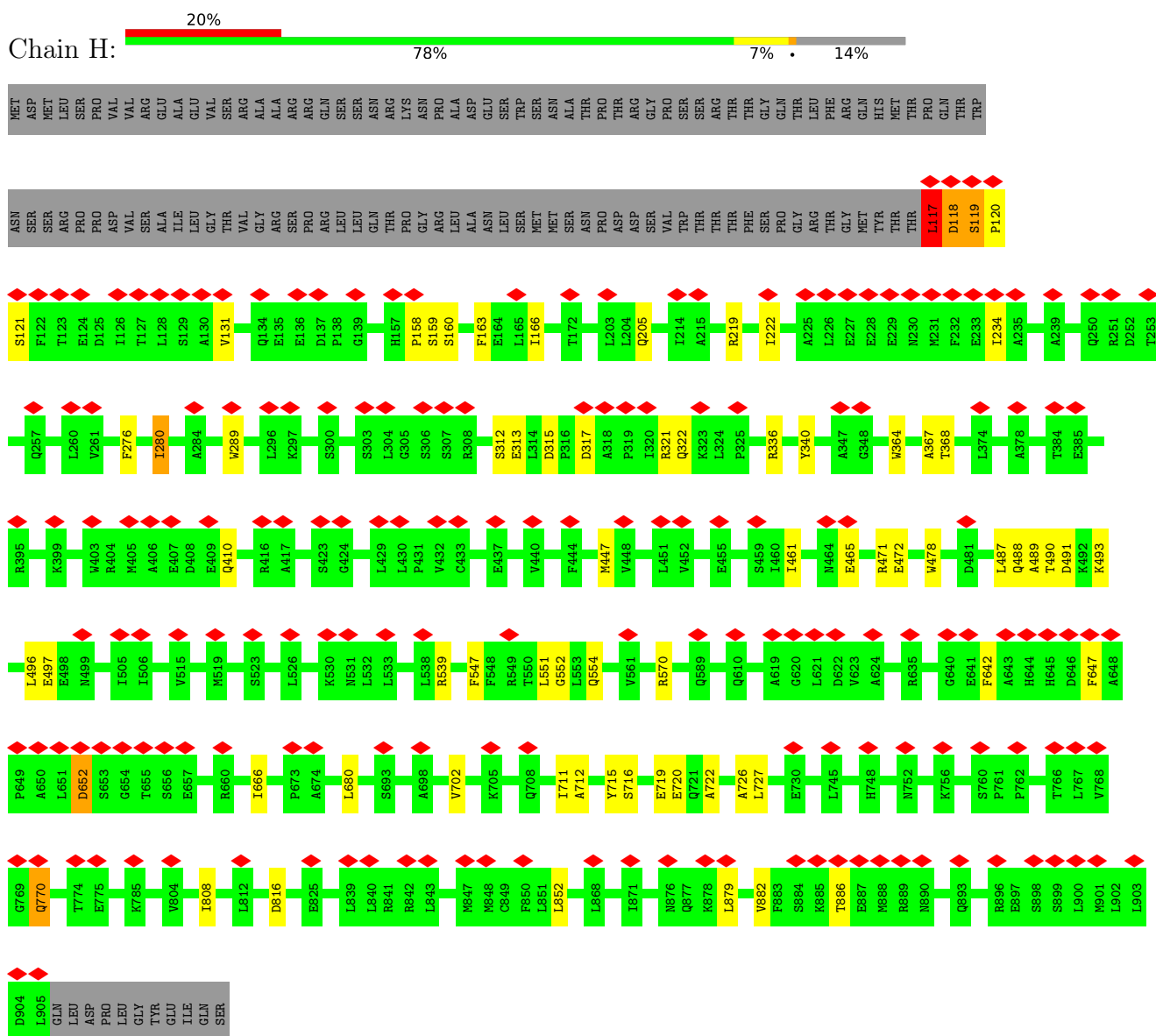
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Mol	Chain	Residues	Atoms						AltConf	Trace
15	f	639	Total	C	H	N	O	S	0	0
			10336	3298	5128	928	954	28		

3 Residue-property plots

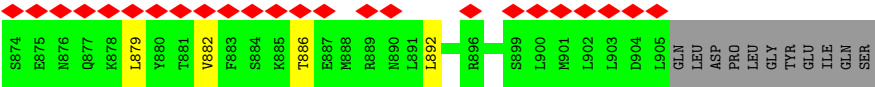
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Nuclear pore complex protein

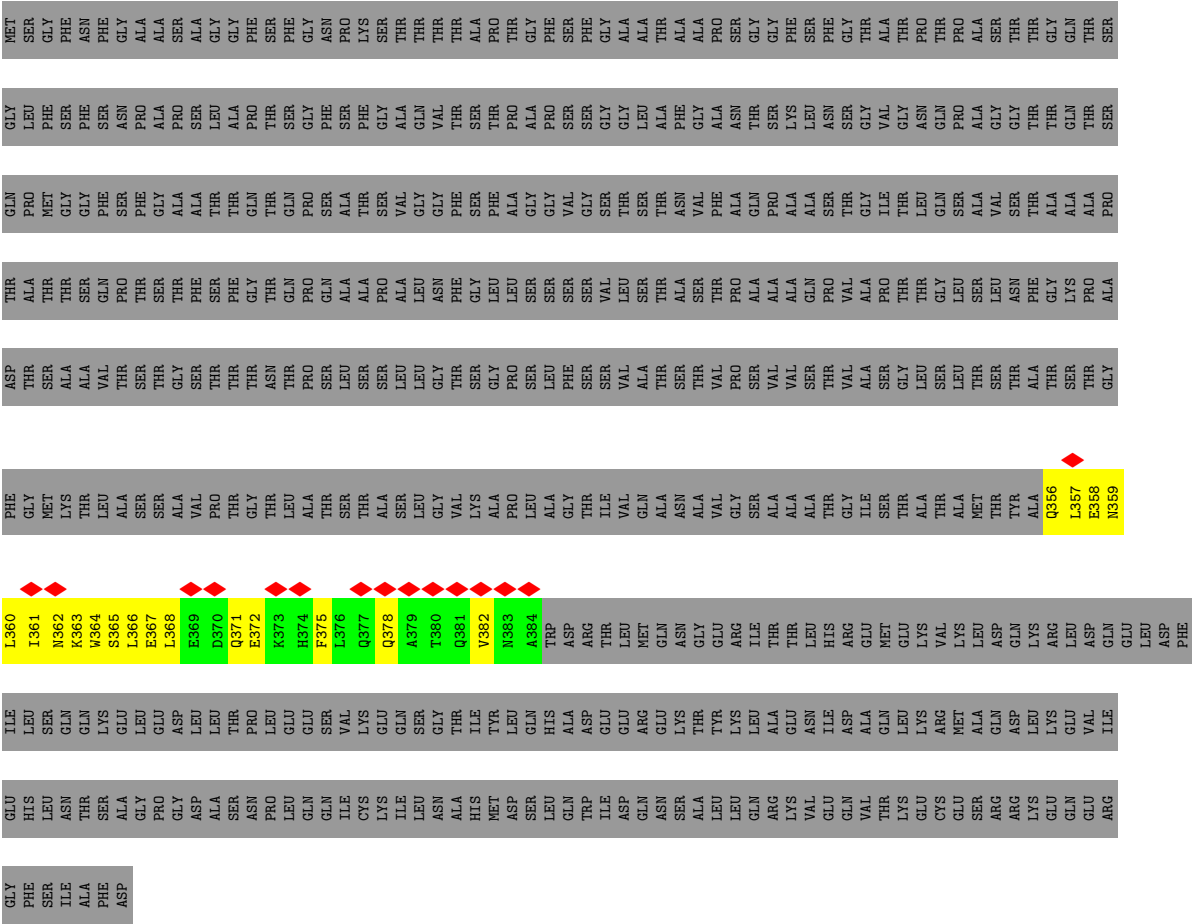


- Molecule 1: Nuclear pore complex protein

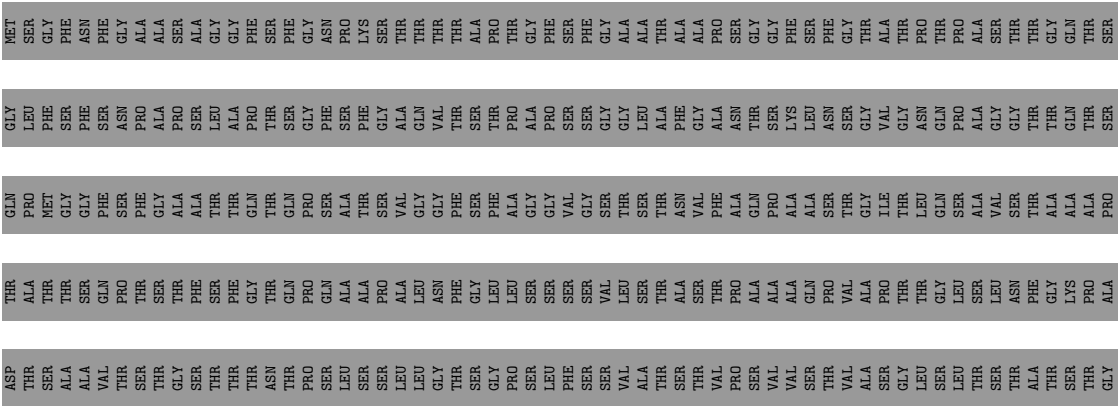


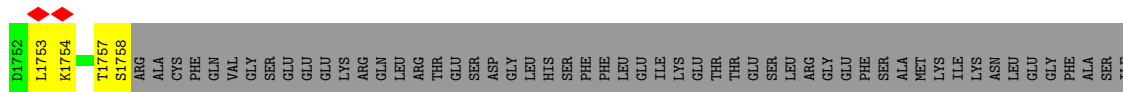


• Molecule 2: Nup62



• Molecule 2: Nup62





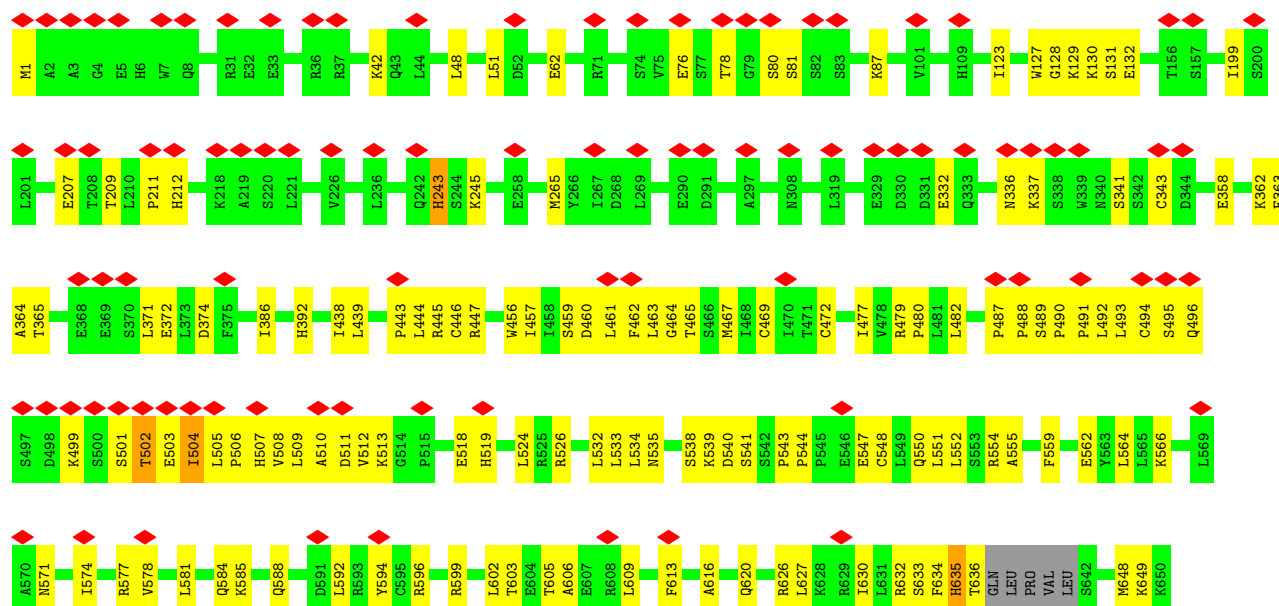


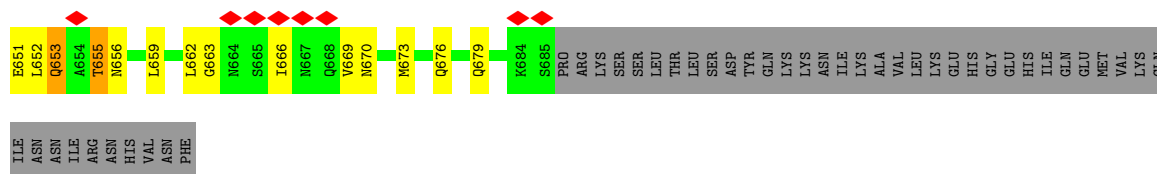
ALA ILE ASP THR THR LYS PRO PRO GLN GLN ALA ALA LYS LEU LEU PRO PRO ALA ALA ASP THR THR LYS PRO PRO GLN GLN ALA ALA LYS LEU LEU PRO PRO VAL VAL LYS GLN SER SER LYS ARG ARG LYS LYS THR THR PRO PRO VAL VAL ARG ARG SER SER LYS LEU LEU ASP ASN PHE PHE LYS LEU LEU ARG ARG SER SER ALA ALA PHE PHE LEU LEU PRO PRO PHE PHE GLU GLU ASP ASP ASP ASP

[illegible]

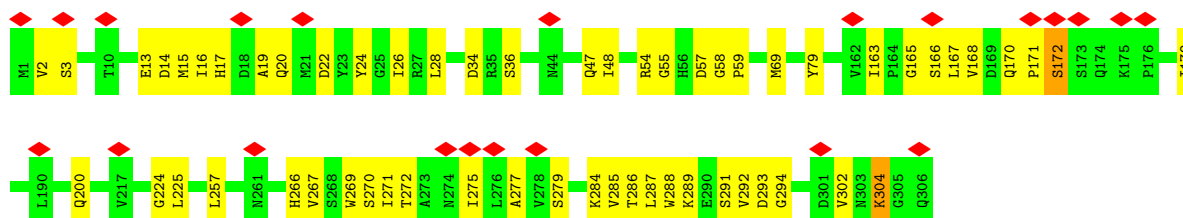
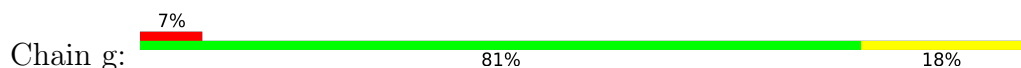
- Molecule 4: Nup88A protein



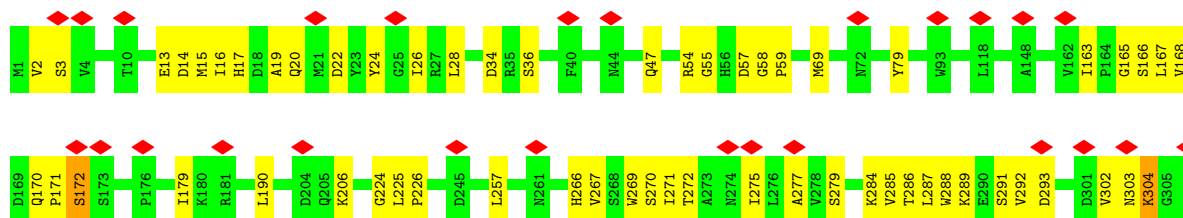
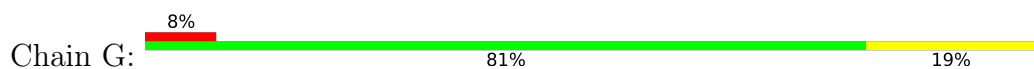




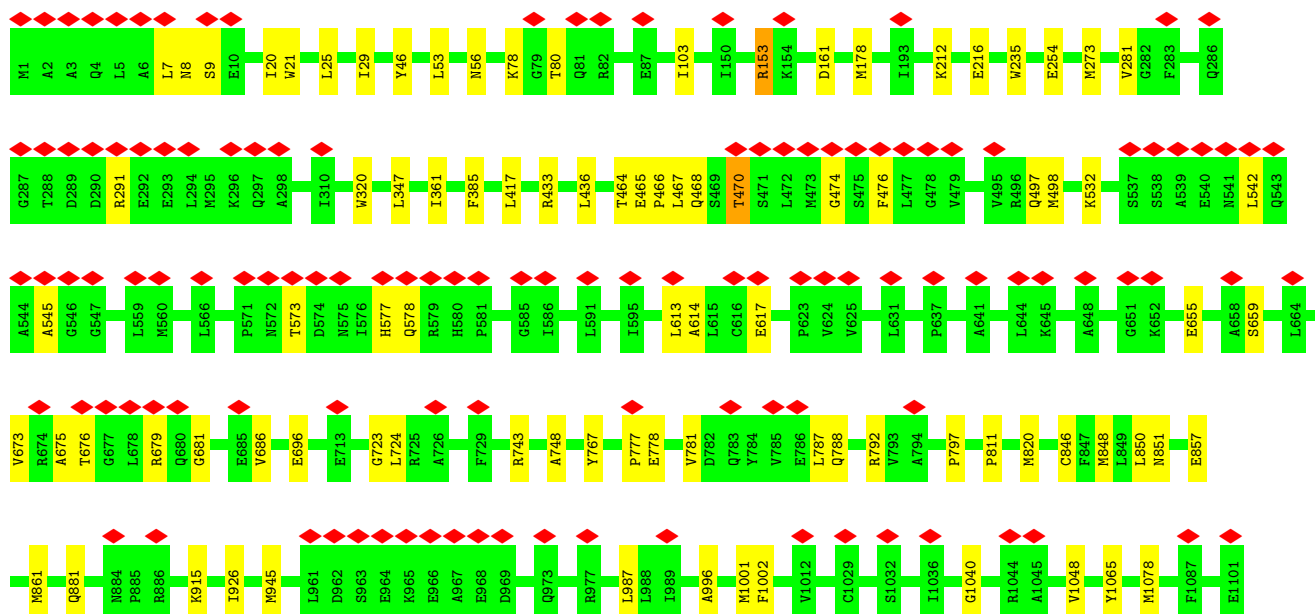
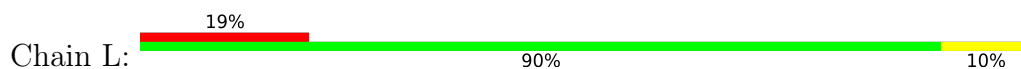
• Molecule 5: Protein SEC13 homolog

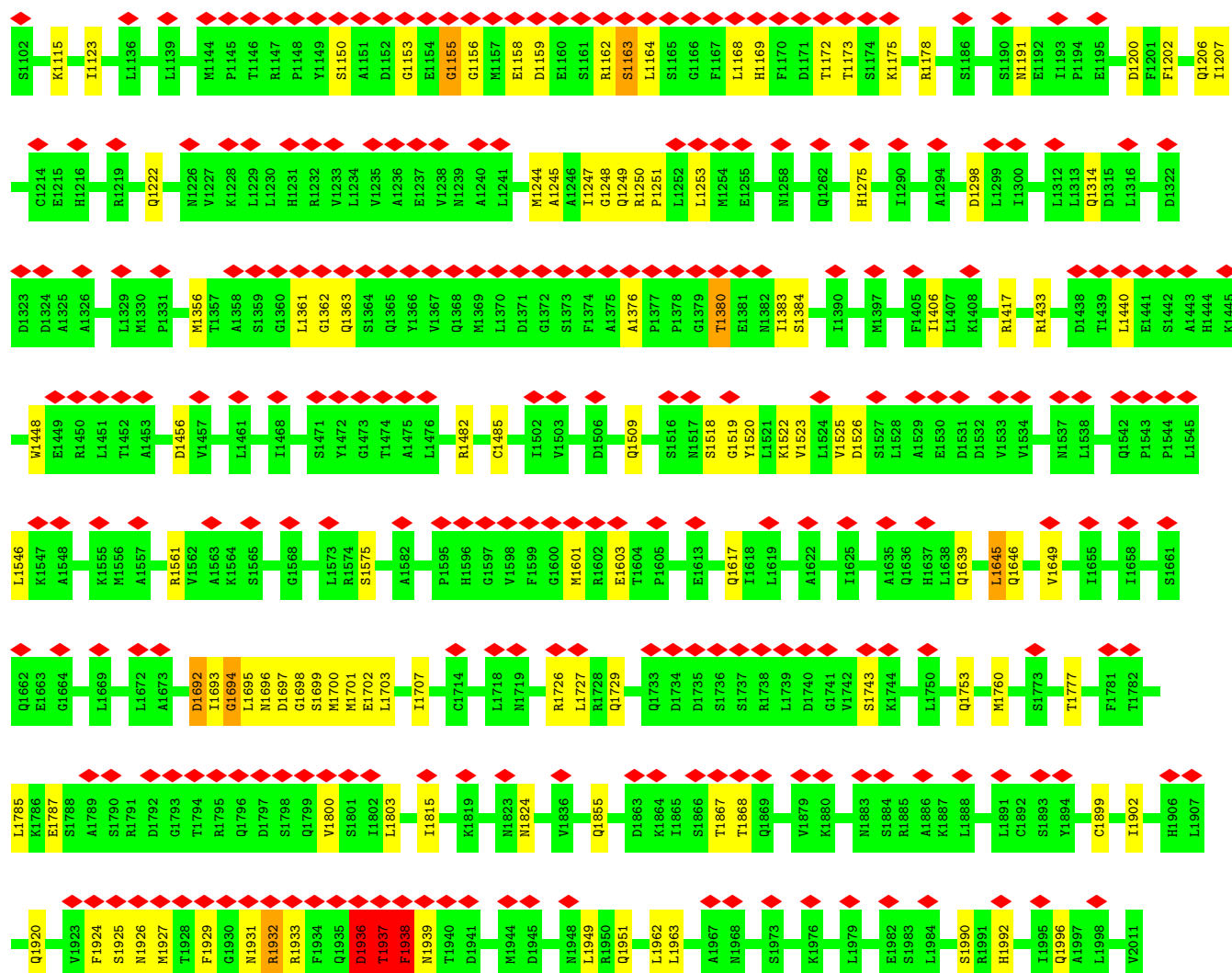


• Molecule 5: Protein SEC13 homolog

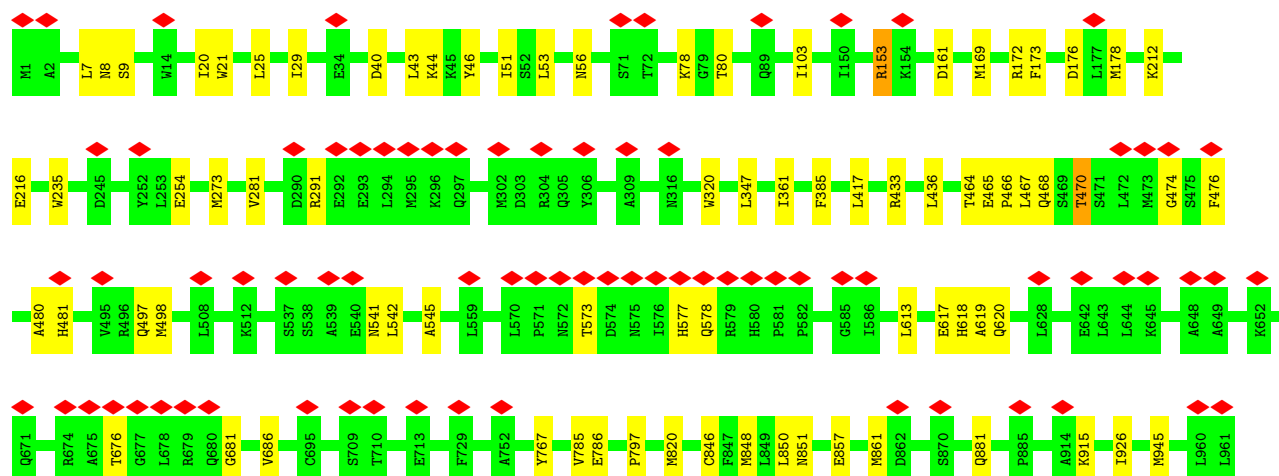


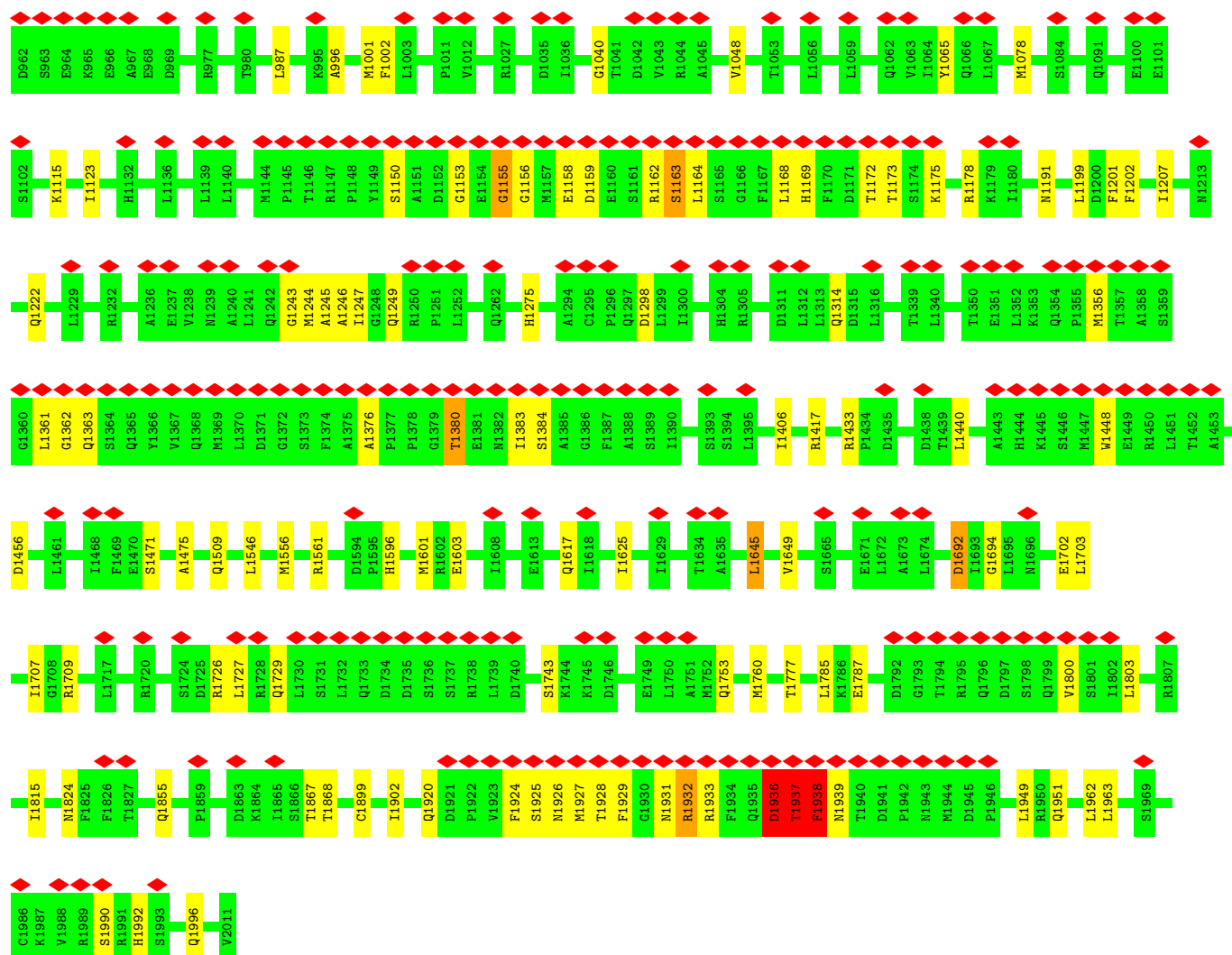
• Molecule 6: Nup205



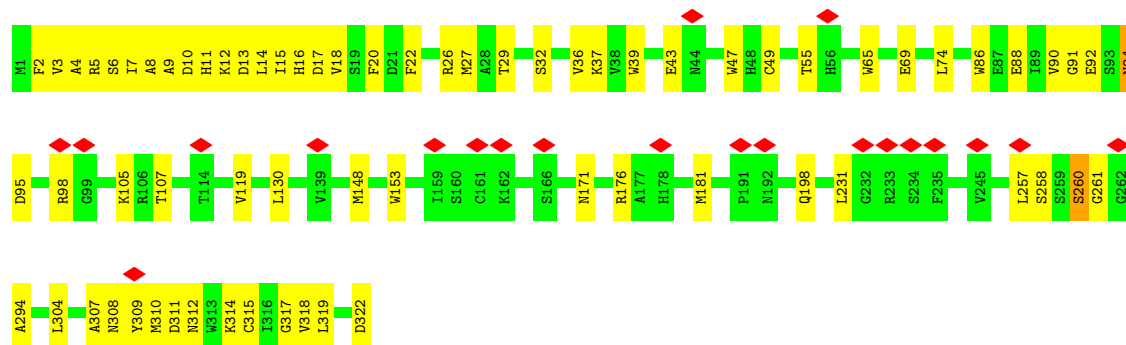
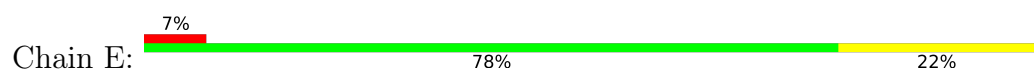


• Molecule 6: Nup205

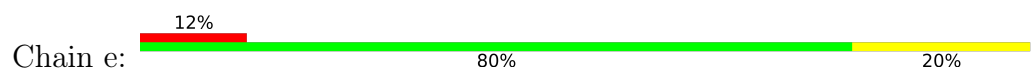


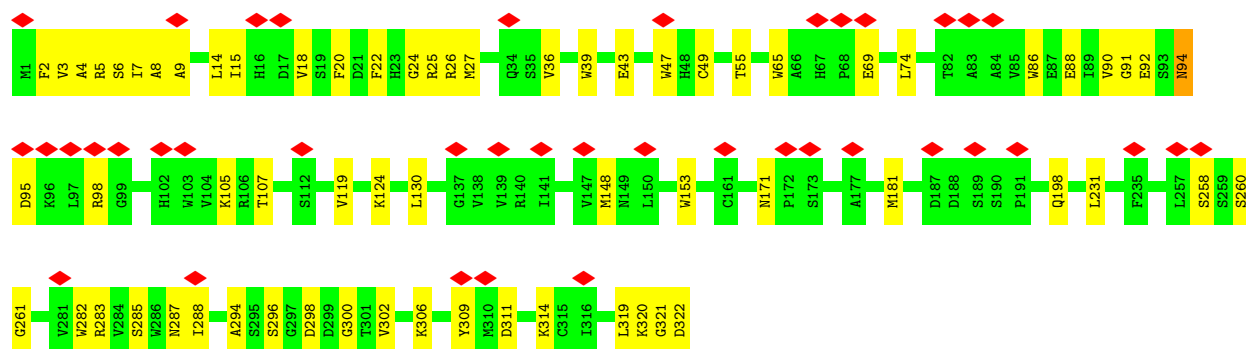


• Molecule 7: Nucleoporin SEH1-A

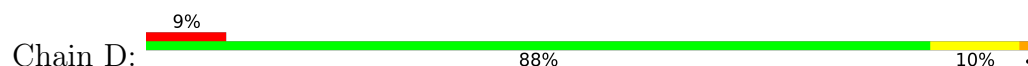


• Molecule 7: Nucleoporin SEH1-A

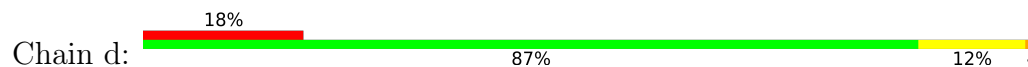




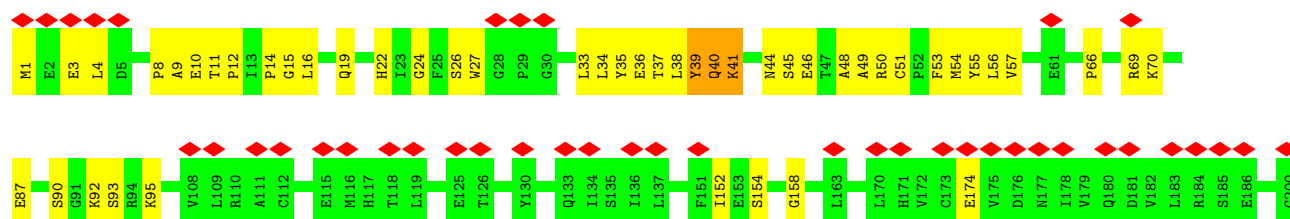
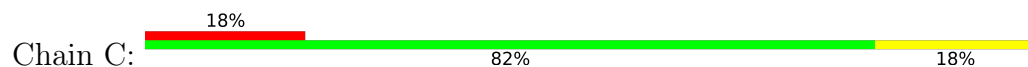
• Molecule 8: Nup42

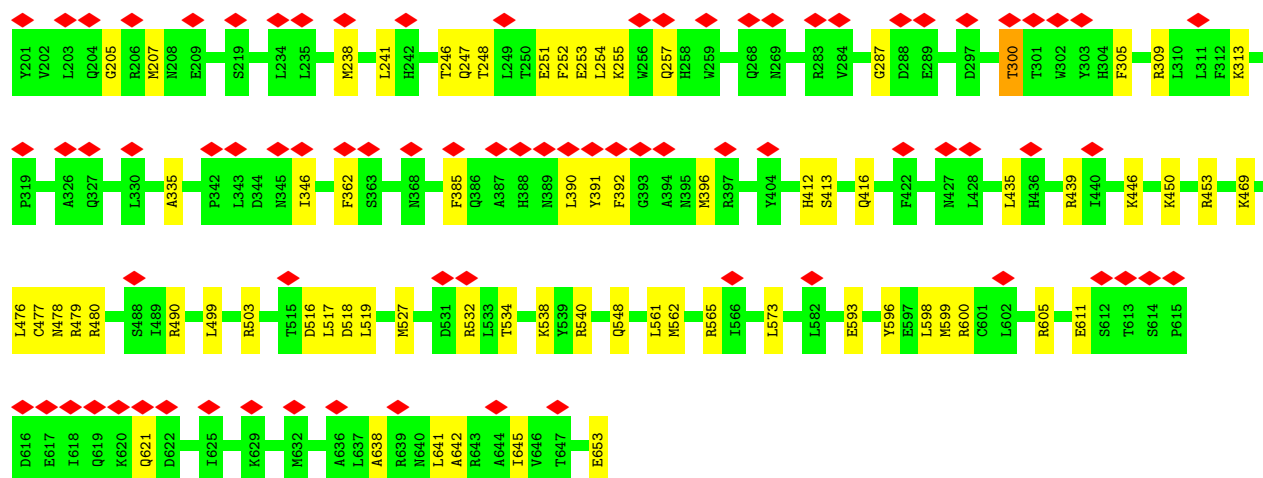


• Molecule 8: Nup42

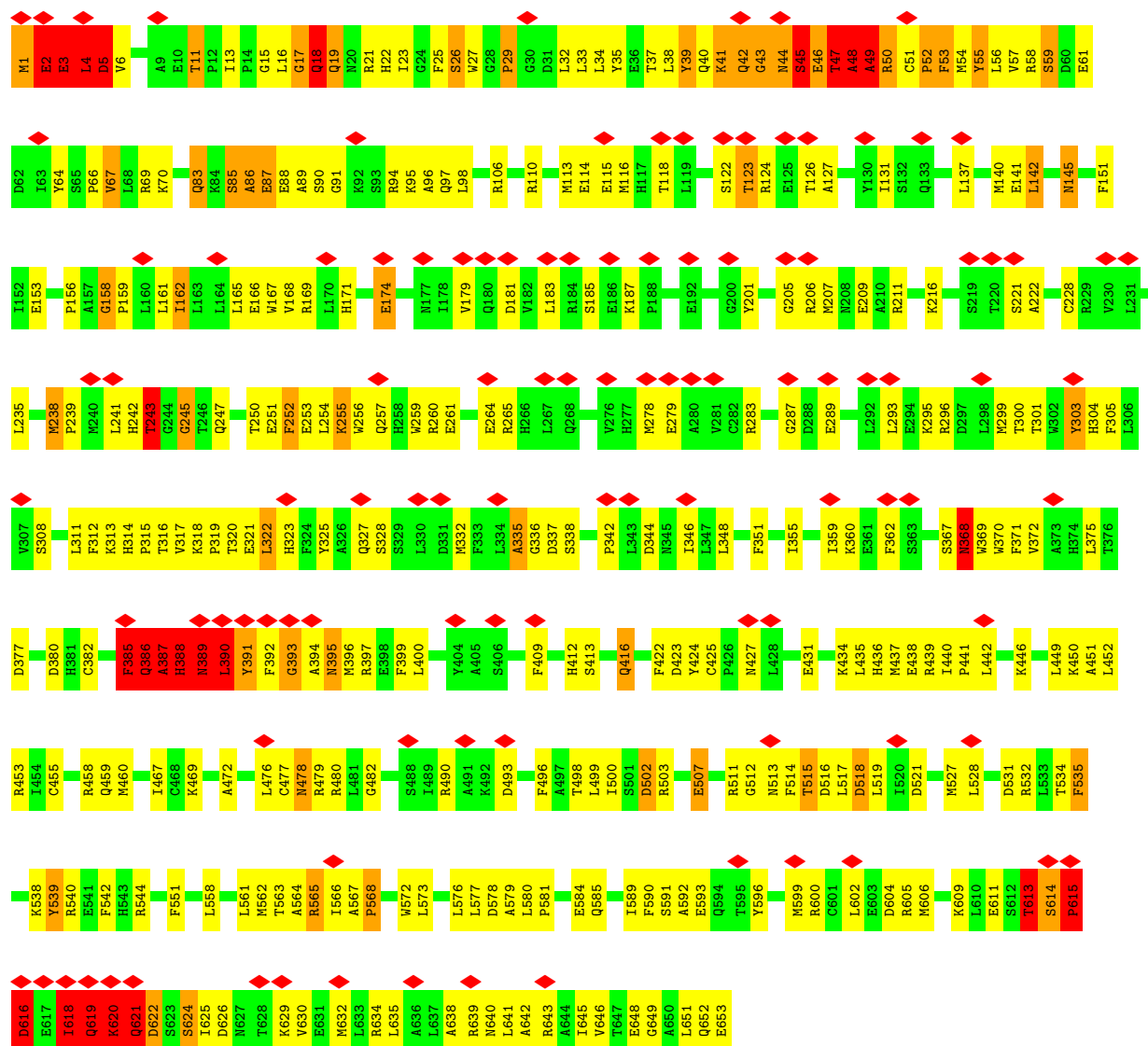


• Molecule 9: Nuclear pore complex protein Nup85





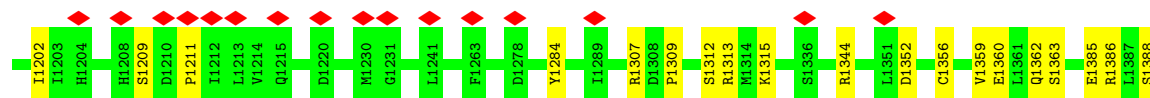
• Molecule 9: Nuclear pore complex protein Nup85



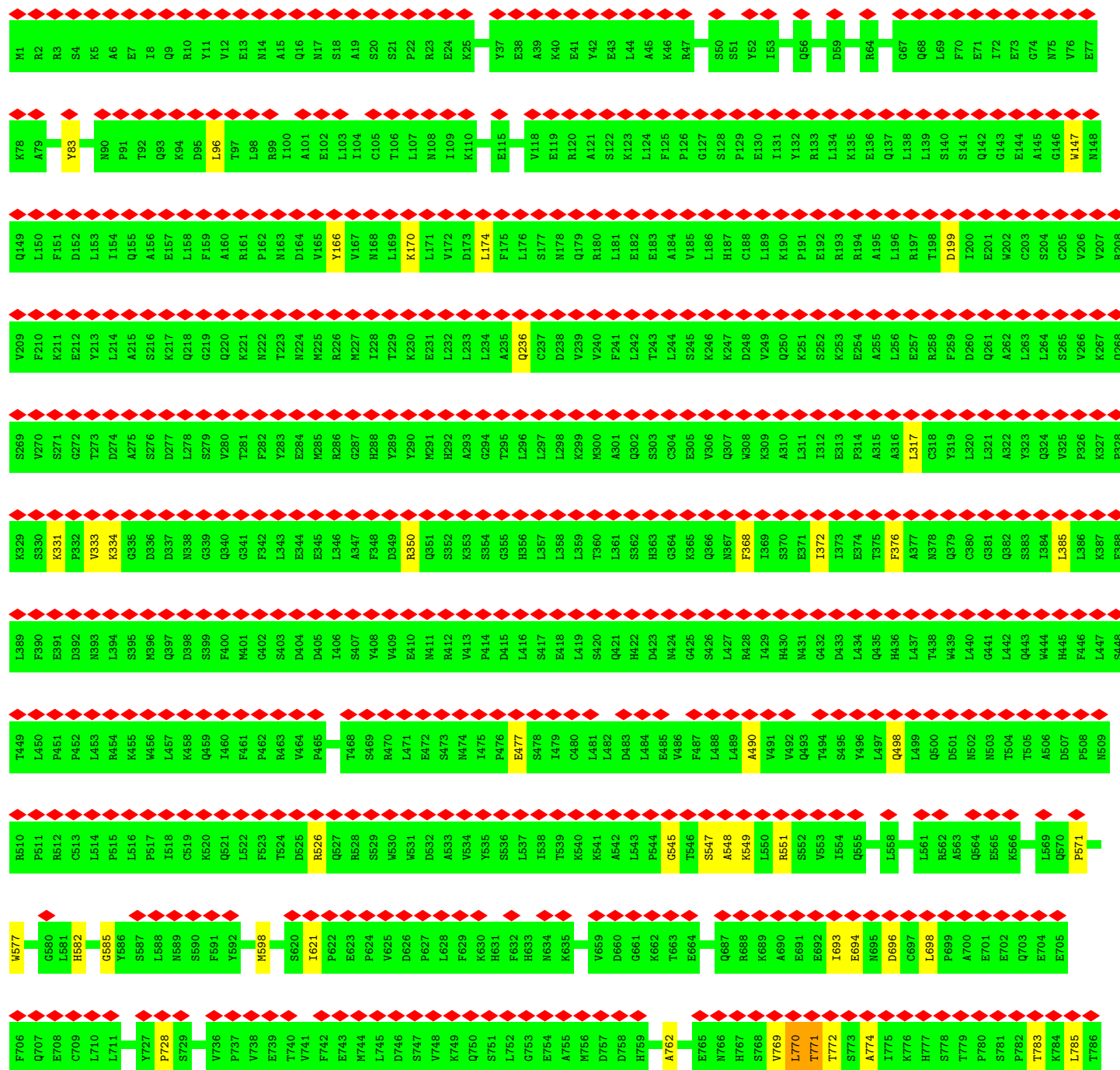
Chain U:



LEU	LYS	PHE	GLN	TYR	CYS	LEU	LEU	PHE	THR	THR	CYS	PRO	ALA	PRO	ALA	PRO	VAL	ASP	ASP	ASP	ARG	THR	TYR	MET
LEU	LEU	GLN	LYS	ILE	ILE	ARG	ARG	ALA	ALA	ALA	THR	ILE	CYS	ILE	CYS	ILE	MET	THR	THR	THR	GLY	GLN	PRO	
ALA	GLN	GLU	SER	SER	ASP	MET	LYS	GLY	THR	LEU	ARG	GLN	THR	GLN	THR	GLN	GLN	THR	THR	ASP	PRO	PRO	GLY	
ARG	LEU	LEU	ASN	ILE	CYS	CYS	GLN	LEU	LEU	ILE	ARG	ILE	ILE	PRO	ILE	ILE	THR	VAL	VAL	SER	LYS	LEU	GLY	
SER	SER	ASN	ALA	ILE	ALA	GLN	ASN	ASN	ASN	ASN	PRO	PRO	SER	SER	PRO	PRO	VAL	ARG	ARG	ASP	ALA	LEU	ALA	
ASN	ASN	SER	VAL	VAL	VAL	ALA	ASP	ALA	ALA	ALA	THR	THR	CYS	PRO	PRO	PRO	VAL	ASN	ASN	SER	GLY	LEU	PRO	
TYR	ASP	TYR	LEU	ASP	VAL	LEU	LEU	PRO	PRO	PRO	PRO	PRO	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	GLN	
GLU	GLU	LYS	ASP	GLY	ASP	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	
I1031																								
I1034																								
A1035																								
D1044																								
E1051																								
E1058																								
R1073																								
D1076																								
W1079																								
K1084																								
R1086																								
V1094																								
H1102																								
K1123																								
S1124																								
T1127																								
M1128																								
S1129																								
T1130																								
A1132																								
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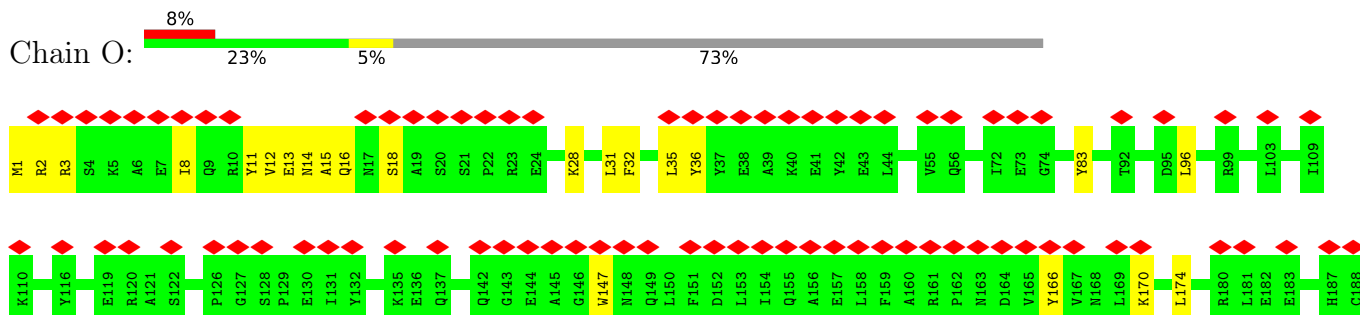


● Molecule 11: Nup358





- Molecule 11: Nup358

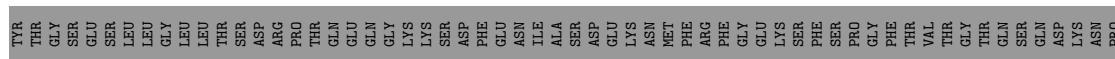






LYS	VAL	GLU	GLN	LEU	ALA	VAL	ARG	PHE	LYS	THR	LYS	GLU	LEU	THR	ASP	SER	PHE	GLN	ASN	LYS	PHE	GLU	GLU	CYS	GLN	HIS	ASN	LEU	GLN	GLU	GLU	SER	ASN	PRO	GLN	HIS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Chain Q: 7% 23% 73%





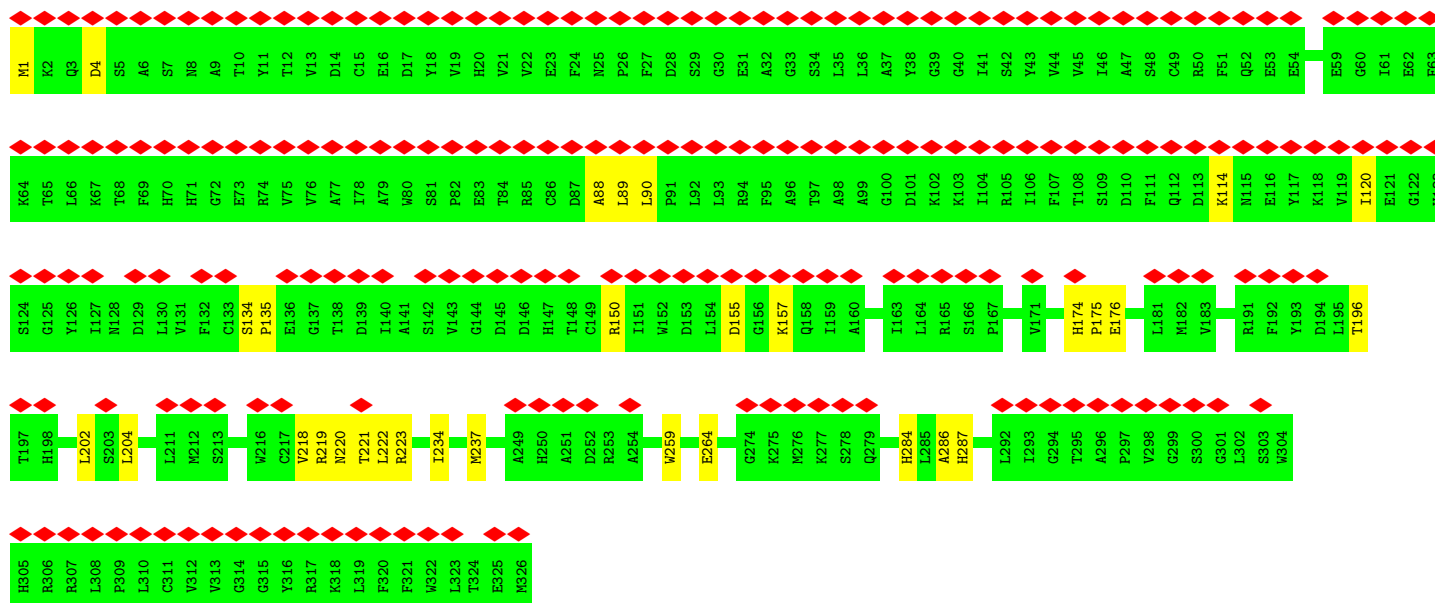




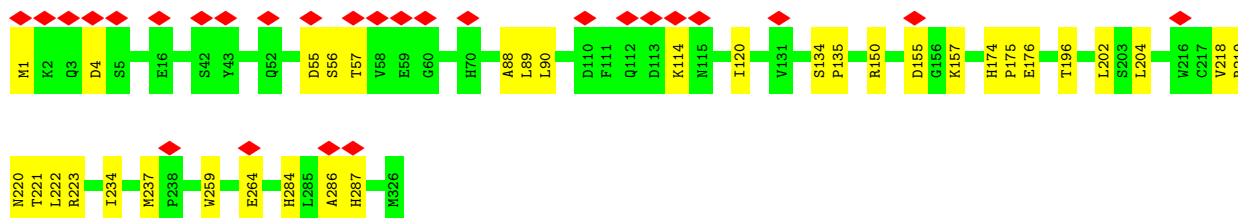
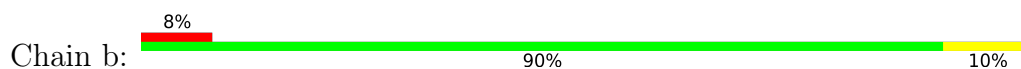


- Molecule 12: Nup37

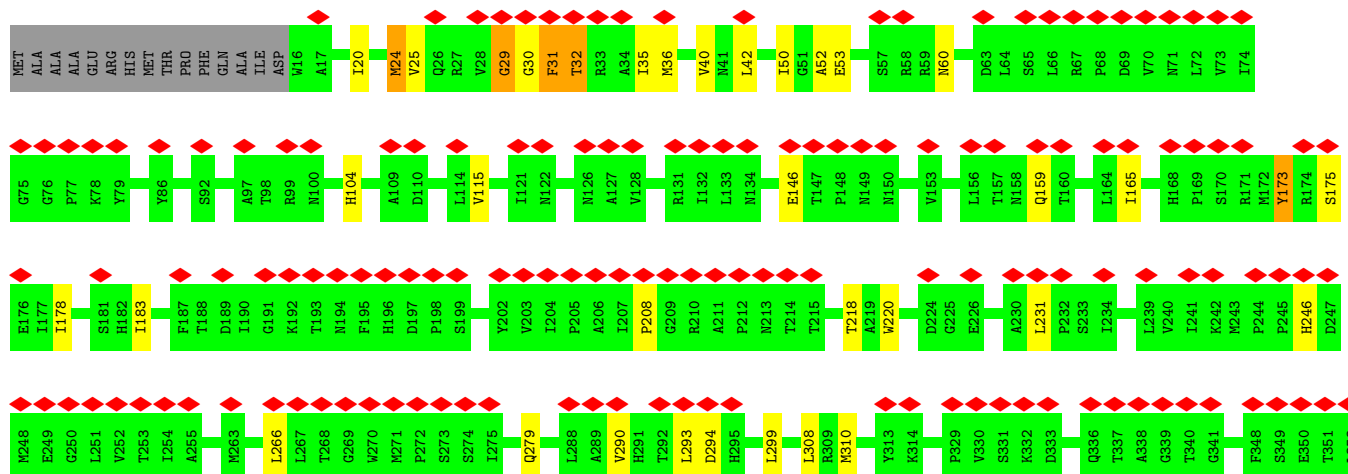
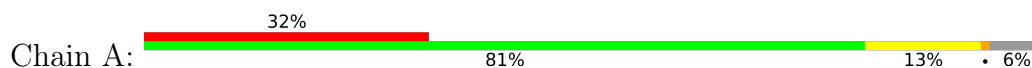


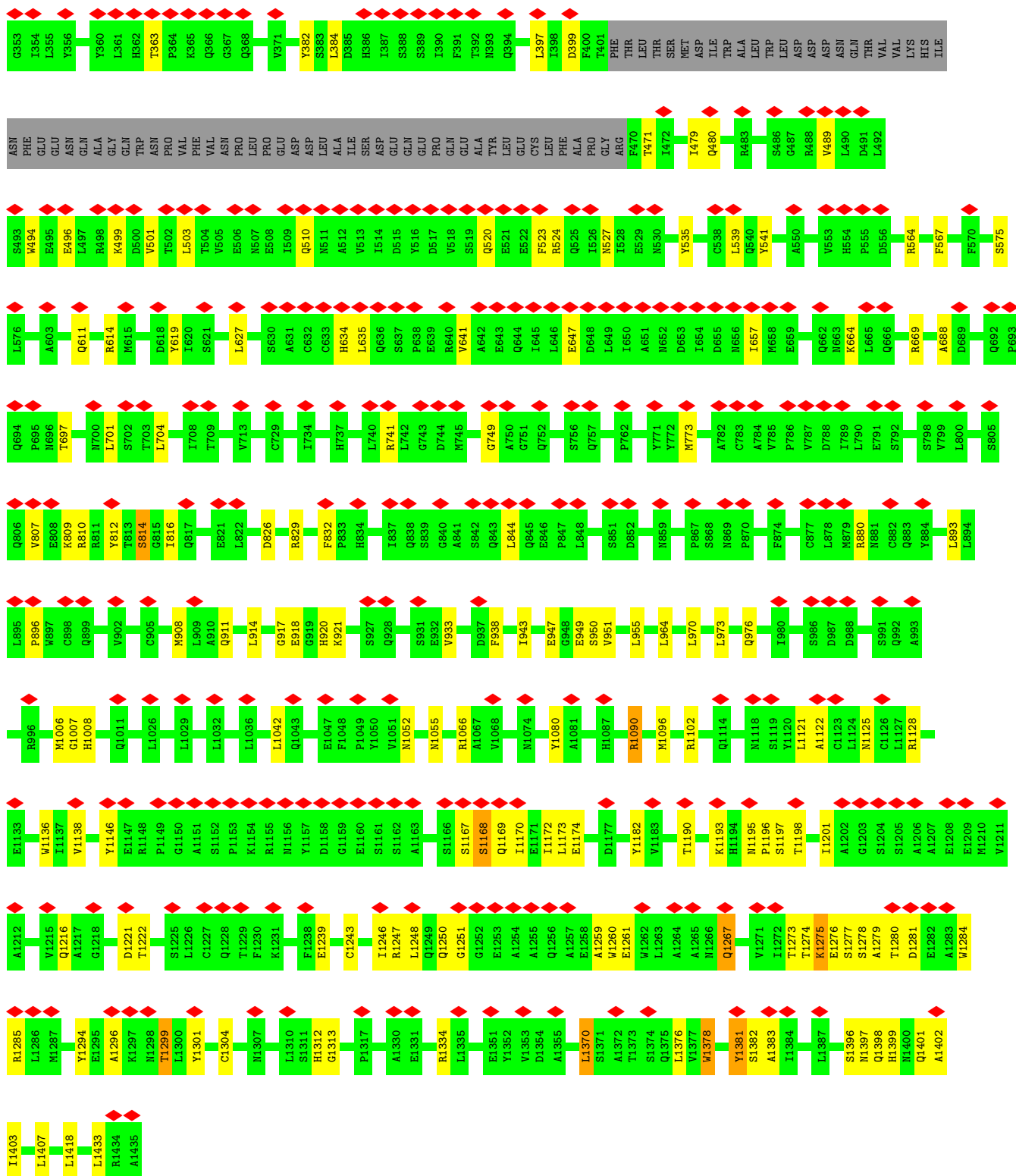


• Molecule 12: Nup37

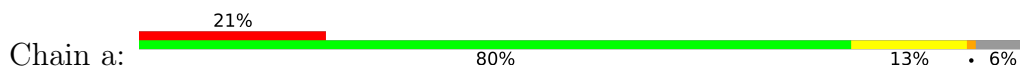


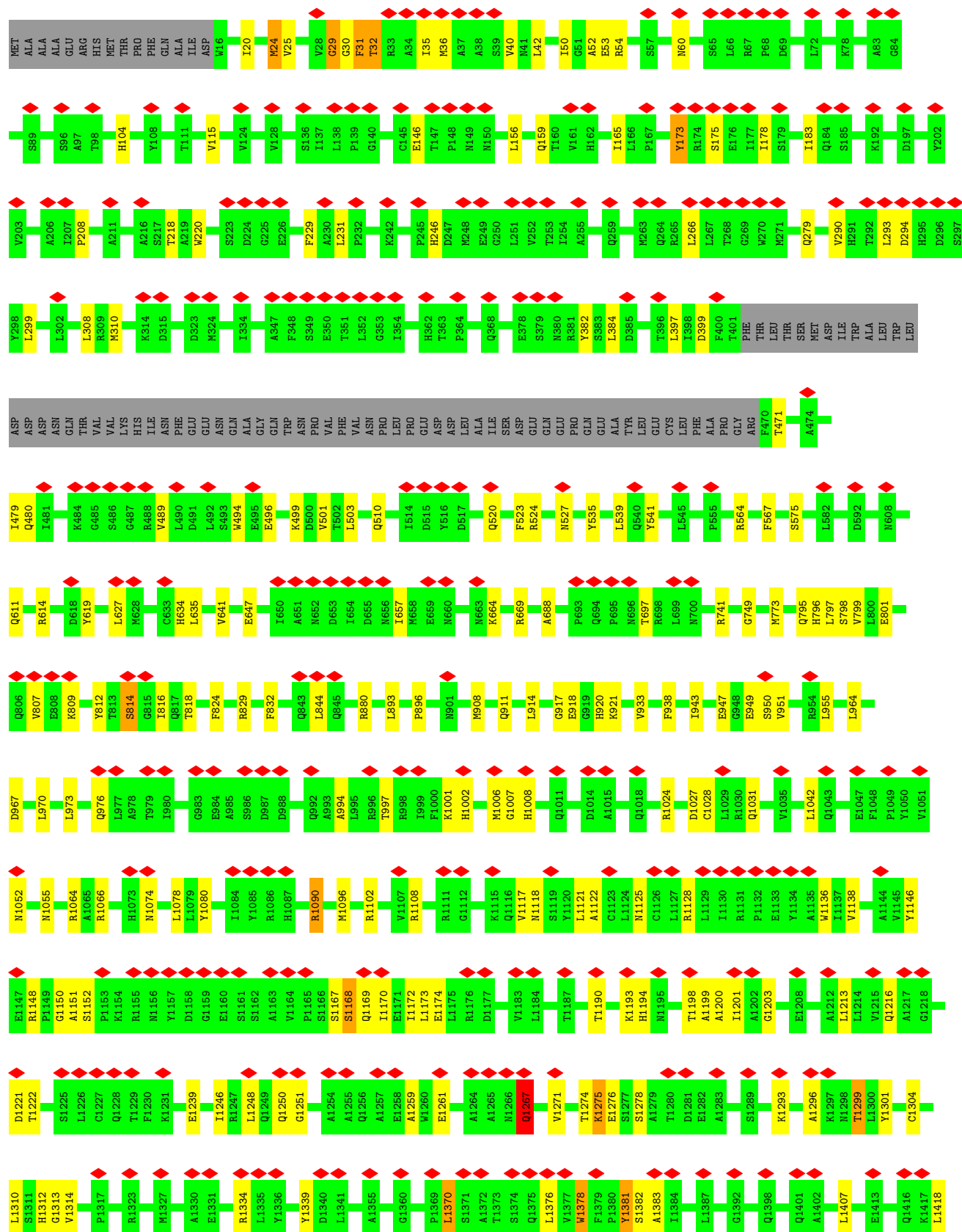
• Molecule 13: Nup160



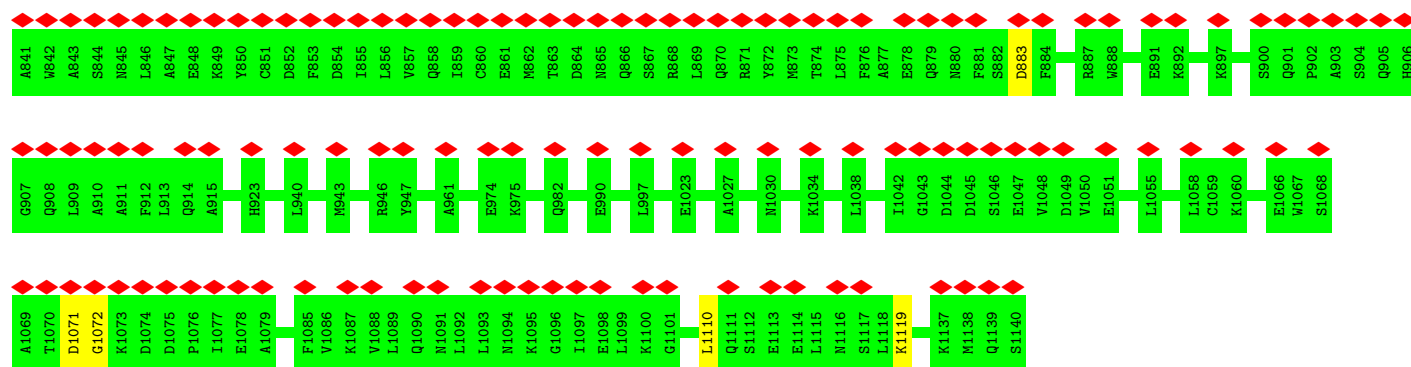


• Molecule 13: Nup160

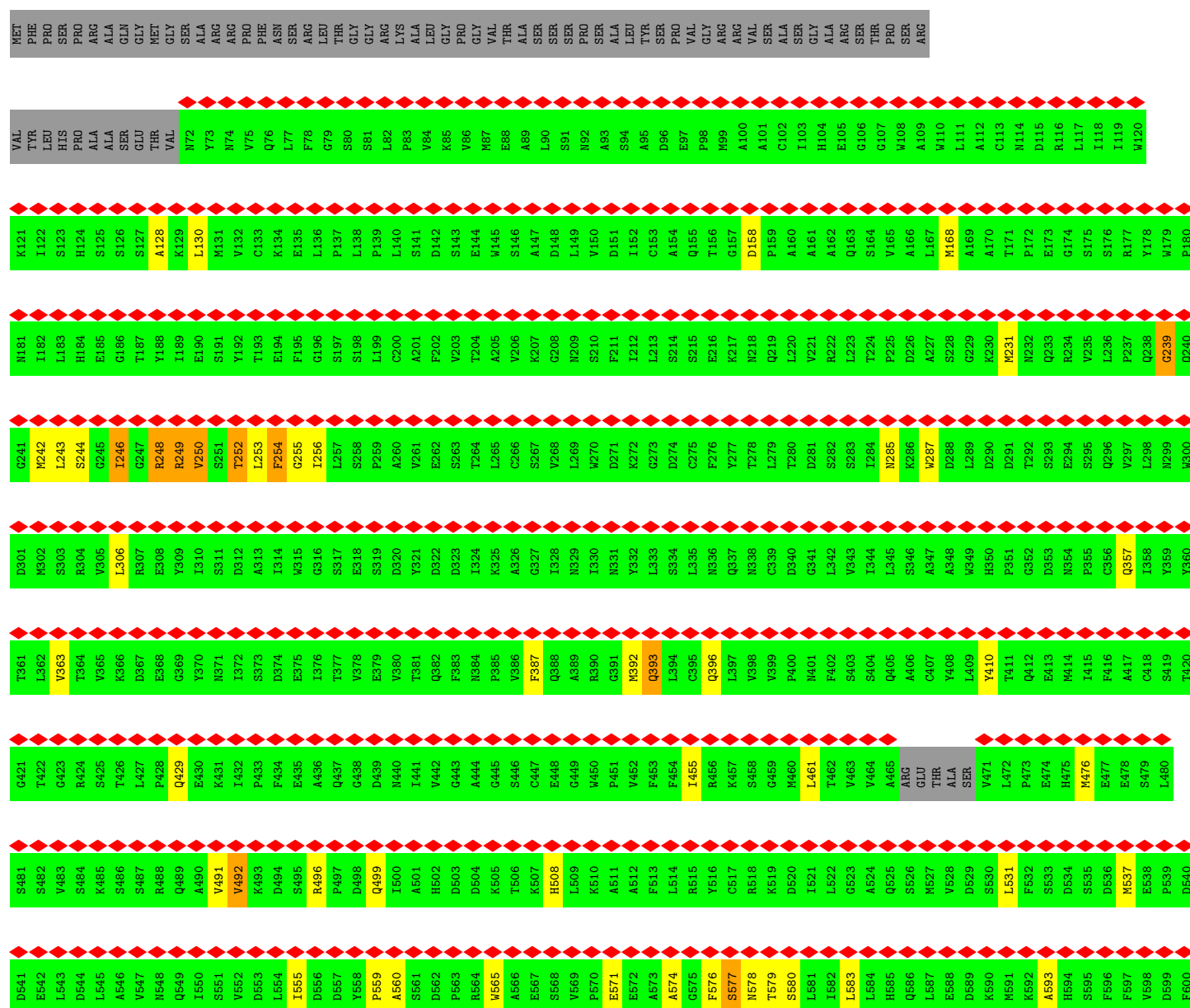
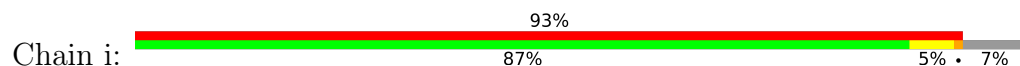


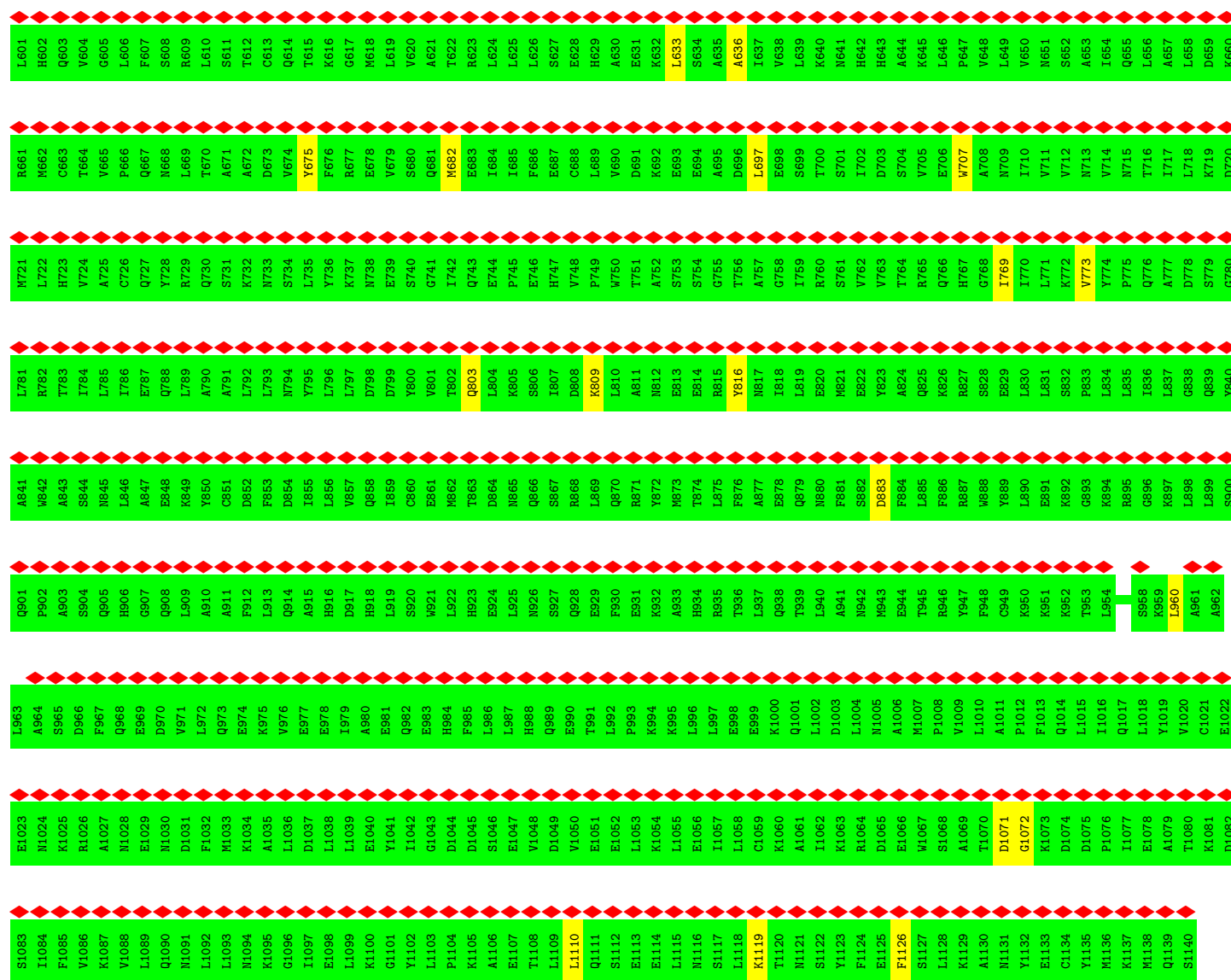


L781	W721	R661	L601	D541	S481
R782	L722	M662	H602	E542	S482
R783	C663	M662	H602	E542	S482
I784	W724	T664	V604	D544	V483
L785	A725	V665	G605	L545	S484
I786	C726	P666	L606	A546	K485
Q787	Q727	Q667	F607	V547	S486
Q788	W728	M668	S608	N548	S487
L789	R729	L669	H609	Q549	R488
A790	Q730	T670	L610	I550	Q489
A791	S731	A671	S611	S551	A490
L792	K732	A672	T612	V552	V491
L793	N733	D673	G613	D553	V492
W794	S734	V674	Q614	L554	K493
Y795	L735	V675	T615	I555	D494
L796	W736	F676	K616	D556	S495
L797	K737	R677	G617	D557	R496
D798	N738	E678	H618	V558	P497
D799	E739	V679	L619	P559	D498
Y800	S740	S680	V620	A560	Q499
T802	I742	Q681	A621	S561	I500
Q803	Q743	M682	T622	D562	A501
L804	E744	L684	L623	P563	H502
K805	P745	L685	L625	R564	D503
S806	E746	F686	L626	V565	D504
I807	H747	E687	S627	A566	K505
D808	W748	C588	E628	E567	T506
K809	P749	L689	H629	S568	K507
L810	W750	V690	A630	V569	H508
A811	T751	D691	E631	P570	L509
N812	A752	K692	L632	E571	K510
E813	S753	E693	L633	E572	A511
E814	S754	E594	S634	A573	A512
R815	G755	A695	A635	A574	F513
Y816	T756	D696	A636	G575	L514
N817	A757	L697	A637	F576	R515
I818	G758	E598	L637	S577	Y516
L819	I759	S699	V638	N578	C517
E820	R760	T700	L639	T579	R518
M821	S761	S701	K640	S580	K519
E822	V762	I702	N641	S581	D520
R823	V763	D703	H642	I521	L522
A824	T764	S704	H643	L582	G523
Q825	R765	V705	A644	L583	A524
K826	Q766	E706	K645	L584	Q525
R827	H767	W707	L646	H585	S526
S828	G768	A708	P647	Q586	M527
E829	I769	N709	V648	L587	V528
L830	I770	T710	L649	E588	D529
L831	L771	L711	V650	D589	S530
S832	K772	V712	N651	K590	L531
P833	V773	N713	S652	M591	F532
L834	Y774	V714	A653	K592	S533
L835	P775	N715	T654	H594	D534
L836	Q776	T716	Q655	S595	S535
L837	A777	T717	L656	F596	D536
Q838	D778	L718	L657	F597	M537
Q839	S779	K719	L658	V598	E538
Y840	G780	D720	D659	D599	P539
			V660	F600	D540

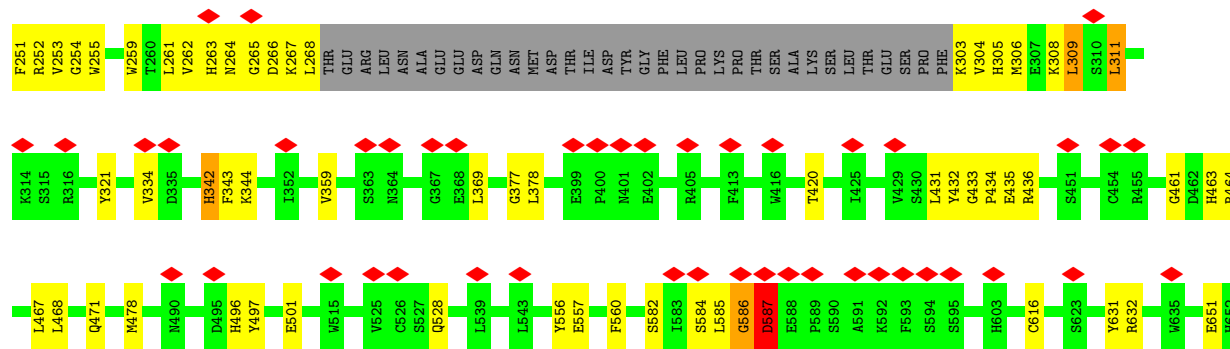
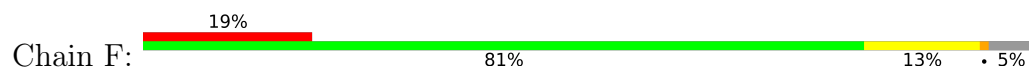


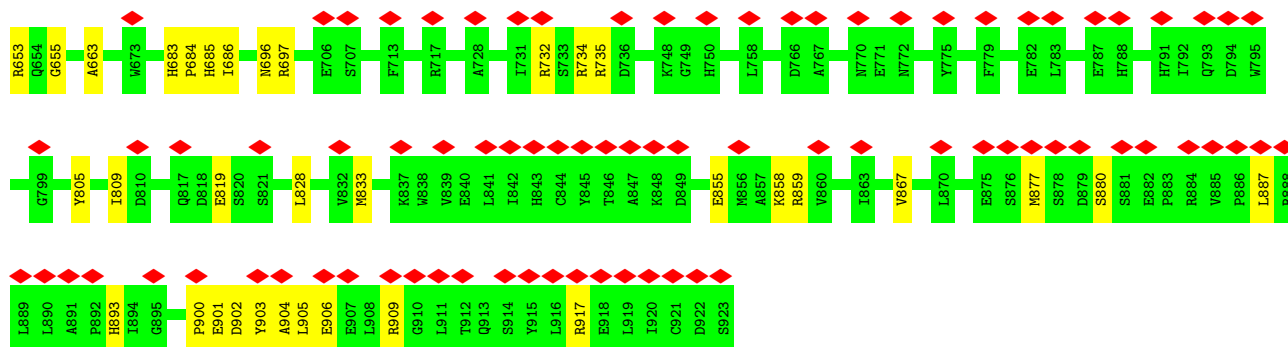
• Molecule 14: Nup133



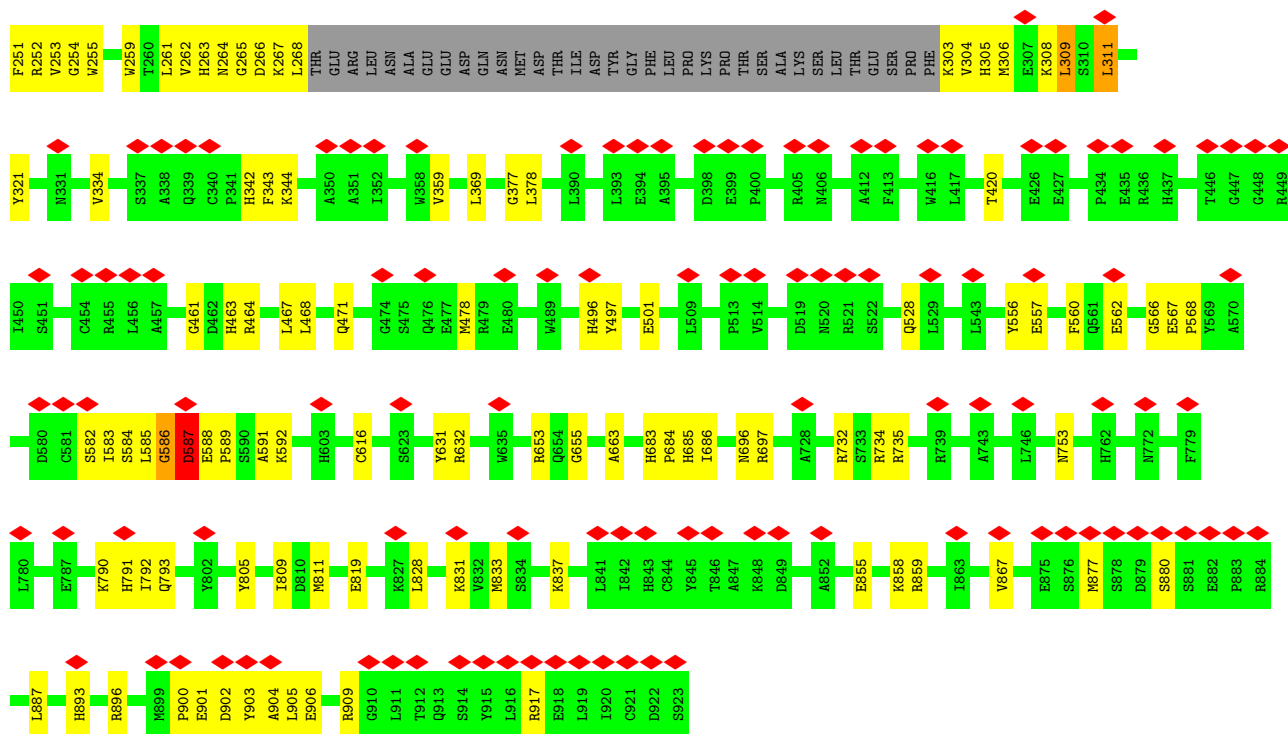
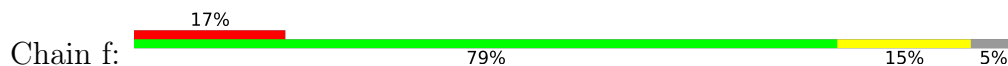


• Molecule 15: Nuclear pore complex protein Nup96





• Molecule 15: Nuclear pore complex protein Nup96



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	333214	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	4.753	Depositor
Minimum map value	-0.227	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.092	Depositor
Recommended contour level	0.366	Depositor
Map size (Å)	840.0, 840.0, 840.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.8, 2.8, 2.8	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	H	0.73	0/6553	1.21	6/8867 (0.1%)
1	h	0.73	0/6553	1.21	6/8867 (0.1%)
2	T	0.71	1/1086 (0.1%)	1.25	1/1457 (0.1%)
2	t	0.66	0/247	1.28	0/333
3	S	1.04	1/1178 (0.1%)	1.47	1/1567 (0.1%)
3	s	0.73	0/258	1.20	0/343
4	R	0.71	0/5490	1.17	3/7427 (0.0%)
4	r	0.70	0/3755	1.14	1/5107 (0.0%)
5	G	0.69	0/2454	1.13	3/3349 (0.1%)
5	g	0.69	0/2454	1.13	3/3349 (0.1%)
6	L	0.79	0/16272	1.30	27/22021 (0.1%)
6	l	0.79	0/16272	1.30	27/22021 (0.1%)
7	E	0.71	0/2592	1.16	3/3515 (0.1%)
7	e	0.71	0/2592	1.16	4/3515 (0.1%)
8	D	0.72	0/2996	1.22	3/4074 (0.1%)
8	d	0.72	0/2996	1.22	3/4074 (0.1%)
9	C	0.73	0/5377	1.22	2/7265 (0.0%)
9	c	1.20	84/5376 (1.6%)	1.44	82/7265 (1.1%)
10	U	0.71	0/2977	1.21	0/4032
11	M	0.74	0/6555	1.24	4/8864 (0.0%)
11	N	0.74	0/6555	1.24	4/8864 (0.0%)
11	O	0.74	0/6555	1.24	4/8864 (0.0%)
11	P	0.74	0/6555	1.24	4/8864 (0.0%)
11	Q	0.74	0/6555	1.24	4/8864 (0.0%)
12	B	0.70	0/2643	1.10	0/3587
12	b	0.70	0/2643	1.10	0/3587
13	A	0.75	0/10962	1.23	11/14884 (0.1%)
13	a	0.74	0/10962	1.23	11/14884 (0.1%)
14	I	0.73	0/5475	1.24	1/7398 (0.0%)
14	i	0.72	0/8561	1.21	6/11601 (0.1%)
15	F	0.77	0/5338	1.26	5/7245 (0.1%)
15	f	0.77	0/5338	1.25	4/7245 (0.1%)
All	All	0.76	86/172175 (0.0%)	1.24	233/233199 (0.1%)

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	H	0	1
1	h	0	1
2	T	0	1
4	R	0	4
4	r	0	3
6	L	0	18
6	l	0	18
8	D	0	7
8	d	0	7
9	C	0	2
9	c	0	41
10	U	0	1
11	M	0	3
11	N	0	3
11	O	0	3
11	P	0	3
11	Q	0	3
12	B	0	3
12	b	0	3
13	A	0	11
13	a	0	11
14	I	0	5
14	i	0	12
15	F	0	2
15	f	0	2
All	All	0	168

The worst 5 of 86 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	S	736	SER	C-N	27.04	1.71	1.33
9	c	393	GLY	C-N	15.72	1.54	1.33
9	c	615	PRO	N-CD	-11.84	1.31	1.47
9	c	59	SER	C-N	11.00	1.48	1.33
9	c	335	ALA	C-N	10.78	1.49	1.33

The worst 5 of 233 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	S	736	SER	O-C-N	-32.83	79.05	122.38
9	c	387	ALA	O-C-N	-24.90	89.47	122.59
9	c	2	GLU	O-C-N	-23.81	90.92	122.59
9	c	3	GLU	O-C-N	-21.67	93.77	122.59
9	c	620	LYS	O-C-N	-18.76	104.48	123.62

There are no chirality outliers.

5 of 168 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	117	LEU	Peptide
1	h	117	LEU	Peptide
4	r	336	ASN	Peptide
4	r	337	LYS	Peptide
4	r	539	LYS	Peptide

5.2 Too-close contacts [i](#)

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	H	6421	6346	6342	288	0
1	h	6421	6346	6342	95	0
2	T	1076	1064	1049	625	0
2	t	244	235	230	223	0
3	S	1169	1164	1149	493	0
3	s	257	261	255	211	0
4	R	5390	5396	5377	1161	0
4	r	3675	3679	3663	405	0
5	G	2387	2270	2260	305	0
5	g	2387	2270	2256	317	0
6	L	15974	16156	16139	518	0
6	l	15974	16156	16148	291	0
7	E	2528	2445	2432	423	0
7	e	2528	2445	2442	318	0
8	D	2927	2800	2795	154	0
8	d	2927	2800	2794	179	0
9	C	5268	5226	5203	721	0
9	c	5267	0	5215	937	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	U	2912	2931	2923	212	0
11	M	6418	6444	6434	192	0
11	N	6418	6444	6442	90	0
11	O	6418	6444	6404	1120	0
11	P	6418	6444	6443	67	0
11	Q	6418	6444	6407	1120	0
12	B	2573	2503	2495	122	0
12	b	2573	2503	2494	145	0
13	A	10746	10745	10720	620	0
13	a	10746	10745	10718	671	0
14	I	5380	5353	5352	16	0
14	i	8398	8274	8272	25	0
15	F	5208	5128	5106	403	0
15	f	5208	5128	5103	492	0
All	All	168654	162589	167404	6833	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 20.

The worst 5 of 6833 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)
7:E:90:VAL:HG12	8:D:127:MET:SD	1.24	1.75
3:s:1732:SER:HA	4:r:548:CYS:SG	1.20	1.70
11:O:786:THR:CG2	11:Q:578:ALA:HB1	1.22	1.68
6:L:1244:MET:SD	13:A:1285:ARG:HG3	1.27	1.67
7:e:90:VAL:HG12	8:d:127:MET:SD	1.24	1.65

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	787/916 (86%)	762 (97%)	17 (2%)	8 (1%)	12	48
1	h	787/916 (86%)	762 (97%)	17 (2%)	8 (1%)	12	48
2	T	126/547 (23%)	124 (98%)	1 (1%)	1 (1%)	16	54
2	t	27/547 (5%)	27 (100%)	0	0	100	100
3	S	136/2037 (7%)	134 (98%)	1 (1%)	1 (1%)	18	56
3	s	30/2037 (2%)	30 (100%)	0	0	100	100
4	R	674/728 (93%)	627 (93%)	30 (4%)	17 (2%)	4	26
4	r	464/728 (64%)	433 (93%)	19 (4%)	12 (3%)	4	25
5	G	304/306 (99%)	293 (96%)	8 (3%)	3 (1%)	12	48
5	g	304/306 (99%)	294 (97%)	7 (2%)	3 (1%)	12	48
6	L	2009/2011 (100%)	1889 (94%)	93 (5%)	27 (1%)	9	42
6	l	2009/2011 (100%)	1889 (94%)	93 (5%)	27 (1%)	9	42
7	E	320/322 (99%)	305 (95%)	10 (3%)	5 (2%)	7	38
7	e	320/322 (99%)	305 (95%)	10 (3%)	5 (2%)	7	38
8	D	373/375 (100%)	345 (92%)	20 (5%)	8 (2%)	5	30
8	d	373/375 (100%)	345 (92%)	20 (5%)	8 (2%)	5	30
9	C	651/653 (100%)	630 (97%)	15 (2%)	6 (1%)	14	51
9	c	651/653 (100%)	614 (94%)	20 (3%)	17 (3%)	4	25
10	U	356/1388 (26%)	352 (99%)	4 (1%)	0	100	100
11	M	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	14	51
11	N	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	14	51
11	O	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	14	51
11	P	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	14	51
11	Q	796/2905 (27%)	768 (96%)	21 (3%)	7 (1%)	14	51
12	B	324/326 (99%)	307 (95%)	15 (5%)	2 (1%)	21	59
12	b	324/326 (99%)	307 (95%)	15 (5%)	2 (1%)	21	59
13	A	1350/1435 (94%)	1268 (94%)	61 (4%)	21 (2%)	7	38
13	a	1350/1435 (94%)	1268 (94%)	61 (4%)	21 (2%)	7	38
14	I	669/1140 (59%)	639 (96%)	19 (3%)	11 (2%)	7	38
14	i	1060/1140 (93%)	997 (94%)	41 (4%)	22 (2%)	5	30
15	F	635/673 (94%)	615 (97%)	16 (2%)	4 (1%)	21	59
15	f	635/673 (94%)	615 (97%)	16 (2%)	4 (1%)	21	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	21028/38851 (54%)	20016 (95%)	734 (4%)	278 (1%)	12	42

5 of 278 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	770	GLN
1	h	770	GLN
4	r	332	GLU
4	r	540	ASP
5	g	172	SER

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	H	704/816 (86%)	696 (99%)	8 (1%)	65	76
1	h	704/816 (86%)	696 (99%)	8 (1%)	65	76
2	T	120/429 (28%)	119 (99%)	1 (1%)	73	80
2	t	27/429 (6%)	27 (100%)	0	100	100
3	S	130/1634 (8%)	130 (100%)	0	100	100
3	s	29/1634 (2%)	29 (100%)	0	100	100
4	R	614/660 (93%)	611 (100%)	3 (0%)	81	83
4	r	424/660 (64%)	424 (100%)	0	100	100
5	G	261/261 (100%)	260 (100%)	1 (0%)	84	84
5	g	261/261 (100%)	260 (100%)	1 (0%)	84	84
6	L	1779/1779 (100%)	1744 (98%)	35 (2%)	48	66
6	l	1779/1779 (100%)	1744 (98%)	35 (2%)	48	66
7	E	280/280 (100%)	280 (100%)	0	100	100
7	e	280/280 (100%)	280 (100%)	0	100	100
8	D	329/329 (100%)	328 (100%)	1 (0%)	86	86
8	d	329/329 (100%)	328 (100%)	1 (0%)	86	86

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	C	580/580 (100%)	578 (100%)	2 (0%)	86	86
9	c	580/580 (100%)	577 (100%)	3 (0%)	81	83
10	U	327/1219 (27%)	327 (100%)	0	100	100
11	M	716/2521 (28%)	713 (100%)	3 (0%)	84	84
11	N	716/2521 (28%)	713 (100%)	3 (0%)	84	84
11	O	716/2521 (28%)	713 (100%)	3 (0%)	84	84
11	P	716/2521 (28%)	713 (100%)	3 (0%)	84	84
11	Q	716/2521 (28%)	713 (100%)	3 (0%)	84	84
12	B	275/275 (100%)	275 (100%)	0	100	100
12	b	275/275 (100%)	275 (100%)	0	100	100
13	A	1184/1256 (94%)	1168 (99%)	16 (1%)	59	72
13	a	1184/1256 (94%)	1169 (99%)	15 (1%)	61	74
14	I	600/993 (60%)	598 (100%)	2 (0%)	86	86
14	i	935/993 (94%)	928 (99%)	7 (1%)	76	81
15	F	571/602 (95%)	567 (99%)	4 (1%)	76	81
15	f	571/602 (95%)	567 (99%)	4 (1%)	76	81
All	All	18712/33612 (56%)	18550 (99%)	162 (1%)	68	79

5 of 162 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	A	231	LEU
15	F	309	LEU
13	A	575	SER
13	a	146	GLU
15	f	887	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 324 such sidechains are listed below:

Mol	Chain	Res	Type
13	a	520	GLN
15	f	762	HIS
13	a	976	GLN
14	I	1017	GLN
14	i	238	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	S	2
4	R	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	R	544:PRO	C	545:PRO	N	4.80
1	S	728:SER	C	729:ARG	N	3.21
1	S	736:SER	C	737:GLU	N	1.71

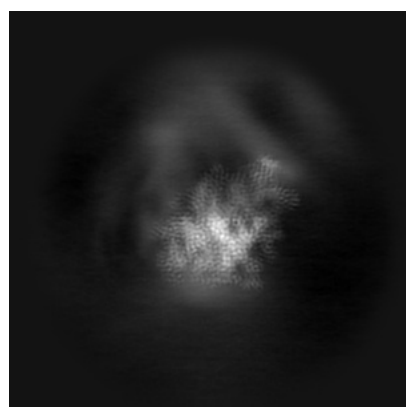
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25817. These allow visual inspection of the internal detail of the map and identification of artifacts.

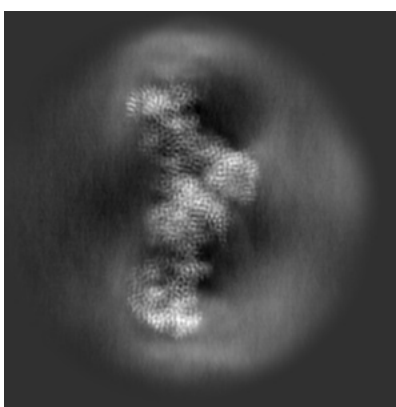
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

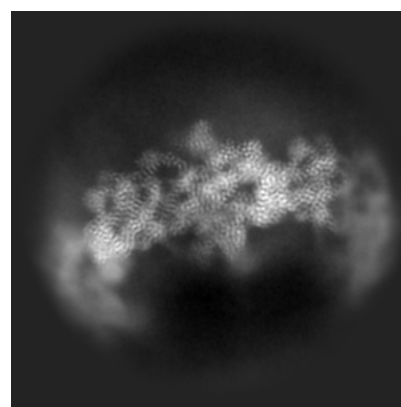
6.1.1 Primary map



X



Y

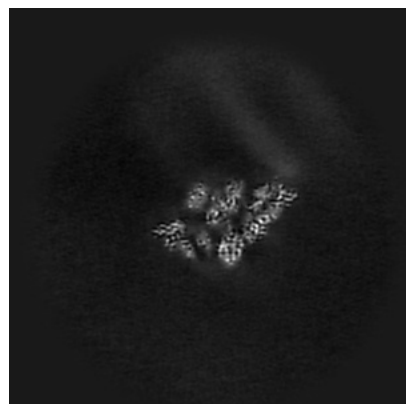


Z

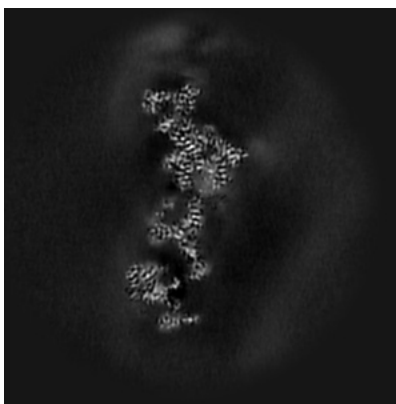
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

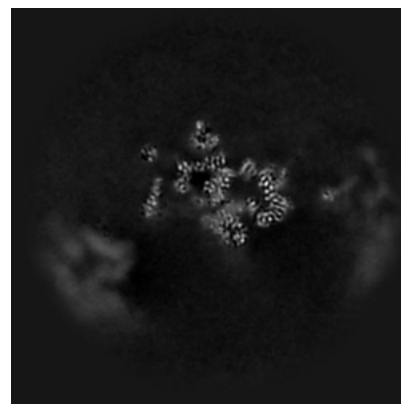
6.2.1 Primary map



X Index: 150



Y Index: 150

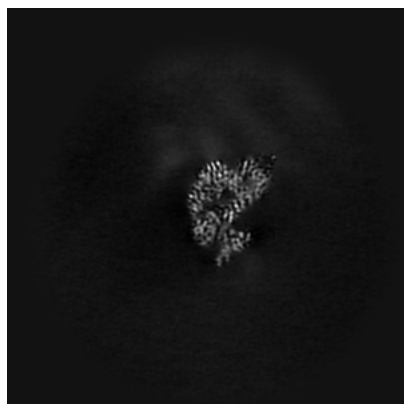


Z Index: 150

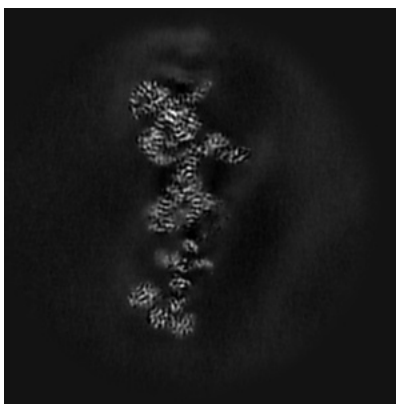
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

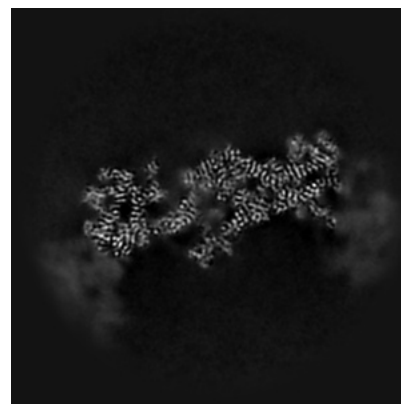
6.3.1 Primary map



X Index: 189



Y Index: 161

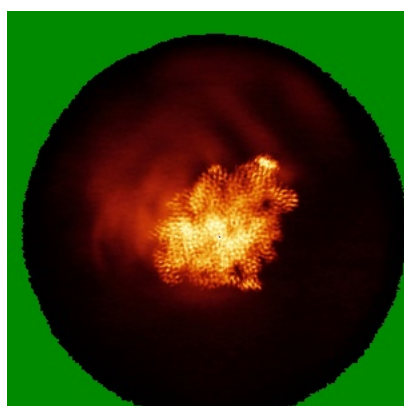


Z Index: 130

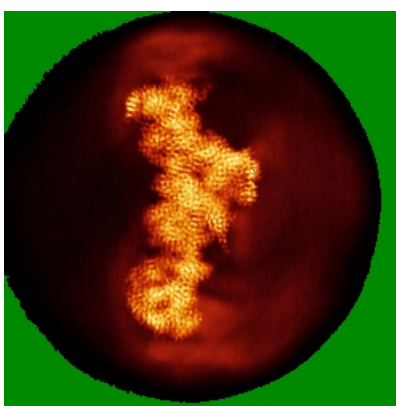
The images above show the largest variance slices of the map in three orthogonal directions.

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

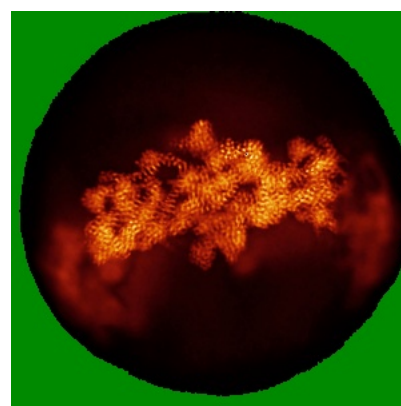
6.4.1 Primary map



X



Y

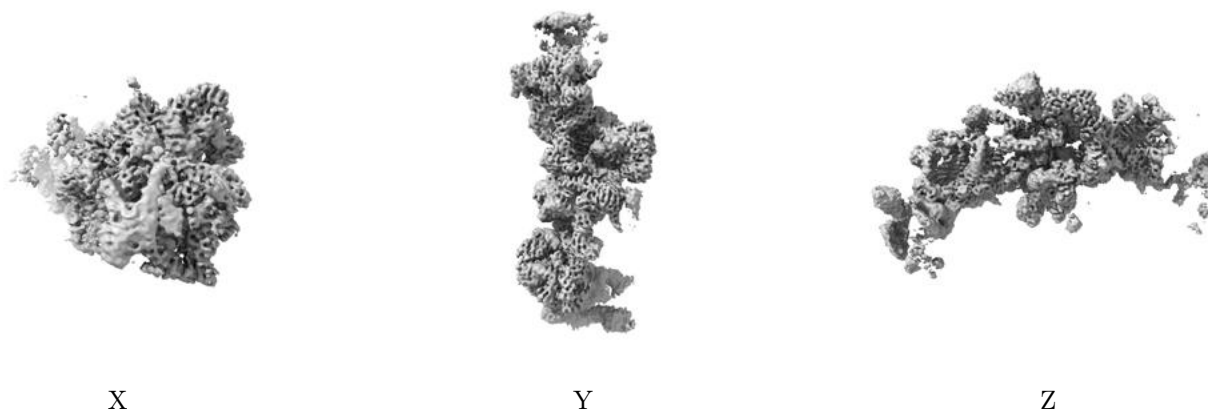


Z

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 0.366. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

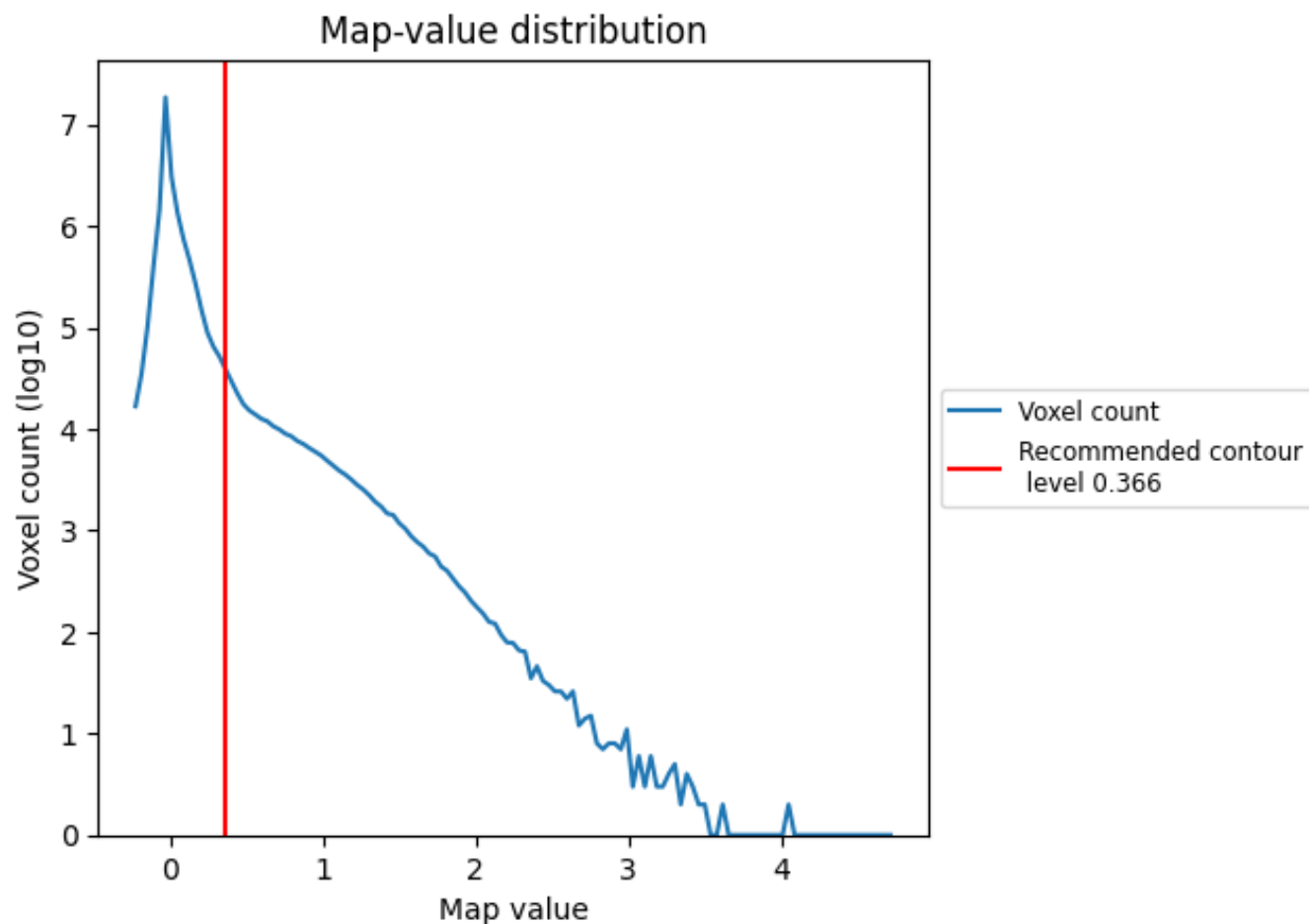
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

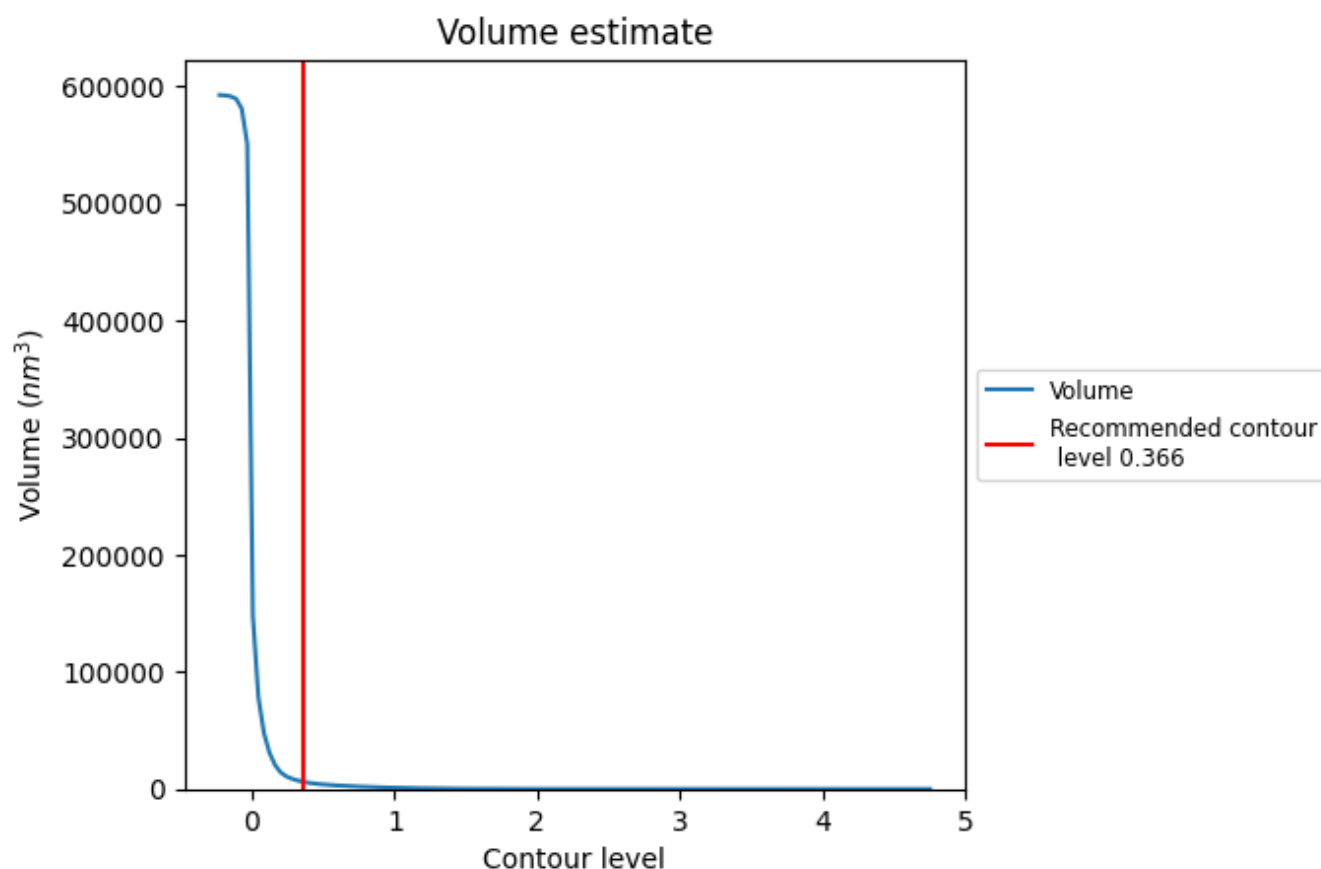
This section contains the results of statistical analysis of the map.

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.

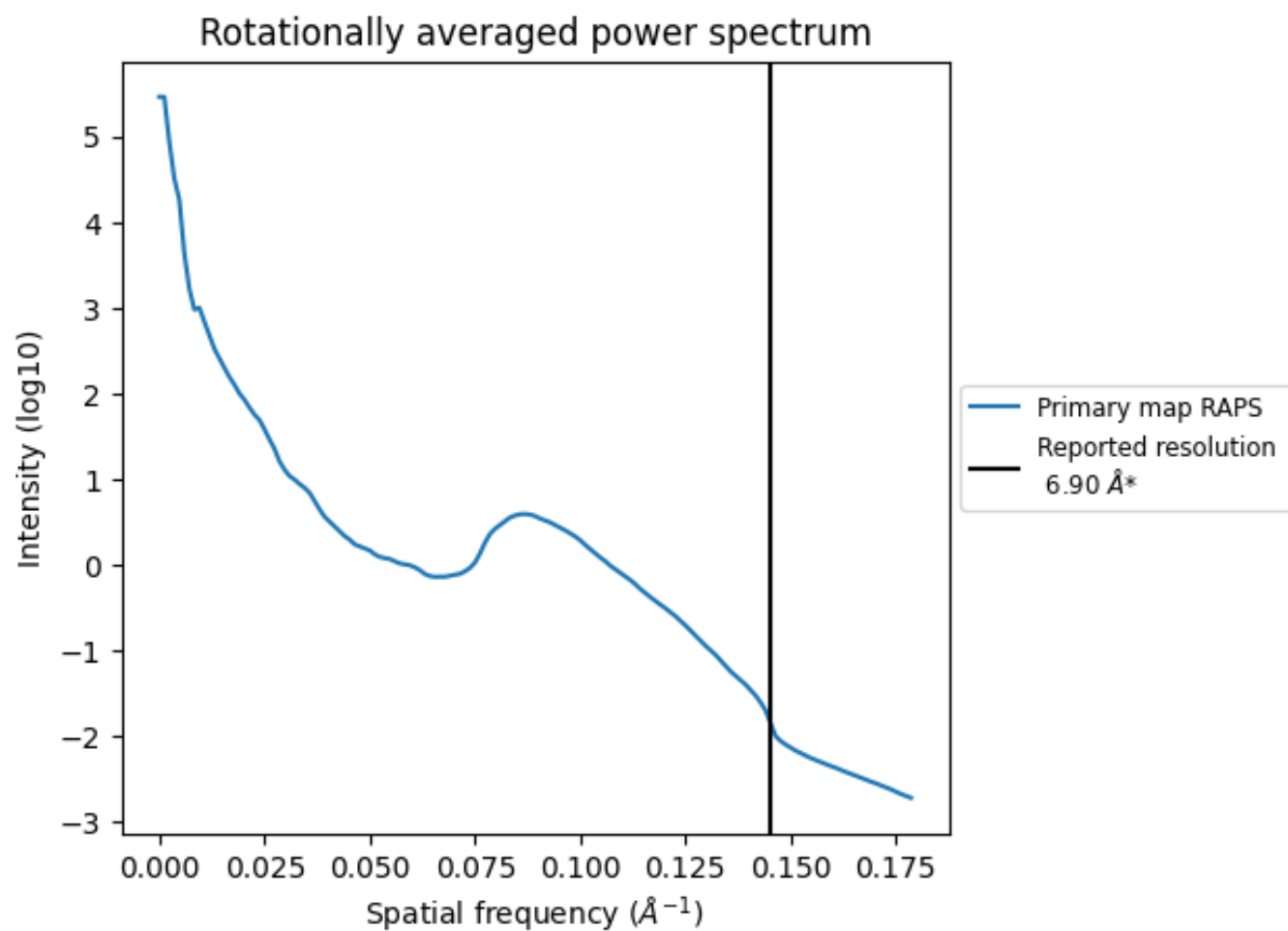
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5957 nm^3 ; this corresponds to an approximate mass of 5381 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 0.145 Å⁻¹

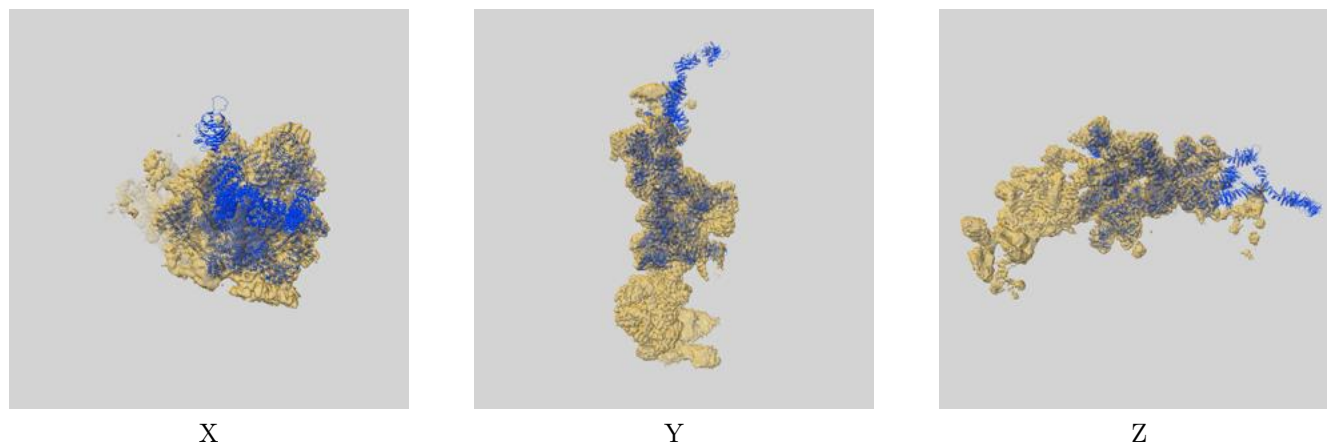
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

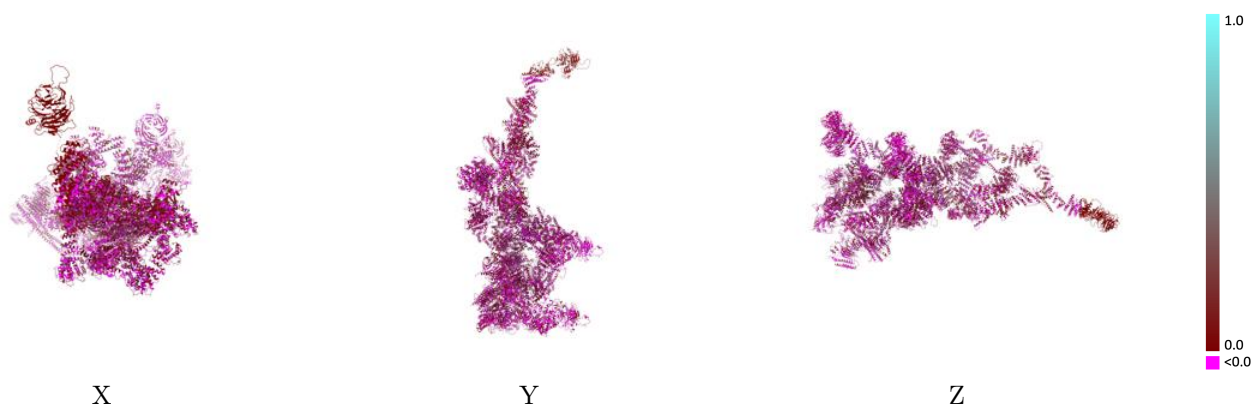
This section contains information regarding the fit between EMDB map EMD-25817 and PDB model 7TDZ. Per-residue inclusion information can be found in section [3](#) on page [9](#).

9.1 Map-model overlay [i](#)



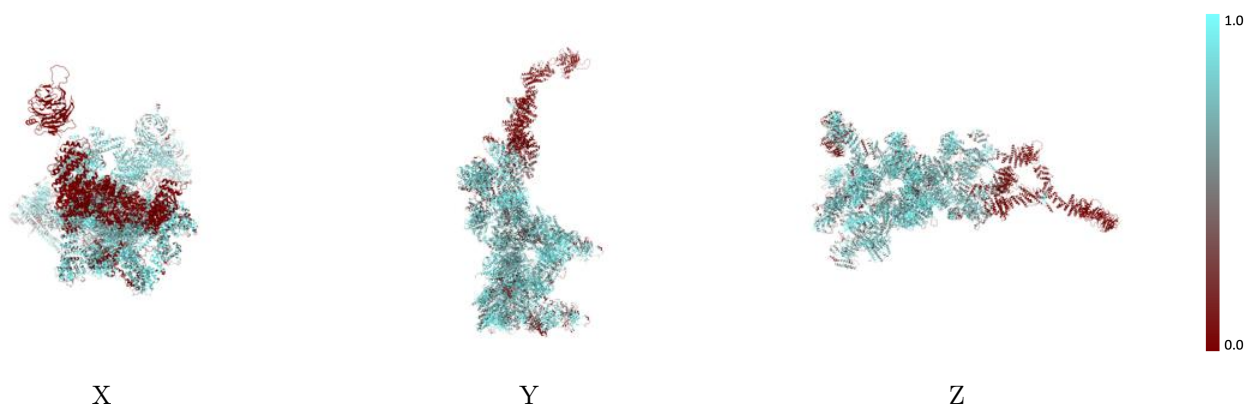
The images above show the 3D surface view of the map at the recommended contour level 0.366 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



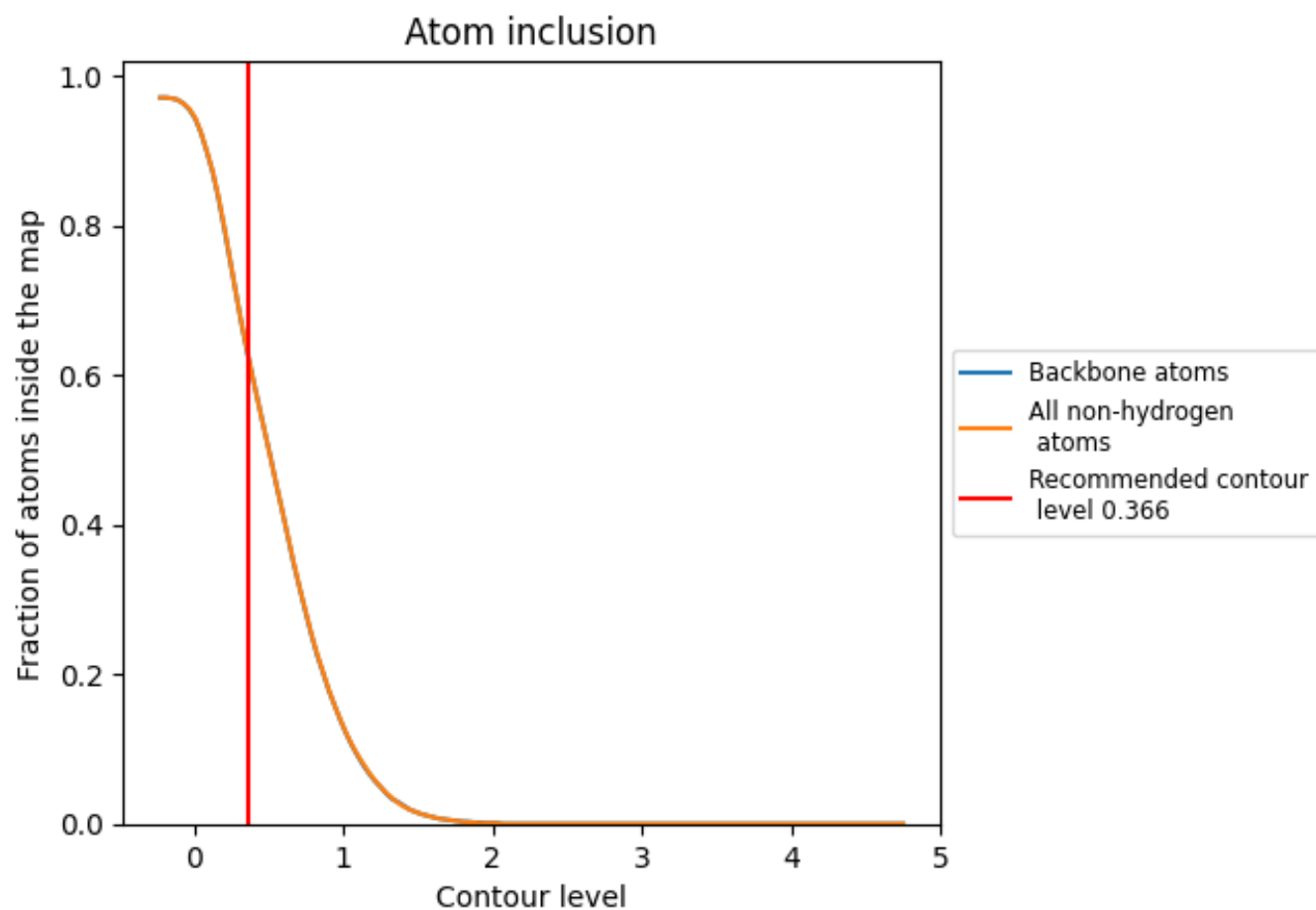
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.366).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 62% 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 (0.366) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6220	 0.0290
A	 0.6040	 -0.0080
B	 0.3250	 -0.0010
C	 0.7390	 0.0430
D	 0.8670	 0.0250
E	 0.8310	 0.0590
F	 0.7000	 0.0550
G	 0.8470	 0.0510
H	 0.6750	 0.0520
I	 0.2370	 0.0510
L	 0.7360	 0.0390
M	 0.7050	 0.0300
N	 0.7150	 0.0430
O	 0.6410	 0.0060
P	 0.2040	 0.0450
Q	 0.6770	 0.0090
R	 0.7800	 0.0310
S	 0.6600	 0.0230
T	 0.6100	 0.0250
U	 0.8410	 0.0100
a	 0.7140	 -0.0090
b	 0.8660	 0.0210
c	 0.7180	 0.0410
d	 0.7220	 0.0360
e	 0.7790	 0.0410
f	 0.7050	 0.0480
g	 0.8340	 0.0730
h	 0.1750	 0.0450
i	 0.0050	 0.0110
l	 0.7800	 0.0320
r	 0.6060	 0.0290
s	 0.5100	 -0.0110
t	 0.4400	 -0.0510

