

## Chapter 2 – Manuscripts

### Supplementary Tables:

#### Proteomic analysis of two divergently responding potato genotypes (*Solanum tuberosum* L.) following osmotic stress application *in vitro*

**Supplementary Table 2: Identification of proteins from all spots with changed abundance amongst the four comparisons.** A Student's t-test was performed (p-value  $\leq 0.05$ ) to determine significant changes in spot volume on the basis of normalized relative spot volume. Only alterations of at least 1.5-fold in spot volume were considered to represent true alterations in protein level. Identification of spots was performed using either the MASCOT search algorithm ([www.matrixscience.com](http://www.matrixscience.com)) for the spots analyzed with the MALDI-TOF-MS/MS ultrafleXtreme™ (Bruker, Bremen, Germany) and with the ProteinLynx Global Server 2.5.3 (Waters Corporation, Eschborn, Germany) for the nLC-ESI-Q-TOF-MS/MS against a potato protein database, which was based upon the sequences from *Solanum tuberosum* group Phureja DM1-3 ([http://solanaceae.plantbiology.msu.edu/pgsc\\_download.shtml](http://solanaceae.plantbiology.msu.edu/pgsc_download.shtml)). Identified proteins were functionally classified with Blast2GO (<https://www.blast2go.com/>).

ID <sup>A</sup>	Genot. <sup>B</sup>	Pep/ Prot <sup>C</sup>	Protein name	PGSC number / EC number <sup>D</sup>	GO annotation <sup>E</sup>	Score <sup>F</sup>	Cal c. PI <sup>G</sup>	CalcM W <sup>H</sup>	Pe p no <sup>I</sup>	Method <sup>J</sup>	Peptides matched <sup>K</sup>	Size <sup>L</sup>	Covera ge % <sup>N</sup>
42	2	Pep	hyoscyamine 6-dioxygenase-like	PGSC0003DMT40003 0676 EC:1.14.11; EC:4.1.1.15	F:glutamate decarboxylase activity; F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors; F:pyridoxal phosphate binding; F:metal ion binding; P:glutamate metabolic process; P:oxidation-reduction process	43	5.54	37857	2	MALDI	R.EVIGAYGDELRR.V R.NAFVVNSGLPITVVSNGK.L	m	25
55	2	Pep	glyceraldehyde-3-phosphate dehydrogenase cytosolic	PGSC0003DMT40004 4944	C:chloroplast; F:glyceraldehyde-3-phosphate dehydrogenase NAD <sup>+</sup> phosphorylating activity; F:NADP binding; F:NAD	57	6.34	36624	2	MALDI	R.VPTADVSVVDLTVR.L K.GILGYTEDDVVSTDFVGDSTR.S	m	10



81	2		700407 proteinase inhibitor ii precursor type a a	PGSC0003DMT40001 1562	C:extracellular region; C:cytoplasmic membrane-bounded vesicle; F:serine-type endopeptidase inhibitor activity; F:peptidase activity; P:negative regulation of endopeptidase activity	6643.650 0	6.79	16648	5	QTOF	FVCEGESDEPK Carbamidomethyl+C3  SLIYPTGCTTCCTGYK Carbamidomethyl+C8, Carbamidomethyl+C11, Carbamidomethyl+C12  GCYYFGK Carbamidomethyl+C2  ICTNCCAGYK Carbamidomethyl+C2, Carbamidomethyl+C5, Carbamidomethyl+C6  GCNYYSSANGAFICEGQSDPK Carbamidomethyl+C2, Carbamidomethyl+C13	m	41.56
96	2	Pep	ribulose- -bisphosphate carboxylase oxygenase large subunit	PGSC0003DMT40008 3063  EC:4.1.1.39	C:mitochondrion; C:chloroplast; F:magnesium ion binding; F:monooxygenase activity; F:ribulose-bisphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	123	7.23	40242	3	MALDI	R.AVYECLR.G Carbamidomethyl C  R.GGLDFTKDDENVNSQPFMR.W  R.FLFCAEALFK.A Carbamidomethyl C	s	9
113	2	Pep	ribulose bisphosphate carboxylase small chain chloroplastic-like	PGSC0003DMT40003 2975  EC:4.1.1.39	C:chloroplast; C:cytoplasmic membrane-bounded vesicle; F:monooxygenase activity; F:protein binding; F:ribulose-bisphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	101	7.60	20306	2	MALDI	K.SPGYYDGR.Y  R.IIGFDNVR.Q	m	27
149	2		tktsoltuame full chloroplastic short tk flags precursor	PGSC0003DMT40005 6799  EC:2.2.1.1	C:chloroplast thylakoid membrane; F:transketolase activity; P:metabolic process	1929.420 0	5.91	79928	3	QTOF	AIGIDFGASAPADK  ESVLPSSVTAR  LPQLAGTSIEGAAK	s	5.40
152	2	Pep	glycine-rich protein 2-like	PGSC0003DMT40000 4028	F:DNA binding; F:RNA binding; F:zinc ion binding;	188	4.82	13741	3	MALDI	K.GFGFITPSDGSSEDLFVHQSGIR.S  R.SLAEGEEVEYQIESGSDGR.A	m	38

					P:regulation of transcription, DNA-templated						R.GYGGGDSGYGGGSR.G		
154	2	Pep	superoxide dismutase	PGSC0003DMT40007 0920  EC:1.15.1.1	C:chloroplast; C:cytoplasmic membrane-bounded vesicle; F:superoxide dismutase activity; F:metal ion binding; P:removal of superoxide radicals; P:oxidation-reduction process	121	6.60	28305	2	MALDI	R.DFGSYDTFVK.E  R.RPDYISIFMEK.L Oxidation M	m	8
159	2	Pep	glycine-rich rna-binding protein grp1a-like	PGSC0003DMT40008 4266	F:nucleotide binding; F:DNA binding; F:RNA binding; P:response to stress	185	7.79	15550	3	MALDI	R.GFGFVTFKDEK.S  R.NITVNEAQR.G  R.EGGGGGYGGGGYGGGGGGY GGGR.R	m	32
165		Pep	chloroplast rubisco activase	PGSC0003DMT40004 9256	C:chloroplast stroma; F:ATP binding	206	8.10	48089	4	MALDI	K.SFQCELVFR.K Carbamidomethyl C  R.VPIIVTGNDSTLYAPLIR.D  K.IVDSFPGQSIDFFGALR.A  R.VYDDEVK.W	s	15
165	2	Pep	nbs-coding resistance gene analog	PGSC0003DMT40003 0826	F:ADP binding	45	8.52	54469	1	MALDI	K.VIPIGMGGIGK.T Oxidation M	s	2
180	2		chloroplast stem loop binding protein of 41 kdachloroplastic like	PGSC0003DMT40006 9189	F:catalytic activity; F:coenzyme binding; P:metabolic process	1188.339 0	8.32	46007	6	QTOF	LETESLLVSR  QVFNISGEK  AFVQVLGNEK  YVTFDGLAK  AADFSTDDMILEK  APISQQLPGESDQDYADFSSK	m	4.39
195	2	Pep	383130 ferredoxin-nadp reductase	PGSC0003DMT40000 9192  EC:1.18.1.2	C:chloroplast thylakoid membrane; C:chloroplast stroma; C:chloroplast envelope; C:thylakoid lumen; C:apoplast; F:nucleotide binding; F:ferredoxin-NADP+ reductase activity; F:polyU RNA binding;	190	8.37	40432	6	MALDI	R.EGQSIGVIADGVDANGKPHK.L  R.LYSIASSALGDFGDSK.T  K.GVCSNFLCDLKPGEVK.I 2 Carbamidomethyl (C)	m	22

				F:electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis activity; F:electron transporter, transferring electrons within the noncyclic electron transport pathway of photosynthesis activity; P:MAPK cascade; P:pentose-phosphate shunt; P:rRNA processing; P:protein targeting to membrane; P:response to cold; P:detection of biotic stimulus; P:plastid organization; P:salicylic acid biosynthetic process; P:photosynthetic electron transport in photosystem I; P:systemic acquired resistance, salicylic acid mediated signaling pathway; P:jasmonic acid mediated signaling pathway; P:response to chitin; P:photosystem II assembly; P:regulation of hydrogen peroxide metabolic process; P:regulation of plant-type hypersensitive response; P:glucosinolate biosynthetic process; P:negative regulation of defense response; P:positive regulation of catalytic activity; P:regulation of multi-organism process; P:defense response to fungus						K.DPNATVIMLATGTGIAPFR.S Oxidation (M)  K.DNTFIYMCGLK.G Carbamidomethyl (C); Oxidation (M)		
202	2	aspartic protease inhibitor 5 like	PGSC0003DMT40002 4601	C:vacuole; F:serine-type endopeptidase inhibitor activity; F:peptidase activity; F:aspartic-type endopeptidase inhibitor activity; P:negative regulation of endopeptidase activity	5425.738 0	7.77	23921	4	QTOF	YNSDVGPSGTPVR  SPNSDAPCPDGVFR Carbamidomethyl+C8  GALGGDVYLK  LCVSYTIWK Carbamidomethyl+C2	m	21.56
207	2	700407 proteinase inhibitor ii precursor type a a,	PGSC0003DMT40001 1562	C:extracellular region; C:cytoplasmic membrane-bounded vesicle; F:serine-type	8279.896 0	6.79	16648	6	QTOF	FVCEGESDEPK Carbamidomethyl+C3	m	51.96

				endopeptidase inhibitor activity; F:peptidase activity; P:proteolysis; P:negative regulation of endopeptidase activity						SLIYPTGCTTCTGYK Carbamidomethyl+C8 Carbamidomethyl+C11 Carbamidomethyl+C12  GCYYFGK Carbamidomethyl+C2  ICTNCCAGYK Carbamidomethyl+C2 Carbamidomethyl+C5 Carbamidomethyl+C6  ACTLECGNLGFGICPR Carbamidomethyl+C2 Carbamidomethyl+C6 Carbamidomethyl+C14  GCNYYSANGAFICEGQSDPK Carbamidomethyl+C2 Carbamidomethyl+C13		
208	2	700407 proteinase inhibitor ii precursor type a a	PGSC0003DMT40001 1562	C:extracellular region; C:cytoplasmic membrane- bounded vesicle; F:serine-type endopeptidase inhibitor activity; F:peptidase activity; P:negative regulation of endopeptidase activity	9003.348 0	6.79	16648	6	QTOF	FVCEGESDEPK Carbamidomethyl+C3  SLIYPTGCTTCTGYK Carbamidomethyl+C8 Carbamidomethyl+C11 Carbamidomethyl+C12  ICTNCCAGYK Carbamidomethyl+C2 Carbamidomethyl+C5 Carbamidomethyl+C6  GCYYFGK Carbamidomethyl+C2  GCNYYSANGAFICEGQSDPK Carbamidomethyl+C2 Carbamidomethyl+C13 Deamidation+N8  SEGSPENRICTNCCAGYK Carbamidomethyl+C10 Carbamidomethyl+C13 Carbamidomethyl+C14 Deamidation+N7	m	46.75
208	2	peptidyl prolyl cis trans isomerase fkbp15 1 like	PGSC0003DMT40002 2512	F:peptidyl-prolyl cis-trans isomerase activity; P:protein	11148.51 00	8.21	16019	5	QTOF	TTTDSSEL	m	38.93

				peptidyl-prolyl isomerization; P:protein folding						LTDGTVFDSSYER			
			EC:5.2.1.8							LGYGESGSPPK			
										SGDVTELQIGVK			
										NDPIEFELGSGQVIK			
208	2		aspartic protease inhibitor 5 like	PGSC0003DMT40002 4601	C:vacuole; F:serine-type endopeptidase inhibitor activity; F:peptidase activity; F:aspartic- type endopeptidase inhibitor activity; P:negative regulation of endopeptidase activity	1953.029 0	7.77	23921	5	QTOF	YNSDVGPSGTPVR	m	20.18
											SPNSDAPCPDGVFR Carbamidomethyl+C8		
											GALGGDVYLGK		
											IISIGR		
											ELNPNSSYR	Deamidation+N3	
											Deamidation+N5		
213	2		ribulose biphosphate carboxylase oxygenase large subunit	PGSC0003DMT40008 3063	C:mitochondrion; C:chloroplast; F:magnesium ion binding; F:monoxygenase activity; F:ribulose-biphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	2783.686 0	730	40242	6	QTOF	VALEACVK	s	12.15
				EC:4.1.1.39							AMHAVIDR		
											DDFIEQDR		
											WSPELAAACEVWK Carbamidomethyl+C9		
											LEGER		
											DDFIEQDRSR		
220	2	Pep	superoxide dismutase	PGSC0003DMT40004 2937	C:mitochondrial matrix; F:superoxide dismutase activity; F:copper ion binding; P:embryo development ending in seed dormancy; P:removal of superoxide radicals; P:oxidation-reduction process	76	7.14	25316	1	MALDI	K.HHQTYYITNYNKA	m	4
				EC:1.15.1.1									
274	2	Pep	chi2_soltu ame: full=endochitinase 2 flags: precursor	PGSC0003DMT40006 9033	C:extracellular region; C:cell wall; C:vacuole; C:cytoplasmic membrane-bounded vesicle; F:chitinase activity; F:chitin binding; P:polysaccharide catabolic process; P:chitin	286	6.18	34095	4	MALDI	R.GPIQISHNYNYGPCGR.A Carbamidomethyl (C)	m	22
				EC:3.2.1.14							R.WQPSGTDQAANR.V		

					catabolic process; P:response to biotic stimulus; P:plant-type hypersensitive response; P:cell wall macromolecule catabolic process						R.VPGFGVITNIINGLECGHGSDSR. V Carbamidomethyl (C)			
											R.YCGILGVSPGDNLDCGNQR.S 2 Carbamidomethyl (C)			
284	2	Prot	catalase isozyme 1-like protein	PGSC0003DMT40007 5611	C:glyoxysome; C:cytoplasmic membrane-bounded vesicle; F:catalase activity; F:heme binding; F:metal ion binding; P:response to oxidative stress; P:hydrogen peroxide catabolic process; P:oxidation-reduction process	66	6.56	56417	7	MALDI	R.GPVLLEDYYLIEK.L	s	16	
				EC:1.11.1.6							R.APGAQTPVICR.F Carbamidomethyl (C)			
											R.FSTVVHER.G			
											R.EGNFDLVGNNVPVFFNR.D			
											K.SFPDTIR.A			
											K.SHIQENWR.I			
											R.HMEGFGVHAYQLINK.E Oxidation (M)			
288	2	Pep	osmotin-like protein	PGSC0003DMT40000 1066	C:extracellular region; C:plant-type cell wall; C:plasmodesma; P:cytokinesis by cell plate formation; P:plant-type cell wall organization; P:cell wall modification	83	7.56	27158	7	MALDI	R.GGFTLHSLTHR.S	m	36	
											R.SFPAPTAHWSGR.V			
											R.VWARTGCTYEHGK.F			
											K.FYCATGDCGGR.I 2 Carbamidomethyl C			
											K.SACEAFKTDEFCCR.N 3 Carbamidomethyl C			
											K.TDEFCCR.N 2 Carbamidomethyl C			
											R.NHYNSPQTCKPSSYSQFFK.H Carbamidomethyl C			
288	2	Prot	osmotin-like protein	PGSC0003DMT40000 1066	C:extracellular region; C:plant-type cell wall; C:plasmodesma; P:cytokinesis by cell plate formation; P:plant-type cell wall organization; P:cell wall modification	105	7.56	27158	9	MALDI	R.GGFTLHSLTHR.S	m	41	
											R.SFPAPTAHWSGR.V			
											R.VWARTGCTYEHGK.F			



											K.FYCATGDCGGR.I Carbamidomethyl (C)	2	
											K.SACEAFKTDEFCCR.N Carbamidomethyl (C)	3	
											K.TDEFCCR.N 2 Carbamidomethyl (C)		
											R.NHYNPQTCKPSSYSQFFK.H Carbamidomethyl (C)		
293	2	Pep	aspartic protease inhibitor 5-like	PGSC0003DMT40002 4601	C:vacuole; F:serine-type endopeptidase inhibitor activity; F:peptidase activity; F:aspartic-type endopeptidase inhibitor activity; P:proteolysis; P:negative regulation of endopeptidase activity	105	8.04	23921	2	MALDI	K.SPNSDAPCPDGVFR.Y Carbamidomethyl (C)	m	12
											R.YNSDVGPSGTPVR.F		
294	2	Pep	carbonic chloroplastic-like isoform x2	PGSC0003DMT40000 1297	C:chloroplast stroma; C:cytoplasmic membrane-bounded vesicle; F:carbonate dehydratase activity; F:zinc ion binding; P:metabolic process; P:carbon utilization	406	6.40	34520	6	MALDI	K.TEKYDTNPALYGELAK.G	m	24
				EC:4.2.1.1							K.YDTNPALYGELAK.G		
											R.VCPSHVLNFQPGAEAFMVR.N Carbamidomethyl (C); Oxidation (M)		
											K.VLADHGDKEFGHQCTACEK.E 2 Carbamidomethyl (C)		
											K.EAVNVSLGNLLTYPFVR.E		
											K.GGYDFVK.G		
298	2		glyceraldehyde 3 phosphate dehydrogenase chloroplastic like	PGSC0003DMT40003 0050	C:chloroplast; F:glyceraldehyde-3-phosphate dehydrogenase NADP+ phosphorylating activity; F:NADP binding; F:NAD binding; P:glucose metabolic process; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	1833.086 0	8.38	42861	7	QTOF	AAALNIVPTSTGAAK	s	18.80
				EC:1.2.1.13							FGIHK		
											GTMTTTHSYTGDQR		
											DSPLDVIAINDTGGVK		
											IIQVVSNR		
											VLITAPGK		
											TSSAVPFGR		

303	2	Pep	ribulose- -bisphosphate carboxylase oxygenase large subunit	PGSC0003DMT40008 3063  EC:4.1.1.39	C:mitochondrion; C:chloroplast; F:magnesium ion binding; F:monooxygenase activity; F:ribulose-bisphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	71	7.23	40242	1	MALDI	K.TFQGPPHGIQVER.D	s	3
305	2	Pep	peptidyl-prolyl cis-trans isomerase cyp20- chloroplastic-like	PGSC0003DMT40001 3412  EC:5.2.1.8	C:chloroplast stromal thylakoid; C:chloroplast thylakoid membrane; C:thylakoid lumen; F:peptidyl-prolyl cis-trans isomerase activity; F:protein histidine kinase binding; P:protein peptidyl-prolyl isomerization; P:protein folding; P:NADPH dehydrogenase complex assembly; P:cysteine biosynthetic process	179	9.16	26510	3	MALDI	K.VYFDISIGNPVGK.L  R.IVIGLYGDDVPQTAENFR.A  K.HVVFGQVLEGMDIVK.L Oxidation M	m	18
324	2		annexin d1 like	PGSC0003DMT40004 5665  EC:1.11.1.7	C:cell wall; C:mitochondrion; C:vacuolar membrane; C:cytosol; C:plasma membrane; C:plasmodesma; C:chloroplast stroma; C:thylakoid; C:apoplast; F:peroxidase activity; F:copper ion binding; F:calcium ion binding; F:ATP binding; F:calcium-dependent phospholipid binding; F:zinc ion binding; F:protein homodimerization activity; P:chromatin assembly or disassembly; P:response to osmotic stress; P:response to oxidative stress; P:Golgi organization; P:response to desiccation; P:response to abscisic acid; P:sterol biosynthetic process; P:cysteine biosynthetic process; P:cellular cation homeostasis; P:oxidation- reduction process; P:calcium ion transmembrane transport; P:potassium ion export	885.6867	5.23	35823	11	QTOF	YGGDEVDLR  AYSDDDEVIR  DAYLAK  QTYAETFGEDLLK  LLVPLVSSYR  ELVLAR  EAYHAR  NAAQR  RDSIPLGR  DAINRR  ASLTVPAEVPSVAEDCEQLR Carbamidomethyl+C16, Acetyl+N- TERM1	m	31.21



				differentiation; P:positive regulation of transcription, DNA-templated						ELMPGGVNSPVR		
387	2	saccharopine dehydrogenase isoform 2	PGSC0003DMT40008 8617	C:chloroplast thylakoid; F:oxidoreductase activity; P:oxidation-reduction process	1054.265 0	6.55	46637	11	QTOF	AVDGTAGEAVSMR	m	24.88
										ELGFGIYS		
										LESEGELER		
										VGGSTAIALSK		
										NAEFAEVNIDDR		
										VLEAAIGTK		
										ASEGTINFILNK		
										EVLQR		
										VVILGGTGR		
										VDLECSGDHNR Carbamidomethyl+C5		
										GASMVSK		
387	2	protein tic chloroplastic like	PGSC0003DMT40000 5492	C:plastid chromosome; C:chloroplast thylakoid membrane; C:chloroplast envelope; P:pentose-phosphate shunt; P:rRNA processing; P:response to blue light; P:chloroplast relocation; P:thylakoid membrane organization; P:stomatal complex morphogenesis; P:response to red light; P:response to far red light; P:chlorophyll biosynthetic process; P:carotenoid biosynthetic process; P:photosynthesis, light reaction; P:glucosinolate biosynthetic process	868.6656	9.35	52530	8	QTOF	ANEESDAQVATVR	m	18.79
										LTEDFSPESYK		
										VVEVFADPSAPSK		
										AGVSDLGAAQELAR		
										AYAEALEK		
										NPFASK		
										VISNDESK		
										MAPTLTSNSFLLSTTPHR		

392	2	Pep	chloroplast rubisco activase	PGSC0003DMT40004 9256	C:chloroplast stroma; F:ATP binding	334	8.10	48089	6	MALDI	K.GLYENASDDQQDIAR.G K.SFQCELVFR.K Carbamidomethyl (C) R.VPIIVTGNDFSTLYAPLIR.D K.FYWAPTR.E K.IVDSFPGQSIDFFGALR.A K.LLGYGNMLVQEENVKR.V Oxidation (M)	m	21
394	2	Prot	threonine dehydratase chloroplastic-like	PGSC0003DMT40003 3801 EC:4.3.1.19	C:chloroplast; F:L-threonine ammonia-lyase activity; F:pyridoxal phosphate binding; P:isoleucine biosynthetic process	106	5.22	64723	10	MALDI	R.GAYNMMSNLSKEELAK.G K.GVITASAGNHAQGVALAGQR.L K.GQGIGTEINR.Q K.QIAPNTK.I K.IIGVEPYGAASMTLSLYEGHR.V Oxidation (M) K.CQELIDGMVLVR.N Carbamidomethyl (C); Oxidation (M) R.NDGISAAIKDVYDEGR.N K.DVYDEGR.N K.LVGS MNITEVTYR.F Oxidation (M) R.KEALVLYR.V	s	20
396	2		glyceraldehyde 3 phosphate dehydrogenase chloroplastic like	PGSC0003DMT40007 5608	C:chloroplast thylakoid membrane; C:chloroplast stroma; C:chloroplast envelope; C:stromule; C:apoplast; F:oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; F:NADP binding; F:NAD binding; P:glucose	2865.675 0	7.47	47896	11	QTOF	AAALNIVPTSTGAAK IVDNETISVDGK ILDEEFIVK DSPLDVVVVNDSSGGVK GISAEDVNAEFR	m	27.11

				metabolic process; P:oxidation-reduction process						YDSMLGTFK		
										VIITAPAK		
										LNGIALR		
										IPTSTR		
										HIQAGAK		
										TNPADKECK Carbamidomethyl+C8		
396	2	glyceraldehyde 3 phosphate dehydrogenase chloroplastic like	PGSC0003DMT400025881	C:chloroplast thylakoid membrane; C:chloroplast stroma; C:chloroplast envelope; C:stromule; C:apoplast; F:oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor; F:NADP binding; F:NAD binding; P:glucose metabolic process; P:oxidation-reduction process	2758.3250	6.55	47976	12	QTOF	AAALNIVPTSTGAAK	m	21.97
										IVDNETISVDGK		
										DSPLDVVVVNDSSGGVK		
										VMDEELGIVK		
										YDSMLGTFK		
										GITAEDVNAAFR		
										VIITAPAK		
										AADGPLK		
										LNGIALR		
										IPTSTR		
										HIQAGAK		
										NSYSFPTQCLSK Carbamidomethyl+C9		
417	2	grip and coiled coil domain containing	PGSC0003DMT400046956		7953.631	4.08	85846	27	QTOF	AEELPSIPATSTESEEK	l	42.18
										EQVDLEASEPQK		
										SVATEELAAPDAK		
										EEASEPAPIAEEK		

ADEPIPTIAEEVK  
QDETPALDVTSK  
TAEGEKEVEETAK  
TTEEVPVK  
LLEATEK  
DIEPIADNGSSK  
DIPELTK  
VLEAEVPK  
APEVVIASR  
IEQEAAEAVTGNEEVIPVDK  
TMEGENVPLTK  
VDENATAEPSVEEAQK  
MDEESPTEVAADNVVTEEK  
ATDTVSSDHPTTVSEQAEK  
STVDAPPSAIIIEELK  
DVTIPTIEAK  
EVPEEVK  
SDEEEKPEADEPAPTIVEEVQK  
SVEPDSEK  
IVDEQPTIEPPPAIAEVNK  
SEVAEK  
EVEETAK  
TVGQDEKVEK

418	2	Prot	elongation factor ts isoform 2	PGSC0003DMT40000 8133	C:chloroplast stroma; C:chloroplast envelope; F:translation elongation factor activity; F:protein binding; P:translational elongation; P:chloroplast relocation; P:thylakoid membrane organization; P:carotenoid biosynthetic process; P:isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; P:ncRNA metabolic process; P:hydrogen peroxide catabolic process	72	4.72	114201	8	MALDI	R.SIQPFGAFIDFGAFTDGLVHVSRL K.LNQGCVVHSATNPFLLAFR.S R.IGVLVEVNCETDFVSR.G Carbamidomethyl (C) R.EIEMQKEDLLSKPEQIR.S K.RLEDLALLEQPYIK.N K.AQEYLR.K R.IGSYIHDSR.I R.IGVLIEVNCETDFVGR.G Carbamidomethyl (C)	s	8
422	2		structural maintenance of chromosomes protein 4 like	PGSC0003DMT40000 3351	C:nucleus; C:chromosome; F:protein binding; F:ATP binding; P:chromosome organization	21.6632	6.14	141514	9	QTOF	GIEESNKEK SFSAVVGPNGSGK LAEK QLDSLRL HEAGR VSVYNER IENAGGER VAFRDNSSK NIANELEK	s	3.37
431	2		linoleate 13s lipxygenase 2 chloroplastic like	PGSC0003DMT40008 1909 EC:1.13.11.12	C:chloroplast thylakoid; C:chloroplast stroma; F:protein binding; F:linoleate 13S- lipxygenase activity; F:metal ion binding; P:oxylipin biosynthetic process; P:oxidation-reduction process	850.6078	6.14	101911	20	QTOF	VYGPPESEITK GVPYSISI CFPSQIQATK DEAFSEVK DVEFAR	m	21.02



										FDQEALPQNLSR		
										IYDYDVYNDLGEADSNDDAK		
										AVVTVQK		
										EIGNYMTVEQAVQQK		
										QTLAGLNPYSIR		
										DPLSETR		
										IFFTNK		
										STFVYVPR		
										AVLSSTEK		
										LVTEWPLR		
										YTMEINALAR		
										DVLLFESPQLVQR		
										SGLFNVVPR		
										LDPK		
										NNSDK		
442	2	heat shock cognate protein 80	PGSC0003DMT40005 7003	C:cytoplasmic membrane- bounded vesicle; F:ATP binding; F:unfolded protein binding; P:protein folding; P:defense response signaling pathway, resistance gene-dependent	7500.347 0	4.76	80221	37	QTOF	ELISNSSDALDK	m	23.75
										EDQLEYLEER		
										EGQNDIYYITGESK		
										AVENSPFLEK		
										FESLTDK		
										EVSNEWSLVNK		
										ADLVNNLGTIAR		
										SGDEMTSLK		

FYEAFSK

GIVDSEDLPLNISR

VIVSDR

DSSMAGYMSSK

VIVTTK

DTSGENLGR

DYVTR

FEGLCK

EIFLR

EEYAAFYK

FAELLR

AVLFVPK

TNNTLTIIDSGIGMTK

APFDLFDTK

MVLYLK

DVLGDK

VEEVDEDKEK

LGIHEDSQNR

DSSMAGYMSSKK

MVLYLKEDQLEYLEER

HFSVEGQLEFK

ADADK

DVLGDKVEK

											EGLKLDSEDEK		
											KAVENSPFLEK		
											ELISNSSDALDKIR		
											RAPFDLFDTK		
											TMEINPENSIMDEL	Oxidation M1	
											TMEINPENSIMDEL	Oxidation M2	
442	2	heat shock cognate protein 80 like	PGSC0003DMT40007 6601	C:cytoplasmic membrane-bounded vesicle; F:ATP binding; F:unfolded protein binding; P:protein folding; P:defense response signaling pathway, resistance gene-dependent	6521.609 0	4.76	80143	28	QTOF	ELISNSSDALDK		m	20.17
											EDQLEYLEER		
											EGQNDIYYITGESK		
											AVENSPFLEK		
											EVSNEWSLVNK		
											ADLVNNLGTIAR		
											FYEAFSK		
											GIVDSEDLPLNISR		
											DSSMAGYMSSK		
											DYVTR		
											FEGLCK		
											EIFLR		
											FQSLTDK		
											EEYAAFYK		
											FAELLR		
											APFDLFDTK		
											DVLGDK		

										TNNTLTIDSGVGMTK		
										LGIHEDSQNR		
										DSSMAGYMSSKK		
										EMLQQNK		
										HFSVEGQLEFK		
										ADADK		
										DVLGDKVEK		
										KAVENSPFEK		
										ELISNSSDALDKIR		
										RAPFDLFDTK		
455	2	transketolase 1	PGSC0003DMT40001 8062	C:chloroplast thylakoid membrane; F:transketolase activity; F:metal ion binding; P:reductive pentose-phosphate cycle	2182.958 0	6.22	80159	15	QTOF	ALPTYTPESPADATR	m	17.29
			EC:2.2.1.1							NLSQQNLNALAK		
										VTTTIGFGSPNK		
										NGNTGYDEIR		
										FLAIDAVEK		
										TPSILALSR		
										SVNTIR		
										FAEYEK		
										ASAAVETLEK		
										YPAEAADLK		
										MFGDFQK		
										AADELK		
										QWGSK		

										SHWSR		
										TDNALVEK		
457	2	transketolase 1	PGSC0003DMT40001 8062	C:chloroplast thylakoid membrane; F:transketolase activity; F:metal ion binding; P:reductive pentose-phosphate cycle  EC:2.2.1.1	728.4799	6.22	80159	11	QTOF	ALPTYTPESPADATR	m	20.24
										VTTTIGFGSPNK		
										NGNTGYDEIR		
										NLSQQNLNALAK		
										SVNTIR		
										FLAIDAVEK		
										FAEYEK		
										AADELK		
										ISALAESR		
										AADELK		
										STTATSFRR		
465	2	tktsoltuame full chloroplastic short tk flags precursor	PGSC0003DMT40005 6799	C:chloroplast thylakoid membrane; F:transketolase activity; F:metal ion binding; P:reductive pentose-phosphate cycle  EC:2.2.1.1	113.8577	5.91	79928	5	QTOF	ALPTYTPESPADATR	s	8.37
										VTTTIGFGSPNK		
										NLSQQNLNALAK		
										AIGIDGFGASAPADK		
										TDAAIVEK		
468	2	tktsoltuame full chloroplastic short tk flags precursor	PGSC0003DMT40005 6799	C:chloroplast thylakoid membrane; F:transketolase activity; F:metal ion binding; P:reductive pentose-phosphate cycle  EC:2.2.1.1	2358.688 0	5.91	79928	13	QTOF	ALPTYTPESPADATR	m	18.76
										NLSQQNLNALAK		
										VTTTIGFGSPNK		
										ESVLPSSVTAR		
										AIGIDGFGASAPADK		

										YAEAAADLK		
										NGNTGYDEIR		
										LPQLAGTSIEGAAK		
										VAVLK		
										TPSILALSR		
										SIITGELPAGWEK		
										TDAAIVEK		
										SVNTIR		
470	2	atp dependent zinc metalloprotease ftshchloroplastic like	PGSC0003DMT40004 4601	C:membrane; F:metalloendopeptidase activity; F:ATP binding; F:microtubule- severing ATPase activity; P:proteolysis; P:cell division	596.8522	6.10	74369	14	QTOF	QVSVDVPDIK	m	16.88
			EC:3.4.24; EC:3.6.4.3							TLLAK		
										EIDDSIDR		
										TEILK		
										FTAVGAR		
										IVEVLEK		
										IVAGMEGTVMTDGK		
										VPAAVPTPAAV		
										ETMTGDEFR		
										VHAGNKK		
										VTLIPR		
										GTGIGGGNDER		
										QLFAR		
										LAEDIDVAVK		

471	2	Prot	atp-dependent zinc metalloprotease ftshchloroplastic-like	PGSC0003DMT40004 4601	C:membrane; F:metalloendopeptidase activity; F:ATP binding; F:microtubule-severing ATPase activity; P:proteolysis; P:cell division	62	6.14	74370	6	MALDI	R.FLEYLDKDR.V  K.AKENAPCIVFVDEIDAVGR.Q Carbamidomethyl (C)  K.ENAPCIVFVDEIDAVGR.Q Carbamidomethyl (C)  R.ADILDSALLRPGR.F  R.AAEEVIFGEPEVTTGAAGDLQIT GLAK.Q  R.AILSEFVEIPAENRVPAAVPTPAA V.-	m	13
473	2		ru large subunit-binding protein subunit chloroplastic	PGSC0003DMT40006 1700	C:cytoplasm; F:ATP binding; P:protein refolding	7607.112 0	5.57	62995	29	QTOF	VVAAGANPVLITR  EVELEDPVENIGAK  NAGVNGSVVSEK  GYVSPYFVTDSEK  IVNDGVTVAR  ALVAELK  NVVLESK  MSVEYENCK Carbamidomethyl+C8  ALSYPK  VEDALNATK  DATTIVGDGSTQEAVNK  VVLTK  VLSSDDPK  SAENSLR  YGAPK	m	42.40

										EELGLTLDK		
										GVVTLEEGK		
										LADLVGVTLGPK		
										VGADIVK		
										LLLVDK		
										GTLANDEEK		
										LQNGVNK		
										EPEAAVAGNPMDNSGYGY		
										VAQIK		
										EVLGHAAK		
										APGFGERK		
										APGFGER		
										RPTILAAAK		
										GIEK		
474	2	ru large subunit binding protein subunit chloroplastic like	PGSC0003DMT40000 6501	C:cytoplasm; F:ATP binding; P:protein refolding	1174.023 0	5.36	64272	7	QTOF	IVNDGVTVAR	m	13.06
										NVVLESK		
										NAGVNGSVVIEK		
										VEDALNATK		
										LLEEAEQDYEK		
										DSTTIVGDGSTQDAVSK		
										ITNAR		
476	2	ru large subunit-binding protein subunit chloroplastic	PGSC0003DMT40006 1700	C:cytoplasm; F:ATP binding; P:protein refolding	3413.156 0	5.57	62995	23	QTOF	VVAAGANPVLITR	m	36.73
										EVELEDPVENIGAK		



										GYVSPYFVTDSEK		
										IVNDGVTVAR		
										DATTIVGDGSTQEAVNK		
										NAGVNGSVVSEK		
										NVVLESK		
										ALVAELK		
										VEDALNATK		
										MSVEYENCK Carbamidomethyl+C8		
										ALSYPLK		
										VLSSDDPK		
										VVLTK		
										EELGLTLDK		
										LADLVGVTLGPK		
										VGADIVK		
										LLLVDK		
										EPEAAVAGNPMDNSGYGY		
										GVVTLLEEGK		
										APGFGER		
										YGAPK		
										GTLANDEEK		
										SAENSLR		
476	2	glucose 6 phosphate isomerase like	PGSC0003DMT400033620	C:cytosol; C:chloroplast stroma; C:chloroplast envelope; F:RNA binding; F:glucose-6-phosphate isomerase activity; F:ATP binding; F:transferase activity;	775.1050	5.32	67598	12	QTOF	VNQGISVYGNK	m	22.56

			EC:5.3.1.9	P:maltose metabolic process; P:polysaccharide catabolic process; P:gluconeogenesis; P:glycolytic process; P:immune response; P:plant-type cell wall organization; P:positive regulation of flower development; P:starch biosynthetic process; P:isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; P:positive regulation of catalytic activity						ALIAEGNCGTPQSIR Carbamidomethyl+C8  VLQVLNEASCK Carbamidomethyl+C10  EMLAGAALMDEANR  EFDLDGNR  QPVEPLTLDEIAER  EAGLIFAK  NGLLEVQK  AAGEVLALQK  GAIANPDEGR  TPSGGR  ESITVTVQEVTPRSVGALVALYER		
477	2	threonine dehydratase chloroplastic like	PGSC0003DMT40003 3801  EC:4.3.1.19	C:chloroplast; F:L-threonine ammonia-lyase activity; F:pyridoxal phosphate binding; P:isoleucine biosynthetic process	1265.118 0	5.04	64723	12	QTOF	GQGTIGTEINR  NDGISAAIK  DVYDEGR  VTELAELGSDK  LVGSMNITEVTYR  SDLEEMIK  QSVFSFK  CQELIDGMVLVR Carbamidomethyl+C1  LNSSNMK  FTSER  SDLEEMIKK	m	17.11

GAYNMMSNLSK Oxidation+M5													
487	2	Pep	adp-glucose pyrophosphorylase small subunit	PGSC0003DMT40007 9823 EC:2.7.7.27	C:amyloplast; C:chloroplast; F:ATP binding; F:glucose-1- phosphate adenyltransferase activity; P:glycogen biosynthetic process; P:starch biosynthetic process	235	6.73	57190	6	MALDI	R.SVLGIIILGGGAGTR.L R.AKPAVPLGANYR.L K.IYVLTQFNSASLNR.H K.KPVPDFSFYDR.S R.SAPIYTQPR.Y K.IHHSVVGRL.S	m	13
507	2		glycine trna ligase mitochondrial like	PGSC0003DMT40003 6931 EC:6.1.1.14	C:cytoplasm; F:glycine-tRNA ligase activity; F:ATP binding; P:glycyl-tRNA aminoacylation	887.9229	5.60	70141	16	QTOF	IDITGTSIGK QAVTNTLER VNVDEVASVIK VVTINK DPNLPAEK DPAQEAQNR NEISPR AAEFR EYGITAPDTK NMVSISK DLYYYNGNK LIIVPAK GVAGLYDYGPPGCAVK Carbamidomethyl+C13 ELGLAFK LFYIPSEK	m	22.54

										MVVEALEAMGEK Oxidation+M1		
508	2	heat shock protein sti like	PGSC0003DMT40001 2208	F:protein binding	7259.621 0	5.82	65090	33	QTOF	QVLSDFQENPK	m	46.46
										NPSNLNLYLK		
										SGLADVQSAQAR		
										CIELDPTFVK Carbamidomethyl+C1		
										GLDIDPNNEGLK		
										YSDALSDAQK		
										LDPQNQELLDGVK		
										LINAGIVQVR		
										MPEEDDEMPEASTER		
										AIELDDGDISFITNR		
										ELEQQEYFSPQIADEER		
										SAAYASLGK		
										CVEQINK Carbamidomethyl+C1		
										GNQFFK		
										LTADASTR		
										TYQEGLK		
										GDLTPEELKER		
										EKEAGNAAYK		
										NPLVMDK		
										YPEAVK		
										GDLTPEELK		
										GYLQQPDFVSMMK		

										LAALPEGLK		
										LNEAEK		
										LAALPEGLKDAEK		
										EAGNAAYK		
										IDPNNEGLK		
										ELEQQEYFSPQIADEEREK		
										AAVYLEMGK		
										AVER		
										NPDTLK		
										MADAEK		
										GYLQQPDFVSMMKDIQK		
										Oxidation+M11		
510	2	heat shock protein sti like	PGSC0003DMT40001 2208	F:protein binding	1153.716 0	5.82	65090	21	QTOF	SGLADVQSAQAR	m	11.74
										QVLSDFQENPK		
										YSDALSDAQK		
										GLDIDPNNEGLK		
										LDPQNQELLDGVK		
										NPSNLNLYLK		
										MPEEDDEMPEASTER		
										SAAYASLGK		
										CVEQINK Carbamidomethyl+Cl		
										LINAGIVQVR		
										GDLTPEELK		

										TYQGLK		
										YPEAVK		
										ELEQQEYFSPQIADEER		
										NPDTLK		
										ADEAK		
										GDLTPEELKER		
										GAVQFFMK		
										HYTESIKR		
										GNQFFK		
										DIQK		
515	2	nadp dependent malic enzyme like	PGSC0003DMT40008 4201	F:malate dehydrogenase decarboxylating NAD+ activity; F:malate dehydrogenase decarboxylating NADP+ activity; F:metal ion binding; F:NAD binding; P:malate metabolic process; P:protein homooligomerization; P:oxidation-reduction process	231.5369	5.62	64057	11	QTOF	GLIVSGR	m	14.34
			EC:1.1.1.38; EC:1.1.1.39; EC:1.1.1.40							AYELGVATR		
										IPVEETR		
										YGSIFK		
										YAESCMYTPNYR Carbamidomethyl+C5		
										ILEVELK		
										EVVEAMACMNK Carbamidomethyl+C8		
										GLLPPVISSQELQEK		
										LFYK		
										LMQSIR		
550	2	gamma aminobutyrate transaminase 2 like	PGSC0003DMT40006 2385	C:chloroplast; F:4-aminobutyrate transaminase activity; F:pyridoxal phosphate	5453.861 0	5.02	33499	11	QTOF	IQAVLK	m	33.66
										NITEVVNK		

			EC:2.6.1.1	binding; P:gamma-aminobutyric acid metabolic process						FQEGLK		
										LGTMFGCDK Carbamidomethyl+C7		
										AFIDSPIIGEIR		
										LANNLENLILK		
										GTGLVLSTEFVDSK		
										YNIKPDLVSIK		
										ALSGGYIPIGAVLVSEEISK		
										IYKEK		
										EKNITEVVNK		
550	2	gamma aminobutyrate transaminase 2 like	PGSC0003DMT40006 4961	C:mitochondrion; F:4-aminobutyrate transaminase activity; F:pyridoxal phosphate binding; P:gamma-aminobutyric acid metabolic process	5081.239 0	6.24	50567	6	QTOF	VFFTNSGSEANDTQVK	m	13.97
			EC:2.6.1.19							FQEGLK		
										LGTMFGCDK Carbamidomethyl+C7		
										LANNLENLILK		
										TTKPSDLAK		
										AEGSYVYDINGK		
557	2	utp alpha d glucose 1 phosphate uridylyltransferase	PGSC0003DMT40003 4699	C:cytoplasm; F:UTP:glucose-1-phosphate uridylyltransferase activity; P:UDP-glucose metabolic process	6067.073 0	5.60	51774	22	QTOF	DINGPEDI	m	40.67
			EC:2.7.7.9							LVTEDFAPLPCK Carbamidomethyl+C11		
										LEIPDGAVIANK		
										NEYCMEVTPK Carbamidomethyl+C4		
										SNPSNPSIELGPEFK		
										TLADVK		
										SVIEVR		

										LVEADALK		
										FLPVK		
										LNGGLGTTMGCTGPK		
										Carbamidomethyl+C11		
										QIEALNAK		
										MEIIPNPK		
										AIGANVPR		
										VANFLGR		
										LNNLK		
										SIPSIIDLSLK		
										MATATLSPADAEK		
										VLQLETAAGAAIK		
										AGFINLVGR		
										EVDGVK		
										LDALLAK		
										ATATLSPADAEK Acetyl+N-TERM1		
565	2	methionine synthase	PGSC0003DMT40007 2279	F:5- methyltetrahydropteroyltriglu- tate-homocysteine S- methyltransferase activity; F:zinc ion binding; P:methionine biosynthetic process; P:methylation	1653.582 0	6.17	84544	23	QTOF	IPSTEEIADR	m	23.14
			EC:2.1.1.14							TLTALK		
										ISEEEYVK		
										EVIAELK		
										GTQTLELIK		
										VSADLR		
										LEAFTK		



											EGLPLR		
											GNASVPAMEMTK		
											LDDEIK		
											AITEEIK		
											VVEVNALAK		
											QMSDAGIK		
											ILPIYK		
											YLFAGVVDGR		
											AITEEIKK		
											LLSVFR		
											DEVEDLEK		
											DEAFFSANAAAQASR		
											ASAALQGS DHR		
											FSYASHK		
											RELK		
											ASHVVGYP R Acetyl+N-TERM1		
568	2	methionine synthase	PGSC0003DMT40007 2279	F:5- methyltetrahydropteroyltrigluta mate-homocysteine S- methyltransferase activity; F:zinc ion binding; P:methionine biosynthetic process; P:methylation	282.2789	6.17	84544	12	QTOF	IPSTEEIADR		m	12.68
			EC:2.1.1.14							GTQTLELIK			
										EVI AELK			
										ISEEEYVK			
										TLTALK			
										VSADLR			
										LEAFTK			

											AGITVIQIDEAALR		
											EGLPLR		
											AVNEYK		
											YLFAGVVDGR		
											ASHVVGYP Acetyl+N-TERM1		
577	2	Pep	PREDICTED: uncharacterized protein At5g39570-like	PGSC0003DMT40000 3630	uncharacterised	410	4.67	40963	7	MALDI	R.KSEYEEPTPEYGSYGR.K	m	43
											R.KSEYEEPKPYGSYGR.K		
											R.KSEYEEPSSEYGSYGR.K		
											R.KSEYEEPTPYGSYGR.K		
											R.KSEYQEPSSEYGR.K		
											R.KTEYEEPTAQYGR.K		
											R.SEEEDYKKPSYER.R		
583	2	Pep	threonine dehydratase chloroplastic-like	PGSC0003DMT40003 3801	C:chloroplast; F:L-threonine ammonia-lyase activity; F:pyridoxal phosphate binding; P:isoleucine biosynthetic process	50	5.22	64723	2	MALDI	R.NDGISAAIKDVYDEGR.N	s	5
											K.TFNFSHNLVAEHK.H		
				EC:4.3.1.19									
583	2		asr4 protein	PGSC0003DMT40001 7057	P:response to stress	6697.709 0	4.74	33936	10	QTOF	TSYGDDTYGEK	m	16.34
											TTYEETTYGESEK		
											NEEDIPVEK		
											TSYGNEEGGYGGVGETTNYEENE SETK		
											EAKEEEEAEK		
											TSYGDSGYGEKPSYGGDDNK		
											TSTYGEK		

										TTTFGDDNKYGEK	
										TSYGEGDDNKYGEK	
										GDDNKYGEK	
583	2	threonine dehydratase chloroplastic like	PGSC0003DMT40003 3801 EC:4.3.1.19	C:chloroplast; F:L-threonine ammonia-lyase activity; F:pyridoxal phosphate binding; P:isoleucine biosynthetic process	2895.097 0	5.04	64723	13	QTOF	GQGTIGTEINR	19.13
										NDGISAAIK	
										LVGSMNITEVTYR	
										VTELAELGSDK	
										DVYDEGR	
										WNITLCR Carbamidomethyl+C6	
										SDLEEMIK	
										SDLEEMIKK	
										KEALVLYR	
										CQELIDGMVLVR Carbamidomethyl+C1	
										QIAPNTK	
										LNSSNMK	
										NENIVAIASGANMDFSK	
583	2	heat shock cognate 70 kda protein 2 like	PGSC0003DMT40002 3039 EC:1.3.1.74	F:ATP binding; F:2-alkenal reductase [NADP] activity; P:oxidation-reduction process	2334.632 0	4.95	71193	16	QTOF	IEEVD	s 14.26
										ELESICNPIIAK Carbamidomethyl+C6	
										ATSVGEK	
										NALENYAYNMR	
										LSKEEIEK	
										VQQLQDFFNGK	

										DNNLLGK		
										ITITNDK		
										CMEPVEK Carbamidomethyl+C1		
										FEELNMDLFR		
										TRDNNLLGK		
										LPEADRK		
										MVTHFVQEFK		
										ITITNDKGR		
										KCMEPVEK Carbamidomethyl+C2		
										MVQEAEKYK		
583	2	heat shock cognate 70 kda	PGSC0003DMT40000 1180	F:ATP binding	776.7247	4.95	71269	10	QTOF	IEEVD	s	14.98
										VQQLQDFENGK		
										DNNLLGK		
										ITITNDK		
										CMEPVEK Carbamidomethyl+C1		
										VSSQLPAADK		
										ITITNDKGR		
										KCMEPVEK Carbamidomethyl+C2		
										MVQEAEKYK		
										FEEKNMDLFR Deamidation+N5		
583	2	endoplasmin homolog	PGSC0003DMT40005 0556	C:mitochondrion; C:vacuolar membrane; C:chloroplast stroma; C:chloroplast envelope; F:ATP binding; F:unfolded protein binding; P:protein folding; P:response to water deprivation; P:response to salt	493.0839	4.70	90856	14	QTOF	GVVDSNDLPLNVS	s	16.31
										LSTSPCVLVSGK Carbamidomethyl+C6		

				stress; P:chloroplast organization; P:de-etiolation; P:response to chlorate; P:protein import into chloroplast stroma; P:ovule development						EETNPENLLPR		
										TESNDYWE		
										FFSSK		
										TIEVEEEEEPK		
										AIYYLATDSLQSAR		
										APVVSRR		
										TAPFLEK		
										DVGVVVRR		
										EVFLR		
										NNIK		
										IYEMMAMALGGR Oxidation+M7		
										AQTLGDTSTLEFMR Oxidation+M13		
583	2	rhodanese like domain containing protein chloroplastlike	PGSC0003DMT40000 0605	P:nucleobase-containing compound metabolic process; P:cellular amino acid metabolic process; P:fatty acid metabolic process; P:coenzyme metabolic process; P:sulfur compound metabolic process; P:phosphate-containing compound metabolic process; P:signal transduction; P:lipid biosynthetic process; P:response to light stimulus; P:plastid organization; P:response to organic substance; P:regulation of metabolic process; P:photosynthesis, light reaction; P:cellular macromolecule metabolic process; P:monocarboxylic acid biosynthetic process; P:defense response to other organism; P:organonitrogen compound	246.8415	4.78	47067	7	QTOF	VEATSPPTPEVNAVPAEVK	m	16.44
										LADDAGAQLLDIR		
										ELVDEIK		
										AAYAIAK		
										MEAINAVR		
										TLQQVDEFLSTK		
										DGAEGPR		

biosynthetic process; P:response to oxygen-containing compound												
619	2	tubulin alpha chain like	PGSC0003DMT40002 2574	C:cytoplasm; C:microtubule; F:GTPase activity; F:structural constituent of cytoskeleton; F:GTP binding; P:microtubule- based process; P:metabolic process; P:protein polymerization	2522.223 0	4.73	49576	7	QTOF	DVNAAVATIK CGINYQPPTVVPGDLAK Carbamidomethyl+C1 EDLAALEK GDVVPK DYEEVGAEADGVGDDDEEY TIQFVDWCPTGFK Carbamidomethyl+C8 LSVDYGK	s	18.22
626	2	ru large subunit binding protein subunit chloroplastic like	PGSC0003DMT40006 1700	C:cytoplasm; F:ATP binding; P:protein refolding	3239.370 0	5.57	62995	14	QTOF	EVELEDPVENIGAK GYVSPYFVTDSEK IVNDGVTVAR MSVEYENCK Carbamidomethyl+C8 NVVLESK ALVAELK VVAAGANPVLITR GVVTLEEGK LLLVDK LADLVGVTLGPK DATTIVGDGSTQEAVNK DLVNVLEDAIR EVLGHAAK NMSK	s	23.37

650	2	Pep	triosephosphate isomerase chloroplastic-like	PGSC0003DMT40000 4042 EC:5.3.1.1	C:mitochondrion; C:cytosol; C:chloroplast stroma; C:thylakoid; C:chloroplast envelope; C:apoplast; F:triosephosphate isomerase activity; P:glycolytic process; P:glycine catabolic process; P:tryptophan catabolic process; P:triglyceride mobilization; P:calcium ion transport; P:Golgi organization; P:response to salt stress; P:chloroplast organization; P:indoleacetic acid biosynthetic process; P:reductive pentose-phosphate cycle; P:isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway; P:cysteine biosynthetic process; P:glycerol catabolic process; P:multicellular organism reproduction; P:regulation of protein localization; P:glyceraldehyde-3-phosphate biosynthetic process; P:primary root development	80	6.89	34647	2	MALDI	K.GGAFTGEISVEQVK.D K.TFDVCFQQLK.A Carbamidomethyl (C)	m	26
652	2	Pep	cysteine protease inhibitor 8-like	PGSC0003DMT40002 6280	F:endorpeptidase inhibitor activity; P:negative regulation of endopeptidase activity	79	5.52	24706	1	MALDI	R.LALNNKPYPFQFTK.V	m	6
652	2	Pep	pigment-binding protein cp26	PGSC0003DMT40006 8129	C:PSII associated light-harvesting complex II; C:photosystem I; C:photosystem II antenna complex; C:plastoglobule; C:integral component of membrane; F:chlorophyll binding; F:metal ion binding; P:rRNA processing; P:response to high light intensity; P:response to sucrose; P:photosynthesis, light harvesting; P:regulation of proton transport; P:nonphotochemical quenching; P:protein-chromophore linkage; P:cysteine biosynthetic process	87	5.98	30392	2	MALDI	R.IFLPDGLLDR.S K.YQAYELIHAR.W	m	7

658	2		oxygen evolving enhancer protein chloroplastic like isoform x1	PGSC0003DMT40000 2421	C:chloroplast thylakoid membrane; C:photosystem II oxygen evolving complex; C:extrinsic component of membrane; F:calcium ion binding; P:photosynthesis	3381.035 0	6.38	30373	10	QTOF	SITDYGSPPEEFLSK ENTDFLPYNGDGFK VDYLLGK LYICK Carbamidomethyl+C4 LQIPAK EIEFPGQVLR QAYFGK WNPSK QYYLSVLTR FVENAATSFZIA	m	31.79
668	2	Pep	chloroplast rubisco activase	PGSC0003DMT40004 9256	C:chloroplast stroma; F:ATP binding	563	8.10	48089	6	MALDI	K.GLYENASDDQQDIAR.G K.SFQCELVFR.K Carbamidomethyl (C) R.VPIIVTGNDSTLYAPLIR.D K.FYWAPTR.E K.IVDSFPGQSIDFFGALR.A K.LLGYGNMLVQEENVKR.V Oxidation (M)	m	19
669	2		protein disulfide isomerase like	PGSC0003DMT40001 0624  EC:5.3.4.1	C:endoplasmic reticulum; F:protein disulfide isomerase activity; P:protein folding; P:cell redox homeostasis	6943.304 0	4.62	54862	19	QTOF	SASGNLSQYNGER SQPIPEVNDEPVK YNDVAVLYK LDATANDLPK YDASDEANR VDSAKDEL	m	37.04



											FFEGTNAK		
											NLAPEYEK		
											SKEDATNLIDEK		
											EDATNLIDEK		
											FENYLTAEK		
											EAAGIVSYLK		
											QVGPASAEIK		
											VQEYNGPR		
											DTLQDMVYNSGK		
											YDASDEANRELSK		
											QYEIQGFPTIK		
											AASELSSHDPPIVLAK		
											GEVDFAHTVDAK		
675	2	Pep	v-type proton atpase subunit b2-like	PGSC0003DMT400008800	C:proton-transporting V-type ATPase, V1 domain; F:ATP binding; F:hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; P:ATP hydrolysis coupled proton transport; P:ATP metabolic process	183	5.45	58410	6	MALDI	K.YQEIVNIR.L	m	16
											R.IFNGSGKPIDNGPILPEAYR.D		
											R.VTLFLNLANPTIER.I		
											R.GYPGYMYTDLATIYER.A		
											Oxidation (M)		
											R.QIYPPINVLPSLSR.L		
											R.KFVSQGAYDTR.N		
05	13	Pep	protein toc75- chloroplastic-like	PGSC0003DMT400078190	C:vacuolar membrane; C:Toc complex; C:integral component of chloroplast outer membrane; F:P-P-bond-hydrolysis-driven protein transmembrane transporter activity;	321	8.42	91403	7	MALDI	K.VSDILFFDR.R	m	13
											K.LGNVCEGNTQYPVVR.R		
											Carbamidomethyl (C)		

					P:chloroplast organization; P:protein import into chloroplast stroma; P:ovule development; P:embryonic morphogenesis						K.FTYGLVMEIITTR.D Oxidation (M) R.VLPSGGISADGPPTLSETGIDR.M R.MAFLQANITR.D Oxidation (M) K.FINGTIVGER.N R.AEYAVDHNSGTGAVFFR.F		
06	13	Pep	probable rhamnose biosynthetic enzyme 1-like	PGSC0003DMT40001 8192	F:dTDP-glucose 4,6-dehydratase activity; P:nucleotide-sugar metabolic process	282	6.75	75660	5	MALDI	K.NNIYGTHVLEACK.V Carbamidomethyl (C) R.SYGLPIITTR.G R.GNNVYGPNQFPEK.L R.DPDASIQFVENRPFNDQR.Y K.EYPNVCTLR.V Carbamidomethyl (C)	m	9
				EC:4.2.1.46									
07	13	Pep	probable rhamnose biosynthetic enzyme 1-like	PGSC0003DMT40005 4753	F:dTDP-glucose 4,6-dehydratase activity; F:UDP-glucose 4,6- dehydratase activity; P:nucleotide-sugar metabolic process	84	6.57	75521	2	MALDI	R.GNNVYGPNQFPEK.L K.QGIPYEYGR.G	m	26
				EC:4.2.1.76; EC:4.2.1.46									
12	13	Pep	dynamamin-related protein 1e- like	PGSC0003DMT40000 4319	F:GTPase activity; F:GTP binding; P:metabolic process	157	7.62	68574	16	MALDI	R.RPLVLQLHK.T K.TDDGQQEYAEFGHMPR.R Oxidation M R.FTDFGTVR.K K.NVDMYAR.R Oxidation M R.IYGVFDNQLPAALR.K R.KLPFDR.Y R.YLSVQNVVR.K	m	29

											R.KVVSEADGYQPHLIAPEQGYR.R		
											R.LIEGALNYFR.G		
											K.RFPSLQSTIAAASNEALEK.F		
											R.KLPQEMETPK.G		
											R.YGEGHFR.R		
											R.IGSNVSSYVNMVSDTLR.N		
											Oxidation M		
											K.ALSELLDEDPALMER.R	Oxidation	
											M		
											K.RLELYK.K		
											R.DEIDSVAVVR.-		
12	13	Prot	dynamamin-related protein 1e-like	PGSC0003DMT40000 4228	F:GTPase activity; F:GTP binding; P:metabolic process	80	6.03	31850	8	MALDI	K.EHLDGGRPGGDR.I	1	26
											R.IYGVFDNQLPAALR.K		
											R.KLPFDR.Y		
											R.YLSVQNVNR.N		
											R.LIEGALNYFR.G		
											R.YGEGHFR.R		
											K.ALSELLDEDPALMER.R	Oxidation	
											(M)		
											K.RLELYK.K		
82	13	Pep	ribulose- -bisphosphate carboxylase oxygenase small subunit	PGSC0003DMT40005 0381	C:chloroplast; C:cytoplasmic membrane-bounded vesicle; F:monoxygenase activity; F:protein binding; F:ribulose-bisphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	284	7.56	20562	4	MALDI	K.SPGYYDGR.Y	m	22
				EC:4.1.1.39							K.NAYPQAWIR.I		
											R.IIGFDNVR.Q		
											R.QVCISFIAKPEGY.-		
											Carbamidomethyl C		

83	13	Pep	ribulose biphosphate carboxylase small chain chloroplastic-like	PGSC0003DMT40003 2975  EC:4.1.1.39	C:chloroplast; C:cytoplasmic membrane-bounded vesicle; F:monoxygenase activity; F:protein binding; F:ribulose- biphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	333	7.60	20306	4	MALDI	K.SPGYYDGR.Y  K.KAYPQAWIR.I  R.IIGFDNVR.Q  R.QVQCISFIAYKPEGY.- Carbamidomethyl C	m	22
101	13	Pep	20 kdachloroplastic-like	PGSC0003DMT40000 4324	C:cytoplasm; P:protein folding	57	8.58	14891	1	MALDI	K.VLFSDINAYEVDLGT DAR.H	m	13
208	13		peptidyl prolyl cis trans isomerase fkbp15 1 like	PGSC0003DMT40002 2512	P:protein folding	11148.51 00	8.21	16019	5	QTOF	TTTDSSEL  LTDGTVFDSSYER  LGYGESGSPPK  SGDVTELQIGVK  NDPIEFELGSGQVIK	m	59.73
221	13	Pep	auxin-binding protein abp19a-like	PGSC0003DMT40003 6428	C:nucleus; C:plant-type cell wall; C:extracellular matrix; C:apoplast; F:manganese ion binding; F:nutrient reservoir activity; P:auxin-activated signaling pathway; P:stomatal complex morphogenesis; P:photosynthesis, light reaction; P:cellular cation homeostasis; P:defense response to bacterium; P:divalent metal ion transport	109	5.83	21506	1	MALDI	K.LVGATTFLEDEATIKK.L	m	7
235	13	Pep	glycolate oxidase	PGSC0003DMT40007 1115  EC:1.1.3.15	F:FMN binding; F:very-long- chain-S-2-hydroxy-acid oxidase activity; F:long-chain-S-2- hydroxy-long-chain-acid oxidase activity; F:medium-chain-S-2- hydroxy-acid oxidase activity; P:oxidation-reduction process	108	9.26	40585	3	MALDI	K.MAHPEGEYATAR.A Oxidation (M)  R.IPVFLDGGVR.R  R.NHIVTDWDTPR.A	m	8
241	13	Pep	2631191 rna-binding family protein isoform 1	PGSC0003DMT40004 4866	F:nucleotide binding; F:nucleic acid binding	199	4.76	53563	3	MALDI	K.VTEYEIIR.D  K.KPSNPASAPAYGSNSR.G	s	18

											R.YGDFGSSEFGGYR.G		
243	13		Monodehydroascorbate reductase	PGSC0003DMT40003 2099	F:oxidoreductase activity; P:oxidation-reduction process	4017.668	8.06	53133	13	QTOF	YEQLYQDNGVK	s	31.76
											YGTLIATGCTASR Carbamidomethyl+C10		
											TFVEQGQANGK		
											TVGGIEVDGQFR		
											EYVVVGGGNAAGYAAR		
											DVADADSLISSLGK		
											HLESGPDGR		
											AYLFPLDK		
											LCIVTK Carbamidomethyl+C2		
											EPYAPYERPALTK		
											LFTPSLAQK		
											EQGIEMLYEDPVTGVDIEK Oxidation+M6		
											SFVAAASFDNENR Deamidation+N10		
313	13	Pep	guanine nucleotide-binding protein subunit beta-like	PGSC0003DMT40007 4094	F:protein binding	46	6.71	35953	2	MALDI	K.DGSHYGVPR.R	m	28
											K.DVLSVAFSVDNR.Q		
338	13	Pep	glutathione s-transferase-like	PGSC0003DMT40003 7918  EC:2.5.1.18	C:cytoplasmic membrane-bounded vesicle; F:glutathione transferase activity; F:protein binding; P:metabolic process; P:auxin-activated signaling pathway	57	5.98	23817	2	MALDI	R.AITQYIAHTYADK.G	m	9
											K.LLDVYESR.L		
338	13	Pep	dehydroascorbate reductase	PGSC0003DMT40006 0193	F:protein binding; F:transferase activity; F:glutathione dehydrogenase ascorbate activity; P:oxidation-reduction process	53	6.32	23439	2	MALDI	K.AAVGAPDVLGDPCFSQR.V Carbamidomethyl C	m	16
											K.YPNPSLIAPPEFASVGSK.L		

EC:1.8.5.1													
349	13	Pep	plastocyanin precursor	PGSC0003DMT40009 2049	C:chloroplast thylakoid membrane; C:cytoplasmic membrane-bounded vesicle; F:copper ion binding; F:electron carrier activity; P:oxidation-reduction process	366	5.04	16970	3	MALDI	K.NNAGFPHNVVFEDEIPAGVDAS K.I K.ISMAEEDLLNAAGETYSVTLSEK. G Oxidation (M) K.GTYTFYCAPHQGAGMVGK.V Carbamidomethyl (C); Oxidation (M)	m	38
375	13	Pep	atp synthase subunit beta	PGSC0003DMT40000 2642	C:chloroplast thylakoid membrane; C:proton-transporting ATP synthase complex, catalytic core F1; F:ATP binding; F:proton-transporting ATP synthase activity, rotational mechanism; F:proton-transporting ATPase activity, rotational mechanism; P:ATP synthesis coupled proton transport; P:ATP hydrolysis coupled proton transport	126	4.78	44598	2	MALDI	R.IGNNEITVLVNDAEK.G K.GSDINPQEAQQTLEIAEANVK.K	s	8
380	13	Pep	ribulose- -biphosphate carboxylase oxygenase large subunit	PGSC0003DMT40008 3063 EC:4.1.1.39	C:mitochondrion; C:chloroplast; F:magnesium ion binding; F:monoxygenase activity; F:ribulose-biphosphate carboxylase activity; P:photorespiration; P:reductive pentose-phosphate cycle; P:oxidation-reduction process	176	7.23	40242	4	MALDI	K.TFQGPPIQVER.D R.GGLDFTKDDENVNSQPFMR.W R.DNGLLLHIHR.A R.DITLGFVDLLR.D	m	14
421	13		probable polyribonucleotide nucleotidyltransferasechloroplastic like	PGSC0003DMT40001 9741 EC:3.1; EC:3.1.13; EC:3.1.15; EC:2.7.7.8	F:3'-5'-exoribonuclease activity; F:RNA binding; F:polyribonucleotide nucleotidyltransferase activity; P:RNA processing; P:mRNA catabolic process; P:regulation of RNA metabolic process; P:purine nucleobase metabolic process; P:pyrimidine nucleobase metabolic process	321.5521	5.79	98592	12	QTOF	SASLSNDNVVSPK GETQSLAVVTLGDK DLLSLEK IGLIGDK EVEALVQK LIEINDK SPQEIR	m	10.51

											QIVDK			
											QALLQAK			
											QASGAVTIR			
											IPVGDR			
											QSTKPRSASLSNDNVVSPK			
											Deamidation+N12			
431	13	Prot	chaperone protein chloroplastic-like	PGSC0003DMT40000 3652	C:cytoplasm; F:ATP binding; P:response to heat; P:protein processing	127	6.17	110252	13	MALDI	R.IVQGDVPQALMNR.K (M)	Oxidation	m	16
											K.YRGEFEDR.L			
											R.CIGATTLDEYRK.Y Carbamidomethyl (C)			
											K.YIEKDPALER.R			
											K.DPALERR.F			
											R.FQQVYVDQPTVEDTVSILR.G			
											R.YELHHGVR.I			
											R.VNLEIQAER.E			
											K.YGSLNTLQR.Q			
											R.AGLSDPHRPIASFMMGPTGVGK. T 2 Oxidation (M)			
											K.ALANYLFNTEEALVR.I			
											R.LIGAPPGYVGYEEGGQLTEIVR.R			
											R.AVFRPEFMNR.V Oxidation (M)			
445	13	Pep	nadh dehydrogenase	PGSC0003DMT40003 4638	C:mitochondrial respiratory chain complex I; C:chloroplast; F:NADH dehydrogenase ubiquinone activity; F:electron carrier activity; F:metal ion binding; F:2 iron, 2 sulfur cluster binding; F:4 iron, 4	68	6.05	79799	2	MALDI	K.ADAFLLVGTQPR.V		m	4
				EC:1.6.5.3							R.ALSEVAGVGLPYDSLGAIR.S			

				sulfur cluster binding; P:ubiquitin-dependent protein catabolic process; P:response to oxidative stress; P:gravitropism; P:photorespiration; P:ATP synthesis coupled electron transport; P:response to misfolded protein; P:proteasome core complex assembly									
466	13	peptidyl prolyl cis trans isomerase fkbp62 like	PGSC0003DMT40005 1809	C:nucleus; C:cytosol; C:cell periphery; F:peptidyl-prolyl cis- trans isomerase activity; F:protein binding; F:phosphatidylinositol-3- phosphate binding; F:phosphatidylinositol-3,5- bisphosphate binding; P:protein peptidyl-prolyl isomerization; P:protein folding; P:response to osmotic stress; P:response to heat; P:response to cytokinin; P:seed germination	2086.306 0	5.05	63456	16	QTOF	TDEEQVIDGLDR VLELDSANVK YEAQLENGTVVVK FTLGQGQVIK EGEGYERPNEGAVVK ALEIDPDNRDVK LLDGTVFTK DLDEVFVK FIEYDTSFSEEEK VQLTVKPQYGFGEK VGEEKEIGNQGLK FIEYDTSFSEEEKK EIGNQGLK TVSNVTDDKK EPEPMSIDSKA Oxidation+M5 EPEPMSIDSK Oxidation+M5	m	26.31	
			EC:5.2.1.8										
466	13	protein executor chloroplastic like	PGSC0003DMT40006 9690	C:thylakoid membrane; F:protein binding; P:singlet	210.2857	5.03	71445	6	QTOF	GPSSTEIENR	m	16.98	



					oxygen-mediated programmed cell death							VNITEEITDDGDSVK		
												NAIDEER		
												VTVGGDSGTNEEGK		
												SIDFEGAAEEGIR		
												ITPGVGR		
470	13	Prot	atp-dependent zinc metalloprotease ftshchloroplast-like	PGSC0003DMT40004 4601	C:membrane; F:metalloendopeptidase activity; F:ATP binding; F:microtubule- severing ATPase activity; P:proteolysis; P:cell division	220	6.14	74370	22	MALDI	R.FLEYLDKDR.V	m	44	
				EC:3.4.24; EC:3.6.4.3							K.VDLFENGTTAIVEAVSPELGNR.V			
											R.VQLPGLSQELLQK.F			
											R.SNGGMGGPGGPNPLAFGQSK.A			
											K.FQMEPNTGVTFDDVAGVDEAK. Q Oxidation (M)			
											K.QDFMEVVEFLK.K Oxidation (M)			
											R.FTAVGAR.I			
											R.VRDLFK.K			
											K.AKENAPCIVFVDEIDAVGR.Q Carbamidomethyl (C)			
											K.ENAPCIVFVDEIDAVGR.Q Carbamidomethyl (C)			
											R.GTGIGGGNDER.E			
											R.ADILDSALLRPGR.F			
											K.KFSDVSLEVIAMR.T Oxidation (M)			
											R.TPGFSGADLANLLNEAAILAGR.R			
											K.EIDDSIDR.I			
											K.SLVAYHEVGHAICGTLTPGHDAV QK.V Carbamidomethyl (C)			

											K.QQLFAR.I		
											R.IVGGLGGR.A		
											R.AAEVIFGEPEVTTGAAGDLQQIT GLAK.Q		
											K.IVEVLEKETMTGDEF.R.A Oxidation (M)		
											K.ETMTGDEF.R.A Oxidation (M)		
											R.AILSEFVEIPAENRVPAAVPTPAA V.-		
478	13	Pep	threonine dehydratase chloroplastic-like	PGSC0003DMT40003 3801	C:chloroplast; F:L-threonine ammonia-lyase activity; F:pyridoxal phosphate binding; P:isoleucine biosynthetic process	189	5.22	64723	5	MALDI	K.GVITASAGNHAQGVLAGQR.L	m	12
				EC:4.3.1.19							K.GQGTIGTEINR.Q		
											R.NDGISAAIKDVYDEGR.N		
											K.LVGSMNITEVTYR.F		
											K.TFNFSHNELVAEHIK.H		
483	13		v type proton atpase catalytic subunit a like	PGSC0003DMT40007 4197	C:proton-transporting V-type ATPase, V1 domain; F:ATP binding; F:proton-transporting ATPase activity, rotational mechanism; P:ATP hydrolysis coupled proton transport; P:ATP metabolic process	2407.394 0	5.08	68594	15	QTOF	LAADTPLLTGQR	m	25.36
				EC:3.6.1; EC:3.6.1.3; EC:3.6.1.15							TTLVANTSNPVAAR		
											YSGALESFYEK		
											YSNSDTVVYVGCGER Carbamidomethyl+C12		
											EDYLAQNAFTPYDK		
											LAEMPADSGYPAYLAAR		
											EISGR		
											LASFYER		
											ITYTLIK		
											TVISQALSK		

										SGDVYIPR		
										WAEALR		
										DMGYNVSMADSTSR		
										SPRPVASK		
										FDPDFINIR		
483	13	nad binding rossmann fold superfamily protein isoform 1	PGSC0003DMT40007 3075	F:catalytic activity; F:coenzyme binding; P:metabolic process	821.9412	7.94	65202	16	QTOF	TPISV	m	21.92
										GIVTTANNGGFASIR		
										FFESLIEK		
										LLFGYEGNSFK		
										TLYFFNGPPSPAK		
										FFEPEIK		
										TLKDGITGK		
										GEDEIR		
										LNPTFK		
										GDSPEMVEYIGMK		
										ASTLLPEYFK		
										VVDVLR		
										ICVAALK Carbamidomethyl+C2		
										NLINA VK		
										RVVDVLR		
										NLINA VKENVCLR Carbamidomethyl+C11, Deamidation+N4		
483	13	ru large subunit-binding protein subunit chloroplastic	PGSC0003DMT40006 1700	C:cytoplasm; F:ATP binding; P:protein refolding	632.0175	5.57	62995	12	QTOF	VVAAGANPVLITR	m	20.87

										EVELEDPVENIGAK		
										GYVSPYFVTDSEK		
										NAGVNGSVVSEK		
										IVNDGVTVAR		
										ELHFNKDGSAIK		
										DLVNVLEDAIR		
										DATTIVGDGSTQEAVNK		
										ALVAELK		
										EVLGHAAK		
										DGSAIK		
										KLQNGVNK		
483	13	t complex protein 1 subunit epsilon like	PGSC0003DMT40002 7968	F:ATP binding; F:unfolded proteinbinding; P:protein folding	627.2056	5.50	24624	9	QTOF	IAEGYEMASR	1	
										YFDDMVQK		
										AVLAVADLER		
										FQTLR		
										SMAEIAVK		
										DVNLDLIK		
										VDIDTVEK		
										QIEDAK		
										LMVELSR		
491	13	far upstream element binding protein 2 like	PGSC0003DMT40003 1096	F:RNA binding	1569.795 0	4.72	82586	9	QTOF	EQPADDNQQTGDVEQSDAK	1	15.55
										YLQYNSGAK		
										DVIAEADAGGSPALVAR		

											LGTIEEEAADV D GSEPK		
											TSLEIENSTQADEPSK		
											IQLVPLPSDGK		
											GDIQESEA EK		
											VGLIIGK		
											ANGLASQNGYEEK Deamidation+N8		
523	13	Pep	catechol oxidase chloroplastic	PGSC0003DMT40007 6054	C:chloroplast thylakoid lumen; F:catechol oxidase activity; F:metal ion binding; P:pigment biosynthetic process; P:oxidation-reduction process	52	6.63	66404	2	MALDI	R.EGSSLYDDKR.N	m	12
				EC:1.10.3.1							R.FDVFLNVDK.T		
557	13	Pep	utp:alpha-d-glucose-1- phosphate uridylyltransferase	PGSC0003DMT40003 4699	C:cytoplasm; F:UTP:glucose-1- phosphate uridylyltransferase activity; P:UDP-glucose metabolic process	110	5.70	51774	2	MALDI	K.VQLLEIAQVPDEHVNEFK.S	m	10
				EC:2.7.7.9							R.SNPSNPSIELGPEFKK.V		
597	13	Pep	145429 phosphoribulose	PGSC0003DMT40002 4090	C:chloroplast thylakoid membrane; C:chloroplast stroma; C:chloroplast envelope; C:stromule; C:apoplast; F:ATP binding; F:phosphoribulokinase activity; P:MAPK cascade; P:carbohydrate metabolic process; P:pentose-phosphate shunt; P:rRNA processing; P:protein targeting to membrane; P:detection of biotic stimulus; P:response to blue light; P:salicylic acid biosynthetic process; P:response to cytokinin; P:photosynthetic electron transport in photosystem I; P:systemic acquired resistance, salicylic acid mediated signaling pathway; P;jasmonic acid mediated signaling pathway;	250	5.82	44838	6	MALDI	R.LTSVFGGAAEPPK.G	m	18
				EC:2.7.1.19							R.ANDFDLMYEQVK.A Oxidation M		
											K.ILVIEGLHPMYDER.V Oxidation M		
											R.KPDFDAYIDPQK.Q		
											K.FYGEVTQQMLK.H Oxidation M		
											K.IRDLYEQIVASR.A		

					P:chloroplast relocation; P:stomatal complex morphogenesis; P:response to red light; P:response to chitin; P:photosystem II assembly; P:response to far red light; P:regulation of hydrogen peroxide metabolic process; P:regulation of plant-type hypersensitive response; P:cysteine biosynthetic process; P:negative regulation of defense response; P:regulation of protein dephosphorylation; P:regulation of multi-organism process; P:defense response to fungus								
608	13	Pep	1-aminocyclopropane-1- carboxylate oxidase	PGSC0003DMT40005 5332	F:oxidoreductase activity; P:oxidation-reduction process	102	5.21	36363	4	MALDI	K.HLPVSNISEVPDLEDDYRK.I  K.VSNYPCKPKPDLIK.G Carbamidomethyl (C)  R.AHTDAGGILLFQDDK.V  K.FVFEDYMK.L Oxidation (M)	m	17
614	13	Pep	quinone oxidoreductase-like protein chloroplastic-like	PGSC0003DMT40007 9606  EC:1.6.5.5	C:chloroplast stroma; C:thylakoid; C:chloroplast envelope; C:stromule; C:apoplast; F:NADPH:quinone reductase activity; F:zinc ion binding; F:enone reductase activity; F:2-alkenal reductase NADP+ activity; P:sulfur amino acid metabolic process; P:glycine catabolic process; P:unsaturated fatty acid biosynthetic process; P:oxidoreduction coenzyme metabolic process; P:vitamin metabolic process; P:cellular amino acid biosynthetic process; P:aromatic amino acid family metabolic process; P:lipoate metabolic process; P:coenzyme biosynthetic process; P:nucleotide metabolic process; P:response to light stimulus; P:jasmonic acid biosynthetic	370	6.48	41008	6	MALDI	K.LESNVAVPDIKEDQVLIK.V  K.VVAAALNPIDFKR.R  K.ATDSPLPTVPGYDVAGVVVK.V  K.AIDGPNQFGSLAEYTAVEEK.L  K.EGGSVVVLTGAVTPPGFR.F  K.VVDAFSHLETGR.A	m	26

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process; P:myo-inositol  
hexakisphosphate biosynthetic  
process; P:chlorophyll  
biosynthetic process;  
P:carotenoid biosynthetic  
process; P:regulation of lipid  
metabolic process; P:isopentenyl  
diphosphate biosynthetic  
process, methylerythritol 4-  
phosphate pathway;  
P:secondary metabolic process;  
P:oxylipin biosynthetic process;  
P:pteridine-containing  
compound metabolic process;  
P:defense response to bacterium;  
P:sulfur compound biosynthetic  
process; P:oxidation-reduction  
process

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**A** = ID represents the number of a protein spot in the 2D PAGE gels. Corresponding spots of all gels are labelled with the same ID.

**B** = Genotype in which the protein was identified. 2 = sensitive genotype 2; 13 = tolerant genotype 13.

**C** = Note, if proteins are identified via peptides or via protein search if they are identified via MALDI-TOF-MS/MS.

**D** = PGSC number and EC number for the identified protein.

**E** = GO annotation according to the search with Blast2GO (<https://www.blast2go.com/>).

**F** = The protein score obtained either via the MASCOT search algorithm ([www.matrixscience.com](http://www.matrixscience.com)) or through the ProteinLynx Global Server 2.5.3 (Water Corporation) against a potato protein database, which was based upon the sequences from *Solanum tuberosum* group Phureja DM1-3, which was completely sequenced by [9].

**G** = Calculated PI obtained either via the MASCOT search algorithm ([www.matrixscience.com](http://www.matrixscience.com)) or through the ProteinLynx Global Server 2.5.3 (Water Corporation) against a potato protein database.

**H** = Calculated MW obtained via the MASCOT search algorithm ([www.matrixscience.com](http://www.matrixscience.com)) or through the ProteinLynx Global Server 2.5.3 (Water Corporation) against a potato protein database.

**I** = Number of peptides matched to the protein through the database search.

**J** = Method with which the protein was identified. MALDI = MALDI-TOF-MS/MS and QTOF = nLC-ESI-Q-TOF-MS/MS.

**K** = Peptide sequences with modifications identified.

**L** = Molecular weight (MW) in gel as compared to the theoretically expected MW.

**m**: MW in gel corresponding to the theoretically expected MW  $\pm$  15 kDa

s: MW in gel lower than theoretically expected

I: MW in gel larger than theoretically expected

**M** = Sequence coverage of a protein by identified peptides.

**Supplementary Table 3: Mean normalizes spot volume and coefficient of variation for the groups `genotype 13 control`, `genotype 13 treatment with 0.2 M sorbitol`, `genotype 2 control` and `genotype 2 treatment with 0.2 M sorbitol`. Spot ID corresponding to the spots labelled on each gel through the Delta2D software (Decodon, Greifswald, Germany).**

Spot ID	Genotype 13 control		Genotype 13 treatment 0.2 M sorbitol		Genotype 2 control		Genotype 2 treatment 0.2 M sorbitol	
	mean Normalized Volume of group `genotype 13 control`	coefficient of variation of group `genotype 13 control`	mean Normalized Volume of group `genotype 13 treatment`	coefficient of variation of group `genotype 13 treatment`	mean Normalized Volume of group `genotype 2 control`	coefficient of variation of group `genotype 2 control`	mean Normalized Volume of group `genotype 2 treatment`	coefficient of variation of group `genotype 2 treatment`
01	0.019	81.6	0.019	12.0	0.020	36.2	0.022	54.4
02	0.017	61.4	0.038	53.1	0.020	59.1	0.016	55.7
03	0.012	22.2	0.026	61.6	0.003	76.5	0.013	72.4
04	0.013	43.8	0.025	37.0	0.014	17.4	0.012	57.0
05	0.029	23.0	0.027	48.1	0.002	11.7	0.008	28.6
06	0.040	55.6	0.063	39.0	0.040	9.9	0.016	41.6
07	0.021	59.2	0.028	33.6	0.007	17.1	0.012	21.8



08	0.011	58.2	0.019	50.4	0.007	17.3	0.017	27.1
09	0.014	25.1	0.016	28.3	0.004	21.5	0.007	48.3
10	0.024	32.0	0.030	29.2	0.007	39.9	0.018	55.5
11	0.026	23.6	0.027	37.5	0.014	28.7	0.011	48.3
12	0.040	13.8	0.038	27.1	0.022	15.3	0.019	26.5
13	0.015	67.0	0.027	40.7	0.002	27.4	0.009	33.0
14	0.016	65.3	0.018	24.4	0.001	52.1	0.010	64.9
15	0.033	62.6	0.037	18.8	0.011	34.1	0.030	20.0
16	0.020	51.2	0.023	47.8	0.024	26.1	0.013	47.6
17	0.044	16.8	0.035	13.1	0.045	47.3	0.027	27.8
18	0.026	39.7	0.025	47.1	0.021	20.0	0.014	33.1
19	0.063	28.1	0.044	33.8	0.051	37.6	0.042	29.7
20	0.028	42.6	0.014	33.5	0.033	38.4	0.017	45.2
21	0.835	28.7	0.791	26.8	0.937	16.1	0.848	30.6
22	0.281	25.6	0.323	23.6	0.229	17.1	0.357	27.6
23	0.389	31.4	0.429	33.2	0.237	21.2	0.270	39.9
24	0.172	72.8	0.096	57.0	0.071	24.0	0.086	11.6
25	0.088	35.6	0.084	47.8	0.071	30.9	0.079	37.6

26	0.043	49.4	0.036	62.4	0.014	18.5	0.033	31.9
27	0.073	82.7	0.037	60.5	0.029	55.8	0.039	40.1
28	0.047	61.8	0.029	56.7	0.013	21.5	0.030	20.0
29	0.165	15.0	0.149	40.3	0.100	34.0	0.091	28.6
30	0.155	37.5	0.158	32.3	0.113	32.1	0.115	18.9
31	0.055	43.4	0.058	32.1	0.036	32.2	0.062	21.4
32	0.084	18.7	0.097	21.5	0.102	23.9	0.105	21.2
33	0.165	13.4	0.160	3.0	0.239	11.3	0.261	9.8
34	0.085	4.0	0.089	5.9	0.084	19.5	0.082	14.4
35	0.025	14.6	0.022	37.5	0.026	24.2	0.028	47.4
36	0.037	13.1	0.030	38.2	0.031	28.4	0.025	35.1
37	0.017	16.3	0.017	50.2	0.022	39.1	0.025	41.7
38	0.088	13.4	0.091	20.2	0.043	24.0	0.051	22.0
39	0.051	29.3	0.046	36.8	0.042	5.2	0.045	18.5
40	0.030	15.4	0.032	44.2	0.023	34.4	0.020	26.0
41	0.085	25.1	0.073	28.3	0.020	25.2	0.033	29.3
42	0.154	28.9	0.146	9.2	0.122	13.7	0.193	12.3
43	0.082	8.6	0.065	14.7	0.064	13.8	0.069	13.6

44	0.067	21.3	0.074	25.7	0.050	10.2	0.059	14.7
45	0.062	16.3	0.062	18.4	0.058	13.4	0.044	18.3
46	0.072	3.6	0.067	28.3	0.081	22.0	0.106	17.1
47	0.015	20.6	0.015	40.3	0.026	49.4	0.041	26.4
48	0.023	36.9	0.035	38.2	0.045	49.0	0.040	14.3
49	0.144	24.8	0.114	13.9	0.116	13.1	0.113	9.3
50	0.052	33.9	0.030	36.4	0.087	9.9	0.073	2.5
51	0.039	74.5	0.015	24.5	0.039	38.6	0.057	4.6
52	0.085	14.4	0.093	19.6	0.086	26.6	0.071	27.4
53	0.036	15.1	0.034	35.7	0.030	28.3	0.046	27.0
54	0.158	14.7	0.144	11.1	0.234	33.4	0.133	8.5
55	0.043	17.9	0.045	41.2	0.017	24.7	0.095	36.6
56	0.080	16.0	0.057	50.5	0.045	39.1	0.025	47.2
57	0.038	29.2	0.036	21.6	0.028	26.2	0.038	16.2
58	0.019	22.1	0.013	35.9	0.054	16.5	0.089	4.9
59	0.472	19.1	0.474	25.4	0.374	7.7	0.222	34.4
60	0.364	7.0	0.340	24.7	0.346	18.9	0.192	18.7
61	0.086	14.1	0.078	18.3	0.073	20.6	0.070	22.2

62	0.047	16.7	0.036	21.5	0.067	5.1	0.051	7.4
63	0.187	18.9	0.162	12.0	0.142	24.7	0.162	14.9
64	0.436	17.8	0.493	32.2	0.324	59.9	0.454	12.6
65	0.157	12.9	0.172	30.5	0.165	28.7	0.134	23.5
66	0.060	18.5	0.068	31.3	0.074	18.4	0.061	16.8
67	0.051	24.8	0.052	21.4	0.044	23.7	0.042	16.3
68	0.337	16.4	0.447	41.6	0.316	61.4	0.465	11.6
69	0.153	15.9	0.196	40.8	0.172	17.8	0.143	8.6
70	0.128	18.2	0.120	11.5	0.132	8.6	0.105	11.7
71	0.080	4.4	0.061	19.6	0.110	47.1	0.101	23.1
72	0.165	22.8	0.157	31.3	0.143	26.2	0.179	68.0
73	0.483	9.9	0.424	12.0	0.518	3.2	0.530	14.5
74	0.229	22.5	0.235	26.1	0.149	6.3	0.168	21.3
75	0.215	21.6	0.204	15.3	0.186	8.3	0.184	8.4
76	0.082	60.5	0.041	66.7	0.063	31.6	0.031	53.3
77	0.038	36.7	0.030	31.1	0.165	10.5	0.178	11.0
78	0.213	29.8	0.224	40.0	0.517	37.2	0.220	14.8
79	0.224	36.6	0.151	38.6	0.150	16.9	0.150	22.2

80	1.093	18.5	1.180	15.8	1.521	10.7	1.373	9.9
81	0.095	29.1	0.105	35.7	0.070	20.9	0.169	7.7
82	0.742	3.5	0.751	7.6	0.107	26.9	0.137	27.1
83	0.877	10.7	0.893	7.8	0.071	103.4	0.079	50.8
84	0.017	9.3	0.016	29.7	0.010	28.3	0.010	28.5
85	0.068	25.5	0.118	33.0	0.110	7.7	0.146	41.8
86	0.097	10.3	0.072	24.6	0.091	27.3	0.068	34.8
87	0.009	43.8	0.011	41.8	0.013	30.1	0.017	67.4
88	0.053	13.7	0.050	25.9	0.053	14.1	0.052	6.4
89	0.079	23.4	0.103	45.1	0.085	25.4	0.105	21.0
90	0.006	36.7	0.009	92.7	0.007	36.8	0.035	38.4
91	0.010	19.5	0.022	50.4	0.015	36.2	0.029	73.2
92	0.024	36.8	0.041	43.6	0.020	50.7	0.036	44.8
93	0.012	45.9	0.012	37.3	0.014	42.8	0.012	18.0
94	0.013	15.7	0.011	55.4	0.013	19.9	0.016	72.0
95	0.016	32.0	0.015	54.3	0.010	75.8	0.011	42.5
96	0.059	46.0	0.182	60.0	0.214	13.5	0.289	43.8
97	0.009	49.5	0.010	62.8	0.017	12.9	0.030	62.0

98	0.039	43.3	0.098	52.1	0.133	11.4	0.199	35.7
99	0.020	29.6	0.026	42.8	0.026	22.9	0.034	15.3
100	0.011	25.0	0.026	60.8	0.026	13.6	0.032	31.9
101	0.106	12.7	0.079	29.0	0.062	12.4	0.049	23.7
102	0.019	46.1	0.027	30.1	0.042	33.0	0.027	38.8
103	0.027	31.8	0.044	55.4	0.066	17.1	0.080	28.1
104	0.109	36.6	0.142	29.9	0.102	25.9	0.125	36.0
105	0.050	15.1	0.050	30.5	0.090	34.0	0.063	24.3
106	0.017	38.9	0.027	38.7	0.026	38.7	0.021	43.7
107	0.549	25.3	0.533	33.0	0.436	25.9	0.348	36.3
108	0.036	15.9	0.029	25.3	0.019	26.8	0.028	42.4
109	0.024	16.2	0.026	15.6	0.026	13.9	0.030	37.6
110	0.019	21.3	0.033	47.8	0.041	19.8	0.023	40.2
111	0.048	10.4	0.039	29.9	0.054	34.9	0.039	34.8
112	0.256	17.2	0.228	18.1	0.228	34.2	0.220	30.6
113	0.028	25.3	0.030	27.4	0.074	21.8	0.045	40.9
114	0.081	38.9	0.083	57.7	0.055	23.2	0.064	41.0
115	0.055	14.0	0.056	30.6	0.056	15.7	0.040	23.7

116	0.017	24.8	0.015	22.0	0.029	49.9	0.020	51.6
117	0.037	26.3	0.030	57.5	0.035	44.7	0.027	63.4
118	0.031	17.2	0.029	35.1	0.053	41.8	0.060	37.5
119	0.411	22.2	0.416	33.4	0.429	31.6	0.333	23.4
120	0.024	19.3	0.014	37.2	0.013	69.9	0.011	61.9
121	0.091	18.3	0.062	46.0	0.039	44.2	0.030	38.4
122	0.054	21.3	0.046	40.7	0.043	46.4	0.059	67.2
123	0.218	26.8	0.092	45.2	0.217	31.6	0.213	42.2
124	0.020	28.9	0.016	39.1	0.015	17.2	0.018	38.7
125	0.061	21.4	0.042	25.8	0.053	30.4	0.046	24.8
126	0.193	12.9	0.189	37.2	0.228	38.6	0.184	54.6
127	0.204	1.9	0.187	37.0	0.225	38.5	0.193	63.0
128	0.062	18.0	0.059	31.5	0.078	60.6	0.069	54.6
129	0.188	29.8	0.212	48.9	0.155	26.0	0.410	34.6
130	0.138	15.7	0.159	21.0	0.127	25.3	0.119	30.4
131	0.160	27.5	0.259	51.3	0.154	22.6	0.186	49.5
132	0.305	4.2	0.306	63.2	0.696	28.6	1.050	30.1
133	0.439	71.5	0.646	67.2	0.235	39.6	0.604	31.0

134	0.109	48.0	0.126	61.3	0.037	42.3	0.045	26.5
135	0.182	38.8	0.284	30.6	0.355	24.5	0.856	37.6
136	0.273	32.7	0.321	32.7	0.016	72.1	0.063	42.0
137	0.033	39.8	0.041	58.9	0.023	35.5	0.064	40.2
138	0.169	24.1	0.154	57.4	0.169	58.8	0.117	87.3
139	0.036	73.9	0.061	43.1	0.079	33.1	0.043	64.9
140	0.396	4.2	0.408	2.1	0.423	14.7	0.479	12.3
141	0.847	9.0	0.849	6.4	0.888	9.8	0.828	4.5
142	0.181	21.2	0.167	44.5	0.224	26.3	0.223	12.1
143	0.210	15.3	0.191	14.0	0.152	30.6	0.210	10.2
144	0.058	20.0	0.092	39.1	0.063	45.5	0.083	9.6
145	0.090	17.8	0.103	38.8	0.086	29.1	0.124	8.6
146	0.059	19.0	0.083	49.9	0.083	29.6	0.110	25.1
147	0.447	12.4	0.463	22.0	0.409	12.2	0.424	11.2
148	0.319	19.5	0.230	21.2	0.222	15.2	0.182	22.2
149	0.017	81.8	0.027	59.0	0.015	24.2	0.050	41.5
150	0.072	14.4	0.084	45.7	0.090	19.4	0.087	6.7
151	0.119	14.6	0.090	8.4	0.125	19.0	0.124	25.5



152	0.215	16.6	0.168	20.6	0.201	10.1	0.268	7.8
153	0.138	30.5	0.126	7.0	0.130	16.6	0.267	13.9
154	0.030	44.8	0.026	65.2	0.186	13.0	0.193	6.7
155	0.051	12.7	0.047	14.1	0.047	11.4	0.042	9.2
156	0.184	8.4	0.152	21.7	0.138	10.5	0.131	22.7
157	0.116	46.1	0.187	56.7	0.121	17.9	0.117	17.5
158	0.154	15.0	0.129	13.6	0.157	17.5	0.168	16.1
159	0.046	28.9	0.038	22.8	0.104	27.1	0.161	22.1
160	0.409	11.8	0.350	16.0	0.373	14.6	0.342	8.5
161	0.018	10.4	0.017	28.2	0.015	48.3	0.020	27.8
162	1.342	10.4	1.388	2.3	1.593	5.2	1.481	6.5
163	0.030	65.2	0.021	19.2	0.036	32.3	0.027	23.6
164	0.050	46.1	0.052	11.6	0.048	42.3	0.041	14.1
165	0.121	30.1	0.155	35.7	0.206	20.3	0.180	20.1
166	0.078	41.4	0.101	50.4	0.116	25.3	0.086	30.7
167	0.186	35.0	0.264	40.7	0.178	67.3	0.269	14.6
168	0.036	74.0	0.023	61.0	0.113	106.3	0.077	33.0
169	0.016	63.3	0.018	34.2	0.044	72.0	0.031	25.0

170	0.408	12.8	0.367	13.8	0.428	11.7	0.299	8.6
171	0.056	8.1	0.061	13.3	0.054	30.1	0.048	45.0
172	0.355	10.2	0.378	19.5	0.323	15.6	0.315	11.5
173	0.111	21.8	0.099	20.2	0.063	69.9	0.070	7.2
174	0.039	19.3	0.034	36.5	0.041	31.1	0.037	33.3
175	0.050	28.5	0.055	48.0	0.049	43.5	0.084	16.1
176	0.023	49.6	0.021	31.3	0.010	56.5	0.023	65.3
177	0.443	10.1	0.428	11.0	0.339	36.4	0.389	11.3
178	0.403	4.8	0.399	5.3	0.444	15.9	0.412	11.5
179	0.402	16.9	0.392	21.2	0.484	8.3	0.343	27.5
180	0.217	28.1	0.218	25.4	0.082	11.7	0.188	7.0
181	0.118	13.9	0.116	19.0	0.095	56.4	0.093	27.5
182	0.022	59.3	0.018	64.8	0.037	35.0	0.030	54.6
183	0.181	11.3	0.169	22.2	0.127	37.8	0.161	42.7
184	0.054	31.4	0.058	25.9	0.060	23.9	0.055	26.9
185	0.900	13.9	0.985	34.2	0.977	36.8	1.045	3.9
186	1.006	22.1	0.952	27.5	0.844	45.4	0.999	25.9
187	0.033	61.2	0.041	26.3	0.041	27.2	0.055	20.4

188	0.056	17.6	0.079	16.9	0.051	38.6	0.066	42.9
189	0.238	4.5	0.237	19.7	0.071	24.2	0.107	20.5
190	0.059	13.0	0.063	38.0	0.076	35.9	0.064	10.0
191	0.028	51.7	0.027	58.3	0.037	18.7	0.040	38.0
192	0.020	33.8	0.018	72.0	0.028	16.7	0.032	16.2
193	0.012	61.9	0.010	47.7	0.021	45.9	0.025	50.0
194	0.036	4.4	0.038	51.3	0.036	56.5	0.052	43.7
195	0.327	15.8	0.272	10.1	0.287	13.5	0.190	6.2
196	0.298	12.8	0.437	44.2	0.381	19.5	0.403	14.0
197	0.120	12.4	0.100	31.7	0.105	20.2	0.080	75.4
198	0.235	3.4	0.204	13.0	0.177	27.0	0.204	14.1
199	0.412	24.1	0.458	18.6	0.358	12.3	0.335	21.3
200	0.112	7.8	0.137	31.0	0.185	29.8	0.239	28.3
201	0.143	40.3	0.137	26.7	0.220	17.9	0.336	14.8
202	0.071	30.2	0.162	41.8	0.113	15.0	0.278	20.2
203	0.073	18.5	0.150	38.4	0.122	10.9	0.380	23.3
204	0.051	43.2	0.098	35.9	0.079	18.0	0.125	19.0
205	0.050	26.2	0.079	27.4	0.040	36.5	0.043	30.6

206	0.743	8.7	0.671	25.3	0.696	27.7	0.542	12.2
207	0.019	35.1	0.040	42.8	0.167	22.9	0.282	17.6
208	0.044	35.4	0.096	34.2	0.080	11.8	0.149	25.5
209	0.138	21.7	0.267	25.4	0.282	15.2	0.220	38.2
210	0.119	25.0	0.140	30.2	0.110	25.2	0.116	30.5
211	0.469	22.2	0.427	20.9	0.429	39.4	0.394	19.1
212	0.456	13.6	0.608	40.5	0.507	33.4	0.573	22.8
213	0.327	31.3	0.622	40.6	0.311	72.3	0.748	20.4
214	0.132	6.9	0.162	34.8	0.183	42.9	0.328	34.4
215	0.156	21.8	0.145	28.1	0.180	28.4	0.165	15.5
216	0.152	17.9	0.237	45.3	0.235	17.7	0.228	38.0
217	0.019	48.3	0.027	37.9	0.040	29.2	0.085	26.8
218	0.298	5.5	0.281	7.7	0.225	22.6	0.238	26.9
219	0.068	28.5	0.105	38.6	0.054	78.9	0.113	18.0
220	0.186	11.9	0.194	14.7	0.294	14.5	0.318	10.2
221	0.310	24.9	0.282	12.7	0.224	9.7	0.188	6.0
222	0.068	46.9	0.129	42.7	0.111	31.2	0.199	9.1
223	0.039	16.8	0.038	60.2	0.011	46.2	0.008	120.4

224	0.082	33.0	0.126	65.2	0.035	68.0	0.042	14.0
225	0.086	21.2	0.077	45.2	0.045	29.1	0.059	48.1
226	0.008	27.0	0.009	63.1	0.009	59.9	0.014	63.9
227	0.006	65.3	0.009	66.1	0.018	15.9	0.044	53.0
228	0.157	55.4	0.167	24.0	0.107	10.7	0.077	22.4
229	0.032	44.0	0.018	73.8	0.018	27.7	0.015	27.5
230	0.056	45.9	0.070	21.7	0.031	40.8	0.059	32.2
231	0.071	32.2	0.095	48.5	0.059	67.6	0.074	27.6
232	0.224	25.6	0.208	25.4	0.143	23.2	0.172	11.2
233	0.047	36.1	0.036	39.2	0.037	22.1	0.047	22.6
234	0.125	41.3	0.098	22.5	0.106	22.1	0.126	28.1
235	0.403	25.4	0.387	29.5	0.228	18.6	0.186	32.4
236	0.145	19.3	0.123	6.2	0.133	11.2	0.146	9.5
237	0.099	60.9	0.090	29.5	0.057	30.9	0.053	30.3
238	0.149	10.5	0.140	29.3	0.109	16.1	0.125	4.4
239	0.193	27.0	0.210	31.8	0.162	18.0	0.199	24.0
240	0.276	18.9	0.379	37.2	0.217	17.6	0.201	30.4
241	0.029	15.9	0.026	52.8	0.018	21.5	0.021	34.3

242	0.117	38.0	0.145	61.0	0.176	20.4	0.212	65.8
243	0.012	5.1	0.025	15.0	0.012	37.3	0.020	34.7
244	0.041	22.5	0.036	33.7	0.033	10.5	0.029	18.7
245	0.294	7.1	0.270	5.3	0.317	15.5	0.173	26.3
246	0.191	24.5	0.199	6.9	0.169	16.8	0.107	35.2
247	0.053	7.0	0.047	32.8	0.040	47.8	0.064	59.2
248	0.193	13.2	0.191	22.2	0.149	15.7	0.159	5.4
249	0.034	19.1	0.014	116.7	0.032	37.3	0.051	77.2
250	0.042	24.3	0.023	22.6	0.038	16.5	0.027	35.2
251	0.089	25.3	0.071	9.1	0.072	15.9	0.074	13.2
252	0.013	46.3	0.023	58.9	0.012	49.5	0.031	46.9
253	0.011	56.0	0.029	33.4	0.022	30.2	0.036	61.0
254	0.041	43.5	0.063	14.4	0.061	6.9	0.120	43.1
255	0.065	18.8	0.073	19.9	0.057	23.1	0.050	5.7
256	0.035	25.9	0.041	20.3	0.040	23.9	0.046	17.4
257	0.133	20.4	0.157	14.4	0.104	8.3	0.123	16.1
258	0.830	52.3	0.669	29.6	0.437	13.3	0.401	23.7
259	0.322	13.6	0.345	18.9	0.310	8.9	0.207	12.9

260	0.101	18.2	0.115	42.4	0.099	42.7	0.083	42.7
261	0.081	27.1	0.094	80.1	0.093	21.4	0.176	44.3
262	0.089	23.9	0.072	22.9	0.068	38.9	0.177	19.0
263	0.197	18.6	0.233	19.4	0.185	32.8	0.151	13.5
264	0.067	13.9	0.052	31.7	0.055	10.5	0.078	27.5
265	0.070	43.3	0.091	31.8	0.062	63.3	0.060	38.9
266	0.080	28.4	0.038	57.2	0.032	43.7	0.019	43.0
267	0.054	46.3	0.063	38.4	0.049	46.8	0.062	42.1
268	0.271	18.8	0.281	19.1	0.236	19.5	0.240	11.1
269	0.091	21.3	0.110	39.3	0.071	21.4	0.072	41.4
270	0.054	30.3	0.043	19.6	0.022	17.7	0.038	19.9
271	0.057	11.5	0.037	47.2	0.013	5.3	0.009	38.6
272	0.156	21.6	0.143	25.4	0.124	6.0	0.108	23.8
273	0.109	18.9	0.092	16.5	0.098	19.9	0.058	11.4
274	0.157	42.5	0.169	21.5	0.237	9.7	0.317	25.3
275	0.054	14.3	0.063	10.9	0.048	20.9	0.079	23.0
276	0.033	10.6	0.041	39.5	0.050	22.2	0.030	21.8
277	0.026	19.3	0.032	21.0	0.017	27.8	0.055	39.0

278	0.025	11.8	0.035	29.4	0.021	57.1	0.027	40.6
279	0.175	12.9	0.219	20.4	0.199	8.8	0.274	41.7
280	0.066	10.4	0.082	13.9	0.090	17.0	0.090	26.7
281	0.005	14.0	0.007	73.6	0.019	21.5	0.019	86.8
282	0.064	18.2	0.064	8.5	0.070	16.8	0.062	23.4
283	0.015	12.6	0.014	30.4	0.010	68.5	0.012	67.7
284	0.004	59.0	0.006	67.3	0.019	23.0	0.032	69.1
285	0.076	28.6	0.084	24.0	0.058	31.8	0.060	7.0
286	0.126	30.7	0.112	28.6	0.100	15.8	0.047	36.2
287	0.053	18.6	0.063	24.3	0.065	25.4	0.075	33.2
288	0.061	31.9	0.068	27.7	0.102	17.6	0.143	20.4
289	0.024	37.0	0.019	52.6	0.030	22.5	0.028	47.6
290	0.149	17.4	0.158	20.5	0.102	13.6	0.102	14.2
291	0.192	19.3	0.191	16.2	0.208	21.3	0.298	24.0
292	0.044	39.9	0.039	23.9	0.058	24.6	0.025	46.7
293	0.049	30.4	0.050	30.1	0.053	7.0	0.162	19.4
294	0.624	7.9	0.694	27.6	0.890	12.0	1.145	13.5
295	0.020	33.6	0.024	15.3	0.018	27.0	0.016	8.9



296	0.228	9.1	0.297	28.1	0.228	22.3	0.317	15.3
297	1.268	7.5	1.354	4.9	1.578	9.8	1.266	10.4
298	0.123	10.5	0.176	40.1	0.134	19.9	0.288	19.0
299	0.030	22.8	0.074	45.9	0.106	30.7	0.070	21.3
300	0.164	26.9	0.161	24.4	0.171	10.3	0.140	23.8
301	0.741	21.7	0.735	10.4	0.791	10.0	0.686	9.7
302	0.876	33.6	1.097	28.1	1.044	22.1	1.178	16.4
303	0.208	14.0	0.505	42.1	0.438	13.5	0.392	26.1
304	0.014	39.5	0.035	45.2	0.020	40.1	0.042	46.2
305	0.163	33.0	0.207	12.7	0.262	9.5	0.327	27.6
306	0.275	16.9	0.308	8.2	0.219	15.9	0.201	11.4
307	0.060	17.5	0.067	12.4	0.027	44.9	0.070	43.6
308	0.058	24.0	0.087	43.3	0.062	19.7	0.105	21.8
309	0.116	14.5	0.118	18.0	0.085	6.5	0.122	8.8
310	0.202	11.9	0.237	14.1	0.139	34.3	0.153	11.9
311	0.067	35.0	0.060	33.5	0.030	53.8	0.044	32.6
312	0.126	24.9	0.127	14.7	0.114	16.6	0.114	17.2
313	0.094	15.6	0.090	35.9	0.054	25.6	0.049	14.6

314	0.034	28.8	0.034	43.5	0.025	28.4	0.019	33.4
315	0.077	27.0	0.069	16.0	0.054	21.4	0.047	28.3
316	0.041	41.3	0.056	59.2	0.062	29.2	0.054	13.2
317	0.328	18.8	0.391	28.9	0.288	43.9	0.312	35.4
318	0.161	15.4	0.199	34.6	0.118	35.8	0.184	24.0
319	0.031	36.4	0.042	27.0	0.026	58.7	0.048	54.5
320	0.142	25.4	0.122	11.0	0.122	18.3	0.178	29.9
321	0.194	21.4	0.196	25.8	0.196	18.0	0.193	29.0
322	0.738	16.0	0.874	15.6	0.959	3.7	0.805	23.6
323	0.148	10.6	0.164	24.6	0.174	10.9	0.365	10.7
324	0.029	27.7	0.033	18.1	0.025	34.4	0.072	18.4
325	0.029	59.0	0.070	39.7	0.039	15.4	0.070	22.7
326	0.117	12.9	0.131	41.5	0.120	35.3	0.099	23.3
327	0.331	18.1	0.302	33.7	0.261	31.8	0.264	17.0
328	0.102	11.1	0.109	31.7	0.076	16.2	0.139	16.3
329	0.031	20.5	0.027	24.2	0.011	24.3	0.014	43.1
330	0.100	9.6	0.114	13.5	0.095	18.0	0.099	11.7
331	0.010	60.1	0.010	47.9	0.054	56.7	0.096	82.5

332	0.086	12.8	0.097	26.6	0.083	41.0	0.087	30.1
333	0.074	18.6	0.110	50.7	0.095	23.6	0.107	32.8
334	0.456	26.0	0.589	23.5	0.440	13.4	0.542	18.2
335	0.014	60.7	0.021	25.8	0.015	57.1	0.029	30.1
336	0.094	45.3	0.109	43.2	0.083	67.1	0.096	88.2
337	0.027	32.2	0.021	52.3	0.022	40.7	0.008	52.2
338	0.219	9.7	0.199	34.5	0.139	9.8	0.161	40.7
339	0.064	24.4	0.083	53.3	0.054	17.9	0.060	48.8
340	0.442	12.5	0.462	16.6	0.411	20.0	0.344	18.2
341	0.047	31.8	0.043	13.3	0.041	15.6	0.038	40.7
342	0.011	22.9	0.013	39.3	0.009	32.9	0.020	37.6
343	0.162	13.3	0.167	21.9	0.175	19.1	0.161	18.2
344	0.046	7.7	0.061	20.2	0.047	20.1	0.037	15.3
345	0.113	17.5	0.135	4.5	0.091	22.7	0.130	16.5
346	0.103	16.0	0.128	14.5	0.124	13.3	0.140	22.0
347	0.029	15.1	0.027	12.4	0.003	108.1	0.014	21.2
348	0.021	31.8	0.022	15.7	0.026	31.2	0.029	29.5
349	0.322	8.8	0.159	63.2	0.211	29.0	0.014	78.3

350	0.400	14.3	0.329	45.7	0.103	12.3	0.196	29.7
351	0.361	22.4	0.373	18.9	0.011	39.6	0.008	51.0
352	0.022	57.3	0.023	58.7	0.010	22.6	0.116	43.0
353	0.038	15.6	0.039	35.5	0.016	46.1	0.080	50.1
354	0.101	28.0	0.153	15.6	0.165	18.6	0.244	24.1
355	0.036	20.4	0.038	35.3	0.057	14.8	0.054	31.2
356	0.119	9.8	0.135	17.2	0.128	42.3	0.094	37.2
357	0.422	43.2	0.593	22.9	0.929	21.8	1.386	12.0
358	0.335	1.2	0.310	22.8	0.276	8.9	0.283	20.4
359	0.319	38.9	0.464	30.7	0.468	8.1	0.577	17.9
360	0.546	12.5	0.628	17.6	0.684	5.2	0.734	18.0
361	0.293	10.2	0.374	33.1	0.454	11.8	0.439	32.0
362	0.068	47.6	0.079	36.4	0.100	36.4	0.092	43.1
363	0.046	23.3	0.061	31.5	0.080	27.7	0.088	15.6
364	0.029	60.8	0.077	65.4	0.142	17.6	0.091	16.8
365	0.657	15.0	0.688	2.3	0.552	14.7	0.543	7.4
366	0.155	26.7	0.234	36.8	0.202	11.7	0.225	18.3
367	0.152	18.0	0.197	18.3	0.207	18.5	0.229	20.3

368	0.048	38.2	0.040	64.0	0.040	32.7	0.019	77.0
369	0.175	10.9	0.202	20.5	0.202	17.4	0.296	37.7
370	0.072	37.5	0.023	99.8	0.044	45.9	0.020	58.2
371	2.179	7.4	2.118	12.6	2.416	7.7	1.975	10.3
372	0.067	25.9	0.046	62.9	0.050	41.5	0.039	70.6
373	0.381	15.9	0.394	33.9	0.461	9.1	0.516	21.6
374	0.044	35.4	0.059	47.9	0.035	53.5	0.049	52.7
375	0.104	17.4	0.104	15.0	0.069	22.5	0.076	17.6
376	0.137	27.9	0.106	50.6	0.295	17.2	0.075	50.7
377	0.152	25.5	0.113	19.7	0.054	22.1	0.062	54.5
378	0.029	48.3	0.028	48.8	0.119	48.8	0.070	47.6
379	0.152	12.1	0.207	25.9	0.152	24.0	0.212	22.9
380	0.351	19.1	0.220	17.1	0.330	23.1	0.108	22.5
381	0.343	17.4	0.229	23.1	0.250	22.1	0.108	36.9
382	0.280	26.3	0.222	15.3	0.256	15.9	0.227	2.8
383	0.055	48.5	0.033	15.3	0.049	9.4	0.044	7.7
384	0.046	25.2	0.042	5.6	0.055	15.2	0.027	8.5
385	0.204	13.0	0.192	5.3	0.191	17.1	0.148	12.6

386	0.154	20.6	0.128	19.5	0.142	18.8	0.072	13.0
387	0.220	18.3	0.181	23.6	0.133	40.3	0.281	7.8
388	0.084	27.4	0.075	3.0	0.086	11.1	0.080	16.2
389	0.041	12.8	0.039	23.7	0.031	36.8	0.022	26.2
390	0.116	14.4	0.122	12.3	0.082	49.1	0.069	33.5
391	0.046	53.2	0.033	21.5	0.054	18.7	0.073	17.1
392	0.217	12.3	0.224	16.2	0.247	8.1	0.163	20.1
393	0.124	20.9	0.103	25.1	0.094	27.9	0.109	8.9
394	0.058	18.1	0.048	41.7	0.073	35.1	0.104	22.7
395	0.015	57.3	0.014	60.4	0.037	20.7	0.054	8.4
396	0.028	45.7	0.036	48.7	0.040	26.1	0.065	11.8
397	0.040	14.4	0.036	37.0	0.031	24.7	0.036	9.4
398	0.302	12.3	0.303	17.4	0.414	9.2	0.407	13.6
399	0.075	6.8	0.068	22.3	0.136	35.8	0.142	25.4
400	0.026	28.2	0.024	20.4	0.020	38.1	0.012	29.8
401	0.091	15.4	0.085	10.7	0.089	27.4	0.080	10.3
402	0.090	7.2	0.071	5.6	0.070	27.4	0.056	23.4
403	0.070	15.5	0.062	24.5	0.069	22.8	0.109	30.0

404	0.142	15.0	0.114	11.4	0.143	28.6	0.110	13.5
405	0.159	26.4	0.136	9.7	0.160	5.0	0.135	11.7
406	0.091	14.2	0.101	2.3	0.101	9.5	0.085	10.3
407	0.074	15.0	0.081	7.5	0.095	11.8	0.088	10.1
408	0.108	21.3	0.100	31.4	0.056	47.0	0.084	15.5
409	0.165	24.1	0.149	11.4	0.131	36.4	0.103	13.3
410	0.170	29.6	0.179	21.2	0.183	4.2	0.203	9.9
411	0.179	16.9	0.167	5.0	0.130	7.9	0.133	6.8
412	0.298	3.7	0.312	10.6	0.267	14.5	0.289	12.6
413	0.110	14.6	0.099	28.0	0.109	11.1	0.091	24.8
414	0.073	12.4	0.070	25.9	0.086	14.0	0.121	17.3
415	0.099	21.6	0.093	15.3	0.127	20.1	0.087	14.0
416	0.396	11.3	0.366	8.1	0.424	12.1	0.298	6.6
417	0.039	43.5	0.017	50.6	0.017	40.1	0.042	29.7
418	0.104	22.9	0.087	23.1	0.113	24.3	0.060	20.7
419	0.080	17.7	0.060	31.4	0.084	30.2	0.072	10.6
420	0.024	15.4	0.012	14.3	0.012	19.1	0.008	55.6
421	0.089	32.9	0.041	19.5	0.051	34.6	0.028	49.7

422	0.028	7.6	0.022	13.6	0.024	8.2	0.005	61.4
423	0.022	45.5	0.002	57.2	0.033	16.4	0.007	33.2
424	0.022	54.5	0.020	109.3	0.053	23.7	0.033	32.5
425	0.040	48.9	0.040	29.2	0.047	36.7	0.020	21.4
426	0.049	31.7	0.041	44.9	0.054	32.4	0.026	48.7
427	0.049	24.4	0.038	49.6	0.034	18.2	0.019	35.5
428	0.076	25.3	0.054	34.2	0.057	51.2	0.028	67.4
429	0.022	30.8	0.019	43.4	0.024	42.4	0.011	20.7
430	0.028	23.9	0.011	30.6	0.016	41.1	0.009	63.8
431	0.035	42.2	0.014	11.9	0.020	28.0	0.004	59.1
432	0.071	26.1	0.067	53.1	0.082	55.9	0.037	20.1
433	0.070	15.0	0.026	37.0	0.036	28.8	0.025	54.3
434	0.247	37.6	0.139	21.4	0.196	75.1	0.107	56.6
435	0.190	19.3	0.129	27.8	0.154	32.5	0.084	58.4
436	0.032	38.2	0.011	34.5	0.011	52.4	0.015	58.0
437	0.082	46.4	0.068	35.9	0.018	56.7	0.068	41.7
438	0.171	30.2	0.132	21.8	0.145	14.6	0.057	48.7
439	0.021	23.5	0.011	42.2	0.005	59.1	0.013	76.1



440	0.047	33.3	0.042	32.1	0.047	26.6	0.024	37.8
441	0.119	28.8	0.094	23.3	0.105	16.0	0.060	37.0
442	0.326	16.8	0.235	26.5	0.262	5.7	0.149	21.0
443	0.012	48.8	0.012	102.1	0.013	26.5	0.060	37.9
444	0.016	48.2	0.025	20.4	0.019	61.7	0.060	37.6
445	0.058	32.6	0.048	15.2	0.047	79.2	0.019	16.5
446	0.024	39.2	0.022	78.7	0.042	33.8	0.016	30.2
447	0.133	19.0	0.097	6.4	0.104	15.2	0.068	23.3
448	0.092	14.0	0.106	16.7	0.106	5.3	0.049	33.0
449	0.019	61.7	0.015	52.5	0.017	79.4	0.006	24.3
450	0.024	23.6	0.020	17.2	0.019	31.2	0.011	43.4
451	0.014	86.6	0.008	13.6	0.043	41.6	0.032	37.3
452	0.029	34.5	0.031	19.2	0.027	19.4	0.019	21.6
453	0.023	59.6	0.026	27.4	0.027	30.3	0.017	42.0
454	0.842	9.0	0.709	8.1	0.641	12.0	0.495	7.0
455	0.254	21.7	0.230	10.0	0.241	10.8	0.156	24.7
456	0.443	18.5	0.478	21.6	0.630	23.0	0.454	5.2
457	0.121	23.4	0.113	5.1	0.114	12.6	0.065	25.5

458	0.018	46.6	0.024	28.1	0.015	37.8	0.013	36.4
459	0.043	25.1	0.048	20.2	0.045	8.4	0.028	22.7
460	0.054	23.9	0.047	5.1	0.065	17.1	0.058	6.5
461	0.026	28.3	0.025	48.3	0.018	87.6	0.017	22.5
462	0.013	43.5	0.013	35.3	0.022	42.0	0.011	24.7
463	0.008	59.7	0.010	39.3	0.013	62.2	0.012	58.9
464	0.037	22.8	0.031	27.1	0.027	28.8	0.017	26.9
465	0.050	31.6	0.058	23.3	0.071	24.1	0.040	2.6
466	0.037	16.6	0.021	31.8	0.013	44.5	0.014	12.3
467	0.085	31.0	0.070	13.4	0.099	10.5	0.066	17.4
468	0.015	38.4	0.034	46.1	0.040	17.4	0.024	16.6
469	0.012	61.5	0.016	40.7	0.023	20.5	0.022	23.7
470	0.059	21.4	0.041	13.7	0.031	10.8	0.006	28.5
471	0.031	21.8	0.024	6.8	0.026	7.8	0.007	111.7
472	0.039	30.8	0.038	16.3	0.058	9.8	0.053	13.4
473	0.190	8.1	0.161	28.3	0.172	8.0	0.093	33.8
474	0.101	13.2	0.090	11.8	0.097	14.0	0.023	50.4
475	0.028	36.6	0.019	57.1	0.019	13.3	0.011	66.2

476	0.055	15.9	0.046	25.2	0.039	12.4	0.019	20.0
477	0.282	32.1	0.351	31.7	0.507	13.8	0.285	21.3
478	0.179	55.3	0.249	16.4	0.050	41.3	0.088	47.1
479	0.289	32.0	0.230	35.3	0.222	21.1	0.143	24.4
480	0.014	39.5	0.023	41.7	0.022	27.9	0.024	15.0
481	0.027	32.3	0.027	21.9	0.025	21.3	0.021	19.5
482	0.024	28.9	0.024	28.2	0.022	53.9	0.013	12.1
483	0.005	50.7	0.011	13.9	0.017	25.8	0.019	21.7
484	0.053	33.9	0.044	11.2	0.048	38.2	0.029	26.8
485	0.039	15.1	0.028	68.4	0.041	24.2	0.033	20.2
486	0.078	32.9	0.084	12.7	0.066	14.3	0.052	18.4
487	0.068	9.4	0.080	8.5	0.095	13.6	0.121	14.9
488	0.115	14.4	0.129	15.6	0.119	4.2	0.089	10.8
489	0.061	19.4	0.044	17.1	0.027	31.6	0.035	33.1
490	0.062	13.7	0.041	24.8	0.034	17.3	0.032	22.8
491	0.080	14.9	0.052	17.1	0.036	21.0	0.035	37.7
492	0.033	10.3	0.021	14.1	0.019	14.3	0.021	31.0
493	0.086	9.1	0.059	22.6	0.046	10.3	0.050	39.4

494	0.043	15.2	0.024	48.1	0.032	32.7	0.019	51.5
495	0.071	6.7	0.059	95.4	0.021	94.9	0.007	38.7
496	0.028	51.1	0.024	31.6	0.022	16.2	0.026	13.2
497	0.015	43.1	0.014	38.4	0.018	11.8	0.017	14.8
498	0.159	20.9	0.132	5.8	0.174	13.7	0.128	20.8
499	0.776	13.9	0.652	16.4	0.624	8.6	0.488	19.2
500	0.100	14.0	0.081	22.3	0.083	25.0	0.067	13.3
501	0.058	28.6	0.047	33.1	0.006	42.8	0.021	62.4
502	0.013	37.4	0.010	12.4	0.022	16.4	0.009	37.8
503	0.034	78.9	0.022	36.1	0.039	26.6	0.027	50.6
504	0.044	54.5	0.027	17.3	0.018	46.8	0.019	48.8
505	0.027	11.6	0.024	25.6	0.028	28.1	0.023	41.4
506	0.017	54.5	0.011	26.2	0.009	9.9	0.007	50.7
507	0.016	23.7	0.014	21.1	0.020	12.4	0.011	16.5
508	0.016	43.8	0.015	42.7	0.038	14.9	0.023	3.8
509	0.018	9.4	0.022	34.8	0.003	31.9	0.005	89.6
510	0.015	57.9	0.008	11.8	0.022	21.3	0.008	35.6
511	0.034	47.2	0.025	27.2	0.014	23.3	0.008	44.8

512	0.011	30.6	0.011	67.7	0.011	47.6	0.014	55.4
513	0.033	169.6	0.003	156.9	0.023	88.5	0.006	57.2
514	0.015	5.5	0.025	41.5	0.007	31.1	0.012	64.6
515	0.049	43.4	0.041	13.6	0.062	7.5	0.040	8.2
516	0.038	12.4	0.038	12.3	0.032	70.1	0.042	18.2
517	0.013	62.8	0.016	37.4	0.004	37.9	0.013	55.3
518	0.045	34.5	0.033	21.1	0.033	34.9	0.019	16.8
519	0.050	22.8	0.041	22.7	0.022	75.9	0.029	11.6
520	0.021	44.2	0.011	11.5	0.014	77.4	0.014	16.7
521	0.029	43.2	0.025	27.0	0.020	35.4	0.021	51.8
522	0.028	33.8	0.027	29.8	0.018	71.2	0.023	54.4
523	0.024	34.0	0.023	82.9	0.002	135.5	0.006	59.3
524	0.053	26.6	0.037	23.7	0.022	16.3	0.019	58.9
525	0.287	20.5	0.206	10.7	0.212	13.0	0.168	20.5
526	0.245	12.7	0.199	32.8	0.220	8.5	0.186	28.6
527	0.664	20.9	0.613	27.7	0.461	36.9	0.575	33.8
528	0.829	28.9	0.849	32.2	0.564	28.9	0.723	41.6
529	0.306	27.4	0.287	27.2	0.211	29.9	0.261	29.3

530	0.071	49.3	0.036	20.2	0.055	75.4	0.017	55.7
531	0.271	27.4	0.171	15.8	0.296	69.6	0.170	17.7
532	0.055	18.5	0.047	23.9	0.031	16.4	0.044	24.6
533	0.063	23.9	0.061	18.1	0.062	17.6	0.058	12.0
534	0.040	28.0	0.040	18.0	0.037	13.6	0.039	17.5
535	0.033	42.7	0.030	34.6	0.031	24.4	0.034	12.7
536	0.044	24.6	0.041	27.0	0.017	69.6	0.013	34.9
537	0.035	33.4	0.033	9.7	0.037	12.7	0.030	14.5
538	0.147	26.4	0.134	21.1	0.120	62.0	0.176	14.7
539	0.033	10.0	0.023	30.1	0.038	18.5	0.015	78.6
540	0.018	38.3	0.016	29.9	0.022	16.0	0.012	55.4
541	0.022	53.3	0.019	27.4	0.009	19.3	0.016	57.6
542	0.064	24.6	0.073	35.2	0.028	25.3	0.034	36.7
543	0.026	38.4	0.027	52.9	0.002	74.1	0.015	67.1
544	0.049	106.3	0.025	58.1	0.038	47.5	0.020	64.1
545	0.046	21.0	0.046	32.6	0.034	48.7	0.035	48.6
546	0.033	37.9	0.027	60.2	0.019	30.3	0.006	57.1
547	0.336	25.1	0.370	27.9	0.355	9.0	0.372	45.1

548	0.053	10.5	0.047	38.4	0.045	23.3	0.041	31.7
549	0.134	18.4	0.142	30.4	0.114	23.1	0.072	67.1
550	0.054	62.1	0.056	54.3	0.039	38.6	0.095	10.3
551	0.040	23.2	0.041	27.9	0.032	43.6	0.039	43.2
552	0.048	14.0	0.054	15.2	0.049	38.5	0.075	9.5
553	0.046	23.0	0.045	45.6	0.030	26.8	0.032	45.5
554	0.104	15.3	0.103	24.6	0.102	21.1	0.114	29.4
555	0.036	29.2	0.022	29.5	0.031	22.2	0.008	62.5
556	0.195	37.2	0.102	14.4	0.145	64.7	0.063	32.7
557	0.066	7.7	0.054	7.1	0.092	32.4	0.018	26.5
558	0.124	8.2	0.118	10.3	0.122	40.1	0.121	14.8
559	0.247	16.5	0.209	11.1	0.182	10.8	0.202	15.6
560	0.122	14.2	0.118	11.5	0.178	31.9	0.061	11.8
561	0.056	36.4	0.060	7.0	0.064	12.9	0.099	6.1
562	0.142	23.3	0.137	17.9	0.187	12.4	0.147	7.6
563	0.047	25.6	0.035	19.1	0.034	3.0	0.045	8.5
564	0.029	59.0	0.020	8.6	0.027	57.2	0.014	49.2
565	0.070	31.8	0.045	9.4	0.071	10.4	0.027	34.5

566	0.082	17.2	0.061	14.5	0.080	34.8	0.045	25.1
567	0.027	35.5	0.022	12.0	0.051	67.3	0.015	31.4
568	0.014	58.8	0.017	16.1	0.018	21.4	0.010	13.7
569	0.074	12.2	0.066	7.6	0.061	20.7	0.042	24.8
570	0.111	16.0	0.097	10.8	0.105	69.4	0.052	27.0
571	0.100	21.7	0.086	9.6	0.113	37.9	0.065	12.3
572	0.024	30.0	0.020	26.6	0.015	50.1	0.012	64.9
573	0.172	31.9	0.148	61.5	0.072	57.9	0.033	48.9
574	0.128	28.6	0.098	19.0	0.091	14.9	0.070	32.1
575	0.607	33.1	0.425	68.4	0.669	26.4	0.469	23.0
576	0.215	27.3	0.179	65.8	0.260	14.7	0.141	19.1
577	0.035	58.1	0.046	36.8	0.073	21.1	0.085	21.6
578	0.362	23.6	0.278	22.9	0.406	6.4	0.240	7.6
579	0.417	13.6	0.314	13.5	0.357	8.3	0.394	3.0
580	0.066	14.5	0.078	21.0	0.048	20.2	0.086	19.3
581	0.342	27.4	0.378	3.4	0.519	6.1	0.605	4.1
582	0.021	49.1	0.026	51.7	0.022	18.7	0.032	27.2
583	0.145	59.5	0.277	31.9	0.329	13.4	0.608	8.9



584	0.032	74.4	0.056	65.5	0.012	28.7	0.023	16.4
585	0.273	8.2	0.299	24.1	0.295	15.2	0.222	18.7
586	0.085	6.2	0.084	39.9	0.085	16.3	0.085	20.6
587	0.030	29.2	0.026	35.7	0.025	25.0	0.020	26.1
588	0.070	55.4	0.118	40.6	0.117	17.1	0.206	34.7
589	0.199	4.0	0.207	22.0	0.195	3.8	0.170	9.1
590	0.149	9.1	0.162	13.6	0.186	4.9	0.143	16.3
591	0.200	11.3	0.168	26.1	0.164	15.8	0.099	22.4
592	0.544	8.9	0.497	17.3	0.544	4.3	0.443	16.7
593	0.087	37.6	0.132	24.4	0.158	23.5	0.165	14.4
594	0.103	22.9	0.081	14.7	0.103	10.6	0.060	6.3
595	0.198	14.4	0.173	19.2	0.206	5.5	0.189	7.6
596	0.098	11.0	0.136	18.9	0.136	16.3	0.138	15.1
597	0.066	12.9	0.052	39.5	0.032	43.2	0.029	35.2
598	0.064	25.3	0.057	7.4	0.071	26.0	0.070	25.9
599	0.044	21.6	0.051	26.4	0.054	28.5	0.038	24.6
600	0.190	8.8	0.183	7.7	0.205	12.6	0.194	14.9
601	0.070	11.4	0.062	24.3	0.053	23.6	0.046	17.2

602	0.019	47.7	0.026	73.1	0.043	48.7	0.042	26.2
603	0.301	11.7	0.339	17.3	0.385	6.4	0.333	6.7
604	0.026	35.0	0.016	22.1	0.025	25.7	0.026	24.2
605	0.175	9.2	0.129	8.8	0.137	15.5	0.136	8.3
606	0.258	15.2	0.181	5.6	0.305	10.4	0.260	3.0
607	0.131	18.0	0.171	15.9	0.247	21.6	0.242	11.2
608	0.032	22.8	0.018	15.3	0.026	34.9	0.017	20.0
609	0.117	9.5	0.101	32.6	0.087	15.5	0.062	24.2
610	0.142	32.7	0.140	16.1	0.108	25.7	0.142	13.0
611	0.104	18.4	0.096	37.5	0.068	15.0	0.055	5.9
612	0.110	10.9	0.064	20.0	0.084	4.4	0.082	5.0
613	0.180	15.6	0.166	6.7	0.148	14.5	0.146	14.9
614	0.063	17.1	0.055	16.0	0.042	8.6	0.049	24.0
615	0.036	30.2	0.032	25.1	0.038	25.3	0.049	10.2
616	0.233	19.8	0.218	12.5	0.207	17.4	0.180	3.7
617	0.377	38.8	0.413	73.0	1.196	38.8	0.471	11.6
618	0.177	39.9	0.125	15.6	0.195	19.0	0.146	11.6
619	0.551	43.7	0.488	52.3	0.811	20.3	0.405	10.0

620	0.043	32.1	0.037	18.8	0.051	33.4	0.018	58.2
621	0.093	22.3	0.083	16.6	0.108	17.0	0.117	12.9
622	0.224	57.4	0.139	11.4	0.184	28.7	0.096	11.3
623	0.090	44.2	0.059	11.5	0.098	14.4	0.062	29.3
624	0.081	24.3	0.059	15.3	0.075	25.4	0.035	29.7
625	0.656	7.9	0.767	14.3	0.773	12.3	0.637	7.7
626	0.054	35.3	0.089	19.9	0.144	10.0	0.277	11.3
627	0.163	17.5	0.160	15.1	0.223	13.3	0.168	11.5
628	0.527	6.6	0.406	13.0	0.543	10.2	0.557	10.2
629	0.022	62.1	0.031	27.9	0.033	38.8	0.064	32.0
630	0.068	27.8	0.092	17.4	0.163	16.0	0.195	16.0
631	0.251	29.0	0.220	24.7	0.218	26.0	0.408	16.4
632	0.078	16.1	0.069	41.4	0.124	12.8	0.120	24.7
633	0.141	17.1	0.156	11.1	0.131	28.1	0.157	5.1
634	0.046	12.6	0.043	16.1	0.024	34.5	0.041	13.8
635	0.041	41.9	0.045	27.7	0.051	31.6	0.049	5.9
636	0.509	9.5	0.417	20.0	0.480	16.1	0.551	13.1
637	0.302	17.0	0.335	7.5	0.347	6.2	0.390	5.7

638	0.642	11.5	0.638	11.6	0.678	5.6	0.723	10.9
639	0.288	42.1	0.220	18.9	0.226	8.7	0.283	4.9
640	0.141	4.8	0.114	24.7	0.133	11.9	0.114	13.0
641	0.150	20.5	0.136	27.9	0.145	22.1	0.147	9.3
642	0.078	38.6	0.071	17.0	0.082	14.6	0.055	24.5
643	0.081	34.4	0.043	59.7	0.075	47.7	0.012	56.4
644	0.083	18.1	0.056	47.1	0.063	42.9	0.117	31.6
645	0.176	18.4	0.182	30.1	0.147	20.7	0.204	21.8
646	0.535	1.4	0.520	10.7	0.449	11.1	0.447	10.5
647	0.047	41.0	0.030	32.3	0.036	40.7	0.016	18.2
648	0.112	6.8	0.129	18.7	0.147	11.6	0.135	23.6
649	0.065	7.9	0.050	13.8	0.034	13.9	0.033	12.1
650	0.145	11.2	0.148	14.1	0.160	14.2	0.243	10.7
651	0.290	12.8	0.226	23.6	0.374	31.3	0.225	19.8
652	0.338	14.1	0.281	13.2	0.283	8.5	0.510	10.3
653	0.417	11.7	0.491	28.8	0.533	32.8	0.379	22.9
654	0.014	70.7	0.036	86.5	0.047	58.4	0.036	35.9
655	0.203	12.6	0.242	12.3	0.163	8.6	0.281	8.5

656	0.068	16.4	0.073	16.7	0.075	39.4	0.085	16.4
657	0.374	32.6	0.349	9.5	0.351	6.5	0.366	8.2
658	0.082	8.4	0.066	39.0	0.082	21.0	0.046	28.1
659	0.272	6.9	0.240	20.1	0.234	15.0	0.229	9.2
660	0.308	15.5	0.357	28.1	0.458	23.2	0.372	11.8
661	0.229	28.0	0.235	16.0	0.327	33.1	0.298	5.9
662	0.061	21.1	0.074	18.2	0.101	26.9	0.080	7.3
663	0.302	9.7	0.271	17.6	0.261	20.5	0.230	11.8
664	0.116	10.9	0.112	11.4	0.058	19.0	0.077	9.9
665	0.015	59.5	0.019	58.4	0.037	41.4	0.058	7.9
666	0.106	20.6	0.108	12.2	0.095	11.5	0.112	14.5
667	0.155	30.7	0.154	13.5	0.204	8.9	0.196	18.3
668	0.855	8.9	0.815	18.9	0.938	4.3	0.625	7.5
669	0.104	13.2	0.147	16.4	0.109	22.7	0.189	22.4
670	0.311	14.4	0.306	31.8	0.279	8.6	0.245	12.8
671	0.383	48.1	0.394	19.2	0.398	13.6	0.364	16.7
672	0.170	24.4	0.169	55.6	0.123	35.0	0.067	41.7
673	0.086	11.4	0.112	12.1	0.138	13.7	0.152	9.4

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674	0.144	11.3	0.144	32.7	0.190	19.9	0.289	31.3
675	0.312	20.1	0.255	53.2	0.336	7.7	0.219	14.2
676	0.170	14.0	0.122	15.7	0.202	11.1	0.380	24.1
677	0.563	22.5	0.379	38.0	0.445	17.8	0.590	27.9
678	0.284	18.7	0.243	19.2	0.292	8.4	0.229	16.8
679	0.253	18.3	0.185	21.7	0.227	24.8	0.400	10.9