

Apoplast Fluid Proteins Control									
Id-No. Protein	Accession No.	pI:	MW (kDa)	Seq. Coverage %	Mascot MS/MS Score	No. of MS/MS Peptides	MS/MS Peptide sequence	Range	Protein Identification
56-8 60-20	GRMZM2G076348_P01	6.34	28.60	10.60	138.14	3	K.AGYFVVVPDFLK.G R.AYVSGAASSSR.A R.AVVLASDVFGYEAPLLR.Q	59-69 70-86 95-105	Endo1,3;1,4 β -D-glucanase
57-20	GRMZM2G161335	5.02	50.00	2.40	59.81	1	R.TDLTDLVDLIK.S	450-460	DIMBOA-UDP glucosyltransferase BX9
52-3 53-17 59-16	GRMZM2G016890	6.24	64.20	24.20	742.70	15	R.YGIVYVDR.N R.FSISWPR.I K.EGGINPDGIK.Y K.YGGFLDK.S K.SIVEDYTYFAK.V K.VCFDNFGDKVK.N R.IGLAFDVMGR.V R.VPYGTSFLDK.Q R.VPYGTSFLDKQAEER.S R.GDYPFSMR.S K.LAGSYNMLGLNYYTSR.F K.NKYGNPPIYITENGIGDVDTK.E K.YGNPPIYITENGIGDVDTK.E K.ETPLPMEAALNDYK.R K.RLDYIQR.H	53-60 151-157 165-174 207-213 217-227 228-238 310-319 320-329 320-334 350-357 375-390 449-469 451-469 470-483 484-490	β -Glucosidase1 GDIMBOA β -glucosidase
52-11/12	GRMZM2G136895	6.65	38.60	8.0	153.06	3	R.AIGEVVSNEAR.A R.GQETPGEDPLLTSK.Y R.AVTNNLVTLMR.L	142-152 180-193 360-370	β -D-Xylosidase
51-10/11	GRMZM2G115065	5.64	22.90	4.70	71.57	1	R.IGEATALEVR.A	135-144	Glycosyl hydrolase family
52-6	GRMZM2G120962	6.08	63.30	14.20	413.90	8	R.FSISWSR.I R.ILPNGTLEGGINPYGIK.Y K.YGGFLDER.I R.AHAEAVDLYNK.Y R.IGLAFDVMGR.V K.SAFTDQQAEQR.S R.GDYPFSMR.S K.DLLMIMK.N	144-150 151-167 200-207 300-309 315-325 314-348 341-348 433-439	Exo- β -glucanase

57-19	GRMZM2G453805	3.89	30.30	4.40	68.06	1	R.FNDVQNNYSSQVK.G	280-292	Chitinase
57-16	GRMZM2G132093	4.95	14.00	14.80	120.76	2	R.NQAVVDENVEK.L K.VLEVYEAR.L	35-45 49-56	Glutathione S-transferase
57-9	GRMZM2G116273	5.34	23.80	29.00	224.16	4	R.CATALEEAGSDYEIVPINFATAEHK.S R.NPFGQVPALQDGDLYLFESR.A K.VLEVYEAR.L K.VAALMKPSA	18-42 50-69 142-149 206-214	Glutathione S-transferase
52-10/11 53-11	GRMZM2G135108	6.65	38.60	21.70	423.62	6	R.TCPTAETIVQQTVAAAF.R.N R.DSVVLSSGGLGYQVPAGR.R K.AYAFLLK.S K.YYVGLTNNLGLFK.S K.ALVDSEFVR.S K.MGQIEVLTGTQGEIR.R	35-52 132-148 233-239 269-281 294-301 317-331	Peroxidase
53-20/22	GRMZM2G044049	9.08	39.60	2.70	53.86	1	R.DAVFFLSGSK.V	176-185	Putative class III secretory peroxidase
54-11	GRMZM2G085967	8.84	35.40	17.10	264.25	6	K.AHIPHAPDVASTLLR.T R.GGPDDADPSLDPLYAAK.L R.GGPDDADPSLDPLYAAK.L R.TFDLSYYR.G R.GLFQSDAALITDAASK.A R.GLFQSDAALITDAASK.A	46-60 211-227 244-260 251-258 265-280 298-313	Peroxidase 39 precursor
54-13	GRMZM2G088765	4.30	36.00	8.60 %	231.71	3	K.QVLVDAVQSDTR.I R.IFASLIR.L R.GILNSDQELK.S	52-63 64-70 272-281	Peroxidase
54-16	GRMZM2G048474	6.20	38.10	5.20	113.56	1	K.EAPVNIGLAAFDVL EEIK.A	96-113	Putative class III secretory peroxidase
54-17 56-7 57-17 59-14/15	GRMZM2G108207	6.25	37.50	8.70	107.52	2	R.DAVVASGGPFFEVLGR.R R.FALNQAAFFDQFAR.S	144-160 293-306	Anionic Peroxidase
52-16/17 54-19/21	GRMZM2G168073	5.50	27.40	6.50	57.09	1	R.GFEVIDAAK.A R.VLFTSDASLLTSPATAK.L	37-45 200-216	Putative class III secretory peroxidase
56-4/5	GRMZM2G133475	9.70	33.50	24.70	275.57	6	R.SGVNSAVRQEPR.V R.GFVVVNSIK.A R.DGVVALGGPSWTVLLGR.R R.DGVVALGGPSWTVLLGRR.D R.DSTASFPQTSDLPPPTSSLR.Q R.SFASSTSAFNATAMVK.M	49-60 103-111 134-150 134-151 152-172 279-297	Peroxidase 66 precursor

56-7	GRMZM2G108219	5.61	38.70	8.80	190.37	3	R.DAVVASGGPFFEVPLGR.R R.DAVVASGGPFFEVPLGRR.D R.FALNQAFFDQFAR.S	147-163 147-164 299-312	Peroxidase precursor
56-10	GRMZM2G427815	6.22	33.20	13.80	110.12	3	K.SAVNAAVQKENR.M R.DSVVALGGPSWTVPLGR.R K.MGNLSPLTGSQQQIR.L	42-53 131-147 299-313	Peroxidase
58-13	GRMZM2G126261	5.36	26.40	6.70	67.71	1	R.DGVVALGGPSWTVLLGR.R	67-83	Peroxidase 66 precursor
54-9	GRMZM2G103342	9.66	38.00	19.60	330.78	5	R.VVSCADIVALAAR.E R.DGLAPASNAAVLAALPPPTSK.V K.VPTLLSFLAK.I R.LFPTQDPTLNK.F R.TPNAFDNKYYVDLLNR.E	132-144 163-183 184-193 222-232 257-272	Peroxidase 12
56-12/13 58-9/11	GRMZM2G108153	5.25	35.50	8.60	117.82	2	R.SSVDAALQQNVR.L R.DAVSLSGGPSFTVPLGR.L R.CSSFGDVAGPATDDVTR.C	58-69 141-157 211-227	Peroxidase
54-6/7	GRMZM2G025441	10.4 6	33.40	24.00	433.63	5	K.AAVTAAVAQEAR.M R.DSVVALGGPSWR.V R.TDLVALSGAHTIGLAQCK.N R.GLLHSDQQLFNGGATDGLVR.T R.MGNISPLTGTQQQIR.R	45-66 132-143 185-202 261-280 300-314	Peroxidase
54-14/15	AC196475.3_FGP004	5.41	39.50	6.00	122.09	2	K.NAIELGLLEVLQK.E R.LLASVDVVR.C	35-47 85-93	O-Methyltransferase
51-1/2 54-1/2	GRMZM2G149751-P01	5.45	84.40	14.90	553.31	9	K.FALESFWDGK.S R.GTQTLGLVTSAGFPAGK.Y K.YLFAGVVDGR.N K.SWLAFAAQK.V K.VVEVDALAK.A K.ALAGQKDEAYFAANAAAQASR.K K.KLNLPIPTTTIGSFQTVELR.R K.LNLPIPTTTIGSFQTVELR.R K.YGAGIGPGVYDIHSPR.I	19-28 271-287 288-297 350-358 359-367 368-388 427-448 428-448 690-705	Putative homocysteine methyltransferase, methionine synthase
52-9	GRMZM2G149751-P02	8.89	60.00	10.30	355.07	5	R.QNLEPLFEQYINNLR.R K.ADTLTDEINFLR.A R.NLDLDSIIAEVK.A K.AQYEEIAQR.S K.YEELQITAGR.H	208-222 288-299 327-338 339-347 360-369	Putative homocysteine methyltransferase, methionine synthase

54-12	GRMZM2G149751-P05	5.39	85.90	6.10	234.02	3	K.TLTSLSSVTAYGFDLVR.G K.YLFAGVVDGR.N K.LNLPILPTTTIGSFQTVELR.R	254-270 288-297 428-448	Putative homocysteine methyltransferase, methionine synthase
51-4	GRMZM2G165747	5.81	84.40	11.50	382.00	7	K.FALESFWDGK.S K.YLFAGVVDGR.N K.SWLAFAAQK.V K.ALAGQKDEAYFAANAAAQASR.R K.KLNLPVLPTTTIGSFQTVELR.R K.LNLPVLPTTTIGSFQTVELR.R K.YGAGIGPGVYDIHSPR	19-28 287-296 349-357 367-387 426-447 427-447 689-704	Putative homocysteine methyltransferase, methionine synthase
53-8	GRMZM2G067225	6.60	53.00	22.40	596.09	8	K.DVPGSYGLPLVGAVR.D R.DRLDFYYFQQQDK.Y R.SNFSSLLATVEAELAK.G K.QALDTAEGLGLSR.E K.VLFPGLLANVASGGEK.L K.VTLAAVER.M R.VFGDTAGDFVPDR.F K.ELLGTSVIFTGVTK.A	14-28 29-41 146-161 253-265 286-301 321-328 387-399 461-474	Cytochrome P450
Apoplast Fluid Proteins BOA									
Protein-Id Spot No.- Protein No.	Accession No.	pI:	MW (kDa)	Seq. Coverage %	Mascot MS/MS Score	No. of MS/MS Peptides	MS/MS Peptide sequence	Range	Protein Identification
68-6 69-16 72-11	GRMZM2G076348	6.34	28.60	15.20	281.12	4	R.AYVSGAASSSR.A R.AVVLASDVFGYEAPLLR.Q K.AGYFVVVPDFLK.G K.TAETALAYMVSWFNK.H	59-69 70-86 95-106 247-261	Endo1,3;1,4 β-D- glucanase
65-12	GRMZM2G111143	5.72	40.60	5.80	86.89	2	R.TFETYVFSLFDENQKPGPVAER.N R.NFGIFNTDLTPK.Y	312-332 334-345	Glucan endo-1,3- beta-glucosidase precursor

64-5 65-10	GRMZM2G016890	6.25	64.20	14.70	490.68	8	R.FSISWPR.I K.EGGINPDGIK.Y K.YGGFLDK.S K.SIVEDYTYFAK.V R.VPYGTSFLDK.Q R.GDYPFSMR.S R.IGLAFDVMGR.V K.LAGSYNMLGLNYYTSR.F K.ETPLPMEALNDYK.R	151-157 165-174 207-213 217-227 310-319 320-329 350-357 375-390 470-483	β-Glucosidase1 GDIMBOA β- glucosidase
64-14	GRMZM2G017186	9.96	32.60	8.7	94.95	2	R.DYYIGSLLSGGGSVPR.K R.IGAATALEVR.A	76-91 140-149	Exohydrolase II
64-7 65-13	GRMZM2G120962	6.08	63.30	9.0	234.34	5	R.FSISWSR.I R.ILPNGTLEGGINPYGIK.Y R.GDYPFSMR.S K.YGGFLDER.I R.IGLAFDVMGR.V	144-150 151-167 200-207 300-309 341-348	Exo-β -glucanase
64-11	GRMZM2G136895	5.55	47.50	8.0	148.94	3	R.AIGEVVSNEAR.A R.GQETPGEDPLLTSK.Y R.AVTNNLVTLMR.L	142-152 180-193 360-370	β-D-Gylosidase
69-16/17	GRMZM2G453805	3.89	30.30	4.4	101.09	1	R.FNDVQNNYSSQVK.G	280-292	Chitinase glucosyl hydrolase
69-10/11	GRMZM2G116273	5.34	23.80	17.30	189.34	3	R.NPFGQVPALQDGDLYLFESR.A K.VLEVYEAR.L K.VAALMKPSA.	50-69 142-149 206-214	Glutathione S- transferase
70-12/13 69-7	GRMZM2G132093	5.73	24.60	20.60	259.98	4	K.VYGWAISPFVSR.A K.VPVLEDGDLTLFESR.A R.NQAVVDENVEK.L K.VLEVYEAR.L	8-19 57-71 130-140 144-151	Glutathione S- transferase
65-11	GRMZM2G135108	6.65	38.60	13.90	212.23	4	R.TCPTAETIVQQTVAAAF.R.N R.DSVVLSGGLGYQVPAGR.R K.AYAFLLK.S K.ALVDSEFVR.S	35-52 132-148 233-239 294-301	Peroxidase
67-5/6	GRMZM2G025441	10.46	33.40	16.5	214.5	4	K.AAVTAAVAQEAR.M R.GFGVVDNIK.A R.DSVVALGGPSWR.V R.GLLHSDQQLFNGGATDGLVR.T	45-56 101-109 132-143 261-280	Peroxidase
66-11/12	GRMZM2G085967	7.71	30.30	17.90	177.76	3	R.DSVGVIGPFWVSVPTGR.R R.GGPDDADPSLDPLYAAK.L R.GLFQSDAALITDAASK.A	80-96 163-179 217-232	Peroxidase

67-10 68-10	GRMZM2G108207	6.25	37.50	8.70	191.78	2	R.DAVVASGGPFFEVLGR.R R.FALNQAAFFDQFAR.S	144-160 293-306	Peroxidase
67-11 70-15/16	GRMZM2G126261	5.41	39.50	6.70	90.57	1	R.DGVVALGGPSWTVLLGR.R	67-83	Peroxidase
68-14/15	GRMZM2G427815	6.22	33.40	5.60	83.02	2	K.SAVNAAVQK.E R.GFDVIANIK.A	42-50 100-108	Peroxidase
66-12/13	GRMZM2G088765	4.30	36.00	7.70	123.13	3	R.IFASLIR.L R.GFGVVDAK.A R.GILNSDQELK.S	64-70 108-116 272-281	Peroxidase
67-9	AC197758.3_FGP004	6.87	34.70	11.40	146.44	1	R.GFEVIDAVK.S R.DSVVILGGPTWDVK.V K.DMVALSGAHTIGQAR.C	112-120 143-156 197-211	Peroxidase
67-11 68-8 71-9	GRMZM2G133475	9.70	33.50	12.80	193.51	3	R.GFVVVNSIK.A R.DGVVALGGPSWTVLLGR.R K.MGNLSPQTGTQGQIR.R	103-111 134-150 298-312	Peroxidase
67-14/17	GRMZM2G070603	9.11	35.30	4.80	60.90	1	R.GLFQSDAALLADATTR.E	270-285	Peroxidase
68-12	GRMZM2G405459	9.77	33.10	14.00	132.06	2	R.DGVNLLSGPTWAVQLGR.R R.TASQSAANSNLPSPSSSAAALVSAFA SK.G	130-146 151-178	Peroxidase
66-8/9	GRMZM2G103342	9.66	38.00	14.10	304.56	5	R.YPPLAPGLSFDFYK.K R.EFLASAVR.Q R.QNVGLAAALIR.L K.VPTLLSFLAK.I K.YYVDLLNR.E	31-44 56-63 64-74 184-193 265-272	Peroxidase
68-13/14	GRMZM2G108153	5.25	35.50	8.60	104.29	2	R.SSVDAALQQNVR.L R.DAVSLSGGPSFTVPLGR.L	58-69 141-157	Peroxidase
66-14/16 67-12/14	AC196475.3_FGP004	5.41	39.50	3.60	90.57	1	K.NAIELGLLEVQLK.E	2	O-Methyltransferase
63-3 64-7/8 66-7/9	GRMZM2G149751-P01	5.45	84.40	13.30	433.25	7	K.FALESFWDGK.S K.WFDTNYHFIVPELGPNTK.F R.GTQTLGLVTSAGFPAGK.Y K.YLFAGVVDGR.N K.LNLPILPTTTIGSFPQTVELR.R K.YGAGIGPGVYDIHSPR.I R.IPSAEEIADR.I	19-28 112-129 271-287 288-297 428-448 690-705 706-715	Putative methionine synthase
67-10	GRMZM2G149751-P02	5.45	49.70	6.31	151.09	3	K.FALESFWDGK.S R.GTQTLGLVTSAGFPAGK.Y K.YLFAGVVDGR.N	19-28 271-287 288-297	Putative methionine synthase

63-2	GRMZM2G149751-P05	5.39	85.90	17.30	516.71	9	K.FALESFWDGK.S K.WFDTNYHFIVPELGPNTK.F R.GTQTLGLVTSAGFPAGK.Y K.YLFAGVVDGR.N K.VVEVDALAK.A K.ALAGQKDEAYFAANAAQASR.K K.LNLPILPTTTIGSFPQTVELR.R K.YGAGIGPGVYDIHSPR.I R.IPSAEEIADRIDK.M	19-28 112-129 271-287 288-297 359-367 368-388 428-448 690-705 706-718	Putative methionine synthase
63-6	GRMZM2G112149	5.78	84.60	7.5	234.83	4	K.FALESFWDGK.S K.YLFAGVVDGR.N K.LNLPVLPTTTIGSFPQTVELR.R K.YGAGIGPGVYDIHSPR.I	19-28 287-296 427-447 689-704	Methionine synthase
65-9	GRMZM2G067225	6.60	53.00	18.00	342.00	6	K.DVPGSYGLPLVGAVR.D R.SNFSSLLATVEAELAK.G K.QALDTAEGLGLSR.E K.VLFPGLLANVASGGEK.L K.DLLVESHDAVFQVR.K R.VFGDTAGDFVPDR.F	14-28 146-161 253-265 286-301 356-369 387-399	Cytochrom P450
Cell wall salt extract proteins, control									
Id-No. Protein	Accession No.	pI:	MW (kDa)	Seq. Coverage %	Mascot MS/MS Score	No. of MS/MS Peptides	MS/MS Peptide sequence	Range	Protein Identification
75-11/14	GRMZM2G115065	5.64	22.90	4.7	77.61	1	R.IGEATALEVR.A	135-144	Glycosyl hydrolase
81-12 80-11 79-30 76-18	GRMZM2G076348	6.34	28.60	4.5	60.02	6	R.AYVSGAASSSR.A R.AVVLASDVFGYEAPLLR.Q K.AGYFVVVPDFLK.G K.AVCLSHPYSVTADDMK.E K.AAEDAKPLFAALK.K K.IFQGVVEHGFACR.Y	59-69 70-26 95-106 128-140 169-184 225-236	Endo1,3;1,4 β-D-glucanase
80-28	GRMZM2G004699	6.20	34.10	5.7	92.70	2	R.IYLWFDPTK.E R.DLDAAQYR.R	140-148 255-262	Xyloglucan-endo-transglycosylase

81-34	GRMZM2G409642	8.65	45.30	3.2	65.88	1	R.ILTTNLWSAELSK.L	134-146	UPD-glucose-6-dehydrogenase
77-7 78-26	GRMZM2G118003	9.37	56.40	25.70	655.59	11	K.GANWLGLSR.A K.GFVFGTATSAYQVEGAASTNGR.G K.SLNFDAYR.F R.FSISWSR.I K.YGGWLSAK.M K.MADLFTDYADFCFK.T R.IVALLGYDTGSNPPQR.C K.GSADYIGINEYTSSYMK.G R.SYIGQLK.K K.FGIVYVDFNTLER.H K.ASAYWFR.D	28-37 43-64 104-111 112-118 166-173 174-187 204-219 330-346 437-443 474-486 490-496	β-Glucosidase
76-9/12	GRMZM2G147687	7.12	66.90	9.30	299.64	4	R.IGEATALEVR.A R.GFVISDWEGIDR.I R.YTEFIDDLTTQVQNK.V K.FTMGLFENPYPDSSLAGELGK.Q	149-158 301-312 342-356 375-395	Glycosyl hydrolase
82-6 83-25/27	GRMZM2G175134	9.01	21.40	22.90	261.28	4	R.DLFGPGALER.A K.LLDIYEQR.L R.LGEEAFLAGGK.F K.FTLADLSHLPNADR.L	27-36 110-117 118-128 129-142	Glutathione S-transferase
82-12 83-17/26	GRMZM2G096247	7.87	25.80	15	195.18	3	R.YVCTQFPNDGNK.S K.SLYGSGALER.A K.QVLDVYDEILSR.N	75-86 87-96 148-159	Glutathione S-transferase
82-20	GRMZM2G126763	7.86	20.20	12.40	98.20	2	K.SLYGSGALER.A K.QVLDVYDEILSK.N	38-47 99-110	Glutathione S-transferase
82-10/11	GRMZM2G126781	9.01	21.40	17.60	207.40	4	K.LRDPTGQVTFK.H R.YLCTQFPDDGYK.K R.YLCTQFPDDGYKK.L K.LYGTGSLER.A	50-60 75-86 75-87 88-96	Glutathione S-transferase
76-17 77-18/19 80-1/2	GRMZM2G108207	6.25	37.50	31.30	645.21	9	R.DIGIAAGLIR.I K.VSCADITTLATR.D R.DAVVASGGPFFEVLGR.R R.SLDTADLVALSGAHTVGR.G K.DASAAQVLDVR.T R.TPNAFDNK.Y R.TPNAFDNKYYFDLIAK.Q K.SDQGLINDQTTK.R R.FALNQAAFFDQFAR.S	68-77 132-143 144-160 193-210 244-254 255-262 255-270 276-287 293-306	Peroxidase

77-19/20 78-30/31	GRMZM2G135108	6.65	38.60	5	80.05	1	R.TCPTAETIVQQTVAAAF.R.N	35-52	Peroxidase
77-20/22	GRMZM2G044049	9.08	39.60	3.5	65.62	1	K.SDAALLTSTETAR.M	312-324	Peroxidase
77-21/25	GRMZM2G168073	5.50	27.40	3.5	55.64	1	R.GFEVIDAAK.A	37-45	Peroxidase
78-4 79-25/26	GRMZM2G394500	8.09	38.00	40.40	700.38	9	K.TAPINIGLAAFEVIDEIK.A R.CPGTVSCADIVVYAAR.D R.DASSLLSNGHVHFAAPAGR.L R.DLPDSTFTVSELIR.N R.LSAPPAQIVPAYR.N K.CAAAAGGADDPVVANNVRDEDPR.A R.AVAAAFPSFLGK.L R.DFLDNSYYHNNLAR.I R.IVTFNSDWQLLTEK.E	100-117 124-139 140-158 172-185 218-230 237-259 260-271 277-290 291-304	Peroxidase
78-5 79-13	GRMZM2G085967	8.84	35.40	28.40	545.91	7	K.EGFYDYSCPQAEK.I K.AHIPHAPDVASTLLR.T R.GFGFIDR.I K.ECPGVVSCADIVALAAR.D R.DSVGVIGGPFWSVPTGR.R R.TFDLSYYR.G R.GLFQSDAALITDAASK.A	26-38 46-60 97-103 111-127 128-144 251-258 265-280	Peroxidase
78-21/22 80-19/21 81-25/26 82-21/22 84-29	GRMZM2G055487	6.80	30.80	10.90	163.25	2	R.ALSVAPSLAGPLLR.M R.GFGFIER.V K.GPFWAVPLGR.R R.TFDLGYYANVAK.R	4-17 54-60 92-101 208-219	Peroxidase
79-1	GRMZM2G025441	10.46	33.40	37.10	747.02	8	K.AAVTAAVAQEAR.M R.GFGVVDNIK.A K.AQVEAVCPGVVSCADILAVAAR.D R.DSVVALGGPSWR.V R.TDLVALSGAHTIGLAQCK.N R.GLLHSDQQLFNGGATDGLVR.T R.RFSGDFAAAMIR.M R.FSGDFAAAMIR.M R.MGNISPLTGTQGQIR.R	45-56 101-109 110-131 132-143 185-202 261-280 288-299 289-299 300-299	Peroxidase

75-6 78-3 79-2	GRMZM2G103342	9.66	38.00	33.10	739.41	11	R.YPPLAPGLSFDFYK.K R.QNVGLAAALIR.L R.VVSCADIVALAAR.E R.DGLAPASNAAVLAALPPPTSK.V K.VPTLLSFLAK.I K.FFAGQLYR.T R.TPNAFDNK.Y R.TPNAFDNKYYVDLLNR.E K.YYVDLLNR.E K.MGQVNVLTGSQGQVR.A R.ESVALGGGPAYK.L	31-44 64-74 132-144 145-156 163-183 184-193 233-240 257-264 257-272 265-272 313-327	Peroxidase
91-16 92-2	GRMZM2G108219	5.61	38.70	33.50	655.90	9	R.WHVAEALR.R R.DIGIAAGLIR.I R.AAVHAVCGPTVSCADITTLATR.D R.DAVVASGGPFFEVPLGR.R R.SLDKADLVALSGAHTVGR.G K.CASDPSGNVVTQVLDVR.T R.TPNAFDNK.Y R.TPNAFDNKYYFDLIAK.Q R.FALNQAAFFDQFAR.S	62-69 71-80 125-146 147-163 196-213 244-260 261-268 261-276 299-312	Peroxidase
79-4 80-12/13	GRMZM2G089982	9.59	35.70	29.70	483.81	7	K.EIVQSIVAQAVAK.E R.GFEVIDQIK.A K.AALEAACPGTVSCADIVALAAR.D R.DSTALVGGPYWDVPLGR.R R.SGGDNNLFPLDFITPAK.F K.GLLSSDEILLTK.S K.SAETAALVK.A	44-56 104-112 113-134 135-151 239-255 269-280 281-289	Peroxidase
79-8	GRMZM2G410175	6.20	35.00	22.30	392.69	7	R.FYGGSCPSVEDVVR.K R.ALSVAPSLAGPLLR.M R.GFGFIER.V R.DAVWLSK.G K.GPFWAVPLGR.R R.DTDPELDR.A R.TFDLGYANVAK.R	25-38 44-57 94-100 125-131 132-141 211-218 247-258	Peroxidase

80-4/5	GRMZM2G108123	9.48	36.60	39.50	538.41	10	R.TAVQAALR.R R.EIALAAGLLR.I R.IFFHDCFPQGCDASVLLK.G R.ALQLIDDIR.A K.VHAACGPTVSCADVTALATR.A R.AAVVASGGPSYPVPLGQR.D R.DVADLVALSGAHTVGR.A R.ADSQEDDFAR.Q R.LQQLDVVTPDADFNVYYK.N R.DPTTAPIVR.C	51-58 60-69 70-87 105-113 136-153 136-153 189-204 214-223 236-253 271-279	Peroxidase
80-8/9	GRMZM2G023840	9.48	36.60	34.00	456.97	8	R.LHFHDCFVK.G R.GFEVIDEIK.A K.AALEAACPGTVSCADILALAAR.D K.LQGLDIVDLVALLGSHTIGDSR.C R.SGGDQNLFFLDPVTPFK.F K.FDNQYYK.N K.LYAANQDIFFQHFR.S K.MGNISPLTGANGEIR.K	76-84 113-121 122-143 191-212 248-264 265-271 299-313 318-332	Peroxidase
80-6	GRMZM2G405459	9.77	33.10	34.00	516.30	6	R.AGMAAAVQQEPR.M K.SQVEAACPGTVSCADILALAAR.D R.DGVNLLSGPTWAVQLGR.R R.TASQSAANSNLPSPSSSAAALVSAFAS K.G R.DLVALSGAHTIGAAR.C K.MGSIGPLTGSSGEIR.A	43-54 108-129 130-146 151-178 184-198 300-314	Peroxidase
79-29/33	AC196475.3_FGP004	5.41	39.50	53.6	53.58	1	K.NAIELGLLEVLR.E	35-47	O-Methyltransferase
76-15	GRMZM2G149751-P02	6.31	49.70	8.10	138.32	3	K.FALESFWDGK.S K.ALGVDTVPVLVGPVSYLLLSKPAK.G K.YLFAGVVDGR.N	19-28 146-169 288-297	Putative methionine synthase
Cell wall salt extract proteins, BOA									
Id-No. Protein	Accession No.	pI:	MW (kDa)	Seq. Coverage %	Mascot MS/MS Score	No. of MS/MS Peptides	MS/MS Peptide sequence	Range	Protein Identification
88-9	GRMZM2G147687	7.12	66.90	3.5	178.14	2	R.IGEATALEVR.A R.GFVISDWEGIDR.I	184-193 336-347	Glycosyl hydrolase

89-12	GRMZM2G118003	9.37	56.40	20.50	446.99	8	K.GANWLGLSR.A K.SLNFDAYR.F R.FSISWSR.I K.MADLFTDYADFCFK.T R.IVALLGYDTGSNPPQR.C R.CAAGGNSATEPYIVAHNFLLAHATAVAR. K.FGIVYVDFNTLER.H K.ASAYWFR.D	28-37 104-111 112-118 174-187 204-219 223-250 474-486 490-496	β-Glucosidase
93/92-10	GRMZM2G076348-P01	6.34	28.60	15.20	210.26	5	R.AYVSGAASSSR.A R.AVVLASDVFGYEAPLLR.Q K.AGYFVVVPDFLK.G K.AAEDAKPLFAALK.K K.IFQGVEHGFACR.Y	59-69 70-86 95-106 128-140 225-236	Endo1,3;1,4 β-D-glucanase
92-24	GRMZM2G004699	6.15	36.20	9.30	71.97	2	K.STGTGFQTR.G R.DLDAAQYR.R	63-71 255-265	Xyloglucan-endo-transglycosylase
93-13 94-11/12	GRMZM2G096247	7.87	25.80	199.50	18.60	4	R.VLTCLFEK.K R.YVCTQFPNDGNK.S K.SLYGSGALER.A K.QVLDVYDEILSR. N	19-26 75-86 87-96 148-159	Glutathione S-transferase
94-5 93-14/16	GRMZM2G175134	9.01	21.40	191.79	15.40	3	R.DLFGPGALER.A K.LLDIYEQR.L R.LGEEAFLAGGK.F	27-36 110-117 118-128	Glutathione S-transferase
94-13/14	GRMZM2G126763	7.86	20.20	125.42	12.40	2	K.SLYGSGALER.A K.QVLDVYDEILSK.N	38-47 99-110	Glutathione S-transferase
95-12/13 96-20	GRMZM2G119499	7.91	36.60	142.30	6.70	2	K.QGNPYLIGTGALER.A K.LLDIYEQR.L	106-119 217-224	Glutathione S-transferase
96-28/29	GRMZM2G055487	6.80	30.80	85.47	4.2	1	R.TFDLGYYANVAK.R	208-219	Peroxidase
88-15/17 91-15/	GRMZM2G108207	6.25	37.50	611.1	27.6	8	R.DIGIAAGLIR.I K.VSCADITTLATR.D R.DAVVASGGPFFEVLGR.R R.SLDTADLVALSGAHTVGR.G K.DASAAQVLDVR.T R.TPNAFDNK.Y R.TPNAFDNKYYFDLIAK.Q R.FALNQAAFFDQFAR.S	68-77 132-143 144-1160 193-210 244-254 255-270 293-306	Peroxidase

91-16 92-2	GRMZM2G108219	5.61	38.70	556.51	31.30	8	R.DIGIAAGLIR.I R.AAVHAVCGPTVSCADITTLATR.D R.DAVVASGGPFFEVPLGR.R R.SLDKADLVALSGAHTVGR.G K.CASDPSGNVVTQVLDVR.T R.TPNAFDNK.Y R.TPNAFDNKYYFDLIAK.Q R.FALNQAAFFDQFAR.S	71-80 125-146 147-163 196-213 244-260 261-268 261-276 299-312	Peroxidase
92-4	GRMZM2G108123	9.48	36.60	468.13	29.10	7	R.TAVQAALR.R R.EIALAAGLLR.I K.VHAACGPTVSCADVTALATR.A R.AAVVASGGPSYPVPLGQR.D R.DVADLVALSGAHTVGR.A R.ADSQEDDFAR.Q R.LQQLDVVTPDAFDNVYYK.N	51-58 60-69 116-135 136-153 189-204 214-223 236-253	Peroxidase
92-15/16	GRMZM2G405459	9.77	33.10	219.27	17.10	3	R.AGMAAAVQQEPR.M R.TASQSAANSNLPSPSSSAAALVSAFASK. G R.DLVALSGAHTIGAAR.C	43-54 151-178 184-198	Peroxidase
90-8 91-5	GRMZM2G103342	9.66	38.00	604.27	27.30	9	K.VPTLLSFLAK.I K.FFAGQLYR.T R.TPNAFDNKYYVDLLNR.E K.YYVDLLNR.E K.MGQVNVLTGSQGQVR.A R.YPPLAPGLSFDFYK.K R.QNVGLAAALIR.L R.VVSCADIVALAAR.E R.ESVALGGGPAYK.L	31-44 64-74 132-144 145-156 184-193 233-240 257-272 265-272 313-327	Peroxidase
91-8	GRMZM2G025441	10.46	33.40	478.54	20.60	5	K.AAVTAAVAQEAR.M R.GFGVVDNIK.A R.DSVVALGGPSWR.V R.TDLVALSGAHTIGLAQCK.N R.MGNISPLTGTQGQIR.R	45-56 101-109 132-143 185-202 300-314	Peroxidase
91-12	GRMZM2G089982	9.59	35.70	374.02	24.60	6	K.EIVQSIVAQAVAK.E R.GFEVIDQIK.A K.AALEAACPGTVSCADIVALAAR.D R.SGGDNNLFPLDFITPAK.F K.GLLSSDEILLTK.S K.SAETAALVK.A	44-56 104-112 113-134 239-255 269-280 281-289	Peroxidase

90-10/11 91-27/28	GRMZM2G085967	8.84	35.40	344.62	19.2	7	K.AHIPHAPDVASTLLR.T R.DSVGVIGGPFWSVPTGR.R R.GFGFIDR.I K.ECPGVVSCADIVALAAR.D R.GGPDDADPSLDPLYAAK.L R.TFDLSYYR.G R.GLFQSDAALITDAASK.A	46-60 80-96 97-103 111-127 163-179 251-258 265-280	Peroxidase
91-27/29	GRMZM2G168073	5.50	27.40	117.37	15.00	2	R.TLDFLPPPTSSLPELVQSFAAK.G R.VLFTSDASLLTSPATAK.L	97-118 200-216	Peroxidase
91-36/38	GRMZM2G070603	9.11	35.30	74.34	4.80	1	R.GLFQSDAALLADATTR.E	270-285	Peroxidase
88-17/19 90-9	GRMZM2G394500	6.20	31.50	376.34	25.10	5	K.TAPINIGLAAFEVIDEIK.A R.DLPDSTFTVSELIR.N R.LSAPPAQIVPAYR.N R.DFLDNSYYHNNLAR.I R.IVTFNSDWQLLTEK.E	37-54 109-122 155-167 214-227 228-241	Peroxidase
90-13 91-14/15 92-15/16 93-21	GRMZM2G410175	6.20	35.00	326.71	20.10	6	R.FYGGQSCPSVEDVVR.K R.ALSVAPSLAGPLL.R.M R.GFGFIER.V K.GPFWAVPLGR.R R.DTDPELDR.A R.TFDLGYYANVAK.R	25-38 44-57 94-100 132-141 211-218 247-258	Peroxidase
89-15/16	GRMZM2G044049	9.08	39.60	65.66	3.50	1	K.SDAALLTSTETAR.M	312-324	Peroxidase
91-32/35 92-12/14 96-40/44	GRMZM2G023840	9.84	36.60	327.54	31.10	6	R.GFEVIDEIK.A K.AALEAACPATVSCADILALAAR.D K.LQGLDIVDLVALLGSHTIGDSR.C R.SGGDQNLFFLDPVTPFK.F R.GLLSSDEVLLTGSGATADLVK.L K.LYAAANQDIFFQHAR.S	113-121 122-143 191-212 248-264 278-298 299-313	Peroxidase
92-29/35	GRMZM2G054123	5.43	42.50	66.37	3.80	1	R.FVIGGPHGDAGLTGR.K	240-254	S-adenosylmeth- ionine synthetase