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Review

Comprehensive post-genomic data analysis approaches integrating biochemical pathway maps

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Abstract

Post-genomic era research is focusing on studies to attribute functions to genes and their encoded proteins, and to describe the regulatory networks controlling metabolic, protein synthesis and signal transduction pathways. To facilitate the analysis of experiments using post-genomic technologies, new concepts for linking the vast amount of raw data to a biological context have to be developed. Visual representations of pathways help biologists to understand the complex relationships between components of metabolic networks, and provide an invaluable resource for the integration of transcriptomics, proteomics and metabolomics data sets. Besides providing an overview of currently available bioinformatic tools for plant scientists, we introduce `BioPathAt`, a newly developed visual interface that allows the knowledge-based analysis of genome-scale data by integrating biochemical pathway maps (`BioPathAtMAPS` module) with a manually scrutinized gene-function database (`BioPathAtDB`) for the model plant *Arabidopsis thaliana*. In addition, we discuss approaches for generating a biochemical pathway knowledge database for *A. thaliana* that includes, in addition to accurate annotation, condensed experimental information regarding in vitro and in vivo gene/protein function.

Keywords: *Arabidopsis thaliana*; Cruciferae; Biochemical pathways; Bioinformatics; `BioPathAt`; Gene function; Metabolite profiling; Metabolomics; Microarray; Proteomics

Contents

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1. Introduction

Owing to their obligate phototrophic and sessile lifestyle, plants have evolved numerous unique adaptations to help cope with unavoidable stresses that are imposed upon them. Developmental, abiotic and biotic signals can directly or indirectly influence changes in biochemical pathways leading to the production of bioactive primary and secondary metabolites (Croteau et al., 2000). Post-genomic technologies provide an unprecedented opportunity to acquire measurements that can accurately describe the complex networks regulating such biochemical pathways in plants. The results from post-genomic experiments investigating biochemical processes should provide researchers with quantitative information regarding global transcript, protein and metabolite patterns, transcriptional and translational modifications, protein–DNA and protein–protein interactions, and enzymatic activities (Burbulis and Winkel-Shirley, 1999; Koller et al., 2002; MacCoss et al., 2002; Conrads et al., 2003; Hendricks et al., 2003; Aebersold and Mann, 2003; Tao and Aebersold, 2003; Cutler, 2003; Weckwerth, 2003). Combined with experimental information regarding plant phenotype, the subcellular localization and tissue specific-accumulation of transcripts, proteins and metabolites, a high-resolution network of biochemical processes would emerge. However, the toolbox for the knowledge-based analysis of post-genomic experiments is still in its infancy. Thus, strategies need to be developed that allow visualizing and processing the complexity of post-genomic data sets that are obtained today and also leave room for future expansion. Biochemical pathway maps are a powerful tool to provide a biological context for the display of post-genomic data sets.

2. Approaches and tools for the integrative analysis of biochemical pathways

2.1. Kyoto Encyclopedia of Genes and Genomes (KEGG)

The most prominent examples of generic maps are the Roche Applied Science Wall Charts (“Biochemical Pathways” and “Cellular and Molecular Processes” at http://www.expasy.org/cgi-bin/search-biochem-index) and the Kyoto Encyclopedia of Genes and Genomes maps (KEGG; available at http://www.genome.ad.jp/kegg/; Kanehisa et al., 2002). With the advent of the post-genomic era the KEGG maps have been integrated into a software that allows the visualization of mRNA expression data in a biochemical map environment (http://www.genome.ad.jp/kegg/expression/). The user can choose from a selection of organisms for each metabolic map and known genes of the selected organism are indicated by green color in a box that also shows the EC number of the encoded enzyme. Microarray data can then be overlaid in the same box. For *Arabidopsis thaliana* researchers this tool has a critical disadvantage: KEGG was initially developed to represent various microbial (and animal) pathways and only a few plant-specific pathways have been integrated thus far. In addition, gene annotations for *A. thaliana* in KEGG are often homology-based and rarely scrutinized manually for accuracy, which can cause misannotations of individual members of gene families.

2.2. AraCyc

A very useful tool has been developed based on the AraCyc biochemical pathway database, which now features more than 170 pathways, of which more than 20 have been assessed manually for accuracy (http://

www.arabidopsis.org:1555/expression.html; Mueller et al., 2003). This database was built upon the Pathway Tools software suite which itself provides comprehensive information regarding biochemical pathways in the form of Pathway Genome Databases (Karp et al., 2002a). The reference for the development of AraCyc was MetaCyc (http://metacyc.org; Karp et al., 2002b), a database that describes metabolic pathways occurring in more than 150 organisms. Since its automatic build, AraCyc has been manually edited and now contains over 180 pathways with more than 1100 reactions. Its key advantages are the use of controlled vocabulary for describing enzymes, compounds, and subcellular compartments, and the convenient `PERL` module for formulating queries and batch-loading of data. However, there are still gaps in many of the AraCyc pathways, which will have to be filled using manual annotation efforts based on reports published in the last couple of years. An additional module, the AraCyc Expression Viewer, allows the user to overlay mRNA expression data on the AraCyc pathway diagrams. Although this tool is quite useful to provide a bird's eye view of experimentally observed changes in expression levels, the versatility of its visualization interface is quite limited, especially at the level of presenting the dynamics of isogene patterns.

2.3. MAPMAN

One of the comprehensive open-source software packages with relevance for *A. thaliana* researchers is MAPMAN (http://gabi.rzpd.de/projects/MapMan/; Thimm et al., 2004). Within MAPMAN, *A. thaliana* genes are grouped into over 200 hierarchical categories (BINs) by a module called TRANSCRIPTSCAVENGER, and hundreds of metabolites are linked to pathways using the METABOLITESCAVENGER module. The IMAGEANNOTATOR module allows the user to import the contents of the SCAVENGER modules, experimental data and diagrams/maps onto which experimental data can be displayed. The uploading of experimental data into MAPMAN is straightforward and, in our trial runs, the

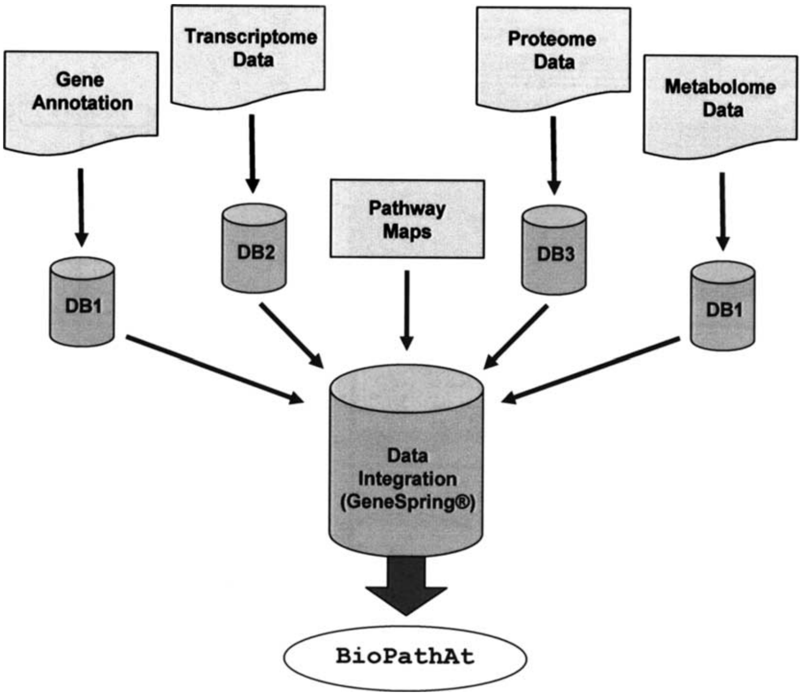
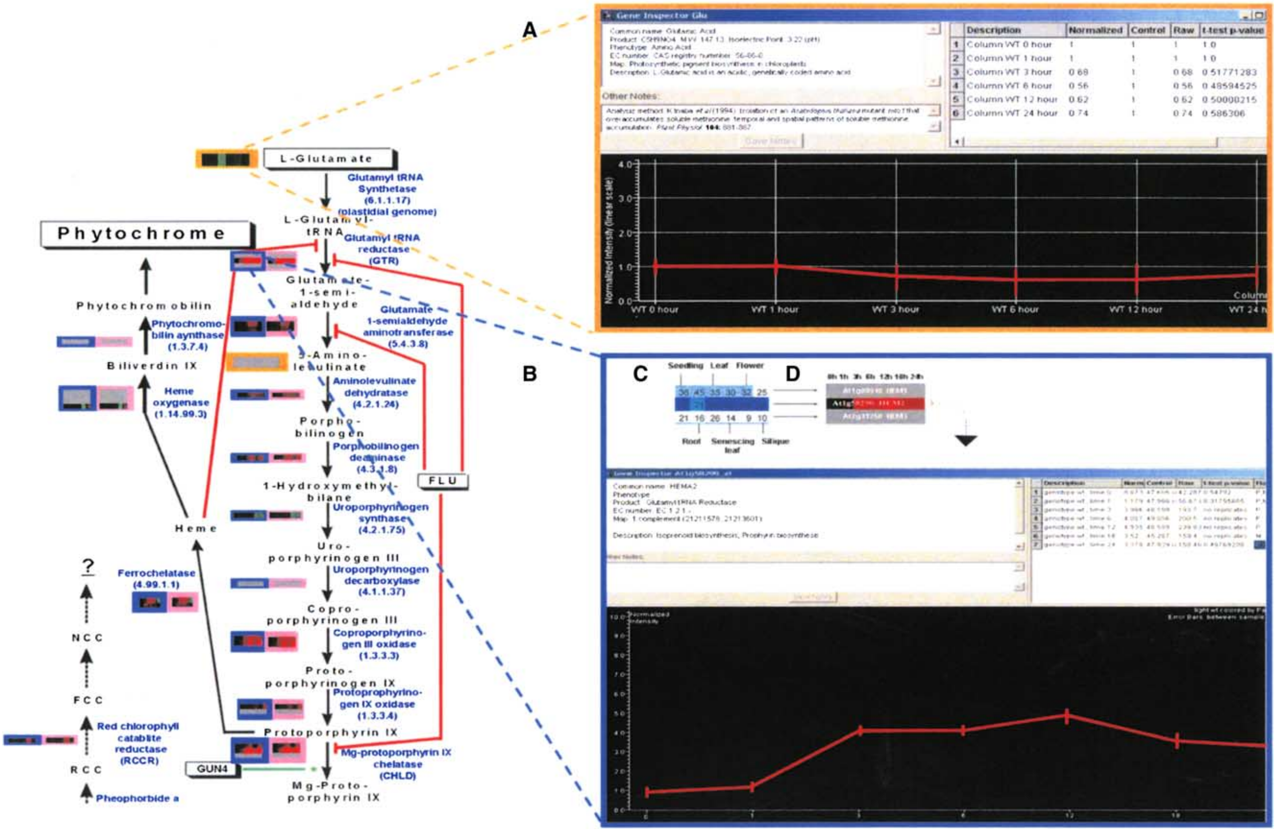


Fig. 1. Flowchart illustrating post-genomic data integration and analysis using `BioPathAt`. It is highly desirable to filter all data sets to remove unreliable data points and then to normalize the data either to specific control experiments or to the median expression level for each gene. To upload data sets into Genespring®, each measured element must have a unique identification code. The total of all identification codes for element must be typed into a text tab-delimited file, the "Genome Definition File" (for details regarding the format for this file see the GeneSpring® application tutorial section). The normalized and filtered data should be merged into one table and imported into GeneSpring™ as a "Custom File". The pathway maps are saved as image files and imported into GeneSpring® using the "New Pathway" function. Follow the GeneSpring® tutorial for addition of expression boxes to the maps.

software has been operating without major problems. However, MAPMAN has several disadvantages for users interested in the regulation of biochemical pathways. Pathways are treated as separate entities in BINs and MAPMAN does not feature an adequate tool for the visualization of their interactions in networks (e.g., the effect of transcriptional regulators on the expression of their target genes). Because MAPMAN is a user-driven tool, pathway details would have to be added by the user, which can be both an advantage (the user determines the level of detail) and a disadvantage (assembling information about pathway networks and drawing network interactions is very time-consuming). Analyses of hundreds of experiments in parallel, which are essential for screening mutant populations or for analyzing the effects of single nucleotide polymorphisms (Henikoff and Comai, 2003), cannot be visualized satisfactorily using MAPMAN. Despite these current shortcomings, the MAPMAN software package works very well to obtain a quick overview as to which pathways are affected in an experiment for which mRNA expression and/or metabolite profiling data have been acquired.

2.4. MetNet

An impressive tool in development, which features advanced visualization and statistical analysis tools for the analysis of post-genomic data sets obtained with *A. thaliana*, is the `MetNet` package (http://www.public.iastate.edu/~mash/MetNet/exchange.html; Wurtele et al., 2003). It integrates statistical and clustering packages and will eventually include capabilities to model metabolic and regulatory networks. `MetNet` has a JAVA-based interface to a database (`MetNetDB`) that contains information on known interactions in metabolic and regulatory networks. The `FCModeler` module captures input for `MetNetDB` and converts it into a graphical format. Interaction network modeling is performed in the `Matlab`™ analysis program, which uses fuzzy logic functions. `GGobi` is a module for multivari-



Common name: Glutamic Acid
Product: C5H9NO4 MW 147.13 Isoelectric Point 3.22 (pH)
Phenotype: Amino Acid
EC number: CAS registry number: 56-86-0
Map: Photosynthetic pigment biosynthesis in chloroplasts
Description: L-Glutamic acid is an acidic, genetically coded amino acid

Other Notes:
Analysis method: K Inaba *et al* (1994) Isolation of an *Arabidopsis thaliana* mutant, mto1 that overaccumulates soluble methionine: temporal and spatial patterns of soluble methionine accumulation. *Plant Physiol* **104**: 881-887

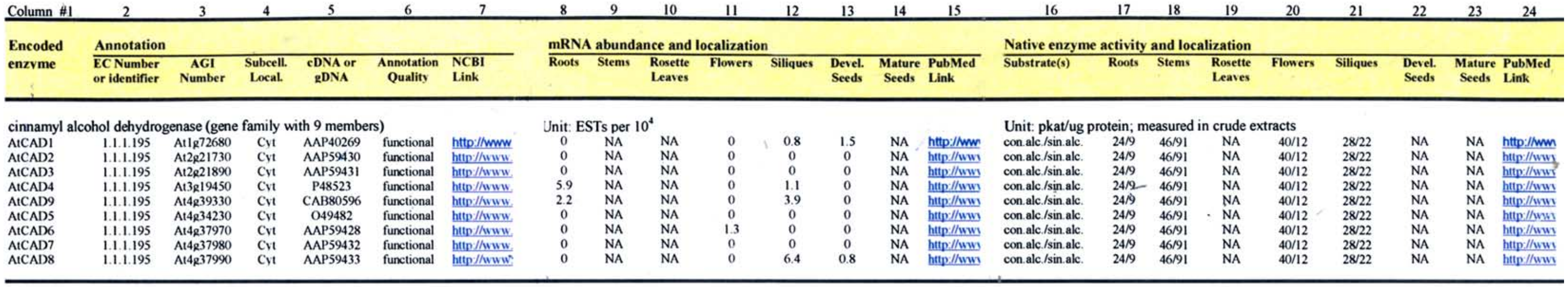
	Description	Normalized	Control	Raw	t-test p-value
1	Column WT 0 hour	1	1	1	1.0
2	Column WT 1 hour	1	1	1	1.0
3	Column WT 3 hour	0.68	1	0.68	0.51771283
4	Column WT 6 hour	0.56	1	0.56	0.48594525
5	Column WT 12 hour	0.62	1	0.62	0.50000215
6	Column WT 24 hour	0.74	1	0.74	0.586306

Common name: HEMA2
Phenotype
Product: Glutamyl tRNA Reductase
EC number: EC 1.2.1.-
Map: 1 complement (21211578..21213601)

Description: Isoprenoid biosynthesis; Prophyrin biosynthesis

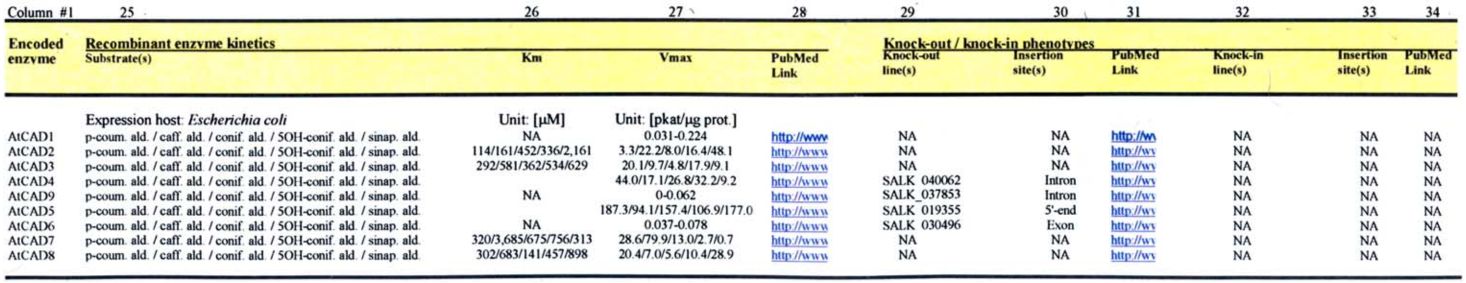
Fig. 2. Example of the `BioPathAt` concept using an extract of pigment biosynthetic pathways in *Arabidopsis thaliana* chloroplasts. For details see text in Section 3.3.

Table 1
Gene-function annotation table for genes involved in biochemical pathways in *Arabidopsis thaliana* using the cinnamyl alcohol dehydrogenase (CAD) gene family as an example



Column #1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
Encoded enzyme	**Annotation**						**mRNA abundance and localization**								**Native enzyme activity and localization**								
	EC Number or identifier	**AGI Number**	**Subcell. Local.**	**cDNA or gDNA**	**Annotation Quality**	**NCBI Link**	**Roots**	**Stems**	**Rosette Leaves**	**Flowers**	**Siliques**	**Devel. Seeds**	**Mature Seeds**	**PubMed Link**	**Substrate(s)**	**Roots**	**Stems**	**Rosette Leaves**	**Flowers**	**Siliques**	**Devel. Seeds**	**Mature Seeds**	**PubMed Link**
cinnamyl alcohol dehydrogenase (gene family with 9 members)							Unit: ESTs per 10^4								Unit: pkat/ug protein; measured in crude extracts								
AtCAD1	1.1.1.195	At1g72680	Cyt	AAP40269	functional	http://www	0	NA	NA	0	0.8	1.5	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD2	1.1.1.195	At2g21730	Cyt	AAP59430	functional	http://www.	0	NA	NA	0	0	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD3	1.1.1.195	At2g21890	Cyt	AAP59431	functional	http://www.	0	NA	NA	0	0	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD4	1.1.1.195	At3g19450	Cyt	P48523	functional	http://www.	5.9	NA	NA	0	1.1	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD9	1.1.1.195	At4g39330	Cyt	CAB80596	functional	http://www.	2.2	NA	NA	0	3.9	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD5	1.1.1.195	At4g34230	Cyt	O49482	functional	http://www.	0	NA	NA	0	0	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD6	1.1.1.195	At4g37970	Cyt	AAP59428	functional	http://www.	0	NA	NA	1.3	0	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD7	1.1.1.195	At4g37980	Cyt	AAP59432	functional	http://www.	0	NA	NA	0	0	0	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww
AtCAD8	1.1.1.195	At4g37990	Cyt	AAP59433	functional	http://www	0	NA	NA	0	6.4	0.8	NA	http://ww	con.alc./sin.alc.	24/9	46/91	NA	40/12	28/22	NA	NA	http://ww

Table 1. Continued.



Column #1	25	26	27	28	29	30	31	32	33	34
Encoded enzyme	**Recombinant enzyme kinetics**				**Knock-out / knock-in phenotypes**					
	Substrate(s)	**Km**	**Vmax**	**PubMed Link**	**Knock-out line(s)**	**Insertion site(s)**	**PubMed Link**	**Knock-in line(s)**	**Insertion site(s)**	**PubMed Link**
	Expression host: *Escherichia coli*	Unit: [µM]	Unit: [pkat/µg prot.]							
AtCAD1	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	NA	0.031-0.224	http://www	NA	NA	http://w	NA	NA	NA
AtCAD2	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	114/161/452/336/2,161	3.3/22.2/8.0/16.4/48.1	http://www	NA	NA	http://w	NA	NA	NA
AtCAD3	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	292/581/362/534/629	20.1/9.7/4.8/17.9/9.1	http://www	NA	NA	http://w	NA	NA	NA
AtCAD4	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.		44.0/17.1/26.8/32.2/9.2	http://www	SALK 040062	Intron	http://w	NA	NA	NA
AtCAD9	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	NA	0-0.062	http://www	SALK_037853	Intron	http://w	NA	NA	NA
AtCAD5	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.		187.3/94.1/157.4/106.9/177.0	http://www	SALK 019355	5'-end	http://w	NA	NA	NA
AtCAD6	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	NA	0.037-0.078	http://www	SALK 030496	Exon	http://w	NA	NA	NA
AtCAD7	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	320/3,685/675/756/313	28.6/79.9/13.0/2.7/0.7	http://www	NA	NA	http://w	NA	NA	NA
AtCAD8	p-coum. ald. / caff. ald. / conif. ald. / 5OH-conif. ald. / sinap. ald.	302/683/141/457/898	20.4/7.0/5.6/10.4/28.9	http://www	NA	NA	http://w	NA	NA	NA

For details see text. *Abbreviations*: alt. spl., alternative splicing variants exist; Chl, chloroplast; Cyt, cytosolic; Cyt/ER, cytoplasm/endoplasmic reticulum; En, chloroplast envelope membrane; Gly, glyoxisomal; Lum, lumenal; Memb, membrane-bound or membrane-associated; Mil, mitochondrial; NA, not available; Nuc, nuclear; Per, peroxisomal; Sec, secreted, Str, stroma; Ton, tonoplast; Thy, thylakoid; Vac, vacuolar.

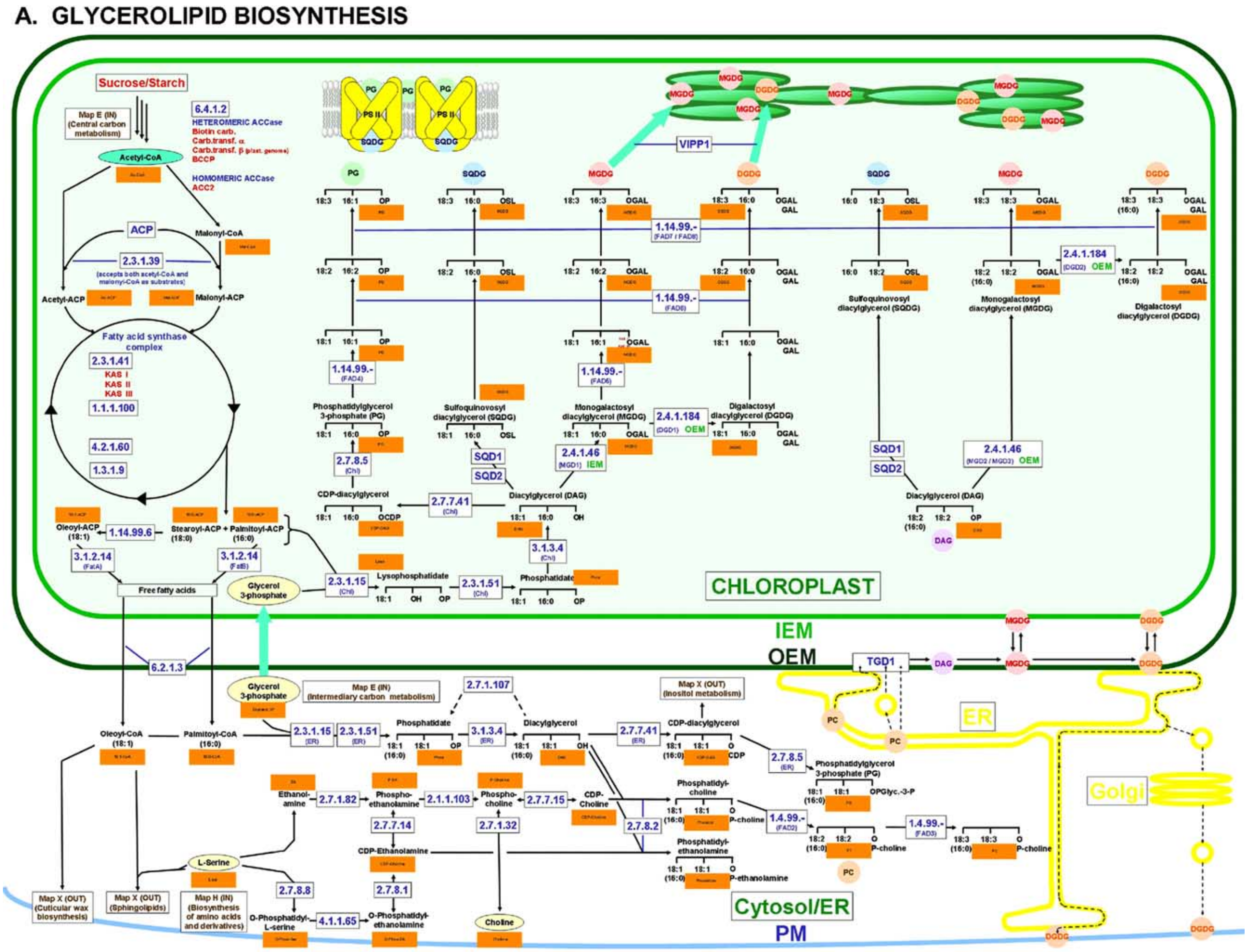
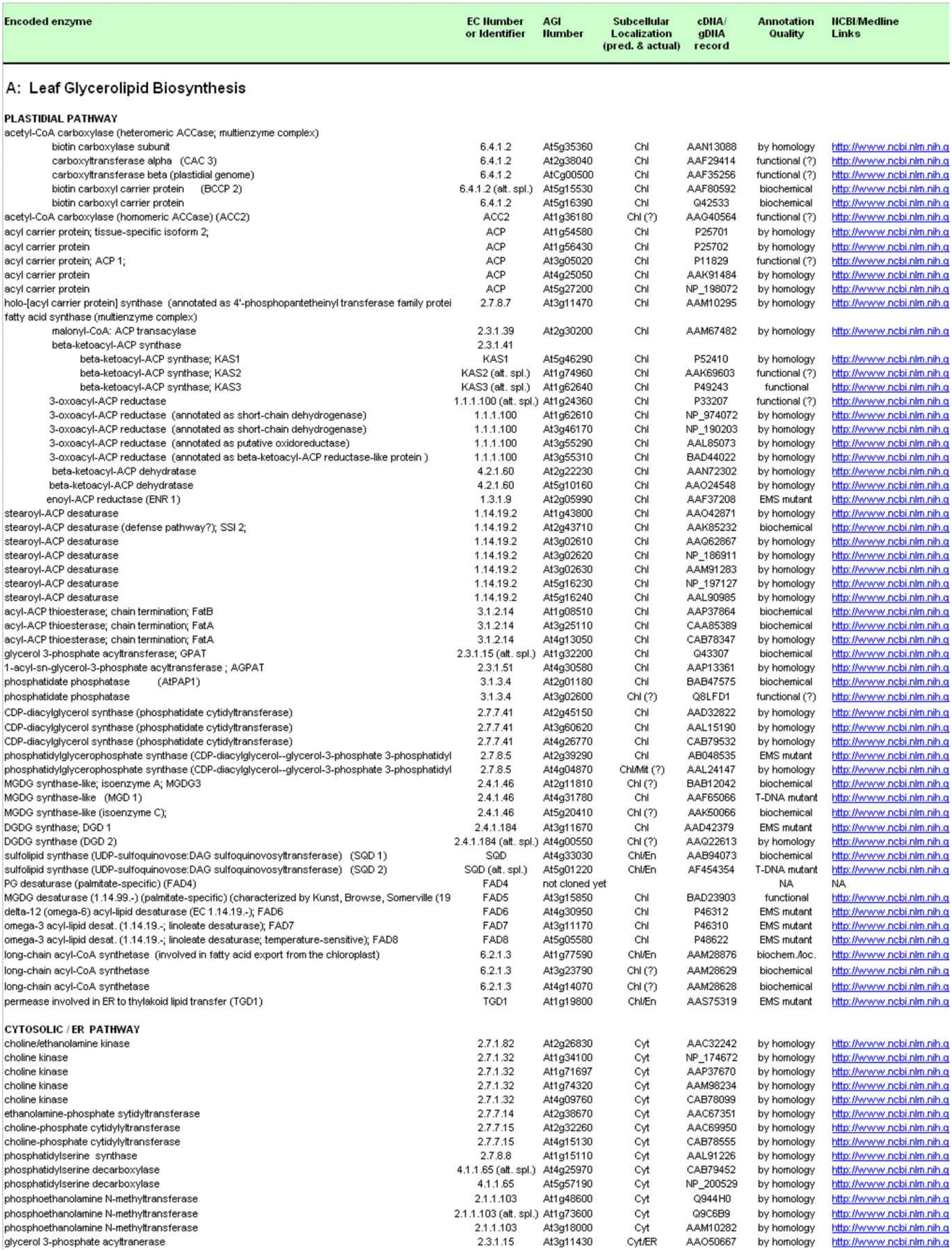


Fig. 3. Selection of biochemical pathway maps featured in `BioPathAtMAPS` and corresponding gene annotation tables featured in `BioPathAtDB`. For legends to pathway maps and annotation tables see Fig. 2 and Table 1, respectively.

ate analysis, which is linked to R, a language and environment for statistical computing and graphics. Currently, only a limited number of metabolic and regulatory pathways have been integrated into `MetNet` but the first full production version promises to be an invaluable tool for *A. thaliana* researchers.

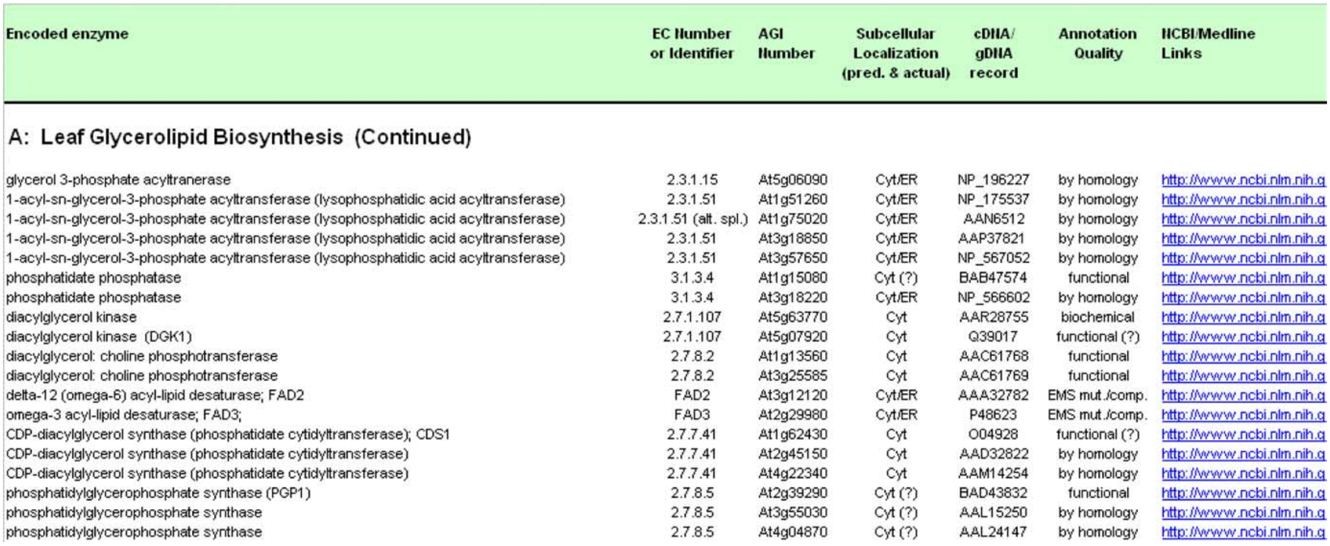
3. BioPathAt, a novel tool for post-genomic data integration

Although several bioinformatic tools for the analysis of genome-scale data sets in a biochemical pathway context have been developed over the last couple of years, we felt that the currently available tools have critical limitations in providing details about the role of specific isogenes/isozymes in the regulation of biochemical networks. Ideally, bioinformatic tools and gene function databases are integrated into one common software package, thus allowing a holistic analysis of data generated using different technologies. Thus, several options were explored to evaluate which software package would be most suitable to integrate biochemical map visualization capabilities. GeneSpring®, a commercial software package, is among the most widely used software packages in the core facilities of academic and industrial institutions (Dresen et al., 2003). It provides a host of statistical tools (e.g., *t*-tests, 2-way ANOVA tests, 1-way post-hoc tests, class prediction tools, R-based scripts) and data can be clustered to uncover expression patterns using various algorithms (e.g., hierarchical clustering, self-organizing maps, k-means, principal components analysis (PCA), QT clustering). With the pathway viewer module genes and their expression patterns can be visually characterized based on their location within a biochemical pathway. Users can import custom annotation and design their own pathway diagrams or directly import publicly available pathway maps. MIAME is a community-accepted standard that describes the minimal information that is needed to fully describe a gene expression experiment (Brazma et al., 2001) and the user can customize MIAME-compliant



Encoded enzyme	**EC Number or Identifier**	**AGI Number**	**Subcellular Localization (pred. & actual)**	**cDNA/ gDNA record**	**Annotation Quality**	**NCBI/Medline Links**
A: Leaf Glycerolipid Biosynthesis						
PLASTIDIAL PATHWAY						
acetyl-CoA carboxylase (heteromeric ACCase; multienzyme complex)						
biotin carboxylase subunit	6.4.1.2	At5g35360	Chl	AAN13088	by homology	http://www.ncbi.nlm.nih.g
carboxyltransferase alpha (CAC 3)	6.4.1.2	At2g38040	Chl	AAF29414	functional (?)	http://www.ncbi.nlm.nih.g
carboxyltransferase beta (plastidial genome)	6.4.1.2	AtCg00500	Chl	AAF35256	functional (?)	http://www.ncbi.nlm.nih.g
biotin carboxyl carrier protein (BCCP 2)	6.4.1.2 (alt. spl.)	At5g15530	Chl	AAF80592	biochemical	http://www.ncbi.nlm.nih.g
biotin carboxyl carrier protein	6.4.1.2	At5g16390	Chl	Q42533	biochemical	http://www.ncbi.nlm.nih.g
acetyl-CoA carboxylase (homomeric ACCase) (ACC2)	ACC2	At1g36180	Chl (?)	AAG40564	functional (?)	http://www.ncbi.nlm.nih.g
acyl carrier protein; tissue-specific isoform 2;	ACP	At1g54580	Chl	P25701	by homology	http://www.ncbi.nlm.nih.g
acyl carrier protein	ACP	At1g56430	Chl	P25702	by homology	http://www.ncbi.nlm.nih.g
acyl carrier protein; ACP 1;	ACP	At3g05020	Chl	P11829	functional (?)	http://www.ncbi.nlm.nih.g
acyl carrier protein	ACP	At4g25050	Chl	AAK91484	by homology	http://www.ncbi.nlm.nih.g
acyl carrier protein	ACP	At5g27200	Chl	NP_198072	by homology	http://www.ncbi.nlm.nih.g
holo-[acyl carrier protein] synthase (annotated as 4'-phosphopantetheinyl transferase family protei	2.7.8.7	At3g11470	Chl	AAM10295	by homology	http://www.ncbi.nlm.nih.g
fatty acid synthase (multienzyme complex)						
malonyl-CoA: ACP transacylase	2.3.1.39	At2g30200	Chl	AAM67482	by homology	http://www.ncbi.nlm.nih.g
beta-ketoacyl-ACP synthase	2.3.1.41					
beta-ketoacyl-ACP synthase; KAS1	KAS1	At5g46290	Chl	P52410	by homology	http://www.ncbi.nlm.nih.g
beta-ketoacyl-ACP synthase; KAS2	KAS2 (alt. spl.)	At1g74960	Chl	AAK69603	functional (?)	http://www.ncbi.nlm.nih.g
beta-ketoacyl-ACP synthase; KAS3	KAS3 (alt. spl.)	At1g62640	Chl	P49243	functional	http://www.ncbi.nlm.nih.g
3-oxoacyl-ACP reductase	1.1.1.100 (alt. spl.)	At1g24360	Chl	P33207	functional (?)	http://www.ncbi.nlm.nih.g
3-oxoacyl-ACP reductase (annotated as short-chain dehydrogenase)	1.1.1.100	At1g62610	Chl	NP_974072	by homology	http://www.ncbi.nlm.nih.g
3-oxoacyl-ACP reductase (annotated as short-chain dehydrogenase)	1.1.1.100	At3g46170	Chl	NP_190203	by homology	http://www.ncbi.nlm.nih.g
3-oxoacyl-ACP reductase (annotated as putative oxidoreductase)	1.1.1.100	At3g55290	Chl	AAL85073	by homology	http://www.ncbi.nlm.nih.g
3-oxoacyl-ACP reductase (annotated as beta-ketoacyl-ACP reductase-like protein)	1.1.1.100	At3g55310	Chl	BAD44022	by homology	http://www.ncbi.nlm.nih.g
beta-ketoacyl-ACP dehydratase	4.2.1.60	At2g22230	Chl	AAN72302	by homology	http://www.ncbi.nlm.nih.g
beta-ketoacyl-ACP dehydratase	4.2.1.60	At5g10160	Chl	AAO24548	by homology	http://www.ncbi.nlm.nih.g
enoyl-ACP reductase (ENR 1)	1.3.1.9	At2g05990	Chl	AAF37208	EMS mutant	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase	1.14.19.2	At1g43800	Chl	AAO42871	by homology	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase (defense pathway?); SSI 2;	1.14.19.2	At2g43710	Chl	AAK85232	biochemical	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase	1.14.19.2	At3g02610	Chl	AAQ62867	by homology	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase	1.14.19.2	At3g02620	Chl	NP_186911	by homology	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase	1.14.19.2	At3g02630	Chl	AAM91283	by homology	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase	1.14.19.2	At5g16230	Chl	NP_197127	by homology	http://www.ncbi.nlm.nih.g
stearoyl-ACP desaturase	1.14.19.2	At5g16240	Chl	AAL90985	by homology	http://www.ncbi.nlm.nih.g
acyl-ACP thioesterase; chain termination; FatB	3.1.2.14	At1g08510	Chl	AAP37864	biochemical	http://www.ncbi.nlm.nih.g
acyl-ACP thioesterase; chain termination; FatA	3.1.2.14	At3g25110	Chl	CAA85389	biochemical	http://www.ncbi.nlm.nih.g
acyl-ACP thioesterase; chain termination; FatA	3.1.2.14	At4g13050	Chl	CAB78347	by homology	http://www.ncbi.nlm.nih.g
glycerol 3-phosphate acyltransferase; GPAT	2.3.1.15 (alt. spl.)	At1g32200	Chl	Q43307	biochemical	http://www.ncbi.nlm.nih.g
1-acyl-sn-glycerol-3-phosphate acyltransferase ; AGPAT	2.3.1.51	At4g30580	Chl	AAP13361	by homology	http://www.ncbi.nlm.nih.g
phosphatidate phosphatase (AtPAP1)	3.1.3.4	At2g01180	Chl	BAB47575	biochemical	http://www.ncbi.nlm.nih.g
phosphatidate phosphatase	3.1.3.4	At3g02600	Chl (?)	Q8LFD1	functional (?)	http://www.ncbi.nlm.nih.g
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase)	2.7.7.41	At2g45150	Chl	AAD32822	by homology	http://www.ncbi.nlm.nih.g
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase)	2.7.7.41	At3g60620	Chl	AAL15190	by homology	http://www.ncbi.nlm.nih.g
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase)	2.7.7.41	At4g26770	Chl	CAB79532	by homology	http://www.ncbi.nlm.nih.g
phosphatidylglycerophosphate synthase (CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl	2.7.8.5	At2g39290	Chl	AB048535	EMS mutant	http://www.ncbi.nlm.nih.g
phosphatidylglycerophosphate synthase (CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl	2.7.8.5	At4g04870	Chl/Mit (?)	AAL24147	by homology	http://www.ncbi.nlm.nih.g
MGDG synthase-like; isoenzyme A; MGDG3	2.4.1.46	At2g11810	Chl (?)	BAB12042	biochemical	http://www.ncbi.nlm.nih.g
MGDG synthase-like (MGD 1)	2.4.1.46	At4g31780	Chl	AAF65066	T-DNA mutant	http://www.ncbi.nlm.nih.g
MGDG synthase-like (isoenzyme C);	2.4.1.46	At5g20410	Chl (?)	AAK50066	biochemical	http://www.ncbi.nlm.nih.g
DGDG synthase; DGD 1	2.4.1.184	At3g11670	Chl	AAD42379	EMS mutant	http://www.ncbi.nlm.nih.g
DGDG synthase (DGD 2)	2.4.1.184 (alt. spl.)	At4g00550	Chl (?)	AAQ22613	by homology	http://www.ncbi.nlm.nih.g
sulfolipid synthase (UDP-sulfoquinovose:DAG sulfoquinovosyltransferase) (SQD 1)	SQD	At4g33030	Chl/En	AAB94073	biochemical	http://www.ncbi.nlm.nih.g
sulfolipid synthase (UDP-sulfoquinovose:DAG sulfoquinovosyltransferase) (SQD 2)	SQD (alt. spl.)	At5g01220	Chl/En	AF454354	T-DNA mutant	http://www.ncbi.nlm.nih.g
PG desaturase (palmitate-specific) (FAD4)	FAD4	not cloned yet			NA	NA
MGDG desaturase (1.14.99.-) (palmitate-specific) (characterized by Kunst, Browse, Somerville (19	FAD5	At3g15850	Chl	BAD23903	functional	http://www.ncbi.nlm.nih.g
delta-12 (omega-6) acyl-lipid desaturase (EC 1.14.19.-); FAD6	FAD6	At4g30950	Chl	P46312	EMS mutant	http://www.ncbi.nlm.nih.g
omega-3 acyl-lipid desat. (1.14.19.-; linoleate desaturase); FAD7	FAD7	At3g11170	Chl	P46310	EMS mutant	http://www.ncbi.nlm.nih.g
omega-3 acyl-lipid desat. (1.14.19.-; linoleate desaturase; temperature-sensitive); FAD8	FAD8	At5g05580	Chl	P48622	EMS mutant	http://www.ncbi.nlm.nih.g
long-chain acyl-CoA synthetase (involved in fatty acid export from the chloroplast)	6.2.1.3	At1g77590	Chl/En	AAM28876	biochem./loc.	http://www.ncbi.nlm.nih.g
long-chain acyl-CoA synthetase	6.2.1.3	At3g23790	Chl (?)	AAM28629	biochemical	http://www.ncbi.nlm.nih.g
long-chain acyl-CoA synthetase	6.2.1.3	At4g14070	Chl (?)	AAM28628	biochemical	http://www.ncbi.nlm.nih.g
permease involved in ER to thylakoid lipid transfer (TGD1)	TGD1	At1g19800	Chl/En	AAS75319	EMS mutant	http://www.ncbi.nlm.nih.g
CYTOSOLIC / ER PATHWAY						
choline/ethanolamine kinase	2.7.1.82	At2g26830	Cyt	AAC32242	by homology	http://www.ncbi.nlm.nih.g
choline kinase	2.7.1.32	At1g34100	Cyt	NP_174672	by homology	http://www.ncbi.nlm.nih.g
choline kinase	2.7.1.32	At1g71697	Cyt	AAP37670	by homology	http://www.ncbi.nlm.nih.g
choline kinase	2.7.1.32	At1g74320	Cyt	AAM98234	by homology	http://www.ncbi.nlm.nih.g
choline kinase	2.7.1.32	At4g09760	Cyt	CAB78099	by homology	http://www.ncbi.nlm.nih.g
ethanolamine-phosphate sytidyltransferase	2.7.7.14	At2g38670	Cyt	AAC67351	by homology	http://www.ncbi.nlm.nih.g
choline-phosphate cytidylyltransferase	2.7.7.15	At2g32260	Cyt	AAC69950	by homology	http://www.ncbi.nlm.nih.g
choline-phosphate cytidylyltransferase	2.7.7.15	At4g15130	Cyt	CAB78555	by homology	http://www.ncbi.nlm.nih.g
phosphatidylserine synthase	2.7.8.8	At1g15110	Cyt	AAL91226	by homology	http://www.ncbi.nlm.nih.g
phosphatidylserine decarboxylase	4.1.1.65 (alt. spl.)	At4g25970	Cyt	CAB79452	by homology	http://www.ncbi.nlm.nih.g
phosphatidylserine decarboxylase	4.1.1.65	At5g57190	Cyt	NP_200529	by homology	http://www.ncbi.nlm.nih.g
phosphoethanolamine N-methyltransferase	2.1.1.103	At1g48600	Cyt	Q944H0	by homology	http://www.ncbi.nlm.nih.g
phosphoethanolamine N-methyltransferase	2.1.1.103 (alt. spl.)	At1g73600	Cyt	Q9C6B9	by homology	http://www.ncbi.nlm.nih.g
phosphoethanolamine N-methyltransferase	2.1.1.103	At3g18000	Cyt	AAM10282	by homology	http://www.ncbi.nlm.nih.g
glycerol 3-phosphate acyltranerase	2.3.1.15	At3g11430	Cyt/ER	AAO50667	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



A: Leaf Glycerolipid Biosynthesis (Continued)

Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
glycerol 3-phosphate acyltranerase	2.3.1.15	At5g06090	Cyt/ER	NP_196227	by homology	http://www.ncbi.nlm.nih.g
1-acyl-sn-glycerol-3-phosphate acyltransferase (lysophosphatidic acid acyltransferase)	2.3.1.51	At1g51260	Cyt/ER	NP_175537	by homology	http://www.ncbi.nlm.nih.g
1-acyl-sn-glycerol-3-phosphate acyltransferase (lysophosphatidic acid acyltransferase)	2.3.1.51 (alt. spl.)	At1g75020	Cyt/ER	AAN6512	by homology	http://www.ncbi.nlm.nih.g
1-acyl-sn-glycerol-3-phosphate acyltransferase (lysophosphatidic acid acyltransferase)	2.3.1.51	At3g18850	Cyt/ER	AAP37821	by homology	http://www.ncbi.nlm.nih.g
1-acyl-sn-glycerol-3-phosphate acyltransferase (lysophosphatidic acid acyltransferase)	2.3.1.51	At3g57650	Cyt/ER	NP_567052	by homology	http://www.ncbi.nlm.nih.g
phosphatidate phosphatase	3.1.3.4	At1g15080	Cyt (?)	BAB47574	functional	http://www.ncbi.nlm.nih.g
phosphatidate phosphatase	3.1.3.4	At3g18220	Cyt/ER	NP_566602	by homology	http://www.ncbi.nlm.nih.g
diacylglycerol kinase	2.7.1.107	At5g63770	Cyt	AAR28755	biochemical	http://www.ncbi.nlm.nih.g
diacylglycerol kinase (DGK1)	2.7.1.107	At5g07920	Cyt	Q39017	functional (?)	http://www.ncbi.nlm.nih.g
diacylglycerol: choline phosphotransferase	2.7.8.2	At1g13560	Cyt	AAC61768	functional	http://www.ncbi.nlm.nih.g
diacylglycerol: choline phosphotransferase	2.7.8.2	At3g25585	Cyt	AAC61769	functional	http://www.ncbi.nlm.nih.g
delta-12 (omega-6) acyl-lipid desaturase; FAD2	FAD2	At3g12120	Cyt/ER	AAA32782	EMS mut./comp.	http://www.ncbi.nlm.nih.g
omega-3 acyl-lipid desaturase; FAD3;	FAD3	At2g29980	Cyt/ER	P48623	EMS mut./comp.	http://www.ncbi.nlm.nih.g
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase); CDS1	2.7.7.41	At1g62430	Cyt	O04928	functional (?)	http://www.ncbi.nlm.nih.g
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase)	2.7.7.41	At2g45150	Cyt	AAD32822	by homology	http://www.ncbi.nlm.nih.g
CDP-diacylglycerol synthase (phosphatidate cytidyltransferase)	2.7.7.41	At4g22340	Cyt	AAM14254	by homology	http://www.ncbi.nlm.nih.g
phosphatidylglycerophosphate synthase (PGP1)	2.7.8.5	At2g39290	Cyt (?)	BAD43832	functional	http://www.ncbi.nlm.nih.g
phosphatidylglycerophosphate synthase	2.7.8.5	At3g55030	Cyt (?)	AAL15250	by homology	http://www.ncbi.nlm.nih.g
phosphatidylglycerophosphate synthase	2.7.8.5	At4g04870	Cyt (?)	AAL24147	by homology	http://www.ncbi.nlm.nih.g

B. CHLOROPLAST (protein import, folding, maturation; transcription/translation)

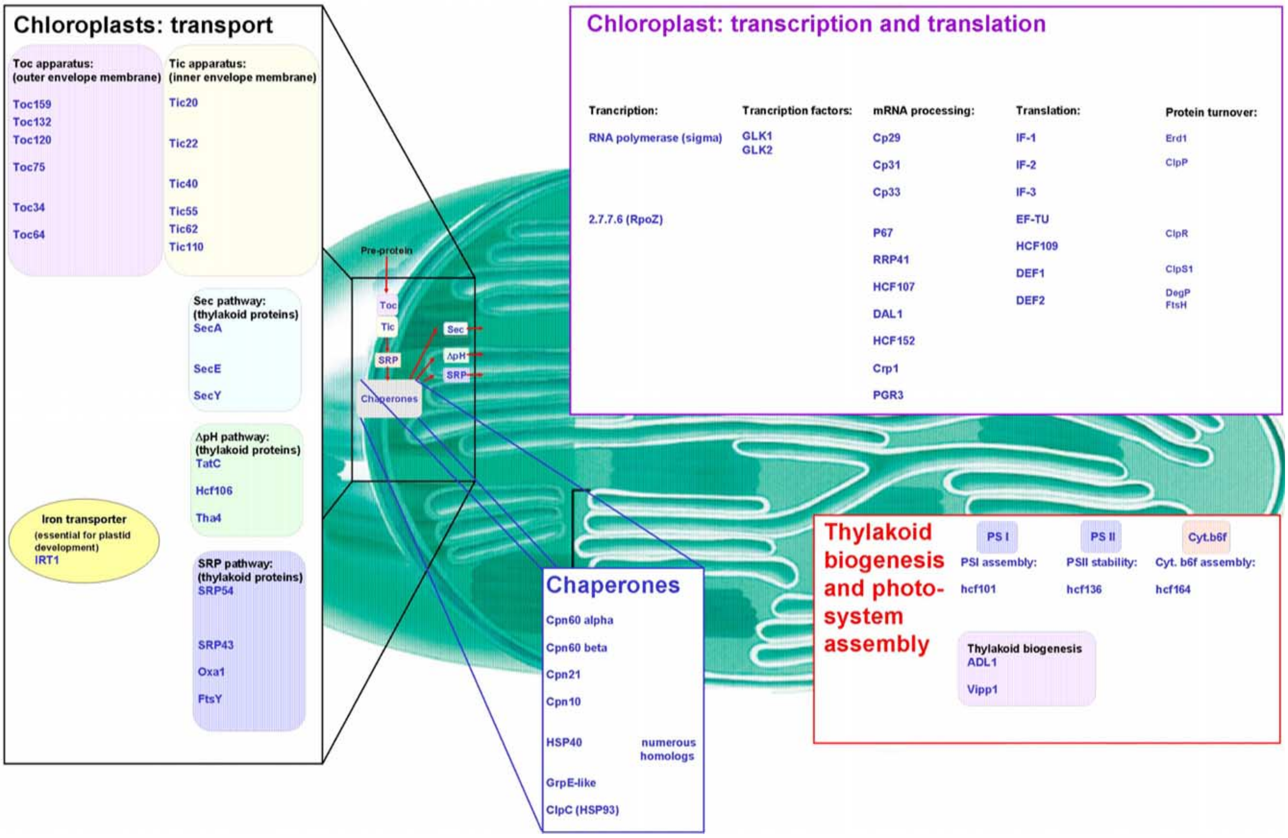
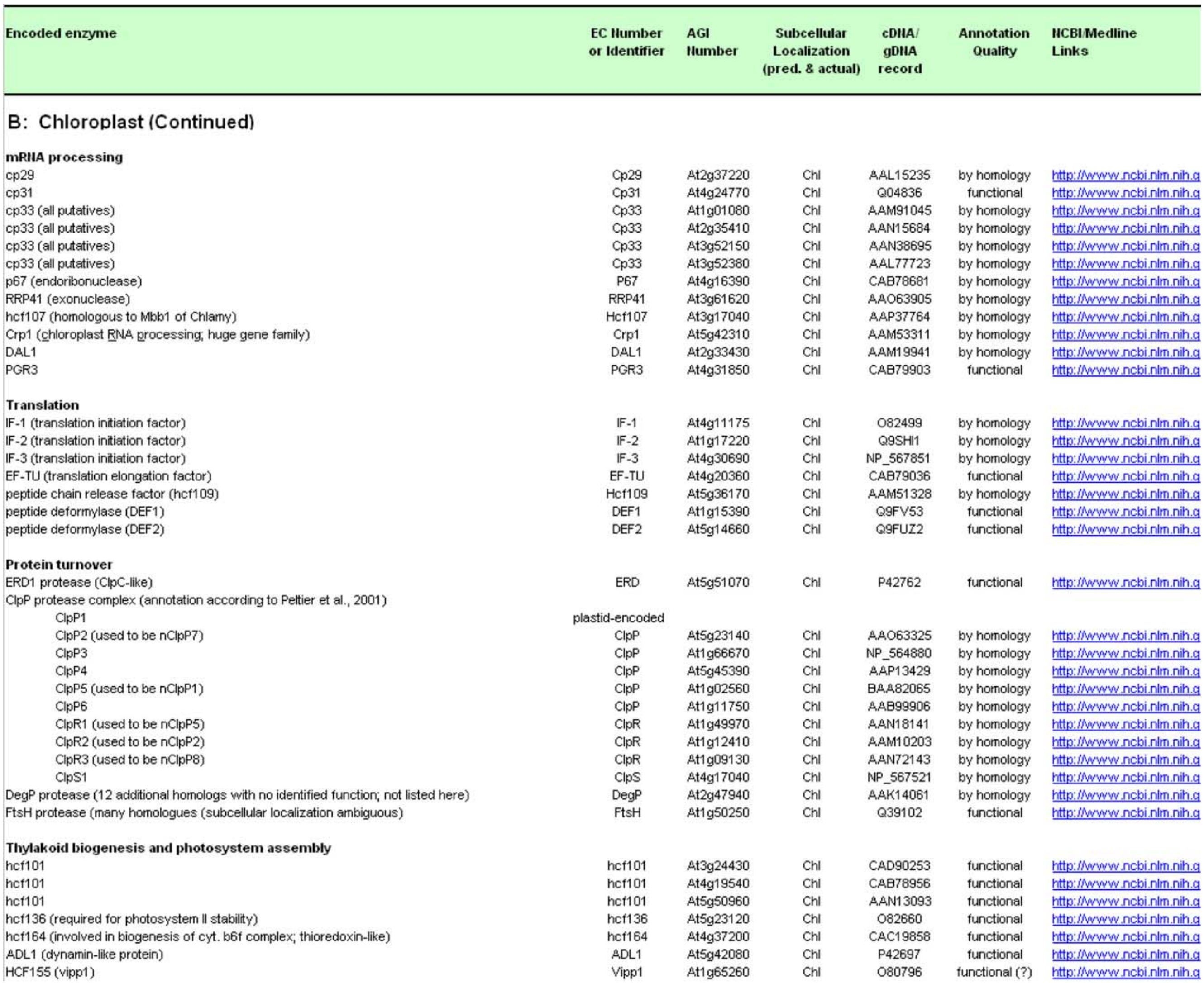


Fig. 3 (*continued*)

Encoded enzyme	**EC Number or Identifier**	**AGI Number**	**Subcellular Localization (pred. & actual)**	**cDNA/ gDNA record**	**Annotation Quality**	**NCBI/Medline Links**
B: Chloroplast (protein import, folding, maturation; transcription/translation)						
Protein import via envelope membrane						
Toc apparatus						
Toc159 (outer envelope membrane protein OEP86)	Toc159	At4g02510	Chl/En	AAM91483	by homology	http://www.ncbi.nlm.nih.g
Toc159 homolog Toc132 (unknown function)	Toc132	At2g16640	Chl/En	AAM20511	by homology	http://www.ncbi.nlm.nih.g
Toc159 homolog Toc120	Toc120	At3g16620	Chl/En	AAS97961	by homology	http://www.ncbi.nlm.nih.g
Toc75 (outer envelope membrane protein OEP75)	Toc75	At4g09080	Chl/En	CAB78032	by homology	http://www.ncbi.nlm.nih.g
(> 75 % homology; import-associated channel homolog)	Toc75	At3g46740	Chl/En	AAP21166	by homology	http://www.ncbi.nlm.nih.g
(> 60 % homology)	Toc75	At1g35860	Chl/En	NP_174821	by homology	http://www.ncbi.nlm.nih.g
Toc34 (GTP-binding protein)	Toc34	At5g05000	Chl/En	Q38906	functional	http://www.ncbi.nlm.nih.g
Toc34 (GTP-binding protein)	Toc34	At1g02280	Chl/En	AAL08304	by homology	http://www.ncbi.nlm.nih.g
Toc64 (homology to pea protein)	Toc64	At1g08980	Chl/En	AAO42800	by homology	http://www.ncbi.nlm.nih.g
Toc64 (homology to pea protein)	Toc64	At3g17970	Chl/En	NP_188424	by homology	http://www.ncbi.nlm.nih.g
Toc64 (homology to pea protein)	Toc64	At5g09420	Chl/En	NP_196504	by homology	http://www.ncbi.nlm.nih.g
Tic apparatus						
Tic20	Tic20	At1g04940	Chl/En	NP_171986	by homology	http://www.ncbi.nlm.nih.g
Tic20	Tic20	At4g03320	Chl/En	AAK32801	by homology	http://www.ncbi.nlm.nih.g
Tic22	Tic22	At3g23710	Chl/En	NP_189013	by homology	http://www.ncbi.nlm.nih.g
Tic22	Tic22	At4g33350	Chl/En	AAO63837	by homology	http://www.ncbi.nlm.nih.g
Tic40	Tic40	At5g16620	Chl/En	AAM13009	by homology	http://www.ncbi.nlm.nih.g
Tic55 (Rieske iron sulfur protein)	Tic55	At2g24820	Chl/En	AAD23030	by homology	http://www.ncbi.nlm.nih.g
Tic62	Tic62	At3g18890	Chl/En	AAP37762	by homology	http://www.ncbi.nlm.nih.g
Tic110 (IEP110)	Tic110	At1g06950	Chl/En	AAM20701	by homology	http://www.ncbi.nlm.nih.g
Pathway for nuclear-encoded, thylakoid-localized proteins						
Sec (secretory) pathway						
SecA-type chloroplast protein transport factor	SecA	At1g21650	Chl	AAM20701	by homology	http://www.ncbi.nlm.nih.g
SecA-type chloroplast protein transport factor	SecA	At4g01800	Chl	CAB77750	by homology	http://www.ncbi.nlm.nih.g
SecE-like protein translocase precursor (Sec61)	SecE	At4g14870	Chl	AAM20124	by homology	http://www.ncbi.nlm.nih.g
SecY preprotein translocase	SecY	At2g18710	Chl	Q38885	functional	http://www.ncbi.nlm.nih.g
Delta-pH pathway						
TatC (twin arginine translocation)	TatC	At2g01110	Chl	BAB62074	functional	http://www.ncbi.nlm.nih.g
Hcf106	Hcf106	At5g52440	Chl	AAD32652	functional	http://www.ncbi.nlm.nih.g
Tha4	Tha4	At5g28750	Chl	AAG40358	by homology	http://www.ncbi.nlm.nih.g
SRP (signal recognition particle)-dependent pathway for integral membrane proteins						
SRP54 (54 kDa)	SRP54	At1g15310	Chl	P49967	functional	http://www.ncbi.nlm.nih.g
SRP54 (54 kDa)	SRP54	At1g48900	Chl	AAK96524	by homology	http://www.ncbi.nlm.nih.g
SRP54 (54 kDa)	SRP54	At5g49500	Chl	P49966	functional	http://www.ncbi.nlm.nih.g
SRP43 (CAO)	SRP43	At2g47450	Chl	AAD01509	functional	http://www.ncbi.nlm.nih.g
Oxa1 (albino3; alb3; psbX)	Oxa1	At2g28800	Chl/Th	AAB61458	functional	http://www.ncbi.nlm.nih.g
FtsY	FtsY	At2g45770	Chl/En	CAB40382	functional	http://www.ncbi.nlm.nih.g
Transporters required for plastid development						
IRT1 (Fe transport protein)	IRT1	At4g19690	Chl/En	Q38856	functional	http://www.ncbi.nlm.nih.g
Protein folding / chaperonins						
Cpn60 (HSP60) (two subunits)						
alpha subunit (Rubisco subunit-binding)	Cpn60	At2g28000	Chl	P21238	functional	http://www.ncbi.nlm.nih.g
alpha subunit	Cpn60	At5g18820	Chl	NP_197383	by homology	http://www.ncbi.nlm.nih.g
beta subunit (Rubisco subunit-binding)	Cpn60	At5g56500	Chl	NP_200461	by homology	http://www.ncbi.nlm.nih.g
beta subunit	Cpn60	At1g55490	Chl	P21240	functional	http://www.ncbi.nlm.nih.g
Hsp93 (ClpC)	ClpC	At3g48870	Chl	AAL10478	by homology	http://www.ncbi.nlm.nih.g
	ClpC	At5g50920	Chl	AAM26692	by homology	http://www.ncbi.nlm.nih.g
Cpn21 (Cpn10, 20kDa protein)	Cpn21	At5g20720	Chl	O65282	functional	http://www.ncbi.nlm.nih.g
10 kDa chaperonin (Cpn10)	Cpn10	At1g14980	Chl/Mit (?)	P34893	functional	http://www.ncbi.nlm.nih.g
10 kDa chaperonin (Cpn10)	Cpn10	At1g23100	Chl/Cyt (?)	AAO50554	by homology	http://www.ncbi.nlm.nih.g
10 kDa chaperonin (Cpn10)	Cpn10	At3g60210	Chl (?)	AAO64777	by homology	http://www.ncbi.nlm.nih.g
10 kDa chaperonin (Cpn10)	Cpn10	At2g44650	Chl	AAC27467	by homology	http://www.ncbi.nlm.nih.g
HSP40 (DnaJ-like)	> 40 seq. in Arabidopsis; subcellular local. in several cases ambiguous					NA
GrpE-like chaperone	GrpE	At1g36390	Chl	AAM51251	by homology	http://www.ncbi.nlm.nih.g
GrpE-like chaperone	GrpE	At4g26780	Chl	AAP04032	by homology	http://www.ncbi.nlm.nih.g
GrpE-like chaperone	GrpE	At5g17710	Chl	AAL34228	by homology	http://www.ncbi.nlm.nih.g
GrpE-like chaperone	GrpE	At5g55200	Chl	AAM10113	by homology	http://www.ncbi.nlm.nih.g
Transcription						
RNA polymerase (Sigma factor)						
(SIG1; Isono et al., 1997; sigma factor 2; Allison, 2000; sigA; Hakimi et al., 2000; sigB; Tan	RNAPolySigma	At1g08540	Chl	AAB69385	functional	http://www.ncbi.nlm.nih.g
(SIG2; Isono et al., 1997; sigma factor 1; Allison, 2000)	RNAPolySigma	At1g64860	Chl	AAG40388	functional	http://www.ncbi.nlm.nih.g
(Sigma factor 70; SIG6)	RNAPolySigma	At2g36990	Chl	AAM14121	by homology	http://www.ncbi.nlm.nih.g
(Sigma factor C; genome project; SIG3; Isono et al., 1997 and Allison, 2000)	RNAPolySigma	At3g53920	Chl	AAM91534	functional	http://www.ncbi.nlm.nih.g
(SIG4)	RNAPolySigma	At5g13730	Chl	AF101075	functional (?)	http://www.ncbi.nlm.nih.g
(SIG5; Hakimi et al., 2000)	RNAPolySigma	At5g24120	Chl	CAA77213	by homology	http://www.ncbi.nlm.nih.g
RpoZ (RPOPT)	2.7.7.6	At2g24120	Chl	O24600	functional	http://www.ncbi.nlm.nih.g
Transcriptional regulators						
GLK (AtGLK2; golden 2-like; GARP superfam. of TFs (required for plastid developm.)	GLK	At5g44190	Chl	AAK16744	functional	http://www.ncbi.nlm.nih.g
AtGLK1 (golden 2-like)	GLK	At2g20570	Chl	AAK96791	functional	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
B: Chloroplast (Continued)						
mRNA processing						
cp29	Cp29	At2g37220	Chl	AAL15235	by homology	http://www.ncbi.nlm.nih.g
cp31	Cp31	At4g24770	Chl	Q04836	functional	http://www.ncbi.nlm.nih.g
cp33 (all putatives)	Cp33	At1g01080	Chl	AAM91045	by homology	http://www.ncbi.nlm.nih.g
cp33 (all putatives)	Cp33	At2g35410	Chl	AAN15684	by homology	http://www.ncbi.nlm.nih.g
cp33 (all putatives)	Cp33	At3g52150	Chl	AAN38695	by homology	http://www.ncbi.nlm.nih.g
cp33 (all putatives)	Cp33	At3g52380	Chl	AAL77723	by homology	http://www.ncbi.nlm.nih.g
p67 (endoribonuclease)	P67	At4g16390	Chl	CAB78681	by homology	http://www.ncbi.nlm.nih.g
RRP41 (exonuclease)	RRP41	At3g61620	Chl	AAO63905	by homology	http://www.ncbi.nlm.nih.g
hcf107 (homologous to Mbb1 of Chlamy)	Hcf107	At3g17040	Chl	AAP37764	by homology	http://www.ncbi.nlm.nih.g
Crp1 (chloroplast RNA processing; huge gene family)	Crp1	At5g42310	Chl	AAM53311	by homology	http://www.ncbi.nlm.nih.g
DAL1	DAL1	At2g33430	Chl	AAM19941	by homology	http://www.ncbi.nlm.nih.g
PGR3	PGR3	At4g31850	Chl	CAB79903	functional	http://www.ncbi.nlm.nih.g
Translation						
IF-1 (translation initiation factor)	IF-1	At4g11175	Chl	O82499	by homology	http://www.ncbi.nlm.nih.g
IF-2 (translation initiation factor)	IF-2	At1g17220	Chl	Q9SHI1	by homology	http://www.ncbi.nlm.nih.g
IF-3 (translation initiation factor)	IF-3	At4g30690	Chl	NP_567851	by homology	http://www.ncbi.nlm.nih.g
EF-TU (translation elongation factor)	EF-TU	At4g20360	Chl	CAB79036	functional	http://www.ncbi.nlm.nih.g
peptide chain release factor (hcf109)	Hcf109	At5g36170	Chl	AAM51328	by homology	http://www.ncbi.nlm.nih.g
peptide deformylase (DEF1)	DEF1	At1g15390	Chl	Q9FV53	functional	http://www.ncbi.nlm.nih.g
peptide deformylase (DEF2)	DEF2	At5g14660	Chl	Q9FUZ2	functional	http://www.ncbi.nlm.nih.g
Protein turnover						
ERD1 protease (ClpC-like)	ERD	At5g51070	Chl	P42762	functional	http://www.ncbi.nlm.nih.g
ClpP protease complex (annotation according to Peltier et al., 2001)						
ClpP1	plastid-encoded					
ClpP2 (used to be nClpP7)	ClpP	At5g23140	Chl	AAO63325	by homology	http://www.ncbi.nlm.nih.g
ClpP3	ClpP	At1g66670	Chl	NP_564880	by homology	http://www.ncbi.nlm.nih.g
ClpP4	ClpP	At5g45390	Chl	AAP13429	by homology	http://www.ncbi.nlm.nih.g
ClpP5 (used to be nClpP1)	ClpP	At1g02560	Chl	BAA82065	by homology	http://www.ncbi.nlm.nih.g
ClpP6	ClpP	At1g11750	Chl	AAB99906	by homology	http://www.ncbi.nlm.nih.g
ClpR1 (used to be nClpP5)	ClpR	At1g49970	Chl	AAN18141	by homology	http://www.ncbi.nlm.nih.g
ClpR2 (used to be nClpP2)	ClpR	At1g12410	Chl	AAM10203	by homology	http://www.ncbi.nlm.nih.g
ClpR3 (used to be nClpP8)	ClpR	At1g09130	Chl	AAN72143	by homology	http://www.ncbi.nlm.nih.g
ClpS1	ClpS	At4g17040	Chl	NP_567521	by homology	http://www.ncbi.nlm.nih.g
DegP protease (12 additional homologs with no identified function; not listed here)	DegP	At2g47940	Chl	AAK14061	by homology	http://www.ncbi.nlm.nih.g
FtsH protease (many homologues (subcellular localization ambiguous)	FtsH	At1g50250	Chl	Q39102	functional	http://www.ncbi.nlm.nih.g
Thylakoid biogenesis and photosystem assembly						
hcf101	hcf101	At3g24430	Chl	CAD90253	functional	http://www.ncbi.nlm.nih.g
hcf101	hcf101	At4g19540	Chl	CAB78956	functional	http://www.ncbi.nlm.nih.g
hcf101	hcf101	At5g50960	Chl	AAN13093	functional	http://www.ncbi.nlm.nih.g
hcf136 (required for photosystem II stability)	hcf136	At5g23120	Chl	O82660	functional	http://www.ncbi.nlm.nih.g
hcf164 (involved in biogenesis of cyt. b6f complex; thioredoxin-like)	hcf164	At4g37200	Chl	CAC19858	functional	http://www.ncbi.nlm.nih.g
ADL1 (dynamin-like protein)	ADL1	At5g42080	Chl	P42697	functional	http://www.ncbi.nlm.nih.g
HCF155 (vipp1)	Vipp1	At1g65260	Chl	O80796	functional (?)	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

attributes from a window in GeneSpring®. Similar standards have been proposed for the documentation of proteomics (Taylor et al., 2003) and metabolomics (Bino et al., 2004) experiments, and both formats can potentially be uploaded into GeneSpring®. Other commercial software packages feature similar capabilities (and are just as expensive) but we did not find comparable capabilities in any of the currently available open-source software packages. Thus, an integration of *A. thaliana*-specific biochemical pathway maps into GeneSpring® appeared to be the most sensible short-term approach to provide the *A. thaliana* research community with a tool for the analysis of complex post-genomic data sets in the context of well-annotated biochemical pathways.

3.1. Biochemical pathway maps (BioPathAtMAPS)

The experimental evidence regarding the presence of pathways in *A. thaliana* was evaluated and matched with the occurrence predicted based on the apparent coding capacity of the entirely sequenced genome (The Arabidopsis Genome Initiative, 2000). Maps were generated to represent current knowledge regarding numerous pathways involved in light perception, metabolism, protein trafficking, and signal transduction (`BioPathAtMAPS` module). In `BioPathAt` biochemical pathways are treated as modules that can be reassembled in various ways so that separate maps can be used to visualize the connections between path-

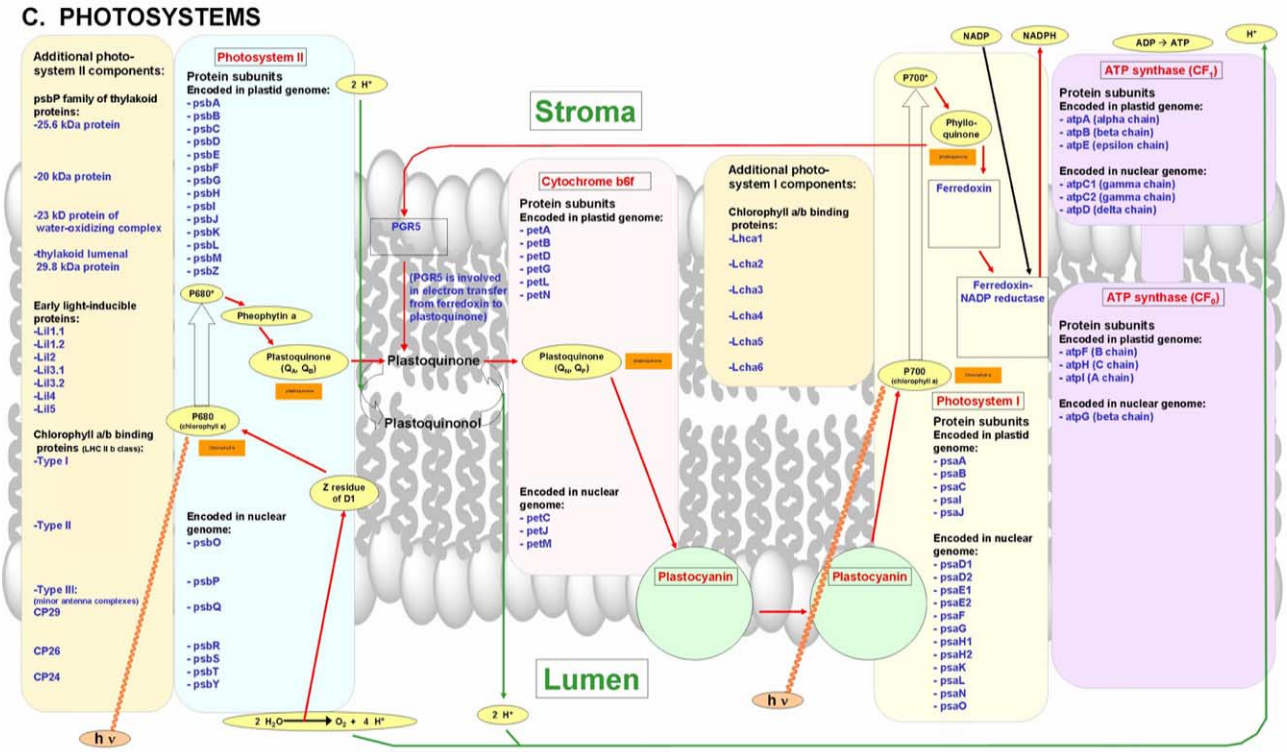
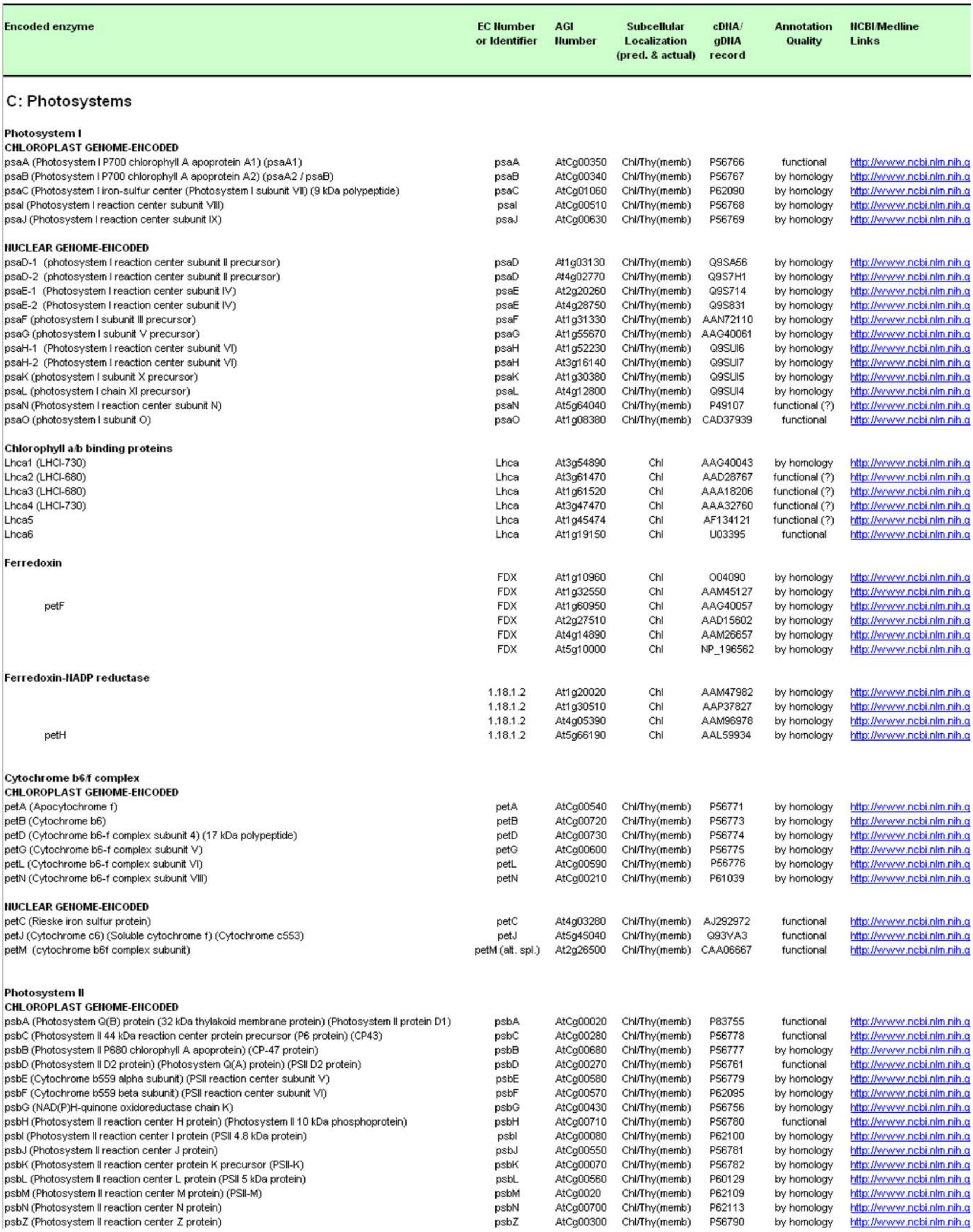


Fig. 3 (*continued*)

ways in different biological contexts. For example, one map shows glycerolipid biosynthesis in the leaf cytosol and chloroplasts, whereas another map summarizes reactions converting storage triacylglycerols into sucrose in seeds. Overview maps (e.g., intermediary carbon metabolism) show full details for certain featured pathways (e.g., glycolysis/gluconeogenesis, pentose phosphate pathway, Calvin cycle, TCA cycle) and provide links to other pathways derived from intermediates of the featured pathways (e.g., amino acids, isoprenoids, nucleotides). Images of the currently available biochemical pathway maps are shown in the Fig. 3. `BioPathAtMAPS` files (and future updates) can be downloaded at http://www.ibc.wsu.edu/research/lange/index.html.

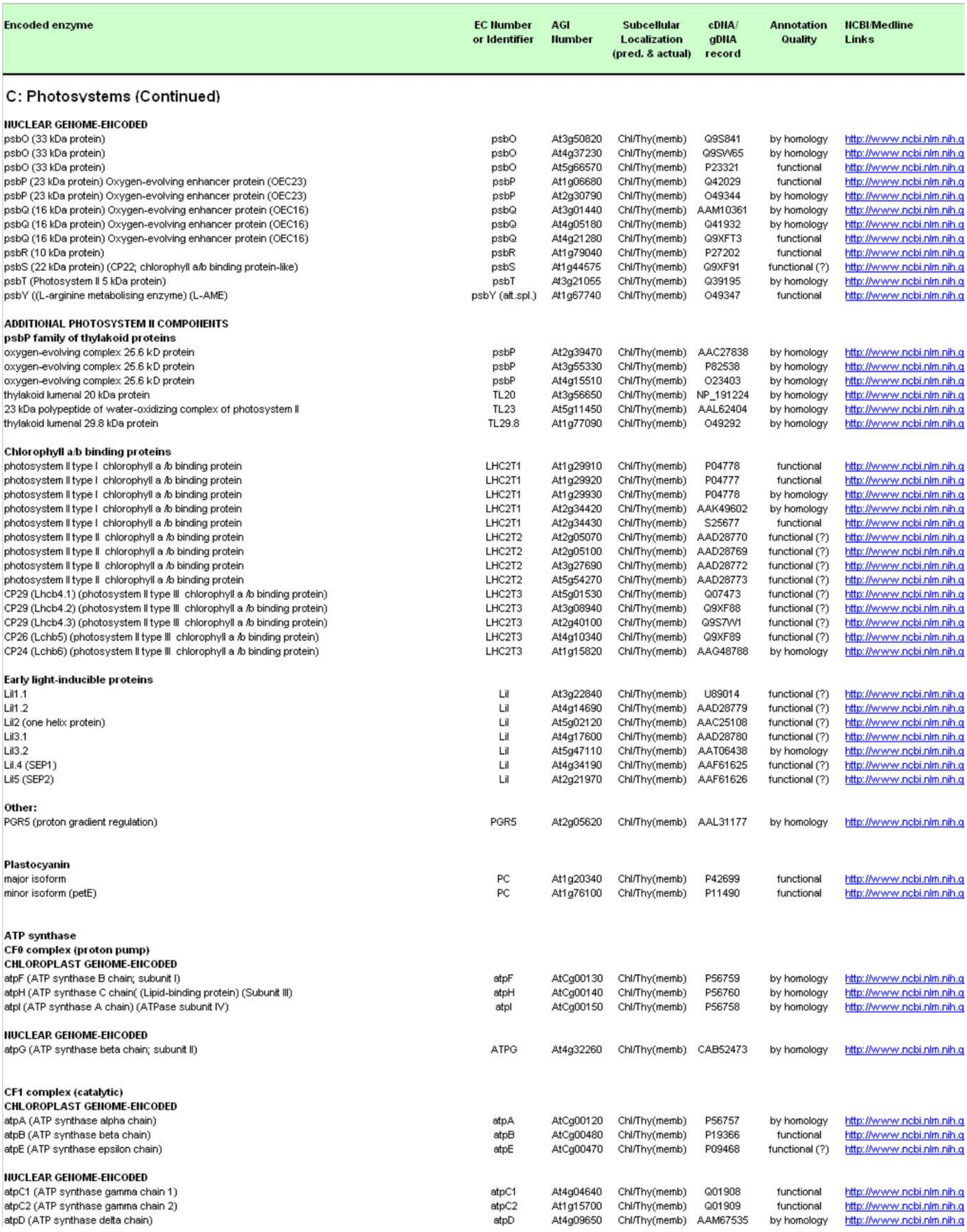
3.2. *A. thaliana gene/enzyme function database (BioPathAtDB)*

It is noteworthy that experimental evidence is available for only about 10% of all genes in *A. thaliana* and only another 40% of *A. thaliana* genes display sufficient homology to those of other organisms so that a sequence-based annotation might be feasible (Wortman et al., 2003). However, recent publications have underscored that the annotation of gene sequences in the public databases as having a particular or putative function in a specific biochemical pathway must be viewed with considerable caution (Mekhedov et al., 2000; Aubourg et al., 2002; Lange and Ghassemian, 2003; Raes et al., 2003; Costa et al., 2003; Dunn et al., 2004; Kim et al., 2004). Integrative genome annotation involves keyword and sequence-based searches against public databases, the use of algorithms that predict the subcellular localization of enzymes, and a manual evaluation of available annotation based on published literature and knowledge about the tissue-specific mRNA expression. Our laboratory has performed a comprehensive in silico analysis for genes involved in pathways that lead to the production of various isoprenoids in *A. thaliana* (Lange and Ghassemian, 2003) and we have used the same thorough approach to generate gene annotation tables for additional pathways (photosynthesis, uptake of pre-proteins into chloroplasts; plastidial gene expression machinery; intermediary carbon metabolism [incl. glycolysis, pentose phosphate pathway, citric acid cycle, glyoxylate cycle]; biosynthesis of amino acids; carbohydrate metabolism [monosaccharides, phytic acid, ascorbic



Encoded enzyme	**EC Number or Identifier**	**AGI Number**	**Subcellular Localization (pred. & actual)**	**cDNA/ gDNA record**	**Annotation Quality**	**NCBI/Medline Links**
C: Photosystems						
Photosystem I						
CHLOROPLAST GENOME-ENCODED						
psaA (Photosystem I P700 chlorophyll A apoprotein A1) (psaA1)	psaA	AtCg00350	Chl/Thy(memb)	P56766	functional	http://www.ncbi.nlm.nih.g
psaB (Photosystem I P700 chlorophyll A apoprotein A2) (psaA2 / psaB)	psaB	AtCg00340	Chl/Thy(memb)	P56767	by homology	http://www.ncbi.nlm.nih.g
psaC (Photosystem I iron-sulfur center (Photosystem I subunit VII) (9 kDa polypeptide)	psaC	AtCg01060	Chl/Thy(memb)	P62090	by homology	http://www.ncbi.nlm.nih.g
psaI (Photosystem I reaction center subunit VIII)	psaI	AtCg00510	Chl/Thy(memb)	P56768	by homology	http://www.ncbi.nlm.nih.g
psaJ (Photosystem I reaction center subunit IX)	psaJ	AtCg00630	Chl/Thy(memb)	P56769	by homology	http://www.ncbi.nlm.nih.g
NUCLEAR GENOME-ENCODED						
psaD-1 (photosystem I reaction center subunit II precursor)	psaD	At1g03130	Chl/Thy(memb)	Q9SA56	by homology	http://www.ncbi.nlm.nih.g
psaD-2 (photosystem I reaction center subunit II precursor)	psaD	At4g02770	Chl/Thy(memb)	Q9S7H1	by homology	http://www.ncbi.nlm.nih.g
psaE-1 (Photosystem I reaction center subunit IV)	psaE	At2g20260	Chl/Thy(memb)	Q9S714	by homology	http://www.ncbi.nlm.nih.g
psaE-2 (Photosystem I reaction center subunit IV)	psaE	At4g28750	Chl/Thy(memb)	Q9S831	by homology	http://www.ncbi.nlm.nih.g
psaF (photosystem I subunit III precursor)	psaF	At1g31330	Chl/Thy(memb)	AAN72110	by homology	http://www.ncbi.nlm.nih.g
psaG (photosystem I subunit V precursor)	psaG	At1g55670	Chl/Thy(memb)	AAG40061	by homology	http://www.ncbi.nlm.nih.g
psaH-1 (Photosystem I reaction center subunit VI)	psaH	At1g52230	Chl/Thy(memb)	Q9SUI6	by homology	http://www.ncbi.nlm.nih.g
psaH-2 (Photosystem I reaction center subunit VI)	psaH	At3g16140	Chl/Thy(memb)	Q9SUI7	by homology	http://www.ncbi.nlm.nih.g
psaK (photosystem I subunit X precursor)	psaK	At1g30380	Chl/Thy(memb)	Q9SUI5	by homology	http://www.ncbi.nlm.nih.g
psaL (photosystem I chain XI precursor)	psaL	At4g12800	Chl/Thy(memb)	Q9SUI4	by homology	http://www.ncbi.nlm.nih.g
psaN (Photosystem I reaction center subunit N)	psaN	At5g64040	Chl/Thy(memb)	P49107	functional (?)	http://www.ncbi.nlm.nih.g
psaO (photosystem I subunit O)	psaO	At1g08380	Chl/Thy(memb)	CAD37939	functional	http://www.ncbi.nlm.nih.g
Chlorophyll a/b binding proteins						
Lhca1 (LHCI-730)	Lhca	At3g54890	Chl	AAG40043	by homology	http://www.ncbi.nlm.nih.g
Lhca2 (LHCI-680)	Lhca	At3g61470	Chl	AAD28767	functional (?)	http://www.ncbi.nlm.nih.g
Lhca3 (LHCI-680)	Lhca	At1g61520	Chl	AAA18206	functional (?)	http://www.ncbi.nlm.nih.g
Lhca4 (LHCI-730)	Lhca	At3g47470	Chl	AAA32760	functional (?)	http://www.ncbi.nlm.nih.g
Lhca5	Lhca	At1g45474	Chl	AF134121	functional (?)	http://www.ncbi.nlm.nih.g
Lhca6	Lhca	At1g19150	Chl	U03395	functional	http://www.ncbi.nlm.nih.g
Ferredoxin						
	FDX	At1g10960	Chl	O04090	by homology	http://www.ncbi.nlm.nih.g
	FDX	At1g32550	Chl	AAM45127	by homology	http://www.ncbi.nlm.nih.g
petF	FDX	At1g60950	Chl	AAG40057	by homology	http://www.ncbi.nlm.nih.g
	FDX	At2g27510	Chl	AAD15602	by homology	http://www.ncbi.nlm.nih.g
	FDX	At4g14890	Chl	AAM26657	by homology	http://www.ncbi.nlm.nih.g
	FDX	At5g10000	Chl	NP_196562	by homology	http://www.ncbi.nlm.nih.g
Ferredoxin-NADP reductase						
	1.18.1.2	At1g20020	Chl	AAM47982	by homology	http://www.ncbi.nlm.nih.g
	1.18.1.2	At1g30510	Chl	AAP37827	by homology	http://www.ncbi.nlm.nih.g
	1.18.1.2	At4g05390	Chl	AAM96978	by homology	http://www.ncbi.nlm.nih.g
petH	1.18.1.2	At5g66190	Chl	AAL59934	by homology	http://www.ncbi.nlm.nih.g
Cytochrome b6/f complex						
CHLOROPLAST GENOME-ENCODED						
petA (Apocytochrome f)	petA	AtCg00540	Chl/Thy(memb)	P56771	by homology	http://www.ncbi.nlm.nih.g
petB (Cytochrome b6)	petB	AtCg00720	Chl/Thy(memb)	P56773	by homology	http://www.ncbi.nlm.nih.g
petD (Cytochrome b6-f complex subunit 4) (17 kDa polypeptide)	petD	AtCg00730	Chl/Thy(memb)	P56774	by homology	http://www.ncbi.nlm.nih.g
petG (Cytochrome b6-f complex subunit V)	petG	AtCg00600	Chl/Thy(memb)	P56775	by homology	http://www.ncbi.nlm.nih.g
petL (Cytochrome b6-f complex subunit VI)	petL	AtCg00590	Chl/Thy(memb)	P56776	by homology	http://www.ncbi.nlm.nih.g
petN (Cytochrome b6-f complex subunit VIII)	petN	AtCg00210	Chl/Thy(memb)	P61039	by homology	http://www.ncbi.nlm.nih.g
NUCLEAR GENOME-ENCODED						
petC (Rieske iron sulfur protein)	petC	At4g03280	Chl/Thy(memb)	AJ292972	functional	http://www.ncbi.nlm.nih.g
petJ (Cytochrome c6) (Soluble cytochrome f) (Cytochrome c553)	petJ	At5g45040	Chl/Thy(memb)	Q93VA3	functional	http://www.ncbi.nlm.nih.g
petM (cytochrome b6f complex subunit)	petM (alt. spl.)	At2g26500	Chl/Thy(memb)	CAA06667	functional	http://www.ncbi.nlm.nih.g
Photosystem II						
CHLOROPLAST GENOME-ENCODED						
psbA (Photosystem Q(B) protein (32 kDa thylakoid membrane protein) (Photosystem II protein D1)	psbA	AtCg00020	Chl/Thy(memb)	P83755	functional	http://www.ncbi.nlm.nih.g
psbC (Photosystem II 44 kDa reaction center protein precursor (P6 protein) (CP43)	psbC	AtCg00280	Chl/Thy(memb)	P56778	functional	http://www.ncbi.nlm.nih.g
psbB (Photosystem II P680 chlorophyll A apoprotein) (CP-47 protein)	psbB	AtCg00680	Chl/Thy(memb)	P56777	by homology	http://www.ncbi.nlm.nih.g
psbD (Photosystem II D2 protein) (Photosystem Q(A) protein) (PSII D2 protein)	psbD	AtCg00270	Chl/Thy(memb)	P56761	functional	http://www.ncbi.nlm.nih.g
psbE (Cytochrome b559 alpha subunit) (PSII reaction center subunit V)	psbE	AtCg00580	Chl/Thy(memb)	P56779	by homology	http://www.ncbi.nlm.nih.g
psbF (Cytochrome b559 beta subunit) (PSII reaction center subunit VI)	psbF	AtCg00570	Chl/Thy(memb)	P62095	by homology	http://www.ncbi.nlm.nih.g
psbG (NAD(P)H-quinone oxidoreductase chain K)	psbG	AtCg00430	Chl/Thy(memb)	P56756	by homology	http://www.ncbi.nlm.nih.g
psbH (Photosystem II reaction center H protein) (Photosystem II 10 kDa phosphoprotein)	psbH	AtCg00710	Chl/Thy(memb)	P56780	functional	http://www.ncbi.nlm.nih.g
psbI (Photosystem II reaction center I protein (PSII 4.8 kDa protein)	psbI	AtCg00080	Chl/Thy(memb)	P62100	by homology	http://www.ncbi.nlm.nih.g
psbJ (Photosystem II reaction center J protein)	psbJ	AtCg00550	Chl/Thy(memb)	P56781	by homology	http://www.ncbi.nlm.nih.g
psbK (Photosystem II reaction center protein K precursor (PSII-K)	psbK	AtCg00070	Chl/Thy(memb)	P56782	by homology	http://www.ncbi.nlm.nih.g
psbL (Photosystem II reaction center L protein (PSII 5 kDa protein)	psbL	AtCg00560	Chl/Thy(memb)	P60129	by homology	http://www.ncbi.nlm.nih.g
psbM (Photosystem II reaction center M protein) (PSII-M)	psbM	AtCg0020	Chl/Thy(memb)	P62109	by homology	http://www.ncbi.nlm.nih.g
psbN (Photosystem II reaction center N protein)	psbN	AtCg00700	Chl/Thy(memb)	P62113	by homology	http://www.ncbi.nlm.nih.g
psbZ (Photosystem II reaction center Z protein)	psbZ	AtCg00300	Chl/Thy(memb)	P56790	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
C: Photosystems (Continued)						
NUCLEAR GENOME-ENCODED						
psbO (33 kDa protein)	psbO	At3g50820	Chl/Thy(memb)	Q9S841	by homology	http://www.ncbi.nlm.nih.g
psbO (33 kDa protein)	psbO	At4g37230	Chl/Thy(memb)	Q9SW65	by homology	http://www.ncbi.nlm.nih.g
psbO (33 kDa protein)	psbO	At5g66570	Chl/Thy(memb)	P23321	functional	http://www.ncbi.nlm.nih.g
psbP (23 kDa protein) Oxygen-evolving enhancer protein (OEC23)	psbP	At1g06680	Chl/Thy(memb)	Q42029	functional	http://www.ncbi.nlm.nih.g
psbP (23 kDa protein) Oxygen-evolving enhancer protein (OEC23)	psbP	At2g30790	Chl/Thy(memb)	O49344	by homology	http://www.ncbi.nlm.nih.g
psbQ (16 kDa protein) Oxygen-evolving enhancer protein (OEC16)	psbQ	At3g01440	Chl/Thy(memb)	AAM10361	by homology	http://www.ncbi.nlm.nih.g
psbQ (16 kDa protein) Oxygen-evolving enhancer protein (OEC16)	psbQ	At4g05180	Chl/Thy(memb)	Q41932	by homology	http://www.ncbi.nlm.nih.g
psbQ (16 kDa protein) Oxygen-evolving enhancer protein (OEC16)	psbQ	At4g21280	Chl/Thy(memb)	Q9XFT3	functional	http://www.ncbi.nlm.nih.g
psbR (10 kDa protein)	psbR	At1g79040	Chl/Thy(memb)	P27202	functional	http://www.ncbi.nlm.nih.g
psbS (22 kDa protein) (CP22; chlorophyll a/b binding protein-like)	psbS	At1g44575	Chl/Thy(memb)	Q9XF91	functional (?)	http://www.ncbi.nlm.nih.g
psbT (Photosystem II 5 kDa protein)	psbT	At3g21055	Chl/Thy(memb)	Q39195	by homology	http://www.ncbi.nlm.nih.g
psbY ((L-arginine metabolising enzyme) (L-AME)	psbY (alt.spl.)	At1g67740	Chl/Thy(memb)	O49347	functional	http://www.ncbi.nlm.nih.g
ADDITIONAL PHOTOSYSTEM II COMPONENTS						
psbP family of thylakoid proteins						
oxygen-evolving complex 25.6 kD protein	psbP	At2g39470	Chl/Thy(memb)	AAC27838	by homology	http://www.ncbi.nlm.nih.g
oxygen-evolving complex 25.6 kD protein	psbP	At3g55330	Chl/Thy(memb)	P82538	by homology	http://www.ncbi.nlm.nih.g
oxygen-evolving complex 25.6 kD protein	psbP	At4g15510	Chl/Thy(memb)	O23403	by homology	http://www.ncbi.nlm.nih.g
thylakoid lumenal 20 kDa protein	TL20	At3g56650	Chl/Thy(memb)	NP_191224	by homology	http://www.ncbi.nlm.nih.g
23 kDa polypeptide of water-oxidizing complex of photosystem II	TL23	At5g11450	Chl/Thy(memb)	AAL62404	by homology	http://www.ncbi.nlm.nih.g
thylakoid lumenal 29.8 kDa protein	TL29.8	At1g77090	Chl/Thy(memb)	O49292	by homology	http://www.ncbi.nlm.nih.g
Chlorophyll a/b binding proteins						
photosystem II type I chlorophyll a /b binding protein	LHC2T1	At1g29910	Chl/Thy(memb)	P04778	functional	http://www.ncbi.nlm.nih.g
photosystem II type I chlorophyll a /b binding protein	LHC2T1	At1g29920	Chl/Thy(memb)	P04777	functional	http://www.ncbi.nlm.nih.g
photosystem II type I chlorophyll a /b binding protein	LHC2T1	At1g29930	Chl/Thy(memb)	P04778	by homology	http://www.ncbi.nlm.nih.g
photosystem II type I chlorophyll a /b binding protein	LHC2T1	At2g34420	Chl/Thy(memb)	AAK49602	by homology	http://www.ncbi.nlm.nih.g
photosystem II type I chlorophyll a /b binding protein	LHC2T1	At2g34430	Chl/Thy(memb)	S25677	functional	http://www.ncbi.nlm.nih.g
photosystem II type II chlorophyll a /b binding protein	LHC2T2	At2g05070	Chl/Thy(memb)	AAD28770	functional (?)	http://www.ncbi.nlm.nih.g
photosystem II type II chlorophyll a /b binding protein	LHC2T2	At2g05100	Chl/Thy(memb)	AAD28769	functional (?)	http://www.ncbi.nlm.nih.g
photosystem II type II chlorophyll a /b binding protein	LHC2T2	At3g27690	Chl/Thy(memb)	AAD28772	functional (?)	http://www.ncbi.nlm.nih.g
photosystem II type II chlorophyll a /b binding protein	LHC2T2	At5g54270	Chl/Thy(memb)	AAD28773	functional (?)	http://www.ncbi.nlm.nih.g
CP29 (Lhcb4.1) (photosystem II type III chlorophyll a /b binding protein)	LHC2T3	At5g01530	Chl/Thy(memb)	Q07473	functional (?)	http://www.ncbi.nlm.nih.g
CP29 (Lhcb4.2) (photosystem II type III chlorophyll a /b binding protein)	LHC2T3	At3g08940	Chl/Thy(memb)	Q9XF88	functional (?)	http://www.ncbi.nlm.nih.g
CP29 (Lhcb4.3) (photosystem II type III chlorophyll a /b binding protein)	LHC2T3	At2g40100	Chl/Thy(memb)	Q9S7W1	functional (?)	http://www.ncbi.nlm.nih.g
CP26 (Lchb5) (photosystem II type III chlorophyll a /b binding protein)	LHC2T3	At4g10340	Chl/Thy(memb)	Q9XF89	functional (?)	http://www.ncbi.nlm.nih.g
CP24 (Lchb6) (photosystem II type III chlorophyll a /b binding protein)	LHC2T3	At1g15820	Chl/Thy(memb)	AAG48788	by homology	http://www.ncbi.nlm.nih.g
Early light-inducible proteins						
Lil1.1	Lil	At3g22840	Chl/Thy(memb)	U89014	functional (?)	http://www.ncbi.nlm.nih.g
Lil1.2	Lil	At4g14690	Chl/Thy(memb)	AAD28779	functional (?)	http://www.ncbi.nlm.nih.g
Lil2 (one helix protein)	Lil	At5g02120	Chl/Thy(memb)	AAC25108	functional (?)	http://www.ncbi.nlm.nih.g
Lil3.1	Lil	At4g17600	Chl/Thy(memb)	AAD28780	functional (?)	http://www.ncbi.nlm.nih.g
Lil3.2	Lil	At5g47110	Chl/Thy(memb)	AAT06438	by homology	http://www.ncbi.nlm.nih.g
Lil.4 (SEP1)	Lil	At4g34190	Chl/Thy(memb)	AAF61625	functional (?)	http://www.ncbi.nlm.nih.g
Lil5 (SEP2)	Lil	At2g21970	Chl/Thy(memb)	AAF61626	functional (?)	http://www.ncbi.nlm.nih.g
Other:						
PGR5 (proton gradient regulation)	PGR5	At2g05620	Chl/Thy(memb)	AAL31177	by homology	http://www.ncbi.nlm.nih.g
Plastocyanin						
major isoform	PC	At1g20340	Chl/Thy(memb)	P42699	functional	http://www.ncbi.nlm.nih.g
minor isoform (petE)	PC	At1g76100	Chl/Thy(memb)	P11490	functional	http://www.ncbi.nlm.nih.g
ATP synthase						
CF0 complex (proton pump)						
CHLOROPLAST GENOME-ENCODED						
atpF (ATP synthase B chain; subunit I)	atpF	AtCg00130	Chl/Thy(memb)	P56759	by homology	http://www.ncbi.nlm.nih.g
atpH (ATP synthase C chain((Lipid-binding protein) (Subunit III)	atpH	AtCg00140	Chl/Thy(memb)	P56760	by homology	http://www.ncbi.nlm.nih.g
atpI (ATP synthase A chain) (ATPase subunit IV)	atpI	AtCg00150	Chl/Thy(memb)	P56758	by homology	http://www.ncbi.nlm.nih.g
NUCLEAR GENOME-ENCODED						
atpG (ATP synthase beta chain; subunit II)	ATPG	At4g32260	Chl/Thy(memb)	CAB52473	by homology	http://www.ncbi.nlm.nih.g
CF1 complex (catalytic)						
CHLOROPLAST GENOME-ENCODED						
atpA (ATP synthase alpha chain)	atpA	AtCg00120	Chl/Thy(memb)	P56757	by homology	http://www.ncbi.nlm.nih.g
atpB (ATP synthase beta chain)	atpB	AtCg00480	Chl/Thy(memb)	P19366	functional	http://www.ncbi.nlm.nih.g
atpE (ATP synthase epsilon chain)	atpE	AtCg00470	Chl/Thy(memb)	P09468	functional (?)	http://www.ncbi.nlm.nih.g
NUCLEAR GENOME-ENCODED						
atpC1 (ATP synthase gamma chain 1)	atpC1	At4g04640	Chl/Thy(memb)	Q01908	functional	http://www.ncbi.nlm.nih.g
atpC2 (ATP synthase gamma chain 2)	atpC2	At1g15700	Chl/Thy(memb)	Q01909	functional	http://www.ncbi.nlm.nih.g
atpD (ATP synthase delta chain)	atpD	At4g09650	Chl/Thy(memb)	AAM67535	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

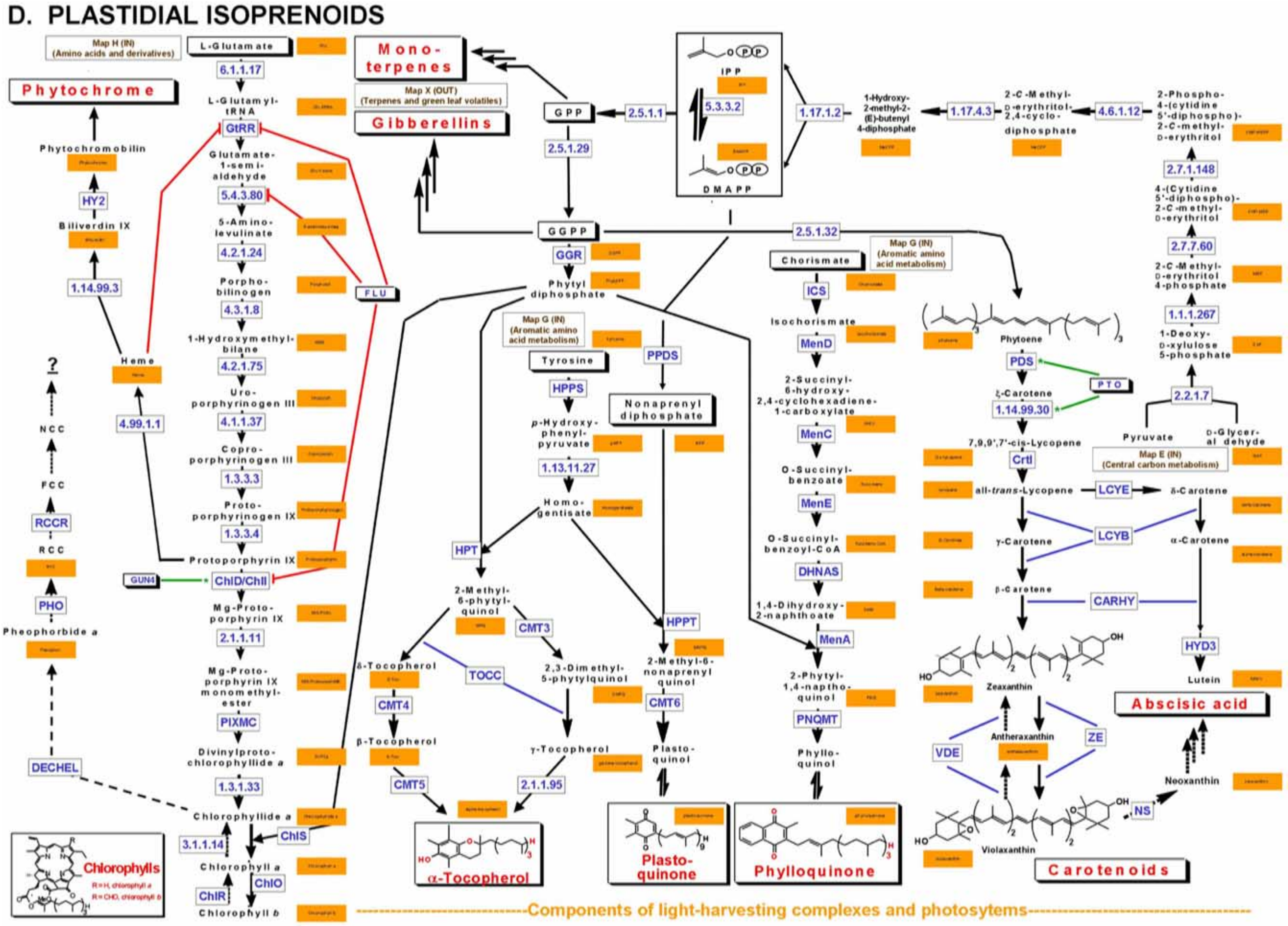
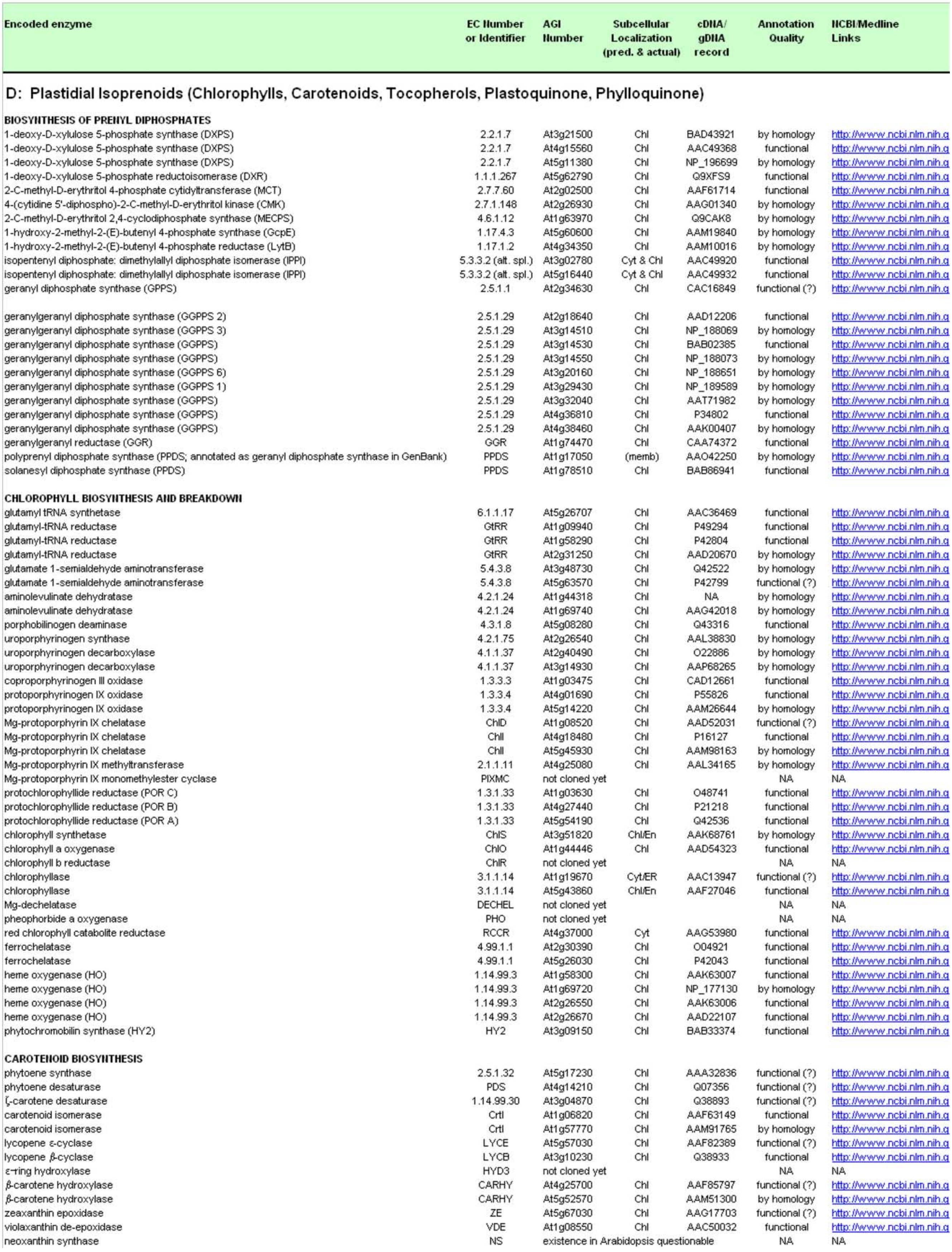


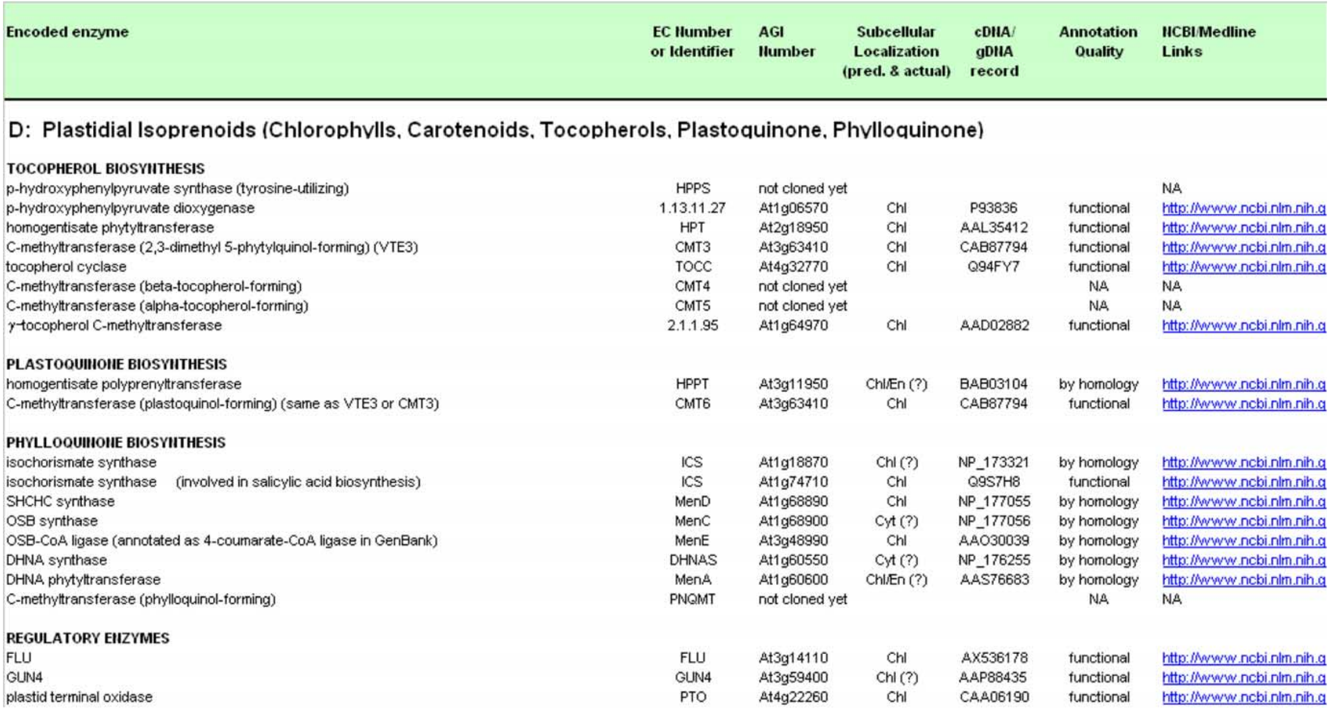
Fig. 3 (*continued*)

acid, cell wall polymers], phenylpropanoids [incl. flavonoids and anthocyanins], leaf glycerolipids, and conversion of seed storage lipids into sucrose). A gene list for genes encoding the proteins represented in the `BioPathAtMAPS` module was compiled using literature keyword and sequence-based searches in the TAIR *A. thaliana* database (http://www.arabidopsis.org/Blast/). If no *A. thaliana* gene for a protein of interest was annotated based on biochemical data, the gene from the nearest relative (putative ortholog) was used as the reference protein sequence to identify the *A. thaliana* gene. For this purpose, a protein sequence database covering biochemical pathways in all plants was generated with data from NCBI (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Protein). These protein sequences were then compared (`BLASTp`; Altschul et al., 1990) with the predicted *A. thaliana* proteins. The `BLASTp` alignments were processed with `PERL` scripts to extract the top 10 hits. A separate `BLASTp` search was run against full-length cDNA databases (http://rarge.gsc.riken.go.jp/blast/blast.pl; http://signal.salk.edu/dblast.html). Genes encoding members of enzyme families in *A. thaliana* were aligned, using the `CLUSTALW` algorithm (Thompson et al., 1994), with those homologs from other plants for which a biochemical function had already been established. `BLASTp` results and sequence alignments where manually scrutinized for the quality of hits. The subcellular localization of proteins was predicted using the `PSORT` (http://psort.nibb.ac.jp/form.html) and `TargetP` (http://www.cbs.dtu.dk/services/TargetP/) programs, and was manually updated when experimental data were in disagreement with the computational prediction. For roughly 1500 genes the annotation table underlying `BioPathAtDB` is shown in the Fig. 3. `BioPathAtDB` (and future updates) can be downloaded from the Lange laboratory



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
D: Plastidial Isoprenoids (Chlorophylls, Carotenoids, Tocopherols, Plastoquinone, Phylloquinone)						
BIOSYNTHESIS OF PRENYL DIPHOSPHATES						
1-deoxy-D-xylulose 5-phosphate synthase (DXPS)	2.2.1.7	At3g21500	Chl	BAD43921	by homology	http://www.ncbi.nlm.nih.g
1-deoxy-D-xylulose 5-phosphate synthase (DXPS)	2.2.1.7	At4g15560	Chl	AAC49368	functional	http://www.ncbi.nlm.nih.g
1-deoxy-D-xylulose 5-phosphate synthase (DXPS)	2.2.1.7	At5g11380	Chl	NP_196699	by homology	http://www.ncbi.nlm.nih.g
1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR)	1.1.1.267	At5g62790	Chl	Q9XFS9	functional	http://www.ncbi.nlm.nih.g
2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (MCT)	2.7.7.60	At2g02500	Chl	AAF61714	functional	http://www.ncbi.nlm.nih.g
4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase (CMK)	2.7.1.148	At2g26930	Chl	AAG01340	by homology	http://www.ncbi.nlm.nih.g
2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECPS)	4.6.1.12	At1g63970	Chl	Q9CAK8	by homology	http://www.ncbi.nlm.nih.g
1-hydroxy-2-methyl-2-(E)-butenyl 4-phosphate synthase (GcpE)	1.17.4.3	At5g60600	Chl	AAM19840	by homology	http://www.ncbi.nlm.nih.g
1-hydroxy-2-methyl-2-(E)-butenyl 4-phosphate reductase (LytB)	1.17.1.2	At4g34350	Chl	AAM10016	by homology	http://www.ncbi.nlm.nih.g
isopentenyl diphosphate: dimethylallyl diphosphate isomerase (IPPI)	5.3.3.2 (alt. spl.)	At3g02780	Cyt & Chl	AAC49920	functional	http://www.ncbi.nlm.nih.g
isopentenyl diphosphate: dimethylallyl diphosphate isomerase (IPPI)	5.3.3.2 (alt. spl.)	At5g16440	Cyt & Chl	AAC49932	functional	http://www.ncbi.nlm.nih.g
geranyl diphosphate synthase (GPPS)	2.5.1.1	At2g34630	Chl	CAC16849	functional (?)	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS 2)	2.5.1.29	At2g18640	Chl	AAD12206	functional	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS 3)	2.5.1.29	At3g14510	Chl	NP_188069	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS)	2.5.1.29	At3g14530	Chl	BAB02385	functional	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS)	2.5.1.29	At3g14550	Chl	NP_188073	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS 6)	2.5.1.29	At3g20160	Chl	NP_188651	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS 1)	2.5.1.29	At3g29430	Chl	NP_189589	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS)	2.5.1.29	At3g32040	Chl	AAT71982	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS)	2.5.1.29	At4g36810	Chl	P34802	functional	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS)	2.5.1.29	At4g38460	Chl	AAK00407	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl reductase (GGR)	GGR	At1g74470	Chl	CAA74372	functional	http://www.ncbi.nlm.nih.g
polyprenyl diphosphate synthase (PPDS; annotated as geranyl diphosphate synthase in GenBank)	PPDS	At1g17050	(memb)	AAO42250	by homology	http://www.ncbi.nlm.nih.g
solanesyl diphosphate synthase (PPDS)	PPDS	At1g78510	Chl	BAB86941	functional	http://www.ncbi.nlm.nih.g
CHLOROPHYLL BIOSYNTHESIS AND BREAKDOWN						
glutamyl tRNA synthetase	6.1.1.17	At5g26707	Chl	AAC36469	functional	http://www.ncbi.nlm.nih.g
glutamyl-tRNA reductase	GtRR	At1g09940	Chl	P49294	functional	http://www.ncbi.nlm.nih.g
glutamyl-tRNA reductase	GtRR	At1g58290	Chl	P42804	functional	http://www.ncbi.nlm.nih.g
glutamyl-tRNA reductase	GtRR	At2g31250	Chl	AAD20670	by homology	http://www.ncbi.nlm.nih.g
glutamate 1-semialdehyde aminotransferase	5.4.3.8	At3g48730	Chl	Q42522	by homology	http://www.ncbi.nlm.nih.g
glutamate 1-semialdehyde aminotransferase	5.4.3.8	At5g63570	Chl	P42799	functional (?)	http://www.ncbi.nlm.nih.g
aminolevulinate dehydratase	4.2.1.24	At1g44318	Chl	NA	by homology	http://www.ncbi.nlm.nih.g
aminolevulinate dehydratase	4.2.1.24	At1g69740	Chl	AAG42018	by homology	http://www.ncbi.nlm.nih.g
porphobilinogen deaminase	4.3.1.8	At5g08280	Chl	Q43316	functional	http://www.ncbi.nlm.nih.g
uroporphyrinogen synthase	4.2.1.75	At2g26540	Chl	AAL38830	by homology	http://www.ncbi.nlm.nih.g
uroporphyrinogen decarboxylase	4.1.1.37	At2g40490	Chl	O22886	by homology	http://www.ncbi.nlm.nih.g
uroporphyrinogen decarboxylase	4.1.1.37	At3g14930	Chl	AAP68265	by homology	http://www.ncbi.nlm.nih.g
coproporphyrinogen III oxidase	1.3.3.3	At1g03475	Chl	CAD12661	functional	http://www.ncbi.nlm.nih.g
protoporphyrinogen IX oxidase	1.3.3.4	At4g01690	Chl	P55826	functional	http://www.ncbi.nlm.nih.g
protoporphyrinogen IX oxidase	1.3.3.4	At5g14220	Chl	AAM26644	by homology	http://www.ncbi.nlm.nih.g
Mg-protoporphyrin IX chelatase	ChlD	At1g08520	Chl	AAD52031	functional (?)	http://www.ncbi.nlm.nih.g
Mg-protoporphyrin IX chelatase	ChlI	At4g18480	Chl	P16127	functional	http://www.ncbi.nlm.nih.g
Mg-protoporphyrin IX chelatase	ChlI	At5g45930	Chl	AAM98163	by homology	http://www.ncbi.nlm.nih.g
Mg-protoporphyrin IX methyltransferase	2.1.1.11	At4g25080	Chl	AAL34165	by homology	http://www.ncbi.nlm.nih.g
Mg-protoporphyrin IX monomethylester cyclase	PIXMC	not cloned yet			NA	NA
protochlorophyllide reductase (POR C)	1.3.1.33	At1g03630	Chl	O48741	functional	http://www.ncbi.nlm.nih.g
protochlorophyllide reductase (POR B)	1.3.1.33	At4g27440	Chl	P21218	functional	http://www.ncbi.nlm.nih.g
protochlorophyllide reductase (POR A)	1.3.1.33	At5g54190	Chl	Q42536	functional	http://www.ncbi.nlm.nih.g
chlorophyll synthetase	ChlS	At3g51820	Chl/En	AAK68761	by homology	http://www.ncbi.nlm.nih.g
chlorophyll a oxygenase	ChlO	At1g44446	Chl	AAD54323	functional	http://www.ncbi.nlm.nih.g
chlorophyll b reductase	ChlR	not cloned yet			NA	NA
chlorophyllase	3.1.1.14	At1g19670	Cyt/ER	AAC13947	functional (?)	http://www.ncbi.nlm.nih.g
chlorophyllase	3.1.1.14	At5g43860	Chl/En	AAF27046	functional	http://www.ncbi.nlm.nih.g
Mg-dechelatase	DECHEL	not cloned yet			NA	NA
pheophorbide a oxygenase	PHO	not cloned yet			NA	NA
red chlorophyll catabolite reductase	RCCR	At4g37000	Cyt	AAG53980	functional	http://www.ncbi.nlm.nih.g
ferrochelatase	4.99.1.1	At2g30390	Chl	O04921	functional	http://www.ncbi.nlm.nih.g
ferrochelatase	4.99.1.1	At5g26030	Chl	P42043	functional	http://www.ncbi.nlm.nih.g
heme oxygenase (HO)	1.14.99.3	At1g58300	Chl	AAK63007	functional	http://www.ncbi.nlm.nih.g
heme oxygenase (HO)	1.14.99.3	At1g69720	Chl	NP_177130	by homology	http://www.ncbi.nlm.nih.g
heme oxygenase (HO)	1.14.99.3	At2g26550	Chl	AAK63006	functional	http://www.ncbi.nlm.nih.g
heme oxygenase (HO)	1.14.99.3	At2g26670	Chl	AAD22107	functional	http://www.ncbi.nlm.nih.g
phytochromobilin synthase (HY2)	HY2	At3g09150	Chl	BAB33374	functional	http://www.ncbi.nlm.nih.g
CAROTENOID BIOSYNTHESIS						
phytoene synthase	2.5.1.32	At5g17230	Chl	AAA32836	functional (?)	http://www.ncbi.nlm.nih.g
phytoene desaturase	PDS	At4g14210	Chl	Q07356	functional (?)	http://www.ncbi.nlm.nih.g
ζ-carotene desaturase	1.14.99.30	At3g04870	Chl	Q38893	functional (?)	http://www.ncbi.nlm.nih.g
carotenoid isomerase	CrtI	At1g06820	Chl	AAF63149	functional	http://www.ncbi.nlm.nih.g
carotenoid isomerase	CrtI	At1g57770	Chl	AAM91765	by homology	http://www.ncbi.nlm.nih.g
lycopene ε-cyclase	LYCE	At5g57030	Chl	AAF82389	functional (?)	http://www.ncbi.nlm.nih.g
lycopene β-cyclase	LYCB	At3g10230	Chl	Q38933	functional	http://www.ncbi.nlm.nih.g
ε-ring hydroxylase	HYD3	not cloned yet			NA	NA
β-carotene hydroxylase	CARHY	At4g25700	Chl	AAF85797	functional (?)	http://www.ncbi.nlm.nih.g
β-carotene hydroxylase	CARHY	At5g52570	Chl	AAM51300	by homology	http://www.ncbi.nlm.nih.g
zeaxanthin epoxidase	ZE	At5g67030	Chl	AAG17703	functional (?)	http://www.ncbi.nlm.nih.g
violaxanthin de-epoxidase	VDE	At1g08550	Chl	AAC50032	functional	http://www.ncbi.nlm.nih.g
neoxanthin synthase	NS	existence in Arabidopsis questionable			NA	NA

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
D: Plastidial Isoprenoids (Chlorophylls, Carotenoids, Tocopherols, Plastoquinone, Phylloquinone)						
TOCOPHEROL BIOSYNTHESIS						
p-hydroxyphenylpyruvate synthase (tyrosine-utilizing)	HPPS	not cloned yet				NA
p-hydroxyphenylpyruvate dioxygenase	1.13.11.27	At1g06570	Chl	P93836	functional	http://www.ncbi.nlm.nih.g
homogentisate phytyltransferase	HPT	At2g18950	Chl	AAL35412	functional	http://www.ncbi.nlm.nih.g
C-methyltransferase (2,3-dimethyl 5-phytylquinol-forming) (VTE3)	CMT3	At3g63410	Chl	CAB87794	functional	http://www.ncbi.nlm.nih.g
tocopherol cyclase	TOCC	At4g32770	Chl	Q94FY7	functional	http://www.ncbi.nlm.nih.g
C-methyltransferase (beta-tocopherol-forming)	CMT4	not cloned yet			NA	NA
C-methyltransferase (alpha-tocopherol-forming)	CMT5	not cloned yet			NA	NA
γ-tocopherol C-methyltransferase	2.1.1.95	At1g64970	Chl	AAD02882	functional	http://www.ncbi.nlm.nih.g
PLASTOQUINONE BIOSYNTHESIS						
homogentisate polyprenyltransferase	HPPT	At3g11950	Chl/En (?)	BAB03104	by homology	http://www.ncbi.nlm.nih.g
C-methyltransferase (plastoquinol-forming) (same as VTE3 or CMT3)	CMT6	At3g63410	Chl	CAB87794	functional	http://www.ncbi.nlm.nih.g
PHYLLOQUINONE BIOSYNTHESIS						
isochorismate synthase	ICS	At1g18870	Chl (?)	NP_173321	by homology	http://www.ncbi.nlm.nih.g
isochorismate synthase (involved in salicylic acid biosynthesis)	ICS	At1g74710	Chl	Q9S7H8	functional	http://www.ncbi.nlm.nih.g
SHCHC synthase	MenD	At1g68890	Chl	NP_177055	by homology	http://www.ncbi.nlm.nih.g
OSB synthase	MenC	At1g68900	Cyt (?)	NP_177056	by homology	http://www.ncbi.nlm.nih.g
OSB-CoA ligase (annotated as 4-coumarate-CoA ligase in GenBank)	MenE	At3g48990	Chl	AAO30039	by homology	http://www.ncbi.nlm.nih.g
DHNA synthase	DHNAS	At1g60550	Cyt (?)	NP_176255	by homology	http://www.ncbi.nlm.nih.g
DHNA phytyltransferase	MenA	At1g60600	Chl/En (?)	AAS76683	by homology	http://www.ncbi.nlm.nih.g
C-methyltransferase (phylloquinol-forming)	PNQMT	not cloned yet			NA	NA
REGULATORY ENZYMES						
FLU	FLU	At3g14110	Chl	AX536178	functional	http://www.ncbi.nlm.nih.g
GUN4	GUN4	At3g59400	Chl (?)	AAP88435	functional	http://www.ncbi.nlm.nih.g
plastid terminal oxidase	PTO	At4g22260	Chl	CAA06190	functional	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

website (http://www.ibc.wsu.edu/research/lange/index.html).

3.3. Displaying post-genomic data sets using BioPathAt

To integrate microarray, proteomics and metabolite profiling data as one data set, the gene identifiers for the *A. thaliana* genome (AGI numbers), the enzyme identifiers (EC numbers) and metabolite identifiers (compound names) were loaded into GeneSpring® using the "Genome Definition File" (Fig. 1). Biochemical pathway maps from the `BioPathAtMAPS` module and an artificial data set (containing normalized and filtered microarray, protein expression and metabolite profiling data) were also imported into GeneSpring®. Our custom *A. thaliana* gene annotation database (`BioPathAtDB`) was linked to the Affymetrix GeneChip® ID table (ftp://ftp.arabidopsis.org/home/tair/Microarrays/Affymetrix/) via the AGI numbers and was also uploaded into GeneSpring®. Dynamic boxes, which are used to visualize patterns of mRNA abundances, protein expression and metabolite pools, were placed on the biochemical pathway maps according to the GeneSpring® tutorial on "Pathways". The dynamic rectangular boxes representing genes (blue frames) and encoded enzymes (pink frames) are positioned next the biochemical reaction arrow, whereas boxes indicating metabolite pools (orange frames) are next to the compound name. Gene and protein expression patterns are displayed in dynamic rectangular boxes (blue and pink frames, respectively) using colors to represent changes of expression from a mean or control value (red for up-regulation and green for down-regulation) and color intensity to represent the level of the change (inset A). Information is shown regarding the identity of the selected gene and the expression values (relative to an experimental control) at different time points (numerically as well as graphically in the horizontal orientation). It should be noted that on some maps only the EC numbers of enzymes are displayed (as opposed to the full enzyme name as shown in Fig. 2). Genes representing different isozymes are stacked on top of each other (inset B) in the same order as they are listed in the gene annotation table. Actual gene expression or protein abundance values can also be uploaded and the intensity of expression can be indicated numerically as well as by the intensity of blue color. As an example, the transcript levels of the three genes encoding glutamyl tRNA reductase in *A. thaliana* are shown for a variety of different tissues (inset C). Dynamic metabolite boxes contain information regarding the commonly used name of the compound, its accurate mass and elemental composi-

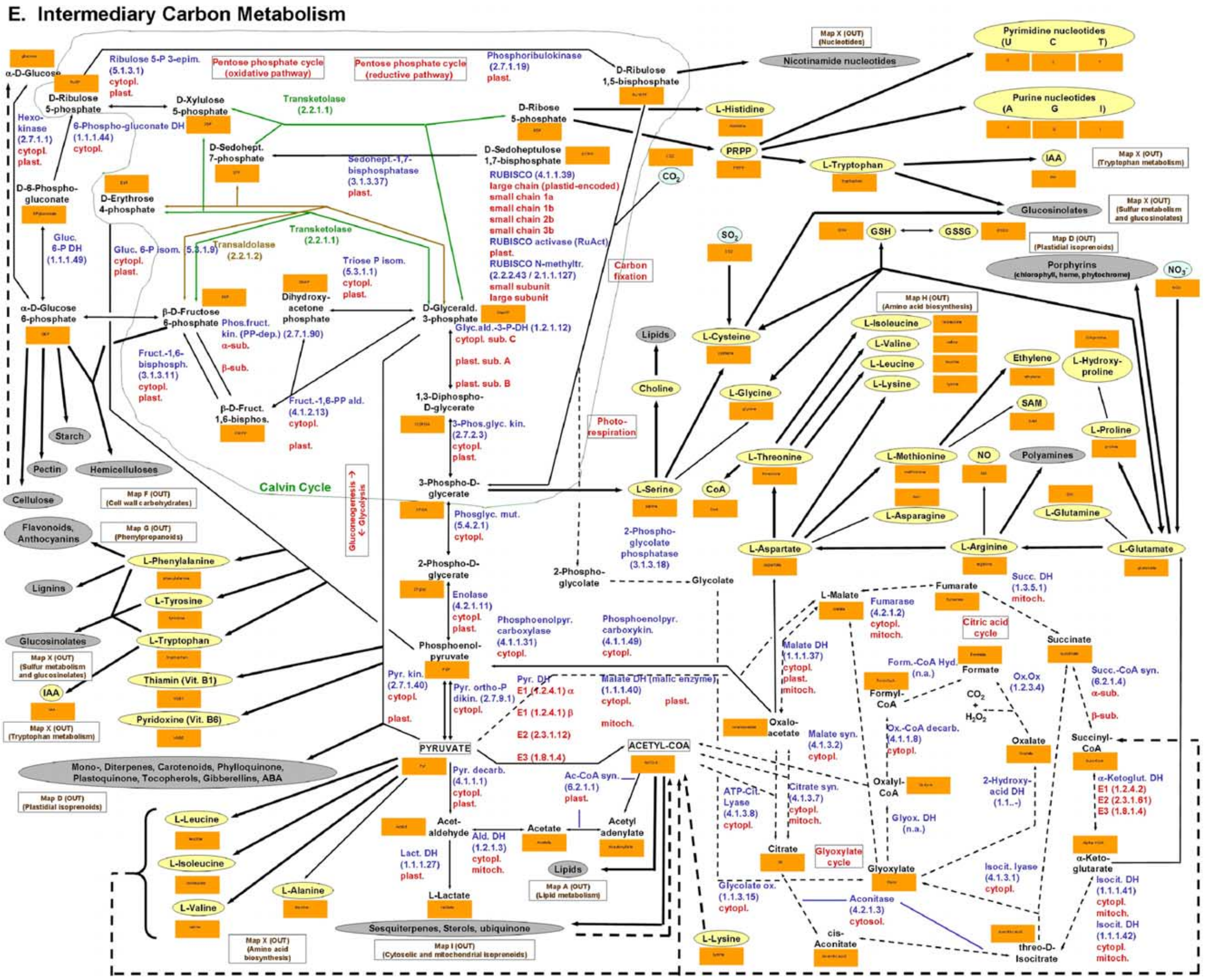
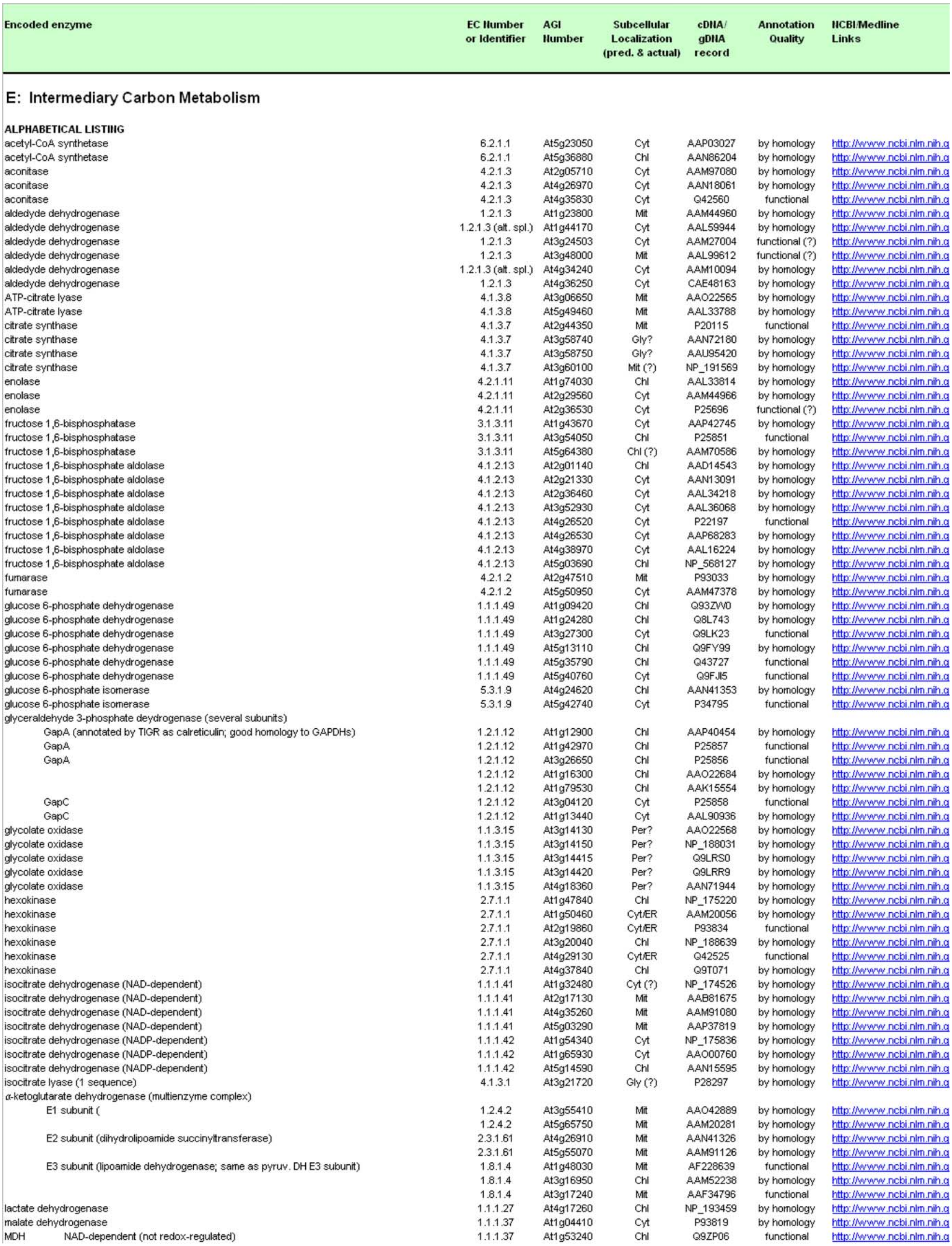


Fig. 3 (*continued*)

tion, its structure, the method of analysis used, and the measured pool size (relative to an experimental control) at different time points (numerically as well as graphically) (inset D). Enzyme activators are connected to a biochemical reaction arrow by green lines and an asterisk (e.g., GUN4; Larkin et al., 2003) and enzyme repressors are indicated by red lines with an orthogonal bar (e.g., FLU; Meskauskiene et al., 2001). This approach to a graphic representation of genomic data is highly flexible and allows the user to define the level of complexity to be visualized. For example, if only mRNA expression data are acquired in a specific experiment, the boxes representing enzymes and metabolites can be omitted. However, if flux control analysis experiments have been performed in addition to acquiring microarray and metabolite profiling data, extra boxes displaying flux values can be placed on top of reaction arrows. A selection of biochemical pathway maps and the corresponding annotation tables in given in Fig. 3.

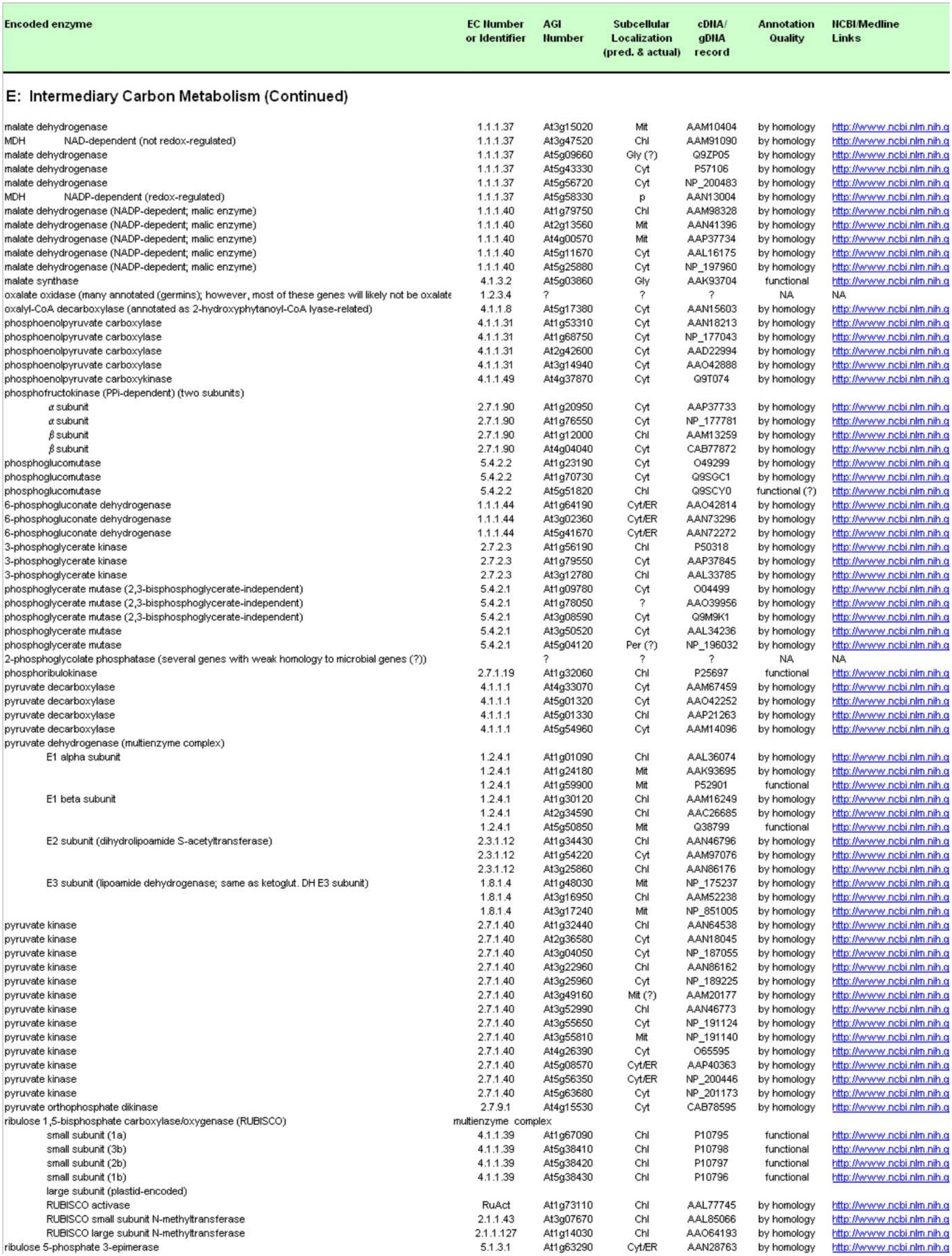
3.4. Further developments

`BioPathAtDB` currently contains annotation information for genes/enzymes involved in various biochemical pathways in *A. thaliana*. However, a gene/enzyme function database should also integrate experimental knowledge regarding the role of specific isogenes/isozymes in regulating biochemical networks. To provide all essential functional information in one database, ongoing efforts are focused on expanding `BioPathAtDB` to include experimental data on expression patterns (organ- and tissue-specificity of



Encoded enzyme	**EC Number or Identifier**	**AGI Number**	**Subcellular Localization (pred. & actual)**	**cDNA/ gDNA record**	**Annotation Quality**	**NCBI/Medline Links**
E: Intermediary Carbon Metabolism						
ALPHABETICAL LISTING						
acetyl-CoA synthetase	6.2.1.1	At5g23050	Cyt	AAP03027	by homology	http://www.ncbi.nlm.nih.g
acetyl-CoA synthetase	6.2.1.1	At5g36880	Chl	AAN86204	by homology	http://www.ncbi.nlm.nih.g
aconitase	4.2.1.3	At2g05710	Cyt	AAM97080	by homology	http://www.ncbi.nlm.nih.g
aconitase	4.2.1.3	At4g26970	Cyt	AAN18061	by homology	http://www.ncbi.nlm.nih.g
aconitase	4.2.1.3	At4g35830	Cyt	Q42560	functional	http://www.ncbi.nlm.nih.g
aldedyde dehydrogenase	1.2.1.3	At1g23800	Mit	AAM44960	by homology	http://www.ncbi.nlm.nih.g
aldedyde dehydrogenase	1.2.1.3 (alt. spl.)	At1g44170	Cyt	AAL59944	by homology	http://www.ncbi.nlm.nih.g
aldedyde dehydrogenase	1.2.1.3	At3g24503	Cyt	AAM27004	functional (?)	http://www.ncbi.nlm.nih.g
aldedyde dehydrogenase	1.2.1.3	At3g48000	Mit	AAL99612	functional (?)	http://www.ncbi.nlm.nih.g
aldedyde dehydrogenase	1.2.1.3 (alt. spl.)	At4g34240	Cyt	AAM10094	by homology	http://www.ncbi.nlm.nih.g
aldedyde dehydrogenase	1.2.1.3	At4g36250	Cyt	CAE48163	by homology	http://www.ncbi.nlm.nih.g
ATP-citrate lyase	4.1.3.8	At3g06650	Mit	AAO22565	by homology	http://www.ncbi.nlm.nih.g
ATP-citrate lyase	4.1.3.8	At5g49460	Mit	AAL33788	by homology	http://www.ncbi.nlm.nih.g
citrate synthase	4.1.3.7	At2g44350	Mit	P20115	functional	http://www.ncbi.nlm.nih.g
citrate synthase	4.1.3.7	At3g58740	Gly?	AAN72180	by homology	http://www.ncbi.nlm.nih.g
citrate synthase	4.1.3.7	At3g58750	Gly?	AAU95420	by homology	http://www.ncbi.nlm.nih.g
citrate synthase	4.1.3.7	At3g60100	Mit (?)	NP_191569	by homology	http://www.ncbi.nlm.nih.g
enolase	4.2.1.11	At1g74030	Chl	AAL33814	by homology	http://www.ncbi.nlm.nih.g
enolase	4.2.1.11	At2g29560	Cyt	AAM44966	by homology	http://www.ncbi.nlm.nih.g
enolase	4.2.1.11	At2g36530	Cyt	P25696	functional (?)	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphatase	3.1.3.11	At1g43670	Cyt	AAP42745	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphatase	3.1.3.11	At3g54050	Chl	P25851	functional	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphatase	3.1.3.11	At5g64380	Chl (?)	AAM70586	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At2g01140	Chl	AAD14543	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At2g21330	Cyt	AAN13091	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At2g36460	Cyt	AAL34218	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At3g52930	Cyt	AAL36068	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At4g26520	Cyt	P22197	functional	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At4g26530	Cyt	AAP68283	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At4g38970	Cyt	AAL16224	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At5g03690	Chl	NP_568127	by homology	http://www.ncbi.nlm.nih.g
fumarase	4.2.1.2	At2g47510	Mit	P93033	by homology	http://www.ncbi.nlm.nih.g
fumarase	4.2.1.2	At5g50950	Cyt	AAM47378	by homology	http://www.ncbi.nlm.nih.g
glucose 6-phosphate dehydrogenase	1.1.1.49	At1g09420	Chl	Q93ZW0	by homology	http://www.ncbi.nlm.nih.g
glucose 6-phosphate dehydrogenase	1.1.1.49	At1g24280	Chl	Q8L743	by homology	http://www.ncbi.nlm.nih.g
glucose 6-phosphate dehydrogenase	1.1.1.49	At3g27300	Cyt	Q9LK23	functional	http://www.ncbi.nlm.nih.g
glucose 6-phosphate dehydrogenase	1.1.1.49	At5g13110	Chl	Q9FY99	by homology	http://www.ncbi.nlm.nih.g
glucose 6-phosphate dehydrogenase	1.1.1.49	At5g35790	Chl	Q43727	functional	http://www.ncbi.nlm.nih.g
glucose 6-phosphate dehydrogenase	1.1.1.49	At5g40760	Cyt	Q9FJI5	functional	http://www.ncbi.nlm.nih.g
glucose 6-phosphate isomerase	5.3.1.9	At4g24620	Chl	AAN41353	by homology	http://www.ncbi.nlm.nih.g
glucose 6-phosphate isomerase	5.3.1.9	At5g42740	Cyt	P34795	functional	http://www.ncbi.nlm.nih.g
glyceraldehyde 3-phosphate deydrogenase (several subunits)						
GapA (annotated by TIGR as calreticulin; good homology to GAPDHs)	1.2.1.12	At1g12900	Chl	AAP40454	by homology	http://www.ncbi.nlm.nih.g
GapA	1.2.1.12	At1g42970	Chl	P25857	functional	http://www.ncbi.nlm.nih.g
GapA	1.2.1.12	At3g26650	Chl	P25856	functional	http://www.ncbi.nlm.nih.g
	1.2.1.12	At1g16300	Chl	AAO22684	by homology	http://www.ncbi.nlm.nih.g
	1.2.1.12	At1g79530	Chl	AAK15554	by homology	http://www.ncbi.nlm.nih.g
GapC	1.2.1.12	At3g04120	Cyt	P25858	functional	http://www.ncbi.nlm.nih.g
GapC	1.2.1.12	At1g13440	Cyt	AAL90936	by homology	http://www.ncbi.nlm.nih.g
glycolate oxidase	1.1.3.15	At3g14130	Per?	AAO22568	by homology	http://www.ncbi.nlm.nih.g
glycolate oxidase	1.1.3.15	At3g14150	Per?	NP_188031	by homology	http://www.ncbi.nlm.nih.g
glycolate oxidase	1.1.3.15	At3g14415	Per?	Q9LRS0	by homology	http://www.ncbi.nlm.nih.g
glycolate oxidase	1.1.3.15	At3g14420	Per?	Q9LRR9	by homology	http://www.ncbi.nlm.nih.g
glycolate oxidase	1.1.3.15	At4g18360	Per?	AAN71944	by homology	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At1g47840	Chl	NP_175220	by homology	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At1g50460	Cyt/ER	AAM20056	by homology	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At2g19860	Cyt/ER	P93834	functional	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At3g20040	Chl	NP_188639	by homology	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At4g29130	Cyt/ER	Q42525	functional	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At4g37840	Chl	Q9T071	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NAD-dependent)	1.1.1.41	At1g32480	Cyt (?)	NP_174526	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NAD-dependent)	1.1.1.41	At2g17130	Mit	AAB81675	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NAD-dependent)	1.1.1.41	At4g35260	Mit	AAM91080	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NAD-dependent)	1.1.1.41	At5g03290	Mit	AAP37819	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NADP-dependent)	1.1.1.42	At1g54340	Cyt	NP_175836	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NADP-dependent)	1.1.1.42	At1g65930	Cyt	AAO00760	by homology	http://www.ncbi.nlm.nih.g
isocitrate dehydrogenase (NADP-dependent)	1.1.1.42	At5g14590	Chl	AAN15595	by homology	http://www.ncbi.nlm.nih.g
isocitrate lyase (1 sequence)	4.1.3.1	At3g21720	Gly (?)	P28297	by homology	http://www.ncbi.nlm.nih.g
α-ketoglutarate dehydrogenase (multienzyme complex)						
E1 subunit (	1.2.4.2	At3g55410	Mit	AAO42889	by homology	http://www.ncbi.nlm.nih.g
	1.2.4.2	At5g65750	Mit	AAM20281	by homology	http://www.ncbi.nlm.nih.g
E2 subunit (dihydrolipoamide succinyltransferase)	2.3.1.61	At4g26910	Mit	AAN41326	by homology	http://www.ncbi.nlm.nih.g
	2.3.1.61	At5g55070	Mit	AAM91126	by homology	http://www.ncbi.nlm.nih.g
E3 subunit (lipoamide dehydrogenase; same as pyruv. DH E3 subunit)	1.8.1.4	At1g48030	Mit	AF228639	functional	http://www.ncbi.nlm.nih.g
	1.8.1.4	At3g16950	Chl	AAM52238	by homology	http://www.ncbi.nlm.nih.g
	1.8.1.4	At3g17240	Mit	AAF34796	functional	http://www.ncbi.nlm.nih.g
lactate dehydrogenase	1.1.1.27	At4g17260	Chl	NP_193459	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At1g04410	Cyt	P93819	by homology	http://www.ncbi.nlm.nih.g
MDH NAD-dependent (not redox-regulated)	1.1.1.37	At1g53240	Chl	Q9ZP06	functional	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
E: Intermediary Carbon Metabolism (Continued)						
malate dehydrogenase	1.1.1.37	At3g15020	Mit	AAM10404	by homology	http://www.ncbi.nlm.nih.g
MDH NAD-dependent (not redox-regulated)	1.1.1.37	At3g47520	Chl	AAM91090	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At5g09660	Gly (?)	Q9ZP05	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At5g43330	Cyt	P57106	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At5g56720	Cyt	NP_200483	by homology	http://www.ncbi.nlm.nih.g
MDH NADP-dependent (redox-regulated)	1.1.1.37	At5g58330	p	AAN13004	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase (NADP-depedent; malic enzyme)	1.1.1.40	At1g79750	Chl	AAM98328	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase (NADP-depedent; malic enzyme)	1.1.1.40	At2g13560	Mit	AAN41396	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase (NADP-depedent; malic enzyme)	1.1.1.40	At4g00570	Mit	AAP37734	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase (NADP-depedent; malic enzyme)	1.1.1.40	At5g11670	Cyt	AAL16175	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase (NADP-depedent; malic enzyme)	1.1.1.40	At5g25880	Cyt	NP_197960	by homology	http://www.ncbi.nlm.nih.g
malate synthase	4.1.3.2	At5g03860	Gly	AAK93704	functional	http://www.ncbi.nlm.nih.g
oxalate oxidase (many annotated (germins); however, most of these genes will likely not be oxalate	1.2.3.4	?	?	?	NA	NA
oxalyl-CoA decarboxylase (annotated as 2-hydroxyphytanoyl-CoA lyase-related)	4.1.1.8	At5g17380	Cyt	AAN15603	by homology	http://www.ncbi.nlm.nih.g
phosphoenolpyruvate carboxylase	4.1.1.31	At1g53310	Cyt	AAN18213	by homology	http://www.ncbi.nlm.nih.g
phosphoenolpyruvate carboxylase	4.1.1.31	At1g68750	Cyt	NP_177043	by homology	http://www.ncbi.nlm.nih.g
phosphoenolpyruvate carboxylase	4.1.1.31	At2g42600	Cyt	AAD22994	by homology	http://www.ncbi.nlm.nih.g
phosphoenolpyruvate carboxylase	4.1.1.31	At3g14940	Cyt	AAO42888	by homology	http://www.ncbi.nlm.nih.g
phosphoenolpyruvate carboxykinase	4.1.1.49	At4g37870	Cyt	Q9T074	by homology	http://www.ncbi.nlm.nih.g
phosphofructokinase (PPi-dependent) (two subunits)						
α subunit	2.7.1.90	At1g20950	Cyt	AAP37733	by homology	http://www.ncbi.nlm.nih.g
α subunit	2.7.1.90	At1g76550	Cyt	NP_177781	by homology	http://www.ncbi.nlm.nih.g
β subunit	2.7.1.90	At1g12000	Chl	AAM13259	by homology	http://www.ncbi.nlm.nih.g
β subunit	2.7.1.90	At4g04040	Cyt	CAB77872	by homology	http://www.ncbi.nlm.nih.g
phosphoglucomutase	5.4.2.2	At1g23190	Cyt	O49299	by homology	http://www.ncbi.nlm.nih.g
phosphoglucomutase	5.4.2.2	At1g70730	Cyt	Q9SGC1	by homology	http://www.ncbi.nlm.nih.g
phosphoglucomutase	5.4.2.2	At5g51820	Chl	Q9SCY0	functional (?)	http://www.ncbi.nlm.nih.g
6-phosphogluconate dehydrogenase	1.1.1.44	At1g64190	Cyt/ER	AAO42814	by homology	http://www.ncbi.nlm.nih.g
6-phosphogluconate dehydrogenase	1.1.1.44	At3g02360	Cyt/ER	AAN73296	by homology	http://www.ncbi.nlm.nih.g
6-phosphogluconate dehydrogenase	1.1.1.44	At5g41670	Cyt/ER	AAN72272	by homology	http://www.ncbi.nlm.nih.g
3-phosphoglycerate kinase	2.7.2.3	At1g56190	Chl	P50318	by homology	http://www.ncbi.nlm.nih.g
3-phosphoglycerate kinase	2.7.2.3	At1g79550	Cyt	AAP37845	by homology	http://www.ncbi.nlm.nih.g
3-phosphoglycerate kinase	2.7.2.3	At3g12780	Chl	AAL33785	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase (2,3-bisphosphoglycerate-independent)	5.4.2.1	At1g09780	Cyt	O04499	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase (2,3-bisphosphoglycerate-independent)	5.4.2.1	At1g78050	?	AAO39956	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase (2,3-bisphosphoglycerate-independent)	5.4.2.1	At3g08590	Cyt	Q9M9K1	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase	5.4.2.1	At3g50520	Cyt	AAL34236	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase	5.4.2.1	At5g04120	Per (?)	NP_196032	by homology	http://www.ncbi.nlm.nih.g
2-phosphoglycolate phosphatase (several genes with weak homology to microbial genes (?))		?	?	?	NA	NA
phosphoribulokinase	2.7.1.19	At1g32060	Chl	P25697	functional	http://www.ncbi.nlm.nih.g
pyruvate decarboxylase	4.1.1.1	At4g33070	Cyt	AAM67459	by homology	http://www.ncbi.nlm.nih.g
pyruvate decarboxylase	4.1.1.1	At5g01320	Cyt	AAO42252	by homology	http://www.ncbi.nlm.nih.g
pyruvate decarboxylase	4.1.1.1	At5g01330	Chl	AAP21263	by homology	http://www.ncbi.nlm.nih.g
pyruvate decarboxylase	4.1.1.1	At5g54960	Cyt	AAM14096	by homology	http://www.ncbi.nlm.nih.g
pyruvate dehydrogenase (multienzyme complex)						
E1 alpha subunit	1.2.4.1	At1g01090	Chl	AAL36074	by homology	http://www.ncbi.nlm.nih.g
	1.2.4.1	At1g24180	Mit	AAK93695	by homology	http://www.ncbi.nlm.nih.g
	1.2.4.1	At1g59900	Mit	P52901	functional	http://www.ncbi.nlm.nih.g
E1 beta subunit	1.2.4.1	At1g30120	Chl	AAM16249	by homology	http://www.ncbi.nlm.nih.g
	1.2.4.1	At2g34590	Chl	AAC26685	by homology	http://www.ncbi.nlm.nih.g
	1.2.4.1	At5g50850	Mit	Q38799	functional	http://www.ncbi.nlm.nih.g
E2 subunit (dihydrolipoamide S-acetyltransferase)	2.3.1.12	At1g34430	Chl	AAN46796	by homology	http://www.ncbi.nlm.nih.g
	2.3.1.12	At1g54220	Cyt	AAM97076	by homology	http://www.ncbi.nlm.nih.g
	2.3.1.12	At3g25860	Chl	AAN86176	by homology	http://www.ncbi.nlm.nih.g
E3 subunit (lipoamide dehydrogenase; same as ketoglut. DH E3 subunit)	1.8.1.4	At1g48030	Mit	NP_175237	by homology	http://www.ncbi.nlm.nih.g
	1.8.1.4	At3g16950	Chl	AAM52238	by homology	http://www.ncbi.nlm.nih.g
	1.8.1.4	At3g17240	Mit	NP_851005	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At1g32440	Chl	AAN64538	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At2g36580	Cyt	AAN18045	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g04050	Cyt	NP_187055	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g22960	Chl	AAN86162	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g25960	Cyt	NP_189225	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g49160	Mit (?)	AAM20177	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g52990	Chl	AAN46773	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g55650	Cyt	NP_191124	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At3g55810	Mit	NP_191140	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At4g26390	Cyt	O65595	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At5g08570	Cyt/ER	AAP40363	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At5g56350	Cyt/ER	NP_200446	by homology	http://www.ncbi.nlm.nih.g
pyruvate kinase	2.7.1.40	At5g63680	Cyt	NP_201173	by homology	http://www.ncbi.nlm.nih.g
pyruvate orthophosphate dikinase	2.7.9.1	At4g15530	Cyt	CAB78595	by homology	http://www.ncbi.nlm.nih.g
ribulose 1,5-bisphosphate carboxylase/oxygenase (RUBISCO)	multienzyme complex					
small subunit (1a)	4.1.1.39	At1g67090	Chl	P10795	functional	http://www.ncbi.nlm.nih.g
small subunit (3b)	4.1.1.39	At5g38410	Chl	P10798	functional	http://www.ncbi.nlm.nih.g
small subunit (2b)	4.1.1.39	At5g38420	Chl	P10797	functional	http://www.ncbi.nlm.nih.g
small subunit (1b)	4.1.1.39	At5g38430	Chl	P10796	functional	http://www.ncbi.nlm.nih.g
large subunit (plastid-encoded)						
RUBISCO activase	RuAct	At1g73110	Chl	AAL77745	by homology	http://www.ncbi.nlm.nih.g
RUBISCO small subunit N-methyltransferase	2.1.1.43	At3g07670	Chl	AAL85066	by homology	http://www.ncbi.nlm.nih.g
RUBISCO large subunit N-methyltransferase	2.1.1.127	At1g14030	Chl	AAO64193	by homology	http://www.ncbi.nlm.nih.g
ribulose 5-phosphate 3-epimerase	5.1.3.1	At1g63290	Cyt/ER	AAN28763	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
E: Intermediary Carbon Metabolism (Continued)						
ribulose 5-phosphate 3-epimerase	5.1.3.1	At3g01850	Cyt/ER	AAN72185	by homology	http://www.ncbi.nlm.nih.g
ribulose 5-phosphate 3-epimerase	5.1.3.1	At5g61410	Chl	AAM14320	by homology	http://www.ncbi.nlm.nih.g
sedoheptulose 1,7-bisphosphatase	3.1.3.37	At3g55880	Chl	AAN15722	by homology	http://www.ncbi.nlm.nih.g
succinate dehydrogenase (two subunits)						
flavoprotein subunit	1.3.5.1	At2g18450	Mit	AAO64873	by homology	http://www.ncbi.nlm.nih.g
flavoprotein subunit	1.3.5.1	At5g66760	Mit	O82663	by homology	http://www.ncbi.nlm.nih.g
iron protein subunit	1.3.5.1	At3g27380	Mit (?)	AAL34227	by homology	http://www.ncbi.nlm.nih.g
iron protein subunit	1.3.5.1	At5g40650	Mit	AAM67569	by homology	http://www.ncbi.nlm.nih.g
succinyl-CoA synthetase (two subunits)						
α subunit	6.2.1.4	At5g08300	Mit (?)	P53586	by homology	http://www.ncbi.nlm.nih.g
α subunit	6.2.1.4	At5g23250	Mit	AAM47926	by homology	http://www.ncbi.nlm.nih.g
β subunit	6.2.1.4	At2g20420	Mit	O82662	by homology	http://www.ncbi.nlm.nih.g
transaldolase	2.2.1.2	At5g13420	Chl	AAM45123	by homology	http://www.ncbi.nlm.nih.g
transketolase	2.2.1.1	At2g45290	Chl	AAB82634	by homology	http://www.ncbi.nlm.nih.g
transketolase	2.2.1.1	At3g60750	Chl	AAN18173	by homology	http://www.ncbi.nlm.nih.g
triosephosphate isomerase	5.3.1.1	At2g21170	Chl	Q9SKP6	by homology	http://www.ncbi.nlm.nih.g
triosephosphate isomerase	5.3.1.1	At3g55440	Cyt	P48491	by homology	http://www.ncbi.nlm.nih.g

F. Cell Wall Carbohydrates

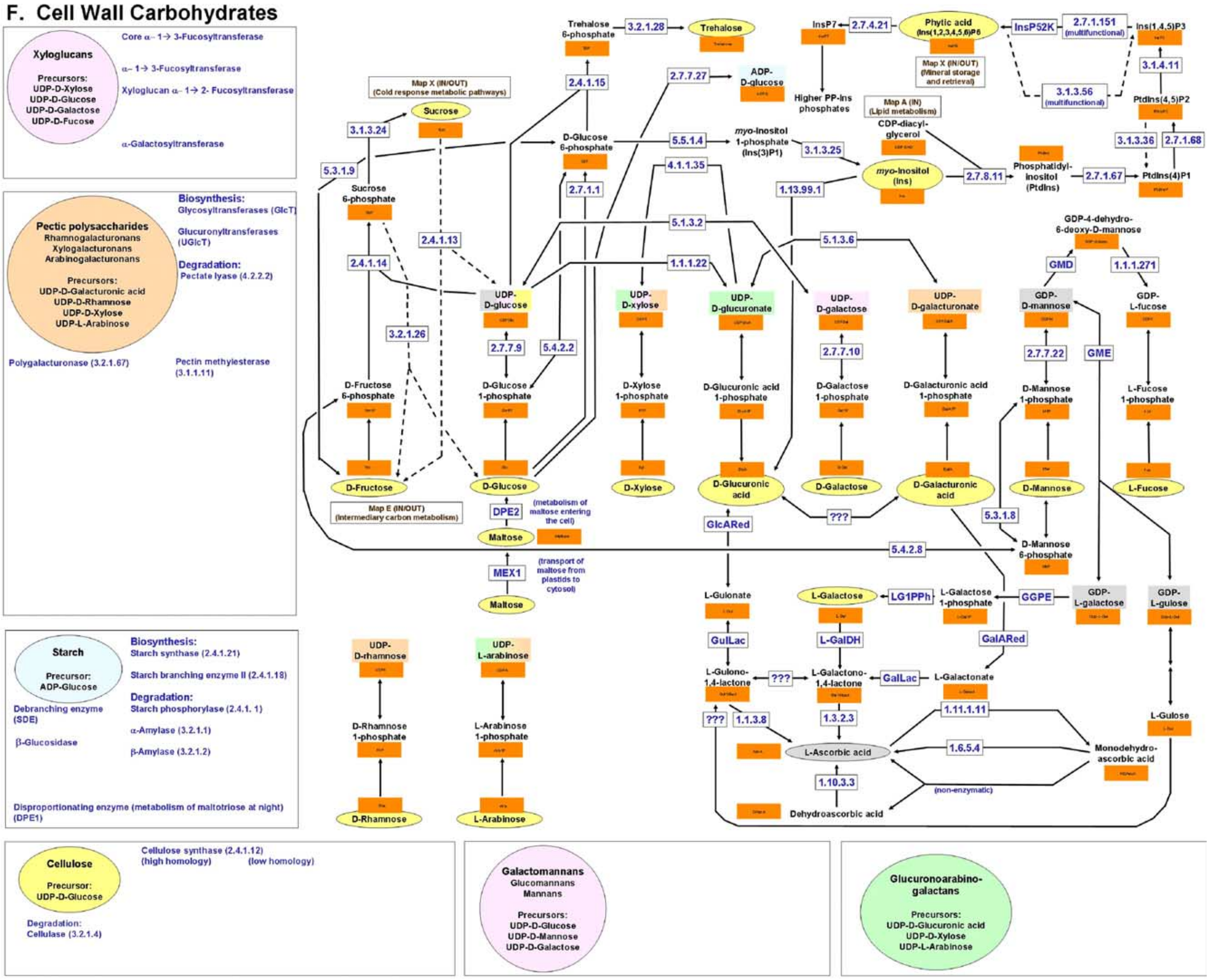
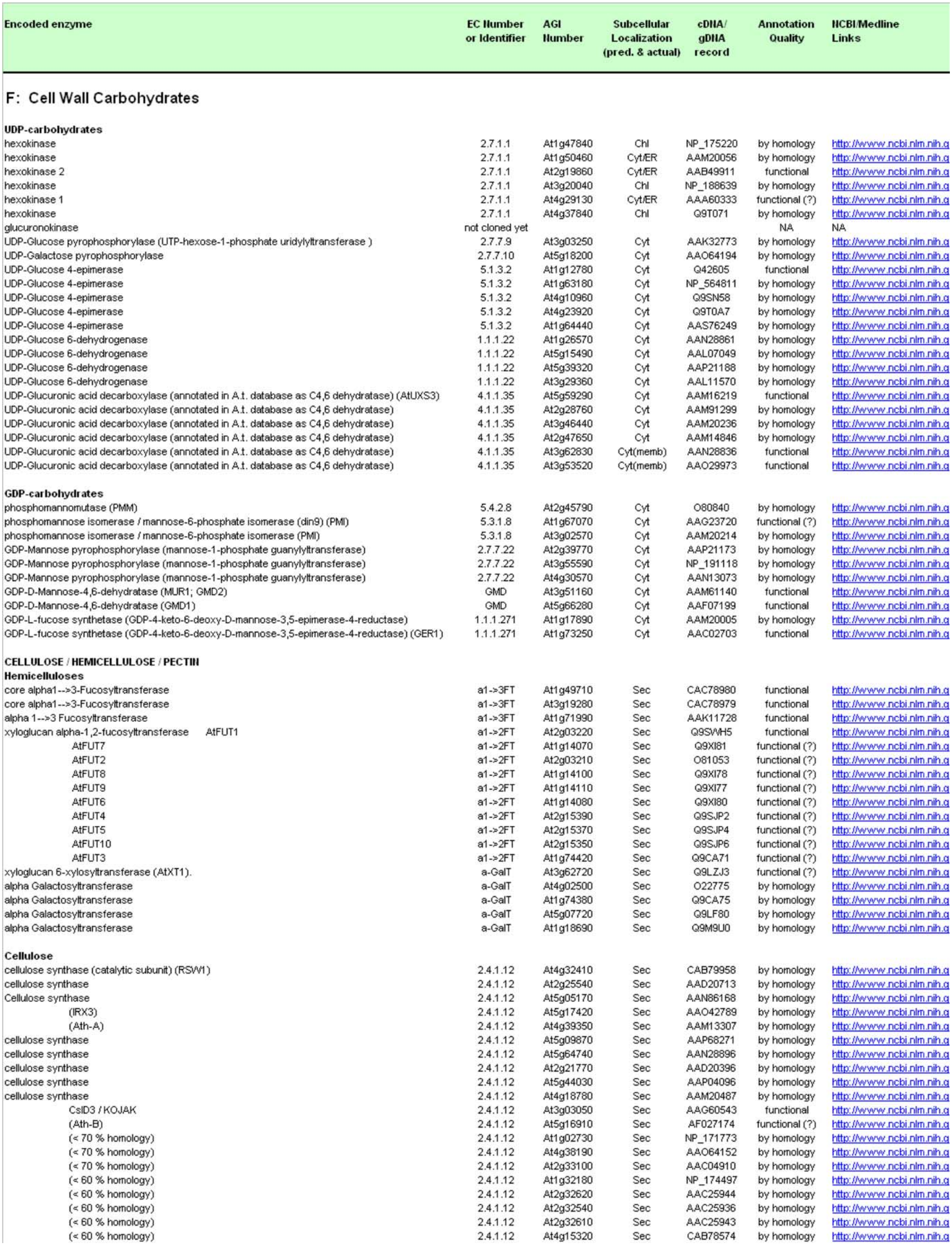
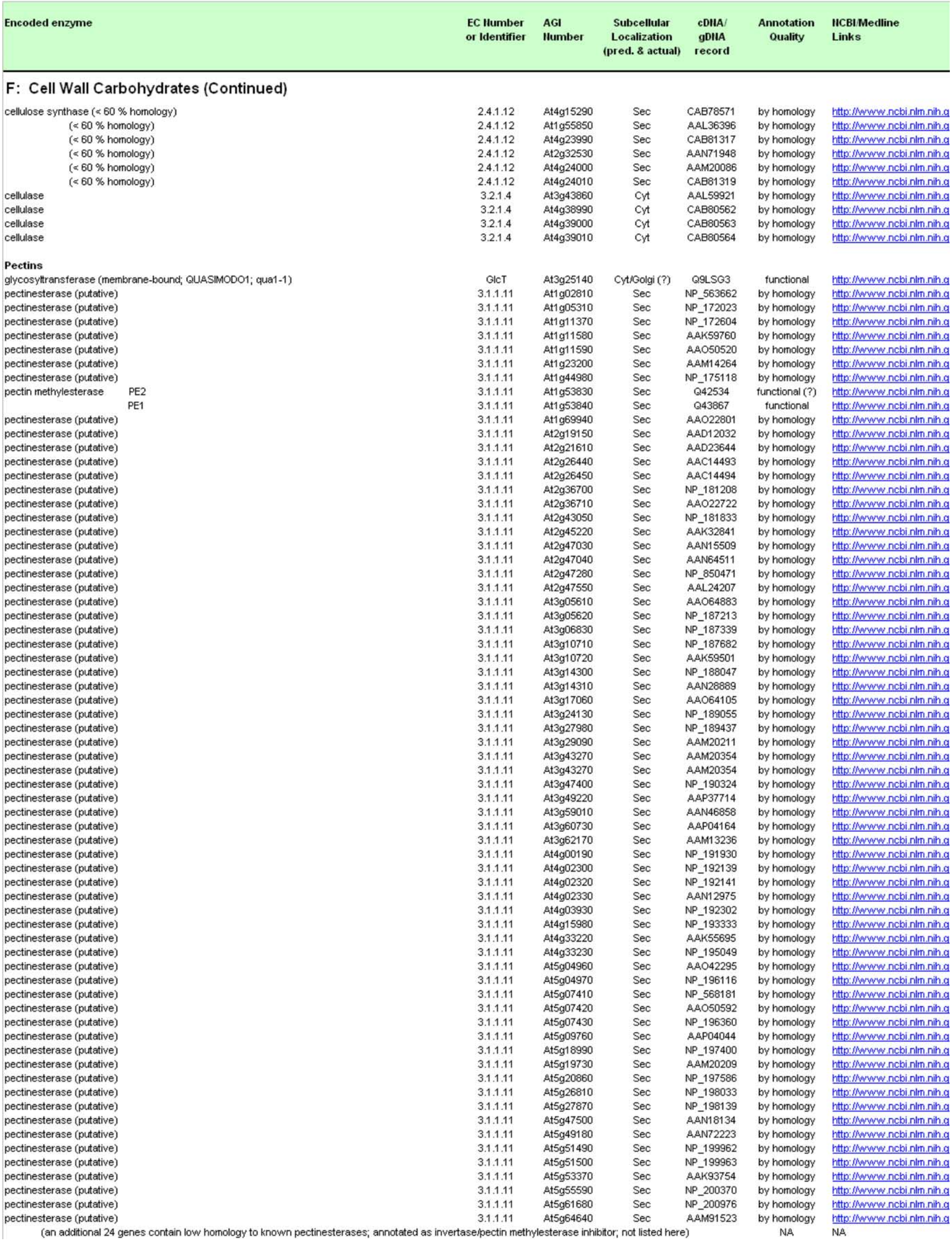


Fig. 3 (*continued*)



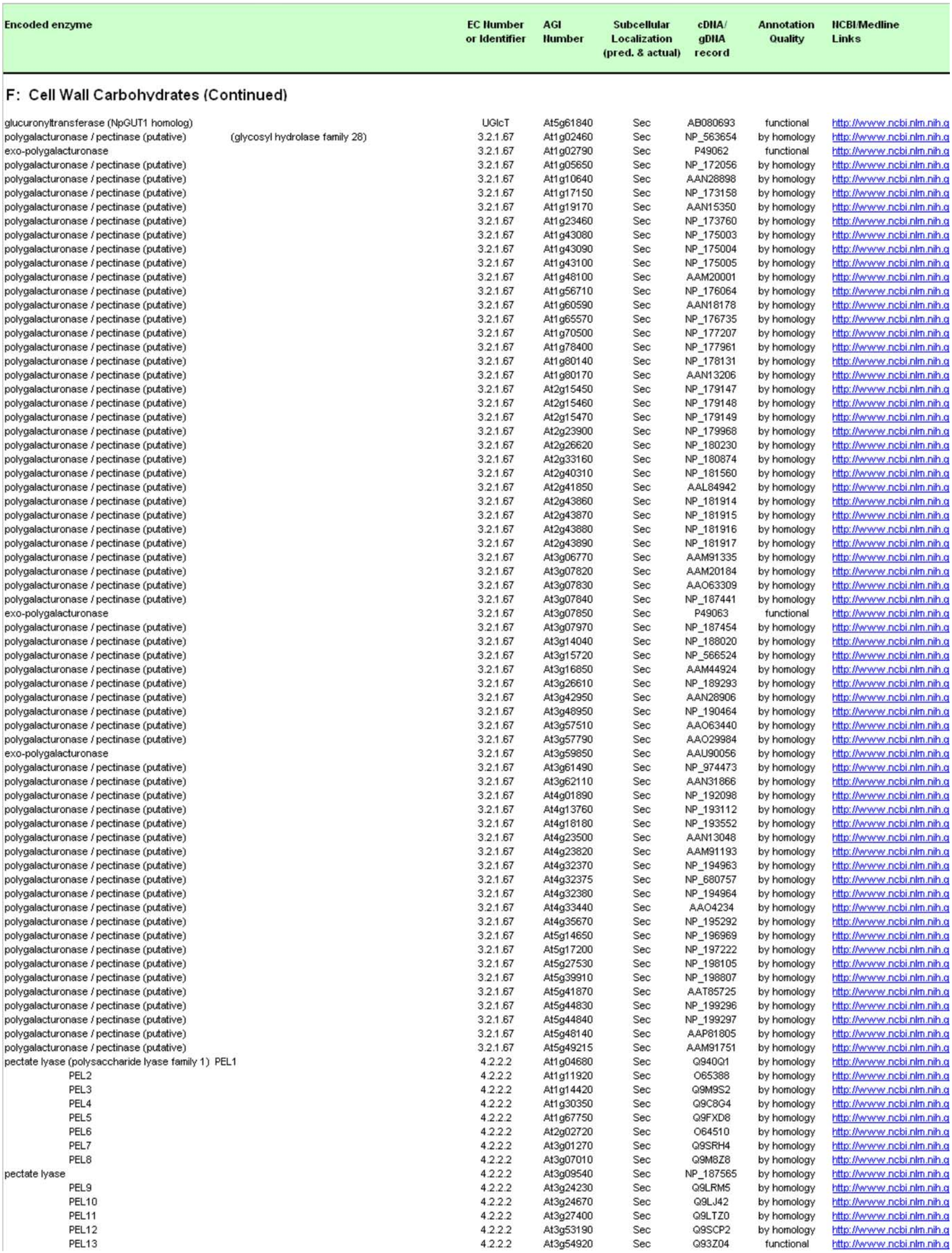
Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
F: Cell Wall Carbohydrates						
UDP-carbohydrates						
hexokinase	2.7.1.1	At1g47840	Chl	NP_175220	by homology	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At1g50460	Cyt/ER	AAM20056	by homology	http://www.ncbi.nlm.nih.g
hexokinase 2	2.7.1.1	At2g19860	Cyt/ER	AAB49911	functional	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At3g20040	Chl	NP_188639	by homology	http://www.ncbi.nlm.nih.g
hexokinase 1	2.7.1.1	At4g29130	Cyt/ER	AAA60333	functional (?)	http://www.ncbi.nlm.nih.g
hexokinase	2.7.1.1	At4g37840	Chl	Q9T071	by homology	http://www.ncbi.nlm.nih.g
glucuronokinase	not cloned yet				NA	NA
UDP-Glucose pyrophosphorylase (UTP-hexose-1-phosphate uridylyltransferase)	2.7.7.9	At3g03250	Cyt	AAK32773	by homology	http://www.ncbi.nlm.nih.g
UDP-Galactose pyrophosphorylase	2.7.7.10	At5g18200	Cyt	AAO64194	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 4-epimerase	5.1.3.2	At1g12780	Cyt	Q42605	functional	http://www.ncbi.nlm.nih.g
UDP-Glucose 4-epimerase	5.1.3.2	At1g63180	Cyt	NP_564811	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 4-epimerase	5.1.3.2	At4g10960	Cyt	Q9SN58	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 4-epimerase	5.1.3.2	At4g23920	Cyt	Q9T0A7	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 4-epimerase	5.1.3.2	At1g64440	Cyt	AAS76249	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 6-dehydrogenase	1.1.1.22	At1g26570	Cyt	AAN28861	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 6-dehydrogenase	1.1.1.22	At5g15490	Cyt	AAL07049	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 6-dehydrogenase	1.1.1.22	At5g39320	Cyt	AAP21188	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose 6-dehydrogenase	1.1.1.22	At3g29360	Cyt	AAL11570	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucuronic acid decarboxylase (annotated in A.t. database as C4,6 dehydratase) (AtUXS3)	4.1.1.35	At5g59290	Cyt	AAM16219	functional	http://www.ncbi.nlm.nih.g
UDP-Glucuronic acid decarboxylase (annotated in A.t. database as C4,6 dehydratase)	4.1.1.35	At2g28760	Cyt	AAM91299	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucuronic acid decarboxylase (annotated in A.t. database as C4,6 dehydratase)	4.1.1.35	At3g46440	Cyt	AAM20236	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucuronic acid decarboxylase (annotated in A.t. database as C4,6 dehydratase)	4.1.1.35	At2g47650	Cyt	AAM14846	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucuronic acid decarboxylase (annotated in A.t. database as C4,6 dehydratase)	4.1.1.35	At3g62830	Cyt(memb)	AAN28836	functional	http://www.ncbi.nlm.nih.g
UDP-Glucuronic acid decarboxylase (annotated in A.t. database as C4,6 dehydratase)	4.1.1.35	At3g53520	Cyt(memb)	AAO29973	functional	http://www.ncbi.nlm.nih.g
GDP-carbohydrates						
phosphomannomutase (PMM)	5.4.2.8	At2g45790	Cyt	O80840	by homology	http://www.ncbi.nlm.nih.g
phosphomannose isomerase / mannose-6-phosphate isomerase (din9) (PMI)	5.3.1.8	At1g67070	Cyt	AAG23720	functional (?)	http://www.ncbi.nlm.nih.g
phosphomannose isomerase / mannose-6-phosphate isomerase (PMI)	5.3.1.8	At3g02570	Cyt	AAM20214	by homology	http://www.ncbi.nlm.nih.g
GDP-Mannose pyrophosphorylase (mannose-1-phosphate guanylyltransferase)	2.7.7.22	At2g39770	Cyt	AAP21173	by homology	http://www.ncbi.nlm.nih.g
GDP-Mannose pyrophosphorylase (mannose-1-phosphate guanylyltransferase)	2.7.7.22	At3g55590	Cyt	NP_191118	by homology	http://www.ncbi.nlm.nih.g
GDP-Mannose pyrophosphorylase (mannose-1-phosphate guanylyltransferase)	2.7.7.22	At4g30570	Cyt	AAN13073	by homology	http://www.ncbi.nlm.nih.g
GDP-D-Mannose-4,6-dehydratase (MUR1; GMD2)	GMD	At3g51160	Cyt	AAM61140	functional	http://www.ncbi.nlm.nih.g
GDP-D-Mannose-4,6-dehydratase (GMD1)	GMD	At5g66280	Cyt	AAF07199	functional	http://www.ncbi.nlm.nih.g
GDP-L-fucose synthetase (GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase)	1.1.1.271	At1g17890	Cyt	AAM20005	by homology	http://www.ncbi.nlm.nih.g
GDP-L-fucose synthetase (GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase) (GER1)	1.1.1.271	At1g73250	Cyt	AAC02703	functional	http://www.ncbi.nlm.nih.g
CELLULOSE / HEMICELLULOSE / PECTIN						
Hemicelluloses						
core alpha1-->3-Fucosyltransferase	a1->3FT	At1g49710	Sec	CAC78980	functional	http://www.ncbi.nlm.nih.g
core alpha1-->3-Fucosyltransferase	a1->3FT	At3g19280	Sec	CAC78979	functional	http://www.ncbi.nlm.nih.g
alpha 1-->3 Fucosyltransferase	a1->3FT	At1g71990	Sec	AAK11728	functional	http://www.ncbi.nlm.nih.g
xyloglucan alpha-1,2-fucosyltransferase AtFUT1	a1->2FT	At2g03220	Sec	Q9SWH5	functional	http://www.ncbi.nlm.nih.g
AtFUT7	a1->2FT	At1g14070	Sec	Q9XI81	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT2	a1->2FT	At2g03210	Sec	O81053	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT8	a1->2FT	At1g14100	Sec	Q9XI78	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT9	a1->2FT	At1g14110	Sec	Q9XI77	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT6	a1->2FT	At1g14080	Sec	Q9XI80	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT4	a1->2FT	At2g15390	Sec	Q9SJP2	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT5	a1->2FT	At2g15370	Sec	Q9SJP4	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT10	a1->2FT	At2g15350	Sec	Q9SJP6	functional (?)	http://www.ncbi.nlm.nih.g
AtFUT3	a1->2FT	At1g74420	Sec	Q9CA71	functional (?)	http://www.ncbi.nlm.nih.g
xyloglucan 6-xylosyltransferase (AtXT1).	a-GalT	At3g62720	Sec	Q9LZJ3	functional (?)	http://www.ncbi.nlm.nih.g
alpha Galactosyltransferase	a-GalT	At4g02500	Sec	O22775	by homology	http://www.ncbi.nlm.nih.g
alpha Galactosyltransferase	a-GalT	At1g74380	Sec	Q9CA75	by homology	http://www.ncbi.nlm.nih.g
alpha Galactosyltransferase	a-GalT	At5g07720	Sec	Q9LF80	by homology	http://www.ncbi.nlm.nih.g
alpha Galactosyltransferase	a-GalT	At1g18690	Sec	Q9M9U0	by homology	http://www.ncbi.nlm.nih.g
Cellulose						
cellulose synthase (catalytic subunit) (RSW1)	2.4.1.12	At4g32410	Sec	CAB79958	by homology	http://www.ncbi.nlm.nih.g
cellulose synthase	2.4.1.12	At2g25540	Sec	AAD20713	by homology	http://www.ncbi.nlm.nih.g
Cellulose synthase	2.4.1.12	At5g05170	Sec	AAN86168	by homology	http://www.ncbi.nlm.nih.g
(IRX3)	2.4.1.12	At5g17420	Sec	AAO42789	by homology	http://www.ncbi.nlm.nih.g
(Ath-A)	2.4.1.12	At4g39350	Sec	AAM13307	by homology	http://www.ncbi.nlm.nih.g
cellulose synthase	2.4.1.12	At5g09870	Sec	AAP68271	by homology	http://www.ncbi.nlm.nih.g
cellulose synthase	2.4.1.12	At5g64740	Sec	AAN28896	by homology	http://www.ncbi.nlm.nih.g
cellulose synthase	2.4.1.12	At2g21770	Sec	AAD20396	by homology	http://www.ncbi.nlm.nih.g
cellulose synthase	2.4.1.12	At5g44030	Sec	AAP04096	by homology	http://www.ncbi.nlm.nih.g
cellulose synthase	2.4.1.12	At4g18780	Sec	AAM20487	by homology	http://www.ncbi.nlm.nih.g
CslD3 / KOJAK	2.4.1.12	At3g03050	Sec	AAG60543	functional	http://www.ncbi.nlm.nih.g
(Ath-B)	2.4.1.12	At5g16910	Sec	AF027174	functional (?)	http://www.ncbi.nlm.nih.g
(< 70 % homology)	2.4.1.12	At1g02730	Sec	NP_171773	by homology	http://www.ncbi.nlm.nih.g
(< 70 % homology)	2.4.1.12	At4g38190	Sec	AAO64152	by homology	http://www.ncbi.nlm.nih.g
(< 70 % homology)	2.4.1.12	At2g33100	Sec	AAC04910	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At1g32180	Sec	NP_174497	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At2g32620	Sec	AAC25944	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At2g32540	Sec	AAC25936	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At2g32610	Sec	AAC25943	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At4g15320	Sec	CAB78574	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



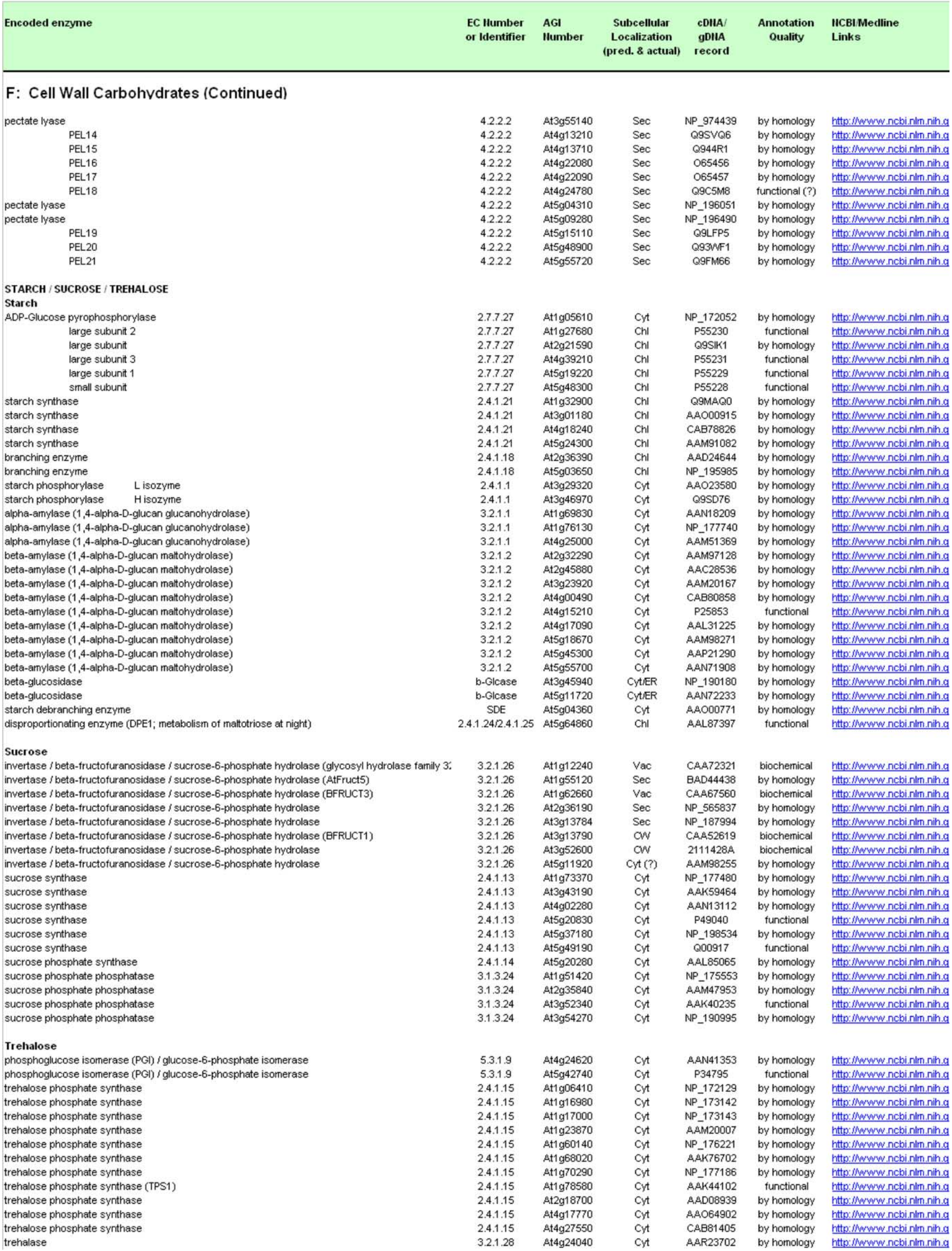
Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
F: Cell Wall Carbohydrates (Continued)						
cellulose synthase (< 60 % homology)	2.4.1.12	At4g15290	Sec	CAB78571	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At1g55850	Sec	AAL36396	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At4g23990	Sec	CAB81317	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At2g32530	Sec	AAN71948	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At4g24000	Sec	AAM20086	by homology	http://www.ncbi.nlm.nih.g
(< 60 % homology)	2.4.1.12	At4g24010	Sec	CAB81319	by homology	http://www.ncbi.nlm.nih.g
cellulase	3.2.1.4	At3g43860	Cyt	AAL59921	by homology	http://www.ncbi.nlm.nih.g
cellulase	3.2.1.4	At4g38990	Cyt	CAB80562	by homology	http://www.ncbi.nlm.nih.g
cellulase	3.2.1.4	At4g39000	Cyt	CAB80563	by homology	http://www.ncbi.nlm.nih.g
cellulase	3.2.1.4	At4g39010	Cyt	CAB80564	by homology	http://www.ncbi.nlm.nih.g
Pectins						
glycosyltransferase (membrane-bound; QUASIMODO1; qua1-1)	GlcT	At3g25140	Cyt/Golgi (?)	Q9LSG3	functional	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g02810	Sec	NP_563662	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g05310	Sec	NP_172023	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g11370	Sec	NP_172604	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g11580	Sec	AAK59760	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g11590	Sec	AAO50520	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g23200	Sec	AAM14264	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g44980	Sec	NP_175118	by homology	http://www.ncbi.nlm.nih.g
pectin methylesterase PE2	3.1.1.11	At1g53830	Sec	Q42534	functional (?)	http://www.ncbi.nlm.nih.g
PE1	3.1.1.11	At1g53840	Sec	Q43867	functional	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At1g69940	Sec	AAO22801	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g19150	Sec	AAD12032	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g21610	Sec	AAD23644	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g26440	Sec	AAC14493	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g26450	Sec	AAC14494	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g36700	Sec	NP_181208	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g36710	Sec	AAO22722	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g43050	Sec	NP_181833	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g45220	Sec	AAK32841	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g47030	Sec	AAN15509	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g47040	Sec	AAN64511	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g47280	Sec	NP_850471	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At2g47550	Sec	AAL24207	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g05610	Sec	AAO64883	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g05620	Sec	NP_187213	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g06830	Sec	NP_187339	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g10710	Sec	NP_187682	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g10720	Sec	AAK59501	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g14300	Sec	NP_188047	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g14310	Sec	AAN28889	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g17060	Sec	AAO64105	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g24130	Sec	NP_189055	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g27980	Sec	NP_189437	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g29090	Sec	AAM20211	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g43270	Sec	AAM20354	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g43270	Sec	AAM20354	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g47400	Sec	NP_190324	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g49220	Sec	AAP37714	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g59010	Sec	AAN46858	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g60730	Sec	AAP04164	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At3g62170	Sec	AAM13236	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g00190	Sec	NP_191930	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g02300	Sec	NP_192139	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g02320	Sec	NP_192141	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g02330	Sec	AAN12975	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g03930	Sec	NP_192302	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g15980	Sec	NP_193333	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g33220	Sec	AAK55695	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At4g33230	Sec	NP_195049	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g04960	Sec	AAO42295	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g04970	Sec	NP_196116	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g07410	Sec	NP_568181	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g07420	Sec	AAO50592	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g07430	Sec	NP_196360	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g09760	Sec	AAP04044	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g18990	Sec	NP_197400	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g19730	Sec	AAM20209	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g20860	Sec	NP_197586	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g26810	Sec	NP_198033	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g27870	Sec	NP_198139	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g47500	Sec	AAN18134	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g49180	Sec	AAN72223	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g51490	Sec	NP_199962	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g51500	Sec	NP_199963	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g53370	Sec	AAK93754	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g55590	Sec	NP_200370	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g61680	Sec	NP_200976	by homology	http://www.ncbi.nlm.nih.g
pectinesterase (putative)	3.1.1.11	At5g64640	Sec	AAM91523	by homology	http://www.ncbi.nlm.nih.g
(an additional 24 genes contain low homology to known pectinesterases; annotated as invertase/pectin methylesterase inhibitor; not listed here)					NA	NA

Fig. 3 (*continued*)



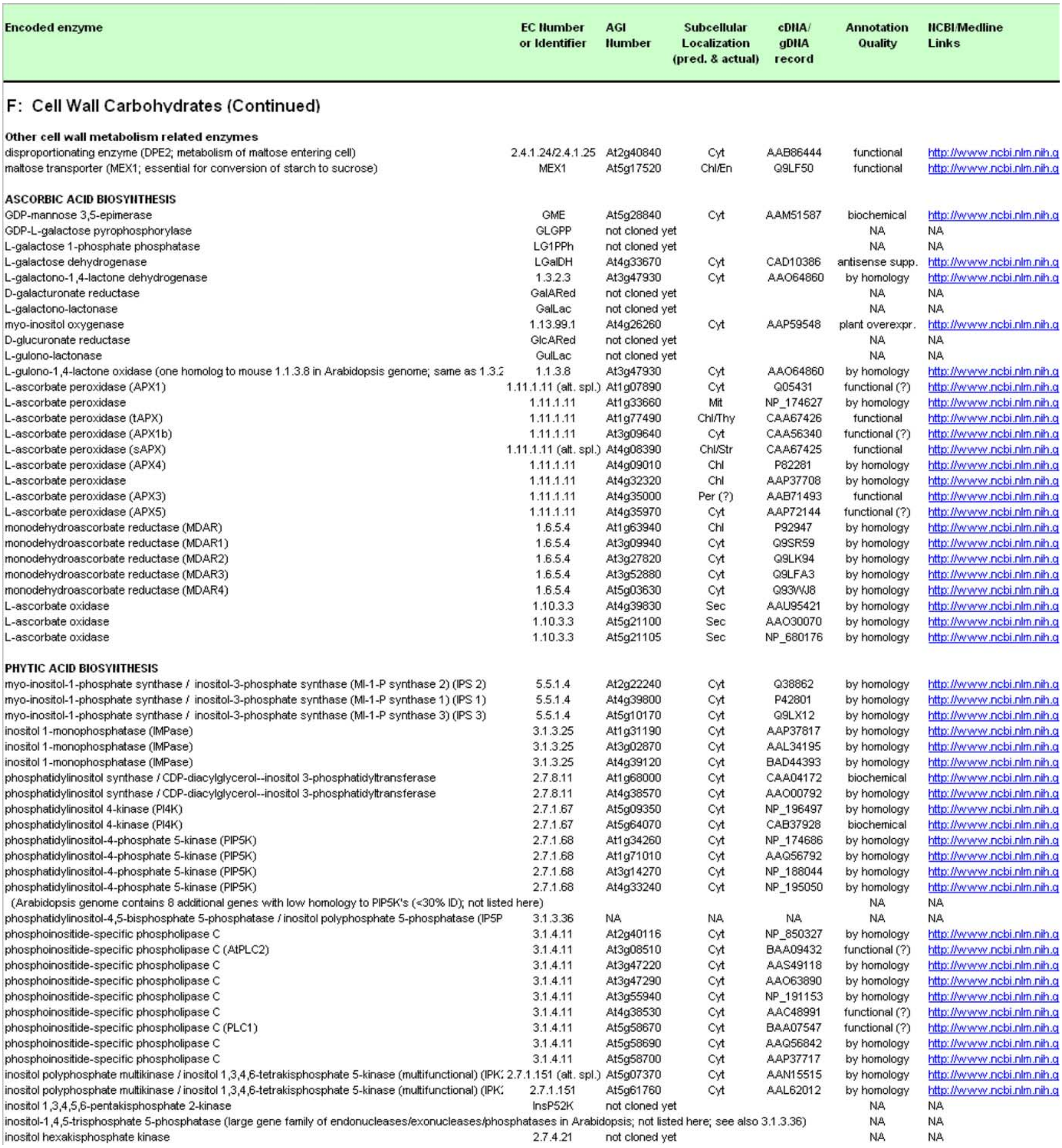
Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
F: Cell Wall Carbohydrates (Continued)						
glucuronyltransferase (NpGUT1 homolog)	UGlcT	At5g61840	Sec	AB080693	functional	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative) (glycosyl hydrolase family 28)	3.2.1.67	At1g02460	Sec	NP_563654	by homology	http://www.ncbi.nlm.nih.g
exo-polygalacturonase	3.2.1.67	At1g02790	Sec	P49062	functional	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g05650	Sec	NP_172056	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g10640	Sec	AAN28898	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g17150	Sec	NP_173158	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g19170	Sec	AAN15350	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g23460	Sec	NP_173760	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g43080	Sec	NP_175003	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g43090	Sec	NP_175004	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g43100	Sec	NP_175005	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g48100	Sec	AAM20001	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g56710	Sec	NP_176064	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g60590	Sec	AAN18178	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g65570	Sec	NP_176735	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g70500	Sec	NP_177207	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g78400	Sec	NP_177961	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g80140	Sec	NP_178131	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At1g80170	Sec	AAN13206	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g15450	Sec	NP_179147	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g15460	Sec	NP_179148	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g15470	Sec	NP_179149	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g23900	Sec	NP_179968	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g26620	Sec	NP_180230	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g33160	Sec	NP_180874	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g40310	Sec	NP_181560	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g41850	Sec	AAL84942	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g43860	Sec	NP_181914	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g43870	Sec	NP_181915	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g43880	Sec	NP_181916	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At2g43890	Sec	NP_181917	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g06770	Sec	AAM91335	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g07820	Sec	AAM20184	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g07830	Sec	AAO63309	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g07840	Sec	NP_187441	by homology	http://www.ncbi.nlm.nih.g
exo-polygalacturonase	3.2.1.67	At3g07850	Sec	P49063	functional	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g07970	Sec	NP_187454	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g14040	Sec	NP_188020	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g15720	Sec	NP_566524	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g16850	Sec	AAM44924	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g26610	Sec	NP_189293	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g42950	Sec	AAN28906	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g48950	Sec	NP_190464	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g57510	Sec	AAO63440	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g57790	Sec	AAO29984	by homology	http://www.ncbi.nlm.nih.g
exo-polygalacturonase	3.2.1.67	At3g59850	Sec	AAU90056	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g61490	Sec	NP_974473	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At3g62110	Sec	AAN31866	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g01890	Sec	NP_192098	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g13760	Sec	NP_193112	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g18180	Sec	NP_193552	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g23500	Sec	AAN13048	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g23820	Sec	AAM91193	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g32370	Sec	NP_194963	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g32375	Sec	NP_680757	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g32380	Sec	NP_194964	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g33440	Sec	AAO4234	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At4g35670	Sec	NP_195292	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g14650	Sec	NP_196969	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g17200	Sec	NP_197222	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g27530	Sec	NP_198105	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g39910	Sec	NP_198807	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g41870	Sec	AAT85725	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g44830	Sec	NP_199296	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g44840	Sec	NP_199297	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g48140	Sec	AAP81805	by homology	http://www.ncbi.nlm.nih.g
polygalacturonase / pectinase (putative)	3.2.1.67	At5g49215	Sec	AAM91751	by homology	http://www.ncbi.nlm.nih.g
pectate lyase (polysaccharide lyase family 1) PEL1	4.2.2.2	At1g04680	Sec	Q940Q1	by homology	http://www.ncbi.nlm.nih.g
PEL2	4.2.2.2	At1g11920	Sec	O65388	by homology	http://www.ncbi.nlm.nih.g
PEL3	4.2.2.2	At1g14420	Sec	Q9M9S2	by homology	http://www.ncbi.nlm.nih.g
PEL4	4.2.2.2	At1g30350	Sec	Q9C8G4	by homology	http://www.ncbi.nlm.nih.g
PEL5	4.2.2.2	At1g67750	Sec	Q9FXD8	by homology	http://www.ncbi.nlm.nih.g
PEL6	4.2.2.2	At2g02720	Sec	O64510	by homology	http://www.ncbi.nlm.nih.g
PEL7	4.2.2.2	At3g01270	Sec	Q9SRH4	by homology	http://www.ncbi.nlm.nih.g
PEL8	4.2.2.2	At3g07010	Sec	Q9M8Z8	by homology	http://www.ncbi.nlm.nih.g
pectate lyase	4.2.2.2	At3g09540	Sec	NP_187565	by homology	http://www.ncbi.nlm.nih.g
PEL9	4.2.2.2	At3g24230	Sec	Q9LRM5	by homology	http://www.ncbi.nlm.nih.g
PEL10	4.2.2.2	At3g24670	Sec	Q9LJ42	by homology	http://www.ncbi.nlm.nih.g
PEL11	4.2.2.2	At3g27400	Sec	Q9LTZ0	by homology	http://www.ncbi.nlm.nih.g
PEL12	4.2.2.2	At3g53190	Sec	Q9SCP2	by homology	http://www.ncbi.nlm.nih.g
PEL13	4.2.2.2	At3g54920	Sec	Q93Z04	functional	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
F: Cell Wall Carbohydrates (Continued)						
pectate lyase	4.2.2.2	At3g55140	Sec	NP_974439	by homology	http://www.ncbi.nlm.nih.g
PEL14	4.2.2.2	At4g13210	Sec	Q9SVQ6	by homology	http://www.ncbi.nlm.nih.g
PEL15	4.2.2.2	At4g13710	Sec	Q944R1	by homology	http://www.ncbi.nlm.nih.g
PEL16	4.2.2.2	At4g22080	Sec	O65456	by homology	http://www.ncbi.nlm.nih.g
PEL17	4.2.2.2	At4g22090	Sec	O65457	by homology	http://www.ncbi.nlm.nih.g
PEL18	4.2.2.2	At4g24780	Sec	Q9C5M8	functional (?)	http://www.ncbi.nlm.nih.g
pectate lyase	4.2.2.2	At5g04310	Sec	NP_196051	by homology	http://www.ncbi.nlm.nih.g
pectate lyase	4.2.2.2	At5g09280	Sec	NP_196490	by homology	http://www.ncbi.nlm.nih.g
PEL19	4.2.2.2	At5g15110	Sec	Q9LFP5	by homology	http://www.ncbi.nlm.nih.g
PEL20	4.2.2.2	At5g48900	Sec	Q93WF1	by homology	http://www.ncbi.nlm.nih.g
PEL21	4.2.2.2	At5g55720	Sec	Q9FM66	by homology	http://www.ncbi.nlm.nih.g
STARCH / SUCROSE / TREHALOSE						
Starch						
ADP-Glucose pyrophosphorylase	2.7.7.27	At1g05610	Cyt	NP_172052	by homology	http://www.ncbi.nlm.nih.g
large subunit 2	2.7.7.27	At1g27680	Chl	P55230	functional	http://www.ncbi.nlm.nih.g
large subunit	2.7.7.27	At2g21590	Chl	Q9SIK1	by homology	http://www.ncbi.nlm.nih.g
large subunit 3	2.7.7.27	At4g39210	Chl	P55231	functional	http://www.ncbi.nlm.nih.g
large subunit 1	2.7.7.27	At5g19220	Chl	P55229	functional	http://www.ncbi.nlm.nih.g
small subunit	2.7.7.27	At5g48300	Chl	P55228	functional	http://www.ncbi.nlm.nih.g
starch synthase	2.4.1.21	At1g32900	Chl	Q9MAQ0	by homology	http://www.ncbi.nlm.nih.g
starch synthase	2.4.1.21	At3g01180	Chl	AAO00915	by homology	http://www.ncbi.nlm.nih.g
starch synthase	2.4.1.21	At4g18240	Chl	CAB78826	by homology	http://www.ncbi.nlm.nih.g
starch synthase	2.4.1.21	At5g24300	Chl	AAM91082	by homology	http://www.ncbi.nlm.nih.g
branching enzyme	2.4.1.18	At2g36390	Chl	AAD24644	by homology	http://www.ncbi.nlm.nih.g
branching enzyme	2.4.1.18	At5g03650	Chl	NP_195985	by homology	http://www.ncbi.nlm.nih.g
starch phosphorylase L isozyme	2.4.1.1	At3g29320	Cyt	AAO23580	by homology	http://www.ncbi.nlm.nih.g
starch phosphorylase H isozyme	2.4.1.1	At3g46970	Cyt	Q9SD76	by homology	http://www.ncbi.nlm.nih.g
alpha-amylase (1,4-alpha-D-glucan glucanohydrolase)	3.2.1.1	At1g69830	Cyt	AAN18209	by homology	http://www.ncbi.nlm.nih.g
alpha-amylase (1,4-alpha-D-glucan glucanohydrolase)	3.2.1.1	At1g76130	Cyt	NP_177740	by homology	http://www.ncbi.nlm.nih.g
alpha-amylase (1,4-alpha-D-glucan glucanohydrolase)	3.2.1.1	At4g25000	Cyt	AAM51369	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At2g32290	Cyt	AAM97128	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At2g45880	Cyt	AAC28536	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At3g23920	Cyt	AAM20167	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At4g00490	Cyt	CAB80858	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At4g15210	Cyt	P25853	functional	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At4g17090	Cyt	AAL31225	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At5g18670	Cyt	AAM98271	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At5g45300	Cyt	AAP21290	by homology	http://www.ncbi.nlm.nih.g
beta-amylase (1,4-alpha-D-glucan maltohydrolase)	3.2.1.2	At5g55700	Cyt	AAN71908	by homology	http://www.ncbi.nlm.nih.g
beta-glucosidase	b-Glcase	At3g45940	Cyt/ER	NP_190180	by homology	http://www.ncbi.nlm.nih.g
beta-glucosidase	b-Glcase	At5g11720	Cyt/ER	AAN72233	by homology	http://www.ncbi.nlm.nih.g
starch debranching enzyme	SDE	At5g04360	Cyt	AAO00771	by homology	http://www.ncbi.nlm.nih.g
disproportionating enzyme (DPE1; metabolism of maltotriose at night)	2.4.1.24/2.4.1.25	At5g64860	Chl	AAL87397	functional	http://www.ncbi.nlm.nih.g
Sucrose						
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase (glycosyl hydrolase family 3:	3.2.1.26	At1g12240	Vac	CAA72321	biochemical	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase (AtFruct5)	3.2.1.26	At1g55120	Sec	BAD44438	by homology	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase (BFRUCT3)	3.2.1.26	At1g62660	Vac	CAA67560	biochemical	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase	3.2.1.26	At2g36190	Sec	NP_565837	by homology	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase	3.2.1.26	At3g13784	Sec	NP_187994	by homology	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase (BFRUCT1)	3.2.1.26	At3g13790	CW	CAA52619	biochemical	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase	3.2.1.26	At3g52600	CW	2111428A	biochemical	http://www.ncbi.nlm.nih.g
invertase / beta-fructofuranosidase / sucrose-6-phosphate hydrolase	3.2.1.26	At5g11920	Cyt (?)	AAM98255	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At1g73370	Cyt	NP_177480	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At3g43190	Cyt	AAK59464	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At4g02280	Cyt	AAN13112	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At5g20830	Cyt	P49040	functional	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At5g37180	Cyt	NP_198534	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At5g49190	Cyt	Q00917	functional	http://www.ncbi.nlm.nih.g
sucrose phosphate synthase	2.4.1.14	At5g20280	Cyt	AAL85065	by homology	http://www.ncbi.nlm.nih.g
sucrose phosphate phosphatase	3.1.3.24	At1g51420	Cyt	NP_175553	by homology	http://www.ncbi.nlm.nih.g
sucrose phosphate phosphatase	3.1.3.24	At2g35840	Cyt	AAM47953	by homology	http://www.ncbi.nlm.nih.g
sucrose phosphate phosphatase	3.1.3.24	At3g52340	Cyt	AAK40235	functional	http://www.ncbi.nlm.nih.g
sucrose phosphate phosphatase	3.1.3.24	At3g54270	Cyt	NP_190995	by homology	http://www.ncbi.nlm.nih.g
Trehalose						
phosphoglucose isomerase (PGI) / glucose-6-phosphate isomerase	5.3.1.9	At4g24620	Cyt	AAN41353	by homology	http://www.ncbi.nlm.nih.g
phosphoglucose isomerase (PGI) / glucose-6-phosphate isomerase	5.3.1.9	At5g42740	Cyt	P34795	functional	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g06410	Cyt	NP_172129	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g16980	Cyt	NP_173142	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g17000	Cyt	NP_173143	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g23870	Cyt	AAM20007	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g60140	Cyt	NP_176221	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g68020	Cyt	AAK76702	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At1g70290	Cyt	NP_177186	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase (TPS1)	2.4.1.15	At1g78580	Cyt	AAK44102	functional	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At2g18700	Cyt	AAD08939	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At4g17770	Cyt	AAO64902	by homology	http://www.ncbi.nlm.nih.g
trehalose phosphate synthase	2.4.1.15	At4g27550	Cyt	CAB81405	by homology	http://www.ncbi.nlm.nih.g
trehalase	3.2.1.28	At4g24040	Cyt	AAR23702	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
F: Cell Wall Carbohydrates (Continued)						
Other cell wall metabolism related enzymes						
disproportionating enzyme (DPE2; metabolism of maltose entering cell)	2.4.1.24/2.4.1.25	At2g40840	Cyt	AAB86444	functional	http://www.ncbi.nlm.nih.g
maltose transporter (MEX1; essential for conversion of starch to sucrose)	MEX1	At5g17520	Chl/En	Q9LF50	functional	http://www.ncbi.nlm.nih.g
ASCORBIC ACID BIOSYNTHESIS						
GDP-mannose 3,5-epimerase	GME	At5g28840	Cyt	AAM51587	biochemical	http://www.ncbi.nlm.nih.g
GDP-L-galactose pyrophosphorylase	GLGPP	not cloned yet			NA	NA
L-galactose 1-phosphate phosphatase	LG1PPh	not cloned yet			NA	NA
L-galactose dehydrogenase	LGalDH	At4g33670	Cyt	CAD10386	antisense supp.	http://www.ncbi.nlm.nih.g
L-galactono-1,4-lactone dehydrogenase	1.3.2.3	At3g47930	Cyt	AAO64860	by homology	http://www.ncbi.nlm.nih.g
D-galacturonate reductase	GalARed	not cloned yet			NA	NA
L-galactono-lactonase	GalLac	not cloned yet			NA	NA
myo-inositol oxygenase	1.13.99.1	At4g26260	Cyt	AAP59548	plant overexpr.	http://www.ncbi.nlm.nih.g
D-glucuronate reductase	GlcARed	not cloned yet			NA	NA
L-gulono-lactonase	GulLac	not cloned yet			NA	NA
L-gulono-1,4-lactone oxidase (one homolog to mouse 1.1.3.8 in Arabidopsis genome; same as 1.3.2	1.1.3.8	At3g47930	Cyt	AAO64860	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (APX1)	1.11.1.11 (alt. spl.)	At1g07890	Cyt	Q05431	functional (?)	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase	1.11.1.11	At1g33660	Mit	NP_174627	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (tAPX)	1.11.1.11	At1g77490	Chl/Thy	CAA67426	functional	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (APX1b)	1.11.1.11	At3g09640	Cyt	CAA56340	functional (?)	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (sAPX)	1.11.1.11 (alt. spl.)	At4g08390	Chl/Str	CAA67425	functional	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (APX4)	1.11.1.11	At4g09010	Chl	P82281	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase	1.11.1.11	At4g32320	Chl	AAP37708	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (APX3)	1.11.1.11	At4g35000	Per (?)	AAB71493	functional	http://www.ncbi.nlm.nih.g
L-ascorbate peroxidase (APX5)	1.11.1.11	At4g35970	Cyt	AAP72144	functional (?)	http://www.ncbi.nlm.nih.g
monodehydroascorbate reductase (MDAR)	1.6.5.4	At1g63940	Chl	P92947	by homology	http://www.ncbi.nlm.nih.g
monodehydroascorbate reductase (MDAR1)	1.6.5.4	At3g09940	Cyt	Q9SR59	by homology	http://www.ncbi.nlm.nih.g
monodehydroascorbate reductase (MDAR2)	1.6.5.4	At3g27820	Cyt	Q9LK94	by homology	http://www.ncbi.nlm.nih.g
monodehydroascorbate reductase (MDAR3)	1.6.5.4	At3g52880	Cyt	Q9LFA3	by homology	http://www.ncbi.nlm.nih.g
monodehydroascorbate reductase (MDAR4)	1.6.5.4	At5g03630	Cyt	Q93WJ8	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate oxidase	1.10.3.3	At4g39830	Sec	AAU95421	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate oxidase	1.10.3.3	At5g21100	Sec	AAO30070	by homology	http://www.ncbi.nlm.nih.g
L-ascorbate oxidase	1.10.3.3	At5g21105	Sec	NP_680176	by homology	http://www.ncbi.nlm.nih.g
PHYTIC ACID BIOSYNTHESIS						
myo-inositol-1-phosphate synthase / inositol-3-phosphate synthase (MI-1-P synthase 2) (IPS 2)	5.5.1.4	At2g22240	Cyt	Q38862	by homology	http://www.ncbi.nlm.nih.g
myo-inositol-1-phosphate synthase / inositol-3-phosphate synthase (MI-1-P synthase 1) (IPS 1)	5.5.1.4	At4g39800	Cyt	P42801	by homology	http://www.ncbi.nlm.nih.g
myo-inositol-1-phosphate synthase / inositol-3-phosphate synthase (MI-1-P synthase 3) (IPS 3)	5.5.1.4	At5g10170	Cyt	Q9LX12	by homology	http://www.ncbi.nlm.nih.g
inositol 1-monophosphatase (IMPase)	3.1.3.25	At1g31190	Cyt	AAP37817	by homology	http://www.ncbi.nlm.nih.g
inositol 1-monophosphatase (IMPase)	3.1.3.25	At3g02870	Cyt	AAL34195	by homology	http://www.ncbi.nlm.nih.g
inositol 1-monophosphatase (IMPase)	3.1.3.25	At4g39120	Cyt	BAD44393	by homology	http://www.ncbi.nlm.nih.g
phosphatidylinositol synthase / CDP-diacylglycerol--inositol 3-phosphatidyltransferase	2.7.8.11	At1g68000	Cyt	CAA04172	biochemical	http://www.ncbi.nlm.nih.g
phosphatidylinositol synthase / CDP-diacylglycerol--inositol 3-phosphatidyltransferase	2.7.8.11	At4g38570	Cyt	AAO00792	by homology	http://www.ncbi.nlm.nih.g
phosphatidylinositol 4-kinase (PI4K)	2.7.1.67	At5g09350	Cyt	NP_196497	by homology	http://www.ncbi.nlm.nih.g
phosphatidylinositol 4-kinase (PI4K)	2.7.1.67	At5g64070	Cyt	CAB37928	biochemical	http://www.ncbi.nlm.nih.g
phosphatidylinositol-4-phosphate 5-kinase (PIP5K)	2.7.1.68	At1g34260	Cyt	NP_174686	by homology	http://www.ncbi.nlm.nih.g
phosphatidylinositol-4-phosphate 5-kinase (PIP5K)	2.7.1.68	At1g71010	Cyt	AAQ56792	by homology	http://www.ncbi.nlm.nih.g
phosphatidylinositol-4-phosphate 5-kinase (PIP5K)	2.7.1.68	At3g14270	Cyt	NP_188044	by homology	http://www.ncbi.nlm.nih.g
phosphatidylinositol-4-phosphate 5-kinase (PIP5K)	2.7.1.68	At4g33240	Cyt	NP_195050	by homology	http://www.ncbi.nlm.nih.g
(Arabidopsis genome contains 8 additional genes with low homology to PIP5K's (<30% ID); not listed here)					NA	NA
phosphatidylinositol-4,5-bisphosphate 5-phosphatase / inositol polyphosphate 5-phosphatase (IP5P	3.1.3.36	NA	NA	NA	NA	NA
phosphoinositide-specific phospholipase C	3.1.4.11	At2g40116	Cyt	NP_850327	by homology	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C (AtPLC2)	3.1.4.11	At3g08510	Cyt	BAA09432	functional (?)	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C	3.1.4.11	At3g47220	Cyt	AAS49118	by homology	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C	3.1.4.11	At3g47290	Cyt	AAO63890	by homology	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C	3.1.4.11	At3g55940	Cyt	NP_191153	by homology	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C	3.1.4.11	At4g38530	Cyt	AAC48991	functional (?)	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C (PLC1)	3.1.4.11	At5g58670	Cyt	BAA07547	functional (?)	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C	3.1.4.11	At5g58690	Cyt	AAQ56842	by homology	http://www.ncbi.nlm.nih.g
phosphoinositide-specific phospholipase C	3.1.4.11	At5g58700	Cyt	AAP37717	by homology	http://www.ncbi.nlm.nih.g
inositol polyphosphate multikinase / inositol 1,3,4,6-tetrakisphosphate 5-kinase (multifunctional) (IPK	2.7.1.151 (alt. spl.)	At5g07370	Cyt	AAN15515	by homology	http://www.ncbi.nlm.nih.g
inositol polyphosphate multikinase / inositol 1,3,4,6-tetrakisphosphate 5-kinase (multifunctional) (IPK	2.7.1.151	At5g61760	Cyt	AAL62012	by homology	http://www.ncbi.nlm.nih.g
inositol 1,3,4,5,6-pentakisphosphate 2-kinase	InsP52K	not cloned yet			NA	NA
inositol-1,4,5-trisphosphate 5-phosphatase (large gene family of endonucleases/exonucleases/phosphatases in Arabidopsis; not listed here; see also 3.1.3.36)					NA	NA
inositol hexakisphosphate kinase	2.7.4.21	not cloned yet			NA	NA

Fig. 3 (*continued*)

transcript abundance [based on Northern Blots, ESTs, RT-PCR and microarrays], enzyme presence [based on proteomics data] and enzyme activity [based on biochemical assays with purified, native protein or crude protein extracts]), biochemical characteristics of recombinantly expressed isozymes (substrate specificity,

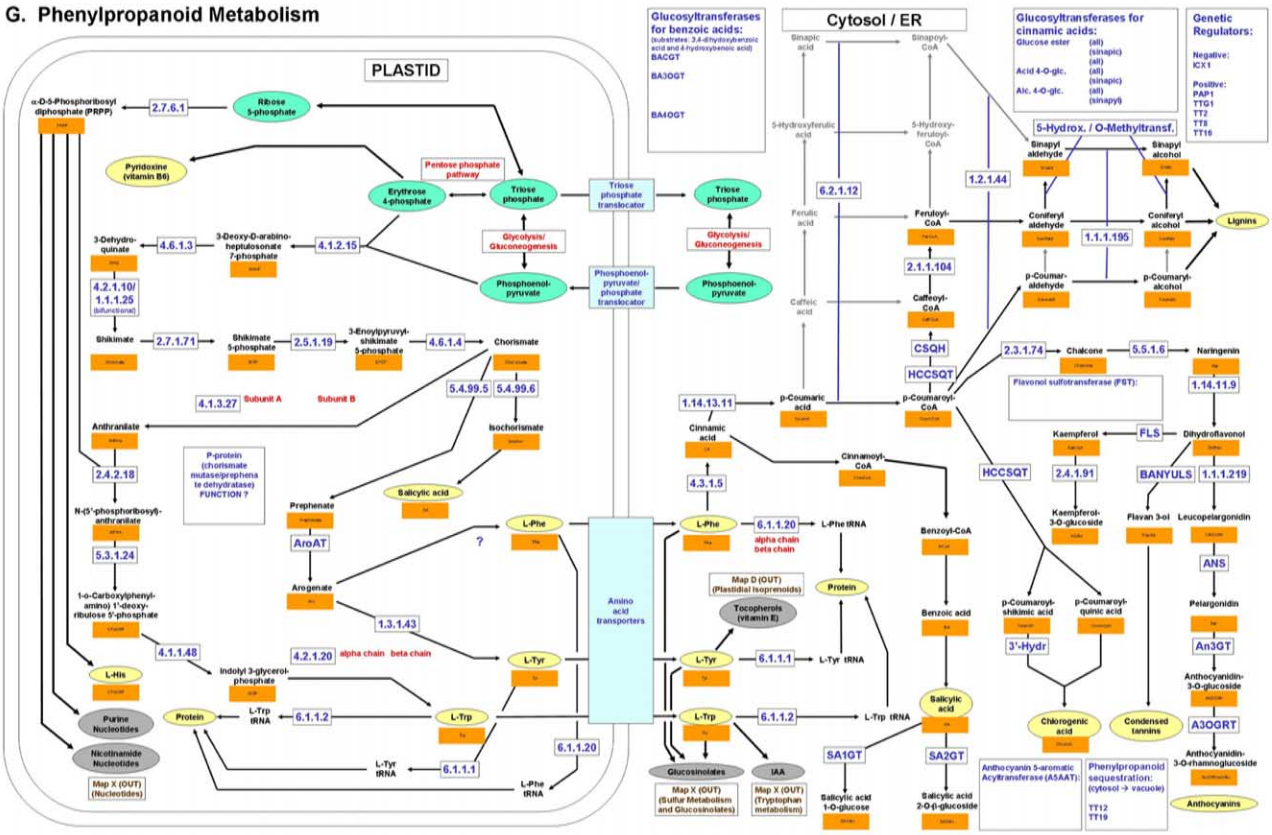
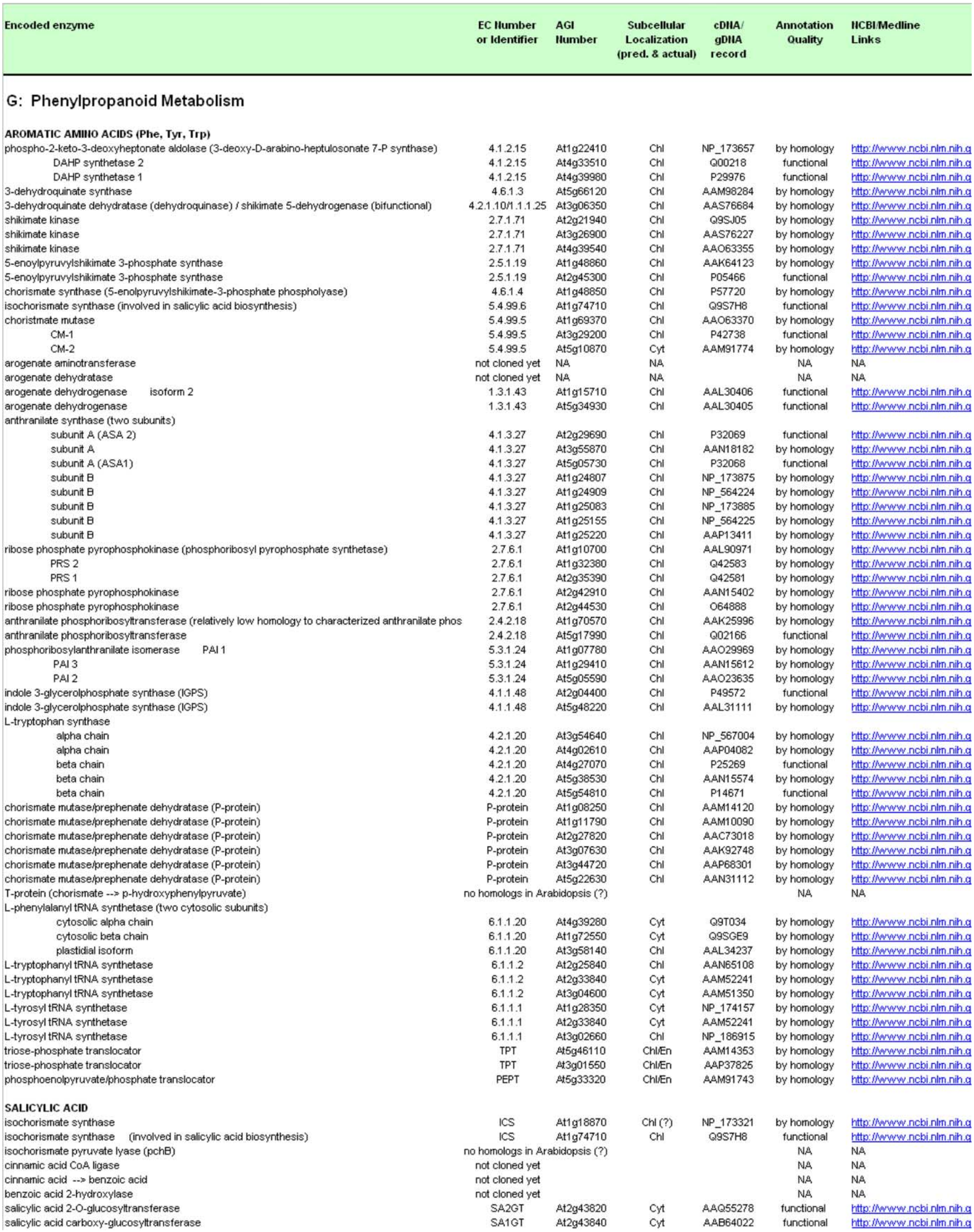

G. Phenylpropanoid Metabolism

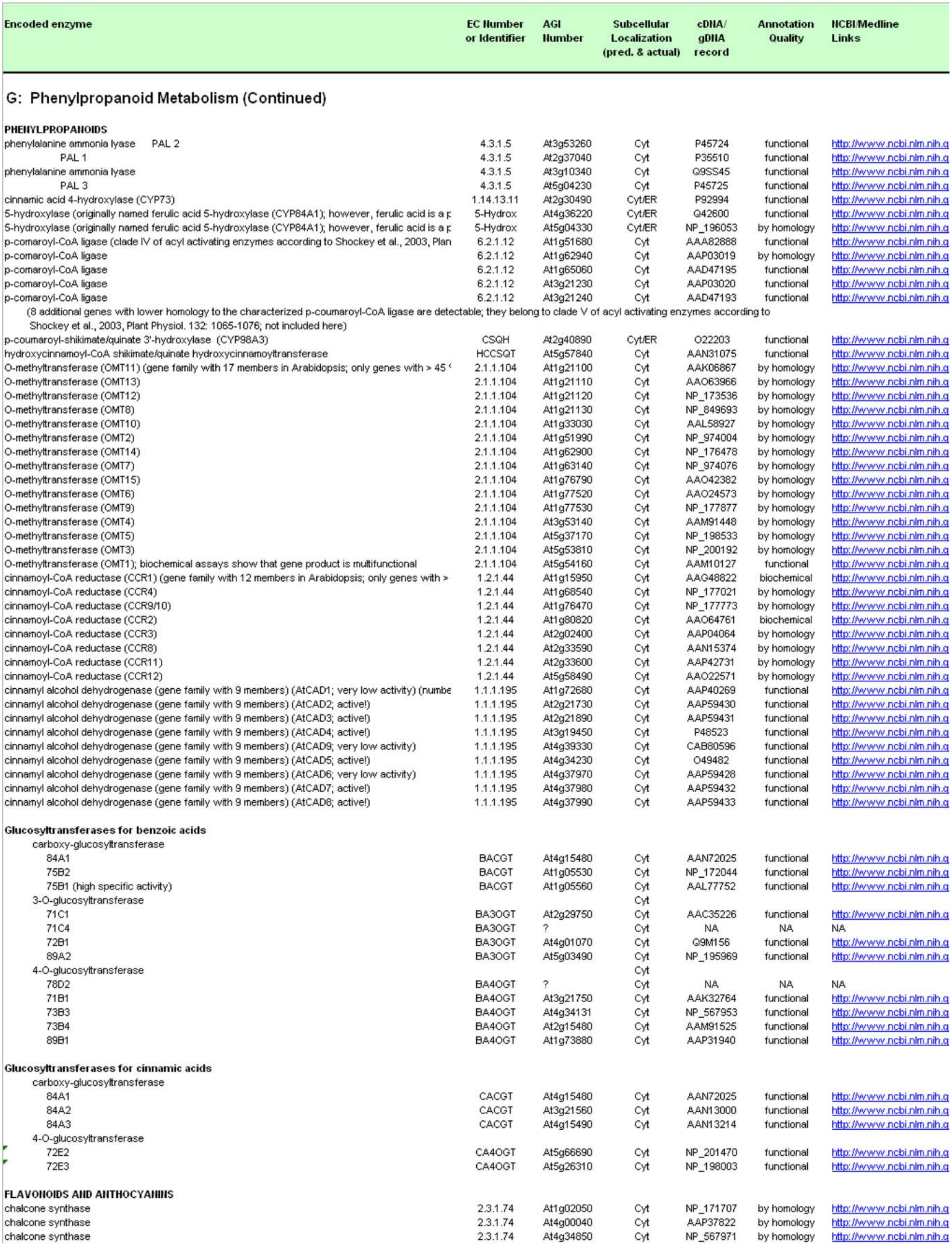
Fig. 3 (*continued*)

K_m, V_{max}), phenotypic characterization of knock-out or knock-in mutants, and links to the relevant literature (Table 1). Information is given about the enzyme name (column 1), the EC number (column 2), the AGI number of the gene(s) encoding the enzyme (column 3), the predicted or demonstrated subcellular localization (column 4; question marks are added when prediction algorithms do not yield ambiguous scores), the accession number of the peptide record for a full-length cDNA sequence (if available) or a genomic DNA sequence (column 5), a comment if the annotation was derived solely based on homology to enzymes of known function, or if the function was identified by biochemical assays or characterization of mutants (column 6), and a link to relevant GenBank records (column 7). Columns 8–15 provide experimental information on the tissue-specific expression patterns of the CAD genes and a link to the PubMed record of the relevant literature (Costa et al., 2003). Columns 16–24 summarize data regarding the tissue-specific expression and substrate specificity of native CAD (note that the individual isozymes could not be distinguished; the activity values shown are thus the same for all isozymes), with a link to the PubMed record of the publication from which the data were extracted (Sibout et al., 2003). By contrast, columns 25–28 show the substrate specificity for the recombinant isozymes expressed in *Escherichia coli* (literature link: Kim et al., 2004). Columns 29 to 34 display data and links regarding the phenotypic characterization of knock-out and knock-in mutants in specific CAD genes (literature link: Kim et al., 2004). A complementary database containing experimental information regarding the organ- and tissue-specific pool sizes of metabolites involved in *A. thaliana* biochemical pathways (`BioPathAtMETDB`) is also in development. Because gene–protein and protein–protein interaction data are sparse for *A. thaliana*, attempts will be made to integrate putatively relevant data sets from other model organisms (yeast, animals) into `BioPathAtDB`.



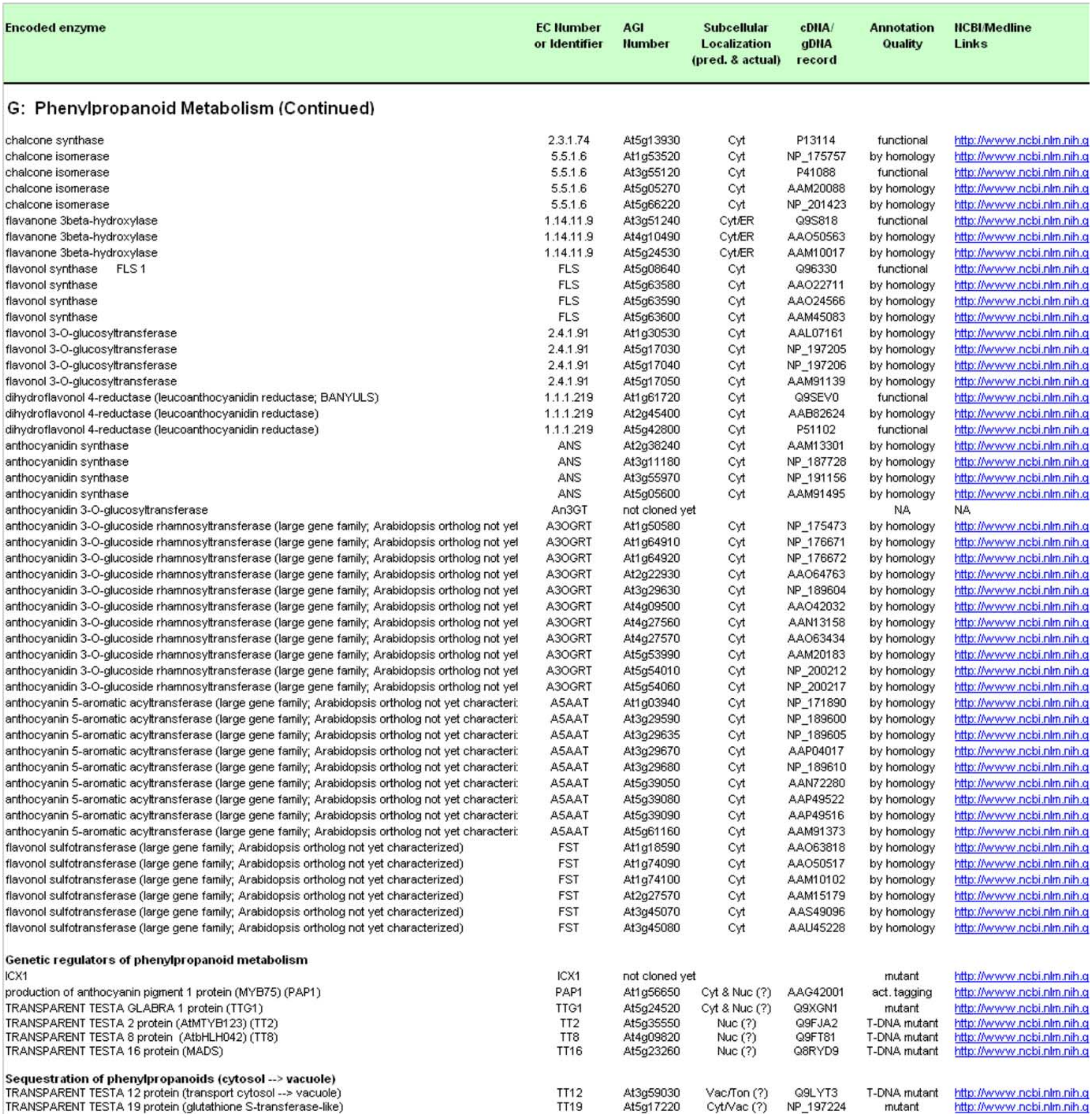
Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
G: Phenylpropanoid Metabolism						
AROMATIC AMINO ACIDS (Phe, Tyr, Trp)						
phospho-2-keto-3-deoxyheptonate aldolase (3-deoxy-D-arabino-heptulosonate 7-P synthase)	4.1.2.15	At1g22410	Chl	NP_173657	by homology	http://www.ncbi.nlm.nih.g
DAHP synthetase 2	4.1.2.15	At4g33510	Chl	Q00218	functional	http://www.ncbi.nlm.nih.g
DAHP synthetase 1	4.1.2.15	At4g39980	Chl	P29976	functional	http://www.ncbi.nlm.nih.g
3-dehydroquinate synthase	4.6.1.3	At5g66120	Chl	AAM98284	by homology	http://www.ncbi.nlm.nih.g
3-dehydroquinate dehydratase (dehydroquinase) / shikimate 5-dehydrogenase (bifunctional)	4.2.1.10/1.1.1.25	At3g06350	Chl	AAS76684	by homology	http://www.ncbi.nlm.nih.g
shikimate kinase	2.7.1.71	At2g21940	Chl	Q9SJ05	by homology	http://www.ncbi.nlm.nih.g
shikimate kinase	2.7.1.71	At3g26900	Chl	AAS76227	by homology	http://www.ncbi.nlm.nih.g
shikimate kinase	2.7.1.71	At4g39540	Chl	AAO63355	by homology	http://www.ncbi.nlm.nih.g
5-enoylpyruvylshikimate 3-phosphate synthase	2.5.1.19	At1g48860	Chl	AAK64123	by homology	http://www.ncbi.nlm.nih.g
5-enoylpyruvylshikimate 3-phosphate synthase	2.5.1.19	At2g45300	Chl	P05466	functional	http://www.ncbi.nlm.nih.g
chorismate synthase (5-enolpyruvylshikimate-3-phosphate phospholyase)	4.6.1.4	At1g48850	Chl	P57720	by homology	http://www.ncbi.nlm.nih.g
isochorismate synthase (involved in salicylic acid biosynthesis)	5.4.99.6	At1g74710	Chl	Q9S7H8	functional	http://www.ncbi.nlm.nih.g
choristmate mutase	5.4.99.5	At1g69370	Chl	AAO63370	by homology	http://www.ncbi.nlm.nih.g
CM-1	5.4.99.5	At3g29200	Chl	P42738	functional	http://www.ncbi.nlm.nih.g
CM-2	5.4.99.5	At5g10870	Cyt	AAM91774	by homology	http://www.ncbi.nlm.nih.g
arogenate aminotransferase	not cloned yet	NA	NA		NA	NA
arogenate dehydratase	not cloned yet	NA	NA		NA	NA
arogenate dehydrogenase isoform 2	1.3.1.43	At1g15710	Chl	AAL30406	functional	http://www.ncbi.nlm.nih.g
arogenate dehydrogenase	1.3.1.43	At5g34930	Chl	AAL30405	functional	http://www.ncbi.nlm.nih.g
anthranilate synthase (two subunits)						
subunit A (ASA 2)	4.1.3.27	At2g29690	Chl	P32069	functional	http://www.ncbi.nlm.nih.g
subunit A	4.1.3.27	At3g55870	Chl	AAN18182	by homology	http://www.ncbi.nlm.nih.g
subunit A (ASA1)	4.1.3.27	At5g05730	Chl	P32068	functional	http://www.ncbi.nlm.nih.g
subunit B	4.1.3.27	At1g24807	Chl	NP_173875	by homology	http://www.ncbi.nlm.nih.g
subunit B	4.1.3.27	At1g24909	Chl	NP_564224	by homology	http://www.ncbi.nlm.nih.g
subunit B	4.1.3.27	At1g25083	Chl	NP_173885	by homology	http://www.ncbi.nlm.nih.g
subunit B	4.1.3.27	At1g25155	Chl	NP_564225	by homology	http://www.ncbi.nlm.nih.g
subunit B	4.1.3.27	At1g25220	Chl	AAP13411	by homology	http://www.ncbi.nlm.nih.g
ribose phosphate pyrophosphokinase (phosphoribosyl pyrophosphate synthetase)	2.7.6.1	At1g10700	Chl	AAL90971	by homology	http://www.ncbi.nlm.nih.g
PRS 2	2.7.6.1	At1g32380	Chl	Q42583	by homology	http://www.ncbi.nlm.nih.g
PRS 1	2.7.6.1	At2g35390	Chl	Q42581	by homology	http://www.ncbi.nlm.nih.g
ribose phosphate pyrophosphokinase	2.7.6.1	At2g42910	Chl	AAN15402	by homology	http://www.ncbi.nlm.nih.g
ribose phosphate pyrophosphokinase	2.7.6.1	At2g44530	Chl	O64888	by homology	http://www.ncbi.nlm.nih.g
anthranilate phosphoribosyltransferase (relatively low homology to characterized anthranilate phos	2.4.2.18	At1g70570	Chl	AAK25996	by homology	http://www.ncbi.nlm.nih.g
anthranilate phosphoribosyltransferase	2.4.2.18	At5g17990	Chl	Q02166	functional	http://www.ncbi.nlm.nih.g
phosphoribosylanthranilate isomerase PAI 1	5.3.1.24	At1g07780	Chl	AAO29969	by homology	http://www.ncbi.nlm.nih.g
PAI 3	5.3.1.24	At1g29410	Chl	AAN15612	by homology	http://www.ncbi.nlm.nih.g
PAI 2	5.3.1.24	At5g05590	Chl	AAO23635	by homology	http://www.ncbi.nlm.nih.g
indole 3-glycerolphosphate synthase (IGPS)	4.1.1.48	At2g04400	Chl	P49572	functional	http://www.ncbi.nlm.nih.g
indole 3-glycerolphosphate synthase (IGPS)	4.1.1.48	At5g48220	Chl	AAL31111	by homology	http://www.ncbi.nlm.nih.g
L-tryptophan synthase						
alpha chain	4.2.1.20	At3g54640	Chl	NP_567004	by homology	http://www.ncbi.nlm.nih.g
alpha chain	4.2.1.20	At4g02610	Chl	AAP04082	by homology	http://www.ncbi.nlm.nih.g
beta chain	4.2.1.20	At4g27070	Chl	P25269	functional	http://www.ncbi.nlm.nih.g
beta chain	4.2.1.20	At5g38530	Chl	AAN15574	by homology	http://www.ncbi.nlm.nih.g
beta chain	4.2.1.20	At5g54810	Chl	P14671	functional	http://www.ncbi.nlm.nih.g
chorismate mutase/prephenate dehydratase (P-protein)	P-protein	At1g08250	Chl	AAM14120	by homology	http://www.ncbi.nlm.nih.g
chorismate mutase/prephenate dehydratase (P-protein)	P-protein	At1g11790	Chl	AAM10090	by homology	http://www.ncbi.nlm.nih.g
chorismate mutase/prephenate dehydratase (P-protein)	P-protein	At2g27820	Chl	AAC73018	by homology	http://www.ncbi.nlm.nih.g
chorismate mutase/prephenate dehydratase (P-protein)	P-protein	At3g07630	Chl	AAK92748	by homology	http://www.ncbi.nlm.nih.g
chorismate mutase/prephenate dehydratase (P-protein)	P-protein	At3g44720	Chl	AAP68301	by homology	http://www.ncbi.nlm.nih.g
chorismate mutase/prephenate dehydratase (P-protein)	P-protein	At5g22630	Chl	AAN31112	by homology	http://www.ncbi.nlm.nih.g
T-protein (chorismate --> p-hydroxyphenylpyruvate)	no homologs in Arabidopsis (?)				NA	NA
L-phenylalanyl tRNA synthetase (two cytosolic subunits)						
cytosolic alpha chain	6.1.1.20	At4g39280	Cyt	Q9T034	by homology	http://www.ncbi.nlm.nih.g
cytosolic beta chain	6.1.1.20	At1g72550	Cyt	Q9SGE9	by homology	http://www.ncbi.nlm.nih.g
plastidial isoform	6.1.1.20	At3g58140	Chl	AAL34237	by homology	http://www.ncbi.nlm.nih.g
L-tryptophanyl tRNA synthetase	6.1.1.2	At2g25840	Chl	AAN65108	by homology	http://www.ncbi.nlm.nih.g
L-tryptophanyl tRNA synthetase	6.1.1.2	At2g33840	Cyt	AAM52241	by homology	http://www.ncbi.nlm.nih.g
L-tryptophanyl tRNA synthetase	6.1.1.2	At3g04600	Cyt	AAM51350	by homology	http://www.ncbi.nlm.nih.g
L-tyrosyl tRNA synthetase	6.1.1.1	At1g28350	Cyt	NP_174157	by homology	http://www.ncbi.nlm.nih.g
L-tyrosyl tRNA synthetase	6.1.1.1	At2g33840	Cyt	AAM52241	by homology	http://www.ncbi.nlm.nih.g
L-tyrosyl tRNA synthetase	6.1.1.1	At3g02660	Chl	NP_186915	by homology	http://www.ncbi.nlm.nih.g
triose-phosphate translocator	TPT	At5g46110	Chl/En	AAM14353	by homology	http://www.ncbi.nlm.nih.g
triose-phosphate translocator	TPT	At3g01550	Chl/En	AAP37825	by homology	http://www.ncbi.nlm.nih.g
phosphoenolpyruvate/phosphate translocator	PEPT	At5g33320	Chl/En	AAM91743	by homology	http://www.ncbi.nlm.nih.g
SALICYLIC ACID						
isochorismate synthase	ICS	At1g18870	Chl (?)	NP_173321	by homology	http://www.ncbi.nlm.nih.g
isochorismate synthase (involved in salicylic acid biosynthesis)	ICS	At1g74710	Chl	Q9S7H8	functional	http://www.ncbi.nlm.nih.g
isochorismate pyruvate lyase (pchB)	no homologs in Arabidopsis (?)				NA	NA
cinnamic acid CoA ligase	not cloned yet				NA	NA
cinnamic acid --> benzoic acid	not cloned yet				NA	NA
benzoic acid 2-hydroxylase	not cloned yet				NA	NA
salicylic acid 2-O-glucosyltransferase	SA2GT	At2g43820	Cyt	AAQ55278	functional	http://www.ncbi.nlm.nih.g
salicylic acid carboxy-glucosyltransferase	SA1GT	At2g43840	Cyt	AAB64022	functional	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
G: Phenylpropanoid Metabolism (Continued)						
PHENYLPROPANOIDS						
phenylalanine ammonia lyase PAL 2	4.3.1.5	At3g53260	Cyt	P45724	functional	http://www.ncbi.nlm.nih.g
PAL 1	4.3.1.5	At2g37040	Cyt	P35510	functional	http://www.ncbi.nlm.nih.g
phenylalanine ammonia lyase	4.3.1.5	At3g10340	Cyt	Q9SS45	functional	http://www.ncbi.nlm.nih.g
PAL 3	4.3.1.5	At5g04230	Cyt	P45725	functional	http://www.ncbi.nlm.nih.g
cinnamic acid 4-hydroxylase (CYP73)	1.14.13.11	At2g30490	Cyt/ER	P92994	functional	http://www.ncbi.nlm.nih.g
5-hydroxylase (originally named ferulic acid 5-hydroxylase (CYP84A1); however, ferulic acid is a p	5-Hydrox	At4g36220	Cyt/ER	Q42600	functional	http://www.ncbi.nlm.nih.g
5-hydroxylase (originally named ferulic acid 5-hydroxylase (CYP84A1); however, ferulic acid is a p	5-Hydrox	At5g04330	Cyt/ER	NP_196053	by homology	http://www.ncbi.nlm.nih.g
p-comaroyl-CoA ligase (clade IV of acyl activating enzymes according to Shockey et al., 2003, Plan	6.2.1.12	At1g51680	Cyt	AAA82888	functional	http://www.ncbi.nlm.nih.g
p-comaroyl-CoA ligase	6.2.1.12	At1g62940	Cyt	AAP03019	by homology	http://www.ncbi.nlm.nih.g
p-comaroyl-CoA ligase	6.2.1.12	At1g65060	Cyt	AAD47195	functional	http://www.ncbi.nlm.nih.g
p-comaroyl-CoA ligase	6.2.1.12	At3g21230	Cyt	AAP03020	functional	http://www.ncbi.nlm.nih.g
p-comaroyl-CoA ligase	6.2.1.12	At3g21240	Cyt	AAD47193	functional	http://www.ncbi.nlm.nih.g
(8 additional genes with lower homology to the characterized p-coumaroyl-CoA ligase are detectable; they belong to clade V of acyl activating enzymes according to Shockey et al., 2003, Plant Physiol. 132: 1065-1076; not included here)						
p-coumaroyl-shikimate/quinate 3'-hydroxylase (CYP98A3)	CSQH	At2g40890	Cyt/ER	O22203	functional	http://www.ncbi.nlm.nih.g
hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyltransferase	HCCSQT	At5g57840	Cyt	AAN31075	functional	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT11) (gene family with 17 members in Arabidopsis; only genes with > 45 °	2.1.1.104	At1g21100	Cyt	AAK06867	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT13)	2.1.1.104	At1g21110	Cyt	AAO63966	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT12)	2.1.1.104	At1g21120	Cyt	NP_173536	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT8)	2.1.1.104	At1g21130	Cyt	NP_849693	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT10)	2.1.1.104	At1g33030	Cyt	AAL58927	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT2)	2.1.1.104	At1g51990	Cyt	NP_974004	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT14)	2.1.1.104	At1g62900	Cyt	NP_176478	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT7)	2.1.1.104	At1g63140	Cyt	NP_974076	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT15)	2.1.1.104	At1g76790	Cyt	AAO42382	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT6)	2.1.1.104	At1g77520	Cyt	AAO24573	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT9)	2.1.1.104	At1g77530	Cyt	NP_177877	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT4)	2.1.1.104	At3g53140	Cyt	AAM91448	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT5)	2.1.1.104	At5g37170	Cyt	NP_198533	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT3)	2.1.1.104	At5g53810	Cyt	NP_200192	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (OMT1); biochemical assays show that gene product is multifunctional	2.1.1.104	At5g54160	Cyt	AAM10127	functional	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR1) (gene family with 12 members in Arabidopsis; only genes with >	1.2.1.44	At1g15950	Cyt	AAG48822	biochemical	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR4)	1.2.1.44	At1g68540	Cyt	NP_177021	by homology	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR9/10)	1.2.1.44	At1g76470	Cyt	NP_177773	by homology	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR2)	1.2.1.44	At1g80820	Cyt	AAO64761	biochemical	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR3)	1.2.1.44	At2g02400	Cyt	AAP04064	by homology	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR8)	1.2.1.44	At2g33590	Cyt	AAN15374	by homology	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR11)	1.2.1.44	At2g33600	Cyt	AAP42731	by homology	http://www.ncbi.nlm.nih.g
cinnamoyl-CoA reductase (CCR12)	1.2.1.44	At5g58490	Cyt	AAO22571	by homology	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD1; very low activity) (numbe	1.1.1.195	At1g72680	Cyt	AAP40269	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD2; active!)	1.1.1.195	At2g21730	Cyt	AAP59430	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD3; active!)	1.1.1.195	At2g21890	Cyt	AAP59431	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD4; active!)	1.1.1.195	At3g19450	Cyt	P48523	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD9; very low activity)	1.1.1.195	At4g39330	Cyt	CAB80596	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD5; active!)	1.1.1.195	At4g34230	Cyt	O49482	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD6; very low activity)	1.1.1.195	At4g37970	Cyt	AAP59428	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD7; active!)	1.1.1.195	At4g37980	Cyt	AAP59432	functional	http://www.ncbi.nlm.nih.g
cinnamyl alcohol dehydrogenase (gene family with 9 members) (AtCAD8; active!)	1.1.1.195	At4g37990	Cyt	AAP59433	functional	http://www.ncbi.nlm.nih.g
Glucosyltransferases for benzoic acids						
carboxy-glucosyltransferase						
84A1	BACGT	At4g15480	Cyt	AAN72025	functional	http://www.ncbi.nlm.nih.g
75B2	BACGT	At1g05530	Cyt	NP_172044	functional	http://www.ncbi.nlm.nih.g
75B1 (high specific activity)	BACGT	At1g05560	Cyt	AAL77752	functional	http://www.ncbi.nlm.nih.g
3-O-glucosyltransferase			Cyt			
71C1	BA3OGT	At2g29750	Cyt	AAC35226	functional	http://www.ncbi.nlm.nih.g
71C4	BA3OGT	?	Cyt	NA	NA	NA
72B1	BA3OGT	At4g01070	Cyt	Q9M156	functional	http://www.ncbi.nlm.nih.g
89A2	BA3OGT	At5g03490	Cyt	NP_195969	functional	http://www.ncbi.nlm.nih.g
4-O-glucosyltransferase			Cyt			
78D2	BA4OGT	?	Cyt	NA	NA	NA
71B1	BA4OGT	At3g21750	Cyt	AAK32764	functional	http://www.ncbi.nlm.nih.g
73B3	BA4OGT	At4g34131	Cyt	NP_567953	functional	http://www.ncbi.nlm.nih.g
73B4	BA4OGT	At2g15480	Cyt	AAM91525	functional	http://www.ncbi.nlm.nih.g
89B1	BA4OGT	At1g73880	Cyt	AAP31940	functional	http://www.ncbi.nlm.nih.g
Glucosyltransferases for cinnamic acids						
carboxy-glucosyltransferase						
84A1	CACGT	At4g15480	Cyt	AAN72025	functional	http://www.ncbi.nlm.nih.g
84A2	CACGT	At3g21560	Cyt	AAN13000	functional	http://www.ncbi.nlm.nih.g
84A3	CACGT	At4g15490	Cyt	AAN13214	functional	http://www.ncbi.nlm.nih.g
4-O-glucosyltransferase						
72E2	CA4OGT	At5g66690	Cyt	NP_201470	functional	http://www.ncbi.nlm.nih.g
72E3	CA4OGT	At5g26310	Cyt	NP_198003	functional	http://www.ncbi.nlm.nih.g
FLAVONOIDS AND ANTHOCYANINS						
chalcone synthase	2.3.1.74	At1g02050	Cyt	NP_171707	by homology	http://www.ncbi.nlm.nih.g
chalcone synthase	2.3.1.74	At4g00040	Cyt	AAP37822	by homology	http://www.ncbi.nlm.nih.g
chalcone synthase	2.3.1.74	At4g34850	Cyt	NP_567971	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

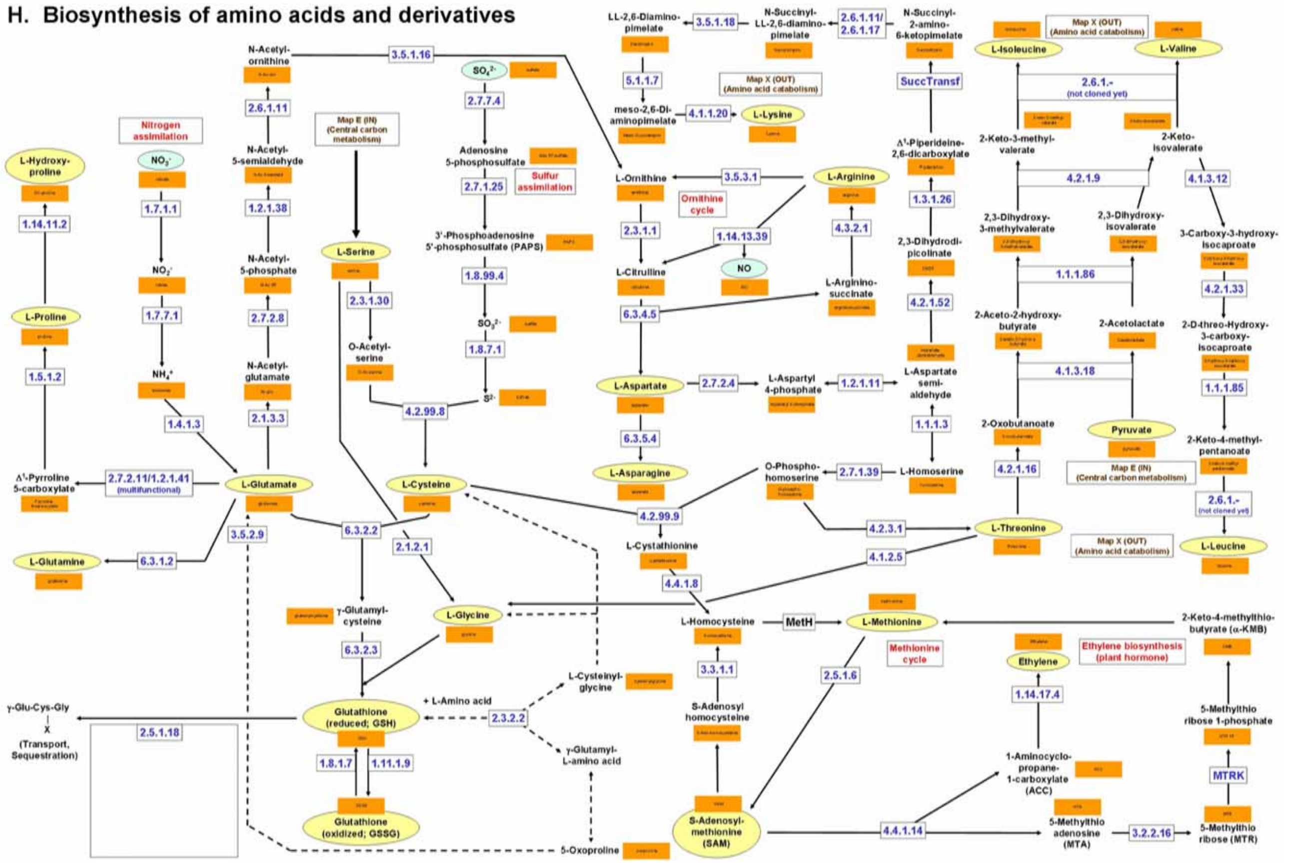


Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
G: Phenylpropanoid Metabolism (Continued)						
chalcone synthase	2.3.1.74	At5g13930	Cyt	P13114	functional	http://www.ncbi.nlm.nih.g
chalcone isomerase	5.5.1.6	At1g53520	Cyt	NP_175757	by homology	http://www.ncbi.nlm.nih.g
chalcone isomerase	5.5.1.6	At3g55120	Cyt	P41088	functional	http://www.ncbi.nlm.nih.g
chalcone isomerase	5.5.1.6	At5g05270	Cyt	AAM20088	by homology	http://www.ncbi.nlm.nih.g
chalcone isomerase	5.5.1.6	At5g66220	Cyt	NP_201423	by homology	http://www.ncbi.nlm.nih.g
flavanone 3beta-hydroxylase	1.14.11.9	At3g51240	Cyt/ER	Q9S818	functional	http://www.ncbi.nlm.nih.g
flavanone 3beta-hydroxylase	1.14.11.9	At4g10490	Cyt/ER	AAO50563	by homology	http://www.ncbi.nlm.nih.g
flavanone 3beta-hydroxylase	1.14.11.9	At5g24530	Cyt/ER	AAM10017	by homology	http://www.ncbi.nlm.nih.g
flavonol synthase FLS 1	FLS	At5g08640	Cyt	Q96330	functional	http://www.ncbi.nlm.nih.g
flavonol synthase	FLS	At5g63580	Cyt	AAO22711	by homology	http://www.ncbi.nlm.nih.g
flavonol synthase	FLS	At5g63590	Cyt	AAO24566	by homology	http://www.ncbi.nlm.nih.g
flavonol synthase	FLS	At5g63600	Cyt	AAM45083	by homology	http://www.ncbi.nlm.nih.g
flavonol 3-O-glucosyltransferase	2.4.1.91	At1g30530	Cyt	AAL07161	by homology	http://www.ncbi.nlm.nih.g
flavonol 3-O-glucosyltransferase	2.4.1.91	At5g17030	Cyt	NP_197205	by homology	http://www.ncbi.nlm.nih.g
flavonol 3-O-glucosyltransferase	2.4.1.91	At5g17040	Cyt	NP_197206	by homology	http://www.ncbi.nlm.nih.g
flavonol 3-O-glucosyltransferase	2.4.1.91	At5g17050	Cyt	AAM91139	by homology	http://www.ncbi.nlm.nih.g
dihydroflavonol 4-reductase (leucoanthocyanidin reductase; BANYULS)	1.1.1.219	At1g61720	Cyt	Q9SEV0	functional	http://www.ncbi.nlm.nih.g
dihydroflavonol 4-reductase (leucoanthocyanidin reductase)	1.1.1.219	At2g45400	Cyt	AAB82624	by homology	http://www.ncbi.nlm.nih.g
dihydroflavonol 4-reductase (leucoanthocyanidin reductase)	1.1.1.219	At5g42800	Cyt	P51102	functional	http://www.ncbi.nlm.nih.g
anthocyanidin synthase	ANS	At2g38240	Cyt	AAM13301	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin synthase	ANS	At3g11180	Cyt	NP_187728	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin synthase	ANS	At3g55970	Cyt	NP_191156	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin synthase	ANS	At5g05600	Cyt	AAM91495	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucosyltransferase	An3GT	not cloned yet			NA	NA
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At1g50580	Cyt	NP_175473	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At1g64910	Cyt	NP_176671	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At1g64920	Cyt	NP_176672	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At2g22930	Cyt	AAO64763	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At3g29630	Cyt	NP_189604	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At4g09500	Cyt	AAO42032	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At4g27560	Cyt	AAN13158	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At4g27570	Cyt	AAO63434	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At5g53990	Cyt	AAM20183	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At5g54010	Cyt	NP_200212	by homology	http://www.ncbi.nlm.nih.g
anthocyanidin 3-O-glucoside rhamnosyltransferase (large gene family; Arabidopsis ortholog not yet	A3OGRT	At5g54060	Cyt	NP_200217	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At1g03940	Cyt	NP_171890	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At3g29590	Cyt	NP_189600	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At3g29635	Cyt	NP_189605	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At3g29670	Cyt	AAP04017	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At3g29680	Cyt	NP_189610	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At5g39050	Cyt	AAN72280	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At5g39080	Cyt	AAP49522	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At5g39090	Cyt	AAP49516	by homology	http://www.ncbi.nlm.nih.g
anthocyanin 5-aromatic acyltransferase (large gene family; Arabidopsis ortholog not yet characteri:	A5AAT	At5g61160	Cyt	AAM91373	by homology	http://www.ncbi.nlm.nih.g
flavonol sulfotransferase (large gene family; Arabidopsis ortholog not yet characterized)	FST	At1g18590	Cyt	AAO63818	by homology	http://www.ncbi.nlm.nih.g
flavonol sulfotransferase (large gene family; Arabidopsis ortholog not yet characterized)	FST	At1g74090	Cyt	AAO50517	by homology	http://www.ncbi.nlm.nih.g
flavonol sulfotransferase (large gene family; Arabidopsis ortholog not yet characterized)	FST	At1g74100	Cyt	AAM10102	by homology	http://www.ncbi.nlm.nih.g
flavonol sulfotransferase (large gene family; Arabidopsis ortholog not yet characterized)	FST	At2g27570	Cyt	AAM15179	by homology	http://www.ncbi.nlm.nih.g
flavonol sulfotransferase (large gene family; Arabidopsis ortholog not yet characterized)	FST	At3g45070	Cyt	AAS49096	by homology	http://www.ncbi.nlm.nih.g
flavonol sulfotransferase (large gene family; Arabidopsis ortholog not yet characterized)	FST	At3g45080	Cyt	AAU45228	by homology	http://www.ncbi.nlm.nih.g
Genetic regulators of phenylpropanoid metabolism						
ICX1	ICX1	not cloned yet			mutant	http://www.ncbi.nlm.nih.g
production of anthocyanin pigment 1 protein (MYB75) (PAP1)	PAP1	At1g56650	Cyt & Nuc (?)	AAG42001	act. tagging	http://www.ncbi.nlm.nih.g
TRANSPARENT TESTA GLABRA 1 protein (TTG1)	TTG1	At5g24520	Cyt & Nuc (?)	Q9XGN1	mutant	http://www.ncbi.nlm.nih.g
TRANSPARENT TESTA 2 protein (AtMTYB123) (TT2)	TT2	At5g35550	Nuc (?)	Q9FJA2	T-DNA mutant	http://www.ncbi.nlm.nih.g
TRANSPARENT TESTA 8 protein (AtbHLH042) (TT8)	TT8	At4g09820	Nuc (?)	Q9FT81	T-DNA mutant	http://www.ncbi.nlm.nih.g
TRANSPARENT TESTA 16 protein (MADS)	TT16	At5g23260	Nuc (?)	Q8RYD9	T-DNA mutant	http://www.ncbi.nlm.nih.g
Sequestration of phenylpropanoids (cytosol --> vacuole)						
TRANSPARENT TESTA 12 protein (transport cytosol --> vacuole)	TT12	At3g59030	Vac/Ton (?)	Q9LYT3	T-DNA mutant	http://www.ncbi.nlm.nih.g
TRANSPARENT TESTA 19 protein (glutathione S-transferase-like)	TT19	At5g17220	Cyt/Vac (?)	NP_197224	mutant	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

4. Future directions

Transcriptome analyses, which use microarray technology to assess transcriptional activity across a large number of genes, can yield important insights into the regulation of metabolic pathways at the transcriptional level. However, in plant cells, numerous posttranscriptional modifications take place that can not be studied with microarrays. Among these, mRNA stability and translatability, posttranslational protein modifications and the impact of modulators on enzyme activities play important roles in regulating flux through



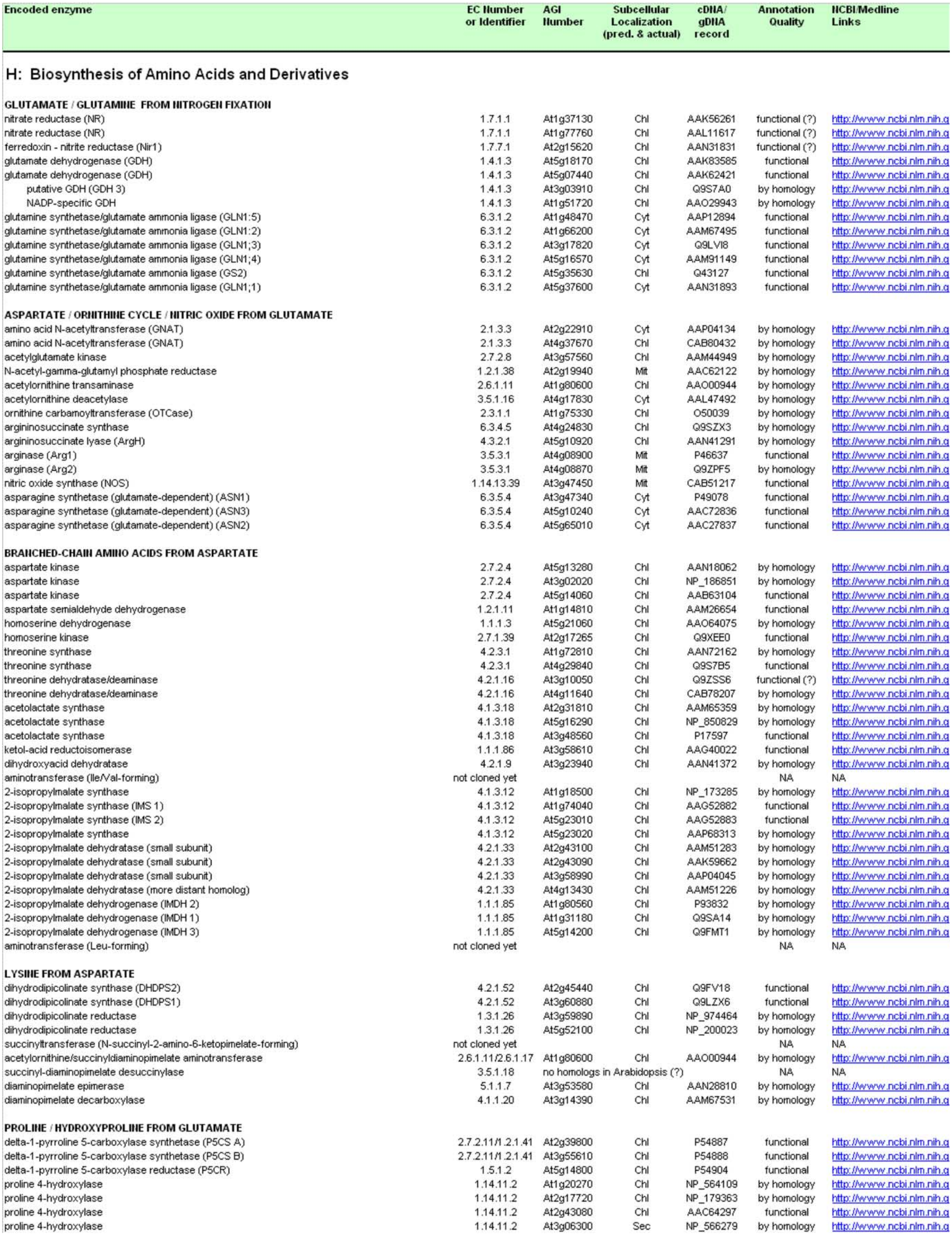
H. Biosynthesis of amino acids and derivatives

Fig. 3 (*continued*)

metabolic pathways (Burbulis and Winkel-Shirley, 1999; Chiba et al., 2003; Hendricks et al., 2003). Thus, only the integration of several genomic technologies can provide an accurate assessment of the functional relevance of experiment-induced changes in transcript patterns.

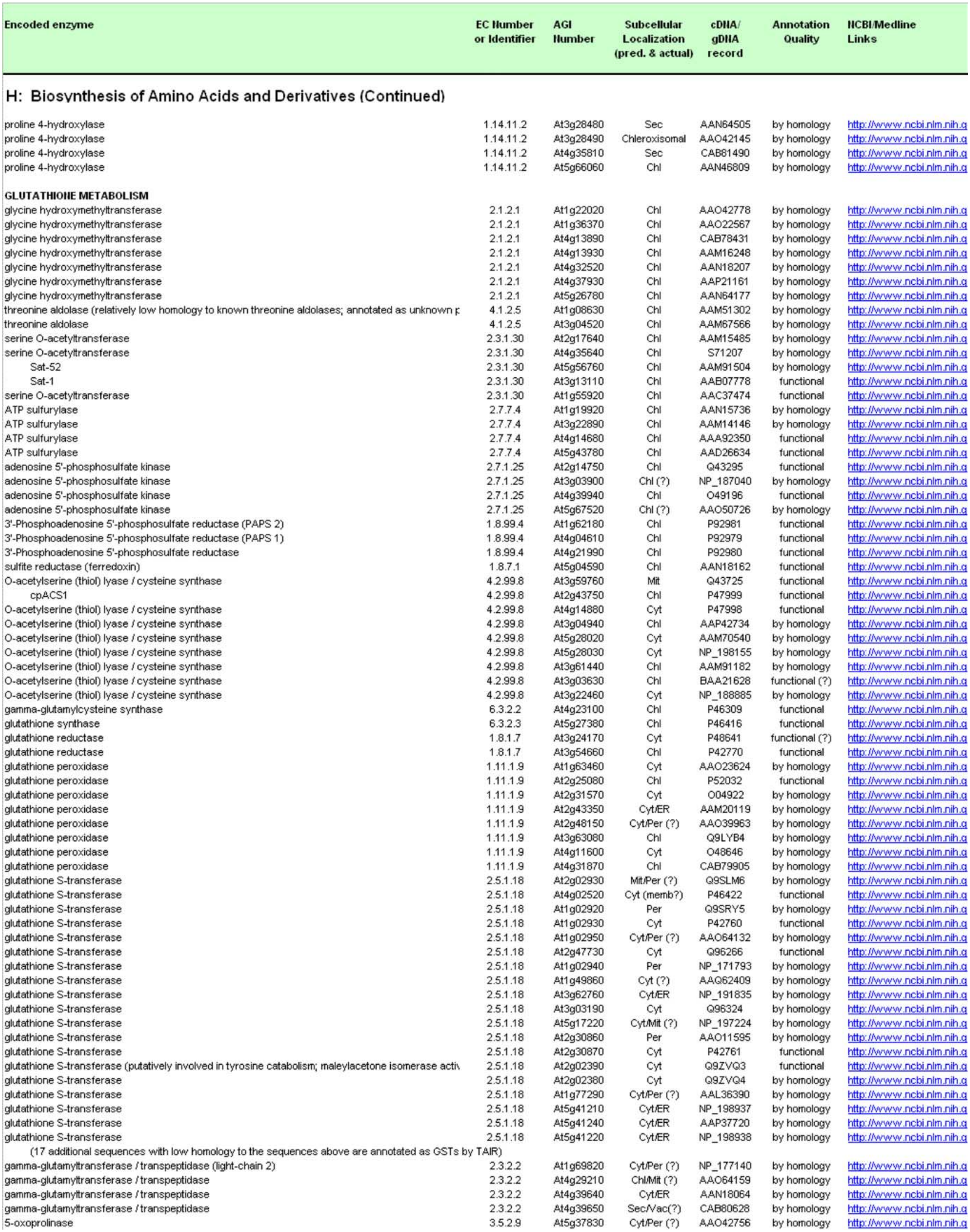
Proteomics aims at profiling the enzyme complement of cells or tissues and provides essential information beyond the transcriptional level. Proteomics with *A. thaliana* has focused mainly on efforts to catalogue the enzyme complement of different ecotypes (Chevalier et al., 2004), organs (Gallardo et al., 2002), subcellular compartments (Froehlich et al., 2003) or protein complexes (Zolla et al., 2002). These studies are consistent with the literature using other organisms in that they confirm that only the more abundant proteins are detected and information on the enzymes involved in less abundant biochemical pathways remains incomplete (Koller et al., 2002). Another caveat is that comparative proteomics, which leads to the identification of proteins that change in abundance in developmental or physiological contexts, is still in its infancy (Lonosky et al., 2004). However, continued advancements in technologies (Aebersold and Mann, 2003), sample fractionation (Wienkoop et al., 2004), algorithms for the detection of posttranslational modifications (MacCoss et al., 2002) and quantification (Tao and Aebersold, 2003; Cutler, 2003) are expected to increase the utility of proteomics as a global profiling tool dramatically.

Metabolomics sets out to determine how (all) metabolite levels respond to genetic or environmental changes and, from the data, to generate new hypotheses. However, there are three major complications: (1) there is no direct relationship between metabolites and genes in the way there is between genes and mRNAs and proteins. Metabolite levels are determined by the activities of all the enzymes of a pathway and by effectors that act on these enzymes; (2) the plant metabolome is much larger than that of yeast, where there are far fewer metabolites than genes or proteins (<600 metabolites vs. 6000 genes; Oliver



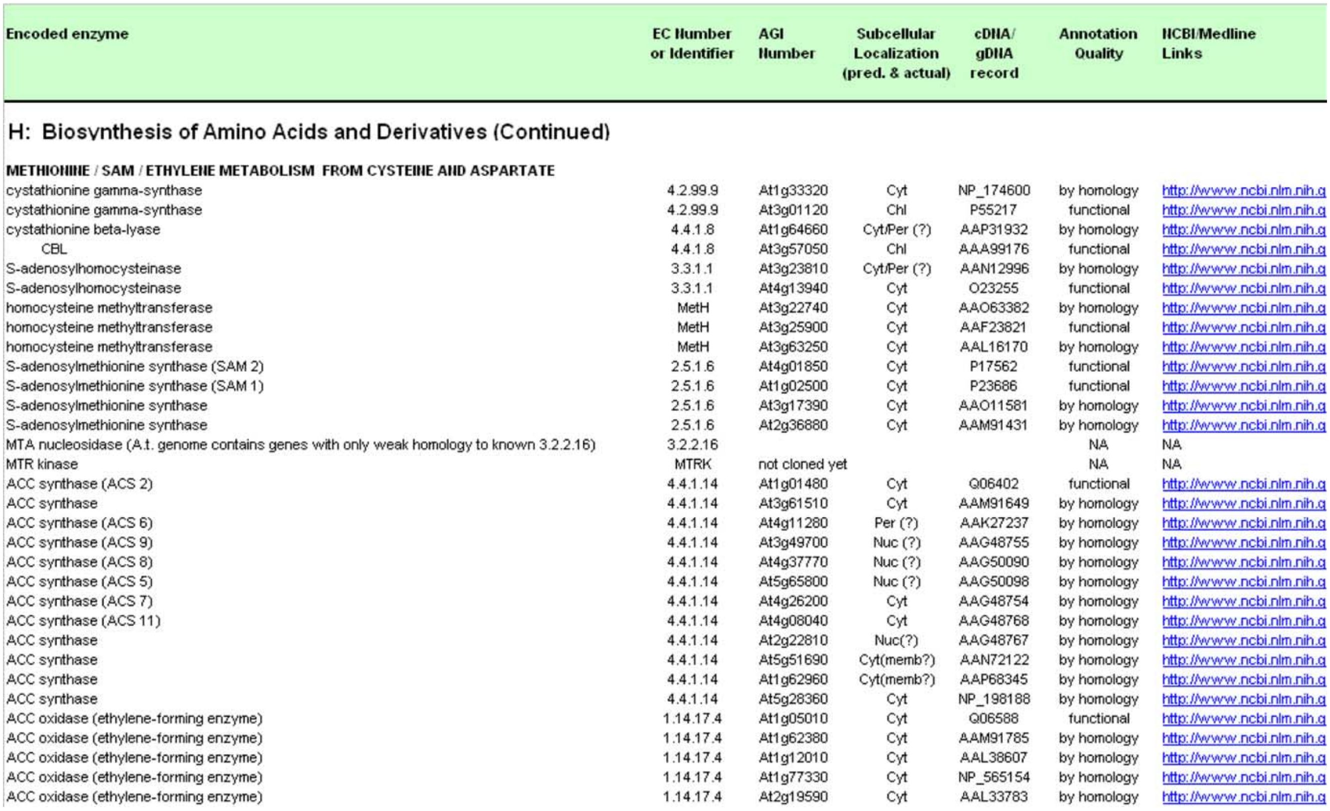
Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
H: Biosynthesis of Amino Acids and Derivatives						
GLUTAMATE / GLUTAMINE FROM NITROGEN FIXATION						
nitrate reductase (NR)	1.7.1.1	At1g37130	Chl	AAK56261	functional (?)	http://www.ncbi.nlm.nih.g
nitrate reductase (NR)	1.7.1.1	At1g77760	Chl	AAL11617	functional (?)	http://www.ncbi.nlm.nih.g
ferredoxin - nitrite reductase (Nir1)	1.7.7.1	At2g15620	Chl	AAN31831	functional (?)	http://www.ncbi.nlm.nih.g
glutamate dehydrogenase (GDH)	1.4.1.3	At5g18170	Chl	AAK83585	functional	http://www.ncbi.nlm.nih.g
glutamate dehydrogenase (GDH)	1.4.1.3	At5g07440	Chl	AAK62421	functional	http://www.ncbi.nlm.nih.g
putative GDH (GDH 3)	1.4.1.3	At3g03910	Chl	Q9S7A0	by homology	http://www.ncbi.nlm.nih.g
NADP-specific GDH	1.4.1.3	At1g51720	Chl	AAO29943	by homology	http://www.ncbi.nlm.nih.g
glutamine synthetase/glutamate ammonia ligase (GLN1:5)	6.3.1.2	At1g48470	Cyt	AAP12894	functional	http://www.ncbi.nlm.nih.g
glutamine synthetase/glutamate ammonia ligase (GLN1:2)	6.3.1.2	At1g66200	Cyt	AAM67495	functional	http://www.ncbi.nlm.nih.g
glutamine synthetase/glutamate ammonia ligase (GLN1;3)	6.3.1.2	At3g17820	Cyt	Q9LVI8	functional	http://www.ncbi.nlm.nih.g
glutamine synthetase/glutamate ammonia ligase (GLN1;4)	6.3.1.2	At5g16570	Cyt	AAM91149	functional	http://www.ncbi.nlm.nih.g
glutamine synthetase/glutamate ammonia ligase (GS2)	6.3.1.2	At5g35630	Chl	Q43127	functional	http://www.ncbi.nlm.nih.g
glutamine synthetase/glutamate ammonia ligase (GLN1;1)	6.3.1.2	At5g37600	Cyt	AAN31893	functional	http://www.ncbi.nlm.nih.g
ASPARTATE / ORNITHINE CYCLE / NITRIC OXIDE FROM GLUTAMATE						
amino acid N-acetyltransferase (GNAT)	2.1.3.3	At2g22910	Cyt	AAP04134	by homology	http://www.ncbi.nlm.nih.g
amino acid N-acetyltransferase (GNAT)	2.1.3.3	At4g37670	Chl	CAB80432	by homology	http://www.ncbi.nlm.nih.g
acetylglutamate kinase	2.7.2.8	At3g57560	Chl	AAM44949	by homology	http://www.ncbi.nlm.nih.g
N-acetyl-gamma-glutamyl phosphate reductase	1.2.1.38	At2g19940	Mit	AAC62122	by homology	http://www.ncbi.nlm.nih.g
acetylornithine transaminase	2.6.1.11	At1g80600	Chl	AAO00944	by homology	http://www.ncbi.nlm.nih.g
acetylornithine deacetylase	3.5.1.16	At4g17830	Cyt	AAL47492	by homology	http://www.ncbi.nlm.nih.g
ornithine carbamoyltransferase (OTCase)	2.3.1.1	At1g75330	Chl	O50039	by homology	http://www.ncbi.nlm.nih.g
argininosuccinate synthase	6.3.4.5	At4g24830	Chl	Q9SZX3	by homology	http://www.ncbi.nlm.nih.g
argininosuccinate lyase (ArgH)	4.3.2.1	At5g10920	Chl	AAN41291	by homology	http://www.ncbi.nlm.nih.g
arginase (Arg1)	3.5.3.1	At4g08900	Mit	P46637	functional	http://www.ncbi.nlm.nih.g
arginase (Arg2)	3.5.3.1	At4g08870	Mit	Q9ZPF5	by homology	http://www.ncbi.nlm.nih.g
nitric oxide synthase (NOS)	1.14.13.39	At3g47450	Mit	CAB51217	functional	http://www.ncbi.nlm.nih.g
asparagine synthetase (glutamate-dependent) (ASN1)	6.3.5.4	At3g47340	Cyt	P49078	functional	http://www.ncbi.nlm.nih.g
asparagine synthetase (glutamate-dependent) (ASN3)	6.3.5.4	At5g10240	Cyt	AAC72836	functional	http://www.ncbi.nlm.nih.g
asparagine synthetase (glutamate-dependent) (ASN2)	6.3.5.4	At5g65010	Cyt	AAC27837	functional	http://www.ncbi.nlm.nih.g
BRANCHED-CHAIN AMINO ACIDS FROM ASPARTATE						
aspartate kinase	2.7.2.4	At5g13280	Chl	AAN18062	by homology	http://www.ncbi.nlm.nih.g
aspartate kinase	2.7.2.4	At3g02020	Chl	NP_186851	by homology	http://www.ncbi.nlm.nih.g
aspartate kinase	2.7.2.4	At5g14060	Chl	AAB63104	functional	http://www.ncbi.nlm.nih.g
aspartate semialdehyde dehydrogenase	1.2.1.11	At1g14810	Chl	AAM26654	functional	http://www.ncbi.nlm.nih.g
homoserine dehydrogenase	1.1.1.3	At5g21060	Chl	AAO64075	by homology	http://www.ncbi.nlm.nih.g
homoserine kinase	2.7.1.39	At2g17265	Chl	Q9XEE0	functional	http://www.ncbi.nlm.nih.g
threonine synthase	4.2.3.1	At1g72810	Chl	AAN72162	by homology	http://www.ncbi.nlm.nih.g
threonine synthase	4.2.3.1	At4g29840	Chl	Q9S7B5	functional	http://www.ncbi.nlm.nih.g
threonine dehydratase/deaminase	4.2.1.16	At3g10050	Chl	Q9ZSS6	functional (?)	http://www.ncbi.nlm.nih.g
threonine dehydratase/deaminase	4.2.1.16	At4g11640	Chl	CAB78207	by homology	http://www.ncbi.nlm.nih.g
acetolactate synthase	4.1.3.18	At2g31810	Chl	AAM65359	by homology	http://www.ncbi.nlm.nih.g
acetolactate synthase	4.1.3.18	At5g16290	Chl	NP_850829	by homology	http://www.ncbi.nlm.nih.g
acetolactate synthase	4.1.3.18	At3g48560	Chl	P17597	functional	http://www.ncbi.nlm.nih.g
ketol-acid reductoisomerase	1.1.1.86	At3g58610	Chl	AAG40022	functional	http://www.ncbi.nlm.nih.g
dihydroxyacid dehydratase	4.2.1.9	At3g23940	Chl	AAN41372	by homology	http://www.ncbi.nlm.nih.g
aminotransferase (Ile/Val-forming)	not cloned yet				NA	NA
2-isopropylmalate synthase	4.1.3.12	At1g18500	Chl	NP_173285	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate synthase (IMS 1)	4.1.3.12	At1g74040	Chl	AAG52882	functional	http://www.ncbi.nlm.nih.g
2-isopropylmalate synthase (IMS 2)	4.1.3.12	At5g23010	Chl	AAG52883	functional	http://www.ncbi.nlm.nih.g
2-isopropylmalate synthase	4.1.3.12	At5g23020	Chl	AAP68313	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydratase (small subunit)	4.2.1.33	At2g43100	Chl	AAM51283	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydratase (small subunit)	4.2.1.33	At2g43090	Chl	AAK59662	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydratase (small subunit)	4.2.1.33	At3g58990	Chl	AAP04045	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydratase (more distant homolog)	4.2.1.33	At4g13430	Chl	AAM51226	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydrogenase (IMDH 2)	1.1.1.85	At1g80560	Chl	P93832	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydrogenase (IMDH 1)	1.1.1.85	At1g31180	Chl	Q9SA14	by homology	http://www.ncbi.nlm.nih.g
2-isopropylmalate dehydrogenase (IMDH 3)	1.1.1.85	At5g14200	Chl	Q9FMT1	by homology	http://www.ncbi.nlm.nih.g
aminotransferase (Leu-forming)	not cloned yet				NA	NA
LYSINE FROM ASPARTATE						
dihydrodipicolinate synthase (DHDPS2)	4.2.1.52	At2g45440	Chl	Q9FV18	functional	http://www.ncbi.nlm.nih.g
dihydrodipicolinate synthase (DHDPS1)	4.2.1.52	At3g60880	Chl	Q9LZX6	functional	http://www.ncbi.nlm.nih.g
dihydrodipicolinate reductase	1.3.1.26	At3g59890	Chl	NP_974464	by homology	http://www.ncbi.nlm.nih.g
dihydrodipicolinate reductase	1.3.1.26	At5g52100	Chl	NP_200023	by homology	http://www.ncbi.nlm.nih.g
succinyltransferase (N-succinyl-2-amino-6-ketopimelate-forming)	not cloned yet				NA	NA
acetylornithine/succinyldiaminopimelate aminotransferase	2.6.1.11/2.6.1.17	At1g80600	Chl	AAO00944	by homology	http://www.ncbi.nlm.nih.g
succinyl-diaminopimelate desuccinylase	3.5.1.18	no homologs in Arabidopsis (?)			NA	NA
diaminopimelate epimerase	5.1.1.7	At3g53580	Chl	AAN28810	by homology	http://www.ncbi.nlm.nih.g
diaminopimelate decarboxylase	4.1.1.20	At3g14390	Chl	AAM67531	by homology	http://www.ncbi.nlm.nih.g
PROLINE / HYDROXYPROLINE FROM GLUTAMATE						
delta-1-pyrroline 5-carboxylase synthetase (P5CS A)	2.7.2.11/1.2.1.41	At2g39800	Chl	P54887	functional	http://www.ncbi.nlm.nih.g
delta-1-pyrroline 5-carboxylase synthetase (P5CS B)	2.7.2.11/1.2.1.41	At3g55610	Chl	P54888	functional	http://www.ncbi.nlm.nih.g
delta-1-pyrroline 5-carboxylase reductase (P5CR)	1.5.1.2	At5g14800	Chl	P54904	functional	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At1g20270	Chl	NP_564109	by homology	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At2g17720	Chl	NP_179363	by homology	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At2g43080	Chl	AAC64297	functional	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At3g06300	Sec	NP_566279	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
H: Biosynthesis of Amino Acids and Derivatives (Continued)						
proline 4-hydroxylase	1.14.11.2	At3g28480	Sec	AAN64505	by homology	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At3g28490	Chleroxisomal	AAO42145	by homology	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At4g35810	Sec	CAB81490	by homology	http://www.ncbi.nlm.nih.g
proline 4-hydroxylase	1.14.11.2	At5g66060	Chl	AAN46809	by homology	http://www.ncbi.nlm.nih.g
GLUTATHIONE METABOLISM						
glycine hydroxymethyltransferase	2.1.2.1	At1g22020	Chl	AAO42778	by homology	http://www.ncbi.nlm.nih.g
glycine hydroxymethyltransferase	2.1.2.1	At1g36370	Chl	AAO22567	by homology	http://www.ncbi.nlm.nih.g
glycine hydroxymethyltransferase	2.1.2.1	At4g13890	Chl	CAB78431	by homology	http://www.ncbi.nlm.nih.g
glycine hydroxymethyltransferase	2.1.2.1	At4g13930	Chl	AAM16248	by homology	http://www.ncbi.nlm.nih.g
glycine hydroxymethyltransferase	2.1.2.1	At4g32520	Chl	AAN18207	by homology	http://www.ncbi.nlm.nih.g
glycine hydroxymethyltransferase	2.1.2.1	At4g37930	Chl	AAP21161	by homology	http://www.ncbi.nlm.nih.g
glycine hydroxymethyltransferase	2.1.2.1	At5g26780	Chl	AAN64177	by homology	http://www.ncbi.nlm.nih.g
threonine aldolase (relatively low homology to known threonine aldolases; annotated as unknown p	4.1.2.5	At1g08630	Chl	AAM51302	by homology	http://www.ncbi.nlm.nih.g
threonine aldolase	4.1.2.5	At3g04520	Chl	AAM67566	by homology	http://www.ncbi.nlm.nih.g
serine O-acetyltransferase	2.3.1.30	At2g17640	Chl	AAM15485	by homology	http://www.ncbi.nlm.nih.g
serine O-acetyltransferase	2.3.1.30	At4g35640	Chl	S71207	by homology	http://www.ncbi.nlm.nih.g
Sat-52	2.3.1.30	At5g56760	Chl	AAM91504	by homology	http://www.ncbi.nlm.nih.g
Sat-1	2.3.1.30	At3g13110	Chl	AAB07778	functional	http://www.ncbi.nlm.nih.g
serine O-acetyltransferase	2.3.1.30	At1g55920	Chl	AAC37474	functional	http://www.ncbi.nlm.nih.g
ATP sulfurylase	2.7.7.4	At1g19920	Chl	AAN15736	by homology	http://www.ncbi.nlm.nih.g
ATP sulfurylase	2.7.7.4	At3g22890	Chl	AAM14146	by homology	http://www.ncbi.nlm.nih.g
ATP sulfurylase	2.7.7.4	At4g14680	Chl	AAA92350	functional	http://www.ncbi.nlm.nih.g
ATP sulfurylase	2.7.7.4	At5g43780	Chl	AAD26634	functional	http://www.ncbi.nlm.nih.g
adenosine 5'-phosphosulfate kinase	2.7.1.25	At2g14750	Chl	Q43295	functional	http://www.ncbi.nlm.nih.g
adenosine 5'-phosphosulfate kinase	2.7.1.25	At3g03900	Chl (?)	NP_187040	by homology	http://www.ncbi.nlm.nih.g
adenosine 5'-phosphosulfate kinase	2.7.1.25	At4g39940	Chl	O49196	functional	http://www.ncbi.nlm.nih.g
adenosine 5'-phosphosulfate kinase	2.7.1.25	At5g67520	Chl (?)	AAO50726	by homology	http://www.ncbi.nlm.nih.g
3'-Phosphoadenosine 5'-phosphosulfate reductase (PAPS 2)	1.8.99.4	At1g62180	Chl	P92981	functional	http://www.ncbi.nlm.nih.g
3'-Phosphoadenosine 5'-phosphosulfate reductase (PAPS 1)	1.8.99.4	At4g04610	Chl	P92979	functional	http://www.ncbi.nlm.nih.g
3'-Phosphoadenosine 5'-phosphosulfate reductase	1.8.99.4	At4g21990	Chl	P92980	functional	http://www.ncbi.nlm.nih.g
sulfite reductase (ferredoxin)	1.8.7.1	At5g04590	Chl	AAN18162	functional	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At3g59760	Mit	Q43725	functional	http://www.ncbi.nlm.nih.g
cpACS1	4.2.99.8	At2g43750	Chl	P47999	functional	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At4g14880	Cyt	P47998	functional	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At3g04940	Chl	AAP42734	by homology	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At5g28020	Cyt	AAM70540	by homology	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At5g28030	Cyt	NP_198155	by homology	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At3g61440	Chl	AAM91182	by homology	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At3g03630	Chl	BAA21628	functional (?)	http://www.ncbi.nlm.nih.g
O-acetylserine (thiol) lyase / cysteine synthase	4.2.99.8	At3g22460	Cyt	NP_188885	by homology	http://www.ncbi.nlm.nih.g
gamma-glutamylcysteine synthase	6.3.2.2	At4g23100	Chl	P46309	functional	http://www.ncbi.nlm.nih.g
glutathione synthase	6.3.2.3	At5g27380	Chl	P46416	functional	http://www.ncbi.nlm.nih.g
glutathione reductase	1.8.1.7	At3g24170	Cyt	P48641	functional (?)	http://www.ncbi.nlm.nih.g
glutathione reductase	1.8.1.7	At3g54660	Chl	P42770	functional	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At1g63460	Cyt	AAO23624	by homology	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At2g25080	Chl	P52032	functional	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At2g31570	Cyt	O04922	by homology	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At2g43350	Cyt/ER	AAM20119	by homology	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At2g48150	Cyt/Per (?)	AAO39963	by homology	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At3g63080	Chl	Q9LYB4	by homology	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At4g11600	Cyt	O48646	by homology	http://www.ncbi.nlm.nih.g
glutathione peroxidase	1.11.1.9	At4g31870	Chl	CAB79905	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At2g02930	Mit/Per (?)	Q9SLM6	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At4g02520	Cyt (memb?)	P46422	functional	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At1g02920	Per	Q9SRY5	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At1g02930	Cyt	P42760	functional	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At1g02950	Cyt/Per (?)	AAO64132	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At2g47730	Cyt	Q96266	functional	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At1g02940	Per	NP_171793	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At1g49860	Cyt (?)	AAQ62409	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At3g62760	Cyt/ER	NP_191835	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At3g03190	Cyt	Q96324	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At5g17220	Cyt/Mit (?)	NP_197224	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At2g30860	Per	AAO11595	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At2g30870	Cyt	P42761	functional	http://www.ncbi.nlm.nih.g
glutathione S-transferase (putatively involved in tyrosine catabolism; maleylacetone isomerase activ	2.5.1.18	At2g02390	Cyt	Q9ZVQ3	functional	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At2g02380	Cyt	Q9ZVQ4	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At1g77290	Cyt/Per (?)	AAL36390	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At5g41210	Cyt/ER	NP_198937	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At5g41240	Cyt/ER	AAP37720	by homology	http://www.ncbi.nlm.nih.g
glutathione S-transferase	2.5.1.18	At5g41220	Cyt/ER	NP_198938	by homology	http://www.ncbi.nlm.nih.g
(17 additional sequences with low homology to the sequences above are annotated as GSTs by TAIR)						
gamma-glutamyltransferase / transpeptidase (light-chain 2)	2.3.2.2	At1g69820	Cyt/Per (?)	NP_177140	by homology	http://www.ncbi.nlm.nih.g
gamma-glutamyltransferase / transpeptidase	2.3.2.2	At4g29210	Chl/Mit (?)	AAO64159	by homology	http://www.ncbi.nlm.nih.g
gamma-glutamyltransferase / transpeptidase	2.3.2.2	At4g39640	Cyt/ER	AAN18064	by homology	http://www.ncbi.nlm.nih.g
gamma-glutamyltransferase / transpeptidase	2.3.2.2	At4g39650	Sec/Vac(?)	CAB80628	by homology	http://www.ncbi.nlm.nih.g
5-oxoprolinase	3.5.2.9	At5g37830	Cyt/Per (?)	AAO42756	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
H: Biosynthesis of Amino Acids and Derivatives (Continued)						
METHIONINE / SAM / ETHYLENE METABOLISM FROM CYSTEINE AND ASPARTATE						
cystathionine gamma-synthase	4.2.99.9	At1g33320	Cyt	NP_174600	by homology	http://www.ncbi.nlm.nih.g
cystathionine gamma-synthase	4.2.99.9	At3g01120	Chl	P55217	functional	http://www.ncbi.nlm.nih.g
cystathionine beta-lyase	4.4.1.8	At1g64660	Cyt/Per (?)	AAP31932	by homology	http://www.ncbi.nlm.nih.g
CBL	4.4.1.8	At3g57050	Chl	AAA99176	functional	http://www.ncbi.nlm.nih.g
S-adenosylhomocysteinase	3.3.1.1	At3g23810	Cyt/Per (?)	AAN12996	by homology	http://www.ncbi.nlm.nih.g
S-adenosylhomocysteinase	3.3.1.1	At4g13940	Cyt	O23255	functional	http://www.ncbi.nlm.nih.g
homocysteine methyltransferase	MetH	At3g22740	Cyt	AAO63382	by homology	http://www.ncbi.nlm.nih.g
homocysteine methyltransferase	MetH	At3g25900	Cyt	AAF23821	functional	http://www.ncbi.nlm.nih.g
homocysteine methyltransferase	MetH	At3g63250	Cyt	AAL16170	by homology	http://www.ncbi.nlm.nih.g
S-adenosylmethionine synthase (SAM 2)	2.5.1.6	At4g01850	Cyt	P17562	functional	http://www.ncbi.nlm.nih.g
S-adenosylmethionine synthase (SAM 1)	2.5.1.6	At1g02500	Cyt	P23686	functional	http://www.ncbi.nlm.nih.g
S-adenosylmethionine synthase	2.5.1.6	At3g17390	Cyt	AAO11581	by homology	http://www.ncbi.nlm.nih.g
S-adenosylmethionine synthase	2.5.1.6	At2g36880	Cyt	AAM91431	by homology	http://www.ncbi.nlm.nih.g
MTA nucleosidase (A.t. genome contains genes with only weak homology to known 3.2.2.16)	3.2.2.16				NA	NA
MTR kinase	MTRK	not cloned yet			NA	NA
ACC synthase (ACS 2)	4.4.1.14	At1g01480	Cyt	Q06402	functional	http://www.ncbi.nlm.nih.g
ACC synthase	4.4.1.14	At3g61510	Cyt	AAM91649	by homology	http://www.ncbi.nlm.nih.g
ACC synthase (ACS 6)	4.4.1.14	At4g11280	Per (?)	AAK27237	by homology	http://www.ncbi.nlm.nih.g
ACC synthase (ACS 9)	4.4.1.14	At3g49700	Nuc (?)	AAG48755	by homology	http://www.ncbi.nlm.nih.g
ACC synthase (ACS 8)	4.4.1.14	At4g37770	Nuc (?)	AAG50090	by homology	http://www.ncbi.nlm.nih.g
ACC synthase (ACS 5)	4.4.1.14	At5g65800	Nuc (?)	AAG50098	by homology	http://www.ncbi.nlm.nih.g
ACC synthase (ACS 7)	4.4.1.14	At4g26200	Cyt	AAG48754	by homology	http://www.ncbi.nlm.nih.g
ACC synthase (ACS 11)	4.4.1.14	At4g08040	Cyt	AAG48768	by homology	http://www.ncbi.nlm.nih.g
ACC synthase	4.4.1.14	At2g22810	Nuc(?)	AAG48767	by homology	http://www.ncbi.nlm.nih.g
ACC synthase	4.4.1.14	At5g51690	Cyt(memb?)	AAN72122	by homology	http://www.ncbi.nlm.nih.g
ACC synthase	4.4.1.14	At1g62960	Cyt(memb?)	AAP68345	by homology	http://www.ncbi.nlm.nih.g
ACC synthase	4.4.1.14	At5g28360	Cyt	NP_198188	by homology	http://www.ncbi.nlm.nih.g
ACC oxidase (ethylene-forming enzyme)	1.14.17.4	At1g05010	Cyt	Q06588	functional	http://www.ncbi.nlm.nih.g
ACC oxidase (ethylene-forming enzyme)	1.14.17.4	At1g62380	Cyt	AAM91785	by homology	http://www.ncbi.nlm.nih.g
ACC oxidase (ethylene-forming enzyme)	1.14.17.4	At1g12010	Cyt	AAL38607	by homology	http://www.ncbi.nlm.nih.g
ACC oxidase (ethylene-forming enzyme)	1.14.17.4	At1g77330	Cyt	NP_565154	by homology	http://www.ncbi.nlm.nih.g
ACC oxidase (ethylene-forming enzyme)	1.14.17.4	At2g19590	Cyt	AAL33783	by homology	http://www.ncbi.nlm.nih.g

I. Isoprenoid Biosynthesis in the Cytosol and in Mitochondria

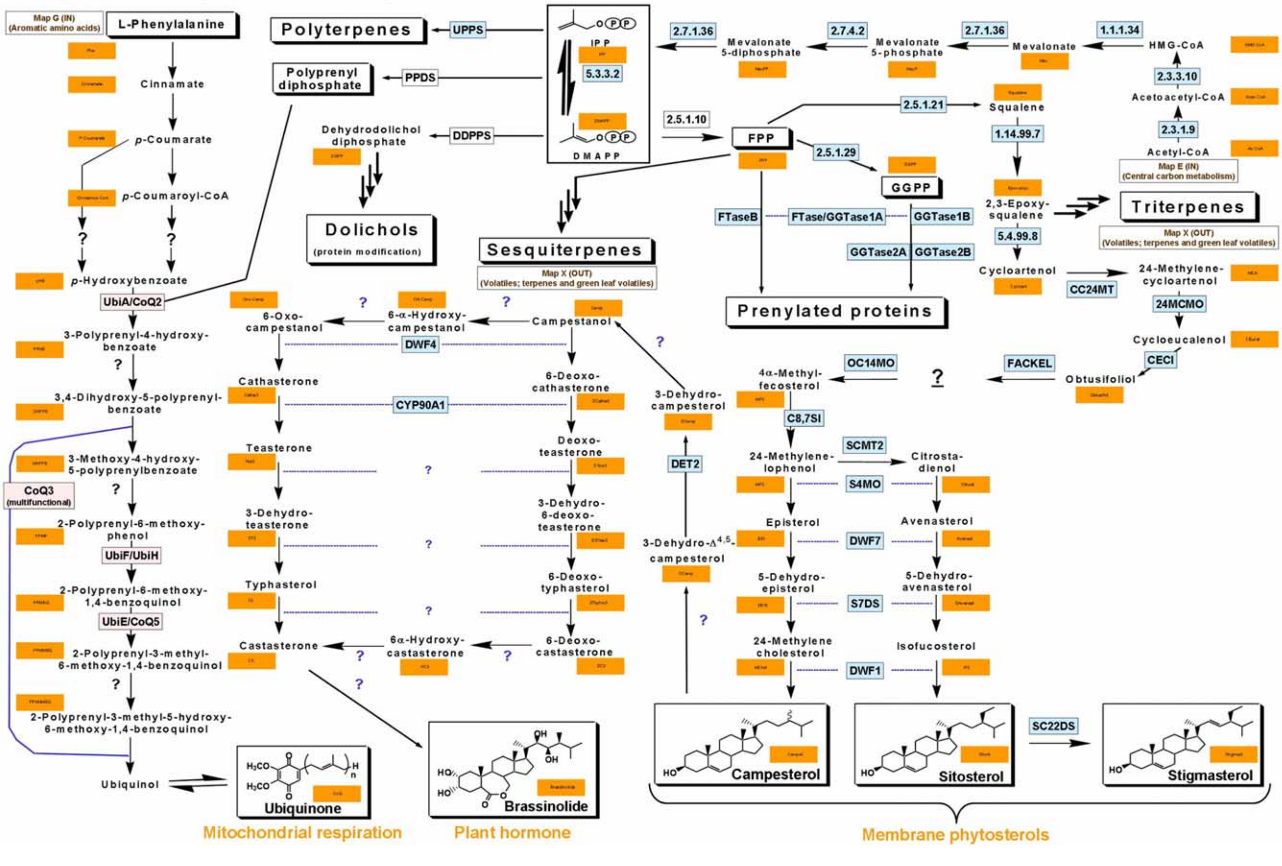
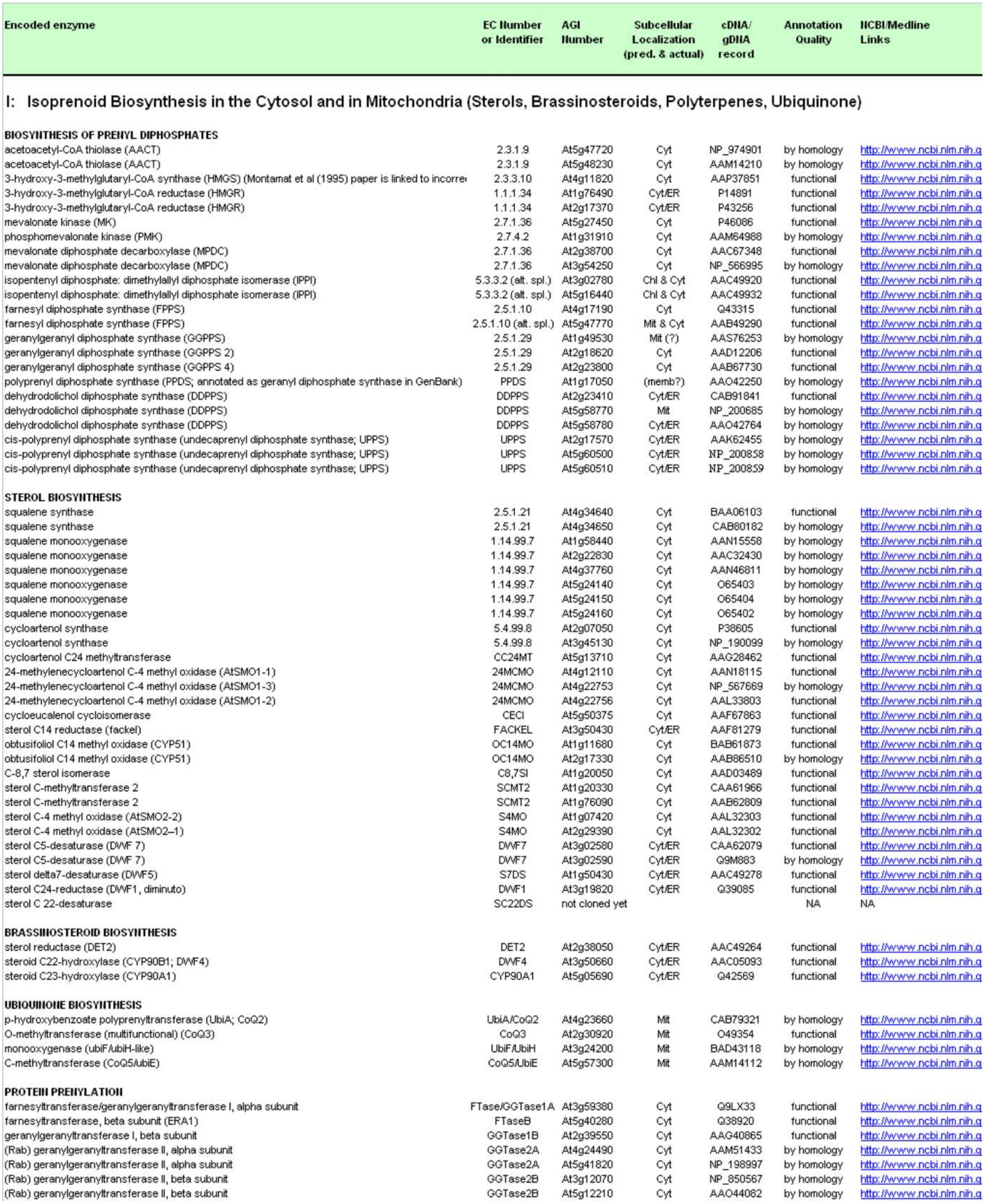


Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
I: Isoprenoid Biosynthesis in the Cytosol and in Mitochondria (Sterols, Brassinosteroids, Polyterpenes, Ubiquinone)						
BIOSYNTHESIS OF PRENYL DIPHOSPHATES						
acetoacetyl-CoA thiolase (AACT)	2.3.1.9	At5g47720	Cyt	NP_974901	by homology	http://www.ncbi.nlm.nih.g
acetoacetyl-CoA thiolase (AACT)	2.3.1.9	At5g48230	Cyt	AAM14210	by homology	http://www.ncbi.nlm.nih.g
3-hydroxy-3-methylglutaryl-CoA synthase (HMGS) (Montamat et al (1995) paper is linked to incorre	2.3.3.10	At4g11820	Cyt	AAP37851	functional	http://www.ncbi.nlm.nih.g
3-hydroxy-3-methylglutaryl-CoA reductase (HMGR)	1.1.1.34	At1g76490	Cyt/ER	P14891	functional	http://www.ncbi.nlm.nih.g
3-hydroxy-3-methylglutaryl-CoA reductase (HMGR)	1.1.1.34	At2g17370	Cyt/ER	P43256	functional	http://www.ncbi.nlm.nih.g
mevalonate kinase (MK)	2.7.1.36	At5g27450	Cyt	P46086	functional	http://www.ncbi.nlm.nih.g
phosphomevalonate kinase (PMK)	2.7.4.2	At1g31910	Cyt	AAM64988	by homology	http://www.ncbi.nlm.nih.g
mevalonate diphosphate decarboxylase (MPDC)	2.7.1.36	At2g38700	Cyt	AAC67348	functional	http://www.ncbi.nlm.nih.g
mevalonate diphosphate decarboxylase (MPDC)	2.7.1.36	At3g54250	Cyt	NP_566995	by homology	http://www.ncbi.nlm.nih.g
isopentenyl diphosphate: dimethylallyl diphosphate isomerase (IPPI)	5.3.3.2 (alt. spl.)	At3g02780	Chl & Cyt	AAC49920	functional	http://www.ncbi.nlm.nih.g
isopentenyl diphosphate: dimethylallyl diphosphate isomerase (IPPI)	5.3.3.2 (alt. spl.)	At5g16440	Chl & Cyt	AAC49932	functional	http://www.ncbi.nlm.nih.g
farnesyl diphosphate synthase (FPPS)	2.5.1.10	At4g17190	Cyt	Q43315	functional	http://www.ncbi.nlm.nih.g
farnesyl diphosphate synthase (FPPS)	2.5.1.10 (alt. spl.)	At5g47770	Mit & Cyt	AAB49290	functional	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS)	2.5.1.29	At1g49530	Mit (?)	AAS76253	by homology	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS 2)	2.5.1.29	At2g18620	Cyt	AAD12206	functional	http://www.ncbi.nlm.nih.g
geranylgeranyl diphosphate synthase (GGPPS 4)	2.5.1.29	At2g23800	Cyt	AAB67730	functional	http://www.ncbi.nlm.nih.g
polyprenyl diphosphate synthase (PPDS; annotated as geranyl diphosphate synthase in GenBank)	PPDS	At1g17050	(memb?)	AAO42250	by homology	http://www.ncbi.nlm.nih.g
dehydrodolichol diphosphate synthase (DDPPS)	DDPPS	At2g23410	Cyt/ER	CAB91841	functional	http://www.ncbi.nlm.nih.g
dehydrodolichol diphosphate synthase (DDPPS)	DDPPS	At5g58770	Mit	NP_200685	by homology	http://www.ncbi.nlm.nih.g
dehydrodolichol diphosphate synthase (DDPPS)	DDPPS	At5g58780	Cyt/ER	AAO42764	by homology	http://www.ncbi.nlm.nih.g
cis-polyprenyl diphosphate synthase (undecaprenyl diphosphate synthase; UPPS)	UPPS	At2g17570	Cyt/ER	AAK62455	by homology	http://www.ncbi.nlm.nih.g
cis-polyprenyl diphosphate synthase (undecaprenyl diphosphate synthase; UPPS)	UPPS	At5g60500	Cyt/ER	NP_200858	by homology	http://www.ncbi.nlm.nih.g
cis-polyprenyl diphosphate synthase (undecaprenyl diphosphate synthase; UPPS)	UPPS	At5g60510	Cyt/ER	NP_200859	by homology	http://www.ncbi.nlm.nih.g
STEROL BIOSYNTHESIS						
squalene synthase	2.5.1.21	At4g34640	Cyt	BAA06103	functional	http://www.ncbi.nlm.nih.g
squalene synthase	2.5.1.21	At4g34650	Cyt	CAB80182	by homology	http://www.ncbi.nlm.nih.g
squalene monooxygenase	1.14.99.7	At1g58440	Cyt	AAN15558	by homology	http://www.ncbi.nlm.nih.g
squalene monooxygenase	1.14.99.7	At2g22830	Cyt	AAC32430	by homology	http://www.ncbi.nlm.nih.g
squalene monooxygenase	1.14.99.7	At4g37760	Cyt	AAN46811	by homology	http://www.ncbi.nlm.nih.g
squalene monooxygenase	1.14.99.7	At5g24140	Cyt	O65403	by homology	http://www.ncbi.nlm.nih.g
squalene monooxygenase	1.14.99.7	At5g24150	Cyt	O65404	by homology	http://www.ncbi.nlm.nih.g
squalene monooxygenase	1.14.99.7	At5g24160	Cyt	O65402	by homology	http://www.ncbi.nlm.nih.g
cycloartenol synthase	5.4.99.8	At2g07050	Cyt	P38605	functional	http://www.ncbi.nlm.nih.g
cycloartenol synthase	5.4.99.8	At3g45130	Cyt	NP_190099	by homology	http://www.ncbi.nlm.nih.g
cycloartenol C24 methyltransferase	CC24MT	At5g13710	Cyt	AAG28462	functional	http://www.ncbi.nlm.nih.g
24-methylenecycloartenol C-4 methyl oxidase (AtSMO1-1)	24MCMO	At4g12110	Cyt	AAN18115	functional	http://www.ncbi.nlm.nih.g
24-methylenecycloartenol C-4 methyl oxidase (AtSMO1-3)	24MCMO	At4g22753	Cyt	NP_567669	by homology	http://www.ncbi.nlm.nih.g
24-methylenecycloartenol C-4 methyl oxidase (AtSMO1-2)	24MCMO	At4g22756	Cyt	AAL33803	functional	http://www.ncbi.nlm.nih.g
cycloeucalenol cycloisomerase	CECI	At5g50375	Cyt	AAF67863	functional	http://www.ncbi.nlm.nih.g
sterol C14 reductase (fackel)	FACKEL	At3g50430	Cyt/ER	AAF81279	functional	http://www.ncbi.nlm.nih.g
obtusifoliol C14 methyl oxidase (CYP51)	OC14MO	At1g11680	Cyt	BAB61873	functional	http://www.ncbi.nlm.nih.g
obtusifoliol C14 methyl oxidase (CYP51)	OC14MO	At2g17330	Cyt	AAB86510	by homology	http://www.ncbi.nlm.nih.g
C-8,7 sterol isomerase	C8,7SI	At1g20050	Cyt	AAD03489	functional	http://www.ncbi.nlm.nih.g
sterol C-methyltransferase 2	SCMT2	At1g20330	Cyt	CAA61966	functional	http://www.ncbi.nlm.nih.g
sterol C-methyltransferase 2	SCMT2	At1g76090	Cyt	AAB62809	functional	http://www.ncbi.nlm.nih.g
sterol C-4 methyl oxidase (AtSMO2-2)	S4MO	At1g07420	Cyt	AAL32303	functional	http://www.ncbi.nlm.nih.g
sterol C-4 methyl oxidase (AtSMO2–1)	S4MO	At2g29390	Cyt	AAL32302	functional	http://www.ncbi.nlm.nih.g
sterol C5-desaturase (DWF 7)	DWF7	At3g02580	Cyt/ER	CAA62079	functional	http://www.ncbi.nlm.nih.g
sterol C5-desaturase (DWF 7)	DWF7	At3g02590	Cyt/ER	Q9M883	by homology	http://www.ncbi.nlm.nih.g
sterol delta7-desaturase (DWF5)	S7DS	At1g50430	Cyt/ER	AAC49278	functional	http://www.ncbi.nlm.nih.g
sterol C24-reductase (DWF1, diminuto)	DWF1	At3g19820	Cyt/ER	Q39085	functional	http://www.ncbi.nlm.nih.g
sterol C 22-desaturase	SC22DS	not cloned yet			NA	NA
BRASSINOSTEROID BIOSYNTHESIS						
sterol reductase (DET2)	DET2	At2g38050	Cyt/ER	AAC49264	functional	http://www.ncbi.nlm.nih.g
steroid C22-hydroxylase (CYP90B1; DWF4)	DWF4	At3g50660	Cyt/ER	AAC05093	functional	http://www.ncbi.nlm.nih.g
steroid C23-hydroxylase (CYP90A1)	CYP90A1	At5g05690	Cyt/ER	Q42569	functional	http://www.ncbi.nlm.nih.g
UBIQUINONE BIOSYNTHESIS						
p-hydroxybenzoate polyprenyltransferase (UbiA; CoQ2)	UbiA/CoQ2	At4g23660	Mit	CAB79321	by homology	http://www.ncbi.nlm.nih.g
O-methyltransferase (multifunctional) (CoQ3)	CoQ3	At2g30920	Mit	O49354	functional	http://www.ncbi.nlm.nih.g
monooxygenase (ubiF/ubiH-like)	UbiF/UbiH	At3g24200	Mit	BAD43118	by homology	http://www.ncbi.nlm.nih.g
C-methyltransferase (CoQ5/ubiE)	CoQ5/UbiE	At5g57300	Mit	AAM14112	by homology	http://www.ncbi.nlm.nih.g
PROTEIN PRENYLATION						
farnesyltransferase/geranylgeranyltransferase I, alpha subunit	FTase/GGTase1A	At3g59380	Cyt	Q9LX33	functional	http://www.ncbi.nlm.nih.g
farnesyltransferase, beta subunit (ERA1)	FTaseB	At5g40280	Cyt	Q38920	functional	http://www.ncbi.nlm.nih.g
geranylgeranyltransferase I, beta subunit	GGTase1B	At2g39550	Cyt	AAG40865	functional	http://www.ncbi.nlm.nih.g
(Rab) geranylgeranyltransferase II, alpha subunit	GGTase2A	At4g24490	Cyt	AAM51433	by homology	http://www.ncbi.nlm.nih.g
(Rab) geranylgeranyltransferase II, alpha subunit	GGTase2A	At5g41820	Cyt	NP_198997	by homology	http://www.ncbi.nlm.nih.g
(Rab) geranylgeranyltransferase II, beta subunit	GGTase2B	At3g12070	Cyt	NP_850567	by homology	http://www.ncbi.nlm.nih.g
(Rab) geranylgeranyltransferase II, beta subunit	GGTase2B	At5g12210	Cyt	AAO44082	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

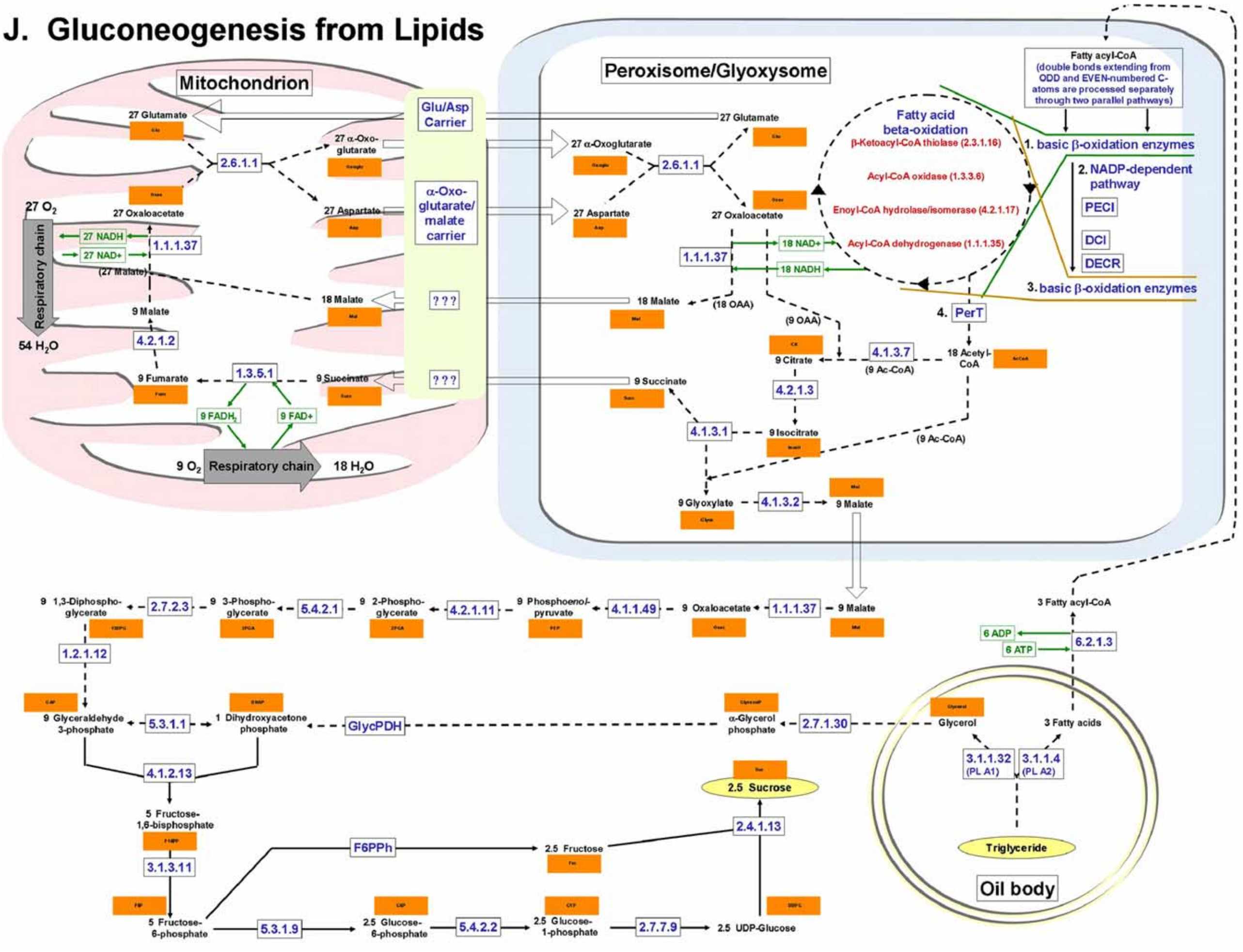
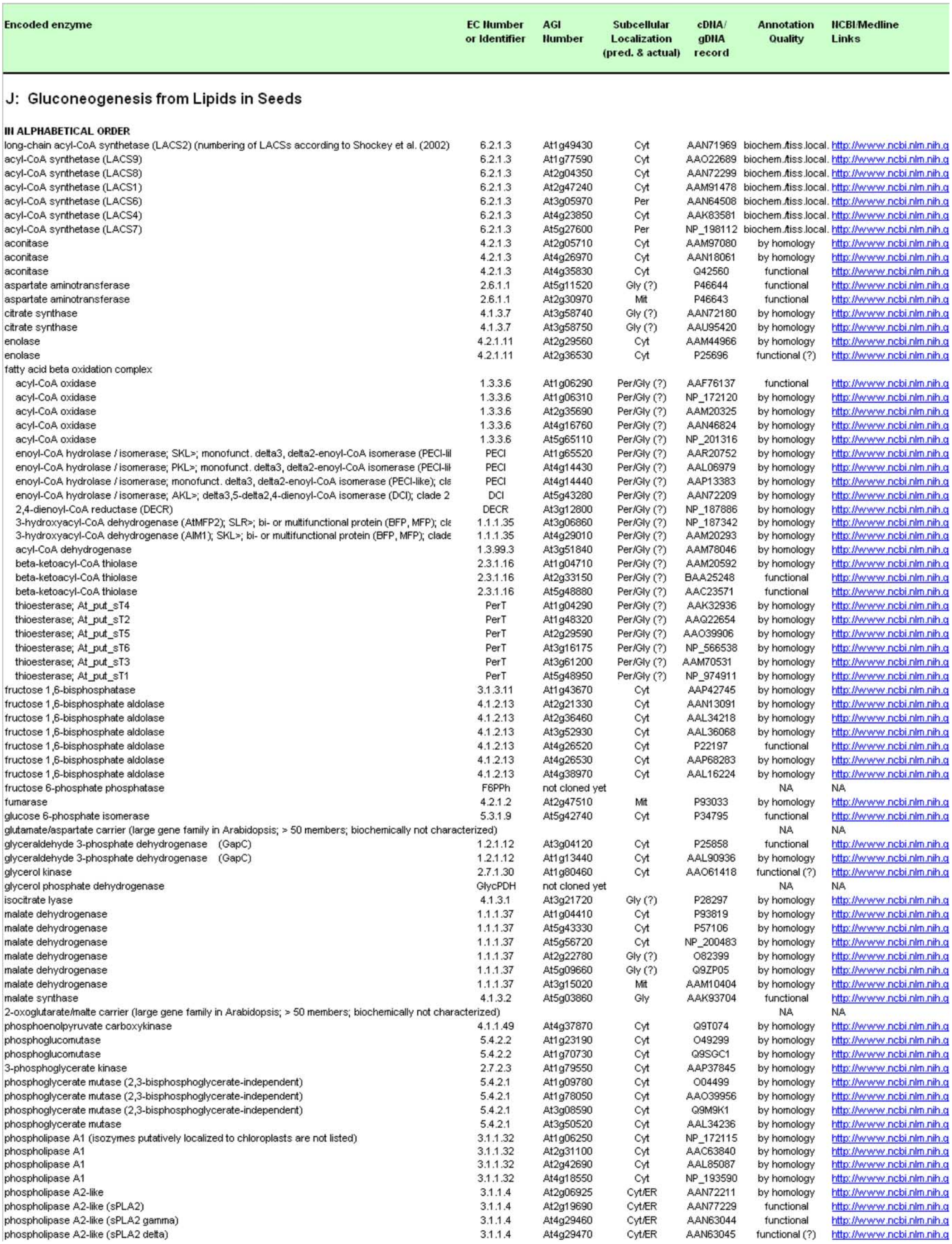

J. Gluconeogenesis from Lipids

Fig. 3 (*continued*)

et al., 1998). The size of the plant metabolome reflects the vast array of secondary compounds that plants produce, but estimates vary widely (2000–7000 in *A. thaliana*); (3) unlike nucleic acids and proteins, metabolites have a vast range of chemical structures and properties. Therefore, there is no single extraction or analysis technique that is suitable for all low molecular weight metabolites. Chromatographic metabolite separations combined with detection by nuclear magnetic resonance and/or mass spectrometry are powerful means of generating multivariate metabolic data, but further development is required before high-throughput metabolic studies at a global scale can be attempted (Weckwerth, 2003). In a scaled-back strategy, stable pools of key metabolites (which define branch points in pathways or are metabolic end-products) from several different metabolic pathways are measured, thus providing a snapshot of the metabolic state of a cell, tissue or organ (Golan et al., 2003).

The aim of 'omics' technologies is to extract latent biochemical information that is of diagnostic or prognostic value, thus reflecting 'actual' biological events rather than the 'potential' for the occurrence of such events. Metabolic changes are 'actual' end points, whereas gene and protein expression changes are generally only indicators of the potential for an end-point change, which can sometimes be misleading (Laule et al., 2003). Therefore, metabolomics bridges the gap between the 'omics' platform technologies and experimental phenotype. Measurements of metabolite pools and the integration of transcriptome and proteome data will bring a new level of understanding to the cellular biology of model organisms. As the size of the experimental databases increases, repeated patterns of gene, protein and metabolite abundance will emerge and will provide insight into the networks that regulate metabolic pathways. Ultimately, models will be developed that allow the rational design of bioengineering strategies to achieve the desired flux

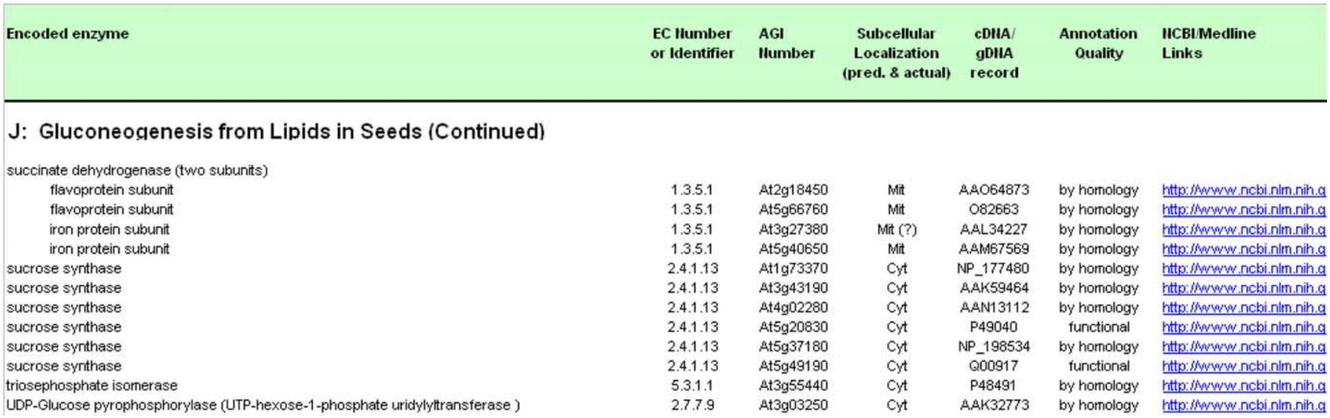


J: Gluconeogenesis from Lipids in Seeds

IN ALPHABETICAL ORDER

Encoded enzyme	**EC Number or Identifier**	**AGI Number**	**Subcellular Localization (pred. & actual)**	**cDNA/ gDNA record**	**Annotation Quality**	**NCBI/Medline Links**
long-chain acyl-CoA synthetase (LACS2) (numbering of LACSs according to Shockey et al. (2002)	6.2.1.3	At1g49430	Cyt	AAN71969	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
acyl-CoA synthetase (LACS9)	6.2.1.3	At1g77590	Cyt	AAO22689	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
acyl-CoA synthetase (LACS8)	6.2.1.3	At2g04350	Cyt	AAN72299	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
acyl-CoA synthetase (LACS1)	6.2.1.3	At2g47240	Cyt	AAM91478	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
acyl-CoA synthetase (LACS6)	6.2.1.3	At3g05970	Per	AAN64508	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
acyl-CoA synthetase (LACS4)	6.2.1.3	At4g23850	Cyt	AAK83581	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
acyl-CoA synthetase (LACS7)	6.2.1.3	At5g27600	Per	NP_198112	biochem./tiss.local.	http://www.ncbi.nlm.nih.g
aconitase	4.2.1.3	At2g05710	Cyt	AAM97080	by homology	http://www.ncbi.nlm.nih.g
aconitase	4.2.1.3	At4g26970	Cyt	AAN18061	by homology	http://www.ncbi.nlm.nih.g
aconitase	4.2.1.3	At4g35830	Cyt	Q42560	functional	http://www.ncbi.nlm.nih.g
aspartate aminotransferase	2.6.1.1	At5g11520	Gly (?)	P46644	functional	http://www.ncbi.nlm.nih.g
aspartate aminotransferase	2.6.1.1	At2g30970	Mit	P46643	functional	http://www.ncbi.nlm.nih.g
citrate synthase	4.1.3.7	At3g58740	Gly (?)	AAN72180	by homology	http://www.ncbi.nlm.nih.g
citrate synthase	4.1.3.7	At3g58750	Gly (?)	AAU95420	by homology	http://www.ncbi.nlm.nih.g
enolase	4.2.1.11	At2g29560	Cyt	AAM44966	by homology	http://www.ncbi.nlm.nih.g
enolase	4.2.1.11	At2g36530	Cyt	P25696	functional (?)	http://www.ncbi.nlm.nih.g
fatty acid beta oxidation complex						
acyl-CoA oxidase	1.3.3.6	At1g06290	Per/Gly (?)	AAF76137	functional	http://www.ncbi.nlm.nih.g
acyl-CoA oxidase	1.3.3.6	At1g06310	Per/Gly (?)	NP_172120	by homology	http://www.ncbi.nlm.nih.g
acyl-CoA oxidase	1.3.3.6	At2g35690	Per/Gly (?)	AAM20325	by homology	http://www.ncbi.nlm.nih.g
acyl-CoA oxidase	1.3.3.6	At4g16760	Per/Gly (?)	AAN46824	by homology	http://www.ncbi.nlm.nih.g
acyl-CoA oxidase	1.3.3.6	At5g65110	Per/Gly (?)	NP_201316	by homology	http://www.ncbi.nlm.nih.g
enoyl-CoA hydrolase / isomerase; SKL>; monofunct. delta3, delta2-enoyl-CoA isomerase (PECI-lil	PECI	At1g65520	Per/Gly (?)	AAR20752	by homology	http://www.ncbi.nlm.nih.g
enoyl-CoA hydrolase / isomerase; PKL>; monofunct. delta3, delta2-enoyl-CoA isomerase (PECI-lik	PECI	At4g14430	Per/Gly (?)	AAL06979	by homology	http://www.ncbi.nlm.nih.g
enoyl-CoA hydrolase / isomerase; monofunct. delta3, delta2-enoyl-CoA isomerase (PECI-like); cla	PECI	At4g14440	Per/Gly (?)	AAP13383	by homology	http://www.ncbi.nlm.nih.g
enoyl-CoA hydrolase / isomerase; AKL>; delta3,5-delta2,4-dienoyl-CoA isomerase (DCI); clade 2	DCI	At5g43280	Per/Gly (?)	AAN72209	by homology	http://www.ncbi.nlm.nih.g
2,4-dienoyl-CoA reductase (DECR)	DECR	At3g12800	Per/Gly (?)	NP_187886	by homology	http://www.ncbi.nlm.nih.g
3-hydroxyacyl-CoA dehydrogenase (AtMFP2); SLR>; bi- or multifunctional protein (BFP, MFP); cla	1.1.1.35	At3g06860	Per/Gly (?)	NP_187342	by homology	http://www.ncbi.nlm.nih.g
3-hydroxyacyl-CoA dehydrogenase (AIM1); SKL>; bi- or multifunctional protein (BFP, MFP); clade	1.1.1.35	At4g29010	Per/Gly (?)	AAM20293	by homology	http://www.ncbi.nlm.nih.g
acyl-CoA dehydrogenase	1.3.99.3	At3g51840	Per/Gly (?)	AAM78046	by homology	http://www.ncbi.nlm.nih.g
beta-ketoacyl-CoA thiolase	2.3.1.16	At1g04710	Per/Gly (?)	AAM20592	by homology	http://www.ncbi.nlm.nih.g
beta-ketoacyl-CoA thiolase	2.3.1.16	At2g33150	Per/Gly (?)	BAA25248	functional	http://www.ncbi.nlm.nih.g
beta-ketoacyl-CoA thiolase	2.3.1.16	At5g48880	Per/Gly (?)	AAC23571	functional	http://www.ncbi.nlm.nih.g
thioesterase; At_put_sT4	PerT	At1g04290	Per/Gly (?)	AAK32936	by homology	http://www.ncbi.nlm.nih.g
thioesterase; At_put_sT2	PerT	At1g48320	Per/Gly (?)	AAQ22654	by homology	http://www.ncbi.nlm.nih.g
thioesterase; At_put_sT5	PerT	At2g29590	Per/Gly (?)	AAO39906	by homology	http://www.ncbi.nlm.nih.g
thioesterase; At_put_sT6	PerT	At3g16175	Per/Gly (?)	NP_566538	by homology	http://www.ncbi.nlm.nih.g
thioesterase; At_put_sT3	PerT	At3g61200	Per/Gly (?)	AAM70531	by homology	http://www.ncbi.nlm.nih.g
thioesterase; At_put_sT1	PerT	At5g48950	Per/Gly (?)	NP_974911	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphatase	3.1.3.11	At1g43670	Cyt	AAP42745	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At2g21330	Cyt	AAN13091	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At2g36460	Cyt	AAL34218	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At3g52930	Cyt	AAL36068	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At4g26520	Cyt	P22197	functional	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At4g26530	Cyt	AAP68283	by homology	http://www.ncbi.nlm.nih.g
fructose 1,6-bisphosphate aldolase	4.1.2.13	At4g38970	Cyt	AAL16224	by homology	http://www.ncbi.nlm.nih.g
fructose 6-phosphate phosphatase	F6PPh	not cloned yet			NA	NA
fumarase	4.2.1.2	At2g47510	Mit	P93033	by homology	http://www.ncbi.nlm.nih.g
glucose 6-phosphate isomerase	5.3.1.9	At5g42740	Cyt	P34795	functional	http://www.ncbi.nlm.nih.g
glutamate/aspartate carrier (large gene family in Arabidopsis; > 50 members; biochemically not characterized)					NA	NA
glyceraldehyde 3-phosphate dehydrogenase (GapC)	1.2.1.12	At3g04120	Cyt	P25858	functional	http://www.ncbi.nlm.nih.g
glyceraldehyde 3-phosphate dehydrogenase (GapC)	1.2.1.12	At1g13440	Cyt	AAL90936	by homology	http://www.ncbi.nlm.nih.g
glycerol kinase	2.7.1.30	At1g80460	Cyt	AAO61418	functional (?)	http://www.ncbi.nlm.nih.g
glycerol phosphate dehydrogenase	GlycPDH	not cloned yet			NA	NA
isocitrate lyase	4.1.3.1	At3g21720	Gly (?)	P28297	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At1g04410	Cyt	P93819	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At5g43330	Cyt	P57106	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At5g56720	Cyt	NP_200483	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At2g22780	Gly (?)	O82399	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At5g09660	Gly (?)	Q9ZP05	by homology	http://www.ncbi.nlm.nih.g
malate dehydrogenase	1.1.1.37	At3g15020	Mit	AAM10404	by homology	http://www.ncbi.nlm.nih.g
malate synthase	4.1.3.2	At5g03860	Gly	AAK93704	functional	http://www.ncbi.nlm.nih.g
2-oxoglutarate/malte carrier (large gene family in Arabidopsis; > 50 members; biochemically not characterized)					NA	NA
phosphoenolpyruvate carboxykinase	4.1.1.49	At4g37870	Cyt	Q9T074	by homology	http://www.ncbi.nlm.nih.g
phosphoglucomutase	5.4.2.2	At1g23190	Cyt	O49299	by homology	http://www.ncbi.nlm.nih.g
phosphoglucomutase	5.4.2.2	At1g70730	Cyt	Q9SGC1	by homology	http://www.ncbi.nlm.nih.g
3-phosphoglycerate kinase	2.7.2.3	At1g79550	Cyt	AAP37845	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase (2,3-bisphosphoglycerate-independent)	5.4.2.1	At1g09780	Cyt	O04499	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase (2,3-bisphosphoglycerate-independent)	5.4.2.1	At1g78050	Cyt	AAO39956	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase (2,3-bisphosphoglycerate-independent)	5.4.2.1	At3g08590	Cyt	Q9M9K1	by homology	http://www.ncbi.nlm.nih.g
phosphoglycerate mutase	5.4.2.1	At3g50520	Cyt	AAL34236	by homology	http://www.ncbi.nlm.nih.g
phospholipase A1 (isozymes putatively localized to chloroplasts are not listed)	3.1.1.32	At1g06250	Cyt	NP_172115	by homology	http://www.ncbi.nlm.nih.g
phospholipase A1	3.1.1.32	At2g31100	Cyt	AAC63840	by homology	http://www.ncbi.nlm.nih.g
phospholipase A1	3.1.1.32	At2g42690	Cyt	AAL85087	by homology	http://www.ncbi.nlm.nih.g
phospholipase A1	3.1.1.32	At4g18550	Cyt	NP_193590	by homology	http://www.ncbi.nlm.nih.g
phospholipase A2-like	3.1.1.4	At2g06925	Cyt/ER	AAN72211	by homology	http://www.ncbi.nlm.nih.g
phospholipase A2-like (sPLA2)	3.1.1.4	At2g19690	Cyt/ER	AAN77229	functional	http://www.ncbi.nlm.nih.g
phospholipase A2-like (sPLA2 gamma)	3.1.1.4	At4g29460	Cyt/ER	AAN63044	functional	http://www.ncbi.nlm.nih.g
phospholipase A2-like (sPLA2 delta)	3.1.1.4	At4g29470	Cyt/ER	AAN63045	functional (?)	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)



Encoded enzyme	EC Number or Identifier	AGI Number	Subcellular Localization (pred. & actual)	cDNA/ gDNA record	Annotation Quality	NCBI/Medline Links
J: Gluconeogenesis from Lipids in Seeds (Continued)						
succinate dehydrogenase (two subunits)						
flavoprotein subunit	1.3.5.1	At2g18450	Mit	AAO64873	by homology	http://www.ncbi.nlm.nih.g
flavoprotein subunit	1.3.5.1	At5g66760	Mit	O82663	by homology	http://www.ncbi.nlm.nih.g
iron protein subunit	1.3.5.1	At3g27380	Mit (?)	AAL34227	by homology	http://www.ncbi.nlm.nih.g
iron protein subunit	1.3.5.1	At5g40650	Mit	AAM67569	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At1g73370	Cyt	NP_177480	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At3g43190	Cyt	AAK59464	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At4g02280	Cyt	AAN13112	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At5g20830	Cyt	P49040	functional	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At5g37180	Cyt	NP_198534	by homology	http://www.ncbi.nlm.nih.g
sucrose synthase	2.4.1.13	At5g49190	Cyt	Q00917	functional	http://www.ncbi.nlm.nih.g
triosephosphate isomerase	5.3.1.1	At3g55440	Cyt	P48491	by homology	http://www.ncbi.nlm.nih.g
UDP-Glucose pyrophosphorylase (UTP-hexose-1-phosphate uridylyltransferase)	2.7.7.9	At3g03250	Cyt	AAK32773	by homology	http://www.ncbi.nlm.nih.g

Fig. 3 (*continued*)

through specific biochemical pathways of interest. Tools utilizing biochemical pathway maps for data integration can provide the biological context for such models.

5. Note added in proof

During the final stages of the revision of this article, a new analysis tool for microarray data was published (Zimmermann et al., 2004). The GENEVESTIGATOR toolbox is available at http://www.genevestigator.ethz.ch.

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