

1 Review

2 Endogenous control mechanisms of FAK and PYK2 3 and their relevance to cancer development and therapy

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11 Abstract:

12 Focal adhesion kinase (FAK) and its close paralogue, proline-rich tyrosine kinase 2 (PYK2), are key
13 regulators of aggressive spreading and metastasis of cancer cells. While targeted small-molecule
14 inhibitors of FAK and PYK2 are showing promising antitumor activity, their clinical long-term
15 efficacy may be undermined by the strong capacity of cancer cells to evade anti-kinase drugs. In
16 healthy cells, the expression and/or function of FAK and PYK2 is tightly controlled through
17 modulation of gene expression, competing alternatively spliced forms, non-coding RNAs, and
18 proteins that directly or indirectly affect kinase activation or protein stability. The molecular factors
19 involved are frequently deregulated in cancer cells. Here, we review the endogenous mechanisms
20 controlling FAK and PYK2, and discuss how these mechanisms could inspire or improve anticancer
21 therapies.

22 **Keywords:** dimerization; miRNA; motility; anoikis; chaperon; PTEN; FIP200; LKB1; PI3K; regulation

23

24 1. Introduction

25 Focal Adhesion Kinase (FAK) is a multi-domain non-receptor protein tyrosine kinase (PTK) found in
26 metazoan, but also the unicellular eukaryote *Capsaspora owczarzaki* [1,2]. FAK is a multifunctional
27 protein that integrates and transduces signals perceived through integrin or growth factor receptors
28 into adapted cytoplasmic and nuclear responses. This mechanism allows FAK to functionally link
29 adhesion, migration and survival of cells [3,4]. In particular, its ability to override apoptosis
30 following cell detachment (anoikis) makes FAK an essential factor in embryogenesis and wound
31 healing. While present in low levels in most adult tissues, FAK is overexpressed in most types of
32 cancer in which its capacity to override anoikis and to drive cell motility promotes aggressive
33 invasiveness and metastasis of cancer cells [5–8]. The observation that tumor-specific overexpression
34 of FAK is linked to tumor invasiveness has made FAK a promising target for small-molecule
35 inhibition [7,9]. Initial proof-of-principle studies have highlighted that inhibition of FAK not only
36 reduces tumor spreading, but it also makes cancer cells more susceptible to chemotherapy [10,11].
37 However, most available inhibitors lack either specificity or efficacy, and their precise molecular
38 mechanism remains in many cases poorly defined [10]. Moreover, proline-rich tyrosine kinase 2
39 (PYK2), a close paralogue to FAK in vertebrates [12], can functionally compensate for loss of FAK in
40 some settings and may thus override inhibition of FAK [13,14]. FAK and PYK2 have different tissue
41 distributions. Whereas FAK is widely expressed, expression of PYK2 is more restricted with major
42 occurrences and roles in the brain, osteoclasts, macrophages and lymphocytes [15]. Both can have
43 different, or even opposing, cellular roles; for example, FAK activation promotes cell cycle

44 progression and survival, whereas PYK2 generally inhibits such events [5,16–21]. Hence, (tissue-)
45 specific inhibition of FAK or PYK2 might be required for an inhibitor to achieve desired therapeutic
46 effects.

47 In this review, we summarize current understanding of the endogenous mechanisms used by cells to
48 contain aberrant FAK and PYK2 activity. Thorough understanding of these mechanisms might lead
49 to the design of new or improved therapeutic interventions that could block aggressive spreading of
50 cancer cells. The multitude of cellular functions and locations of FAK and PYK2 have been
51 comprehensively described in recent reviews [22–25]. We thus only briefly outline the general
52 molecular mechanism for FAK and PYK2 activation. We focus our review on how this mechanism is
53 controlled by cellular factors, including alternatively spliced forms, interacting proteins and
54 non-coding RNAs. We also discuss if and how the current knowledge of endogenous control
55 mechanisms of FAK and/or PYK2 could assist the development anti-cancer strategies.

56 1.1 Mechanistic bases for activation of FAK and PYK2

57 PYK2 evolved from FAK through gene duplication and subsequent specialization in vertebrates [12].
58 In humans, both proteins share 46% sequence identity (65% similarity) and have the same
59 three-domain organization [25–27]: an N-terminal band 4.1, ezrin, radixin, moesin (FERM) domain, a
60 central catalytic kinase domain and a C-terminal focal adhesion targeting (FAT) domain (reviewed
61 in detail by [4,23,25]). The domains are connected by long linkers that also contain important ligand
62 binding sites (**Figure 1**) [25,28,29]. Owing to the common origin and high sequence similarity of FAK
63 and PYK2, the basic principles for their (in)activation likely remain conserved.

64 Both proteins harbor binding sites for many ligands (more than 50 have been described for FAK [23])
65 and nuclear localization and export signals [30,31], allowing them to function as molecular scaffolds
66 in various locations in the cell. Enzymatic kinase activity is required only for a subset of actions. In
67 FAK, the FERM domain can directly bind to the kinase domain and inhibit its function [28]. Key
68 residues for the FERM:kinase interaction are conserved between FAK and PYK2 (in particular FAK
69 F596/PYK2 F599; [23]), suggesting that this FERM:kinase association also exists in PYK2.
70 Experimental evidence for this association in PYK2 is however lacking [32–34]. In both proteins,
71 kinase activity is generally initiated by autophosphorylation of a tyrosine situated in the
72 FERM-kinase linker (FAK Y397 and PYK2 Y402). Together with a proline-rich region (PR1) situated
73 upstream in the same linker, the phosphotyrosine (pY) forms a high-affinity binding site that
74 recruits and activates Src kinases *via* a dual interaction with their SH2 and SH3 domains [25]. The
75 bound and activated Src kinase is responsible for much of the kinase activity associated with FAK or
76 PYK2. Importantly, autophosphorylation can only proceed *in trans*, and it requires FAK/PYK2
77 dimerization and/or clustering. In FAK, dimers are formed through FERM:FERM and FERM:FAT
78 interactions (**Figure 2**). In PYK2, FERM domains form crystallographic dimers that are identical to
79 the FAK FERM:FERM domains (PDB 4EQU), suggesting that the FERM:FERM mechanism might be
80 conserved. Self-association of FAK and PYK2 is controlled by ligands. In FAK,
81 trans-autophosphorylation, and hence kinase-dependent functions, occur mostly at focal adhesions
82 to which FAK is recruited, enriched and primed for dimerization *via* interactions between its FAT
83 domain and the leucine-aspartic acid (LD) motifs of paxillin [35]. Additionally, clustering of FAK is
84 promoted through interactions between the FERM domain and membrane-associated
85 phospholipids [36]. Although the FAT domain in PYK2 can bind to paxillin [37], PYK2 is not as
86 strongly localized to focal adhesions as FAK is in most cell types. Conceptually similar
87 recruitment/clustering mechanisms appear to lead to activation of FAK and PYK2 at other
88 transmembrane receptor complexes, such as T-cell immune synapses [38,39], or to activation of
89 PYK2 in post-synaptic densities [40]. In addition, FAK and PYK2 play roles in various other cellular
90 locations, including endosomes, adherens junctions, the microtubule organizing center and the
91 nucleus [3,26]. Some of these functions (e.g. at nascent adhesions or in the nucleus) are
92 kinase-independent.

93

94 A major difference between FAK and PYK2 is that the latter can be activated by calcium ions (Ca²⁺).
95 The exact molecular mechanism for activation of PYK2 by Ca²⁺ remains unclear and controversial.
96 The current view is that Ca²⁺ does not bind directly to PYK2, but binds through calmodulin (which
97 has been reported to bind to either the FERM or kinase domain of PYK2) or through Ca²⁺-activated
98 PYK2-modifying kinases (PKC, CaMKII, PKA), phosphatases (calcineurin, PP1) or Ca²⁺-activated
99 ligands (PSD-95) [23,41].

100 In summary, FAK and PYK2 are versatile protein scaffolds with kinase-dependent and
101 kinase-independent functions. Although the details may differ, the underlying mechanism for the
102 control and activation of kinase activity appears to be preserved between FAK and PYK2. Activation
103 of the kinase function requires trans-autophosphorylation. Cellular ligands can trigger
104 trans-autophosphorylation by stabilizing a weak intrinsic propensity for self-association of FAK or
105 PYK2 and/or by increasing the local protein concentration. Consequently, endogenous inhibitory
106 mechanisms can prevent kinase activation by lowering FAK and/or PYK2 protein concentrations, by
107 reinforcing inactivating autoinhibitory interactions, by competing with activating ligands, by
108 dephosphorylating the Src-recruiting tyrosine or by displacing FAK/PYK2 from their sites of
109 activation (**Figure 1**).

110 2. FRNK and PRNK

111 Both the FAK and PYK2 genes (*PTK2* and *PTK2B*, respectively) can produce shorter protein forms
112 that lack the FERM and kinase domains [42,43]. These autonomously expressed non-catalytic
113 C-terminal portions presumably originate from alternative transcription initiation sites [44] and are
114 called the FAK-related non-kinase (FRNK) and the PYK2-related non-kinase (PRNK). Starting at
115 residues 693 and 780 of the canonical FAK and PYK2 isoforms, respectively, they include ligand
116 binding sites (proline-rich sites PR2 and PR3 for FRNK and PR3 for PRNK), sites of phosphorylation
117 (most prominently Y861 and S910 in FAK, Y849 and S866 in PYK2) and the FAT domain (**Figure 1**).
118 PR2 and PR3 mediate the binding of different SH3-containing proteins, such as p130cas or Graf
119 [43,45–49]. The FAT domain is sufficient to localize to focal adhesions, through interactions mainly
120 with paxillin, but also with cofactors or alternative ligands, such as talin or Rgnef/p190RhoGef [50–
121 52]. Alternative interactions can also localize FAT to other structures, such as the T-cell receptor
122 complex [1,38,53], or the growth cone of developing axons [54]. FRNK and PRNK maintain these
123 functions, although without any regulatory influence from the other FAK/PYK2 regions. The
124 production of these truncated forms was therefore suggested to lead to a direct competition of FRNK
125 or PRNK with FAK and/or PYK2 at sites that attract their FAT domains. Indeed, immunostaining
126 showed that FRNK and PRNK localize to focal adhesions [42,43]. By competitively displacing FAK
127 or PYK2, the alternative spliced variants lower the local concentrations of FAK and PYK2 and hence
128 lower the propensity for trans-autophosphorylation of FAK and, possibly, PYK2. Accordingly,
129 western-blot analysis indicates a lowering of FAK Y397 phosphorylation, a key step in FAK
130 activation, at increasing FRNK levels [55,56]. Moreover, by displacing FAK or PYK2 and by forming
131 incomplete signalling complexes, FRNK and PRNK promote the disassembly of focal adhesions.
132 Indeed, the expression of FRNK and PRNK correlates with focal adhesion turnover [42,43,57].

133 In addition to displacing FAK from common binding sites, FRNK may also act by directly binding to
134 FAK. In rat aortic smooth muscle cells, FRNK co-immunoprecipitates with FAK [56]. This
135 association is decreased by phosphorylation of FRNK S217 by extracellular signal-regulated kinase
136 (ERK) and increased five-fold by the S217A mutation. In cells, autophosphorylation of FAK was
137 reduced by expression of FRNK, and even more so by expression of the S217A mutant form of FRNK
138 [56]. The molecular basis for this phosphorylation-dependent interaction is unknown, but it might
139 involve competition of FRNK with the intramolecular FERM:FAT interaction that promotes FAK for
140 autophosphorylation by reinforcing FAK dimers. In size exclusion chromatography, dimerization of
141 recombinant FAK was indeed weakened by the presence of recombinant FAT domains [35]. FRNK
142 S217 corresponds to Erk-phosphorylated S910 in the canonical FAK isoform. This serine is situated
143 five residues upstream of the four-helix FAT domain. The S910PPP motif weakly interacts with the

144 FAT domain [58] and, when phosphorylated on S910, constitutes a proline-isomerase binding site
145 [56,59]. Phosphorylation of FRNK S217 could therefore affect the FRNK:FAK association in various
146 direct or indirect ways.

147 The possibility that a similar mechanism of competitive binding also exists for PRNK and PYK2 has
148 not been tested. If this mechanism does exist, then this association would be regulated differently,
149 because the PYK2 serine 866, that is also phosphorylated and located just N-terminal of its FAT
150 domain, is not situated in an Erk phosphorylation motif [60].

151 3. Proteases

152 FAK and PYK2 are cleaved by several proteases. Some of the resulting fragments resemble FRNK or
153 PRNK.

154 3.1. Caspases

155 Cysteine aspartate-specific proteases (caspases) play an important role in programmed cell death
156 (apoptosis). During apoptosis, caspases cleave critical repair and structural proteins that bolster cell
157 survival. It has been shown that FAK is cleaved in the early stages of myc-induced apoptosis [61–63].
158 Sensitivity profiling of protease inhibitors showed that FAK is cleaved by caspase-3, 6, 7 and 8, with
159 caspase-7 by far the most active [64,65]. Caspase-3, 7 and 8 generated 85 kDa and 33 kDa fragments
160 [64,65]. Caspase-6 cleaved FAK with low efficiency, generating a 77 kDa fragment [65]. Generated
161 cleavage products and cleavage site consensus suggested that the 85-kDa cleavage happened after
162 D772 and that the 77 kDa cleavage occurred after D704 (**Figure 1**) [65]. Accordingly, the D772A
163 mutation was not cleavable by caspase-3 [65]. It is expected that the separation from the FAT domain
164 weakens the attachment of the FERM-kinase domain fragment to focal adhesions (and other
165 FAT-targeted sites), leading to turnover of these structures. The 35 kDa fragment generated from
166 FAK cleavage resembles FRNK and may act similarly. Indeed, western-blot analysis indicated a
167 decrease in FAK Y397 phosphorylation levels in HeLa cells transfected with the 35 kDa fragment
168 [65]. Direct evidence for caspase cleavage of PYK2 is currently lacking.

169 3.2. Calpain

170 Calpain, a calcium-dependent cysteine protease, cleaves both FAK and PYK2 [66,67]. When either
171 purified calpain I or calpain II were added to FAK, four fragments were generated with sizes of 90
172 kDa, 50 kDa, 40 kDa, and 35 kDa, and the cleavage was blocked by the calpain inhibitor, calpastatin
173 [67]. Antibodies against the FAK kinase domain reacted with the 90-kDa and 50-kDa bands while
174 antibodies against the C-terminus of FAK bound to the 35-kDa band [67]. An 80 kDa and a 75 kDa
175 PYK2 cleavage products were observed in human platelets, and when treated with the calpain
176 inhibitor calpeptin, the bands were no longer present [68].

177 4. Regulation through post-translational modifications

178 In addition to irreversible protease cleavage, FAK and PYK2 are subjected to several types of
179 post-translational modifications. FAK, but not PYK2, has been reported to be acetylated on residue
180 A2 [60] and SUMOylated on K152 in the FERM domain [69]. SUMOylation was mediated by the
181 SUMO ligase protein inhibitor of activated STAT1 (PIAS1) that interacted with FAK in cells and *in*
182 *vitro*. SUMOylation was increased in suspended cells and correlated with increased nuclear presence
183 of FAK and increased FAK Y397 phosphorylation independently of cell adhesion [69]. The
184 mechanistic bases for this effect remain to be determined, but since K157 is in the vicinity of the
185 FERM:kinase interaction site [28], its SUMOylation might interfere with the ‘closed’ autoinhibitory
186 FAK conformation.

187 The major post-translational modification however is (de)phosphorylation [70]. According to the
188 UniProt database, FAK and PYK2 are phosphorylated on serines (8 on FAK; 6 on PYK2), threonines
189 (FAK: 2; PYK2: 2) and tyrosines (FAK: 8; PYK2: 8). Regulation through phosphorylation was
190 previously reviewed in detail [25,60,71,72]. Here, we present a very broad overview. Tyrosine
191 phosphorylation is generally associated with activating characteristics, starting of course with the
192 autophosphorylation of the FERM-kinase linker tyrosine (Y397 and Y402 in FAK and PYK2,
193 respectively). Src-mediated phosphorylation of a tyrosine in the first FAT helix (FAK-Y925 and
194 PYK2-Y881) triggers activation of mitogen-activated protein (MAP) kinases *via* the
195 phosphotyrosine-binding adapter protein Grb2 [73–76]. In FAK, phosphorylation of S910 by Erk
196 recruits the proline-isomerase PIN1 and subsequently the protein tyrosine phosphatase (PTP-PEST),
197 which then counteracts FAK phosphorylation and activation, thus closing a negative feedback loop
198 [59]. In PYK2, a nuclear export signal in its kinase-FAT linker is activated by phosphorylation of S778
199 by protein kinase A (PKA) and deactivated by the phosphatase calcineurin [31]. Conversely,
200 PKC-mediated phosphorylation of FAK on S722 promoted nuclear localization [77].
201 (De)phosphorylation therefore regulates nuclear localization of PYK2 and FAK, although based on
202 different mechanisms. Phosphorylation can also alter the protein structure, as seen for the case of
203 the FAK activation loop tyrosines. Their phosphorylation not only increases the kinase catalytic
204 activity by restructuring the activation loop, but it also prevents the kinase domain from forming an
205 inhibitory interaction with the FERM domain [28].

206 While most kinases or phosphatases probably form only transient or short-lived complexes with
207 FAK and/or PYK2, the tyrosine-kinases Src and Fyn durably attach to the Y397-phosphorylated
208 FERM-kinase linker. They are associated with a kinase-active state [25,71,78–80]. In the following,
209 we highlight one other kinase and one phosphatase that also have lasting associations with FAK or
210 PYK2 and show inhibitory effects.

211 4.1. Liver kinase β 1 (LKB1)

212 The liver kinase β 1 (LKB1) or STK11 is a multifunctional serine/threonine kinase that links energy
213 sensing and cell polarity [81–83]. In particular, LKB1 stabilizes cell polarity under energy stress.
214 Given that loss of cell polarity increases unidirectional ‘exploratory’ migration, LKB1 controls cell
215 movements during embryogenesis and wound healing [81–83]. LKB1 also counteracts cancer cell
216 metastasis and is the third most frequently mutated gene in lung adenocarcinoma [84–86]. Rather
217 than through phosphorylation of its activation loop, LKB1 (**Figure 3**) is activated allosterically
218 through an association with the pseudo-kinase STRAD α , which is tethered to LKB1 by the
219 scaffolding protein MO25 α [87]. In addition, LKB1 activity and localization are affected by
220 post-translational modification [81,83]. SUMOylation of LKB1 K178, in response to energy stress,
221 promotes the interaction between LKB1 and the AMP-activated protein kinase (AMPK). The
222 resulting phosphorylation and activation of AMPK help to maintain the energy balance in a cell
223 during energy stress [88]. Furthermore, live cell imaging experiments show that farnesylation on
224 C430 within the LKB1 C-terminus is required for its co-localization with actin at the leading edges of
225 migrating cells. The LKB1 kinase activity is required to stabilize the actin colocalization of LKB1 and
226 to promote mesenchymal polarization and directed cell migration [82,83].

227 Initially, LKB1 was linked to FAK through the observation that the FAK adhesion pathway is
228 upregulated in LKB1 $^{-/-}$ mice in a mutant Kirsten rat sarcoma (KRAS) background [89]. Subsequent
229 analyses confirmed that the presence and activation of LKB1 represses phosphorylation of FAK
230 Y397, Y861 and Y925 [82,90]. The current model proposes that farnesylation colocalizes LKB1 with
231 actin at the leading cell edge of migratory cells, where the LKB1 kinase activity indirectly decreases
232 FAK activation. Inactivation of FAK decreases focal-adhesion turnover and hence stabilizes focal
233 adhesions at the leading edge. Conversely, loss of LKB1 farnesylation or kinase activity results in
234 FAK hyperphosphorylation and leads to cells that present a more exploratory behaviour with loss of
235 directional persistence [81,82].

236 The exact mechanisms by which LKB1 negatively affects FAK activation are unclear. FAK and LKB1
237 can co-immunoprecipitate each other, suggesting that they colocalize within the same protein
238 complex. However, the FAK:LKB1 interaction may not be direct, as indicated by commercially
239 available purified FAK and LKB1/MO25 α /STRAD α proteins not binding each other *in vitro* [82]. A
240 possibility would be that the effect of LKB1 is mediated by its downstream substrates. Activation of
241 AMPK or its family members (e.g., MARK1 and MARK4) correlates with inhibition of FAK
242 phosphorylation in several systems, including human liver cancer cell lines and muscle cells [90–
243 93]. The details of these inhibitory pathways through AMPK or MARKs remain incompletely
244 established. Intriguingly, one study could recapitulate the FAK pY397-suppressing effect of LKB1 by
245 expressing just the LKB1 N-terminal arm region (residues 1-47) in LKB1-null H157 cells, suggesting
246 that, at least in this setting, LKB1 kinase activity was not needed [82]. The possibility of an interaction
247 between PYK2 and LKB1 has not yet been explored, although PYK2 activation has been observed
248 following AMPK activation in muscle cells [94,95].

249 4.2. PTEN

250 The phosphatase and tensin homolog deleted on chromosome 10 (PTEN) (**Figure 3**) exerts a dual
251 function as both a lipid and a protein phosphatase [96,97]. As a lipid phosphatase, PTEN converts
252 phosphoinositide(3,4,5)P3 to phosphoinositide(4,5)P2, and is therefore the antagonist of the
253 phosphoinositide-3 kinase (PI3K). PI3K directly associates with FAK through its PR motifs [98]
254 promoting cell survival via the activation of the PI3K/Akt pathway. This association has an
255 important effect on maintaining cell adhesion to integrins, which is, in some tissues like endothelial
256 cells, indispensable for cell survival [99].

257 PTEN affects cell migration and invasiveness by dampening this FAK/PI3K pathway. The most
258 commonly observed effect of PTEN on FAK might be indirect through its lipid-phosphatase-based
259 downregulation of the PI3K pathway [100]. As an additional indirect mechanism, PTEN was shown
260 to inhibit FAK expression levels in myeloma and gastric cancers [101,102]. However, PTEN can also
261 form a complex with Y397-phosphorylated FAK in glioma, breast cancer and colon carcinoma cells
262 [103,104]. This interaction leads to dephosphorylation of pY397 following cell detachment in these
263 cells. The FAK:PTEN association was compatible with the FAK:paxillin association, but it competed
264 with binding of PI3K and Src to FAK [103,104]. Both the p85 subunit of the PI3K and the SH2-SH3
265 fragment of Src kinase bind to the Y397-phosphorylated FERM-linker fragment [25,71,78,79,105,106],
266 suggesting that PTEN binding involves the same region. Moreover, it has been observed that FAK
267 phosphorylates PTEN at Y336 with a positive effect on PTEN stability and phosphatase activity
268 [107,108]. Y336 is located in the phospholipid-binding region of the C2 domain (**Figure 3**). In
269 principle, the introduction of a negative charge in this position is expected to hamper association
270 with negatively charged lipid headgroups. Future research is needed to clarify the underlying
271 molecular mechanisms causing the multiple effects of the FAK:PTEN association.

272 5. Regulation through non-catalytic protein interactions

273 FAK or PYK2 also have a large number of interaction partners that do not post-translationally
274 modify them. Many of these partners either control subcellular localization, or attach to FAK or
275 PYK2 to form active signalling complexes [25,71,106]. So far, to our knowledge, only one
276 non-catalytic protein has been identified as an inhibitor of FAK and PYK2 activation, namely FIP200.

277 5.1. RB1CC1 / FIP200

278 *In vitro* and *in vivo* protein interaction assays led to the discovery of a 200 kDa ligand for both FAK
279 and PYK2, named the FAK family kinase-interacting protein (FIP200) [109]. The 1,594 residue FIP200
280 is predicted to contain an N-terminal ubiquitin-like domain (ULD) but would otherwise be mostly
281 composed of loops and long helices, possibly forming coiled-coiled structural elements [109,110]

282 (Figure 3). Accordingly, FIP200, also known as the RB1-inducible coiled-coil protein 1 (RB1CC1), is a
283 non-catalytic scaffolding protein. It regulates a wide range of cellular events, such as growth,
284 proliferation, apoptosis and autophagy, through interactions with signaling proteins (e.g. PYK2,
285 FAK, ActA, p53, TSC1, ASK1, TRAF2 and Stathmin) [111].

286 Immunofluorescence analyses of FIP200 indicated mostly a diffuse localization in the cytoplasm
287 [109]. But the presence of a consensus nuclear localization signal implies an alternative function for
288 FIP200 in the nucleus, where it may act as a transcription factor [109,110,112,113]. Additionally,
289 FIP200 polyclonal antibody pull-downs revealed a partial colocalization of the protein in focal
290 contacts where it may regulate FAK and vinculin [114]. FIP200 binding decreases the kinase activity
291 of FAK and PYK2 [109,114] and the autophosphorylation levels of FAK [114]. During cell adhesion
292 to fibronectin, FAK activation correlates with increased dissociation of FAK and FIP200 [111,114].

293 Given that FIP200 inhibits both FAK and PYK2, which can have opposing functions, for example in
294 the promotion of the cell cycle and apoptosis, the outcome of their inhibition by FIP200 may be
295 highly cell-type specific. For example, overexpression of FIP200 in glioblastoma cells (where PYK2
296 has dominant functions) leads to inhibition of apoptosis [115], whereas in breast cancer cells, FIP200
297 acts as a tumor suppressor gene [113].

298 Although the direct interaction with FIP200 appears to inhibit both FAK and PYK2 in a similar
299 manner, the way in which FIP200 physically binds them might differ (Figure 3). In one study, the
300 FIP C-terminal (CT-FIP; residues 1374-1591) interacts strongly with the PYK2 kinase domain.
301 However, CT-FIP only binds to the N-terminal region of FAK, while the FAK kinase domain
302 (403-672aa) binds to the FIP200 N-terminus (NT-FIP; 1-638aa) and the middle domain (MD-FIP;
303 639-1373) [114]. Conversely, NT-FIP and MD-FIP did not show affinity for PYK2. The apparent
304 differences might however only be caused by a change in relative affinity of the fragments of FIP200
305 for FAK or PYK2. For example, although CT-FIP did not display significant binding to the FAK
306 kinase, it could reduce its enzymatic activity when present at high concentrations in *in vitro* kinase
307 assays [114,115]. The differences in binding affinity might have important functional implications in
308 cases where FAK and PYK2 are present, but these functions might be different. For example, in
309 retinoblastoma cells, the interaction of CT-FIP with PYK2 is stronger, and hence preferred, than the
310 interaction of the other two domains of FIP200 with FAK [109,114,115].

311 6. Chaperones

312 Although the focus of this review is on endogenous inhibitory mechanisms, we also consider
313 chaperones that enhance the activation of FAK. The housekeeping function of chaperones as protein
314 stabilizers is deregulated in many cancers, and hence therapeutically lowering their action to normal
315 levels may produce tumor-inhibiting effects [116].

316 Molecular chaperones can interact with exposed hydrophobic patches of misfolded proteins and
317 help them (re)establish their native and functional three-dimensional structure. While chaperones
318 commonly release refolded clients, some remain associated with structurally fragile proteins to
319 sustain their function. Thus, chaperones maintain cellular proteins in their functional state and
320 prevent their degradation [117,118]. Overexpression of chaperones, in particular of inducible heat
321 shock proteins (HSPs), is prevalent in cancer cells where proteotoxic stress is endemic [116,119]. The
322 resulting increase in protein stability and function may enhance the action of overexpressed and/or
323 mutated oncogenes and more generally help creating a protective and resistant cytoplasmic
324 environment [120]. Inversely, a decrease in the expression of molecular chaperones is associated
325 with accumulation of misfolded proteins and the onset of neurodegenerative diseases [120].

326

327 In a systematic survey of the kinome, FAK and PYK2 were identified as 'weak clients' for HSP90
328 and its kinase-specific cochaperone, CDC37 [118]. Xiong et al. (2014) reported an interaction
329 between HSP90 β and FAK in breast cancer cells. FAK bound to the HSP90 β middle domain
330 (residues 233-620), in agreement with a structural analysis of the complex formed by HSP90, CDC37
331 and a client cyclin-dependent kinase (CDK4) [121]. The HSP90 β interaction protects FAK from
332 ubiquitylation-dependent proteasomal degradation. Inhibition of both HSP90 β and FAK reduces
333 tumor growth in breast cancer cells [122].

334 Chaperones can also have more indirect effects on FAK activity. Caino et al. showed that inhibition
335 of mitochondrial HSP90 chaperones, including the tumor necrosis factor receptor-associated
336 protein-1 (TRAP-1), leads to an energy stress-triggered activation of the LKB1-AMPK pathway
337 [123]. AMPK phosphorylates and activates the Unc-51 like autophagy activating kinase (ULK1),
338 which in turn phosphorylates FIP200. These events activate the autophagy-initiating complex
339 between ULK1, FIP200 and autophagy related protein 13 (atg13), and they allow activated FIP200 to
340 maintain FAK in an inactive unphosphorylated state [123]. Increased expression and function of
341 mitochondrial HSP90, as observed in some cancers, lead to sufficient ATP production in
342 nutrient-scarce tumor cells to avoid triggering activation of the LKB1-AMPK pathway. This releases
343 the inhibitory effect of FIP200 on FAK, results in increased cytoskeletal dynamics and enhances
344 tumor cell invasion to bone or liver in mice disease models [123].

345 Additionally, heat shock proteins HSP70 and Mamalian relative DNA J (MRJ, also named DNAJB6)
346 exert an oncogenic effect on colon cancer cells. HSP70 and MRJ interact with the urokinase-type
347 plasminogen activator receptor (uPAR) to activate FAK, c-Src, H-Ras, AKT and MAPK cell signaling
348 pathways, regulating cell adhesion and migration [124]. Another example is the molecular
349 chaperone Cosmc. Cosmc is necessary for the formation of the active T-synthase, which catalyses the
350 production of T antigen. Increased expression of T antigen is correlated with tumor metastasis and
351 poor prognosis in colorectal cancer. The forced expression of Cosmc in colon cancer cell lines
352 increases T antigen expression resulting in increased activation of FAK, PI3K/Akt and MAPK kinase
353 (MEK)/ERK signaling pathways [125]. Cosmc-induced tumor cell migration and invasion suggest
354 that Cosmc may serve as a potential target for colorectal cancer. The exact mechanisms that lead to
355 FAK Y397 phosphorylation through either HSP70/MRJ or Cosmc under these conditions have not
356 yet been determined. Given that in both cases FAK activation involves the PI3K and MAPK
357 pathways, the molecular routes may be overlapping or converging.

358 7. Transcriptional regulation of FAK and PYK2

359 The normal or alternative intronic promoters of the *PTK2* and *PTK2B* genes are controlled in a tissue
360 and developmental stage-dependent manner [44]. Factors that activate the *PTK2* promoter include
361 the nuclear factor- κ B (NF- κ B), argonaute 2 (AGO2), PEA3 and NANOG [12,126–128]. Overactivity of
362 these *PTK2* transcription factors is associated with tumorigenesis, and their silencing can block
363 tumorigenesis and metastasis [10]. The major repressor of the human *PTK2* and *PTK2B* promoters
364 is the stress-induced tumor suppressor p53 [129–131]. Two putative binding sites for p53 have been
365 identified in the *PTK2* promoter [132]. In turn, nuclear FAK promotes degradation of p53 by linking
366 it to the E3 ubiquitin ligase Mdm2, using the FERM domain as a scaffold. FERM-triggered
367 proteosomal degradation of p53 leads to cell proliferation and survival under cellular stress [133]. A
368 strong correlation between FAK overexpression and p53 mutations has been observed in human
369 breast cancer [134]. While loss or damage of p53 is closely associated with the development of
370 tumors, forced overexpression can cause premature aging [135]. However, therapeutic restoration of
371 a functional p53 pool at endogenous levels can have tumor-suppressive effects [136].

372

373

374 8. non-coding RNA

375 Non-coding RNA (ncRNA) are RNA molecules that are not translated into proteins [137]. ncRNAs
376 include transfer RNA (tRNA), ribosomal RNA (rRNA) and small RNAs. ncRNAs are further
377 classified according to their length and function, and they include long non-coding RNA (lncRNA),
378 micro-RNA (miRNA), small-interfering RNA (siRNA) and piwi-interacting RNA (piRNA). Small
379 RNAs can regulate gene expression at the transcriptional and post-transcriptional level, but they can
380 also affect protein function through direct binding and scaffolding. Many ncRNAs are abnormally
381 expressed in cancer, leading to a large-scale deregulation of protein genes, most prominently the
382 tumor suppressor p53 [138]. Here, we focus on those ncRNAs that directly alter expression and
383 function of FAK or PYK2; we note that many other ncRNAs have pleiotropic effects that may also
384 affect FAK or PYK2.

385 8.1. microRNA

386 miRNAs contain about 20 nucleotides and are transcribed from miRNA genes or coding gene
387 introns. miRNAs post-transcriptionally downregulate target genes by either destabilizing and
388 degrading their mRNA or by binding to the 3'-untranslated region (3'UTR) of their mRNA, thus
389 inhibiting translation [139,140]. miRNAs are implicated in various cellular processes such as
390 development, cell proliferation, and differentiation. They also regulate junction protein gene
391 expression and ECM processes, thus helping to maintain the integrity of the cellular structure
392 [141,142]. By inhibiting gene translation, many miRNAs act as tumor suppressors and their
393 downregulation in cancer cells generally promotes cancer formation and metastasis [143].
394 Conversely, forced upregulation of miRNA can have tumor-suppressive effects, making miRNAs
395 interesting therapeutic targets and prognostic markers for anti-cancer therapy.

396 8.1.1. Tumor-suppressor miRNAs acting directly on FAK

397 *miR-7*. One of the most studied microRNAs regulating FAK is miRNA-7 (miR-7). miR-7 is encoded
398 by three DNA loci (9q21, 15q26 and 19q13) producing the same mature 23-nucleotide miR-7
399 sequence. miR-7 is enriched in various normal tissues and implicated in organ development and
400 other biological processes (reviewed by [144]). miR-7 can directly bind to 3'UTR of FAK mRNA,
401 repressing FAK protein expression [145]. miR-7 is also involved in the growth, migration, and
402 invasion of many cancer types. miR-7 downregulates glioblastoma and colon cancer cell
403 invasiveness by repressing FAK protein expression [145,146]. Forced expression of miR-7
404 significantly reduced endogenous FAK protein expression in breast cancer cell lines, inhibited
405 primary breast tumor growth and invasiveness, and repressed metastatic migration of breast cancer
406 xenografts [147]. In non-small-cell lung carcinoma (NSCLC) cells, miR-7 suppresses cell
407 proliferation, migration and invasion by downregulating FAK expression and inhibiting the
408 activation of the ERK/MAPK signaling pathway [148]. The inverse relation between miR-7
409 expression and tumor growth and invasiveness suggests that miR-7 can be used as a diagnostic
410 marker for certain cancers [144]. miR-7 also positively affects radiation therapy outcomes as it
411 increases cancer cell radiosensitivity [149], phenocopying an effect observed for FAK-targeting
412 inhibitors [150–152].

413 *miR-1298*. miR-1298 was identified in a global miRNA functional screen as selectively lethal to cells
414 expressing mutated KRAS, which is an oncogene mutated in 20% of human cancers, mainly NSCLC
415 and colorectal cancers. miR-1298 acts a tumor suppressor in KRAS-driven NSCLC and colorectal
416 cancer cells by directly targeting the mRNA of both FAK and the Laminin subunit beta 3 (LAMB3),
417 lowering their protein expression levels [153]. Interestingly, only expression of LAMB3, but not
418 FAK, was upregulated by KRAS; yet silencing of either FAK or LAMB3 recapitulated
419 miR-1298-induced cell-death in KRAS-dependent cancer cells. However, FAK Y925 phosphorylation

420 also links FAK activation via Grb2 to activation of the RAS pathway [154], and FAK signaling is a
421 requirement for the maintenance of KRAS-dependent adenocarcinomas [155].

422 *miR-543*. miR-543 expression is decreased in tumorous endometrium tissue and associated with
423 impaired cancer cell invasion *in vitro*. miR-543 binds to the 3'UTR of FAK and of the TWIST1
424 oncogene, decreasing their expression at both the mRNA and protein level. This repression resulted
425 in impaired tumor cell proliferation, migration and invasion in cancer cell lines [156].

426 *miR-379-5p*. Underexpression of miR-379-5p in hepatocellular carcinoma (HCC) correlated with the
427 tumor node-metastasis (TNM) stage and metastasis. miR-397-5p inhibits tumor migration and
428 invasion in HCC cells by direct binding to the 3'UTR of FAK inhibiting FAK translation while the
429 mRNA level is not affected. This inhibition suppresses AKT activation and hence inhibits the
430 PI3K/AKT pathway. Introduction of miR-397-5p represses HCC metastasis and EMT *in vivo* [157].

431 *miR-193b*. A recent study showed that miR-193b is downregulated in liposarcoma while its
432 reintroduction induces apoptosis in liposarcoma cells. miR-193b functions by directly targeting FAK
433 mRNA regulating the oncogenic FAK/SRC/BCAR1 signaling pathway [158].

434 8.1.2 miRNAs indirectly regulating FAK.

435 Rather than directly suppressing FAK expression by binding to FAK mRNA, miRNAs can indirectly
436 affect FAK targeting by activating upstream effectors. For instance, miR-205 and miR-940 negatively
437 regulate Src kinase expression. miR-205 is suppressed in renal and prostate cancer. Its inhibition
438 increases cell adhesion in normal keratinocytes, whereas its overexpression reduces tumor growth *in*
439 *vivo* [159–161]. miR-205 binds to Src 3'UTR, degrading its mRNA, decreasing Src protein expression
440 and hence activating FAK and paxillin [159–161]. The exosomal miR-940 also inhibits the expression
441 of Src at the mRNA and protein levels in ovarian cancer, thus decreasing the activation of
442 downstream proteins such as FAK, paxillin and Akt [162].

443 8.1.3. Oncogenic miRNAs acting on FAK

444 Although most FAK-targeting miRNAs act as tumor suppressors by lowering FAK expression
445 and/or activation, some miRNAs show oncogenic effects by targeting cellular inhibitors of FAK
446 [163,164]. The miR-130 family (miR-130b, miR-301a and miR-301b) is one example that is
447 upregulated in bladder cancer tissues. The miR-130 family activates FAK and the Akt signaling
448 pathway by targeting PTEN either directly through binding to its mRNA (miR-130b) or indirectly by
449 repressing PTEN expression (miR-301a/b). High expression of miR-130 increased migration and
450 invasion of bladder cancer cells [163] and the progression of malignant melanoma [164].

451 Several other miRNAs have been found to influence the activation of FAK by repressing or
452 activating an upstream effector of FAK. Due to space limitations, these miRNAs are listed in Table 1
453 but not elaborated in the text.

454 8.1.4. miRNA regulators of PYK2

455 Not many miRNAs are known to regulate the expression of PYK2. However, PYK2 is a direct target
456 of miRNA-23b, which binds to its 515-522 3'UTR. Overexpression of miR-23b decreases the protein
457 level of PYK2, but not of FAK, and results in reduced cell proliferation, migration and invasion of
458 hepatocellular carcinoma and glioblastoma cells. Additionally, elevated expression of miR-517a and
459 miR-517c resulted in decreased PYK2 expression, suggesting that these miRNAs play a tumor
460 suppressor role in hepatocellular carcinoma [165].

461

462 8.2. *lncRNAs*

463 lncRNAs with more than 200 nucleotides, commonly called lncRNAs, are implicated in many
464 biological and pathological processes [166]. The oncogenic lncRNA metastasis-associated lung
465 adenocarcinoma transcript 1 (MALAT1) promotes vasculogenic mimicry and angiogenesis by
466 increasing the expression of VE-cadherin and b-catenin on cell membranes, as well as by increasing
467 levels of metalloproteases MMP2/9 and MT1-MMP and of phosphorylated ERK, FAK, and paxillin.
468 These events promote gastric cancer tumor growth and metastasis [167]. lncRNA H19 is a
469 competing endogenous RNA (ceRNA) for miR-138. Given that miR-138 targets FAK and suppresses
470 its expression, the action of lncRNA H19 increases FAK expression and osteogenesis of bone marrow
471 mesenchymal stem cells under tension [168]. lncRNA can also act by directly binding to proteins.
472 Upregulation of the lncRNA CASC9 in esophageal squamous cell carcinoma (ESCC) was correlated
473 with metastasis and poor prognosis. CASC9 upregulates the laminin subunit LAMC2 by recruiting
474 the transcriptional coactivator CREB-binding protein (CBP) to the LAMC2 promoter. LAMC2
475 upregulation is associated with phosphorylation of FAK and activation of the PI3K/AKT pathway
476 [169]. Phenotypically, CASC9 therefore produces opposing effects to those of miR-1298 (see above).

477 9. Discussion

478 By linking cell motility and survival, FAK and PYK2 promote cancer cell survival and invasiveness.
479 In particular FAK, but also to some extent PYK2, have been recognized as anti-cancer targets, and
480 first small-molecule inhibitors are currently in clinical trials. However, drug efficacy and specificity
481 remains low in several cases, and their exact mechanism of action is not always well understood
482 [10,170]. Moreover, the application of anti-cancer drugs designed to selectively inhibit single kinases
483 can trigger large-scale signal network rewiring, leading to bypass mechanisms that render the drug
484 ineffective [171,172].

485 Stringent endogenous control of kinase activity is essential for normal cellular function and
486 homeostasis. Evoking naturally evolved endogenous control mechanisms for therapeutic purposes
487 may trigger fewer escape manoeuvres in diseased cells than experienced by targeted kinase
488 inhibitors. Endogenous mechanisms that (negatively) regulate the activity of FAK and PYK2 in
489 normal or diseased cells might inspire improved or additional therapeutic interventions (**Figure 2**).

490 FAK and PYK2 have numerous kinase-dependent and kinase-independent biological roles (**Figure**
491 **4**), which can vary with cellular status, cell type and subcellular location. Among these roles, FAK
492 and PYK2 can have opposing, redundant or synergistic effects, depending on the cell type and
493 condition. Accordingly, cells use different general or specifically adapted mechanisms to control
494 FAK and/or PYK2. The general mechanisms involve chaperones, proteases, and
495 kinases/phosphatases (such as the Src, LKB1 or PTEN). Therapeutic strategies that target these
496 regulatory mechanisms will likely provoke pleiotropic effects, which might not always be
497 counterproductive in diseased cells, but would generally be difficult to predict and may adversely
498 affect healthy tissue.

499 Inhibitors specifically targeting the p53 or Mdm2 binding site on the FERM domain of nuclear FAK
500 are also promising in treating cancers without deleterious mutations of p53, because a first inhibitor
501 of the putative p53 binding site on FAK FERM showed tumor-suppressive effects by dampening
502 FAK-induced p53 degradation [173]. However, the structural basis for these interactions needs to be
503 clarified to allow using them as templates for the rational design of inhibitory small-molecule
504 mimics.

505 An alternative strategy is to target the self-association mechanisms of FAK and PYK2 needed for
506 their trans-autophosphorylation. Such allosteric protein-protein interaction inhibitors could directly
507 manipulate the molecular control mechanisms of FAK or PYK2, without the risk of severe off-target

508 side effects commonly associated with inhibitors of kinase domains. For FAK, such protein-protein
509 interaction inhibitors could target the FERM or FAT domains, which are required for
510 trans-autophosphorylation, or could stabilize the inhibitory FERM:kinase association [28,35,174].
511 Indeed, compounds have been developed that target these mechanisms, including molecules that
512 block access to Y397 or inhibit interactions of the FAT or FERM domains [173,175–179]. Although
513 these compounds lacked efficacy and required micromolar concentrations, they displayed
514 tumor-suppressive activity in xenograft mouse models, and enhanced the effect of conventional
515 chemotherapy. However, their specificity and mode of action remain poorly understood [175].

516 Another promising approach to utilizing endogenous mechanisms for controlling the spread and
517 metastasis of cancer cells may be based on ncRNAs. Their mode of action through direct binding to
518 mRNA is simple and sufficiently well understood, and detailed descriptions of their
519 tumor-suppressive effects are rapidly accumulating. Therapeutic miRNAs or siRNAs are already
520 emerging as next-generation biopharmaceuticals that can rapidly move from the bench to the clinic,
521 with about 20 different molecules currently in clinical trials. Although none of these 20 ncRNAs are
522 targeting FAK or PYK2, most of them are used to treat cancers, and two are specifically silencing
523 kinases (SYK and PKN3) [180,181]. These proofs of concept for ncRNA-based therapeutics combined
524 with the accruing evidence for tumor-suppressive effects of miRNA-mediated inhibition of FAK
525 and/or PYK2 provide a strong incentive for the development of FAK- and/or PYK2-specific
526 anti-cancer mi/siRNA therapies. Moreover, the biological capacities of the almost 20,000 potentially
527 functional human lncRNAs are only beginning to emerge [182]. In particular, their capacity to act as
528 ceRNA or to directly bind to proteins (see, for example [183]) might provide interesting regulatory
529 effects with therapeutic potential. Although to date no lncRNA has been discovered that directly
530 binds to FAK or PYK2, RNA aptamers can potently and selectively inhibit kinases through
531 positioning of an adenine nucleotide into the ATP-binding pocket [184], and more than 40 kinases
532 were identified as non-classical RNA binding proteins in a screen of the *Arabidopsis thaliana*
533 proteome [185]. Efficient and specific *in vivo* delivery of ncRNAs faces many challenges, including
534 poor tissue penetration, rapid degradation, immunotoxicity, reliance on cellular factors required for
535 miRNA function and possible off-target effects [186]. Nonetheless, advances in tissue delivery
536 methods and methods for ncRNA bioengineering and recombinant production (e.g., [187]), indicate
537 that ncRNAs are promising nature-inspired agents that can enrich our toolkit of selective therapeutic
538 inhibitors of FAK and PYK2.

539

540 **Acknowledgements**

541 We thank V. Unkefer for editorial proof reading, and J-A. Girault, S. Hong, B.W. Quereshi and A.A.
542 Momin for suggestions and discussions. This publication was supported by King Abdullah
543 University of Science and Technology (KAUST) through the baseline funds and Award No
544 URF/1/2602-01-01 from the Office of Sponsored Research (OSR).

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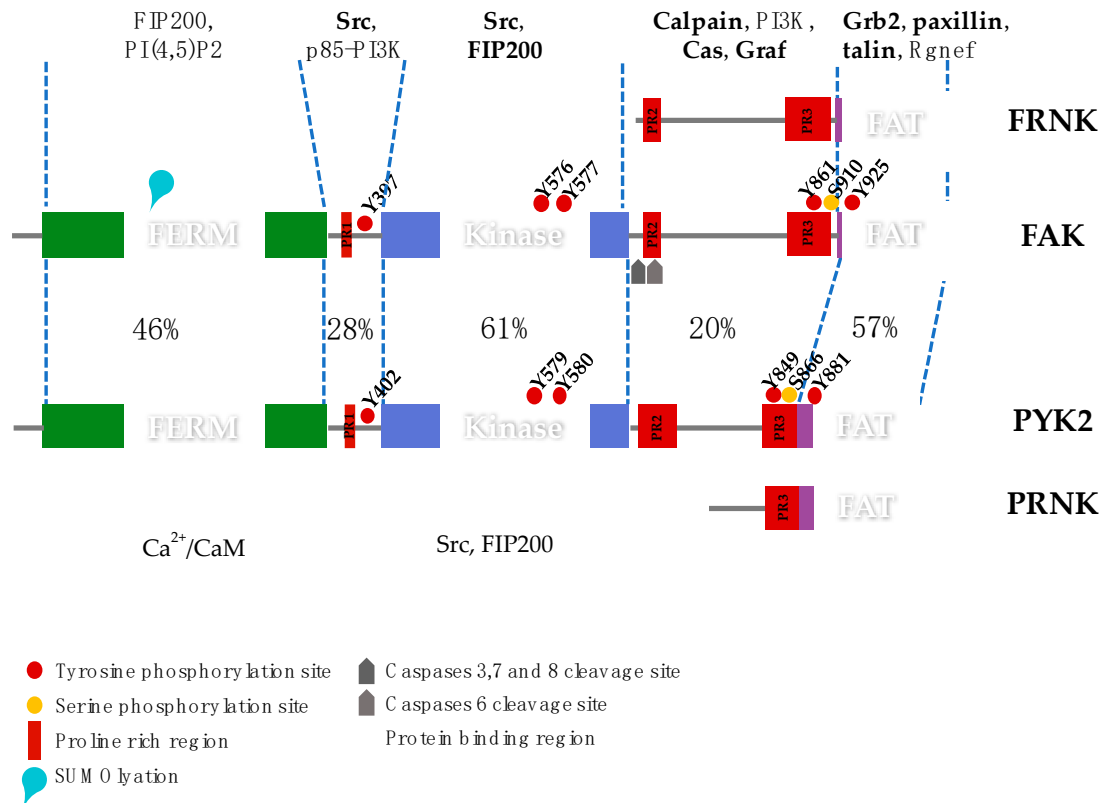
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1269 **Table 1.** FAK/PYK2 based endogenous inhibitors.

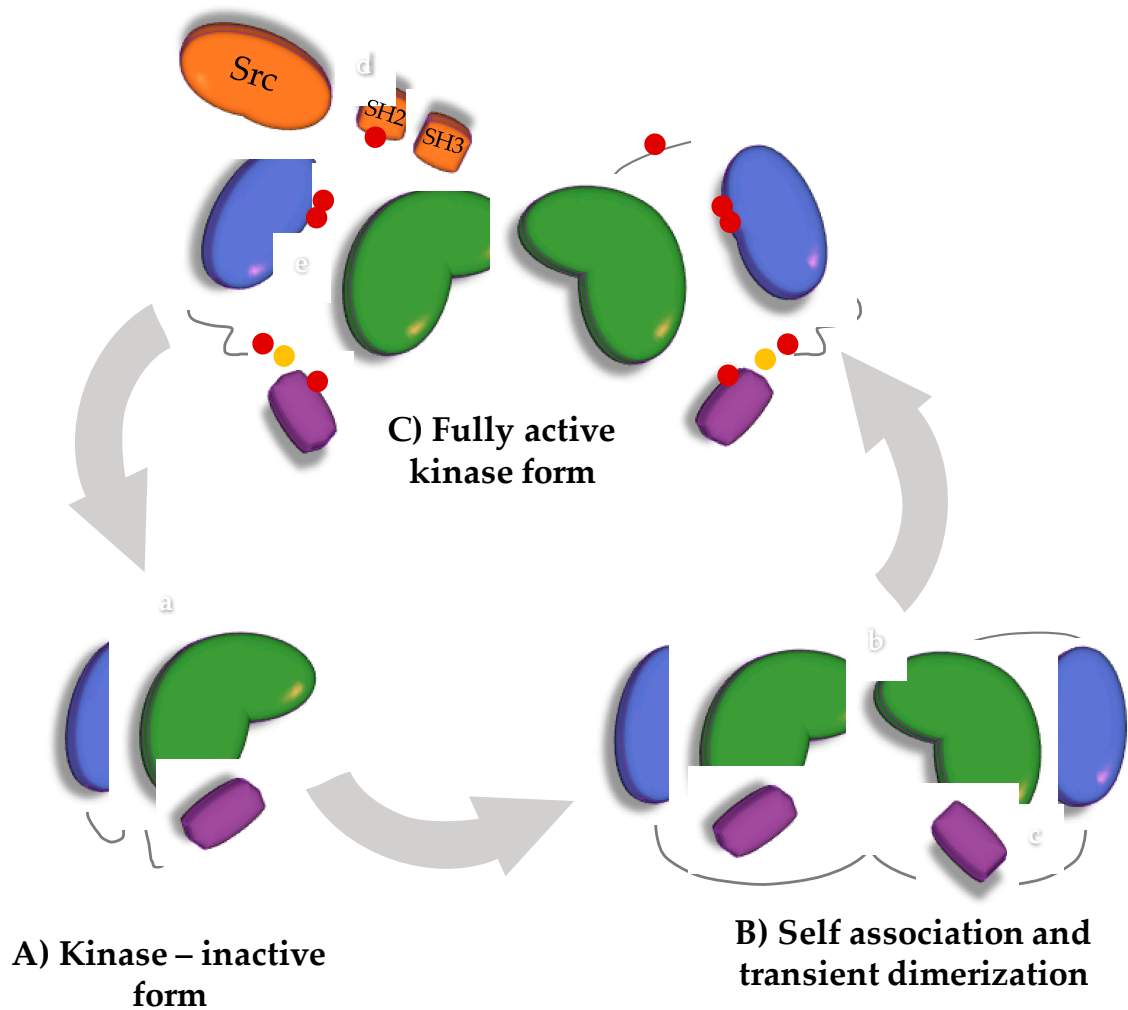
miRNA	Cell type	Target site(s)	Role	Ref
miR-9	Ovarian serous carcinoma	TLN1, FAK, Akt	Tumor suppressor	[188]
miR-16	Glioma	p-FAK, p-Akt expression, nuclear factor- κ B, Slug	Tumor suppressor	[189]
miR-17-3p	Cardiac fibroblasts	Par4, CEBPB, FAK, N-cadherin, vimentin, Oct4, Sca-1, E-cadherin	Oncogene	[190]
miR-21	Breast cancer lymph node metastasis	CDK5RAP1, CDK5 activator p39, FAK	Oncogene	[191]
miR-34a	Neuroblastoma, colorectal cancer	VEGF, FAK	Tumor suppressor	[192,193]
miR-92b	Esophageal squamous cell carcinoma	ITGAV, FAK, Rac1	Tumor suppressor	[194]
miR-124	Glioma	Capn4, -FAK, MMP2, vimentin, N-cadherin	Tumor suppressor	[195]
miR-130a	Hemangioma	TFPI2, FAK, PI3K, Rac1, mdm2	Oncogene	[196]
miR-133b	Osteosarcoma	BCL2L2, MCL-1, IGF1R, MET, FAK, Akt	Tumor suppressor	[197]
miR-134	Hepatocellular carcinoma	ITGB1, FAK and RhoA	Tumor suppressor	[198]
miR-138	Ewing's sarcoma, head and neck squamous cell carcinoma	RhoC, FAK, Src, Erk(1/2)	Tumor suppressor	[168,199–202]
miR-141	Renal cell carcinoma	EphA2, p-FAK, p-AKT, MMP2/9	Tumor suppressor	[203]
miR-141/200c cluster	Breast cancer	VEGF-A, FAK, PI3K, Akt	Oncogene	[204]

miR-145	Glioma	CTGF, SPARC, FAK	Tumor suppressor	[205]
miR-150	Lung cancer	Src, FAK, Ras, ERK	Oncogene	[206]
miR-151-5p	Gastric cancer, hepatocellular carcinoma	FAK (host genet), RhoGDIA, Rac1, Cdc42, Rho GTPases	Oncogene	[207–209]
miR-187	Ovarian cancer	Dab2, E-cadherin, vimentin, FAK	Tumor suppressor	[210]
miR-199a-5p	Breast cancer	Ets-1, FAK/Src/Akt/mTOR	Tumor suppressor	[211]
miR-202	Esophageal squamous cell carcinoma	LAMA1, FAK-PI3K-Akt	Tumor suppressor	[212]
MiR-221 and miR-26b	Mesenchymal stem cells	PTEN, FAK, PI3K, Akt		[213]
miR-296-3p	Lung Adenocarcinoma	PRKCA, FAK-Ras-c-Myc	Tumor suppressor	[214]
miR-375	Mesenchymal stem cells	FAK, paxillin, PDK1, Akt		[215]
miR-383	Glioma	VEGF/VEGFR2, FAK, Src	Tumor suppressor	[216]
miR-425-5p	Hepatocellular carcinoma	SCAI, integrin β 1-Fak/Src-RhoA/CDC42, PTEN-AKT, TIMP2-MMP2/MMP9	Oncogene	[217]
miR-491-5p	Oral squamous cell carcinoma	GIT1, paxillin, FAK, EGF/EGFR- ERK1/2, MMP2/9	Tumor suppressor	[218]
miR-542-3p	Colon cancer	ILK, FAK/c-Src	Tumor suppressor	[219]
miR-647	Gastric cancer	ANK2, FAK, MMP2, MMP12, CD44, SNAIL1,	Tumor suppressor	[220,221]
miR-708	Metastatic breast cancer	Neuronatin, ERK, FAK	Tumor suppressor	[222]



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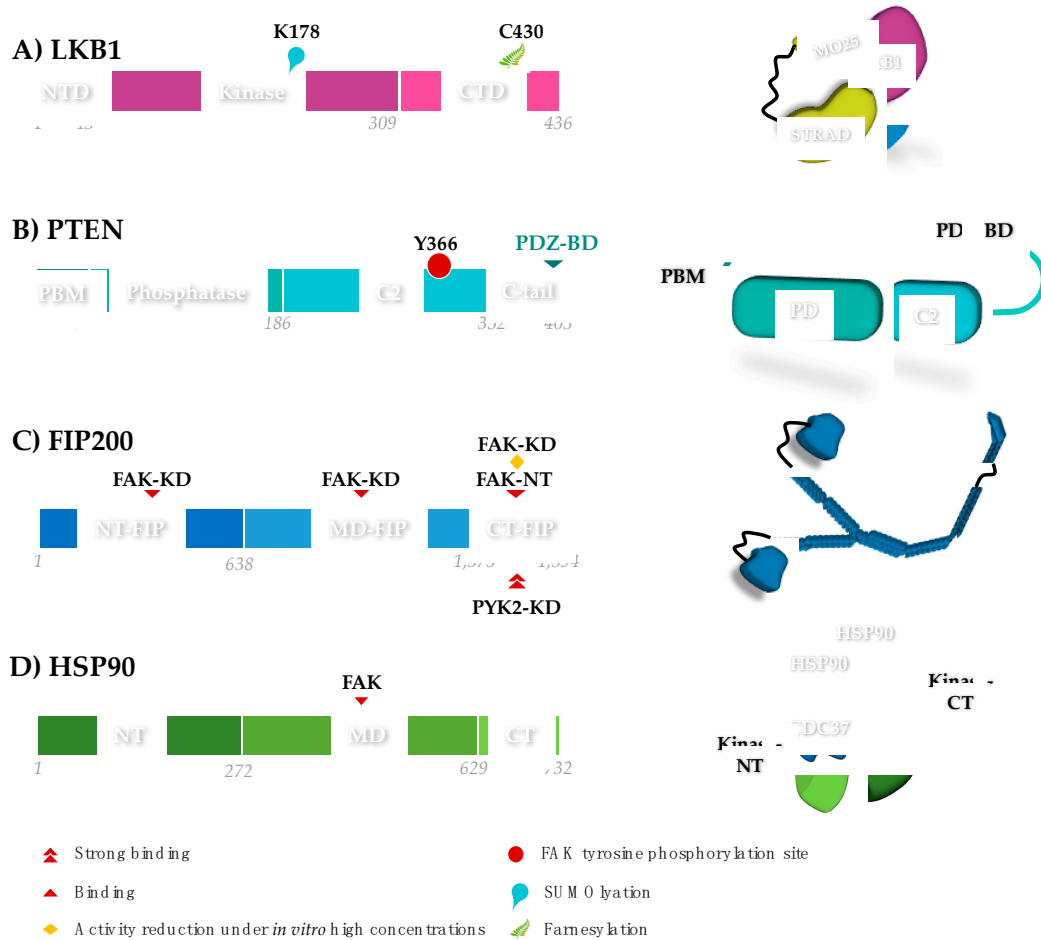
Figure 1. Schematic domain structure of FAK and PYK2. The three folded domains are shown in green, blue and magenta. Interaction motifs, sites of post-translational modification, and binding sites of ligands discussed in the text are shown. The % numbers give the sequence identity between corresponding regions of FAK and PYK2. The alternatively transcribed products FRNK and PRNK are schematically represented with respect to FAK and PYK2. Protein ligand names in bold indicate that these proteins were shown to bind to both, FAK and PYK2. Protein names not in bold have so far only been shown to be ligands for FAK (if above the FAK drawing) or PYK2 ($\text{Ca}^{2+}/\text{CaM}$).



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Figure 2. Canonical FAK activation scheme. (A) In the absence of integrin activation, an interaction between the FERM and kinase domain (indicated by a white lower-case 'a' in a red triangle) inhibits FAK kinase activity. Ligand-mediated recruitment and clustering of FAK at focal adhesions promotes transient dimerization by stabilizing weak FERM:FERM interactions (lower-case 'b' in triangle) and promoting FERM:FAT binding *in trans* (lower-case c). FAK clustering and self-association allows trans-autophosphorylation of Y397 (red dot) in the FERM-kinase linker. When phosphorylated, Y397 and PR1 form a bidentate binding site for the SH2 and SH3 domains of Src (lower-case d). Recruitment-activated Src phosphorylates the activation loop of the FAK kinase domain (lower-case e) and other tyrosines on FAK, resulting in an open FAK conformation and full enzymatic activity. Triggered signaling may result in additional FAK modifications (e.g. serine phosphorylation; yellow dot), and may ultimately lead to dephosphorylation and/or displacement of FAK from focal adhesions (back to the closed monomeric inactive conformation of A), or to proteolytic cleavage and degradation (not shown).



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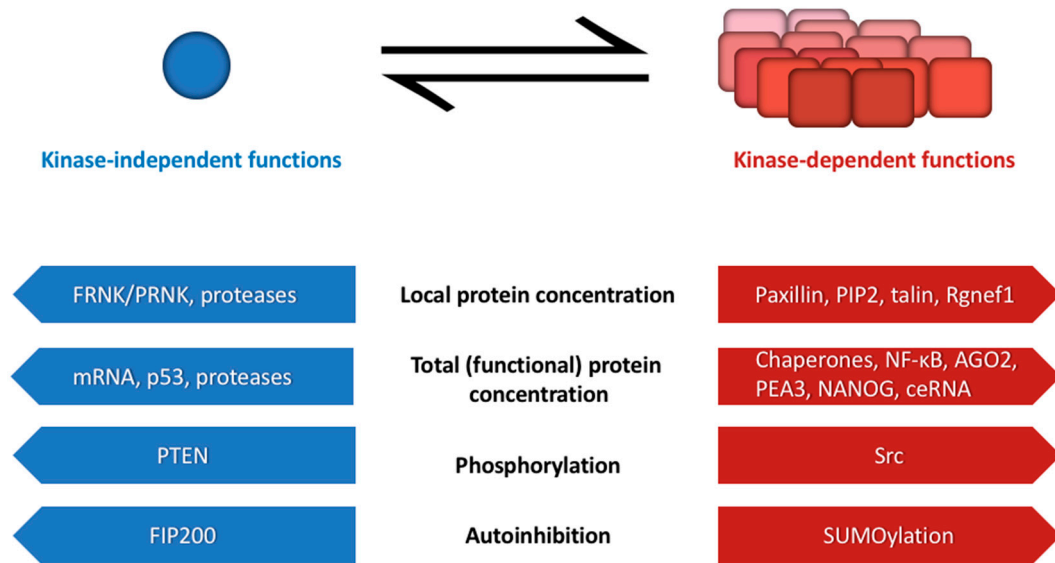
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Figure 3. Schematic domain structures (left) and 3D architectures (right) of protein regulators of FAK: LKB1, PTEN and FIP200 are negative regulators. LKB1 is shown as part of the activating complex formed with MO25 α and STRAD α (according to PDB accession 2wtk). The presented 3-dimensional structure of FIP200 (blue) is highly speculative, based on secondary structure predictions and homology modeling. The stabilizing function of HSP90 is upregulated in cancers. HSP90 is displayed with the kinase-specific adaptor CDC37, maintaining the separated N-terminal (NT) and C-terminal (CT) lobe of a kinase domain (taken from PDB 5fwl). Binding sites and posttranscriptional modifications relevant for their interaction with FAK and PY2 are indicated. Abbreviations are: LKB1: NTD, N-terminal domain; CTD, C-terminal domain. PTEN: PD, phosphatase domain; PBM, PI(4,5)P2-binding module; PDZ-BD: PDZ binding domain. FIP200/HSP90: NT, N-terminal domain; MD: middle domain; CT, C-terminal domain. FAK: KD, kinase domain; NT, N-terminal fragment.

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1309 **Figure 4. Schematic overview of the endogenous mechanisms promoting either**
 1310 **kinase-independent or kinase-dependent functions of FAK or PYK2.** *Top panel:* Kinase-inactive
 1311 FAK/PYK2 is illustrated by a blue sphere. Kinase-active FAK/PYK2 are shown as clustered square
 1312 dimers in shades of red. *Bottom panel:* Promoters of kinase-independent and kinase-dependent
 1313 functions are presented in blue and red, respectively, next to the mechanism or function they affect.
 1314 The direction of the arrowheads indicates decrease (left) or increase (right) of the indicated
 1315 mechanism/function. This list is incomplete, as the factors with unknown molecular mechanism are
 1316 not shown (e.g. LKB1).

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