

Table S1. Detected post-translational modifications (PTMs) on proteasome subunits of *Arabidopsis*.

Subunits	Gene-ID	Quantity	Types, Locations of PTMs
Rpt1a	AT1G53750	6	V ² nt, K ¹³ ub, S ⁹⁶ ph, T ¹²⁵ ph, C ³⁷⁰ ro, K ⁴⁰⁰ ub
Rpt1b	AT1G53780	2	S ²⁸⁹ ph, C ⁵⁶³ ro
Rpt2a	AT4G29040	3	G ² my, H ¹²³ nt, K ³⁵³ nt
Rpt2b	AT2G20140	3	G ² my, H ¹²³ nt, K ³⁵³ nt
Rpt3	AT5G58290	7	A ² na/nt, S ¹⁶ ph, A ¹⁸ nt, K ⁷⁰ ac, C ³⁶⁹ no, K ³⁸⁷ ac
Rpt4a	AT5G43010	6	T ² nt/na, K ⁴⁸ ac, S ⁸⁰ ph, K ²⁰³ ub, K ³⁰⁴ nt
Rpt4b	AT1G45000	4	K ⁴⁸ ac, S ⁸⁰ ph, K ²⁰³ ub, K ³⁰⁴ nt
Rpt5a	AT3G05530	7	A ² na/nt, C ⁵⁰ no, S ⁵² ph, C ²²⁵ ro, T ²⁹⁴ nt, N ³⁰⁰ nt
Rpt5b	AT1G09100	3	A ² na/nt, C ²²⁴ ro
Rpt6a	AT5G19990	4	A ² na/nt, C ¹⁹ ro/no
Rpt6b	AT5G20000	2	A ² na/nt
Rpn1a	AT2G20580	8	S ⁴⁰ ph, M ¹⁰⁷ mo, K ¹¹³ ac, K ¹⁶⁸ ac, K ²¹⁸ ub, T ³⁴³ ph, S ³⁵⁹ ph, C ⁶²¹ no
Rpn1b	AT4G28470	3	M ⁷² mo, T ³⁴³ ph, S ³⁵⁹ ph
Rpn2a	AT1G08410	0	
Rpn2b	AT2G32730	11	A ² na, K ²⁷⁹ ac, T ³¹⁸ nt, S ⁴¹² nt, A ⁴³³ nt, K ⁷³⁰ ac, S ^{876/878/891/896} ph,
Rpn10	AT4G38630	12	K ⁹⁰³ nt V ² nt, K ¹³⁰ ac, S ¹³⁶ ph, S ¹⁸⁷ nt, T ¹⁸⁸ nt, D ²⁵⁸ nt, S ^{263/265/363} ph, K ^{379/380/386} ub
Subunits	Gene-ID	Quantity	Types, Locations of PTMs
Rpn3a	AT1G20200	9	T ² nt, T ¹² ph, S ^{14/16/19/20} ph, T ^{22/24} ph, C ²⁴⁰ no
Rpn3b	AT1G75990	8	T ^{12/14} ph, S ^{16/19} ph, T ²² ph, S ²³ ph, T ²⁴ ph, C ²³⁹ no
Rpn5a	AT5G09900	6	G ² na/nt, S ⁴ ph, K ¹⁹ ub, C ²³⁴ no, K ³²⁰ ac
Rpn5b	AT5G64760	2	K ¹⁹ ub, C ²³⁴ no
Rpn6	AT1G29150	5	V ² na/nt, C ^{51/332} no, M ³⁶⁴ mo
Rpn7	AT4G24820	1	M ¹ na
Rpn8a	AT5G05780	3	M ¹ na, S ²¹⁸ ph, Y ²¹⁹ ph
Rpn8b	AT3G11270	1	M ¹ na
Rpn9a	AT5G45620	1	A ² na
Rpn9b	AT4G19006	3	A ² na/nt, A ³ na
Rpn11	AT5G23540	2	K ²³⁸ ub, S ²⁶⁵ ph
Rpn12a	AT1G64520	2	M ¹ na, C ¹⁹⁰ no
Rpn12b	AT5G42040	1	C ¹⁵⁶ no
PAA1	AT5G35590	2	K ^{33/181} ac
PAA2	AT2G05840	1	K ¹⁸¹ ac
PAB1	AT1G16470	5	G ² na, K ⁵⁰ ac, K ⁹² ub, K ^{165/171} ac
PAB2	AT1G79210	5	G ² na, K ⁵⁰ ac, K ⁹² ub, K ¹⁶⁵ ac, K ¹⁷¹ ac
PAC1	AT3G22110	8	K ⁴⁰ ub, K ¹⁹⁸ ac, M ²⁰⁰ mo, T ²¹⁸ ph, S ^{220/232} ph, T ²³⁴ ph, k ²³⁹ ac
PAC2	AT4G15160	0	
PAD1	AT3G51260	3	K ²⁹ ub, L ⁹⁹ nt, K ¹⁷⁶ ac
PAD2	AT5G66140	3	K ²⁹ ub, L ⁹⁹ nt, K ¹⁷⁶ ac
PAE1	AT1G53850	3	K ⁵² ac, K ⁶⁶ ub, E ⁹⁵ na
PAE2	AT3G14290	4	K ⁵² ac, K ^{66/185} ub, E ⁹⁵ na
PAF1	AT5G42790	7	M ¹ na, K ⁵¹ ub, S ⁹⁰ ph/nt, S ⁹² ph, k ¹⁶⁹ ub/ac
PAF2	AT1G47250	7	M ¹ na, K ⁵¹ ub, S ⁹⁰ ph/nt, S ⁹² ph, K ¹⁶⁹ ub/ac
PAG1	AT2G27020	6	S ² ph/na/nt, K ^{173/240} ac, M ²⁴⁶ mo
PBA1	AT4G31300	4	T ¹³ nt, S ⁵⁸ ph/nt, S ⁶⁰ ph
PBB1	AT3G27430	4	T ⁴⁰ nt, G ⁵⁰ nt, G ⁸⁴ nt, A ⁸⁵ nt
PBB2	AT5G40580	4	T ⁴⁰ nt, G ⁵⁰ nt, G ⁸⁴ nt, A ⁸⁵ nt
PBE2	AT3G26340	5	K ^{47/53} ub, T ⁵⁸ nt, K ^{89/128} ac
PBF1	AT3G60820	2	V ¹¹⁵ nt, S ¹⁶³ ph
PBD2	AT4G14800	0	

PBD1	AT3G22630	1	M ³⁶ mo
PBC1	AT1G21720	2	S ² na, K ⁹⁸ ac
PBE1	AT1G13060	2	K ^{89/128} ac
PBC2	AT1G77440	2	S ² na, K ⁹⁸ ac
PBG1	AT1G56450	2	S ^{234/235} ph
UMP1-like	AT1G67250	0	
UMP1-like	AT5G38650.1	0	

Illustrated example: V²nt, V: modified valine; 2: second amino acid of protein sequence; nt: PTM types.

Abbreviation of different PTMs: ac/lysine acetylation, bu/lysine 2-hydroxyisobutyrylation, ca/carbonylation, ma/lysine malonylation, me/lysine methylation, mo/methionine oxidation, my/myristoylation, na/N-terminal acetylation, ng/N-glycosylation, no/S-nitrosylation, nt/N-terminus proteolysis, nu/N-terminal ubiquitination, og/O-GlcNAcylation, ph/phosphorylation, ro/reversible cysteine oxidation, sg/S-glutathionylation, sm/lysine SUMOylation, su/lysine succinylation, ub/lysine ubiquitination.