

1 **Frontotemporal dementia mutant tau (P301L) locks Fyn in an open, active conformation**
2 **conductive to nanoclustering**

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15 **Abstract**

16 Fyn is a Src kinase that controls critical signalling cascades and its postsynaptic enrichment
17 underpins synaptotoxicity in Alzheimer's disease (AD) and frontotemporal dementia (FTLD-
18 tau). Previously, we found that pathogenic FTLD tau mutant (P301L) expression promotes
19 aberrant trapping of Fyn in nanoclusters within hippocampal dendrites via an unknown
20 mechanism (Padmanabhan et al., 2019). Here, we imaged Fyn-mEos2 using single particle
21 tracking photoactivated localization microscopy (sptPALM) to demonstrate that
22 nanoclustering of Fyn in hippocampal dendrites is promoted by Fyn's open, primed
23 conformation. Disrupting the auto-inhibitory, closed conformation of Fyn through phospho-
24 inhibition, and perturbation of Fyn's SH3 domain increases, Fyn's nanoscale trapping.
25 However, inhibition of Fyn's catalytic domain has no impact on its mobility. Tau-P301L
26 promotes Fyn lateral trapping via Fyn opening and ensuing increased catalytic activation.
27 Pathogenic tau may therefore drive synaptotoxicity by locking Fyn in an open, catalytically
28 active conformation, leading to postsynaptic entrapment and aberrant signalling cascades.

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32 **Introduction**

33 Fyn is a member of the Src family of kinases (SFKs), a group of enzymes that regulate signal
34 transduction by catalysing the phosphorylation of tyrosine residues. Fyn is expressed in
35 numerous cell-types, including lymphocytes, neurons and glia, and like other SFKs, is an
36 intracellular, membrane-associated enzyme characterised by four conserved motifs known as
37 Src homology domains (SH1, SH2, SH3 and SH4) (Figure 1A i). The SH1 domain is the
38 catalytic domain responsible for the phosphorylation of tyrosine residues from target proteins
39 and is connected via a polyproline type II (PPII) helix linker region to the SH2 domain (Figure
40 1A ii-iii). The SH2 and SH3 domains control the interaction of Fyn with its substrates, and the
41 N-terminal SH4 domain is responsible for the association with the plasma membrane through
42 myristylation and palmitoylation, thereby facilitating the interaction between Fyn and its
43 membrane-associated substrates (Sato et al., 2009). The kinase activity of Fyn is also controlled
44 by the transition between a closed (assembled) (Figure 1A ii) and an open (extended)
45 conformation that can bind to its substrates and execute its catalytic activity (Figure 1Aiii).
46 This transition is controlled by two conserved tyrosine phosphorylation sites with opposing
47 roles. Dephosphorylation of Y531 in the C-terminal tail opens Fyn, resulting in its priming.
48 This extended-primed form of Fyn is activated by trans-autophosphorylation of Y420, located
49 in a central “activation loop” of the SH1 catalytic domain (Young et al., 2001). In the open
50 conformation, the SH2 and SH3 domains are displaced and are free to interact with external
51 ligands (Yadav & Miller, 2007). Conversely, two intramolecular interactions with the SH2 and
52 SH3 domains are essential for downregulation of the kinase activity (Engen et al., 2008;
53 Huculeci et al., 2016). Phosphorylation of Y531 allows this residue to interact with the SH2
54 domain and stabilises an assembled conformation whereby kinase activity is decreased by
55 conformational changes at the active site of the catalytic domain. The second downregulatory
56 interaction includes the SH3 domain and the PPII helix linker. Interestingly, this intramolecular

57 interaction resembles the standard binding mode of SH3 domains to target sequences rich in
58 proline and other hydrophobic amino acids (P-X-X-P motif, where P is proline and X is any
59 amino acid). These sequences generally form a PPII helix which associates with the
60 hydrophobic surface of the SH3 domain (Engen et al., 2008).

61

62 Fyn is responsible for integrating multiple signalling cascades. In neurons, Fyn facilitates cell-
63 to-cell communication by promoting the scaffolding of the N-methyl-D-aspartate (NMDA)
64 receptor through phosphorylation of the NR2B subunit of the receptor at the Y1472 epitope.
65 This increases the affinity of NR2B with postsynaptic density protein 95 (PSD95) and, as a
66 consequence, facilitates the stabilisation of NMDA receptor clusters at the membrane, thereby
67 maintaining postsynaptic excitatory currents (Tezuka et al., 1999). Fyn is also implicated in
68 mediating neurodegeneration. Overactive Fyn is believed to exacerbate cell death by promoting
69 excess activation of NMDA receptors, leading to aberrant calcium entry into the postsynapse
70 and neuronal excitotoxicity (Xia & Gotz, 2014). Fyn has also been shown to play a critical role
71 in the neurotoxicity of Alzheimer's disease (AD) and frontal temporal lobar degeneration with
72 tau (FTLD-tau) (Briner et al., 2020; Polanco et al., 2018). Fyn promotes neurotoxicity
73 downstream of the amyloid-beta ($A\beta$) peptide, which forms extracellular amyloid plaques, and
74 the microtubule-associated protein tau (MAPT). Hyperphosphorylated tau accumulates into
75 neurofibrillary tangles (NFTs), a key hallmark of the toxicity associated with AD and FTLD-
76 tau (Gotz et al., 2001). In transgenic mouse lines that replicate AD pathology, knockout of Fyn
77 has been shown to protect against the loss of presynaptic terminals and to delay premature
78 mortality (Chin et al., 2004). Hippocampal slices from Fyn knockout mice have been shown to
79 resist the toxic effects of treatment with toxic $A\beta$ oligomers (Um et al., 2012). Similarly,
80 pharmacological inhibition of Fyn rescues the behavioural deficits observed in AD mice

81 (Kaufman et al., 2015). Conversely, overexpression of Fyn exacerbated the neuronal deficits
82 present in AD mice (Chin et al., 2005; Kaufman et al., 2015).

83

84 Increasing evidence suggests that Fyn works as a key partner in tau-mediated pathology. Fyn
85 interacts with tau through its SH2 and SH3 domains and P-X-X-P motifs located in the proline-
86 rich region of tau (Bhaskar et al., 2005; Lau et al., 2016; Lee et al., 1998). This interaction
87 mediates phosphorylation of tau at residue Y18, one of the epitopes associated with the
88 formation of NFTs in AD patients (Bhaskar et al., 2010; Lee et al., 2004; Miyamoto et al.,
89 2017; Neddens et al., 2018), and potentiates its association with Fyn (Usardi et al., 2011).
90 Subcellular compartmentalisation of Fyn and tau also appears to be crucial for their toxicity.
91 Mis-localisation of tau into dendritic spines mediates the synaptic dysfunction associated with
92 AD and FTLN-tau (Fransdemiche et al., 2014; Hoover et al., 2010; Miller et al., 2014; Xia et
93 al., 2015). Fyn regulates the phosphorylation and dendritic distribution of tau through its
94 activation by A β during AD (Larson et al., 2012). Alternatively, a previous study found that
95 tau itself controls the localisation of Fyn to dendrites, and that disruption of postsynaptic
96 targeting of Fyn mitigates A β toxicity (Ittner et al., 2010).

97

98 Altered organisation of receptors and signalling molecules in nanodomains is emerging as a
99 key regulator of neuronal toxicity (Shrivastava et al., 2017). Several proteins involved in AD
100 show aberrant clustering associated with the pathology. The metabotropic glutamate receptor
101 mGluR5, for example, shows increased clustering when binding to A β (Renner et al., 2010);
102 and the amyloid precursor protein (APP) organises into regulatory nanodomains that control
103 the availability of APP molecules for proteolytic processing (Kedia et al., 2020). In this respect,
104 tau has been shown to control the lateral trapping of Fyn into nanodomains within the dendrites
105 and spines of hippocampal neurons, with single molecule imaging of Fyn-mEos2 showing

106 enhanced mobility and decreased clustering in tau knockout neurons. Importantly, expression
107 of an FTLD tau mutant (P301L) aberrantly increases the number of Fyn nanoclusters in spines,
108 an effect that is likely to contribute to NMDA-mediated excitotoxicity (Padmanabhan et al.,
109 2019). However, whether the nanoscale spatiotemporal organisation of Fyn is involved in its
110 efficient transactivation remained to be established, and the mechanisms underlying the Fyn-
111 tau toxic partnership have not yet been fully elucidated.

112

113 In this study, we used single-particle tracking photoactivated localization microscopy
114 (sptPALM) to determine how the nanoscale organisation of Fyn is affected by its activity and
115 conformation in the dendrites of live hippocampal neurons. Through pharmacological
116 inhibition, blocking phosphorylation of the Y420 residue, preventing binding of ATP to the
117 K299 epitope, or introducing a phosphorylation-inhibitory mutant to render Fyn constitutively
118 open, we evaluated whether preventing the catalytic activity or altering the overall
119 conformation can modulate Fyn mobility dynamics in neurons. Our results demonstrate that
120 the SH3 domain is essential for maintaining a closed conformation and interacting with Fyn-
121 binding proteins such as the FTLD-associated P301L mutant tau. Fyn entry into an opened,
122 primed conformation is associated with its nanoscale entrapment. This extended and confined
123 molecular configuration is compatible with the binding of pathological mutant tau to Fyn.
124 Taken together, our findings suggest a molecular mechanism in which binding of P301L tau to
125 Fyn in the dendritic compartment exacerbates Fyn's toxic effects in FTLD-tau.

126

127 **Results**

128

129 **The catalytic activity of Fyn does not alter the nanoscale organisation of Fyn in**
130 **hippocampal dendrites**

131 We recently discovered that Fyn displays a nanocluster organisation in the dendritic spines of
132 hippocampal neurons that is dynamically regulated by neuronal maturation (Padmanabhan et
133 al., 2019). In this study, we investigate whether changes in Fyn activity affect the nanoscale
134 organisation of Fyn in live neurons. Fyn-mEos2 was expressed in hippocampal neurons,
135 together with mCardinal or GFP as a cytoplasmic marker, and we performed sptPALM in an
136 oblique illumination configuration. We imaged mature neurons at DIV19-22 and selected
137 secondary dendrites with mature spines for analysis (Figure 1B). Fyn-mEos2 molecules were
138 randomly photoconverted from a green- to a red-emitting state in response to constant weak
139 illumination at 405 nm at a low spatial density. The photoconverted molecules were tracked in
140 the red-emitting channel at 561 nm excitation at 50 Hz for a duration of 320 s (16,000 frames),
141 in order to resolve the nanoscale distribution and dynamics of Fyn at a high spatiotemporal
142 resolution in live neurons (Figure 1C).

143

144 Given that Fyn has a critical role in integrating a multitude of signalling pathways in neurons
145 (Li & Gotz, 2017), we first sought to determine whether its catalytic activity was involved in
146 promoting its nanoclustering at the post-synapse. Based on experiments performed with other
147 SFKs, it is established that mutations of specific residues in the SH1 domain have profound
148 effects on the activity of these enzymes, without affecting their conformation (Engen et al.,
149 2008; Nika et al., 2010; Sicheri & Kuriyan, 1997). Trans-autophosphorylation of Y420 located
150 at the central “activation loop” of the catalytic domain is required for the transition from an
151 open, primed to an opened, active form able to phosphorylate its substrates (Nika et al., 2010;

152 Young et al., 2001). To determine if the trans-autophosphorylation of Y420 in the catalytic
153 SH1 domain controls the nanoclustering of Fyn, we introduced a phospho-inhibitory mutation
154 (Y420F) to generate a ‘kinase-inactivated’ Fyn enzyme (Figure 2A-B). Our results showed that
155 this mutation did not affect the mobility of Fyn in dendritic branches of hippocampal neurons
156 (Figure 2C i-ii). Similarly, no changes in the mobility of Fyn-mEos2 were observed in dendritic
157 spines (Figure 2D i-ii). To further evaluate the importance of Fyn activity, we generated a
158 ‘kinase-dead’ Fyn by introducing the mutation K299M, designed to block interaction with
159 ATP, thereby creating an inactive enzyme unable to phosphorylate other substrates (Figure 2A)
160 (Jin et al., 2017; Twamley et al., 1992; Twamley-Stein et al., 1993). Similarly, the Fyn-K299M-
161 mEos2 mutation had no effect on the mobility compared to wild-type Fyn-mEos2 in dendrites
162 (Figure 2C i-ii) and spines (Figure 2D i-ii). Blockade of Fyn activity was also achieved by
163 incubating neurons with 3-(4-chlorophenyl)-1-(1,1-dimethylethyl)-1H-pyrazolo[3,4-
164 d]pyrimidin-4-amine (PP2) (10 μ M, 30 minutes), a potent and specific pharmacological
165 inhibitor of SFK’s kinase catalytic activity (Hanke et al., 1995; Jin et al., 2017; Tomatis et al.,
166 2013). We used the structurally related inactive analogue 1-phenyl-1H-pyrazolo[3,4-
167 d]pyrimidin-4-amine (PP3) (10 μ M) as a control that does not inhibit Src family members
168 (Figure 2 – Figure 1 supplement) (Bain et al., 2003). PP2 is an ATP-competitive inhibitor that
169 interacts with the hydrophobic pocket near the ATP-binding cleft of the SH1 domain, thereby
170 preventing the binding of the substrate ATP to the enzyme (Zhu et al., 1999). No alterations in
171 Fyn-mEos2 mobility were observed in the dendrites of hippocampal neurons in response to
172 PP2 or PP3 treatment (Figure 2-Figure 1 supplement) suggesting that the catalytic activity had
173 no influence on the nanoscale organisation of Fyn at the synapse. Overall, these results further
174 support the notion that the catalytic activity of Fyn does not influence its nanoscale organisation
175 at the post-synapse.

176

177 **Induction to an open, primed conformation promotes the nanoscale entrapment of Fyn**
178 **in hippocampal dendrites and spines**

179 The closed conformation of Fyn is primarily maintained through phosphorylation of the Y531
180 epitope in the C-terminal tail, which stabilises the interaction of the C-terminal domain of Fyn
181 with its SH2 region. To constitutively force an open conformation, we introduced a phospho-
182 inhibitory mutation (Y531F) into the C-terminal domain of Fyn (Figure 3A). The opened-
183 primed conformation rapidly facilitates the trans-autophosphorylation on Y420 that results in
184 a fully active enzyme. In the presence of the Y531F mutation, Fyn is unable to return to its
185 inactive-closed conformation, resulting in a ‘constitutively-active’ form of Fyn (Nakazawa et
186 al., 2001; Xia & Gotz, 2014). To examine the effect of Y531F-induced constitutively open
187 conformation on the mobility of Fyn in dendrites, we performed sptPALM of Fyn-Y531F-
188 mEos2. We observed a significant decrease in Fyn mobility, indicating that the open
189 conformation of Fyn is essential for mediating the nanoscale lateral trapping of Fyn within
190 dendrites (Figure 3C i-ii) and spines (Figure 3D i-ii). To evaluate whether the kinase activity
191 of Fyn played a role in its immobilization, or whether this effect was solely associated with a
192 change in the conformation towards an extended one, we created the mutant Fyn-Y531F-
193 K299M, that remains constitutively opened but with an inactive catalytic domain (Figure 3A).
194 This double mutant also showed significantly lower mobility than the wild-type Fyn in
195 dendrites (Figure 3C i-ii) and spines (Figure 3D i-ii). Interestingly, our results revealed an
196 attenuation of the opened Fyn immobilization in the presence of the K299M mutation (Figure
197 3C-D). This observation suggests that modifying the catalytic domain through the K299M
198 mutation somehow interferes with Fyn’s open conformation. In summary, these results
199 demonstrate that the nanoscale organisation of Fyn is principally controlled by its entry into an
200 open, primed conformation through dephosphorylation of the Y531 epitope.

201

202 To determine if the changes in mobility observed with the Y531F mutant were a product of an
203 alteration in the lateral trapping of Fyn-mEos2 molecules, we compared the frequency
204 distribution (%) of inter-frame step lengths taken by Fyn-WT-mEos2 and Fyn-Y531F-mEos2
205 throughout our acquisitions. Interestingly, the average inter-frame step size of Fyn-WT-mEos2
206 throughout its lifespan was not significantly different from that of the Y531F mutant (Figure
207 4A), suggesting that the changes in mobility of the Y531F mutant may be due a perturbation
208 in the nanoclustering of Fyn-mEos2. To investigate this, we used Density-Based Spatial
209 Clustering of Applications with Noise (DBSCAN) to quantify the size and density of Fyn-
210 mEos2 nanoclusters (Figure 4B-D). This approach involved evaluating the spatial distribution
211 of Fyn-mEos2 trajectory centroids, which allowed us to determine which of those trajectories
212 were confined within spatial clusters, and to derive metrics on cluster number, area, density
213 and trajectory mobility. DBSCAN analysis confirmed that wild-type Fyn had decreased
214 mobility when organised in small nanoclusters at the synapse (Figure 4B) that occupy an
215 average area of $0.271 \pm 0.016 \mu\text{m}^2$. Within these nanoclusters, the mobility and displacement
216 of Fyn were restricted (Figure 4C i). The Y531F mutation, which induces an active, open
217 conformation, caused Fyn-mEos2 to have a significantly lower mobility (MSD) within
218 nanoclusters (Figure 4C ii). Furthermore, the Y531F mutation caused Fyn-mEos2 to be
219 packaged into smaller nanoclusters ($0.124 \pm 0.006 \mu\text{m}^2$) with increased trajectory membership
220 (Figure 4D i) and of significantly higher density (Figure 4D ii-iii). These results led us to
221 conclude that the decreased mobility of Fyn-mEos2 observed in its open conformation was due
222 to increased nanoclustering propensity, rather than a decrease in the size of the inter-frame
223 steps of Fyn-mEos2 molecules.

224

225 **Alteration of the SH3 domain renders Fyn more immobile in dendrites**

226 The intramolecular interaction between the SH3 domain and the PPII helix linker is also
227 essential to stabilise the inactive, closed conformation of Fyn and other SFKs (Moroco et al.,
228 2014; Young et al., 2001). As a consequence, displacement of the SH3 domain from the helix
229 linker has been reported to facilitate the activation of these kinases (Briggs & Smithgall, 1999;
230 Moroco et al., 2014). The SH3 domain is also involved in the interaction of Fyn with its
231 substrates such as the heterogeneous nuclear ribonucleoprotein A2 (hnRNPA2) (Amaya et al.,
232 2018), p85 α (Morton et al., 1996), the palmitoyl-acyl transferase DHHC5 (Brigidi et al., 2015),
233 tau (Lee et al., 1998; Reynolds et al., 2008) and P301L mutant tau (Bhaskar et al., 2005). As
234 displacement of the SH3 domain has been used to activate Fyn molecules and other SFKs
235 (Moroco et al., 2014), we wanted to explore whether direct alterations of this domain affects
236 the nanoscale organisation of Fyn. To investigate this, we performed sptPALM on a Fyn
237 protein lacking the SH3 domain (Fyn- Δ SH3-mEos2) (Figure 5A, B). Deletion of the SH3
238 domain resulted in a decreased mobility of Fyn (Figure 5C, D). In accordance to what has been
239 observed through alteration of the SH3 domain in other SFKs (Moroco et al., 2014), our results
240 may suggest that the absence of the SH3 domain destabilises the closed conformation of Fyn.
241 Similar to the Y531F mutation, this could facilitate the transition of Fyn to the open, primed
242 conformation, leading to Fyn's immobilisation.

243

244 Due to the importance of the SH3:helix linker interaction in stabilising the closed conformation
245 of SFKs, several strategies have been developed to manipulate the activity of these enzymes
246 based on the creation of small molecules that selectively bind the SH3 domain (Huang et al.,
247 2016; Kukenshoner et al., 2017; Moroco et al., 2014; Yadav & Miller, 2007). The G9
248 monobody was specifically generated to interact with the SH3 domain, displaying high
249 specificity for Fyn among other kinases (Huang et al., 2012). To further evaluate how
250 alterations of the SH3-PPII helix linker interaction affects the nanoscale organisation of Fyn,

251 we created a mEos2 tagged version of the G9 monoclonal antibody (Figure 6A). As a control, we used a
252 mEos2-tagged anti-GFP nanobody co-transfected with Fyn-GFP in HEK293 cells (Figure 6A,
253 B). Our results demonstrate that the anti-GFP-mEos2 nanobody, co-expressed with Fyn-GFP,
254 displays similar mobility to Fyn-mEos2 alone. However, co-expression of Fyn-GFP together
255 with the mEos2 G9 anti-Fyn-mEos2 monoclonal antibodies targeting the SH3 domain, resulted in a
256 significant decrease in the MSD of Fyn-GFP in HEK293T cells (Figure 6C). This result
257 suggests that binding of monoclonal antibodies to the SH3 domain of Fyn causes an increase in the
258 immobilisation of Fyn molecules. Interfering with the SH3-PPII helix linker region may
259 therefore facilitate the acquisition of a conformation conducive to lateral trapping of extended-
260 primed Fyn molecules.

261

262 **Overexpression of wild-type and FTLN-tau mutant (P301L) tau promotes an open** 263 **conformation and immobilisation of Fyn in hippocampal dendrites**

264 Previous findings suggest that aberrant nanoclustering is enhanced by the presence of a FTLN
265 mutant form of tau (P301L) (Padmanabhan et al., 2019). This mutant tau binds to the SH3
266 domain of Fyn with higher affinity than wild-type tau (Bhaskar et al., 2005). To further evaluate
267 the effect of wild-type and P301L mutant tau on the mobility of Fyn-mEos2, we co-expressed
268 wild-type tau and P301L mutant tau with Fyn-mEos2 in hippocampal neurons and performed
269 sptPALM imaging (Figure 7A). Wild-type tau caused a significant decrease in the mobility of
270 Fyn-mEos2 (Figure 7B, C). In accordance with our previous findings, this decrease was
271 accentuated in the presence of P301L tau (Figure 7B, C), which has an increased binding
272 capacity to Fyn (Bhaskar et al., 2005). This is interesting as tau binds Fyn through its SH3
273 domain, which causes a decrease in Fyn mobility when disrupted. These results suggest that
274 the intramolecular interaction between the SH3 and PPII helix linker regions plays a key role
275 in controlling the nanoscale organisation of Fyn, and that wild-type and P301L mutant tau

276 drives the nanoclustering of Fyn by displacing this interaction and thus stabilising an open and
277 highly immobile Fyn conformation. We co-expressed Fyn and tau or tau-P301L in HEK293T
278 cells and observed that the total expression of Fyn increased in the presence of P301L mutant
279 tau, and that the proportion of phosphorylated Fyn (Y420) was also higher (Figure 7D). Taken
280 together, these findings suggest that the interaction of Fyn with P301L tau exposes and primes
281 the Y420 epitope for phosphorylation, a process which is associated with increased
282 nanoclustering in hippocampal neurons.

283

284 **Discussion**

285 Fyn is an SFK whose activity integrates multiple signalling cascades. However, when
286 dysregulated, Fyn has been associated with the development of neurological disorders such as
287 AD and tau pathologies (Haass & Mandelkow, 2010; Ittner & Gotz, 2011). We recently
288 provided the first conceptual framework for how the nanoscale organisation of Fyn is altered
289 during tau-mediated neurodegeneration (Padmanabhan et al., 2019). However, it is not known
290 whether the nanoscale spatiotemporal organization of Fyn is required for its efficient signal
291 transduction, and the mechanisms driving the toxic partnership of Fyn and tau remains
292 unsolved. Our new results now suggest that the transition of Fyn into an open conformation
293 facilitates its organization into nanoclusters, and that the binding of toxic P301L mutant tau
294 associated with FTLN-tau locks Fyn into an open, immobile and catalytically active
295 conformation, thereby providing a rational explanation for the resulting initiation of aberrant
296 toxic signalling cascades.

297

298 The kinase activity of Fyn and other SFKs is controlled by the transition between two opposing
299 configurations (from closed/inactive to open/primed). This transition allows SFKs to bind their
300 substrates and execute their catalytic activity (Sicheri & Kuriyan, 1997). Closed Fyn is locked

301 through two intramolecular interactions between the SH2 domain bound to phosphorylated
302 Y531 at the C-terminal tail, and the interaction between the hydrophobic residues from the
303 SH3 domain with the proline-rich PPII helix linker (Engen et al., 2008). Our results showed
304 that altering any of the locking interactions reduces the mobility of Fyn, suggesting that its
305 transition into an open, primed conformation promotes its lateral entrapment. Opening of SFKs
306 triggers their catalytic activity because the SH2 and SH3 domains become accessible to interact
307 with external ligands (Yadav & Miller, 2007), and the SH1 catalytic domain can be activated
308 immediately after trans-autophosphorylation of Y420 (Young et al., 2001). In contrast, we
309 found that the catalytic activity of the SH1 domain has little impact on the mobility of Fyn.
310 This finding was demonstrated by the observations that (1) neither genetic or pharmacological
311 suppression of Fyn activity had an impact on Fyn mobility, and (2) creation of an open-but-
312 inactive Fyn through addition of the “kinase-dead” K299M mutant on top of the “open” Y531F
313 mutant had little effect on Fyn immobilisation. Taken together, our findings indicate that the
314 nanoscale organisation of Fyn is only affected by changes in its conformation, and that
315 acquisition of an open, extended structure induces its lateral trapping in dendritic nanoclusters.
316 In addition, as conformation and activity changes are interdependent in SFK enzymes, it is
317 likely that the nanoclustering of Fyn facilitates its catalytic activity, being required to initiate
318 its downstream signalling at the post-synapse.

319
320 The fact that SFKs are broadly expressed and share a common negative regulatory mechanism
321 based on intramolecular interactions involving the SH2:tail and SH3:linker has motivated
322 extensive research in exploiting these properties, to design strategies based on the creation of
323 synthetic SH2/SH3-binding small molecules to finely control the activity of SFKs (Huang et
324 al., 2016; Kukenshoner et al., 2017; Moroco et al., 2014; Yadav & Miller, 2007). Interestingly,
325 monobodies (Huang et al., 2016; Huang et al., 2012) and peptoid-based ligands (Li &

326 Lawrence, 2005) that are highly selective for the Fyn SH3 domain have already been generated
327 to modulate the activity of Fyn kinase. We used a mEos2-tagged version of the G9 monobody
328 created specifically to selectively bind Fyn SH3 domain (Huang et al., 2012). As Fyn interacts
329 with tau through its SH2 and SH3 domains (Bhaskar et al., 2005; Lau et al., 2016; Lee et al.,
330 1998), it is conceivable that binding of our G9-mEos2 monobody to the SH3 domain could
331 induce a steric effect that interferes with the conformational mobility of Fyn in a similar way
332 to tau. Our results indicate that binding of the G9-mEos2 monobody reduces the mobility of
333 Fyn molecules, reinforcing the idea that alteration of their closed state by interfering with the
334 intramolecular SH3:linker promotes an open-primed and immobilised Fyn conformation. The
335 equilibrium dissociation constant (K_D) for G9 monobodies bound to the Fyn SH3 domain
336 calculated using isothermal titration calorimetry is 0.166 μ M (Huang et al., 2012). In a different
337 study using surface plasmon resonance, the K_D values calculated for WT tau and tau P301L
338 bound to the SH3 domain of Fyn were 6.77 μ M and 0.16 μ M, respectively (Bhaskar et al.,
339 2005). Although different techniques were used, these results suggest that G9 monobodies bind
340 to the SH3 domain of Fyn with higher affinity than tau, and at comparable level as the FTLN
341 mutant tau. These results are in line with our observations where overexpression of the mutant
342 P301L tau decreased Fyn mobility to a similar extent as G9 monobodies do.

343

344 Interaction between tau and Fyn contribute to neurodegeneration associated with AD (Ittner et
345 al., 2010) and FTLN-tau (Liu et al., 2020; Tang et al., 2020). Manipulating this interaction has
346 been suggested as a potential therapeutical intervention. Decreasing either tau (Rapoport et al.,
347 2002) or Fyn (Lambert et al., 1998; Um et al., 2012), for example, protects against A β toxicity
348 in AD. However, undesired effects such as memory deficits associated with the absence of Fyn
349 (Grant et al., 1992) suggest that further investigations are required to achieve more desirable
350 therapeutic results. The recent development of a cell-permeable peptide inhibitor of the Fyn-

351 tau interaction yielded promising results, reducing the endogenous Fyn-tau interaction and tau
352 phosphorylation (Rush et al., 2020). G9 monoclonal antibodies have also been used, demonstrating
353 efficiency in inhibiting Fyn-tau binding (Cochran et al., 2014). Our findings on Fyn mobility
354 using G9 monoclonal antibodies against the SH3 domain are in line with these results and add the analysis
355 of nanoscale mobility using super-resolution microscopy as a powerful new tool to evaluate
356 potential therapeutic candidates.

357

358 Nanoclustering has been linked to the increased activity of multiple pre- and postsynaptic
359 molecules, including AMPA receptors (Nair et al., 2013), syntaxin1A (Bademosi et al., 2017)
360 and Munc18-1 (Chai et al., 2016). In particular, nanoclustering of syntaxin1A, which is
361 associated with increased exocytosis, is driven by analogous mechanisms to those observed for
362 Fyn. Syntaxin1A, a soluble N-ethylmaleimide-sensitive factor attachment protein receptor
363 (SNARE) that drives vesicle fusion at the presynapse, switches from an inactive, closed
364 conformation to an open conformation that can bind other SNARE proteins to initiate the fusion
365 of synaptic vesicles with the plasma membrane. Interaction with the chaperone Munc18-1
366 promotes the folding of syntaxin1A into a closed and inactive state. Detachment of Munc18-1
367 facilitates the entry into an open conformation that allows syntaxin1A to interact with other
368 SNARE proteins and form nanoclusters, thereby driving exocytosis at the presynapse (Kasula
369 et al., 2016; Padmanabhan et al., 2020). Similarly, Fyn molecules fluctuate between a closed
370 and an open conformation, the latter being enzymatically active and more immobile, and tau
371 working as a molecular chaperone that modulates this transition.

372

373 We have previously reported that Fyn is organised in compacted nanodomains in dendrites
374 (Padmanabhan et al., 2019), suggesting molecular crowding (Goose & Sansom, 2013; Li et al.,
375 2016), spine geometry (Byrne et al., 2011) and interaction with neighbouring proteins as

376 mechanisms that regulate the trapping and nanodomain organization of Fyn. Extension of Fyn
377 molecules exposes their SH2 and SH3 motifs (Huculeci et al., 2016), and our results indicate
378 that opening this conformation induces lateral trapping of Fyn into nanoclusters. However, it
379 is unclear which interactions are responsible for this effect. Self-association has been described
380 for other SFKs, with the formation of dimers enabling rapid potentiation of their activity when
381 the enzymes adopt an open conformation (Irtegun et al., 2013). This suggests that
382 multimerisation of opened, primed Fyn molecules could facilitate their clustering in dendrites.
383 PSD95 is another possible candidate, as it stabilises molecules at the post-synapse and forms
384 spine nanodomains of comparable size and frequency to those of Fyn (Hruska et al., 2018; Nair
385 et al., 2013). Both PSD95 and Fyn associate with the plasma membrane following
386 palmitoylation of specific residues (Sato et al., 2009; Tezuka et al., 1999; Topinka & Brecht,
387 1998) and PSD95 interacts with the SH2 domain of Fyn (Tezuka et al., 1999). This suggests
388 that entry into an open conformation may induce Fyn to bind to PSD95, resulting in their
389 postsynaptic nanoclustering. Tau also interacts with Fyn, and has previously been shown to
390 control its localisation and nanoclustering in dendrites (Ittner et al., 2010; Padmanabhan et al.,
391 2019). However, it is unclear whether this effect reflects a direct interaction with tau or is
392 caused by tau's regulation of the cytoskeleton in neurons. In this respect, tau interacts with
393 actin (Cabrales Fontela et al., 2017; Elie et al., 2015) and the P301L mutant tau induces aberrant
394 presynaptic actin polymerisation that is capable of crosslinking synaptic vesicles and restricting
395 their mobilisation (Zhou et al., 2017). The actin cytoskeleton modulates nanoclustering of
396 membrane proteins (Torreno-Pina et al., 2016), opening the possibility that it could also
397 modulate the nanoscale organisation of Fyn. Further work is therefore needed to evaluate the
398 potential involvement of the actin cytoskeleton in Fyn nanoclustering. Analysis of the kinetic
399 parameters of the interaction between the SH3 domain of Fyn and pseudo-phosphorylated
400 forms of tau and mutant forms associated with FTLT-tau, showed increased binding affinities

401 when compared to wild-type tau, with the FTL D-tau mutant variant P301L having the highest
402 SH3 affinity (Bhaskar et al., 2005). The interaction between Fyn and tau has been extensively
403 characterised in terms of the residues responsible for this binding (Bhaskar et al., 2005;
404 Cochran et al., 2014; Lau et al., 2016; Lee et al., 1998; Usardi et al., 2011; Wang et al., 2019)
405 and the amino acids that are phosphorylated as a consequence (Lee et al., 2004). However, the
406 crystal structure that would provide a detailed representation of how Fyn and tau interact is still
407 missing. Although we lack precise structural information of Fyn-tau binding, it is therefore
408 tempting to speculate that P301L tau may stabilize an open conformation, thereby promoting
409 nanoclustering of Fyn at the post-synapse (Figure 8). Unfortunately, our temporal and spatial
410 resolution limits do not allow us to determine whether the P301L mutant tau preferentially
411 interacts with Fyn in its open state, or the binding of the mutant tau induces a conformational
412 change that extends the structure of Fyn. Although it is possible that the nanoclustering of Fyn
413 is facilitated by other interactions, our previous results suggest that P301L tau preferentially
414 drives the cluster state of Fyn in hippocampal dendrites (Padmanabhan et al., 2019). Our new
415 findings reveal the formation of a more immobile and active form of Fyn through interaction
416 with P301L mutant tau, when compared to wild-type tau. Interestingly, in a FTL D-tau
417 transgenic mice model, the loss of dendritic spines associated with impairment of spine
418 plasticity occurs in the absence of detected hyperphosphorylated tau species or NFTs
419 (Hoffmann et al., 2013). These findings are in line with observations from brain tissue of AD
420 patients (Blazquez-Llorca et al., 2011; Merino-Serrais et al., 2013). Prefibrillar tau species such
421 as tau monomers, dimers and higher order oligomeric aggregates are responsible for the
422 neurotoxic effects in AD (Polanco et al., 2018), and have been suggested as a cause for the
423 impairment in spine plasticity. However, our findings further suggest the neurotoxicity from
424 P301L tau-mediated Fyn over-activity as a plausible complementary new mechanism
425 responsible for the early loss in spine plasticity and morphology defects. Overall, the results

426 presented in here support the idea that the ability of the tau to associate with Fyn is increased
427 in FTLD-tau, altering the nanoscale organisation of Fyn and promoting an aberrant over-
428 activity that potentiates neurodegeneration.

429

430

431 **Experimental procedures**

432 **Animal ethics and mouse strains**

433 All experimental procedures were conducted under the guidelines of the Australian Code of
434 Practice for the Care and Use of Animals for Scientific purposes and were approved by the
435 University of Queensland Animal Ethics Committee (QBI/254/16/NHMRC). Wild-type mice
436 (C57Bl/6 strain) used throughout the study were maintained on a 12-h light/dark cycle and
437 housed in a PC2 facility with *ad libitum* access to food and water.

438

439 **Primary hippocampal cultures**

440 Primary hippocampal neurons were prepared as described previously (Joensuu et al., 2017;
441 Padmanabhan et al., 2019). Briefly, pregnant dams (C57Bl/6 mice) were euthanised using
442 cervical dislocation, from which embryos (E16) were extracted and dissected in 1x Hank's
443 buffered salt solution (HBSS), 10 mM HEPES pH 7.3, 100 U/ml penicillin-100 µg/ml
444 streptomycin (GIBCO-Thermo Fisher Scientific). Subsequently, the dissected hippocampal
445 tissue was digested with trypsin (0.25% for 10 minutes). Digestion was halted by addition of
446 Fetal Bovine Serum (FBS) (5%) (GIBCO-Thermo Fisher Scientific) with DNase I (Sigma) to
447 prevent tissue clumping. The digested hippocampal tissue was left to incubate (37°C for 10
448 minutes). Following this, the hippocampal tissue was triturated and centrifuged (120 g, 7 min)
449 and resuspended in neurobasal media, 100 U/ml penicillin-100 µg/ml streptomycin, 1x
450 GlutaMAX supplement (GIBCO-Thermo Fisher Scientific), 1x B27 (GIBCO-Thermo Fisher
451 Scientific) and Foetal Bovine Serum (FBS) (5%) (GIBCO-Thermo Fisher Scientific). Neurons
452 were seeded in Poly-L-Lysine coated 29 mm glass-bottom dishes (Cellvis, CA, USA) at a
453 density of $0.8-1 \times 10^5$ neurons. A full media change was performed 2 hours after seeding using
454 culturing media (Neurobasal Medium, 100 U/ml penicillin-100 µg/ml streptomycin, 1x
455 GlutaMAX supplement, 1x B27).

456

457 **Heterologous cell cultures**

458 HEK-293T cells were maintained in DMEM media (GIBCO-Thermo Fisher Scientific)
459 supplemented with FBS (10%), 1x GlutaMAX and 100 U/ml penicillin-100 µg/ml
460 streptomycin. Cells were transfected using the Lipofectamine™ LTX reagent according to the
461 manufacturer's instructions (Invitrogen-Thermo Fisher Scientific).

462

463 **Plasmids and reagents**

464 The plasmid that codes for an FN3 monobody targeted against Fyn SH3 domain was a generous
465 gift from Emeritus Professor Brian Kay (University of Illinois at Chicago, Illinois, US). The
466 FN3 monobody was subcloned into the mEos2-N1 plasmid (Kasula et al., 2016) by inserting
467 BamHI and EcoRI restriction sites at the N- and C-termini of the monobody, followed by
468 BamHI/EcoRI digestion and ligation into mEos2 vector. Fyn mutant constructs were generated
469 by site-directed mutagenesis, using the QuikChange II site-directed mutagenesis kit (Agilent),
470 on the mEos2 donor vector containing full-length human Fyn isoform 1 (Padmanabhan et al.,
471 2019) as a template. All the resulting plasmids were sequenced using the service of the AEGRC
472 sequencing facility (The University of Queensland). PP2 and PP3 reagents were purchased
473 from Calbiochem (Merck/Millipore).

474

475 **Western blotting**

476 HEK293T cells were seeded in a 6 well plate and co-transfected with three combinations of
477 plasmid (2 µg, 24 hrs with Opti-MEM and lipofectamine LTX with Plus Reagent): Fyn-mEos2
478 + GFP, Fyn-mEos2 + tau-GFP or Fyn-mEos2 + tau-P301L-GFP. HEK293T cells were isolated
479 following trypsin digestion. Protein homogenates were boiled at 95°C in Laemmli buffer, run
480 on a Tris-Glycine Precast Gel (4-15%, Bio-Rad) at 150V and subsequently transferred to a

481 PVDF-FL membrane (Millipore), which was incubated in blocking buffer (Odyssey, TBS) for
482 1 hour at room temperature. Subsequently, membranes were incubated with primary antibody.
483 Membranes were stained for total Fyn (1:1000 rabbit anti-Fyn, Cell Signalling Technology),
484 active Src (1:1000 rabbit anti-phosphor-Y16, Santa Cruz), GAPDH (1:1000 mouse anti-
485 GAPDH, abcam #189095) and GFP (1:1000 rabbit anti-GFP, Millipore #AB3080P); in
486 blocking buffer overnight (4°C). Membranes went through TBS-T washes (5x) and incubated
487 in secondary antibody (1:10000 donkey anti-mouse 680, Li-Cor Biosciences #32212 and
488 donkey anti-rabbit 800, Li-Cor Biosciences #68023) with in Odyssey (TBS) blocking buffer (1
489 hour at room temperature). Fyn activity was measured as a ratio of phosphorylated Y416
490 intensity to total Fyn intensity, normalised to GAPDH.

491

492 **Single-particle tracking Photo-activated Localization Microscopy (sptPALM)**

493 Neurons were transfected at DIV 14 using lipofectamine 2000 (ThermoFisher Scientific) (2 µg
494 of GFP or mCardinal with 3 µg Fyn-mEos2 for 4 hrs) and were subsequently left to incubate
495 for 24 hrs prior to imaging. Acquisitions (16 000 frames at 50Hz) were taken at 37°C on the
496 Roper Scientific TIRF microscope fitted with an iLas² double illuminator (Roper Scientific), a
497 CFI Apo 100x/1.49N.A. oil-immersion objective (Nikon Instruments) and an evolve 512 Delta
498 EMCCD cameras (Photometrics). A Perfect Focus System (Nikon) and an iLas2 double laser
499 illuminator (Roper Scientific) was used for 360°C TIRF illumination. MetaMorph software
500 (version 7.10.2, Molecular Devices) was used for image acquisition. A TIRF-quality ultra-flat
501 quadruple beam splitter (ZT405/488/561/647rpc; Chroma Technology) for distortion-free
502 reflection of lasers and QUAD emission filter (ZET405/488/561/640m; Chroma) were used.
503 Transfected neurons were identified based on their GFP transfection using excitation with a
504 491-nm laser. For sptPALM, Fyn-mEos2 was photoactivated with low-levels 405-nm laser
505 excitation (100 mW Vortran Laser Technology, 1-3% of initial laser power). Photoactivated

506 Fyn-mEos2 molecules were subsequently photoconverted using 561-nm laser (150 mW Cobolt
507 Jive, 70% of initial laser power).

508

509 **Data analysis**

510 Tracking of single molecules of Fyn-mEos2 was performed in accordance with previous
511 publications (Nair et al., 2013). Wavelet-based segmentation was used to detect single
512 localizations of Fyn-mEos2. Following this, tracks of Fyn-mEos2 were computed using
513 simulated annealing-based tracking algorithm implemented in PALM-Tracer, a software that
514 operates in MetaMorph (Molecular Devices). Tracks lasting a minimum of eight frames were
515 reconstructed and used to calculate the mean-square displacement (MSD) of Fyn-mEos2 using
516 the equation $MSD(t) = a + 4Dt$, where D is the diffusion coefficient, a =y intercept and t =time.
517 Trajectories with $\text{Log}_{10}[D] > -1.6$ were considered to be mobile, allowing us to plot a frequency
518 distribution histogram of $\text{Log}_{10}[D]$ and calculate the relative portion of mobile to immobile
519 Fyn-mEos2 molecules (Bademosi et al., 2017; Constals et al., 2015). Fyn nanoclustering was
520 quantified and visualised from sptPALM data using custom Python scripting based around the
521 Density-Based Spatial Clustering of Applications with Noise (DBSCAN) functionality of the
522 Python SciKit-Learn module (scikit-learn.org). Spatial centroids for each trajectory (with a
523 minimum of eight steps) in a region of interest were clustered using DBSCAN with empirically
524 determined “Goldilocks” values of $\epsilon = 0.1 \mu\text{m}$ (radius around each centroid to check for other
525 centroids) and $\text{MinPts} = 3$ (minimum number of centroids within this radius to be considered
526 a cluster). For each DBSCAN cluster, a convex hull of all the localizations comprising the
527 clustered trajectories was used to determine the cluster area.

528

529 **Statistics**

530 The D'Agostino and Pearson test was used to test for normality. For statistical analysis between
531 two groups, a Student's t-test was used. For multiple comparisons, a one-way ANOVA was
532 used with the Tukey's test for corrections for multiple comparisons. Statistical comparisons
533 were performed on a per-cell basis (Fig 2-3, 5-7) and a per-cluster basis (Fig 4). The neurons
534 analysed for each experiment were derived from a dissection of a minimum of five embryos.
535 Unless otherwise stated, values are represented as the mean \pm SEM. The tests used are indicated
536 in the respective figure legends. For all statistical comparisons, $p < 0.05$ was considered to be
537 statistically significant. The tests used are indicated in the respective figure legends. Data were
538 considered significant at $p < 0.05$. Statistical tests were performed, and figures were made using
539 GraphPad Prism 7. A summary of statistical analyses is provided in Supplementary table 1.

540

541

542 **Figure legends**

543

544 **Figure 1.** Single molecule imaging photoactivated localization microscopy (sptPALM) of Fyn-
545 mEos2 co-transfected with GFP in secondary dendritic branches and spines of hippocampal
546 neurons (DIV19-22). **A.** Illustration showing the structure and conformation of Fyn-mEos2.
547 Key epitopes found in the SH1 domain and C terminus of Fyn are highlighted. **(i)** Secondary
548 structure and domain alignment of Fyn. **(ii)** Tertiary structure of Fyn, closed conformation **(iii)**
549 Tertiary structure of Fyn, open conformation. mEos2 is conjugated to the C-terminus of Fyn.
550 **B.** Panels depict GFP epifluorescence and intensity, diffusion coefficient and tracking maps of
551 Fyn-mEos2 (note: hotter colours within diffusion coefficient maps designate regions of low
552 mobility). Scale bar = 4 μm (dendrites) and 1 μm (spines). **C.** Frequency distribution (%) of
553 postsynaptic Fyn-mEos2 mobility, $\text{Log}_{10}[\text{D}](\mu\text{m}^2\text{s}^{-1})$, where [D] is the diffusion coefficient. **(i-**

554 **iii)** Examples of frequency of diffusion of Fyn-mEos2 from individual neurons. **(iv)** Averaged
555 frequency distribution. Mobile:immobile fraction threshold is set at $-1.6 \mu\text{m}^2 \text{s}^{-1}$.

556

557 **Figure 2.** Inhibition of the catalytic (SH1) domain does not impact the mobility of Fyn-mEos2
558 **A.** Illustration depicting K299M and Y420F mutants in closed conformation of Fyn. **B.**
559 Intensity and diffusion coefficient maps for Fyn-mEos2 (wild-type, K299M, Y420F). **C.**
560 Mobility of Fyn-mEos2 in dendrites. **D.** Mobility of Fyn-mEos2 in spines. **(i)** Frequency
561 distribution of $\text{Log}_{10} [D](\mu\text{m}^2\text{s}^{-1})$ where $[D]$ is the diffusion coefficient, together with the
562 immobile fraction (%). **(ii)** Mean square displacement (MSD) of Fyn-mEos2 over time (0.14
563 sec) with corresponding area under curve (AUC) $[(\mu\text{m}^2 \text{s}) \times 100]$. Error bars are standard errors
564 of the mean (SEM). Mean \pm SEM values were obtained for neurons transfected with Fyn-WT-
565 mEos2 (n = 14), Fyn-K299M-mEos2 (n=12) and Fyn-Y420F-mEos2 (n=8). Statistical
566 comparisons were performed using a Student's t test.

567

568 **Figure 2 – Figure supplement 1.** Pharmacological inhibition of the catalytic activity of Fyn
569 with pyrazolopyrimidine 2 (PP2) does not impact its mobility. **A.** Illustration depicting the
570 pharmacological inhibition of Fyn in closed and open conformation with PP2. **B.** Mobility of
571 Fyn-mEos2. **(i)** Frequency distribution of $\text{Log}_{10}[D](\mu\text{m}^2\text{s}^{-1})$ where $[D]$ is the diffusion
572 coefficient **(ii)** the immobile fraction (%). Error bars are standard errors of the mean (SEM).
573 Mean \pm SEM values were obtained for neurons transfected with Fyn-WT-mEos2 treated with
574 PP3 (n=9) and PP2 (n=11). Statistical comparisons were performed using the Student's t test.

575

576 **Figure 3.** Phosphorylation of the Y531 epitope controls the lateral entrapment of Fyn-mEos2
577 in the dendrites and spines of hippocampal neurons. **A.** Illustration depicting **(i)** the Y531
578 epitope in the closed conformation of Fyn and **(ii)** the Y531F mutation triggering an open

579 conformation of Fyn. **B.** Intensity and diffusion coefficient maps of Fyn-mEos2 localisations
580 within spines of hippocampal dendrites. Scale bar = 1 μm . **C.** Mobility of Fyn-mEos2 in
581 hippocampal dendrites. **(i)** Frequency distribution of diffusion coefficient values together with
582 immobile fraction (%). **(ii)** Mean square displacement (MSD) of Fyn-mEos2 over time (0.14
583 s) with the corresponding area under curve (AUC) [$(\mu\text{m}^2 \text{ s}) \times 100$]. **D.** Mobility of Fyn-mEos2
584 in hippocampal spines. **(i)** Frequency distribution of diffusion coefficient values together with
585 immobile fraction (%). **(ii)** Mean square displacement (MSD) of Fyn-mEos2 over time (0.14
586 s) with the corresponding area under curve (AUC) [$(\mu\text{m}^2 \text{ s}) \times 100$]. Error bars are standard
587 errors of the mean (SEM). Mean \pm SEM values were obtained for neurons transfected with
588 Fyn-WT-mEos2 (n = 8), Fyn-Y531F-mEos2 (n=14) and Y531F-K299M-mEos2 (n=9).
589 Statistical comparisons were performed using a one-way ANOVA and Tukey's test for
590 comparisons between groups.

591

592 **Figure 4.** Nanoclustering and step length distribution of Fyn-mEos2 in the dendrites of
593 hippocampal neurons revealed by density-based clustering analysis (DBSCAN). The Y531F
594 mutation, which induces entry of Fyn into an open, active conformation, increases the density
595 and decreases the size of Fyn-mEos2 nanoclusters. **A.** Frequency distribution of step lengths
596 (μm) of Fyn-mEos2. No change in the frequency distribution of steps taken was observed
597 between Fyn-WT-mEos2 and Fyn-Y531F-mEos2. **B.** Spatial distribution of Fyn-mEos2
598 nanoclusters in the dendrites and spines. Scale bar = 1 μm . **C. (i)** Mean square displacement
599 (MSD) (μm^2) over time (200 ms) plotted for clustered and unclustered populations of Fyn-
600 mEos2. **(ii)** Average cluster MSD AUC ($\mu\text{m}^2\text{s}$) for Fyn-WT-mEos2 and Fyn-Y531F-mEos2.
601 **D.** Nanocluster dynamics of Fyn-WT-mEos2 and Fyn-Y531F-mEos2. **(i)** Cluster membership
602 (trajectory number). **(ii)** Cluster density (trajectories/ μm^2). **(iii)** Cluster area (μm^2).
603 Nanoclusters were significantly denser for Fyn-Y531F-mEos2 compared to Fyn-WT-mEos2.

604 Error bars are standard errors of the mean (SEM). Mean \pm SEM values were obtained from n
605 = 823 nanoclusters (Fyn-WT-mEos2) and n=698 (Fyn-Y531F-mEos2) from 5 neurons.
606 Statistical comparisons were performed using a Student's t test.

607

608 **Figure 5.** Deletion of the SH3 domain promotes the lateral trapping of Fyn-mEos2. **A.**
609 Schematic showing deletion of the SH3 domain (Δ SH3). **B.** Intensity and diffusion coefficient
610 maps of Fyn-mEos2 (WT, Δ SH3) in hippocampal neurons. Scale bar = 1 μ m. **C.** Frequency
611 distribution of diffusion coefficient values, where [D]=diffusion coefficient, together with the
612 immobile fraction (%). **D.** Mean square displacement (MSD) over time (0.14 s) with
613 corresponding area under curve (AUC) [$(\mu\text{m}^2 \text{ s}) \times 100$] of Fyn-mEos2 (WT, Δ SH3) in
614 hippocampal dendrites (DIV18-22). Error bars are standard errors of the mean (SEM). Mean \pm
615 SEM values were obtained from neurons transfected with Fyn-WT-mEos2 (n=19) and Fyn-
616 Δ SH3-mEos2 (n = 13). Statistical comparisons were performed using a one-way ANOVA and
617 Tukey's test for comparisons between groups.

618

619 **Figure 6.** Binding of anti-Fyn intrabodies to the SH3 domain decreases the mobility of Fyn-
620 GFP in HEK293T cells. **A.** Schematic depicting binding of anti-Fyn-mEos2 intrabodies to the
621 SH3 domain and anti-GFP-mEos2 intrabodies to Fyn-GFP. **B.** Anti-GFP-mEos2 and anti-Fyn
622 (SH3)-mEos2 tracking of Fyn-GFP in HEK293T cells. Scale bar = 4 μ m for epifluorescence
623 and 1 μ m for track panels. **C. (i)** Frequency distribution of diffusion coefficient values together
624 with immobile fraction (%) and **(ii)** MSD over time (0.14 sec) with AUC [$(\mu\text{m}^2 \text{ s}) \times 100$] of
625 Fyn-mEos2, anti-GFP-mEos2/Fyn-GFP or anti-SH3-mEos2/Fyn-GFP in HEK293T cells.
626 Error bars are standard errors of the mean (SEM). Mean \pm SEM values were obtained from
627 HEK293T cells transfected with Fyn-mEos2 (n=11), Fyn-GFP treated with anti-GFP-mEos2

628 (n=7) or anti-Fyn-mEos2 (n=7). Statistical comparisons were performed using a one-way
629 ANOVA and Tukey's test.

630

631 **Figure 7.** Overexpression of tau (WT, P301L) decreases the mobility and increases activity of
632 Fyn. **A.** Intensity map of Fyn-mEos2 co-expressed with GFP, tau-WT-GFP and tau-P301L-
633 GFP in the spines of mouse hippocampal neurons (DIV19-22). Scale bar = 1 μm . **B.** Frequency
634 distribution (%) of $\text{Log}_{10} [D]$ of Fyn-mEos2 with immobile fraction (%). **C.** Mean square
635 displacement (MSD) of Fyn-mEos2 over time (0.14 sec) and area under curve (AUC) [$(\mu\text{m}^2 \text{s})$
636 $\times 100$]. **D.** Increased phosphorylation at the Y16 epitope in the presence of tau P301L. Western
637 blot of Fyn in protein extracts derived from HEK293 cells co-transfected with Fyn-WT-mEos2
638 and GFP, tau-WT-GFP or tau-P301L-GFP. Fyn-Y420F-mEos2 was also co-transfected with
639 GFP as a control. Activity of Fyn determined by quantifying proportion of active Fyn (anti-
640 Y416) relative to total Fyn, normalised to GAPDH. Co-expression of tau-P301L increased the
641 proportion of active Fyn. Error bars are standard errors of the mean (SEM). Mean \pm SEM
642 values were obtained from neurons transfected with Fyn-mEos2+GFP (n = 12), Fyn-
643 mEos2+tau-WT-GFP (n=4) or Fyn-mEos2+tau-P301L-GFP (n=15), and HEK293 protein
644 lysates (n=3 for each group). Statistical comparisons between tau-transfections (A-C) were
645 performed using a one-way ANOVA and Tukey's test for multiple comparisons. A Student's
646 t test was performed for statistical comparisons of Y16 phosphorylation (D).

647

648 **Figure 8.** Model for the lateral entrapment of Fyn, mediated by entry into an open
649 conformation. Tau P301L (brown) binds to the SH3 domain (green) of Fyn and displaces the
650 interaction of SH3 with the linker region (red), which stabilises the open conformation of Fyn.
651 The open conformation of Fyn bound to tau P301L exposes the SH2 domain (blue) of Fyn to
652 interact with additional binding proteins, and positions tau P301L N-termini in close proximity

653 with Fyn's catalytic domain. This extended conformation also causes the lateral entrapment of
654 Fyn.

655

656 **Article and author information**

657

658 **Authors contribution**

659 R.M.M. and F.A.M. were involved in conceptualisation of the project, design and supervision
660 of the research. R.M.M. and C.S. performed super-resolution experiments. C.S. and R.M.M.
661 analysed the data. T.W. contributed with analytic tools and analysis of the data. R.S.G. created
662 specific plasmids. C.S., R.M.M., and F.A.M. wrote the paper. C.S., R.M.M, F.A.M and J.G.
663 reviewed and edited the manuscript. F.A.M and J.G acquired required funding.

664

665 **Conflict of interest**

666 The authors declare no competing financial interests to disclose.

667

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684

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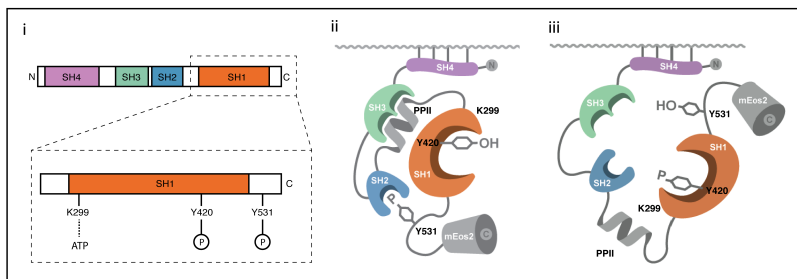
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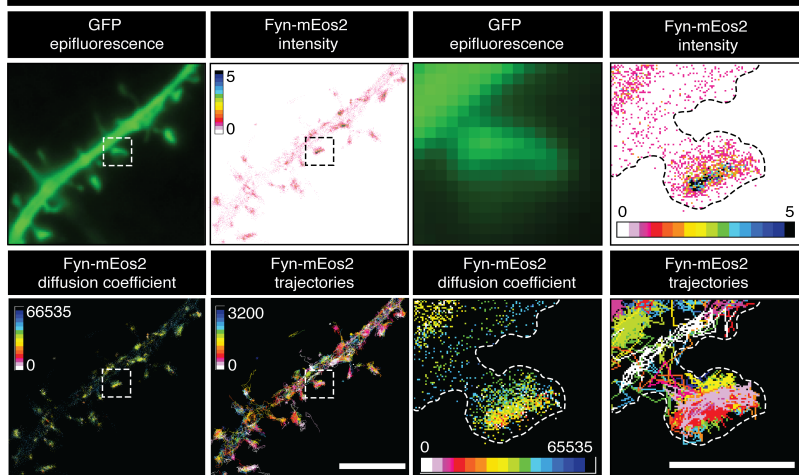
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A Fyn kinase structure and conformation



B Single particle tracking of Fyn-mEos2



C Fyn-mEos2 postsynaptic mobility (diffusion coefficient)

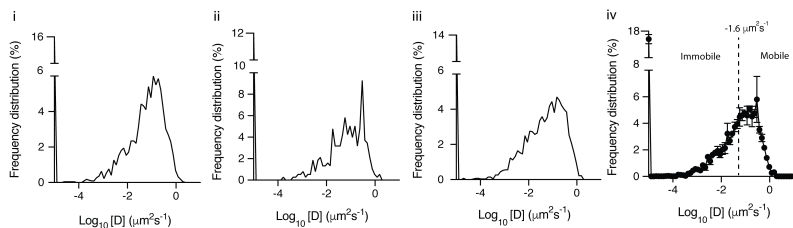


Figure 1

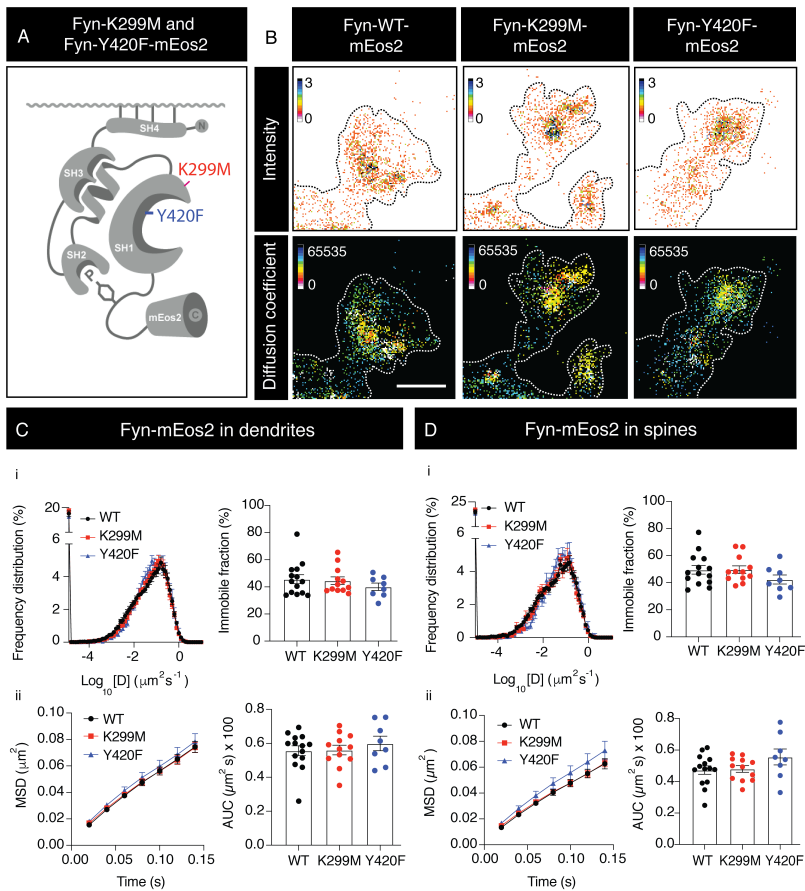
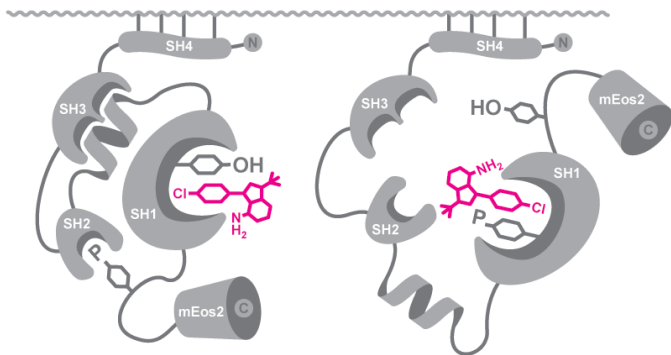
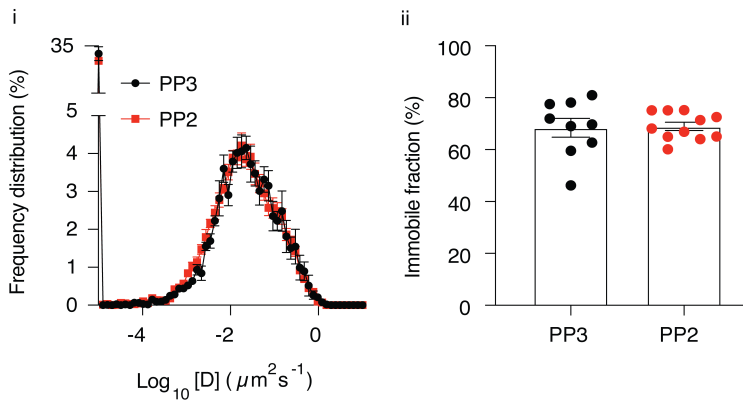


Figure 2

A Pharmacological inhibition of Fyn-mEos2 with pyrazolopyrimidine 2 (PP2)



B Fyn-mEos2 mobility during PP2 treatment



Supplemental figure 1
(Figure 2)

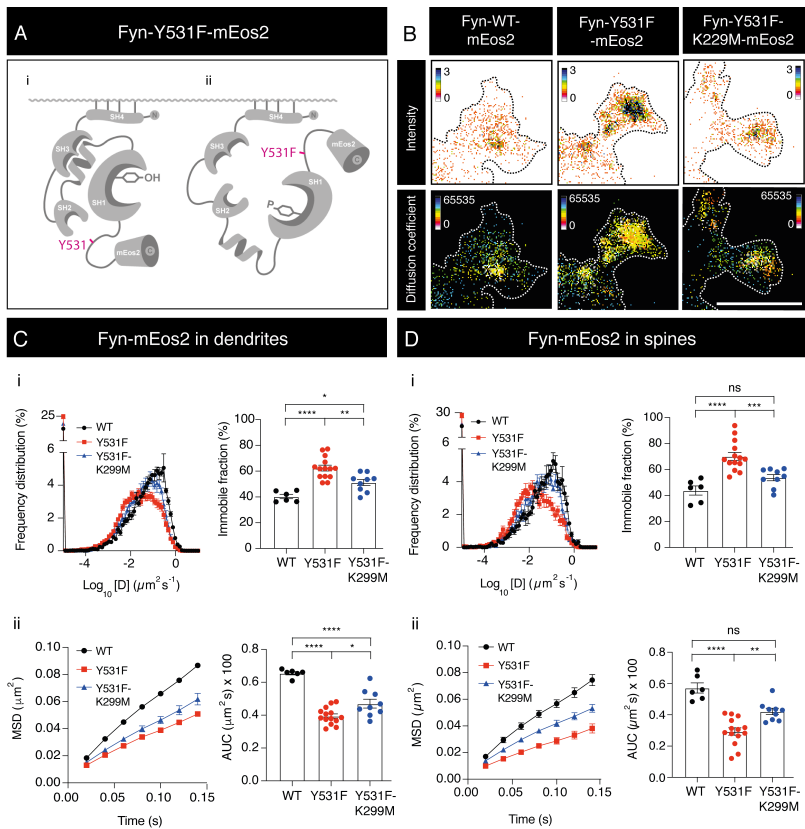


Figure 3

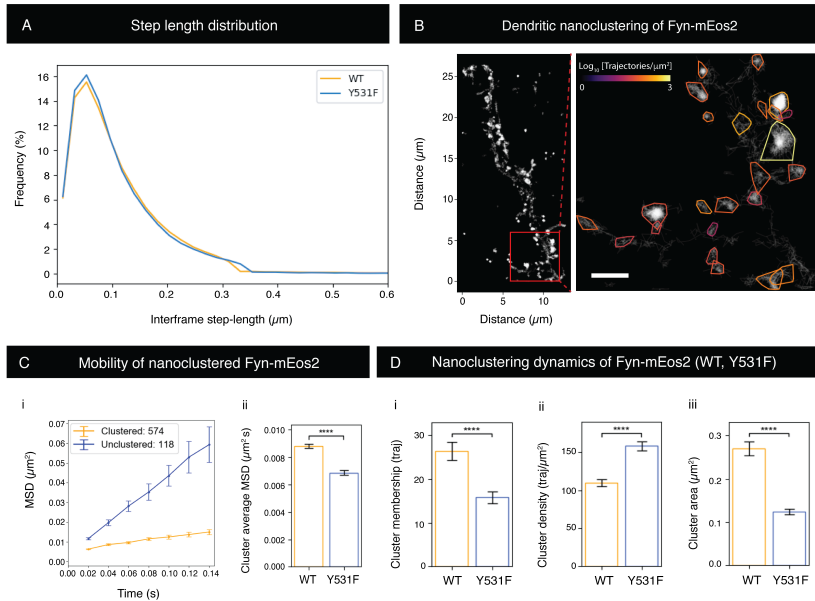


Figure 4

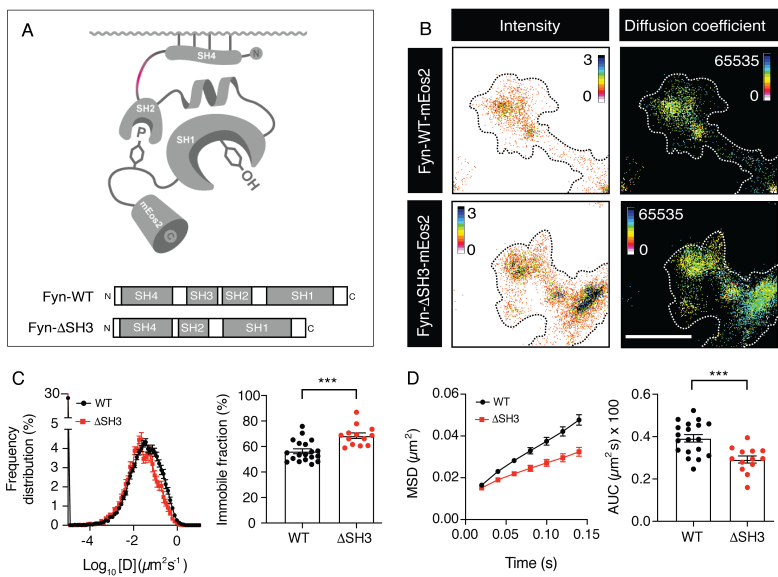


Figure 5

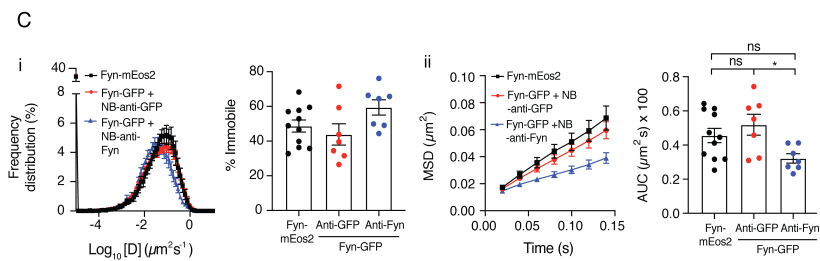
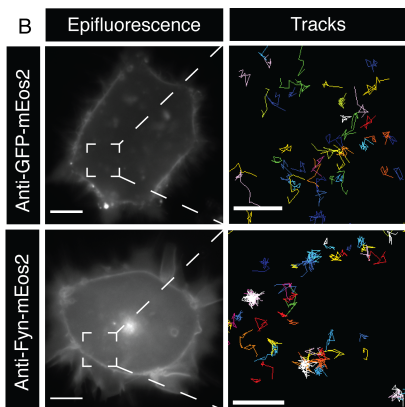
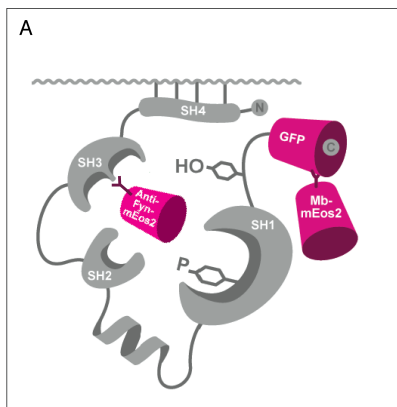


Figure 6

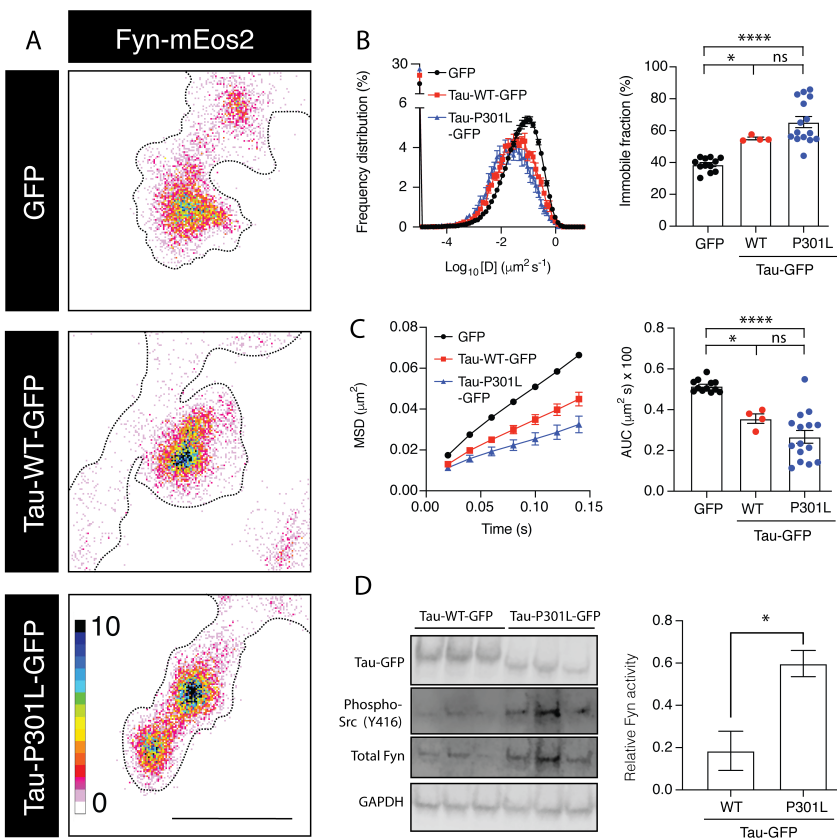


Figure 7

Hypothetical model: tau P301L controls the conformation and mobility state of Fyn kinase

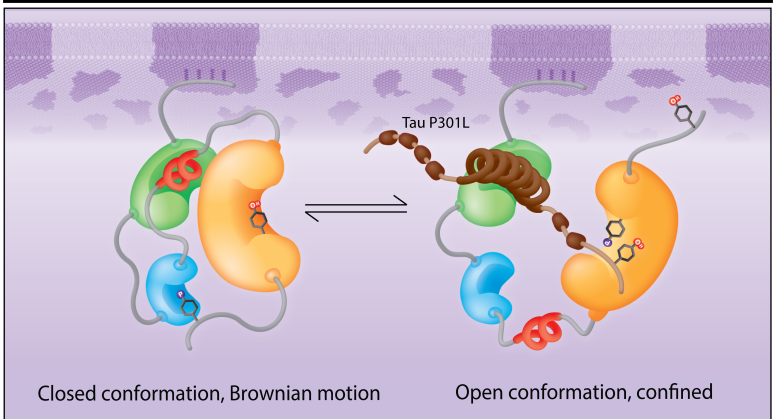


Figure 8