

<b>Novel Ara ESTs (12-21-00)*</b>					
<b>EST Name</b>	<b>Accession Number</b>	<b>Annotation</b>	<b>Annotated Organism</b>	<b>Seq Length</b>	<b>Insert Size</b>
AA01D07	NP_005830.1	unknown	Homo sapiens	980	0.3
AA03A03	AAF13218.1	Spen RNP motif protein long isoform	Drosophila melanogaster	774	0.65
AF04D01	S67483	adenosinetriphosphatase 2	Plasmodium falciparum	999	1.79
AF04D11	P09063	dihydrolipoamide dehydrogenase	Pseudomonas putida	972	1.97
AA03H01	188878	mucin protein	Homo sapiens	787	2.65
AA04A06	O22060	sucrose-phosphate synthase 1	Citrus unshiu	713	0.33
AA04C06	CAA49544	unknown	Plasmodium falciparum	1318	1.73
AA04H07	S54157	extensin	cowpea	1498	0.44
AA04H11	NP_012089.1	unknown	Saccharomyces cerevisiae	1489	2.13
AA05A01	S25299	extensin	Lycopersicon esculentum	880	0.16
AA05B02	AAF12875.1	maturase	Arachis pintoi	1129	0.74
AA05H12	212657	smooth muscle caldesmon	Gallus gallus	1169	>1
AA06G09	BAA78744.1	unknown	ORYZA SATIVA	692	0.71
AA07A01	727264	hydroxyproline-rich glycoprotein	Phaseolus vulgaris	774	0.43
AA07D05	CAB08179	unknown	Planktothrix agardhii	720	>0.7
AA10D08	AAF46987.1	unknown	Drosophila melanogaster	702	1.05
AA10F11	2289161	unknown	Oryctolagus cuniculus	711	0.98
AA11A03	2648379	isochorismatase	Archaeoglobus fulgidus	600	0.76
AA12D07	P48189	photosystem II reaction center M protein	Zea mays	711	0.62
AA17C07	AAF53718.1	unknown	Drosophila melanogaster	709	1.25
AB04E05	BAA17246	fibrillin	Synechocystis sp.	738	2.09
AB05G08	CAA75593.1	MtN5 protein	Medicago truncatula	573	1.94
AB07B12	Q06852	cell surface glycoprotein 1	Clostridium thermocellum	792	1.67
AB07H05	P12471	chlorophyll a/b binding protein	Glycine max	707	2.11
AB08B02	NP_012089.1	unknown	Saccharomyces cerevisiae	982	1.69
AB08F08	BAA18426.1	unknown	Synechocystis sp.	713	1.1
AB14A07	CAB76401.1	unknown	Scenedesmus obliquus	1060	0.49
AB14B04	1209265K	chorion protein A6	Bombyx mori	1077	1.26
AB14B10	AAA36487.1	profilaggrin	Homo sapiens	1633	1.4
AB14G02	A34615	profilaggrin	Rattus norvegicus	1067	0.97
AC01E01	Q28640	histidine-rich glycoprotein	Oryctolagus cuniculus	842	>0.8
AC03D02	AAF21309.1	seed maturation protein PM23	Glycine max	692	0.85
AC03G07	AAD28279.1	glutathione S-transferase GST-msolf1	Manduca sexta	680	1.26
AC03G12	AAD28279.1	glutathione S-transferase GST-msolf1	Manduca sexta	693	1.1
AC04E01	BAA83718.1	RNA binding protein	Homo sapiens	1197	1.48

AC06A08	S54157	extensin	cowpea (fragment)	1211	1.21
AC06A10	AAC17422.1	SH3-philo protein	Mus musculus	857	1.61
AC06A12	AAF37578.1	splicing regulatory protein, serine/arginine-rich	Rattus norvegicus	1014	3
AC06B11	NP_004759.1	arginine/serine-rich splicing factor 11	Homo sapiens	1180	0.48
AC06E07	AAB40929.1	LimA protein	Dictyostelium discoideum	1462	0.98
AC06F08	S54157	extensin	cowpea (fragment)	1593	1.41
AC06F12	AAF19255.1	small nuclear ribonucleoprotein, U1, 70K protein	Homo sapiens	1352	1.13
AF01B07	T35921	oxidoreductase	Streptomyces coelicolor	974	1.14
AF01C02	CAB05975.1	cytochrome b	Histeromerus mystacinus	815	0.48
AF02G10	P00772	elastase 1	Sus scrofa	869	1.99
AF04H01	Q05046	chaperonin CPN60-2: mitochondrial	Cucurbita sp.	984	2.18
AF04H09	O49884	ribosomal protein, 60S, L30	Lupinus luteus	991	1.04
*Novel Arabidopsis transcripts from cDNA libraries:					
AA - Leaves, 200mM NaCl, 20 hours					
AB - Leaves, 200mM NaCl, 3-6-9-12 hours					
AC - Leaves/Roots, 150mM NaCl, 20 hours					
AF - Roots, 200mM NaCl, 6 hours					
The 49 novel transcripts were found in an EST population of 3, 392 sequences from libraries after "subtractive screening" (see also: <a href="http://www.stress-genomics.org">http://www.stress-genomics.org</a> ). The sequences were compared with Arabidopsis sequences among non-redundant sequences in GenBank.					
The clones/ESTs will be available through the Arabidopsis Stock Center at Ohio State University.					