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Connecting the dots: from nanodomains to physiological functions of REMORINs

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► **To cite this version:**

Paul Gouguet, Julien Gronnier, Anthony Legrand, Artemis Perraki, Marie-Dominique Jolivet, et al.. Connecting the dots: from nanodomains to physiological functions of REMORINs. *Plant Physiology*, 2021, 185 (3), pp.632-649. 10.1093/plphys/kiaa063 . hal-02996729

HAL Id: hal-02996729

<https://hal.science/hal-02996729v1>

Submitted on 9 Nov 2020

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1 Connecting the dots: from nanodomains to physiological functions
2 of REMORINS

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36

37 **Abstract**

38 REMORINs (REMs) are a plant-specific protein family, proposed regulators of
39 membrane-associated molecular assemblies and well-established markers of
40 plasma membrane nanodomains. REMs have been shown to play a diverse set
41 of functions in plant interactions with pathogens and symbionts, responses to
42 abiotic stresses, hormones signaling and cell-to-cell communication. In this
43 review, we extensively highlight the roles and reported associations of REMs
44 throughout the literature. We subsequently discuss the physiological functions
45 of REMORINs, the mechanisms underlying their nanodomain-organization and
46 their putative function as regulators of nanodomain-associated molecular
47 assemblies. Furthermore, we discuss how REMORINs phosphorylation may
48 regulate their functional versatility. Overall, through data-mining and
49 comparative analysis of the literature, we suggest how to further study the
50 molecular mechanisms underpinning the functions of REMs.

51

52 **Advances Box**

- 53 • REMORINs are membrane-bound plant-specific proteins family involved
54 in response to biotic (bacteria, viruses, fungi, oomycetes, mycorrhizae) and
55 abiotic stresses (cold, mannitol, salt...), as well as developmental cues.
56 • REMORINs are strongly embedded in the inner-leaflet of the plasma
57 membrane by an unconventional mechanism involving anionic lipids and
58 sterols, and are proposed as nanodomain-organizing proteins.
59 • REMORINs are highly phosphorylated proteins containing intrinsically
60 disordered regions, which likely play a role in scaffolding protein complexes.
61 • REMORINs regulate cell-to-cell communication through plasmodesmata.

62

63 **Outstanding Questions Box**

- 64 • What are the molecular mechanisms underlying the formation of diverse
65 and coexisting REMORIN nanodomains?
66 • How can REMORIN functional versatility be explained?
67 • What are the consequences of the phosphorylation(s) of REMORIN's
68 intrinsically disordered regions in term of 3D structure, protein-protein
69 interaction and nanodomain organization?
70 • How do REMORINs regulate cell-to-cell communication through
71 plasmodesmata?

72

73 **One-sentence summary**

74 This review collates and discusses all the available information on the plant-
75 specific plasma membrane-bound family of REMORIN proteins involved in a
76 plethora of cellular processes, likely as scaffolding factors.

77

78	DISCOVERY OF REMORINS
79	REMORINS LOCALIZE IN DIVERSE AND COEXISTING NANODOMAINS
80	Mechanisms of REMs' Association to PM Nanodomains
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104 REMORINS DISCOVERY

105

106 In this review on the plant-specific multigenic-family of REMORIN proteins (REMs), it is
107 first important to remember how these proteins were discovered and came to be studied.
108 REMs were first identified in tomato (*Solanum lycopersicum*) and potato (*Solanum*
109 *tuberosum*) by Edward Farmer, Gregory Pearce and Clarence Ryan at the Institute of
110 Biological Chemistry, Washington University, USA in 1989, in a will of identifying molecular
111 actors involved in the perception of polygalacturonides by plant cells (Farmer et al., 1989).
112 Polygalacturonides (PGA) are leaf pectic polysaccharides present in the plant cell wall which
113 are released during wounding and pathogen attack. These cell wall compounds are
114 molecules that the plant cell may perceive as an attack warning for a large range of
115 pathogens (Voxeur and Höfte, 2016). It had been reported that PGA treatments were
116 sufficient to induce the local and systemic release of proteinase inhibitors (Ryan and An,
117 1988). The plant secretes these proteinase inhibitors in order to counteract the potential
118 proteases produced by the pathogens attacking the plant. Considering that these
119 polysaccharides are not able to diffuse as fast as the systemic response is triggered, Farmer
120 et al. investigated whether any signaling mechanism such as phosphorylation was activated
121 at the plasma membrane (PM) of PGA-treated cells. Investigating phosphorylation events at
122 the PM would enable the isolation of proteins able to perceive or relay the release of PGA in
123 the apoplast. This would permit to subsequently explore the molecular agents involved in
124 the systemic reaction triggered by wounding. It was in these *in vitro* phosphorylation assays
125 on isolated tomato- and potato-PM that a clear band appeared on an electrophoresis gel at
126 the molecular weight of 34 kilodaltons. This *phosphorylated protein* of 34 kilodaltons was
127 therefore first called *pp34* (Farmer et al., 1989). Consequently, *pp34* was used as a marker
128 for the plant-response to wounding, and by proxy, for the response to the most efficient
129 PGA elicitor: α -1,4-D-polygalacturonic acid (Farmer et al., 1991). By post-phosphorylation
130 hydrolysis of *pp34* and 2D electrophoresis, it was detected that the major phosphorylated
131 residue in consequence to PGA treatment was Threonine with an 11-fold increase in
132 phosphorylation (Farmer et al., 1991). The potato (*Solanum tuberosum* L.) *pp34* was then
133 purified after biochemical purification using a combination of phenol extraction and re-
134 solubilization after trichloroacetic acid (TCA) precipitation (Jacinto et al., 1993) and cloned by
135 (Reymond et al., 1996). The sequence of *pp34* turned out to be one of a hydrophilic protein

136 but unintuitively, still tightly bound to the PM. *Pp34* was then renamed REMORIN in
137 reference to the work of J.L. Borges, “Book of Imaginary Beings” (*El libro de los seres*
138 *imaginarios*, J.L. Borges, 1969), in which a remora or “suckerfish” is depicted as attaching
139 itself to vessels and larger fish (Raffaele et al., 2007). The name REMORIN was therefore
140 chosen by analogy to its binding to the PM whilst displaying an overall hydrophilic residue
141 profile (Reymond et al., 1996). Concurrently to the experiments of Farmer et al., Alliotte et al.
142 isolated a similar protein in *Arabidopsis thaliana* termed DNA-binding protein (*dbp*). This
143 gene would be later known as AtREM1.3 (At2g45820) and was first characterized as a DNA-
144 binding protein due to its highly-hydrophilic nature permitting electrostatic interactions with
145 DNA and its amino-acid composition similar to Histone 1 proteins (Alliotte et al., 1989).

146

147 Genome-wide analyses have shown that the REM family is specific to the land-plant
148 lineage (Raffaele et al., 2007). REM proteins present a highly-conserved C-terminal domain
149 and a divergent N-terminal domain, which has been the basis for their phylogenetic
150 classification into 6 separate groups (Raffaele et al., 2007). For example, we count 19
151 OsREMs in rice *Oryza sativa* and 16 AtREMs in *Arabidopsis thaliana*. Note that during the
152 writing of this review we found a 17th AtREM in the *A. thaliana* genome belonging to Group
153 2. We named it AtREM2.1 (At1g63295), see supplemental figure 1. Land plants have been
154 evolving for 450-500 million years from an ancestral Charophycean algae (Delwiche and
155 Cooper, 2015). BLAST analysis and keyword searches have identified no REM homologues in
156 algal genomes (Raffaele et al., 2007), and a recent BLAST-analysis in *Oestrecoccus*
157 *lucimarinus*, *Chlorella vulgaris*, *Volvox carteri*, *Chlamydomonas reinhardtii*, *Ulva spp*, and
158 *Micromonas pusilla* has confirmed this statement (data not shown). Hence, the symbolism of
159 the name REMORIN would come to be even more poignant, considering that the REM clade
160 appears to have emerged in the first land plants (Raffaele et al., 2007). Naming this protein
161 after a fish can be perceived as somewhat of an ironic twist if taken into account the
162 putative role REMORIN proteins could have played in the adaptation of photosynthetic algae
163 during the “plant land invasion” (Wellman, 2010).

164

165 Since their discovery in the late 1980’s, REMs have been the subject of ever-increasing
166 attention (Figure 1). Be they directly the subject of studies or found in different screens of
167 “omics” approaches, REMs are consistently found in a large variety of academic inquiries,

168 providing grist to the mill to the idea that they could play a central role in plant development
169 and adaptation. The first REMORIN protein identified in potato, which would be later named
170 StREM1.3 for *Solanum tuberosum* REMORIN of Group 1 isoform 3. REMORIN's polyanion
171 binding capacity, originally linked to binding cell wall compounds (Reymond et al., 1996)
172 would be later mitigated by the discovery of REMORIN's presence as intrinsically inserted
173 within the PM inner-leaflet (Raffaele et al., 2009). Nevertheless, the recent discovery of
174 Group 1 REMs in a proteomic analysis of *A. thaliana* extracellular vesicles may potentially
175 change our view of REMORIN's strictly-PM function (Rutter and Innes, 2017; Rutter and
176 Innes, 2018).

177

178 In this review, we address the different characteristics that have been described for REMs
179 as well as an overview of the physiological roles that REMs may participate in. We will
180 discuss how REMs are anchored to the PM and cluster into PM-nanodomains, how they are
181 phosphorylated and the subsequent role of these post-translational modifications. Finally,
182 we will develop a number of perspectives on how REMs should be further studied in order to
183 better understand the many physiological conditions involving REMs.

184

185 **REMORINS LOCALIZE IN DIVERSE AND COEXISTING NANODOMAINS**

186

187 REMORINS predominantly associate with the PM (Raffaele et al., 2009; Marín et al., 2012;
188 Jarsch et al., 2014; Konrad et al., 2014; Perraki et al., 2014). Additionally to its PM
189 localization, StREM1.3 has been used to immobilize ER-PM contact sites by using bi-
190 molecular fluorescence complementation (BiFC) (Tao et al. 2019). Moreover, isoforms from
191 Group 1 and Group 6 REMs have been shown to be partially associated with the PD-PM
192 compartment in rice and in *Solanaceae* (Raffaele et al., 2009; Fernandez-Calvino et al., 2011;
193 Gui et al., 2014; Perraki et al., 2018). Nonetheless, translocation into the nucleus upon
194 interaction with α -importins (Marín et al., 2012) and re-localization to intracellular foci upon
195 perception of an immunogenic epitope of bacterial flagellum (Albers et al., 2019) have been
196 reported for Group 1 and Group 4 REMs, respectively.

197 Identification of Group 1 REMs in detergent-resistant membrane fractions (DRMs; a
198 biochemical counterpart of membrane sub-compartmentalization) from tobacco first
199 suggested a lateral organization of REMs into clusters at the PM (Mongrand et al., 2004).

200 REMs' co-purification with DRM appears to be dependent on the presence of phytosterols as
201 it was reported to be absent of DRMs in the sterol methyl-transferase mutant *smt1* albeit
202 still present in this fraction in the sterol glycosylation mutant *ugt80A2;B1* (Zauber et al.,
203 2014). AtREM1.2 also appeared to have a sterol- and very-long-chain-fatty-acid -dependent
204 patterning at the PM considering the "smoothing out" of its canonical patchy localization at
205 the PM under fenpropimorph and metazachlor treatments (Grison et al., 2015).

206 Electron microscopy immuno-localization, stimulated-emission depletion (STED)
207 microscopy and photoactivated localization microscopy (PALM) studies have all showed that
208 Group 1 REMs were organized into nanodomains around about 70-90 nm in diameter in
209 *Arabidopsis* and *Solanaceae* species (Raffaele et al., 2009; Demir and Horntrich, 2013;
210 Gronnier et al., 2017). Members of other groups in *Arabidopsis* and *Medicago* are organized
211 in PM domains that can be distinguished in density, size and shape (Jarsch et al., 2014).
212 Interestingly, evolutionary distant REMs (belonging to distinct groups *e.g.* groups 1 and 6)
213 localize in separate nanodomains hinting to that distinct REMs cluster into separate domains
214 in order to play independent functions (Jarsch et al., 2014; Bücherl et al., 2017). It must also
215 be noted that REMs of different groups are not found in the DRM-fractions of different plant
216 tissues (Stanislas et al., 2009; Keinath et al., 2010; Srivastava et al., 2013; Takahashi et al.,
217 2013), hinting to a diversity of REM-associated PM-domains and a dynamic-association of
218 REMs within different domains.

219

220 **Mechanisms of REMs Association to PM Nanodomains**

221 A number of works have been performed to understand how highly-hydrophilic REMs
222 could be tightly anchored to the PM and the molecular interactions leading to the clustering
223 of REMs into nanodomains. REMs are anchored to the PM inner-leaflet *via* the
224 unconventional lipid-binding motif called REMORIN C-terminal Anchor (REM-CA) (Raffaele et
225 al., 2009; Konrad et al., 2014; Perraki et al., 2014; Gronnier et al., 2017). In the past few
226 years, several molecular determinants regulating REMs' nanodomain organization have
227 emerged and need to be further studied to fully understand the diversity of REMs'
228 clustering. There are at least four determinants: lipid-binding properties of REM-CA domain
229 (that also can be S-acylated), lipid/lipid interactions, REM-REM oligomerization and REM-
230 cytoskeleton interactions. Here we review the knowledge obtained to explain the molecular
231 mechanisms at play.

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1. The unconventional membrane-anchoring REMORIN C-terminal Anchor domain (REM-CA) and S-acylation

REMs are synthesized in the cytosol as they contain no target-peptides or transmembrane domains (Raffaele et al., 2007). They attached to the PM independently of the conventional secretory pathway (Gronnier et al., 2017). In the case of StREM1.3, the last 28 amino acids (*i.e.* REM-CA) folds in the presence of specific lipids (Gronnier et al., 2017). This folding occurring during REM's interaction with the PM leads, or is concomitant, to REM-nanodomain formation. This is driven by protein-lipid interactions between the REM-CA and the PM's inner-leaflet lipids: negatively-charged phosphoinositides (PIPs), notably the Phosphatidylinositol-4-phosphate (PI4P), and sterols, notably sitosterol (Raffaele et al., 2009; Legrand et al., 2019), (Figure 2). REM-CA binds to PI4P with a yet unknown stoichiometry through its Lysine/Arginine residues by electrostatic interactions partially folds into an alpha helix in the presence of PI4P and sitosterol and also inserts itself into the hydrophobic core of the bilayer (Gronnier et al., 2017). Conceptually, with PIPs bearing mostly saturated acyl-chains (Furt et al., 2010), and their reported ability to cluster together to form nanodomains (Bilkova et al., 2017) together with the possibility for sitosterol to be recruited in the bilayer, as was shown *in vitro* for cholesterol (Engberg et al., 2016); REMs could be either targeted to pre-existing nanodomains or participate in the organization of their own lipid environments. Both the latter and former possibilities for REMs' association to PM-nanodomains still remain open questions.

The presence of cysteine residues in the conserved REMORIN_C domain of many REMs raised the possibility of membrane association due to S-acylation. AtREM1.2 was the first REM to be found to be S-acylated (Hemsley et al., 2013). SYMREM1 (MtREM2.2) as well as AtREM1.3, AtREM4.2, AtREM6.1 and AtREM6.3 have been described to be strictly PM localized thanks to their REM-CA moieties. AtREM1.2 and AtREM6.4 were also shown to need their REM-CA domains to localize at the PM, and all lost strict-PM localization when the REM-CA Cysteines residues were substituted by Alanine residues (Konrad et al., 2014). Yet for SYMREM1, the Cysteine substitution did not reduce its PM-localization and moreover did not change its segregation pattern in the PM, hinting to a more complex PM association mechanism. Interestingly, AtREM6.4, which localizes to PM, has its localization altered to intracellular vesicles when mutated at a C-terminal Cysteine residue (Konrad et al., 2014).

264 Altered localization when S-acylation is abolished *via* 2-bromopalmitate was also observed
265 with the rice REM OsREM6.6 (Gui et al., 2015). This alteration of localization of S-acylation-
266 deficient REM is reminiscent of the observation of the mutant NbREM1.1^{C206A} and its
267 relocalization to RFP-ATG8e-tagged vesicles (Fu et al., 2018). It is important to note that
268 NbREM1.1^{C206A} is no longer organized in nanodomains nor co-purifies with the DRM
269 biochemical fraction (Fu et al., 2018). This highlights the importance of the REM-CA as a
270 moiety strongly determinant of REM's general membrane affinity as well as REM's
271 organization within these membranes. This idea is virtually illustrated in Fu et al. 2018 by the
272 difference between NbREM1.1 and NbREM1.1^{C206A} respective localization in both *N.*
273 *benthamiana* epidermal cells and *N. benthamiana* protoplasts. Their localization varies from
274 organized PM-domains to smooth PM-localization, respectively for wild-type NbREM1.1 and
275 from smooth PM-localization to ER localization for the S-acylation mutant. These cell-
276 dependent localization variations could be explained by different membrane and cell-wall
277 compositions between these different cell types and also by the tissue-dependent native
278 expression and localization patterns (Bariola et al., 2004; Jarsch et al., 2014). It must be
279 noted that many other REMs do not have predicted S-acylation sites in their REMORIN_C
280 domain (Konrad et al., 2014; Gronnier et al., 2017).

281

282 2. REM Oligomerization

283

284 REM oligomerization is highly important for its stability and function. The first evidence of
285 this phenomenon was reported in Bariola et al. (2004) where the REMORIN_C coiled-coil
286 domain of Group 1 REMs was first explicated as such and proposed to participate in the
287 formation of REM multimers. Electronic microscopy and glutaraldehyde crosslinking assays
288 evidenced REM multimerization *via* the C-terminal region of two Group 1 REMs *i.e.*
289 StREM1.3 and SIREM1.2 (Bariola et al., 2004). This multimerization has been discussed in a
290 few papers with yet no *in vivo* proof of the order of oligomerization (Jaillais and Ott, 2020).
291 Bariola et al. (2004) argue *via* analytical ultracentrifugation of recombinant proteins and
292 cross-linking experiments on isolated PM that Group 1 REMs associate into dimers,
293 tetramers or higher-order oligomeric structures *via* their coiled-coil domains. Alternatively,
294 Perraki et al. (2012) developed the hypothesis that StREM1.3 would trimerize either before

295 or after the anchoring event at the PM. This hypothesis was upheld by gel filtration assays
296 with the *E. coli* purified 6His-tagged StREM1.3 protein.

297 In our current view, StREM1.3 is homo-trimeric in solution and in certain assembled
298 configurations (Bariola et al., 2004; Martinez et al., 2018), bundling three REM-CA domains
299 together. This trimeric hypothesis was further developed in Martinez et al. (2018) upon *in*
300 *silico* modelling confirmed by Solid-State NMR in conjunction with cryo-Electron Microscopy
301 (cryo-EM) and *in vivo* observations of mutations in the coiled-coil domain that impairs PM-
302 association (Figure 2). These *in vivo* observations seem to corroborate the hypothesis that in
303 a minimal state, the trimeric form is necessary for the anchoring to the PM. Cryo-EM further
304 revealed a possible lateral association of the trimeric REMs in the presence of an N-terminal
305 6His-tag (Martinez et al., 2018), yet the presence of a 6His-tag may also alter the oligomeric
306 behavior of proteins (Amor-Mahjoub et al., 2006). This casts a doubt on the trimer observed
307 by gel filtration. In any case, the existence *in vivo* of homo-oligomers and higher-order
308 oligomers has not been invalidated by the latest data. Because of steric hindrance between
309 the oligomers and the lipid headgroups, as well as considering protein-lipid interactions, the
310 overall REM orientation is likely rather perpendicular to the PM, placing the REM-CA
311 domains of the oligomeric REMs symmetrically on the lipid headgroups (Figure 2). Formation
312 of higher-order oligomers, i.e. oligomers of trimers, as a mean to drive nanoclustering
313 cannot be excluded but has yet to be tested. Interactions between the REM trimers are likely
314 to further stabilize nanodomain clustering.

315

316 Group 1 AtREMs have been found to form oligomers in a large-scale study of PM protein
317 oligomerization in leaves (McBride et al. 2017). AtREM1.2, AtREM1.3 and AtREM1.4 were
318 predicted to form oligomeric complexes according to their ratio of the calculated mass to
319 the apparent mass (R_{app}) score which calculates a ratio between the predicted molecular
320 mass of the monomer and the measured molecular mass of the complex in which the
321 protein is found. AtREM1.2, AtREM1.3 and AtREM1.4 were found in different complexes to
322 have R_{app} scores ranging on average from 35 to 60 for AtREM1.2, 25 for AtREM1.3 and 30 to
323 95 for AtREM1.4 (McBride et al. 2017). This data may suggest that in addition to being
324 homo-oligomerized, Group 1 REMs are also forming multi-protein complexes. This idea has
325 already been suggested in the literature, notably in Lefebvre et al. (2010) where REMs are

326 compared to caveolins considering the common properties they share: small, oligomeric,
327 lipid raft-associated scaffold proteins that can form filamentous structures.

328

329 3. REM Association with the Cytoskeleton

330

331 In the seminal work of Jarsch et al. (2014), the subcellular localization of all Arabidopsis

332 REMs was studied, and certain members displayed characteristic patterns at the PM.

333 Observed filamentous exclusion zones (Jarsch et al., 2014) at the surface of the PM have led
334 to think that REMs could be associated in some way with the cortical cytoskeleton. A
335 localization dependent on microtubule polymerization has been reported for AtREM6.6
336 (Jarsch et al., 2014) as well as for AtREM1.2 (Szymanski et al., 2015) using the microtubule
337 depolymerizing drug oryzalin. Oryzalin treatment substantially mislocalized these REMs, that
338 were originally at the PM in domains (AtREM1.2; Szymanski et al., 2015) or forming strands
339 in the cytosol (AtREM6.6; Jarsch et al., 2014). An association with the actin cytoskeleton may
340 also be hypothesized considering the localization of the N-terminal regions of AtREM4.2 and
341 AtREM6.5 (Jarsch et al., 2014).

342 This interplay between the cortical cytoskeleton and PM-nanodomains fits with the
343 “fences and pickets” paradigm (Kusumi et al., 2012), where REMs could play a role as a
344 putative scaffold protein. This interplay with actin has been further demonstrated for other
345 REMs such as SYMREM1 (also termed MtREM2.2), a crucial actor involved in bacterial
346 symbiosis establishment in *Medicago truncatula*. MtREM2.2’s association to PM-
347 nanodomains has been shown to be destabilized by the actin depolymerizing drug,
348 latrunculin B, yet not by the microtubule depolymerizing drug, oryzalin. MtREM2.2’s
349 presence at the PM was also shown to be essential for the establishment of FLOT4-LYK3
350 domains that are dependent on the contact between FLOT4 and the actin cytoskeleton
351 (Liang et al., 2018). The rice Group 6 REM, OsREM6.6 or GSD1, has also been shown to
352 interact with the actin cytoskeleton. It was shown to bind OsACT1 *in planta* as long as its
353 REM-CA region was S-acylated (Gui et al., 2015). Treatment with cytochalasin D (a potent
354 inhibitor of actin polymerization) completely disrupted the punctate localization pattern of
355 AtREM1.2 and AtREM1.3 to a more uniform distribution with smaller punctate patterns of
356 lower intensity (Szymanski et al., 2015). Additionally, AtREM1.2 was shown to associate with
357 the actin cytoskeleton under viral infection (Cheng et al., 2020). This data reveals the strong

358 relationship between REMs' anchoring to the PM and the actin cytoskeleton in order to
359 ensure their function.

360

361 **THE BIOLOGICAL FUNCTIONS OF REMORINS**

362 **Plant-Microbe Interactions**

363 Numerous studies have reported the implication of REMs in plant interactions with
364 microorganisms such as bacteria, viruses or filamentous pathogens/symbionts (*i.e.* fungi and
365 oomycetes).

366 1. Bacteria:

367 The involvement of REMs in plant-bacteria interactions has mainly been studied in the
368 context of Group 2 REMs implicated in the establishment of bacterial symbiosis in legumes.
369 Yet several studies have also reported the involvement of Group 1 REMs in responses to
370 pathogenic bacteria.

371 *Group 2 REMs & Bacterial Symbiosis*

372

373 The particular Group 2 REMs, merely constituted of a REMORIN C_DOMAIN (Raffaele et
374 al., 2007), have been characterized by their role in the establishment of infection threads (IT)
375 during the symbiosis of *M. truncatula* and *Lotus japonicus* with *Rhizobiaceae* family bacteria
376 by participating in the formation of a root nodule (Lefebvre et al., 2010; Tóth et al., 2012).
377 SYMREM1 (MtREM2.2) in *M. truncatula* has been shown to be specifically expressed in roots
378 and nodules with an expression strongly induced by Nod factors treatment (Lefebvre et al.
379 2010), which are lipo-chitooligosaccharides produced by symbiotic bacteria or fungi in order
380 to initiate symbiosis (for review: Oldroyd 2013). Furthermore, MtREM2.2 knock-down lines
381 were shown to strongly reduce nodule establishment and growth (Lefebvre et al. 2010).
382 Analogously overexpression of Group 2 REM LjSYMREM1 significantly increased the number
383 of nodules per root in *L. japonicus*, establishing these orthologs as key players for symbiosis
384 in legumes (Tóth et al., 2012). In this context, MtREM2.2 has been further characterized at
385 the molecular level. It has been described as a scaffold protein due to its interaction with
386 three receptor-like kinases (RLKs) essential for nodule establishment and maintenance *i.e.*
387 NFP, DMI2 and LYK3 (Lefebvre et al., 2010). This interaction has recently been further
388 associated to the effective role of these membrane-bound receptors and MtREM2.2 along
389 with FLOT4 (FLOTILLIN 4) in the initiation of IT (Liang et al., 2018). MtREM2.2 is believed to

390 stabilize the interactions between FLOT4 and both NFP and LYK3 which would prevent the
391 RLKs' endocytosis and ensure nodulation-promoting signaling (Liang et al., 2018; see Figure
392 3A).

393

394 *Group 1 REMs & Bacterial Pathogenicity*

395

396 Considering the presence of Group 1 REMs within PM-nanodomains (Raffaele et al., 2009)
397 that are known to host many proteins involved in plant innate immunity such as RLKs and
398 other innate immunity-associated proteins (Morel et al., 2006; Stanislas et al., 2009; Keinath
399 et al., 2010), their involvement in these processes was long suspected. Under treatment by
400 the ubiquitous bacterial elicitor flagellin (flg22), AtREM1.3 was found to be differentially
401 phosphorylated up to 3-fold more on its Threonine 58 and approximately 1.5-fold on its
402 Serine 14 (Benschop et al., 2007). It must be noted that this large-scale phosphoproteomics
403 screen did detect other *A. thaliana* REMs such as AtREM1.2, AtREM5.1, AtREM6.1, AtREM6.2
404 and AtREM6.4 but they were not reproducibly differentially phosphorylated under flg22 or
405 xylanase treatments (Benschop et al., 2007). It is interesting to find a differential
406 phosphorylation status between AtREM1.3 and AtREM1.2 considering that they colocalize *in*
407 *vivo* (Jarsch et al., 2014). However, AtREM1.2 possesses Alanines at the two phosphosites
408 detected to be differentially phosphorylated under flg22 treatment (*i.e.* Ser14 and Thr58)
409 (Benschop et al., 2007; Raffaele et al., 2007). This suggests that there may be (a) specific
410 kinase(s) triggered under flg22 treatment that could recognize these sites. Moreover, a
411 thread of evidence leads to the implication of AtREM1.2 and AtREM1.3 in the cell's response
412 to bacterial infection. AtREM1.2 has been shown to be significantly up regulated at the
413 protein level in plants over-expressing the *Pseudomonas syringae* effector gene AvrRPM1
414 (Widjaja et al., 2009). Different AtREM1.2 post-transnationally modified peptides (putative
415 phospho-peptides) were recovered in this screen for low-abundant proteins involved in
416 plant defense, confirming the implication of AtREM1.2 in the general response to bacterial
417 infection (Widjaja et al., 2009), see supplementary table 1.

418 The AtREM1.2 has been shown to interact with RPM1 (RESISTANCE TO PSEUDOMONAS
419 SYRINGAE PV. MACULICOLA 1)- INTERACTING PROTEIN 4 (RIN4), an interacting partner of
420 RPM1 involved in bacterial disease resistance known as a negative-regulator of Pathogen-
421 associated Molecular Pattern (PAMP)-Triggered Immunity (PTI), more precisely PTI linked to

422 *Pseudomonas syringae* (Mackey et al., 2002; Liu et al., 2009a; Lee et al., 2015). In response
423 to bacterial attack and notably to the presence of the bacterial effector AvrRpm1 or AvrB,
424 RIN4 is known to be hyper-phosphorylated, thereby leading to RPM1-mediated resistance
425 (Mackey et al., 2002). RIN4 is also known to contain a protein cleavage site that can be
426 targeted by the *P. syringae* effector AvrRpt2 (as well as AtREM6.1; *in silico* prediction
427 (Chisholm et al., 2005) and induce RPS2-mediated resistance (Mackey et al., 2002). Induced-
428 phosphorylation of AtREM1.2 by the expression of avirulence pathogen genes is dependent
429 of RPM1 nucleotide binding site leucine rich repeat (NB-LRR) immune receptor (Widjaja et
430 al., 2009). Overall these data may suggest that AtREM1.2 lies at the crossroads of Effector-
431 Triggered Immunity (ETI) and PTI.

432 Additionally, AtREM1.2 and AtREM1.3 along with RIN4 have been identified as interactors
433 of the *P. syringae* effector HopF2b^{PtODC3000} via the proximity-dependent biotin identification
434 (BioID) technique that uses the *E. coli* biotin ligase BirA* to biotinylate potential interacting
435 proteins that come in proximity to BirA*-fused bait protein, here HopF2b^{PtODC3000} (Khan et al.,
436 2018). This triggers the questions whether bacterial effector proteins may target REMs to
437 suppress their function in immunity or if REMs are involved in perceiving bacterial effector
438 proteins. The implication of REMs in bacterial immunity remains to be deciphered further.

439 In *Solanaceae*, REMs have scarcely been reported as being involved in bacterial
440 interactions except for the potato REM StREMa4 (StREM1.4) that has been described as
441 differentially regulated under *Ralstonia solanacearum* infection (Kong et al., 2016).
442 StREM1.4's expression has been shown to be upregulated at 6- and 72-hours post-infection
443 and mainly expressed in the vascular bundle of leaves and the phloem of stems (Kong et al.,
444 2016). This data suggests that StREM1.4 may be involved in the regulation of innate
445 immunity/cell-to-cell communication in the latter tissues considering its high-homology to
446 StREM1.3 and the fact that *R. solanacearum* is a bacterial pathogen that colonizes the
447 vascular tissue of *S. tuberosum* plants.

448

449 2. Viruses

450 The first REM to be shown as implicated in the context of viral infection has been
451 StREM1.3. It has been demonstrated that its overexpression, leads to the limiting of the cell-
452 to-cell movement of *Potato Virus X* (PVX) (Raffaele et al., 2009) and, had a general effect on
453 the gating of PD even in the presence of viral movement proteins such as 30K from the

454 *Tobacco Mosaic Virus* (TMV) or Hc-Pro from the *Potato Virus Y* (PVY) (Perraki et al., 2014). In
455 addition to limiting PVX cell-to-cell movement, StREM1.3 has also recently been shown to
456 limit TMV cell-to-cell propagation (Perraki et al., 2018). Over-expression of StREM1.3 was
457 shown not to impair the silencing suppressor activity of the PVX-encoded TRIPLE-GENE
458 BLOCK protein 1 (TGBp1) (Perraki et al., 2012), but rather to induce the increase in callose
459 accumulation at PD pit-fields (Perraki et al., 2018). Furthermore, StREM1.3's capacity in
460 hindering PVX cell-to-cell movement has been shown to be abolished by altering the
461 electrostatic properties of the REM-CA, thereby modifying its localization pattern at the PM
462 (Gronnier et al., 2017). Yet, StREM1.3 was shown to physically interact with the PVX
463 movement protein TGBp1 with or without an impaired REM-CA domain (Perraki et al., 2012).

464 *Solanaceae* Group 1 REMs have also been studied in the context of *Tenuivirus* infection.
465 *N. benthamiana* NbREM1.1 and NbREM1.2 were shown to be degraded during *Rice Stripe*
466 *Virus* (RSV) infection in consequence to the interference of the RSV-encoded protein, NSvc4,
467 with the S-acylation of these Group 1 REMs' REM-CA. The degradation of NbREM1.1 and
468 NbREM1.2 *via* the autophagy pathway led to RSV circumventing NbREM1-associated
469 resistance (Fu et al., 2018). In contrast, a recent study has underlined the effect of the
470 tobacco REM NtREM1.2 on the cell-to-cell movement of a *Tobamovirus*, the *Tomato Mosaic*
471 *Virus* (ToMV) (Sasaki et al., 2018). ToMV infection and the overexpression of ToMV
472 movement proteins separately affected NtREM1.2's localization by inducing its aggregation
473 at the PM. Dissimilarly to StREM1.3, which is known to localize in a patchy pattern at the PM
474 and is present in PM-nanodomains, NtREM1.2 localized in a uniform fashion throughout the
475 PM regardless of N-terminal or C-terminal fusion to fluorescent tags. Considering the high
476 sequence conservation of the C-terminal region, this suggested that the N-terminal region
477 was involved in NtREM1.2's characteristic localization. Interestingly, NtREM1.2 was shown to
478 interact and colocalize with ToMV's 30-kDa movement protein at PD using BiFC and aniline
479 blue staining. *Agrobacterium*-mediated transient expression of NtREM1.2 was also shown to
480 slightly increase ToMV infection foci size (Sasaki et al., 2018). Moreover, in ToMV infected
481 cells, NtREM1.2 aggregates occur close to tubular ER structures and are associated with
482 ToMV's 30-kDa movement protein bodies that appeared to be linked to the Endoplasmic
483 Reticulum-Actin network (Sasaki et al., 2018). Finally, *A. thaliana* AtREM1.2 has been shown
484 to play a role in *Turnip Mosaic Virus* (TuMV) cell-to-cell movement by competing with the
485 TuMV protein VPg, in the actin-dependent regulation of PD aperture (Cheng et al., 2020).

486 Group 4 REMs have been reported as positive regulators of viral infection. AtREM4.1 and
487 AtREM4.2 were shown to be susceptibility factors during *Beet Curly Top Virus* and *Beet*
488 *Severe curly Top Virus* infection. This was shown using single- and double- knock-out and
489 overexpressing lines for AtREM4.1 and AtREM4.2. This effect of Group 4 REMs on geminiviral
490 infection could be linked to SnRK1, an important positive regulator of plant stress involved in
491 antiviral defense, which could phosphorylate AtREM4.1 *in vitro* (Son et al., 2014).

492

493 3. Fungi and Oomycetes

494 REMs have been reported to be **directly** implicated in interactions with filamentous
495 pathogens/symbionts.

496 *Filamentous pathogens*

497

498 StREM1.3 has long been established as a marker of *Phytophthora infestans* haustoria (Lu
499 et al., 2012; Bozkurt et al., 2014). The extrahaustorial membrane (EHM) is a host PM-derived
500 membrane formed by the protrusions of the oomycete (haustoria) within the plant cell
501 known to occur in the early stages of the infection and are thought to be a hub for nutrient
502 intake as well as effector delivery by the pathogen (Dagdaz et al., 2016). StREM1.3 has been
503 observed to label haustoria approximately 50 % of the time and specifically label non-calloxic
504 haustoria (Bozkurt et al., 2014). Moreover, the overexpression of StREM1.3 in *N.*
505 *benthamiana* and tomato increased susceptibility to *P. infestans* infection (Bozkurt et al.,
506 2014). Nevertheless, the true role of StREM1.3 during *P. infestans* has yet to be precisely
507 determined. Interestingly, recent studies showed the specific recruitment of
508 phosphoinositides (PIPs) to the plant-pathogen interfacial membrane during fungal infection
509 (Qin et al., 2020). Different PIPs were found enriched at EHM. Researchers demonstrated
510 that among the two PM phosphoinositides in Arabidopsis, Phosphatidylinositol 4,5-
511 bisphosphate (PI(4,5)P₂) was dynamically up-regulated at powdery mildew infection sites
512 and recruited to the EHM, whereas PI4P is absent in the EHM. Furthermore, the depletion of
513 PI(4,5)P₂ in the *pip5k1 pip5k2* mutant lines inhibited fungal pathogen development and
514 caused disease resistance, independent of cell death-associated defenses, involving
515 impaired host susceptibility. The fact that REMs both bind to PIPs and are involved in
516 immune responses to fungi **prompted** to examine in detail the link between these two
517 observations.

518

519 The first report of the implication of REMs in plant-fungal interactions was a maize Group
520 6 REM ZmREM6.3 that was found in a QTL (Quantitative Trait Loci) analysis for resistance to
521 northern leaf blight caused by the fungal pathogen *Setosphaeria turcica* (Jamann et al.,
522 2016). The importance of Remorins for the resistance of maize to fungal pathogens has also
523 been highlighted by the importance of ZmREM1.3 in the resistance to *Puccinia polyspora*
524 (Wang et al., 2019). AtREM1.3 was also found to interact with ergosterol, a fungal
525 metabolite toxic for plants (Khoza et al., 2019). Cucumber (*Curcumis sativus*) CsREMs that
526 presumably (*i.e.* closest ortholog annotations found using NCBI *BLASTp*) belong to Group 4
527 (Sequence ID: XP_004134586.1) and Group 1 (Sequence ID: XP_004133871.1; closest *A.*
528 *thaliana* ortholog: AtREM1.2) have been found to be present in a QTL genomic segment
529 termed *Pm5.1* and to be differentially expressed upon powdery mildew (*Podosphaera fusca*)
530 infection (Xu et al., 2017). These REMs are proposed to participate in the resistance to
531 powdery mildew conferred by the *Pm5.1* segment (Xu et al., 2017).

532 A recent study showed that overexpression of tomato (*Solanum lycopersicum*) SIREM1
533 increased susceptibility to the necrotrophic fungus *Botrytis cinerea* (Cai et al., 2020).
534 Heterologous expression of SIREM1 increased ROS accumulation and triggered other cell-
535 death regulators, suggesting a positive role of SIREM1 in plant cell-death and providing clues
536 for understanding the PCD molecular regulatory networks in plants.

537 Along with herbivores, pathogenic insects and bacteria, filamentous pathogens are
538 known for wounding plant tissue, yet out of all the latter-named pathogens, they are
539 particularly known for the diverse cell wall-degrading enzymes they are able to synthesize
540 and secrete (for review Kubicek et al., 2014). Therefore, the initial discovery of Group 1
541 REMs as being phosphorylated subsequently to the presence of cell wall degradation
542 products (*e.g.* PGA; Reymond et al., 1995) hints to the association of Group 1 REMs to the
543 response to fungal attack. An emerging field of research has been concentrating on the
544 vesicular exchanges that may occur during plant pathogen interactions. These extracellular
545 vesicles (EVs) are produced by the host and the pathogen and may contain a number of
546 defense compounds such as defense proteins, metabolites or interfering-RNAs involved in
547 post-transcriptional gene silencing (for review, Rutter and Innes, 2018; Rybak and Robatzek,
548 2019; Cui et al., 2020). Congruently, EVs have been reported to accumulate in large numbers
549 at the pathogenic fungi penetration sites produced by appressoria and haustoria (Meyer et

550 al., 2009; Micali et al., 2011). The presence of AtREM1.2 and AtREM1.3 in *A. thaliana*
551 **extracellular vesicles** alongside stress related proteins and compounds may well be a telltale
552 sign of Group 1 REMs' direct involvement in plant defense (Rutter and Innes, 2017). Coming
553 back to the recorded PGA-binding capacity of Group 1 REMs (Reymond et al., 1996), it could
554 have initially seemed unlikely that their presence in EVs is linked to this phenomenon
555 considering that AtREMs were not found to be phosphorylated under PGA-treatment, unlike
556 REMs from other species (Reymond et al., 1996). Nonetheless, more recent
557 phosphoproteomes of oligogalacturonide (OGA)-treated plants have been established and
558 have found AtREM1.3 and AtREM1.2 to be phosphorylated under OGA (degree of
559 polymerization = 9-15) treatment (Kohorn et al., 2016; Mattei et al., 2016). One of the
560 canonical markers of extracellular vesicles, PENETRATION3 (PEN3) was also found to be
561 phosphorylated under OGA treatment (Kohorn et al., 2016; Mattei et al., 2016). PEN3 is an
562 ATP Binding Cassette ABC transporter family protein and is thought to participate in the
563 transport of defense compounds along with other EV-resident proteins such as GTR1
564 (GLUCOSINOLATE TRANSPORTER1; At3g47960) and EPITHIOSPECIFIC MODIFIER1 (ESM1;
565 At3g14210) involved in glucosinolate biosynthesis and transport (Rutter & Innes 2017).
566 Moreover, RIN4 has also been found in the EV proteome along with EARLY-RESPONSIVE TO
567 DEHYDRATION4 (ERD4; At1g30360) which are known to interact with AtREM1.2 (Liu et al.,
568 2009b; Khan et al., 2018). This data may open new perspectives in understanding Group 1
569 REMs' role in link to wounding response.

570 **A recent protein- and metabolite-profiling of tomato and lettuce infected with**
571 ***Verticillium dahlia*, a soilborne fungal pathogen, showed that REMs were expressed in the**
572 **incompatible interaction together with lignin biosynthesis, phenylpropanoid, and**
573 **carbohydrate methylation pathways. Authors proposed that this response allows the**
574 **strengthening of plant cell walls, likely critical to confer resistance to *V. dahliae* (Hu et al.,**
575 **2019).**

576

577 *Filamentous symbionts*

578

579 A couple of papers have reported the implication of REMs in the establishment of
580 mycorrhizal symbiosis. The oak (*Quercus robur*) Group 4 REM QrREM4.1 (Accession number:
581 Qrob_P0167880.2) was transcriptionally detected in roots undergoing ectomycorrhizal

582 symbiosis with *Piloderma croceum* (Tarkka et al., 2013). An ortholog of Group 1 REMs
583 (Accession number: AFK42693.1) has been reported to be transcriptionally up-regulated in *L.*
584 *japonicus* roots 3-weeks post-inoculation with the ectomycorrhizal symbiotic fungi *Glomus*
585 *intraradices* (Kistner et al., 2005).

586

587 **Hormone Signaling & Abiotic Stress**

588 Throughout the relatively extensive literature that links the expression of REMs to
589 hormone signaling and/or abiotic stress, several patterns may be found. Considering the
590 overlapping nature of these types of events, we will proceed by grouping REMs by phylum in
591 order to describe the relevant data present in the literature.

592 1. Group 1 REMs

593 Group 1 REMs have been found to be transcriptionally up regulated in a large variety of
594 abiotic stress conditions. AtREM1.3 was initially found to be induced under water deficit
595 conditions (Reymond et al., 2000; Bray, 2002) as well as under cold, mannitol and salt stress
596 (Kreps et al., 2002). These types of stress are reminiscent of abscisic acid (ABA)-signaling
597 conditions. AtREM1.3 transcription has also been shown to be induced by auxin treatment in
598 the shoot apex, particularly in regions undergoing cell division (Alliotte et al., 1989). This
599 same isoform had also been found to interact with ARR4, an Arabidopsis response-regulator
600 induced by cytokinin treatment (Yamada et al., 1998). The *arr4* mutant displays an elongated
601 petiole phenotype (Verma et al., 2015). Group 1 REM isoforms from crops have evidenced to
602 be involved in hormonal signaling linked to development and stress responses. The tomato
603 SIREM1.2 has recently been shown to be involved in fruit ripening by interacting with the
604 ethylene biosynthesis proteins SAM1, ACS2 and ACO1. The overexpression was also shown
605 to up-regulate key genes involved in ethylene, lycopene biosynthesis and ripening regulators
606 (ACS2, ACS4, ACO1, ACO3, RIN, NOR, CNR, TAGL1, SIDML2, SIMS11) resulting in an effective
607 increase in the ethylene and lycopene content of fruit (Cai et al., 2018). This same tomato
608 REM isoform was found to be consequently transcriptionally upregulated (more than 9-fold)
609 in tomato plants overexpressing CaPIF1, a pepper zinc-finger transcription factor known to
610 be involved in resistance to bacterial infections (Oh et al., 2005; Seong et al., 2007). The
611 resulting CaPIF1 overexpressing lines were characterized by an enhanced resistance to cold
612 stress (Seong et al., 2007).

613 The functional characterization of a mulberry (*Morus indica*) Group 1 isoform MiREM1
614 evidenced its transcriptional upregulation under a number of abiotic stresses and hormone
615 treatments *e.g.* air drying, ABA, SA, BR treatments and mannitol and salt stress in the aerial
616 parts of the plant. Heterologous overexpression of MiREM1 in *A. thaliana* conferred
617 resistance to salt stress and drought in the extent that the overexpressing lines better
618 recovered from drought stress and maintained a higher fresh weight and root length than
619 the wild-type lines during salt stress (Checker and Khurana, 2013).

620 The potato StREM1.4 (or StREMa4) was found to be transcriptionally up regulated under
621 MeJA treatment up to 7-fold at 3 days post-treatment. On the other hand, ABA and SA
622 increased StREM1.4 transcription roughly 20-fold at 4 days and 4-fold at 5 days, respectively.
623 Interestingly, *in situ* hybridization of StREM1.4 transcripts revealed its presence in the
624 vascular bundles of leaves and phloem of stems (Kong et al., 2016). In strong correlation
625 with this study, AtREM1.2's lipid-dependent presence and organization at the PM was
626 shown to be a major determinant of SA-dependent closure of PD (Huang et al., 2019).
627 Likewise, the rice Group 1 isoform OsREM1.5 was found to be more than 2-fold up-regulated
628 by ABA and BR treatments (Lin et al., 2003). The up-regulation of Group 1 REM isoforms
629 seems to be a common feature in the aerial tissues under a variety of hormone treatments
630 and abiotic stresses, yet a study performed on barley aleurone (*Hordeum vulgare L. cv*
631 *Himalaya*) showed downregulation of the Group 1 REM HvREM1 upon ABA and GA
632 treatments (Chen and An, 2006).

633

634 2. Group 4 REMs

635

636 Group 4 REMs also appear to be induced by abiotic stresses and hormone treatments in
637 different plant species. AtREM4.1 and AtREM4.2 are transcriptionally upregulated by
638 drought, osmotic, salt stress and ABA treatment (Reymond et al., 2000; Bray 2002; Son et al.,
639 2014). In soy (*Glycine max*), GmREM4 transcript abundance was overall shown to increase in
640 drought conditions over a 20 hour-period and even more under “severe drought”
641 conditions. In addition, GmREM4 always followed diurnal oscillations with minimal
642 expression in the middle of the light period (Marcolino-Gomes et al., 2014). More than just
643 showing a transcriptional increase of Group 4 REMs during drought stress, this study brings
644 to light a circadian regulation of REMs, likely to be crucial for their function.

645 The rice (*Oryza sativa*) OsREM4.1 was shown to be up regulated by ABA treatment *via* the
646 bZIP transcription factor OsZIP23, which can bind the OsREM4.1 promoter. OsREM4.1
647 overexpression inhibited BR signaling by inhibiting OsSERK1 and OsBRI1 complex formation.
648 This REM effect is undermined by the phosphorylation of REM. Under high ABA
649 concentrations, OsREM4.1 is up regulated by OsZIP23 and inhibits the formation of the
650 OsSERK1/OsBRI1 complex. Under high BR concentrations, BR stabilizes the OsSERK1/OsBRI1
651 complex, which activates the phosphorylation of OsREM4.1 by OsBRI1, thereby reducing
652 OsREM4.1's affinity for OsSERK1 and enabling the BR signaling cascade. This system
653 maintains a dynamic equilibrium between ABA and BR signaling (Gui et al., 2016a), see
654 Figure 3B.

655 Overexpressing in rice a C-repeat binding factor (CBF)/dehydration-responsive element
656 binding protein (DREB) of the Antarctic plant *Deschampsia antarctica*, DaCBF7, enhanced cold
657 recovery and induced the strong up regulation of OsREM4.1 (5- to 10-fold higher than in WT
658 lines regardless of stress) (Byun et al., 2015). In maize (*Zea mays* L.), Group 4 REM
659 ZmREM4.1 transcripts were found in several tissues: Kranz mesophyll, bundle sheath,
660 vascular parenchyma, companion cells and sieve elements, with a specific accumulation
661 between the Kranz mesophyll and the bundle sheath. REM was shown to be transcriptionally
662 repressed in a maize cold-sensitive line after 28h (Bilska-Kos et al., 2016).

663

664 3. Group 6 REMs

665

666 The Group 6 REM SiREM6 (*Setaria italica*, fox-tail millet) has been found to be
667 transcriptionally up regulated under salt (NaCl 150mM), cold (4°C), ABA (100μM) and
668 osmotic (PEG 20% v/v) stress up to 12h post-stress. Yet this up regulation was weakly
669 observed under drought stress and SiREM6 overexpression did not impact drought tolerance
670 (under 300mM mannitol). SiREM6 overexpression in *A. thaliana* increased germination rate
671 and seedling biomass as well as seedling survival under salt stress. These characteristics
672 were linked to an increase in proline content and a reduction in electrolyte leakage.
673 Additionally, overexpression of SiREM6 in *A. thaliana* enhanced sensitivity to ABA treatment
674 (Yue et al., 2014). In rice (*Oryza sativa*), OsREM6.5 was also found to be highly upregulated
675 during drought stress (7.8-fold) and ABA treatment (9.5-fold) (Wu et al., 2006).

676 In *Populus euphratica*, a salt-resistant poplar, PeREM6.5 was induced by NaCl stress.
677 Interestingly, PeREM6.5 recombinant protein significantly increased the H⁺-ATPase
678 hydrolytic activity and proton transport activity in *P. euphratica* PM vesicles. Yeast two-
679 hybrid assays showed that PeREM6.5 interacted with RPM1-interacting protein 4 (PeRIN4)
680 and PeREM6.5 induced an increase in H⁺-ATPase activity that was moreover enhanced by
681 PeRIN4 recombinant protein. Finally, overexpression of PeREM6.5 in *A. thaliana* improved
682 salt tolerance. PeREM6.5, by regulating H⁺-ATPase activity in the PM, may therefore enhance
683 the plant capacity to maintain ionic homeostasis under salinity (Zhang et al., 2020).

684

685 More generally, a recent genome-wide analysis of the wheat genome *Triticum aestivum*
686 revealed that 12 members of the TaREM family of different groups were regulated during
687 cold acclimation in wheat in four different tissues (roots, crowns, stems, and leaves), with
688 the highest expression in roots (Badawi et al., 2019). This study provides valuable resources
689 for functional analysis aimed at understanding the role of TaREMs in stress adaptation.

690

691 **Cell-to-Cell Communication**

692

693 Throughout the different contexts that implicate the presence of REMs in the plants'
694 adaptation to the various aforementioned stimuli, one constant seems to stand out, which
695 may well explain the fact that REMs are so ubiquitously present in such diverse contexts:
696 cell-to-cell communication.

697 The first direct evidence of the implication of REMs in cell-to-cell communication was
698 revealed by the ability of StREM1.3 to hinder PVX cell-to-cell movement as well as GFP
699 diffusion in non-virally-infected plants in *N. benthamiana* leaf epidermal cells (Perraki et al.,
700 2012; Perraki et al., 2014). This capacity was shown to be dependent of the REMORIN_C
701 domain, shown to be responsible for its anchoring to the cytosolic leaflet of the PM (Perraki
702 et al., 2012; Gronnier et al., 2017). Conversely, Group 4 REMs have been evidenced to
703 potentially have an opposite effect on cell-to-cell connectivity. OsREM4.1 transcripts were
704 found to be localized in situ near PD linking cells from the Kranz mesophyll and the bundle
705 sheath (Bilska-Kos et al., 2016). This interface is a crucial zone for the systemic diffusion of
706 macromolecules necessary for plant development and for the plant-wide adaptation to

707 various biotic or abiotic stimuli. These observations could explain the data demonstrating
708 that AtREM4.1/4.2 positively regulate BSCTV and BCTV systemic infection in *A. thaliana* (Son
709 et al. 2014). This tissue-specific expression, REM group specificity and evidence of REMs'
710 involvement in cell-to-cell communication seem to be the key to understanding this
711 characteristic of REM function. Moreover, REM transcript and protein levels were shown to
712 increase in mature, ageing and senescing tissues, as well as in source parts of tobacco leaves,
713 where a majority of mature- and branched-PD are present (Raffaele et al., 2009). These
714 results suggest that tobacco Group 1 REMs predominantly associate with mature-branched-
715 PD.

716 The Group 6 REM OsREM6.6 was shown to be a strong regulator of PD permeability in
717 rice via the characterization of a tissue-specific expression mutant line. The mutant termed
718 GSD-1 (for grain setting defect 1) was shown to have an altered and ubiquitous expression of
719 OsREM6.6, which is natively only expressed in phloem companion cells, thereby inducing an
720 accumulation of starch and free-sugars in the leaf blades and consequently a reduction of
721 starch accumulation in grains (Gui et al., 2014).

722 The only occurrence in the literature of Group 5 REMs in regard to development and
723 indirectly cell-to-cell communication, has been the identification of Long Panicle 1 (LP1 or
724 OsREM5.3) displaying higher expression (6-fold) in young panicles correlated with smaller-
725 sized panicles while a mutant LP1 version, lacking this overexpression, correlated with longer
726 panicles (Liu et al., 2016). Reminiscent of the importance of cell-to-cell communication
727 regulation in plant development, the overexpression of the *A. thaliana* transposase
728 DAYSLEEPER was found to induce a more than 65-fold increase in transcript abundance of
729 AtREM6.7. The over- or null-expression of DAYSLEEPER induced very severe developmental
730 defects. These defects included slow growth, no expansion of the cotyledons or
731 development of abnormal flowers and leaves for the null mutants, and delayed flowering,
732 altered cauline leaves, fasciation and partial to total sterility for the overexpressing lines. An
733 intriguing phenotype of the latter lines was reduced petal and sepal growth along with the
734 margins of the sepals appearing petaloid (Bundock and Hooykaas, 2005). These defects
735 could possibly be induced by an alteration of PD conductivity in the meristematic zones
736 considering the known effect of Group 6 REMs on PD conductance (Gui et al., 2014).

737

738 **STRUCTURAL AND BIOLOGICAL IMPLICATION OF REM PHOSPHORYLATION**

739

740 Since the first identification of REM as an *in vitro* phosphorylated protein, pp34 (Farmer
741 et al., 1989), members of all REM groups have been detected in phosphoproteomes from
742 diverse tissues and biological contexts, revealing phosphorylation as a major *in vivo*
743 regulatory mechanism of REMs (see supplementary table 1 for a compilation of REM
744 phosphoproteomic data). A recent study established a phosphorylation pattern of 14
745 AtREMs in steady-state conditions from 30 different plant tissues (Mergner et al., 2020).
746 Apart from this broad-scale analysis, other studies have shown that, for some residues, the
747 phosphorylation of REMs is modulated by stress conditions such as flg22 and OG treatment,
748 nitrogen deprivation, ABA, H₂O₂, cold, osmotic and salt stresses (Benschop et al., 2007;
749 Kohorn et al., 2016; Menz et al., 2016; Nikonorova et al., 2018; Wang et al., 2020, see
750 supplementary table 1), suggesting functional roles of phosphorylation that remain to be
751 explored. Interestingly, most of the phosphorylation has been observed in the N-terminal
752 domain of REMs (Figure 4).

753 Sequence analysis and *in vitro* assays showed that AtREM1.3 contains an intrinsically
754 disordered N-terminal region (IDR) (Marín and Ott, 2012). Sequence prediction analysis
755 suggests that most REMs have an IDR in their N-terminal domain (Marín and Ott, 2012). IDR
756 regions are flexible and extended protein segments that provide dynamic structural
757 remodeling and protein-protein interaction plasticity. (Iakoucheva et al., 2004; Dyson and
758 Wright, 2005). They are often regulated *via* protein phosphorylation that may act as a
759 regulatory switch, leading to structural changes such as folding and the sequestration of
760 binding sites (Bah et al., 2015). Because they facilitate multiple protein recognition and
761 binding by acting as adaptable interaction surfaces, IDR regions are often found in hub
762 proteins that link interaction networks and integrate signals (Kim et al., 2008). REMs are
763 found to be phosphorylated *in vivo* mainly at IDR regions at the N terminus (Figure 4). REMs'
764 basal and signal-induced phosphorylation regions could regulate interactions with its protein
765 partners upon stimulus (Figure 4). This, and the fact that REMs participate in different plant
766 signaling networks, ground the idea that they act as PM-bound-complex signaling "hubs"
767 able to interact with many different proteins, at specific times and locations, and in response
768 to specific stimuli. However, little is known about how REMs integrate diverse signaling cues
769 in plants and how their specific functions are regulated. Only few studies drew a link
770 between REM phosphorylation and intracellular signaling. Marín and Ott. (2012) showed

771 that AtREM1.3 phosphorylation at S66 located in the IDR region led to a reduced affinity for
772 importins in yeast two-hybrid assays. However, the impact of this phosphorylation on the
773 structure, and subcellular localization of AtREM1.3 remains to be investigated.

774 Gui et al. (2016) demonstrated that OsREM4.1 is phosphorylated by OsBRI1 to inhibit
775 OsREM4.1 interaction with OsSERK1, leading to OsBRI1-OsSERK1 complex formation and
776 subsequent activation of the brassinosteroid signaling pathway, (Gui et al., 2016, Figure 3B).
777 While the phosphosites remains to be identified, this model connects REM phosphorylation,
778 hormone-signaling balance and rice development, giving an important insight on one of the
779 functional roles of REM phosphorylation in rice.

780 In Perraki et al. 2018, it was shown that PVX activated kinases responsible for StREM1.3's
781 phosphorylation potentially on S74/T86/S91 sites and that expression of the
782 phosphomimetic but not the phosphoablative mutant of StREM1.3 hampered virus cell-to-
783 cell propagation to similar levels with the WT form. Importantly, the calcium-dependent
784 protein kinase AtCPK3, which could phosphorylate StREM1.3 *in vitro* on S74/T86/S91, could
785 also restrict PVX cell-to-cell movement in a REM-dependent manner. This suggests that
786 AtCPK3 orthologue in potato could regulate StREM1.3 *in vivo* for anti-viral defense.
787 Moreover, the phosphorylation mutants had an impact on the localization of REM at PD and
788 on callose deposition, associating phosphostatus, protein mobility, PD permeability and cell-
789 to-cell viral propagation (Perraki et al., 2018, Figure 3C).

790 Although multiple REM phosphosites have been described in phosphoproteomes or with
791 directed approaches, only few REM-associated kinases have been identified (see
792 supplementary table 1). A recent large-scale phosphoproteomic study identified 8
793 Arabidopsis kinases (CPK11, MPK6, OST1, SnRK2.4, SOS2, OXI1, CKL2, CRKL2) that could
794 phosphorylate, *in vitro*, AtREM phosphopeptides generated *in vivo* (Wang et al. 2020).
795 Additional kinases responsible for REM phosphorylation have been described in rice, *N.*
796 *benthiana*, *M. truncatula*, *L. japonicus* and *A. thaliana* (SnRK1.2, AtCPK3 and various RLKs)
797 (Mehlmer et al., 2010; Tóth et al., 2012; Son et al., 2014; Gui et al., 2016; Perraki et al., 2018;
798 Albers et al., 2019, see a summary Figure 5. However, all these data have been obtained *in*
799 *vitro* and will require further validation. In particular, *in vivo* interaction by BiFC between
800 REMs and protein kinases has been reported for some of them (Tóth et al., 2012; Perraki et
801 al., 2018; Albers et al., 2019). These kinases can phosphorylate a unique REM or several of
802 them and *vice versa* (Mehlmer et al., 2010; Tóth et al., 2012; Son et al., 2014; Gui et al.,

803 2016a; Perraki et al., 2018; Albers et al., 2019; Wang et al., 2020) (supplementary Table 1).
804 Interestingly, while most of those kinases are associated with DRMs, (Majeran et al., 2018)
805 some of them are rather soluble, suggesting that DRM association could be triggered by
806 protein interaction, including through REMs.

807 Indeed REM has been suggested to be a scaffold protein, interacting with several receptor
808 complexes in PM nanodomains (Bücherl et al., 2017; Liang et al., 2018) SYMREM1
809 (MtREM2.2) interacts with LYK3, NFP and DMI, three Medicago **RLKs** essential to sense
810 bacterial elicitors (Lefebvre et al., 2010), Figure 3A. These interactions could potentially be a
811 recruiting process of RLKs to specific nanodomains to initiate bacterial symbiosis (Liang et
812 al., 2018). The interplay between REMs and RLKs deserves to be further investigated,
813 considering the fact that they often present overlapping PM-domain localisation and that
814 REM phosphorylation is induced upon stress (Benschop et al., 2007; Kohorn et al., 2016).
815 This capacity of protein-protein interaction through the N-terminal regions presenting high-
816 scores of intrinsic disorder, see Figure 4 (Raffaele et al., 2007, Marín and Ott, 2012) and the
817 regulation phosphorylation (Reymond et al., 1996; Marín and Ott, 2012; Gui et al., 2016a;
818 Kohorn et al., 2016; Perraki et al., 2018) are characteristics reminiscent of scaffold proteins,
819 like 14-3-3 family proteins. This analogy holds on the cases where REMs' interaction capacity
820 was reported to differ upon phosphorylation of either the interaction partner(s) or the REM
821 isoform itself (Gui et al., 2016; Liang et al., 2018). 14-3-3 family proteins are involved in
822 phospho-relay events in potentially different ways, preeminently in facilitating and hindering
823 protein-protein interaction by binding to the phosphorylated residues of interaction
824 partners (Lozano-Durán and Robatzek, 2015).

825

826 **PERSPECTIVES**

827 The amount of data that has been accumulated since the cloning of the first REM in 1996
828 on the characteristics and the cellular and physiological role of REMs is very heterogeneous.
829 Although many articles have shown REMs as being involved in a number of physiological
830 processes, either biotic or abiotic, a clear role for the REM family has not yet arose from the
831 ever-increasing amount of data (Figure 1). Nevertheless, many trails have emerged from the
832 30 years of research on REMs that show great promise in the everlasting search for REMs'
833 functionalities. One of these functionalities stands out, considering the multiple instances

834 where REMs are linked to intercellular connectivity. These instances reinforce the idea that
835 the establishment of REMs as a genetic family could have been important for the adaptation
836 of photosynthetic algae during the land plant invasion that occurred approximately 475
837 million years ago (Steemans et al., 2009). Indeed, the control of water and solute exchanges
838 between cells and tissues was a major necessary adaptation in order to handle water fluxes
839 in dry land. The development of complex PD along with a complex vasculature necessary for
840 the establishment of root systems and hormone signaling were the fundamental
841 developments that enabled adaptation and establishment of Embryophytes (Rensing et al.,
842 2008). Moreover, the fact REMs are found to be involved in biotic interactions, notably with
843 symbiotic fungi and bacteria (see section “Plant-Microbe Interactions”), is also a clue to their
844 potential involvement in the conquest of land by plants considering the hypothetical
845 importance of symbiotic microorganisms in helping the first rootless land plants to secure
846 nutrients (for review Rensing 2018).

847

848 **1. Genetics**

849 A major weakness in the functional study of REMs is the lack of genetic tools. To study
850 Group 1 REMs, the most notable problematic is currently the lack of KO-lines for each Group
851 1 isoform although the generation of these lines is currently ongoing with the recently
852 published CRISPR-Cas9 KO-lines for two Group 1 REMs in *N. benthamiana* (Fu et al., 2018)
853 and the quadruple CRISPR-Cas9 KO-line for all four Group 1 REMs in *A. thaliana* soon
854 available (T. Ott, personal communication). KO lines for each REM Group will be essential for
855 our understanding of the role played by each REM Group that could entail not only different
856 possible cellular functions but also different tissue specificities (*e.g.* Gui et al., 2014). Several
857 REM Groups such as Group 5 and Group 3 could consequently become less illusive as to their
858 function. The generation of KO-lines should be combined with gain-of-function assays as
859 those undertaken in the characterization of OsREM6.6 (or GSD1; Gui et al., 2014) and
860 OsREM4.1 (Gui et al., 2016) in order to develop true functional approaches in deciphering
861 the cellular and physiological purposes of REMs.

862

863 **2. Protein-Protein Interactions**

864 REMs are suspected to be involved in protein-protein interactions considering their N-
865 terminal regions that present high-scores of intrinsic disorder (Raffaele et al., 2007; Marín et
866 al., 2012) and the fact that members of several REM Groups have been found to be
867 phosphorylated (see Figure 3, supplementary table 1). These characteristics are reminiscent
868 of scaffold proteins and notably of 14-3-3 family proteins. Recently, GRF10 (14-3-3 epsilon)
869 was shown to interact with AtREM1.2 and, to be crucial for its partitioning at the PM (Huang
870 et al., 2019). REMs and 14-3-3 family proteins could indeed co-depend on each other
871 considering REMs' interaction capacity was reported to vary upon phosphorylation of either
872 the interaction partner(s) or the REM isoform itself (Gui et al., 2016; Liang et al., 2018;). In
873 both cases, the REM isoforms *i.e.* OsREM4.1 or MtREM2.2 interact with receptor-like kinases
874 (RLKs), OsSERK1 (Gui et al., 2016) and LYK3 and NFP (Liang et al., 2018), respectively (Figure
875 3). The interplay between REMs and RLKs deserves to be further investigated considering
876 their common phosphorylation and PM-domain association under biotic/stress stimuli
877 (Benschop et al., 2007; Kohorn et al., 2016).

878 Considering that phosphorylation is at the center of the interaction events recorded for
879 REMs, it seems crucial to develop phospho-dependent interactomic screens for REMs. This
880 advancement would enable us to understand the different phospho-dependent protein-
881 protein interaction regulation levels that are highly probable to occur for many REM
882 isoforms. This type of screen should importantly be performed under different stress
883 conditions and in different tissues as REMs' interactions with its cognate partners appear to
884 be highly determined by plant development and stress.

885

886 **3. The PM's complexity**

887 Important advancements have recently been established in the deciphering of the PM-
888 anchoring properties of REMs (Perraki et al., 2012; Gronnier et al., 2017; Martinez et al.,
889 2018; Legrand et al., 2019), clear problematics have arisen. In as much as REMs are
890 dependent of their C-terminal region or REM-CA for their anchoring to the PM, more must
891 be developed in the understanding of the exact biophysical properties that govern this
892 anchoring. Critically, decrypting the determinants of the PM-nanodomain association of
893 REMs is a top priority, as it has already been shown to be a determining factor of REM
894 function (Gronnier et al., 2017; Fu et al., 2018). In particular, affiliating the presence of

895 Group 1 REMs in PM-nanodomains with their observed effect on the accumulation of callose
896 at PD pit-fields (Gronnier et al., 2017; Perraki et al., 2018) raises a critical question: how does
897 a protein, present in the PM inner-leaflet, influence enzymatic activities (*i.e.* callose
898 synthesis/degradation) occurring in the cell wall or, at best in the PM outer-leaflet?

899 Several hypotheses may be explored to answer this question: 1) Can Group 1 REMs or
900 their interaction partners regulate callose synthases present at PD pit-fields in order to
901 stimulate callose deposition? 2) Can Group 1 REMs or their interaction partners regulate the
902 activity or localization of β -1,3-glucanases? This latter question can be a particularly
903 interesting hypothesis to investigate considering the different subcellular and extracellular
904 localizations of β -1,3-glucanases (for review: (Zavaliev et al., 2011). Group 1 REMs could
905 potentially regulate the extracellular secretion of β -1,3-glucanases as it was reported in
906 Zavaliev et al. 2013 in response to salicylic acid treatments. Yet some β -1,3-glucanases have
907 been reported to be glycosylphosphatidylinositol (GPI)-anchored proteins *i.e.* inserted *via* a
908 lipid moiety within the PM outer-leaflet associated with PD in a tissue-dependent manner
909 (Levy et al., 2007). The enrichment of GPI-anchored proteins in the DRM biochemical
910 fraction (for review on plant GPI-anchored proteins: Yeats et al., 2018) licenses the
911 hypothesis that there could be a form of registration between the inner-leaflet PM-domains
912 containing REMs and the outer-leaflet PM-domains containing GPI-anchored β -1,3-
913 glucanases. In this context, the concept of registration refers to the presence of each
914 component in a common PM-domain that spans from one PM-leaflet to the other. There
915 could therefore be interaction *in trans* between inner- and outer-leaflet proteins *via* the
916 interdigitation of very-long-chain acyl chains of the lipids that are present in these PM-
917 domains. This functional mechanism has been demonstrated in animal cells by showing the
918 necessity of phosphatidylserine with a very-long-chain acyl moiety in order to register a GPI-
919 anchored protein to a lipid-protein complex that virtually anchored the GPI-anchored
920 protein to the actin cytoskeleton (Raghupathy et al., 2015). More than just a presence in
921 common biochemical fractions, the registration hypothesis is supported by StREM1.3's
922 modification in PM-dynamics under a phosphorylated state (Perraki et al., 2018), hinting to a
923 regulation of StREM1.3's PM-lateral-segregation *via* the cortical cytoskeleton. This
924 modification in PM-dynamics could possibly modify the PM-dynamics of PM-outer-leaflet-
925 associated proteins *e.g.* GPI-anchored β -1,3-glucanases. Ultimately, elucidating not only the
926 protein-protein- but also the protein-lipid-interactions necessary for REMs' PM-

927 nanodomain-association constitutes a great challenge that will participate in the unfurling of
928 the complex and dynamic molecular mechanisms that govern REMs particular role(s) at the
929 PM.

930 Considering the fact that REMs of different groups label plethora of PM-domains (Jarsch
931 et al., 2014), new methodologies must be developed in order to study these PM-based
932 events and interactions: these methodologies should include: 1) cutting edge proteomic and
933 lipidomic techniques (e.g. identifying lipids in close interaction with proteins) including
934 phosphoproteomics and the study of lipidated proteins (myristoylation, palmitoylation,
935 isoprenylation, and GPI-anchoring; reviewed in Ray et al. 2017); 2) biophysical tools to study
936 lipid–protein interactions *via* surface plasmon resonance (e.g. Lenarčič et al. 2017), liposome
937 binding assays and lipid blotting assays (e.g. Perraki et al., 2012), solid-state NMR, Langmuir
938 monolayer tensiometry, and Fourier transform infrared spectrometry (e.g. Gronnier et al.,
939 2017; methods reviewed in Zhou & Hancock 2018); 3) 3D structures of the membrane-
940 bound interacting complexes including specific lipid-protein complexes by solid-state NMR;
941 4) generation of mutants impaired in PM-domain-association and the use of super-
942 resolution imaging to visualize the *in vivo* segregation and dynamics of PM-components,
943 which should be a focus in order to better understand the molecular interplay occurring at
944 the protein and lipid clustering sites that are PM-domains. These important tools can
945 considerably be assisted by *in silico* modeling such as molecular dynamics simulations (for
946 review: Ulmschneider & Ulmschneider 2018). Notably, the study of the PM-bound cancer-
947 related protein K-RAS is particularly noteworthy as it exemplifies the use of these different
948 methodologies in order to decipher the precise molecular mechanisms underlying K-RAS
949 function (e.g. Zhou et al., 2015; Zhou et al., 2017; Maxwell et al., 2018).

950

951 **ACKNOWLEDGEMENTS**

952 This work was sustained by CNRS (Centre National de la Recherche Scientifique) and the
953 University of Bordeaux. This work has benefited from the facilities of the Bordeaux
954 Metabolome/lipidome Facility-MetaboHUB (ANR-11-INBS-0010). AFD, AL, JG and PG were
955 supported by grants from the French Ministère de l'Enseignement Supérieur et de la
956 Recherche (MESR). JG was supported by EMBO LTF 438-2018 and ERC-2017-COG IMMUNO-
957 PEPTALK ID: 773153. SM, BH, MB and VG are supported by ANR project Phospho-REM
958 domain (ANR 2019). SG, SM, VG are supported by ANR project Potymove The IPS2 (MB)
959 benefits from the support of the LabEx Saclay Plant Sciences-SPS (ANR-10-LABX-0040-SPS).
960 BH was supported by the CNRS Momentum.

961

962 **Author Contributions**

963 PG and JG developed the rationale of the review and wrote the text with the help of all
964 the co-authors. JG did the phylogenetic analysis (Supp Figure 1). SM did the Figure 1. AL and
965 BH did the Figure 2 and wrote the corresponding text. PG did the Figure 3. AP did the Figures
966 4 and 5. MDJ and MB gathered the data for the supp table 1 and wrote the corresponding
967 text. AFD and SGR wrote the virus part. SM and VG supervised the writing and figures. All
968 authors read and corrected the manuscript.

969

970 **FIGURE LEGENDS**

971 **Figure 1. Cumulative number of articles and reviews dealing directly or indirectly with**
972 **REMORIN genes since the discovery of REMs in 1984, and the cloning of the first REM in**
973 **1996.** Source PubMed (<https://www.ncbi.nlm.nih.gov/pubmed>)

974

975 **Figure 2: Molecular driving forces for the formation of StREM1.3-enriched PM**
976 **nanodomains based on structural analysis.** (A) StREM1.3 (blue) clusters at the PM's inner
977 leaflet into nanodomains (red rectangle) enriched in phytosterols and phosphoinositides,
978 the most common being sitosterol and PI4P (Palta et al., 1993, Furt et al., 2010, 2011,
979 Gronnier et al., 2017; Legrand et al., 2019). The overall REM orientation is likely to be
980 perpendicular to the membrane plane to minimize steric hindrance, though the precise
981 angle distribution is unknown. Lipids herein are more ordered than the bulk of the PM
982 and the membrane therefore is slightly thicker even though the PM's complex
983 composition may greatly attenuate this tendency (Gronnier et al., 2018, Legrand et al.,
984 2019). (B) StREM1.3 forms homo-trimers through a coiled-coil domain (Martinez et al.,
985 2018) bundling together three REM C-terminal membrane anchors (RemCA) (Gronnier et
986 al., 2017) and three intrinsically-disordered domains (IDD) bearing phosphorylation sites
987 (Perraki et al., 2018). REM-CA binds to PI4P through electrostatic interactions involving,
988 notably, positively charged amino-acids K192 and K193, as proposed in the right panel by
989 molecular dynamics (Gronnier et al., 2017). The most C-terminal part (region 2) of REM-
990 CA is embedded inside the inner leaflet, as supported by solid-state NMR and molecular
991 dynamics (Gronnier et al., 2017). Nanodomain-associated PIPs being enriched in
992 saturated acyl chains (Furt et al., 2010), sitosterol is also recruited. The left panel shows
993 hydrophobic contacts between the three L155 residues (red), which are critical to the
994 coiled-coil's structure, supporting membrane-association (Martinez et al. 2019).
995 Membrane binding is accompanied by an enrichment in PI4P and sitosterol in the vicinity
996 of the binding site (Legrand et al., 2019). A relative impoverishment in such lipids in the
997 surrounding bulk membrane would therefore be a logical consequence. Note here that
998 only REM molecules are presented, and the other PM proteins are omitted.

1000 **Figure 3. Proposed model for REM-mediated signaling.** (A) Group 2 REM in *Medicago*
 1001 *truncatula*. Constitutively-expressed FLOT4 forms a primary PM-scaffold that is unable to
 1002 recruit LYK3 in the absence of SYMREM1. Nod factor (NF) perception by NFP and LYK3
 1003 PM-receptors triggers the activation of a symbiosis-specific signalling cascade that leads
 1004 to the expression of MtREM2.2. Due to its ability to directly bind LYK3, MtREM2.2 actively
 1005 recruits the receptor into the FLOT4 domain. In *MtREM2.2* mutants, LYK3 is destabilized
 1006 and endocytosed upon rhizobial inoculation. Illustrations adapted from Liang et al. 2018;
 1007 (B) Group 4 REM in *Oriza sativa*. OsREM4.1 protein is PM-localized in association with
 1008 OsBRI1-OsSERK1 complex . Upon elevated ABA levels, the ABA-responsive transcription
 1009 factor OsZIP23 is activated and upregulates OsREM4.1 expression. OsREM4.1 protein
 1010 interacts with OsSERK1 and interferes with OsBRI1-OsSERK1 active complex formation,
 1011 repressing therefore BR signaling initiation. Increased BR levels, causes the binding of BR to
 1012 the extracellular domain of OsBRI1 and the activation of OsBRI1 kinase to phosphorylate
 1013 OsREM4.1. The phosphorylated OsREM4.1, has lower binding affinity to OsSERK1, and
 1014 therefore the OsREM4.1- OsSERK1 complex is dissociated. Therefore, OsSERK1 is able to
 1015 interact with OsBRI1 to form the OsBRI1- OsSERK1 receptor kinase complex, and activate
 1016 BR signaling. OsREM4.1 function is similar to BKI1, which upon BR binding to BRI1, is
 1017 phosphorylated and released from the PM, allowing the BRI1/SERK complex to form.
 1018 Illustrations adapted from Gui et al. 2016; (C). Group 1 REM in *Nicotiana benthamiana*.
 1019 Proposed model for the molecular mechanisms involved in the StREM1.3-dependent
 1020 limiting of PVX cell-to-cell movement according to the data from (Raffaele et al. 2009;
 1021 Perraki et al. 2012; Gronnier et al. 2017; Perraki et al. 2018. Perception of PVX leads to
 1022 the production of a calcium burst that activates a group 2 calcium-dependent protein
 1023 kinase (here CPK3), which in turn phosphorylates group 1 REMs. Group 1 REMs'
 1024 phosphorylated state increases its PM-mobility and interacts with phospho-REM
 1025 Interacting Proteins (RIP). These interactions cause an increase in callose deposition at
 1026 the plasmodesmata.

1027

1028 **Figure 4. Phosphorylation of Arabidopsis REMs occurs mostly at Intrinsic disordered**
1029 **regions at its N terminus.** Graphs show the intrinsic disorder probability on the
1030 Arabidopsis REM proteins that were found to be phosphorylated up to date by *in vivo*
1031 studies. *In vivo* phosphorylation site positions on REM sequences are indicated by
1032 asterisk. Intrinsic disorder predictions were calculated using the PrDOS-Protein disorder
1033 prediction server (<http://prdos.hgc.jp/cgi-bin/top.cgi>). Coiled-coil predictions were
1034 calculated using the COILS program ([https://embnet.vital-](https://embnet.vital-it.ch/software/COILS_form.html)
1035 [it.ch/software/COILS_form.html](https://embnet.vital-it.ch/software/COILS_form.html)). REM-CA prediction was estimated based on homology
1036 with the REM-CA protein from potato StREM1.3.

1037

1038 **Figure 5. REM proteins are involved in independent signaling pathways and are**
1039 **phosphorylated by different kinases.** Schematic representation of all the known
1040 interactions between REM proteins from groups 1, 2, 4 and protein kinases (PK), that
1041 were described in plant immunity, symbiosis and hormonal signaling.

1042

1043 **SUPPLEMENTARY INFORMATION**

1044 **Figure 1. Phylogenetic tree showing the position of the new REM (At1g63295) found in**
1045 **the *A. thaliana* genome.** This new REM appears to belong to the group 2, therefore, we
1046 named it AtREM2.1.

1047

1048 **Table 1: Compilation of phosphoproteomics data sets on REMs of different plant**
1049 **species.** (Nühse et al., 2004; Benschop et al., 2007; Niittylä et al., 2007; Nühse et al.,
1050 2007; Sugiyama et al., 2008; Whiteman et al., 2008; Li et al., 2009; Reiland et al., 2009;
1051 Chen et al., 2010; Grimsrud et al., 2010; Mehlmer et al., 2010; Nakagami et al., 2010;
1052 Reiland et al., 2011; Engelsberger and Schulze, 2012; Lan et al., 2012; Mayank et al., 2012;
1053 Tóth et al., 2012; Yang et al., 2013; Son et al., 2014; Wang et al., 2014; Choudhary et al.,
1054 2015; Hou et al., 2015; Lu et al., 2015; Marcon et al., 2015; Roitinger et al., 2015; Ye et al.,
1055 2015; Gui et al., 2016b; Kohorn et al., 2016; Maronedze et al., 2016; Mattei et al., 2016;
1056 Nukarinen et al., 2016; Qiu et al., 2016; Vu et al., 2016; Xiang et al., 2016; Qiu et al., 2017;
1057 Nikonorova et al., 2018; Perraki et al., 2018; Song et al., 2018; Wang et al., 2018; Albers et
1058 al., 2019; Gupta et al., 2019; Wong et al., 2019; Cai et al., 2020; Mergner et al., 2020;
1059 Wang et al., 2020)

1060

1061 **REFERENCES**

- 1062 **Albers P, Üstün S, Witzel K, Kraner M, Börnke F** (2019) A Remorin from *Nicotiana*
 1063 *benthamiana* Interacts with the *Pseudomonas* Type-III Effector Protein HopZ1a and is
 1064 Phosphorylated by the Immune-Related Kinase PBS1. *Mol Plant-Microbe Interact* **32**:
 1065 1229–1242
- 1066 **Alliotte T, Tiré C, Engler G, Peleman J, Caplan a, Van Montagu M, Inzé D** (1989) An Auxin-
 1067 Regulated Gene of *Arabidopsis thaliana* Encodes a DNA-Binding Protein. *Plant Physiol*
 1068 **89**: 743–52
- 1069 **Amor-Mahjoub M, Suppini JP, Gomez-Vrielyunck N, Ladjimi M** (2006) The effect of the
 1070 hexahistidine-tag in the oligomerization of HSC70 constructs. *J Chromatogr B Anal*
 1071 *Technol Biomed Life Sci* **844**: 328–334
- 1072 **Badawi MA, Agharbaoui Z, Zayed M, Li Q, Byrns B, Zou J, Fowler DB, Danyluk J, Sarhan F**
 1073 (2019) Genome-Wide Identification and Characterization of the Wheat Remorin (Ta
 1074 REM) Family during Cold Acclimation . *Plant Genome* **12**: 180040
- 1075 **Bah A, Vernon RM, Siddiqui Z, Krzeminski M, Muhandiram R, Zhao C, Sonenberg N, Kay LE,**
 1076 **Forman-Kay JD** (2015) Folding of an intrinsically disordered protein by phosphorylation
 1077 as a regulatory switch. *Nature* **519**: 106–109
- 1078 **Bariola PA, Retelska D, Stasiak A, Kammerer RA, Fleming A, Hijri M, Frank S, Farmer EE**
 1079 (2004) Remorins form a novel family of coiled coil-forming oligomeric and filamentous
 1080 proteins associated with apical, vascular and embryonic tissues in plants. *Plant Mol Biol*
 1081 **55**: 579–594
- 1082 **Benschop JJ, Mohammed S, O’Flaherty M, Heck AJR, Slijper M, Menke FLH** (2007)
 1083 Quantitative Phosphoproteomics of Early Elicitor Signaling in *Arabidopsis*. *Mol Cell*
 1084 *Proteomics* **6**: 1198–1214
- 1085 **Bilkova E, Pleskot R, Rissanen S, Sun S, Czogalla A, Cwiklik L, Róg T, Vattulainen I, Cremer**
 1086 **PS, Jungwirth P, et al** (2017) Calcium Directly Regulates Phosphatidylinositol 4,5-
 1087 Bisphosphate Headgroup Conformation and Recognition. *J Am Chem Soc* **139**: 4019–
 1088 4024
- 1089 **Bilska-Kos A, Grzybowski M, Jończyk M, Sowiński P** (2016) In situ localization and changes
 1090 in the expression level of transcripts related to intercellular transport and phloem
 1091 loading in leaves of maize (*Zea mays* L.) treated with low temperature. *Acta Physiol*
 1092 *Plant*. doi: 10.1007/s11738-016-2151-5
- 1093 **Bozkurt TO, Richardson A, Dagdas YF, Mongrand S, Kamoun S, Raffaele S** (2014) The Plant
 1094 Membrane-Associated REMORIN1.3 Accumulates in Discrete Perihyphal Domains
 1095 and Enhances Susceptibility to *Phytophthora infestans*. *Plant Physiol* **165**: 1005–1018
- 1096 **Bray EA** (2002) Classification of genes differentially expressed during water-deficit stress in
 1097 *Arabidopsis thaliana*: An analysis using microarray and differential expression data. *Ann*
 1098 *Bot* **89**: 803–811
- 1099 **Bücherl CA, Jarsch IK, Schudoma C, Segonzac C, Mbengue M, Robotze S, MacLean D, Ott T,**
 1100 **Zipfe C** (2017) Plant immune and growth receptors share common signalling
 1101 components but localise to distinct plasma membrane nanodomains. *Elife* **6**: 1–28
- 1102 **Bundock P, Hooykaas P** (2005) An *Arabidopsis* hAT-like transposase is essential for plant
 1103 development. *Nature* **436**: 282–284
- 1104 **Byun MY, Lee J, Cui LH, Kang Y, Oh TK, Park H, Lee H, Kim WT** (2015) Constitutive
 1105 expression of DaCBF7, an Antarctic vascular plant *Deschampsia antarctica* CBF homolog,
 1106 resulted in improved cold tolerance in transgenic rice plants. *Plant Sci* **236**: 61–74
- 1107 **Cai J, Chen T, Wang Y, Qin G, Tian S** (2020) SIREM1 triggers cell death by activating an

1108 oxidative burst and other regulators. *Plant Physiol* pp.00120.2020

1109 **Checker VG, Khurana P** (2013) Molecular and functional characterization of mulberry EST

1110 encoding remorin (MiREM) involved in abiotic stress. *Plant Cell Rep* **32**: 1729–41

1111 **Chen K, An YQC** (2006) Transcriptional responses to gibberellin and abscisic acid in Barley

1112 aleurone. *J Integr Plant Biol* **48**: 591–612

1113 **Chen Y, Hoehenwarter W, Weckwerth W** (2010) Comparative analysis of phytohormone-

1114 responsive phosphoproteins in *Arabidopsis thaliana* using TiO₂-phosphopeptide

1115 enrichment and mass accuracy precursor alignment. *Plant J* **63**: 1–17

1116 **Cheng G, Yang Z, Zhang H, Zhang J, Xu J** (2020) Remorin interacting with PCaP1 impairs

1117 Turnip mosaic virus intercellular movement but is antagonised by VPg. *New Phytol* **225**:

1118 2122–2139

1119 **Chisholm ST, Dahlbeck D, Krishnamurthy N, Day B, Sjolander K, Staskawicz BJ** (2005)

1120 Molecular characterization of proteolytic cleavage sites of the *Pseudomonas syringae*

1121 effector AvrRpt2. *Proc Natl Acad Sci* **102**: 2087–2092

1122 **Choudhary MK, Nomura Y, Wang L, Nakagami H, Somers DE** (2015) Quantitative circadian

1123 phosphoproteomic analysis of *Arabidopsis* reveals extensive clock control of key

1124 components in physiological, metabolic, and signaling pathways. *Mol Cell Proteomics*

1125 **14**: 2243–2260

1126 **Cui Y, Gao J, He Y, Jiang L** (2020) Plant extracellular vesicles. *Protoplasma* **257**: 3–12

1127 **Dagdas YF, Beihaj K, Maqbool A, Chaparro-Garcia A, Pandey P, Petre B, Tabassum N, Cruz-**

1128 **Mireles N, Hughes RK, Sklenar J, et al** (2016) An effector of the irish potato famine

1129 pathogen antagonizes a host autophagy cargo receptor. *Elife* **5**: 1–23

1130 **Delwiche CF, Cooper ED** (2015) The evolutionary origin of a terrestrial flora. *Curr Biol* **25**:

1131 R899–R910

1132 **Demir F, Horntrich C** (2013) *Arabidopsis* nanodomain-delimited ABA signaling pathway

1133 regulates the anion channel SLAH3. *Proc* doi: 10.6019/PXD000211

1134 **Dyson HJ, Wright PE** (2005) Intrinsically unstructured proteins and their functions. *Nat Rev*

1135 *Mol Cell Biol* **6**: 197–208

1136 **Engberg O, Hautala V, Yasuda T, Dehio H, Murata M, Slotte JP, Nyholm TKM** (2016) The

1137 Affinity of Cholesterol for Different Phospholipids Affects Lateral Segregation

1138 in Bilayers. *Biophys J* **111**: 546–556

1139 **Engelsberger WR, Schulze WX** (2012) Nitrate and ammonium lead to distinct global dynamic

1140 phosphorylation patterns when resupplied to nitrogen-starved *Arabidopsis* seedlings.

1141 *Plant J* **69**: 978–995

1142 **Farmer E, Pearce G, Ryan C** (1989) In vitro phosphorylation of plant plasma membrane

1143 proteins in response to the proteinase inhibitor inducing factor. *Proc ...* **86**: 1539–1542

1144 **Farmer EE, Moloshok TD, Saxton MJ, Ryan CA** (1991) Oligosaccharide signaling in plants.

1145 Specificity of oligouronide-enhanced plasma membrane protein phosphorylation. *J Biol*

1146 *Chem* **266**: 3140-3145.

1147 **Fernandez-Calvino L, Faulkner C, Walshaw J, Saalbach G, Bayer E, Benitez-Alfonso Y, Maule**

1148 **A** (2011) *Arabidopsis* plasmodesmal proteome. *PLoS One*. doi:

1149 10.1371/journal.pone.0018880

1150 **Fu S, Xu Y, Li C, Li Y, Wu J, Zhou X** (2018) Rice Stripe Virus Interferes with S-acylation of

1151 Remorin and Induces Its Autophagic Degradation to Facilitate Virus Infection. *Mol Plant*

1152 **11**: 269–287

1153 **Furt F, König S, Bessoule JJ, Sargueil F, Zallot R, Stanislas T, Noirot E, Lherminier J, Simon-**

1154 **Plas F, Heilmann I, et al** (2010) Polyphosphoinositides are enriched in plant membrane

rafts and form microdomains in the plasma membrane. *Plant Physiol* **152**: 2173–2187

1156 **Grimsrud PA, den Os D, Wenger CD, Swaney DL, Schwartz D, Sussman MR, Ané JM, Coon JJ**
 1157 (2010) Large-scale Phosphoprotein analysis in *Medicago truncatula* roots provides
 1158 insight into in vivo kinase activity in legumes. *Plant Physiol* **152**: 19–28

1159 **Grisson MS, Brocard L, Fouillen L, Nicolas W, Wewer V, Dörmann P, Nacir H, Benitez-Alfonso**
 1160 **Y, Claverol S, Germain V, et al** (2015) Specific Membrane Lipid Composition Is
 1161 Important for Plasmodesmata Function in *Arabidopsis*. *Plant Cell Online* **27**:
 1162 tpc.114.135731

1163 **Gronnier J, Crowet JM, Habenstein B, Nasir MN, Bayle V, Hosy E, Platre MP, Gouguet P,**
 1164 **Raffaele S, Martinez D, et al** (2017) Structural basis for plant plasma membrane protein
 1165 dynamics and organization into functional nanodomains. *Elife* **6**: 1–24

1166 **Gui J, Liu C, Shen J, Li L** (2014) Grain setting defect1, Encoding a Remorin Protein, Affects the
 1167 Grain Setting in Rice through Regulating Plasmodesmatal Conductance. *Plant Physiol*
 1168 **166**: 1463–1478

1169 **Gui J, Zheng S, Liu C, Shen J, Li J, Li L** (2016a) OsREM4.1 Interacts with OsSERK1 to
 1170 Coordinate the Interlinking between Abscisic Acid and Brassinosteroid Signaling in Rice.
 1171 *Dev Cell* **38**: 201–213

1172 **Gui J, Zheng S, Liu C, Shen J, Li J, Li L** (2016b) OsREM4.1 Interacts with OsSERK1 to
 1173 Coordinate the Interlinking between Abscisic Acid and Brassinosteroid Signaling in Rice.
 1174 *Dev Cell* **38**: 201–213

1175 **Gui J, Zheng S, Shen J, Li L** (2015) Grain setting defect1 (GSD1) function in rice depends on S-
 1176 acylation and interacts with actin 1 (OsACT1) at its C-terminal. *Front Plant Sci* **6**: 1–11

1177 **Gupta R, Min CW, Kim YJ, Kim ST** (2019) Identification of Msp1-induced signaling
 1178 components in rice leaves by integrated proteomic and phosphoproteomic analysis. *Int*
 1179 *J Mol Sci* **20**: 1–17

1180 **Hemsley PA, Weimar T, Lilley KS, Dupree P, Grierson CS** (2013) A proteomic approach
 1181 identifies many novel palmitoylated proteins in *Arabidopsis*. *New Phytol* **197**: 805–814

1182 **Hou Y, Qiu J, Tong X, Wei X, Nallamilli BR, Wu W, Huang S, Zhang J** (2015) A comprehensive
 1183 quantitative phosphoproteome analysis of rice in response to bacterial blight. *BMC*
 1184 *Plant Biol* **15**: 1–15

1185 **Hu X, Puri KD, Gurung S, Klosterman SJ, Wallis CM, Britton M, Durbin-Johnson B, Phinney**
 1186 **B, Salemi M, Short DPG, et al** (2019) Proteome and metabolome analyses reveal
 1187 differential responses in tomato -*Verticillium dahliae*-interactions. *J Proteomics* **207**:
 1188 103449

1189 **Huang D, Sun Y, Ma Z, Ke M, Cui Y, Chen Z, Chen C, Ji C, Tran TM, Yang L, et al** (2019)
 1190 Salicylic acid-mediated plasmodesmal closure via Remorin-dependent lipid
 1191 organization. *Proc Natl Acad Sci U S A* **116**: 21274–21284

1192 **Iakoucheva LM, Radivojac P, Brown CJ, O'Connor TR, Sikes JG, Obradovic Z, Dunker AK**
 1193 (2004) The importance of intrinsic disorder for protein phosphorylation. *Nucleic Acids*
 1194 *Res* **32**: 1037–1049

1195 **Jacinto T, Farmer E, Ryan C** (1993) Purification of potato leaf plasma membrane protein
 1196 pp34, a protein phosphorylated in response to oligogalacturonide signals for defense
 1197 and development. *Plant Physiol* **139**: 1393–1397

1198 **Jaillais Y, Ott T** (2020) The Nanoscale Organization of the Plasma Membrane and Its
 1199 Importance in Signaling: A Proteolipid Perspective. *Plant Physiol* **182**: 1682–1696

1200 **Jamann TM, Luo X, Morales L, Kolkman JM, Chung CL, Nelson RJ** (2016) A remorin gene is
 1201 implicated in quantitative disease resistance in maize. *Theor Appl Genet* **129**: 591–602

1202 **Jarsch IK, Konrad SSA, Stratil TF, Urbanus SL, Szymanski W, Braun P, Braun K-HK-H, Ott T**
1203 (2014) Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and
1204 Diverse Microdomains in Arabidopsis and Nicotiana benthamiana. *Plant Cell* **26**: 1698–
1205 1711

1206 **Keinath NF, Kierszniowska S, Lorek J, Bourdais G, Kessler SA, Shimosato-Asano H,**
1207 **Grossniklaus U, Schulze WX, Robatzek S, Panstruga R** (2010) PAMP (Pathogen-
1208 associated Molecular Pattern)-induced changes in plasma membrane
1209 compartmentalization reveal novel components of plant immunity. *J Biol Chem* **285**:
1210 39140–39149

1211 **Khan M, Youn J-Y, Gingras A-C, Subramaniam R, Desveaux D** (2018) In planta proximity
1212 dependent biotin identification (BioID). *Sci Rep* **8**: 9212

1213 **Khoza TG, Dubery IA, Piater LA** (2019) Identification of candidate ergosterol-responsive
1214 proteins associated with the plasma membrane of arabidopsis Thaliana. *Int J Mol Sci* **20**:
1215 1–22

1216 **Kim PM, Sboner A, Xia Y, Gerstein M** (2008) The role of disorder in interaction networks: A
1217 structural analysis. *Mol Syst Biol* **4**: 179

1218 **Kistner C, Winzer T, Pitzschke A, Mulder L, Sato S, Kaneko T, Tabata S, Sandal N, Stoudgard**
1219 **J, Webb KJ, et al** (2005) Seven Lotus japonicus Genes Required for Transcriptional
1220 Reprogramming of the Root during Fungal and Bacterial Symbiosis. *Plant Cell* **17**: 2217–
1221 2229

1222 **Kohorn BD, Hoon D, Minkoff BB, Sussman MR, Kohorn SL** (2016) Rapid Oligo-Galacturonide
1223 Induced Changes in Protein Phosphorylation in Arabidopsis. *Mol Cell Proteomics* **15**:
1224 1351–1359

1225 **Kong CY, Luo Y ping, Duan TT, Xue Z, Gao XD, Zhao X, Gao G** (2016) Potato remorin gene
1226 StREMa4 cloning and its spatiotemporal expression pattern under Ralstonia
1227 solanacearum and plant hormones treatment. *Phytoparasitica* **44**: 575–584

1228 **Konrad SSA, Popp C, Stratil TF, Jarsch IK, Thallmair V, Folgmann J, Marín M, Ott T** (2014) S-
1229 acylation anchors remorin proteins to the plasma membrane but does not primarily
1230 determine their localization in membrane microdomains. *New Phytol* **203**: 758–769

1231 **Kreps JA, Wu Y, Chang H, Zhu T, Wang X, Harper JF, Mesa T, Row M, Diego S, California**
1232 **JAK, et al** (2002) Transcriptome Changes for Arabidopsis in Response to Salt, Osmotic,
1233 and Cold Stress. *Plant Physiol* **130**: 2129–2141

1234 **Kubicek CP, Starr TL, Glass NL** (2014) Plant Cell Wall–Degrading Enzymes and Their Secretion
1235 in Plant-Pathogenic Fungi. *Annu Rev Phytopathol* **52**: 427–451

1236 **Kusumi A, Fujiwara TK, Chadda R, Xie M, Tsunoyama TA, Kalay Z, Kasai RS, Suzuki KGN**
1237 (2012) Dynamic Organizing Principles of the Plasma Membrane that Regulate Signal
1238 Transduction: Commemorating the Fortieth Anniversary of Singer and Nicolson’s Fluid-
1239 Mosaic Model. *Annu Rev Cell Dev Biol* **28**: 215–250

1240 **Lan P, Li W, Wen TN, Schmidt W** (2012) Quantitative phosphoproteome profiling of iron-
1241 deficient arabidopsis roots. *Plant Physiol* **159**: 403–417

1242 **Lee D, Bourdais G, Yu G, Robatzek S, Coaker G** (2015) Phosphorylation of the Plant Immune
1243 Regulator RPM1-INTERACTING PROTEIN4 Enhances Plant Plasma Membrane H⁺ -
1244 ATPase Activity and Inhibits Flagellin-Triggered Immune Responses in Arabidopsis. *Plant*
1245 *Cell* **27**: 2042–2056

1246 **Lefebvre B, Timmers T, Mbengue M, Moreau S, Hervé C, Tóth K, Bittencourt-Silvestre J,**
1247 **Klaus D, Deslandes L, Godiard L, et al** (2010) A remorin protein interacts with symbiotic
1248 receptors and regulates bacterial infection. *Proc Natl Acad Sci U S A* **107**: 2343–8

- 1249 **Legrand A, Martinez D, Grélard A, Berbon M, Morvan E, Tawani A, Loquet A, Mongrand S,**
1250 **Habenstein B** (2019) Nanodomain Clustering of the Plant Protein Remorin by Solid-
1251 State NMR. *Front Mol Biosci* **6**: 1–14
- 1252 **Lenarčič T, Albert I, Böhm H, Hodnik V, Pirc K, Zavec AB, Podobnik M, Pahovnik D, Žagar E,**
1253 **Pruitt R, et al** (2017) Eudicot plant-specific sphingolipids determine host selectivity of
1254 microbial NLP cytolysins. *Science* (80-) **358**: 1431–1434
- 1255 **Levy A, Erlanger M, Rosenthal M, Epel BL** (2007) A plasmodesmata-associated β -1,3-
1256 glucanase in Arabidopsis. *Plant J* **49**: 669–682
- 1257 **Li H, Wai SW, Zhu L, Hong WG, Ecker J, Li N** (2009) Phosphoproteomic analysis of ethylene-
1258 regulated protein phosphorylation in etiolated seedlings of Arabidopsis mutant ein2
1259 using two-dimensional separations coupled with a hybrid quadrupole time-of-flight
1260 mass spectrometer. *Proteomics* **9**: 1646–1661
- 1261 **Liang P, Stratil TF, Popp C, Marín M, Folgmann J, Mysore KS, Wen J, Ott T** (2018) Symbiotic
1262 root infections in *Medicago truncatula* require remorin-mediated receptor stabilization
1263 in membrane nanodomains. *Proc Natl Acad Sci* **115**: 5289–5294
- 1264 **Lin F, Xu SL, Ni WM, Chu ZQ, Xu ZH, Xue HW** (2003) Identification of ABA-responsive genes
1265 in rice shoots via cDNA macroarray. *Cell Res* **13**: 59–68
- 1266 **Liu E, Liu Y, Wu G, Zeng S, Tran Thi TG, Liang L, Liang Y, Dong Z, She D, Wang H, et al** (2016)
1267 Identification of a Candidate Gene for Panicle Length in Rice (*Oryza sativa* L.) Via
1268 Association and Linkage Analysis. *Front Plant Sci* **7**: 1–13
- 1269 **Liu J, Elmore JM, Coaker G** (2009a) Investigating the functions of the RIN4 protein complex
1270 during plant innate immune responses. *Plant Signal Behav* **4**: 1107–1110
- 1271 **Liu J, Elmore JM, Fuglsang AT, Palmgren MG, Staskawicz BJ, Coaker G** (2009b) RIN4
1272 functions with plasma membrane H⁺-ATPases to regulate stomatal apertures during
1273 pathogen attack. *PLoS Biol.* doi: 10.1371/journal.pbio.1000139
- 1274 **Lozano-Durán R, Robatzek S** (2015) 14-3-3 Proteins in Plant-Pathogen Interactions. *Mol*
1275 *Plant-Microbe Interact* **28**: 511–518
- 1276 **Lu Q, Ding S, Reiland S, Rödiger A, Roschitzki B, Xue P, Gruitsem W, Lu C, Baginsky S** (2015)
1277 Identification and characterization of chloroplast casein kinase II from *Oryza sativa*
1278 (rice). *J Exp Bot* **66**: 175–187
- 1279 **Lu YJ, Schornack S, Spallek T, Geldner N, Chory J, Schellmann S, Schumacher K, Kamoun S,**
1280 **Robatzek S** (2012) Patterns of plant subcellular responses to successful oomycete
1281 infections reveal differences in host cell reprogramming and endocytic trafficking. *Cell*
1282 *Microbiol* **14**: 682–697
- 1283 **Mackey D, Iii BFH, Wiig A, Dangl JL, Hill C, Carolina N** (2002) RIN4 interacts with
1284 *Pseudomonas syringae* type III effector molecules and is required for RPM1-mediated
1285 resistance in Arabidopsis. *Cell* **108**: 743–754
- 1286 **Majeran W, Le Caer JP, Ponnala L, Meinel T, Giglione C** (2018) Targeted profiling of
1287 Arabidopsis thaliana subproteomes illuminates co- and posttranslationally N-terminal
1288 myristoylated proteins. *Plant Cell* **30**: 543–562
- 1289 **Marcolino-Gomes J, Rodrigues FA, Fuganti-Pagliarini R, Bendix C, Nakayama TJ, Celaya B,**
1290 **Molinari HBC, De Oliveira MCN, Harmon FG, Nepomuceno A** (2014) Diurnal oscillations
1291 of soybean circadian clock and drought responsive genes. *PLoS One.* doi:
1292 10.1371/journal.pone.0086402
- 1293 **Marcon C, Malik WA, Walley JW, Shen Z, Paschold A, Smith LG, Piepho HP, Briggs SP,**
1294 **Hochholdinger F** (2015) A high-resolution tissue-specific proteome and
1295 phosphoproteome atlas of maize primary roots reveals functional gradients along the

1296 root axes. *Plant Physiol* **168**: 233–246

1297 **Marín M, Ott T** (2012) Phosphorylation of intrinsically disordered regions in remorin
1298 proteins. *Front Plant Sci* **3**: 86

1299 **Marín M, Thallmair V, Ott T** (2012) The intrinsically disordered N-terminal region of
1300 AtREM1.3 remorin protein mediates protein-protein interactions. *J Biol Chem* **287**:
1301 39982–39991

1302 **Maroundedze C, Groen AJ, Thomas L, Lilley KS, Gehring C** (2016) A Quantitative
1303 Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in *Arabidopsis*
1304 *thaliana*. *Mol Plant* **9**: 621–623

1305 **Martinez D, Legrand A, Gronnier J, Decossas M, Gouguet P, Lambert O, Berbon M, Verron**
1306 **L, Grélard A, Germain V, et al** (2018) Coiled-coil oligomerization controls localization of
1307 the plasma membrane REMORINs. *J Struct Biol* 0–1

1308 **Mattei B, Spinelli F, Pontiggia D, De Lorenzo G** (2016) Comprehensive Analysis of the
1309 Membrane Phosphoproteome Regulated by Oligogalacturonides in *Arabidopsis*
1310 *thaliana*. *Front Plant Sci*. doi: 10.3389/fpls.2016.01107

1311 **Maxwell KN, Zhou Y, Hancock JF** (2018) Clustering of Rac1: Selective Lipid Sorting Drives
1312 Signaling. *Trends Biochem Sci* **43**: 75–77

1313 **Mayank P, Grossman J, Wuest S, Boisson-Dernier A, Roschitzki B, Nanni P, Nühse T,**
1314 **Grossniklaus U** (2012) Characterization of the phosphoproteome of mature *Arabidopsis*
1315 pollen. *Plant J* **72**: 89–101

1316 **Mehlmer N, Wurzinger B, Stael S, Hofmann-Rodrigues D, Csaszar E, Pfister B, Bayer R,**
1317 **Teige M** (2010) The Ca²⁺-dependent protein kinase CPK3 is required for MAPK-
1318 independent salt-stress acclimation in *Arabidopsis*. *Plant J* **63**: 484–498

1319 **Menz J, Li Z, Schulze WX, Ludewig U** (2016) Early nitrogen-deprivation responses in
1320 *Arabidopsis* roots reveal distinct differences on transcriptome and (phospho-)
1321 proteome levels between nitrate and ammonium nutrition. *Plant J* **88**: 717–734

1322 **Mergner J, Frejno M, List M, Papacek M, Chen X, Chaudhary A, Samaras P, Richter S,**
1323 **Shikata H, Messerer M, et al** (2020) Mass-spectrometry-based draft of the *Arabidopsis*
1324 proteome. *Nature* **579**: 409–414

1325 **Meyer D, Pajonk S, Micali C, O’Connell R, Schulze-Lefert P** (2009) Extracellular transport and
1326 integration of plant secretory proteins into pathogen-induced cell wall compartments.
1327 *Plant J* **57**: 986–999

1328 **Micali CO, Neumann U, Grunewald D, Panstruga R, O’Connell R** (2011) Biogenesis of
1329 a specialized plant-fungal interface during host cell internalization of *Golovinomyces*
1330 *orontii* haustoria. *Cell Microbiol* **13**: 210–226

1331 **Mongrand S, Morel J, Laroche J, Claverol S, Carde J-P, Hartmann M-A, Bonneau M, Simon-**
1332 **Plas F, Lessire R, Bessoule J-J** (2004) Lipid rafts in higher plant cells: purification and
1333 characterization of Triton X-100-insoluble microdomains from tobacco plasma
1334 membrane. *J Biol Chem* **279**: 36277–86

1335 **Morel J, Clavero S, Mongrand S, Furt F, Fromentin J, Bessoule JJ, Blein JP, Simon F** (2006)
1336 Proteomics of plant detergent-resistant membranes. *Mol Cell Proteomics* **5**: 1396–1411

1337 **Nakagami H, Sugiyama N, Mochida K, Daudi A, Yoshida Y, Toyoda T, Tomita M, Ishihama Y,**
1338 **Shirasu K** (2010) Large-scale comparative phosphoproteomics identifies conserved
1339 phosphorylation sites in plants. *Plant Physiol* **153**: 1161–1174

1340 **Niittylä T, Fuglsang AT, Palmgren MG, Frommer WB, Schulze WX** (2007) Temporal analysis
1341 of sucrose-induced phosphorylation changes in plasma membrane proteins of
1342 *Arabidopsis*. *Mol Cell Proteomics* **6**: 1711–1726

1343 **Nikonorova N, Van Den Broeck L, Zhu S, Van De Cotte B, Dubois M, Gevaert K, Inzé D, De**
1344 **Smet I** (2018) Early mannitol-triggered changes in the Arabidopsis leaf
1345 (phospho)proteome reveal growth regulators. *J Exp Bot* **69**: 4591–4607

1346 **Nühse TS, Bottrill AR, Jones AME, Peck SC** (2007) Quantitative phosphoproteomic analysis
1347 of plasma membrane proteins reveals regulatory mechanisms of plant innate immune
1348 responses. *Plant J* **51**: 931–940

1349 **Nühse TS, Stensballe A, Jensen ON, Peck SC** (2004) Phosphoproteomics of the arabidopsis
1350 plasma membrane and a new phosphorylation site database W inside box sign. *Plant*
1351 *Cell* **16**: 2394–2405

1352 **Nukarinen E, Ngele T, Pedrotti L, Wurzinger B, Mair A, Landgraf R, Börnke F, Hanson J,**
1353 **Teige M, Baena-Gonzalez E, et al** (2016) Quantitative phosphoproteomics reveals the
1354 role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy
1355 deprivation. *Sci Rep* **6**: 1–19

1356 **Oh SK, Jeong MP, Young HJ, Lee S, Chung E, Kim SY, Seung HY, Choi D** (2005) A plant EPF-
1357 type zinc-finger protein, CaPIF1, involved in defence against pathogens. *Mol Plant*
1358 *Pathol* **6**: 269–285

1359 **Perraki A, Binaghi M, Mecchia M a, Gronnier J, German-Retana S, Mongrand S, Bayer E,**
1360 **Zelada AM, Germain V** (2014) StRemorin1.3 hampers Potato virus X TGBp1 ability to
1361 increase plasmodesmata permeability, but does not interfere with its silencing
1362 suppressor activity. *FEBS Lett* **588**: 1699–705

1363 **Perraki A, Gronnier J, Gouguet P, Boudsocq M, Deroubaix F, Simon V, Legrand A, German-**
1364 **Retana S, Zipfel C, Bayer EMF, et al** (2018) REM1 .3's phospho-status defines its plasma
1365 membrane nanodomain organization and activity in restricting PVX cell-to-cell
1366 movement. *PLoS Pathog.*

1367 **Qin L, Zhou Z, Li Q, Zhai C, Liu L, Quilichini TD, Gao P, Kessler SA, Jaillais Y, Datla R, et al**
1368 (2020) Specific Recruitment of Phosphoinositide Species to the Plant-Pathogen
1369 Interfacial Membrane Underlies Arabidopsis Susceptibility to Fungal Infection. *Plant Cell*
1370 **32**: tpc.00970.2019

1371 **Qiu J, Hou Y, Tong X, Wang Y, Lin H, Liu Q, Zhang W, Li Z, Nallamilli BR, Zhang J** (2016)
1372 Quantitative phosphoproteomic analysis of early seed development in rice (*Oryza sativa*
1373 L.). *Plant Mol Biol* **90**: 249–265

1374 **Qiu J, Hou Y, Wang Y, Li Z, Zhao J, Tong X, Lin H, Wei X, Ao H, Zhang J** (2017) A
1375 comprehensive proteomic survey of aba-induced protein phosphorylation in rice (*Oryza*
1376 *sativa* L.). *Int J Mol Sci* **18**: 1–16

1377 **Raffaele S, Bayer E, Lafarge D, Cluzet S, German Retana S, Boubekour T, Leborgne-Castel N,**
1378 **Carde J-P, Lherminier J, Noirot E, et al** (2009) Remorin, a solanaceae protein resident in
1379 membrane rafts and plasmodesmata, impairs potato virus X movement. *Plant Cell* **21**:
1380 1541–55

1381 **Raffaele S, Mongrand S, Gamas P, Niebel A, Ott T** (2007) Genome-wide annotation of
1382 remorins, a plant-specific protein family: evolutionary and functional perspectives.
1383 *Plant Physiol* **145**: 593–600

1384 **Raghupathy R, Anilkumar AA, Polley A, Singh PP, Yadav M, Johnson C, Suryawanshi S,**
1385 **Saikam V, Sawant SD, Panda A, et al** (2015) Transbilayer Lipid Interactions Mediate
1386 Nanoclustering of Lipid-Anchored Proteins. *Cell* **161**: 581–594

1387 **Ray A, Jatana N, Thukral L** (2017) Lipidated proteins: Spotlight on protein-membrane
1388 binding interfaces. *Prog Biophys Mol Biol* **128**: 74–84

1389 **Reiland S, Finazzi G, Endler A, Willig A, Baerenfaller K, Grossmann J, Gerrits B, Rutishauser**

1390 **D, Gruissem W, Rochaix JD, et al** (2011) Comparative phosphoproteome profiling
1391 reveals a function of the STN8 kinase in fine-tuning of cyclic electron flow (CEF). Proc
1392 Natl Acad Sci U S A **108**: 12955–12960

1393 **Reiland S, Messerli G, Baerenfaller K, Gerrits B, Endler A, Grossmann J, Gruissem W,**
1394 **Baginsky S** (2009) Large-scale arabidopsis phosphoproteome profiling reveals novel
1395 chloroplast kinase substrates and phosphorylation networks1[w]. Plant Physiol **150**:
1396 889–903

1397 **Rensing SA** (2018) Great moments in evolution: the conquest of land by plants. Curr Opin
1398 Plant Biol **42**: 49–54

1399 **Rensing SA, Lang D, Zimmer AD** (2008) Conquest of Land by Plants. Science (80-) **319**: 64–69

1400 **Reymond P, Grünberger S, Paul K, Müller M, Farmer EE** (1995) Oligogalacturonide defense
1401 signals in plants: large fragments interact with the plasma membrane in vitro. Proc Natl
1402 Acad Sci U S A **92**: 4145–4149

1403 **Reymond P, Kunz B, Paul-Pletzer K, Grimm R, Eckerskorn C, Farmer EE** (1996) Cloning of a
1404 cDNA encoding a plasma membrane-associated, uronide binding phosphoprotein with
1405 physical properties similar to viral movement proteins. Plant Cell ... **8**: 2265–2276

1406 **Reymond P, Weber H, Damond M, Farmer EE** (2000) Differential Gene Expression in
1407 Response to Mechanical Wounding and Insect Feeding in Arabidopsis. Plant Cell **12**:
1408 707–719

1409 **Roitinger E, Hofer M, Köcher T, Pichler P, Novatchkova M, Yang J, Schlögelhofer P,**
1410 **Mechtler K** (2015) Quantitative phosphoproteomics of the ataxia telangiectasia-
1411 mutated (ATM) and ataxia telangiectasia-mutated and Rad3-related (ATR) dependent
1412 DNA damage response in arabidopsis thaliana. Mol Cell Proteomics **14**: 556–571

1413 **Rutter BD, Innes RW** (2017) Extracellular Vesicles Isolated from the Leaf Apoplast Carry
1414 Stress-Response Proteins. Plant Physiol **173**: 728–741

1415 **Rutter BD, Innes RW** (2018) Extracellular vesicles as key mediators of plant–microbe
1416 interactions. Curr Opin Plant Biol **44**: 16–22

1417 **Ryan CA, An G** (1988) Molecular biology of wound-inducible proteinase inhibitors in plants.
1418 Plant Cell Environ **11**: 345–349

1419 **Rybak K, Robatzek S** (2019) Functions of extracellular vesicles in immunity and virulence.
1420 Plant Physiol **179**: 1236–1247

1421 **Sasaki N, Takashima E, Nyunoya H** (2018) Altered Subcellular Localization of a Tobacco
1422 Membrane Raft-Associated Remorin Protein by Tobamovirus Infection and Transient
1423 Expression of Viral Replication and Movement Proteins. Front Plant Sci **9**: 1–16

1424 **Seong ES, Baek KH, Oh SK, Jo SH, Yi SY, Park JM, Joung YH, Lee S, Cho HS, Choi D** (2007)
1425 Induction of enhanced tolerance to cold stress and disease by overexpression of the
1426 pepper CaPIF1 gene in tomato. Physiol Plant **129**: 555–566

1427 **Son S, Oh C, An C** (2014) Arabidopsis thaliana Remorins Interact with SnRK1 and Play a Role
1428 in Susceptibility to Beet Curly Top Virus and Beet Severe Curly Top Virus. plant Pathol J
1429 **30**: 269–278

1430 **Song G, Brachova L, Nikolau BJ, Jones AM, Walley JW** (2018) Heterotrimeric G-Protein-
1431 Dependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots.
1432 Proteomics **18**: 1–14

1433 **Srivastava V, Malm E, Sundqvist G, Bulone V** (2013) Quantitative Proteomics Reveals that
1434 Plasma Membrane Microdomains From Poplar Cell Suspension Cultures Are Enriched in
1435 Markers of Signal Transduction, Molecular Transport, and Callose Biosynthesis. Mol Cell
1436 Proteomics **12**: 3874–3885

- 1437 **Stanislas T, Bouyssie D, Rossignol M, Vesa S, Fromentin J, Morel J, Pichereaux C, Monsarrat**
1438 **B, Simon-Plas F** (2009) Quantitative Proteomics Reveals a Dynamic Association of
1439 Proteins to Detergent-resistant Membranes upon Elicitor Signaling in Tobacco. *Mol Cell*
1440 *Proteomics* **8**: 2186–2198
- 1441 **Stemmans P, Hérissé A Le, Melvin J, Miller MA, Paris F, Verniers J, Wellman CH** (2009)
1442 Origin and radiation of the earliest vascular land plants. *Science* (80-) **324**: 353
- 1443 **Sugiyama N, Nakagami H, Mochida K, Daudi A, Tomita M, Shirasu K, Ishihama Y** (2008)
1444 Large-scale phosphorylation mapping reveals the extent of tyrosine phosphorylation in
1445 Arabidopsis. *Mol Syst Biol*. doi: 10.1038/msb.2008.32
- 1446 **Szymanski WG, Zauber H, Erban A, Gorka M, Wu XN, Schulze WX** (2015) Cytoskeletal
1447 components define protein location to membrane microdomains. *Mol Cell Proteomics*
1448 **14**: M114.046904-
- 1449 **Takahashi D, Kawamura Y, Uemura M** (2013) Detergent-resistant plasma membrane
1450 proteome to elucidate microdomain functions in plant cells. *Front Plant Sci* **4**: 27
- 1451 **Tarkka MT, Herrmann S, Wubet T, Feldhahn L, Recht S, Kurth F, Mailänder S, Bönn M, Neef**
1452 **M, Angay O, et al** (2013) OakContigDF159.1, a reference library for studying differential
1453 gene expression in *Quercus robur* during controlled biotic interactions: Use for
1454 quantitative transcriptomic profiling of oak roots in ectomycorrhizal symbiosis. *New*
1455 *Phytol* **199**: 529–540
- 1456 **Tóth K, Stratil TF, Madsen EB, Ye J, Popp C, Antolín-Llovera M, Grossmann C, Jensen ON,**
1457 **Schüßler A, Parniske M, et al** (2012) Functional domain analysis of the remorin protein
1458 LjSYMREM1 in *lotus japonicus*. *PLoS One*. doi: 10.1371/journal.pone.0030817
- 1459 **Ulmschneider JP, Ulmschneider MB** (2018) Molecular Dynamics Simulations Are Redefining
1460 Our View of Peptides Interacting with Biological Membranes. *Acc Chem Res* **51**: 1106–
1461 1116
- 1462 **Verma V, Sivaraman J, Srivastava AK, Sadanandom A, Kumar PP** (2015) Destabilization of
1463 interaction between cytokinin signaling intermediates AHP1 and ARR4 modulates
1464 Arabidopsis development. *New Phytol* **206**: 726–737
- 1465 **Voxeur A, Höfte H** (2016) Cell wall integrity signaling in plants: “To grow or not to grow
1466 that’s the question.” *Glycobiology* **26**: 950–960
- 1467 **Vu LD, Stes E, Van Bel M, Nelissen H, Maddelein D, Inzé D, Coppens F, Martens L, Gevaert**
1468 **K, De Smet I** (2016) Up-to-Date Workflow for Plant (Phospho)proteomics Identifies
1469 Differential Drought-Responsive Phosphorylation Events in Maize Leaves. *J Proteome*
1470 *Res* **15**: 4304–4317
- 1471 **Wang K, Yang Z, Qing D, Ren F, Liu S, Zheng Q, Liu J, Zhang W, Dai C, Wu M, et al** (2018)
1472 Quantitative and functional posttranslational modification proteomics reveals that
1473 TREP1 plays a role in plant touch-delayed bolting. *Proc Natl Acad Sci U S A* **115**:
1474 E10265–E10274
- 1475 **Wang K, Zhao Y, Li M, Gao F, Yang M kun, Wang X, Li S, Yang P** (2014) Analysis of
1476 phosphoproteome in rice pistil. *Proteomics* **14**: 2319–2334
- 1477 **Wang P, Hsu CC, Du Y, Zhu P, Zhao C, Fu X, Zhang C, Paez JS, Macho AP, Andy Tao W, et al**
1478 (2020) Mapping proteome-wide targets of protein kinases in plant stress responses.
1479 *Proc Natl Acad Sci U S A* **117**: 3270–3280
- 1480 **Wang S, Chen Z, Tian L, Ding Y, Zhang J, Zhou J, Liu P, Chen Y, Wu L** (2019) Comparative
1481 proteomics combined with analyses of transgenic plants reveal ZmREM1.3 mediates
1482 maize resistance to southern corn rust. *Plant Biotechnol J* **17**: 2153–2168
- 1483 **Wellman CH** (2010) The invasion of the land by plants: When and where? *New Phytol* **188**:

1484 306–309

1485 **Whiteman SA, Serazetdinova L, Jones AME, Sanders D, Rathjen J, Peck SC, Maathuis FJM**

1486 (2008) Identification of novel proteins and phosphorylation sites in a tonoplast enriched

1487 membrane fraction of *Arabidopsis thaliana*. *Proteomics* **8**: 3536–3547

1488 **Widjaja I, Naumann K, Roth U, Wolf N, Mackey D, Dangl JL, Scheel D, Lee J** (2009)

1489 Combining subproteome enrichment and Rubisco depletion enables identification of

1490 low abundance proteins differentially regulated during plant defense. *Proteomics* **9**:

1491 138–147

1492 **Wong MM, Bhaskara GB, Wen TN, Lin WD, Nguyen TT, Chong GL, Verslues PE** (2019)

1493 Phosphoproteomics of *Arabidopsis* Highly ABA-Induced1 identifies AT-Hook-Like10

1494 phosphorylation required for stress growth regulation. *Proc Natl Acad Sci U S A* **116**:

1495 2354–2363

1496 **Wu C-Q, Hu H-H, Zeng Y, Liang D-C, Xie K-B, Zhang J-W, Chu Z-H, Xiong L-Z** (2006)

1497 Identification of Novel Stress-responsive Transcription Factor Genes in Rice by cDNA

1498 Array Analysis. *J Integr Plant Biol* **48**: 1216–1224

1499 **Xiang Y, Song B, Née G, Kramer K, Finkemeier I, Soppe WJJ** (2016) Sequence polymorphisms

1500 at the REDUCED DORMANCY5 pseudophosphatase underlie natural variation in

1501 *Arabidopsis* dormancy. *Plant Physiol* **171**: 2659–2670

1502 **Xu Q, Xu X, Shi Y, Qi X, Chen X** (2017) Elucidation of the molecular responses of a cucumber

1503 segment substitution line carrying Pm5.1 and its recurrent parent triggered by powdery

1504 mildew by comparative transcriptome profiling. *BMC Genomics* **18**: 1–14

1505 **Yamada H, Hanaki N, Imamura A, Ueguchi C, Mizuno T** (1998) An *Arabidopsis* protein that

1506 interacts with the cytokinin-inducible response regulator, ARR4, implicated in the His-

1507 Asp phosphorylay signal transduction. *FEBS Lett* **436**: 76–80

1508 **Yang Z, Guo G, Zhang M, Liu CY, Hu Q, Lam H, Cheng H, Xue Y, Li J, Li N** (2013) Stable

1509 isotope metabolic labeling-based quantitative phosphoproteomic analysis of

1510 *arabidopsis* mutants reveals ethylene-regulated time-dependent phosphoproteins and

1511 putative substrates of constitutive triple response 1 kinase. *Mol Cell Proteomics* **12**:

1512 3559–3582

1513 **Ye J, Zhang Z, Long H, Zhang Z, Hong Y, Zhang X, You C, Liang W, Ma H, Lu P** (2015)

1514 Proteomic and phosphoproteomic analyses reveal extensive phosphorylation of

1515 regulatory proteins in developing rice anthers. *Plant J* **84**: 527–544

1516 **Yeats TH, Bacic A, Johnson KL** (2018) Plant glycosylphosphatidylinositol anchored proteins at

1517 the plasma membrane-cell wall nexus. *J Integr Plant Biol* **60**: 649–669

1518 **Yue J, Li C, Liu Y, Yu J** (2014) A remorin gene SiREM6, the target gene of SiARDP, from foxtail

1519 millet (*Setaria italica*) promotes high salt tolerance in transgenic *Arabidopsis*. *PLoS One*

1520 **9**: e100772

1521 **Zauber H, Burgos A, Garapati P, Schulze WX** (2014) Plasma membrane lipid-protein

1522 interactions affect signaling processes in sterol-biosynthesis mutants in *Arabidopsis*

1523 *thaliana*. *Front Plant Sci* **5**: 1–18

1524 **Zavaliev R, Levy A, Gera A, Epel BL** (2013) Subcellular dynamics and role of *Arabidopsis* β -

1525 1,3-glucanases in cell-to-cell movement of tobamoviruses. *Mol Plant Microbe Interact*

1526 **26**: 1016–30

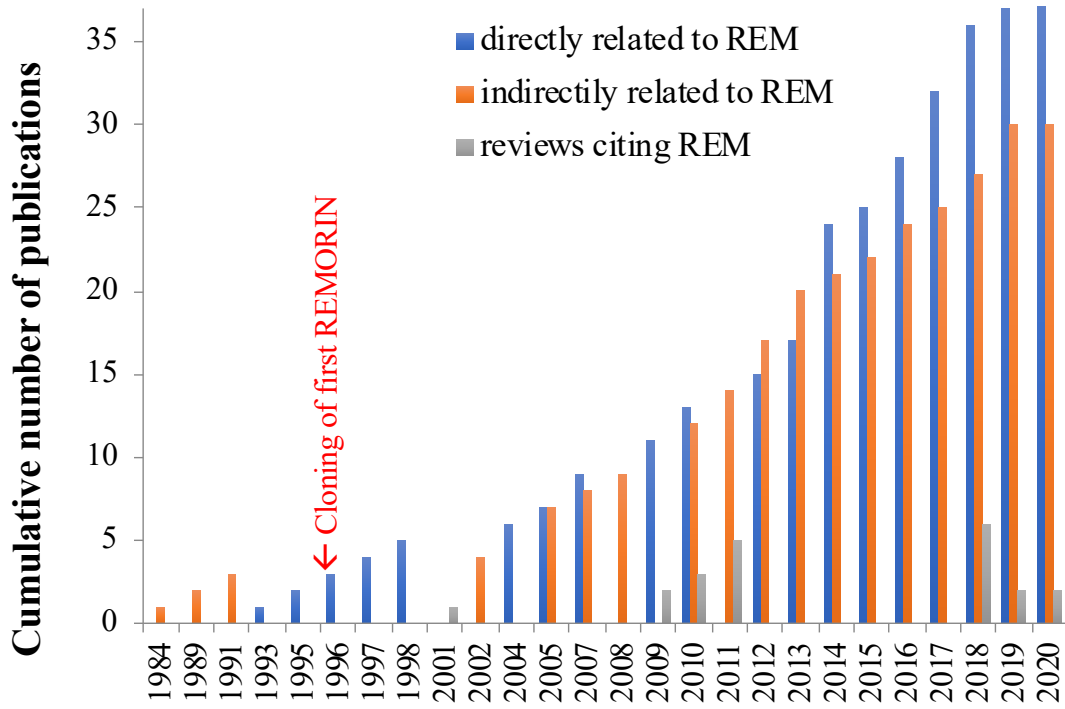
1527 **Zavaliev R, Ueki S, Epel BL, Citovsky V** (2011) Biology of callose (β -1,3-glucan) turnover at

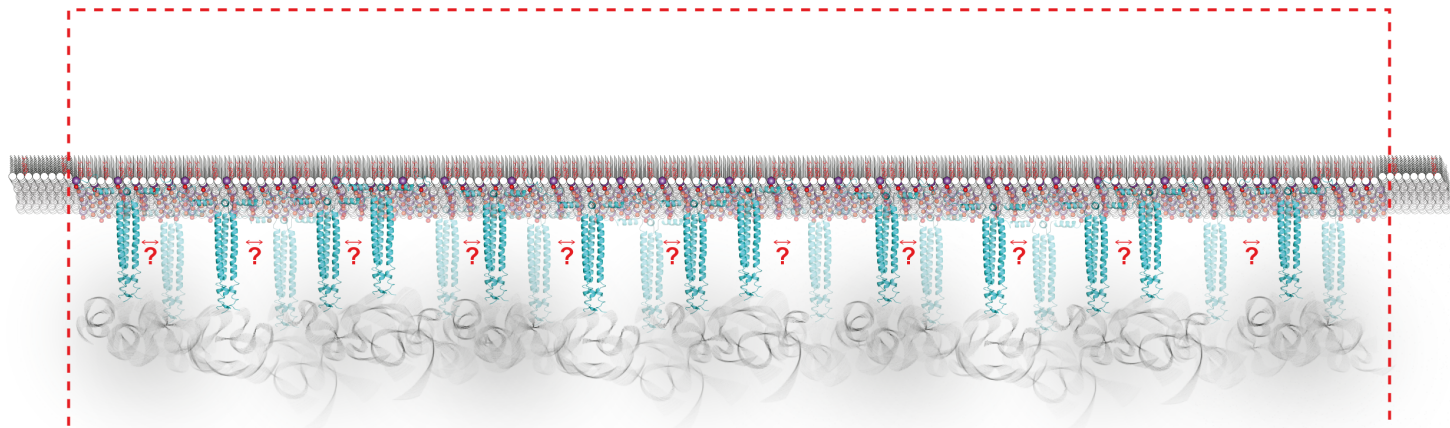
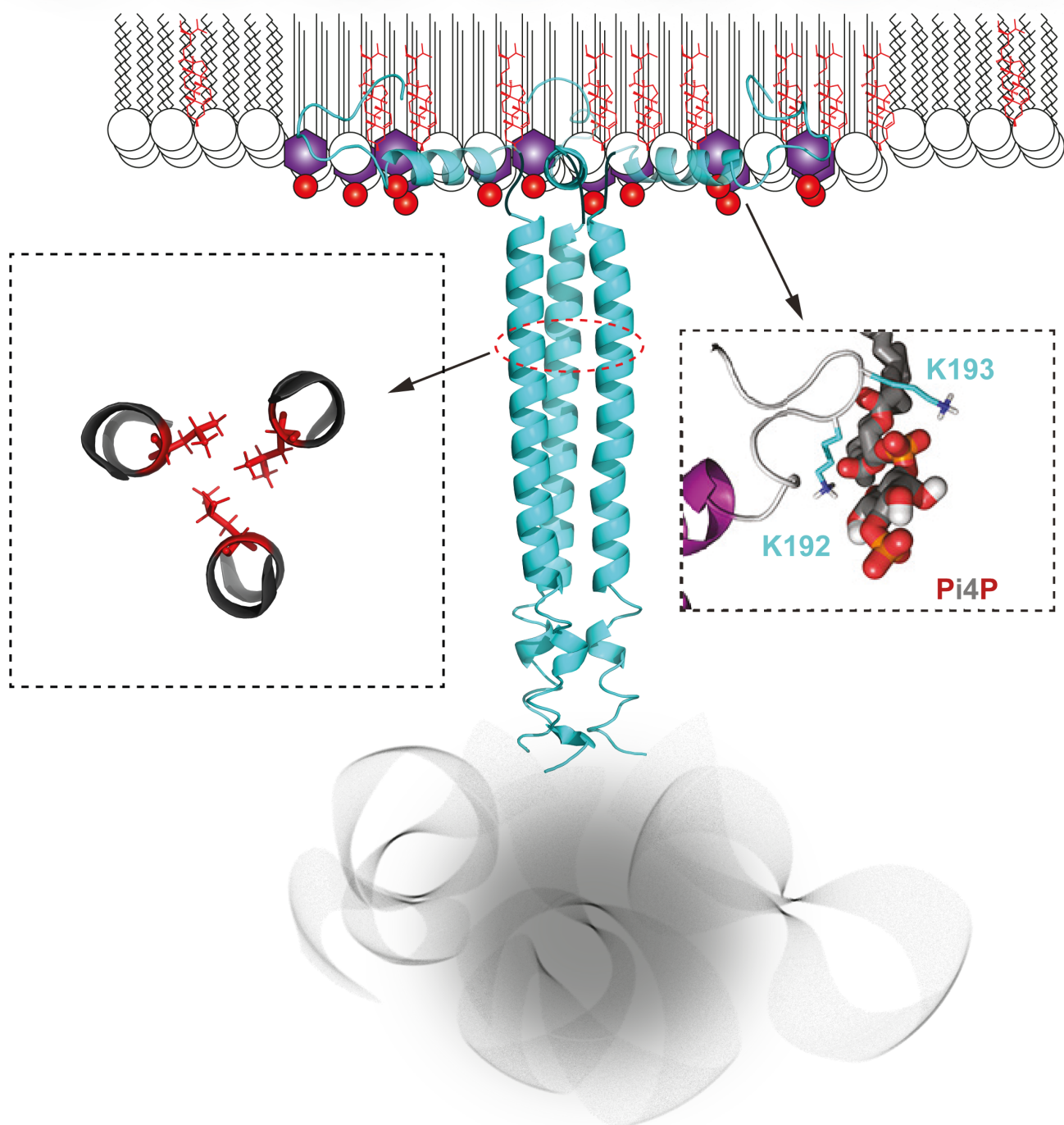
1528 plasmodesmata. *Protoplasma* **248**: 117–130

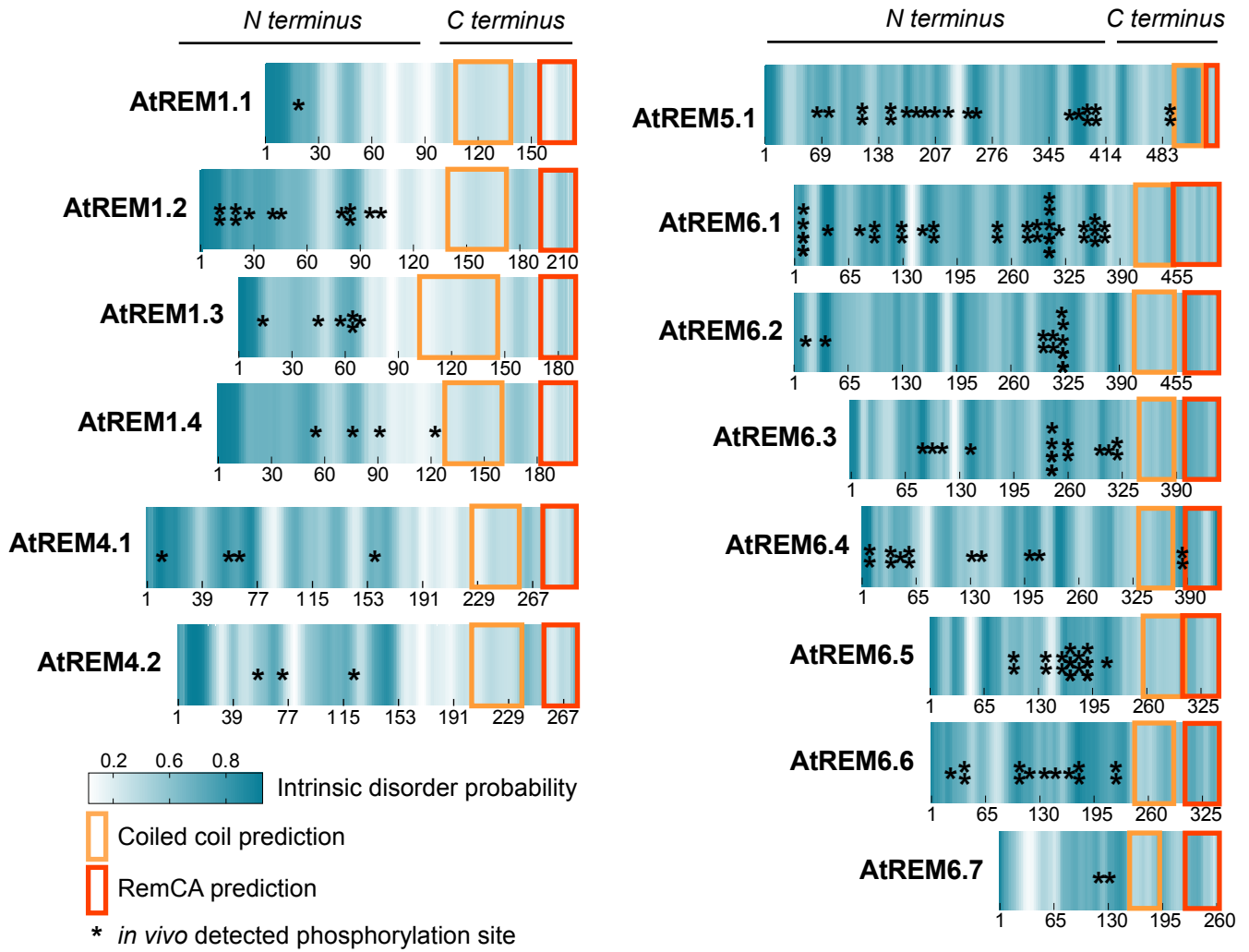
1529 **Zhang H, Deng C, Wu X, Yao J, Zhang Y, Zhang Y, Deng S, Zhao N, Zhao R, Zhou X, et al**

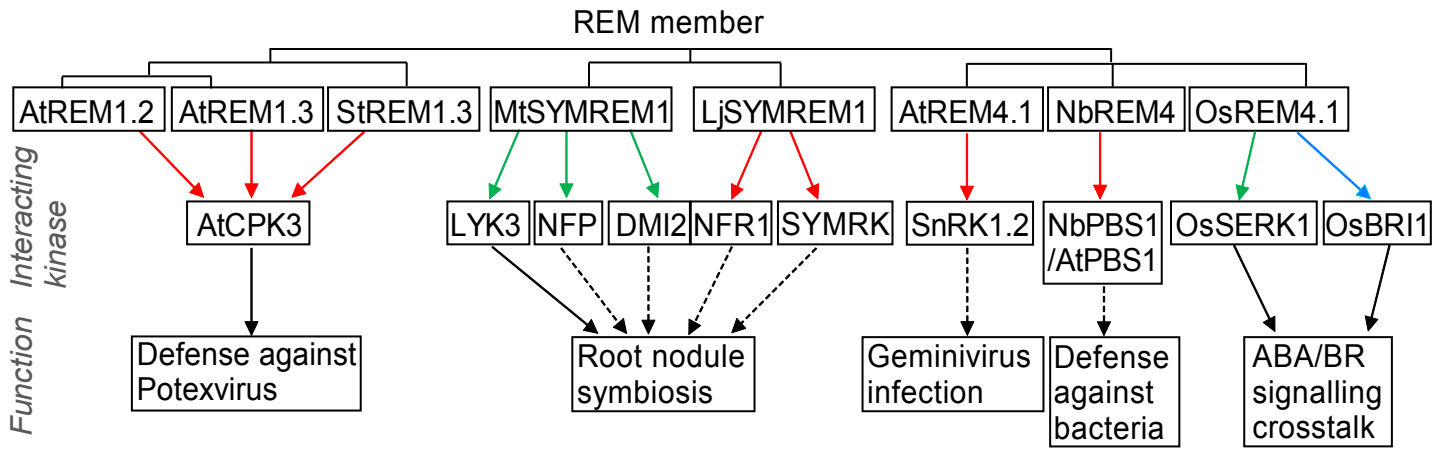
1530 (2020) *Populus euphratica* remorin 6.5 activates plasma membrane H⁺-ATPases to

1531 mediate salt tolerance. *Tree Physiol* 1–49
1532 **Zhou Y, Hancock JF** (2018) Deciphering lipid codes: K-Ras as a paradigm. *Traffic* **19**: 157–165
1533 **Zhou Y, Prakash P, Liang H, Cho K-J, Gorfe AA, Hancock JF** (2017) Lipid-Sorting Specificity
1534 Encoded in K-Ras Membrane Anchor Regulates Signal Output. *Cell* **168**: 239–251
1535 **Zhou Y, Wong CO, Cho KJ, Van Der Hoeven D, Liang H, Thakur DP, Luo J, Babic M, Zinsmaier**
1536 **KE, Zhu MX, et al** (2015) Membrane potential modulates plasma membrane
1537 phospholipid dynamics and K-Ras signaling. *Science* (80-) **349**: 873–876
1538



A**B**





- The PK interacts with and phosphorylates REM
- The PK phosphorylates REM
- The PK interacts with REM
- The PK and REM function together in the biological context
- The PK and REM function in the same biological context but the link of PK/REM in the function is not yet demonstrated

Parsed Citations

Albers P, Üstün S, Witzel K, Kraner M, Börnke F (2019) A Remorin from *Nicotiana benthamiana* Interacts with the *Pseudomonas* Type-III Effector Protein HopZ1a and is Phosphorylated by the Immune-Related Kinase PBS1. *Mol Plant-Microbe Interact* 32: 1229–1242

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Alliotte T, Tiré C, Engler G, Peleman J, Caplan a, Van Montagu M, Inzé D (1989) An Auxin-Regulated Gene of *Arabidopsis thaliana* Encodes a DNA-Binding Protein. *Plant Physiol* 89: 743–52

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Amor-Mahjoub M, Suppini JP, Gomez-Vrielyunck N, Ladjimi M (2006) The effect of the hexahistidine-tag in the oligomerization of HSC70 constructs. *J Chromatogr B Anal Technol Biomed Life Sci* 844: 328–334

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Badawi MA, Agharbaoui Z, Zayed M, Li Q, Byrns B, Zou J, Fowler DB, Danyluk J, Sarhan F (2019) Genome-Wide Identification and Characterization of the Wheat Remorin (TaREM) Family during Cold Acclimation. *Plant Genome* 12: 180040

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bah A, Vernon RM, Siddiqui Z, Krzeminski M, Muhandiram R, Zhao C, Sonenberg N, Kay LE, Forman-Kay JD (2015) Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. *Nature* 519: 106–109

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bariola PA, Retelska D, Stasiak A, Kammereer RA, Fleming A, Hijri M, Frank S, Farmer EE (2004) Remorins form a novel family of coiled coil-forming oligomeric and filamentous proteins associated with apical, vascular and embryonic tissues in plants. *Plant Mol Biol* 55: 579–594

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Benschop JJ, Mohammed S, O'Flaherty M, Heck AJR, Slijper M, Menke FLH (2007) Quantitative Phosphoproteomics of Early Elicitor Signaling in *Arabidopsis*. *Mol Cell Proteomics* 6: 1198–1214

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bilkova E, Pleskot R, Rissanen S, Sun S, Czogalla A, Cwiklik L, Róg T, Vattulainen I, Cremer PS, Jungwirth P, et al (2017) Calcium Directly Regulates Phosphatidylinositol 4,5-Bisphosphate Headgroup Conformation and Recognition. *J Am Chem Soc* 139: 4019–4024

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bilska-Kos A, Grzybowski M, Jończyk M, Sowiński P (2016) In situ localization and changes in the expression level of transcripts related to intercellular transport and phloem loading in leaves of maize (*Zea mays* L.) treated with low temperature. *Acta Physiol Plant*. doi: 10.1007/s11738-016-2151-5

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bozkurt TO, Richardson A, Dagdas YF, Mongrand S, Kamoun S, Raffaele S (2014) The Plant Membrane-Associated REMORIN1.3 Accumulates in Discrete Perhaustorial Domains and Enhances Susceptibility to *Phytophthora infestans*. *Plant Physiol* 165: 1005–1018

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bray EA (2002) Classification of genes differentially expressed during water-deficit stress in *Arabidopsis thaliana*: An analysis using microarray and differential expression data. *Ann Bot* 89: 803–811

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bücherl CA, Jarsch IK, Schudoma C, Segonzac C, Mbengue M, Robatzke S, MacLean D, Ott T, Zipfe C (2017) Plant immune and growth receptors share common signalling components but localise to distinct plasma membrane nanodomains. *Elife* 6: 1–28

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bundock P, Hooykaas P (2005) An *Arabidopsis* hAT-like transposase is essential for plant development. *Nature* 436: 282–284

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Byun MY, Lee J, Cui LH, Kang Y, Oh TK, Park H, Lee H, Kim WT (2015) Constitutive expression of DaCBF7, an Antarctic vascular plant *Deschampsia antarctica* CBF homolog, resulted in improved cold tolerance in transgenic rice plants. *Plant Sci* 236: 61–74

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Cai J, Chen T, Wang Y, Qin G, Tian S (2020) SIREM1 triggers cell death by activating an oxidative burst and other regulators. *Plant*

Physiol pp.00120.2020

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Checker VG, Khurana P (2013) Molecular and functional characterization of mulberry EST encoding remorin (MiREM) involved in abiotic stress. Plant Cell Rep 32: 1729–41

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Chen K, An YQC (2006) Transcriptional responses to gibberellin and abscisic acid in Barley aleurone. J Integr Plant Biol 48: 591–612

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Chen Y, Hoehenwarter W, Weckwerth W (2010) Comparative analysis of phytohormone-responsive phosphoproteins in Arabidopsis thaliana using TiO2-phosphopeptide enrichment and mass accuracy precursor alignment. Plant J 63: 1–17

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Cheng G, Yang Z, Zhang H, Zhang J, Xu J (2020) Remorin interacting with PCaP1 impairs Turnip mosaic virus intercellular movement but is antagonised by VPg. New Phytol 225: 2122–2139

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Chisholm ST, Dahlbeck D, Krishnamurthy N, Day B, Sjolander K, Staskawicz BJ (2005) Molecular characterization of proteolytic cleavage sites of the Pseudomonas syringae effector AvrRpt2. Proc Natl Acad Sci 102: 2087–2092

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Choudhary MK, Nomura Y, Wang L, Nakagami H, Somers DE (2015) Quantitative circadian phosphoproteomic analysis of Arabidopsis reveals extensive clock control of key components in physiological, metabolic, and signaling pathways. Mol Cell Proteomics 14: 2243–2260

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Cui Y, Gao J, He Y, Jiang L (2020) Plant extracellular vesicles. Protoplasma 257: 3–12

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Dagdas YF, Beihaj K, Maqbool A, Chaparro-Garcia A, Pandey P, Petre B, Tabassum N, Cruz-Mireles N, Hughes RK, Sklenar J, et al (2016) An effector of the irish potato famine pathogen antagonizes a host autophagy cargo receptor. Elife 5: 1–23

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Delwiche CF, Cooper ED (2015) The evolutionary origin of a terrestrial flora. Curr Biol 25: R899–R910

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Demir F, Horntrich C (2013) Arabidopsis nanodomain-delimited ABA signaling pathway regulates the anion channel SLAH3. Proc doi: 10.6019/PXD000211

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Dyson HJ, Wright PE (2005) Intrinsically unstructured proteins and their functions. Nat Rev Mol Cell Biol 6: 197–208

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Engberg O, Hautala V, Yasuda T, Dehio H, Murata M, Slotte JP, Nyholm TKM (2016) The Affinity of Cholesterol for Different Phospholipids Affects Lateral Segregation in Bilayers. Biophys J 111: 546–556

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Engelsberger WR, Schulze WX (2012) Nitrate and ammonium lead to distinct global dynamic phosphorylation patterns when resupplied to nitrogen-starved Arabidopsis seedlings. Plant J 69: 978–995

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Farmer E, Pearce G, Ryan C (1989) In vitro phosphorylation of plant plasma membrane proteins in response to the proteinase inhibitor inducing factor. Proc ... 86: 1539–1542

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Farmer EE, Moloshok TD, Saxton MJ, Ryan CA (1991) Oligosaccharide signaling in plants. Specificity of oligouronide-enhanced plasma membrane protein phosphorylation. J Biol Chem 266: 3140–3145.

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

- Fernandez-Calvino L, Faulkner C, Walshaw J, Saalbach G, Bayer E, Benitez-Alfonso Y, Maule A (2011) Arabidopsis plasmodesmal proteome. PLoS One. doi: 10.1371/journal.pone.0018880**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Fu S, Xu Y, Li C, Li Y, Wu J, Zhou X (2018) Rice Stripe Virus Interferes with S-acylation of Remorin and Induces Its Autophagic Degradation to Facilitate Virus Infection. Mol Plant 11: 269–287**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Furt F, König S, Bessoule JJ, Sargueil F, Zallot R, Stanislas T, Noirot E, Lherminier J, Simon-Plas F, Heilmann I, et al (2010) Polyphosphoinositides are enriched in plant membrane rafts and form microdomains in the plasma membrane. Plant Physiol 152: 2173–2187**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Grimsrud PA, den Os D, Wenger CD, Swaney DL, Schwartz D, Sussman MR, Ané JM, Coon JJ (2010) Large-scale Phosphoprotein analysis in Medicago truncatula roots provides insight into in vivo kinase activity in legumes. Plant Physiol 152: 19–28**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Grison MS, Brocard L, Fouillen L, Nicolas W, Wewer V, Dörmann P, Nacir H, Benitez-Alfonso Y, Claverol S, Germain V, et al (2015) Specific Membrane Lipid Composition Is Important for Plasmodesmata Function in Arabidopsis. Plant Cell Online 27: tpc.114.135731**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Gronnier J, Crowet JM, Habenstein B, Nasir MN, Bayle V, Hosy E, Platre MP, Gouguet P, Raffaele S, Martinez D, et al (2017) Structural basis for plant plasma membrane protein dynamics and organization into functional nanodomains. Elife 6: 1–24**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Gui J, Liu C, Shen J, Li L (2014) Grain setting defect1, Encoding a Remorin Protein, Affects the Grain Setting in Rice through Regulating Plasmodesmatal Conductance. Plant Physiol 166: 1463–1478**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Gui J, Zheng S, Liu C, Shen J, Li J, Li L (2016a) OsREM4.1 Interacts with OsSERK1 to Coordinate the Interlinking between Abscisic Acid and Brassinosteroid Signaling in Rice. Dev Cell 38: 201–213**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Gui J, Zheng S, Liu C, Shen J, Li J, Li L (2016b) OsREM4.1 Interacts with OsSERK1 to Coordinate the Interlinking between Abscisic Acid and Brassinosteroid Signaling in Rice. Dev Cell 38: 201–213**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Gui J, Zheng S, Shen J, Li L (2015) Grain setting defect1 (GSD1) function in rice depends on S-acylation and interacts with actin 1 (OsACT1) at its C-terminal. Front Plant Sci 6: 1–11**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Gupta R, Min CW, Kim YJ, Kim ST (2019) Identification of Msp1-induced signaling components in rice leaves by integrated proteomic and phosphoproteomic analysis. Int J Mol Sci 20: 1–17**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Hemsley PA, Weimar T, Lilley KS, Dupree P, Grierson CS (2013) A proteomic approach identifies many novel palmitoylated proteins in Arabidopsis. New Phytol 197: 805–814**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Hou Y, Qiu J, Tong X, Wei X, Nallamilli BR, Wu W, Huang S, Zhang J (2015) A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. BMC Plant Biol 15: 1–15**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Hu X, Puri KD, Gurung S, Klosterman SJ, Wallis CM, Britton M, Durbin-Johnson B, Phinney B, Salemi M, Short DPG, et al (2019) Proteome and metabolome analyses reveal differential responses in tomato -Verticillium dahliae-interactions. J Proteomics 207: 103449**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Huang D, Sun Y, Ma Z, Ke M, Cui Y, Chen Z, Chen C, Ji C, Tran TM, Yang L, et al (2019) Salicylic acid-mediated plasmodesmal closure via Remorin-dependent lipid organization. Proc Natl Acad Sci U S A 116: 21274–21284**
Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Iakoucheva LM, Radivojac P, Brown CJ, O'Connor TR, Sikes JG, Obradovic Z, Dunker AK (2004) The importance of intrinsic disorder for protein phosphorylation. *Nucleic Acids Res* 32: 1037–1049

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jacinto T, Farmer E, Ryan C (1993) Purification of potato leaf plasma membrane protein pp34, a protein phosphorylated in response to oligogalacturonide signals for defense and development. *Plant Physiol* 1393–1397

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jaillais Y, Ott T (2020) The Nanoscale Organization of the Plasma Membrane and Its Importance in Signaling: A Proteolipid Perspective. *Plant Physiol* 182: 1682–1696

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jamann TM, Luo X, Morales L, Kolkman JM, Chung CL, Nelson RJ (2016) A remorin gene is implicated in quantitative disease resistance in maize. *Theor Appl Genet* 129: 591–602

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jarsch IK, Konrad SSA, Stratil TF, Urbanus SL, Szymanski W, Braun P, Braun K-HK-H, Ott T (2014) Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and Diverse Microdomains in *Arabidopsis* and *Nicotiana benthamiana*. *Plant Cell* 26: 1698–1711

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Keinath NF, Kierszniowska S, Lorek J, Bourdais G, Kessler SA, Shimosato-Asano H, Grossniklaus U, Schulze WX, Robatzek S, Panstruga R (2010) PAMP (Pathogen-associated Molecular Pattern)-induced changes in plasma membrane compartmentalization reveal novel components of plant immunity. *J Biol Chem* 285: 39140–39149

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Khan M, Youn J-Y, Gingras A-C, Subramaniam R, Desveaux D (2018) In planta proximity dependent biotin identification (BioID). *Sci Rep* 8: 9212

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Khoza TG, Dubery IA, Piater LA (2019) Identification of candidate ergosterol-responsive proteins associated with the plasma membrane of *Arabidopsis thaliana*. *Int J Mol Sci* 20: 1–22

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kim PM, Sboner A, Xia Y, Gerstein M (2008) The role of disorder in interaction networks: A structural analysis. *Mol Syst Biol* 4: 179

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kistner C, Winzer T, Pitzschke A, Mulder L, Sato S, Kaneko T, Tabata S, Sandal N, Stoudgard J, Webb KJ, et al (2005) Seven *Lotus japonicus* Genes Required for Transcriptional Reprogramming of the Root during Fungal and Bacterial Symbiosis. *Plant Cell* 17: 2217–2229

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kohorn BD, Hoon D, Minkoff BB, Sussman MR, Kohorn SL (2016) Rapid Oligo-Galacturonide Induced Changes in Protein Phosphorylation in *Arabidopsis*. *Mol Cell Proteomics* 15: 1351–1359

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kong CY, Luo Y ping, Duan TT, Xue Z, Gao XD, Zhao X, Gao G (2016) Potato remorin gene StREMa4 cloning and its spatiotemporal expression pattern under *Ralstonia solanacearum* and plant hormones treatment. *Phytoparasitica* 44: 575–584

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Konrad SSA, Popp C, Stratil TF, Jarsch IK, Thallmair V, Folgmann J, Marin M, Ott T (2014) S-acylation anchors remorin proteins to the plasma membrane but does not primarily determine their localization in membrane microdomains. *New Phytol* 203: 758–769

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kreps JA, Wu Y, Chang H, Zhu T, Wang X, Harper JF, Mesa T, Row M, Diego S, California JAK, et al (2002) Transcriptome Changes for *Arabidopsis* in Response to Salt, Osmotic, and Cold Stress. *Plant Physiol* 130: 2129–2141

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kubicek CP, Starr TL, Glass NL (2014) Plant Cell Wall-Degrading Enzymes and Their Secretion in Plant-Pathogenic Fungi. *Annu Rev*

Phytopathol 52: 427–451

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Kusumi A, Fujiwara TK, Chadda R, Xie M, Tsunoyama TA, Kalay Z, Kasai RS, Suzuki KGN (2012) Dynamic Organizing Principles of the Plasma Membrane that Regulate Signal Transduction: Commemorating the Fortieth Anniversary of Singer and Nicolson's Fluid-Mosaic Model. Annu Rev Cell Dev Biol 28: 215–250

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lan P, Li W, Wen TN, Schmidt W (2012) Quantitative phosphoproteome profiling of iron-deficient arabidopsis roots. Plant Physiol 159: 403–417

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lee D, Bourdais G, Yu G, Robatzek S, Coaker G (2015) Phosphorylation of the Plant Immune Regulator RPM1-INTERACTING PROTEIN4 Enhances Plant Plasma Membrane H⁺ -ATPase Activity and Inhibits Flagellin-Triggered Immune Responses in Arabidopsis. Plant Cell 27: 2042–2056

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lefebvre B, Timmers T, Mbengue M, Moreau S, Hervé C, Tóth K, Bittencourt-Silvestre J, Klaus D, Deslandes L, Godiard L, et al (2010) A remorin protein interacts with symbiotic receptors and regulates bacterial infection. Proc Natl Acad Sci U S A 107: 2343–8

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Legrand A, Martinez D, Grélard A, Berbon M, Morvan E, Tawani A, Loquet A, Mongrand S, Habenstein B (2019) Nanodomain Clustering of the Plant Protein Remorin by Solid-State NMR. Front Mol Biosci 6: 1–14

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lenarčič T, Albert I, Böhm H, Hodnik V, Pirc K, Zavec AB, Podobnik M, Pahovnik D, Žagar E, Pruitt R, et al (2017) Eudicot plant-specific sphingolipids determine host selectivity of microbial NLP cytolysins. Science (80-) 358: 1431–1434

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Levy A, Erlanger M, Rosenthal M, Epel BL (2007) A plasmodesmata-associated β -1,3-glucanase in Arabidopsis. Plant J 49: 669–682

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Li H, Wai SW, Zhu L, Hong WG, Ecker J, Li N (2009) Phosphoproteomic analysis of ethylene-regulated protein phosphorylation in etiolated seedlings of Arabidopsis mutant ein2 using two-dimensional separations coupled with a hybrid quadrupole time-of-flight mass spectrometer. Proteomics 9: 1646–1661

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Liang P, Stratil TF, Popp C, Marín M, Folgmann J, Mysore KS, Wen J, Ott T (2018) Symbiotic root infections in Medicago truncatula require remorin-mediated receptor stabilization in membrane nanodomains. Proc Natl Acad Sci 115: 5289–5294

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lin F, Xu SL, Ni WM, Chu ZQ, Xu ZH, Xue HW (2003) Identification of ABA-responsive genes in rice shoots via cDNA macroarray. Cell Res 13: 59–68

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Liu E, Liu Y, Wu G, Zeng S, Tran Thi TG, Liang L, Liang Y, Dong Z, She D, Wang H, et al (2016) Identification of a Candidate Gene for Panicle Length in Rice (Oryza sativa L.) Via Association and Linkage Analysis. Front Plant Sci 7: 1–13

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Liu J, Elmore JM, Coaker G (2009a) Investigating the functions of the RIN4 protein complex during plant innate immune responses. Plant Signal Behav 4: 1107–1110

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Liu J, Elmore JM, Fuglsang AT, Palmgren MG, Staskawicz BJ, Coaker G (2009b) RIN4 functions with plasma membrane H⁺-ATPases to regulate stomatal apertures during pathogen attack. PLoS Biol. doi: 10.1371/journal.pbio.1000139

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lozano-Durán R, Robatzek S (2015) 14-3-3 Proteins in Plant-Pathogen Interactions. Mol Plant-Microbe Interact 28: 511–518

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Lu Q, Ding S, Reiland S, Rödiger A, Roschitzki B, Xue P, Gruitsem W, Lu C, Baginsky S (2015) Identification and characterization of chloroplast casein kinase II from *Oryza sativa* (rice). *J Exp Bot* 66: 175–187

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lu YJ, Schornack S, Spallek T, Geldner N, Chory J, Schellmann S, Schumacher K, Kamoun S, Robatzek S (2012) Patterns of plant subcellular responses to successful oomycete infections reveal differences in host cell reprogramming and endocytic trafficking. *Cell Microbiol* 14: 682–697

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Mackey D, Iii BFH, Miig A, Dangl JL, Hill C, Carolina N (2002) RIN4 interacts with *Pseudomonas syringae* type III effector molecules and is required for RPM1-mediated resistance in *Arabidopsis*. *Cell* 108: 743–754

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Majeran W, Le Caer JP, Ponnala L, Meinell T, Giglione C (2018) Targeted profiling of *Arabidopsis thaliana* subproteomes illuminates co- and posttranslationally N-terminal myristoylated proteins. *Plant Cell* 30: 543–562

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Marcolino-Gomes J, Rodrigues FA, Fuganti-Pagliarini R, Bendix C, Nakayama TJ, Celaya B, Molinari HBC, De Oliveira MCN, Harmon FG, Nepomuceno A (2014) Diurnal oscillations of soybean circadian clock and drought responsive genes. *PLoS One*. doi: 10.1371/journal.pone.0086402

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Marcon C, Malik WA, Walley JW, Shen Z, Paschold A, Smith LG, Piepho HP, Briggs SP, Hochholdinger F (2015) A high-resolution tissue-specific proteome and phosphoproteome atlas of maize primary roots reveals functional gradients along the root axes. *Plant Physiol* 168: 233–246

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Marín M, Ott T (2012) Phosphorylation of intrinsically disordered regions in remorin proteins. *Front Plant Sci* 3: 86

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Marín M, Thallmair V, Ott T (2012) The intrinsically disordered N-terminal region of AtREM1.3 remorin protein mediates protein-protein interactions. *J Biol Chem* 287: 39982–39991

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Maronedze C, Groen AJ, Thomas L, Lilley KS, Gehring C (2016) A Quantitative Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in *Arabidopsis thaliana*. *Mol Plant* 9: 621–623

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Martinez D, Legrand A, Gronnier J, Decossas M, Gouguet P, Lambert O, Berbon M, Verron L, Grélard A, Germain V, et al (2018) Coiled-coil oligomerization controls localization of the plasma membrane REMORINs. *J Struct Biol* 0–1

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Mattei B, Spinelli F, Pontiggia D, De Lorenzo G (2016) Comprehensive Analysis of the Membrane Phosphoproteome Regulated by Oligogalacturonides in *Arabidopsis thaliana*. *Front Plant Sci*. doi: 10.3389/fpls.2016.01107

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Maxwell KN, Zhou Y, Hancock JF (2018) Clustering of Rac1: Selective Lipid Sorting Drives Signaling. *Trends Biochem Sci* 43: 75–77

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Mayank P, Grossman J, Wuest S, Boisson-Dernier A, Roschitzki B, Nanni P, Nühse T, Grossniklaus U (2012) Characterization of the phosphoproteome of mature *Arabidopsis* pollen. *Plant J* 72: 89–101

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Mehlmer N, Wurzinger B, Stael S, Hofmann-Rodrigues D, Csaszar E, Pfister B, Bayer R, Teige M (2010) The Ca²⁺-dependent protein kinase CPK3 is required for MAPK-independent salt-stress acclimation in *Arabidopsis*. *Plant J* 63: 484–498

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Menz J, Li Z, Schulze WX, Ludewig U (2016) Early nitrogen-deprivation responses in *Arabidopsis* roots reveal distinct differences on transcriptome and (phospho-) proteome levels between nitrate and ammonium nutrition. *Plant J* 88: 717–734

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Mergner J, Frejno M, List M, Papacek M, Chen X, Chaudhary A, Samaras P, Richter S, Shikata H, Messerer M, et al (2020) Mass-spectrometry-based draft of the *Arabidopsis* proteome. *Nature* 579: 409–414

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Meyer D, Pajonk S, Micali C, O'Connell R, Schulze-Lefert P (2009) Extracellular transport and integration of plant secretory proteins into pathogen-induced cell wall compartments. *Plant J* 57: 986–999

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Micali CO, Neumann U, Grunewald D, Panstruga R, O'Connell R (2011) Biogenesis of a specialized plant-fungal interface during host cell internalization of *Golovinomyces orontii* haustoria. *Cell Microbiol* 13: 210–226

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Mongrand S, Morel J, Laroche J, Claverol S, Carde J-P, Hartmann M-A, Bonneau M, Simon-Plas F, Lessire R, Bessoule J-J (2004) Lipid rafts in higher plant cells: purification and characterization of Triton X-100-insoluble microdomains from tobacco plasma membrane. *J Biol Chem* 279: 36277–86

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Morel J, Clavero S, Mongrand S, Furt F, Fromentin J, Bessoule JJ, Blein JP, Simon F (2006) Proteomics of plant detergent-resistant membranes. *Mol Cell Proteomics* 5: 1396–1411

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nakagami H, Sugiyama N, Mochida K, Daudi A, Yoshida Y, Toyoda T, Tomita M, Ishihama Y, Shirasu K (2010) Large-scale comparative phosphoproteomics identifies conserved phosphorylation sites in plants. *Plant Physiol* 153: 1161–1174

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Niittylä T, Fuglsang AT, Palmgren MG, Frommer WB, Schulze WX (2007) Temporal analysis of sucrose-induced phosphorylation changes in plasma membrane proteins of *Arabidopsis*. *Mol Cell Proteomics* 6: 1711–1726

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nikonorova N, Van Den Broeck L, Zhu S, Van De Cotte B, Dubois M, Gevaert K, Inzé D, De Smet I (2018) Early mannitol-triggered changes in the *Arabidopsis* leaf (phospho)proteome reveal growth regulators. *J Exp Bot* 69: 4591–4607

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nühse TS, Bottrill AR, Jones AME, Peck SC (2007) Quantitative phosphoproteomic analysis of plasma membrane proteins reveals regulatory mechanisms of plant innate immune responses. *Plant J* 51: 931–940

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nühse TS, Stensballe A, Jensen ON, Peck SC (2004) Phosphoproteomics of the *Arabidopsis* plasma membrane and a new phosphorylation site database W inside box sign. *Plant Cell* 16: 2394–2405

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nukarinen E, Ngele T, Pedrotti L, Wurzinger B, Mair A, Landgraf R, Börnke F, Hanson J, Teige M, Baena-Gonzalez E, et al (2016) Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. *Sci Rep* 6: 1–19

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Oh SK, Jeong MP, Young HJ, Lee S, Chung E, Kim SY, Seung HY, Choi D (2005) A plant EPF-type zinc-finger protein, CaPIF1, involved in defence against pathogens. *Mol Plant Pathol* 6: 269–285

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Perraki A, Binaghi M, Mecchia M a, Gronnier J, German-Retana S, Mongrand S, Bayer E, Zelada AM, Germain V (2014) StRemorin1.3 hampers Potato virus X TGBp1 ability to increase plasmodesmata permeability, but does not interfere with its silencing suppressor activity. *FEBS Lett* 588: 1699–705

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Perraki A, Gronnier J, Gouguet P, Boudsocq M, Deroubaix F, Simon V, Legrand A, German-Retana S, Zipfel C, Bayer EMF, et al (2018) REM1.3's phospho-status defines its plasma membrane nanodomain organization and activity in restricting PVX cell-to-cell movement. *PLoS Pathog.*

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Qin L, Zhou Z, Li Q, Zhai C, Liu L, Quilichini TD, Gao P, Kessler SA, Jaillais Y, Datla R, et al (2020) Specific Recruitment of Phosphoinositide Species to the Plant-Pathogen Interfacial Membrane Underlies Arabidopsis Susceptibility to Fungal Infection. Plant Cell 32: tpc.00970.2019

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Qiu J, Hou Y, Tong X, Wang Y, Lin H, Liu Q, Zhang W, Li Z, Nallamilli BR, Zhang J (2016) Quantitative phosphoproteomic analysis of early seed development in rice (*Oryza sativa* L.). Plant Mol Biol 90: 249–265

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Qiu J, Hou Y, Wang Y, Li Z, Zhao J, Tong X, Lin H, Wei X, Ao H, Zhang J (2017) A comprehensive proteomic survey of aba-induced protein phosphorylation in rice (*Oryza sativa* L.). Int J Mol Sci 18: 1–16

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Raffaele S, Bayer E, Lafarge D, Cluzet S, German Retana S, Boubekeur T, Leborgne-Castel N, Carde J-P, Lherminier J, Noirot E, et al (2009) Remorin, a solanaceae protein resident in membrane rafts and plasmodesmata, impairs potato virus X movement. Plant Cell 21: 1541–55

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Raffaele S, Mongrand S, Gamas P, Niebel A, Ott T (2007) Genome-wide annotation of remorins, a plant-specific protein family: evolutionary and functional perspectives. Plant Physiol 145: 593–600

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Raghupathy R, Anilkumar AA, Polley A, Singh PP, Yadav M, Johnson C, Suryawanshi S, Saikam V, Sawant SD, Panda A, et al (2015) Transbilayer Lipid Interactions Mediate Nanoclustering of Lipid-Anchored Proteins. Cell 161: 581–594

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Ray A, Jatana N, Thukral L (2017) Lipidated proteins: Spotlight on protein-membrane binding interfaces. Prog Biophys Mol Biol 128: 74–84

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Reiland S, Finazzi G, Endler A, Willig A, Baerenfaller K, Grossmann J, Gerrits B, Rutishauser D, Gruissem W, Rochaix JD, et al (2011) Comparative phosphoproteome profiling reveals a function of the STN8 kinase in fine-tuning of cyclic electron flow (CEF). Proc Natl Acad Sci U S A 108: 12955–12960

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Reiland S, Messerli G, Baerenfaller K, Gerrits B, Endler A, Grossmann J, Gruissem W, Baginsky S (2009) Large-scale arabidopsis phosphoproteome profiling reveals novel chloroplast kinase substrates and phosphorylation networks1[w]. Plant Physiol 150: 889–903

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Rensing SA (2018) Great moments in evolution: the conquest of land by plants. Curr Opin Plant Biol 42: 49–54

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Rensing SA, Lang D, Zimmer AD (2008) Conquest of Land by Plants. Science (80-) 319: 64–69

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Reymond P, Grünberger S, Paul K, Müller M, Farmer EE (1995) Oligogalacturonide defense signals in plants: large fragments interact with the plasma membrane in vitro. Proc Natl Acad Sci U S A 92: 4145–4149

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Reymond P, Kunz B, Paul-Pletzer K, Grimm R, Eckerskorn C, Farmer EE (1996) Cloning of a cDNA encoding a plasma membrane-associated, uronide binding phosphoprotein with physical properties similar to viral movement proteins. Plant Cell ... 8: 2265–2276

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Reymond P, Weber H, Damond M, Farmer EE (2000) Differential Gene Expression in Response to Mechanical Wounding and Insect Feeding in Arabidopsis. Plant Cell 12: 707–719

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Roitinger E, Hofer M, Köcher T, Pichler P, Novatchkova M, Yang J, Schlögelhofer P, Mechtler K (2015) Quantitative phosphoproteomics of the ataxia telangiectasia-mutated (ATM) and ataxia telangiectasia-mutated and Rad3-related (ATR) dependent DNA damage response in arabidopsis thaliana. Mol Cell Proteomics 14: 556–571

- Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Rutter BD, Innes RW (2017) Extracellular Vesicles Isolated from the Leaf Apoplast Carry Stress-Response Proteins. Plant Physiol 173: 728–741**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Rutter BD, Innes RW (2018) Extracellular vesicles as key mediators of plant–microbe interactions. Curr Opin Plant Biol 44: 16–22**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Ryan CA, An G (1988) Molecular biology of wound-inducible proteinase inhibitors in plants. Plant Cell Environ 11: 345–349**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Rybak K, Robatzek S (2019) Functions of extracellular vesicles in immunity and virulence. Plant Physiol 179: 1236–1247**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Sasaki N, Takashima E, Nyunoya H (2018) Altered Subcellular Localization of a Tobacco Membrane Raft-Associated Remorin Protein by Tobamovirus Infection and Transient Expression of Viral Replication and Movement Proteins. Front Plant Sci 9: 1–16**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Seong ES, Baek KH, Oh SK, Jo SH, Yi SY, Park JM, Joung YH, Lee S, Cho HS, Choi D (2007) Induction of enhanced tolerance to cold stress and disease by overexpression of the pepper CaPIF1 gene in tomato. Physiol Plant 129: 555–566**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Son S, Oh C, An C (2014) Arabidopsis thaliana Remorins Interact with SnRK1 and Play a Role in Susceptibility to Beet Curly Top Virus and Beet Severe Curly Top Virus. plant Pathol J 30: 269–278**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Song G, Brachova L, Nikolau BJ, Jones AM, Walley JW (2018) Heterotrimeric G-Protein-Dependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots. Proteomics 18: 1–14**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Srivastava V, Malm E, Sundqvist G, Bulone V (2013) Quantitative Proteomics Reveals that Plasma Membrane Microdomains From Poplar Cell Suspension Cultures Are Enriched in Markers of Signal Transduction, Molecular Transport, and Callose Biosynthesis. Mol Cell Proteomics 12: 3874–3885**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Stanislas T, Bouyssié D, Rossignol M, Vesa S, Fromentin J, Morel J, Pichereaux C, Monsarrat B, Simon-Plas F (2009) Quantitative Proteomics Reveals a Dynamic Association of Proteins to Detergent-resistant Membranes upon Elicitor Signaling in Tobacco. Mol Cell Proteomics 8: 2186–2198**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Stemans P, Hérisse A Le, Melvin J, Miller MA, Paris F, Verniers J, Wellman CH (2009) Origin and radiation of the earliest vascular land plants. Science (80-) 324: 324–325**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Sugiyama N, Nakagami H, Mochida K, Daudi A, Tomita M, Shirasu K, Ishihama Y (2008) Large-scale phosphorylation mapping reveals the extent of tyrosine phosphorylation in Arabidopsis. Mol Syst Biol. doi: 10.1038/msb.2008.32**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Szymanski WG, Zauber H, Erban A, Gorka M, Wu XN, Schulze WX (2015) Cytoskeletal components define protein location to membrane microdomains. Mol Cell Proteomics 14: M114.046904-**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Takahashi D, Kawamura Y, Uemura M (2013) Detergent-resistant plasma membrane proteome to elucidate microdomain functions in plant cells. Front Plant Sci 4: 27**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)
- Tarkka MT, Herrmann S, Wubet T, Feldhahn L, Recht S, Kurth F, Mailänder S, Bönn M, Neef M, Angay O, et al (2013) OakContigDF159.1, a reference library for studying differential gene expression in Quercus robur during controlled biotic interactions: Use for quantitative transcriptomic profiling of oak roots in ectomycorrhizal symbiosis. New Phytol 199: 529–540**

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Tóth K, Stratil TF, Madsen EB, Ye J, Popp C, Antolín-Llovera M, Grossmann C, Jensen ON, Schüßler A, Parniske M, et al (2012) Functional domain analysis of the remorin protein LjSYMREM1 in lotus japonicus. PLoS One. doi: 10.1371/journal.pone.0030817

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Ulmschneider JP, Ulmschneider MB (2018) Molecular Dynamics Simulations Are Redefining Our View of Peptides Interacting with Biological Membranes. Acc Chem Res 51: 1106–1116

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Verma V, Sivaraman J, Srivastava AK, Sadanandom A, Kumar PP (2015) Destabilization of interaction between cytokinin signaling intermediates AHP1 and ARR4 modulates Arabidopsis development. New Phytol 206: 726–737

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Voxeur A, Höfte H (2016) Cell wall integrity signaling in plants: “To grow or not to grow that’s the question.” Glycobiology 26: 950–960

Vu LD, Stes E, Van Bel M, Nelissen H, Maddelein D, Inzé D, Coppens F, Martens L, Gevaert K, De Smet I (2016) Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. J Proteome Res 15: 4304–4317

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang K, Yang Z, Qing D, Ren F, Liu S, Zheng Q, Liu J, Zhang W, Dai C, Wu M, et al (2018) Quantitative and functional posttranslational modification proteomics reveals that TREP1 plays a role in plant touch-delayed bolting. Proc Natl Acad Sci U S A 115: E10265–E10274

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang K, Zhao Y, Li M, Gao F, Yang M kun, Wang X, Li S, Yang P (2014) Analysis of phosphoproteome in rice pistil. Proteomics 14: 2319–2334

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang P, Hsu CC, Du Y, Zhu P, Zhao C, Fu X, Zhang C, Paez JS, Macho AP, Andy Tao W, et al (2020) Mapping proteome-wide targets of protein kinases in plant stress responses. Proc Natl Acad Sci U S A 117: 3270–3280

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang S, Chen Z, Tian L, Ding Y, Zhang J, Zhou J, Liu P, Chen Y, Wu L (2019) Comparative proteomics combined with analyses of transgenic plants reveal ZmREM1.3 mediates maize resistance to southern corn rust. Plant Biotechnol J 17: 2153–2168

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wellman CH (2010) The invasion of the land by plants: When and where? New Phytol 188: 306–309

Whiteman SA, Serazetdinova L, Jones AME, Sanders D, Rathjen J, Peck SC, Maathuis FJM (2008) Identification of novel proteins and phosphorylation sites in a tonoplast enriched membrane fraction of Arabidopsis thaliana. Proteomics 8: 3536–3547

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Widjaja I, Naumann K, Roth U, Wolf N, Mackey D, Dangl JL, Scheel D, Lee J (2009) Combining subproteome enrichment and Rubisco depletion enables identification of low abundance proteins differentially regulated during plant defense. Proteomics 9: 138–147

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wong MM, Bhaskara GB, Wen TN, Lin WD, Nguyen TT, Chong GL, Verslues PE (2019) Phosphoproteomics of Arabidopsis Highly ABA-Induced1 identifies AT-Hook-Like10 phosphorylation required for stress growth regulation. Proc Natl Acad Sci U S A 116: 2354–2363

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wu C-Q, Hu H-H, Zeng Y, Liang D-C, Xie K-B, Zhang J-W, Chu Z-H, Xiong L-Z (2006) Identification of Novel Stress-responsive Transcription Factor Genes in Rice by cDNA Array Analysis. J Integr Plant Biol 48: 1216–1224

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Xiang Y, Song B, Née G, Kramer K, Finkemeier I, Soppe WJJ (2016) Sequence polymorphisms at the REDUCED DORMANCY5 pseudophosphatase underlie natural variation in Arabidopsis dormancy. Plant Physiol 171: 2659–2670

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Xu Q, Xu X, Shi Y, Qi X, Chen X (2017) Elucidation of the molecular responses of a cucumber segment substitution line carrying Pm5.1 and its recurrent parent triggered by powdery mildew by comparative transcriptome profiling. BMC Genomics 18: 1–14

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Yamada H, Hanaki N, Imamura A, Ueguchi C, Mizuno T (1998) An Arabidopsis protein that interacts with the cytokinin-inducible response regulator, ARR4, implicated in the His-Asp phosphorylation signal transduction. FEBS Lett 436: 76–80

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Yang Z, Guo G, Zhang M, Liu CY, Hu Q, Lam H, Cheng H, Xue Y, Li J, Li N (2013) Stable isotope metabolic labeling-based quantitative phosphoproteomic analysis of arabidopsis mutants reveals ethylene-regulated time-dependent phosphoproteins and putative substrates of constitutive triple response 1 kinase. Mol Cell Proteomics 12: 3559–3582

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Ye J, Zhang Z, Long H, Zhang Z, Hong Y, Zhang X, You C, Liang W, Ma H, Lu P (2015) Proteomic and phosphoproteomic analyses reveal extensive phosphorylation of regulatory proteins in developing rice anthers. Plant J 84: 527–544

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Yeats TH, Bacic A, Johnson KL (2018) Plant glycosylphosphatidylinositol anchored proteins at the plasma membrane-cell wall nexus. J Integr Plant Biol 60: 649–669

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Yue J, Li C, Liu Y, Yu J (2014) A remorin gene SiREM6, the target gene of SiARDP, from foxtail millet (*Setaria italica*) promotes high salt tolerance in transgenic Arabidopsis. PLoS One 9: e100772

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zauber H, Burgos A, Garapati P, Schulze WX (2014) Plasma membrane lipid-protein interactions affect signaling processes in sterol-biosynthesis mutants in Arabidopsis thaliana. Front Plant Sci 5: 1–18

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zavaliev R, Levy A, Gera A, Epel BL (2013) Subcellular dynamics and role of Arabidopsis β -1,3-glucanases in cell-to-cell movement of tobamoviruses. Mol Plant Microbe Interact 26: 1016–30

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zavaliev R, Ueki S, Epel BL, Citovsky V (2011) Biology of callose (β -1,3-glucan) turnover at plasmodesmata. Protoplasma 248: 117–130

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhang H, Deng C, Wu X, Yao J, Zhang Y, Zhang Y, Deng S, Zhao N, Zhao R, Zhou X, et al (2020) Populus euphratica remorin 6.5 activates plasma membrane H⁺-ATPases to mediate salt tolerance. Tree Physiol 1–49

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhou Y, Hancock JF (2018) Deciphering lipid codes: K-Ras as a paradigm. Traffic 19: 157–165

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhou Y, Prakash P, Liang H, Cho K-J, Gorfé AA, Hancock JF (2017) Lipid-Sorting Specificity Encoded in K-Ras Membrane Anchor Regulates Signal Output. Cell 168: 239–251

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhou Y, Wong CO, Cho KJ, Van Der Hoeven D, Liang H, Thakur DP, Luo J, Babic M, Zinsmaier KE, Zhu MX, et al (2015) Membrane potential modulates plasma membrane phospholipid dynamics and K-Ras signaling. Science (80-) 349: 873–876

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Albers P, Üstün S, Witzel K, Kraner M, Börnke F (2019) A Remorin from *Nicotiana benthamiana* Interacts with the *Pseudomonas* Type-III Effector Protein HopZ1a and is Phosphorylated by the Immune-Related Kinase PBS1. Mol Plant-Microbe Interact 32: 1229–1242

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Alliotte T, Tiré C, Engler G, Peleman J, Caplan a, Van Montagu M, Inzé D (1989) An Auxin-Regulated Gene of Arabidopsis thaliana Encodes a DNA-Binding Protein. Plant Physiol 89: 743–52

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Amor-Mahjoub M, Suppini JP, Gomez-Vrielyunck N, Ladjimi M (2006) The effect of the hexahistidine-tag in the oligomerization of HSC70 constructs. J Chromatogr B Anal Technol Biomed Life Sci 844: 328–334

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Badawi MA, Agharbaoui Z, Zayed M, Li Q, Byrns B, Zou J, Fowler DB, Danyluk J, Sarhan F (2019) Genome-Wide Identification and Characterization of the Wheat Remorin (Ta REM) Family during Cold Acclimation . Plant Genome 12: 180040

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bah A, Vernon RM, Siddiqui Z, Krzeminski M, Muhandiram R, Zhao C, Sonenberg N, Kay LE, Forman-Kay JD (2015) Folding of an intrinsically disordered protein by phosphorylation as a regulatory switch. Nature 519: 106–109

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bariola PA, Retelska D, Stasiak A, Kammerer RA, Fleming A, Hijri M, Frank S, Farmer EE (2004) Remorins form a novel family of coiled coil-forming oligomeric and filamentous proteins associated with apical, vascular and embryonic tissues in plants. Plant Mol Biol 55: 579–594

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Benschop JJ, Mohammed S, O'Flaherty M, Heck AJR, Slijper M, Menke FLH (2007) Quantitative Phosphoproteomics of Early Elicitor Signaling in Arabidopsis. Mol Cell Proteomics 6: 1198–1214

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bilkova E, Pleskot R, Rissanen S, Sun S, Czogalla A, Cwiklik L, Róg T, Vattulainen I, Cremer PS, Jungwirth P, et al (2017) Calcium Directly Regulates Phosphatidylinositol 4,5-Bisphosphate Headgroup Conformation and Recognition. J Am Chem Soc 139: 4019–4024

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bilska-Kos A, Grzybowski M, Jończyk M, Sowiński P (2016) In situ localization and changes in the expression level of transcripts related to intercellular transport and phloem loading in leaves of maize (Zea mays L.) treated with low temperature. Acta Physiol Plant. doi: 10.1007/s11738-016-2151-5

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bozkurt TO, Richardson A, Dagdas YF, Mongrand S, Kamoun S, Raffaele S (2014) The Plant Membrane-Associated REMORIN1.3 Accumulates in Discrete Perihyphal Domains and Enhances Susceptibility to Phytophthora infestans. Plant Physiol 165: 1005–1018

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bray EA (2002) Classification of genes differentially expressed during water-deficit stress in Arabidopsis thaliana: An analysis using microarray and differential expression data. Ann Bot 89: 803–811

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bücherl CA, Jarsch IK, Schudoma C, Segonzac C, Mbengue M, Robatzke S, MacLean D, Ott T, Zipfe C (2017) Plant immune and growth receptors share common signalling components but localise to distinct plasma membrane nanodomains. Elife 6: 1–28

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Bundock P, Hooykaas P (2005) An Arabidopsis hAT-like transposase is essential for plant development. Nature 436: 282–284

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Byun MY, Lee J, Cui LH, Kang Y, Oh TK, Park H, Lee H, Kim WT (2015) Constitutive expression of DaCBF7, an Antarctic vascular plant Deschampsia antarctica CBF homolog, resulted in improved cold tolerance in transgenic rice plants. Plant Sci 236: 61–74

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Cai J, Chen T, Wang Y, Qin G, Tian S (2020) SIREM1 triggers cell death by activating an oxidative burst and other regulators. Plant Physiol pp.00120.2020

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Checker VG, Khurana P (2013) Molecular and functional characterization of mulberry EST encoding remorin (MiREM) involved in abiotic stress. Plant Cell Rep 32: 1729–41

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Chen K, An YQC (2006) Transcriptional responses to gibberellin and abscisic acid in Barley aleurone. J Integr Plant Biol 48: 591–612

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Chen Y, Hoehenwarter W, Weckwerth W (2010) Comparative analysis of phytohormone-responsive phosphoproteins in Arabidopsis thaliana using TiO2-phosphopeptide enrichment and mass accuracy precursor alignment. Plant J 63: 1–17

Pubmed: [Author and Title](#)

- Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Cheng G, Yang Z, Zhang H, Zhang J, Xu J (2020) Remorin interacting with PCaP1 impairs Turnip mosaic virus intercellular movement but is antagonised by VPg. *New Phytol* 225: 2122–2139**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Chisholm ST, Dahlbeck D, Krishnamurthy N, Day B, Sjolander K, Staskawicz BJ (2005) Molecular characterization of proteolytic cleavage sites of the *Pseudomonas syringae* effector AvrRpt2. *Proc Natl Acad Sci* 102: 2087–2092**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Choudhary MK, Nomura Y, Wang L, Nakagami H, Somers DE (2015) Quantitative circadian phosphoproteomic analysis of *Arabidopsis* reveals extensive clock control of key components in physiological, metabolic, and signaling pathways. *Mol Cell Proteomics* 14: 2243–2260**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Cui Y, Gao J, He Y, Jiang L (2020) Plant extracellular vesicles. *Protoplasma* 257: 3–12**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Dagdas YF, Beihaj K, Maqbool A, Chaparro-Garcia A, Pandey P, Petre B, Tabassum N, Cruz-Mireles N, Hughes RK, Sklenar J, et al (2016) An effector of the Irish potato famine pathogen antagonizes a host autophagy cargo receptor. *Elife* 5: 1–23**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Delwiche CF, Cooper ED (2015) The evolutionary origin of a terrestrial flora. *Curr Biol* 25: R899–R910**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Demir F, Horntrich C (2013) *Arabidopsis* nanodomain-delimited ABA signaling pathway regulates the anion channel SLAH3. *Proc* doi: 10.6019/PXD000211**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Dyson HJ, Wright PE (2005) Intrinsically unstructured proteins and their functions. *Nat Rev Mol Cell Biol* 6: 197–208**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Engberg O, Hautala V, Yasuda T, Dehio H, Murata M, Slotte JP, Nyholm TKM (2016) The Affinity of Cholesterol for Different Phospholipids Affects Lateral Segregation in Bilayers. *Biophys J* 111: 546–556**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Engelsberger WR, Schulze WX (2012) Nitrate and ammonium lead to distinct global dynamic phosphorylation patterns when resupplied to nitrogen-starved *Arabidopsis* seedlings. *Plant J* 69: 978–995**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Farmer E, Pearce G, Ryan C (1989) In vitro phosphorylation of plant plasma membrane proteins in response to the proteinase inhibitor inducing factor. *Proc ...* 86: 1539–1542**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Farmer EE, Moloshok TD, Saxton MJ, Ryan CA (1991) Oligosaccharide signaling in plants. Specificity of oligouronide-enhanced plasma membrane protein phosphorylation. *J Biol Chem* 266: 3140–3145.**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Fernandez-Calvino L, Faulkner C, Walshaw J, Saalbach G, Bayer E, Benitez-Alfonso Y, Maule A (2011) *Arabidopsis* plasmodesmal proteome. *PLoS One*. doi: 10.1371/journal.pone.0018880**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Fu S, Xu Y, Li C, Li Y, Wu J, Zhou X (2018) Rice Stripe Virus Interferes with S-acylation of Remorin and Induces Its Autophagic Degradation to Facilitate Virus Infection. *Mol Plant* 11: 269–287**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)
- Furt F, König S, Bessoule JJ, Sargueil F, Zallot R, Stanislas T, Noirot E, Lherminier J, Simon-Plas F, Heilmann I, et al (2010) Polyphosphoinositides are enriched in plant membrane rafts and form microdomains in the plasma membrane. *Plant Physiol* 152: 2173–2187**
Pubmed: [Author and Title](#)
Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Grimsrud PA, den Os D, Wenger CD, Swaney DL, Schwartz D, Sussman MR, Ané JM, Coon JJ (2010) Large-scale Phosphoprotein analysis in *Medicago truncatula* roots provides insight into in vivo kinase activity in legumes. *Plant Physiol* 152: 19–28

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Grison MS, Brocard L, Fouillen L, Nicolas W, Wewer V, Dörmann P, Nacir H, Benitez-Alfonso Y, Claverol S, Germain V, et al (2015) Specific Membrane Lipid Composition Is Important for Plasmodesmata Function in *Arabidopsis*. *Plant Cell Online* 27: tpc.114.135731

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Gronnier J, Crowet JM, Habenstein B, Nasir MN, Bayle V, Hosy E, Platre MP, Gouguet P, Raffaele S, Martinez D, et al (2017) Structural basis for plant plasma membrane protein dynamics and organization into functional nanodomains. *Elife* 6: 1–24

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Gui J, Liu C, Shen J, Li L (2014) Grain setting defect1, Encoding a Remorin Protein, Affects the Grain Setting in Rice through Regulating Plasmodesmatal Conductance. *Plant Physiol* 166: 1463–1478

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Gui J, Zheng S, Liu C, Shen J, Li J, Li L (2016a) OsREM4.1 Interacts with OsSERK1 to Coordinate the Interlinking between Abscisic Acid and Brassinosteroid Signaling in Rice. *Dev Cell* 38: 201–213

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Gui J, Zheng S, Liu C, Shen J, Li J, Li L (2016b) OsREM4.1 Interacts with OsSERK1 to Coordinate the Interlinking between Abscisic Acid and Brassinosteroid Signaling in Rice. *Dev Cell* 38: 201–213

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Gui J, Zheng S, Shen J, Li L (2015) Grain setting defect1 (GSD1) function in rice depends on S-acylation and interacts with actin 1 (OsACT1) at its C-terminal. *Front Plant Sci* 6: 1–11

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Gupta R, Min CW, Kim YJ, Kim ST (2019) Identification of Msp1-induced signaling components in rice leaves by integrated proteomic and phosphoproteomic analysis. *Int J Mol Sci* 20: 1–17

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Hemsley PA, Weimar T, Lilley KS, Dupree P, Grierson CS (2013) A proteomic approach identifies many novel palmitoylated proteins in *Arabidopsis*. *New Phytol* 197: 805–814

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Hou Y, Qiu J, Tong X, Wei X, Nallamilli BR, Wu W, Huang S, Zhang J (2015) A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight. *BMC Plant Biol* 15: 1–15

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Hu X, Puri KD, Gurung S, Klosterman SJ, Wallis CM, Britton M, Durbin-Johnson B, Phinney B, Salemi M, Short DPG, et al (2019) Proteome and metabolome analyses reveal differential responses in tomato -*Verticillium dahliae*-interactions. *J Proteomics* 207: 103449

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Huang D, Sun Y, Ma Z, Ke M, Cui Y, Chen Z, Chen C, Ji C, Tran TM, Yang L, et al (2019) Salicylic acid-mediated plasmodesmal closure via Remorin-dependent lipid organization. *Proc Natl Acad Sci U S A* 116: 21274–21284

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Iakoucheva LM, Radivojac P, Brown CJ, O'Connor TR, Sikes JG, Obradovic Z, Dunker AK (2004) The importance of intrinsic disorder for protein phosphorylation. *Nucleic Acids Res* 32: 1037–1049

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jacinto T, Farmer E, Ryan C (1993) Purification of potato leaf plasma membrane protein pp34, a protein phosphorylated in response to oligogalacturonide signals for defense and development. *Plant Physiol* 1393–1397

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jaillais Y, Ott T (2020) The Nanoscale Organization of the Plasma Membrane and Its Importance in Signaling: A Proteolipid Perspective. *Plant Physiol* 182: 1682–1696

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jamann TM, Luo X, Morales L, Kolkman JM, Chung CL, Nelson RJ (2016) A remorin gene is implicated in quantitative disease resistance in maize. *Theor Appl Genet* 129: 591–602

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Jarsch IK, Konrad SSA, Stratil TF, Urbanus SL, Szymanski W, Braun P, Braun K-HK-H, Ott T (2014) Plasma Membranes Are Subcompartmentalized into a Plethora of Coexisting and Diverse Microdomains in *Arabidopsis* and *Nicotiana benthamiana*. *Plant Cell* 26: 1698–1711

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Keinath NF, Kierszniowska S, Lorek J, Bourdais G, Kessler SA, Shimosato-Asano H, Grossniklaus U, Schulze WX, Robatzek S, Panstruga R (2010) PAMP (Pathogen-associated Molecular Pattern)-induced changes in plasma membrane compartmentalization reveal novel components of plant immunity. *J Biol Chem* 285: 39140–39149

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Khan M, Youn J-Y, Gingras A-C, Subramaniam R, Desveaux D (2018) In planta proximity dependent biotin identification (BioID). *Sci Rep* 8: 9212

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Khoza TG, Dubery IA, Piater LA (2019) Identification of candidate ergosterol-responsive proteins associated with the plasma membrane of *Arabidopsis thaliana*. *Int J Mol Sci* 20: 1–22

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kim PM, Sboner A, Xia Y, Gerstein M (2008) The role of disorder in interaction networks: A structural analysis. *Mol Syst Biol* 4: 179

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kistner C, Winzer T, Pitzschke A, Mulder L, Sato S, Kaneko T, Tabata S, Sandal N, Stoudgard J, Webb KJ, et al (2005) Seven Lotus japonicus Genes Required for Transcriptional Reprogramming of the Root during Fungal and Bacterial Symbiosis. *Plant Cell* 17: 2217–2229

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kohorn BD, Hoon D, Minkoff BB, Sussman MR, Kohorn SL (2016) Rapid Oligo-Galacturonide Induced Changes in Protein Phosphorylation in *Arabidopsis*. *Mol Cell Proteomics* 15: 1351–1359

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kong CY, Luo Y ping, Duan TT, Xue Z, Gao XD, Zhao X, Gao G (2016) Potato remorin gene StREMa4 cloning and its spatiotemporal expression pattern under *Ralstonia solanacearum* and plant hormones treatment. *Phytoparasitica* 44: 575–584

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Konrad SSA, Popp C, Stratil TF, Jarsch IK, Thallmair V, Folgmann J, Marin M, Ott T (2014) S-acylation anchors remorin proteins to the plasma membrane but does not primarily determine their localization in membrane microdomains. *New Phytol* 203: 758–769

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kreps JA, Wu Y, Chang H, Zhu T, Wang X, Harper JF, Mesa T, Row M, Diego S, California JAK, et al (2002) Transcriptome Changes for *Arabidopsis* in Response to Salt, Osmotic, and Cold Stress. *Plant Physiol* 130: 2129–2141

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kubicek CP, Starr TL, Glass NL (2014) Plant Cell Wall-Degrading Enzymes and Their Secretion in Plant-Pathogenic Fungi. *Annu Rev Phytopathol* 52: 427–451

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Kusumi A, Fujiwara TK, Chadda R, Xie M, Tsunoyama TA, Kalay Z, Kasai RS, Suzuki KGN (2012) Dynamic Organizing Principles of the Plasma Membrane that Regulate Signal Transduction: Commemorating the Fortieth Anniversary of Singer and Nicolson's Fluid-Mosaic Model. *Annu Rev Cell Dev Biol* 28: 215–250

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lan P, Li W, Wen TN, Schmidt W (2012) Quantitative phosphoproteome profiling of iron-deficient *Arabidopsis* roots. *Plant Physiol* 159: 403–417

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lee D, Bourdais G, Yu G, Robatzek S, Coaker G (2015) Phosphorylation of the Plant Immune Regulator RPM1-INTERACTING

PROTEIN4 Enhances Plant Plasma Membrane H⁺-ATPase Activity and Inhibits Flagellin-Triggered Immune Responses in Arabidopsis. Plant Cell 27: 2042–2056

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lefebvre B, Timmers T, Mbengue M, Moreau S, Hervé C, Tóth K, Bittencourt-Silvestre J, Klaus D, Deslandes L, Godiard L, et al (2010) A remorin protein interacts with symbiotic receptors and regulates bacterial infection. Proc Natl Acad Sci U S A 107: 2343–8

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Legrand A, Martinez D, Grélard A, Berbon M, Morvan E, Tawani A, Loquet A, Mongrand S, Habenstein B (2019) Nanodomain Clustering of the Plant Protein Remorin by Solid-State NMR. Front Mol Biosci 6: 1–14

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lenarčič T, Albert I, Böhm H, Hodnik V, Pirc K, Zavec AB, Podobnik M, Pahovnik D, Žagar E, Pruitt R, et al (2017) Eudicot plant-specific sphingolipids determine host selectivity of microbial NLP cytolysins. Science (80-) 358: 1431–1434

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Levy A, Erlanger M, Rosenthal M, Epel BL (2007) A plasmodesmata-associated β -1,3-glucanase in Arabidopsis. Plant J 49: 669–682

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Li H, Wai SW, Zhu L, Hong WG, Ecker J, Li N (2009) Phosphoproteomic analysis of ethylene-regulated protein phosphorylation in etiolated seedlings of Arabidopsis mutant ein2 using two-dimensional separations coupled with a hybrid quadrupole time-of-flight mass spectrometer. Proteomics 9: 1646–1661

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Liang P, Stratil TF, Popp C, Marin M, Folgmann J, Mysore KS, Wen J, Ott T (2018) Symbiotic root infections in Medicago truncatula require remorin-mediated receptor stabilization in membrane nanodomains. Proc Natl Acad Sci 115: 5289–5294

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lin F, Xu SL, Ni WM, Chu ZQ, Xu ZH, Xue HW (2003) Identification of ABA-responsive genes in rice shoots via cDNA macroarray. Cell Res 13: 59–68

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Liu E, Liu Y, Wu G, Zeng S, Tran Thi TG, Liang L, Liang Y, Dong Z, She D, Wang H, et al (2016) Identification of a Candidate Gene for Panicle Length in Rice (Oryza sativa L.) Via Association and Linkage Analysis. Front Plant Sci 7: 1–13

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Liu J, Elmore JM, Coaker G (2009a) Investigating the functions of the RIN4 protein complex during plant innate immune responses. Plant Signal Behav 4: 1107–1110

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Liu J, Elmore JM, Fuglsang AT, Palmgren MG, Staskawicz BJ, Coaker G (2009b) RIN4 functions with plasma membrane H⁺-ATPases to regulate stomatal apertures during pathogen attack. PLoS Biol. doi: 10.1371/journal.pbio.1000139

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lozano-Durán R, Robatzek S (2015) 14-3-3 Proteins in Plant-Pathogen Interactions. Mol Plant-Microbe Interact 28: 511–518

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lu Q, Ding S, Reiland S, Rödiger A, Roschitzki B, Xue P, GUISSEM W, Lu C, BAGINSKY S (2015) Identification and characterization of chloroplast casein kinase II from Oryza sativa (rice). J Exp Bot 66: 175–187

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Lu YJ, Schornack S, Spallek T, Geldner N, Chory J, Schellmann S, Schumacher K, Kamoun S, Robatzek S (2012) Patterns of plant subcellular responses to successful oomycete infections reveal differences in host cell reprogramming and endocytic trafficking. Cell Microbiol 14: 682–697

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Mackey D, Iii BFH, Wieg A, Dangl JL, Hill C, Carolina N (2002) RIN4 interacts with Pseudomonas syringae type III effector molecules and is required for RPM1-mediated resistance in Arabidopsis. Cell 108: 743–754

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Majeran W, Le Caer JP, Ponnala L, Meinzel T, Giglione C (2018) Targeted profiling of Arabidopsis thaliana subproteomes illuminates co- and posttranslationally N-terminal myristoylated proteins. Plant Cell 30: 543–562

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Marcolino-Gomes J, Rodrigues FA, Fuganti-Pagliarini R, Bendix C, Nakayama TJ, Celaya B, Molinari HBC, De Oliveira MCN, Harmon FG, Nepomuceno A (2014) Diurnal oscillations of soybean circadian clock and drought responsive genes. PLoS One. doi: 10.1371/journal.pone.0086402

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Marcon C, Malik WA, Walley JW, Shen Z, Paschold A, Smith LG, Piepho HP, Briggs SP, Hochholdinger F (2015) A high-resolution tissue-specific proteome and phosphoproteome atlas of maize primary roots reveals functional gradients along the root axes. Plant Physiol 168: 233–246

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Marín M, Ott T (2012) Phosphorylation of intrinsically disordered regions in remorin proteins. Front Plant Sci 3: 86

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Marín M, Thallmair V, Ott T (2012) The intrinsically disordered N-terminal region of AtREM1.3 remorin protein mediates protein-protein interactions. J Biol Chem 287: 39982–39991

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Marondedze C, Groen AJ, Thomas L, Lilley KS, Gehring C (2016) A Quantitative Phosphoproteome Analysis of cGMP-Dependent Cellular Responses in Arabidopsis thaliana. Mol Plant 9: 621–623

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Martinez D, Legrand A, Gronnier J, Decossas M, Gougnet P, Lambert O, Berbon M, Verron L, Grélard A, Germain V, et al (2018) Coiled-coil oligomerization controls localization of the plasma membrane REMORINs. J Struct Biol 0–1

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Mattei B, Spinelli F, Pontiggia D, De Lorenzo G (2016) Comprehensive Analysis of the Membrane Phosphoproteome Regulated by Oligogalacturonides in Arabidopsis thaliana. Front Plant Sci. doi: 10.3389/fpls.2016.01107

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Maxwell KN, Zhou Y, Hancock JF (2018) Clustering of Rac1: Selective Lipid Sorting Drives Signaling. Trends Biochem Sci 43: 75–77

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Mayank P, Grossman J, Wuest S, Boisson-Dernier A, Roschitzki B, Nanni P, Nühse T, Grossniklaus U (2012) Characterization of the phosphoproteome of mature Arabidopsis pollen. Plant J 72: 89–101

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Mehlmer N, Wurzinger B, Stael S, Hofmann-Rodrigues D, Csaszar E, Pfister B, Bayer R, Teige M (2010) The Ca²⁺-dependent protein kinase CPK3 is required for MAPK-independent salt-stress acclimation in Arabidopsis. Plant J 63: 484–498

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Menz J, Li Z, Schulze WX, Ludewig U (2016) Early nitrogen-deprivation responses in Arabidopsis roots reveal distinct differences on transcriptome and (phospho-) proteome levels between nitrate and ammonium nutrition. Plant J 88: 717–734

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Mergner J, Frejno M, List M, Papacek M, Chen X, Chaudhary A, Samaras P, Richter S, Shikata H, Messerer M, et al (2020) Mass-spectrometry-based draft of the Arabidopsis proteome. Nature 579: 409–414

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Meyer D, Pajonk S, Micali C, O'Connell R, Schulze-Lefert P (2009) Extracellular transport and integration of plant secretory proteins into pathogen-induced cell wall compartments. Plant J 57: 986–999

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Micali CO, Neumann U, Grunewald D, Panstruga R, O'Connell R (2011) Biogenesis of a specialized plant-fungal interface during host cell internalization of Golovinomyces orontii haustoria. Cell Microbiol 13: 210–226

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Mongrand S, Morel J, Laroche J, Claverol S, Carde J-P, Hartmann M-A, Bonneau M, Simon-Plas F, Lessire R, Bessoule J-J (2004) Lipid rafts in higher plant cells: purification and characterization of Triton X-100-insoluble microdomains from tobacco plasma membrane. J Biol Chem 279: 36277–86

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Morel J, Clavero S, Mongrand S, Furt F, Fromentin J, Bessoule JJ, Blein JP, Simon F (2006) Proteomics of plant detergent-resistant membranes. Mol Cell Proteomics 5: 1396–1411

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nakagami H, Sugiyama N, Mochida K, Daudi A, Yoshida Y, Toyoda T, Tomita M, Ishihama Y, Shirasu K (2010) Large-scale comparative phosphoproteomics identifies conserved phosphorylation sites in plants. Plant Physiol 153: 1161–1174

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Niittylä T, Fuglsang AT, Palmgren MG, Frommer WB, Schulze WX (2007) Temporal analysis of sucrose-induced phosphorylation changes in plasma membrane proteins of Arabidopsis. Mol Cell Proteomics 6: 1711–1726

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nikonorova N, Van Den Broeck L, Zhu S, Van De Cotte B, Dubois M, Gevaert K, Inzé D, De Smet I (2018) Early mannitol-triggered changes in the Arabidopsis leaf (phospho)proteome reveal growth regulators. J Exp Bot 69: 4591–4607

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nühse TS, Bottrill AR, Jones AME, Peck SC (2007) Quantitative phosphoproteomic analysis of plasma membrane proteins reveals regulatory mechanisms of plant innate immune responses. Plant J 51: 931–940

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nühse TS, Stensballe A, Jensen ON, Peck SC (2004) Phosphoproteomics of the Arabidopsis plasma membrane and a new phosphorylation site database Winside box sign. Plant Cell 16: 2394–2405

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Nukarinen E, Ngele T, Pedrotti L, Wurzinger B, Mair A, Landgraf R, Börnke F, Hanson J, Teige M, Baena-Gonzalez E, et al (2016) Quantitative phosphoproteomics reveals the role of the AMPK plant ortholog SnRK1 as a metabolic master regulator under energy deprivation. Sci Rep 6: 1–19

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Oh SK, Jeong MP, Young HJ, Lee S, Chung E, Kim SY, Seung HY, Choi D (2005) A plant EPF-type zinc-finger protein, CaPIF1, involved in defence against pathogens. Mol Plant Pathol 6: 269–285

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Perraki A, Binaghi M, Mecchia M a, Gronnier J, German-Retana S, Mongrand S, Bayer E, Zelada AM, Germain V (2014) StRemorin1.3 hampers Potato virus X TGBp1 ability to increase plasmodesmata permeability, but does not interfere with its silencing suppressor activity. FEBS Lett 588: 1699–705

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Perraki A, Gronnier J, Gouguet P, Boudsocq M, Deroubaix F, Simon V, Legrand A, German-Retana S, Zipfel C, Bayer EMF, et al (2018) REM1.3's phospho-status defines its plasma membrane nanodomain organization and activity in restricting PVX cell-to-cell movement. PLoS Pathog.

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Qin L, Zhou Z, Li Q, Zhai C, Liu L, Quilichini TD, Gao P, Kessler SA, Jaillais Y, Datla R, et al (2020) Specific Recruitment of Phosphoinositide Species to the Plant-Pathogen Interfacial Membrane Underlies Arabidopsis Susceptibility to Fungal Infection. Plant Cell 32: tpc.00970.2019

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Qiu J, Hou Y, Tong X, Wang Y, Lin H, Liu Q, Zhang W, Li Z, Nallamilli BR, Zhang J (2016) Quantitative phosphoproteomic analysis of early seed development in rice (*Oryza sativa* L.). Plant Mol Biol 90: 249–265

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Qiu J, Hou Y, Wang Y, Li Z, Zhao J, Tong X, Lin H, Wei X, Ao H, Zhang J (2017) A comprehensive proteomic survey of aba-induced protein phosphorylation in rice (*Oryza sativa* L.). Int J Mol Sci 18: 1–16

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Raffaele S, Bayer E, Lafarge D, Cluzet S, German Retana S, Boubekeur T, Leborgne-Castel N, Carde J-P, Lherminier J, Noirot E, et al (2009) Remorin, a solanaceae protein resident in membrane rafts and plasmodesmata, impairs potato virus X movement. Plant Cell 21: 1541–55

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Raffaele S, Mongrand S, Gamas P, Niebel A, Ott T (2007) Genome-wide annotation of remorins, a plant-specific protein family: evolutionary and functional perspectives. Plant Physiol 145: 593–600

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Raghupathy R, Anilkumar AA, Polley A, Singh PP, Yadav M, Johnson C, Suryawanshi S, Saikam V, Sawant SD, Panda A, et al (2015) Transbilayer Lipid Interactions Mediate Nanoclustering of Lipid-Anchored Proteins. Cell 161: 581–594

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Ray A, Jatana N, Thukral L (2017) Lipidated proteins: Spotlight on protein-membrane binding interfaces. Prog Biophys Mol Biol 128: 74–84

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Reiland S, Finazzi G, Endler A, Willig A, Baerenfaller K, Grossmann J, Gerrits B, Rutishauser D, Gruissem W, Rochaix JD, et al (2011) Comparative phosphoproteome profiling reveals a function of the STN8 kinase in fine-tuning of cyclic electron flow (CEF). Proc Natl Acad Sci U S A 108: 12955–12960

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Reiland S, Messerli G, Baerenfaller K, Gerrits B, Endler A, Grossmann J, Gruissem W, Baginsky S (2009) Large-scale arabidopsis phosphoproteome profiling reveals novel chloroplast kinase substrates and phosphorylation networks1[w]. Plant Physiol 150: 889–903

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Rensing SA (2018) Great moments in evolution: the conquest of land by plants. Curr Opin Plant Biol 42: 49–54

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Rensing SA, Lang D, Zimmer AD (2008) Conquest of Land by Plants. Science (80-) 319: 64–69

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Reymond P, Grünberger S, Paul K, Müller M, Farmer EE (1995) Oligogalacturonide defense signals in plants: large fragments interact with the plasma membrane in vitro. Proc Natl Acad Sci U S A 92: 4145–4149

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Reymond P, Kunz B, Paul-Pletzer K, Grimm R, Eckerskorn C, Farmer EE (1996) Cloning of a cDNA encoding a plasma membrane-associated, uronide binding phosphoprotein with physical properties similar to viral movement proteins. Plant Cell ... 8: 2265–2276

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Reymond P, Weber H, Damond M, Farmer EE (2000) Differential Gene Expression in Response to Mechanical Wounding and Insect Feeding in Arabidopsis. Plant Cell 12: 707–719

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Roitinger E, Hofer M, Köcher T, Pichler P, Novatchkova M, Yang J, Schlögelhofer P, Mechtler K (2015) Quantitative phosphoproteomics of the ataxia telangiectasia-mutated (ATM) and ataxia telangiectasia-mutated and Rad3-related (ATR) dependent DNA damage response in arabidopsis thaliana. Mol Cell Proteomics 14: 556–571

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Rutter BD, Innes RW (2017) Extracellular Vesicles Isolated from the Leaf Apoplast Carry Stress-Response Proteins. Plant Physiol 173: 728–741

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Rutter BD, Innes RW (2018) Extracellular vesicles as key mediators of plant–microbe interactions. Curr Opin Plant Biol 44: 16–22

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Ryan CA, An G (1988) Molecular biology of wound-inducible proteinase inhibitors in plants. Plant Cell Environ 11: 345–349

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Rybak K, Robatzek S (2019) Functions of extracellular vesicles in immunity and virulence. Plant Physiol 179: 1236–1247

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Sasaki N, Takashima E, Nyunoya H (2018) Altered Subcellular Localization of a Tobacco Membrane Raft-Associated Remorin Protein by Tobamovirus Infection and Transient Expression of Viral Replication and Movement Proteins. Front Plant Sci 9: 1–16

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Seong ES, Baek KH, Oh SK, Jo SH, Yi SY, Park JM, Joung YH, Lee S, Cho HS, Choi D (2007) Induction of enhanced tolerance to cold stress and disease by overexpression of the pepper CaPIF1 gene in tomato. Physiol Plant 129: 555–566

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Son S, Oh C, An C (2014) Arabidopsis thaliana Remorins Interact with SnRK1 and Play a Role in Susceptibility to Beet Curly Top Virus and Beet Severe Curly Top Virus. plant Pathol J 30: 269–278

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Song G, Brachova L, Nikolau BJ, Jones AM, Walley JW (2018) Heterotrimeric G-Protein-Dependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots. Proteomics 18: 1–14

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Srivastava V, Malm E, Sundqvist G, Bulone V (2013) Quantitative Proteomics Reveals that Plasma Membrane Microdomains From Poplar Cell Suspension Cultures Are Enriched in Markers of Signal Transduction, Molecular Transport, and Callose Biosynthesis. Mol Cell Proteomics 12: 3874–3885

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Stanislas T, Bouyssié D, Rossignol M, Vesa S, Fromentin J, Morel J, Pichereaux C, Monsarrat B, Simon-Plas F (2009) Quantitative Proteomics Reveals a Dynamic Association of Proteins to Detergent-resistant Membranes upon Elicitor Signaling in Tobacco. Mol Cell Proteomics 8: 2186–2198

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Steemans P, Hérissé A Le, Melvin J, Miller MA, Paris F, Verniers J, Wellman CH (2009) Origin and radiation of the earliest vascular land plants. Science (80-) 324: 353

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Sugiyama N, Nakagami H, Mochida K, Daudi A, Tomita M, Shirasu K, Ishihama Y (2008) Large-scale phosphorylation mapping reveals the extent of tyrosine phosphorylation in Arabidopsis. Mol Syst Biol. doi: 10.1038/msb.2008.32

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Szymanski WG, Zauber H, Erban A, Gorka M, Wu XN, Schulze WX (2015) Cytoskeletal components define protein location to membrane microdomains. Mol Cell Proteomics 14: M114.046904-

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Takahashi D, Kawamura Y, Uemura M (2013) Detergent-resistant plasma membrane proteome to elucidate microdomain functions in plant cells. Front Plant Sci 4: 27

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Tarkka MT, Herrmann S, Wubet T, Feldhahn L, Recht S, Kurth F, Mailänder S, Bönn M, Neef M, Angay O, et al (2013) OakContigDF159.1, a reference library for studying differential gene expression in Quercus robur during controlled biotic interactions: Use for quantitative transcriptomic profiling of oak roots in ectomycorrhizal symbiosis. New Phytol 199: 529–540

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Tóth K, Stratil TF, Madsen EB, Ye J, Popp C, Antolín-Llovera M, Grossmann C, Jensen ON, Schüßler A, Parniske M, et al (2012) Functional domain analysis of the remorin protein LjSYMREM1 in lotus japonicus. PLoS One. doi: 10.1371/journal.pone.0030817

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Ulmschneider JP, Ulmschneider MB (2018) Molecular Dynamics Simulations Are Redefining Our View of Peptides Interacting with Biological Membranes. Acc Chem Res 51: 1106–1116

Pubmed: [Author and Title](#)

Google Scholar: [Author Only](#) [Title Only](#) [Author and Title](#)

Verma V, Sivaraman J, Srivastava AK, Sadanandom A, Kumar PP (2015) Destabilization of interaction between cytokinin signaling intermediates AHP1 and ARR4 modulates Arabidopsis development. New Phytol 206: 726–737

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Voxeur A, Höfte H (2016) Cell wall integrity signaling in plants: “To grow or not to grow that’s the question.” *Glycobiology* 26: 950–960

Vu LD, Stes E, Van Bel M, Nelissen H, Maddelein D, Inzé D, Coppens F, Martens L, Gevaert K, De Smet I (2016) Up-to-Date Workflow for Plant (Phospho)proteomics Identifies Differential Drought-Responsive Phosphorylation Events in Maize Leaves. *J Proteome Res* 15: 4304–4317

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang K, Yang Z, Qing D, Ren F, Liu S, Zheng Q, Liu J, Zhang W, Dai C, Wu M, et al (2018) Quantitative and functional posttranslational modification proteomics reveals that TREP1 plays a role in plant touch-delayed bolting. *Proc Natl Acad Sci U S A* 115: E10265–E10274

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang K, Zhao Y, Li M, Gao F, Yang M kun, Wang X, Li S, Yang P (2014) Analysis of phosphoproteome in rice pistil. *Proteomics* 14: 2319–2334

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang P, Hsu CC, Du Y, Zhu P, Zhao C, Fu X, Zhang C, Paez JS, Macho AP, Andy Tao W, et al (2020) Mapping proteome-wide targets of protein kinases in plant stress responses. *Proc Natl Acad Sci U S A* 117: 3270–3280

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wang S, Chen Z, Tian L, Ding Y, Zhang J, Zhou J, Liu P, Chen Y, Wu L (2019) Comparative proteomics combined with analyses of transgenic plants reveal ZmREM1.3 mediates maize resistance to southern corn rust. *Plant Biotechnol J* 17: 2153–2168

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wellman CH (2010) The invasion of the land by plants: When and where? *New Phytol* 188: 306–309

Whiteman SA, Serazetdinova L, Jones AME, Sanders D, Rathjen J, Peck SC, Maathuis FJM (2008) Identification of novel proteins and phosphorylation sites in a tonoplast enriched membrane fraction of *Arabidopsis thaliana*. *Proteomics* 8: 3536–3547

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Widjaja I, Naumann K, Roth U, Wolf N, Mackey D, Dangl JL, Scheel D, Lee J (2009) Combining subproteome enrichment and Rubisco depletion enables identification of low abundance proteins differentially regulated during plant defense. *Proteomics* 9: 138–147

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wong MM, Bhaskara GB, Wen TN, Lin WD, Nguyen TT, Chong GL, Verslues PE (2019) Phosphoproteomics of *Arabidopsis* Highly ABA-Induced1 identifies AT-Hook-Like10 phosphorylation required for stress growth regulation. *Proc Natl Acad Sci U S A* 116: 2354–2363

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Wu C-Q, Hu H-H, Zeng Y, Liang D-C, Xie K-B, Zhang J-W, Chu Z-H, Xiong L-Z (2006) Identification of Novel Stress-responsive Transcription Factor Genes in Rice by cDNA Array Analysis. *J Integr Plant Biol* 48: 1216–1224

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Xiang Y, Song B, Née G, Kramer K, Finkemeier I, Soppe WJJ (2016) Sequence polymorphisms at the REDUCED DORMANCY5 pseudophosphatase underlie natural variation in *Arabidopsis* dormancy. *Plant Physiol* 171: 2659–2670

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Xu Q, Xu X, Shi Y, Qi X, Chen X (2017) Elucidation of the molecular responses of a cucumber segment substitution line carrying Pm5.1 and its recurrent parent triggered by powdery mildew by comparative transcriptome profiling. *BMC Genomics* 18: 1–14

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Yamada H, Hanaki N, Imamura A, Ueguchi C, Mizuno T (1998) An *Arabidopsis* protein that interacts with the cytokinin-inducible response regulator, ARR4, implicated in the His-Asp phosphorylation signal transduction. *FEBS Lett* 436: 76–80

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Yang Z, Guo G, Zhang M, Liu CY, Hu Q, Lam H, Cheng H, Xue Y, Li J, Li N (2013) Stable isotope metabolic labeling-based quantitative phosphoproteomic analysis of *Arabidopsis* mutants reveals ethylene-regulated time-dependent phosphoproteins and putative substrates of constitutive triple response 1 kinase. *Mol Cell Proteomics* 12: 3559–3582

Pubmed: [Author and Title](#)
Google Scholar: [Author Only Title Only Author and Title](#)

Ye J, Zhang Z, Long H, Zhang Z, Hong Y, Zhang X, You C, Liang W, Ma H, Lu P (2015) Proteomic and phosphoproteomic analyses reveal

extensive phosphorylation of regulatory proteins in developing rice anthers. Plant J 84: 527–544

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Yeats TH, Bacic A, Johnson KL (2018) Plant glycosylphosphatidylinositol anchored proteins at the plasma membrane-cell wall nexus. J Integr Plant Biol 60: 649–669

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Yue J, Li C, Liu Y, Yu J (2014) A remorin gene SiREM6, the target gene of SiARDP, from foxtail millet (*Setaria italica*) promotes high salt tolerance in transgenic Arabidopsis. PLoS One 9: e100772

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zauber H, Burgos A, Garapati P, Schulze WX (2014) Plasma membrane lipid-protein interactions affect signaling processes in sterol-biosynthesis mutants in Arabidopsis thaliana. Front Plant Sci 5: 1–18

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zavaliev R, Levy A, Gera A, Epel BL (2013) Subcellular dynamics and role of Arabidopsis β -1,3-glucanases in cell-to-cell movement of tobamoviruses. Mol Plant Microbe Interact 26: 1016–30

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zavaliev R, Ueki S, Epel BL, Citovsky V (2011) Biology of callose (β -1,3-glucan) turnover at plasmodesmata. Protoplasma 248: 117–130

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhang H, Deng C, Wu X, Yao J, Zhang Y, Zhang Y, Deng S, Zhao N, Zhao R, Zhou X, et al (2020) Populus euphratica remorin 6.5 activates plasma membrane H⁺-ATPases to mediate salt tolerance. Tree Physiol 1–49

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhou Y, Hancock JF (2018) Deciphering lipid codes: K-Ras as a paradigm. Traffic 19: 157–165

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhou Y, Prakash P, Liang H, Cho K-J, Gorfe AA, Hancock JF (2017) Lipid-Sorting Specificity Encoded in K-Ras Membrane Anchor Regulates Signal Output. Cell 168: 239–251

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)

Zhou Y, Wong CO, Cho KJ, Van Der Hoeven D, Liang H, Thakur DP, Luo J, Babic M, Zinsmaier KE, Zhu MX, et al (2015) Membrane potential modulates plasma membrane phospholipid dynamics and K-Ras signaling. Science (80-) 349: 873–876

Pubmed: [Author and Title](#)

Google Scholar: [Author Only Title Only Author and Title](#)