

APPENDIX A

Identification and characterization of a soybean protein with adenylyl cyclase activity

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Rank	Locus	Gene Ontology Terms	r-value	Annotation and Description
-	Glyma.07G251000		1.00	GmAC
1	Glyma.05G029300	RNAM; PTM	0.80	Uncharacterized protein
2	Glyma.07G184300	PF; RCd; RH	0.79	Mitochondrial HSO70
3	Glyma.03G150600	PyRBP; RtC; TE	0.79	GTP binding elongation factor Tu family protein
4	Glyma.17G023300		0.77	Uncharacterized protein
5	Glyma.03G186500	RNAM; mRNAEN; PIN	0.75	WD-40 repeat family protein
6	Glyma.20G168100	RNAM; EDSD	0.74	Ribosomal protein 1
7	Glyma.18G278400		0.74	PPR superfamily protein
8	Glyma.08G123100	CD; HM; PM; EM; PM; PU	0.74	T-complex protein 1 alpha subunit
9	Glyma.07G128300	FOF; HM; RFD	0.73	Uncharacterized protein
10	Glyma.16G208700	CPMP; PF; rRNAP	0.73	CPN60 chaperonin family protein
11	Glyma.13G237800	EDSD; rRNAP; RSSUA	0.73	Ribosomal protein S6e
12	Glyma.18G090400	HA; PF; PTM; PyRBP; RH	0.73	Co-chaperone GrpE family protein
13	Glyma.17G105700	EDSD; ESED	0.72	Elongation factor family protein
14	Glyma.07G261900	RNAM; RNAP; CD; ESED; HM; mRNAEN; mRNAS; MMI; PM; EM, DIN: DM: DTM: DL!: BED	0.71	Uncharacterized protein
15	Glyma.02G251000	CD; ESED; HLM; PM; PTM; RoFD	0.71	Mitochondrial glycoprotein family protein
16	Glyma.02G004400	CD; HLM; PM; RoFD	0.71	TTR-like superfamily protein
17	Glyma.08G364000	CWM; CPMP; CO; G; PPCP; PF;	0.71	CPN60 chaperonin family protein
18	Glyma.03G164500	RNAM; PNF; rRNAP	0.71	Nucleolar RNA-binding Nop10p family protein
19	Glyma.19G125400	PIN; RSS	0.70	Nascent polypeptide-associated complex
20	Glyma.17G097600	RNAM; PTM	0.70	Uncharacterized protein
21	Glyma.15G129100	RNAM; EDSD; ESD; mRNAEN; MF; PIN' AP	0.70	WD40 repeat-like superfamily protein
22	Glyma.02G079000	RNAM; RB; T	0.70	S18 ribosomal protein
23	Glyma.06G193200	CD; CP; LRF; NA	0.70	NAP1-related protein 2
24	Glyma.18G002000	CA; rRNAP; RC; ROS; RSS; RWD; SG	0.69	Glycine-rich RNA binding protein
25	Glyma.17G099200	CD; CP; LRF; NA	0.69	NAP1-related protein
26	Glyma.11G014400	RNAM; NA; PM; PF	0.69	FK506 binding protein
27	Glyma.20G081800	N-tPM; PyRBP	0.69	NTF2 family protein

Table S1. List of the top 50 genes co-expressed with Glyma.07G251000.

28	Glyma.10G106900	RCd	0.69	S-formylglutathione hydrolase
29	Glyma.01G190500	PyRBP	0.69	Uncharacterized protein
30	Glyma.16G088000	RH; ROS; RWD; SG	0.68	Rotamase FKBP 1
31	Glyma.06G018400	NBP; RB	0.68	Uncharacterized protein
32	Glyma.01G029200	CPMP; HM; NBP; PU; T	0.68	Ubiquitin family protein
33	Glyma.19G213200	RNAM; CS; HM; NBP; PyRBP; RB	0.68	L19e family protein
34	Glyma.08G050100	CPMP; CO; G; Gly; PPCP; PF; RCd;	0.68	CPN60 chaperonin family protein
35	Glyma.14G065700	CD; ESECD; HLM; PM; PTM; RoFD	0.68	Mitochondrial glycoprotein family protein
36	Glyma.02G124500	CO; DE; EDSD; OD; PF; PICS; RCd;	0.68	Chaperone htpG family protein
37	Glyma.04G139900	RNAM; ECrRNAP; rRNAP	0.66	Ribosomal RNA processing Brix domain protein
38	Glyma.08G232000	RNAM; CD; CG; LRF; MO; PTM;	0.66	Prohibitin 3
39	Glyma.05G241100	RNAM; AT; PR; PTM; PyRBP;	0.66	Translocase 40
40	Glyma.09G024000	RNAM; CWM	0.66	Ribosomal L13 protein family
41	Glyma.01G032500	CO; G; PPCP; tRNA AA; TtRNA AA	0.66	Threonyl-tRNA synthatase
42	Glyma.10G127800		0.66	Heat shock protein 60
43	Glyma.08G152100	C-MPF; ESC; ESD; ESECD; NMF;	0.66	Gametophytic factor 2
44	Glyma.07G043800	ECITS1; PIN; rRNAE; rSSUA	0.66	40s ribosomal protein SAB
45	Glyma.06G075300	EDSD; ESED; FOF; HM; LS; mRNAEN; MMI; MSO; PM; PRVR; PU; PNBP; RFD; RF; SDP; SG; SMSP: VRPTM	0.66	SHK1 binding protein 1
46	Glyma.19G125000	FOF; HLM; HM; RFD	0.65	WD40 repeat-like superfamily protein
47	Glyma.08G035500	CD; HM; PM; PR; PM; PU	0.65	S-adenosyl-L-methyltransferase
48	Glyma.03G013100	RNAS; MBP; PS	0.65	Uncharacterized protein
49	Glyma.06G133600	EDSD; PU; T	0.64	Ubiquitin-like domain-containing protein
50	Glyma.05G134100	RNAM	0.64	CX9C domain-containing protein

CO = Cytoskeleton organization; G = Gluconeogenesis; PPCP = Proteasomal protein catabolic process; RNAM = RNA methylation; T = Translation; HLM = Histone lysine methylation; PM = photomorphogenesis; RoFD = Regulation of flower development; tRNA AA = tRNA aminoacylation; TtRNA AA = Threonyl-tRNA aminoacylation; RB = Ribosome biogenesis; N-tPM = N-terminal protein myristoylation; PTM = Protein targeting to mitochondrion; DE = De-etiolation; EDSD = Embryo development ending in seed dormancy; OD = Ovule development; PF = Protein folding; PICS = Protein import into chloroplast stroma; RH = Response to heat; RSS = Response to salt stress; RWD = Response to water deprivation; ESED = Embryo sac egg cell differentiation; MBP = Methionine biosynthetic process; PS = Protein sumoylation; PyRBP = Pyrimidine ribonucleotide biosynthetic process; RtC = Response to cadmium ion; PNF = Polar nucleus fusion; rRNAP = rRNA processing; TE = Translational elongation; mRNAS = mRNA splicing; PIN = Protein import into nucleus; NBP = Nucleotide biosynthetic process; ECrRNAP = Endonucleolytic cleavage involved in rRNA processing; PNBP = Purine nucleotide biosynthetic process; AT = Anion transport; PR = Photorespiration; RAT = Regulation of anion transport; TT = Transmembrane transport; CRAS = Cellular response to abscisic acid stimulus; SG = Seed germination; FO = Floral organ formation; HM = Histone modification; LS = Lipid storage; mRNAEN = mRNA export from nucleus; MMI = Maintenance of meristem identity; MSO = Meristem development; SDP = Seed dormancy process; SMSP = Sugar mediated signaling pathway; VRPTM = Vegetative to reproductive phase transition of meristem; CD = Cell differentiation; CP = Cell proliferation; LFF = Lateral root formation; NA = Nucleosome assembly; RNAS = RNA splicing; ECITS1 = Endonucleolytic cleavage in ITS1; rRNAE = rRNA export from nucleus; SIC = Response to cadmium ion; CWM = Cell wall modification; SD = Synergid death; CPMP = Cellular protein metabolic process; GI = Glycolysis; RCd = Response to cadmium ion