

Supplemental material

Type II-Metacaspases are involved in cell stress but not in cell death in the unicellular green algae *Dunaliella tertiolecta*

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Table S1. Inhibition of Rase and Kase enzymatic activities with reversible and irreversible protease inhibitors presenting different target inhibition sites, at different final concentrations.

Inhibitor	Compound	Target protoein inhibition	Type of inhibition
PMSF	Phenylmethylsulfonyl fluoride	Serine-proteases	Reversible
Z-VAD-FMK	Benzoyloxycarbonyl-Val-Ala-Asp (OMe) fluoromethylketone	Caspases	Irreversible
4A-PMSF	4-(2-Aminoethyl)benzenesulfonyl fluoride hydrochloride	Serin-proteases	Irreversible
BOC-D-FMK	Boc-Asp(OMe) fluoromethylketone	Caspases	Irreversible
E64	Trans-Epoxysuccinyl-L-leucylamido(4-guanidino) butane	Cisteinyl-proteases	Irreversible
Leupeptin	Leupeptin	Serine & cisteinyl-proteases	Reversible
Benzamidine	Benzamidine	Poly-ADPribose polymerase (PARP)	Reversible

Table S2. In-gel-Rase activity bands (zymograms) analyses by MALDI (matrix-assisted laser desorption ionization) source and tandem time-of-flight (TOF/TOF) mass analyses. For protein identification, peptide lists from the MS analysis were submitted to the Mascot search engine version 2.1 (Matrix Science, London, UK) integrated in GPS ExplorerTM v3.5 (AB Sciex). A combined (MS+MS/MS) type analysis was run by aligning similar fragments with those sequences uploaded in NCBI nr Uniprot databases restricted to Viridiplantae as search criteria. For each Rase substrate the 10 most probable matching proteins found are shown. The protein score C.I. % is the confidence interval for the protein scores that the Mascot search engine assigns to each identification. Values above 99% are considered as significant high identity.

Zymogram	Band/Species	Protein Score C.I.%	Protein name	M.W. (kDa)	Accession number
RVRR	1/D.t	99.812	Phytochrome B, partial [<i>Tarenaya hassleriana</i>]	117.1	AAW56607.1
	1/D.t	99.746	Homeodomain-like superfamily protein [<i>Arabidopsis thaliana</i>]	447.1	NP_974216.1
	1/D.t	99.598	110 kDa 4SNC-Tudor domain protein [<i>Pisum sativum</i>]	108.6	BAC06184.1
	1/D.t	99.198	Asparaginyl-tRNA synthetase, partial [<i>Hyacinthus orientalis</i>]	10.0	AAT08691.1
	1/D.t	99.058	Hypothetical protein PHYPA_024096 [<i>Physcomitrella patens</i>]	78.6	PNR34279.1
	1/D.t	98.918	THO complex subunit 4A-like isoform X1 [<i>Physcomitrella patens</i>]	28.9	XP_024365628.1
	1/D.t	98.841	Unknown protein [<i>Arabidopsis thaliana</i>]	13.9	AAD23025.2
	1/D.t	98.541	CDT1-like protein a, chloroplastic [<i>Oryza sativa Japonica Group</i>]	64.5	XP_015634451.1
	1/D.t	97.345	Hypothetical protein VITISV_010874 [<i>Vitis vinifera</i>]	37.3	CAN82058.1
	1/D.t	97.22	Retrotransposon protein, putative, Ty3-gypsy subclass [<i>Oryza sativa Japonica Group</i>]	17.3	ABA96803.1
RVRR	2/D.t	99.794	PREDICTED: uncharacterized protein LOC100248586 [<i>Vitis vinifera</i>]	54.4	XP_002267983.1
	2/D.t	98.893	Protein PHOSPHATE STARVATION RESPONSE 3-like [<i>Physcomitrella patens</i>]	62.1	XP_024363632.1
	2/D.t	98.507	Micronuclear linker histone polyprotein, putative [<i>Solanum bulbocastanum</i>]	17.6	AAP45160.2
	2/D.t	98.076	(-)limonene synthase [<i>Picea abies</i>]	73.4	AAS47694.1
	2/D.t	96.733	PREDICTED: protein yippee-like At4g27745 [<i>Oryza brachyantha</i>]	12.7	XP_006662984.1
	2/D.t	94.323	Kinesin-like protein KIN-12F [<i>Physcomitrella patens</i>]	309.8	XP_024374937.1
	2/D.t	93.33	Disease resistance gene analog, partial [<i>Zizania latifolia</i>]	18.6	ABB69771.1
	2/D.t	89.429	Uncharacterized protein LOC4336466 isoform X1 [<i>Oryza sativa Japonica Group</i>]	15.1	XP_015633835.1
	2/D.t	89.429	Hypothetical protein VITISV_024824 [<i>Vitis vinifera</i>]	58.3	CAN61722.1
	2/D.t	88.139	Pentatricopeptide repeat-containing protein At4g18520, chloroplastic-like [<i>Physcomitrella patens</i>]	57.5	XP_024379060.1

RVRR	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.4/53.0	NP_051067.1
	3/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Arabis hirsuta</i>]	53.4/53.0	YP_001123207.1
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Olimarabidopsis pumila</i>]	53.4/53.0	YP_001123123.1
	3/A. <i>t_{oe1}</i>	100	Ribulosebisphosphate carboxylase, partial [<i>Arabidopsis thaliana</i>]	48.0	BAA19595.1
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Crucihimalaya himalaica</i>]	48.0/47.6	BAA19596.1
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Polanisia dodecandra</i>]	49.9/49.6	AAO38787.1
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Heliotrichia pubescens</i>]	52.0/51.5	CAJ86804.1
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Tarenaya hassleriana</i>]	52.1/51.6	AAA84103.2
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema grandiflorum</i>]	49.8/49.4	AAO38786.1
	3/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Rorippa indica</i>]	48.0/47.6	BAA19601.1
RVRR	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C2 [<i>Arabidopsis thaliana</i>]	36.9	NP_172801.1
	4/A. <i>t_{oe1}</i>	100	RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	36.9	P04796.2
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) [<i>Arabidopsis thaliana</i>]	37.0	AAM65189.1
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C2 [<i>Arabidopsis thaliana</i>]	33.9	NP_001077530.1
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase, partial [<i>Pachycladon cheesemanii</i>]	14.5	ABM98111.1
	4/A. <i>t_{oe1}</i>	100	Cytosolic glyceraldehyde-3-phosphate dehydrogenase, partial [<i>Leavenworthia crassa</i>]	13.5	AAC32382.1
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase, partial [<i>Pachycladon radicum</i>]	14.5	ABM98114.1
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase, partial [<i>Brassica napus</i>]	17.6	AAZ05899.1
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase, partial [<i>Brassica rapa subsp. Pekinensis</i>]	18.5	AAN05699.1
	4/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase, partial [<i>Leavenworthia crassa</i>]	8.5	AAC34080.1
RVRR	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.0	NP_051067.1

	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Arabidopsis lyrata</i> subsp. <i>Lyrata</i>]	47.5	AAO19421.1
	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Lepidium africanum</i>]	48.4	CAJ86805.1
	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Erysimum capitatum</i>]	49.5	AAO38783.1
	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema saxatile</i>]	51.6	AAS88130.1
	5/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Arabis hirsuta</i>]	53.0	YP_001123207.1
	5/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Draba nemorosa</i>]	53.0	YP_001123558.1
	5/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema grandiflorum</i>]	53.7	YP_001123038.1
	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema grandiflorum</i>]	49.4	AAO38786.1
	5/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Chamira circaeoides</i>]	50.0	CAJ86803.1
GRR	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.0	NP_051067.1
	6/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Draba nemorosa</i>]	53.0	YP_001123558.1
	6/A. <i>t_{oe1}</i>	100	Ribulosebisphosphate carboxylase, partial [<i>Arabidopsis thaliana</i>]	47.6	BAA19595.1
	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Olimarabidopsis pumila</i>]	52.9	YP_001123123.1
	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Limnanthes douglasii</i>]	52.1	AAA84354.2
	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Scutellaria alpina</i>]	52.4	CAA85705.1
	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Sebaea sp.</i> Forest 560]	51.6	CAJ86855.1
	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema saxatile</i>]	51.6	AAS88130.1

	6/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Crucihimalaya wallichii</i>]	53.0	YP_001123470.1
	6/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema cordifolium</i>]	53.3	YP_001122954.1
GRR	7/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C subunit 1 [<i>Arabidopsis thaliana</i>]	36.9	NP_187062.1
	7/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C2 [<i>Arabidopsis thaliana</i>]	33.9	NP_001077530.1
	7/A. <i>t_{oe1}</i>	100	Recname: Full=Glyceraldehyde-3-phosphate dehydrogenase; Short=GAPDH	39.1	P34783.1
	7/A. <i>t_{oe1}</i>	100	Putative glyceraldehyde-3-phosphate dehydrogenase [<i>Arabidopsis thaliana</i>]	17.3	BAD94800.1
	7/A. <i>t_{oe1}</i>	100	Putative cytosolic fructose-bisphosphate aldolase, partial [<i>Populus x canadensis</i>]	8.8	ABD35813.1
	7/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C subunit, partial [<i>Arabidopsis thaliana</i>]	8.7	BAD94315.1
	7/A. <i>t_{oe1}</i>	100	Recname: Full=Glyceraldehyde-3-phosphate dehydrogenase, cytosolic	36.9	P04796.2
	7/A. <i>t_{oe1}</i>	100	Aldolase superfamily protein [<i>Arabidopsis thaliana</i>]	38.4	NP_181187.1
	7/A. <i>t_{oe1}</i>	100	Aldolase superfamily protein [<i>Arabidopsis thaliana</i>]	28.7	NP_001118453.1
	7/A. <i>t_{oe1}</i>	100	Glyceraldehyde-3-phosphate dehydrogenase C subunit (gapc) [<i>Arabidopsis thaliana</i>]	37.0	AAM65189.1
GRR	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.0	NP_051067.1
	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema saxatile</i>]	51.6	AAS88130.1
	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Capsella bursa-pastoris</i>]	53.0	YP_001123381.1
	8/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Draba nemorosa</i>]	53.0	YP_001123558.1
	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Crucihimalaya wallichii</i>]	53.0	YP_001123470.1
	8/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema cordifolium</i>]	53.3	YP_001122954.1
	8/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema grandiflorum</i>]	53.7	YP_001123038.1
	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Chamira circaeoides</i>]	50.0	CAJ86803.1
	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Heliosperma pubescens</i>]	51.5	CAJ86804.1

	8/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Olimarabidopsis pumila</i>]	53.0	YP_001123123.1
QRR	9/ <i>D.t</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema arabicum</i>]	53.4	YP_009356788.1
	9/ <i>D.t</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase [<i>Arabis hirsuta</i>]	52.9	YP_001123207.1
	9/ <i>D.t</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Capsella bursa-pastoris</i>]	53.0	YP_001123381.1
	9/ <i>D.t</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema grandiflorum</i>]	53.7	YP_001123038.1
	9/ <i>D.t</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Draba nemorosa</i>]	52.9	YP_001123558.1
	9/ <i>D.t</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Arabidopsis thaliana</i>]	51.9	AMR44347.1
	9/ <i>D.t</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Crucihimalaya himalaica</i>]	47.6	BAA19596.1
	9/ <i>D.t</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Rorippa indica</i>]	47.6	BAA19601.1
	9/ <i>D.t</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Lepidium africanum</i>]	69.6	CAJ86805.1
	9/ <i>D.t</i>	100	Ribulosebisphosphate carboxylase, partial (chloroplast) [<i>Armoracia rusticana</i>]	49.5	AAB71403.1
QRR	10/ <i>D.t</i>	99.363	PREDICTED: dextran box ATP-dependent RNA helicase dextrin 10 isoform X1 [<i>Vitis vinifera</i>]	112.6	XP_002266524.2
	10/ <i>D.t</i>	99.252	Hypothetical protein VITISV_035836 [<i>Vitis vinifera</i>]	101.8	CAN80939.1
	10/ <i>D.t</i>	97.986	THO complex subunit 2-like isoform X1 [<i>Physcomitrella patens</i>]	191.7	XP_024388620.1
	10/ <i>D.t</i>	97.464	Unknown [<i>Picea sitchensis</i>]	19.4	ABK26501.1
	10/ <i>D.t</i>	97.345	Unnamed protein product [<i>Arabidopsis thaliana</i>]	26.0	BAB11390.1
	10/ <i>D.t</i>	96.808	Putative transcription factor, partial [<i>Platanus x hispanica</i>]	21.8	CAL25350.1
	10/ <i>D.t</i>	96.162	DEAD-box ATP-dependent RNA helicase 39 isoform X1 [<i>Oryza sativa Japonica Group</i>]	68.2	XP_015613578.1
	10/ <i>D.t</i>	95.056	Hypothetical protein VITISV_040528 [<i>Vitis vinifera</i>]	48.5	CAN78754.1
	10/ <i>D.t</i>	94.94	Hypothetical protein PHYPA_012615, partial [<i>Physcomitrella patens</i>]	107.9	PNR48141.1
	10/ <i>D.t</i>	94.94	Hypothetical protein VITISV_031913 [<i>Vitis vinifera</i>]	190.1	CAN71787.1
QRR	11/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.0	NP_051067.1

	11/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Draba nemorosa</i>]	53.0	YP_001123558.1
	11/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema saxatile</i>]	51.6	AAS88130.1
	11/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Arabis hirsuta</i>]	53.0	YP_001123207.1
	11/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Capsella bursa-pastoris</i>]	53.0	YP_001123381.1
	11/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema cordifolium</i>]	53.3	YP_001122954.1
	11/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema grandiflorum</i>]	53.7	YP_001123038.1
	11/A. <i>t_{oe1}</i>	100	Ribulosebisphosphate carboxylase, partial [<i>Arabidopsis thaliana</i>]	47.6	BAA19595.1
	11/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Arabis stelleri</i>]	47.6	BAA19597.1
	11/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Rorippa indica</i>]	47.6	BAA19601.1
QRR	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.0	NP_051067.1
	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema saxatile</i>]	51.6	AAS88130.1
	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Olimarabidopsis pumila</i>]	53.0	YP_001123123.1
	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Crucihimalaya wallichii</i>]	53.0	YP_001123470.1
	12/A. <i>t_{oe1}</i>	100	Large subunit of riblose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema grandiflorum</i>]	53.7	YP_001123038.1
	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Arabis stelleri</i>]	47.6	BAA19597.1
	12/A. <i>t_{oe1}</i>	100	Ribulosebisphosphate carboxylase, partial [<i>Arabidopsis thaliana</i>]	47.6	BAA19595.1
	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Polanisia dodecandra</i>]	49.6	AAO38787.1
	12/A. <i>t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Chamira circaeoides</i>]	50.0	CAJ86803.1

	12/ <i>A.t_{oe1}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Heliotrope pubescens</i>]	51.5	CAJ86804.1
QRR	13/ <i>A.t_{wt}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Arabidopsis thaliana</i>]	53.0	NP_051067.1
	13/ <i>A.t_{wt}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Capsella bursa-pastoris</i>]	53.0	YP_001123381.1
	13/ <i>A.t_{wt}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Crucihimalaya wallichii</i>]	53.0	YP_001123470.1
	13/ <i>A.t_{wt}</i>	100	Large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Draba nemorosa</i>]	53.0	YP_001123558.1
	13/ <i>A.t_{wt}</i>	100	Large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema cordifolium</i>]	53.3	YP_001122954.1
	13/ <i>A.t_{wt}</i>	100	Large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Aethionema grandiflorum</i>]	53.7	YP_001123038.1
	13/ <i>A.t_{wt}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [<i>Aethionema saxatile</i>]	51.6	AAS88130.1
	13/ <i>A.t_{wt}</i>	100	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast) [<i>Olimarabidopsis pumila</i>]	53.0	YP_001123123.1
	13/ <i>A.t_{wt}</i>	100	Large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase (chloroplast) [<i>Arabis hirsuta</i>]	53.0	YP_001123207.1
	13/ <i>A.t_{wt}</i>	100	Ribulosebisphosphate carboxylase, partial [<i>Arabidopsis thaliana</i>]	47.6	BAA19595.1

Figure S1. Clustal Omega (v1.2.4, EMBL-EBI) multiple sequence alignment of Type II metacaspases from *Arabidopsis thaliana* and *Dunaliella salina* showing the conserved catalytic amino acid residues HYSGHGT and CHSG of the catalytic diad.

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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
AMC8sp|Q9SA41|1-381
AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
-----MGRSALLIGCNYPGTTKAALQGCVNDWDFKQTLMECMGFDEDNIAIMVDTDQE
MDQQGMVKRRLAVLVCNYPNTRNELHGCINDVLAMKETILSRFGFKQDDIEVLTDEPES
-----MAKKALLIGINYPGTTAELRGCVNDVHRMVKCLIELYGFANKDIVIMIDTDES
-----MAKKALLIGINYPGTTAELRGCVNDVHRMVKCLVDRFGFAEEDITVLIIDTDES
-----MTKKAVLIGINYPGTTKAELRGCVNDVRRMVKCLVERYGFSEENITVLIIDTDES
-----MAKKALLIGINYPGTTKAELRGCVNDVRRMVKCLVERYGFSEENIKMLIDTDES
-----MAKKAVLIGINYPGTTKAELRGCVNDVRRVHKSLVDRFGFERNITEIDTDES
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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
AMC8sp|Q9SA41|1-381
AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
YPQPTGKNIRAYLNKMVDEA--EDGDLLFLHYSGHGTQLPTDDP--EEPDGKNECICPSD
KVPTGANIKAALRRMVDKAQAGSGDILFFHYSGHGTRIPSVKS--AHFKQDEAIVPCD
CIOPTGKNICDLDNLIASG--QSCDFLVFHYSGHGTRIPPGIEDSEDPTGFDECITPCD
YTQPTGKNIRQALSELIKPA--KSCDVLFVHYSGHGTRVPETG-EEDDTGFDECIVPCD
STQPTGKNIRRALADLVEA--DSCDVLFVHYSGHGTRLPETG-EDDDTGFDECIVPCD
SICKTGKNIRQALLDLVEPA--KSCDVLFVHYSGHGTRLPETG-EDDDTGYDECIVPCD
STKPTGKNIRRALLNLVEA--KPGDVLFVHYSGHGTRLPETG-EDDDTGYDECIVPCD
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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
AMC8sp|Q9SA41|1-381
AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
LDVISDNDLTKIFAPLSKKNVKLTFVADCHSGTLLDHKEVIITGPKDNRPPPQAN--A
FNLTIDDFRELVNL--PKGTSFTMISDSCHSGGLIDKEKEQIGPSSVSNISP-----
MNLIKDDQFREMSRV-KEGCQLTIISDSCHSGGLIDKEKEQIGESHMKPVDKVKEQIEE
LNPPIPDDDFRDIVLVEQV-PEGCQITIVSDSCHSGGLIDKEKEQIGESTTTKPNRESKV---
MNLIITDDDFRDIVDKV-PPGCRMTIIISDSCHSGGLIDKEKEQIGESTKKEAEDEDES---
MNLIITDDDFRDIVDMV-PKDCPITIISDSCHSGGLIDKEKEQIGESTKKKD-----
MNLIITDEFRDLVEKV-PKEAHITIISDSCHSGGLIDKEKEQIGESTKKKPKE-----
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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
AMC8sp|Q9SA41|1-381
AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
RSME-----A-----LQAALGAGDDSRDIQIR
-----AIETTNKTITSR
SHMKQPKLGIASTYFLNIVMNLATCGVSKSQR--DRGGGEESFRGEIELEKDETLDIKTR
---SSFEFEFKNCLHSIFVKLALFCGIGSSH-----VETREIVEVGEDEVVRSR
-EESSRFGRFKFLRSKVEGAIERSGFHIGGNKDEDEAEIETKEIELEDGETIHAKDK
-SGDSSTIN-----KETEAELIEVGNR
-SGGSSGLGIKGTVREAAELESKGIAIPHHKDEK---DENTKELKLEDGAKVHVNVN
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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
AMC8sp|Q9SA41|1-381
AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
SPLPEVYKELLSGKLGG--VDFGDLPVSLIKGFGDESMERWARLFPVIADLQKRQDTSK
ALFFKAVLDHLSLTGITT--SDIGTHLLEFGRDAGLKFRLPAMDLMDEL-----YLPFESYLSLLKEQTGQTNIEPVRIRQTLKLKFGEDPSPNQRGLSDLG-----N-----
YPLPLERFIELLKQQTGQDNIEVGKIRPSSLFDAGFDDSSPKVKKFMVILGKLQAGNG--SPLQLTLDILKQQTGNDIEVGKIRPTLFDMFDDSSPKVKKFMVILSNIQETTTIQ
SPLQLTLDILKQNTGNNDIEVGKIRPTLFNVFGEDASPVKVKKFMVILTKLQEGKT---**:: . *. * :
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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
AMC8sp|Q9SA41|1-381
AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
T-----LNTLRESA-----ETLVGL-KKAREPLNENVG
-----TMTAREKHVDSG
-----CEVDAGDGSASRLNAVTDNG
--QSTLLGKIEESARGYIEETLND-EHYMKPAMQAQVKSDREIYGG--RSSNG-LFPDRG
-EEGGLMGMLGKLASFLEGKLN-EDYVKPAMQTHVGSKEEVYAG--GSRGSVPLPDSG
TVSDEVLGSVENLAQEFLQKLSDDVK--P-----AIQDVYAG--AINGA--LPDNG
--EGGILGMIGKLAQEFLKHKLNDDEEVKPMKTHVGNKQEVYAG--ASNGS--LADNG
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Dusal.0158s00011.1
AMC9sp|Q9FYE1|1-325
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AMC7sp|Q6XPT5|1-403
AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
ILLSGCLERECAADVRRK--NSVPHGAFSHAVNMLLRQMHKDGIATNRSVNLGVRESL
ILMSGCQADETSADVGVG--NGKAYGAFSNAIQRLVLEN--EGAMKNQKLVMMARDVLE
ILLSGCQTDQSRSEDVYVT-RTGKAYGAFSDAIQMILSAPRKDKKKITNKELVSEARVFLK
ILLSGCQTDETSADVKKKG--EAFGAFSNAIQMVLS-DHKDKITNKEMVLRAREILK
ILLISGCQTDQTSADATPAGKPTEAYGAMSNSIQTILEET-D--GEISNREMVTARKALK
ILLISGCQTDQTSADASPPGHPELAYGALTNAIQIIIGET-K--GKISNKDLVLIKARKLLR
ILLISGCQTDQTSADASPQGHPEMAYGAFTNAVQIILET-K--GMITYKELVLKARKLLR
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AMC4sp|O64517|1-418
AMC6sp|O64519|1-368
AMC5sp|O64518|1-410
KSGLKQSPCLEGSEKWAADFVLCDEEGSI*
RLGFHQHPCLYCSQNADATFLSQP-----
KRGYSQRPGLYCSDQNAFVDPKFCY-----
KQMFQRPGLYCNDRFVNPAPFIC-----
KQGFTQQPGLYCHDGYANAPFIC-----
KQGFDQRPGLYCNDAVNARFIC-----
KQGFSQRPGLYCSDSFVNAPFIC-----
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