

9 Anhang

Anhang 8.1:

Auf den folgenden zwei Seiten (Seite 150-151) sind die Ergebnisse der BLAST-Analyse der Testsequenzierung der 48 Pistill cNDA-Klone dargestellt (vgl. 3.2.2.1).

sequence name	cluster size	BLAST-Hit	putative gene/function	e-value	start query [nt]	start subject [aa]	length subject [aa]	frame
P-c4		At1g05680	putative indole-3-acetate beta-glucosyltransferase	1,70E-65	164	144	453	2
P-h11		At1g06680	23 kDa polypeptide of oxygen-evolving complex (OEC)	1,70E-90	165	16	263	3
P-h12		At1g09640	unknown protein	2,70E-37	200	340	414	2
P-g7		At1g10360	putative glutathione S-transferase TSI-1	2,30E-31	178	95	227	1
P-g1		At1g12900	glyceraldehyde 3-phosphate dehydrogenase A, chloroplast precursor,	1,50E-82	199	75	399	1
P-f4		At1g21461	unknown protein	1,90E-68	197	44	247	2
P-c6		At1g25310	hypothetical protein	2,80E-42	188	63	151	2
P-a2		At1g42970	putative glyceraldehyde-3-phosphate dehydrogenase	1,50E-19	187	405	447	1
P-h4		At1g55460	putative protein	9,40E-67	199	221	411	1
P-b5	1	At1g60000	unknown protein	1,20E-66	171	25	258	3
P-b6		At1g60000	unknown protein	4,90E-86	189	25	258	3
P-c3		At1g61680	hypothetical protein	4,70E-81	183	166	474	3
P-b1		At1g72640	hypothetical protein	7,60E-22	222	1	153	3
P-c2		At1g73450		4,30E-67	196	820	1155	1
P-h1		At2g01930	unknown protein	1,60E-78	163	81	283	1
P-f3		At2g18170	MAP kinase (ATMPK7)	1,00E-91	156	9	368	3
P-h9		At2g21330	fructose biphosphate aldolase like protein	9,40E-83	180	171	399	3
P-d7		At2g27030	calmodulin	2,00E-29	192	6	149	3
P-e1		At2g28790	thauamin like protein	2,30E-70	168	7	249	3
P-d11		At2g36800	putative glucosyl transferase	1,20E-65	496	105	495	-3
P-g11		At2g42530	cold-regulated protein cor1.5b precursor	3,90E-68	242	1	141	1
P-d2		At3g06510	beta glucosidase like protein	4,40E-22	196	572	622	1
P-d3		At3g10920	putative [Mn] superoxide dismutase	2,70E-85	189	1	231	3
P-e6		At3g10985	unknown protein	2,40E-52	273	1	110	3
P-b7		At3g13200	unknown protein	2,60E-72	242	1	230	2
P-f5		At3g25070	unknown protein	8,70E-97	224	1	211	2
P-b2		At3g26070	unknown protein	1,80E-65	136	36	242	1
P-d1		At3g44190	unknown protein	1,20E-74	208	217	367	1
P-h8		At3g47470	light-harvesting chlorophyll a/b-binding protein	7,40E-90	160	29	251	1
P-g2		At3g47810	putative protein	1,80E-49	332	1	190	2
P-b4		At3g55430	beta-1,3-glucanase - like protein	2,20E-85	197	249	449	2
P-d12		At3g62800	unknown protein	7,30E-67	194	228	355	2
P-a8		At4g01710	unknown protein	4,80E-65	195	2	132	3

P-d5	At4g03430	putative pre-mRNA splicing factor	1,80E-68	183	810	1029	3
P-g5	At4g08810	putative protein	1,90E-52	189	269	552	3
P-h5	At4g10280	unknown protein	3,40E-07	244	40	140	1
P-f9	At4g24770	31 kDa RNA binding protein (rbp31)	6,00E-65	196	6	329	1
P-e5	At4g35980	putative protein	2,20E-74	179	222	512	2
P-f6	At5g01530	chlorophyll a/b-binding protein CP29	3,40E-60	221	1	290	2
P-h2	At5g02960	unknown protein	3,70E-71	255	1	142	3
P-d4	At5g05230	unknown protein	4,10E-40	197	163	248	2
P-e1	At5g18380	40S RIBOSOMAL PROTEIN S16	5,80E-67	233	1	146	2
P-f2	At5g18380	40S RIBOSOMAL PROTEIN S16	1,10E-71	247	1	146	1
P-g8	At5g40340	unknown protein	2,70E-64	197	421	1008	2
P-e7	At5g47070	protein serine/threonine kinase-like	1,90E-61	197	218	410	2
P-f8	At5g47570	unknown protein	8,70E-64	202	1	125	1
P-a11	At5g61410	ribulose-5-phosphate-3-epimerase	7,70E-72	183	109	281	3
P-e5	At5g66730	zinc finger protein	7,90E-86	192	99	500	3

Anhang 8.2:

Auf den folgenden zwölf Seiten (Seite 152 - 163) sind die Ergebnisse der BLAST-Analyse der Testsequenzierung der 576 Infloreszenz cNDA-Klone dargestellt (vgl. 3.2.2.2).

sequence name	cluster size	BLAST-Hit	putative gene/function	e-value	start query [nt]	start subject [aa]	length subject [aa]	frame
atm6_E1	1	At1g01620	hypothetical protein	3,00E-82	41	1	286	2
atm4_D5	1	At1g02780	ribosomal protein L19, putative	1,00E-77	6	1	214	3
atm3_H9	1	At1g03430	putative AHP2	3,00E-19	260	1	192	2
atm4_F8	1	At1g03680	putative thioredoxin-m	3,00E-79	81	1	179	3
atm5_B4	3	At1g04270	putative 40S ribosomal protein S15	1,00E-61	69	1	152	3
atm5_C3	1	At1g04270	putative 40S ribosomal protein S15	4,00E-68	69	1	152	3
atm5_C4	1	At1g04270	putative 40S ribosomal protein S15	4,00E-74	69	1	152	3
atm5_E12	1	At1g04770	hypothetical protein	3,00E-68	48	1	302	3
atm1_E1	1	At1g05850	class I chitinase, putative	1,00E-87	115	1	321	1
atm2_G12	1	At1g06680	23 kDa polypeptide of oxygen-evolving complex (OEC)	6,00E-55	34	1	263	1
atm1_G7	2	At1g06760	histone H1, putative	1,00E-31	65	1	274	2
atm1_G8	1	At1g06760	histone H1, putative	2,00E-34	65	1	274	2
atm5_B9	2	At1g07890	L-ascorbate peroxidase	7,00E-81	78	1	250	3
atm5_C2	1	At1g07890	L-ascorbate peroxidase	1,00E-76	28	1	250	1
atm1_H4	1	At1g08110	glyoxalase I, putative	1,00E-87	45	1	185	3
atm4_C12	3	At1g09310	unknown protein	3,00E-64	10	1	179	1
atm5_A5	1	At1g09310	unknown protein	6,00E-66	28	1	179	1
atm5_H12	1	At1g09310	unknown protein	1,00E-59	38	1	179	2
atm1_D11	1	At1g12080	unknown protein	4,00E-04	61	1	138	1
atm3_E12	2	At1g13930	putative hydroxyproline-rich glycoprotein	1,00E-58	36	1	155	3
atm5_F9	1	At1g13930	putative hydroxyproline-rich glycoprotein	8,00E-58	39	1	155	3
atm1_F1	1	At1g14320	hypothetical protein	e-103	9	1	220	3
atm1_G10	3	At1g15820	hypothetical protein	5,00E-78	213	1	258	3
atm3_D9	1	At1g15820	hypothetical protein	3,00E-58	23	1	258	2
atm5_D9	1	At1g15820	hypothetical protein	2,00E-75	23	1	258	2
atm6_A11	1	At1g16460	putative thiosulfate sulfurtransferase	1,00E-56	163	1	318	1
atm1_A9	2	At1g20630	hypothetical protein	e-113	73	1	492	1
atm3_A11	1	At1g20630	hypothetical protein	1,00E-69	63	1	492	3
atm5_F4	1	At1g24020	pollen allergen-like protein	1,00E-73	45	1	155	3
atm4_F11	1	At1g27950	hypothetical protein	7,00E-74	13	1	193	1
atm3_H5	1	At1g29910	chlorophyll a/b-binding protein	6,00E-73	22	1	267	1
atm4_F7	1	At1g31330	photosystem I subunit III precursor, putative	5,00E-65	61	1	221	1
atm4_C6	1	At1g36240	60S ribosomal protein L30, putative	1,00E-56	41	1	112	2

atm3_B4	1	At1g52230	photosystem I subunit VI precursor	1,00E-59	10	1	145	1
atm5_E5	1	At1g52300	60S ribosomal protein L37, putative	6,00E-35	36	1	95	3
atm2_H10	1	At1g52600		1,00E-45	99	1	180	3
atm3_C12	1	At1g55360	unknown protein	2,00E-54	220	1	422	1
atm2_D3	1	At1g55520	transcription initiation factor TFIIID-2	1,00E-53	82	1	200	1
atm6_A6	2	At1g56580	unknown protein	3,00E-60	41	1	166	2
atm6_A7		At1g56580	unknown protein	3,00E-63	41	1	166	2
atm1_B4	1	At1g61170		2,00E-50	54	1	251	3
atm1_C5	2	At1g62370	hypothetical protein	1,00E-79	127	1	204	1
atm1_C6		At1g62370	hypothetical protein	1,00E-62	127	1	204	1
atm1_C7	1	At1g62370	hypothetical protein	1,00E-41	127	1	204	1
atm2_F11	2	At1g63290	putative D-ribose-5-phosphate	2,00E-66	33	1	227	3
atm3_A9		At1g65290		1,00E-64	14	1	126	2
atm2_F7	1	At1g67050	hypothetical protein	3,00E-41	73	1	264	1
atm1_H9	1	At1g67060	hypothetical protein	1,00E-74	97	1	182	1
atm2_E2		At1g70600	60S ribosomal protein L27A	1,00E-80	39	1	146	3
atm2_A8	1	At1g74670	GASTT-like protein	1,00E-33	219	1	80	3
atm3_G9	1	At1g75880	anter-specific proline-rich -like protein (APG-like)	2,00E-48	94	1	374	1
atm3_F8	1	At1g77270	hypothetical protein	3,00E-06	241	1	558	1
atm1_A8	1	At1g78040	similar to phosphoglycerate mutase 1 spP31217; similar	5,00E-95	44	1	171	2
atm1_D2	2	At1g79040	hypothetical protein	3,00E-57	34	1	140	1
atm2_B3		At1g79040	hypothetical protein	1,00E-48	38	1	140	2
atm6_D3	1	At1g79550	hypothetical protein	9,00E-27	109	1	401	1
atm3_C8	1	At1g80920	J8-like protein	6,00E-38	118	1	163	1
atm3_H10	1	At2g01350	putative nicotinate-nucleotide pyrophosphorylase	8,00E-68	89	1	323	2
atm3_D3	1	At2g02400	putative cinnamoyl-CoA reductase	e-103	15	1	318	3
atm4_E3	1	At2g06520	hypothetical protein	4,00E-37	45	1	116	3
atm4_D8		At2g15300	putative receptor-like protein kinase	4,00E-44	137	1	744	2
atm3_E4	1	At2g20820	unknown protein	1,00E-35	51	1	112	3
atm3_G8	1	At2g20870	unknown protein	2,00E-70	18	1	140	3
atm1_H3	1	At2g20920	unknown protein	e-103	32	1	287	2
atm6_B4	1	At2g21190	putative ER lumen protein retaining receptor	e-123	30	1	263	3
atm2_B4	1	At2g21660	glycine-rich RNA binding protein	4,00E-44	36	1	176	3
atm1_A5	1	At2g23780	putative RING zinc finger protein	2,00E-78	134	1	227	2
atm2_A12	1	At2g23930	putative small nuclear ribonucleoprotein E	1,00E-31	63	1	80	3
atm1_C8	1	At2g27750	unknown protein	5,00E-35	82	1	113	1

atm3 C10	1	A12g28950	putative expansin				2,00E-64	42	1	257	3
atm3 G1		A12g29550	tubulin beta-7 chain				4,00E-76	45	1	449	3
atm2 E11	1	A12g29960	cyclophilin				1,00E-67	23	1	201	2
atm4 B6	1	A12g30570	photosystem II reaction center 6.1KD protein				2,00E-40	54	1	133	3
atm1 F7	3	A12g30860	glutathione S-transferase				e-108	30	1	215	3
atm1 G4		A12g30860	glutathione S-transferase				e-109	30	1	215	3
atm3 E7		A12g30860	glutathione S-transferase				2,00E-83	31	1	215	1
atm5 H3	1	A12g31360	delta 9 desaturase				4,00E-74	40	1	311	1
atm4 F5	1	A12g31610	40S ribosomal protein; contains C-terminal domain				6,00E-97	55	1	250	1
atm4 G9	1	A12g32060	40S ribosomal protein S12				4,00E-64	51	1	144	3
atm3 A1	1	A12g33150	3-ketoacyl-CoA thiolase				2,00E-73	101	1	462	2
atm6 A1	1	A12g33450	putative chloroplast 50S ribosomal protein L28				5,00E-64	15	1	140	3
atm3 A10	2	A12g34420	photosystem II type I chlorophyll a/b binding protein				3,00E-94	42	1	265	3
atm6 E3		A12g34420	photosystem II type I chlorophyll a/b binding protein				5,00E-65	34	1	265	1
atm1 F9	1	A12g35370	glycine decarboxylase complex H-protein				2,00E-57	24	1	165	3
atm5 D4	1	A12g38270	unknown protein				6,00E-82	9	1	293	3
atm6 C1	1	A12g38530	putative nonspecific lipid-transfer protein				1,00E-48	41	1	118	2
atm3 G4	4	A12g38540	putative nonspecific lipid-transfer protein				3,00E-64	24	1	118	3
atm4 B4		A12g38540	putative nonspecific lipid-transfer protein				2,00E-64	33	1	118	3
atm5 B7		A12g38540	putative nonspecific lipid-transfer protein				3,00E-64	49	1	118	1
atm5 H9		A12g38540	putative nonspecific lipid-transfer protein				2,00E-64	49	1	118	1
atm6 B8	1	A12g39760	hypothetical protein				e-107	23	1	408	2
atm2 D6	1	A12g41430	dehydration-induced protein (ERD15)				5,00E-50	77	1	163	2
atm1 D1	1	A12g41470	unknown protein				2,00E-89	67	1	365	1
atm1 F12	1	A12g42540	cold-regulated protein cor15a precursor				3,00E-56	69	1	139	3
atm4 A7		A13g02470	S-adenosylmethionine decarboxylase				2,00E-06	667	1	366	1
atm5 F7	1	A13g02600	putative phosphatidate phosphohydrolyase				2,00E-60	101	1	314	2
atm1 D9	1	A13g04710	ankyrin-like protein				7,00E-59	127	1	456	1
atm3 H4	1	A13g08030	unknown protein				6,00E-79	74	1	365	2
atm4 C9	1	A13g11400	putative eukaryotic translation initiation factor 3				1,00E-82	98	1	294	2
atm6 B9	1	A13g11940	putative 40S ribosomal protein S5				e-104	24	1	207	3
atm3 B6	1	A13g12145	leucine-rich repeat protein FLR1				6,00E-89	1	1	203	1
atm6 D9	1	A13g12370	hypothetical protein				1,00E-58	132	1	171	3
atm2 B9	2	A13g17970	phosphoprotein phosphatase, putative				1,00E-52	112	1	143	1
atm2 D1		A13g17970	phosphoprotein phosphatase, putative				9,00E-57	112	1	143	1
atm2 A6	1	A13g22210	hypothetical protein				1,00E-25	16	1	69	1

atm2_D10	1	At3g26740	light regulated protein, putative	1,00E-56	35	1	141	2
atm3_E10	1	At3g27160	unknown protein	2,00E-52	41	1	183	2
atm5_D7	1	At3g27850	50S ribosomal protein L12-C	1,00E-69	40	1	187	1
atm6_G5	1	At3g44310	nitrilase 1	1,00E-36	14	1	346	2
atm5_F12	1	At3g46010	actin depolymerizing factor 1 (ADF1)	1,00E-45	87	1	139	3
atm5_B1	1	At3g47470	CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR homolog	7,00E-62	81	1	251	3
atm4_C5	1	At3g48890	putative progesterone-binding protein homolog.Atmp2	2,00E-96	27	1	233	3
atm4_G1	1	At3g49010	60S ribosomal protein L13, BBC1 protein	2,00E-98	36	1	206	3
atm1_B5	4	At3g49270	hypothetical protein	2,00E-23	189	1	121	3
atm1_F8		At3g49270	hypothetical protein	2,00E-64	168	1	121	3
atm2_H1		At3g49270	hypothetical protein	1,00E-29	189	1	121	3
atm2_H2		At3g49270	hypothetical protein	3,00E-51	189	1	121	3
atm6_B5	1	At3g52590	ubiquitin / ribosomal protein CEP52	1,00E-69	14	1	128	2
atm2_H4	1	At3g56680	putative protein	1,00E-33	219	1	353	3
atm3_G7	1	At3g56940	leucine zipper-containing protein AT103	6,00E-65	31	1	409	1
atm2_C3	2	At3g58680	transcriptional coactivator - like protein	4,00E-69	57	1	142	3
atm6_F1		At3g58680	transcriptional coactivator - like protein	4,00E-74	48	1	142	3
atm3_A8	1	At3g60500	nucleolar autoantigen - like protein	1,00E-80	120	1	438	3
atm6_B3	1	At4g00430	probable plasma membrane intrinsic protein 1c	2,00E-78	8	1	295	2
atm4_C3	1	At4g03210	putative xyloglucan endotransglycosylase	e-101	36	1	290	3
atm1_G6		At4g03280	putative component of cytochrome B6-F complex	2,00E-74	14	1	229	2
atm1_F2	1	At4g03520	putative M-type thioredoxin	2,00E-83	61	1	186	1
atm2_A1		At4g05320	polyubiquitin (ubq10)	7,00E-40	53	1	464	2
atm2_B1	2	At4g10340	chlorophyll a/b-binding protein - like	9,00E-38	23	1	280	2
atm6_E6		At4g10340	chlorophyll a/b-binding protein - like	2,00E-65	40	1	280	1
atm3_A12	1	At4g12800	probable photosystem I chain XI precursor	6,00E-62	9	1	219	3
atm5_F3	1	At4g15140	putative protein	2,00E-63	6	1	175	3
atm5_G10	1	At4g16500	cysteine proteinase inhibitor like protein	1,00E-28	13	1	117	1
atm6_D4	1	At4g17390	60S ribosomal protein L15 homolog	1,00E-77	17	1	204	2
atm3_C3	1	At4g18140	putative protein	9,00E-55	74	1	307	2
atm2_H5	1	At4g21620	putative protein	2,00E-15	21	1	131	3
atm1_E7	1	At4g22880	putative leucoanthocyanidin dioxygenase (LDOX)	3,00E-69	134	1	356	2
atm5_H6	1	At4g23630	putative protein	6,00E-23	77	1	275	2
atm5_C1	2	At4g23670	putative major latex protein	9,00E-64	40	1	151	1
atm5_D10		At4g23670	putative major latex protein	2,00E-75	40	1	151	1
atm4_D12	1	At4g25030	putative protein	3,00E-60	48	1	344	3

atm5_H11	1	At4g28340	hypothetical protein	3,00E-23	124	1	159	1
atm2_H7	1	At4g29040	26S proteasome subunit 4-like protein	2,00E-50	12	1	443	3
atm3_C9	1	At4g32150	synaptobrevin-like protein	4,00E-58	198	1	219	3
atm1_D4	1	At4g32470	ubiquitin-cytochrome c reductase - like protein	2,00E-49	52	1	122	1
atm5_E6	1	At4g33865	ribosomal S29 subunit	1,00E-30	18	1	56	3
atm2_D12	1	At4g34870	peptidylprolyl isomerase (cyclophilin)	1,00E-74	39	1	172	3
atm3_F1	1	At4g36800	ubiquitin--protein ligase-like protein	9,00E-74	57	1	183	3
atm3_C5	1	At4g39980	2-dehydro-3-deoxyphosphoheptanate aldolase	1,00E-63	178	1	525	1
atm1_H5	1	At5g02790	putative protein	e-116	115	1	235	1
atm3_G6	1	At5g02840	putative protein	6,00E-56	68	1	307	2
atm4_B10	2	At5g04800	40S ribosomal protein S17	1,00E-74	86	1	141	2
atm4_B11		At5g04800	40S ribosomal protein S17	2,00E-72	86	1	141	2
atm3_G11	1	At5g07550	glycine-rich protein PUTG1	9,00E-46	37	1	106	1
atm1_H6	2	At5g10980	histon H3 protein	9,00E-72	65	1	136	2
atm1_H7		At5g10980	histon H3 protein	3,00E-52	65	1	136	2
atm3_F2	1	At5g14150	putative protein	9,00E-36	143	1	383	2
atm4_C10	1	At5g15090	voltage-dependent anion-selective channel protein hsr2	7,00E-98	58	1	274	1
atm1_A12	1	At5g20290	putative protein	3,00E-41	30	1	222	3
atm6_A4	1	At5g20740	ripening-related protein - like	6,00E-70	12	1	205	3
atm5_C11		At5g22430	unknown protein	7,00E-73	31	1	172	1
atm6_E4		At5g22430	unknown protein	1,00E-67	37	1	172	1
atm2_E8	1	At5g23120	photosystem II stability/assembly factor HCF136	5,00E-26	30	1	403	3
atm3_B8	2	At5g24780	vegetative storage protein Vsp1	8,00E-83	8	1	270	2
atm5_B8	1	At5g27850	60S ribosomal protein - like	e-100	4	1	187	1
atm1_A7		At5g38410	ribulose biphosphate carboxylase small chain 3b	1,00E-81	40	1	181	1
atm3_G10	1	At5g40580	20S proteasome beta subunit PBB2	3,00E-66	41	1	274	2
atm6_B2	1	At5g40950	50S ribosomal protein L27	8,00E-96	23	1	198	2
atm4_A9	1	At5g42780	putative protein	2,00E-89	8	1	242	2
atm5_H4	1	At5g45775	ribosomal protein L11-like	2,00E-83	45	1	182	3
atm3_D6	1	At5g47570	unknown protein	4,00E-56	22	1	125	1
atm3_F12	1	At5g47700	60S acidic ribosomal protein P1-like protein	1,00E-35	73	1	113	1
atm3_A5	1	At5g50040	putative protein	2,00E-72	2	1	175	2
atm5_G4	1	At5g50680	ubiquitin activating enzyme	3,00E-68	17	1	320	2
atm6_H5	1	At5g51410	arginine-aspartate-rich RNA binding protein-like	5,00E-18	151	1	334	1
atm2_B5	1	At5g54290	cytochrome c biogenesis protein precursor (gb AAF35369.1)	e-101	26	1	354	2
atm3_D10	1	At5g54580	putative protein	2,00E-56	113	1	156	2

atm6 C4	2	At5g54770	thiazole biosynthetic enzyme precursor (ARA6) (sp Q38814)	4,00E-47	12	1	349	3
atm6 C8		At5g54770	thiazole biosynthetic enzyme precursor (ARA6) (sp Q38814)	9,00E-53	27	1	349	3
atm2 C8	1	At5g56020	putative protein	1,00E-44	52	1	230	1
atm4 D1	1	At5g58500	putative protein	3,00E-89	78	1	182	3
atm4 A2	1	At5g59310	nonspecific lipid-transfer protein precursor - like	1,00E-56	22	1	110	1
atm3 G5	1	At5g60360	AALP protein	8,00E-44	184	1	358	1
atm2 E6	1	At5g60750	putative protein	4,00E-69	157	1	319	1
atm6 A10	1	At5g61240	CF-5 disease resistance protein - like	9,00E-66	10	1	380	1
atm5 G8	1	At5g61660	structural protein - like	1,00E-04	127	1	105	1
atm4 A5	1	At5g62300	ribosomal protein S20 - like	2,00E-66	58	1	124	1
atm2 B7	1	At5g64080	putative protein	3,00E-73	2	1	173	2
atm4 H8	1	At5g66290	unknown protein	4,00E-77	77	1	202	2
atm6 A3	1	At5g66320	GATA-binding transcription factor-like protein	1,00E-19	139	1	339	1
atm3 B12	1	At5g66880	protein kinase, 41K (EC 2.7.1.-) (pir S71172)	2,00E-57	128	1	361	2
atm1 H1	1	At5g67330	natural resistance-associated macrophage protein	5,00E-39	60	1	512	3
atm4 B5	1	At2g21250	putative NADPH dependent mannose 6-phosphate reductase	e-115	2	2	309	2
atm6 D1	1	At2g47400	putative chloroplast protein CPI2	6,00E-54	2	2	124	2
atm1 C4	1	At3g01470	homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5)	0,004	513	2	272	3
atm6 E5	1	At4g04020	putative fibrillin	2,00E-86	2	2	318	2
atm3 H3	1	At4g04610	5'-adenylylsulfate reductase	3,00E-53	29	2	465	2
atm3 D4	1	At4g21580	putative NADPH quinone oxidoreductase	8,00E-85	2	2	325	2
atm3 C2	1	At1g67290	hypothetical protein	1,00E-44	1	3	615	1
atm1 E12	1	At5g52930	fructose biphosphate aldolase - like protein	1,00E-78	1	3	358	1
atm5 G5	1	At5g06270	putative protein	3,00E-39	2	4	122	2
atm5 F5	1	At1g11850	unknown protein	5,00E-07	2	5	108	2
atm1 H11	1	At1g42970	hypothetical protein	e-107	2	5	447	2
atm4 B3	1	At1g44575	photosystem II 22kDa protein, putative	7,00E-35	1	6	265	1
atm6 A5	2	At3g20670	histone H2A, putative	7,00E-55	2	6	132	2
atm4 D4	1	At4g29350	profilin 2	5,00E-70	77	6	131	2
atm1 D3	1	At1g22300	hypothetical protein	2,00E-70	71	7	254	2
atm2 C10	2	At1g70600	60S ribosomal protein L27A	7,00E-81	1	7	146	1
atm2 D7	1	At2g45960	aquaporin (plasma membrane intrinsic protein 1B)	2,00E-82	151	7	286	1
atm2 E10	2	At4g33220	pectinesterase - like protein	9,00E-14	215	8	477	2
atm2 H9		At4g33220	pectinesterase - like protein	6,00E-29	215	8	477	2
atm3 F11	1	At2g47170	ADP-ribosylation factor 1	8,00E-78	2	9	181	2
atm3 E1	1	At5g11420	putative protein	1,00E-48	87	9	366	3

				e-112	2	11	235
atm4 B9	1	At1g16470	multicatalytic endopeptidase				
atm3 H6	1	At5g14470	putative protein	8,00E-70	22	11	366
atm4 E7	1	At5g47200	ras-related small GTP-binding protein-like	2,00E-80	1	11	159
atm6 G3	1	At1g12760	hypothetical protein	0,098	18	13	368
atm5 A11	2	At1g29930	hypothetical protein	1,00E-81	82	13	267
atm3 E6	1	At5g65260	poly(A)-binding protein II-like	3,00E-69	66	13	220
atm4 F3	1	At2g22090	putative RNA-binding protein	5,00E-67	1	14	347
atm3 D1	1	At5g61410	ribulose-5-phosphate-3-epimerase	5,00E-48	115	14	280
atm2 F2	9	At1g67090	hypothetical protein	4,00E-94	51	15	180
atm2 F9		At1g67090	hypothetical protein	2,00E-65	51	15	180
atm3 B11		At1g67090	hypothetical protein	3,00E-64	60	15	180
atm5 B10		At1g67090	hypothetical protein	5,00E-91	48	15	180
atm5 D8		At1g67090	hypothetical protein	4,00E-80	48	15	180
atm6 C5		At1g67090	hypothetical protein	3,00E-89	49	15	180
atm6 E12		At1g67090	hypothetical protein	3,00E-33	48	15	180
atm6 G10		At1g67090	hypothetical protein	3,00E-88	48	15	180
atm1 B6	2	At5g38430	ribulose biphosphate carboxylase small chain 1b	1,00E-91	53	15	181
atm1 B8		At5g38430	ribulose biphosphate carboxylase small chain 1b	3,00E-88	53	15	181
atm4 F12	1	At1g62500	putative proline-rich cell wall protein (pir S2985);	0,014	2	16	297
atm6 A12	1	At5g26000	myrosinase precursor	8,00E-81	66	16	541
atm1 D6	1	At3g11630	putative 2-cys peroxidoxin	3,00E-59	76	17	266
atm3 E9	1	At1g16650	Hypothetical protein	6,00E-44	87	18	489
atm3 H2	1	At1g23390	unknown protein	1,00E-94	39	18	394
atm6 H4		At1g29930	hypothetical protein	8,00E-68	1	18	267
atm3 D12	1	At3g62870	60S RIBOSOMAL PROTEIN L7A protein	2,00E-46	47	19	256
atm3 A7	1	At2g23150	putative metal ion transporter (NRAMP)	8,00E-61	65	20	509
atm4 G7	1	At4g34670	Putative S-phase-specific ribosomal protein	1,00E-42	121	20	262
atm4 B12	1	At5g49440	unknown protein	5,00E-77	421	22	181
atm1 D5	1	At1g62940	4-coumarate coenzyme A ligase, putative	5,00E-94	1	24	542
atm2 H11	1	At5g02380	metallothionein 2b	9,00E-28	136	24	77
atm1 C2	1	At3g09390	metallothionein-like protein	4,00E-25	71	25	81
atm1 C2	1	At3g09390	metallothionein-like protein	5,00E-26	71	25	81
atm5 A9	1	At1g60170		2,00E-67	119	27	511
atm2 D5	1	At3g56800	calmodulin-3	7,00E-65	99	27	149
atm3 E2	1	At4g18270	putative protein	3,00E-24	1	28	313
atm3 C4	1	At3g21020	unknown protein	0,94	239	29	310

atm3_H12	1	At5g44080	bZIP protein AtbZIP13			2,1	155	31	315	-2
atm1_E8	1	At3g15630	unknown protein			8,00E-39	2	32	107	2
atm3_H11	1	At3g61470	Lhca2 protein			2,00E-78	124	32	257	1
atm3_B7	1	At5g63040	putative protein			2,00E-30	246	34	366	3
atm5_E4	1	At1g78630	Hypothetical protein			3,00E-93	3	38	241	3
atm1_C11	1	At3g16950	dihydroliipoamide dehydrogenase [pd1			9,00E-16	3	38	570	3
atm4_B2	1	At1g04850	unknown protein			4,00E-06	411	40	400	3
atm2_A10	2	At3g57490	40S ribosomal protein S2 homolog			8,00E-56	168	42	276	3
atm2_A9		At3g57490	40S ribosomal protein S2 homolog			2,00E-70	168	42	276	3
atm1_E5	2	At4g34620	putative ribosomal protein S16			9,00E-36	3	42	113	3
atm1_E6		At4g34620	putative ribosomal protein S16			8,00E-36	3	42	113	3
atm4_B1	1	At3g12930	hypothetical protein			1,00E-84	3	46	238	3
atm5_F1	1	At2g41840	40S ribosomal protein S2			3,00E-37	184	48	285	1
atm2_C12	2	At1g25170				1,00E-34	585	51	469	-1
atm1_G1	3	At2g45180	putative proline-rich protein			1,00E-44	164	52	134	2
atm1_G2		At2g45180	putative proline-rich protein			1,00E-44	164	52	134	2
atm4_A1		At2g45180	putative proline-rich protein			1,00E-44	167	52	134	2
atm2_D11		At1g25170				4,00E-27	573	53	469	-2
atm4_C7	1	At5g14740	CARBONIC ANHYDRASE 2			2,00E-79	142	53	331	1
atm6_E11	1	At5g23750	putative protein			1,00E-04	220	55	202	1
atm6_A8		At3g20670	histone H2A, putative			5,00E-10	166	60	132	1
atm5_A2	1	At4g21960	peroxidase prx1			e-109	3	63	323	3
atm5_C9	1	At5g60910	MAD box containing protein NAP1-1 - like			2,00E-37	60	63	154	3
atm6_A9	1	At1g24070	glucosyltransferase, putative			1,00E-46	5	69	552	2
atm4_H9	1	At1g18210	hypothetical protein			1,00E-42	2	76	170	2
atm2_C7	3	At5g22430	unknown protein			8,00E-35	19	79	172	1
atm2_F4	1	At1g05680	putative indole-3-acetate beta-glucosyltransferase			e-100	1	80	453	1
atm2_G10	2	At5g21940	putative protein			1,00E-59	3	80	264	3
atm2_G9		At5g21940	putative protein			9,00E-54	3	80	264	3
atm1_A11	1	At3g24830	60S ribosomal protein, putative			3,00E-66	1	83	206	1
atm6_B7	1	At5g09810	ACTIN 2/7 (sp P53492)			e-130	2	85	377	2
atm4_A3	1	At1g70490	putative ADP-ribosylation factor 1			6,00E-49	1	86	181	1
atm3_F3	1	At3g55770	transcription factor L2			1,00E-53	2	86	199	2
atm1_A6	2	At5g38410	ribulose biphosphate carboxylase small chain 3b			3,00E-81	323	96	181	2
atm3_E3	1	At5g16710	valine-tRNA ligase-like protein			2,00E-81	3	97	1093	3
atm1_B3	2	At4g03280	putative component of cytochrome B6-F complex			9,00E-89	238	100	229	1

atm4 C1	1	A13g16240	delta tonoplast integral protein (delta-TIP)	3,00E-67	1	101	250	1
atm5 C12	1	A11g30630	coatamer-like protein, epsilon subunit	2,00E-85	1	107	292	1
atm4 F4	1	A11g76970		4,00E-92	1	113	387	1
atm4 D10	1	A13g60390	homeobox-leucine zipper protein HAI3	0,27	296	117	315	-3
atm6 D12	1	A11g10890	unknown protein	1,00E-06	3	118	592	3
atm6 G6	1	A13g50500	protein kinase SPK-2	3,00E-99	1	119	362	1
atm4 G8		A11g67090	hypothetical protein	1,00E-29	3	123	180	3
atm1 G12	1	A13g01980	unknown protein	3,00E-90	5	123	296	2
atm3 E5	1	A13g13800	hydrolase, putative	3,00E-38	14	125	282	2
atm5 H1	1	A14g32260	H+-transporting ATP synthase chain 9 - like protein	6,00E-26	1	125	219	1
atm1 D7	3	A14g05320	polyubiquitin (ubq10)	e-107	3	126	464	3
atm3 A4	1	A14g26970	putative aconitase	7,00E-43	108	133	907	3
atm2 C2	1	A12g35020	putative UDP-N-acetylglucosamine pyrophosphorylase	9,00E-66	107	134	502	2
atm1 C10	1	A14g08590	putative zinc finger protein	3,6	307	135	432	1
atm5 C7	1	A13g08580	adenylate translocator	6,00E-96	1	138	381	1
atm5 A3		A15g62700	tubulin beta-2/beta-3 chain (sp P29512)	6,00E-91	3	144	450	3
atm6 H10		A15g62700	tubulin beta-2/beta-3 chain (sp P29512)	e-102	3	144	450	3
atm1 F3	1	A13g51410	putative protein	2,00E-24	36	145	255	3
atm3 B5	1	A13g62530	putative protein	3,00E-63	103	150	342	1
atm1 F10	2	A15g16840	putative protein	1,00E-46	2	150	259	2
atm1 F11		A15g16840	putative protein	1,00E-46	2	150	259	2
atm1 D12	1	A15g24770	vegetative storage protein Vsp2	1,00E-64	2	150	265	2
atm3 F5	1	A11g69680	hypothetical protein	6,00E-14	1	152	186	1
atm1 G9	2	A12g29550	tubulin beta-7 chain	e-104	41	152	449	2
atm5 D11	1	A12g44720	unknown protein	2,00E-11	4	152	239	1
atm2 D4	1	A13g01500	carbonic anhydrase, chloroplast precursor	e-103	2	154	336	2
atm3 B2	1	A15g38420	ribulose biphosphate carboxylase small chain 2b	2,00E-08	1	157	181	1
atm6 C9	1	A11g28290	proline-rich protein, putative	2,2	511	162	359	1
atm3 A6	1	A11g67870	unknown protein	0,005	346	163	191	1
atm4 B8	1	A15g08680	H+-transporting ATP synthase beta chain (mitochondrial)	7,00E-91	1	164	559	1
atm2 E12	1	A11g62050	hypothetical protein	3,00E-69	1	167	605	1
atm2 F8	1	A15g23940	acyltransferase	3,00E-93	2	169	484	2
atm1 H2	1	A15g20720	chloroplast Cpm21 protein	3,00E-39	1	174	253	1
atm1 B2	1	A11g27580	hypothetical protein	5,00E-10	52	175	380	1
atm5 F10	1	A13g49850	MYB-like protein	6,1	503	175	295	2
atm5 G3	1	A11g12830	unknown protein	2,5	334	176	213	1

atm1_F6	1	At1g76010	unknown protein	6,00E-36	1	178	350	1
atm4_C4	1	At4g11320	cysteine proteinase-like protein	5,00E-74	2	178	371	2
atm3_F6	1	At5g37490	putative protein	1,00E-55	1	178	435	1
atm6_G1	1	At3g12290	hypothetical protein	8,00E-62	2	183	299	2
atm2_B2	1	At5g02240	putative protein	2,00E-29	1	184	376	1
atm5_A8	1	At5g05610	nucleic acid binding protein-like	2,00E-32	2	186	241	2
atm1_C1	2	At5g01530	chlorophyll a/b-binding protein CP29	2,00E-54	2	187	290	2
atm1_C3		At5g01530	chlorophyll a/b-binding protein CP29	1,00E-54	2	187	290	2
atm5_E10		At5g24780	vegetative storage protein Vsp1	1,00E-42	1	189	270	1
atm5_G7	1	At1g56340	hypothetical protein	1,00E-80	2	194	425	2
atm2_A11	1	At4g39280	phenylalanyl-trna synthetase - like protein	2,00E-52	31	197	428	1
atm3_B1	3	At5g62700	tubulin beta-2/beta-3 chain (sp P29512)	1,00E-92	1	197	450	1
atm1_D8		At4g05320	polyubiquitin (ubq10)	2,00E-99	3	202	464	3
atm1_E11	1	At3g47080	putative protein	9,00E-72	2	203	515	2
atm1_A2	1	At3g10410	putative serine carboxypeptidase precursor	3,00E-78	1	209	516	1
atm6_B10	1	At1g76930	extensin	0,37	510	213	373	-1
atm3_H8	1	At3g07340	unknown protein	3,00E-89	2	213	456	2
atm4_F9	1	At3g58660	putative protein	4,00E-40	3	213	446	3
atm5_D5	1	At3g12610	hypothetical protein	5,00E-80	2	231	372	2
atm3_H7	1	At2g30200	putative malonyl-CoA:Acyl carrier protein transacylase	2,00E-16	477	232	367	-1
atm4_C11	1	At3g50660	steroid 22-alpha-hydroxylase (DWF4)	1,00E-89	2	239	513	2
atm3_E11	1	At1g69870	putative peptide transporter	5,00E-80	1	243	644	1
atm5_E1	2	At3g20920	hypothetical protein	1,00E-65	3	245	365	3
atm5_E2		At3g20920	hypothetical protein	5,00E-65	3	245	365	3
atm2_B8	1	At1g11860	aminomethyltransferase-like precursor protein	1,00E-89	3	248	408	3
atm5_G1		At3g02470	S-adenosylmethionine decarboxylase	3,00E-53	3	248	366	3
atm3_D7	1	At5g47210	putative protein	4,00E-40	2	248	357	2
atm3_C7	1	At3g21670	nitrate transporter	7,00E-82	3	274	590	3
atm1_E10	1	At1g03900	unknown protein	0,23	2	276	585	2
atm4_D2	2	At3g21600	unknown protein	2,00E-32	2	289	374	2
atm4_D3		At3g21600	unknown protein	2,00E-32	2	289	374	2
atm5_F2	1	At1g09840	shaggy-like protein kinase, kappa	7,00E-77	1	290	421	1
atm6_A2	1	At3g54190	putative protein	1,00E-92	3	292	454	3
atm1_G3	1	At4g34110	poly(A)-binding protein	5,00E-86	2	292	629	2
atm6_E10	1	At5g08410	lipic acid synthase - like protein	2,00E-26	27	294	477	3
atm1_F4	2	At5g44190	putative protein	4	319	299	386	-2

atm1_F5		At1g44190	putative protein		4,1	319	299	386	-2
atm5_C10	1	At1g08510	acyl-(acyl carrier protein) thioesterase, putative		2,00E-60	1	304	412	1
atm5_B12	1	At3g02350	hypothetical protein		e-124	2	304	561	2
atm5_G9	1	At5g08570	pyruvate kinase		1,00E-90	3	304	510	3
atm2_G3	3	At3g02470	S-adenosylmethionine decarboxylase		2,00E-15	1	311	366	1
atm3_A3	1	At1g55530			2,2	2	312	351	2
atm4_A8	1	At1g26250	hypothetical protein		1,1	245	316	443	2
atm1_A1	1	At1g21750	putative protein disulfide isomerase precursor		4,00E-33	1	319	501	1
atm2_A3	1	At2g16570	amidophosphoribosyltransferase		8,00E-71	2	320	566	2
atm6_F7	1	At4g32940	gamma-VPE (vacuolar processing enzyme)		6,00E-95	2	322	494	2
atm4_A11	1	At1g52400	beta-glucosidase, putative		e-108	3	323	528	3
atm3_C1	1	At1g60200			8,00E-55	2	332	781	2
atm3_G3	1	At3g54220	SCARECROW1		7,00E-79	2	339	653	2
atm1_E9	1	At4g23040	putative protein		1,00E-67	2	339	577	2
atm2_G5	1	At2g26460	unknown protein		e-109	1	349	585	1
atm2_E4	2	At2g29650	putative Na ⁺ -dependent inorganic phosphate cotransporter		1,00E-81	3	350	512	3
atm2_E5		At2g29650	putative Na ⁺ -dependent inorganic phosphate cotransporter		4,00E-81	3	350	512	3
atm6_B12	1	At3g55940	phosphoinositide-specific phospholipase C - like protein		4,00E-50	761	353	584	-1
atm6_C7	1	At5g56030	HEAT SHOCK PROTEIN 81-2 (HSP81-2)(spP55737)		1,00E-64	2	355	699	2
atm4_A12	1	At5g57655	xylose isomerase		2,00E-58	3	355	472	3
atm5_H10	1	At3g09440	heat-shock protein (At-hsc70-3)		1,00E-68	2	364	649	2
atm4_E2	1	At3g19420	putative tyrosine phosphatase		e-112	3	369	611	3
atm5_A10	1	At3g13870	root hair defective 3		2,00E-96	1	380	802	1
atm5_E7	1	At5g35630	glutamate-ammonia ligase (EC 6.3.1.2) precursor,		4,00E-22	129	385	430	3
atm5_E8	1	At5g35630	glutamate-ammonia ligase (EC 6.3.1.2) precursor,		4,00E-22	129	385	430	3
atm4_H5	1	At2g27350	unknown protein		2,00E-53	60	392	522	3
atm5_D1	1	At1g05560	hypothetical protein		1,00E-61	2	404	519	2
atm6_G9	1	At4g38430	putative protein		1,00E-72	1	406	548	1
atm2_B6	1	At4g38770	extensin - like protein		3,00E-05	407	433	448	2
atm6_D2	1	At3g55980	putative protein		1,00E-66	3	436	586	3
atm2_C5	1	At3g53230	CDC48 - like protein		9,00E-86	5	441	815	2
atm3_G2	1	At2g45810	putative ATP-dependent RNA helicase		2,00E-32	1	457	528	1
atm3_F4	1	At5g51150	putative protein		1,00E-18	2	470	531	2
atm4_E12	1	At5g50310	putative protein		1,00E-40	250	477	596	1
atm5_E11	1	At1g08540	plastid RNA polymerase sigma-subunit (SIG1)		1,00E-22	2	481	572	2
atm3_B3	1	At2g01570	putative RGA1, gibberellin response modulation protein		5,00E-48	1	488	587	1

atm3 B10	1	At4g04310	putative transposon protein	8,5	574	529	1011	-2
atm1 C12	1	At3g48670	putative protein	6,00E-49	1	541	644	1
atm6 F4	1	At5g02500	dnaK-type molecular chaperone hsc70.1	1,00E-46	1	548	651	1
atm2 A7	1	At5g63410	putative protein	8,00E-32	2	557	637	2
atm6 C10	1	At5g17920	5-methyltetrahydropteroyltriglutamate--homocysteine	1,00E-66	1	559	765	1
atm6 B11	1	At1g51570	anthranilate phosphoribosyltransferase, putative	e-104	3	574	776	3
atm3 F7	1	At3g45140	lipoygenase AtLOX2	e-108	3	580	870	3
atm2 D8	2	At3g16000	myosin heavy chain-like protein	9,00E-51	137	596	724	2
atm2 E1		At3g16000	myosin heavy chain-like protein	9,00E-46	103	596	724	1
atm1 A3	1	At4g24190	HSP90-like protein	3,00E-52	140	600	823	2
atm3 D5	1	At1g29350	unknown protein	3,00E-77	3	614	858	3
atm1 E3	7	At2g18790	phytochrome B	e-110	128	619	1172	2
atm2 B11		At2g18790	phytochrome B	e-100	81	619	1172	3
atm2 D9		At2g18790	phytochrome B	1,00E-70	85	619	1172	1
atm3 A2		At2g18790	phytochrome B	8,00E-53	146	619	1172	2
atm3 H1		At2g18790	phytochrome B	3,00E-72	140	619	1172	2
atm4 D9		At2g18790	phytochrome B	e-110	110	619	1172	2
atm5 H8		At2g18790	phytochrome B	e-100	128	619	1172	2
atm5 B2	1	At4g16250	phytochrome D	5,00E-66	123	623	1164	3
atm3 C6	1	At1g07110	hypothetical protein	7,00E-45	112	656	744	1
atm5 A4	1	At1g15690	hypothetical protein	1,00E-47	2	679	770	2
atm1 A4	1	At5g05170	cellulose synthase catalytic subunit (gb/AAC39336.1)	e-115	2	772	1065	2
atm1 G5	1	At3g26240	hypothetical protein	1,00E-88	3	775	922	3
atm6 G12	1	At3g28770	hypothetical protein	4,00E-09	176	919	2081	2
atm4 G4	1	At3g14570	hypothetical protein	3,00E-48	2	1171	1973	2

Anhang 8.3

Schematische Darstellung der ersten Zeilen der HTML-Tabelle 1 (Proteinexpressions-Unterbibliothek):
http://gabi.rz-berlin.mpg.de/projects/Arabidopsis_Proteomics/ArabidopsisExpressionCloneSet.shtml

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
sequence name	GenBank accNo	cluster number	cluster size	cluster and Blast comparison	AGIs in cluster	first stopcodon position [aa]	BLAST Hit	putative genefunction	e-value	start query [nt]	start subject [aa]	length subject [aa]	direction	frame
201a01.p1	CK121741	5504	1	+	At3g20530	56	At3g20530	protein kinase, putative	3e-84	245	2	386	forward	2
201a04.p1	CK121740	5503	1	+	At1g67400 At3g43400	-	At1g67400	unknown protein	e-120	118	61	328	forward	1
201a05.p1	CK121742	5505	1	+	At2g33540	145	At2g33540	CTD phosphatase-like 3 (CPL3)	6e-77	19	1104	1241	forward	1
201a07.p1	CK121743	5506	1	+	At1g68530	-	At1g68530	very-long-chain fatty acid condensing enzyme (CUT1)	e-152	4	158	497	forward	1
201a08.p1	CK121744	118	1	+	At1g74920	66	At1g74920	betaine aldehyde dehydrogenase like protein	9e-34	16	442	501	forward	1
201a09.p1	CK121745	5508	1	+	At5g66170	145	At5g66170	senescence-associated protein sen1-like protein	2e-73	25	1	136	forward	1
201a10.p1	CK121746	5509	1	+	At1g02205	218	At1g02205	CER1 protein	e-117	16	414	625	forward	1
201a13.p1	CK121747	2471	3	+	At2g46020	-	At2g46020	putative SNF2 subfamily transcriptional activator	e-147	4	941	1245	forward	1
201a16.p1	CK121748	5511	1	+	At1g71220	101	At1g71220	putative UDP-glucose: glycoprotein glucosyltransferase	2e-50	22	1582	1674	forward	1
201a19.p1	CK121749	5513	1	+	At2g37470	99	At2g37470	putative histone H2B	4e-49	140	31	138	forward	2

Anhang 8.4:

Schematische Darstellung der ersten Zeilen der HTML-Tabelle 2 (Uniklonset):

http://gabi.rz-berlin.mpg.de/projects/Arabidopsis_Proteomics/ArabidopsisExpressionUniCloneSet.shtml

Das Format wurde an DIN A 4 angepaßt, die Inhalte sind identisch.

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
unigene name	sequence name	GenBank accNo	cluster number	Blast cluster and comparison	AGIs in cluster	first stopcodon position	Results from BLAST against MIPS annotated protein sequences		e-value	start query	start subject	length subject	Results from BLAST against TIGR5 annotated protein sequences		e-value
							BLAST-Hit	putative genefunction					BLAST-Hit	putative genefunction	
311_A01	A01201a04.p1	CK121740	5503	+	At1g67400	-	At1g67400	unknown protein	e-120	118	61	328	At1g67400	phagocytosis and cell motility protein ELMO1-related (Mus musculus)	0.0
311_A03	A03201a05.p1	CK121742	5505	+	At2g33540	145	At2g33540	CTD phosphatase-like 3 (CPL3)	6e-77	19	1104	1241	At2g33540	CTD phosphatase-like protein 3 (CPL3) identical to thaliana GI:22212705; contains Pfam profile PF03031; NLI interacting factor	0.0
311_A05	A05201a07.p1	CK121743	5506	+	At1g68530	-	At1g68530	very-long-chain fatty acid condensing enzyme (CUT1)	e-152	4	158	497	At1g68530	very-long-chain fatty acid condensing enzyme (CUT1) identical to very-long-chain fatty acid for cuticular wax biosynthesis and pollen fertility; Millar, A. A., et al., Plant Cell (1999)	0.0
311_A07	A07201a09.p1	CK121745	5508	+	At5g66170	145	At5g66170	senescence-associated protein sen1-like protein	2e-73	25	1	136	At5g66170	senescence-associated family protein. contains similarity to ketoconazole-resistant protein GI:928938 and senescence-associated protein GI:1046268 from (Arabidopsis thaliana)	0.0
311_A09	A09201a10.p1	CK121746	5509	+	At1g02205	218	At1g02205	CER1 protein	e-117	16	414	625	At1g02205	CER1 protein identical to maize gl1 homolog (glossy1 locus) GI:1209703 and CER1 GI:1199467 from (Arabidopsis thaliana)	0.0
311_A11	A11201a16.p1	CK121748	5511	+	At1g71220	101	At1g71220	putative UDP-glucose: glycoprotein glucosyltransferase	2e-50	22	1582	1674	At1g71220	UDP-glucose:glycoprotein glucosyltransferase. putative similar to UDP-glucose:glycoprotein glucosyltransferase precursor GB:Q09332 (SPQ09332) from Drosophila melanogaster. (gi:7670746) and (gi:11346464) from Homo sapiens citrate synthase, mitochondrial, putative strong similarity to SP120115 Citrate synthase, mitochondrial precursor (Arabidopsis thaliana); contains Pfam profile PF02085: Citrate synthase	e-160
311_A13	A13201a23.p1	CK121751	5515	+	At2g44350	-	At2g44350	citrate synthase	e-125	19	42	473	At2g44350	SECI14 cytosolic factor family protein / phosphoglycerate transfer family protein similar to polyphosphoinositide binding protein Ssh2p (GI:2739046) (Glycine max); contains Pfam PF00650: CRAL/TRIO domain; contains Pfam PF03765: CRAL/TRIO, N-terminus	0.0
311_A15	A15201a01.p1	CK121752	155	+	At3g51670	235	At3g51670	putative protein	e-128	22	183	409	At3g51670		0.0

Anhang

Anhang 8.5:

Ermittlung der durchschnittlichen Proteinkonzentration von drei 96er Platten mittels Bradford-Test. Ausgehend von den Platten 311-313 wurde jeweils von der Quadranten A2 die Konzentration [$\mu\text{g/ml}$] bestimmt. n.b.= nicht bestimmbar

311_A2 [$\mu\text{g/ml}$]												
	1	2	3	4	5	6	7	8	9	10	11	12
A	98	103	185	50,2	14,3	35,8	22,7	81,2	72,9	68,1	21,5	40,6
B	112	13,1	135	40,6	7,17	172	58,5	226	43	40,6	121	69,3
C	216	227	154	102	141	47,8	141	20,3	88,4	115	57,3	33,5
D	39,4	44,2	14,3	9,56	140	103	160	117	2,39	16,7	200	41,8
E	51,4	117	39,4	98	105	64,5	9,56	198	25,1	50,2	14,3	84,8
F	75,3	28,7	141	63,3	115	47,8	161	178	40,6	93,2	8,36	92
G	20,3	n.b.	1,19	47,8	41,8	51,4	84,8	n.b.	n.b.	n.b.	26,3	n.b.
H	59,7	28,7	1,19	119	23,9	72,9	3,58	34,6	71,7	98	21,5	60,9
312_A2 [$\mu\text{g/ml}$]												
	1	2	3	4	5	6	7	8	9	10	11	12
A	278	51,4	71,7	170	104	254	9,56	118	15,5	172	165	64,5
B	130	129	111	254	71,7	39,4	76,5	225	46,6	168	58,5	172
C	55	208	231	106	226	184	145	148	220	74,1	111	198
D	111	155	170	190	26,3	274	191	71,7	10,8	32,3	50,2	37
E	151	195	82,4	157	161	214	34,6	180	162	137	135	45,4
F	57,3	111	219	166	65,7	62,1	270	127	87,2	n.b.	159	31,1
G	225	174	32,3	35,8	8,36	121	57,3	124	194	162	164	173
H	81,2	128	148	179	133	122	108	124	186	155	137	51,4
313_A2 [$\mu\text{g/ml}$]												
	1	2	3	4	5	6	7	8	9	10	11	12
A	1,19	153	32,3	28,7	168	46,6	87,2	241	179	71,7	293	116
B	200	286	123	213	151	95,6	185	56,2	166	188	200	17,9
C	145	104	33,5	82,4	167	207	104	114	75,3	8,36	68,1	197
D	146	213	n.b.	89,6	177	136	102	56,2	121	19,1	75,3	52,6
E	253	148	43	137	280	17,9	47,8	133	147	8,36	110	103
F	200	254	63,3	88,4	140	165	n.b.	134	164	110	146	96,8
G	49	205	208	135	238	106	57,3	157	60,9	102	96,8	108
H	n.b.	72,9	56,2	145	151	289	33,5	81,2	88,4	76,5	125	59,7