



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:56 PM UTC

PDB ID : 5IJO / pdb_00005ijo
EMDB ID : EMD-8085
Title : Alternative composite structure of the inner ring of the human nuclear pore complex (16 copies of Nup188, 16 copies of Nup205)
Authors : Kosinski, J.; Mosalaganti, S.; von Appen, A.; Beck, M.
Deposited on : 2016-03-02
Resolution : 21.40 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

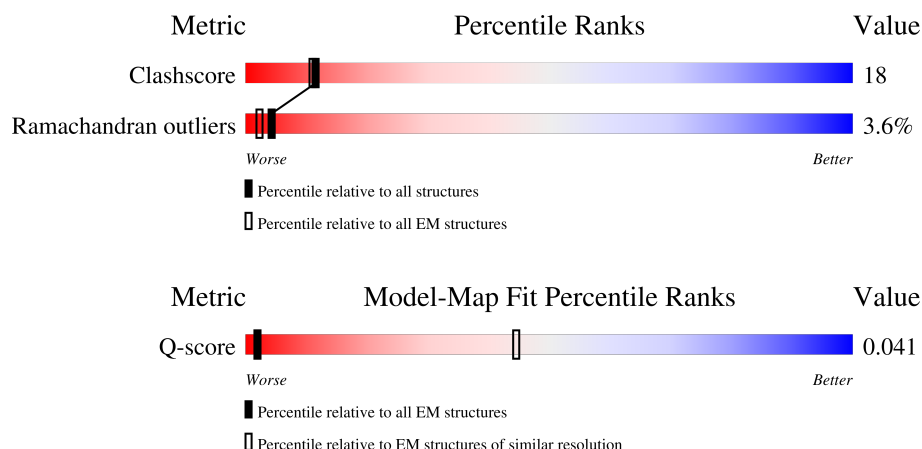
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 21.40 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	-
Q-score	-	25397	9 (21.00 - 21.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1391	
1	B	1391	
1	E	1391	
1	K	1391	
1	Q	1391	

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Mol	Chain	Length	Quality of chain
1	W	1391	
2	C	819	
2	I	819	
2	O	819	
2	U	819	
3	D	2012	
3	P	2012	
4	F	507	
4	L	507	
4	R	507	
4	X	507	
5	G	599	
5	M	599	
5	S	599	
5	Y	599	
6	H	522	
6	N	522	
6	T	522	
6	Z	522	
7	J	1749	
7	V	1749	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 76526 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 Nuclear pore complex protein Nup155.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	650	Total	C	N	O	0	0
			3214	1914	650	650		
1	B	650	Total	C	N	O	0	0
			3214	1914	650	650		
1	E	1083	Total	C	N	O	0	0
			5366	3200	1083	1083		
1	K	1083	Total	C	N	O	0	0
			5366	3200	1083	1083		
1	Q	1083	Total	C	N	O	0	0
			5366	3200	1083	1083		
1	W	1083	Total	C	N	O	0	0
			5366	3200	1083	1083		

- Molecule 2 is a protein called Nuclear pore complex protein Nup93.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	636	Total	C	N	O	0	0
			3152	1880	636	636		
2	I	636	Total	C	N	O	0	0
			3152	1880	636	636		
2	O	636	Total	C	N	O	0	0
			3152	1880	636	636		
2	U	636	Total	C	N	O	0	0
			3152	1880	636	636		

- Molecule 3 is a protein called Nuclear pore complex protein Nup205.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	D	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		
3	P	1028	Total	C	N	O	0	0
			5094	3038	1028	1028		

- Molecule 4 is a protein called Nucleoporin p54.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	F	335	Total	C	N	O	0	0
			1658	988	335	335		
4	L	335	Total	C	N	O	0	0
			1658	988	335	335		
4	R	335	Total	C	N	O	0	0
			1658	988	335	335		
4	X	335	Total	C	N	O	0	0
			1658	988	335	335		

- Molecule 5 is a protein called Nucleoporin p58/p45.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	171	Total	C	N	O	0	0
			853	511	171	171		
5	M	171	Total	C	N	O	0	0
			853	511	171	171		
5	S	171	Total	C	N	O	0	0
			853	511	171	171		
5	Y	171	Total	C	N	O	0	0
			853	511	171	171		

- Molecule 6 is a protein called Nuclear pore glycoprotein p62.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	H	169	Total	C	N	O	0	0
			842	504	169	169		
6	N	169	Total	C	N	O	0	0
			842	504	169	169		
6	T	169	Total	C	N	O	0	0
			842	504	169	169		
6	Z	169	Total	C	N	O	0	0
			842	504	169	169		

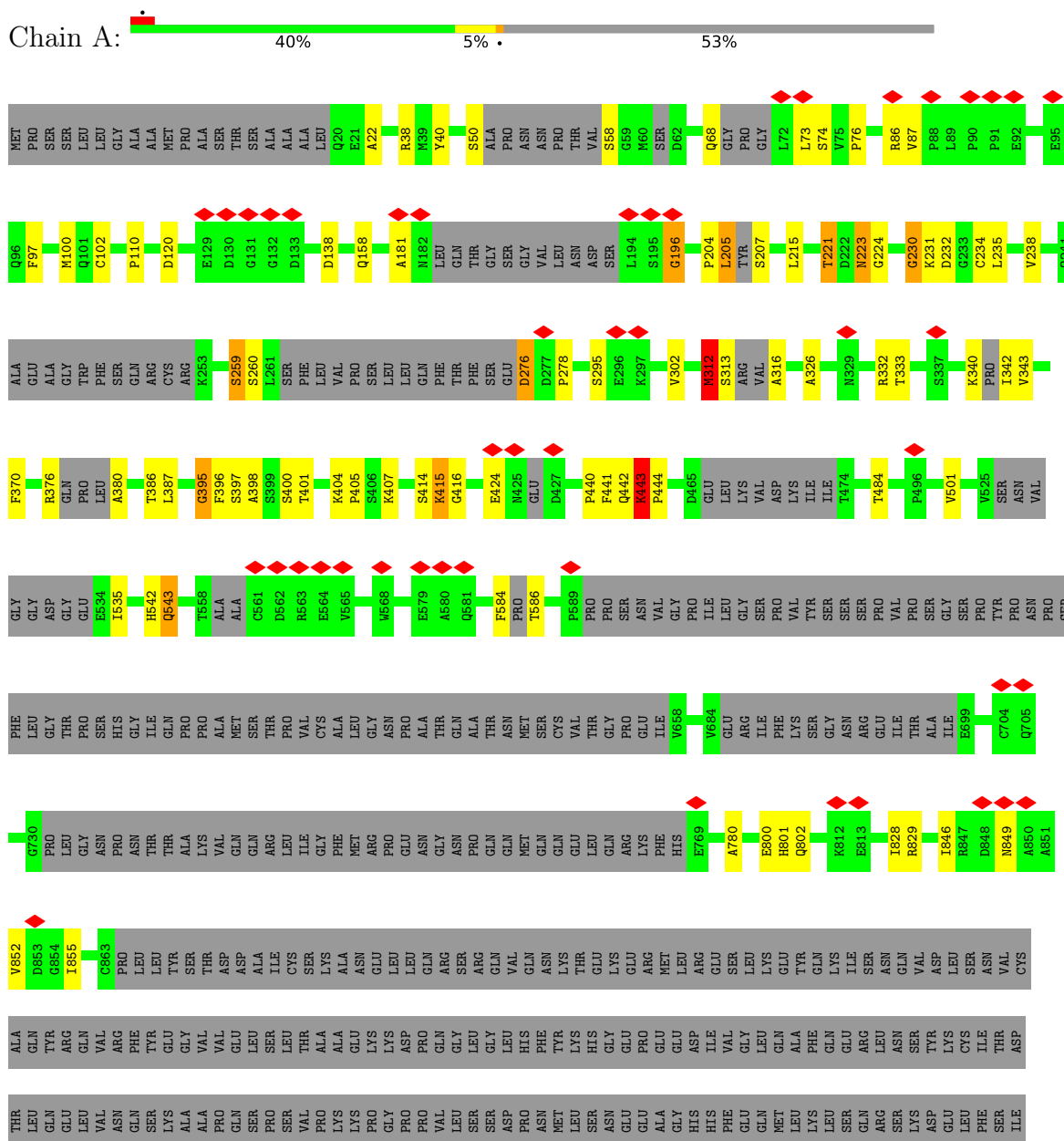
- Molecule 7 is a protein called Nucleoporin NUP188 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	J	1256	Total	C	N	O	0	0
			6213	3701	1256	1256		
7	V	1256	Total	C	N	O	0	0
			6213	3701	1256	1256		

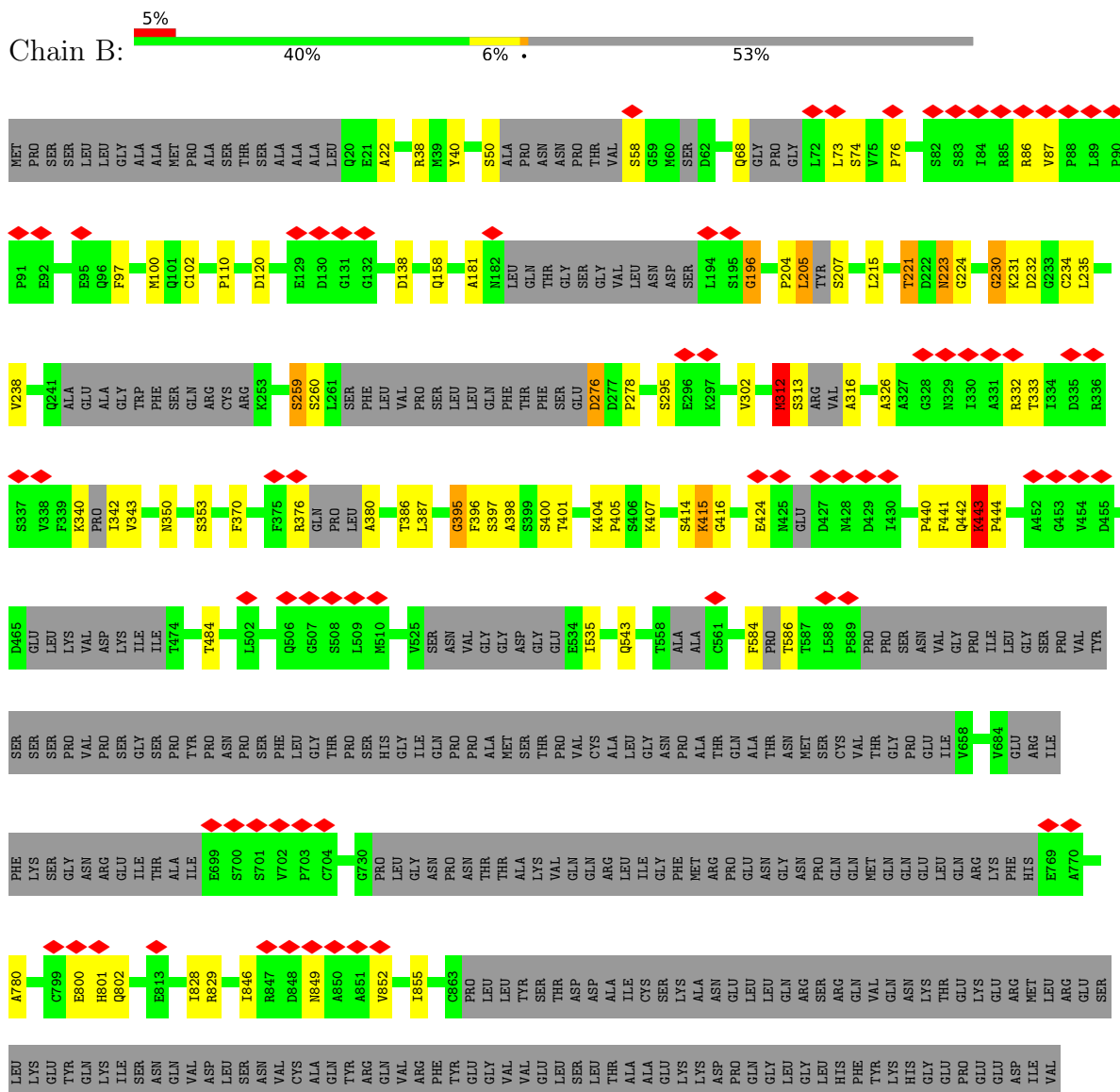
3 Residue-property plots

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 Nup155

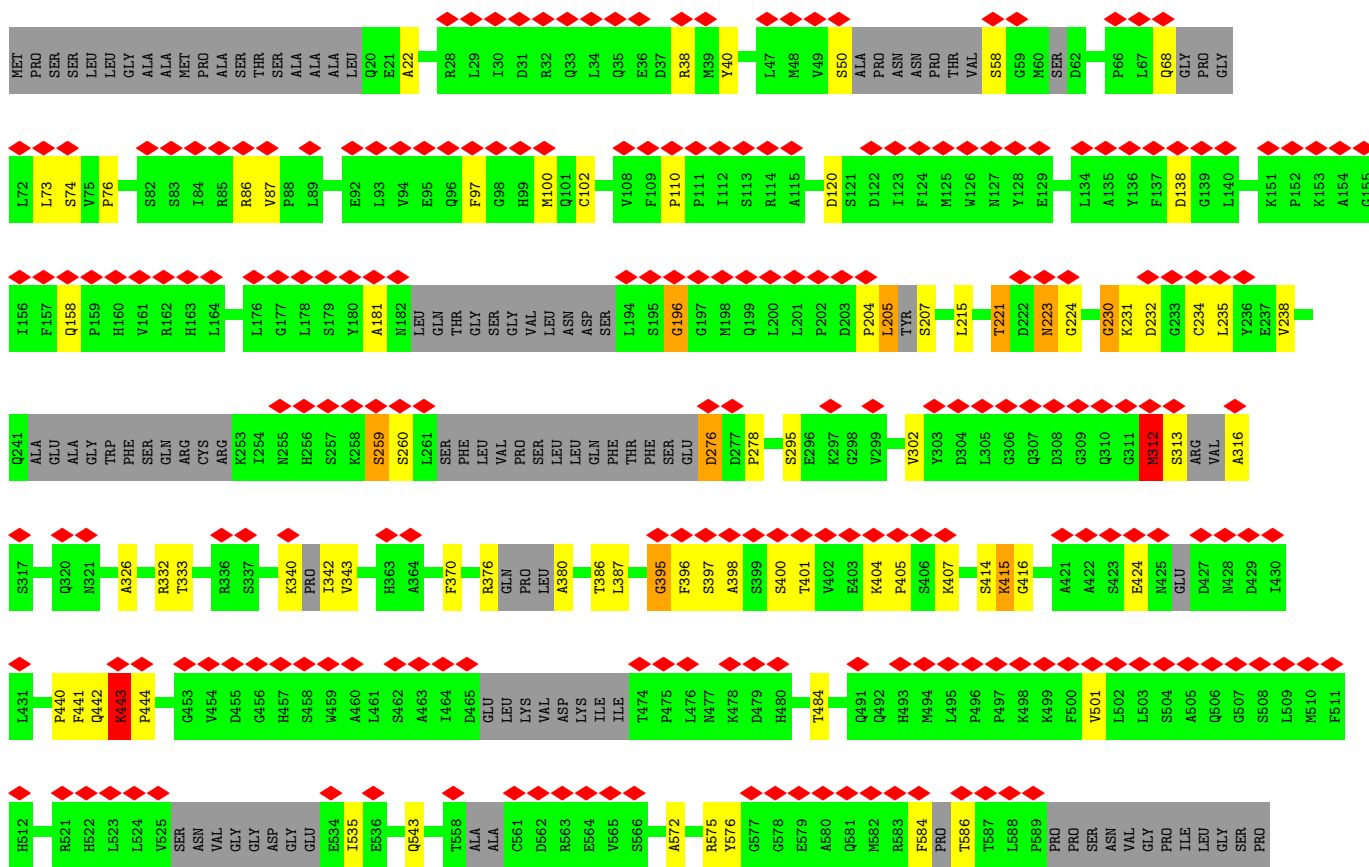


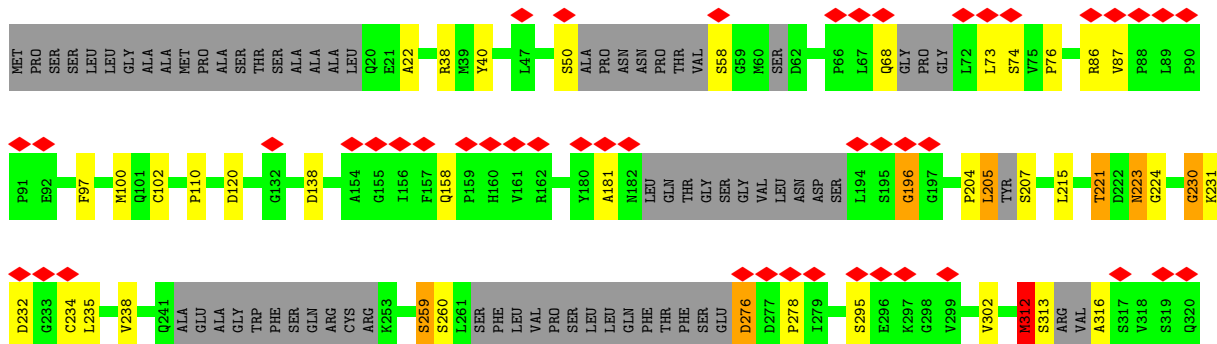
- Molecule 1: Nuclear pore complex protein Nup155

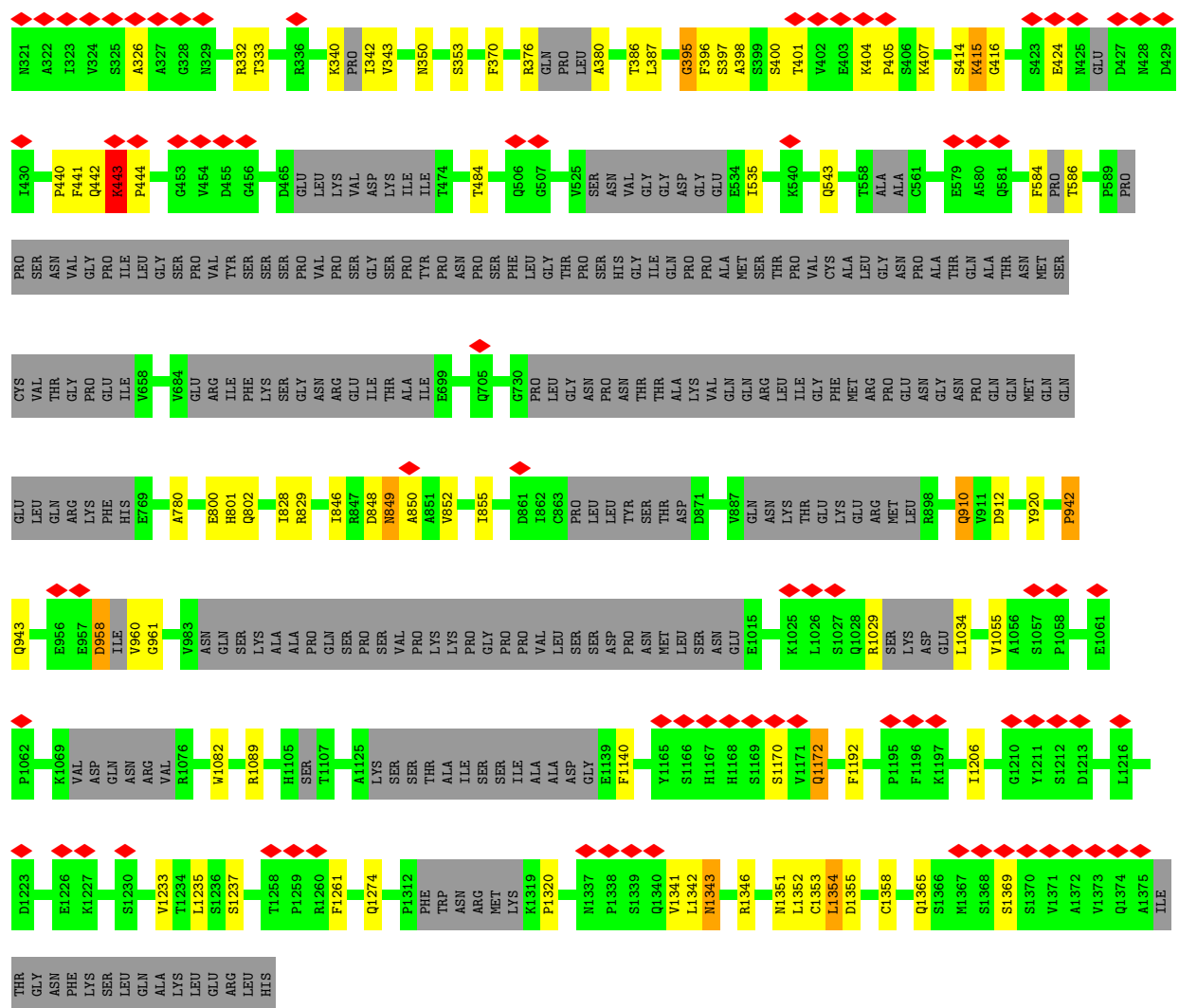




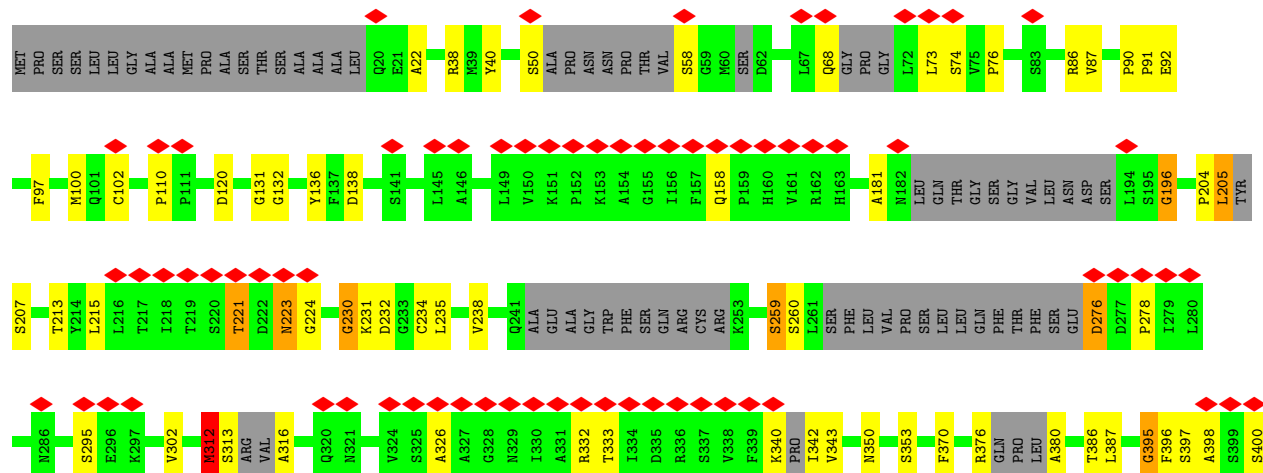
- Molecule 1: Nuclear pore complex protein Nup155

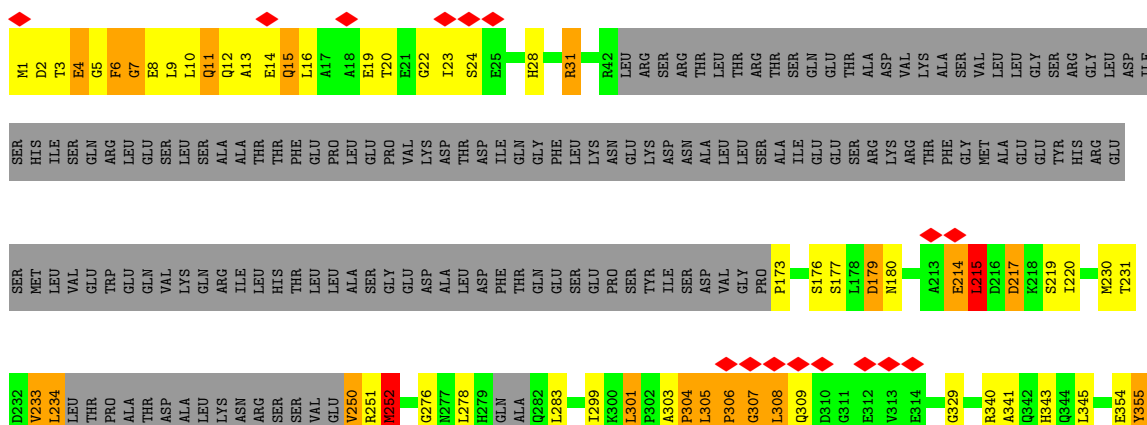


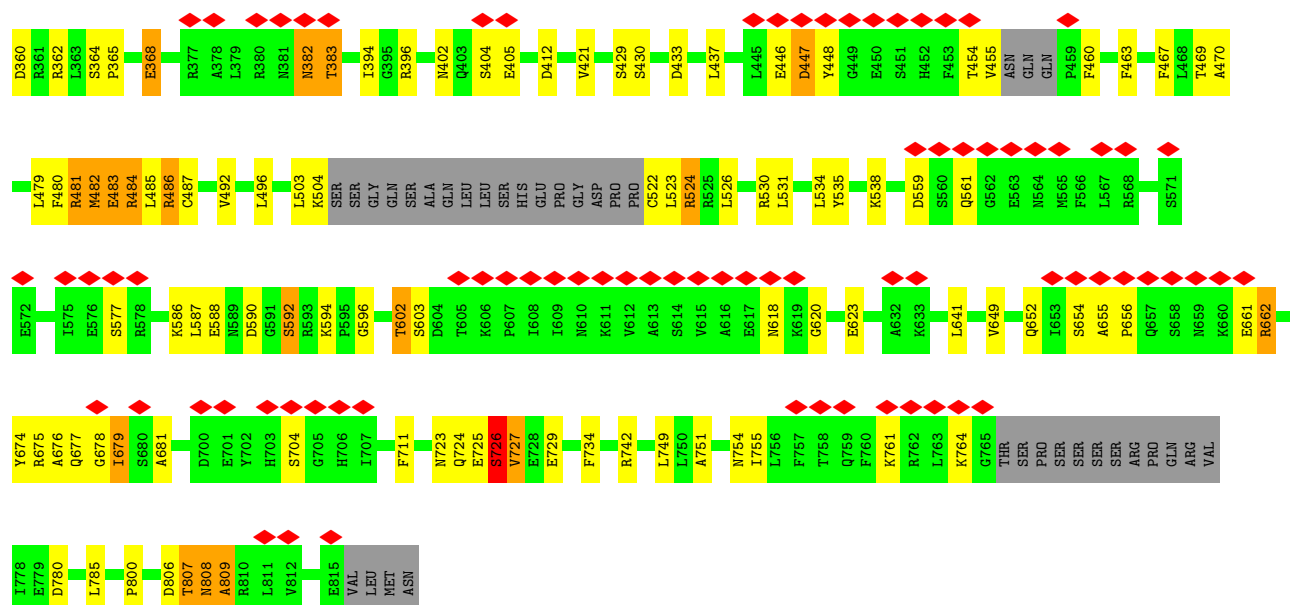




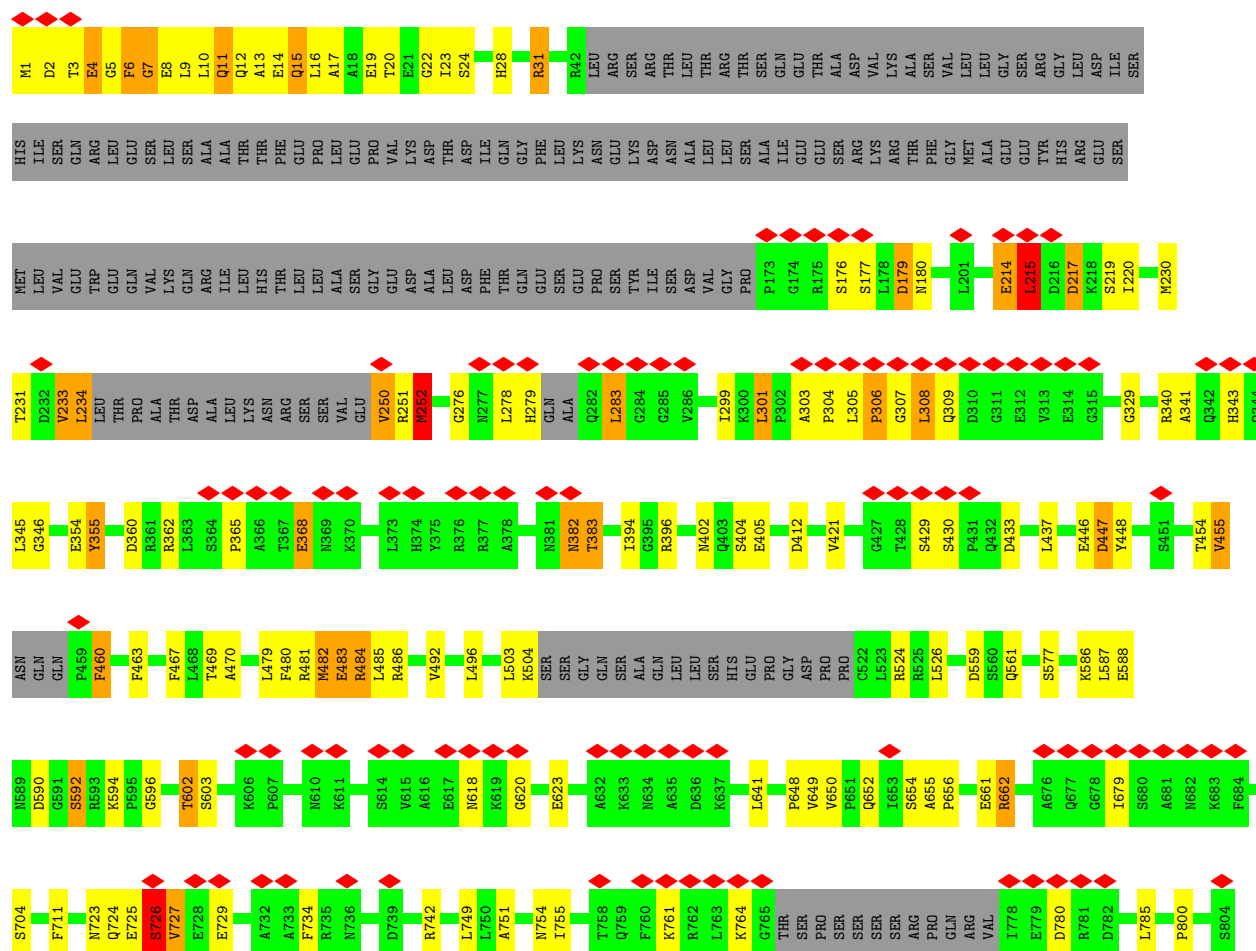
• Molecule 1: Nuclear pore complex protein Nup155

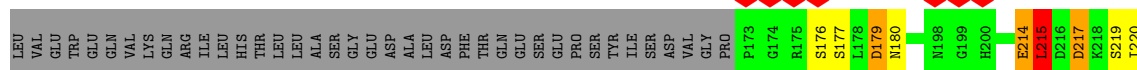


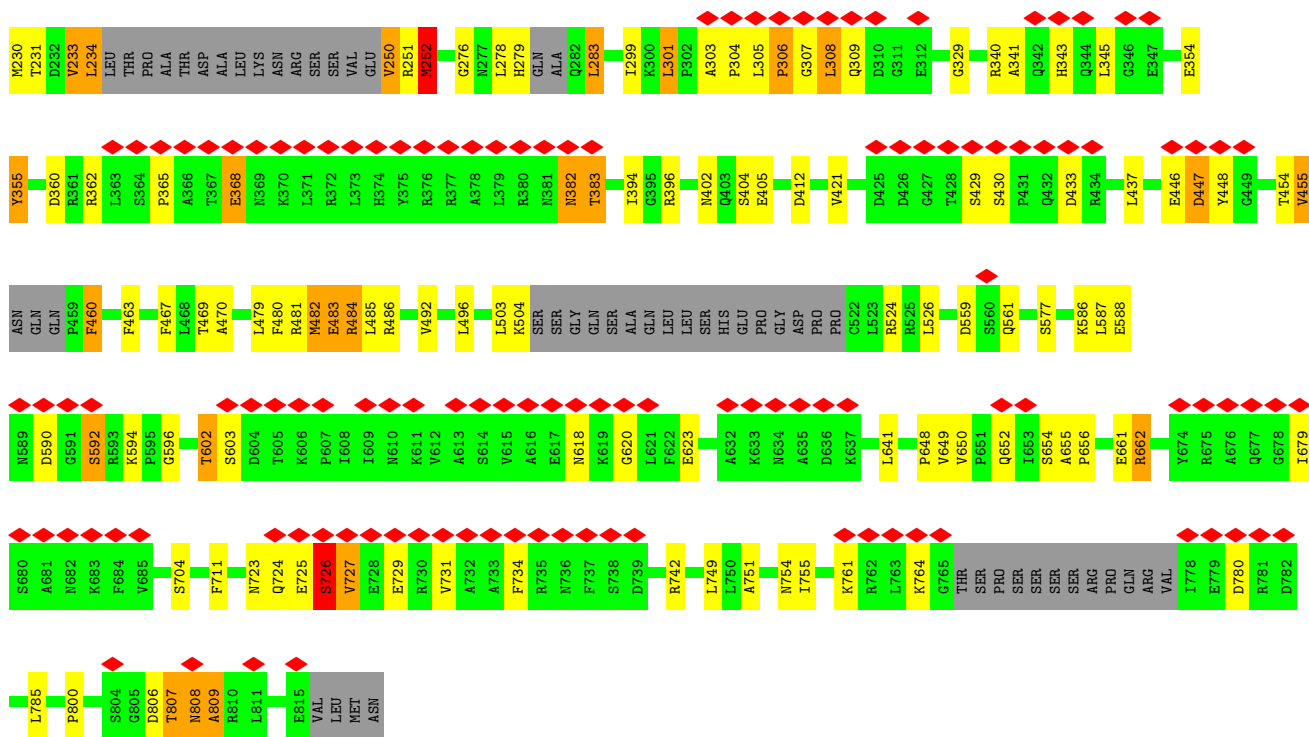




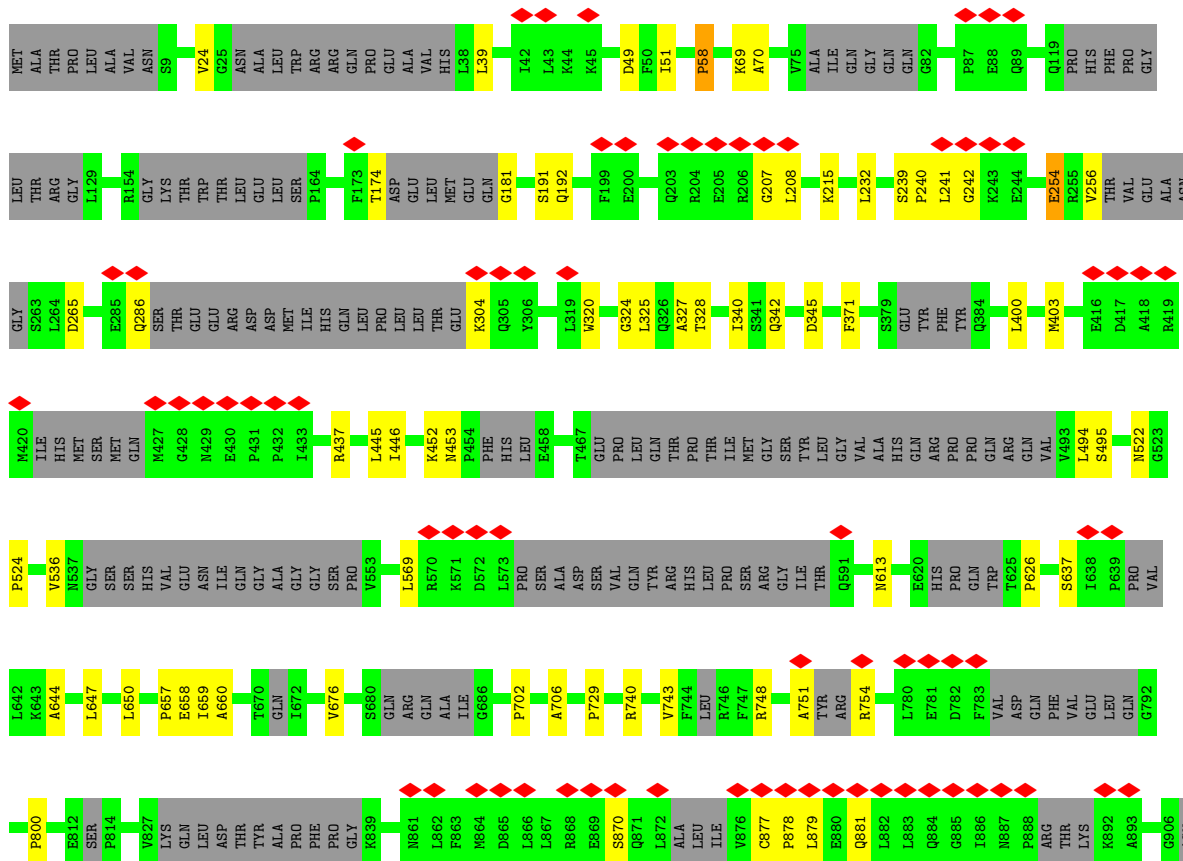
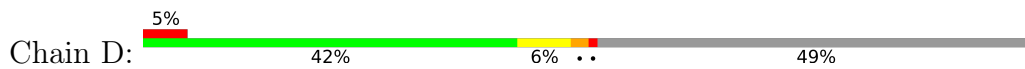
• Molecule 2: Nuclear pore complex protein Nup93



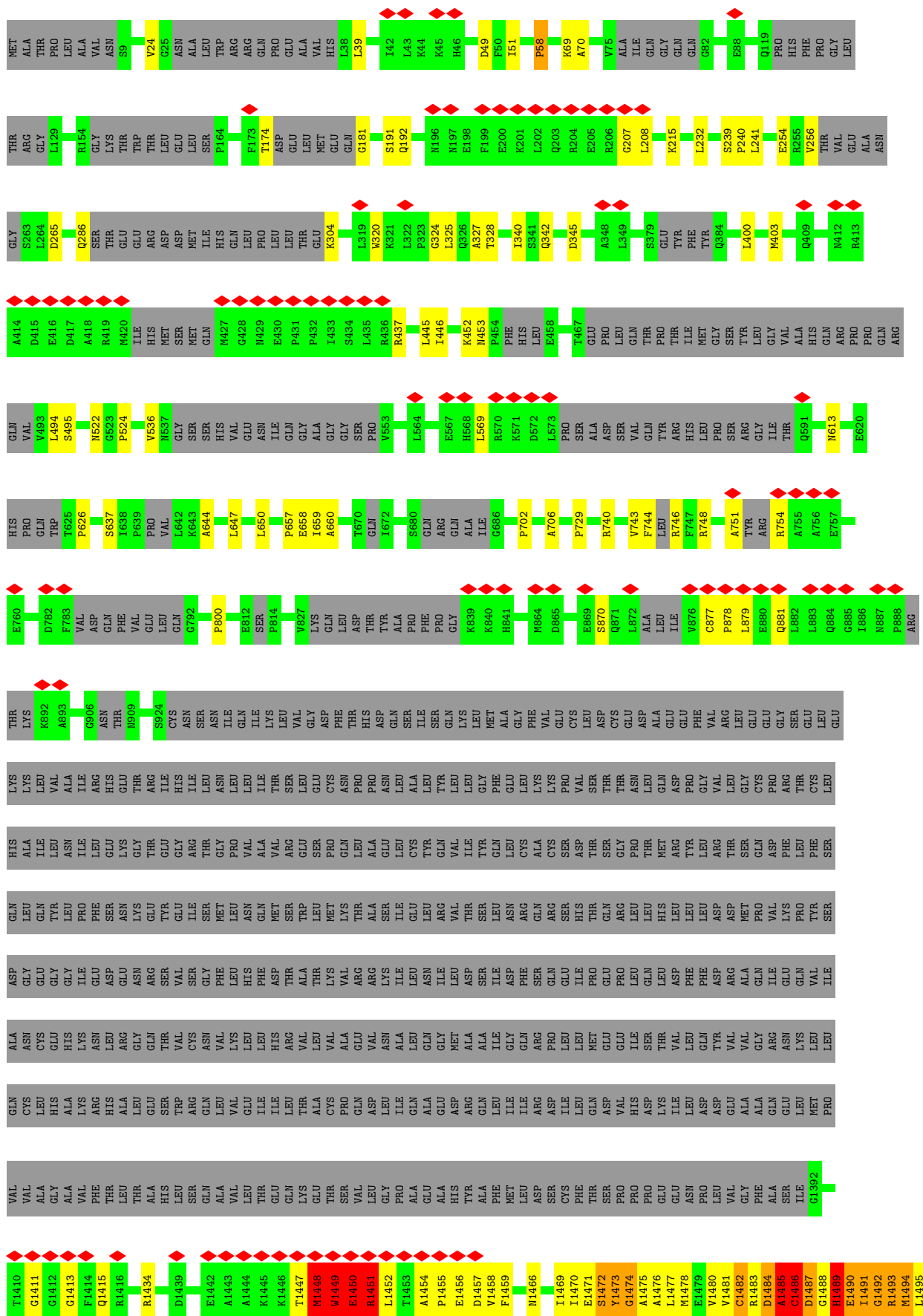




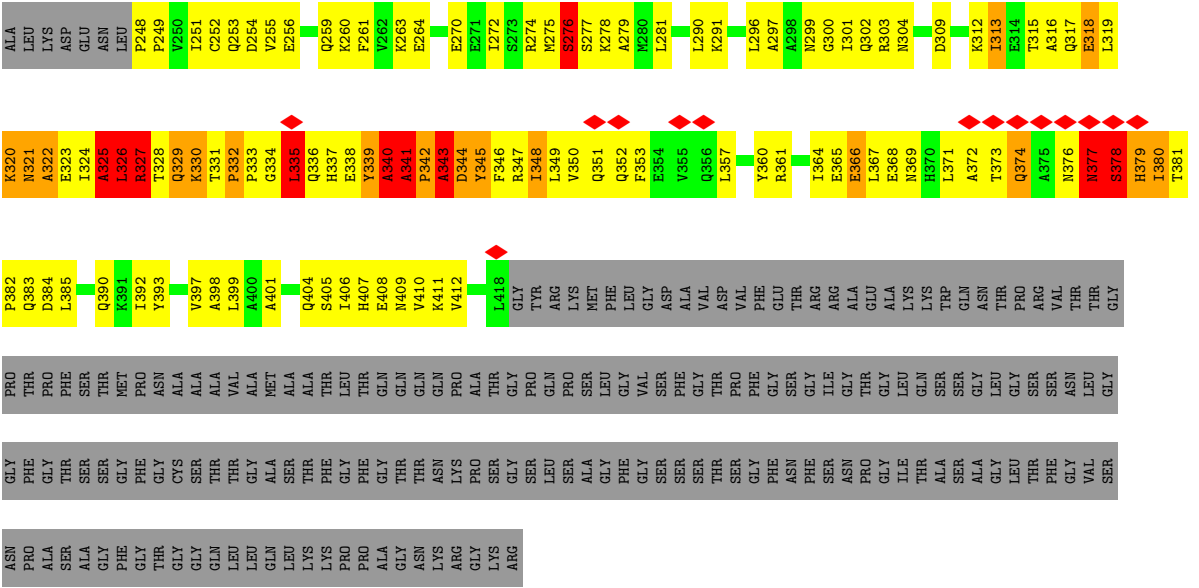
- Molecule 3: Nuclear pore complex protein Nup205



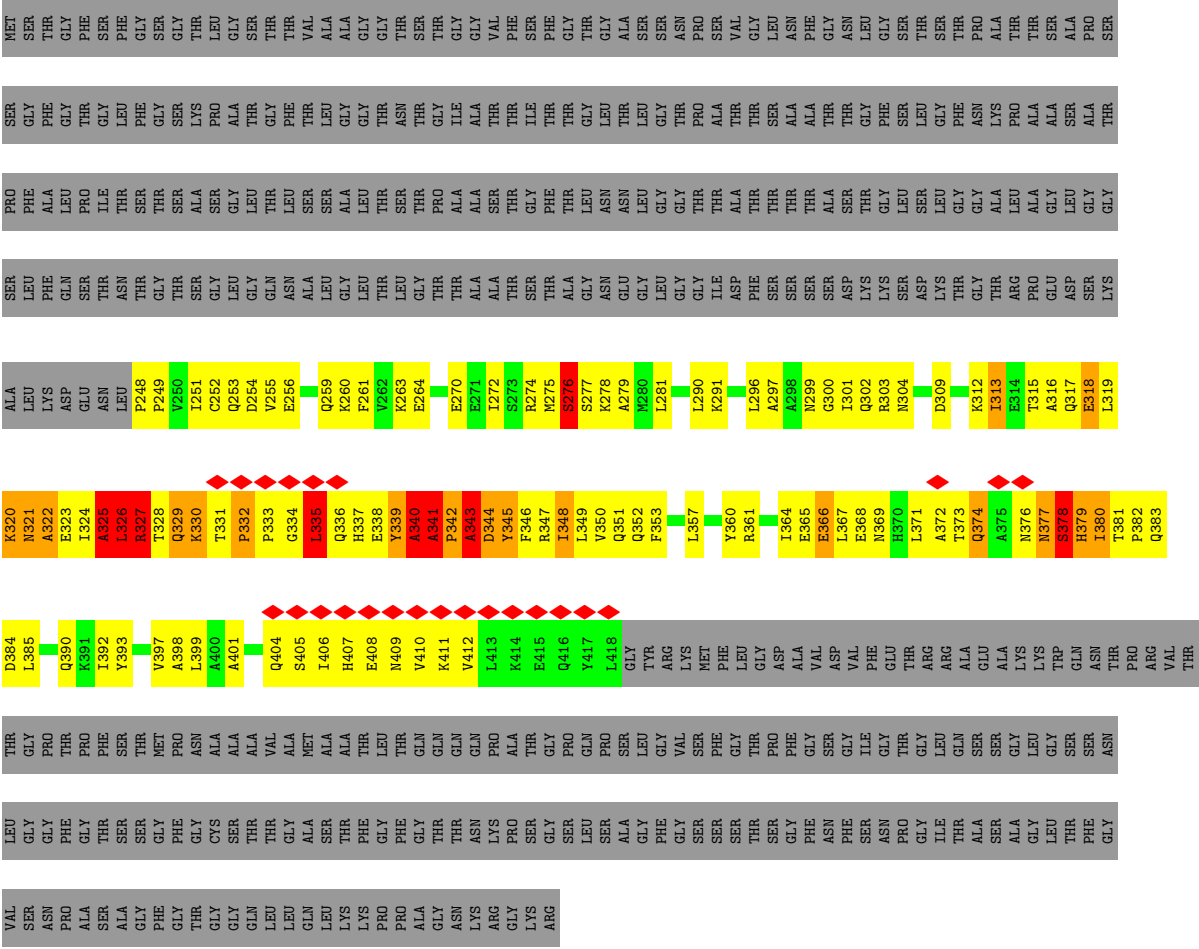




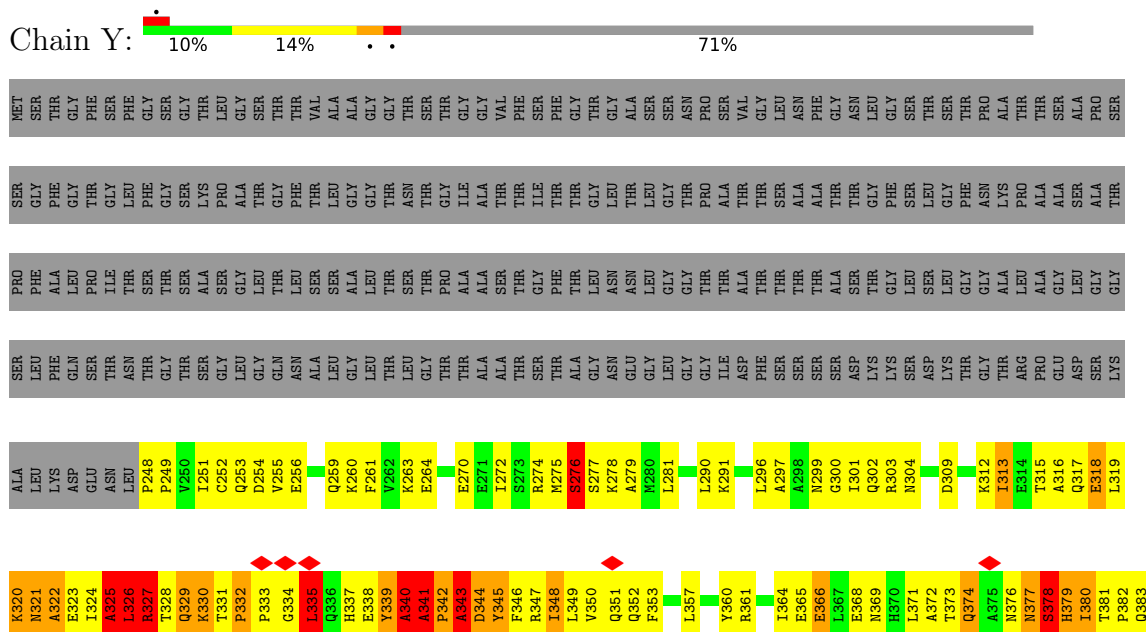


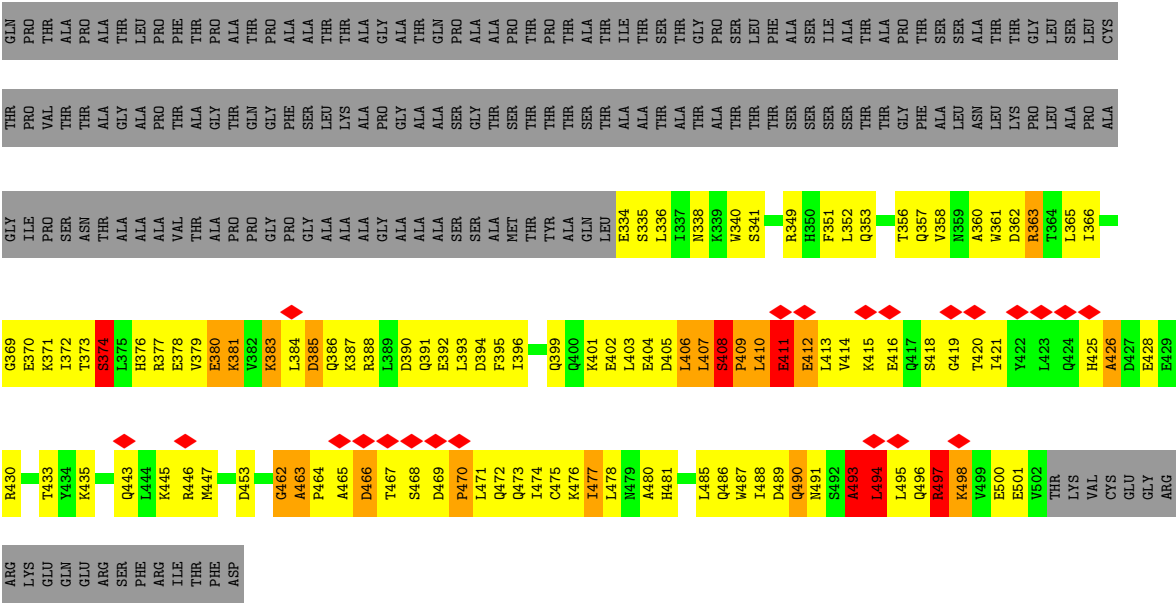


• Molecule 5: Nucleoporin p58/p45

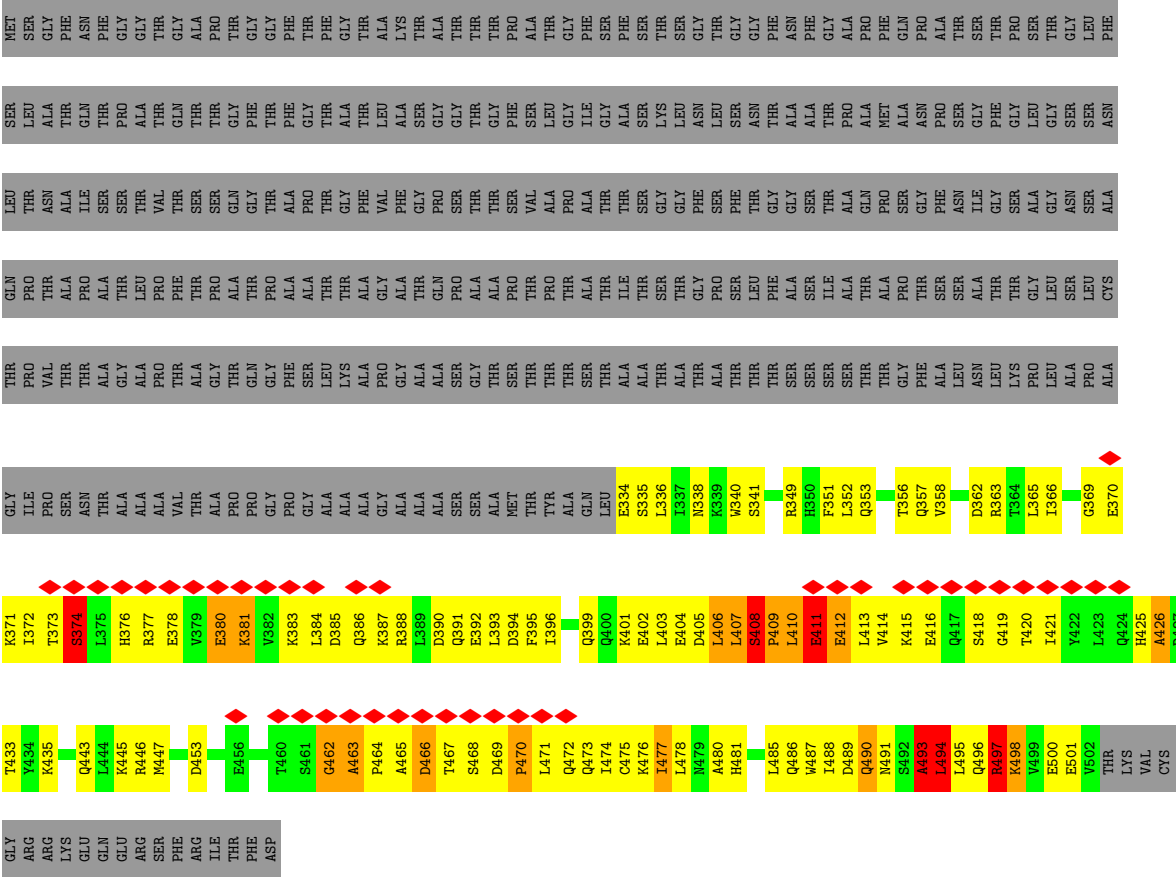


• Molecule 5: Nucleoporin p58/p45



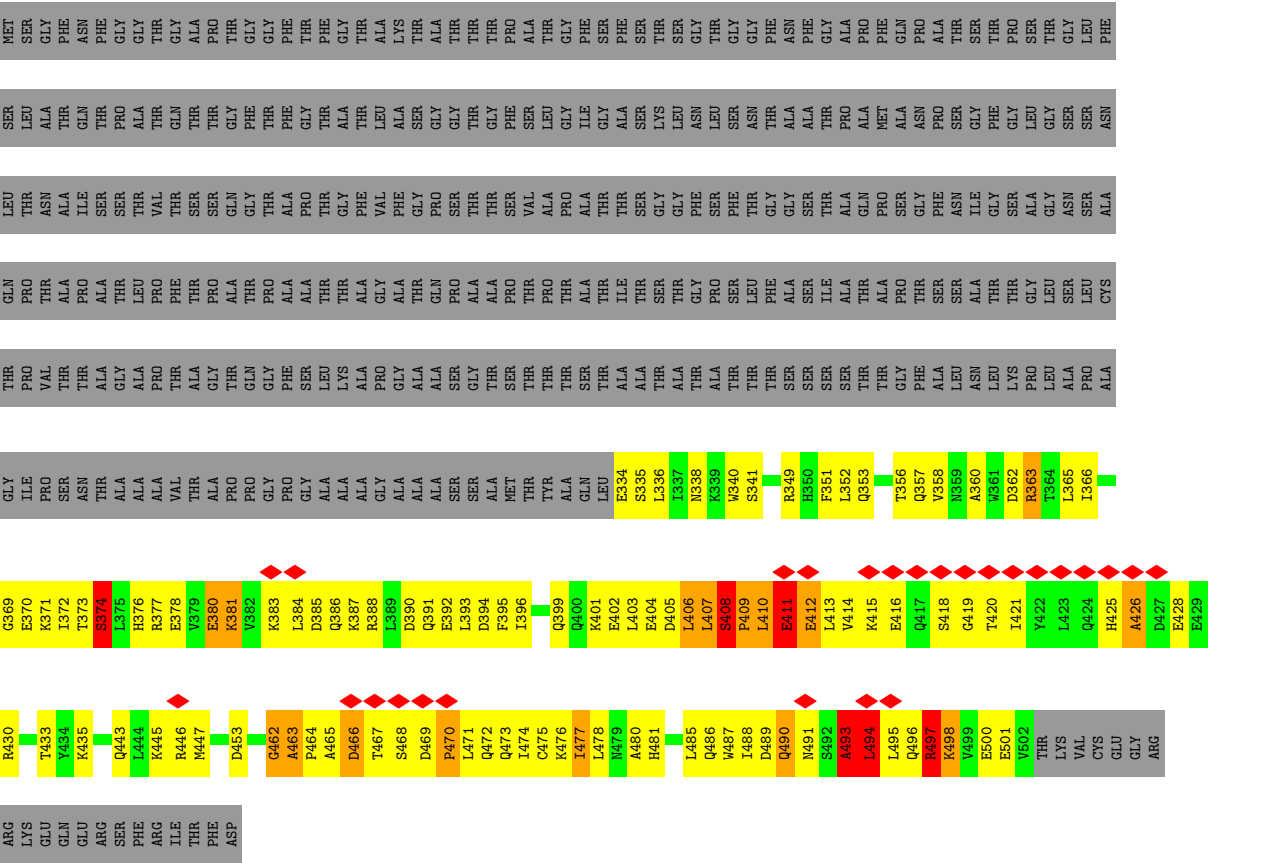


• Molecule 6: Nuclear pore glycoprotein p62

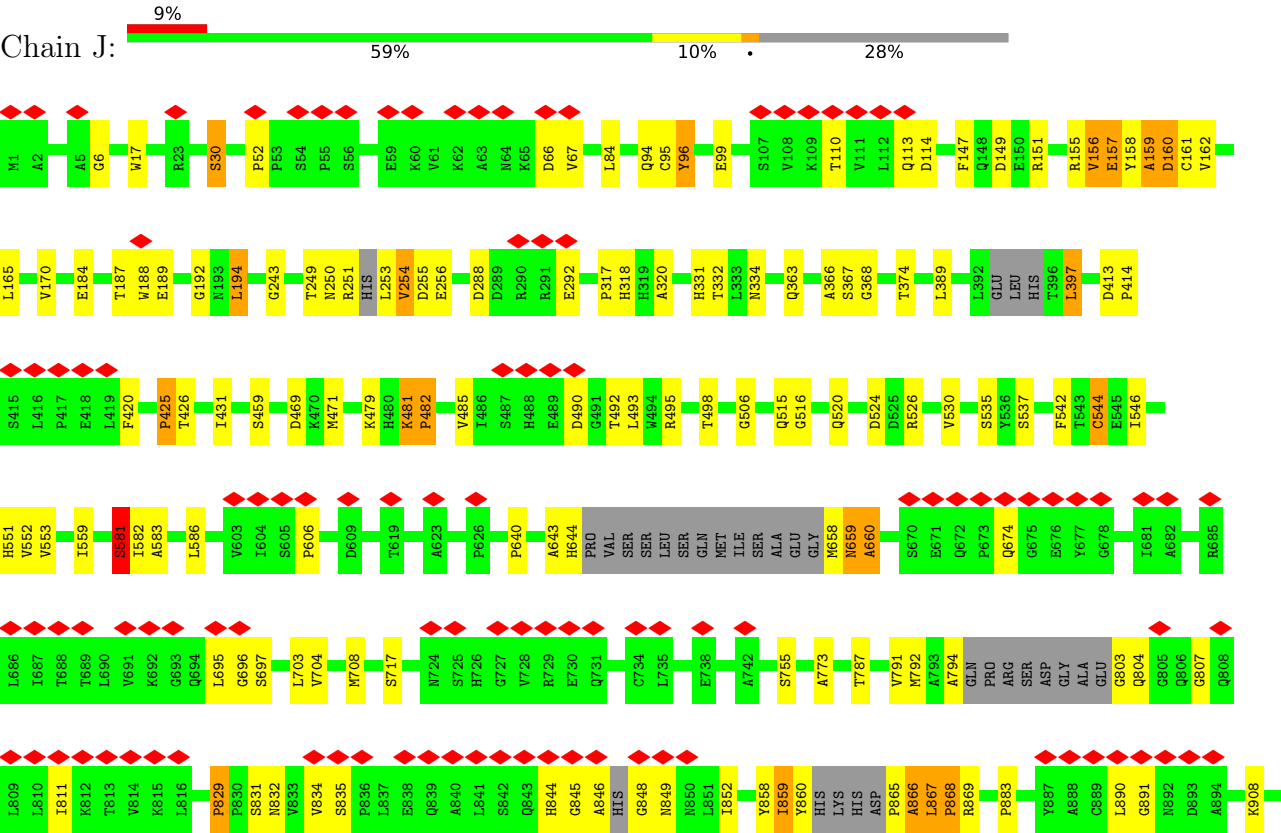


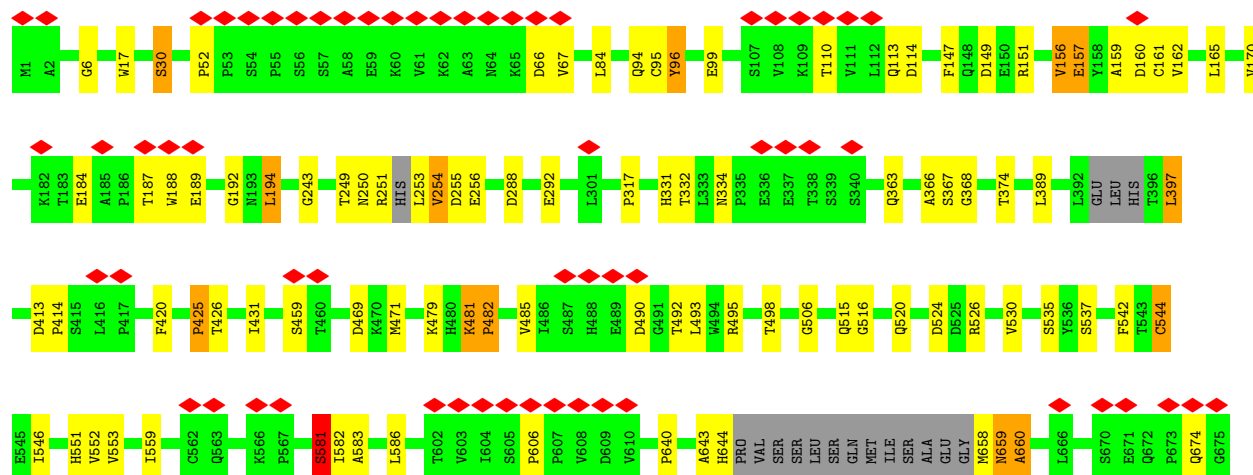
• Molecule 6: Nuclear pore glycoprotein p62





● Molecule 7: Nucleoporin NUP188 homolog







4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, Not provided	
Number of subtomograms used	8400	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 ($e^-/\text{\AA}^2$)	3	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	315.784	Depositor
Minimum map value	0.000	Depositor
Average map value	1.328	Depositor
Map value standard deviation	10.659	Depositor
Recommended contour level	36.6	Depositor
Map size ($\text{\AA}$)	964.8, 964.8, 964.8	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	6.7, 6.7, 6.7	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	1.57	1/3195 (0.0%)	1.85	64/4421 (1.4%)
1	B	1.57	1/3195 (0.0%)	1.85	63/4421 (1.4%)
1	E	1.56	1/5338 (0.0%)	1.82	91/7399 (1.2%)
1	K	1.56	1/5338 (0.0%)	1.82	92/7399 (1.2%)
1	Q	1.56	1/5338 (0.0%)	1.81	90/7399 (1.2%)
1	W	1.56	1/5338 (0.0%)	1.82	91/7399 (1.2%)
2	C	1.86	32/3143 (1.0%)	2.23	155/4369 (3.5%)
2	I	1.86	32/3143 (1.0%)	2.23	156/4369 (3.6%)
2	O	1.86	32/3143 (1.0%)	2.23	157/4369 (3.6%)
2	U	1.86	31/3143 (1.0%)	2.23	155/4369 (3.5%)
3	D	2.03	103/5066 (2.0%)	2.99	296/7020 (4.2%)
3	P	2.03	101/5066 (2.0%)	2.99	292/7020 (4.2%)
4	F	6.66	342/1655 (20.7%)	5.59	475/2302 (20.6%)
4	L	6.65	342/1655 (20.7%)	5.59	478/2302 (20.8%)
4	R	6.66	341/1655 (20.6%)	5.59	477/2302 (20.7%)
4	X	6.66	341/1655 (20.6%)	5.59	477/2302 (20.7%)
5	G	6.74	153/852 (18.0%)	5.79	240/1190 (20.2%)
5	M	6.69	154/852 (18.1%)	5.78	242/1190 (20.3%)
5	S	6.69	152/852 (17.8%)	5.78	240/1190 (20.2%)
5	Y	6.69	154/852 (18.1%)	5.78	242/1190 (20.3%)
6	H	5.53	133/841 (15.8%)	5.00	246/1174 (21.0%)
6	N	5.53	134/841 (15.9%)	5.00	247/1174 (21.0%)
6	T	5.52	133/841 (15.8%)	5.00	246/1174 (21.0%)
6	Z	5.53	134/841 (15.9%)	5.00	248/1174 (21.1%)
7	J	1.56	4/6201 (0.1%)	1.96	159/8622 (1.8%)
7	V	1.56	4/6201 (0.1%)	1.96	160/8622 (1.9%)
All	All	3.10	2858/76240 (3.7%)	3.03	5879/105862 (5.6%)

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	A	0	1
1	B	0	1
1	E	0	1
1	K	0	1
1	Q	0	1
1	W	0	1
2	C	1	4
2	I	1	4
2	O	1	4
2	U	1	4
3	D	0	21
3	P	0	20
4	F	10	40
4	L	10	40
4	R	10	40
4	X	10	40
5	G	9	10
5	M	9	10
5	S	9	10
5	Y	9	10
6	H	5	5
6	N	5	5
6	T	5	4
6	Z	5	5
7	J	0	3
7	V	0	3
All	All	100	288

The worst 5 of 2858 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	379	HIS	CA-C	72.10	2.49	1.52
5	S	379	HIS	CA-C	72.09	2.49	1.52
5	G	379	HIS	CA-C	72.06	2.49	1.52
5	Y	379	HIS	CA-C	72.03	2.49	1.52
4	F	453	TYR	CA-C	70.43	2.47	1.52

The worst 5 of 5879 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Y	341	ALA	CA-C-N	-52.59	63.45	119.19
5	Y	341	ALA	C-N-CA	-52.59	63.45	119.19
5	S	341	ALA	CA-C-N	-52.57	63.47	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	S	341	ALA	C-N-CA	-52.57	63.47	119.19
5	G	341	ALA	CA-C-N	-52.52	63.52	119.19

5 of 100 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	11	GLN	CA
4	F	200	THR	CA
4	F	210	VAL	CA
4	F	211	GLU	CA
4	F	305	ASP	CA

5 of 288 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	259	SER	Mainchain
1	B	259	SER	Mainchain
2	C	4	GLU	Mainchain
2	C	6	PHE	Mainchain
2	C	7	GLY	Mainchain

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	A	3214	0	1424	27	0
1	B	3214	0	1424	28	0
1	E	5366	0	2364	69	0
1	K	5366	0	2360	82	0
1	Q	5366	0	2364	73	0
1	W	5366	0	2364	65	0
2	C	3152	0	1403	163	0
2	I	3152	0	1408	37	0
2	O	3152	0	1405	94	0
2	U	3152	0	1408	37	0
3	D	5094	0	2272	130	0
3	P	5094	0	2273	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	1658	0	715	180	0
4	L	1658	0	715	178	0
4	R	1658	0	714	181	0
4	X	1658	0	715	179	0
5	G	853	0	384	58	0
5	M	853	0	384	58	0
5	S	853	0	384	60	0
5	Y	853	0	384	58	0
6	H	842	0	365	38	0
6	N	842	0	365	41	0
6	T	842	0	365	39	0
6	Z	842	0	365	39	0
7	J	6213	0	2770	91	0
7	V	6213	0	2770	88	0
All	All	76526	0	33864	1962	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 18.

The worst 5 of 1962 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)
5:S:366:GLU:CA	5:S:366:GLU:CB	1.76	1.64
4:F:451:GLU:CA	4:F:451:GLU:CB	1.77	1.63
6:N:490:GLN:CA	6:N:490:GLN:CB	1.75	1.62
4:F:454:TYR:CA	4:F:454:TYR:CB	1.77	1.62
4:X:447:VAL:CA	4:X:447:VAL:CB	1.78	1.62

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	A	612/1391 (44%)	562 (92%)	38 (6%)	12 (2%)	6	31
1	B	612/1391 (44%)	562 (92%)	38 (6%)	12 (2%)	6	31
1	E	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	K	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	Q	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
1	W	1027/1391 (74%)	947 (92%)	58 (6%)	22 (2%)	5	30
2	C	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	I	618/819 (76%)	516 (84%)	58 (9%)	44 (7%)	1	11
2	O	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
2	U	618/819 (76%)	516 (84%)	59 (10%)	43 (7%)	1	11
3	D	972/2012 (48%)	899 (92%)	59 (6%)	14 (1%)	9	40
3	P	972/2012 (48%)	899 (92%)	59 (6%)	14 (1%)	9	40
4	F	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	L	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	R	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
4	X	329/507 (65%)	286 (87%)	21 (6%)	22 (7%)	1	12
5	G	169/599 (28%)	153 (90%)	10 (6%)	6 (4%)	2	20
5	M	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	S	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
5	Y	169/599 (28%)	153 (90%)	11 (6%)	5 (3%)	3	23
6	H	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	N	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	T	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
6	Z	167/522 (32%)	152 (91%)	8 (5%)	7 (4%)	2	17
7	J	1232/1749 (70%)	1111 (90%)	75 (6%)	46 (4%)	2	20
7	V	1232/1749 (70%)	1111 (90%)	75 (6%)	46 (4%)	2	20
All	All	14872/25656 (58%)	13360 (90%)	970 (6%)	542 (4%)	4	20

5 of 542 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	332	ARG
1	A	443	LYS
1	A	543	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	802	GLN
1	B	332	ARG

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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
4	F	6
4	L	6
4	R	6
4	X	6
2	C	3

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
2	I	3
2	O	3
2	U	3
5	M	3
5	Y	3
5	G	3
5	S	3
6	H	3
6	N	3
6	T	3
6	Z	3

The worst 5 of 60 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	483:GLU	C	484:ARG	N	4.02
1	I	483:GLU	C	484:ARG	N	4.02
1	O	483:GLU	C	484:ARG	N	4.02
1	U	483:GLU	C	484:ARG	N	4.02
1	C	447:ASP	C	448:TYR	N	3.63

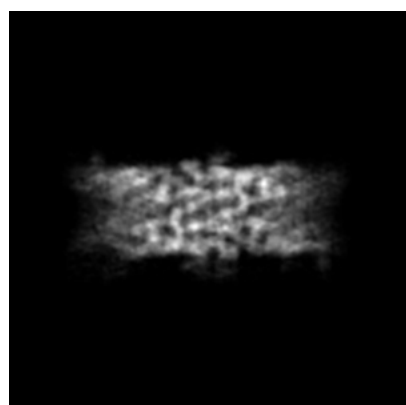
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8085. 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](#)

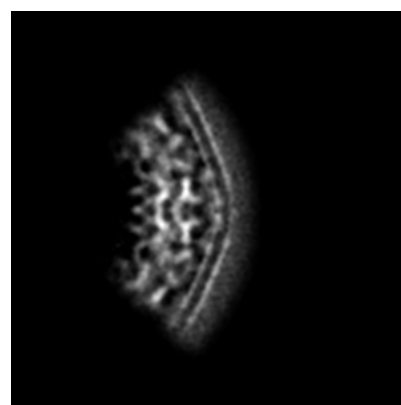
6.1.1 Primary map



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: 72



Y Index: 72

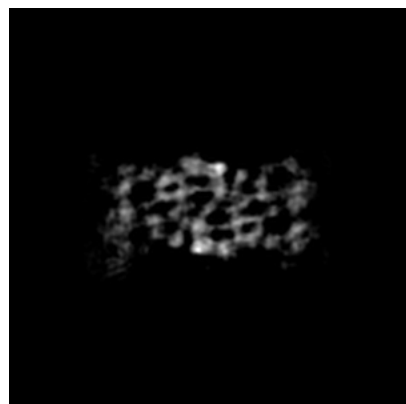


Z Index: 72

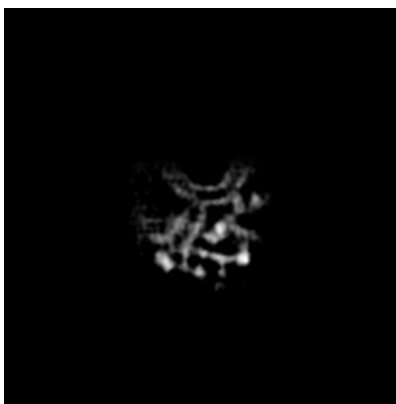
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 53



Y Index: 76

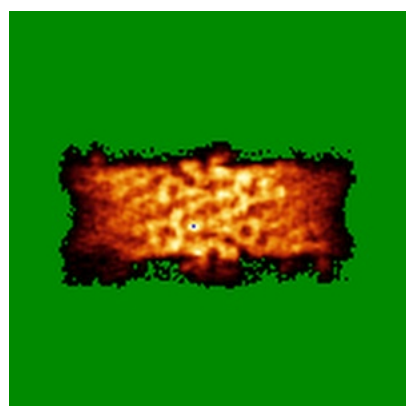


Z Index: 78

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

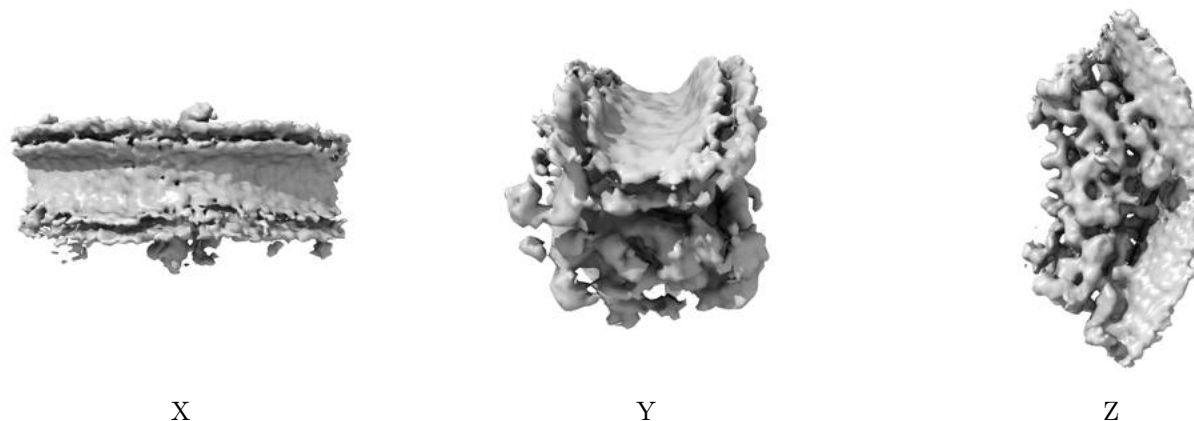


Z

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

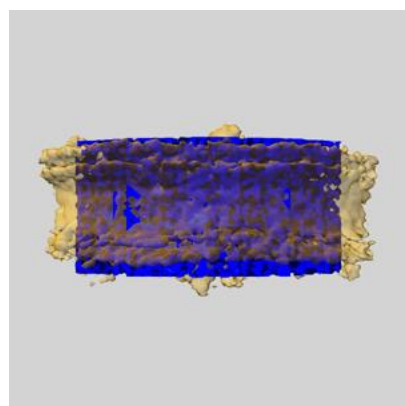
6.6 Mask visualisation [i](#)

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

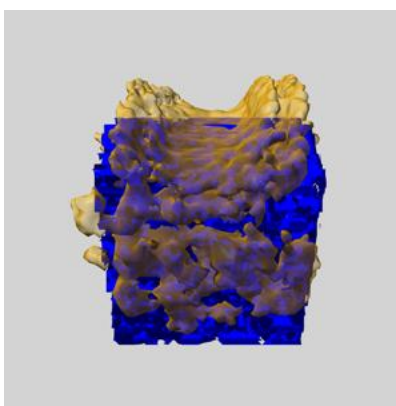
A mask typically either:

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

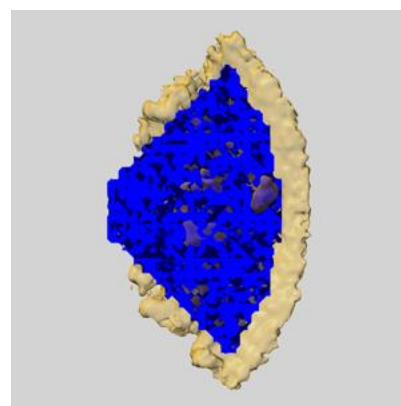
6.6.1 emd_8085_msk_1.map [i](#)



X



Y

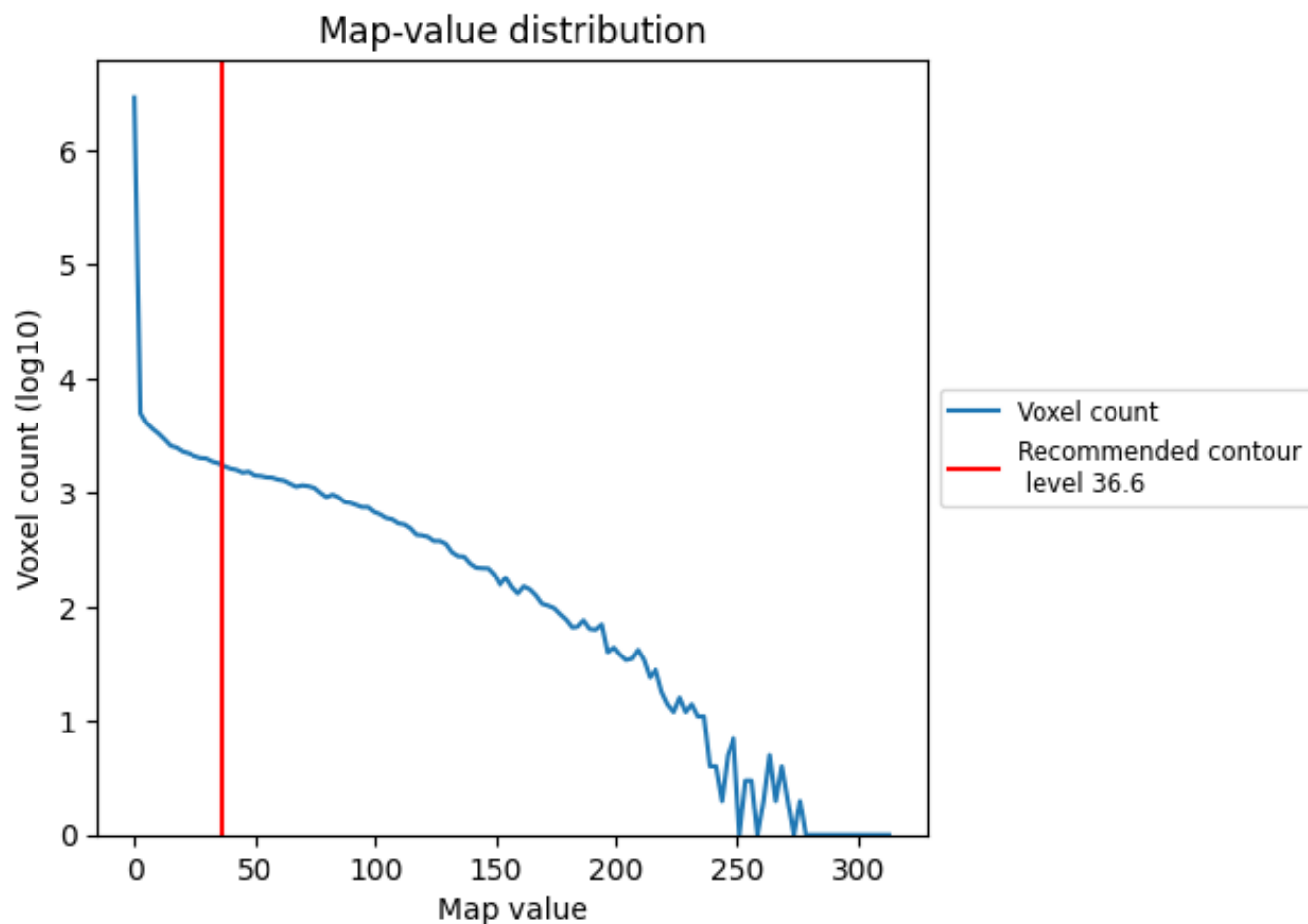


Z

7 Map analysis [i](#)

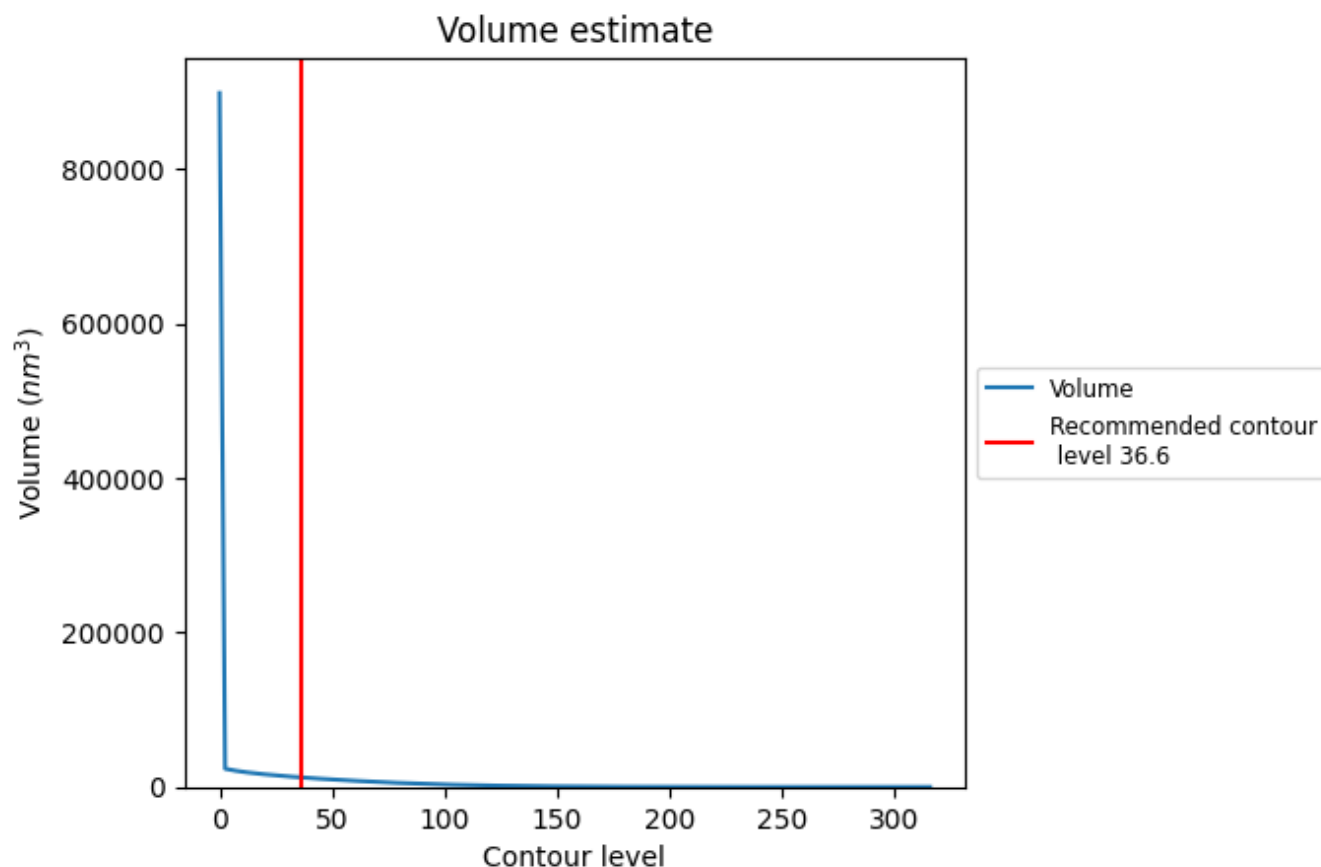
This section contains the results of statistical analysis of the map.

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.

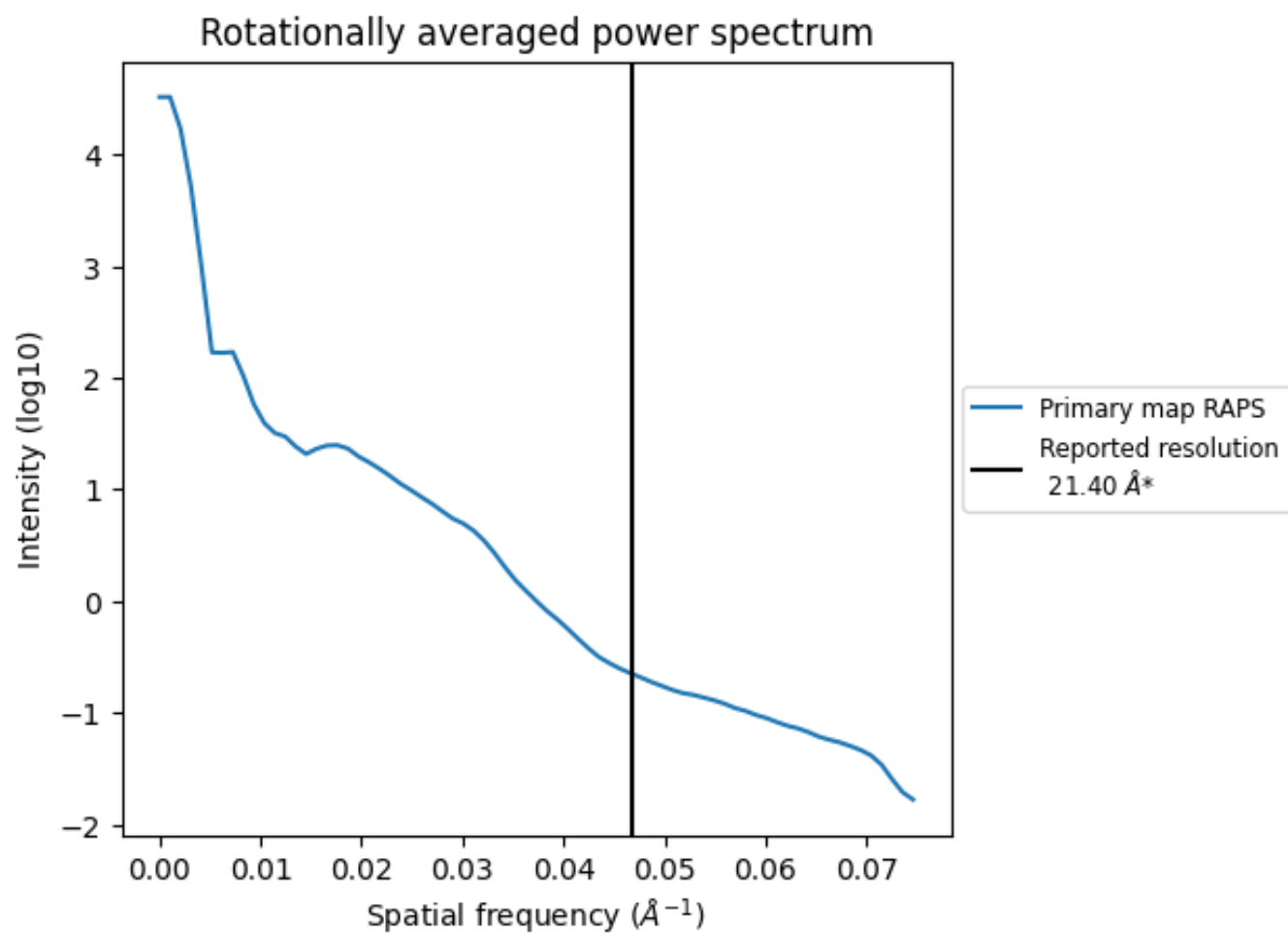
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 12255 nm^3 ; this corresponds to an approximate mass of 11070 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 0.047 Å⁻¹

8 Fourier-Shell correlation ⓘ

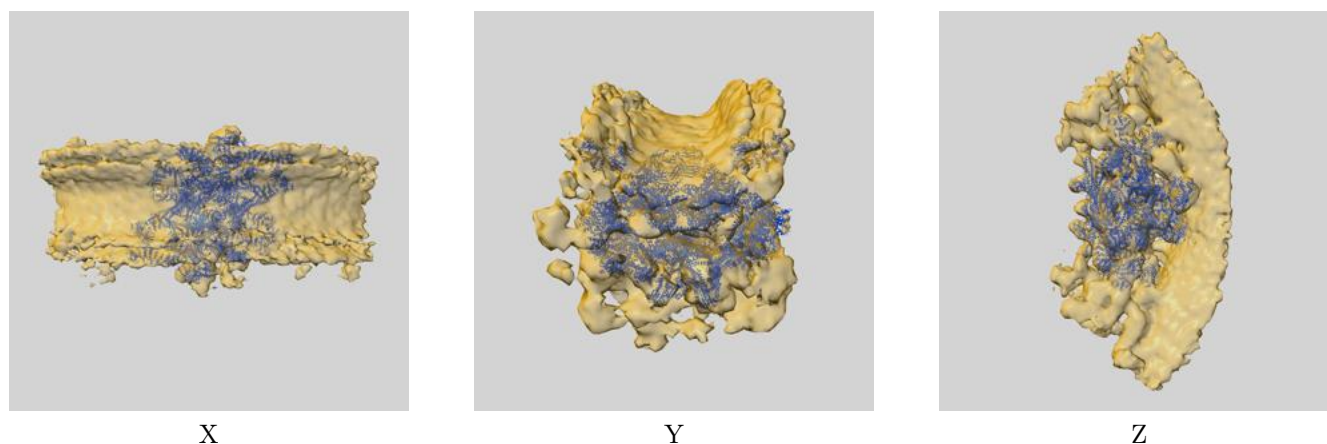
This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit ⓘ

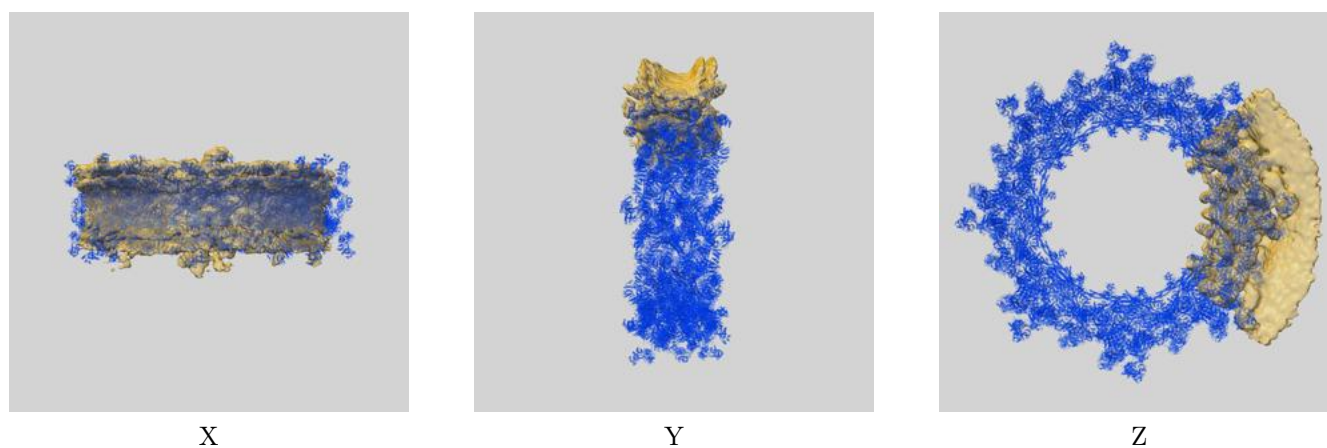
This section contains information regarding the fit between EMDB map EMD-8085 and PDB model 5IJO. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlays

9.1.1 Map-model overlay ⓘ

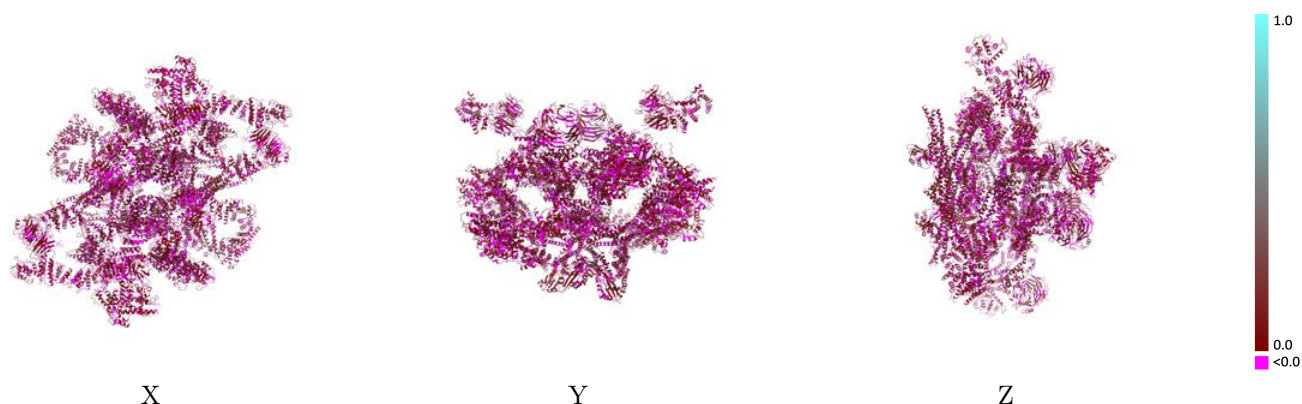


9.1.2 Map-model assembly overlay ⓘ



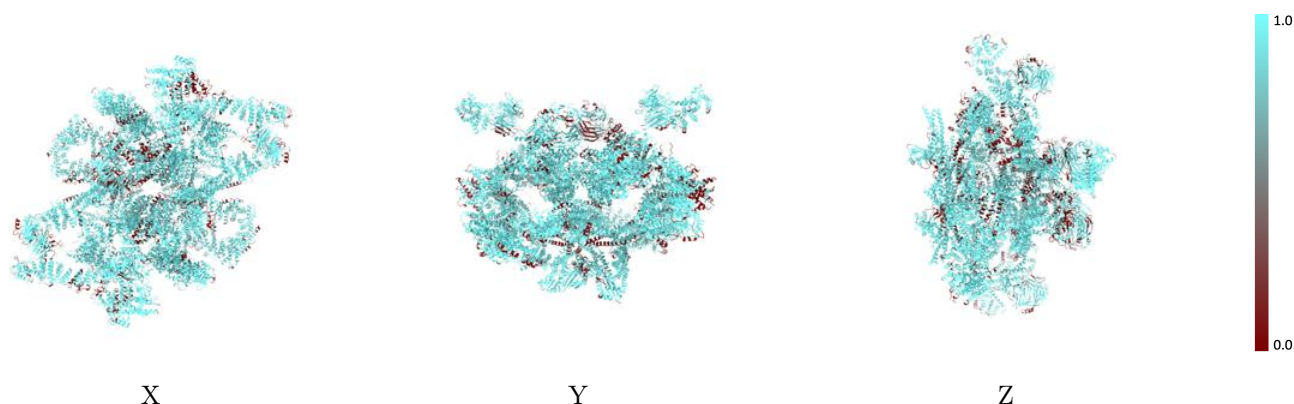
The images above show the 3D surface view of the map at the recommended contour level 36.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



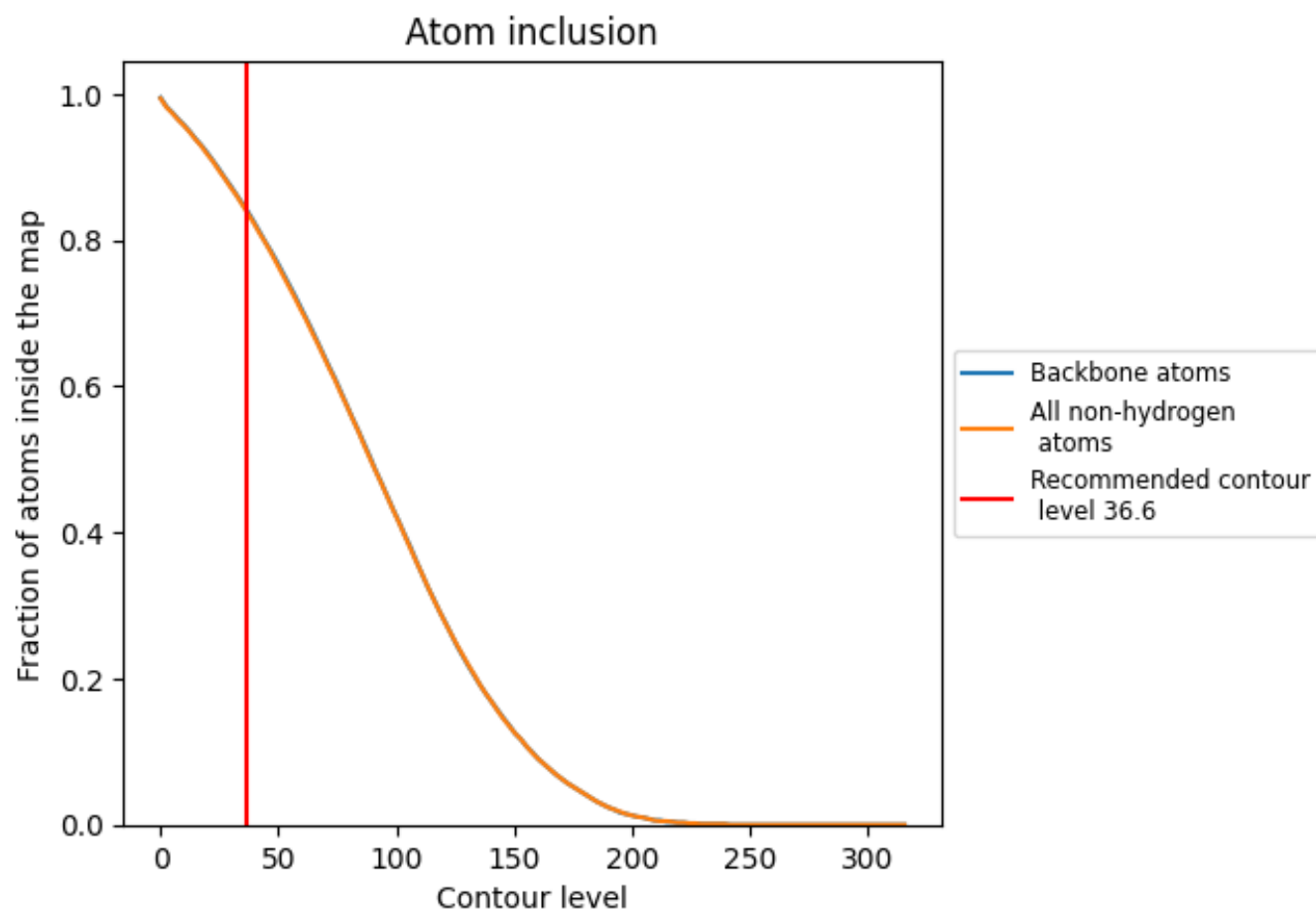
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (36.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 84% 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 (36.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8390	 0.0410
A	 0.9290	 0.0440
B	 0.8790	 0.0450
C	 0.8490	 0.0370
D	 0.8980	 0.0440
E	 0.8660	 0.0390
F	 0.8100	 0.0350
G	 0.9040	 0.0420
H	 0.7990	 0.0240
I	 0.8270	 0.0450
J	 0.8780	 0.0480
K	 0.5460	 0.0180
L	 0.7990	 0.0280
M	 0.8450	 0.0490
N	 0.8730	 0.0700
O	 0.8780	 0.0410
P	 0.8970	 0.0520
Q	 0.8810	 0.0420
R	 0.7760	 0.0280
S	 0.9330	 0.0520
T	 0.7480	 0.0290
U	 0.8000	 0.0390
V	 0.9040	 0.0470
W	 0.7750	 0.0340
X	 0.8370	 0.0380
Y	 0.9000	 0.0550
Z	 0.8490	 0.0460

