

# PROTEASOME NOMENCLATURE & DATA TABLE



## 20S Proteasome

NOMENCLATURE						GENE		1° Acc. # (human)	Seq. length (amino acids)	MW (Da)
Baumeister <i>et al.</i> <sup>1</sup>	'Old' human	Coux <i>et al.</i> <sup>2</sup>	Groll <i>et al.</i> <sup>3</sup>	Miscellaneous	UnProtKB <sup>4</sup>	Human	Yeast (S.c.)			
<b>20S <math>\alpha</math>-type subunits</b>										
$\alpha$ 1	iota	Pro- $\alpha$ 6	$\alpha$ 1_sc	Pros27, p27k, C7, Prs2, Y8, Prs2, Sc11	$\alpha$ 6	PSMA6	PRS2	P60900	246	27399
$\alpha$ 2	C3	Pro- $\alpha$ 2	$\alpha$ 2_sc	Pre8, Prs4, Y7	$\alpha$ 2	PSMA2	PRS4	P25787	233	25767
$\alpha$ 3	C9	Pro- $\alpha$ 4	$\alpha$ 3_sc	Pre9, Prs5, Y13	$\alpha$ 4	PSMA4	PRS5	P25789	261	29484
$\alpha$ 4	C6	Pro- $\alpha$ 3	$\alpha$ 4_sc	XAPC-7, Pre6	$\alpha$ 7	PSMA7	PRE6	O14818	248	27887
$\alpha$ 5	zeta	Pro- $\alpha$ 1	$\alpha$ 5_sc	Pup2, Doa5	$\alpha$ 5	PSMA5	PUP2	P28066	241	26411
$\alpha$ 6	C2	Pro- $\alpha$ 5	$\alpha$ 6_sc	nu, Pros30, p30k, Pre5	$\alpha$ 1	PSMA1	PRE5	P25786	263	29556
$\alpha$ 7	C8	Pro- $\alpha$ 7	$\alpha$ 7_sc	Pre10, Prs1, C1, Prc1	$\alpha$ 3	PSMA3	PRS1	P25788	254	28302
<b>20S <math>\beta</math>-type subunits</b>										
$\beta$ 1	Y	Pro- $\beta$ 3	$\beta$ 1_sc	delta, Lmp9, Pre3	$\beta$ 6	PSMB6	PRE3	P28072	239/205	25358/21904
$\beta$ 1i	Lmp2	Pro- $\beta$ 3		Ring12	$\beta$ 9	PSMB9	-	P28065	219/199	23264/21276
$\beta$ 2	Z	Pro- $\beta$ 2	$\beta$ 2_sc	Lmp19, MC14, Pup1	$\beta$ 7	PSMB7	PUP1	Q99436	277/234	29965/25218
$\beta$ 2i	MECL-1	Pro- $\beta$ 2		Lmp10	$\beta$ 10	PSMB10	-	P40306	273/234	28936/24648
$\beta$ 3	C10	Pro- $\beta$ 6	$\beta$ 3_sc	theta, Pup3	$\beta$ 3	PSMB3	PUP3	P49720	205	22949
$\beta$ 4	C7	Pro- $\beta$ 4	$\beta$ 4_sc	Pre1, C11	$\beta$ 2	PSMB2	PRE1	P49721	201	22836
$\beta$ 5	X	Pro- $\beta$ 1	$\beta$ 5_sc	epsilon, Lmp17, MB1, Pre2, Doa3, Prg1	$\beta$ 5	PSMB5	PRE2	P28074	208/204	22897/22458
$\beta$ 5i	Lmp7	Pro- $\beta$ 1		Ring10, Y2, C13	$\beta$ 8	PSMB8	-	P28062	276/204	30354/22660
$\beta$ 6	C5	Pro- $\beta$ 5	$\beta$ 6_sc	gamma, Pre7, Prs3, C5, Pts1	$\beta$ 1	PSMB1	PRS3	P20618	241	26489
$\beta$ 7	N3	Pro- $\beta$ 7	$\beta$ 7_sc	beta, Pros26, Pre4	$\beta$ 4	PSMB4	PRE4	P28070	264/219	29192/24380

## 19S Proteasome

NOMENCLATURE					GENE		1° Acc. # (human)	Seq. length (amino acids)	MW (Da)
Finley <i>et al.</i> <sup>5</sup>	Dubiel <i>et al.</i> <sup>6</sup>	Miscellaneous	UnProtKB <sup>4</sup>	Human	Yeast (S.c.)				
<b>19S (PA700) regulator ATPase subunits</b>									
Rpt1	S7	p48, Mss1, Yta3, Cim5	Subunit 7	PSMC2	CIM5	P35998	432	48503	
Rpt2	S4	p56, Yhs4, Yta5, Mts2	Subunit 4	PSMC1	YTA5	P62191	440	49185	
Rpt3	S6b	S6, p48, Tbp7, Yta2, Ynt1, MS73	Subunit 6b	PSMC4	YTA2	P43686	418	47336	
Rpt4	S10b	p42, Sug2, Pcs1, Crl13,	Subunit 10b	PSMC6	SUG2	P62333	389	44173	
Rpt5	S6a	S6', p50, Tbp1, Yta1	Subunit 6a	PSMC3	YTA1	P17980	439	49204	
Rpt6	S8	p45, Trip1, Sug1, Cim3, Crl3, Tby1, Tbp10, m56	Subunit 8	PSMC5	SUG1	P62195	406	45626	
<b>19S (PA700) regulator non-ATPase subunits</b>									
Rpn1	S2	p97, Trap2, Nas1, Hrd2, Rpd1, Mts4	Subunit 2	PSMD2	HRD2	Q13200	908	100200	
Rpn2	S1	p112, Sen3	Subunit 1	PSMD1	SEN3	Q99460	953	105836	
Rpn3	S3	p58, Sun2	Subunit 3	PSMD3	SUN2	O43242	534	60978	
Rpn4		Son1, Ufd5			RPN4	Q03465(Sc)	531	60153	
Rpn5		p55, Nas5	Subunit 12	PSMD12	YDL147W	O00232	455	52773	
Rpn6	S9	p44.5, Nas4/6?	Subunit 11	PSMD11	YDL097C	O00231	421	47333	
Rpn7	S10a	p44, HUMORF07	Subunit 6	PSMD6		Q15008	389	45531	
Rpn8	S12	p40, Mov-34h, Nas3	Subunit 7	PSMD7	YOR261C	P51665	324	37025	

## 19S Proteasome continued

NOMENCLATURE				GENE		1° Acc. # (human)	Seq. length (amino acids)	MW (Da)
Finley <i>et al.</i> <sup>5</sup>	Dubiel <i>et al.</i> <sup>6</sup>	Miscellaneous	UniProtKB <sup>4</sup>	Human	Yeast (S.c.)			
<b>19S (PA700) regulator non-ATPase subunits continued</b>								
Rpn9	S11	p40.5, Les1, Nas7	Subunit 13	PSMD13		Q9UNM6	376	42918
Rpn10	S5a	p54, ASF1, Sun1, Mcb1, Mbp1	Subunit 4	PSMD4	SUN1	P55036	377	40736
Rpn11	S13	Poh1, Mpr1, Pad1h	Subunit 14	PSMD14	MPR1	O00487	310	34577
Rpn12	S14	p31, Nin1, Mts3	Subunit 8	PSMD8	NIN1	P48556	257	30005
Rpn13		YLR421C			RPN13	O13563(Sc)	156	17902
	S5b	p50.5	Subunit 5	PSMD5		Q16401	503	56065
	S15	p27-L	Subunit 9	PSMD9	NAS2	O00233	223	24654
		p28, Gankyrin, Nas6	Subunit 10	PSMD10		O75832	226	24428

## 11S Activator

NOMENCLATURE					GENE (human)	1° Acc. # (human)	Seq. length (amino acids)	MW (Da)
Dubiel <i>et al.</i> <sup>6</sup>	Ma <i>et al.</i> <sup>8</sup>	Realini <i>et al.</i> <sup>9</sup>	Kandil <i>et al.</i> <sup>10</sup>	UniProtKB <sup>4</sup>				
11S $\alpha$	PA28 $\alpha$	REG $\alpha$		Subunit 1	PSME1	O06323	249	28723
11S $\beta$	PA28 $\beta$	REG $\beta$		Subunit 2	PSME 2	Q9UL46	238	27230
11S $\gamma$	PA28 $\gamma$	REG $\gamma$	Ki antigen	Subunit 3	PSME 3	P61289	254	29506

## COP9 Signalosome

NOMENCLATURE						GENE (human)	Homology to 19S subunit	1° Acc. # (human)	Seq. length (amino acids)	MW (Da)
Dubiel <i>et al.</i> <sup>6</sup>	'Old' human	A. thaliana	Drosophila	Mouse	UniProtKB <sup>4</sup>					
Csn1	Sgn1, Gps1	Fus6, COP11	DCH1	COPS1, Mfh	Subunit 1	GPS1	Rpn7	Q13098	471	53372
Csn2	Sgn2, Trip15, hAlien	Subunit 2	DCH2, Alien	COPS2	Subunit 2	COPS2	Rpn6	P61201	443	51597
Csn3	Sgn3	Subunit 3	DCH3	COPS3	Subunit 3	COPS3	Rpn3	Q9UNS2	422	47742
Csn4	Sgn4	COP8, FUS4	DCH4	COPS4	Subunit 4	COPS4	Rpn5	Q9BT78	406	46269
Csn5	Sgn5, JAB1	AJH1, AJH2	DCH5	COPS5, Jab1	Subunit 5	COPS5	Rpn11	Q92905	334	37579
Csn6	Sgn6, HVIP	Subunit 6	DCH6	COPS6	Subunit 6	COPS6	Rpn8	Q7L5N1	327	36163
Csn7a	Sgn7	FUS5	DCH7	COPS7a	Subunit 7a	COPS7a	Rpn9	Q9JWB8	275	30277
Csn7b	Sgn7			COPS7b	Subunit 7b	COPS7b	Rpn9	Q9H9Q2	264	29622
Csn8	Sgn8, hCOP9	COP9, Fus7	DCH8	COPS8	Subunit 8	COPS8	Rpn12	Q99627	209	23226

## TPPII

NOMENCLATURE		UniProtKB <sup>4</sup>	GENE (human)	1° Acc. # (human)	Seq. length (amino acids)	MW (Da)
TPP-II	Tripeptidyl aminopeptidase					
		Tripeptidyl peptidase 2	TPP2	P29144	1248	138219

### Literature References:

- The proteasome: paradigm of a self-compartmentalizing protease: W. Baumeister, *et al.*; *Cell* **92**, 367 (1998)
- Phylogenetic relationships of the amino acid sequences of prosome (proteasome, MCP) subunits: O. Coux, *et al.*; *Mol. Gen. Genet.* **245**, 769 (1994)
- Structure of 20S proteasome from yeast at 2.4Å resolution: M. Groll, *et al.*; *Nature* **386**, 463 (1997)
- UniProtKB - the Universal Protein Resource at <http://www.ebi.uniprot.org/index.shtml>
- Unified nomenclature for subunits of the *Saccharomyces cerevisiae* proteasome regulatory particle: D. Finley, *et al.*; *Trends Biochem. Sci.* **23**, 244 (1998)
- Subunits of the regulatory complex of the 26S protease: W. Dubiel, *et al.*; *Mol. Biol. Reports* **21**, 27 (1995)
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- Identification, purification, and characterization of a protein activator (PA28) of the 20S proteasome (macropain): C.P. Ma, *et al.*; *J. Biol. Chem.* **267**, 10515 (1992)
- Characterization of the recombinant REG $\alpha$ , REG $\beta$ , and REG $\gamma$  proteasome activators: C. Realini, *et al.*; *J. Biol. Chem.* **272**, 25483 (1997)
- PA28 subunits of the mouse proteasome: primary structures and chromosomal localization of the genes: E. Kandil, *et al.*; *Immunogenetics* **46**, 337 (1997)
- Unified nomenclature for the COP9 signalosome and its subunits: an essential regulator of development: X.-W. Deng, *et al.*; *Trends in Genetics* **16**, 202 (2000)

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