TABLE 1-continued

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
3027	LIB3602-004-Q1-K1-B2	1172494	BLASTX	150	3.00E−09	50	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE (PHS) (4-ALPHA-HYDROXY-TETRAHYDROPTERIN DEHYDRATASE) (PHENYLALANINE HYDROXYLASE-STIMULATING PROTEIN) (PCD) >gi|476742|gb|AAA25937.1| (M88627) phenylalanine hydroxylase [*Pseudomonas aeruginosa*]
3028	LIB3602-003-Q1-K1-E2	6939228	BLASTX	452	6.00E−45	61	(AC020579) putative phosphoribosylformylglycinamidine synthase [*Arabidopsis thaliana*]
3029	LIB3602-028-Q6-K1-D4	7487199	BLASTX	265	7.00E−23	42	hypothetical protein T19L18.24 - *Arabidopsis thaliana* >gi|3413717|gb|AAC31240.1| (AC004747) unknown protein [*Arabidopsis thaliana*]
3030	LIB3602-113-Q1-K1-B1	7439979	BLASTX	371	2.00E−35	97	glycine-rich RNA-binding protein, low-temperature-responsive - barley >gi|1229138|gb|AAB07749.1| (U49482) low temperature-responsive RNA-binding protein [*Hordeum vulgare*]
3031	LIB3602-080-Q6-K6-A7	4502327	BLASTX	453	7.00E−45	49	AU RNA-binding protein/enoyl-Coenzyme A hydratase precursor >gi|2135070|pir||I37195 AU-specific RNA-binding protein/enoyl-CoA hydratase (EC 4.2.1.17) homolog - human >gi|780241|emb|CAA56260.1| (X79888) AU-binding protein/Enoyl-CoA hydratase [Homo sapien
3032	LIB3602-102-Q1-K1-E6	6822051	BLASTX	328	9.00E−46	64	(AL132957) fructose-bisphosphatase precursor [*Arabidopsis thaliana*]
3033	LIB3602-083-Q6-K6-C2	3063365	BLASTX	452	1.00E−44	49	(AB003712) elongation factor-1alpha [*Ampharetidae* sp.]
3034	LIB3602-111-Q1-K1-G12	4580461	BLASTX	343	4.00E−32	44	(AC006081) unknown protein [*Arabidopsis thaliana*]
3035	LIB3602-039-Q6-K1-C5	7487355	BLASTX	186	1.00E−13	57	hypothetical protein T22J18.13 - *Arabidopsis thaliana* >gi|3287688|gb|AAC25516.1| (AC003979) Contains similarity to ycf37 gene product gb|1001425 from *Synechocystis* sp. genome gb|D63999. ESTs gb|T43026, gb|R64902, gb|Z18169 and gb|N37374 come from this ge
3036	LIB3602-060-Q6-K1-C3	6513923	BLASTX	490	3.00E−49	67	(AC011664) putative mitochondrial processing peptidase [*Arabidopsis thaliana*]
3037	LIB3602-091-Q6-K6-A1	7503664	BLASTX	168	2.00E−11	32	hypothetical protein F47C12.1 - *Caenorhabditis elegans* >gi|1397258|gb|AAC24388.1| (U61946) contains multiple regions of similarity to EGF-type repeats (PS: PS00022) and sushi (SCR) repeats [*Caenorhabditis elegans*]
3038	LIB3602-077-Q6-K6-F4	7019692	BLASTX	479	7.00E−48	61	(AL 138647) putative protein [*Arabidopsis thaliana*]
3039	LIB3602-004-Q1-K1-E6	3914557	BLASTX	231	4.00E−36	76	RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi|1155265|gb|AAA85273.1| (U40219) possible apospory-associated protein [*Pennisetum ciliare*]
3040	LIB3602-004-Q1-K1-D8	6862923	BLASTX	258	6.00E−22	56	(AC018907) unknown protein [*Arabidopsis thaliana*]
3041	LIB3602-009-Q6-K1-F6	2828267	BLASTX	262	3.00E−23	75	(Y14044) geranylgeranyl reductase [*Arabidopsis thaliana*]
3042	LIB3602-102-Q1-K1-A1	7019693	BLASTX	304	7.00E−28	64	(AL138647) putative protein [*Arabidopsis thaliana*]
3043	LIB3602-016-Q6-K1-H4	6862921	BLASTX	170	9.00E−12	54	(AC018907) hypothetical protein [*Arabidopsis thaliana*]

Table 1 Legend
SEQ ID No.: Refers to the sequence identification number of nucleic acids listed in the Sequence Listing.
Clone ID: Refers to an assigned cDNA clone ID number.
NCBI gi: Refers to National Center for Biotechnology Information GenBank Identifier number which is the best match for a given nucleotide sequence.
Method: Refers to the method used in the sequence comparison of the designated nucleotide sequence with the designated GenBank sequence.
BLAST Score: Refers to the BLAST score that is generated by sequence comparison of the designated nucleotide sequence with the designated GenBank sequence using the method referenced in the "Method" column.
E value: The expected number of distinct segment pairs between two sequences with a score above the bit score for BLAST match.
% ident: Refers to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison to generate the statistical scores presented.
NCBI gi Description: A description of the database entry referenced in the "NCBI gi" column.
ⓟ indicates text missing or illegible when filed