



## wwPDB EM Validation Summary Report ⓘ

Oct 5, 2023 – 12:44 PM EDT

PDB ID : 8TJ5  
EMDB ID : EMD-41300  
Title : Inner spoke ring of the yeast NPC  
Authors : Akey, C.W.; Echeverria, I.; Ouch, C.; Fernandez-Martinez, J.; Rout, M.P.  
Deposited on : 2023-07-20  
Resolution : 6.60 Å (reported)  
Based on initial model : .

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

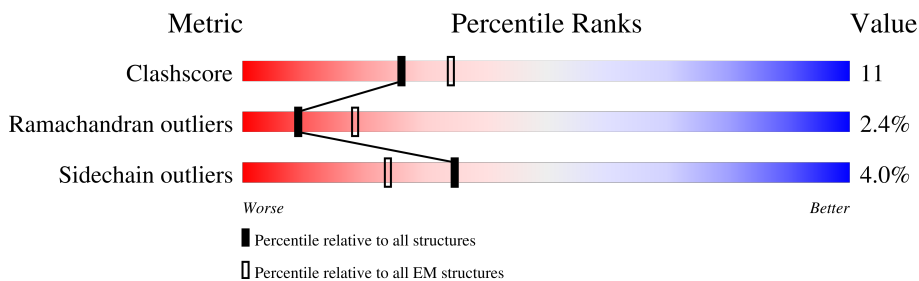
EMDB validation analysis : 0.0.1.dev50  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

# 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 6.60 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.



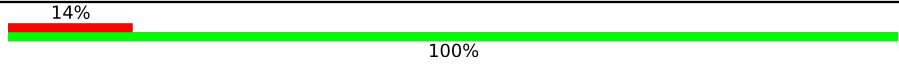

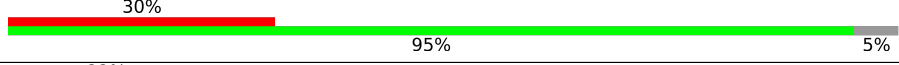
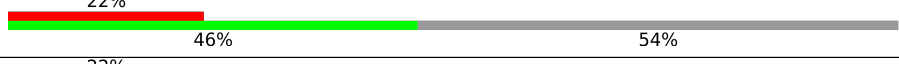
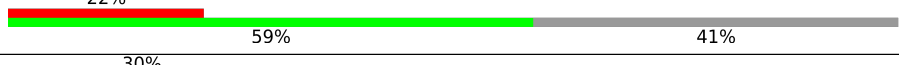
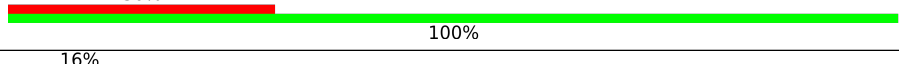
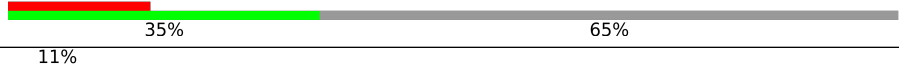

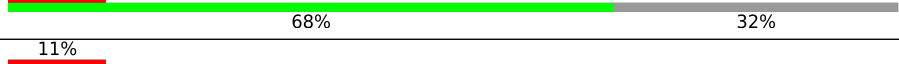


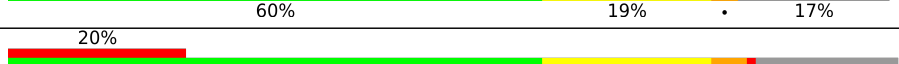
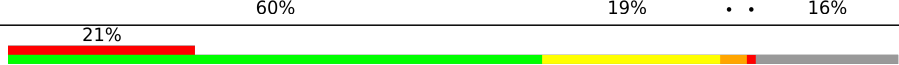

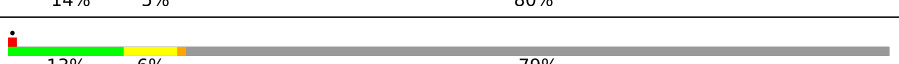


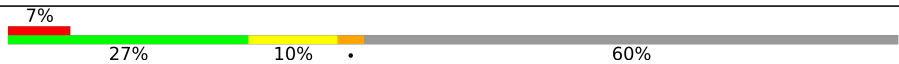







Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	3	37	
1	4	37	
1	7	37	
1	8	37	
1	a	37	
1	b	37	
1	c	37	
1	d	37	






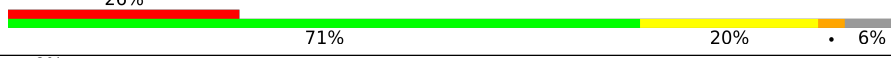
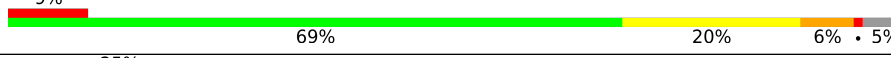






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Mol	Chain	Length	Quality of chain
1	e	37	
1	f	37	
1	g	37	
1	h	37	
1	i	37	
1	j	37	
1	k	37	
1	l	37	
1	m	37	
1	n	37	
2	0	1502	
2	Y	1502	
3	1	1391	
3	Z	1391	
4	A	823	
4	D	823	
4	G	823	
4	J	823	
5	B	541	
5	E	541	
5	H	541	
5	K	541	
6	C	472	
6	F	472	
6	I	472	

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Mol	Chain	Length	Quality of chain
6	L	472	 27% 8% 63%
7	M	1683	 14% 71% 23% . .
7	O	1683	 13% 72% 22% . .
8	N	1655	 13% 74% 21% . .
8	P	1655	 13% 75% 21% . .
9	Q	839	 26% 71% 20% . 6%
9	R	839	 9% 69% 20% 6% . 5%
9	S	839	 25% 70% 20% . 6%
9	T	839	 9% 69% 20% 6% . 5%
10	U	475	 12% 6% . 80%
10	W	475	 12% 6% . . 80%
11	V	528	 8% 6% . 83%
11	X	528	 8% 6% . 83%

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 138272 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 Spoke connector.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	7	17	Total	C	N	O	0	0
			85	51	17	17		
1	3	16	Total	C	N	O	0	0
			80	48	16	16		
1	8	17	Total	C	N	O	0	0
			85	51	17	17		
1	4	16	Total	C	N	O	0	0
			80	48	16	16		
1	a	8	Total	C	N	O	0	0
			40	24	8	8		
1	b	35	Total	C	N	O	0	0
			175	105	35	35		
1	k	13	Total	C	N	O	0	0
			65	39	13	13		
1	c	17	Total	C	N	O	0	0
			85	51	17	17		
1	m	25	Total	C	N	O	0	0
			125	75	25	25		
1	d	22	Total	C	N	O	0	0
			110	66	22	22		
1	e	37	Total	C	N	O	0	0
			185	111	37	37		
1	f	8	Total	C	N	O	0	0
			40	24	8	8		
1	g	35	Total	C	N	O	0	0
			175	105	35	35		
1	l	13	Total	C	N	O	0	0
			65	39	13	13		
1	h	17	Total	C	N	O	0	0
			85	51	17	17		
1	n	25	Total	C	N	O	0	0
			125	75	25	25		
1	j	37	Total	C	N	O	0	0
			185	111	37	37		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	i	22	Total	C	N	O	0	0
			110	66	22	22		

- Molecule 2 is a protein called Nucleoporin NUP170.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Y	1246	Total	C	N	O	S	0	0
			10015	6434	1644	1901	36		
2	0	1246	Total	C	N	O	S	0	0
			10015	6434	1644	1901	36		

- Molecule 3 is a protein called Nucleoporin NUP157.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Z	1164	Total	C	N	O	S	0	0
			9319	5964	1544	1778	33		
3	1	1164	Total	C	N	O	S	0	0
			9319	5964	1544	1778	33		

- Molecule 4 is a protein called Nucleoporin NSP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	163	Total	C	N	O	S	0	0
			1315	814	220	280	1		
4	D	169	Total	C	N	O	S	0	0
			1345	832	226	286	1		
4	G	163	Total	C	N	O	S	0	0
			1315	814	220	280	1		
4	J	169	Total	C	N	O	S	0	0
			1347	833	226	287	1		

- Molecule 5 is a protein called Nucleoporin NUP57.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		
5	E	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		
5	H	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		
5	K	217	Total	C	N	O	S	0	0
			1771	1115	317	336	3		

- Molecule 6 is a protein called Nucleoporin NUP49/NSP49.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	166	Total	C	N	O	S	0	0
			1347	863	217	265	2		
6	F	173	Total	C	N	O	S	0	0
			1381	883	224	272	2		
6	I	166	Total	C	N	O	S	0	0
			1347	863	217	265	2		
6	L	173	Total	C	N	O	S	0	0
			1381	883	224	272	2		

- Molecule 7 is a protein called Nucleoporin NUP192.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	1659	Total	C	N	O	S	0	0
			13334	8597	2155	2542	40		
7	O	1659	Total	C	N	O	S	0	0
			13334	8597	2155	2542	40		

- Molecule 8 is a protein called Nucleoporin NUP188.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	1640	Total	C	N	O	S	0	0
			13181	8518	2115	2519	29		
8	P	1641	Total	C	N	O	S	0	0
			13190	8524	2117	2520	29		

- Molecule 9 is a protein called Nucleoporin NIC96.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	791	Total	C	N	O	S	0	0
			5961	3768	1032	1144	17		
9	R	800	Total	C	N	O	S	0	0
			5983	3783	1037	1146	17		
9	S	791	Total	C	N	O	S	0	0
			5961	3768	1032	1144	17		
9	T	801	Total	C	N	O	S	0	0
			5988	3786	1038	1147	17		

- Molecule 10 is a protein called Nucleoporin NUP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	U	94	745	486	120	137	2	0	0
10	W	94	745	486	120	137	2	0	0

- Molecule 11 is a protein called Nucleoporin 59.

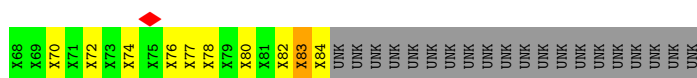
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	V	90	710	459	117	131	3	0	0
11	X	90	710	459	117	131	3	0	0



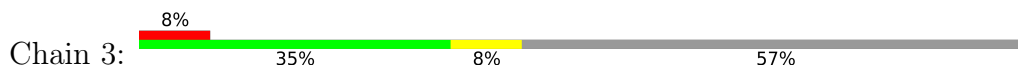
### 3 Residue-property plots [i](#)

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

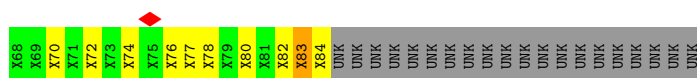
- Molecule 1: Spoke connector



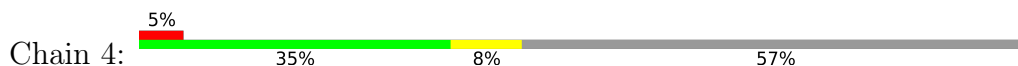
- Molecule 1: Spoke connector



- Molecule 1: Spoke connector



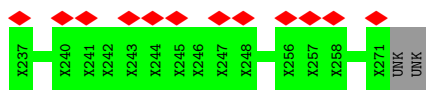
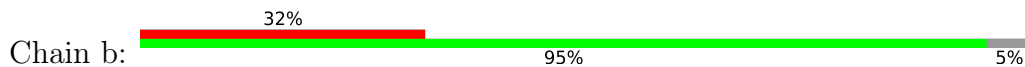
- Molecule 1: Spoke connector



- Molecule 1: Spoke connector



• Molecule 1: Spoke connector



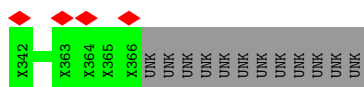
• Molecule 1: Spoke connector



• Molecule 1: Spoke connector



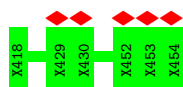
• Molecule 1: Spoke connector



• Molecule 1: Spoke connector



• Molecule 1: Spoke connector

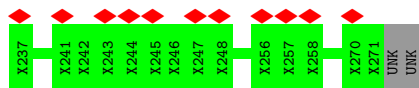
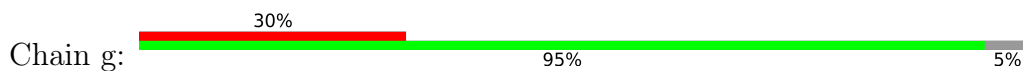


• Molecule 1: Spoke connector





• Molecule 1: Spoke connector



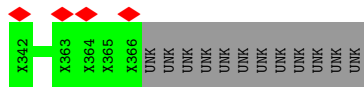
• Molecule 1: Spoke connector



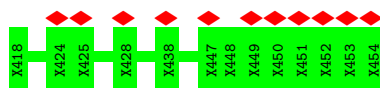
• Molecule 1: Spoke connector



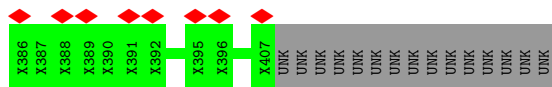
• Molecule 1: Spoke connector



• Molecule 1: Spoke connector



• Molecule 1: Spoke connector



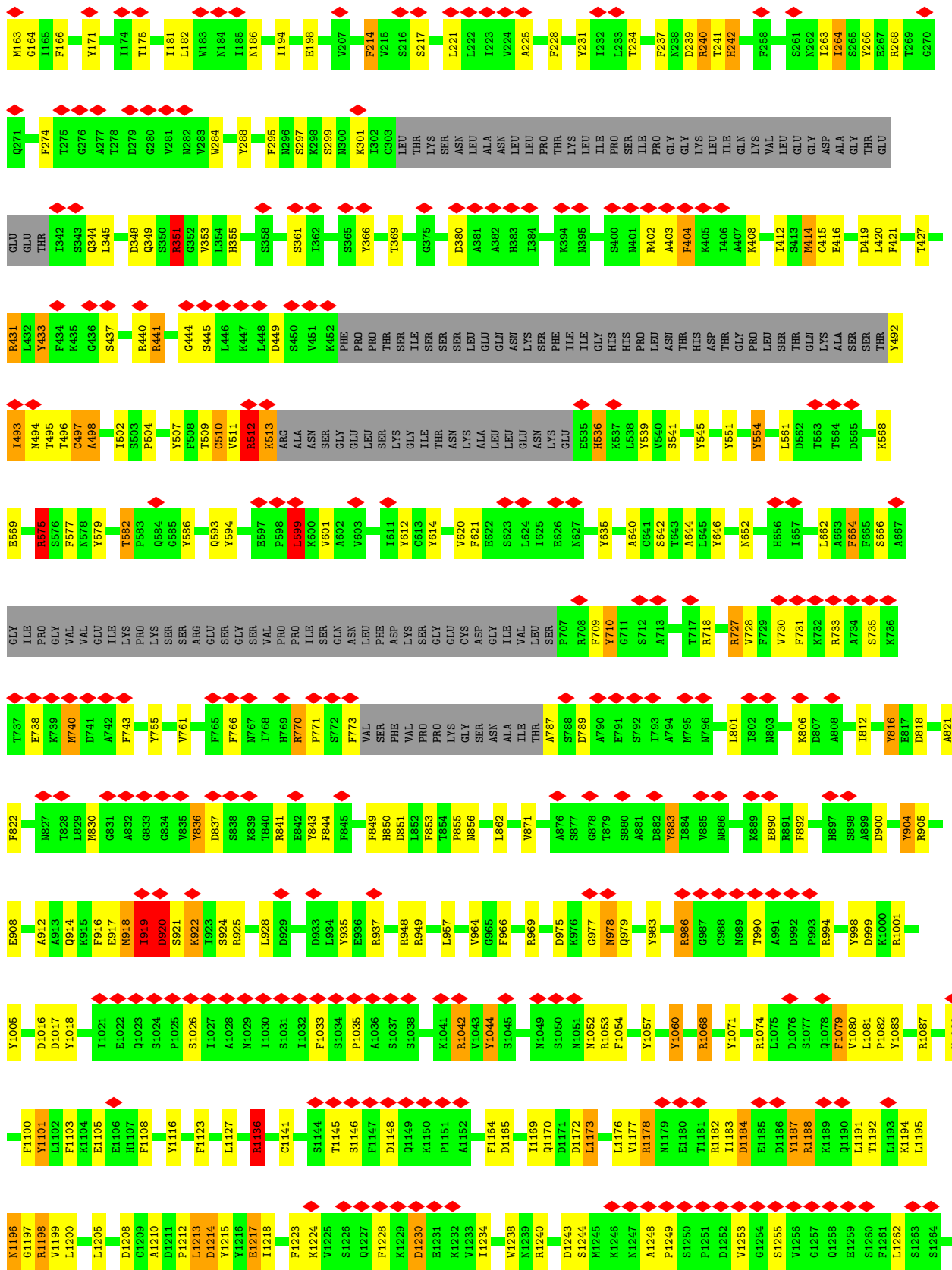
• Molecule 2: Nucleoporin NUP170





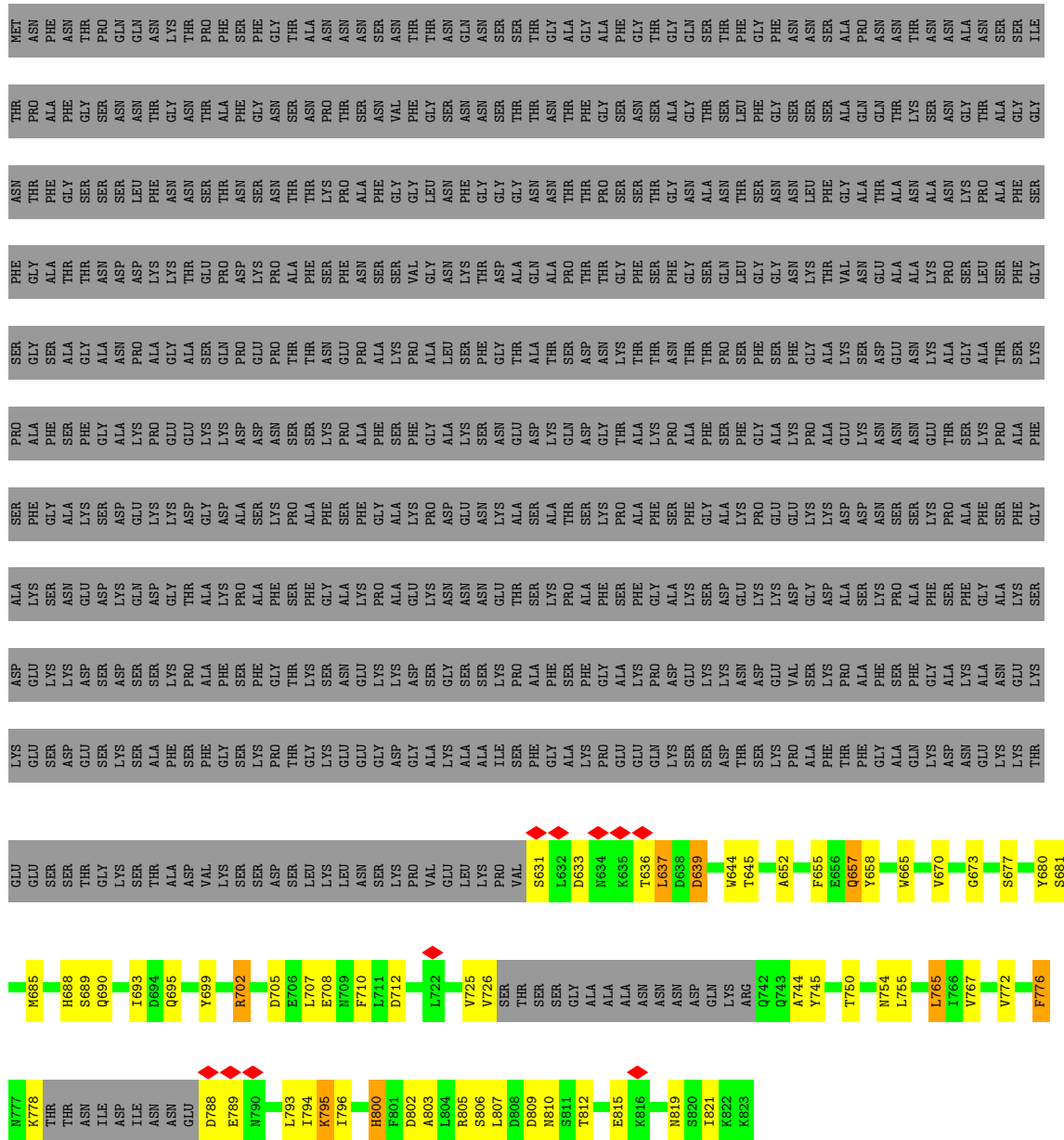




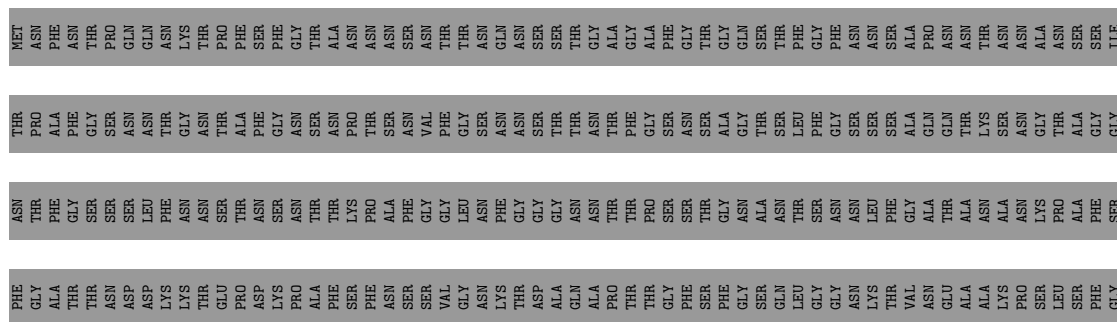




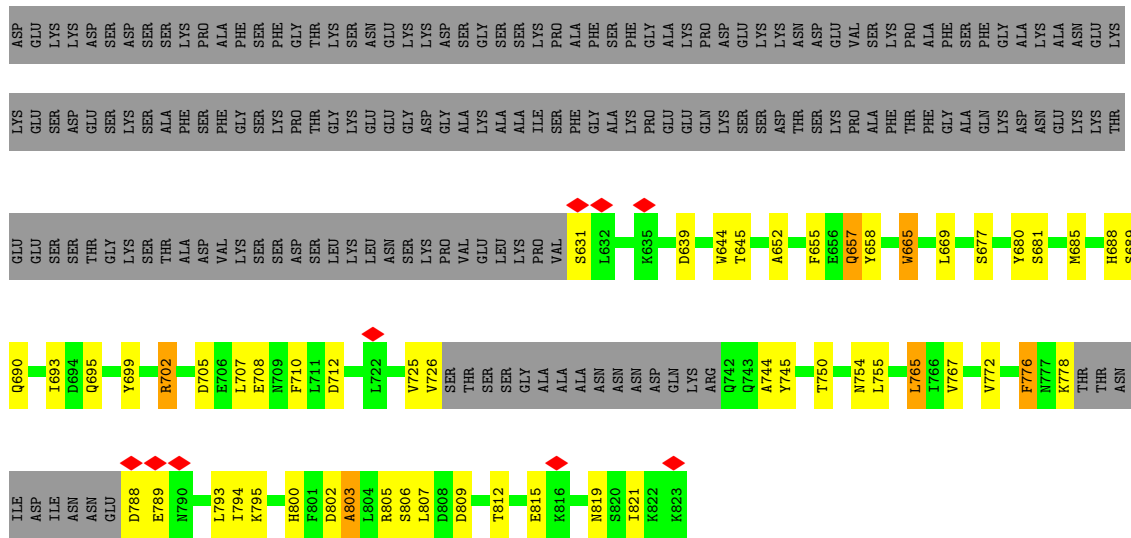




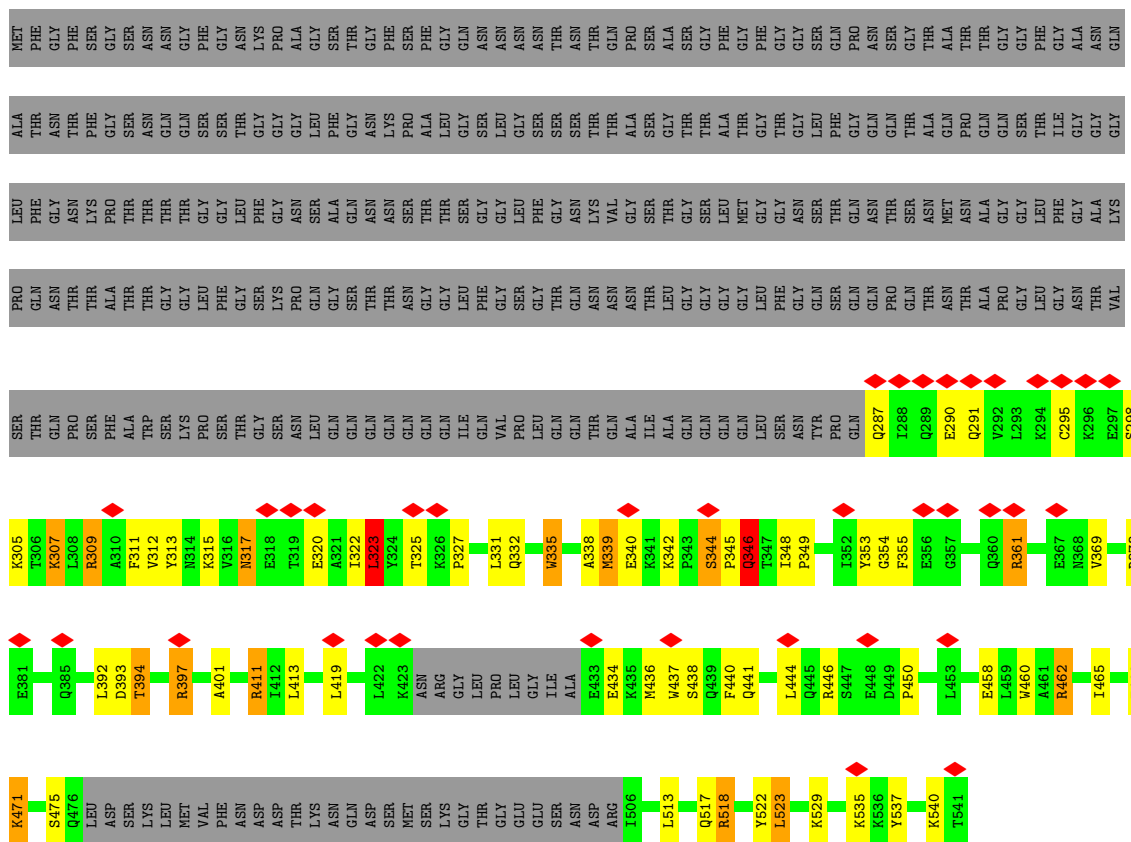
● Molecule 4: Nucleoporin NSP1



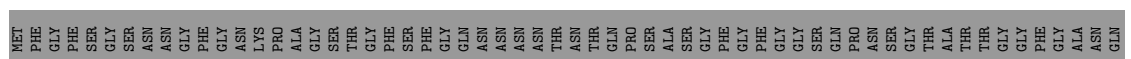




• Molecule 5: Nucleoporin NUP57



• Molecule 5: Nucleoporin NUP57





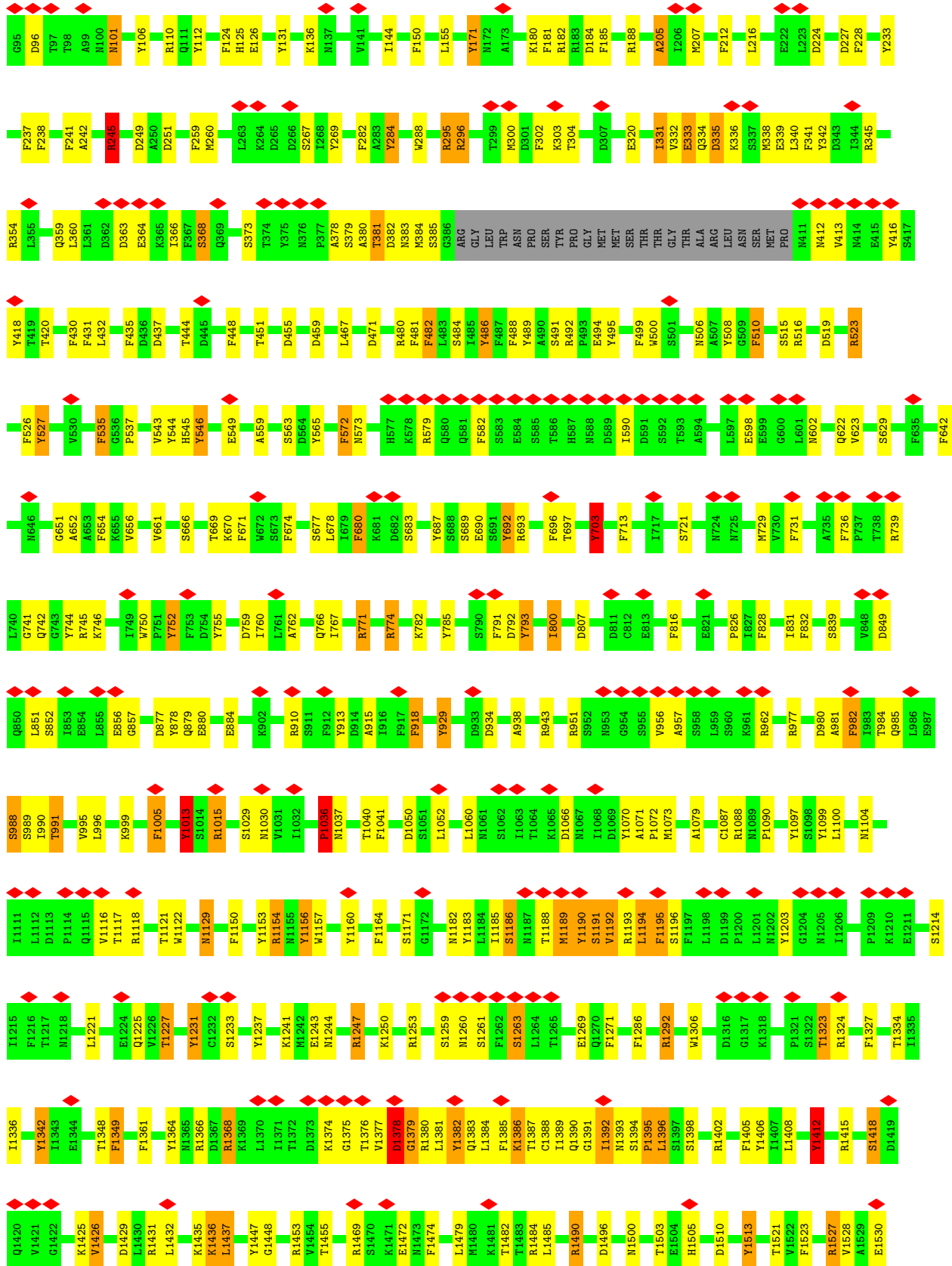


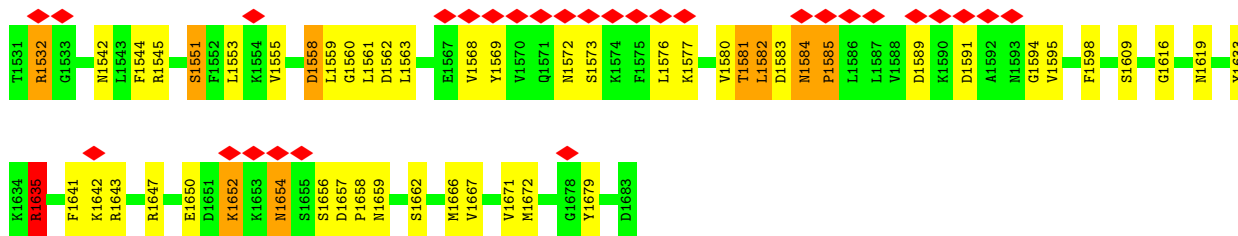




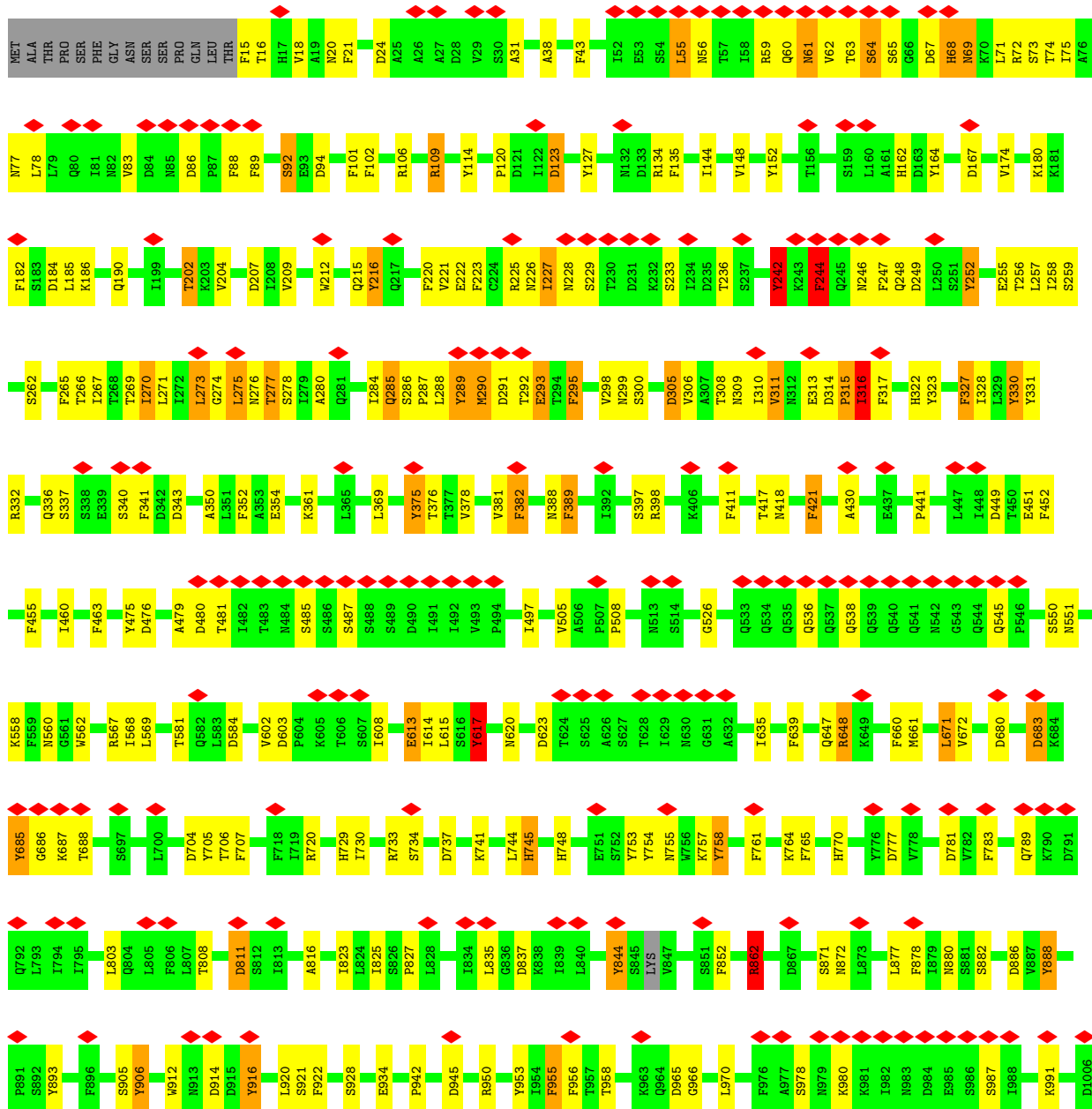
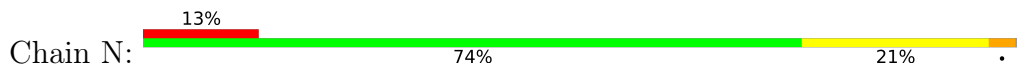


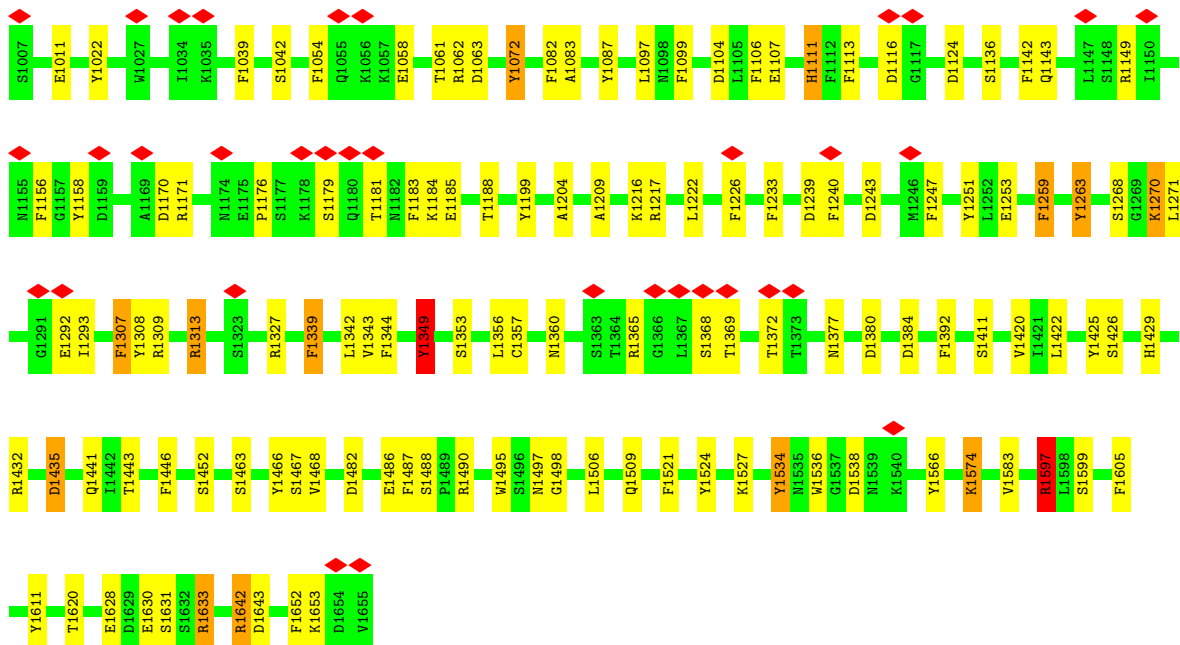




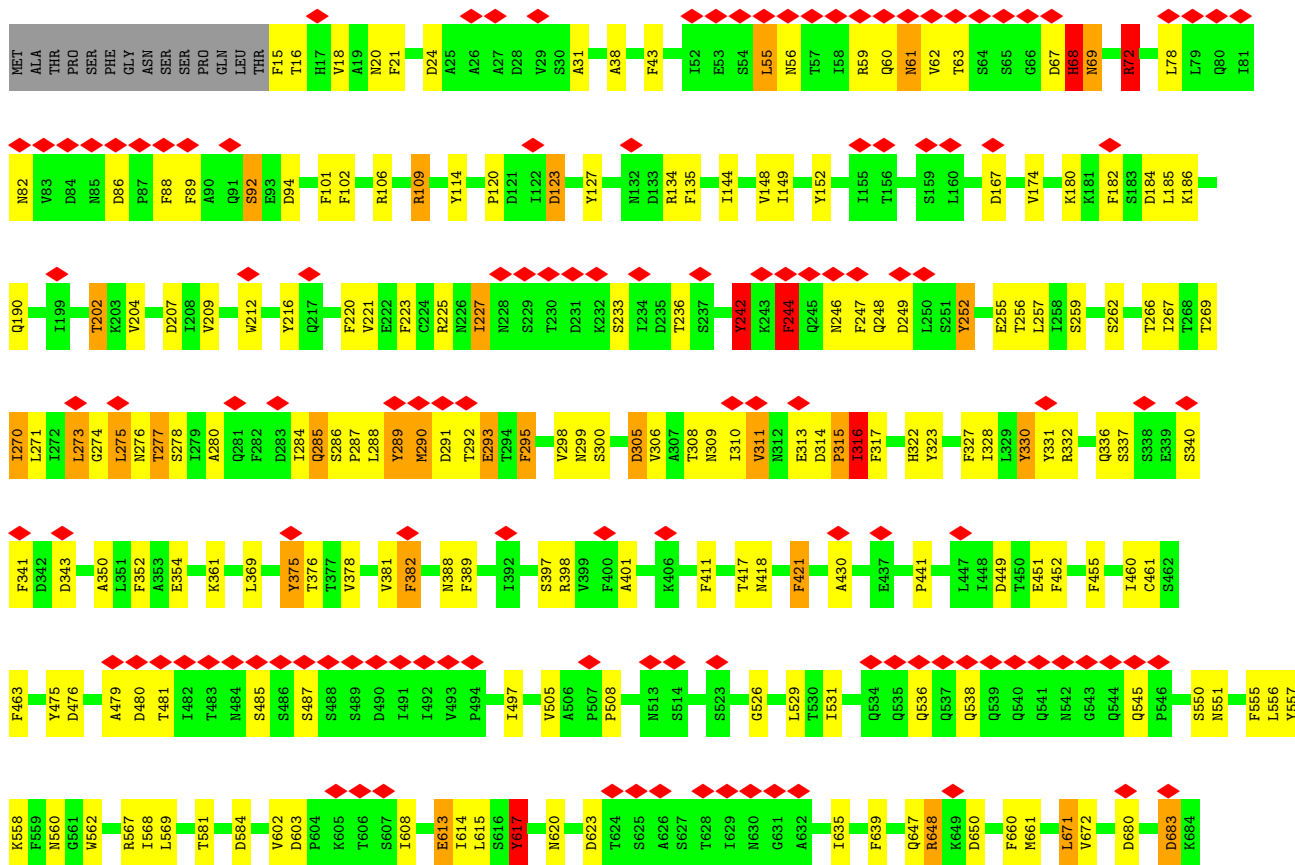
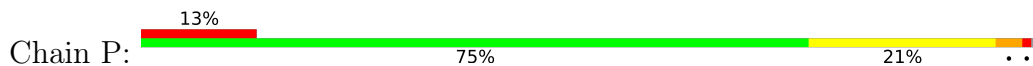


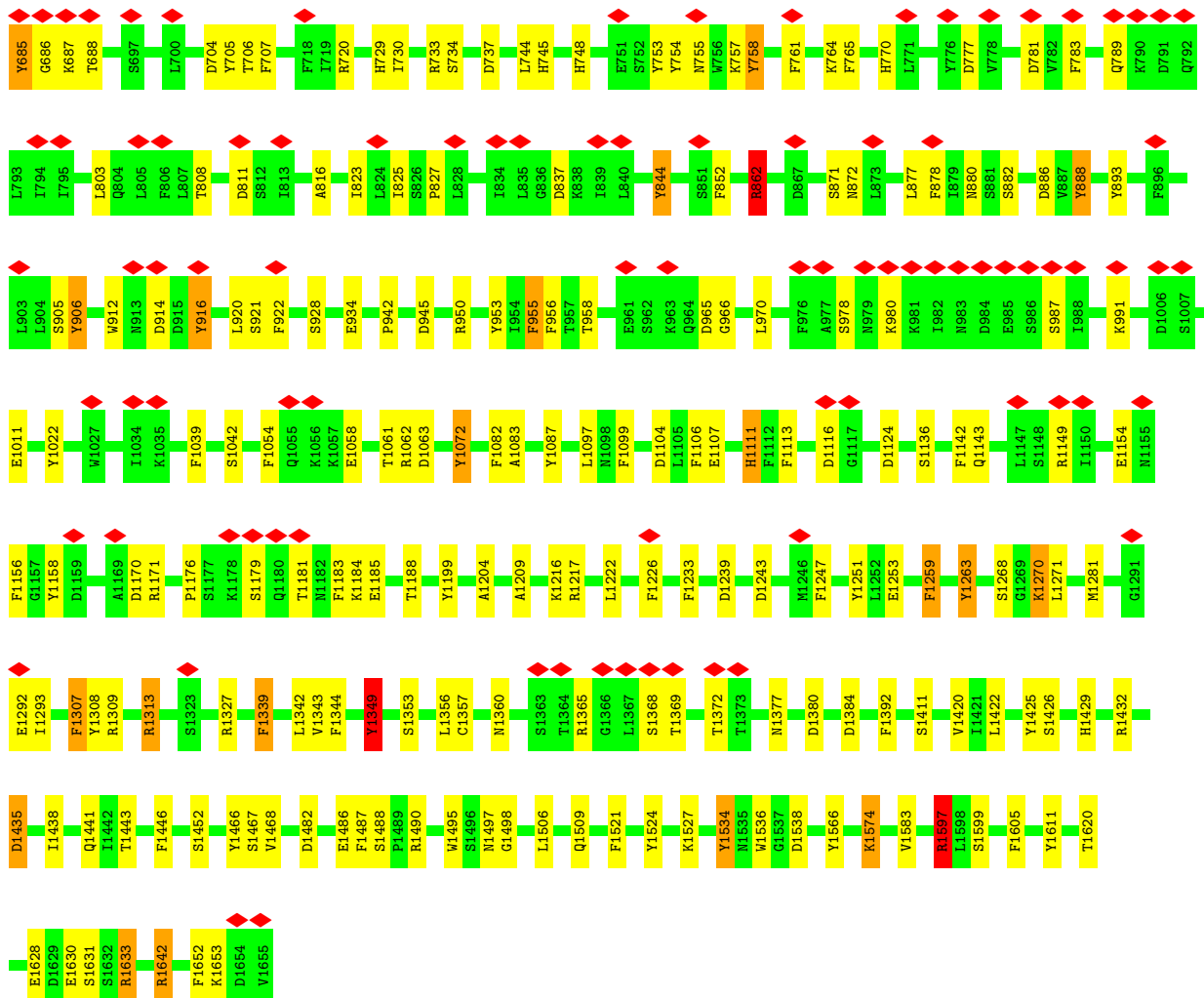
• Molecule 8: Nucleoporin NUP188



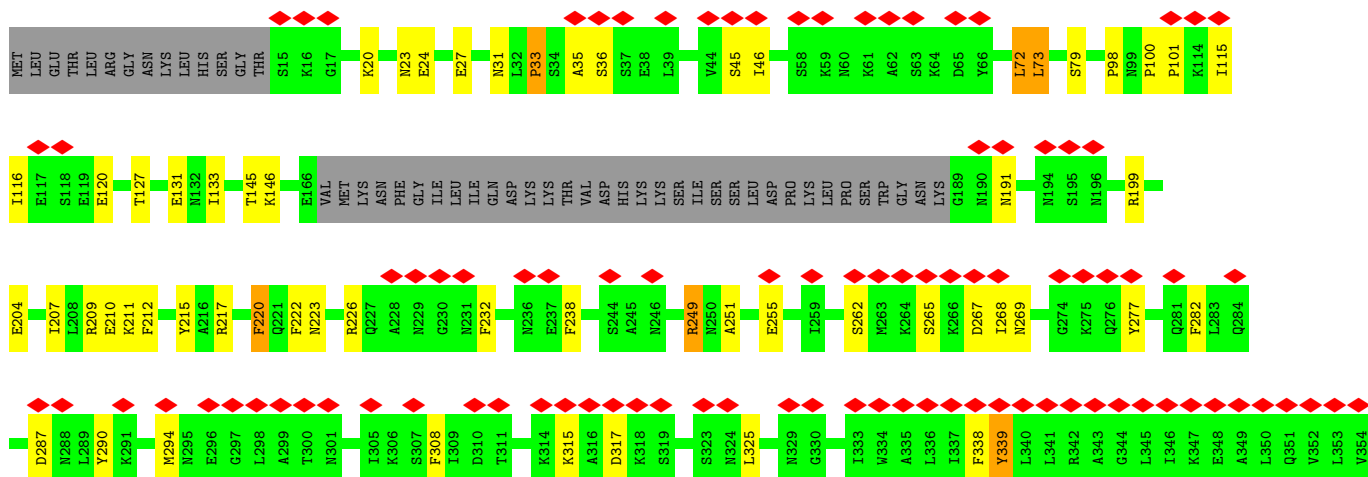


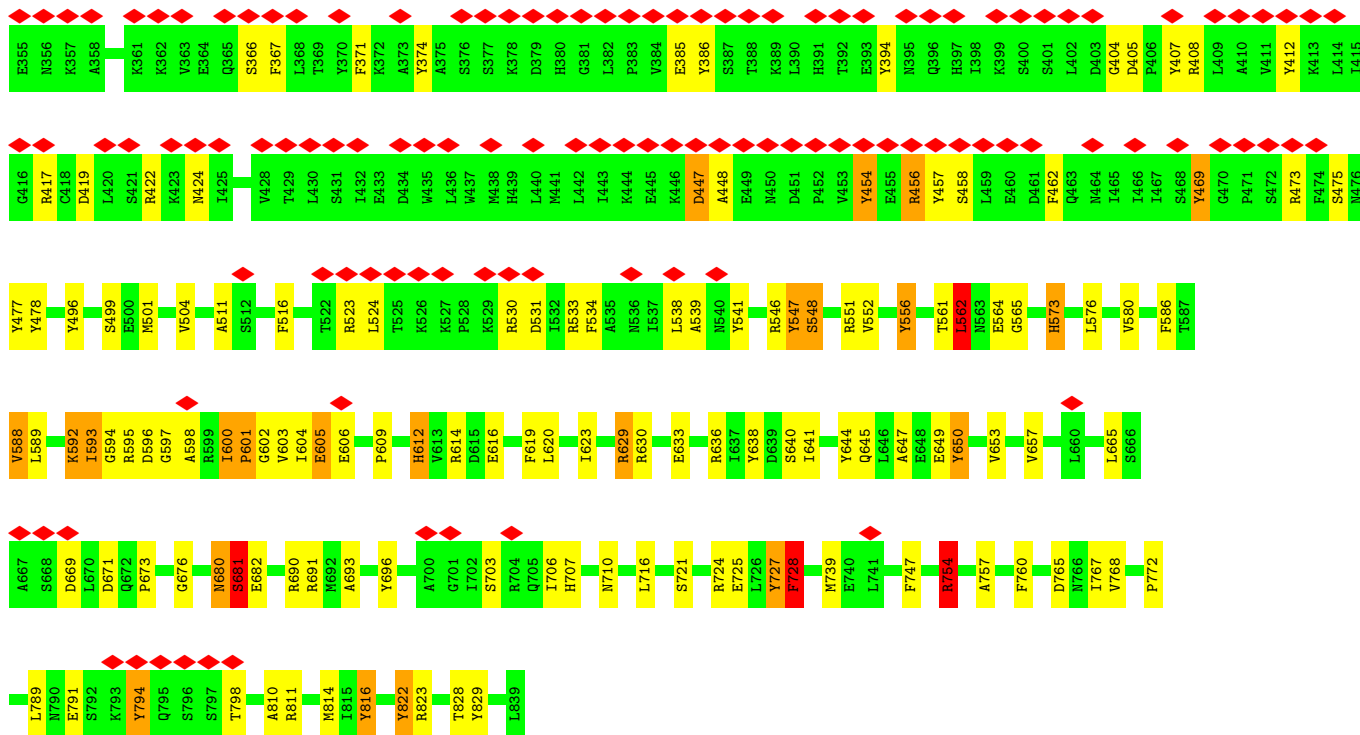
• Molecule 8: Nucleoporin NUP188



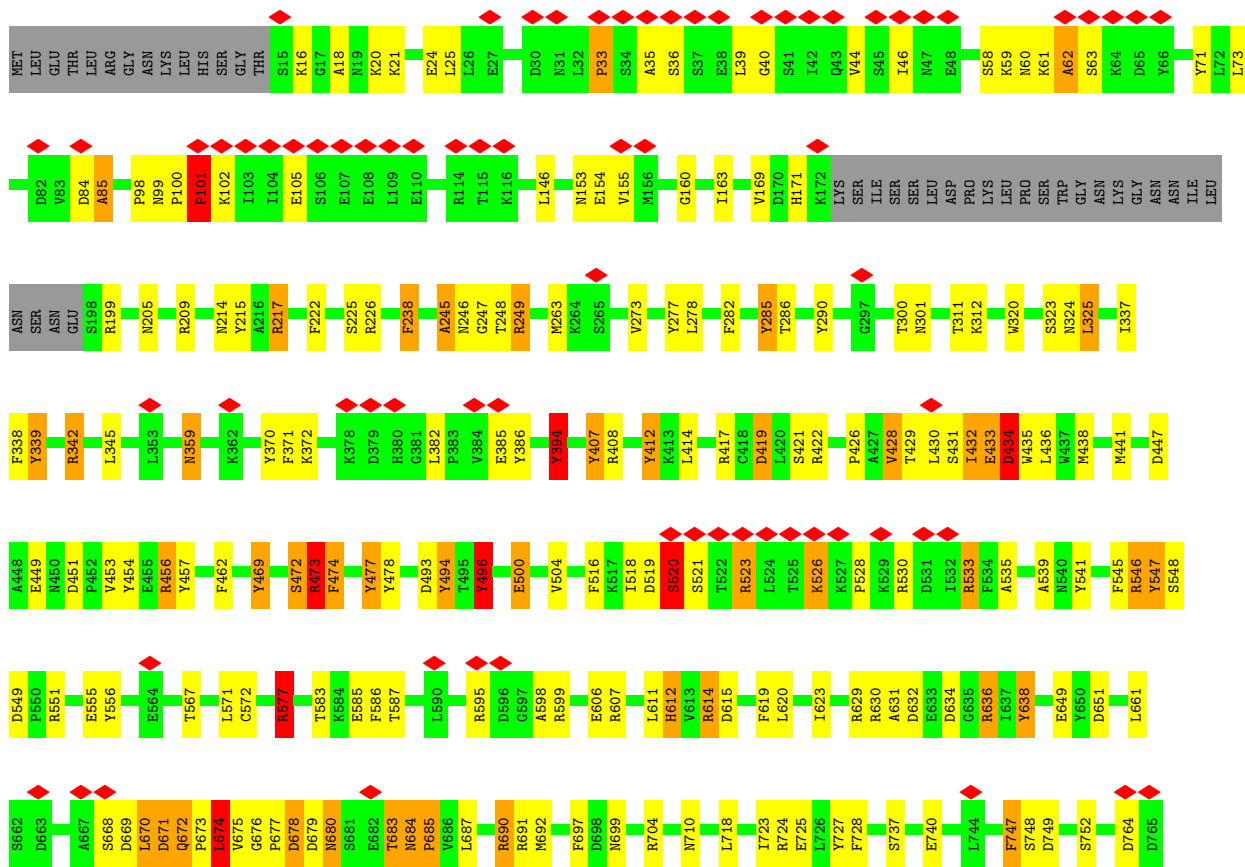


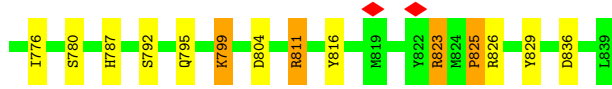
● Molecule 9: Nucleoporin NIC96



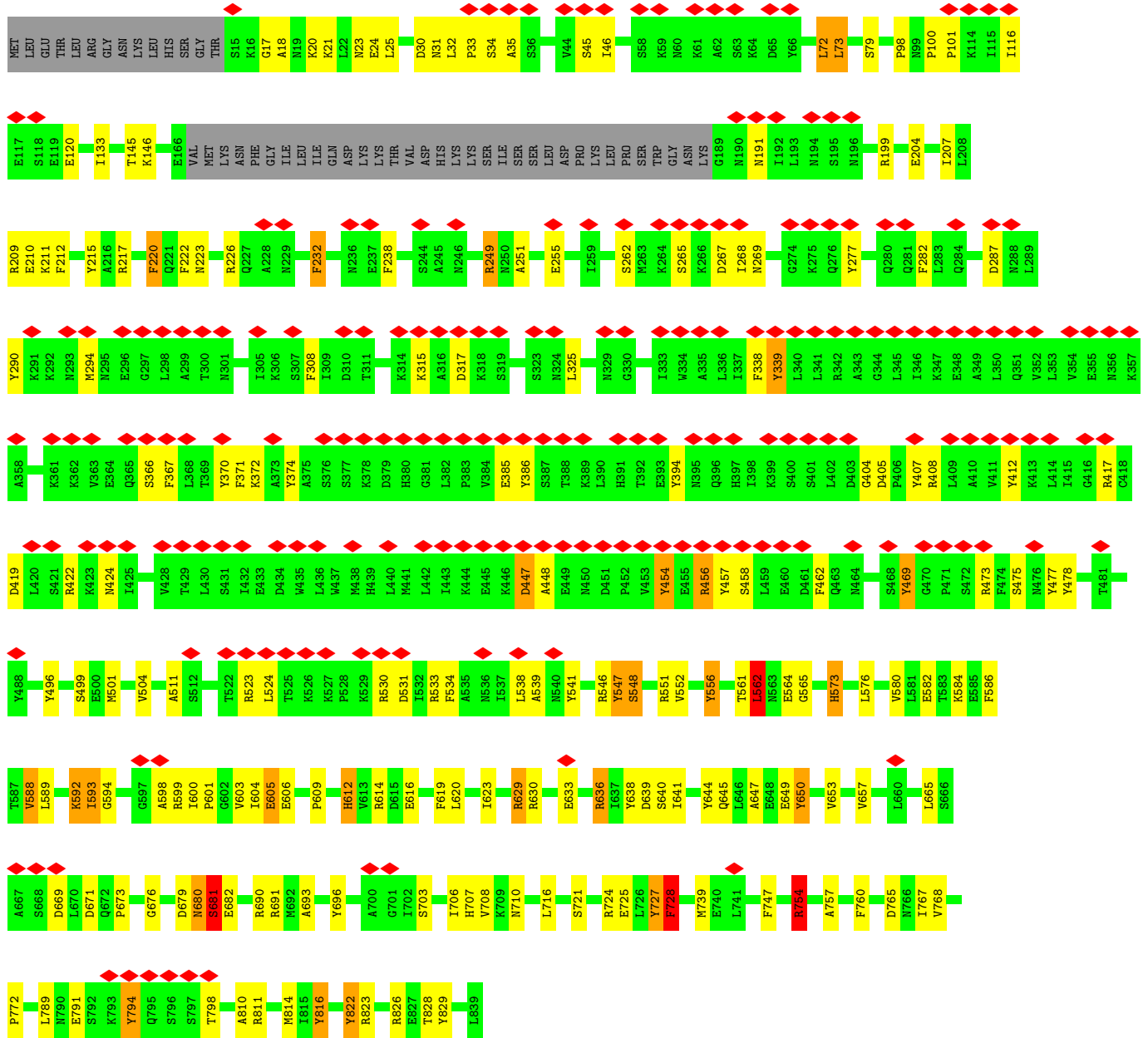


• Molecule 9: Nucleoporin NIC96





• Molecule 9: Nucleoporin NIC96



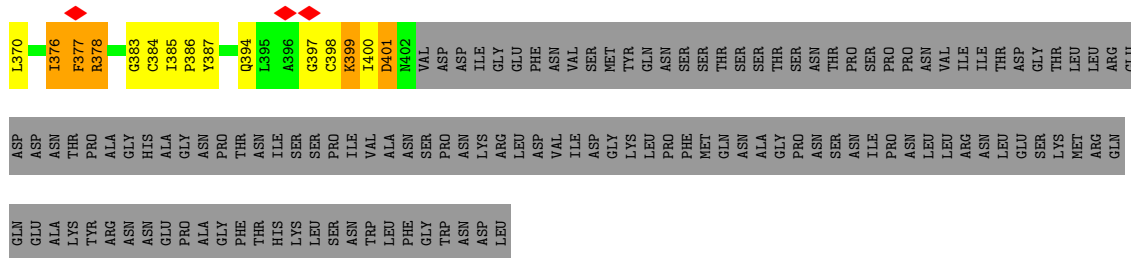
• Molecule 9: Nucleoporin NIC96





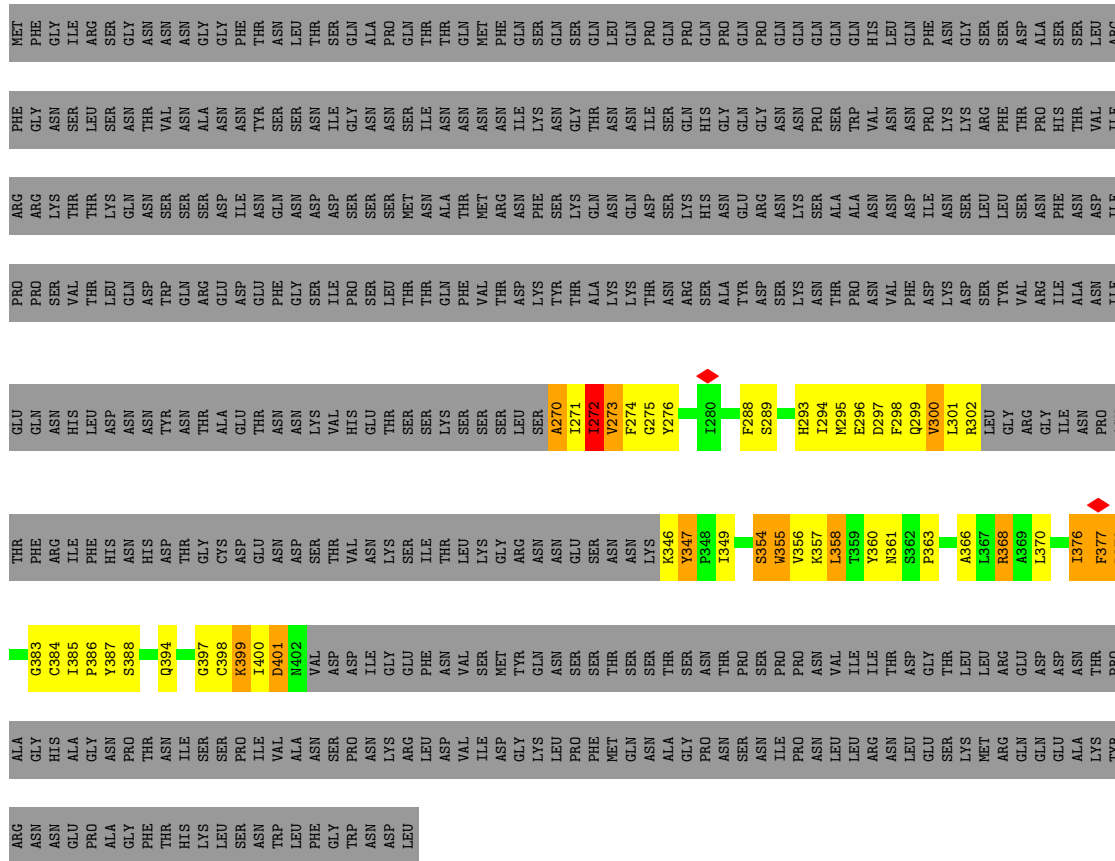






• Molecule 11: Nucleoporin 59

Chain X: 8% 6% • 83%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	208392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF correction applied in RELION during the alignment and reconstruction	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)	3500	Depositor
Magnification	37651	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	5.816	Depositor
Minimum map value	-1.894	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.095	Depositor
Recommended contour level	0.65	Depositor
Map size (Å)	1276.8, 1276.8, 1276.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.66, 2.66, 2.66	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	0	1.68	62/10219 (0.6%)	1.92	243/13825 (1.8%)
2	Y	1.68	61/10219 (0.6%)	1.92	243/13825 (1.8%)
3	1	1.70	68/9504 (0.7%)	1.99	274/12863 (2.1%)
3	Z	1.70	73/9504 (0.8%)	1.98	267/12863 (2.1%)
4	A	1.59	8/1328 (0.6%)	1.86	34/1791 (1.9%)
4	D	1.68	7/1358 (0.5%)	1.84	35/1833 (1.9%)
4	G	1.59	8/1328 (0.6%)	1.86	34/1791 (1.9%)
4	J	1.67	7/1360 (0.5%)	1.83	34/1836 (1.9%)
5	B	1.89	15/1793 (0.8%)	1.92	40/2411 (1.7%)
5	E	1.61	10/1793 (0.6%)	1.82	36/2411 (1.5%)
5	H	1.67	14/1793 (0.8%)	1.83	36/2411 (1.5%)
5	K	1.58	10/1793 (0.6%)	1.80	33/2411 (1.4%)
6	C	1.55	8/1364 (0.6%)	1.80	28/1837 (1.5%)
6	F	1.55	5/1398 (0.4%)	1.84	26/1884 (1.4%)
6	I	1.54	9/1364 (0.7%)	1.79	30/1837 (1.6%)
6	L	1.55	5/1398 (0.4%)	1.85	26/1884 (1.4%)
7	M	1.67	111/13592 (0.8%)	1.89	284/18408 (1.5%)
7	O	1.67	107/13592 (0.8%)	1.89	278/18408 (1.5%)
8	N	1.94	78/13423 (0.6%)	1.85	278/18194 (1.5%)
8	P	1.95	76/13433 (0.6%)	1.86	281/18208 (1.5%)
9	Q	1.67	45/6050 (0.7%)	1.87	133/8208 (1.6%)
9	R	1.63	49/6073 (0.8%)	1.80	113/8244 (1.4%)
9	S	1.67	47/6050 (0.8%)	1.87	138/8208 (1.7%)
9	T	1.63	47/6078 (0.8%)	1.80	111/8251 (1.3%)
10	U	1.42	3/761 (0.4%)	1.67	10/1027 (1.0%)
10	W	1.37	2/761 (0.3%)	1.64	10/1027 (1.0%)
11	V	1.50	6/727 (0.8%)	1.80	18/982 (1.8%)
11	X	1.50	7/727 (1.0%)	1.80	18/982 (1.8%)
All	All	1.72	948/138783 (0.7%)	1.88	3091/187860 (1.6%)

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	7	0	1
1	8	0	1
2	0	0	34
2	Y	0	35
3	1	0	37
3	Z	0	37
4	A	0	1
4	D	0	1
4	G	0	1
4	J	0	1
5	B	0	3
5	E	0	3
5	H	0	3
5	K	0	2
6	C	0	2
6	F	0	1
6	I	0	2
6	L	0	1
7	M	0	44
7	O	0	45
8	N	0	26
8	P	0	27
9	Q	0	16
9	R	0	17
9	S	0	17
9	T	0	17
10	U	0	2
10	W	0	1
11	V	0	1
11	X	0	1
All	All	0	380

The worst 5 of 948 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	P	613	GLU	CG-CD	99.91	3.01	1.51
8	N	613	GLU	CG-CD	99.88	3.01	1.51
5	B	323	LEU	CB-CG	37.01	2.59	1.52
8	N	617	TYR	CG-CD2	34.45	1.83	1.39
8	P	617	TYR	CG-CD2	34.40	1.83	1.39

The worst 5 of 3091 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	323	LEU	CA-CB-CG	23.92	170.32	115.30
9	Q	533	ARG	NE-CZ-NH2	-21.58	109.51	120.30
9	S	533	ARG	NE-CZ-NH2	-21.53	109.53	120.30
9	Q	533	ARG	NE-CZ-NH1	20.88	130.74	120.30
9	S	533	ARG	NE-CZ-NH1	20.78	130.69	120.30

There are no chirality outliers.

5 of 380 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	7	83	UNK	Mainchain
1	8	83	UNK	Mainchain
2	Y	107	TYR	Sidechain
2	Y	127	TYR	Sidechain
2	Y	154	PHE	Sidechain

## 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	3	80	0	18	18	0
1	4	80	0	18	17	0
1	7	85	0	20	34	0
1	8	85	0	20	33	0
1	a	40	0	12	0	0
1	b	175	0	37	0	0
1	c	85	0	18	0	0
1	d	110	0	25	0	0
1	e	185	0	39	0	0
1	f	40	0	12	0	0
1	g	175	0	37	0	0
1	h	85	0	21	0	0
1	i	110	0	24	0	0
1	j	185	0	39	0	0
1	k	65	0	19	0	0
1	l	65	0	19	0	0
1	m	125	0	28	0	0
1	n	125	0	28	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	0	10015	0	10047	88	0
2	Y	10015	0	10047	69	0
3	1	9319	0	9286	182	0
3	Z	9319	0	9286	161	0
4	A	1315	0	1275	17	0
4	D	1345	0	1287	44	0
4	G	1315	0	1275	18	0
4	J	1347	0	1292	31	0
5	B	1771	0	1832	72	0
5	E	1771	0	1832	112	0
5	H	1771	0	1832	30	0
5	K	1771	0	1832	129	0
6	C	1347	0	1376	14	0
6	F	1381	0	1391	37	0
6	I	1347	0	1376	30	0
6	L	1381	0	1391	59	0
7	M	13334	0	13379	337	0
7	O	13334	0	13379	359	0
8	N	13181	0	13422	324	0
8	P	13190	0	13436	262	0
9	Q	5961	0	5621	82	0
9	R	5983	0	5599	194	0
9	S	5961	0	5621	87	0
9	T	5988	0	5600	195	0
10	U	745	0	752	74	0
10	W	745	0	752	89	0
11	V	710	0	692	132	0
11	X	710	0	692	165	0
All	All	138272	0	136036	2816	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 11.

The worst 5 of 2816 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)
8:N:617:TYR:CD1	8:N:617:TYR:CE1	1.75	1.71
8:P:617:TYR:CD1	8:P:617:TYR:CE1	1.76	1.70
8:P:617:TYR:CE1	8:P:617:TYR:CZ	1.79	1.66
8:N:617:TYR:CE1	8:N:617:TYR:CZ	1.79	1.66
8:P:617:TYR:CD1	8:P:617:TYR:CG	1.83	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	
2	0	1244/1502 (83%)	1144 (92%)	65 (5%)	35 (3%)	5	30
2	Y	1244/1502 (83%)	1143 (92%)	66 (5%)	35 (3%)	5	30
3	1	1152/1391 (83%)	1077 (94%)	51 (4%)	24 (2%)	7	36
3	Z	1152/1391 (83%)	1080 (94%)	50 (4%)	22 (2%)	8	38
4	A	157/823 (19%)	151 (96%)	3 (2%)	3 (2%)	8	38
4	D	163/823 (20%)	153 (94%)	4 (2%)	6 (4%)	3	24
4	G	157/823 (19%)	151 (96%)	3 (2%)	3 (2%)	8	38
4	J	163/823 (20%)	153 (94%)	6 (4%)	4 (2%)	5	32
5	B	211/541 (39%)	178 (84%)	22 (10%)	11 (5%)	2	19
5	E	211/541 (39%)	194 (92%)	12 (6%)	5 (2%)	6	33
5	H	211/541 (39%)	180 (85%)	21 (10%)	10 (5%)	2	21
5	K	211/541 (39%)	192 (91%)	13 (6%)	6 (3%)	5	30
6	C	160/472 (34%)	150 (94%)	9 (6%)	1 (1%)	25	66
6	F	167/472 (35%)	159 (95%)	7 (4%)	1 (1%)	25	66
6	I	160/472 (34%)	150 (94%)	9 (6%)	1 (1%)	25	66
6	L	167/472 (35%)	156 (93%)	8 (5%)	3 (2%)	8	40
7	M	1655/1683 (98%)	1536 (93%)	80 (5%)	39 (2%)	6	33
7	O	1655/1683 (98%)	1533 (93%)	78 (5%)	44 (3%)	5	31
8	N	1636/1655 (99%)	1524 (93%)	86 (5%)	26 (2%)	9	44
8	P	1639/1655 (99%)	1524 (93%)	87 (5%)	28 (2%)	9	42
9	Q	785/839 (94%)	717 (91%)	55 (7%)	13 (2%)	9	42
9	R	796/839 (95%)	715 (90%)	54 (7%)	27 (3%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	S	785/839 (94%)	722 (92%)	51 (6%)	12 (2%)	10	46
9	T	797/839 (95%)	719 (90%)	51 (6%)	27 (3%)	3	26
10	U	90/475 (19%)	67 (74%)	18 (20%)	5 (6%)	2	18
10	W	90/475 (19%)	67 (74%)	17 (19%)	6 (7%)	1	15
11	V	86/528 (16%)	70 (81%)	14 (16%)	2 (2%)	6	34
11	X	86/528 (16%)	71 (83%)	13 (15%)	2 (2%)	6	34
All	All	17030/25168 (68%)	15676 (92%)	953 (6%)	401 (2%)	9	33

5 of 401 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	Y	129	SER
2	Y	250	ALA
2	Y	289	SER
2	Y	356	ILE
2	Y	409	ALA

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	0	1130/1353 (84%)	1091 (96%)	39 (4%)	36	59
2	Y	1130/1353 (84%)	1091 (96%)	39 (4%)	36	59
3	1	1051/1250 (84%)	1026 (98%)	25 (2%)	49	69
3	Z	1051/1250 (84%)	1027 (98%)	24 (2%)	50	70
4	A	154/674 (23%)	147 (96%)	7 (4%)	27	52
4	D	154/674 (23%)	144 (94%)	10 (6%)	17	42
4	G	154/674 (23%)	147 (96%)	7 (4%)	27	52
4	J	155/674 (23%)	145 (94%)	10 (6%)	17	42
5	B	196/439 (45%)	178 (91%)	18 (9%)	9	29
5	E	196/439 (45%)	186 (95%)	10 (5%)	24	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	H	196/439 (45%)	180 (92%)	16 (8%)	11	34
5	K	196/439 (45%)	182 (93%)	14 (7%)	14	39
6	C	155/377 (41%)	150 (97%)	5 (3%)	39	61
6	F	155/377 (41%)	151 (97%)	4 (3%)	46	66
6	I	155/377 (41%)	150 (97%)	5 (3%)	39	61
6	L	155/377 (41%)	150 (97%)	5 (3%)	39	61
7	M	1518/1538 (99%)	1456 (96%)	62 (4%)	30	55
7	O	1518/1538 (99%)	1458 (96%)	60 (4%)	31	55
8	N	1538/1557 (99%)	1470 (96%)	68 (4%)	28	53
8	P	1539/1557 (99%)	1474 (96%)	65 (4%)	30	54
9	Q	590/762 (77%)	573 (97%)	17 (3%)	42	64
9	R	582/762 (76%)	560 (96%)	22 (4%)	33	57
9	S	590/762 (77%)	573 (97%)	17 (3%)	42	64
9	T	582/762 (76%)	560 (96%)	22 (4%)	33	57
10	U	80/421 (19%)	72 (90%)	8 (10%)	7	26
10	W	80/421 (19%)	70 (88%)	10 (12%)	4	19
11	V	77/477 (16%)	69 (90%)	8 (10%)	7	25
11	X	77/477 (16%)	68 (88%)	9 (12%)	5	21
All	All	15154/22200 (68%)	14548 (96%)	606 (4%)	35	55

5 of 606 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	O	1386	LYS
9	T	520	SER
7	O	1582	LEU
7	O	1382	TYR
8	P	789	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 216 such sidechains are listed below:

Mol	Chain	Res	Type
2	0	1160	HIS
6	I	374	GLN
9	S	612	HIS

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Mol	Chain	Res	Type
2	0	1369	ASN
3	1	978	ASN

### 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	S	1
9	Q	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	S	101:PRO	C	114:LYS	N	33.71
1	Q	101:PRO	C	114:LYS	N	32.23

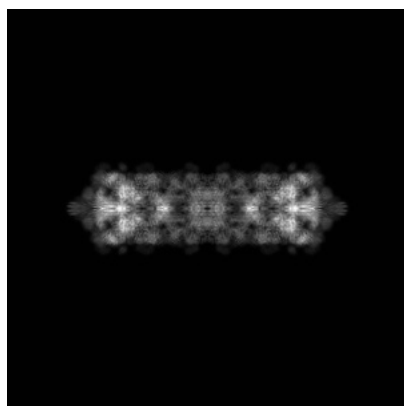
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41300. These allow visual inspection of the internal detail of the map and identification of artifacts.

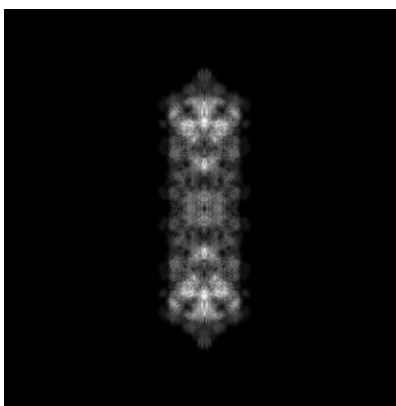
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

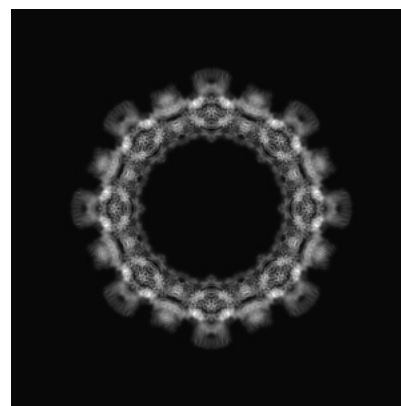
#### 6.1.1 Primary map



X

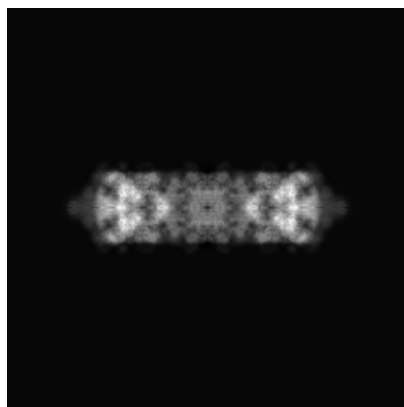


Y

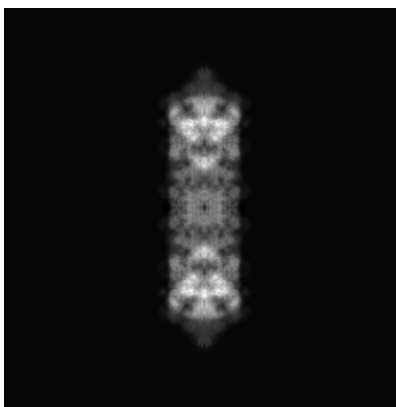


Z

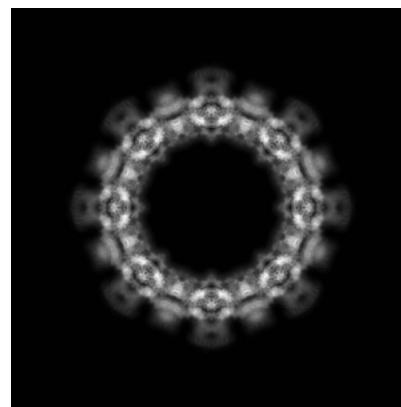
#### 6.1.2 Raw map



X



Y

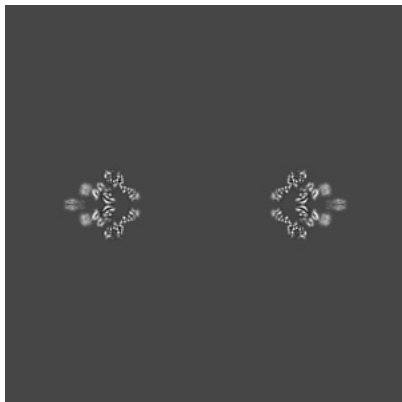


Z

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

## 6.2 Central slices [i](#)

### 6.2.1 Primary map



X Index: 240

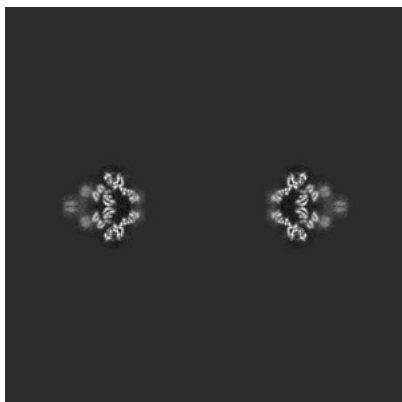


Y Index: 240



Z Index: 240

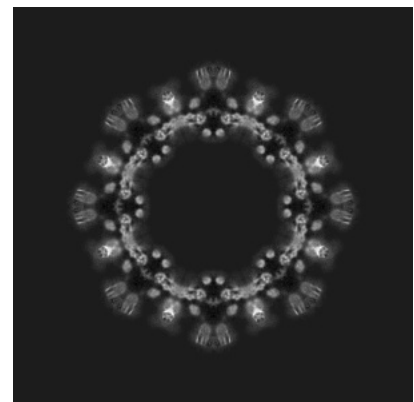
### 6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

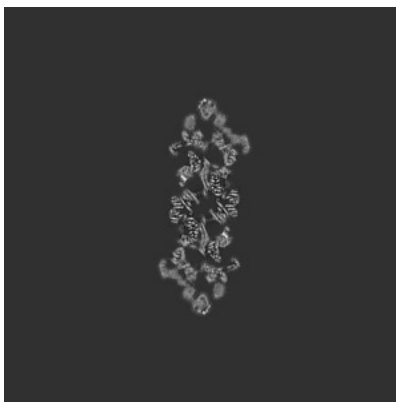
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

### 6.3.1 Primary map



X Index: 139

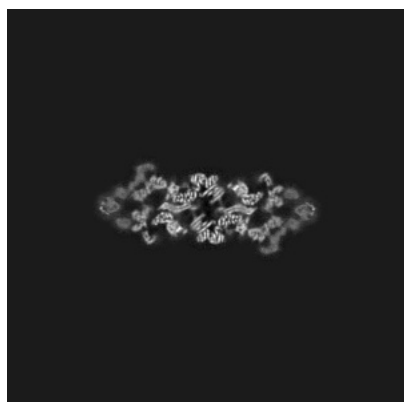


Y Index: 340

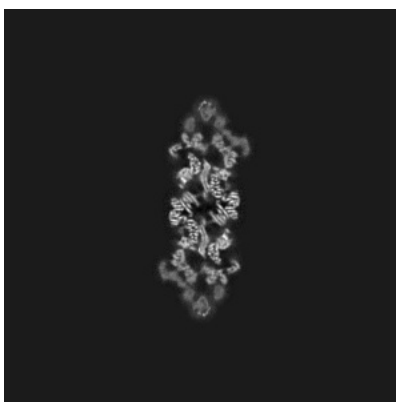


Z Index: 238

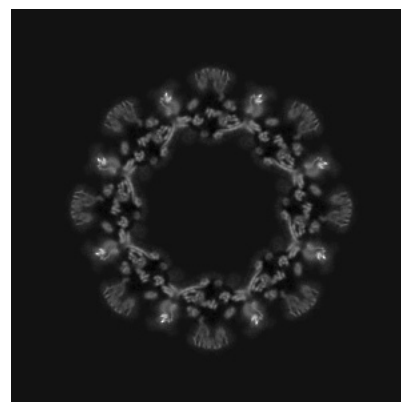
### 6.3.2 Raw map



X Index: 340



Y Index: 340

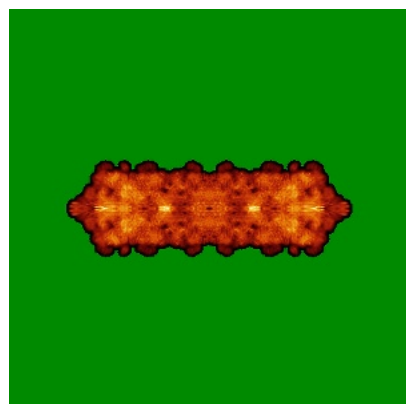


Z Index: 242

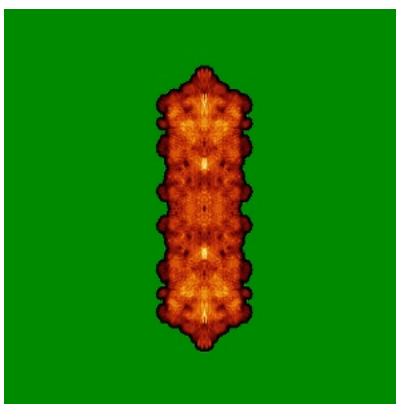
The images above show the largest variance slices of the map in three orthogonal directions.

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

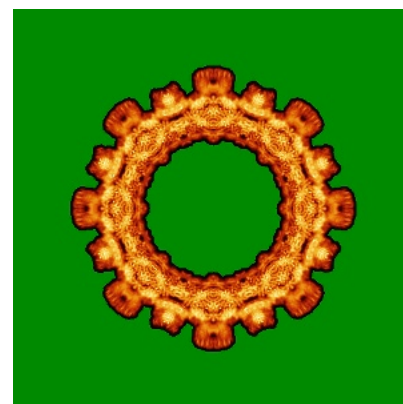
### 6.4.1 Primary map



X

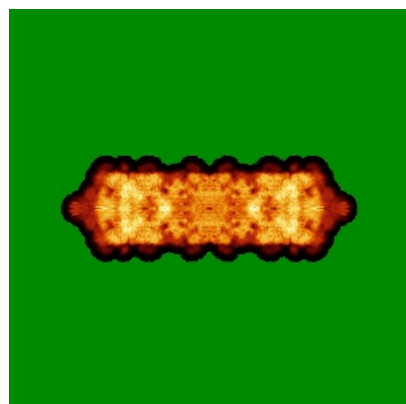


Y

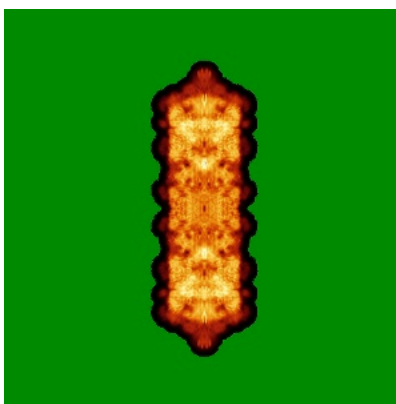


Z

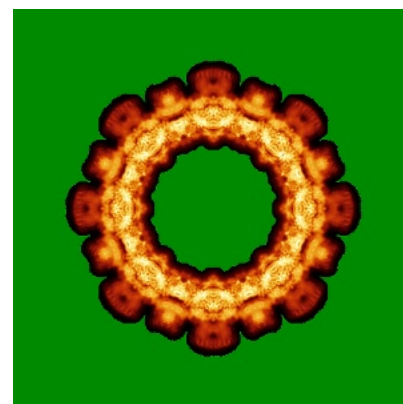
### 6.4.2 Raw map



X



Y

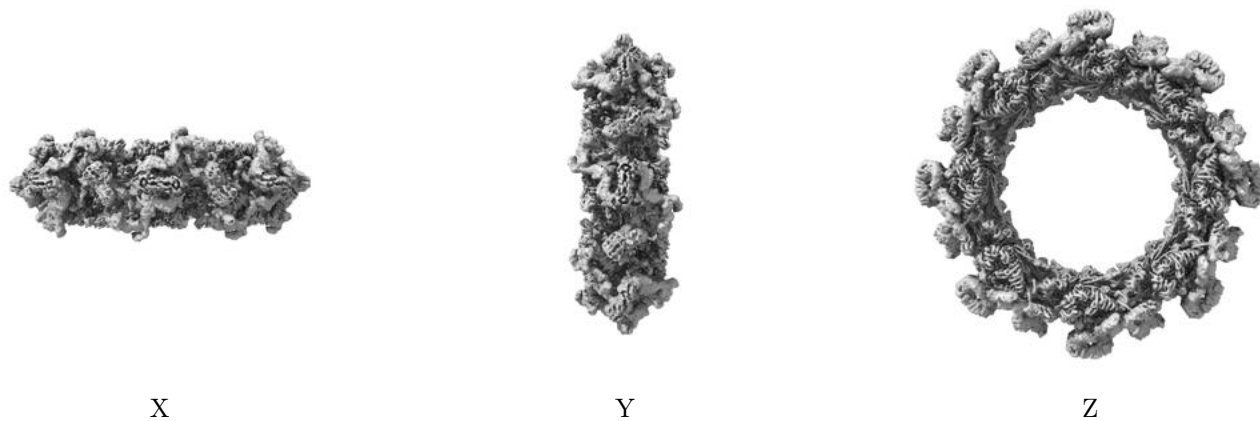


Z

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 0.65. 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](#)

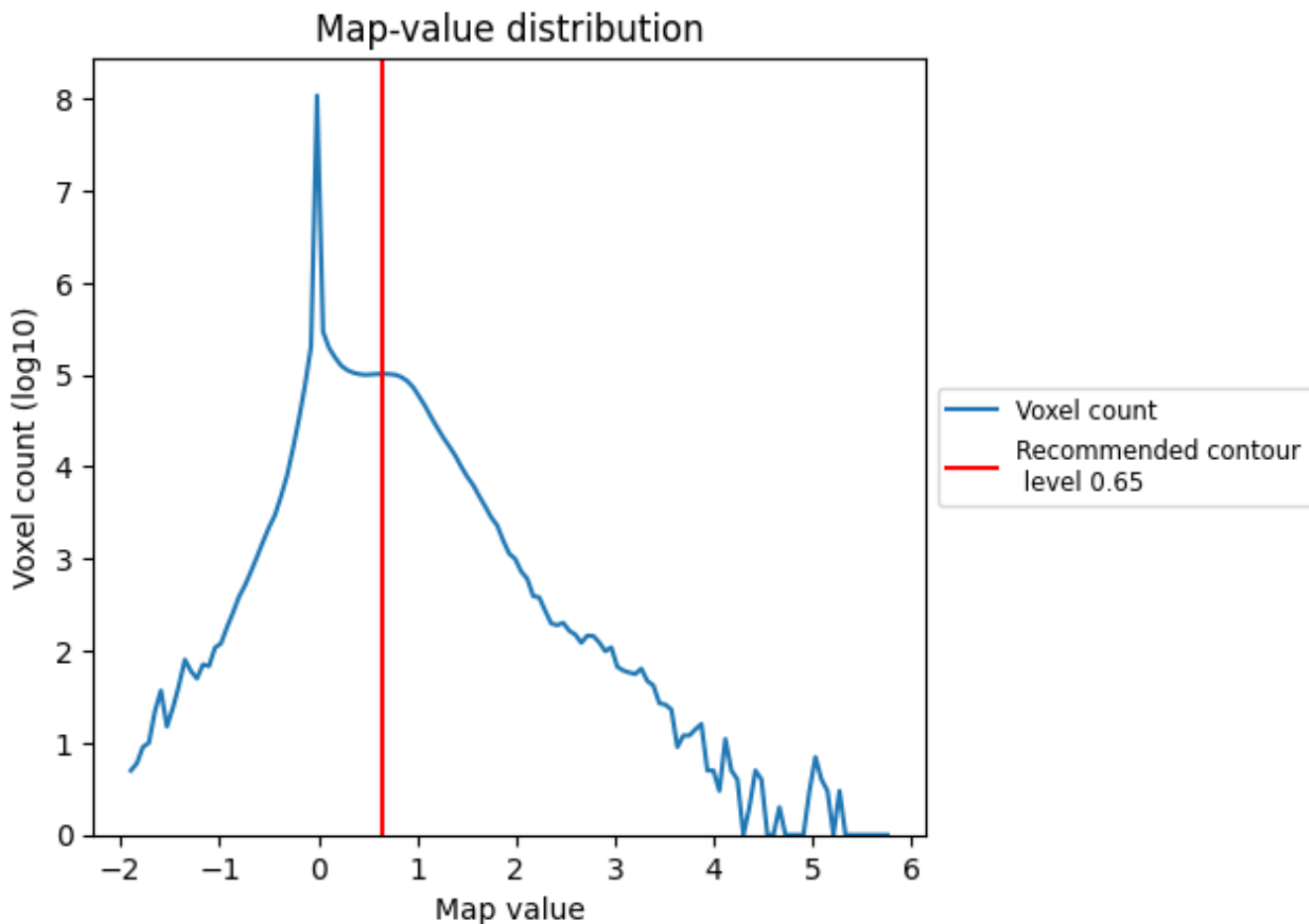
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

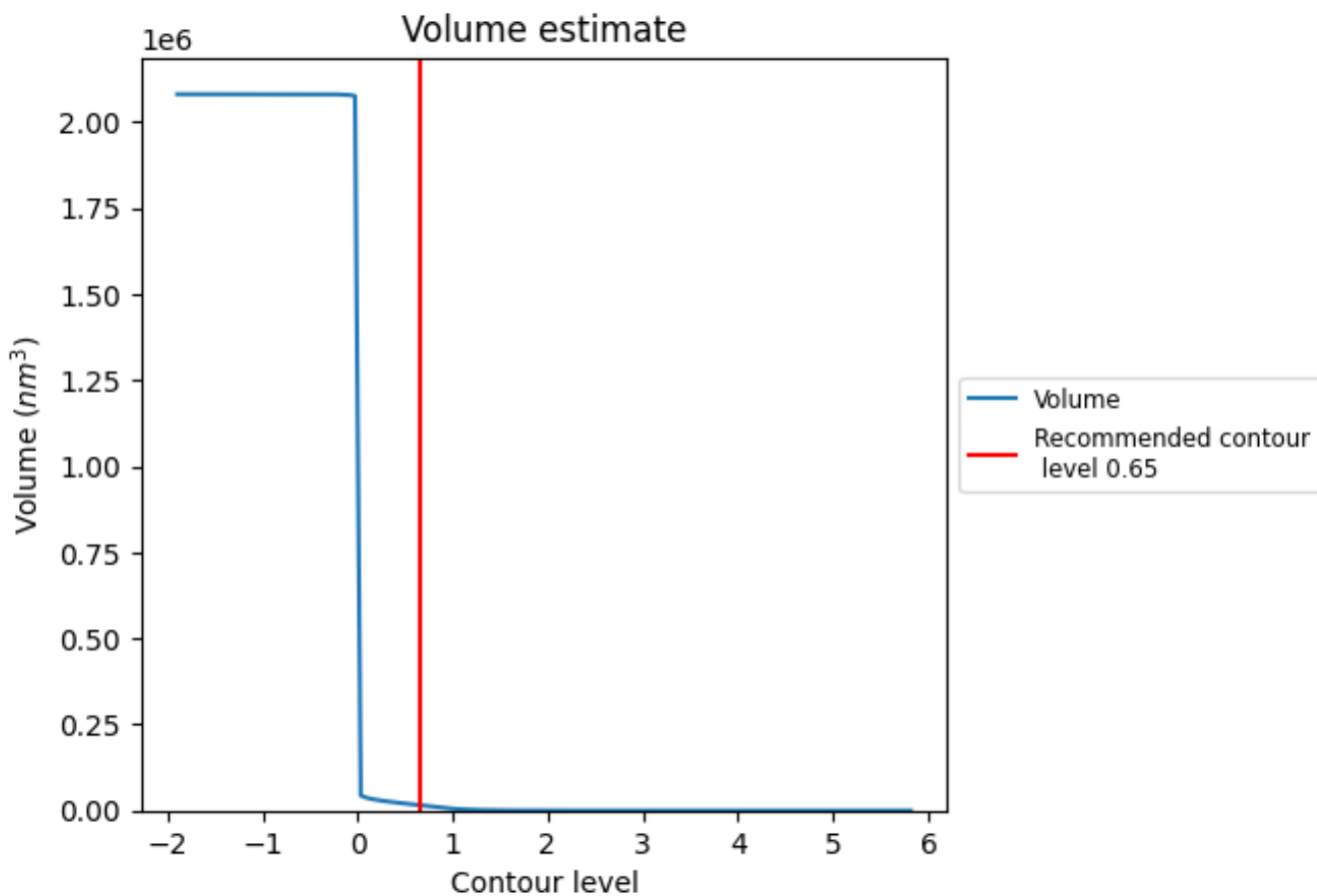
This section contains the results of statistical analysis of the map.

### 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.

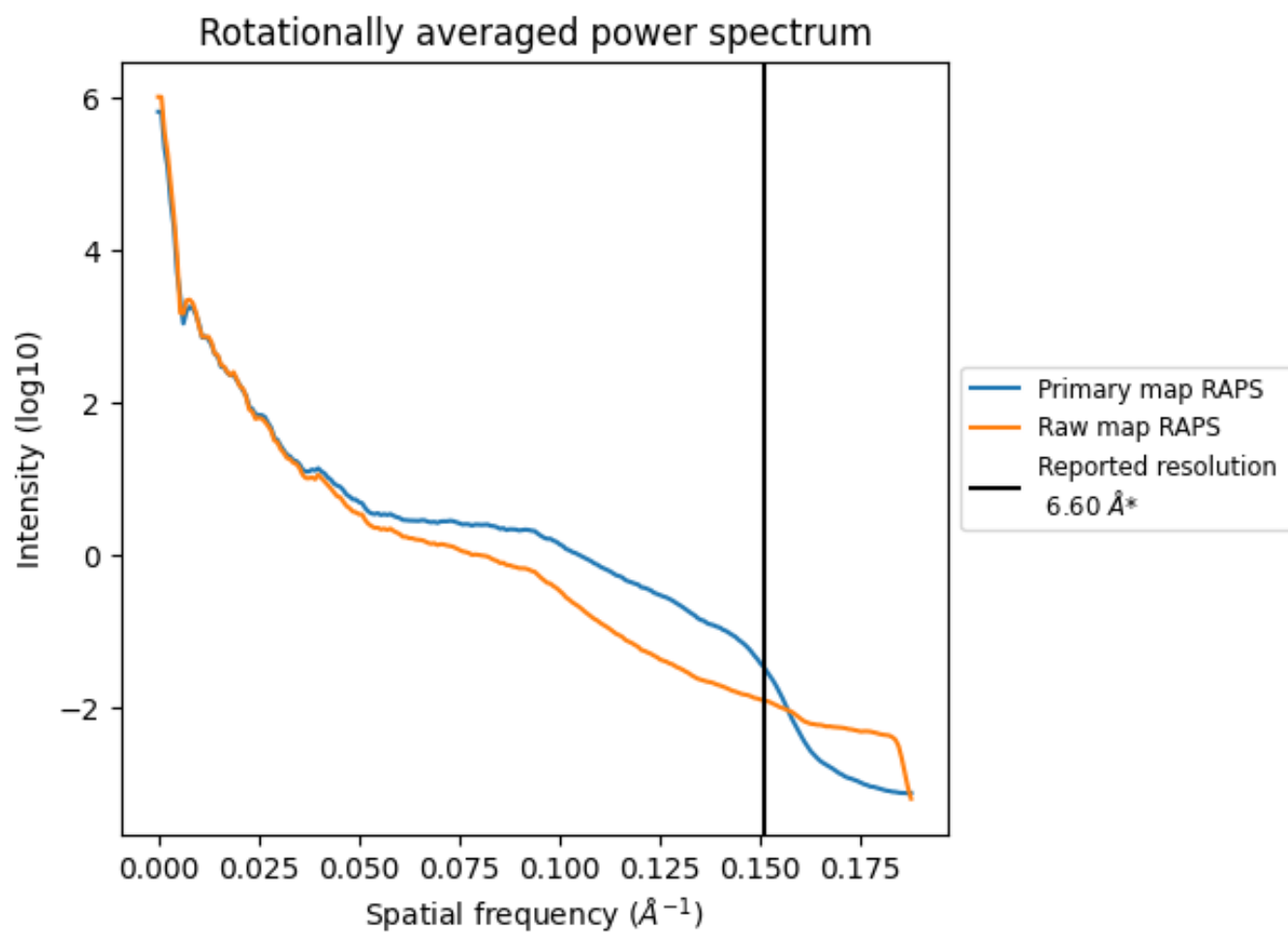
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 15598 nm<sup>3</sup>; this corresponds to an approximate mass of 14090 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum [i](#)

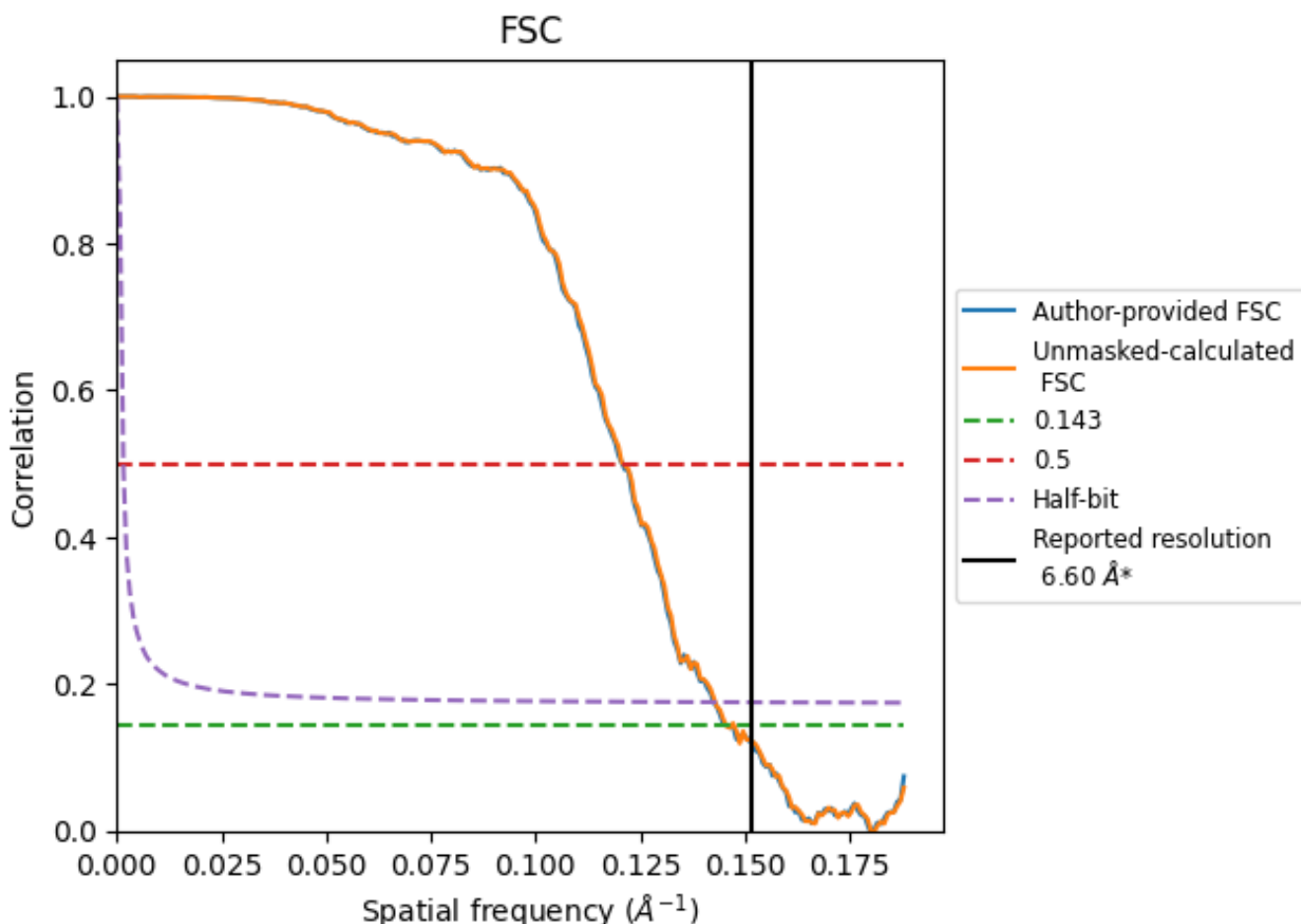


\*Reported resolution corresponds to spatial frequency of 0.152 Å<sup>-1</sup>

## 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 0.152 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

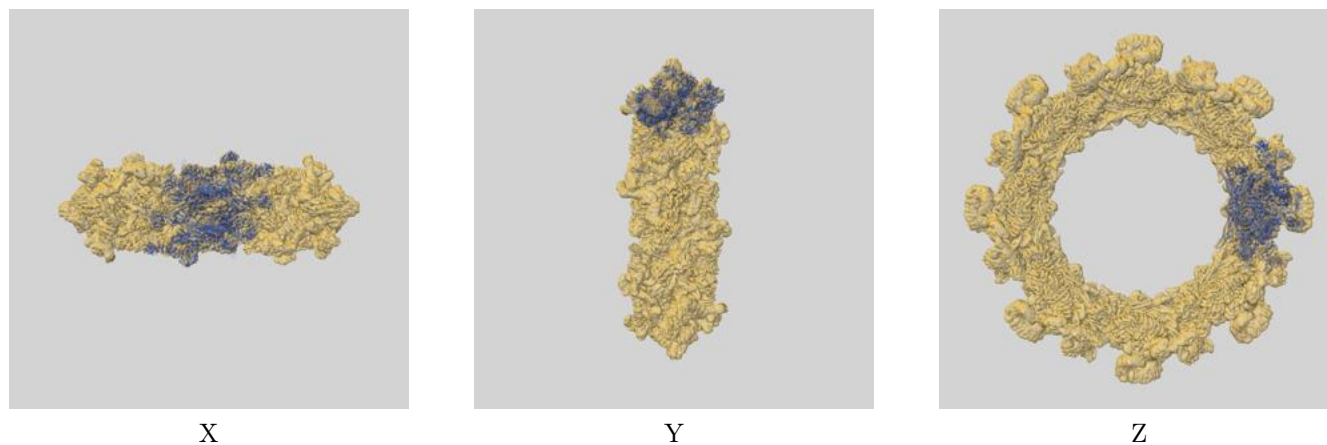
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.60	-	-
Author-provided FSC curve	6.86	8.29	7.02
Unmasked-calculated*	6.87	8.27	6.99

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

## 9 Map-model fit [i](#)

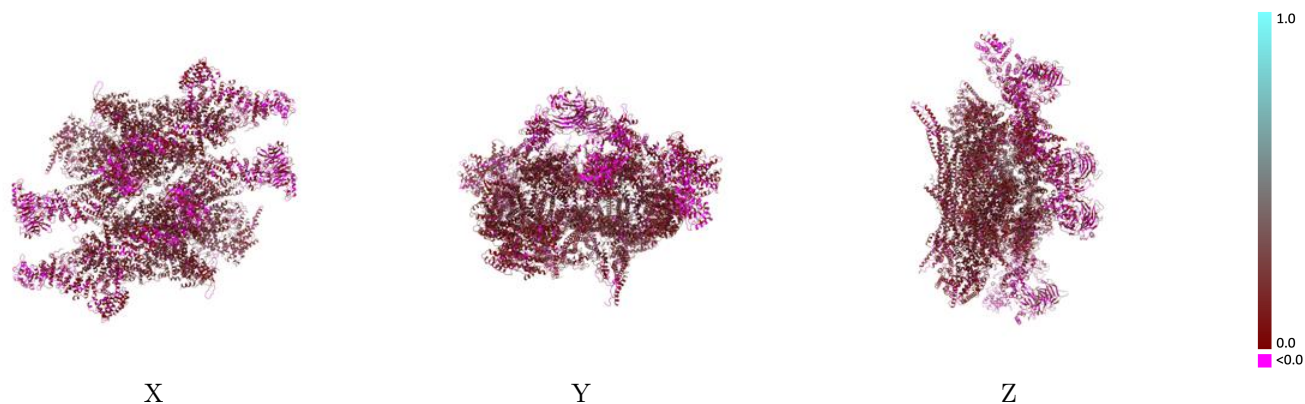
This section contains information regarding the fit between EMDB map EMD-41300 and PDB model 8TJ5. Per-residue inclusion information can be found in section 3 on page 9.

### 9.1 Map-model overlay [i](#)



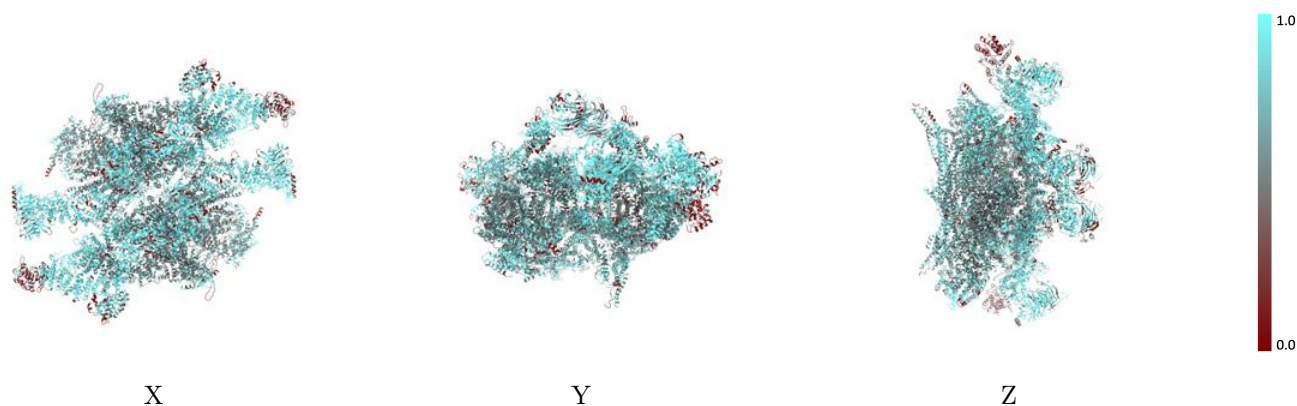
The images above show the 3D surface view of the map at the recommended contour level 0.65 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



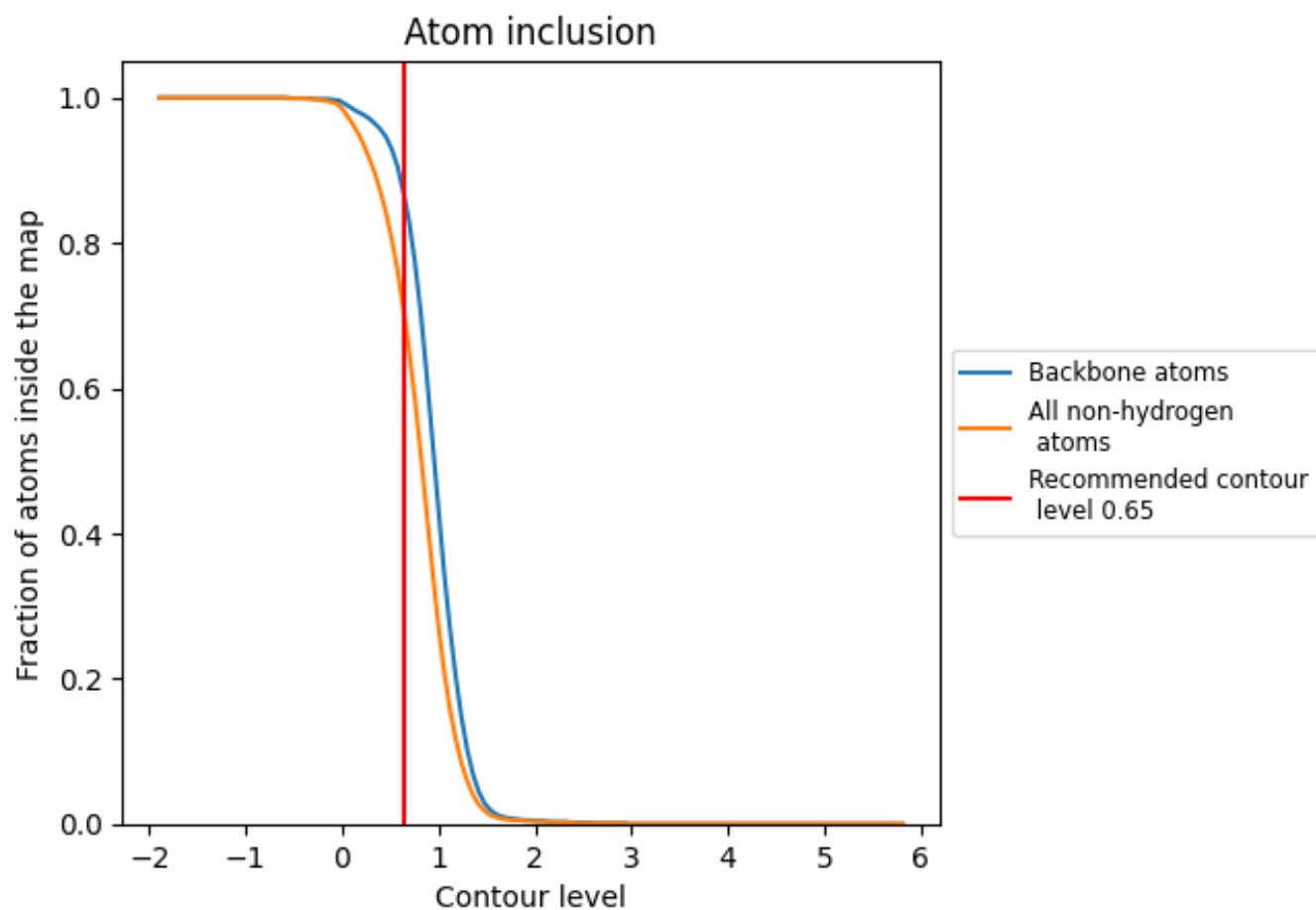
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.65).

## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 86% of all backbone atoms, 70% 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 (0.65) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6970	 0.1130
0	 0.8040	 0.0850
1	 0.7170	 0.0560
3	 0.8380	 0.2750
4	 0.8500	 0.2630
7	 0.8940	 0.1740
8	 0.9180	 0.1870
A	 0.7000	 0.1480
B	 0.6510	 0.1110
C	 0.6650	 0.1440
D	 0.7470	 0.1580
E	 0.7510	 0.1430
F	 0.7260	 0.1430
G	 0.7030	 0.1500
H	 0.6510	 0.1100
I	 0.6750	 0.1400
J	 0.7490	 0.1560
K	 0.7580	 0.1440
L	 0.7310	 0.1430
M	 0.6160	 0.1320
N	 0.6170	 0.1340
O	 0.6190	 0.1330
P	 0.6160	 0.1350
Q	 0.6710	 0.0820
R	 0.8020	 0.1440
S	 0.6720	 0.0830
T	 0.8060	 0.1430
U	 0.9020	 0.0800
V	 0.9080	 0.0570
W	 0.8960	 0.0860
X	 0.9240	 0.0660
Y	 0.8030	 0.0880
Z	 0.7140	 0.0560
a	 0.2500	 0.1860
b	 0.6290	 0.2290



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Chain	Atom inclusion	Q-score
c	 0.4590	 0.1280
d	 0.7460	 0.2710
e	 0.8270	 0.2490
f	 0.2750	 0.2220
g	 0.6400	 0.2240
h	 0.5650	 0.2270
i	 0.6820	 0.2670
j	 0.7030	 0.2170
k	 0.5540	 0.2590
l	 0.6000	 0.2420
m	 0.7360	 0.2080
n	 0.7360	 0.1930