

Table II. Arabidopsis RING-domain-containing Protein Groups Based on Domain Organization

Each RING-domain-containing protein was analyzed for the presence of additional domain and proteins with similar domain organization were placed in groups.






















Group No.	No. of Protein ^a	Representative RING Proteins AGI Code and Domain Organization ^b	Species ^c	Domains	Domain Description and/or Predicted Function
1	140	At2g47700 	At, Bn, Ce, Dm, Hs, Mm, Os, Sc, Sp, XI and Zm	RING 	Zinc binding domain. Protein-protein interactions. Ubiquitin ligase domain. (Lorick et al., 1999)
2.1	3	At3g05670 	At, Ce, Dm, Hs, Mm, Os, Sc, Sp and XI	additional RING /PHD 	Plant homeodomain C4HC3 type. Found in proteins involved in chromatin-mediated transcriptional regulation. Protein-protein interactions. Probable ubiquitin ligase domain. (Aasland et al., 1995; Capili et al., 2001; Lu et al., 2002)
2.2	1	At3g24800 	At	ZNF_ZZ 	Zinc finger domain C-x2-C-x5-C-x2-C type. Found in Dystrophin and CREB-binding protein. Protein-protein interactions. (Ponting et al., 1996)
3	4	At2g44950 	At	AAA ATPase 	ATPase associated with diverse cellular activities. Contains an ATP binding site. (Neuwald et al., 1999)
4.1	6	At5g07270 	At, Ce, Dm, Hs, Mm, Os, and XI	ANK 	Ankyrin repeats. Protein-protein interaction domain. (Bork, 1993)
4.2	1	At5g13530 	At	pKinase 	Serine/threonine and tyrosine protein kinase. Protein phosphorylation.
5	2	At4g21070 	At, Ce, Hs, Mm, Os, and XI	BRCT 	Breast cancer carboxy-terminus domain. Phospho-protein binding domain. Found in proteins involved in cell cycle checkpoint or DNA damage repair. (Callebaut and Mornon, 1997; Yu et al., 2003)
6	20	At5g47050 	At, Bn, Ce, Dm, Hs, Mm, Os, Sc, Sp and XI	Coiled Coil 	Protein-protein interaction /oligomerization motif made up of two to five alpha helices. (Burkhard et al., 2001)
7	2	At5g51450 	At, Ce, Hs, Mm, and XI	CUE 	Ubiquitin binding motif. Found in proteins involved in ubiquitination. (Kang et al., 2003; Shih et al., 2003)
				Transmembrane (TM) 	
8.1	10	At3g16600 	At, Hs, Mm, Os, Sc, and Sp	DEXDc 	DEAD-like helicases. ATP-dependent helicase activity. Found in proteins involved in DNA damage repair. (Rocak and Linder, 2004)




























Table II continued					
Group No.	No. of Protein ^a	Representative RING Proteins AGI Code and Domain Organization ^b	Species ^c	Domains	Domain Description and/or Predicted Function
8.2	2	At5g10370 	At	HELICc 	Helicase superfamily C-terminal domain. Found in a number of helicases. (Rocak and Linder, 2004)
8.3	1	At3g54460 	At and Os	KH  HA2  Fbox  IBR  ZNF_C2H2 	K homology RNA binding domain. KH was first identified in hnRNP K. Proteins usually contains least two copies. (Ostareck-Lederer et al., 1998) Helicase associated domain. Found in a variety of RNA helicases and may be involved in nucleic acid binding. F-box domain found in proteins which are the substrate binding component of the SCF (Skp1-Cullin-F-box) E3 ligase. Interacts with SKP1. (Kipreos and Pagano, 2000) See group 11.1 See group 29.1
9	1	At3g18290 	At and Os	HHE 	Function unknown. Found as tandem repeats in plant, bacteria and yeast proteins. Implicated in cell wall physiology. (Brunskill et al., 1997)
10	1	At3g48030 	At	HIG_1_N  TM 	Hypoxia induced protein conserved region. Found at the N terminus of TM proteins predicted to be involved in the response to hypoxia. (Gracey et al., 2001) See group 7
11.1	29	At3g14250 	At, Dm, Hs, Mm, Os and Sp	IBR 	In Between Ring fingers. Cystiene rich region (C6HC) usually found between two RING domains. Function unknown. (van der Reijden et al., 1999)
11.2	1	At1g32340 	At, Ce, Hs, Mm, Os and Sp	RWD 	RING finger and WD repeat containing proteins and DEXDc-like helicases. Shows similarity to the UBCc domain. Protein interaction domain. (Doerks et al., 2002)
12	5	At1g62310 	At, Mt and Ps	JmjC 	Jumonji C domain. Predicted to be cupin metalloenzyme that may regulate chromatin remodeling. (Clissold and Ponting, 2001)
13	2	At2g21380 	At and Os	KISc  Coiled coil 	Kinesin motor catalytic domain. Involved in cell division and organelle transport. (Block, 1998) See group 6
14	1	At1g18660 	At, Dm, Hs, Mm and Sp	LON 	ATP-dependent protease La (LON) domain. ATP-dependent serine peptidases. (Van Dyck et al., 1994)
15	2	At2g22690 	At and Dd	LisH  CTLH 	Lissencephaly type-1 (Lis1) like homology motif. May be involved in regulating microtubule dynamics. (Reiner, 2000) C-terminal to LisH motif. Function unknown.

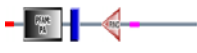






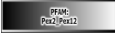




























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Group No.	No. of Protein ^a	Representative RING Proteins AGI Code and Domain Organization ^b	Species ^c	Domains	Domain Description and/or Predicted Function
16	6	At4g09560 	At, Dm, Hs, Mm, Os, Sp and XI	PA  TM	Protease associated domain. Found in plant vacuolar sorting proteins and E3 ligases. (Borchers et al., 2002) See group 7
17.1	1	At1g12470 	At, Ce, Dm, Os, Sc and Sp	PEP3_Vps18 	Region found in Pep3/Vps18 proteins. Found in protein involved in Golgi function and vacuolar sorting. Usually precedes a RING domain. (Warner et al., 1998)
17.2	1	At1g08190 	At, Dm, Le and Os	Clathrin /CLH  WD40 Coiled Coil	Region in Clathrin and VPS. Usually found as one or two repeats in vacuolar membrane proteins. Function unknown. (Warner et al., 1998) See group 28 See group 6
18	2	At1g79810 	At, Ce, Dd, Dm, Hs, Mm, Os, Sc and Sp	PEX 	Similar to the N-terminal region of the Pex2 and Pex12 peroxisomal biogenesis proteins. Region contains two TM domains. (Sparkes and Baker, 2002)
19	1	At4g17910 	At	PPR  TM	Pentatricopeptide repeat domain. Typically found as four or more tandem repeats mainly in plant proteins. Function unknown. (Small and Peeters, 2000) See group 7
20	2	At3g45630 	At, Dm, Hs, Mm, Os and XI	RRM 	RNA recognition motif. Putative RNA binding motif. Found in proteins implicated in regulation of alternative splicing and transcriptional regulation. (Birney et al., 1993)
21	13	At2g41980 	At, Bn, Ce, Dm, Hs, Mm, Os and XI	SINA 	Seven in absentia protein family. Similar to the Drosophila Sina E3 ligase. Protein interactions (Hu et al., 1997)
22	1	Atg2g22010 	At, Ce, Dm and Hs	SPRY 	Domain in SPLa and the ryanodine Receptor. Function unknown. (Ponting et al. 1997)
23	2	At1g02860 	At, Os and Sp	SPX 	Domain named after SYG1/Pho81/XPR1 proteins. Usually found at the amino terminus of a variety of proteins. Function unknown.
24	107	At5g57750 		One/more transmembrane	
25	29	At1g76410 		Signal peptide 	
26	6	At5g39550 	At, Hs, Mm and Os	SRA  PHD	SET and RING finger associated domain. Found in SET domain containing proteins. Histone and chromatin binding domain. (Citterio et al., 2004) See group 2.1

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27.1	9	At2g22680 	At and Os	VWA 	von Willebrand factor type A domain. Protein-protein interactions. Found in cell adhesion and extracellular matrix proteins and intracellular proteins such as copines and Rpn10. (Whittaker and Hynes, 2002)
27.2	5	At1g79380 	At and Os		
28	2	At1g21655 	At, Ce, Dm, Hs, Le, Mm, Os, Sc and XI	WD40 	Found as tandem repeats each containing a central Trp/Asp motif. Phospho-ser/thr binding domain. (Yaffe and Elia, 2001)
29.1	4	At1g77770 	At, Ce, Dm, Hs, Mm, Os, Sc, Sp and XI	ZNF_C2H2 	Zinc finger domain C-x2-C-x12-H-x3-H type. Implicated in nucleic acid binding. (Yaffe and Elia, 2001)
29.2	3	At5g06420 	At, Ce, Dm, Hs, Mm, Os, Ps, Sc and Sp	ZNF_C3H1 	Zinc finger domain C-x8-C-x5-C-x3-H type. Found in proteins involved in cell cycle or cell growth. Nucleic acid binding. (Worthington et al., 1996)
29.3	2	At2g42160 	At, Ce, Dm, Hs, Mm, Os, Sc, Sp and XI	ZNF_UBP 	Ubiquitin C-terminal Hydrolase-like zinc finger. Found in ubiquitin specific proteases and HDAC6. Ubiquitin binding domain. (Seigneurin-Berny et al., 2001; Hook et al., 2002)
				Coiled coil	See group 6
30	3	At5g59550 	At and Os	DUF1117 	Domain of unknown function

^aNumbers do not include the RING-v and RING-D domain-containing proteins. These types of RING proteins either did not contain any other known/detectable domains or only were only found to contain predicted transmembrane domains.

^bDomain organization of each RING protein was determined using the SMART, Pfam or Prosite databases. Schematics were generated using the SMART database. Pink boxes represent regions of low complexity as determined by SMART.

^cSpecies that have RING proteins with similar domain architecture. BLAST searches, SMART and Pfam databases were used to determine the species distribution of each RING group. Abbreviations: At, *Arabidopsis thaliana*; Bn, *Brassica napus*; Ce, *Caenorhabditis elegans*; Dd, *Dictyostelium discoideum*; Dm, *Drosophila melanogaster*; Hs, *Homo sapien*; Le, *Lycopersicon esculentum*; Mm, *Mus musculus*; Mt, *Medicago trunactula*; Os, *Oryza sativa*; Ps, *Pisum sativum*; Sc, *Saccharomyces cerevisiae*; Sp, *Schizosaccharomyces pombe*; XI, *Xenopus laevis*; Zm, *Zea mays*.