

Spot ID	Number of isoforms	GenBank codes	BLASTp description	I/H (S)	R/H (S)	I/H (P)	R/H (P)
5102	1	gi 118406886	glutathione S-transferase, chloroplastic	2.4			
4501	1	gi 14161136	glutamine synthetase		2.9		
5205	1	gi 147772560	triosphosphate isomerase-like protein		2.3		
1810	1	gi 147782269	putative oxalyl-CoA decarboxylase, 2-hydroxyacyl-CoA lyase 1	3.6			
4509	1	gi 147784260	glutamine synthetase leaf isozyme, chloroplastic	3.4			
5202, 3206	2	gi 147784683	Plant Basic Secretory Protein	8.6	2.5		
4004	1	gi 147785904	Molecular chaperone (small heat shock protein) crystallin alpha, hsp20	14.2			
1313	1	gi 147787229	putative plastid lipid-associated protein			2.4	7.2
8504	1	gi 147790682	cysteine peptidase, Peptidase C1A subfamily	2.7			
6810	1	gi 147801802	succinate dehydrogenase			4.9	2.6
3304	1	gi 147805616	Stem-specific protein aluminum-induced protein	2.4			
5510	1	gi 147810287	glycosyl hydrolase family 31 enzyme, alpha-galactosidase	2.5			
2502, 2505	2	gi 147821009	fructokinase, chloroplast		2.4-2.1		
6506	1	gi 147821099	protein disulfide isomerase-like, PDla family, endoplasmic reticulum protein 38 (Erp38) subfamily		2.2		
7414	1	gi 147835129	Cystathionine beta-synthase (CBS) and Cysteine synthase-like protein	3.8			
3405	1	gi 147838052	Putative cyclase, Kynurenine formamidase			2.3	
2601, 2602, 3502, 3505	4	gi 147856329	rubisco activase 2, chloroplastic isoform 1		2.5	3.1-2.5	3.1
2801	1	gi 147860809	chloroplast HSP70		3.6		
2105	1	gi 147866290	thylakoid lumen 18.3 kDa protein	3.2			
3601	1	gi 157838576	anthocyanidin synthase	9.2			
2103, 2105	2	gi 163914213	pathogenesis-related protein 10	2.9-3.2			
1212, 8206	2	gi 1839046	osmotin-like protein	32.8-9.5			
8203, 8204	2	gi 2213852	VVTL1 osmotin-like protein, PR-5 protein	11.6-17.2			
1408	1	gi 225424904	putative metal hydrolase	2.5			
6007, 7003	2	gi 359473856	SNF1-related protein kinase (SnRK1), putative	5.3-2.2			
205, 8208	2	gi 225426793	thaumatin-like protein	7.0-10.1			
4206	1	gi 359476682	soluble inorganic pyrophosphatase-like				6.7
1105	1	gi 225432248	Translationally-controlled tumor protein, putative	5.4	3.2		
3810, 7611	1	gi 225434984	similar to HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding isoform 1	2.6		4.5	4.5
3205, 6303	2	gi 225435177	ascorbate peroxidase		3.8	4.5	8.9
7403	1	gi 225436563	similar to beta-1,3-glucanase	3.2			
6308	1	gi 225436938	endo-1,3,1,4-beta-D-glucanase	3.2			
5705, 5707, 6703, 6707	4	gi 225439064	putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase		3.4	5.6-2.1	2.2
1315	1	gi 225440003	ribonucleoprotein, chloroplast		4.8		
3902	1	gi 225440045	cell division cycle protein 48 homolog			2.9	
2306	1	gi 225441445	probable plastid-lipid-associated protein 13, chloroplastic isoform 2		3.7		
3603	1	gi 225445041	mitochondrial-processing peptidase subunit alpha				4.6
3104	1	gi 225445188	Peroxisiredoxin-2B			8.4	
5203	1	gi 225445670	proteasome subunit beta type-6		3.2		
3208, 5209	1	gi 225446775	oxygen-evolving enhancer protein 2 23-kDa polypeptide of photosystem II	2.1		2.6	
1615	1	gi 225447510	probable acetyl-CoA acetyltransferase, cytosolic 2	3			
4602	1	gi 225448323	actin-101			3.1	5.7
2501, 2503, 2507, 7504	4	gi 225449432	ribulose biphosphate carboxylase/oxygenase activase	2.6	2.9	7.2-2.3	
4201	1	gi 225451299	probable ribose-5-phosphate isomerase			4.8	24.1
6510	1	gi 225451316	auxin-induced protein PCNT115 isoform 1			3.1	2.8
6501	1	gi 225451379	glutamine synthetase cytosolic isozyme 2		2.2		2.8
1201	1	gi 225454408	acidic endochitinase	2.3	2.6		
2607, 2701, 3605	3	gi 225455555	enolase	3.0-3.1-5.8			
1505	1	gi 225456550	UDP-arabinopyranose mutase 1	2.8			
2708	1	gi 225459587	protein disulfide-isomerase	2.5			
4103	1	gi 225459609	similar to PBC1 (20S proteasome beta subunit C1); peptidase isoform 1 beta3		2		
1909, 2903, 2904	3	gi 225460961	aconitate hydratase 2, mitochondrial	2.4-2.3-2.3			
3413	1	gi 225461077	isoform 1, thiazole biosynthetic enzyme, chloroplastic		2.9		
6008	1	gi 225465502	isoform 2 40S ribosomal protein S12	2.8			
2602	1	gi 225466253	isocitrate dehydrogenase [NADP]	2.5			
2504	1	gi 225466690	sedoheptulose-1,7-bisphosphatase, chloroplastic				6.2
6306	1	gi 225468850	isoform 1 putative oxidoreductase GLYR1 isoform 1		2.2		
5104	1	gi 297737681	MLP-LIKE PROTEIN 28	7.1			
4401	1	gi 359475506	proline iminopeptidase		2.5		
5602	1	gi 359478860	26S protease regulatory subunit 6B homolog		2.6		
2611	1	gi 7264740	alcohol dehydrogenase 6	8.4			
2407	1	gi 91983999	ATP synthase CF1 beta subunit, chloroplast	2.3			
1401	1	gi 76559894	isoflavone reductase-like protein 5	2.6			
4703	1	gi 91983977	ATP synthase CF1 alpha subunit, chloroplast	2.8	2.3		
306, 405, 5103, 4108	4	gi 91984000	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit	2.1-2.4	2.7	2.9	

Barbera compared to healthy (H) plants, as revealed by ProQ Diamond (P) and Sypro® Ruby (S) staining. For each protein are reported spot ID, number of isoforms, GenBank code and fold change. Red: up-regulated/up-phosphorylated. Blue: down-regulated/down-phosphorylated. Green shows chloroplast-localized *V. vinifera* proteins according to Plant GOslim term assignment performed by Blast2GO.