

Table 3. Protease-sensitive sites of yeast nups

Fragment ID	Band intensity	Mw of fragment	Cleavage site identification approach	
			Edman Sequence	Mw estimation
Nup192-FL		~197		
A	medium	~168	R405	
B	strong	~150	R579	
C	medium	~104	R962 and 964	
D	medium	~89	R1118	
E	weak	~66	K1283 and R1292	
Nup188-FL		~202		
A	weak	~169		D372-D419
B	strong	~149		D584-D603
Nup170-FL		~185		
A	medium	~170		K99-D115
B	medium	~133	K563	
C	weak	~93	R876	
D	medium	~65	K1126 and K1144 (main)	
Nup157-FL		~178		
A	strong	~164		R52-K80
B	medium	~148		K298-K329
C	weak	~129		K466-K487
D	medium	~120		K527-R575
E	medium	~104		R708-R733
F	weak	~79		D929-D952
Pom152-FL		~177		
A	medium	~163		K108-K117
B	medium	~150		R210-K215
C	medium	~133		K356-K367
D	medium	~114		R518-K543
E	weak	~103		K651-K661
Nic96-FL		~124		
A	weak	~113		K59-K102
B	strong	~100		K152-R198
C	weak	~86		K291-K321
D	weak	~75		K389-K423
E	weak	~60		K514-R546
F	medium	~54		R577-R599
G	medium	~49		R629-D639
H	medium	~42		R704-R724
Nup82-FL		~108		
A	medium	~87		D154-D184
B	strong	~52		D433-K497
Ndc1-FL		~92		
A	strong	~55		R393-D433
B	medium	~33		R582-R587
Pom34-FL		~62		
A	medium	~58		D33-R63

Listed are the sites in the yeast nups most sensitive to the proteases, as shown in Fig. 2. The molecular weight of C-terminal fragments, containing a 26-kDa Protein A tag, was calculated on immunoblot scans using National Institutes of Health IMAGE software. The amino acid residue positions, adjacent to the cleavage site are indicated, where D designates an aspartic

acid, K a lysine, and R an arginine. FL, indicates the full-length Protein A-tagged nup.