

Supplementary Material

Comparative proteomic analysis of latex from *Euphorbia kansui* laticifers at different development stages with and without UV-B treatment via iTRAQ-coupled two-dimensional liquid chromatography–MS/MS

Xueyan Zhao^{A,B}, Yue Zhang^A, Meng Wang^A, Xiaoi Fang^A and Xia Cai^{A,C}

^AKey Laboratory of Resource Biology and Biotechnology in Western China, Ministry of Education, Northwest University, Xi'an, 710069, China.

^BCollaborative Innovation Center of Green Manufacturing Technology for Traditional Chinese Medicine in Shaanxi Province, School of Pharmacy, Shaanxi Institute of International Trade and Commerce, Xianyang, 712046, China.

^CCorresponding author. Email: caix@nwu.edu.cn

Table S1. All the latex proteins identified in *Euphorbia kansui*

Table S2. The KEGG pathways of *Euphorbia kansui* latex proteins

Table S3. The differentially accumulated proteins of *Euphorbia kansui* latex

Table S4. The KEGG pathways of differentially expressed latex proteins between three different comparison groups

Table S5. The primer sequence of genes in qRT-PCR analysis

Table S1 All the latex proteins identified in *Euphorbia kansui*

Number	Accession	Score	Mass	Cov	Peptide	Nr-ID	Nr Score	Nr-annotation
1	Unigene0004237	57478	90321	49.6	26	gij508780017[gb EOY27273.1]	954	Subtilase family protein [Theobroma cacao]
2	Unigene0023113	17264	39535	44.6	9	gij508718200[gb EOY10097.1]	257	Phosphorylase superfamily protein [Theobroma cacao]
3	Unigene0022339	10581	38497	41.1	9	gij309839[gb AAA16342.1]	208	vegetative storage protein [Populus trichocarpa x Populus deltoides]
4	Unigene0050849	7497	16815	59.8	7	gij108710518[gb ABF98313.1]	104	expressed protein [Oryza sativa Japonica Group]
5	Unigene0053141	6975	46801	36	14	gij56385009[gb AAS97959.2]	677	peroxidase precursor [Euphorbia characias]
6	Unigene0035043	6455	37921	37.3	8	gij225437124[ref XP_002273926.1]	264	PREDICTED: chlorophyllase-1 [Vitis vinifera]
7	Unigene0039080	6158	47584	48.9	16	gij225432636[ref XP_002278244.1]	473	PREDICTED: primary amine oxidase [Vitis vinifera]
8	Unigene0013842	5792	65735	28.2	11	gij261264941[gb ACX55829.1]	834	aspartic proteinase 1 [Castanea mollissima]
9	Unigene0045890	5021	31380	43.3	10	gij15226103[ref NP_180896.1]	289	calcosin 3 [Arabidopsis thaliana]
10	Unigene0039081	5010	38418	38.8	9	gij508713761[gb EOY05658.1]	418	Primary amine oxidase isoform 1 [Theobroma cacao]
11	Unigene0045471	4297	51914	50.9	15	gij508713658[gb EOY05555.1]	509	Eukaryotic aspartyl protease family protein isoform 1 [Theobroma cacao]
12	Unigene0020176	4010	42884	47	17	gij508703238[gb EOX95134.1]	463	Alpha/beta-Hydrolases superfamily protein [Theobroma cacao]
13	Unigene0027610	3346	67926	23.5	7	gij20269071[emb CAD29733.1]	556	pectin methylesterase [Sesbania rostrata]
14	Unigene0060497	2684	76576	39.3	17	gij356968738[gb AET43458.1]	949	granule-bound starch synthase 1 [Manihot esculenta]
15	Unigene0009408	2123	50697	45.5	12	gij225436405[ref XP_002271797.1]	352	PREDICTED: lysosomal Pro-X carboxypeptidase [Vitis vinifera]
16	Unigene0021896	1919	39270	18.6	4	gij470118595[ref XP_004295410.1]	331	PREDICTED: GDSL esterase/lipase At1g29660-like [Fragaria vesca subsp. vesca]
17	Unigene0007952	1556	48643	55.7	14	gij359493788[ref XP_002285446.2]	493	PREDICTED: epidermis-specific secreted glycoprotein EP1-like [Vitis vinifera]
18	Unigene0014181	1539	146853	28.4	26	gij508713146[gb EOY05043.1]	1670	Catalytic,carbohydrate kinases,phosphoglucan [Theobroma cacao]
19	Unigene0014507	1462	93237	20.4	14	gij508780017[gb EOY27273.1]	1118	Subtilase family protein [Theobroma cacao]
20	Unigene0011721	1405	115267	15.4	10	gij508711055[gb EOY02952.1]	1478	Glycosyl hydrolase family 38 protein [Theobroma cacao]
21	Unigene0005605	1233	111299	13.1	9	gij508778267[gb EOY25523.1]	1189	Glycosyl hydrolases family 31 protein isoform 1 [Theobroma cacao]
22	Unigene0009803	1197	14821	63	6	gij470134700[ref XP_004303177.1]	142	PREDICTED: xylem serine proteinase 1-like isoform 2 [Fragaria vesca subsp. vesca]
23	Unigene0013179	1189	46113	43.6	11	gij51703306[gb AAR84410.2]	638	glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]
24	Unigene0060990	1148	44359	48.7	14	gij38194890[gb AAR13288.1]	540	Anx1 [Gossypium hirsutum]
25	Unigene0013323	1074	19136	35.2	4	gij400131571[emb CCH50971.1]	192	T4.10 [Malus x robusta]
26	Unigene0053460	1013	63598	24.2	9	gij508699007[gb EOX90903.1]	818	Serine carboxypeptidase S28 family protein [Theobroma cacao]
27	Unigene0051306	1003	44010	55.9	17	gij359807257[ref NP_001241368.1]	405	annexin D4-like [Glycine max]
28	Unigene0061180	994	78977	34	15	gij60592632[dbj BAD90912.1]	1200	vacuolar H ⁺ -ATPase catalytic subunit [Pyrus communis]
29	Unigene0035025	952	68722	21.1	10	gij508726455[gb EOY18352.1]	880	Beta-hexosaminidase 1 isoform 1 [Theobroma cacao]
30	Unigene0003372	943	60440	18.7	6	gij62526575[gb AAx84673.1]	855	cysteine protease CP1 [Manihot esculenta]
31	Unigene0051821	929	79041	15.9	7	gij225441977[ref XP_002265171.1]	861	PREDICTED: pectinesterase 3-like [Vitis vinifera]
32	Unigene0010923	925	18540	26.5	4	gij224076006[ref XP_002304869.1]	66.6	predicted protein [Populus trichocarpa]
33	Unigene0058951	903	84579	22.5	11	gij508724490[gb EOY16387.1]	965	DPP6 N-terminal domain-like protein [Theobroma cacao]
34	Unigene0002542	836	37444	16.9	3	gij225437124[ref XP_002273926.1]	301	PREDICTED: chlorophyllase-1 [Vitis vinifera]
35	Unigene0035285	799	13692	37.3	4	gij470134700[ref XP_004303177.1]	141	PREDICTED: xylem serine proteinase 1-like isoform 2 [Fragaria vesca subsp. vesca]
36	Unigene0029498	790	63266	33.9	11	gij508783946[gb EOY31202.1]	840	Purple acid phosphatase 26 isoform 2 [Theobroma cacao]
37	Unigene0055553	727	83626	20.5	10	gij384371336[gb AFH77957.1]	1066	vacuolar invertase [Manihot esculenta]
38	Unigene0052910	723	43146	34.1	7	gij508776996[gb EOY24252.1]	461	Alpha/beta-Hydrolases superfamily protein isoform 2 [Theobroma cacao]
39	Unigene0000986	703	20330	22.5	3	gij508700251[gb EOX92147.1]	248	Lipase/lipoxygenase, PLAT/LH2 family protein [Theobroma cacao]
40	gij310751740[gb]	688	30030	50.9	8	gij310751740[gb ADP09339.1]	484	actin [Jatropha curcas]

	ADP09339.1]								
41	Unigene0025134	664	106703	16.3	12	gi 508711054 gb EOY02951.1	1228	Glycosyl hydrolase family 38 protein [Theobroma cacao]	
42	Unigene0008378	654	10977	83.3	5	gi 359493788 ref XP_002285446.2	137	PREDICTED: epidermis-specific secreted glycoprotein EPI-like [Vitis vinifera]	
43	Unigene0051610	565	47665	21.5	8	gi 460408038 ref XP_004249455.1	639	PREDICTED: fructose-bisphosphate aldolase cytoplasmic isozyme-like [Solanum lycopersicum]	
44	Unigene0010687	562	38505	27.9	7	gi 508726916 gb EOY18813.1	494	Serine carboxypeptidase-like 49 [Theobroma cacao]	
45	Unigene0053924	562	29863	26.4	4	gi 508711644 gb EOY03541.1	368	Vesicle transport v-SNARE family protein [Theobroma cacao]	
46	Unigene0054117	540	23063	38.2	5	gi 209981339 gb ACJ05350.1	340	actin [Camellia sinensis]	
47	Unigene0005140	515	27354	16.7	3	gi 460404938 ref XP_004247935.1	298	PREDICTED: peroxxygenase-like [Solanum lycopersicum]	
46	Unigene0005801	498	60787	26	9	gi 356536392 ref XP_003536722.1	938	PREDICTED: V-type proton ATPase subunit B 1-like isoform 1 [Glycine max]	
49	Unigene0034090	497	20167	25.3	2	gi 317106727 dbj BAJ53223.1	209	JHL06P13.2 [Jatropha curcas]	
50	Unigene0060976	486	87808	20	9	gi 508726275 gb EOY18172.1	1220	Heat shock cognate protein 70-1 [Theobroma cacao]	
51	Unigene0034309	485	16810	54.5	5	gi 1345501 emb CAA42103.1	230	glycolytic glyceraldehyde 3-phosphate dehydrogenase [Antirrhinum majus]	
52	Unigene0004204	478	87744	21.9	10	gi 392465167 dbj BAM24707.1	1232	Heat shock protein 70 [Nicotiana tabacum]	
53	Unigene0014772	473	77699	19.6	8	gi 508714833 gb EOY06730.1	1163	ATP citrate lyase subunit B 2 isoform 1 [Theobroma cacao]	
54	Unigene0044171	471	50811	20.3	6	gi 508708043 gb EOX99939.1	720	Aldolase superfamily protein [Theobroma cacao]	
55	Unigene0024555	465	93396	21.5	10	gi 211906506 gb ACJ11746.1	1238	luminal binding protein [Gossypium hirsutum]	
56	Unigene0005133	463	31718	23.6	3	gi 157781823 gb ABV72237.1	346	caleosin [Ficus pumila var. awkeotsang]	
57	Unigene0021852	461	4695	52.6	2	gi 255548165 ref XP_002515139.1	48.1	cathepsin B, putative [Ricinus communis]	
58	Unigene0014552	453	49122	23.5	7	gi 198400319 gb ACH87168.1	420	senescence-related protein [Camellia sinensis]	
59	Unigene0058320	438	102739	15.4	9	gi 151347486 gb ABS01352.1	1400	methionine synthase [Carica papaya]	
60	Unigene0000507	437	60126	21.6	6	gi 289600010 gb ADD12953.1	814	2-phospho-D-glycerate hydrolase [Citrus trifoliata]	
61	Unigene0035254	435	16325	44.6	4	gi 449498564 ref XP_004160571.1	129	PREDICTED: uncharacterized LOC101222381 [Cucumis sativus]	
62	Unigene0057648	415	74144	21.7	10	gi 508787185 gb EOY34441.1	1002	RuBisCO large subunit-binding protein subunit alpha isoform 2 [Theobroma cacao]	
63	Unigene0057683	413	62971	17.8	9	gi 356561173 ref XP_003548859.1	833	PREDICTED: lysosomal alpha-mannosidase-like isoform 2 [Glycine max]	
64	Unigene0028283	407	24653	16.7	2	gi 470102209 ref XP_004287550.1	355	PREDICTED: superoxide dismutase [Cu-Zn], chloroplastic-like [Fragaria vesca subsp. vesca]	
65	Unigene0015236	397	92392	15	8	gi 224102795 ref XP_002312804.1	1122	cholesterol transport protein [Populus trichocarpa]	
66	Unigene0052549	378	48671	19.2	5	gi 60396844 gb AAAX19661.1	635	cysteine proteinase [Populus tomentosa]	
67	Unigene0058292	378	55794	23.7	8	gi 470149237 ref XP_004310146.1	719	PREDICTED: transaldolase-like [Fragaria vesca subsp. vesca]	
68	Unigene0010252	374	43046	21.7	5	gi 508721295 gb EOY13192.1	578	Lactate/malate dehydrogenase family protein [Theobroma cacao]	
69	Unigene0053012	369	56621	20.2	5	gi 470145304 ref XP_004308281.1	560	PREDICTED: L-gulonolactone oxidase-like [Fragaria vesca subsp. vesca]	
70	Unigene0010534	358	68222	20.1	8	gi 449434570 ref XP_004135069.1	998	PREDICTED: ATP synthase subunit beta, mitochondrial-like [Cucumis sativus]	
71	Unigene0000233	348	59482	23.1	8	gi 508781499 gb EOY28755.1	728	Sapoin-like aspartyl protease family protein [Theobroma cacao]	
72	Unigene0013493	345	80989	24.5	10	gi 225435794 ref XP_002285746.1	1036	PREDICTED: ruBisCO large subunit-binding protein subunit beta, chloroplastic [Vitis vinifera]	
73	Unigene0045327	345	19563	49.3	6	gi 508784483 gb EOY31739.1	147	Alpha/beta-Hydrolases superfamily protein [Theobroma cacao]	
74	Unigene0034245	341	17846	40.1	4	gi 311615483 gb ABM53666.2	304	copper/zinc superoxide dismutase [Euphorbia characias]	
75	Unigene0011802	341	46793	10.8	4	gi 508703608 gb EOX95504.1	590	Cysteine proteinases superfamily protein [Theobroma cacao]	
76	Unigene0025452	340	32446	31.9	5	gi 288901047 gb ADC68236.1	441	elongation factor 1-alpha [Dendrobium nobile]	
77	Unigene0041825	325	39589	24.1	5	gi 211906536 gb ACJ11761.1	454	class III peroxidase [Gossypium hirsutum]	
78	Unigene0031915	324	47562	13.7	4	gi 359475471 ref XP_002268406.2	519	PREDICTED: triacylglycerol lipase 1-like [Vitis vinifera]	
79	Unigene0042615	317	52137	19.2	5	gi 508711502 gb EOY03399.1	468	Galactose mutarotase-like superfamily protein [Theobroma cacao]	
80	Unigene0026793	317	36562	10.9	2	gi 317106666 dbj BAJ53169.1	482	JHL18108.3 [Jatropha curcas]	
81	Unigene0033989	307	18702	44.9	5	gi 400131571 emb CCH50971.1	97.8	T4.10 [Malus x robusta]	
82	Unigene0030478	305	92268	16.7	9	gi 225456004 ref XP_002279101.1	1225	PREDICTED: stromal 70 kDa heat shock-related protein, chloroplastic-like [Vitis vinifera]	

83	Unigene0035501	304	67310	26.4	9	gj 307566892 gb ADN52612.1	981	acetyl-CoA carboxylase BC subunit [Jatropha curcas]
84	Unigene0027050	300	27738	40.2	6	gj 225430324 ref XP_002285207.1	400	PREDICTED: vesicle-associated membrane protein 713 [Vitis vinifera]
85	Unigene0014554	299	70540	20.5	8	gj 351722359 ref NP_001238009.1	766	protein disulfide isomerase-like protein precursor [Glycine max]
86	Unigene0053361	287	29668	23.6	3	gj 508725757 gb EOY17654.1	332	Biotin/lipoyl attachment domain-containing protein isoform 1 [Theobroma cacao]
87	Unigene0029874	286	74317	16.3	7	gj 502120417 ref XP_004496955.1	1006	PREDICTED: d-3-phosphoglycerate dehydrogenase, chloroplastic-like isoform X1 [Cicer arietinum]
88	Unigene0027361	284	14130	25.2	2	gj 224166603 ref XP_002338954.1	195	vitamin-b12 independent methionine synthase [Populus trichocarpa]
89	Unigene0004780	284	56055	11.4	3	gj 449516613 ref XP_004165341.1	728	PREDICTED: LOW QUALITY PROTEIN: alpha-L-arabinofuranosidase 1-like [Cucumis sativus]
90	Unigene0043750	280	28247	41	7	gj 225463105 ref XP_002264356.1	403	PREDICTED: ras-related protein Rab7 isoform 1 [Vitis vinifera]
91	Unigene0042733	276	70305	16	6	gj 225444135 ref XP_002268361.1	825	PREDICTED: reticuline oxidase-like protein [Vitis vinifera]
92	Unigene0015240	273	94310	12.6	7	gj 508712429 gb EOY04326.1	1152	Glycosyl hydrolase family 81 protein [Theobroma cacao]
93	Unigene0059057	269	40388	22	5	gj 225433918 ref XP_002268097.1	570	PREDICTED: fructokinase-2 [Vitis vinifera]
94	Unigene0053585	268	42289	21	5	gj 357439495 ref XP_003590025.1	607	Malate dehydrogenase [Medicago truncatula]
95	Unigene0052084	258	65523	17.5	7	gj 470136808 ref XP_004304174.1	910	PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating 3-like [Fragaria vesca subsp. vesca]
96	Unigene0005014	243	34314	20.6	4	gj 357481501 ref XP_003611036.1	378	V-type proton ATPase subunit E1 [Medicago truncatula]
97	Unigene0058341	240	70750	13.9	5	gj 225431914 ref XP_002276853.1	963	PREDICTED: dihydrolipoyl dehydrogenase [Vitis vinifera]
98	Unigene0042612	239	22370	39.8	4	gj 343481065 gb AEM44784.1	339	cyclophilin [Momordica charantia]
99	Unigene0013492	234	62542	13.1	4	gj 449444282 ref XP_004139904.1	812	PREDICTED: phosphoglycerate kinase, chloroplastic-like [Cucumis sativus]
100	Unigene0045328	231	19382	29.9	3	gj 508784483 gb EOY31739.1	90.9	Alpha/beta-Hydrolases superfamily protein [Theobroma cacao]
101	Unigene0059717	230	46641	12.6	3	gj 508726787 gb EOY18684.1	635	Adenosine kinase 2 [Theobroma cacao]
102	Unigene0034655	227	48280	13.8	4	gj 508717583 gb EOY09480.1	638	NAD(P)-binding Rossmann-fold superfamily protein isoform 1 [Theobroma cacao]
103	Unigene0014822	226	54945	13.3	4	gj 508722301 gb EOY14198.1	697	Glyceraldehyde-3-phosphate dehydrogenase of plastid 2 isoform 1 [Theobroma cacao]
104	Unigene0011890	225	55795	15.2	4	gj 211906450 gb ACJ11718.1	718	phosphoglycerate kinase [Gossypium hirsutum]
105	Unigene0030324	225	57574	16.6	5	gj 508714708 gb EOY06605.1	687	Pectin lyase-like superfamily protein [Theobroma cacao]
106	Unigene0042995	221	65613	13.1	5	gj 356562585 ref XP_003549550.1	937	PREDICTED: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase-like [Glycine max]
107	Unigene0054226	220	22242	34.3	6	gj 470125885 ref XP_004298928.1	188	PREDICTED: ribonuclease 3-like [Fragaria vesca subsp. vesca]
108	Unigene0042714	218	31883	30.2	5	gj 164604982 dbj BAF98287.1	451	isopentenyl-diphosphate Delta-isomerase [Hevea brasiliensis]
109	Unigene0023484	217	68081	5.3	2	gj 508780729 gb EOY27985.1	771	Xylem bark cysteine peptidase 3 isoform 1 [Theobroma cacao]
110	Unigene0029804	217	31590	21.9	4	gj 356567068 ref XP_003551745.1	385	PREDICTED: syntaxin-51-like [Glycine max]
111	Unigene0053950	205	33832	16.5	3	gj 390098824 gb AFL48185.1	446	triose phosphate isomerase cytosolic isoform-like protein [Capsicum annuum]
112	Unigene0034951	203	59280	11.9	4	gj 508700740 gb EOX92636.1	686	Farnesylcysteine lyase [Theobroma cacao]
113	Unigene0030706	202	47337	16.8	5	gj 508728076 gb EOY19973.1	386	Annexin [Theobroma cacao]
114	Unigene0052520	199	72889	10.7	4	gj 255557893 ref XP_002519975.1	1026	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Ricinus communis]
115	Unigene0028057	198	38737	9.7	2	gj 508705865 gb EOX97761.1	514	Triosephosphate isomerase isoform 2 [Theobroma cacao]
116	Unigene0044263	198	35641	19.5	4	gj 508706840 gb EOX98736.1	450	General regulatory factor 2, OMEGA [Theobroma cacao]
117	Unigene0039388	196	10540	37.1	2	gj 225443421 ref XP_002267740.1	94.7	PREDICTED: subtilisin-like protease [Vitis vinifera]
118	Unigene0003120	194	105182	11.5	6	gj 508720034 gb EOY11931.1	1320	Heat shock protein 81.4 [Theobroma cacao]
119	Unigene0052143	191	96553	7.6	4	gj 449443540 ref XP_004139535.1	1268	PREDICTED: vesicle-fusing ATPase-like [Cucumis sativus]
120	Unigene0051419	190	65305	14	5	gj 211906480 gb ACJ11733.1	936	catalase [Gossypium hirsutum]
121	Unigene0054052	189	63611	14.2	6	gj 429326634 gb AFZ78657.1	938	S-adenosyl-L-homocysteine hydrolase [Populus tomentosa]
122	Unigene0011173	189	13213	36.6	3	gj 449533510 ref XP_004173717.1	183	PREDICTED: polyubiquitin-like, partial [Cucumis sativus]
123	Unigene0009061	188	19619	23	3	gj 284433792 gb ADB85102.1	292	nucleoside diphosphate kinase B [Jatropha curcas]
124	Unigene0044210	187	73964	15.1	5	gj 508776807 gb EOY24063.1	852	Pyruvate kinase isozyme G, chloroplastic [Theobroma cacao]

125	Unigene0001613	186	39814	27.1	6	gi 359483362 ref XP_002273346.2	525	PREDICTED: lactoylglutathione lyase [Vitis vinifera]
126	Unigene0023691	181	53352	15.7	5	gi 470126765 ref XP_004299353.1	672	PREDICTED: malate dehydrogenase, chloroplastic-like [Fragaria vesca subsp. vesca]
127	Unigene0023119	179	13964	29.8	2	gi 313586509 gb ADR71265.1	183	60S ribosomal protein L12A [Hevea brasiliensis]
128	Unigene0031758	178	76712	6.8	3	gi 359483238 ref XP_003632926.1	959	PREDICTED: mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS1-like [Vitis vinifera]
129	Unigene0053546	177	44256	14.9	5	gi 224054174 ref XP_002298128.1	296	2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]
130	Unigene0043808	177	33914	21	4	gi 508712352 gb EOY04249.1	341	Allene oxide cyclase 4 isoform 1 [Theobroma cacao]
131	Unigene0052745	176	33261	10.2	2	gi 502157018 ref XP_004510730.1	385	PREDICTED: ribonuclease 2-like [Cicer arietinum]
132	Unigene0005593	176	33160	11.4	3	gi 508705880 gb EOX97776.1	407	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1 isoform 1 [Theobroma cacao]
133	Unigene0027363	175	72014	17.6	8	gi 224131686 ref XP_002328083.1	965	vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltryglutamate-homocysteine [Populus trichocarpa]
134	Unigene0024554	173	94137	8.8	5	gi 225426230 ref XP_002263323.1	1201	PREDICTED: luminal-binding protein 5 [Vitis vinifera]
135	Unigene0027438	171	28454	42.6	6	gi 508715123 gb EOY07020.1	306	Glutathione peroxidase 2 [Theobroma cacao]
136	Unigene0010760	166	35264	13.6	2	gi 508776820 gb EOY24076.1	456	Tobamovirus multiplication 2A isoform 1 [Theobroma cacao]
137	Unigene0043745	165	35812	22	5	gi 326694865 gb AEA03663.1	493	14-3-3 protein 2 [Hevea brasiliensis]
138	Unigene0010746	163	40461	9.2	2	gi 356528469 ref XP_003532825.1	445	PREDICTED: WW domain-containing oxidoreductase-like isoform 1 [Glycine max]
139	Unigene0034525	161	42358	13.1	3	gi 508710737 gb EOY02634.1	510	Alpha-soluble NSF attachment protein 2 [Theobroma cacao]
140	Unigene0020801	160	18803	21.2	2	gi 225432542 ref XP_002277699.1	243	PREDICTED: basic 7S globulin-like [Vitis vinifera]
141	Unigene0031164	154	20837	22.2	2	gi 224109756 ref XP_002315301.1	296	chorismate synthase [Populus trichocarpa]
142	Unigene0030475	154	63199	16.8	6	gi 233955399 gb ACQ91203.1	762	calreticulin [Carica papaya]
143	Unigene0005909	153	129658	4.5	3	gi 508701576 gb EOX93472.1	1640	Vacuolar protein sorting 11 isoform 1 [Theobroma cacao]
144	Unigene0047967	151	41949	11.8	3	gi 508703238 gb EOX95134.1	472	Alpha/beta-Hydrolases superfamily protein [Theobroma cacao]
145	Unigene0021808	149	24762	14.1	2	gi 225452574 ref XP_002280727.1	278	PREDICTED: protein CREG1 [Vitis vinifera]
146	Unigene0013143	148	48744	14.1	3	gi 502113400 ref XP_004494638.1	639	PREDICTED: GDSL esterase/lipase At1g54790-like isoform X2 [Cicer arietinum]
147	Unigene0001432	145	24388	23.8	4	gi 353441154 gb AEQ94161.1	366	ADP-ribosylation factor [Elaeis guineensis]
148	Unigene0026949	145	38838	9.2	2	gi 508728262 gb EOY20159.1	545	Melibiase family protein isoform 1 [Theobroma cacao]
149	Unigene0010955	143	19175	17.6	2	gi 357511863 ref XP_003626220.1	219	60S ribosomal protein L22-like protein [Medicago truncatula]
150	Unigene0052889	143	93788	5	3	gi 470142472 ref XP_004306931.1	1303	PREDICTED: transketolase, chloroplastic-like [Fragaria vesca subsp. vesca]
151	Unigene0012648	142	99958	6.7	4	gi 359483630 ref XP_002270051.2	922	PREDICTED: beta-amylin synthase [Vitis vinifera]
152	Unigene0059780	142	35186	11.7	2	gi 224140038 ref XP_002323394.1	447	2-cys peroxiredoxin [Populus trichocarpa]
153	Unigene0000676	141	25672	26	4	gi 353441196 gb AEQ94182.1	359	ketol-acid reductoisomerase [Elaeis guineensis]
154	Unigene0027240	141	27640	19	3	gi 508781876 gb EOY29132.1	442	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein isoform 1 [Theobroma cacao]
155	Unigene0013852	141	45371	8.6	2	gi 115463661 ref NP_001055430.1	470	Os05g0388600 [Oryza sativa Japonica Group]
156	Unigene0053540	140	46318	9	3	gi 224054174 ref XP_002298128.1	314	2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]
157	Unigene0060991	137	62755	8.2	2	gi 317106652 dbj BAJ53156.1	885	JHL1011.2 [Jatropha curcas]
158	Unigene0027985	136	61687	11.6	4	gi 15238151 ref NP_198982.1	887	6-phosphogluconate dehydrogenase, decarboxylating 2 [Arabidopsis thaliana]
159	Unigene0043366	135	18570	15.5	2	gi 380085075 gb AFD34188.1	285	Cu/Zn superoxide dismutase [Jatropha curcas]
160	Unigene0030912	133	13488	18.9	2	gi 2674201 gb AAC61786.1	270	glycine-rich RNA-binding protein [Euphorbia esula]
161	Unigene0014173	132	55001	6.6	3	gi 508717505 gb EOY09402.1	734	Pectin lyase-like superfamily protein [Theobroma cacao]
162	Unigene0004642	131	123186	3.1	2	gi 359483029 ref XP_002272000.2	1306	PREDICTED: hypoxia up-regulated protein 1 [Vitis vinifera]
163	Unigene0053536	131	40340	14	4	gi 224054174 ref XP_002298128.1	275	2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]
164	Unigene0021850	127	30510	13.3	3	gi 222424744 dbj BAH20325.1	428	AT1G02305 [Arabidopsis thaliana]
165	Unigene0013851	126	36517	24.2	4	gi 508777909 gb EOY25165.1	439	Syntaxin/t-SNARE family protein [Theobroma cacao]

166	Unigene0057759	126	46960	12.7	3	gi 2246458 gb AAB62812.1	638	S-adenosyl-methionine-sterol-C- methyltransferase [<i>Ricinus communis</i>]
167	Unigene0030697	125	30095	12.8	2	gi 225435249 ref XP_002284989.1	439	PREDICTED: proteasome subunit beta type-4 isoform 1 [<i>Vitis vinifera</i>]
168	Unigene0045329	124	12269	34.4	3	gi 508780794 gb EOY28050.1	99.8	Alpha/beta-Hydrolases superfamily protein [<i>Theobroma cacao</i>]
169	Unigene0005132	123	30111	8	2	gi 15226103 ref NP_180896.1	349	calcosin 3 [<i>Arabidopsis thaliana</i>]
170	Unigene0009131	123	20042	21.1	2	gi 7595792 gb AAF64451.1 AF23992_9_1	281	late-embryogenesis abundant protein [<i>Euphorbia esula</i>]
171	Unigene0005009	122	114314	6.7	5	gi 508775953 gb EOY23209.1	1443	Tripeptidyl peptidase ii [<i>Theobroma cacao</i>]
172	Unigene0027060	121	21710	16.5	2	gi 508702494 gb EOX94390.1	244	Ribosomal protein L14 [<i>Theobroma cacao</i>]
173	Unigene0029486	120	47735	7	2	gi 508786903 gb EOY34159.1	600	RmC-like cupins superfamily protein [<i>Theobroma cacao</i>]
174	Unigene0046877	120	9544	38.1	2	gi 15237236 ref NP_197101.1	63.9	stress-induced protein KIN2 [<i>Arabidopsis thaliana</i>]
175	Unigene0004065	119	78229	4.4	2	gi 359473657 ref XP_002271846.2	1048	PREDICTED: delta(24)-sterol reductase-like [<i>Vitis vinifera</i>]
176	Unigene0029519	119	53612	11.7	3	gi 508703328 gb EOX95224.1	629	Thioredoxin family protein [<i>Theobroma cacao</i>]
177	Unigene0029771	118	53076	6.2	2	gi 449451048 ref XP_004143274.1	766	PREDICTED: S-adenosylmethionine synthase 2-like [<i>Cucumis sativus</i>]
178	Unigene0017186	118	21125	16.8	2	gi 225458649 ref XP_002282833.1	238	PREDICTED: subtilisin-like protease [<i>Vitis vinifera</i>]
179	Unigene0027399	118	26421	19.9	3	gi 23452339 gb AAN33000.1	431	alpha-tubulin 4, partial [<i>Gossypium hirsutum</i>]
180	Unigene0004719	117	52602	5.7	2	gi 31710660 dbj BAJ53113.1	599	JHL07K02.3 [<i>Jatropha curcas</i>]
181	Unigene0021743	117	35678	13.8	2	gi 470117268 ref XP_004294783.1	328	PREDICTED: gamma-interferon-inducible lysosomal thiol reductase-like isoform 1 [<i>Fragaria vesca</i> subsp. <i>vesca</i>]
182	Unigene0015233	115	60658	5.1	2	gi 224102795 ref XP_002312804.1	843	cholesterol transport protein [<i>Populus trichocarpa</i>]
183	Unigene0009490	115	11320	26.6	2	gi 125503270 gb ABN45748.1	135	lipase [<i>Jatropha curcas</i>]
184	Unigene0018434	114	49492	7.1	2	gi 224126143 ref XP_002319765.1	350	hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [<i>Populus trichocarpa</i>]
185	Unigene0015105	114	53995	5.8	2	gi 508718007 gb EOY09904.1	637	Cystathionine beta-synthase family protein isoform 1 [<i>Theobroma cacao</i>]
186	Unigene0044626	113	38857	13.6	3	gi 470144999 ref XP_004308132.1	291	PREDICTED: carboxylesterase 1-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]
187	Unigene0052547	113	25710	12.8	2	gi 356543128 ref XP_003540015.1	348	PREDICTED: 60S ribosomal protein L11-like [<i>Glycine max</i>]
188	gi 223544857 gb EEF46372.1	112	16510	24.2	2	gi 508779700 gb EOY26956.1	242	Profilin 5 [<i>Theobroma cacao</i>]
189	Unigene0050840	112	29228	28.7	5	gi 502121024 ref XP_004497162.1	459	PREDICTED: proteasome subunit alpha type-5-like isoform X1 [<i>Cicer arietinum</i>]
190	Unigene0056317	112	76298	10.2	4	gi 508713472 gb EOY05369.1	1023	Dehydratase family isoform 1 [<i>Theobroma cacao</i>]
191	Unigene0035138	112	19996	25.4	3	gi 225469328 ref XP_002271056.1	245	PREDICTED: FK506-binding protein 2-1 [<i>Vitis vinifera</i>]
192	Unigene0003163	111	121234	7.2	4	gi 356553371 ref XP_003545030.1	1405	PREDICTED: endoplasmic homolog [<i>Glycine max</i>]
193	Unigene0060419	110	81426	5.1	3	gi 508709858 gb EOY01755.1	997	Purple acid phosphatases superfamily protein [<i>Theobroma cacao</i>]
194	Unigene0004160	110	48761	9.9	3	gi 508711023 gb EOY02920.1	678	Vacuolar ATP synthase subunit C (VATC) / V-ATPase C subunit / vacuolar proton pump C subunit (DET3) [<i>Theobroma cacao</i>]
195	Unigene0005700	109	40496	11.2	2	gi 508708933 gb EOY00830.1	506	NAD(P)-binding Rossmann-fold superfamily protein isoform 1 [<i>Theobroma cacao</i>]
196	Unigene0019910	108	19963	19.3	2	gi 225432542 ref XP_002277699.1	255	PREDICTED: basic 7S globulin-like [<i>Vitis vinifera</i>]
197	Unigene0045992	107	19090	26.5	3	gi 470116805 ref XP_004294566.1	210	PREDICTED: outer envelope pore protein 16, chloroplastic-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]
198	Unigene0027293	105	17011	18.5	2	gi 508709070 gb EOY00967.1	191	Serine carboxypeptidase-like 50 [<i>Theobroma cacao</i>]
199	Unigene0027362	103	18296	21.3	2	gi 224131686 ref XP_002328083.1	280	vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroylglutamate-homocysteine [<i>Populus trichocarpa</i>]
200	Unigene0001132	103	28455	8.4	2	gi 508727355 gb EOY19252.1	363	ACT domain-containing protein isoform 1 [<i>Theobroma cacao</i>]
201	Unigene0043668	103	35219	18.7	3	gi 356566130 ref XP_003551288.1	234	PREDICTED: REF/SRPP-like protein At1g67360-like isoform 1 [<i>Glycine max</i>]
202	Unigene0008750	103	28705	15.7	2	gi 356526807 ref XP_003532008.1	415	PREDICTED: proteasome subunit beta type-1-like [<i>Glycine max</i>]

203	Unigene004236	103	105686	4.6	2	gi 281494540 gb ADA72022.1	1549	phospholipase D [<i>Jatropha curcas</i>]
204	Unigene0005939	102	49871	11.8	4	gi 359485106 ref XP_002268471.2	556	PREDICTED: LOW QUALITY PROTEIN: villin-4 [<i>Vitis vinifera</i>]
205	Unigene0000678	102	40652	12.4	3	gi 62321216 dbj BAD94384.1	620	ketol-acid reductoisomerase [<i>Arabidopsis thaliana</i>]
206	Unigene0055590	101	76827	6.4	3	gi 40233152 gb AAR83345.1	1042	cytosolic phosphoglucomutase [<i>Populus tomentosa</i>]
207	Unigene0005077	101	23881	13	2	gi 225434935 ref XP_002283671.1	339	PREDICTED: triosephosphate isomerase, cytosolic isoform 1 [<i>Vitis vinifera</i>]
208	Unigene0008729	101	15350	24.4	2	gi 470133092 ref XP_004302408.1	203	PREDICTED: EG45-like domain containing protein-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]
209	Unigene0026930	100	60753	13.6	5	gi 470124402 ref XP_004298203.1	682	PREDICTED: beta-galactosidase 9-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]
210	Unigene0050639	99	62590	4.4	2	gi 508701346 gb EOX93242.1	758	Aspartic protease isoform 2 [<i>Theobroma cacao</i>]
211	Unigene0051791	98	43828	5.6	2	gi 359496625 ref XP_002263670.2	628	PREDICTED: malate dehydrogenase, glyoxysomal [<i>Vitis vinifera</i>]
212	Unigene0052300	98	57838	9.7	3	gi 359480238 ref XP_002273855.2	781	PREDICTED: probable polygalacturonase-like [<i>Vitis vinifera</i>]
213	Unigene0042801	98	43288	9.3	2	gi 508727703 gb EOY19600.1	548	Alpha/beta-Hydrolases superfamily protein [<i>Theobroma cacao</i>]
214	Unigene0004676	98	107651	5.9	3	gi 508719437 gb EOY11334.1	1360	Mannosylglycoprotein endo-beta-mannosidase isoform 4 [<i>Theobroma cacao</i>]
215	Unigene0014174	97	33796	13.5	3	gi 302122826 gb ADK93079.1	442	14-3-3f protein [<i>Gossypium hirsutum</i>]
216	Unigene0035418	96	15566	39.1	3	gi 284433762 gb ADB85087.1	180	vacuolar ATP synthase subunit G1 [<i>Jatropha curcas</i>]
217	Unigene0034098	96	59989	10.1	3	gi 356536997 ref XP_003537018.1	308	PREDICTED: vinorine synthase-like [<i>Glycine max</i>]
218	Unigene0005602	95	65739	5.7	2	gi 508775190 gb EOY22446.1	810	Arginosuccinate synthase family isoform 1 [<i>Theobroma cacao</i>]
219	Unigene0013392	94	27916	12.4	2	gi 297843056 ref XP_002889409.1	377	Os01g0254000 [<i>Arabidopsis lyrata</i> subsp. <i>lyrata</i>]
220	Unigene0035573	94	80999	5.3	3	gi 449516754 ref XP_004165411.1	755	PREDICTED: peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A-like [<i>Cucumis sativus</i>]
221	Unigene0005892	93	58167	5.6	2	gi 225460716 ref XP_002271286.1	706	PREDICTED: dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial-like isoform 1 [<i>Vitis vinifera</i>]
222	Unigene0042834	93	42464	11.5	3	gi 225427017 ref XP_002271251.1	584	PREDICTED: L-lactate dehydrogenase A [<i>Vitis vinifera</i>]
223	Unigene0003775	93	128741	4.3	3	gi 149789409 gb ABR29876.1	1828	phosphoenolpyruvate carboxylase [<i>Ricinus communis</i>]
224	Unigene0011325	93	39027	10.2	2	gi 16417950 gb AAL18927.1 AF429386_1	527	mevalonate diphosphate decarboxylase [<i>Hevea brasiliensis</i>]
225	Unigene0023873	92	156338	2.5	2	gi 508706004 gb EOX97900.1	2215	Coatomer, alpha subunit [<i>Theobroma cacao</i>]
226	Unigene0000165	92	62135	10.2	3	gi 508718277 gb EOY10174.1	815	Vacuolar ATP synthase subunit H family protein isoform 2 [<i>Theobroma cacao</i>]
227	Unigene0011398	90	58744	5.5	2	gi 255557353 ref XP_002519707.1	862	50 kDa ketoacyl-ACP synthase [<i>Ricinus communis</i>]
228	Unigene0044470	90	34654	12	2	gi 115485231 ref NP_001067759.1	452	Os11g0312400 [<i>Oryza sativa Japonica</i> Group]
229	Unigene0056117	89	131739	4	3	gi 508717326 gb EOY09223.1	1555	Villin 2 isoform 1 [<i>Theobroma cacao</i>]
230	Unigene0005800	89	55727	6.5	2	gi 443908533 gb AGD80034.1	897	alpha-tubulin 1 [<i>Hevea brasiliensis</i>]
231	Unigene0010814	89	33427	13.3	3	gi 225428005 ref XP_002278162.1	460	PREDICTED: proteasome subunit alpha type-7 [<i>Vitis vinifera</i>]
232	Unigene0057666	89	44764	11.4	3	gi 508715071 gb EOY06968.1	514	Late embryogenesis abundant protein, group 2 isoform 1 [<i>Theobroma cacao</i>]
233	Unigene0054565	87	37376	9	2	gi 317106718 dbj BAJ53216.1	311	JHL22C18.7 [<i>Jatropha curcas</i>]
234	Unigene0034113	87	59653	5.6	2	gi 470113403 ref XP_004292913.1	275	PREDICTED: vinorine synthase-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]
235	Unigene0005542	87	49507	8.2	3	gi 508707562 gb EOX99458.1	660	ADP/ATP carrier 3 isoform 1 [<i>Theobroma cacao</i>]
236	Unigene0029325	86	76893	6.8	3	gi 508782453 gb EOY29709.1	817	D-arabinono-1,4-lactone oxidase family protein [<i>Theobroma cacao</i>]
237	Unigene0013158	84	59821	8.7	3	gi 359493457 ref XP_002278756.2	701	PREDICTED: elongation factor 1-gamma-like [<i>Vitis vinifera</i>]
238	Unigene0000984	83	20359	22.5	3	gi 508700251 gb EOX92147.1	251	Lipase/lipoxygenase, PLAT/LH2 family protein [<i>Theobroma cacao</i>]
239	Unigene0009761	83	26142	9	2	gi 225425910 ref XP_002267080.1	129	PREDICTED: vinorine synthase-like [<i>Vitis vinifera</i>]
240	Unigene0003443	82	67997	5.6	2	gi 225457293 ref XP_002284470.1	808	PREDICTED: heparanase-like protein 1-like [<i>Vitis vinifera</i>]
241	Unigene0022620	82	28611	12.8	2	gi 502117080 ref XP_004495692.1	350	PREDICTED: 60S ribosomal protein L18-like [<i>Cicer arietinum</i>]
242	Unigene0005375	80	107048	2.9	2	gi 508706009 gb EOX97905.1	1367	Vacuolar proton ATPase A3 isoform 1 [<i>Theobroma cacao</i>]
243	gi 25538698 ref	80	34289	8.5	2	gi 508722909 gb EOY14806.1	513	20S proteasome alpha subunit F2 [<i>Theobroma cacao</i>]

	XP_002510414.1								
244	Unigene0004679	80	58967	5.8	2	gi 356501255 ref XP_003519441.1	761	PREDICTED: protein disulfide isomerase-like 2-3-like [Glycine max]	
245	Unigene0058305	79	106852	3.4	2	gi 449445987 ref XP_004140753.1	1334	PREDICTED: heat shock protein 83-like [Cucumis sativus]	
246	Unigene0017945	78	9811	31.1	2	gi 84579373 dbj BAE72075.1	126	pear beta-galactosidase3 [Pyrus communis]	
247	Unigene0055634	77	28948	16.7	3	gi 299150759 gb ADJ17723.1	360	beta-hydroxyacyl-acyl carrier protein dehydratase [Hevea brasiliensis]	
248	Unigene0004362	77	46195	9	2	gi 508777788 gb EOY25044.1	603	UDP-D-glucose/UDP-D-galactose 4-epimerase 5 isoform 1 [Theobroma cacao]	
249	Unigene0004983	76	113356	4.2	2	gi 359482944 ref XP_002279789.2	1409	PREDICTED: 97 kDa heat shock protein-like [Vitis vinifera]	
250	Unigene0014196	75	48466	7.5	2	gi 224138226 ref XP_002322761.1	605	cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa]	
251	Unigene0036834	75	21621	14.7	2	gi 359483381 ref XP_002264678.2	226	PREDICTED: beta-glucosidase 46-like [Vitis vinifera]	
252	Unigene0059074	75	66115	4.9	2	gi 508698918 gb EOX90814.1	639	Senescence/dehydration-associated protein-related isoform 3 [Theobroma cacao]	
253	Unigene0001419	75	27333	11.3	2	gi 77744871 gb ABB02389.1	343	temperature-induced lipocalin [Populus balsamifera]	
254	gi 643724340 gb KDP33541.1	74	60380	5.2	2	gi 225430398 ref XP_002285385.1	852	PREDICTED: aspartate aminotransferase, chloroplastic [Vitis vinifera]	
255	Unigene0004548	74	27968	12.1	2	gi 460367695 ref XP_004229706.1	379	PREDICTED: ras-related protein RABH1b-like [Solanum lycopersicum]	
256	Unigene0034192	73	46948	5.9	2	gi 470115755 ref XP_004294057.1	540	PREDICTED: serine carboxypeptidase-like 51-like [Fragaria vesca subsp. vesca]	
257	Unigene0029904	73	13050	25	2	gi 224120292 ref XP_002331012.1	53.5	predicted protein [Populus trichocarpa]	
258	Unigene0058966	72	45141	8.2	2	gi 508782995 gb EOY30251.1	605	Cysteine proteinases superfamily protein [Theobroma cacao]	
259	Unigene0001009	72	28397	12.6	2	gi 508786465 gb EOY33721.1	383	Cyclophilin 5 [Theobroma cacao]	
260	Unigene0029773	72	35431	10.9	2	gi 470137636 ref XP_004304569.1	436	PREDICTED: cytochrome b-c1 complex subunit Rieske-2, mitochondrial-like [Fragaria vesca subsp. vesca]	
261	Unigene0021939	70	37822	8.4	2	gi 225446740 ref XP_002282632.1	451	PREDICTED: V-type proton ATPase subunit D isoform 1 [Vitis vinifera]	
262	Unigene0035177	70	27076	11.8	2	gi 313586553 gb ADR71287.1	374	40S ribosomal protein S5B [Hevea brasiliensis]	
263	Unigene0016294	70	16105	28.1	3	gi 470135226 ref XP_004303424.1	223	PREDICTED: ubiquitin-NEDD8-like protein RUB2-like isoform 2 [Fragaria vesca subsp. vesca]	
264	Unigene0001669	70	13615	21.7	2	gi 284433772 gb ADB85092.1	170	acyl-CoA-binding protein [Jatropha curcas]	
265	Unigene0028097	68	19714	16	2	gi 225440827 ref XP_002282061.1	289	PREDICTED: 40S ribosomal protein S14-like [Vitis vinifera]	
266	Unigene0043697	68	37548	14.7	3	gi 449463779 ref XP_004149609.1	401	PREDICTED: 60S ribosomal protein L6-like [Cucumis sativus]	
267	Unigene0053837	67	55767	7	2	gi 224127758 ref XP_002329170.1	724	acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]	
268	Unigene0000921	67	58592	9.4	3	gi 225432520 ref XP_002280174.1	670	PREDICTED: DUF21 domain-containing protein At4g14240 [Vitis vinifera]	
269	Unigene0042322	66	62264	5.3	2	gi 320148078 emb CBJ20740.1	927	ATPase subunit 1 [Beta vulgaris subsp. maritima]	
270	Unigene0050396	66	22155	20.3	3	gi 386870487 gb AFJ42574.1	265	ubiquitin extension protein 5 [Sesamum indicum]	
271	Unigene0052255	65	108482	2.9	2	gi 468181080 gb AGH29112.1	1542	sucrose synthase [Jatropha curcas]	
272	Unigene0045040	64	51746	7.1	2	gi 408689044 gb AFU81122.1	663	phospholipase C3 [Populus tomentosa]	
273	Unigene0013095	63	45570	6.7	2	gi 209573263 gb ACI62779.1	557	lipase [Jatropha curcas]	
274	Unigene0029603	62	53197	8	3	gi 449458151 ref XP_004146811.1	799	PREDICTED: eukaryotic initiation factor 4A-8-like [Cucumis sativus]	
275	Unigene0043927	62	31654	16.7	3	gi 356554233 ref XP_003545453.1	370	PREDICTED: elongation factor 1-beta 1-like [Glycine max]	
276	Unigene0011128	62	52522	7	2	gi 470114303 ref XP_004293355.1	730	PREDICTED: fumarylacetoacetase-like [Fragaria vesca subsp. vesca]	
277	Unigene0001537	62	59590	4.8	2	gi 18700101 gb AAL77662.1	655	AT5g65760/MPA24_11 [Arabidopsis thaliana]	
278	Unigene0030496	62	20240	29.5	3	gi 15229784 ref NP_189967.1	298	calmodulin 7 [Arabidopsis thaliana]	
279	Unigene0014279	61	42492	8.8	3	gi 225456177 ref XP_002282634.1	573	PREDICTED: aldose 1-epimerase [Vitis vinifera]	
280	Unigene0004496	61	53716	7.1	2	gi 255582193 ref XP_002531889.1	759	Stearoy-ACP desaturase [Ricinus communis]	
281	Unigene0027294	61	41228	7.4	2	gi 470122682 ref XP_004297368.1	421	PREDICTED: serine carboxypeptidase-like 50-like [Fragaria vesca subsp. vesca]	
282	Unigene0029781	61	16274	14.9	2	gi 359497288 ref XP_002263566.2	223	PREDICTED: 70 kDa peptidyl-prolyl isomerase [Vitis vinifera]	
283	Unigene0053109	60	55636	6.4	2	gi 357499179 ref XP_003619878.1	710	Dihydropyrimidine dehydrogenase [Medicago truncatula]	

284	Unigene0031319	59	48552	7.9	2	gj 224808192 gb ACN63187.1	671	farnesyl diphosphate synthase [Euphorbia pekinensis]
285	Unigene0053811	59	62201	6.1	2	gj 356557879 ref XP_003547237.1	754	PREDICTED: DUF21 domain-containing protein At4g14240-like [Glycine max]
286	Unigene0043228	58	42434	8.1	2	gj 225427786 ref XP_002269232.1	576	PREDICTED: NADP-dependent D-sorbitol-6-phosphate dehydrogenase [Vitis vinifera]
287	Unigene0001191	58	29222	16.5	2	gj 307135913 gb ADN33776.1	359	60S ribosomal protein l9 [Cucumis melo subsp. melo]
288	Unigene0039731	58	16391	19.1	2	gj 356505054 ref XP_003521307.1	171	PREDICTED: acid phosphatase 1-like [Glycine max]
289	Unigene0017946	58	38613	7.7	2	gj 525327295 gb AGR44461.1	539	beta-D-galactosidase 2 [Pyrus x bretschneideri]
290	Unigene0024454	56	113121	3.2	2	gj 357451779 ref XP_003596166.1	1623	Elongation factor EF-2 [Medicago truncatula]
291	Unigene0039507	54	20268	18.4	2	gj 470147282 ref XP_004309244.1	162	PREDICTED: carboxylesterase 1-like [Fragaria vesca subsp. vesca]
292	Unigene0059734	54	134627	4.5	3	gj 225430766 ref XP_002267514.1	1634	PREDICTED: vam6/Vps39-like protein [Vitis vinifera]
293	Unigene0003013	54	93492	4.6	2	gj 508702517 gb EOX94413.1	957	Ribophorin II (RPN2) family protein isoform 2 [Theobroma cacao]
294	Unigene0043995	54	54551	7.2	3	gj 508704803 gb EOX96699.1	677	ADP/ATP carrier 2 [Theobroma cacao]
295	Unigene0052669	54	62335	4.2	2	gj 508783589 gb EOY30845.1	836	Leucine-rich repeat family protein [Theobroma cacao]
296	Unigene0053013	52	21030	15.8	2	gj 470145306 ref XP_004308282.1	233	PREDICTED: L-gulonol-1,4-lactone dehydrogenase-like [Fragaria vesca subsp. vesca]
297	Unigene0004438	52	223605	1.7	2	gj 359488807 ref XP_002272790.2	2222	PREDICTED: nuclear pore membrane glycoprotein 210-like [Vitis vinifera]
298	Unigene0061824	52	65315	4.6	2	gj 508714164 gb EOY06061.1	943	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein isoform 1 [Theobroma cacao]
299	Unigene0004547	51	28144	12.1	2	gj 508700212 gb EOX92108.1	396	RAB GTPase H1E isoform 1 [Theobroma cacao]
300	Unigene0013600	50	61727	7.8	3	gj 508783218 gb EOY30474.1	810	Alkaline-phosphatase-like family protein isoform 1 [Theobroma cacao]
301	Unigene0052341	49	96319	4.3	4	gj 508699547 gb EOX91443.1	925	Subtilisin-like serine endopeptidase family protein [Theobroma cacao]
302	Unigene0042140	48	29263	11.6	2	gj 470113403 ref XP_004292913.1	154	PREDICTED: vinorine synthase-like [Fragaria vesca subsp. vesca]
303	Unigene0029617	48	75718	4.2	2	gj 356508007 ref XP_003522754.1	1038	PREDICTED: glucose-6-phosphate isomerase-like [Glycine max]
304	Unigene0043038	47	18689	14.2	2	gj 226498210 ref NP_001152622.1	207	LOC100286263 [Zea mays]
305	Unigene0043785	47	28619	10.2	2	gj 508705109 gb EOX97005.1	397	RAB GTPase 11C [Theobroma cacao]
306	Unigene0053091	47	52938	4.9	2	gj 508722701 gb EOY14598.1	574	Serine protease inhibitor (SERPIN) family protein [Theobroma cacao]
307	Unigene0014379	47	19368	23.1	3	gj 449447418 ref XP_004141465.1	267	PREDICTED: 40S ribosomal protein S19-3-like [Cucumis sativus]
308	Unigene0005076	46	104993	2.3	2	gj 359475494 ref XP_002270199.2	1288	PREDICTED: alpha-L-fucosidase 2-like [Vitis vinifera]
309	Unigene0011730	45	26378	10.8	2	gj 508776965 gb EOY24221.1	378	Ras 5 [Theobroma cacao]
310	Unigene0059811	44	36698	7	2	gj 307566894 gb ADN52613.1	396	acetyl-CoA carboxylase BCCP subunit [Jatropha curcas]
311	Unigene0013491	44	67263	5.7	2	gj 357447035 ref XP_003593793.1	367	Seipin [Medicago truncatula]
312	Unigene0043247	44	21862	18.8	2	gj 449459332 ref XP_004147400.1	253	PREDICTED: 60S ribosomal protein L32-1-like [Cucumis sativus]
313	Unigene0005640	43	78013	4.1	2	gj 508713533 gb EOY05430.1	997	Heat shock protein 60 isoform 1 [Theobroma cacao]
314	Unigene0034612	43	46201	7.9	2	gj 470122736 ref XP_004297395.1	666	PREDICTED: ATP-citrate synthase alpha chain protein 1-like [Fragaria vesca subsp. vesca]
315	Unigene0058354	43	27330	12.8	2	gj 460412868 ref XP_004251818.1	422	PREDICTED: ras-related protein RABBIc-like [Solanum lycopersicum]
316	Unigene0000350	42	21158	11.1	2	gj 6984222 gb AAF34799.1 AF22797_9_1	291	40S ribosomal protein S16 [Euphorbia esula]
317	Unigene0031161	41	36363	8.4	2	gj 460391150 ref XP_004241186.1	608	PREDICTED: tubulin beta-1 chain-like [Solanum lycopersicum]
318	Unigene0027708	40	31120	12.2	2	gj 308191651 dbj BAJ22388.1	376	elongation factor 1 beta [Vigna unguiculata]
319	Unigene0020802	38	27423	6.7	2	gj 225436984 ref XP_002272235.1	311	PREDICTED: basic 7S globulin [Vitis vinifera]
320	Unigene0028318	36	46113	6.9	2	gj 508720533 gb EOY12430.1	686	Inositol-1,4,5-trisphosphate 5-phosphatase 4 isoform 1 [Theobroma cacao]
321	Unigene0023894	35	35915	6.9	2	gj 6752903 gb AAF27931.1 AF22280_5_1	510	14-3-3-like protein [Euphorbia esula]
322	Unigene0030295	34	39257	10.6	2	gj 502161040 ref XP_004511996.1	503	PREDICTED: 40S ribosomal protein S4-1-like [Cicer arietinum]

Table S2 The KEGG pathways of *Euphorbia kansui* latex proteins

Pathway	Count	Pathway ID
Metabolic pathways	92	ko01100
Biosynthesis of secondary metabolites	59	ko01110
Biosynthesis of antibiotics	48	ko01130
Microbial metabolism in diverse environments	37	ko01120
Carbon metabolism	31	ko01200
Biosynthesis of amino acids	28	ko01230
Glycolysis / Gluconeogenesis	23	ko00010
Carbon fixation in photosynthetic organisms	16	ko00710
Protein processing in endoplasmic reticulum	16	ko04141
Ribosome	14	ko03010
Phagosome	14	ko04145
Cysteine and methionine metabolism	13	ko00270
Pyruvate metabolism	12	ko00620
Oxidative phosphorylation	11	ko00190
Pentose phosphate pathway	9	ko00030
Starch and sucrose metabolism	9	ko00500
Citrate cycle (TCA cycle)	8	ko00020
Fructose and mannose metabolism	8	ko00051
Fatty acid metabolism	8	ko01212
Galactose metabolism	7	ko00052
Fatty acid biosynthesis	7	ko00061
Glyoxylate and dicarboxylate metabolism	6	ko00630
Proteasome	6	ko03050
Purine metabolism	5	ko00230
Amino sugar and nucleotide sugar metabolism	5	ko00520
Inositol phosphate metabolism	5	ko00562
Endocytosis	5	ko04144
Selenocompound metabolism	4	ko00450
Propanoate metabolism	4	ko00640
Pantothenate and CoA biosynthesis	4	ko00770
Biotin metabolism	4	ko00780
Terpenoid backbone biosynthesis	4	ko00900
2-Oxocarboxylic acid metabolism	4	ko01210
SNARE interactions in vesicular transport	4	ko04130
Peroxisome	4	ko04146
Plant-pathogen interaction	4	ko04626
Alanine, aspartate and glutamate metabolism	3	ko00250

Glycine, serine and threonine metabolism	3	ko00260
Valine, leucine and isoleucine biosynthesis	3	ko00290
Tyrosine metabolism	3	ko00350
Glutathione metabolism	3	ko00480
Other glycan degradation	3	ko00511
Phenylpropanoid biosynthesis	3	ko00940
RNA transport	3	ko03013
RNA degradation	3	ko03018
Spliceosome	3	ko03040
Pentose and glucuronate interconversions	2	ko00040
Steroid biosynthesis	2	ko00100
Arginine biosynthesis	2	ko00220
Pyrimidine metabolism	2	ko00240
Phenylalanine, tyrosine and tryptophan biosynthesis	2	ko00400
N-Glycan biosynthesis	2	ko00510
Glycerophospholipid metabolism	2	ko00564
Glycosphingolipid biosynthesis - globo series	2	ko00603
Porphyrin and chlorophyll metabolism	2	ko00860
Biosynthesis of unsaturated fatty acids	2	ko01040
Protein export	2	ko03060
Fatty acid elongation	1	ko00062
Valine, leucine and isoleucine degradation	1	ko00280
Lysine degradation	1	ko00310
Arginine and proline metabolism	1	ko00330
Phenylalanine metabolism	1	ko00360
Tryptophan metabolism	1	ko00380
beta-Alanine metabolism	1	ko00410
Cyanoamino acid metabolism	1	ko00460
Glycosaminoglycan degradation	1	ko00531
Glycerolipid metabolism	1	ko00561
Ether lipid metabolism	1	ko00565
Arachidonic acid metabolism	1	ko00590
alpha-Linolenic acid metabolism	1	ko00592
Sphingolipid metabolism	1	ko00600
Glycosphingolipid biosynthesis - ganglio series	1	ko00604
Butanoate metabolism	1	ko00650
Phosphatidylinositol signaling system	1	ko04070

Table S3 The differentially accumulated proteins of *Euphorbia kansui* latex

Laticifers at early stage VS laticifers at later stage (95 decreased proteins)								
Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	fold change
1	Unigene0005077	gj 225434935 ref XP_002283671.1	PREDICTED: triosephosphate isomerase, cytosolic isoform 1 [Vitis vinifera]	23881	13	101	3	2.501
2	Unigene0009131	gj 7595792 gb AAF64451.1 AF239929_1	late-embryogenesis abundant protein [Euphorbia esula]	20042	21.1	123	7	2.318
3	Unigene0027240	gj 508781876 gb EOY29132.1	N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein isoform 1 [Theobroma cacao]	27640	19	141	3	1.933
4	Unigene0043745	gj 326694865 gb AEA03663.1	14-3-3 protein 2 [Hevea brasiliensis]	35812	22	165	4	1.822
5	Unigene0029904	gj 224120292 ref XP_002331012.1	predicted protein [Populus trichocarpa]	13050	25	73	3	3.516
6	Unigene0005939	gj 359485106 ref XP_002268471.2	PREDICTED: LOW QUALITY PROTEIN: villin-4 [Vitis vinifera]	49871	11.8	102	6	2.039
7	Unigene0046877	gj 15237236 ref NP_197101.1	stress-induced protein KIN2 [Arabidopsis thaliana]	9544	38.1	120	4	1.896
8	Unigene0010534	gj 449434570 ref XP_004135069.1	PREDICTED: ATP synthase subunit beta, mitochondrial-like [Cucumis sativus]	68222	20.1	358	12	2.252
9	Unigene0051610	gj 460408038 ref XP_004249455.1	PREDICTED: fructose-bisphosphate aldolase cytoplasmic isozyme-like [Solanum lycopersicum]	47665	21.5	565	18	2.385
10	Unigene0008750	gj 356526807 ref XP_003532008.1	PREDICTED: proteasome subunit beta type-1-like [Glycine max]	28705	15.7	103	4	2.236
11	Unigene0013851	gj 508777909 gb EOY25165.1	Syntaxin/t-SNARE family protein [Theobroma cacao]	36517	24.2	126	5	1.638
12	Unigene0029771	gj 449451048 ref XP_004143274.1	PREDICTED: S-adenosylmethionine synthase 2-like [Cucumis sativus]	53076	6.2	118	4	2.124
13	Unigene0053013	gj 470145306 ref XP_004308282.1	PREDICTED: L-gulonono-1,4-lactone dehydrogenase-like [Fragaria vesca subsp. vesca]	21030	15.8	52	2	5.234
14	Unigene0035138	gj 225469328 ref XP_002271056.1	PREDICTED: FK506-binding protein 2-1 [Vitis vinifera]	19996	25.4	112	5	2.213
15	Unigene0001669	gj 284433772 gb ADB85092.1	acyl-CoA-binding protein [Jatropha curcas]	13615	21.7	70	5	2.795
16	Unigene0001613	gj 359483362 ref XP_002273346.2	PREDICTED: lactoylglutathione lyase [Vitis vinifera]	39814	27.1	186	7	1.882
17	Unigene0004204	gj 392465167 dbj BAM24707.1	Heat shock protein 70 [Nicotiana tabacum]	87744	21.9	478	4	1.583
18	Unigene0052084	gj 470136808 ref XP_004304174.1	PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating 3-like [Fragaria vesca subsp. vesca]	65523	17.5	258	6	2.316
19	Unigene0001009	gj 508786465 gb EOY33721.1	Cyclophilin 5 [Theobroma cacao]	28397	12.6	72	4	2.758
20	Unigene0053361	gj 508725757 gb EOY17654.1	Biotin/lipoyl attachment domain-containing protein isoform 1 [Theobroma cacao]	29668	23.6	287	7	1.726
21	Unigene0010955	gj 357511863 ref XP_003626220.1	60S ribosomal protein L22-like protein [Medicago truncatula]	19175	17.6	143	2	1.963
22	Unigene0009061	gj 284433792 gb ADB85102.1	nucleoside diphosphate kinase B [Jatropha curcas]	19619	23	188	8	1.605
23	Unigene0052520	gj 255557893 ref XP_002519975.1	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Ricinus communis]	72889	10.7	199	6	2.038
24	Unigene0043697	gj 449463779 ref XP_004149609.1	PREDICTED: 60S ribosomal protein L6-like [Cucumis sativus]	37548	14.7	68	3	2.968
25	Unigene0042714	gj 164604982 dbj BAF98287.1	isopentenyl-diphosphate Delta-isomerase [Hevea brasiliensis]	31883	30.2	218	9	2.341
26	Unigene0034192	gj 470115755 ref XP_004294057.1	PREDICTED: serine carboxypeptidase-like 51-like [Fragaria vesca subsp. vesca]	46948	5.9	73	3	2.162
27	Unigene0054117	gj 209981339 gb ACJ05350.1	actin [Camellia sinensis]	23063	38.2	540	4	2.873
28	Unigene0003163	gj 356553371 ref XP_003545030.1	PREDICTED: endoplasmic homolog [Glycine max]	121234	7.2	111	4	2.272

29	Unigene0042801	gj 508727703 gb EOY19600.1	Alpha/beta-Hydrolases superfamily protein [Theobroma cacao]	43288	9.3	98	3	4.422
30	gj 223544857 gb EEF46372.1	gj 508779700 gb EOY26956.1	Profilin 5 [Theobroma cacao]	16510	24.2	112	3	2.331
31	Unigene0027363	gj 224131686 ref XP_002328083.1	vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltriglutamate-homocysteine [Populus trichocarpa]	72014	17.6	175	6	2.203
32	Unigene0031319	gj 224808192 gb ACN63187.1	farnesyl diphosphate synthase [Euphorbia pekinensis]	48552	7.9	59	2	2.127
33	Unigene0014552	gj 198400319 gb ACH87168.1	senescence-related protein [Camellia sinensis]	49122	23.5	453	11	2.457
34	Unigene0005700	gj 508708933 gb EOY00830.1	NAD(P)-binding Rossmann-fold superfamily protein isoform 1 [Theobroma cacao]	40496	11.2	109	3	1.638
35	Unigene0001191	gj 307135913 gb ADN33776.1	60S ribosomal protein 19 [Cucumis melo subsp. melo]	29222	16.5	58	2	2.032
36	Unigene0044626	gj 470144999 ref XP_004308132.1	PREDICTED: carboxylesterase 1-like [Fragaria vesca subsp. vesca]	38857	13.6	113	3	2.397
37	Unigene0001432	gj 353441154 gb AEQ94161.1	ADP-ribosylation factor [Elaeis guineensis]	24388	23.8	145	8	2.499
38	Unigene0058341	gj 225431914 ref XP_002276853.1	PREDICTED: dihydrolipoyl dehydrogenase [Vitis vinifera]	70750	13.9	240	7	1.503
39	Unigene0059717	gj 508726787 gb EOY18684.1	Adenosine kinase 2 [Theobroma cacao]	46641	12.6	230	7	2.498
40	Unigene0053012	gj 470145304 ref XP_004308281.1	PREDICTED: L-gulonolactone oxidase-like [Fragaria vesca subsp. vesca]	56621	20.2	369	10	4.407
41	Unigene0013600	gj 508783218 gb EOY30474.1	Alkaline-phosphatase-like family protein isoform 1 [Theobroma cacao]	61727	7.8	50	3	1.788
42	Unigene0030475	gj 233955399 gb ACQ91203.1	calreticulin [Carica papaya]	63199	16.8	154	14	4.032
43	Unigene0051306	gj 359807257 ref NP_001241368.1	annexin D4-like [Glycine max]	44010	55.9	1003	41	1.984
44	Unigene0009761	gj 225425910 ref XP_002267080.1	PREDICTED: vinorine synthase-like [Vitis vinifera]	26142	9	83	3	1.575
45	Unigene0058320	gj 151347486 gb ABS01352.1	methionine synthase [Carica papaya]	102739	15.4	438	7	2.645
46	Unigene0029519	gj 508703328 gb EOX95224.1	Thioredoxin family protein [Theobroma cacao]	53612	11.7	119	3	3.715
47	Unigene0039388	gj 225443421 ref XP_002267740.1	PREDICTED: subtilisin-like protease [Vitis vinifera]	10540	37.1	196	7	2.353
48	Unigene0028057	gj 508705865 gb EOX97761.1	Triosephosphate isomerase isoform 2 [Theobroma cacao]	38737	9.7	198	5	1.503
49	Unigene0014554	gj 351722359 ref NP_001238009.1	protein disulfide isomerase-like protein precursor [Glycine max]	70540	20.5	299	14	3.622
50	Unigene0054052	gj 429326634 gb AFZ78657.1	S-adenosyl-L-homocysteine hydrolase [Populus tomentosa]	63611	14.2	189	7	2.333
51	Unigene0030496	gj 15229784 ref NP_189967.1	calmodulin 7 [Arabidopsis thaliana]	20240	29.5	62	4	2.123
52	Unigene0000678	gj 62321216 dbj BAD94384.1	ketol-acid reductoisomerase [Arabidopsis thaliana]	40652	12.4	102	4	1.615
53	Unigene0013179	gj 51703306 gb AAR84410.2	glyceraldehyde 3-phosphate dehydrogenase [Daucus carota]	46113	43.6	1189	22	2.71
54	Unigene0012648	gj 359483630 ref XP_002270051.2	PREDICTED: beta-amyrin synthase [Vitis vinifera]	99958	6.7	142	5	1.773
55	Unigene0052255	gj 468181080 gb AGH29112.1	sucrose synthase [Jatropha curcas]	108482	2.9	65	2	2.462
56	Unigene0029603	gj 449458151 ref XP_004146811.1	PREDICTED: eukaryotic initiation factor 4A-8-like [Cucumis sativus]	53197	8	62	3	1.946
57	Unigene0013158	gj 359493457 ref XP_002278756.2	PREDICTED: elongation factor 1-gamma-like [Vitis vinifera]	59821	8.7	84	4	1.625
58	Unigene0057759	gj 2246458 gb AAB62812.1	S-adenosyl-methionine-sterol-C-methyltransferase [Ricinus communis]	46960	12.7	126	4	2.09
59	Unigene0034098	gj 356536997 ref XP_003537018.1	PREDICTED: vinorine synthase-like [Glycine max]	59989	10.1	96	3	1.781
60	Unigene0060976	gj 508726275 gb EOY18172.1	Heat shock cognate protein 70-1 [Theobroma cacao]	87808	20	486	2	2.119
61	Unigene0030697	gj 225435249 ref XP_002284989.1	PREDICTED: proteasome subunit beta type-4 isoform 1 [Vitis vinifera]	30095	12.8	125	3	1.783
62	Unigene0044263	gj 508706840 gb EOX98736.1	General regulatory factor 2, OMEGA [Theobroma cacao]	35641	19.5	198	4	1.957

63	Unigene0005892	gj 225460716 ref XP_002271286.1	PREDICTED: dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial-like isoform 1 [<i>Vitis vinifera</i>]	58167	5.6	93	3	1.506
64	Unigene0030912	gj 267420 gb AAC61786.1	glycine-rich RNA-binding protein [<i>Euphorbia esula</i>]	13488	18.9	133	5	2.574
65	Unigene0043750	gj 225463105 ref XP_002264356.1	PREDICTED: ras-related protein Rab7 isoform 1 [<i>Vitis vinifera</i>]	28247	41	280	11	1.708
66	Unigene0042995	gj 356562585 ref XP_003549550.1	PREDICTED: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase-like [<i>Glycine max</i>]	65613	13.1	221	8	2.436
67	Unigene0011128	gj 470114303 ref XP_004293355.1	PREDICTED: fumarylacetoacetase-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]	52522	7	62	3	2.347
68	Unigene0020801	gj 225432542 ref XP_002277699.1	PREDICTED: basic 7S globulin-like [<i>Vitis vinifera</i>]	18803	21.2	160	3	2.562
69	Unigene0042612	gj 343481065 gb AEM44784.1	cyclophilin [<i>Momordica charantia</i>]	22370	39.8	239	9	1.731
70	Unigene0003120	gj 508720034 gb EOY11931.1	Heat shock protein 81.4 [<i>Theobroma cacao</i>]	105182	11.5	194	8	2.341
71	Unigene0000507	gj 289600010 gb ADD12953.1	2-phospho-D-glycerate hydrolase [<i>Citrus trifoliata</i>]	60126	21.6	437	11	2.15
72	Unigene0053585	gj 357439495 ref XP_003590025.1	Malate dehydrogenase [<i>Medicago truncatula</i>]	42289	21	268	7	2.353
73	Unigene0015240	gj 508712429 gb EOY04326.1	Glycosyl hydrolase family 81 protein [<i>Theobroma cacao</i>]	94310	12.6	273	10	1.561
74	Unigene0010814	gj 225428005 ref XP_002278162.1	PREDICTED: proteasome subunit alpha type-7 [<i>Vitis vinifera</i>]	33427	13.3	89	3	2.084
75	Unigene0025452	gj 288901047 gb ADC68236.1	elongation factor 1-alpha [<i>Dendrobium nobile</i>]	32446	31.9	340	9	2.241
76	Unigene0027438	gj 508715123 gb EOY07020.1	Glutathione peroxidase 2 [<i>Theobroma cacao</i>]	28454	42.6	171	8	2.267
77	Unigene0042834	gj 225427017 ref XP_002271251.1	PREDICTED: L-lactate dehydrogenase A [<i>Vitis vinifera</i>]	42464	11.5	93	4	1.821
78	Unigene0052143	gj 449443540 ref XP_004139535.1	PREDICTED: vesicle-fusing ATPase-like [<i>Cucumis sativus</i>]	96553	7.6	191	9	1.675
79	Unigene0035418	gj 284433762 gb ADB85087.1	vacuolar ATP synthase subunit G1 [<i>Jatropha curcas</i>]	15566	39.1	96	4	1.622
80	Unigene0023119	gj 313586509 gb ADR71265.1	60S ribosomal protein L12A [<i>Hevea brasiliensis</i>]	13964	29.8	179	4	2.573
81	Unigene0009490	gj 125503270 gb ABN45748.1	lipase [<i>Jatropha curcas</i>]	11320	26.6	115	4	1.835
82	Unigene0050840	gj 502121024 ref XP_004497162.1	PREDICTED: proteasome subunit alpha type-5-like isoform X1 [<i>Cicer arietinum</i>]	29228	28.7	112	5	1.796
83	Unigene0014279	gj 225456177 ref XP_002282634.1	PREDICTED: aldose 1-epimerase [<i>Vitis vinifera</i>]	42492	8.8	61	4	1.949
84	Unigene0030706	gj 508728076 gb EOY19973.1	Annexin [<i>Theobroma cacao</i>]	47337	16.8	202	11	2.073
85	Unigene0014772	gj 508714833 gb EOY06730.1	ATP citrate lyase subunit B 2 isoform 1 [<i>Theobroma cacao</i>]	77699	19.6	473	12	2.59
86	Unigene0056117	gj 508717326 gb EOY09223.1	Villin 2 isoform 1 [<i>Theobroma cacao</i>]	131739	4	89	4	1.944
87	Unigene0014379	gj 449447418 ref XP_004141465.1	PREDICTED: 40S ribosomal protein S19-3-like [<i>Cucumis sativus</i>]	19368	23.1	47	3	2.032
88	Unigene0055590	gj 40233152 gb AAR83345.1	cytosolic phosphoglucomutase [<i>Populus tomentosa</i>]	76827	6.4	101	3	2.001
89	Unigene0010252	gj 508721295 gb EOY13192.1	Lactate/malate dehydrogenase family protein [<i>Theobroma cacao</i>]	43046	21.7	374	8	3.885
90	Unigene0034525	gj 508710737 gb EOY02634.1	Alpha-soluble NSF attachment protein 2 [<i>Theobroma cacao</i>]	42358	13.1	161	6	2.273
91	Unigene0004496	gj 255582193 ref XP_002531889.1	Stearoyl-ACP desaturase [<i>Ricinus communis</i>]	53716	7.1	61	3	1.609
92	Unigene0028097	gj 225440827 ref XP_002282061.1	PREDICTED: 40S ribosomal protein S14-like [<i>Vitis vinifera</i>]	19714	16	68	2	2.864
93	Unigene0005014	gj 357481501 ref XP_003611036.1	V-type proton ATPase subunit E1 [<i>Medicago truncatula</i>]	34314	20.6	243	7	1.508
94	Unigene0034245	gj 311615483 gb ABM53666.2	copper/zinc superoxide dismutase [<i>Euphorbia characias</i>]	17846	40.1	341	7	1.778
95	Unigene0043247	gj 449459332 ref XP_004147400.1	PREDICTED: 60S ribosomal protein L32-1-like [<i>Cucumis sativus</i>]	21862	18.8	44	2	2.253

Laticifers at early stage VS laticifers at later stage (5 increased proteins)

Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	Fold change
1	Unigene0025134	gj 508711054 gb EOY02951.1	Glycosyl hydrolase family 38 protein [<i>Theobroma cacao</i>]	106703	16.3	664	9	1.701
2	Unigene0009408	gj 225436405 ref XP_002271797.1	PREDICTED: lysosomal Pro-X carboxypeptidase [<i>Vitis vinifera</i>]	50697	45.5	2123	74	3.802
3	Unigene0030324	gj 508714708 gb EOY06605.1	Pectin lyase-like superfamily protein [<i>Theobroma cacao</i>]	57574	16.6	225	10	1.661

4	Unigene0014181	gj 508713146 gb EOY05043.1	Catalytic,carbohydrate kinases,phosphoglucan [<i>Theobroma cacao</i>]	146853	28.4	1539	63	1.667
5	Unigene0015233	gj 224102795 ref XP_002312804.1	cholesterol transport protein [<i>Populus trichocarpa</i>]	60658	5.1	115	6	1.647
Laticifers at later stage VS laticifers at later stage with UV-B radiation (12 decreased proteins)								
Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	Fold change
1	Unigene0046877	gj 15237236 ref NP_197101.1	stress-induced protein KIN2 [<i>Arabidopsis thaliana</i>]	9544	38.1	120	4	1.793
2	Unigene0057683	gj 356561173 ref XP_003548859.1	PREDICTED: lysosomal alpha-mannosidase-like isoform 2 [<i>Glycine max</i>]	62971	17.8	413	2	1.525
3	Unigene0050639	gj 508701346 gb EOX93242.1	Aspartic protease isoform 2 [<i>Theobroma cacao</i>]	62590	4.4	99	3	1.734
4	Unigene0021896	gj 470118595 ref XP_004295410.1	PREDICTED: GDSL esterase/lipase At1g29660-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]	39270	18.6	1919	77	1.738
5	Unigene0039731	gj 356505054 ref XP_003521307.1	PREDICTED: acid phosphatase 1-like [<i>Glycine max</i>]	16391	19.1	58	3	1.561
6	Unigene0041825	gj 211906536 gb ACJ11761.1	class III peroxidase [<i>Gossypium hirsutum</i>]	39589	24.1	325	8	1.774
7	Unigene0043668	gj 356566130 ref XP_003551288.1	PREDICTED: REF/SRPP-like protein At1g67360-like isoform 1 [<i>Glycine max</i>]	35219	18.7	103	3	1.901
8	Unigene0001669	gj 284433772 gb ADB85092.1	acyl-CoA-binding protein [<i>Jatropha curcas</i>]	13615	21.7	70	5	1.81
9	Unigene0034090	gj 317106727 dbj BAJ53223.1	JHL06P13.2 [<i>Jatropha curcas</i>]	20167	25.3	497	37	1.541
10	Unigene0009803	gj 470134700 ref XP_004303177.1	PREDICTED: xylem serine proteinase 1-like isoform 2 [<i>Fragaria vesca</i> subsp. <i>vesca</i>]	14821	63	1197	23	2.344
11	Unigene0017186	gj 225458649 ref XP_002282833.1	PREDICTED: subtilisin-like protease [<i>Vitis vinifera</i>]	21125	16.8	118	7	1.813
12	Unigene0030324	gj 508714708 gb EOY06605.1	Pectin lyase-like superfamily protein [<i>Theobroma cacao</i>]	57574	16.6	225	10	1.521
Laticifers at later stage VS laticifers at later stage with UV-B radiation (16 increased proteins)								
Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	Fold change
1	Unigene0042801	gj 508727703 gb EOY19600.1	Alpha/beta-Hydrolases superfamily protein [<i>Theobroma cacao</i>]	43288	9.3	98	3	1.675
2	Unigene0053540	gj 224054174 ref XP_002298128.1	2-oxoglutarate-dependent dioxygenase [<i>Populus trichocarpa</i>]	46318	9	140	5	1.802
3	Unigene0053837	gj 224127758 ref XP_002329170.1	acyl:coa ligase acetate-coa synthetase-like protein [<i>Populus trichocarpa</i>]	55767	7	67	2	2.439
4	Unigene0044626	gj 470144999 ref XP_004308132.1	PREDICTED: carboxylesterase 1-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]	38857	13.6	113	3	1.808
5	Unigene0029617	gj 356508007 ref XP_003522754.1	PREDICTED: glucose-6-phosphate isomerase-like [<i>Glycine max</i>]	75718	4.2	48	2	1.639
6	Unigene0053546	gj 224054174 ref XP_002298128.1	2-oxoglutarate-dependent dioxygenase [<i>Populus trichocarpa</i>]	44256	14.9	177	6	1.748
7	Unigene0021852	gj 255548165 ref XP_002515139.1	cathepsin B, putative [<i>Ricinus communis</i>]	4695	52.6	461	10	1.942
8	Unigene0042995	gj 356562585 ref XP_003549550.1	PREDICTED: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase-like [<i>Glycine max</i>]	65613	13.1	221	8	1.57
9	Unigene0031164	gj 224109756 ref XP_002315301.1	chorismate synthase [<i>Populus trichocarpa</i>]	20837	22.2	154	3	1.577
10	Unigene0020801	gj 225432542 ref XP_002277699.1	PREDICTED: basic 7S globulin-like [<i>Vitis vinifera</i>]	18803	21.2	160	3	2.288
11	Unigene0004983	gj 359482944 ref XP_002279789.2	PREDICTED: 97 kDa heat shock protein-like [<i>Vitis vinifera</i>]	113356	4.2	76	4	1.748
12	Unigene0011325	gj 16417950 gb AAL18927.1 AF429386_1	mevalonate diphosphate decarboxylase [<i>Hevea brasiliensis</i>]	39027	10.2	93	2	1.653
13	Unigene0000507	gj 289600010 gb ADD12953.1	2-phospho-D-glycerate hydrolase [<i>Citrus trifoliata</i>]	60126	21.6	437	11	1.645
14	Unigene0008378	gj 359493788 ref XP_002285446.2	PREDICTED: epidermis-specific secreted glycoprotein EPI-like [<i>Vitis vinifera</i>]	10977	83.3	654	18	1.6
15	Unigene0058320	gj 151347486 gb ABS01352.1	methionine synthase [<i>Carica papaya</i>]	102739	15.4	438	7	1.538

Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	Fold change
16	Unigene0024454	gj 357451779 ref XP_003596166.1	Elongation factor EF-2 [<i>Medicago truncatula</i>]	113121	3.2	56	2	1.653
Laticifers at early stage VS laticifers at early stage with UV-B radiation (9 decreased proteins)								
Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	Fold change
1	Unigene0001669	gj 284433772 gb ADB85092.1	acyl-CoA-binding protein [<i>Jatropha curcas</i>]	13615	21.7	70	5	2.232
2	Unigene0042801	gj 508727703 gb EOY19600.1	Alpha/beta-Hydrolases superfamily protein [<i>Theobroma cacao</i>]	43288	9.3	98	3	1.529
3	Unigene0034090	gj 317106727 dbj BAJ53223.1	JHL06P13.2 [<i>Jatropha curcas</i>]	20167	25.3	497	37	1.533
4	Unigene0030475	gj 233955399 gb ACQ91203.1	calreticulin [<i>Carica papaya</i>]	63199	16.8	154	14	1.684
5	Unigene0014552	gj 198400319 gb ACH87168.1	senescence-related protein [<i>Camellia sinensis</i>]	49122	23.5	453	11	1.588
6	Unigene0042612	gj 343481065 gb AEM44784.1	cyclophilin [<i>Momordica charantia</i>]	22370	39.8	239	10	1.629
7	Unigene0010252	gj 508721295 gb EOY13192.1	Lactate/malate dehydrogenase family protein [<i>Theobroma cacao</i>]	43046	21.7	374	8	1.803
8	Unigene0039388	gj 225443421 ref XP_002267740.1	PREDICTED: subtilisin-like protease [<i>Vitis vinifera</i>]	10540	37.1	196	7	1.541
9	Unigene0014554	gj 351722359 ref NP_001238009.1	protein disulfide isomerase-like protein precursor [<i>Glycine max</i>]	70540	20.5	299	14	1.831
Laticifers at early stage (CK1) VS laticifers at early stage with UV-B radiation (T1) (10 increased proteins)								
Number	Accession	Nr-ID	Nr-annotation	Mass	Cov	Score	Quant number	Fold change
1	Unigene0043745	gj 326694865 gb AEA03663.1	14-3-3 protein 2 [<i>Hevea brasiliensis</i>]	35812	22	165	4	1.912
2	Unigene0026930	gj 470124402 ref XP_004298203.1	PREDICTED: beta-galactosidase 9-like [<i>Fragaria vesca</i> subsp. <i>vesca</i>]	60753	13.6	100	5	1.553
3	Unigene0025134	gj 508711054 gb EOY02951.1	Glycosyl hydrolase family 38 protein [<i>Theobroma cacao</i>]	106703	16.3	664	8	1.567
4	Unigene0055634	gj 299150759 gb ADJ17723.1	beta-hydroxyacyl-acyl carrier protein dehydratase [<i>Hevea brasiliensis</i>]	28948	16.7	77	4	1.639
5	Unigene0053540	gj 224054174 ref XP_002298128.1	2-oxoglutarate-dependent dioxygenase [<i>Populus trichocarpa</i>]	46318	9	140	7	1.901
6	Unigene0035418	gj 284433762 gb ADB85087.1	vacuolar ATP synthase subunit G1 [<i>Jatropha curcas</i>]	15566	39.1	96	4	1.587
7	Unigene0009408	gj 225436405 ref XP_002271797.1	PREDICTED: lysosomal Pro-X carboxypeptidase [<i>Vitis vinifera</i>]	50697	45.5	2123	74	4.329
8	Unigene0053546	gj 224054174 ref XP_002298128.1	2-oxoglutarate-dependent dioxygenase [<i>Populus trichocarpa</i>]	44256	14.9	177	6	1.894
9	Unigene0021852	gj 255548165 ref XP_002515139.1	cathepsin B, putative [<i>Ricinus communis</i>]	4695	52.6	461	10	1.949
10	Unigene0059780	gj 224140038 ref XP_002323394.1	2-cys peroxiredoxin [<i>Populus trichocarpa</i>]	35186	11.7	142	4	1.524

Note: Number: protein number; Accession: the sequence of gene in *Euphorbia kansui* transcriptome database (accession number: SRP067381) corresponding to a protein; Nr-ID: the ID of protein in Nr database; Nr-annotation: annotation protein information in Nr database; Mass: protein mass; Cov: sequence coverage of protein; Score: protein identification score; Quant number: The number of peptides used for protein quantitation; Fold change: fold change between different comparison group.

Table S4 The KEGG pathways of differentially expressed latex proteins between three different comparison groups

Pathway (52)	number	Pathway (52)	number
Laticifer at early stage VS laticifer at later stage			
1. Metabolic pathways	32	27. Selenocompound metabolism	2
2. Biosynthesis of secondary metabolites	23	28. Glutathione metabolism	2
3. Biosynthesis of antibiotics	20	29. Starch and sucrose metabolism	2
4. Microbial metabolism in diverse environments	17	30. Inositol phosphate metabolism	2
5. Glycolysis / Gluconeogenesis	12	31. Propanoate metabolism	2
6. Carbon metabolism	12	32. Terpenoid backbone biosynthesis	2
7. Biosynthesis of amino acids	10	33. Biosynthesis of unsaturated fatty acids	2
8. Cysteine and methionine metabolism	7	34. Fatty acid metabolism	2
9. Ribosome	7	35. RNA transport	2
10. Protein processing in endoplasmic reticulum	7	36. Spliceosome	2
11. Pyruvate metabolism	6	37. Steroid biosynthesis	1
12. Carbon fixation in photosynthetic organisms	6	38. Pyrimidine metabolism	1
13. Citrate cycle (TCA cycle)	5	39. Alanine, aspartate and glutamate metabolism	1
14. Proteasome	5	40. Valine, leucine and isoleucine degradation	1
15. Phagosome	5	41. Valine, leucine and isoleucine biosynthesis	1
16. Pentose phosphate pathway	4	42. Lysine degradation	1
17. Fructose and mannose metabolism	3	43. Amino sugar and nucleotide sugar metabolism	1
18. Oxidative phosphorylation	3	44. Arachidonic acid metabolism	1
19. Purine metabolism	3	45. Butanoate metabolism	1
20. Glyoxylate and dicarboxylate metabolism	3	46. Pantothenate and CoA biosynthesis	1
21. Endocytosis	3	47. Biotin metabolism	1
22. Plant-pathogen interaction	3	48. 2-Oxocarboxylic acid metabolism	1
23. Galactose metabolism	2	49. RNA degradation	1
24. Fatty acid biosynthesis	2	50. Phosphatidylinositol signaling system	1

25. Glycine, serine and threonine metabolism	2	51. SNARE interactions in vesicular transport	1
26. Tyrosine metabolism	2	52. Peroxisome	1
Laticifers at early stage VS laticifers at early stage with UV-B radiation (16)			
1. Metabolic pathways	3	1. Metabolic pathways	7
2. Protein processing in endoplasmic reticulum	2	2. Biosynthesis of secondary metabolites	6
3. Phagosome	2	3. Biosynthesis of antibiotics	4
4. Citrate cycle (TCA cycle)	1	4. Glycolysis / Gluconeogenesis	3
5. Fatty acid biosynthesis	1	5. Microbial metabolism in diverse environments	3
6. Oxidative phosphorylation	1	6. Carbon metabolism	3
7. Cysteine and methionine metabolism	1	7. Biosynthesis of amino acids	3
8. Pyruvate metabolism	1	8. Pentose phosphate pathway	2
9. Glyoxylate and dicarboxylate metabolism	1	9. Alanine, aspartate and glutamate metabolism	1
10. Carbon fixation in photosynthetic organisms	1	10. Cysteine and methionine metabolism	1
11. Biotin metabolism	1	11. Lysine degradation	1
12. Biosynthesis of secondary metabolites	1	12. Tyrosine metabolism	1
13. Microbial metabolism in diverse environments	1	13. Phenylalanine, tyrosine and tryptophan biosynthesis	1
14. Biosynthesis of antibiotics	1	14. Selenocompound metabolism	1
15. Carbon metabolism	1	15. Starch and sucrose metabolism	1
16. Fatty acid metabolism	1	16. Other glycan degradation	1
		17. Amino sugar and nucleotide sugar metabolism	1
		18. Butanoate metabolism	1
		19. Terpenoid backbone biosynthesis	1
		20. Phenylpropanoid biosynthesis	1
		21. RNA degradation	1

Table S5 The primer sequence of genes in qRT-PCR analysis

Gene	Protein	Primer sequence
Unigene0008750	Proteasome subunit beta type-1-like	s: TTCTGGTTCCA CTCTCATCATGCC a: ACAGCGTCCTGTGCAGGTAATAAG
Unigene0042714	Isopentenyl diphosphate isomerase Mevalonate disphosphate	s: CGCATCCTCTACAAGGCACCTTC a: TTCACATCACGGACCATGAAGAGC
Unigene0011325	decarboxylase	s: AGGCTGTCGCTTCCATTGTCAAC a: CGAGGCAAGGTT CAGGCAGTG
Unigene0035418	Vacuolar ATP synthase	s: ATTGCTGACTTTCGCGCTCA a: GTGGTCACGTGCTTCAGGAG
Unigene0004204	Heat shock protein 70	s: ATAGGCAATGGCAGCAGCAGTG a: CACAGAGACAAGCCACCAAGGAC s: AAGTGCAAGTCCAAGCCTTATCGG a:
Unigene0043745	14-3-3 protein	AGACAGGTGCTGAGAGGAAGGAAG

Note: the number of gene sequence in *Euphorbia kansui* transcriptome database (accession number: SRP067381).