



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:19 PM UTC

PDB ID : 5A9Q / pdb_00005a9q
EMDB ID : EMD-3103
Title : Human nuclear pore complex
Authors : von Appen, A.; Kosinski, J.; Sparks, L.; Ori, A.; DiGuilio, A.; Vollmer, B.; Mackmull, M.; Banterle, N.; Parca, L.; Kastritis, P.; Buczak, K.; Mosalaganti, S.; Hagen, W.; Andres-Pons, A.; Lemke, E.A.; Bork, P.; Antonin, W.; Glavy, J.S.; Bui, K.H.; Beck, M.
Deposited on : 2015-07-22
Resolution : 23.00 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:

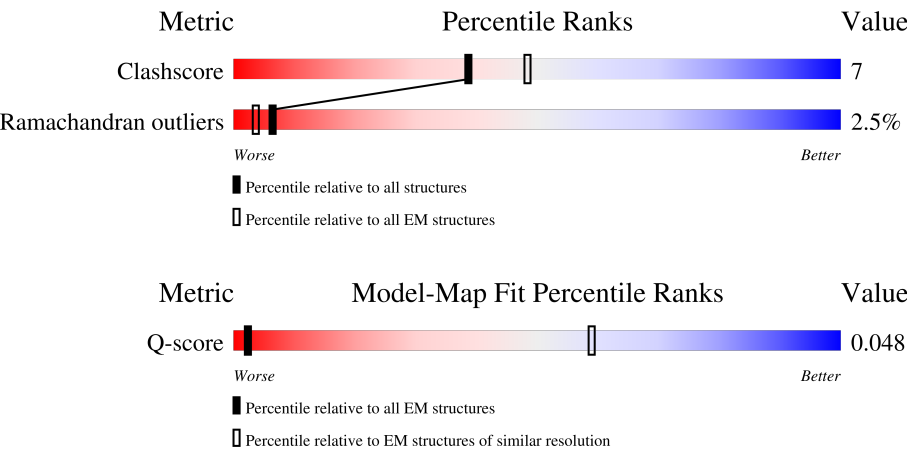
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 23.00 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.



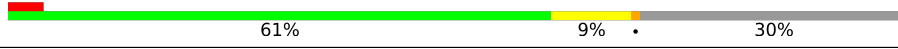
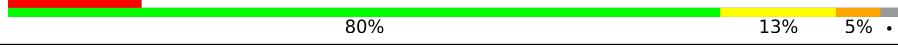
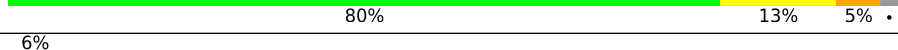
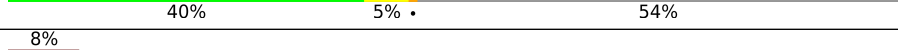
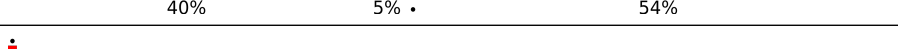
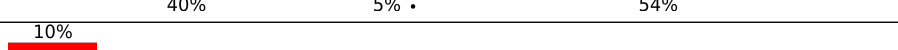
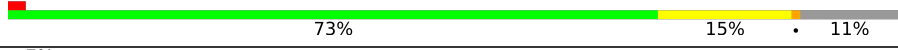
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	17 (22.90 - 23.50)

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	0	380	80%17%
1	9	380	8% 80%17%
1	I	380	80%17%
1	R	380	80%17%
2	1	1436	14% 61%8%30%

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Mol	Chain	Length	Quality of chain
2	J	1436	
2	S	1436	
2	a	1436	
3	2	326	
3	K	326	
3	T	326	
3	b	326	
4	3	1156	
4	C	1156	
4	L	1156	
4	U	1156	
5	4	925	
5	D	925	
5	M	925	
5	V	925	
6	5	937	
6	E	937	
6	N	937	
6	W	937	
7	6	322	
7	F	322	
7	O	322	
7	X	322	
8	7	360	
8	G	360	

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Mol	Chain	Length	Quality of chain
8	P	360	
8	Y	360	
9	8	656	
9	H	656	
9	Q	656	
9	Z	656	
10	A	1391	
10	B	1391	

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 95884 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NUCLEOPORIN NUP43.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	316	Total	C	N	O	0	0
			1562	930	316	316		
1	9	316	Total	C	N	O	0	0
			1562	930	316	316		
1	I	316	Total	C	N	O	0	0
			1562	930	316	316		
1	R	316	Total	C	N	O	0	0
			1562	930	316	316		

- Molecule 2 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP160.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	1009	Total	C	N	O	0	0
			4997	2979	1009	1009		
2	J	1009	Total	C	N	O	0	0
			4997	2979	1009	1009		
2	S	1009	Total	C	N	O	0	0
			4997	2979	1009	1009		
2	a	1009	Total	C	N	O	0	0
			4997	2979	1009	1009		

- Molecule 3 is a protein called NUCLEOPORIN NUP37.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	2	318	Total	C	N	O	0	0
			1566	930	318	318		
3	K	318	Total	C	N	O	0	0
			1566	930	318	318		
3	T	318	Total	C	N	O	0	0
			1566	930	318	318		
3	b	318	Total	C	N	O	0	0
			1566	930	318	318		

- Molecule 4 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP133.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	3	528	Total	C	N	O	0	0
			2629	1573	528	528		
4	C	528	Total	C	N	O	0	0
			2629	1573	528	528		
4	L	528	Total	C	N	O	0	0
			2629	1573	528	528		
4	U	528	Total	C	N	O	0	0
			2629	1573	528	528		

- Molecule 5 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP107.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	4	660	Total	C	N	O	0	0
			3278	1958	660	660		
5	D	660	Total	C	N	O	0	0
			3278	1958	660	660		
5	M	660	Total	C	N	O	0	0
			3278	1958	660	660		
5	V	660	Total	C	N	O	0	0
			3278	1958	660	660		

- Molecule 6 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP96.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	417	Total	C	N	O	0	0
			2073	1239	417	417		
6	E	417	Total	C	N	O	0	0
			2073	1239	417	417		
6	N	417	Total	C	N	O	0	0
			2073	1239	417	417		
6	W	417	Total	C	N	O	0	0
			2073	1239	417	417		

- Molecule 7 is a protein called PROTEIN SEC13 HOMOLOG.

Mol	Chain	Residues	Atoms				AltConf	Trace
7	6	285	Total	C	N	O	0	0
			1402	832	285	285		
7	F	285	Total	C	N	O	0	0
			1402	832	285	285		
7	O	285	Total	C	N	O	0	0
			1402	832	285	285		

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Mol	Chain	Residues	Atoms				AltConf	Trace
7	X	285	Total	C	N	O	0	0
			1402	832	285	285		

- Molecule 8 is a protein called NUCLEOPORIN SEH1.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	7	322	Total	C	N	O	0	0
			1593	949	322	322		
8	G	322	Total	C	N	O	0	0
			1593	949	322	322		
8	P	322	Total	C	N	O	0	0
			1593	949	322	322		
8	Y	322	Total	C	N	O	0	0
			1593	949	322	322		

- Molecule 9 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP85.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	8	434	Total	C	N	O	0	0
			2153	1285	434	434		
9	H	434	Total	C	N	O	0	0
			2153	1285	434	434		
9	Q	434	Total	C	N	O	0	0
			2153	1285	434	434		
9	Z	434	Total	C	N	O	0	0
			2153	1285	434	434		

- Molecule 10 is a protein called NUCLEAR PORE COMPLEX PROTEIN NUP155.

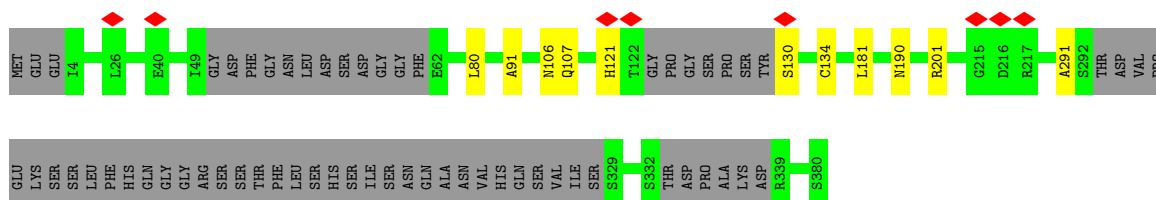
Mol	Chain	Residues	Atoms				AltConf	Trace
10	A	1097	Total	C	N	O	0	0
			5436	3242	1097	1097		
10	B	1097	Total	C	N	O	0	0
			5436	3242	1097	1097		

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.

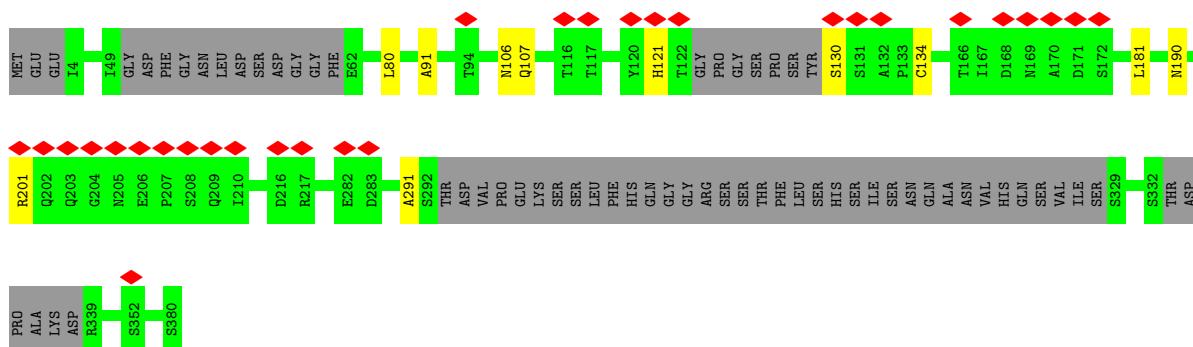
• Molecule 1: NUCLEOPORIN NUP43

Chain 0: 



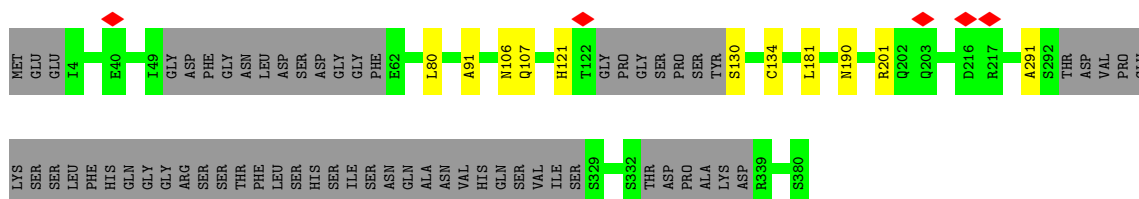
• Molecule 1: NUCLEOPORIN NUP43

Chain 9: 



• Molecule 1: NUCLEOPORIN NUP43

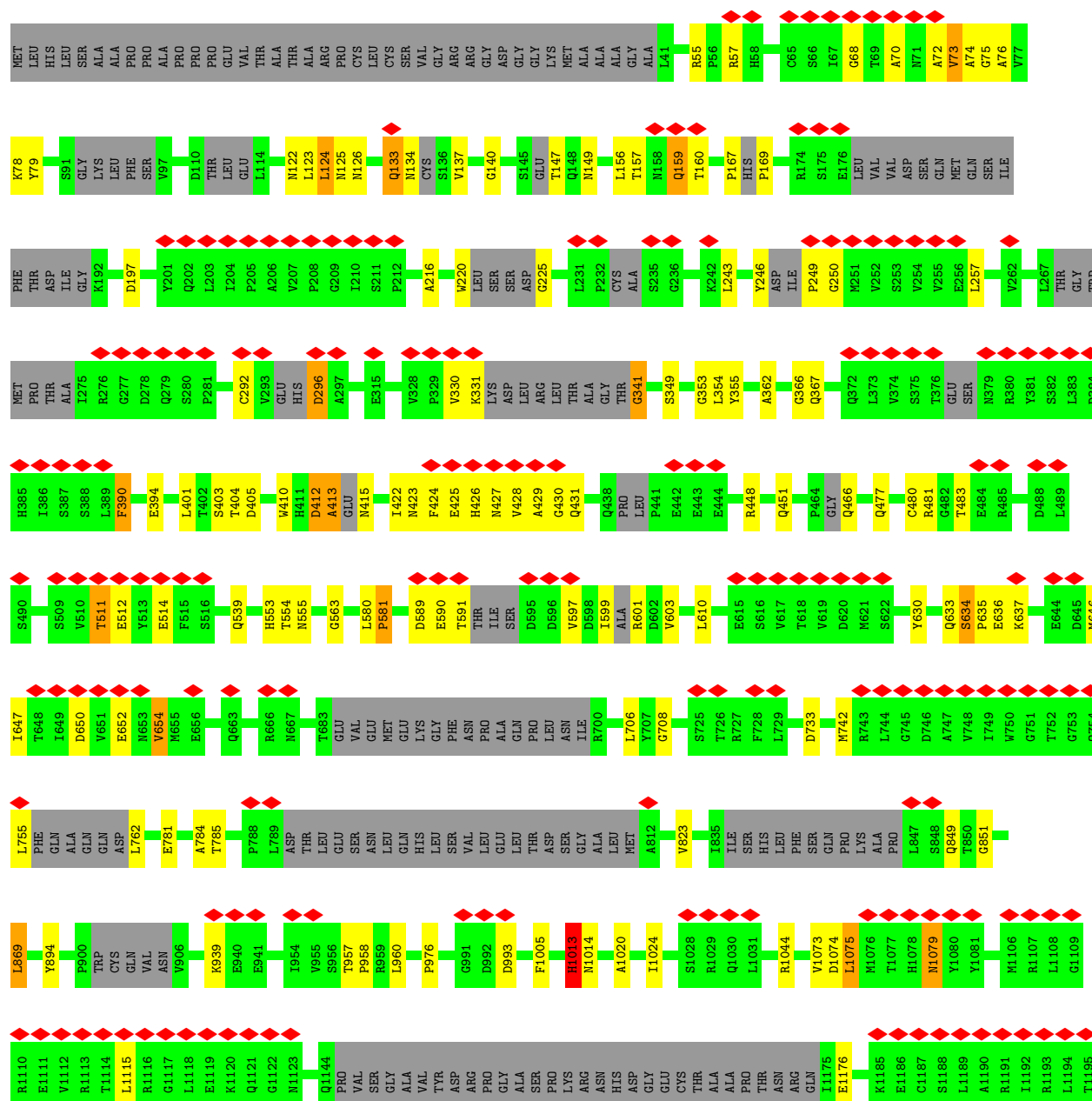
Chain I: 

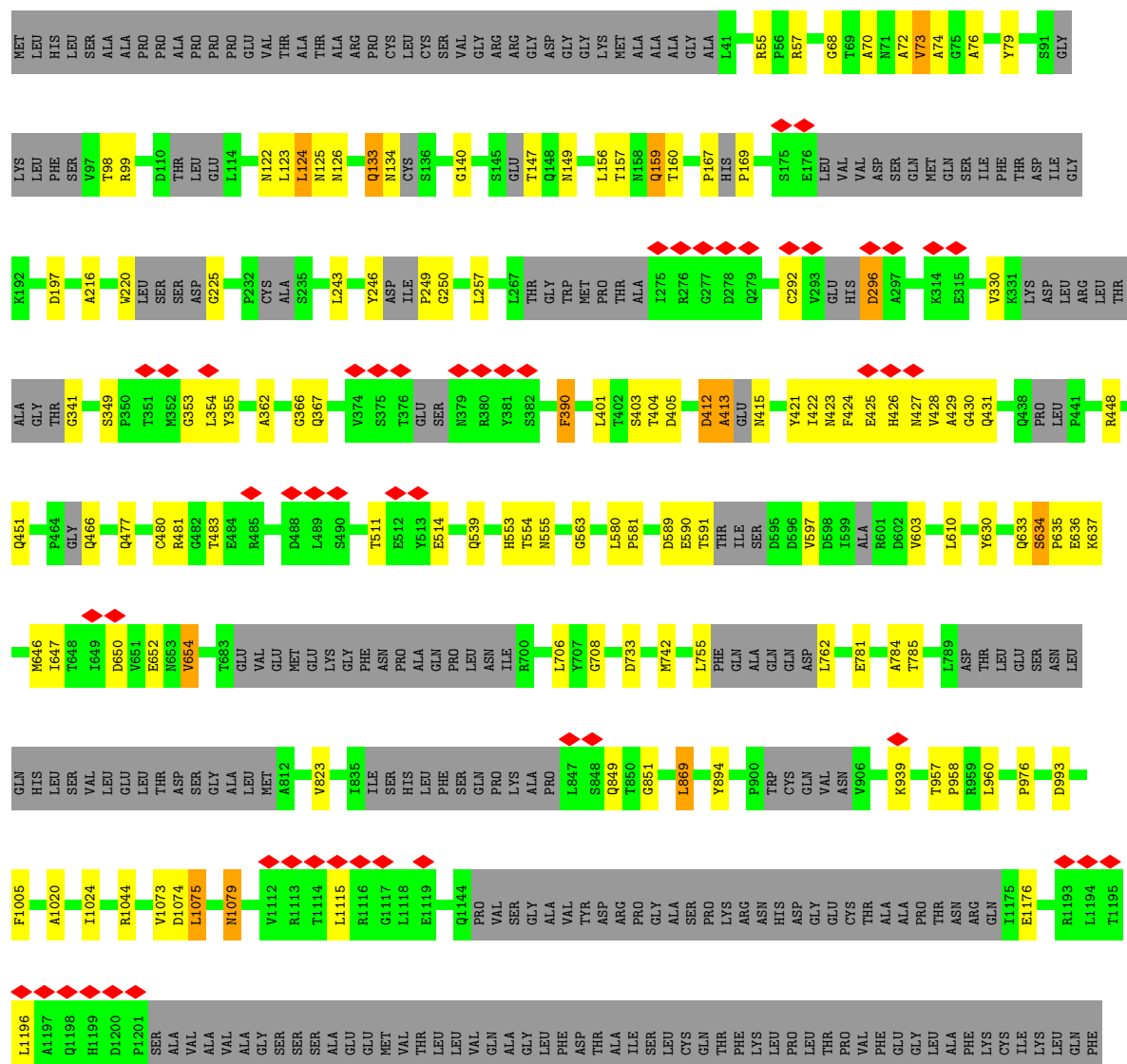


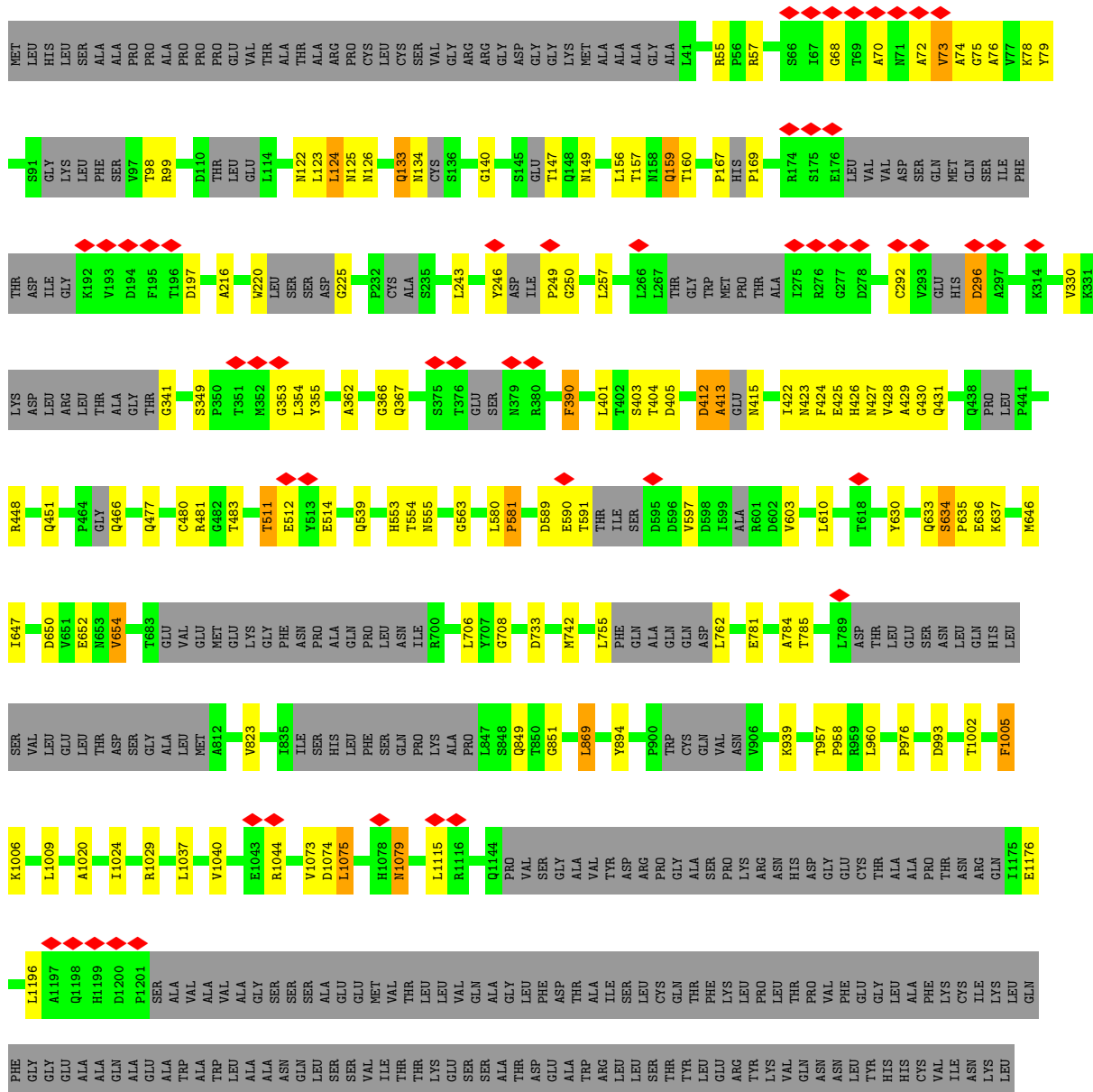
• Molecule 1: NUCLEOPORIN NUP43

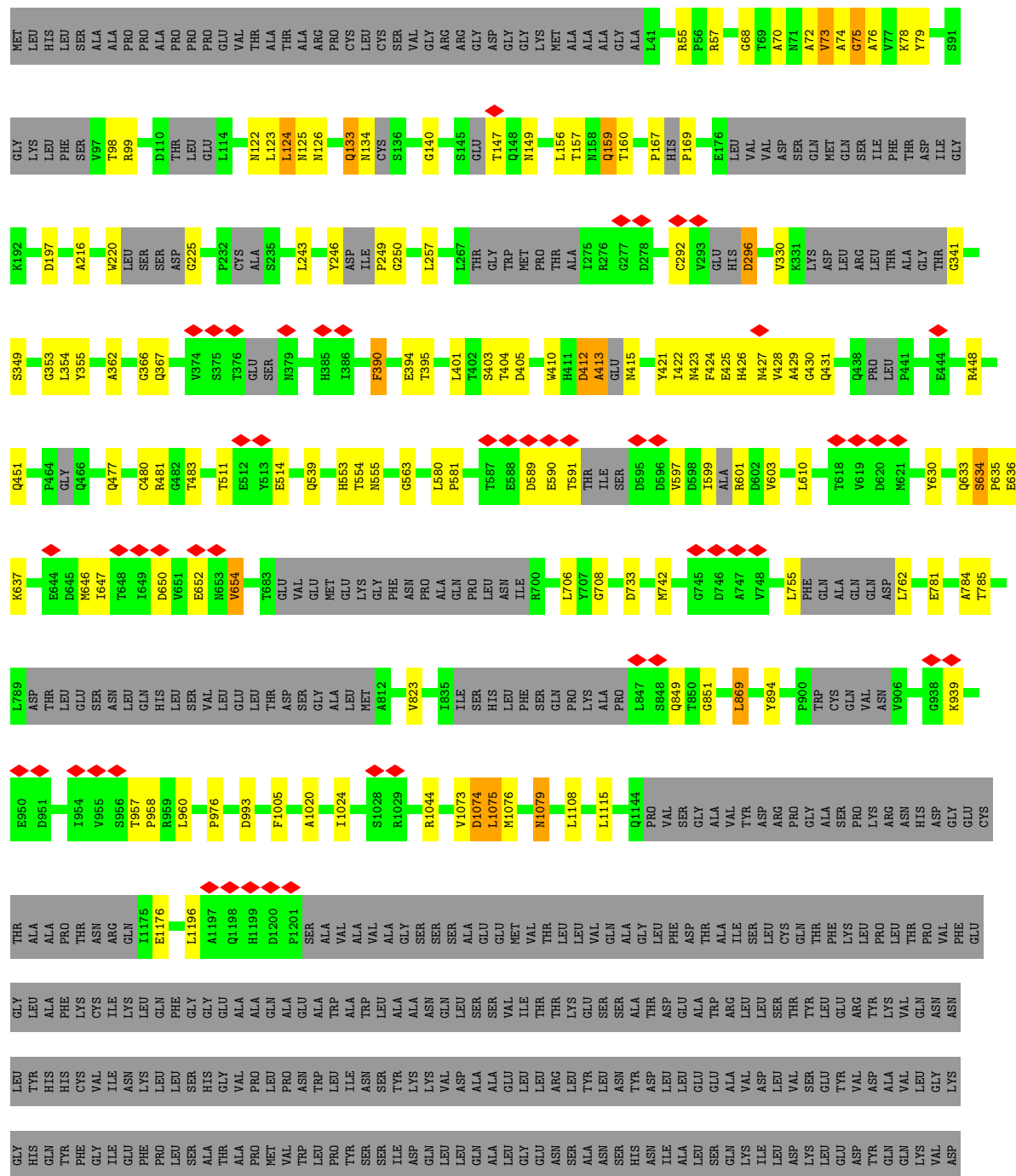
HIS	GLY	GLY	ARG	SER	SER	THR	PHE	LEU	ASN	SER	HIS	SER	ILE	SER	ASN	GLN	ALA	ASN	VAL	HIS	GLM	SER	VAL	ILE	SER	S329	S332	THR	ASP	PRO	ALA	LYS	R339	S380															
MET	GLU	GLY	I4	I49	GLY	ASP	PHE	GLY	ASN	LEU	ASP	SER	ASP	GLY	GLY	PHE	E67	L80	A91	N106	Q107	H121	T122	GLY	PRO	GLY	SER	PRO	ASP	SER	THR	S130	C134	L181	N190	R201	Q202	Q203	A291	S292	THR	ASP	VAL	PRO	GLU	LYS	SER	SER	LEU

Chain 1:





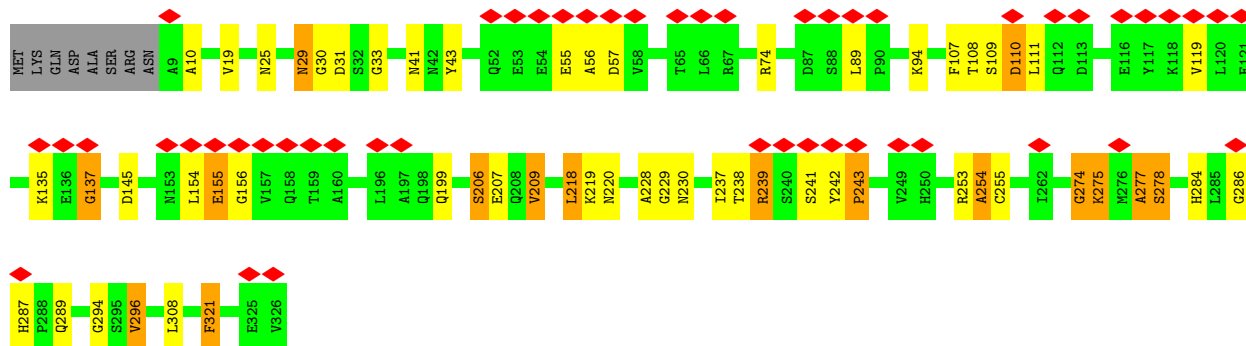




LYS
ALA
THR
GLN
ASP
ARG
ALA
SER
LEU
LEU
TYR
ARG
THR
LEU

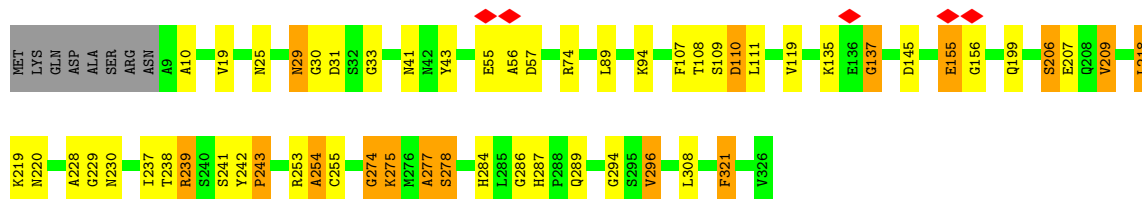
• Molecule 3: NUCLEOPORIN NUP37

Chain 2:  15% 80% 13% 5% .



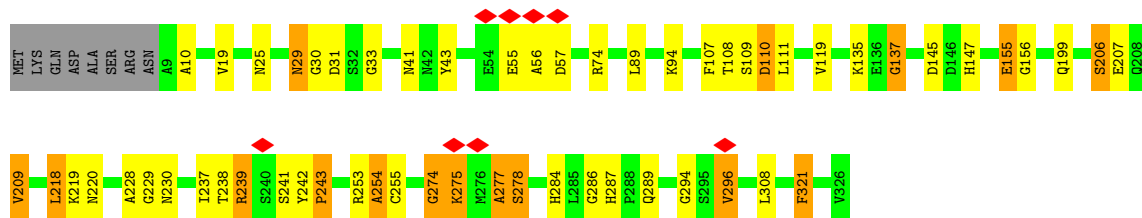
• Molecule 3: NUCLEOPORIN NUP37

Chain K:  80% 13% 5% .



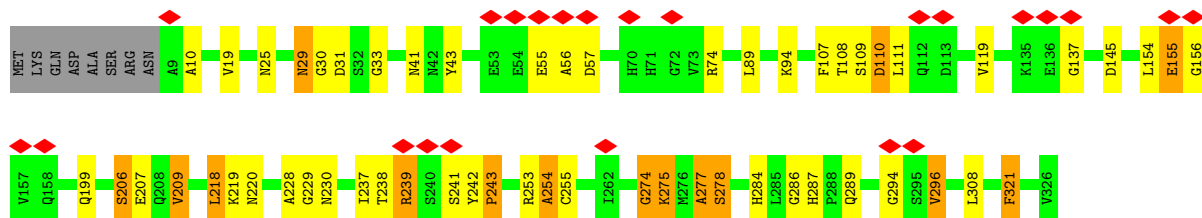
• Molecule 3: NUCLEOPORIN NUP37

Chain T:  80% 13% 5% .

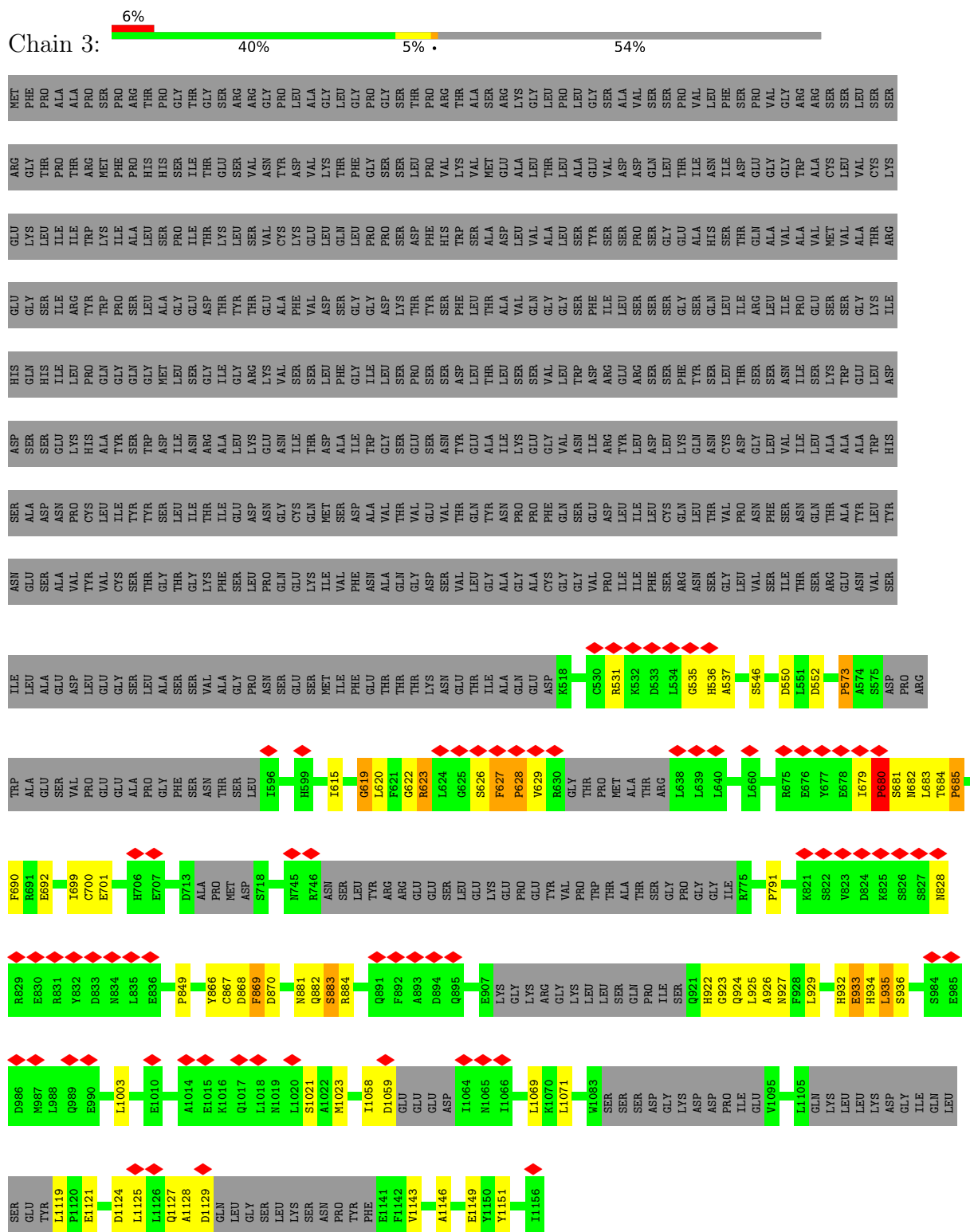


• Molecule 3: NUCLEOPORIN NUP37

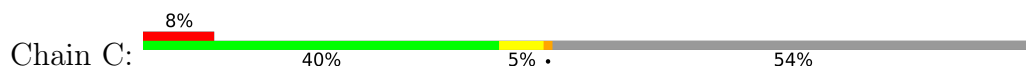
Chain b:  7% 80% 13% 5% .



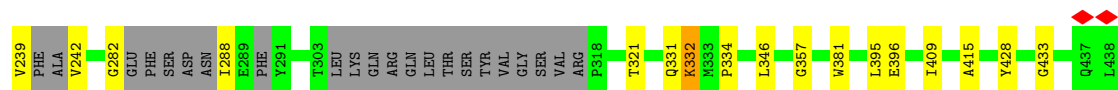
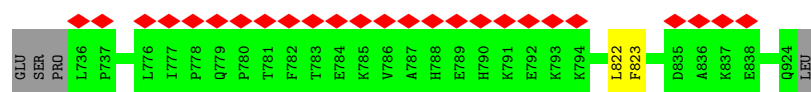
● Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP133



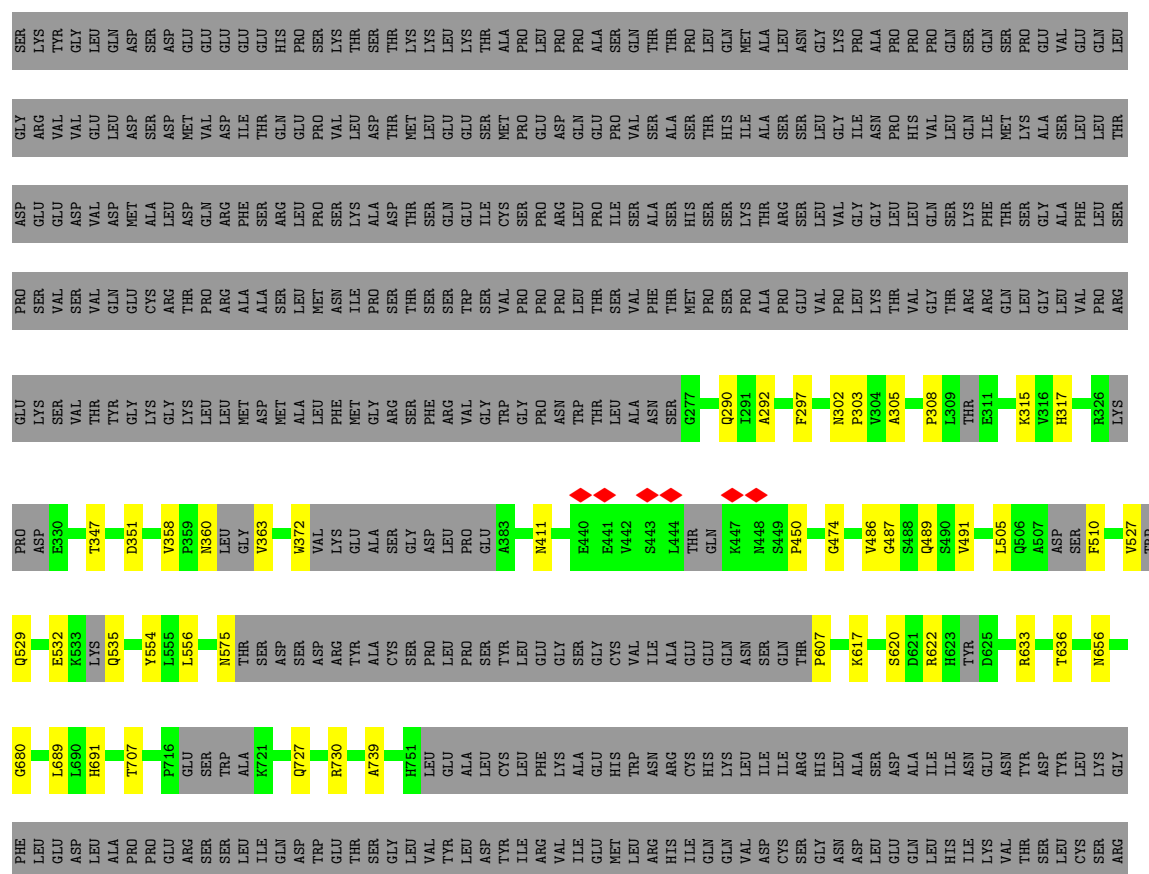
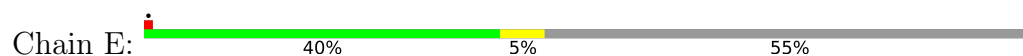
● Molecule 4: NUCLEAR PORE COMPLEX PROTEIN NUP133



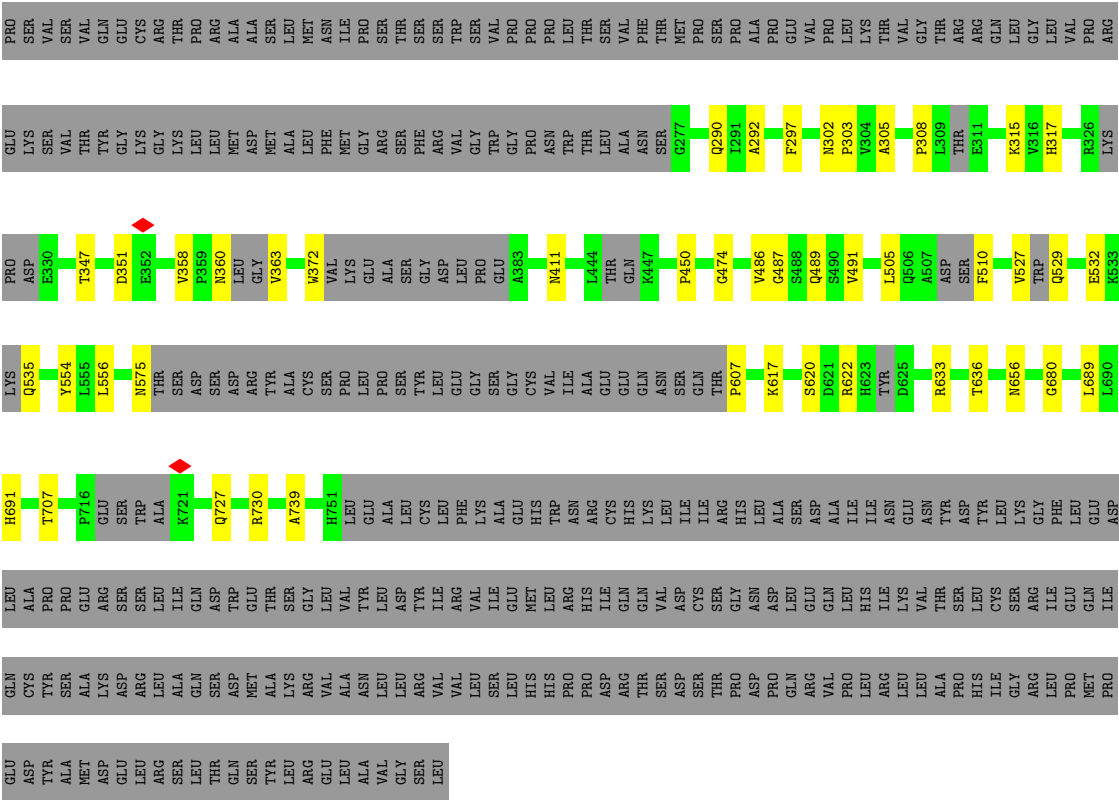
[illegible]



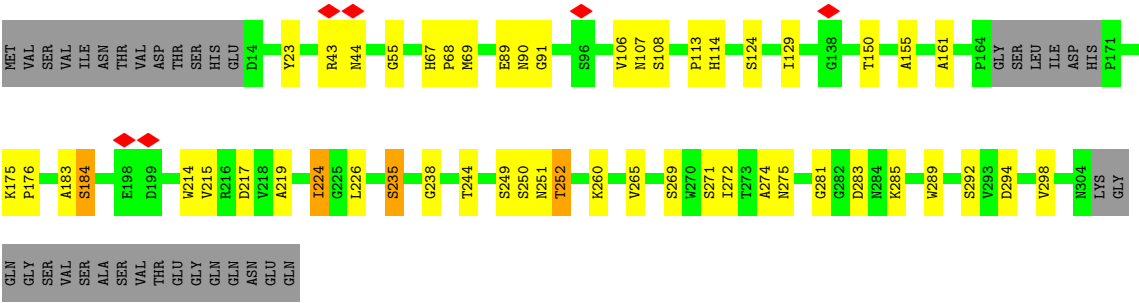
- Molecule 6: NUCLEAR PORE COMPLEX PROTEIN NUP96



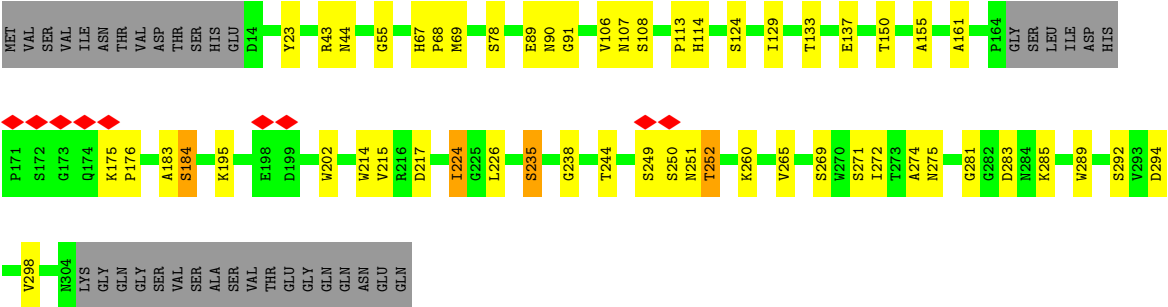




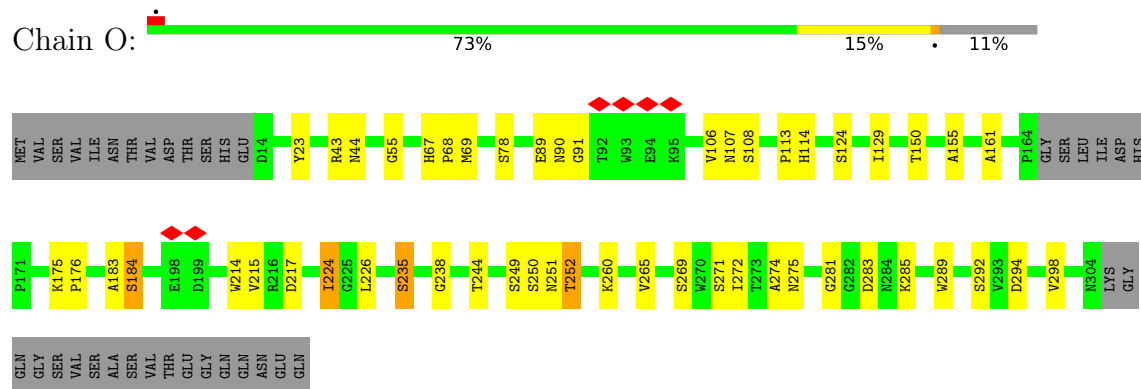
● Molecule 7: PROTEIN SEC13 HOMOLOG



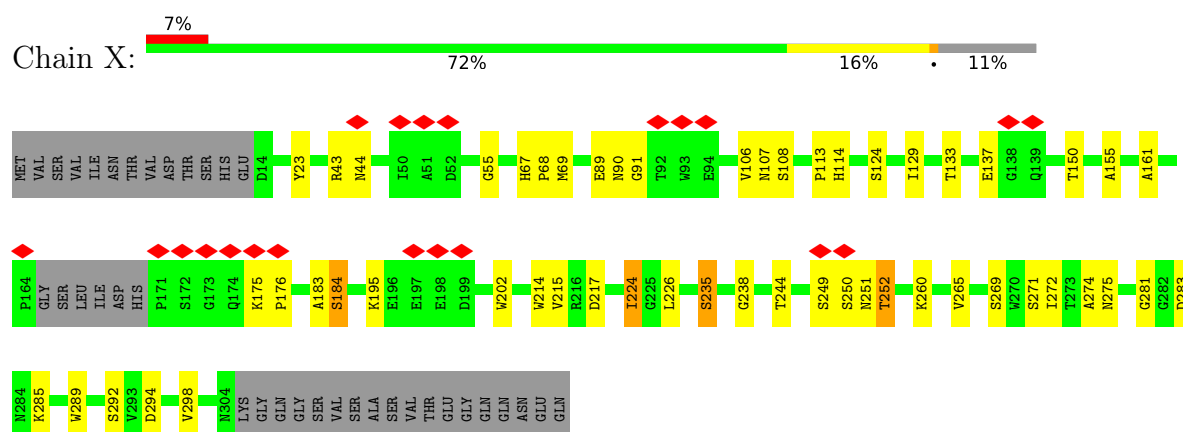
● Molecule 7: PROTEIN SEC13 HOMOLOG



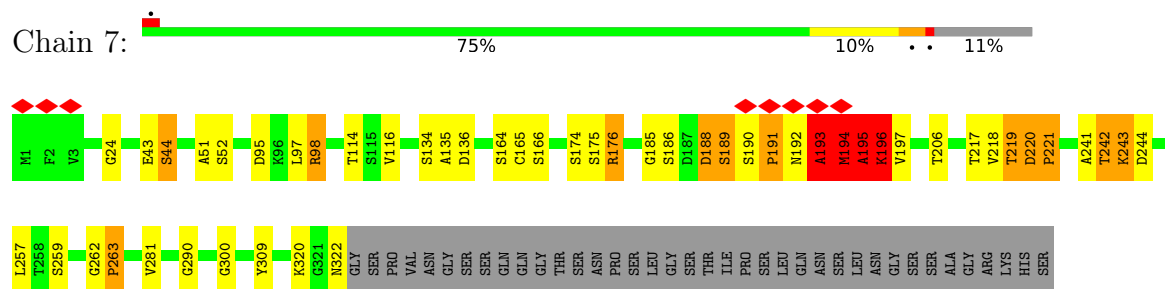
- Molecule 7: PROTEIN SEC13 HOMOLOG



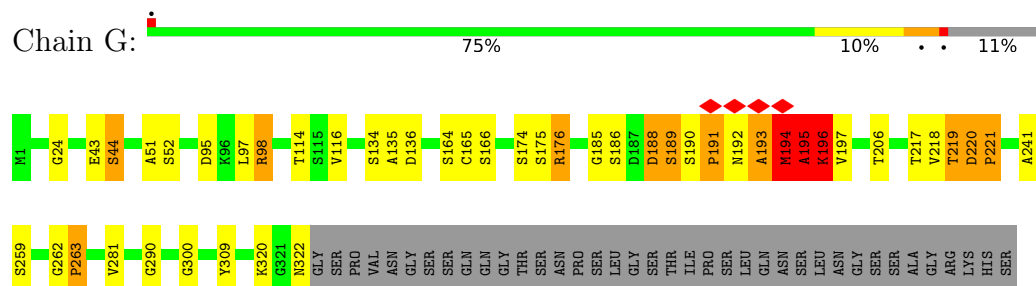
- Molecule 7: PROTEIN SEC13 HOMOLOG



- Molecule 8: NUCLEOPORIN SEH1

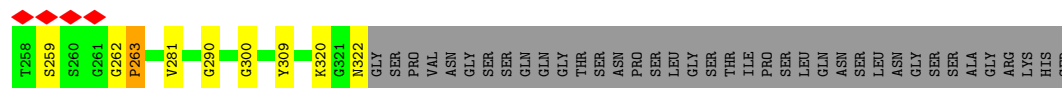


- Molecule 8: NUCLEOPORIN SEH1



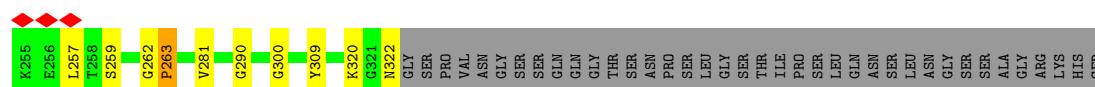
- Molecule 8: NUCLEOPORIN SEH1

Frequency	Percentage
Daily	75%
Weekly	9%
Monthly	11%
Other	4%



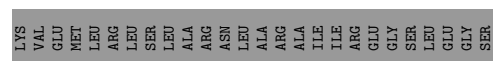
- Molecule 8: NUCLEOPORIN SEH1

Frequency	Percentage
Daily	75%
Weekly	9%
Monthly	11%
Other	5%



- Molecule 9: NUCLEAR PORE COMPLEX PROTEIN NUP85

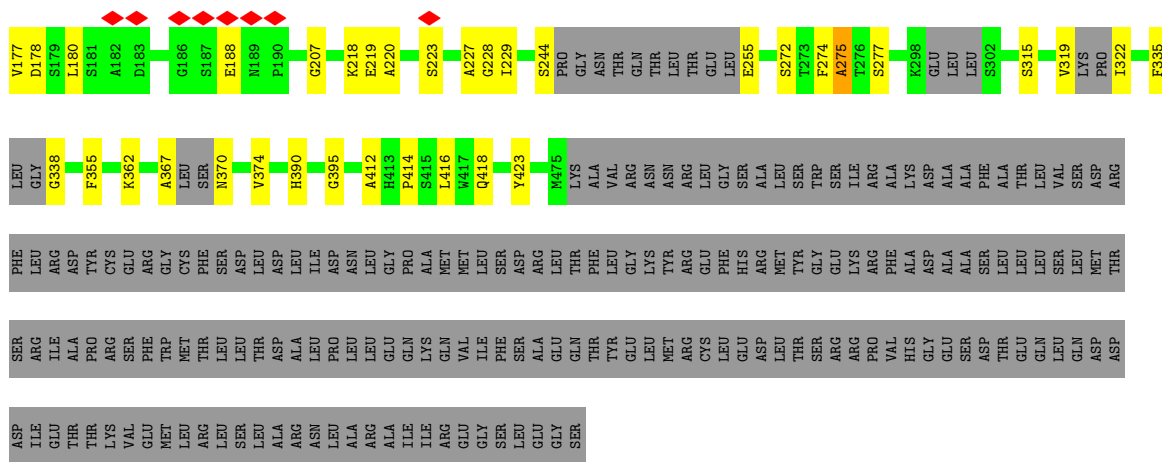
Frequency	Percentage
Daily	58%
Weekly	8%
Monthly	34%



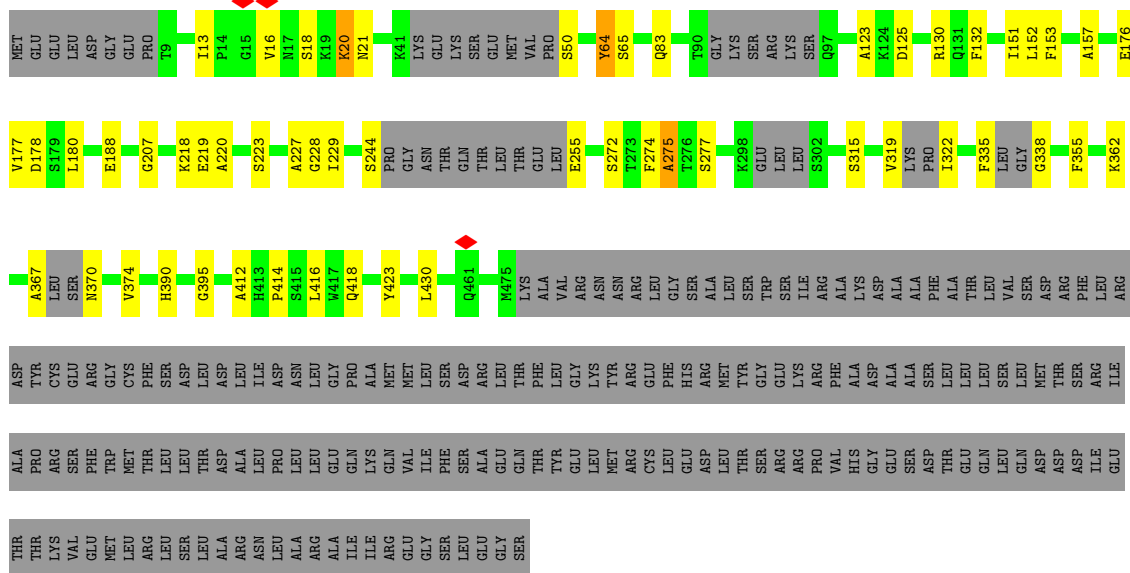
- Molecule 9: NUCLEAR PORE COMPLEX PROTEIN NUP85

Frequency	Percentage
Daily	58%
Weekly	8%
Monthly	34%

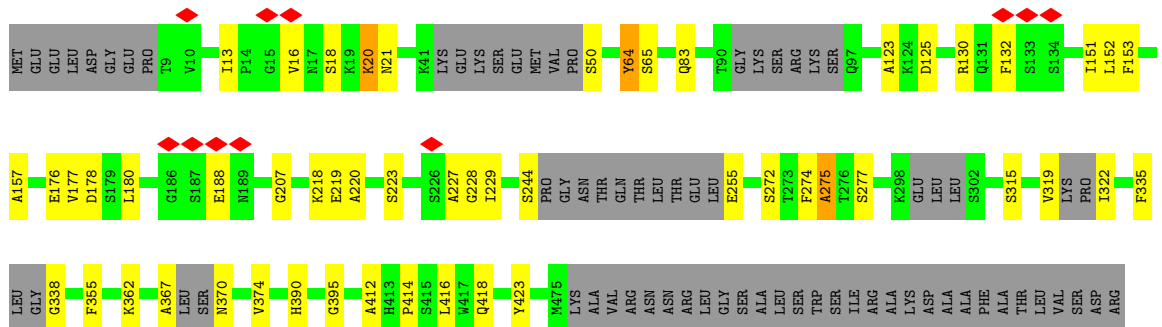




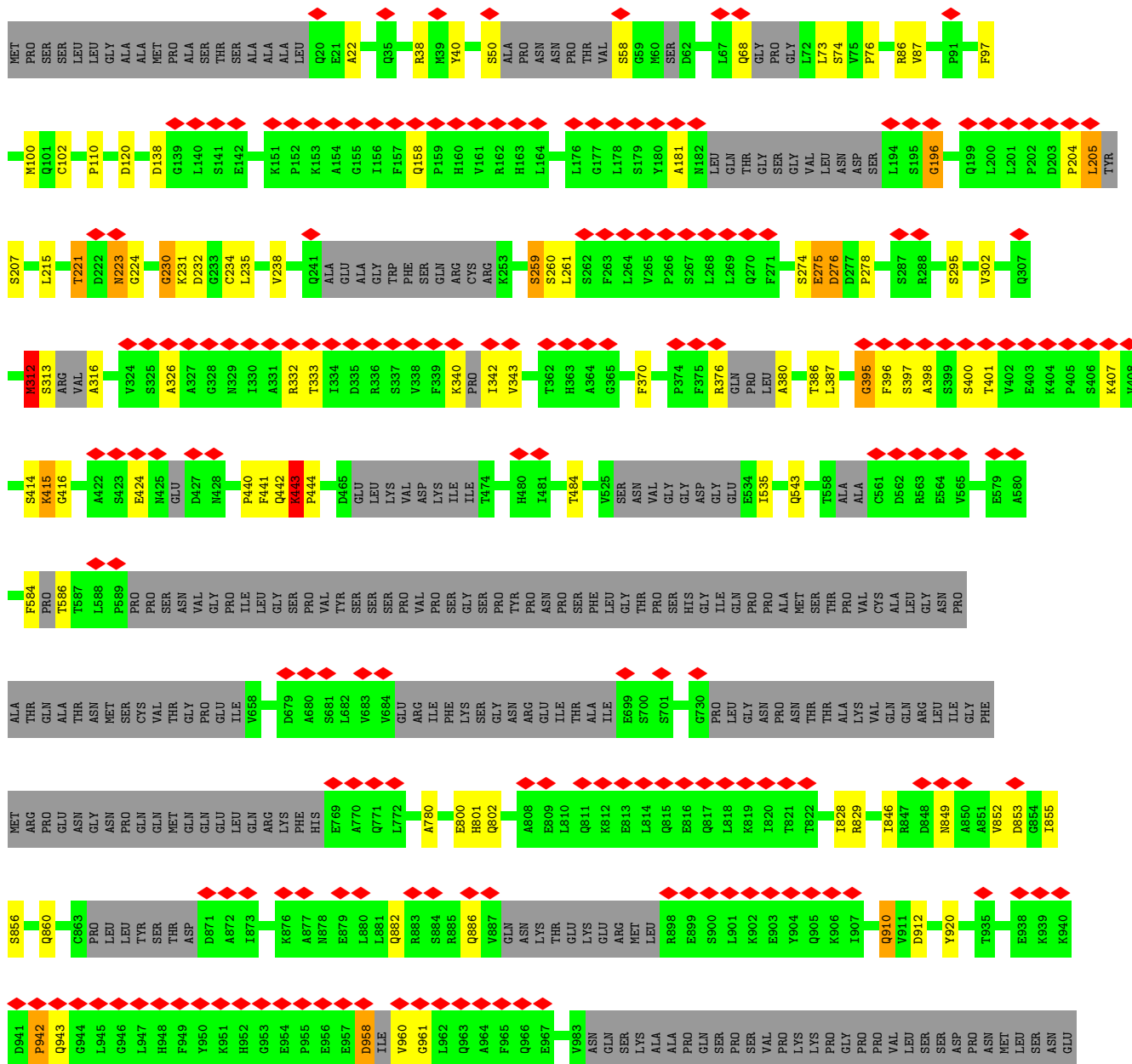
- Molecule 9: NUCLEAR PORE COMPLEX PROTEIN NUP85

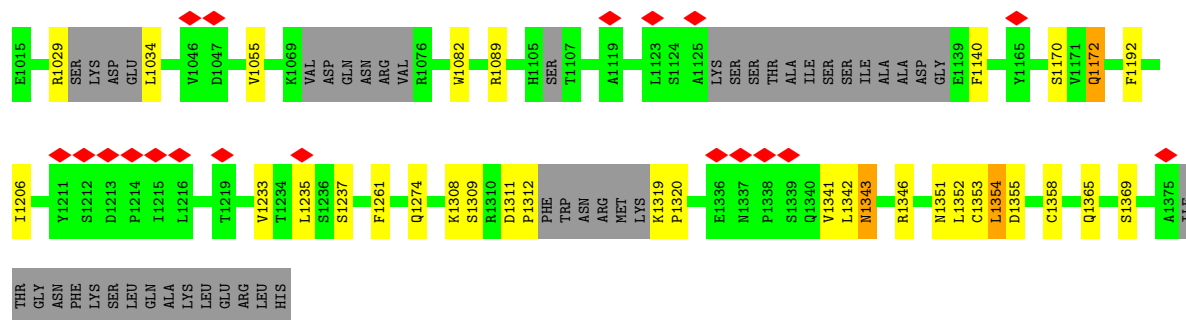


- Molecule 9: NUCLEAR PORE COMPLEX PROTEIN NUP85

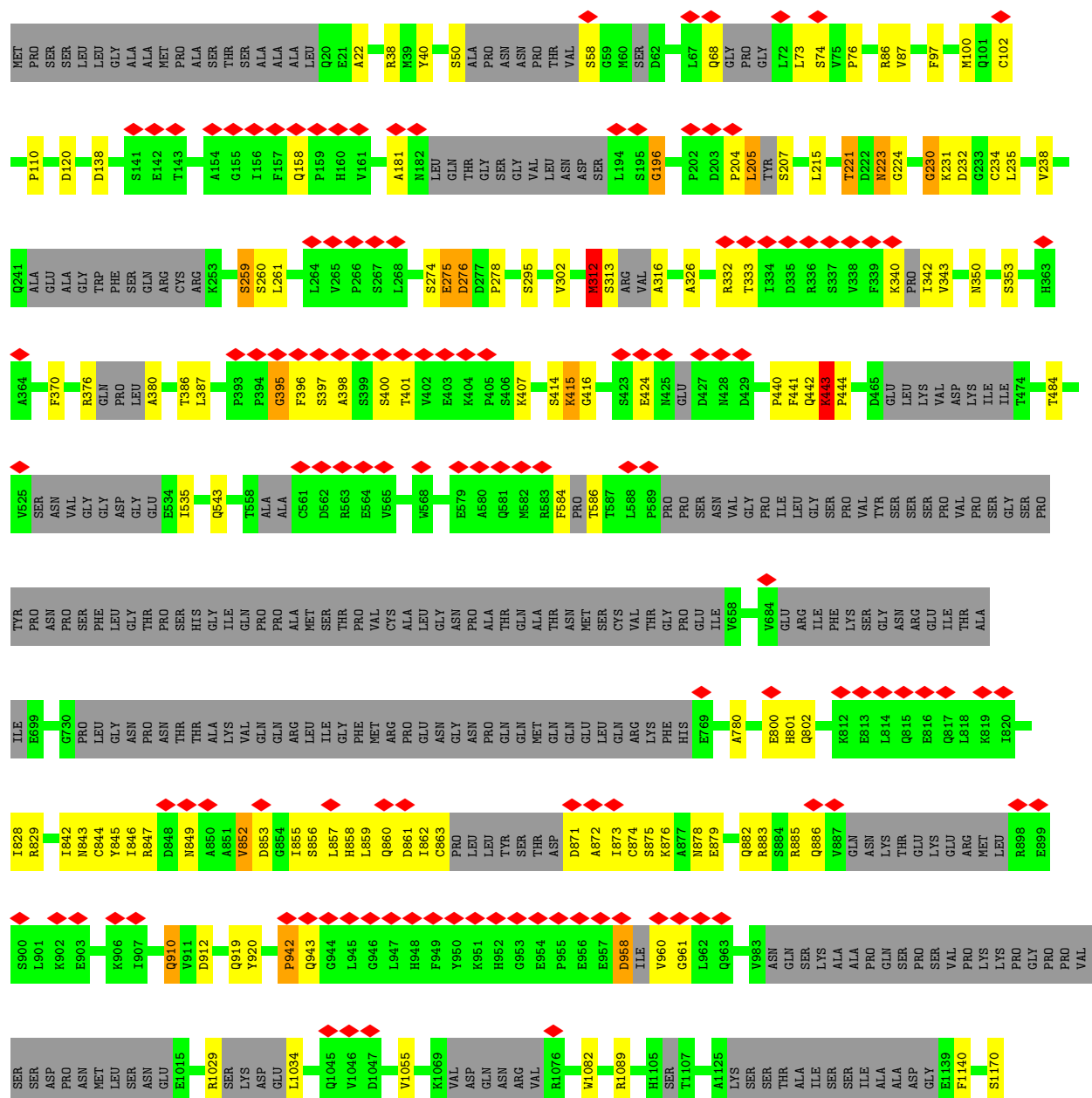


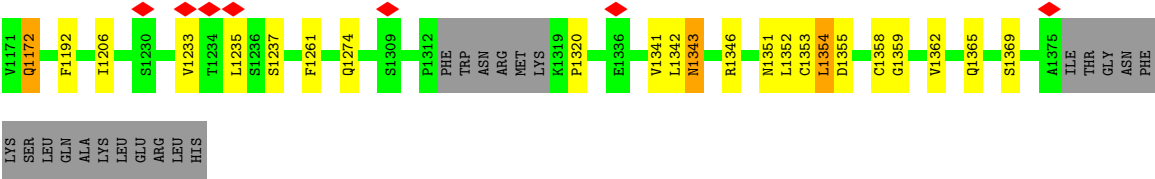
- Molecule 10: NUCLEAR PORE COMPLEX PROTEIN NUP155





• Molecule 10: NUCLEAR PORE COMPLEX PROTEIN NUP155





4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of tilted images used	Not provided	
Resolution determination method	Not provided	
CTF correction method	PHASE FLIPPING OF TILT SERIES	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	110	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum voxel value	15.038	Depositor
Minimum voxel value	-7.184	Depositor
Average voxel value	-0.000	Depositor
Voxel value standard deviation	1.629	Depositor
Recommended contour level	3.5	Depositor
Tomogram size ($\text{\AA}$)	1422.72, 1422.72, 1422.72	wwPDB
Tomogram dimensions	208, 208, 208	wwPDB
Tomogram angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Grid spacing ($\text{\AA}$)	6.8399997, 6.8399997, 6.8399997	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	0	1.22	2/1557 (0.1%)	1.02	2/2161 (0.1%)
1	9	1.22	2/1557 (0.1%)	1.02	2/2161 (0.1%)
1	I	1.22	2/1557 (0.1%)	1.02	2/2161 (0.1%)
1	R	1.22	2/1557 (0.1%)	1.02	2/2161 (0.1%)
2	1	1.59	7/4972 (0.1%)	1.81	108/6892 (1.6%)
2	J	1.60	6/4971 (0.1%)	1.83	107/6889 (1.6%)
2	S	1.58	6/4971 (0.1%)	1.81	106/6889 (1.5%)
2	a	1.59	6/4971 (0.1%)	1.81	104/6889 (1.5%)
3	2	1.53	0/1565	1.91	43/2175 (2.0%)
3	K	1.53	0/1565	1.91	41/2175 (1.9%)
3	T	1.53	0/1565	1.91	42/2175 (1.9%)
3	b	1.53	0/1565	1.91	43/2175 (2.0%)
4	3	0.41	0/2619	1.07	9/3644 (0.2%)
4	C	0.41	0/2619	1.07	8/3644 (0.2%)
4	L	0.41	0/2619	1.07	9/3644 (0.2%)
4	U	0.40	0/2619	1.07	9/3644 (0.2%)
5	4	1.25	0/3266	1.49	32/4540 (0.7%)
5	D	1.23	3/3268 (0.1%)	1.45	30/4546 (0.7%)
5	M	1.25	0/3266	1.49	31/4540 (0.7%)
5	V	1.22	3/3268 (0.1%)	1.45	32/4546 (0.7%)
6	5	1.55	0/2061	1.76	23/2859 (0.8%)
6	E	1.55	0/2061	1.75	23/2859 (0.8%)
6	N	1.55	0/2061	1.76	23/2859 (0.8%)
6	W	1.55	0/2061	1.75	23/2859 (0.8%)
7	6	0.71	0/1400	1.38	18/1943 (0.9%)
7	F	0.72	0/1400	1.42	18/1943 (0.9%)
7	O	0.71	0/1400	1.38	18/1943 (0.9%)
7	X	0.72	0/1400	1.42	17/1943 (0.9%)
8	7	1.64	12/1592 (0.8%)	1.92	41/2217 (1.8%)
8	G	1.64	11/1592 (0.7%)	1.92	41/2217 (1.8%)
8	P	1.65	11/1592 (0.7%)	1.92	41/2217 (1.8%)
8	Y	1.65	13/1592 (0.8%)	1.93	44/2217 (2.0%)
9	8	1.75	1/2145 (0.0%)	1.72	31/2980 (1.0%)
9	H	1.74	1/2145 (0.0%)	1.72	31/2980 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
9	Q	1.75	1/2145 (0.0%)	1.73	33/2980 (1.1%)
9	Z	1.74	1/2145 (0.0%)	1.72	31/2980 (1.0%)
10	A	1.56	1/5409 (0.0%)	1.83	94/7500 (1.3%)
10	B	1.56	1/5409 (0.0%)	1.83	93/7500 (1.2%)
All	All	1.40	92/95527 (0.1%)	1.64	1405/132647 (1.1%)

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
2	1	0	1
2	J	0	1
2	S	0	1
2	a	0	1
3	2	0	1
3	K	0	1
3	T	0	1
3	b	0	1
5	D	0	1
5	V	0	1
10	A	0	1
10	B	0	1
All	All	0	12

The worst 5 of 92 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	8	64	TYR	C-N	40.99	1.89	1.33
9	Q	64	TYR	C-N	40.95	1.89	1.33
9	Z	64	TYR	C-N	40.89	1.89	1.33
9	H	64	TYR	C-N	40.86	1.89	1.33
2	J	124	LEU	CA-C	10.39	1.59	1.53

The worst 5 of 1405 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	276	ASP	O-C-N	28.48	157.40	122.65
10	A	276	ASP	O-C-N	28.43	157.34	122.65
5	M	332	LYS	CA-C-N	14.94	137.84	120.06
5	M	332	LYS	C-N-CA	14.94	137.84	120.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	F	272	ILE	N-CA-C	14.90	125.81	110.62

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	511	THR	Peptide
3	2	286	GLY	Peptide
10	A	259	SER	Mainchain
10	B	259	SER	Mainchain
5	D	480	ARG	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	0	1562	0	681	7	0
1	9	1562	0	681	7	0
1	I	1562	0	681	7	0
1	R	1562	0	681	6	0
2	1	4997	0	2175	37	0
2	J	4997	0	2174	34	0
2	S	4997	0	2174	64	0
2	a	4997	0	2174	45	0
3	2	1566	0	702	21	0
3	K	1566	0	702	21	0
3	T	1566	0	702	20	0
3	b	1566	0	702	19	0
4	3	2629	0	1167	59	0
4	C	2629	0	1167	37	0
4	L	2629	0	1167	39	0
4	U	2629	0	1167	39	0
5	4	3278	0	1440	10	0
5	D	3278	0	1442	11	0
5	M	3278	0	1440	10	0
5	V	3278	0	1442	10	0
6	5	2073	0	907	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	2073	0	907	15	0
6	N	2073	0	907	16	0
6	W	2073	0	907	16	0
7	6	1402	0	648	20	0
7	F	1402	0	648	22	0
7	O	1402	0	648	20	0
7	X	1402	0	648	22	0
8	7	1593	0	731	44	0
8	G	1593	0	731	43	0
8	P	1593	0	731	44	0
8	Y	1593	0	731	43	0
9	8	2153	0	938	20	0
9	H	2153	0	938	20	0
9	Q	2153	0	938	20	0
9	Z	2153	0	938	20	0
10	A	5436	0	2392	68	0
10	B	5436	0	2384	134	0
All	All	95884	0	42333	1013	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 7.

The worst 5 of 1013 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)
10:B:844:CYS:C	10:B:885:ARG:CB	1.81	1.52
4:3:883:SER:CB	4:3:926:ALA:CA	1.90	1.49
10:B:845:TYR:CB	10:B:886:GLN:HA	1.42	1.47
10:B:843:ASN:CB	10:B:919:GLN:CB	1.92	1.46
10:B:860:GLN:N	10:B:874:CYS:N	1.65	1.44

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	0	306/380 (80%)	296 (97%)	10 (3%)	0	100	100
1	9	306/380 (80%)	296 (97%)	10 (3%)	0	100	100
1	I	306/380 (80%)	296 (97%)	10 (3%)	0	100	100
1	R	306/380 (80%)	296 (97%)	10 (3%)	0	100	100
2	1	959/1436 (67%)	873 (91%)	63 (7%)	23 (2%)	4	27
2	J	957/1436 (67%)	873 (91%)	62 (6%)	22 (2%)	5	28
2	S	957/1436 (67%)	873 (91%)	62 (6%)	22 (2%)	5	28
2	a	957/1436 (67%)	873 (91%)	62 (6%)	22 (2%)	5	28
3	2	316/326 (97%)	280 (89%)	15 (5%)	21 (7%)	1	12
3	K	316/326 (97%)	279 (88%)	16 (5%)	21 (7%)	1	12
3	T	316/326 (97%)	280 (89%)	15 (5%)	21 (7%)	1	12
3	b	316/326 (97%)	279 (88%)	16 (5%)	21 (7%)	1	12
4	3	508/1156 (44%)	437 (86%)	55 (11%)	16 (3%)	3	22
4	C	508/1156 (44%)	437 (86%)	56 (11%)	15 (3%)	3	23
4	L	508/1156 (44%)	437 (86%)	56 (11%)	15 (3%)	3	23
4	U	508/1156 (44%)	437 (86%)	56 (11%)	15 (3%)	3	23
5	4	636/925 (69%)	607 (95%)	25 (4%)	4 (1%)	21	59
5	D	640/925 (69%)	607 (95%)	28 (4%)	5 (1%)	16	54
5	M	636/925 (69%)	608 (96%)	24 (4%)	4 (1%)	21	59
5	V	640/925 (69%)	607 (95%)	27 (4%)	6 (1%)	14	51
6	5	393/937 (42%)	363 (92%)	19 (5%)	11 (3%)	4	24
6	E	393/937 (42%)	363 (92%)	19 (5%)	11 (3%)	4	24
6	N	393/937 (42%)	363 (92%)	19 (5%)	11 (3%)	4	24
6	W	393/937 (42%)	363 (92%)	19 (5%)	11 (3%)	4	24
7	6	281/322 (87%)	235 (84%)	38 (14%)	8 (3%)	4	24
7	F	281/322 (87%)	231 (82%)	42 (15%)	8 (3%)	4	24
7	O	281/322 (87%)	235 (84%)	38 (14%)	8 (3%)	4	24
7	X	281/322 (87%)	230 (82%)	43 (15%)	8 (3%)	4	24
8	7	320/360 (89%)	288 (90%)	21 (7%)	11 (3%)	3	21
8	G	320/360 (89%)	288 (90%)	21 (7%)	11 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	P	320/360 (89%)	288 (90%)	21 (7%)	11 (3%)	3	21
8	Y	320/360 (89%)	288 (90%)	21 (7%)	11 (3%)	3	21
9	8	418/656 (64%)	379 (91%)	28 (7%)	11 (3%)	4	25
9	H	418/656 (64%)	379 (91%)	28 (7%)	11 (3%)	4	25
9	Q	418/656 (64%)	379 (91%)	28 (7%)	11 (3%)	4	25
9	Z	418/656 (64%)	379 (91%)	28 (7%)	11 (3%)	4	25
10	A	1043/1391 (75%)	961 (92%)	58 (6%)	24 (2%)	5	28
10	B	1043/1391 (75%)	961 (92%)	58 (6%)	24 (2%)	5	28
All	All	18636/28774 (65%)	16944 (91%)	1227 (7%)	465 (2%)	6	26

5 of 465 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	55	ARG
2	1	73	VAL
2	1	159	GLN
2	1	404	THR
2	1	428	VAL

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
2	J	1
2	a	1
2	S	1
9	8	1
9	H	1
9	Q	1
9	Z	1

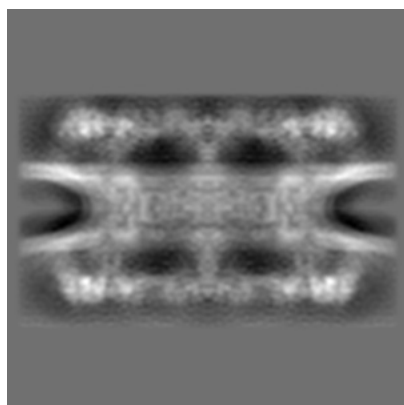
The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	1013:HIS	C	1014:ASN	N	6.20
1	a	1013:HIS	C	1014:ASN	N	6.01
1	S	1013:HIS	C	1014:ASN	N	4.29
1	8	64:TYR	C	65:SER	N	1.89
1	H	64:TYR	C	65:SER	N	1.89

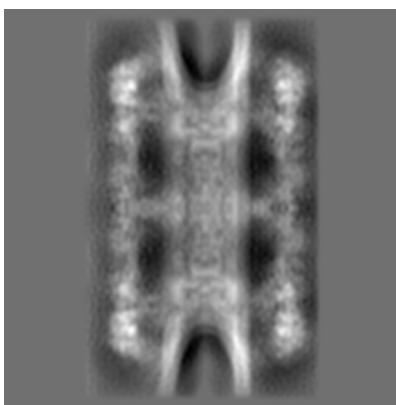
6 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3103. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

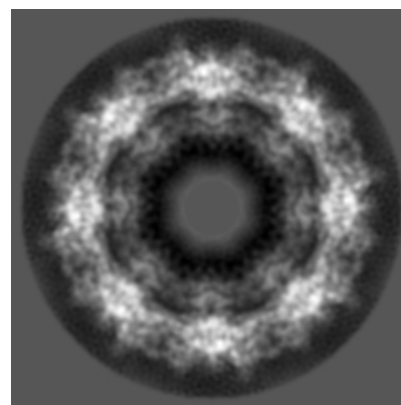
6.1 Orthogonal projections [i](#)



X



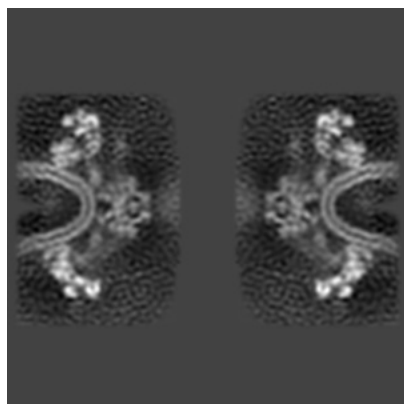
Y



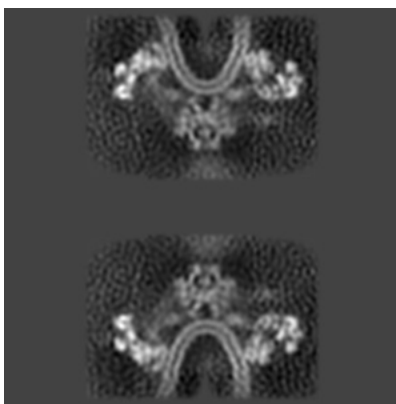
Z

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

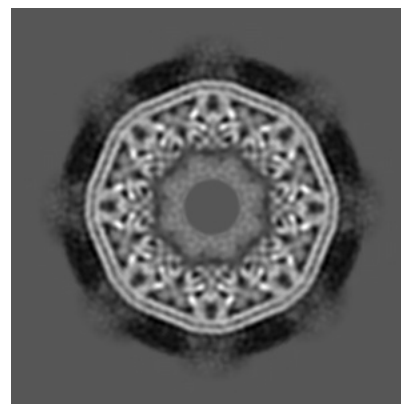
6.2 Central slices [i](#)



X Index: 104



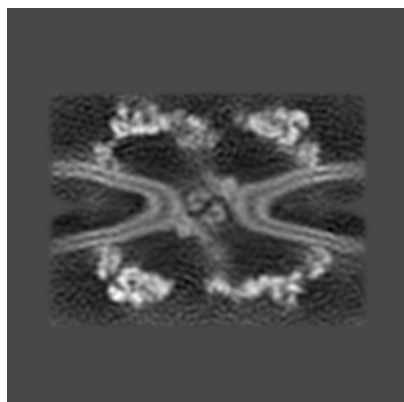
Y Index: 104



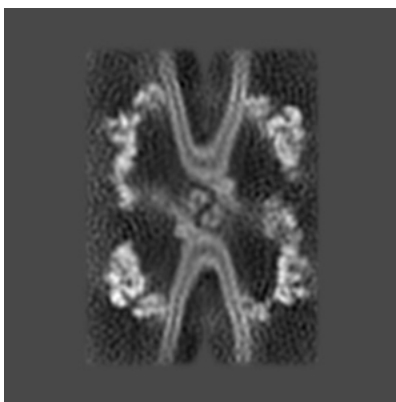
Z Index: 104

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

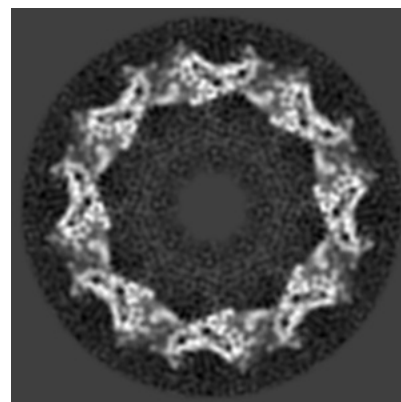
6.3 Largest variance slices [i](#)



X Index: 160



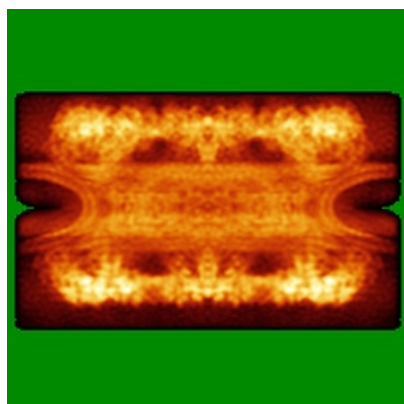
Y Index: 48



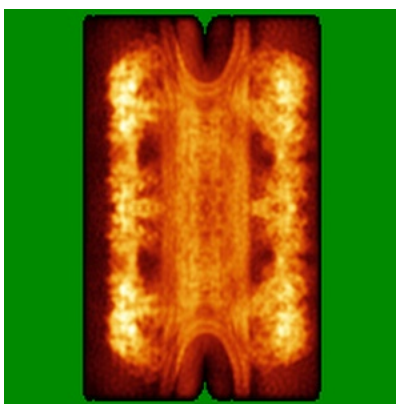
Z Index: 62

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

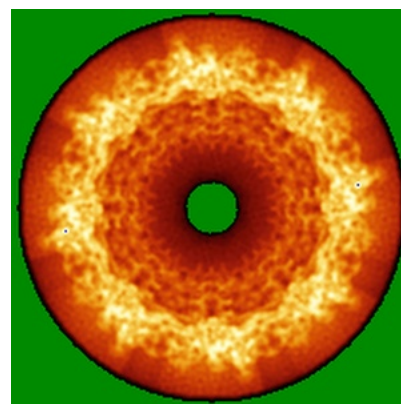
6.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

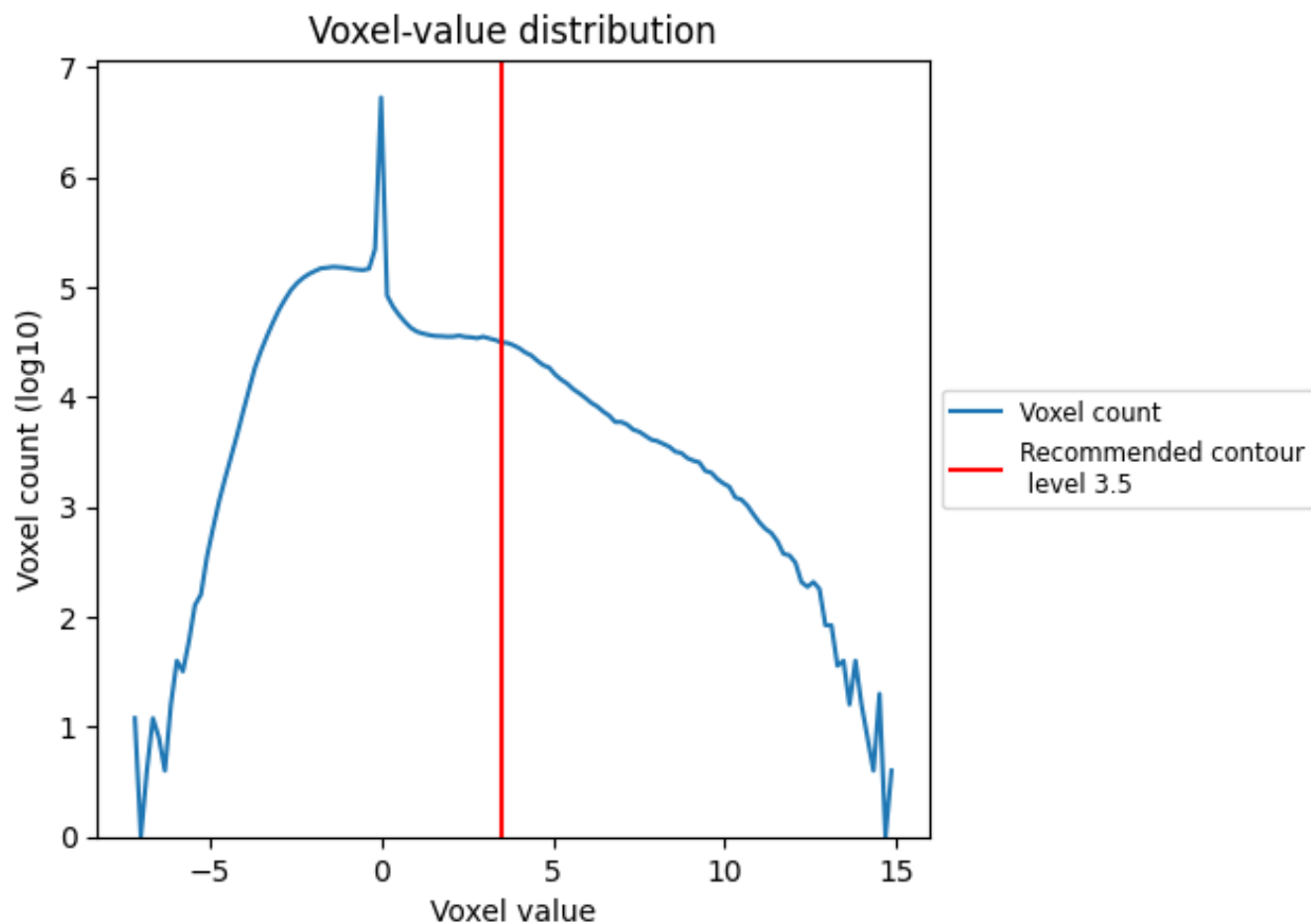
6.5 Mask visualisation [i](#)

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

7 Tomogram analysis [i](#)

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

7.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

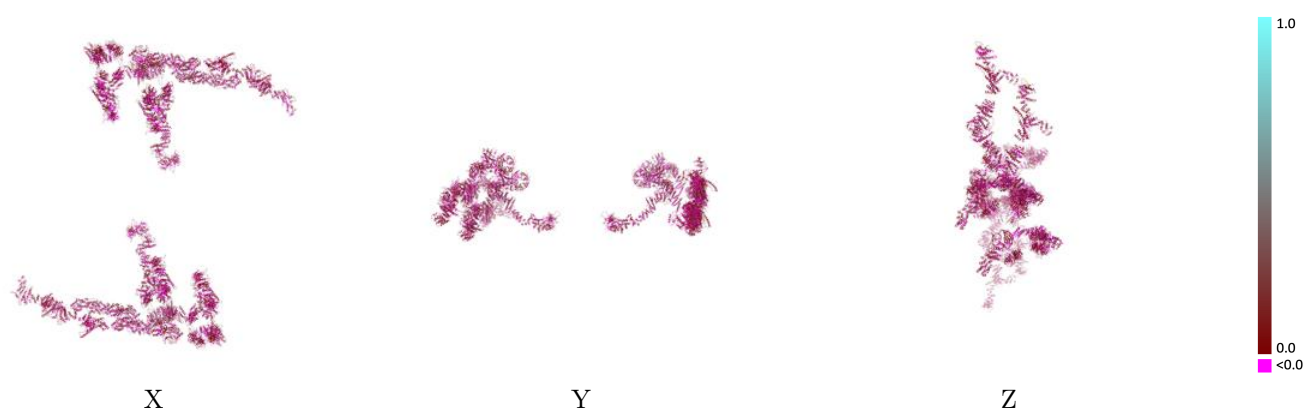
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3103 and PDB model 5A9Q. Per-residue inclusion information can be found in section 3 on page 8.

8.1 Map-model overlay [i](#)

This section was not generated.

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

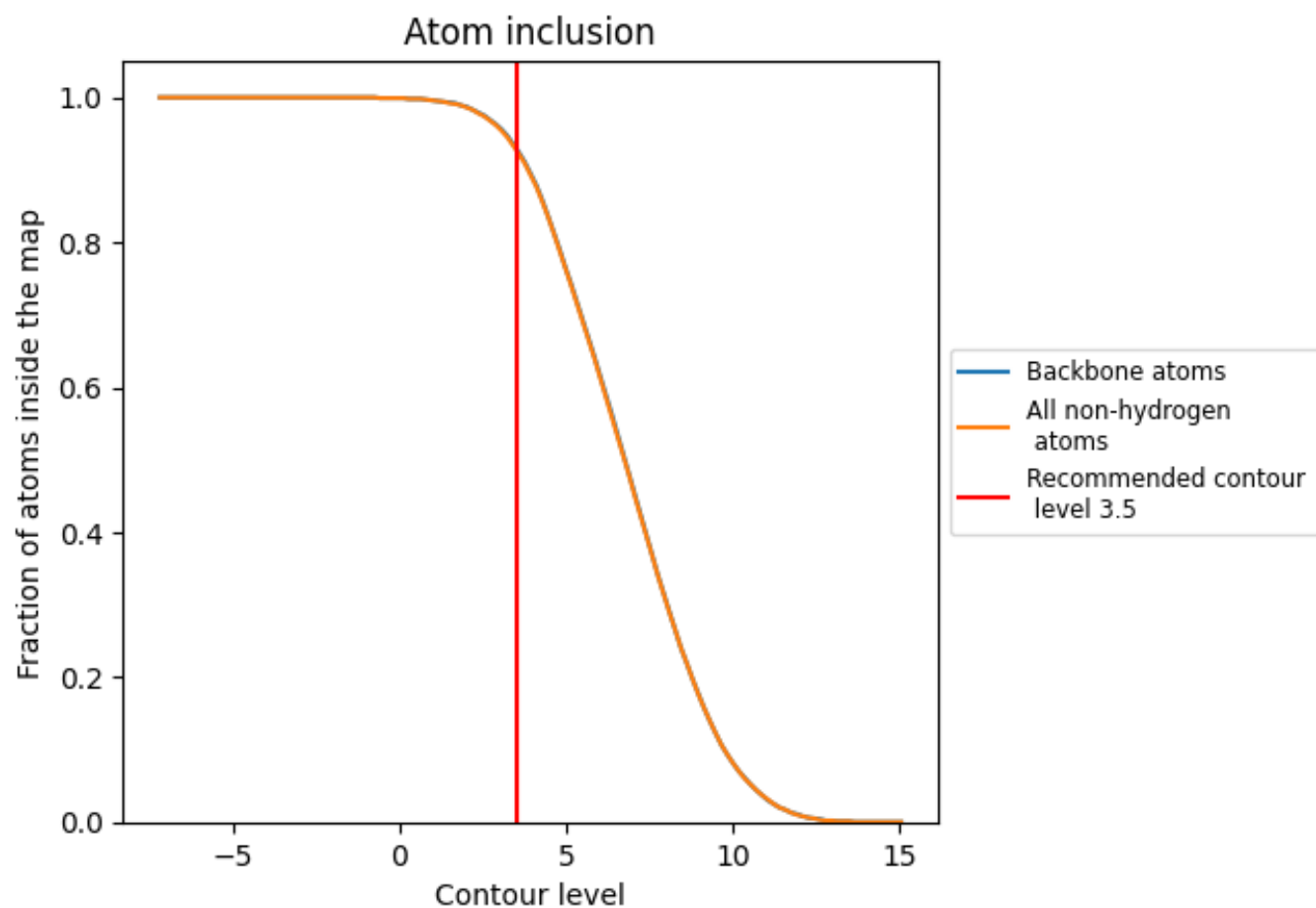


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

8.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 93% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9270	 0.0480
0	 0.9760	 0.0520
1	 0.8030	 0.0300
2	 0.8370	 0.0400
3	 0.8630	 0.0450
4	 0.9590	 0.0580
5	 0.9750	 0.0620
6	 0.9790	 0.0350
7	 0.9740	 0.0520
8	 0.9830	 0.0530
9	 0.9060	 0.0410
A	 0.8030	 0.0510
B	 0.8730	 0.0490
C	 0.8190	 0.0530
D	 0.9520	 0.0540
E	 0.9840	 0.0500
F	 0.9640	 0.0500
G	 0.9840	 0.0520
H	 0.9770	 0.0380
I	 0.9850	 0.0430
J	 0.9470	 0.0400
K	 0.9860	 0.0310
L	 0.9740	 0.0590
M	 0.9840	 0.0630
N	 0.9830	 0.0520
O	 0.9810	 0.0260
P	 0.9660	 0.0570
Q	 0.9920	 0.0490
R	 0.9930	 0.0490
S	 0.9500	 0.0410
T	 0.9720	 0.0500
U	 0.7690	 0.0600
V	 0.9260	 0.0510
W	 0.9930	 0.0550
X	 0.9230	 0.0440



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Chain	Atom inclusion	Q-score
Y	 0.9550	 0.0430
Z	 0.9760	 0.0550
a	 0.9450	 0.0430
b	 0.9270	 0.0400