

TABLE 1 – 2DE PROTEOMICS ANALYSES							
25 µM vs Control							
Spot No.	Protein ID	Mr, Da Theoretical/ experimental	pI Theoretical/ experimental	NCBI GI No.	No. Of peptides	Mascot score	TREND 25 µM Cd vs Control (fold change)
1306	NI						DOWN (0.62)
1405	NI						DOWN (0.53)
2205	H(+)-transporting ATP synthase [Byttneria filipes]	51523	5.12	gi 4995059	6	302	DOWN (0.34)
2401	NI						DOWN (0.30)
3101	Photosystem II oxygen-evolving complex protein 2 - Arabidopsis thaliana (fragment)	1434	9.71	gi 1076373	2	87	DOWN (0.52)
	PsbP [Xerophyta humilis]	26347	6.84	gi 25992740	3	84	
5204	Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2	28079	6.48	gi 131391	4	192	DOWN (0.50)
	PsbP [Xerophyta humilis]	26347	6.84	gi 25992740	2	86	
0305	Ribonucleoprotein [Arabidopsis thaliana]	30699	5.06	gi 15228102	4	214	UP (2.33)
1601	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cakile maritima]	49867	6.12	gi 30959092	6	229	UP (1.58)
	Plastidic glutamine synthetase precursor [Brassica napus]	47758	5.99	gi 1934754	4	197	
	Thylakoid rhodanese-like protein [Arabidopsis thaliana]	49357	5.22	gi 18411523	5	172	
3601	Nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]	54819	4.98	gi 166627	13	542	UP (2.64)
3602	Nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]	54819	4.98	gi 166627	21	844	UP (2.60)
5505	Chloroplast glutamine synthetase [Brassica rapa subsp. chinensis]	47715	5.84	gi 166406194	53	733	UP (2.16)
	Phosphoglycerate kinase 1 [Arabidopsis thaliana]	50195	5.91	gi 15230595	12	649	
6603	Mitochondrial F1 ATP synthase beta subunit [Arabidopsis thaliana]	63560	6.52	gi 17939849	21	1333	UP (2.44)
7206	Carbonic anhydrase 1 [Arabidopsis thaliana]	29827	5.54	gi 30678347	4	186	UP (2.63)
	Putative dehydroascorbate reductase [Brassica rapa subsp. pekinensis]	12029	6.15	gi 33285914	4	179	
	Dehydroascorbate reductase-like protein [Solanum tuberosum]	23596	6.09	gi 76160951	2	111	
	Glutathione S-transferase DHAR2 [Arabidopsis thaliana]	23506	5.79	gi 15222163	2	114	
NI: non identify ID: Identification pI: Isoelectric point							

100 μ M VS CONTROL							
Spot No.	Protein ID	Mr, Da Theoretical/ experimental	pI Theoretical/ experimental	NCBI GI No.	No. Of peptides	Mascot score	TREND 100 VS CONTROL μ M Cd (fold change)
1201	NI						DOWN (0.27)
1305	NI						DOWN (0.29)
2205	H(+)-transporting ATP synthase [Byttneria filipes]	51523	5.12	gi 4995059	6	90	DOWN (0.15)
3303	Photosystem II subunit O-2 [Arabidopsis lyrata subsp. lyrata]	35323	5.93	gi 297819782	10	395	DOWN (0.29)
4503	Annexin I [Brassica napus]	36307	5.34	gi 300433289	12	578	DOWN (0.45)
	Pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]	39448	5.67	gi 520478	2	134	
5204	Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2	28079	6.84	gi 131391	4	192	DOWN (0.50)
	PsbP [Xerophyta humilis]	26347	6.84	gi 25992740	2	86	
5605	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cakile maritima]	49867	6.12	gi 30959092	11	424	DOWN (0.22)
	RecName: Full=ATP synthase subunit beta, chloroplastic; AltName: Full=ATP synthase F1 sector subunit beta; AltName: Full=F-ATPase subunit beta	53799	5.68	gi 29336977	6	274	
6102	Photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum]	26548	5.83	gi 493723	5	238	DOWN (0.60)
6604	ATP synthase CF1 beta subunit [Olimarabidopsis pumila]	53999	5.47	gi 139389425	21	1147	DOWN (0.54)
0303	RNA-binding protein cp31 [Arabidopsis lyrata subsp. lyrata]	33599	4.98	gi 297799522	6	207	UP (1.88)
	GF14 omega [Brassica napus]	29223	4.68	gi 13447104	8	228	
	Ribonucleoprotein [Arabidopsis thaliana]	30699	5.06	gi 15228102	3	176	
0402	Hypothetical protein ARALYDRAFT_914391 [Arabidopsis lyrata subsp. lyrata]	33899	8.62	gi 297799794	9	548	UP (1.78)
1502	Peptidyl-prolyl cis-trans isomerase CYP38 [Arabidopsis thaliana]	48180	5.06	gi 15232123	4	109	UP (1.77)
2102	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Unonopsis rufescens]	52918	6.24	gi 54306684	6	295	UP (4.85)

2402	NI						UP (2.55)
2502	Sedoheptulose-bisphosphatase [Arabidopsis lyrata subsp. lyrata]	42861	6.06	gi 297816906	14	601	UP (2.38)
	Chloroplast elongation factor tub [Arabidopsis lyrata subsp. lyrata]	52228	6.01	gi 297791347	2	103	
	Fructose-1,6-bisphosphatase, cytosolic [Arabidopsis thaliana]	37663	5.28	gi 15218438	3	84	
	Photosystem II stability/assembly factor HCF136 [Arabidopsis thaliana]	44138	6.79	gi 15237225	2	63	
2602	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cakile maritima]	49867	6.12	gi 30959092	11	494	UP (2.38)
	Thylakoid rhodanese-like protein [Arabidopsis thaliana]	49357	5.22	gi 18411523	5	148	
3601	Nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]	54819	4.98	gi 166627	13	542	UP (1.82)
3602	Nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]	54819	4.98	gi 166627	21	844	UP (2.37)
4101	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [Teesdalia nudicaulis]	47039	6.2	gi 371779930	12	518	UP (1.86)
7102	Germin-like protein [Arabidopsis thaliana]	22020	6.81	gi 1755154	2	77	UP (6.41)
7106	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [Cakile maritima]	19888	6.22	gi 371779930	10	452	UP (2.29)
7107	Fe superoxide dismutase 1, partial [Brassica rapa]	22151	5.79	gi 312837924	3	84	UP (2.22)
7206	Carbonic anhydrase 1 [Arabidopsis thaliana]	29827	5.54	gi 30678347	4	186	UP (3.43)
	Putative dehydroascorbate reductase [Brassica rapa subsp. pekinensis]	12029	6.15	gi 33285914	4	179	
	Dehydroascorbate reductase-like protein [Solanum tuberosum]	23596	6.09	gi 76160951	2	111	
	Glutathione S-transferase DHAR2 [Arabidopsis thaliana]	23506	5.79	gi 15222163	2	114	
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0311	RNA-binding protein cp31 [Arabidopsis lyrata subsp. lyrata]	33599	4.89	gi 2977799522	3	89	DOWN (0.36)
1601	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cakile maritima]	49867	6.12	gi 30959092	6	229	DOWN (0.47)
	Plastidic glutamine synthetase precursor [Brassica napus]	47758	5.99	gi 1934754	4	197	
	Thylakoid rhodanese-like protein [Arabidopsis thaliana]	49357	5.22	gi 18411523	5	172	
3303	Photosystem II subunit O-2 [Arabidopsis lyrata subsp. lyrata]	35323	5.93	gi 297819782	10	395	DOWN (0.26)
5605	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cakile maritima]	49867	6.12	gi 30959092	11	424	DOWN (0.24)
	RecName: Full=ATP synthase subunit beta, chloroplastic; AltName: Full=ATP synthase F1 sector subunit beta; AltName: Full=F-ATPase subunit beta	53799	5.68	gi 29336977	6	274	
6603	Mitochondrial F1 ATP synthase beta subunit [Arabidopsis thaliana]	63560	6.52	gi 17939849	21	1333	DOWN (0.27)
7205	Chloroplast beta-carbonic anhydrase [Brassica napus]	36127	5.47	gi 297787439	13	645	DOWN (0.17)
0501	Plastid-lipid associated protein PAP3 [Brassica rapa subsp. campestris]	39278	4.55	gi 14248552	9	437	UP (2.73)
2401	NI						UP (5.07)
2402	NI						UP (3.03)
2703	Sedoheptulose-bisphosphatase [Arabidopsis lyrata subsp. lyrata]	42861	6.06	gi 297816906	12	526	UP (3.35)
4605	Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Cakile maritima]	49867	6.12	gi 30959092	9	407	UP (5.92)
	Tubulin alpha-2/alpha-4 chain [Arabidopsis thaliana]	50194	4.93	gi 15220329	3	140	
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