

Table 1 - Additional data: Bioinformatic analysis of proteins extracted from cell walls of *A. thaliana* cell suspension cultures [8].

Data are from [8]. Proteins were extracted from *A. thaliana* cell walls of cell suspension cultures as described in Figure 1. Two successive extractions were performed : step 1 using CaCl₂, and step 2 using urea. All proteins sequences were analyzed with three bioinformatic programs to predict their sub-cellular localization. Proteins for which predictions by different bioinformatic programs are in conflict are classified as "not clear".

| step 1: CaCl ₂ extract | Predicted subcellular localization | Gene (<i>A. thaliana</i>) | PSORT (a) | TargetP (b) | Predicted signal peptide (c) | Aramemnon (d) |
|-----------------------------------|------------------------------------|--------------------------------|--|--|---------------------------------|-------------------|
| | transmembrane domain | At3g30810 | Golgi (0.900), plasma membrane (0.790), chloroplast thylakoid membrane (0.762) | other (0.796) | 1-20 | yes GPI anchor |
| | | At4g12420 | plasma membrane (0.919) | secretory pathway (0.989) | | |
| | outside | At1g06870 | outside (0.638) | secretory pathway (0.850) | 1-21 | |
| | | At1g21670 | outside (0.820) | secretory pathway (0.973) | 1-21 | |
| | | At1g53070 | outside (0.528) | secretory pathway (0.972) | 1-17 or 1-23 | |
| | | At1g78830 | outside (0.820) | secretory pathway (0.962) | 1-22 | |
| | | At1g78850 | outside (0.820) | secretory pathway (0.973) | 1-22 | |
| | | At2g39700 | outside (0.810) | secretory pathway (0.961) | 1-20 | |
| | | At2g41800 | outside (0.370) | secretory pathway (0.369) | 1-21 | |
| | | At2g44450 | outside (0.820) | secretory pathway (0.853) | 1-22 | |
| | | At2g47050 | outside (0.820) | secretory pathway (0.928) | 1-20 | |
| | | At3g07320 | outside (0.790) | secretory pathway (0.482) | 1-19 | |
| | | At3g08030 | outside (0.820) | secretory pathway (0.985) | 1-21 | |
| | | At3g45960 | outside (0.805) | secretory pathway (0.744) | 1-20 | |
| | | At3g45970 | endoplasmic reticulum (0.820) | secretory pathway (0.854) | 1-20 | |
| | | At3g61820 | outside (0.628) | secretory pathway (0.828) | 1-26 or 1-25 | |
| | | At4g20830 | outside (0.820) | secretory pathway (0.540) | 1-30 | |
| | | At4g25900 | outside (0.820) | secretory pathway (0.924) | 1-20 or 1-24 | |
| | | At4g30270 | outside (0.800) | secretory pathway (0.975) | 1-21 | |
| | At5g06860 | outside (0.733) | secretory pathway (0.964) | 1-21 | | |
| | intracellular | At1g08450 | endoplasmic reticulum (0.910) (C-terminal HDEL) | secretory pathway (0.995) | 1-28 | |
| | | At1g13440 | microbody (0.539) | other (0.610) | | |
| | | At1g30580 | microbody (0.507) | other (0.579) | | |
| | | At2g39050 | microbody (0.515) | other (0.910) | | |
| | | At2g43710 | microbody (0.495) | chloroplast (0.977) | | |
| | | At3g02630 | chloroplast stroma (0.593) | chloroplast (0.779) | | |
| | | At3g26060 | mitochondry (0.679) | chloroplast (0.904) | | |
| | | At3g48380 | mitochondry (0.596) | mitochondry (0.308) | | |
| | | At3g58480 | nucleus (0.760) | other (0.802) | | |
| | | At4g17260 | cytoplasm (0.450) | other (0.435) | | |
| | | At4g37870 | nucleus (0.880) | other (0.849) | | |
| | | At5g08310 | mitochondry (0.789) | mitochondry (0.946) | | |
| | | At5g20080 | mitochondry (0.859) | mitochondry (0.855) | | |
| | At5g46550 | nucleus (0.940) | other (0.504) | | | |
| | At5g55990 | microbody (0.569) | secretory pathway (0.580), other (0.576) | | | |
| | not clear | At4g22410 | cytoplasm (0.450) | secretory pathway (0.922) secretory pathway (0.523), chloroplast (0.307) | 1-26 | |
| | | At5g37990 | endoplasmic reticulum (0.550) | chloroplast (0.307) | 1-15 | |

step 2: urea extract

| | | | | | |
|-----------------------------|----------------------|---|---------------------------|--|-----|
| transmembrane domain | At1g61500 | plasma membrane (0.460) | secretory pathway (0.963) | 1-24 | yes |
| | At1g67880 | plasma membrane (0.790) | other (0.955) | | yes |
| | At3g25560 | plasma membrane (0.460) | secretory pathway (0.742) | 1-32 | yes |
| | At3g57400 | plasma membrane (0.830) | other (0.792) | | yes |
| | At5g08390 | plasma membrane (0.460) | secretory pathway (0.932) | 1-22 | yes |
| | At5g58640 | plasma membrane (0.640) | secretory pathway (0.326) | 1-17 | yes |
| outside | At1g71695 | outside (0.820) | secretory pathway (0.829) | 1-22 or 1-31 | |
| | At2g16430 | outside (0.820) | secretory pathway (0.963) | 1-25 | |
| | At2g44450 | outside (0.820) | secretory pathway (0.853) | 1-22 | |
| | At3g08030 | outside (0.820) | secretory pathway (0.985) | 1-21 | |
| | At3g45970 | endoplasmic reticulum (0.820) | secretory pathway (0.854) | 1-20 | |
| | At3g52500 | outside (0.820) | secretory pathway (0.649) | 1-18 | |
| | At4g08770 | outside (0.633) | secretory pathway (0.955) | 1-22 | |
| | At4g24890 | outside (0.820) | secretory pathway (0.925) | 1-20 or 1-26 | |
| | intracellular | At1g24360 | mitochondry (0.613) | chloroplast (0.545), mitochondry (0.206) | |
| At1g30580 | | microbody (0.507) | other (0.579) | | |
| At1g43800 | | nucleus (0.760) | mitochondry (0.430) | | |
| At1g43800 | | nucleus (0.760) | mitochondry (0.430) | | |
| At1g52960 | | nucleus (0.960) | chloroplast (0.630) | | |
| At1g56070 | | mitochondry (0.360) | other (0.823) | | |
| At1g69290 | | chloroplast (0.840) | chloroplast (0.528) | | |
| At1g72560 | | cytoplasm (0.450) | other (0.872) | | |
| At2g17190 | | cytoplasm (0.650) | other (0.797) | | |
| At2g32920 | | endoplasmic reticulum (0.910) (C-terminal KDEL) | secretory pathway (0.920) | 1-17 or 1-24 | |
| At2g36530 | | endoplasmic reticulum (0.600) | other (0.747) | | |
| At2g43710 | | microbody (0.495) | chloroplast (0.977) | | |
| At2g44350 | | mitochondry (0.883) | mitochondry (0.848) | | |
| At3g04600 | | nucleus (0.940) | other (0.954) | | |
| At3g14440 | | chloroplast (0.905) | chloroplast (0.719) | | |
| At3g15730 | | microbody (0.634) | other (0.614) | | |
| At3g16857 | | nucleus (0.700) | other (0.376) | | |
| At3g57400 | | plasma membrane (0.830) | other (0.792) | | |
| At4g17260 | | cytoplasm (0.450) | chloroplast (0.703) | | |
| At4g31180 | | chloroplast (0.890) | chloroplast (0.876) | | |
| At4g36530 | | microbody (0.594) | other (0.828) | | |
| At4g37870 | | nucleus (0.880) | other (0.849) | | |
| At5g06450 | | microbody (0.640) | other (0.954) | | |
| At5g20080 | | mitochondry (0.859) | mitochondry (0.855) | | |
| At5g26710 | | endoplasmic reticulum (0.550) | chloroplast (0.552) | | |
| At5g28540 | | endoplasmic reticulum (0.910) (C-terminal HDEL) | secretory pathway (0.993) | 1-27 | |
| At5g41550 | | chloroplast (0.520) | mitochondry (0.517) | | |

Colour code:

proteins found at both steps 1 and 2
 proteins found at both steps 1 and 2



(a) PSORT : <http://psort.nibb.ac.jp/form.html> [28]

(b) TargetP: <http://www.cbs.dtu.dk/services/TargetP/> [29]

(c) Two sizes are indicated when different signal peptides are predicted by PSORT and TargetP. The first one is predicted with PSORT.

(d) Aramemnon: <http://aramemnon.botanik.uni-koeln.de/> [30]

Table 2 - Additional data: Bioinformatic analysis of proteins extracted from cell walls of *M. sativa* stems [9].

Data are from [9]. Proteins were extracted from *M. sativa* cell walls of stems as described in Figure 2. Two successive extractions were performed : step 1 using CaCl₂, and step 2 using LiCl. All proteins sequences were analyzed with bioinformatic softwares to predict their sub-cellular localization. When only partial protein sequences or no sequence are available, proteins are classified as "not predictable".

| step 1: CaCl ₂ extract | Predicted subcellular localization | | Gene | Protein | PSORT (a) | TargetP (b) | Predicted signal peptide (c) | Aramemnon (d) | |
|-----------------------------------|------------------------------------|--------|----------------------------------|---------------------------|--|----------------------------------|------------------------------|---------------|----|
| | | | (<i>A. thaliana</i>) | | | | | | |
| | transmembrane domain | | | CAC34417 | plasma membrane (0.460) chloroplast (0.659), plasma membrane (0.650) | secretory pathway (0.986) | 1-20 | yes | |
| | | | | P16002 | plasma membrane (0.790), chloroplast (0.753) | chloroplast (0.924) | | yes | |
| | | | | P26291 | chloroplast (0.753) | chloroplast (0.797) | | yes | |
| | outside | | At1g09560 | AAB51577 | outside (0.609) | secretory pathway (0.960) | 1-23 | | |
| | | | At3g62020 | AAB51752 | plasma membrane (0.685) | secretory pathway (0.970) | 1-21 | no | |
| | | | | BAA81904 | plasma membrane (0.790) | secretory pathway (0.758) | 1-39 | no | |
| | | | | CAA09607 | outside (0.820) | secretory pathway (0.996) | 1-25 or 1-23 | | |
| | | | | CAA10167 | outside (0.790) | secretory pathway (0.963) | 1-16 or 1-22 | | |
| | | | | CAA10287 | outside (0.585) | secretory pathway (0.867) | 1-33 | | |
| | | | | CAC44501 | outside (0.820) | secretory pathway (0.985) | 1-24 | | |
| | | | | CAD29731 | outside (0.714) | secretory pathway (0.982) | 1-23 or 1-26 | | |
| | | | | At1g49750 | NP_175397 | vacuole (0.750), outside (0.666) | secretory pathway (0.239) | 1-15 or 1-22 | |
| | | | | At3g20820 | NP_188718 | vacuole (0.861), outside (0.820) | secretory pathway (0.752) | 1-19 | |
| | | | | At4g34480 | NP_195174 | plasma membrane (0.460) | secretory pathway (0.942) | 1-22 | |
| | | | | At5g14440 | NP_196949 | outside (0.786) | secretory pathway (0.941) | 1-30 | |
| | | | | At5g51890 | NP_200002 | plasma membrane (0.685) | secretory pathway (0.991) | 1-24 | no |
| | | | | At1g09750 | NP_563851 | outside (0.456) | secretory pathway (0.899) | 1-21 or 1-23 | |
| | | | | At1g20850 | NP_564126 | vacuole (0.808), outside (0.786) | secretory pathway (0.987) | 1-26 | |
| | | | | At4g33490 | NP_567922 | outside (0.820) | secretory pathway (0.913) | 1-21 | |
| | | | | | P36907 | outside (0.757) | secretory pathway (0.985) | 1-23 | |
| | | | | | Q01806 | plasma membrane (0.685) | secretory protein (0.983) | 1-30 | no |
| | | | | | Q9S8P4 | outside (0.820) | secretory pathway (0.967) | 1-20 | |
| | | | | | S68805 | outside (0.781) | secretory pathway (0.961) | 1-24 | |
| | | T07086 | outside (0.743) | secretory pathway (0.771) | 1-19 | | | | |
| | | T09642 | vacuole (0.761), outside (0.657) | secretory pathway (0.981) | 1-30 or 1-24 | | | | |

| | | | | |
|------------------------|-----------|---------------------------------------|-------------------------------|--|
| intracellular | AAC49358 | mitochondry (0.555) | chloroplast (0.628) | |
| | AAG34872 | microbody (0.540) | other (0.568) | |
| | AAL77589 | mitochondry (0.679) | chloroplast (0.765) | |
| | CAA09177 | microbody (0.640) | other (0.884) | |
| | At1g16470 | NP_173096 | cytoplasm (0.450) | other (0.703) |
| | At1g23740 | NP_173786 | mitochondry (0.594) | chloroplast (0.568), mitochondry (0.442) |
| | At1g48590 | NP_175292 | mitochondry (0.480) | mitochondry (0.529) |
| | At1g67280 | NP_176896 | mitochondry (0.807) | chloroplast (0.895) |
| | At2g15570 | NP_179159 | chloroplast (0.919) | chloroplast (0.979) |
| | At2g24940 | NP_180066 | cytoplasm (0.450) | other (0.890) |
| | At2g32520 | NP_180811 | microbody (0.570) | other (0.896) |
| | At3g20390 | NP_188674 | mitochondry (0.644) | chloroplast (0.497), mitochondry (0.371) |
| | At3g26060 | NP_189235 | mitochondry (0.679) | chloroplast (0.904) |
| | At3g43810 | NP_189967 | cytoplasm (0.650) | other (0.894) |
| | At3g55330 | NP_191093 | chloroplast (0.647) | chloroplast (0.966) |
| | At4g09010 | NP_192640 | chloroplast (0.512) | chloroplast (0.737) |
| | At5g01650 | NP_195785 | chloroplast (0.890) | other (0.719) |
| | At1g09310 | NP_563841 | cytoplasm (0.650) | other (0.906) |
| | At3g17440 | NP_566578 | endoplasmic reticulum (0.850) | other (0.736) |
| | At3g63190 | NP_567141 | mitochondry (0.838) | chloroplast (0.933) |
| | At5g20080 | NP_568391 | mitochondry (0.859) | mitochondry (0.855) |
| | O65194 | O65194 | chloroplast (0.876) | chloroplast (0.710) |
| | O65198 | O65198 | chloroplast (0.921) | chloroplast (0.941) |
| | P10933 | P10933 | endoplasmic reticulum (0.550) | chloroplast (0.907) |
| | P16048 | P16048 | mitochondry (0.870) | mitochondry (0.645) |
| | P16059 | P16059 | mitochondry (0.750) | chloroplast (0.307), |
| | P29450 | P29450 | chloroplast (0.950) | chloroplast (0.977) |
| | P49231 | P49231 | cytoplasm (0.450) | other (0.818) |
| | P51615 | P51615 | plasma membrane (0.615) | other (0.941) |
| | Q02610 | Q02610 | cytoplasm (0.450) | other (0.404) |
| | Q42971 | Q42971 | endoplasmic reticulum (0.600) | other (0.608) |
| | Q43636 | Q43636 | cytoplasm (0.450) | other (0.907) |
| | T06363 | T06363 | plasma membrane (0.650), | chloroplast (0.505) |
| | T09286 | T09286 | chloroplast (0.539) | mitochondry (0.766) |
| | | mitochondry (0.920) | | |
| not predictable | AAD34458 | encoded by a truncated cDNA | | |
| | AAL06644 | encoded by a truncated cDNA | | |
| | AAL15646 | encoded by a truncated cDNA | | |
| | JC4780 | data not available in usual databases | | |
| | JC4781 | data not available in usual databases | | |
| | JC4782 | data not available in usual databases | | |
| | S22489 | encoded by a truncated cDNA | | |
| | T05957 | encoded by a truncated cDNA | | |
| | T09165 | encoded by a truncated cDNA | | |

step 2: LiCl extract

| | | | | | |
|------------------------|-----------|-----------|---|---------------------------|--------------|
| outside | At1g49750 | NP_175397 | vacuole (0.850), outside (0.666) | secretory pathway (0.239) | 1-15 or 1-22 |
| | | P36907 | outside (0.757) | secretory pathway (0.985) | 1-23 |
| | | T07086 | outside (0.743) | secretory pathway (0.771) | 1-19 |
| | | T07171 | outside (0.820) | secretory pathway (0.981) | 1-23 |
| | | T09665 | outside (0.820) | secretory pathway (0.922) | 1-28 |
| intracellular | At5g41550 | AAD56659 | mitochondry (0.483) | mitochondry (0.839) | |
| | | NP_198970 | chloroplast (0.520) | mitochondry (0.517) | |
| | | T93508 | endoplasmic reticulum (0.910) (C-term HDEL) | secretory pathway (0.991) | 1-20 |
| not predictable | | P04353 | encoded by a truncated cDNA | | |

Colour code:

proteins found at both steps 1 and 2



(a) PSORT : <http://psort.nibb.ac.jp/form.html> [28]

(b) TargetP: <http://www.cbs.dtu.dk/services/TargetP/> [29]

(c) Two sizes are indicated when different signal peptides are predicted by PSORT and TargetP. The first one is predicted with PSORT.

(d) Aramemnon: <http://aramemnon.botanik.uni-koeln.de/> [30]

Table 3 - Bioinformatic analysis of proteins extracted from cell walls of *C. albicans* [20].

Data are from [20]. Proteins were extracted from *C. albicans* cell walls as described in Figure 3. Four successive extractions were performed : step 1 using SDS-DTT, step 2 using NaOH, step 3 using a β -1,3-glucanase and step 4 using an exochitinase. All proteins sequences were analyzed with bioinformatic programs to predict their sub-cellular localization. Proteins for which predictions by different bioinformatic programs are in conflict are classified as "not clear".

| step 1: SDS-DTT extract | Predicted subcellular localization | Accession (a) | PSORT (b) | TargetP (c) | Predicted signal peptide (d) |
|-------------------------|------------------------------------|------------------|--|------------------------------------|------------------------------|
| | outside | CA1541 Phrp * | outside (0.370) | secretory pathway (0.946) | 1-18 |
| | intracellular | CA0362 | cytoplasm (0.650) endoplasmic reticulum (0.910) (C-term HDEL) | other (0.911) | 1-29 or 1-32 |
| | | CA0915 | mitochondry (0.541) | secretory pathway (0.977) | |
| | | CA1015 | nucleus (0.760) | other (0.694), mitochondry (0.271) | |
| | | CA1230 | mitochondry (0.360) | other (0.843) | |
| | | CA1691 | endoplasmic reticulum (0.910) (C-term HDEL) | other (0.789), mitochondry (0.227) | |
| | | CA1755 | microbody (0.300) | secretory pathway (0.955) | 1-23 |
| | | CA2474 | nucleus (0.760) | other (0.798) | |
| | | CA2857 | nucleus (0.980) | other (0.842) | |
| | | CA3081 | cytoplasm (0.650) | other (0.885) | |
| | | CA3208 | mitochondry (0.360) | mitochondry (0.663) | |
| | | CA3483 | mitochondry (0.450) | other (0.275), mitochondry (0.299) | |
| | | CA3534 | cytoplasm (0.450) | other (0.887) | |
| | | CA3874 | cytoplasm (0.450) | other (0.793) | |
| | | CA4671 | mitochondry (0.853) | other (0.834) | |
| | | CA4765 | mitochondry (0.471) | mitochondry (0.716) | |
| | | CA4844 | endoplasmic reticulum (0.550) | other (0.704) | |
| | | CA4862 | mitochondry (0.360) | other (0.934) | |
| | | CA4959 | nucleus (0.600) | other (0.923) | |
| | | CA5135 | cytoplasm (0.450) | other (0.928) | |
| | | CA5180 | cytoplasm (0.450) | other (0.797) | |
| | | CA5892 | mitochondry (0.471) | mitochondry (0.637) | |
| | | CA5950 | microbody (0.800) | other (0.604) | |
| | not predictable | CA2810 | not present in the database | | |
| step 2: NaOH extract | outside | Hsp150p/Pir2p* | | | |
| | intracellular | CA1691 | mitochondry (0.360) | other (0.789), mitochondry (0.227) | |
| | | CA2474 | microbody (0.300) | other (0.798) | |
| | | CA3483 | mitochondry (0.360) | other (0.275), mitochondry (0.299) | |
| | | CA3874 | cytoplasm (0.450) | other (0.793) | |
| | | CA4765 | mitochondry (0.853) | mitochondry (0.716) | |
| | | CA5180 | cytoplasm (0.450) | other (0.797) | |
| | | CA5892 | mitochondry (0.471) | mitochondry (0.637) | |

| | | | | |
|---|----------------------|--|---|--|
| step 3: β-1,3-glucanase extract | outside | putative β -1,3-glucanase* Hsp150p/Pir2p* Phrp * | | |
| | intracellular | CA1691 CA3874 CA5892 | mitochondry (0.360) cytoplasm (0.450) mitochondry (0.471) | other (0.789), mitochondry (0.227) other (0.793) mitochondry (0.637) |
| step 4: exochitinase extract | outside | Hsp150p/Pir2p* Phrp * | | |
| | intracellular | CA1691 CA2474 CA3874 CA5180 CA5892 | mitochondry (0.360) microbody (0.300) cytoplasm (0.450) cytoplasm (0.450) mitochondry (0.471) | other (0.789), mitochondry (0.227) other (0.798) other (0.793) other (0.797) mitochondry (0.637) |

colour code: proteins found in at least 2 fractions
 proteins found in at least 2 fractions

* proteins that failed to be identified to already annotated *C. albicans* proteins

(a) <http://genolist.pasteur.fr/CandidaDB/>

(b) PSORT : <http://psort.nibb.ac.jp/form.html> [28]

(b) TargetP: <http://www.cbs.dtu.dk/services/TargetP/> [29]

(d) Two sizes are indicated when different signal peptides are predicted by PSORT and TargetP. The first one is predicted with PSORT.

Table 4 - Bioinformatic analysis of proteins extracted from cell walls of *A. thaliana* etiolated hypocotyls with salts.

Proteins were extracted from *A. thaliana* cell walls of etiolated hypocotyls as described in Figure 5. Two successive extractions were performed : step 1 using CaCl₂ and step 2 using LiCl. All proteins sequences were analyzed with bioinformatic programs to predict their sub-cellular localization. Proteins for which predictions by different bioinformatic programs are in conflict are classified as "not clear".

| step 1: CaCl ₂ extract | Predicted subcellular localization | Gene (<i>A. thaliana</i>) | PSORT (a) | TargetP (b) | Predicted signal peptide (c) | Aramemnon (d) |
|-----------------------------------|------------------------------------|--------------------------------|---|---------------------------|---------------------------------|------------------|
| | transmembrane domain | At1g23480 | plasma membrane (0.919) | secretory pathway (0.875) | 1-29 | yes |
| | | At1g54010 | plasma membrane (0.685) | secretory pathway (0.991) | 1-29 | yes |
| | | At1g55850 | plasma membrane (0.600) | other (0.787) | | yes |
| | | At1g62660 | plasma membrane (0.790) | other (0.822) | | yes |
| | | At1g79680 | outside (0.820) | secretory pathway (0.929) | 1-26 or 1-24 | yes |
| | | At3g20580 | plasma membrane (0.600) | secretory pathway (0.860) | 1-35 | yes (GPI anchor) |
| | | At3g45970 | endoplasmic reticulum (0.820) | secretory pathway (0.854) | 1-20 | yes |
| | | At4g15320 | plasma membrane (0.600) | other (0.879) | | yes |
| | outside | At1g02335 | plasma membrane (0.685) | secretory pathway (0.933) | 1-22 | no |
| | | At1g03220 | outside (0.820) | secretory pathway (0.912) | 1-22 | |
| | | At1g03230 | outside (0.820) | secretory pathway (0.910) | 1-23 | |
| | | At1g09560 | outside (0.609) | secretory pathway (0.960) | 1-23 | |
| | | At1g09750 | outside (0.456) | secretory pathway (0.899) | 1-21 or 1-23 | |
| | | At1g11580 | outside (0.820) | secretory pathway (0.423) | 1-34 | |
| | | At1g18970 | mitochondry (0.850), plasma membrane (0.650) | secretory pathway (0.932) | 1-27 | no |
| | | At1g20190 | outside (0.820) | secretory pathway (0.961) | 1-20 | |
| | | At1g28290 | outside (0.681) | secretory pathway (0.483) | 1-24 | |
| | | At1g29670 | outside (0.820) | secretory pathway (0.987) | 1-24 | |
| | | At1g33590 | outside (0.738) | secretory pathway (0.963) | 1-24 | no |
| | | At1g65590 | outside (0.819) | secretory pathway (0.948) | 1-24 | |
| | | At1g68560 | outside (0.820) | secretory pathway (0.982) | 1-27 | |
| | | At1g73260 | outside (0.542) | secretory pathway (0.985) | 1-26 | |
| | | At1g76160 | outside (0.820) | secretory pathway (0.984) | 1-23 | |
| | | At1g78830 | outside (0.820) | secretory pathway (0.962) | 1-22 | |
| | | At1g78850 | outside (0.820) | secretory pathway (0.973) | 1-22 | |
| | | At1g78860 | outside (0.652) | secretory pathway (0.981) | 1-22 | |
| | | At2g05580 | outside (0.820) | secretory pathway (0.993) | 1-20 | no |
| | | At2g18140 | outside (0.820) | secretory pathway (0.695) | 1-20 or 1-16 | |
| | | At2g28790 | outside (0.705) | secretory pathway (0.990) | 1-24 or 1-21 | |
| | | At2g30210 | outside (0.820) | secretory pathway (0.983) | 1-25 | |
| | | At2g38530 | plasma membrane (0.685) | secretory pathway (0.967) | 1-23 | no |
| | | At3g08030 | outside (0.820) | secretory pathway (0.985) | 1-21 | |
| | | At3g13790 | outside (0.494) | secretory pathway (0.969) | 1-20 or 1-28 | |
| | | At3g14220 | outside (0.609) | secretory pathway (0.926) | 1-20 or 1-28 | |
| | | At3g14310 | plasma membrane (0.460) | secretory pathway (0.227) | 1-40 or 1-37 | no |
| | | At3g16850 | outside (0.820) | secretory pathway (0.965) | 1-19 or 1-20 | |
| | | At3g18080 | outside (0.370) | secretory pathway (0.374) | 1-23 | |
| | | At3g20370 | outside (0.633) | secretory pathway (0.965) | 1-25 | |

| | | | | | |
|----------------------|------------|---|--|--------------|-----|
| | At3g20820 | outside (0.820) | secretory pathway (0.752) | 1-19 | |
| | At3g21770 | outside (0.820) | secretory pathway (0.967) | 1-27 | |
| | At3g22640 | outside (0.820) | secretory pathway (0.996) | 1-22 | |
| | At3g24480 | outside (0.795) | secretory pathway (0.978) | 1-25 | |
| | At3g25700 | endoplasmic reticulum (0.820) | secretory pathway (0.425) | 1-23 | |
| | At3g43270 | outside (0.820) | secretory pathway (0.979) | 1-24 | |
| | At3g49120 | outside (0.609) | secretory pathway (0.604) | 1-28 or 1-29 | |
| | At3g54400 | outside (0.595) | secretory pathway (0.409) | 1-19 | |
| | At3g55260 | outside (0.738) | secretory pathway (0.805) | 1-22 or 1-20 | |
| | At4g08950 | outside (0.820) | secretory pathway (0.871) | 1-21 | |
| | At4g12880 | outside (0.820) | secretory pathway (0.952) | 1-18 or 1-26 | |
| | At4g13340 | outside (0.820) | secretory pathway (0.945) | 1-20 | |
| | At4g16500 | outside (0.820) | secretory pathway (0.929) | 1-22 | |
| | At4g18970 | plasma membrane (0.685) | secretory pathway (0.980) | 1-22 | no |
| | At4g29270 | outside (0.820) | secretory pathway (0.983) | 1-26 | |
| | At4g30170 | outside (0.695) | secretory pathway (0.980) | 1-25 | |
| | At4g33220 | outside (0.709) | secretory pathway (0.919) | 1-19 | |
| | At5g02260 | plasma membrane (0.685) | secretory pathway (0.969) | 1-20 | no |
| | At5g06230 | plasma membrane (0.790) | secretory pathway (0.744) | 1-38 | |
| | At5g06860 | outside (0.733) | secretory pathway (0.964) | 1-21 | |
| | At5g07030 | outside (0.820) | secretory pathway (0.559) | 1-19 | |
| | At5g09440 | outside (0.820) | secretory pathway (0.812) | 1-19 or 1-23 | |
| | At5g10770 | plasma membrane (0.760) | secretory pathway (0.276) | 1-25 | |
| | At5g11420 | outside (0.820) | secretory pathway (0.989) | 1-22 | |
| | At5g12940 | outside (0.820) | secretory pathway (0.985) | 1-29 or 1-26 | |
| | At5g23210 | outside (0.820) | secretory pathway (0.992) | 1-25 | |
| | At5g25460 | outside (0.820) | secretory pathway (0.979) | 1-19 | |
| | At5g26260 | outside (0.547) | secretory pathway (0.926) | 1-22 or 1-23 | |
| | At5g26280 | outside (0.528) | secretory pathway (0.963) | 1-22 or 1-23 | |
| | At5g34850 | outside (0.748) | secretory pathway (0.870) | 1-16 or 1-22 | |
| | At5g34940 | outside (0.820) | secretory pathway (0.996) | 1-21 | |
| | At5g43060 | outside (0.685) | secretory pathway (0.991) | 1-21 | |
| | At5g44380 | plasma membrane (0.811) | secretory pathway (0.439) | 1-32 | no |
| | At5g63810 | outside (0.819) | secretory pathway (0.887) | 1-29 | |
| | At5g64260 | outside (0.685) | secretory pathway (0.966) | 1-19 or 1-23 | |
| intracellular | At1g67090* | chloroplast (0.923) | chloroplast (0.769) | | |
| | | endoplasmic reticulum (0.910) (C-term KDEL) | secretory pathway (0.952) | 1-24 | |
| | At3g09260 | | other (0.625) | | |
| | At3g16880 | cytoplasm (0.450) | other (0.891) | | |
| | At4g15440 | microbody (0.540) | other (0.493) | | |
| | At4g22165 | microbody (0.640) | other (0.847) | | |
| | At4g23670 | microbody (0.560) | secretory pathway (0.962) | 1-23 | |
| | At4g28520° | outside (0.820) | chloroplast (0.741) | | |
| | At5g38410* | outside (0.370) | chloroplast (0.806) | | |
| | At5g38420* | endoplasmic reticulum (0.550) | chloroplast (0.807) | | |
| | At5g38430* | outside (0.370) | secretory pathway (0.975) | 1-24 or 1-23 | |
| | At5g44120° | outside (0.700) | | | |
| not clear | At2g21540 | plasma membrane (0.700) | other (0.945) | | no |
| | At3g26380 | outside (0.690) | other (0.355), secretory pathway (0.168) | 1-32 | yes |
| | At3g32980 | mitochondry (0.660) | secretory pathway (0.356) | 1-29 | |

step 2: LiCl extract

| | | | | | |
|-----------------------------|-----------------|--|---------------------------|--------------|-----|
| transmembrane domain | At1g54010 | plasma membrane (0.685) | secretory pathway (0.991) | 1-29 | yes |
| | At1g73620 | Golgi (0.900), plasma membrane (0.790) | other (0.532) | | yes |
| | At4g16590 | plasma membrane (0.600) | other (0.879) | | yes |
| | At5g20630 | plasma membrane (0.460) | secretory pathway (0.922) | 1-20 | yes |
| outside | At1g03220 | outside (0.820) | secretory pathway (0.912) | 1-22 | |
| | At1g03230 | outside (0.820) | secretory pathway (0.910) | 1-23 | |
| | At1g09750 | outside (0.456) | secretory pathway (0.899) | 1-21 or 1-23 | |
| | At1g17860 | outside (0.690) | secretory pathway (0.910) | 1-19 | |
| | At1g29670 | outside (0.820) | secretory pathway (0.987) | 1-24 | |
| | At1g47128 | outside (0.771) | secretory pathway (0.993) | 1-21 | |
| | At1g68560 | outside (0.820) | secretory pathway (0.982) | 1-27 | |
| | At1g73260 | outside (0.542) | secretory pathway (0.985) | 1-26 | |
| | At1g78850 | outside (0.820) | secretory pathway (0.973) | 1-22 | |
| | At2g05580 | outside (0.820) | secretory pathway (0.993) | 1-20 | |
| | At2g22170 | outside (0.820) | secretory pathway (0.990) | 1-21 | |
| | At2g28790 | outside (0.705) | secretory pathway (0.994) | 1-24 or 1-21 | |
| | At2g34700 | outside (0.432) | secretory pathway (0.790) | 1-23 or 1-28 | |
| | At3g14310 | plasma membrane (0.460) | secretory pathway (0.227) | 1-40 or 1-37 | no |
| | At3g16850 | outside (0.820) | secretory pathway (0.965) | 1-19 or 1-20 | |
| | At3g21770 | outside (0.820) | secretory pathway (0.967) | 1-27 | |
| | At3g49120 | outside (0.609) | secretory pathway (0.604) | 1-28 or 1-29 | |
| | At3g54400 | outside (0.595) | secretory pathway (0.409) | 1-19 | |
| | At4g30170 | outside (0.695) | secretory pathway (0.980) | 1-25 | |
| | At4g34980 | outside (0.820) | secretory pathway (0.980) | 1-20 | |
| | At5g06860 | outside (0.733) | secretory pathway (0.964) | 1-21 | |
| | At5g07030 | outside (0.820) | secretory pathway (0.559) | 1-19 | |
| | At5g09440 | outside (0.820) | secretory pathway (0.812) | 1-19 or 1-23 | |
| | At5g11420 | outside (0.820) | secretory pathway (0.989) | 1-22 | |
| | At5g25460 | outside (0.820) | secretory pathway (0.979) | 1-19 | |
| | At5g26280 | outside (0.528) | secretory pathway (0.963) | 1-22 or 1-23 | |
| | At5g51260 | outside (0.820) | secretory pathway (0.938) | 1-19 | |
| | At5g59090 | outside (0.820) | secretory pathway (0.978) | 1-24 | |
| At5g66590 | outside (0.820) | secretory pathway (0.973) | 1-23 | | |
| intracellular | At5g20830 | microbody (0.475) | other (0.669) | 1-20 | |
| not clear | At3g42160 | plasma membrane (0.650) | other (0.925) | | no |

colour code:

proteins found at both steps 1 and 2
 proteins found at both steps 1 and 2



* small subunit of RUBISCO

° homolog to storage proteins, most probably vacuolar localization

(a) PSORT : <http://psort.nibb.ac.jp/form.html> [28]

(b) TargetP: <http://www.cbs.dtu.dk/services/TargetP/> [29]

(c) Two sizes are indicated when different signal peptides are predicted by PSORT and TargetP. The first one is predicted with PSORT.

(d) Aramemnon: <http://aramemnon.botanik.uni-koeln.de/> [30]

Table 5 - Bioinformatic analysis of proteins extracted from cell walls of *A. thaliana* etiolated hypocotyls with SDS and DTT.

Proteins were extracted from *A. thaliana* cell walls of etiolated hypocotyls as described in Figure 6. One extraction was performed using SDS and DTT. All proteins sequences were analyzed with bioinformatic programs to predict their sub-cellular localization. Proteins for which predictions by different bioinformatic programs are in conflict are classified as “not clear”.

| step 3: SDS-DTT | Predicted subcellular localization | Gene (<i>A. thaliana</i>) | PSORT (a) | TargetP (b) | Predicted signal peptide (c) | Aramemnon (d) | |
|----------------------|------------------------------------|--------------------------------|---|------------------------------------|---------------------------------|---------------|--|
| transmembrane domain | | At2g25300 | chloroplast thylakoid membrane (0.765), plasma membrane (0.650) | chloroplast (0.573) | | yes | |
| | | At4g33230 | chloroplast thylakoid membrane (0.615), plasma membrane (0.600) | other (0.932) | | yes | |
| | | At4g25080 | endoplasmic reticulum (0.600), mitochondry (0.453), chloroplast (0.376) | chloroplast (0.866) | | yes | |
| | | At2g24820 | mitochondry (0.791), microbody (0.635), chloroplast (0.500) | chloroplast (0.897) | | yes | |
| | | At4g15820 | mitochondry (0.861), chloroplast (0.660), plasma membrane (0.650) | mitochondry (0.537) | | yes | |
| | | At1g72990 | outside (0.820) | mitochondry (0.957) | 1-29 | yes | |
| | | At1g27200 | plasma membrane (0.790) | other (0.521) | | yes | |
| | | At3g05610 | plasma membrane (0.790) | mitochondry (0.537) | | yes | |
| | | At3g61270 | plasma membrane (0.790) | other (0.843) | | yes | |
| | | At4g15320 | plasma membrane (0.600) | other (0.879) | | yes | |
| | | At4g16590 | plasma membrane (0.600) | other (0.879) | | yes | |
| | | At5g41390 | plasma membrane (0.600) | mitochondry (0.750), other (0.544) | | yes | |
| | outside | | At1g66270 | outside (0.820) | secretory pathway (0.976) | 1-24 | |
| | | | At1g71695 | outside (0.820) | secretory pathway (0.829) | 1-22 or 1-31 | |
| | | | At2g46570 | outside (0.370) | secretory pathway (0.868) | 1-20 or 1-29 | |
| | | At3g14040 | outside (0.820) | secretory pathway (0.984) | 1-23 or 1-25 | | |
| | | At4g11310 | outside (0.820) | secretory pathway (0.995) | 1-18 or 1-23 | | |
| | | At4g12880 | outside (0.820) | secretory pathway (0.952) | 1-18 or 1-26 | | |
| | | At4g28790 | outside (0.820) | secretory pathway (0.726) | 1-17 or 1-24 | | |
| | | At4g33810 | outside (0.820) | secretory pathway (0.910) | 1-24 | | |
| | | At5g07030 | outside (0.820) | secretory pathway (0.559) | 1-19 | | |
| | | At5g25460 | outside (0.820) | secretory pathway (0.979) | 1-19 | | |
| | | At5g44020 | mitochondry (0.850), outside (0.820) | secretory pathway (0.845) | 1-16 or 1-21 | | |

| | | | | | |
|---------------|------------|---|------------------------------------|---------------|----|
| intracellular | ArthCp029 | chloroplast | | | |
| | ArthCp030 | chloroplast | | | |
| | At1g55490 | chloroplast (0.864) | chloroplast (0.979) | | |
| | At1g67090* | chloroplast (0.923) | chloroplast (0.769) | | |
| | At2g21170 | chloroplast (0.888) | chloroplast (0.950) | | |
| | At3g04350 | chloroplast (0.842) | other (0.635), chloroplast (0.451) | | |
| | At3g13470 | chloroplast (0.950) | chloroplast (0.924) | | |
| | At3g53460 | chloroplast (0.903) | chloroplast (0.903) | | |
| | At4g15040 | chloroplast (0.496) | other (0.625), chloroplast (0.289) | | |
| | At4g20360 | chloroplast (0.950) | chloroplast (0.975) | | |
| | At5g20720 | chloroplast (0.895) | chloroplast (0.901) | | |
| | At5g54190 | chloroplast (0.924) | chloroplast (0.957) | | |
| | | endoplasmic reticulum (0.910) (C-term KDEL) | secretory pathway (0.952) | 1-24 | |
| | At3g09260 | | secretory pathway (0.962) | 1-23 | |
| | At4g28520° | outside (0.820) | secretory pathway (0.975) | 1-24 or 1-23 | |
| | At5g44120° | outside (0.700) | | | |
| | At1g49240 | cytoplasm (0.450) | other (0.891) | | |
| | At3g18780 | cytoplasm (0.450) | other (0.883) | | |
| | At4g11850 | cytoplasm (0.450) | other (0.806) | | |
| | At5g17920 | cytoplasm (0.450) | other (0.713) | | |
| | At4g02520 | microbody (0.520) | other (0.556) | | |
| | At2g13890 | endoplasmic reticulum (0.850) | other (0.609) | | |
| | At1g13440 | microbody (0.539) | other (0.610) | | |
| | At1g60120 | microbody (0.704) | other (0.753) | | |
| | At1g78380 | microbody (0.640) | other (0.523) | | |
| | At3g02230 | microbody (0.603) | other (0.765) | | |
| | At3g04120 | microbody (0.472) | other (0.619) | | |
| | At3g60120 | microbody (0.640) | other (0.712) | | |
| | At5g58690 | microbody (0.499) | other (0.598) | | |
| | not clear | At3g49400 | plasma membrane (0.650) | other (0.338) | no |
| | | At5g37470 | plasma membrane (0.600) | other (0.973) | no |

colour code:

proteins also extracted by CaCl₂ or LiCl
proteins also extracted by CaCl₂ or LiCl
proteins also extracted by CaCl₂ or LiCl



* small subunit of RUBISCO

° homolog to storage proteins, most probably vacuolar localization

(a) PSORT : <http://psort.nibb.ac.jp/form.html> [28]

(b) TargetP: <http://www.cbs.dtu.dk/services/TargetP/> [29]

(c) Two sizes are indicated when different signal peptides are predicted by PSORT and TargetP. The first one is predicted with PSORT.

(d) Aramemnon: <http://aramemnon.botanik.uni-koeln.de/> [30]