Supplementary Table S2a: Catalytic Particle Subunits
Columns 1 through 4 represent gene name, gene product length in amino acids, molecular weight of the gene product in kDa and codon adaptation index respectively (all according to the *Saccharomyces* Genome Database); columns 5 through 7 represent sequence coverage in % for proteasomes purified from RJD 1144 (WT), RJD 1979 (rad23Δ) and RJD 2480 (rpn10Δ) respectively; columns 8 and 9 represent functional annotation data from the *Saccharomyces* Genome Database; data were filtered by `DTASelect` (Tabb et al. 2002. J Proteome Res 1(1), 21–6) using these parameters: minimum XCORRs of 1.8, 2.5 and 3.5 for singly, doubly and triply charged precursor ions, respectively, minimum Cn of 0.08, and a minimum requirement of two peptides per protein;

Gene	Length	Weight	CAI	WT	rad23Δ	rpn10Δ	Function	Process
PRE1/YER012W	198	22.5	.204	54.0	45.5	44.9	proteasome endopeptidase	ubiquitin-dependent protein catabolism*
PRE2/YPR103W	287	31.6	.21	55.7	66.9	69.0	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE3/YJL001W	215	23.5	.172	82.3	85.6	85.6	proteasome endopeptidase	ubiquitin-dependent protein catabolism*
PRE4/YFR050C	266	29.4	.148	59.8	55.6	52.3	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE5/YMR314W	234	25.6	.159	82.1	85.9	82.1	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE6/YOL038W	254	28.4	.156	68.5	72.4	74.0	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE7/YBL041W	241	26.9	.166	79.7	77.6	71.4	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE8/YML092C	250	27.2	.143	77.2	53.6	60.4	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE9/YGR135W	258	28.7	.182	77.5	70.2	77.1	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PRE10/YOR362C	288	31.5	.192	56.9	66.7	55.2	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PUP1/YOR157C	261	28.3	.179	52.5	54.4	49.4	proteasome endopeptidase	ubiquitin-dependent protein catabolism
PUP2/YGR253C	260	28.6	.162	86.9	86.5	83.8	proteasome endopeptidase	ubiquitin-dependent protein catabolism*
PUP3/YER094C	205	22.6	.159	52.7	48.8	31.2	proteasome endopeptidase	ubiquitin-dependent protein catabolism
SCL1/YGL011C	252	28.0	.178	89.7	90.9	82.1	proteasome endopeptidase	ubiquitin-dependent protein catabolism

Supplementary Table S2b: Regulatory Particle Subunits
Columns 1 through 4 represent gene name, gene product length in amino acids, molecular weight of the gene product in kDa and codon adaptation index respectively (all according to the *Saccharomyces* Genome Database); columns 5 through 7 represent sequence coverage in % for proteasomes purified from RJD 1144 (WT), RJD 1979 (rad23Δ) and RJD 2480 (rpn10Δ) respectively; columns 8 and 9 represent functional annotation data from the *Saccharomyces* Genome Database; data were filtered by `DTASelect` (Tabb et al. 2002. J Proteome Res 1(1), 21–6) using these parameters: minimum XCORRs of 1.8, 2.5 and 3.5 for singly, doubly and triply charged precursor ions, respectively, minimum Cn of 0.08, and a minimum requirement of two peptides per protein;

Gene	Length	Weight	CAI	WT	rad23Δ	rpn10Δ	Function	Process
RPN1/YHR027C	993	109.5	.206	57.4	51.0	50.8	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN2/YIL075C	945	104.2	.176	49.5	41.8	40.6	molecular function unknown	ubiquitin-dependent protein catabolism

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Gene	Length	Weight	CAI	WT	rad23Δ	rpn10Δ	Function	Process
RPN3/YER021W	523	60.4	.183	27.0	20.7	33.8	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN5/YDL147W	445	51.8	.172	42.2	33.3	42.0	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN6/YDL097C	434	49.8	.154	53.7	48.4	45.4	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN7/YPR108W	429	49.0	.186	34.7	33.1	33.6	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN8/YOR261C	338	38.3	.194	75.7	66.0	56.2	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN9/YDR427W	393	45.8	.218	37.7	36.1	43.8	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN10/YHR200W	268	29.7	.108	60.4	31.7	—	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN11/YFR004W	306	34.4	.204	49.0	29.4	35.3	proteasome endopeptidase	ubiquitin-dependent protein catabolism
RPN12/YFR052W	274	31.9	.18	71.9	62.0	70.8	molecular function unknown	ubiquitin-dependent protein catabolism
RPN13/YLR421C	156	17.9	.162	41.7	42.9	62.2	molecular function unknown	proteolysis and peptidolysis
RPT1/YKL145W	467	52.0	.232	56.1	49.3	51.8	adenosinetriphosphatase*	ubiquitin-dependent protein catabolism
RPT2/YDL007W	437	48.8	.155	63.4	65.0	67.3	adenosinetriphosphatase*	ubiquitin-dependent protein catabolism
RPT3/YDR394W	428	47.9	.209	64.3	65.7	62.4	adenosinetriphosphatase*	ubiquitin-dependent protein catabolism
RPT4/YOR259C	437	49.4	.208	56.5	56.5	45.3	adenosinetriphosphatase*	ubiquitin-dependent protein catabolism
RPT5/YOR117W	434	48.3	.195	73.0	63.4	69.4	adenosinetriphosphatase*	ubiquitin-dependent protein catabolism
RPT6/YGL048C	405	45.3	.218	51.4	52.6	50.6	adenosinetriphosphatase*	ubiquitin-dependent protein catabolism

Supplementary Table S2c: Proteasome–Interacting Proteins
Columns 1 through 4 represent gene name, gene product length in amino acids, molecular weight of the gene product in kDa and codon adaptation index respectively (all according to the *Saccharomyces* Genome Database); columns 5 through 7 represent sequence coverage in % for proteasomes purified from RJD 1144 (WT), RJD 1979 (rad23Δ) and RJD 2480 (rpn10Δ) respectively; columns 8 and 9 represent functional annotation data from the *Saccharomyces* Genome Database; data were filtered by `DTASelect` (Tabb et al. 2002. J Proteome Res 1(1), 21–6) using these parameters: minimum XCORRs of 1.8, 2.5 and 3.5 for singly, doubly and triply charged precursor ions, respectively, minimum Cn of 0.08, and a minimum requirement of two peptides per protein;

Gene	Length	Weight	CAI	WT	rad23Δ	rpn10Δ	Function	Process
RAD23/YEL037C	398	42.4	.164	7.0	—	8.8	damaged DNA binding	nucleotide-excision repair, DNA damage recognition
UBP6/YFR010W	499	57.1	.208	23.4	11.6	37.5	ubiquitin-specific protease	deubiquitination