

A>AtRD21 NP_564497 [*Arabidopsis thaliana*]

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MGFLKPTMAILFLAMVAVSSAVDMSIISYDEKHGVSTTGRSEAEVMSIYEAWLVKHGKAQSQNSLVEK
DRRFEIFKDNLRFVDEHNEKNLSYRLGLTRFADLTNDEYRSKYLGAKMEKKERRSLRYEARVGDEL
ESIDWRKKGAVAEVKDQGGCGSCWAFSTIGAVEGINQIVTGLTLTSEQELVDCDTSYNEGCNGGLMDY
AEFEIIKNGGIDTDKDYPYKGVDGTCDQIRKNAKVVTIDSYEDVPTYSEESLKKAVAHQPISIAIEAGGRAF
QLYDSGIFDGSCGTQLDHGVAVGYGTENGKDYWIVRNSWGKSWGESGYLRMARNIASSSGKCGIAEP
SYPIKNGENPPNPGPSPSPIKPPTQCDSYTCPESNTCCLFEYGKYCFAWGCCPEAATCCDDNYSCCP  
HEYPVCSDLQGTCLLSKNSPFSVKALKRKPATPFWSQGRKNIA
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>NbALP DQ094022 [*Nicotiana benthamiana*]

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MSRFSLLLALVVAGGLFAAALAGPATFADENPIRQIVSDGLHELENGILQVVGKTRHALLFARFAHRYGK
RYETVEIKQRFEVFLDNLMIRSHNKKGLSYKLGVNEFTDITWDEFRRDRLGAAQNCSATTKGNLKLTN
VVLPETKDWREAGIVSPVKNQGKCGSCWTFSTTGAEAAYGQAFGKGISLSEQQLVDCAGAFNNFGCNG
GLPSQAFEYIKSNGGLTEEAYPYTGKMLCFSSENVGKVIDSNITGAEDELKYAVALVRPVSIAFE  
VIKGFKQYKSGVTECNTPMDVNHAVLAVGVENGVPYWLIKNSWGADWGDNGYFKMEMGKN  
MCGIATCASYPVVA
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Band	Peptide sequence	Origin	Xcorr**	dCn
3	K.AVAHQPI <u>SIAIEAGGR</u> .A	AtRD21	5.15	0.32
	K.CGIAIE <u>P</u> <u>S</u> <u>Y</u> <u>P</u> <u>I</u> .N	AtRD21	2.52	0.20
	K.DYWIVR.N	AtRD21	2.07	0.01
	K.KAVAHQPI <u>SIAIEAGGR</u> .A	AtRD21	5.48	0.45
	K.NGGIDTD <u>D</u> <u>K</u> <u>D</u> <u>Y</u> <u>P</u> <u>K</u> .G	AtRD21	4.17	0.37
	K.SWGESGYLR.M	AtRD21	2.69	0.20
	K.VVTIDS <u>Y</u> <u>E</u> <u>D</u> <u>V</u> <u>P</u> <u>T</u> <u>Y</u> <u>SE</u> <u>E</u> <u>S</u> <u>L</u> .K	AtRD21	5.10	0.50
	K.VVTIDS <u>Y</u> <u>E</u> <u>D</u> <u>V</u> <u>P</u> <u>T</u> <u>Y</u> <u>SE</u> <u>E</u> <u>S</u> <u>L</u> K.K	AtRD21	4.08	0.27
4	K.AVAHQPI <u>SIAIEAGGR</u> .A	AtRD21	4.55	0.39
	K.CGIAIE <u>P</u> <u>S</u> <u>Y</u> <u>P</u> <u>I</u> .N	AtRD21	3.15	0.15
	K.GVDGTC <u>D</u> <u>Q</u> <u>I</u> <u>R</u> .K	AtRD21	2.65	0.13
	K.KAVAHQPI <u>SIAIEAGGR</u> .A	AtRD21	5.60	0.43
	K.NGGIDTD <u>D</u> <u>K</u> <u>D</u> <u>Y</u> <u>P</u> <u>K</u> .G	AtRD21	4.08	0.15
	K.SWGESGYLR.M	AtRD21	2.85	0.09
	K.VVTIDS <u>Y</u> <u>E</u> <u>D</u> <u>V</u> <u>P</u> <u>T</u> <u>Y</u> <u>SE</u> <u>E</u> <u>S</u> <u>L</u> .K	AtRD21	5.52	0.50
	K.VVTIDS <u>Y</u> <u>E</u> <u>D</u> <u>V</u> <u>P</u> <u>T</u> <u>Y</u> <u>SE</u> <u>E</u> <u>S</u> <u>L</u> K.K	AtRD21	4.86	0.36
5	K.AVAHQPI <u>SIAIEAGGR</u> .A	AtRD21	4.30	0.48
	K.CGIAIE <u>P</u> <u>S</u> <u>Y</u> <u>P</u> <u>I</u> .N	AtRD21	4.28	0.24
	K.DYWIVR.N	AtRD21	2.21	0.07
	K.KAVAHQPI <u>SIAIEAGGR</u> .A	AtRD21	5.66	0.51
	K.NGGIDTD <u>D</u> <u>K</u> <u>D</u> <u>Y</u> <u>P</u> <u>K</u> .G	AtRD21	3.92	0.38
	K.SWGESGYLR.M	AtRD21	2.83	0.26
	K.VVTIDS <u>Y</u> <u>E</u> <u>D</u> <u>V</u> <u>P</u> <u>T</u> <u>Y</u> <u>SE</u> <u>E</u> <u>S</u> <u>L</u> .K	AtRD21	5.37	0.46
	K.VVTIDS <u>Y</u> <u>E</u> <u>D</u> <u>V</u> <u>P</u> <u>T</u> <u>Y</u> <u>SE</u> <u>E</u> <u>S</u> <u>L</u> K.K	AtRD21	4.18	0.35
	K.NM*CGIATC <u>A</u> <u>S</u> <u>Y</u> <u>P</u> <u>V</u> <u>V</u> A	NbALP	3.51	0.42
	K.NMCGIATC <u>A</u> <u>S</u> <u>Y</u> <u>P</u> <u>V</u> <u>V</u> A	NbALP	3.03	0.40
	K.SNGGLD <u>T</u> <u>E</u> <u>E</u> <u>A</u> <u>Y</u> <u>P</u> <u>T</u> <u>G</u> .N	NbALP	4.90	0.47
	K.YAVALVR.P	NbALP	2.73	0.16
	K.YAVALVR <u>P</u> <u>S</u> <u>I</u> <u>A</u> <u>F</u> <u>E</u> <u>V</u> <u>I</u> .G	NbALP	5.09	0.36

Figure S1 Identification of DCG-04 labeled proteases from agroinfiltrated *N. benthamiana*. DCG-04 labeled proteins were purified, digested with trypsin, and analyzed by mass spectrometry. **A)** Sequences of *Arabidopsis* RD21 and *N. benthamiana* ALP (Hao et al., 2006). The signal peptide and prodomain are indicated in light and dark grey, respectively. The identified tryptic peptides and catalytic residues are underlined and boldface, respectively. **B)** Summary of the identified tryptic peptides, with individual scores. *, oxidized methionine; **, X correlation value: >1.5 maybe; >2.5 good; >3.5 excellent; >4.5 no doubt. Only tryptic peptides are shown.