

Table1: List of proteins with significant quantitative changes of hemp leaves in response to Cd. Zn and Si. Seedlings were exposed for one week either to Cd 20 µM, Zn 100 µM or Si 2 mM and proteins were extracted from leaves. MFC: Max Fold Change. Abr.: abbreviation; sol: soluble; mbr: membrane-located.

Accession	Soluble protein name	C-Cd		C-Zn		C-CSi		Cd-CdSi		Zn-ZnSi		Abr.	
		Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC		
ENERGY													
Photosynthesis/CO2 assimilation													
XP_030507415.1	plastocyanin	↘	4.32E-02	4.0								Pc	sol
XP_030507415.1	plastocyanin	↘	8.10E-06	4.4	↘	1.27E-04	2.2					Pc	mbr
XP_030510336.1	ferredoxin-like				↘	1.30E-04	1.7					Fd	mbr
XP_030510578.1	ferredoxin-like	↘	4.28E-02	3.5				↗	3.16E-02	2.4		Fd	sol
XP_030491053.1	oxygen-evolving enhancer protein 3-2_chloroplastic-like	↘	1.45E-03	1.8								OEE	mbr
XP_030496367.1	oxygen-evolving enhancer protein 1_chloroplastic	↘	2.42E-04	1.5								OEE	mbr
XP_030496723.1	photosystem I reaction center subunit N_chloroplastic	↘	1.82E-03	1.6								CR	mbr
XP_030491785.1	photosystem I reaction center subunit VI_chloroplastic-like	↘	1.11E-04	1.5								CR	mbr
XP_030486101.1	ferredoxin--NADP reductase_leaf-type isozyme_chloroplastic-like	↘	1.07E-03	1.5								NADP+ reductase	mbr
XP_030498930.1	protein HHL1_chloroplastic	↘	5.51E-05	1.6								HHL1	mbr
XP_030492156.1	ribulose biphosphate carboxylase/oxygenase activase_chloroplastic isoform X2	↘	8.16E-03	2.2								RCA	sol
XP_030492156.1	ribulose biphosphate carboxylase/oxygenase activase_chloroplastic isoform X2	↘	3.99E-04	1.7								RCA	mbr
XP_030504809.1	ribulose biphosphate carboxylase/oxygenase activase 2_chloroplastic-like	↘	4.65E-03	1.5								RCA	sol
XP_030504809.1	ribulose biphosphate carboxylase/oxygenase activase 2_chloroplastic-like	↘	3.26E-04	1.6	↘	6.95E-04	1.6					RCA	mbr
XP_030501759.1	ribulose biphosphate carboxylase small chain_chloroplastic-like							↗	5.28E-02	1.7		rbcS	sol
XP_030478872.1	ruBisCO large subunit-binding protein subunit beta_chloroplastic	↘	5.53E-03	1.5								rbcL	sol
XP_030478872.1	ruBisCO large subunit-binding protein subunit beta_chloroplastic	↘	3.32E-05	1.5								rbcL	mbr
XP_030495826.1	CBBY-like protein	↘	2.64E-03	1.5								CBBY	sol
XP_030494025.1	ribulose-phosphate 3-epimerase_chloroplastic	↘	1.50E-03	1.5								PPE	mbr
XP_030489666.1	protochlorophyllide reductase_chloroplastic	↘	1.44E-05	2.2	↘	3.77E-05	2.0					POR	mbr
XP_030502075.1	glycine cleavage system H protein_mitochondrial-like	↘	3.48E-03	1.5								GCS-H	mbr
XP_030487982.1	glycerate dehydrogenase						↗	2.01E-02	1.5			GlyDH	mbr
AT5G08280.1	hydroxymethylbilane synthase	↘	3.95E-04	1.6									sol
AT1G03475.1	Coproporphyrinogen III oxidase	↘	4.11E-02	1.6								CPOX	sol
XP_030479749.1	chlorophyll a-b binding protein of LHCII type 1				↗	3.90E-04	2.3						mbr
AJK91475.1	NADH-plastoquinone oxidoreductase subunit I (chloroplast)				↘	8.47E-03	1.6					Ndh	mbr
YP_009143583.1	cytochrome b6 (chloroplast)				↘	9.38E-04	1.5					cytb6f	mbr
AT1G56190.1	phosphoglycerate kinase family protein chr1:21028403-21030454 FORWARD LENGTH=478				↘	9.72E-04	1.5					PGK	mbr
XP_030492934.1	geranylgeranyl diphosphate reductase_chloroplastic				↘	5.50E-04	1.5						mbr

Accession	Soluble protein name	C-Cd		C-Zn		C-CsI		Cd-CdSi		Zn-ZnSi		Abr.		
		Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC			
XP_030508514.1	lignin-forming anionic peroxidase-like	↗	8.04E-03	1.5									sol	
AT5G51970.1	GroES-like zinc-binding alcohol dehydrogenase family protein							↘	5.00E-02	2.1		CADI	sol	
XP_030489850.1	fasciclin-like arabinogalactan protein 10			↘	7.10E-05	1.5						FLA10	mbr	
XP_030510845.1	xylose isomerase	↗	4.69E-02	1.7									sol	
METABOLISM														
Amino acids. nitrogen and glutathione metabolism														
XP_030504084.1	S-adenosylmethionine synthase 1-like					↗	3.89E-02	1.6				SAMS	sol	
AT5G20980.1	methionine synthase 3	↗	3.20E-02	1.7								MS	sol	
XP_030490921.1	alanine aminotransferase 2-like	↗	1.27E-03	1.5								AlaAT	sol	
XP_030492265.1	probable 3-hydroxyisobutyrate dehydrogenase-like 1_ mitochondrial							↗	1.19E-04	2.0			sol	
XP_030480326.1	hydroxyphenylpyruvate reductase-like	↘	3.64E-02	1.6								HPPR	sol	
XP_030491636.1	aminomethyltransferase_ mitochondrial							↗	5.35E-02	1.6			sol	
AT3G03910.1	glutamate dehydrogenase 3	↘	6.43E-03	1.9								GluDH3	sol	
XP_030507269.1	glutamate dehydrogenase 1	↗	3.15E-04	2.0								GluDH1	sol	
XP_030500358.1	glutamine synthetase nodule isozyme	↗	8.02E-04	2.3								GLN	sol	
XP_030497088.1	spermidine synthase 1	↗	2.72E-02	1.6								SPDS	sol	
XP_030507612.1	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1-like									↗	3.90E-02	1.51	MS	sol
XP_030486263.1	LOW QUALITY PROTEIN: ferredoxin--nitrite reductase_ chloroplastic-like									↗	3.27E-02	2.2	NIR	mbr
Purine. pyrimidine. ribonucleotide and deoxyribonucleotide metabolism														
AT3G09820.1	adenosine kinase 1 chr3:3012122-3014624 FORWARD LENGTH=344									↘	4.36E-02	1.94	ADK	sol
PROTEIN SYNTHESIS. PROCESSING. MODIFICATION														
Transcription														
XP_030497012.1	basic transcription factor 3	↘	2.19E-03	2.8								BTF3	mbr	
AT1G72730.1	DEA(D/H)-box RNA helicase family protein	↘	1.13E-03	1.8									mbr	
XP_030503291.1	DEAD-box ATP-dependent RNA helicase 3_ chloroplastic-like	↘	1.49E-04	1.7									mbr	
XP_030481652.1	histone H4	↗	3.91E-02	1.5								H4	mbr	
Protein synthesis (ribosomal proteins. translation. tranlational control. amino-acyl tRNA synthetases)														
XP_030493873.1	RNA-binding protein CP29B_ chloroplastic	↘	3.06E-02	2.1								CP29B	sol	
XP_030499617.1	glycine-rich RNA-binding protein-like	↘	2.37E-03	1.8									sol	
XP_030510025.1	glycine--tRNA ligase_ mitochondrial 1-like	↘	5.82E-03	1.5									sol	
XP_030484196.1	50S ribosomal protein L12-3_ chloroplastic-like	↘	9.11E-05	2.0	↘	1.69E-04	1.7					L12	mbr	
XP_030502076.1	50S ribosomal protein L11_ chloroplastic	↘	1.09E-04	1.8	↘	2.97E-04	1.5					L11	mbr	
AT2G40010.1	Ribosomal protein L10 family protein	↘	8.85E-04	1.6								L10	mbr	
XP_030484291.1	LOW QUALITY PROTEIN: 50S ribosomal protein L9_ chloroplastic	↘	1.02E-04	1.6								L9	mbr	
XP_030504362.1	50S ribosomal protein L4_ chloroplastic isoform X2	↘	4.03E-04	1.5								L4	mbr	
XP_030480118.1	50S ribosomal protein L3_ chloroplastic	↘	7.25E-05	1.5	↘	5.34E-05	1.5					L3	mbr	
XP_030491783.1	30S ribosomal protein S17_ chloroplastic				↘	1.82E-03	1.9					S17	mbr	
XP_030478586.1	30S ribosomal protein S10_ chloroplastic	↘	4.89E-03	1.6	↘	4.53E-04	1.8					S10	mbr	
YP_009143588.1	ribosomal protein S8 (chloroplast)				↘	7.45E-05	1.5					S8	mbr	

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		Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC		
AT2G33800.1	Ribosomal protein S5 family protein	↘	9.73E-06	1.6								S5	mbr
XP_030483051.1	30S ribosomal protein 3_ chloroplastic-like				↘	5.65E-04	1.6						mbr
Protein folding and stabilization													
AT3G48870.1	ATCLPC_ATHSP93-III_ HSP93-III Clp ATPase	↘	1.41E-02	1.8								HSP93	sol
AT5G56030.1	heat shock protein 81-2	↗	1.40E-04	2.7								HSP81	sol
XP_030509817.1	heat shock cognate protein 80	↗	1.71E-03	1.7				↗	1.30E-02	1.7		HSP80	sol
XP_030488797.1	LOW QUALITY PROTEIN: 20 kDa chaperonin_ chloroplastic	↘	9.28E-05	1.6	↘	1.31E-03	1.6						mbr
XP_030487791.1	protein disulfide-isomerase-like	↗	3.12E-05	1.5								PDIL	mbr
XP_030501851.1	luminal-binding protein 5 isoform X1	↗	1.96E-05	1.8	↗	2.77E-04	1.5					LBP5	mbr
AT1G55490.1	Symbols: CPN60B_ LEN1 chaperonin 60 beta chr1:20715717-20718673 REVERSE LENGTH=600				↘	2.70E-04	1.5						mbr
Proteases													
AT3G09790.1	ubiquitin 8 chr3:3004111-3006006 REVERSE LENGTH=631					↘	1.44E-02	1.6				UBQ8	sol
XP_030485940.1	26S proteasome non-ATPase regulatory subunit 4 homolog	↗	1.84E-04	1.8	↗	1.36E-03	1.5					26SP	mbr
XP_030491129.1	kunitz trypsin inhibitor 5-like	↗	2.30E-06	4.1								KT1	mbr
XP_030481504.1	probable mitochondrial-processing peptidase subunit beta_ mitochondrial isoform X2	↗	4.58E-04	1.5									mbr
XP_030488931.1	LOW QUALITY PROTEIN: ATP-dependent Clp protease ATP-binding subunit ClpA homolog CD48_ chloroplastic-like				↘	3.38E-02	1.6					ClpA	sol
XP_030480662.1	ATP-dependent Clp protease proteolytic subunit 4_ chloroplastic				↗	4.61E-03	1.6					Clp4	mbr
XP_030490013.1	cucumis-like				↗	2.36E-05	1.9					Cucumis n	mbr
XP_030477762.1	aspartic proteinase A1-like				↗	1.38E-05	1.6					AP	mbr
TRANSPORT FACILITATION. TRANSPORT MECHANISM. MEMBRANE MODIFICATION													
XP_030488902.1	exportin-2-like	↗	5.23E-03	2.2									sol
XP_030510010.1	patatin-like protein 2 isoform X1	↗	4.50E-05	4.5								PLP2	sol
XP_030481475.1	LOW QUALITY PROTEIN: mitochondrial outer membrane protein porin of 34 kDa-like	↗	1.01E-03	1.9									mbr
XP_030489156.1	alpha-soluble NSF attachment protein 2	↗	9.79E-03	1.5									mbr
XP_030507565.1	clathrin light chain 1	↗	2.58E-04	2.0								CLC1	mbr
XP_030509812.1	putative clathrin assembly protein At5g57200				↘	1.37E-02	1.5						mbr
XP_030487862.1	LOW QUALITY PROTEIN: aquaporin PIP1-2-like				↗	7.61E-04	1.5						mbr
XP_030506023.1	protein TIC110_ chloroplastic				↘	9.97E-05	2.0					TIC	mbr
Ionic homeostasis													
XP_030490597.1	ferritin-3_ chloroplastic-like	↘	3.10E-06	1.5									mbr
XP_030496049.1	V-type proton ATPase catalytic subunit A	↗	2.79E-05	1.6									mbr
XP_030486210.1	V-type proton ATPase subunit B 1				↘	2.42E-05	1.8						mbr
XP_030483484.1	plasma membrane ATPase 4	↗	6.86E-05	2.3									mbr
CELL DIVISION													
XP_030493617.1	cell division control protein 48 homolog D	↘	4.31E-03	1.6									mbr
SIGNAL TRANSDUCTION AND METABOLISM REGULATION													
XP_030482663.1	1-aminocyclopropane-1-carboxylate oxidase	↗	2.40E-02	1.5								ACC oxydase	sol

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		Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC			
XP_030502265.1	thiamine thiazole synthase_chloroplastic	↘	4.96E-02	2.4								THI	sol	
AT1G78300.1	general regulatory factor 2							↗	1.17E-02	1.5			sol	
XP_030510026.1	calcium-dependent protein kinase 2-like	↗	5.53E-06	5.8								CDPK2	mbr	
XP_030508471.1	allene oxide synthase 1_chloroplastic-like	↗	1.75E-02	1.5	↗	1.75E-04	1.5					AOS	mbr	
XP_030492117.1	guanosine nucleotide diphosphate dissociation inhibitor 1				↘	2.56E-03	1.5					GDI1	mbr	
CELL RESCUE. DEFENSE														
XP_030489118.1	pathogenesis-related protein 1-like	↗	4.01E-05	10.9								PR1	sol	
XP_030501451.1	pathogenesis-related protein R major form-like	↗	2.77E-04	6.3								PRR	sol	
AT3G59100.1	glucan synthase-like 11	↘	1.42E-03	1.5								GSL11	sol	
XP_030508841.1	glucan endo-1_3-beta-glucosidase_basic vacuolar isoform-like	↗	5.24E-04	2.7				↗	4.41E-02	1.6		BG	sol	
XP_030494289.1	glucan endo-1_3-beta-glucosidase_basic isoform-like	↗	1.68E-02	2.0								BG	sol	
XP_030494289.1	glucan endo-1_3-beta-glucosidase_basic isoform-like isoform X1	↗	2.27E-03	1.6								BG	sol	
XP_030510675.1	callose synthase 1-like isoform X2				↘	7.57E-05	2.0					CALS	mbr	
XP_030492842.1	thaumatin-like protein 1b	↗	1.56E-03	6.2								TLP	sol	
XP_030502231.1	thaumatin-like protein 1	↗	3.45E-06	2.2								TLP	sol	
XP_030485657.1	endochitinase 2	↗	2.42E-04	4.7								ECH2	sol	
XP_030485657.1	endochitinase 2	↗	6.86E-06	7.1								ECH2	mbr	
XP_030501453.1	protein P21-like	↗	2.74E-05	4.2								PRX	sol	
XP_030479401.1	peroxidase 15-like	↗	3.14E-06	14.9								PRX15	mbr	
XP_030492321.1	peroxidase 12-like	↗	2.52E-05	3.7	↗	7.40E-03	1.5					PRX12	mbr	
XP_030510658.1	cationic peroxidase 2-like	↗	8.43E-03	1.5								PRX	sol	
XP_030510658.1	cationic peroxidase 2-like	↗	1.11E-05	2.3	↗	1.20E-07	3.1			↘	5.09E-04	1.7	PRX2	mbr
XP_030496794.1	probable nucleoredoxin 1	↗	4.05E-04	1.8								Trx	sol	
XP_030496794.1	probable nucleoredoxin 1	↗	2.80E-05	1.9	↗	1.67E-05	2.2					Trx	mbr	
XP_030507761.1	probable aldo-keto reductase 2	↗	2.68E-04	1.5								AKR	sol	
XP_030489998.1	aldehyde dehydrogenase family 7 member A1	↗	8.80E-05	1.7								ALDH	sol	
XP_030493646.1	aldehyde dehydrogenase family 2 member B4_mitochondrial-like	↗	1.43E-03	1.5								ALDH	sol	
XP_030485469.1	peroxiredoxin-2B-like	↘	1.42E-02	1.5								PRN	sol	
XP_030493857.1	peroxiredoxin-2E-2_chloroplastic				↘	1.08E-03	1.5					PRN	mbr	
AT5G28840.1	GDP-D-mannose 3'-5'-epimerase	↗	1.46E-03	1.7								GME	sol	
XP_030491240.1	probable NAD(P)H dehydrogenase (quinone) FQR1-like 1	↗	6.81E-03	1.5									sol	
XP_030481542.1	formate dehydrogenase_mitochondrial	↗	9.59E-03	1.6				↗	3.77E-02	1.5		FDH	sol	
XP_030497100.1	probable mannitol dehydrogenase	↘	1.52E-02	1.7								MTD	sol	
XP_030481127.1	macrophage migration inhibitory factor homolog isoform X1									↗	2.70E-02	1.63	MDL	sol
XP_030501195.1	probable plastid-lipid-associated protein 3_chloroplastic				↗	8.18E-04	1.6						mbr	
OTHERS														
XP_030487929.1	S-norococlaurine synthase-like	↗	5.86E-05	3.7								NCS1	sol	
XP_030478816.1	alpha-humulene synthase-like	↗	2.78E-03	3.1								α-HS	sol	
XP_030491464.1	polyphenol oxidase_chloroplastic-like	↗	1.74E-04	2.0								PPO	mbr	
Phenylpropanoid pathway														
XP_030494389.1	phenylalanine ammonia-lyase-like					↘	2.48E-02	1.9				PAL	sol	

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		Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC	Anova	MFC		
Lignan biosynthesis													
XP_030482060.1	secoisolariciresinol dehydrogenase-like	↗	3.48E-04	2.0								SDH	sol
XP_030481758.1	secoisolariciresinol dehydrogenase-like							↗	1.28E-02	1.5		SDH	sol
NO ASSIGNED FUNCTION													
XP_030496730.1	uncharacterized protein LOC115712571	↗	1.46E-03	1.6									sol
XP_030478572.1	uncharacterized protein LOC115695655					↘	4.57E-02	1.5					sol
XP_030500211.1	uncharacterized protein LOC115715691					↗	3.08E-02	1.5					sol
XP_030489475.1	uncharacterized protein LOC115706092 isoform X2							↗	4.23E-02	1.7			sol
XP_030505388.1	uncharacterized protein LOC115720376	↘	6.17E-04	1.7									mbr
XP_030503597.1	uncharacterized protein LOC115718918	↘	3.96E-04	1.5									mbr
XP_030507137.1	uncharacterized protein LOC115722147	↗	1.19E-05	2.1									mbr
XP_030506176.1	uncharacterized protein LOC115721071				↘	4.49E-03	3.3						mbr
XP_030487836.1	uncharacterized protein LOC115704770				↘	1.21E-04	1.6						mbr
XP_030482857.1	uncharacterized protein LOC115699532				↘	1.07E-03	1.5						mbr
AT1G78150.1	Symbols: unknown protein				↘	3.72E-03	1.5						mbr