

Supplementary data

The Date Palm (*Phoenix dactylifera* L.) leaf proteome: identification of a gender biomarker to screen male parents

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Supplementary data: Identified proteins from the date palm leaf. The spot number corresponds to Figure.1.

Spot Number	Protein name	Organism	NCBI nr Accession number	Mw/pI		score	Number pept matching*	Coverage** (%)
				Theoretical	Estimated			
Metabolism***								
11	Transketolase	<i>Arabidopsis lyrata</i>	gi 2501356	79.94/5.94	81.28/6.03	106	2	4
27	RuBisCO large subunit-binding protein subunit alpha	<i>Triticum aestivum</i>	gi 134102	57.48/4.83	66.06/4.81	263	5	11
28	RuBisCO large subunit-binding protein subunit alpha	<i>Triticum aestivum</i>	gi 134102	57.48/4.83	69.18/4.78	111	3	7
36	Putative 2,3-biphosphoglycerate-independent phosphoglycerate mutase	<i>Arabidopsis thaliana</i>	gi 15231939	60.72/5.53	66.06/5.80	92	2	4
38	Chloroplast ribulose-1,5-bisphosphate carboxylase	<i>Acer rubrum</i>	gi 115334975	47.68/6.85	47.86/4.86	189	4	13
43	Ribulose 1,5-bisphosphate carboxylase	<i>Zea mays</i>	gi 19855036	34.36/6.43	40.73/5.00	60	2	7
44	Rubisco activase precursor	<i>Spinacia oleracea</i>	gi 170129	51.45/6.28	40.73/4.91	69	2	8
52	UTP-glucose-1-phosphate uridylyltransferase	<i>Hordeum vulgare</i>	gi 6136111	51.61/5.20	51.28/5.60	173	3	9
54	UDP-glucose pyrophosphorylase	<i>Oryza sativa</i>	gi 7417426	51.63/5.46	50.11/5.75	90	3	9
55	Phosphoglycerate kinase, chloroplast precursor	<i>Oryza sativa</i>	gi 129915	49.80/6.58	44.66/5.68	85	1	3
56	Phosphoglycerate kinase	<i>Arabidopsis thaliana</i>	gi 15230595	50.08/5.91	44.66/5.73	179	3	7

57	Glutamine synthase	<i>Gossypium hirsutum</i>	gi 211906462	39.19/5.77	39.81/5.66	67	2	8
59	Glutamine synthase	<i>Gossypium hirsutum</i>	gi 211906462	39.19/5.77	39.81/5.83	81	3	8
62	Putative phosphoglycerate kinase	<i>Ricinus communis</i>	gi 255544584	50.00/8.74	44.66/6.05	533	14	29
65	Putative phosphoglycerate kinase	<i>Musa acuminata</i>	gi 102140037	50.04/8.74	44.66/6.23	177	3	10
68	Putative alcohol dehydrogenase	<i>Ricinus communis</i>	gi 255568816	41.55/8.61	36.30/5.46	97	3	9
74	Rubisco activase precursor	<i>Spinacia oleracea</i>	gi 170129	51.45/6.28	46.77/5.13	149	2	7
75	Ribulose biphosphate carboxylase activase	<i>Nicotiana tabacum</i>	gi 170129	51452/6.28	43.65/5.13	91	1	4
77	Putative phosphoribulose kinase	<i>Ricinus communis</i>	gi 255555933	44.82/5.83	36.30/5.10	256	6	11
78	Sedoheptulose-1,7-bisphosphatase	<i>Cucumis sativus</i>	gi 229597543	42.07/5.96	36.30/5.21	155	4	7
79	Sedoheptulose-1,7-bisphosphatase	<i>Cucumis sativus</i>	gi 229597543	42.07/5.96	48.97/5.30	159	5	7
80	Putative alcohol dehydrogenase	<i>Ricinus communis</i>	gi 255568816	41.55/8.61	36.30/5.33	75	2	6
81	Putative alcohol dehydrogenase	<i>Ricinus communis</i>	gi 255568816	41.55/8.61	36.30/5.40	62	2	6
143	Nucleoside diphosphate kinase B	<i>Flaveria bidentis</i>	gi 1346675	16.18/6.43	14.79/6.61	92	1	10
144	Cysteine protease Mir1	<i>Zea diploperennis</i>	gi 76574390	27.78/4.66	16.21/5.83	58	2	8
181	Triose-phosphate isomerase	<i>Arabidopsis thaliana</i>	gi 15226479	33.32/7.67	25.70/5.36	82	1	4
182	Triose-phosphate isomerase	<i>Arabidopsis thaliana</i>	gi 15226479	33.32/7.67	26.30/5.35	75	1	4
191	20S Proteasome subunit alpha-5	<i>Glycine max</i>	gi 12229923	25.96/4.70	24.54/4.61	57	1	4
200	Triose-phosphate isomerase	<i>Arabidopsis thaliana</i>	gi 15226479	33.32/7.67	25.70/5.11	84	1	4
203	Ribulose-1,5-bisphosphate carboxylase	<i>Acer rubrum</i>	gi 115334975	47.68/6.85	31.62/5.45	196	5	12
204	Putative thiamine biosynthesis protein	<i>Oryza sativa</i>	gi 27261025	36.92/5.44	33.11/5.31	123	3	4
205	Putative thiamine biosynthesis protein	<i>Oryza sativa</i>	gi 27261025	36.92/5.44	31.62/5.28	110	2	4
209	Indole-3-glycerol phosphate synthase	<i>Arabidopsis thaliana</i>	gi 15228142	44.54/6.99	34.67/4.76	54	1	2
220	Inorganic pyrophosphatase	<i>Zea mays</i>	gi 226508748	22.75/4.93	25.70/5.58	92	2	15
221	Carbonate dehydratase	<i>Arabidopsis thaliana</i>	gi 15220853	28.81/6.54	24.54/5.66	66	1	5
223	Triose phosphate isomerase	<i>Zea mays</i>	gi 195608720	25.04/7.72	26.91/5.83	84	2	17
227	Carbonate dehydratase	<i>Arabidopsis thaliana</i>	gi 15220853	28.81/6.54	24.54/5.93	71	2	5
228	Carbonate dehydratase	<i>Arabidopsis thaliana</i>	gi 15220853	28.81/6.54	23.17/5.91	63	1	5
229	Triose phosphate isomerase	<i>Solanum tuberosum</i>	gi 77745458	26.99/5.73	26.91/6.05	312	7	19
230	Putative proteasome subunit alpha type	<i>Ricinus communis</i>	gi 255583952	27.33/5.84	28.84/6.16	74	2	9
231	Ribulose-phosphate 3-epimerase	<i>Spinacia oleracea</i>	gi 2833386	30.34/8.23	25.40/6.21	174	6	14
233	Indole-3-glycerol phosphate synthase	<i>Arabidopsis thaliana</i>	gi 26450093	28271/5.72	23.98/6.35	51	1	4
235	ATP-dependent Clp protease proteolytic subunit	<i>Carica papaya</i>	gi 76262827	33.45/7.71	22.13/6.10	61	1	3
248	Indole-3-glycerol phosphate synthase	<i>Arabidopsis thaliana</i>	gi 15228142	44.54/6.99	29.51/6.61	53	1	2

251	Maturase-like protein	<i>Adesmia volckmannii</i>	gi 5817720	61.14/8.98	18.62/6.43	52	1	3
252	Plastidic aldolase	<i>Solanum tuberosum</i>	gi 164470331	42.87/6.38	34.67/6.33	91	2	4
253	Putative NAD-dependent malate dehydrogenase	<i>Solanum tuberosum</i>	gi 21388550	36.14/8.48	34.67/6.61	320	7	21
254	Ribulose 1,5 bisphosphate carboxylase-oxygenase	<i>Gnidia galpinii</i>	gi 118441506	49.71/6.13	33.87/6.30	125	4	13
258	Fructose-bisphosphate aldolase,	<i>Ricinus communis</i>	gi 255543861	42.85/7.55	33.88/6.00	245	4	16
259	Putative NAD-dependent malate dehydrogenase	<i>Solanum tuberosum</i>	gi 21388550	36.14/8.48	34.67/5.95	184	5	15
262	Malate dehydrogenase	<i>Solanum lycopersicum</i>	gi 56562183	48.41/6.23	35.48/5.61	64	1	3
264	NAD-dependent epimerase/dehydratase	<i>Zea mays</i>	gi 226499246	27.75/6.77	27.54/5.43	64	1	3
269	Enolase	<i>Elaeis guineensis</i>	gi 192910834	47.72/5.98	57.54/5.88	200	4	12
271	Glyceraldehyde-3-phosphate dehydrogenase B-subunit	<i>Spinacia oleracea</i>	gi 120664	48.09/6.72	44.66/6.60	192	4	8
273	Maturase-like protein	<i>Adesmia volckmannii</i>	gi 5817720	61.14/8.98	20.41/6.41	55	1	3
274	Ribulose-1,5-bisphosphate carboxylase	<i>Vriesea ospinae</i> var. <i>ospinae</i>	gi 53831798	53.28/6.13	28.18/6.53	948	28	42
275	Ribulose-biphosphate carboxylase	<i>Urospatha sagittifolia</i>	gi 209417487	51.36/6.05	50.11/6.40	582	22	29
276	Ribulose-1,5-bis phosphate carboxylase large subunit	<i>Tupistra grandis</i>	gi 5725121	51.98/6.14	50.11/6.28	194	4	9
277	Ribulose bisphosphate carboxylase large chain	<i>Humiria balsamifera</i>	gi 131979	51.53/6.23	51.28/6.63	459	11	17
278	Rubisco activase	<i>Capsicum annuum</i>	gi 169930138	48.18/8.03	34.67/5.85	103	3	10
Electron transport								
29	V-type proton ATPase catalytic subunit alpha	<i>Zea mays</i>	gi 1352830	61.91/5.89	75.85/5.41	258	4	10
46	ATP synthase beta subunit	<i>Hevea brasiliensis</i>	gi 231586	60.22/5.95	52.48/5.31	170	4	11
47	ATP synthase beta subunit	<i>Hevea brasiliensis</i>	gi 231586	60.22/5.95	52.48/5.31	143	3	9
49	ATP synthase beta subunit	<i>Microcitrus australis</i>	gi 123325687	50.05/5.09	52.48/5.51	244	6	18
51	ATP synthase beta subunit	<i>Cyrtostachys renda</i>	gi 13236768	53.76/5.37	52.48/5.61	619	14	33
71	ATP synthase beta subunit	<i>Phoenix dactylifera</i>	gi 28195665	53.79/5.29	44.66/5.30	514	12	33
Photosynthesis								
92	Putative thylakoid luminal protein	<i>Ricinus communis</i>	gi 255570589	24.33/8.18	14.12/4.83	223	4	24

152	PS II Oxygen-evolving enhancer protein	<i>Fritillaria agrestis</i>	gi 11133884	28.09/8.31	21.87/5.43	142	4	9
160	Thylakoid lumenal 19 kDa protein	<i>Arabidopsis thaliana</i>	gi 92090800	24.96/6.92	18.62/5.85	51	1	5
161	Thylakoid lumenal 19 kDa protein	<i>Arabidopsis thaliana</i>	gi 92090800	24.96/6.92	18.19/5.55	58	1	5
183	Oxygen-evolving enhancer protein 1	<i>Zea mays</i>	gi 195619530	34.49/5.59	30.19/5.36	402	11	24
185	Oxygen evolving enhancer protein 1	<i>Bruguiera gymnorhiza</i>	gi 119952178	35.11/6.48	29.50/5.15	351	10	24
222	PS II Oxygen-evolving enhancer protein 2	<i>Fritillaria agrestis</i>	gi 11133884	28.09/8.31	24.54/5.73	76	2	11
266	Oxygen-evolving enhancer protein 1	<i>Zea mays</i>	gi 195619530	34.49/5.59	30.19/5.58	362	8	21
270	Putative NADH-dependent hydroxypyruvate reductase	<i>Glycine max</i>	gi 29293057	42.17/6.97	52.24/6.53	150	2	6
Transcription/Protein synthesis								
30	RNA polymerase II subunit	<i>Psilotum nudum</i>	gi 56694296	64.86/6.50	75.85/5.50	45	2	4
61	Elongation factor Tu	<i>Glycine max</i>	gi 1169494	52.47/6.33	44.66/5.95	149	4	7
88	RNA polymerase C	<i>Holcus lanatus</i>	gi 242817897	17.95/9.50	12.88/5.05	58	2	15
135	Ribosomal protein L19	<i>Ostreococcus tauri</i>	gi 116058908	24.81/11.4	16.21/6.26	43	2	10
172	30S ribosomal protein S6	<i>Oryza sativa</i>	gi 115456525	23.29/7.79	18.62/4.66	53	1	4
198	Harpin binding protein1	<i>Malus x domestica</i>	gi 38679321	31.29/9.14	26.30/4.15	135	4	12
211	Peptidyl-prolyl cis-trans isomerase	<i>Spinacia oleracea</i>	gi 10720315	49.84/5.29	37.15/4.61	70	2	8
Cell structure								
21	Actin	<i>Zea mays</i>	gi 1498393	37.16/5.57	63.09/5.33	68	8	3
87	Actin	<i>Spirogyra sp. SVCK 253</i>	gi 3127137	40.28/5.72	13.18/5.00	56	1	9
176	Actin	<i>Zea mays</i>	gi 1498393	37.16/5.57	18.19/4.47	68	4	3
224	Actin	<i>Zea mays</i>	gi 168404	41.71/5.22	26.91/5.83	91	3	11
281	Actin	<i>Persea am ericana</i>	gi 281485191	41.62/5.31	44.66/5.40	488	12	42
Disease/Defence								
1	Heat shock protein 70	<i>Cucumis sativus</i>	gi 1143427	75.36/5.15	79.43/4.93	442	10	15
2	Heat shock protein 70	<i>Cucumis sativus</i>	gi 1143427	75.36/5.15	79.43/4.86	477	11	14
3	Heat shock protein 70	<i>Spinacia oleracea</i>	gi 2654208	76.09/5.19	79.43/4.83	361	8	9
4	Heat shock protein 70	<i>Cucumis sativus</i>	gi 1143427	75.36/5.15	79.43/4.81	298	6	11
19	chaperonin-60	<i>Zea mays</i>	gi 22250	60.92/5.67	63.09/5.33	240	5	10
26	Chaperonin 60 alpha subunit	<i>Canavalia lineata</i>	gi 3790441	61.40/5.23	64.56/5.84	329	7	13
67	Mitochondrial aldehyde dehydrogenase	<i>Secale cereale</i>	gi 20530127	59.28/6.58	58.88/6.38	58	2	4

96	Peroxiredoxin	<i>Elaeis guineensis</i>	gi 192910922	17.30/5.18	16.98/5.25	64	2	17
109	Metallothionein-like protein 1	<i>Zea mays</i>	gi 195611028	7.49/4.91	13.18/4.75	45	2	25
110	Metallothionein1	<i>Zea mays</i>	gi 162458060	7.48/4.91	12.02/5.40	68	4	59
118	Cu-Zn Superoxide dismutase	<i>Ipomoea batatas</i>	gi 586004	15.07/5.64	14.79/5.50	74	2	
146	18 kDa heat shock protein	<i>Hordeum vulgare subsp. vulgare</i>	gi 509070	17.97/8.50	16.78/5.53	125	3	11
149	Cu-Zn- Superoxide dismutase	<i>Zantedeschia aethiopica</i>	gi 12230568	22.06/6.17	18.19/5.43	61	1	12
158	Cu-Zn-superoxide dismutase precursor	<i>Pinus pinaster</i>	gi 16798638	22.10/6.11	19.05/5.70	165	5	21
159	Cu-Zn-superoxide dismutase precursor	<i>Pinus pinaster</i>	gi 16798638	22.10/6.11	18.19/5.70	111	4	18
167	Peroxiredoxin	<i>Oryza sativa</i>	gi 115446541	28.07 /5.67	21.87/4.93	130	5	15
168	Peroxiredoxin	<i>Oryza sativa</i>	gi 115446541	28.07 /5.67	21.87/4.93	62	3	6
188	Dehydroascorbate reductase	<i>Malus x domestica</i>	gi 225380890	29.31/8.78	28.18/5.03	65	2	7
219	Cytosolic ascorbate peroxidase	<i>Elaeis guineensis</i>	gi 192912966	27.37/5.42	26.91/5.56	262	9	29
225	Ascorbate peroxidase	<i>Nicotiana tabacum</i>	gi 559005	27.37/5.43	27.54/5.85	127	2	8
244	Mn superoxide dismutase	<i>Nelumbo nucifera</i>	gi 60502316	25.91/6.59	24.54/6.50	69	1	4
246	Salt responsive protein 2	<i>Solanum lycopersicum</i>	gi 195549553	57.13/6.31	27.54/6.56	73	2	4
257	Multicatalytic endopeptidase	<i>Arabidopsis thaliana</i>	gi 2511586	29.12/5.03	31.26/6.11	57	1	4
282	Mn superoxide dismutase	<i>Digitalis lanata</i>	gi 9929159	24.74/8.01	23.98/6.21	81	1	6
283	Chalcone—flavonone isomerase	<i>Paeonia suffruticosa</i>	gi 5921722	27.91 /4.99	25.11/5.28	54	1	3
Unclassified								
20	Predicted protein	<i>Populus trichocarpa</i>	gi 224052861	64.20/5.62	66.06/5.33	243	4	11
35	Predicted protein	<i>Populus trichocarpa</i>	gi 224100535	67.54/6.56	69.18/5.75	124	2	3
64	Predicted protein	<i>Populus trichocarpa</i>	gi 224109060	50.18/8.24	39.81/6.00	283	7	16
66	Predicted protein	<i>Populus trichocarpa</i>	gi 224064707	58.79/6.11	58.88/6.38	145	4	7
170	Predicted protein	<i>Populus trichocarpa</i>	gi 224062828	23.00/5.45	20.65/4.90	52	1	3
173	Predicted protein	<i>Physcomitrella patens subsp. patens</i>	gi 168059196	34.02/4.85	18.19/4.66	71	3	14
201	Predicted protein	<i>Populus trichocarpa</i>	gi 224060355	20.30/4.93	24.54/5.18	57	2	10
265	Predicted protein	<i>Chlamydomonas reinhardtii</i>	gi 159462486	36.34/8.61	26.91/5.36	52	1	2
134	CBS1 domain protein	<i>Hyacinthus orientalis</i>	gi 47027028	22.46/8.58	16.21/6.20	126	3	20
13	Unknown	<i>Arabidopsis thaliana</i>	gi 14532624	85.94/5.48	89.12/5.45	106	2	2
14	Unknown	<i>Arabidopsis thaliana</i>	gi 14532624	85.94/5.48	89.12/5.38	104	3	4
89	Unknown	<i>Glycine max</i>	gi 255630103	23.51/7.60	13.48/5.11	278	4	30
94	Unknown	<i>Glycine max</i>	gi 255629191	21.94/5.80	14.79/4.43	62	3	10

97	Unknown	<i>Picea sitchensis</i>	gi 116781285	25.48/9.11	16.59/5.03	67	1	7
101	Unknown	<i>Oryza sativa</i>	gi 187608845	30.30/5.72	15.13/4.85	65	2	6
106	Unknown	<i>Picea sitchensis</i>	gi 116785879	25.92/7.55	13.80/4.65	57	1	4
107	Unknown	<i>Arabidopsis thaliana</i>	gi 18400907	24.80/4.77	13.18/4.66	50	2	15
127	Unknown	<i>Picea sitchensis</i>	gi 116782330	16.30/5.95	13.48/6.08	101	2	16
139	Unknown	<i>Glycine max</i>	gi 255639105	28262/8.90	17.17/6.60	66	1	7
155	Unknown	<i>Glycine max</i>	gi 255635846	28.42/7.68	22.38/5.83	101	2	8
175	Unknown	<i>Picea sitchensis</i>	gi 116783200	25.83/6.06	18.62/4.50	52	1	6
178	Unknown	<i>Picea sitchensis</i>	gi 116783200	25.83/6.06	18.62/4.38	51	1	6
180	Unknown	<i>Picea sitchensis</i>	gi 116784611	27.19/8.39	24.54/5.38	92	2	7
232	Unknown	<i>Populus trichocarpa</i>	gi 118486197	27.71/5.60	24.54/6.28	117	4	11
234	Unknown	<i>Populus trichocarpa</i>	gi 118486197	27.71/5.60	23.17/6.26	113	3	11
243	Unknown	<i>Populus trichocarpa</i>	gi 118486197	27.71/5.60	24.54/6.50	114	3	11
245	Unknown	<i>Populus trichocarpa</i>	gi 118486197	27.71/5.60	26.30/6.65	95	2	11
284	Unknown	<i>Populus trichocarpa</i>	gi 118486197	27.71/5.60	23.98/6.21	96	3	11
236	Unknown	<i>zea mays</i>	gi 219884075	44.24/8.88	20.89/6.05	62	2	1
7	Hypothetical protein	<i>Vitis vinifera</i>	gi 225455509	74.51/6.34	81.28/5.96	251	4	25
8	Hypothetical protein	<i>Sorghum bicolor</i>	gi 242087069	68.67/5.47	81.28/5.88	266	5	10
9	Hypothetical protein	<i>Vitis vinifera</i>	gi 225455509	74.51/6.76	81.28/5.81	241	5	9
53	Hypothetical protein	<i>Vitis vinifera</i>	gi 225455555	48.08/6.17	57.54/5.73	287	5	19
60	Hypothetical protein	<i>Sorghum bicolor</i>	gi 242090961	49.96/5.89	44.66/5.86	229	6	14
70	Hypothetical protein	<i>Vitis vinifera</i>	gi 225462191	45.88/5.79	45.70/5.25	146	3	9
72	Hypothetical protein	<i>Vitis vinifera</i>	gi 147856329	51.89/5.54	46.77/4.75	115	3	8
76	Hypothetical protein	<i>Vitis vinifera</i>	gi 225462191	45880/5.79	40.73/5.11	76	1	3
82	Hypothetical protein	<i>Vitis vinifera</i>	gi 225462568	19.43/8.34	11.22/4.61	72	2	5
84	Hypothetical protein	<i>Vitis vinifera</i>	gi 225453275	14.62/8.93	10.71/4.91	74	2	20
98	hypothetical protein	<i>Vitis vinifera</i>	gi 225441002	22.49/7.67	16.21/4.81	67	1	5
103	Hypothetical protein	<i>Vitis vinifera</i>	gi 225441002	22.49/7.67	16.21/4.70	67	2	5
162	hypothetical protein	<i>Ricinus communis</i>	gi 255584205	32.15/8.97	22.90/5.26	56	1	3
171	hypothetical protein	<i>Ricinus communis</i>	gi 255580430	13.58/9.63	19.95/4.85	55	1	13
218	hypothetical protein,	<i>Vitis vinifera</i>	gi 225467676	29.82/8.34	28.11/5.63	204	3	19
250	Hypothetical protein	<i>Ipomoea nil</i>	gi 124484375	23.91/9.38	26.00/6.53	62	2	6
255	Hypothetical protein	<i>Vitis vinifera</i>	gi 225457407	43.57/8.13	33.87/6.30	236	8	19

- * Number of peptides identified by mass spectrometry which are present in the protein sequence
- ** Sequence coverage is the percentage of a protein sequence covered by identified peptides
- *** Annotation following criteria of Bevan et al. (1998).