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CaMKII regulation in information processing and storage

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Abstract

The Ca²⁺/Calmodulin(CaM)-dependent protein kinase II (CaMKII) is activated by Ca²⁺/CaM, but becomes partially autonomous (Ca²⁺-independent) upon autophosphorylation at T286. This hallmark feature of CaMKII regulation provides a form of molecular memory and is indeed important in long-term potentiation (LTP) of excitatory synapse strength and memory formation. However, emerging evidence supports a direct role in information processing, while storage of synaptic information may instead be mediated by regulated interaction of CaMKII with the NMDA receptor (NMDAR) complex. These and other CaMKII regulation mechanisms are discussed here in the context of the kinase structure and their impact on post-synaptic functions. Recent findings also implicate CaMKII in long-term depression (LTD), as well as functional roles at inhibitory synapses, lending renewed emphasis on better understanding the spatio-temporal control of CaMKII regulation.

Keywords

CaMKII; NMDA receptor; Autonomy; Long-term Potentiation; Long-term Depression; Learning and Memory

Introduction

CaMKII has sparked the imagination of neuroscientists since its discovery [1, 2]. It is highly expressed in brain and is further enriched at excitatory synapses and their post-synaptic densities (PSDs). Moreover, its stimulation by Ca²⁺/CaM can also generate Ca²⁺-independent autonomous activity that outlasts this initial stimulus [2–4]. Thus, CaMKII is ideally poised to mediate the induction and maintenance of synaptic plasticity underlying learning and memory. Indeed, CaMKII can mediate LTP of excitatory synapse strength [5–9], both by increasing the number of synaptic AMPA receptors (AMPA receptors) [10–12] and their conductance [13–16] (see also [17–21]). Furthermore, knockout mice of CaMKII α , the major isoform in brain, were the first transgenic animals with a behavioral phenotype in learning and memory [22].

Over 25 years of research has firmly connected CaMKII with LTP of excitatory synapses (see Table 1), however, recent findings have expanded this traditional view: CaMKII is also

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required for post-synaptic mechanisms induced by excitatory LTD-stimuli, both for depressing excitatory synapses [23] and for potentiating inhibitory synapses [24, 25]. Further complicating the matter, at least some of the LTP- and LTD-mechanisms require CaMKII autophosphorylation at T286 [25–27]. Thus, the spatial and temporal control of CaMKII regulation in neurons has gained much renewed significance [28]. Despite recent advances on the regulation and structure of CaMKII [29–33], both areas still pose many unsolved riddles. Here, we discuss our current understanding of CaMKII regulation mechanisms in the context of the kinase structure and their role in synaptic functions, with a focus on the CaMKII α isoform. While pre-synaptic [34], pathological [35], cerebellar [36], and non-neuronal [30] functions of CaMKII are emerging, our discussion here is largely restricted to post-synaptic CaMKII mechanisms in hippocampal pyramidal neurons (where the functions of specific CaMKII regulation mechanisms in information processing and storage are understood best).

CaMKII isoforms, variants, subunits and holoenzymes

Four homologous CaMKII isoforms (α , β , γ , and δ) are encoded by separate genes, with alternative splicing in their variable linker domain generating additional diversity [2](Fig. 1a). Splicing can affect targeting and regulation. For instance, the minor splice variant α B contains a nuclear localization signal [37], and the developmental variant β e lacks the F-actin binding found for the major β isoform [38]. Additionally, variants with shorter linkers (such as the major α isoform) appear to be generally less sensitive to Ca²⁺-stimulation [31, 39, 40]. All isoforms are expressed in brain, and CaMKII β and δ are prominent in the cerebellum [36, 41]. However, α and β make up the vast majority of neuronal forebrain CaMKII, with an α : β ratio of ~3:1 and together constituting >1% of total protein [2–4].

CaMKII holoenzymes are formed by 12 subunits via their C-terminal association domains, with the N-terminal kinase domains radiating outward (Fig. 1a,b). This principle arrangement (first visualized 30 years ago [42]) is now well supported by increasingly precise reconstructions based on electron microscopy (EM) and partial crystal structures [31, 32, 43–46]. Lack of any apparent isoform preference in this assembly should lead to mainly heteromeric holoenzymes, with accordingly mixed regulatory and targeting properties [39, 47]. However, formation of CaMKII β homomers is enabled in inhibitory hippocampal interneurons by lack of CaMKII α expression [48, 49]. Formation of CaMKII α homomers in excitatory hippocampal pyramidal neurons is enabled by dendritic localization and translation of only the CaMKII α but not β mRNA [41, 50–52] and by the lack of CaMKII β in a subset of individual neurons [39]. Dendritic translation can be enhanced by neuronal stimulation [53], which may thus specifically increase CaMKII α homomers. Once formed, CaMKII holoenzymes appear to be quite stable, however, subunit exchange has been observed - at least *in vitro* - after cleaving off the kinase domains [44]. Little is known about cellular CaMKII protein turnover and its regulation, but neuronal activity did not significantly affect the ~24 h CaMKII half-life measured in synaptosomes from cortical cultures [54]. However, CaMKII can affect degradation of other synaptic proteins by activating the proteasome and targeting it to spines [55, 56].

Structure and regulation of the CaMKII subunits

Stimulated and autonomous CaMKII activity

Activity of each CaMKII subunit is stimulated individually by direct binding of Ca²⁺/CaM to their regulatory domains (Fig. 1c–e; see also Fig. 3a)[1, 2]. Autophosphorylation at T286 within the regulatory domain transforms CaMKII from one of the lowest to one of the highest affinity CaM binders within the cell [57]. This autophosphorylation also generates autonomous (Ca²⁺-independent) kinase activity. However, contrary to common perception,

such autonomous CaMKII is not fully active, but can instead be significantly further stimulated by $\text{Ca}^{2+}/\text{CaM}$ [29] (Fig. 2). *Vice versa*, T286 phosphorylation also further enhances $\text{Ca}^{2+}/\text{CaM}$ -stimulated activity, albeit to a much lesser extent [58] (Fig. 2). This mechanism still enables molecular memory of past stimulation by autonomous activity, but also prevents complete uncoupling from subsequent Ca^{2+} -signaling. On a molecular level, this indicates a more extensive opening of an inhibitory gate by $\text{Ca}^{2+}/\text{CaM}$ -binding than by T286 phosphorylation alone. The main regulatory effect of the inhibitory gate of CaMKII is to restrict substrate access (although $\text{Ca}^{2+}/\text{CaM}$ also enhances ATP binding and *vice versa*) [2].

Indeed, the regulatory domain blocks the substrate binding site of the CaMKII kinase domain in crystal structures of its basal state [31, 32, 43]. The short regulatory domain is held in place in part through interaction of its N-terminal region around T286 (T286-region) with the T-site, which is located next to the substrate binding S-site on the kinase domain (Fig. 1e). $\text{Ca}^{2+}/\text{CaM}$ -binding to the C-terminal part (CaM-region) of the regulatory domain removes the S-site block, and T286 autophosphorylation prevents complete re-binding of the regulatory region even after dissociation of $\text{Ca}^{2+}/\text{CaM}$. As indicated by an initial structure [59], any part of the regulatory domain can be in a helical conformation. However, recent evidence suggests that only the T286-region is helical in the basal state, while only the CaM-region is helical upon stimulation [32, 33, 60] (Fig. 1d). Such structural transition was also observed in solution [60] and may contribute to the tight regulation of CaMKII activity (~1000fold stimulation by $\text{Ca}^{2+}/\text{CaM}$ over basal activity; Fig. 2). In contrast to the basal state, much less structural information is available for activated CaMKII. One crystal structure of an activated CaMKII [32] provides information about the $\text{Ca}^{2+}/\text{CaM}$ -interaction, the T286 phosphorylation reaction (by a neighboring subunit, see below), and a structural shift of the first helix in the large lobe of the kinase domain (helix D). However, the principal positioning of the regulatory domain in stimulated or autonomous CaMKII remains unclear.

Two new mechanisms for generating autonomy

Two additional mechanisms can generate autonomous CaMKII activity, albeit to a lower level compared to T286 autophosphorylation: (i) oxidation of M281/M282 in CaMKII β (C280/M281 in CaMKII α) [30] and CaMKII binding to the NMDAR subunit GluN2B [61]. M281/M282 are located at the hinge between the kinase and regulatory domains (Fig. 1c–e), and in the oxidized state appear to prevent complete closing of the inhibitory gate. CaMKII binds to GluN2B via its T-site [61, 62] (Fig. 1e), which keeps the regulatory domain displaced, but may also partially impede substrate access [61, 63]. Such a mechanism was described also for CaMKII binding to the neuronal connexin-36 [64] and proposed for binding to the kinesin KIF17 [65]. Both mechanisms (T-site binding and oxidation) require an initial $\text{Ca}^{2+}/\text{CaM}$ stimulus, likely in order to make the relevant residues accessible for modification or interaction. Thus, in the presence of ATP (~4 mM within cells), such $\text{Ca}^{2+}/\text{CaM}$ stimuli should simultaneously trigger generation of higher level autonomy by T286 autophosphorylation. However, the additional mechanisms may enable maintenance of lower level autonomy even after de-phosphorylation of T286.

Forms of completely $\text{Ca}^{2+}/\text{CaM}$ -independent activation

Without requirement of any Ca^{2+} or CaM, CaMKII can be directly activated by gangliosides (especially GT1b), Zn^{2+} [2], or α -actinin [66], at least *in vitro*. Interestingly, α -actinin selectivity stimulates phosphorylation of CaMKII substrates that bind to the T-site (demonstrated only for GluN2B), though not as effectively as does $\text{Ca}^{2+}/\text{CaM}$ [66]. Since α -actinin competes with $\text{Ca}^{2+}/\text{CaM}$ for binding to CaMKII [63], its net effect in presence of

$\text{Ca}^{2+}/\text{CaM}$ is inhibitory for all substrates [63, 66], in addition to participating in mechanisms of substrate selection [29, 66].

Negative regulation of CaMKII activity

Negative regulation of CaMKII activity can be achieved by α -actinin (see above [63, 66]), by the inhibitory protein CaM-KIIN [67–69], or by T305/306 autophosphorylation [70–72]. Similar to GluN2B, binding of the CaM-KIIN α or β isoforms (which share almost identical inhibitory regions [67–69]) to CaMKII involves the T-site of the kinase [33, 73], and thus, prior displacement of the CaMKII regulatory domain is required. However, in contrast to GluN2B, CaM-KIIN binding completely blocks substrate access [33, 69]. CaM-KIIN can be regulated by its expression level [74] and possibly by phosphorylation [69].

The T305/306 residues are located within the CaM-region of the regulatory domain, and a recent crystal structure [32] supports prior biochemical findings that T305/306 phosphorylation inhibits CaM-binding and the notion that, *vice versa*, CaM-binding inhibits T305/306 phosphorylation [2, 71, 72] (see Fig. 1d). As a result, efficient T305/306 autophosphorylation should require autonomous CaMKII with no bound CaM. Indeed, dissociating CaM from T286-phosphorylated CaMKII triggers T305/306 autophosphorylation [71, 72], however, with a reaction rate likely still >100-fold slower compared to the fast ($\sim 12 \text{ sec}^{-1}$) autophosphorylation at T286 [75]. The resulting state of the kinase would be autonomous but without the ability to be further stimulated (Fig. 2). By contrast, making CaMKII autonomous by GluN2B binding inhibits T305/306 autophosphorylation, even after T286-phosphorylation and in absence of CaM [61] {whereas CaMKII binding to calcium/calmodulin-dependent serine protein kinase (Cask) instead promotes T305 phosphorylation [76]}. Protein phosphatases PP1, PP2A and PP2C can dephosphorylate CaMKII (including at T286 to reverse autonomy). This is likely dependent on the subcellular localization [77–80] and with GluN2B binding partially protecting T286, at least from PP1 [81]. As GluN2B-binding also directly increases CaM-affinity [61], the GluN2B-bound form may be the most readily $\text{Ca}^{2+}/\text{CaM}$ -stimulated pool of CaMKII within a neuron.

Regulation within the CaMKII holoenzyme

Frequency detection by T286 autophosphorylation

The holoenzyme assembly (Fig. 1b) has at least one profound effect on CaMKII regulation: T286 autophosphorylation occurs as an inter-subunit reaction within the holoenzyme, which makes it independent of the CaMKII concentration [2]. Importantly, $\text{Ca}^{2+}/\text{CaM}$ -binding has a dual role in this reaction: It is required not only for activation of the subunit acting as the kinase, but also for making T286 accessible on the neighboring subunit acting as the substrate [82, 83] (Fig. 3a). Indeed, this mechanism is supported by the CaMKII structure, which indicates inaccessibility of T286 in the basal state (see Fig. 1e). As a consequence, and in contrast to earlier models, the molecular memory provided by T286 phosphorylation should be relatively short-term: It is fully erased by phosphatases, as rephosphorylation even by a still autonomous neighboring subunit is possible only upon re-binding of $\text{Ca}^{2+}/\text{CaM}$.

Another more intriguing consequence of this dual role of CaM is the decoding of stimulation frequencies by T286 autophosphorylation (Fig. 3b). During sub-maximal low frequency stimulation, some CaMKII subunits within a holoenzyme are activated by $\text{Ca}^{2+}/\text{CaM}$ -binding during the Ca^{2+} -spikes, and inactivated by $\text{Ca}^{2+}/\text{CaM}$ -dissociation during the spike intervals. However, at higher frequencies (with the spike intervals within the range of the CaM dissociation time), $\text{Ca}^{2+}/\text{CaM}$ successively accumulates on the holoenzyme, which increases the chance of $\text{Ca}^{2+}/\text{CaM}$ -binding to neighboring subunits and in turn T286 autophosphorylation. Indeed, such frequency detection was measured in biochemical

experiments with purified CaMKII [31, 40, 47]. Taken together, these mechanisms make T286 autophosphorylation well suited for temporal decoding and for short- but not long-term storage of information.

Two inactive conformations and other holoenzyme-specific effects

Within CaMKII holoenzymes, Ca²⁺/CaM-stimulation of the individual subunits is cooperative, and several potential underlying mechanisms have been proposed [31, 33, 43, 60]. Intriguingly, a recent holoenzyme crystal structure (for CaMKII α without its 30 amino acid linker domain) shows a compact conformation in which each kinase domain folds back to directly interact with two association domains [31] (Fig. 4a). Clearly, this cannot be the only CaMKII α holoenzyme conformation, because the size is significantly smaller than observed previously (15 vs ~20 nm diameter) [31, 44, 45] and because the CaM-binding region is completely inaccessible in this conformation [31]. However, a mutation that prevents the compact conformation reduced the CaM cooperativity not only for the linker-less form, but also for CaMKII α wild type (at least under molecular crowding conditions that mimicked total cellular protein concentration)[31]. This indicates transition between two different inactive CaMKII holoenzyme conformations, one compact and one extended [31] (Fig. 4b,c). Only the extended conformation allows for Ca²⁺/CaM-binding, which in turn appears to promote also transition of neighboring subunits to this CaM-binding competent state [31]. Importantly, any mechanism that affects Ca²⁺/CaM-stimulation of a holoenzyme should contribute to shaping the frequency dependent response. Indeed, this notion is experimentally supported for factors related to the stimulus (spike amplitude and duration) or to the kinase (CaM affinity, autophosphorylation rate) [40, 47], and should also include factors regulating CaM cooperativity [31].

Beyond regulation of CaMKII activity, the various mono-valent protein-protein interactions of individual CaMKII subunits [79, 84] can become multi-valent interactions for CaMKII holoenzymes. Indeed, this appears to promote synaptic localization [62] and to enable crosslinking of binding partners [38, 85, 86], which in turn may contribute to non-catalytic structural functions of CaMKII [34, 87–89], as discussed later.

Function of T286 autophosphorylation in processing of information

A long-standing hypothesis proposed a function for CaMKII stimulation in LTP induction and for CaMKII autonomy in LTP maintenance. Indeed, maintaining the kinase activity that induced LTP [5, 6] should then also be sufficient to maintain the potentiated state, and this intuitive view is supported by experiments that introduced active CaMKII into postsynaptic neurons [90] and by T286A mutant mice [26]. However, recent studies reported that autonomous CaMKII is not fully active [29] and that CaMKII activation after LTP is quickly reversed (within ~1 min) [28]. Furthermore, tatCN21 (a CaM-KIIN derived peptide that inhibits stimulated and autonomous CaMKII activity with equal potency [27, 73]) did not affect LTP maintenance or memory storage/retrieval at concentrations sufficient to inhibit LTP induction and memory formation (5 μ M) [27]. Previous studies are consistent with this conclusion, but used inhibitors that affect autonomous activity less potently [5, 91]. In combination with studies using T286A mutant mice, which clearly indicated a role in LTP and learning/memory [26], the inhibitor studies strongly support a function of T286 autophosphorylation in mediating LTP induction and memory formation rather than LTP maintenance and memory storage. Such a role of CaMKII autonomy in processing rather than storage of synaptic information correlates very suggestively with the biochemistry of its regulation (see previous section): Like LTP, T286 autophosphorylation is more readily induced by high frequency stimulation (HFS) [40, 47]. However, T286 autophosphorylation is important also in other synaptic processes, and storage functions related to LTD and/or cross-synaptic communication remain to be elucidated (see below).

The CaMKII/NMDAR complex in storage of synaptic information

The tatCN21 inhibitor interferes not only with CaMKII activity but also with binding to the NMDAR subunit GluN2B [73]. However, in contrast to inhibition of phosphorylation of regular substrates, inhibition of GluN2B binding is competitive and likely occurs with a higher IC₅₀ [73]. Indeed, transient tatCN21 application persistently disrupts the CaMKII/NMDAR complex in hippocampal slices, but only at higher concentrations (20 μ M) and not at the lower concentrations (5 μ M) sufficient to block LTP induction [27, 92]. Importantly, only the treatment disrupting the CaMKII/NMDAR complex also persistently reduced synaptic strength [27, 92], indicating a direct function of the complex in storage of synaptic information. Only pharmacological treatments allow the temporal resolution required for distinguishing between induction and maintenance effects, but they also raise questions regarding target specificity. However, plausibility of a role for the CaMKII/NMDAR complex in synaptic information storage is supported by independent evidence. Specifically, mutating GluN2B to prevent its interaction with CaMKII impairs enhancement of synaptic strength [93, 94], and the amount of CaMKII localized at individual synapses directly correlates with their strength [95]. Furthermore, while synaptic localization and NMDAR binding of CaMKII are further increased by LTP-stimuli, basal levels of both (localization and binding) are also supported by basal neuronal activity [62, 96, 97]. Accordingly, disrupting the CaMKII/NMDAR complex reduced both potentiated and basal transmission [92]. Thus, while this type of synaptic information storage has a clear and direct link to LTP, it is not restricted to this form of plasticity.

NMDARs are composed of two GluN1 and two GluN2 (or GluN3) subunits. A partial developmental switch from GluN2B to GluN2A is known to be important in synapse maturation [98]. However, even in mature hippocampus, the vast majority of receptors appear to still contain a GluN2B subunit (in tri-heteromeric complexes of GluN1/GluN2A/GluN2B)[99]. CaMKII can bind to GluN1, GluN2A and GluN2B, but the interaction with GluN2B is by far the strongest, followed by the interaction with GluN1 [100–102]. Notably, while the cytoplasmic C-termini of GluN2B and 2A are homologous, their CaMKII binding-sites are not [79, 84]. The major CaMKII binding site on GluN2B (around S1303) [61, 100] is lacking in GluN2A, and this site appears to confer much of the subtype-specific functions [93, 98]. Additionally, CaMKII can bind to several other proteins within the NMDAR complex, including α -actinin, Synaptic Ras GTPase activating protein β (SynGAP β) and synapse-associated protein 97 (SAP97) [79, 84, 103]. It is presently unclear if and how tatCN21 may interfere with these additional CaMKII interactions, but mutating the major binding site on GluN2B was sufficient to reduce CaMKII association with the NMDAR complex (and LTP) to a similar extent as seen with 20 μ M tatCN21 [92, 94]. This indicates that GluN2B is indeed the functionally relevant CaMKII binding partner for maintenance of synaptic strength.

CaMKII, the synaptic tag, and other structural functions related to LTP

As LTP maintenance requires synthesis of new proteins that selectively strengthen only activated synapses but not their neighbors [21], some synaptic tag must enable differentiation between these synapses. Strong evidence indicates that CaMKII activation is required for this tagging [104–106]. CaMKII may induce structural changes that create the tag, be part of the tag itself, or both. CaMKII can induce structural changes by regulating the synaptic scaffolding proteins PSD95 [107, 108] and SAP97 [103, 109] and possibly directly by its interaction with the NMDAR complex (see above) and/or by aggregation of CaMKII holoenzymes into clusters [80, 110–112]. Another attractive structural tagging mechanism is by CaMKII-regulated changes in the spine actin cytoskeleton that indeed result in increased spine size after LTP [113, 114]. CaMKII regulation of actin can occur through regulation of

small GTPases [43, 115–118] and by direct actin-interactions of the CaMKII β isoform [38, 87, 119, 120].

At least some of the structural effects of CaMKII β on spine actin and spine size are independent of its kinase activity [87], and so are some effects of CaMKII α (which does not bind actin) on spine size [88]. Furthermore, hippocampal LTP is normal in mice with activation-incompetent CaMKII β , but impaired in mice that lack CaMKII β (or α) completely [89]. Activation-incompetent CaMKII β can still target α/β -heteromeric holoenzymes to the F-actin cytoskeleton [121], and only the mice with complete CaMKII β loss showed aberrant targeting of the α isoform [89]. Together, this evidence suggests a structural function of heteromeric CaMKII α/β holoenzymes in plasticity, with a physical link to the actin-cytoskeleton provided by the β -subunits and a physical link to PSD-proteins provided largely by the α -subunits.

CaMKII α can interact with a variety of proteins in the PSD, including various proteins in the NMDAR complex (as discussed above) and densin-180 [79, 84]. While GluN2B is currently the only known binding partner that is sufficient to mediate activation-induced synaptic translocation of CaMKII [61, 62], the additional interactions are likely important in shaping structure and function of the PSD protein assembly. Indeed, GluN2B binding alone does not appear sufficient to explain the CaMKII α -specific functions, as this binding is seen for all isoforms [62]. Other CaMKII interactions with the PSD may be α -specific, however, CaMKII β binding has been formally ruled out only for one binding site on densin-180 [86, 122]. While only GluN2B null mice, but not densin-180 null mice, show reduced general synaptic CaMKII α localization, both are impaired in CaMKII-mediated synaptic functions [94, 123].

Taken together, there is now strong evidence for both catalytic and non-catalytic functions of CaMKII in regulating synaptic plasticity. However, catalytic and non-catalytic functions are not as easily distinguished as it may seem at first glance: Some essentially purely structural functions can still require regulation by autophosphorylation and thus kinase activity [88]. Even autophosphorylation-independent structural functions can be regulated by Ca²⁺/CaM [38, 61, 87, 119] and thus be affected by inhibitors like KN93 or by mutations that prevent Ca²⁺/CaM binding. Inhibitors like AC3I or CN peptides directly block not only activity but also CaMKII binding to GluN2B or densin-180 [62, 73, 122]. Even the kinase dead CaMKII K42M mutant (nucleotide binding-incompetent) can report structural rather than catalytic functions, as nucleotide binding is not only required for activity but can also regulate CaMKII protein interactions, for instance with Cask, GluN2B and between CaMKII holoenzymes [76, 112, 124].

Beyond LTP: CaMKII functions in LTD-related mechanisms

Glutamatergic LTD-stimuli cause depression of excitatory glutamatergic synapses and potentiation of inhibitory GABAergic synapses in the same post-synaptic neurons, and CaMKII has recently been implicated in the regulation of both events [23, 24]. The specific CaMKII-mediated downstream signaling steps are currently unclear, but phosphorylation of the AMPAR subunit GluA1 at S567 is an attractive candidate for depressing glutamatergic synapses: Phosphorylation of S567 in loop 1 directly reduces spine localization of the channel [125] (in contrast to LTP-induced phosphorylation at S831 in the C-tail, which enhances channel conductance [14, 15]).

Both metabotropic glutamate receptor (mGluR)- and NMDAR- dependent LTD-stimuli trigger CaMKII autophosphorylation at T286 [23, 25]. The latter was shown to be necessary and sufficient for the NMDAR dependent potentiation of inhibitory synapses [25]. If T286 phosphorylation mediates both LTD- and LTP-mechanisms, then what determines the

opposing effects on synaptic strength? Such differentiation mechanisms could include selective inhibitory phosphorylation at T305/306 during LTD but not LTP. Indeed, overexpressing a constitutively autonomous CaMKII α mutant (T286D) directly induced either synaptic depression or potentiation, depending on if T305/306 phosphorylation was either mimicked (T305/306D) or prevented (T305/306A) by additional mutation [126]. Differential T305/306 phosphorylation would allow further stimulation and full activation of autonomous CaMKII only during LTP, and restrict CaMKII activity to the lower autonomous level during LTD [29] (see Fig. 2). Additionally, it may contribute to the regulation of CaMKII localization [102]. Intriguingly, while T286 autophosphorylation (like LTP) is promoted by HFS (see Fig. 3), T305/306 autophosphorylation (like LTD) should be promoted by low frequency stimulation with longer spike intervals that promote full dissociation of Ca²⁺/CaM, and thus, accessibility of T305/306. Notably, medium frequency stimulations (10 Hz) that did not change synaptic strength in wild type mice caused LTP in T305/306VA-mutant mice and LTD in T305/306D-mutant mice [127]. Additionally, while CaMKII functions in synaptic potentiation involve binding to GluN2B [92–94], functions in synaptic depression may instead require binding to densin-180, as mice lacking this protein are impaired for hippocampal LTD [123].

A pre-synaptic involvement of CaMKII in LTD has been described over 15 years ago [128]. By contrast, and despite several exciting hints described above, CaMKII in post-synaptic LTD is just emerging as a field of study.

CaMKII in global communication between different synapses and receptor systems

CaMKII can communicate the input information of glutamatergic LTD-stimuli to inhibitory synapses, both by increased CaMKII localization to these synapses and by increased GABA_A receptor surface expression [25]. CaMKII can also communicate input information by serotonin, dopamine, and Wnt signaling pathways to glutamatergic synapses. Specifically, CaMKII can mediate 5-HT_{1A} receptor induced suppression of NMDAR function [129], D4-type dopamine receptor-induced bidirectional regulation of AMPARs [127, 130], and Wnt7a-induced increase in spine size [131].

Additional mechanisms involving indirect synapse to synapse communication may occur by more global CaMKII regulation of neuronal functions. For instance, effects on dendritic shape and arborization have been observed that are mediated by CaMKII β - both by its association with F-actin [119] and the centrosome [132], although it should be noted that CaMKII β knock-out mice showed no impairments in dendritic arborization [89]. Additionally, CaMKII can regulate transcription and translation of a variety of genes [133, 134]. For excitation/transcription coupling, Ca²⁺-entry through L-type voltage-dependent Ca²⁺-channels is of special importance [135], and CaMKII can bind and modulate these channels [136, 137]. Finally, while CaMKII translocation to glutamatergic synapses can occur in an input-specific manner [97], a global spread of translocation after regional stimulation has also been observed [138]. Many of the regulatory mechanisms underlying such global effects and their functional consequences await further elucidation. However, CaMKII clearly plays an important role not only in local signaling at individual synapses, but also in more global neuronal signal processing and in synapse to synapse communication.

Directing neuronal plasticity by spatio-temporal regulation of CaMKII?

Traditionally, significant CaMKII T286 phosphorylation (and thus autonomy) was thought to be induced specifically by LTP-stimuli, and then to persist for hours (Fig. 5). Such a view

is supported by experimental evidence [139–141], however, may need to be reassessed in light of recent studies. For instance, a live-imaging study [28] that used a Fluorescence resonance energy transfer (FRET)-based sensor [142] to visualize CaMKII activity in individual spines found that LTP-stimuli induced a sharp rise in CaMKII activation that quickly decayed (with two time-constants of inactivation: 6 sec and 45 sec) [28]. Notably, a previous biochemical study has described a similar decay of autonomous CaMKII activity (Fig. 5), accompanied by decay of T286 phosphorylation [143]. While phospho-T286 immunodetection appeared to remain slightly elevated [143], the difference was not highly significant [143]. While autonomy appeared to decay faster than phospho-T286 immunodetection [143], a direct comparison would require quantification of the phospho-T286 levels [144], ideally at the same time points and in the same samples. Thus, while there is some indication for uncoupling of T286 phosphorylation from autonomous activity after LTP, this still requires further testing. Mechanistically, such uncoupling could be achieved by CaMKII binding to CaM-KIIN, which would block CaMKII activity even if T286 remains phosphorylated [27, 67]. However, this mechanism would not provide reconciliation: Inhibition by CaM-KIIN would still keep the CaMKII autoinhibitory domain displaced [33, 73] and the CaMKII FRET-sensor used in the imaging study [28, 142] should thus still report an active conformation. Reconciliation may be provided instead by LTP-induced increase of both autonomy (or T286 phosphorylation) and total CaMKII activity (or total CaMKII protein) found in biochemical [139] or histological [140] studies. The ratio of phospho-T286 over total CaMKII was found to remain persistently increased only in the soma, but not in dendrites [140], consistent with the fast reversal of CaMKII activity in spines seen by the recent imaging study [28].

By contrast, LTD-stimuli were traditionally thought to cause no significant CaMKII activation [139]. However, recent studies found a slow increase in T286 phosphorylation that peaked ~5 min after LTD-stimuli and then persisted at a lower level [23, 25](Fig. 5). Thus, while both LTP- and LTD-stimuli induce generation of autonomous CaMKII activity, the time course differs significantly (Fig. 5). As CaMKII autonomy is required in both LTP- and LTD-mechanisms [25–27], the opposing outcome on synaptic strength appears to be encoded by such temporal differences. The downstream mechanisms are unclear, but likely include secondary effects on CaMKII regulation, such as differential targeting and/or inhibitory autophosphorylation at T305/306.

Concluding remarks

While we now know many details about CaMKII, both regarding its complex regulation and its various neuronal functions, there is undoubtedly still much to be learned in both areas (Box 1). The most significant advances will likely come from tying together specific regulation mechanisms with specific signaling functions. This will require further elucidating the specific aspects of the complex regulation of CaMKII activity and localization that are engaged in response to different neuronal stimuli. Such information is bound to greatly enhance our understanding of the diverse and distinct functions of CaMKII in neuronal information processing and storage.

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Box 1. Outstanding Questions

- What is the CaMKII holoenzyme structure? Despite significant recent progress [31, 32], the CaMKII holoenzyme structure is known only for one of its inactive conformations. Structures of the activated states of CaMKII will be most meaningful within the holoenzyme structure, which is likely to determine degree of accessibility of the catalytic site.
- What are the differences in spatio-temporal CaMKII regulation after LTP versus LTD stimuli? Recent studies have clearly challenged the traditional view of CaMKII activation after LTP [28, 143] and LTD [23, 25]. However, more work is needed to support this new view, which will also impact our general understanding of the emerging functions of CaMKII beyond LTP at excitatory synapses.
- What mechanisms direct potentiation of excitatory versus inhibitory synapses by autonomous CaMKII? CaMKII functions in potentiating inhibitory synapses also require the T286 autophosphorylation [25], traditionally linked to potentiation of excitatory synapses. Both the differentiating mechanism and the principle downstream mechanisms causing inhibitory synapse potentiation are still unclear.
- What are the mechanisms for depression of excitatory synapses by CaMKII? Arguably, even the mechanisms for potentiation are still incompletely understood. The mechanisms for the new role of CaMKII in depression of excitatory synapses [23] are currently largely speculative.
- Does CaMKII also mediate depression of inhibitory synapses? As glutamatergic LTD-stimuli result in CaMKII-mediated depression of excitatory synapses [23] and potentiation of inhibitory synapses [25], then glutamatergic LTP-stimuli may also require CaMKII not only for potentiation of excitatory synapses but also for depression of inhibitory synapses.

Does T286 autophosphorylation store synaptic information related to LTD? In LTP, CaMKII autonomy appears to have largely an information processing function. However, storage functions in other situations, including in LTD, are unknown.

- Are there functional mechanisms to uncouple T286 autophosphorylation from autonomous activity? One study has suggested such an uncoupling after LTP [143], but this needs to be investigated in more detail. Such uncoupling could be mediated by CaM-KIIN, but the functions of this CaMKII-inhibitory protein are still unclear.
- What are the functions of T286-independent autonomy? CaMKII interaction with the NMDAR is important in regulating plasticity [92–94], however, it is still not clear if this involves the resulting autonomous activity [61] or if it is mediated solely by CaMKII targeting. Oxidation-induced autonomy [30] has yet to be studied in neurons.

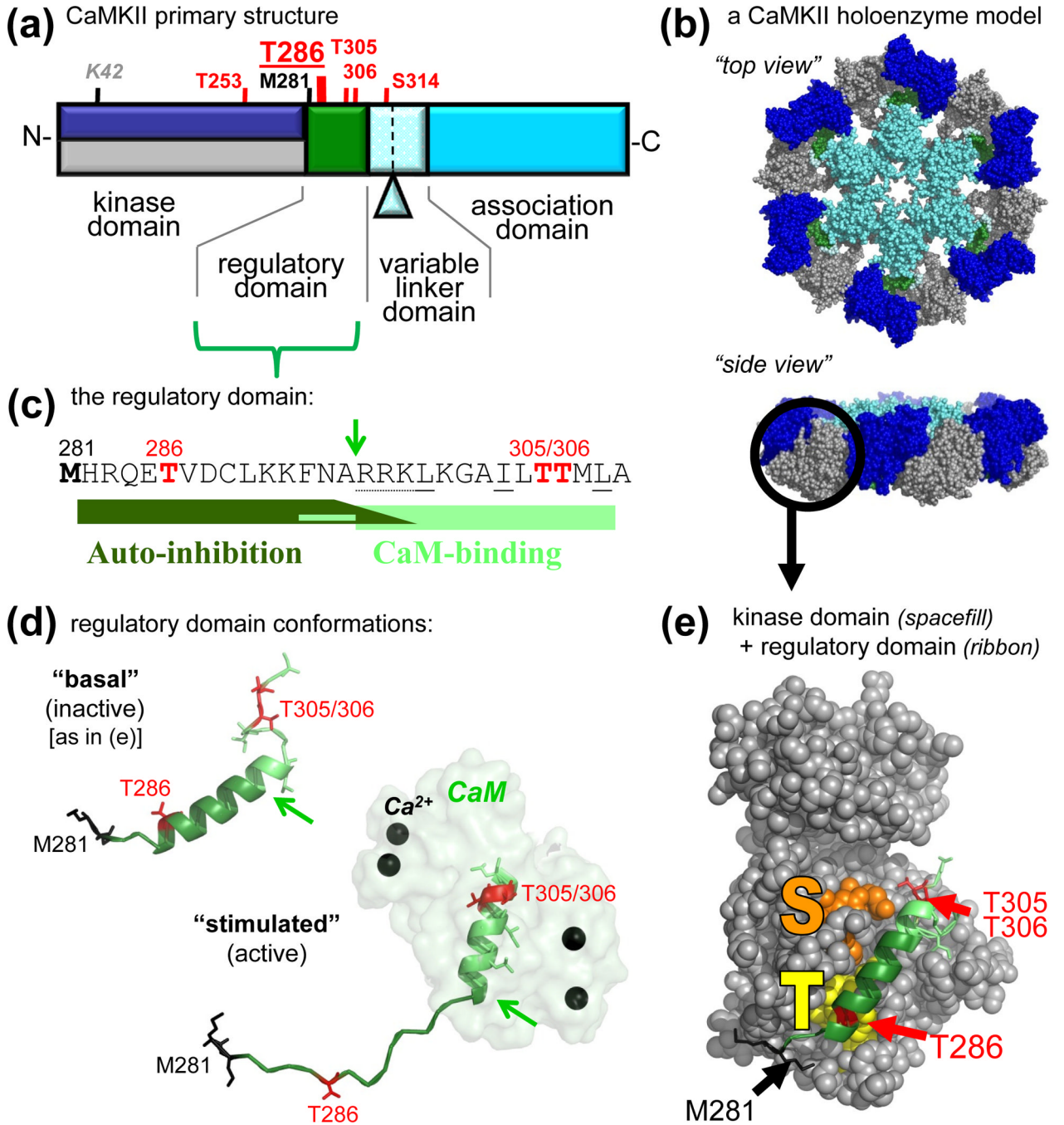


Figure 1. CaMKII structure and regulation. (a) Primary structure of CaMKII α , with an N-terminal kinase domain, followed by a CaM-binding regulatory domain, a variable linker domain (subject to alternative splicing, with the splice insert of α_B indicated), and a C-terminal association domain. Phosphorylation sites (red) and other important residues are indicated (see also Table 1). The other isoforms (β , γ , δ) contain an additional Thr after the third residues, and the numbers of their homologous positions are accordingly higher by one. These other isoforms also show more extensive alternative splicing in the variable domain, which is typically longer. (b) A model of a 12meric CaMKII holoenzyme (in two different view angles), based on several partial crystal structures [44, 46, 59], with the association

domains forming a central hub [44, 46], and the kinases domain [59] radiating outward. The 12meric nature, the particle size, and the principle arrangement is supported by EM studies [44, 45]; however, the precise positioning of the kinase domains in this holoenzyme conformation is unclear (but compare Fig. 4). The reconstruction was kindly provided by Drs. Chao and Kuriyan, and the image is adapted, with permission, from [35]. (c) Sequence of the regulatory domain. The autoinhibitory and CaM-binding regions are indicated. The arrow indicates the N-terminus of the core CaM-binding region (R296; also indicated by arrows in panel d); Ca²⁺/CaM trapping on the T286-phosphorylated form of the kinase also involves F293 [2]. Autoinhibition is maintained in a kinase 1-N294 truncation, but additional C-terminal residues participate in the substrate site block [2] (see also panel e). The oxidation (black) and phosphorylation (red) sites that generate autonomous activity (T286) [2, 29, 30] or inhibit CaM-binding (T306/306) [2, 70–72] are marked. (d) The regulatory domain in the basal (inactive) and stimulated (active) conformation, illustrating a structural transition of the different regions upon Ca²⁺/CaM binding [32]. The positioning relative to the kinase domain is known for the basal state (see panel e) but unclear for the active states. The region shown here for CaMKII δ is identical in CaMKII α . (e) Crystal structure of human CaMKII δ in its basal state, with the regulatory domain (ribbon) held in place in part by interactions with the T286 binding T-site (yellow) and blocking access to the substrate binding S-site (orange). The structural representations in panels d and e are based on Protein Data Bank (PDB) files 2VN9 and 2WEL [32].

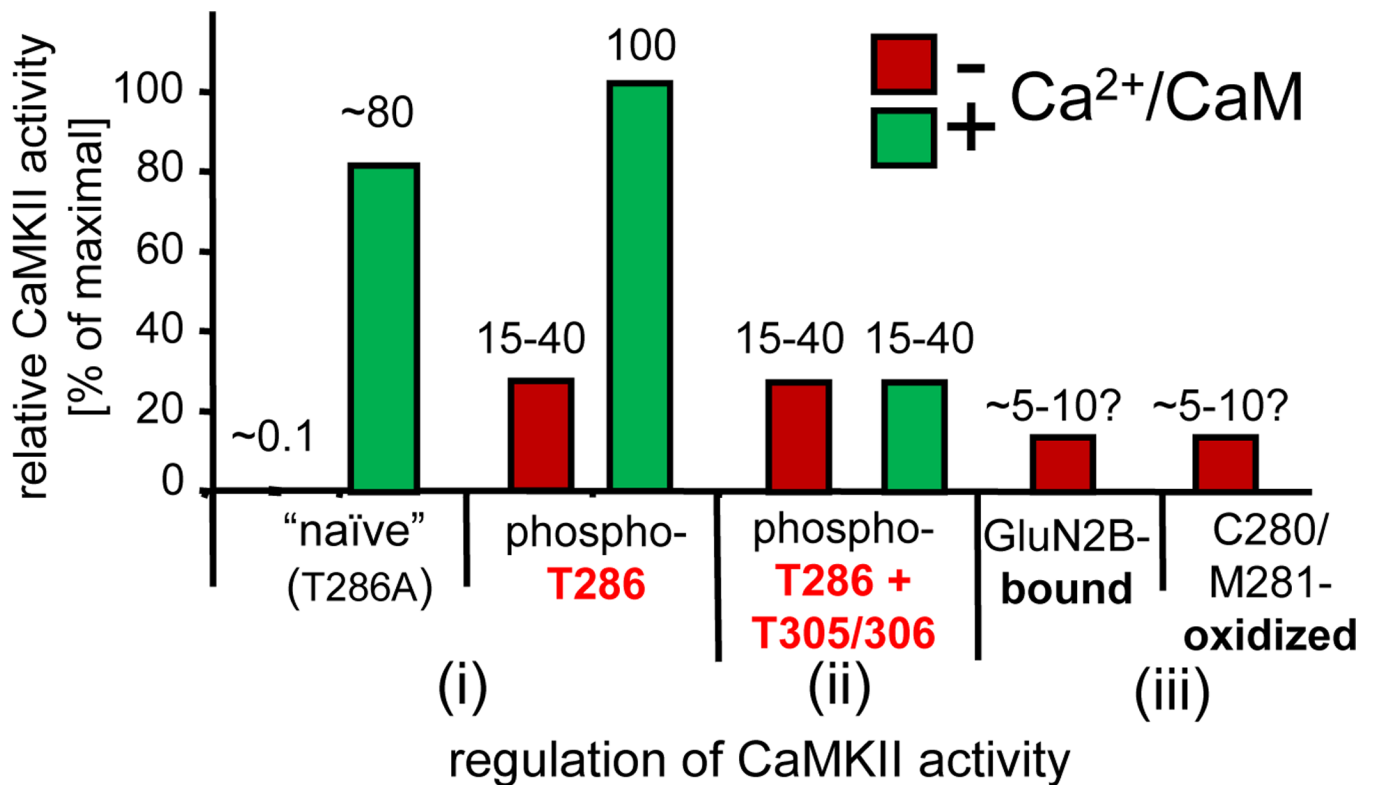
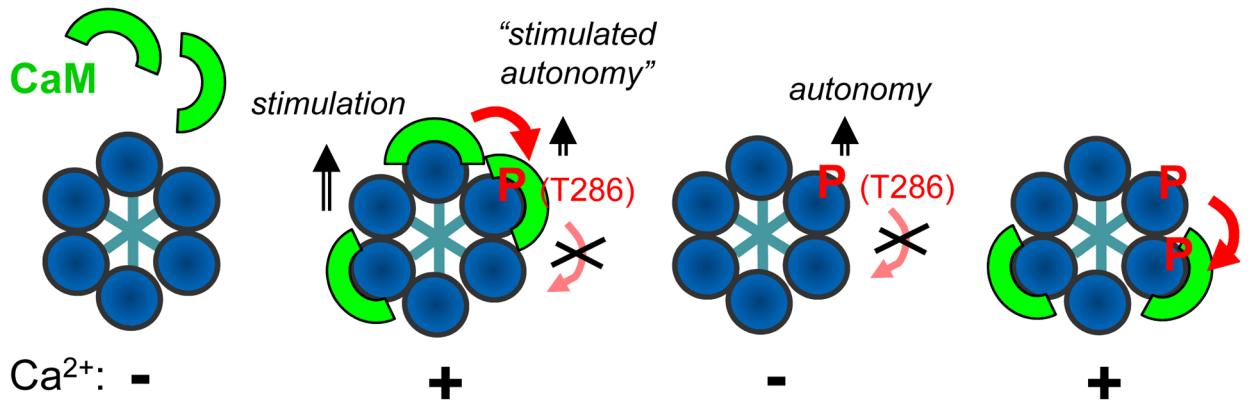
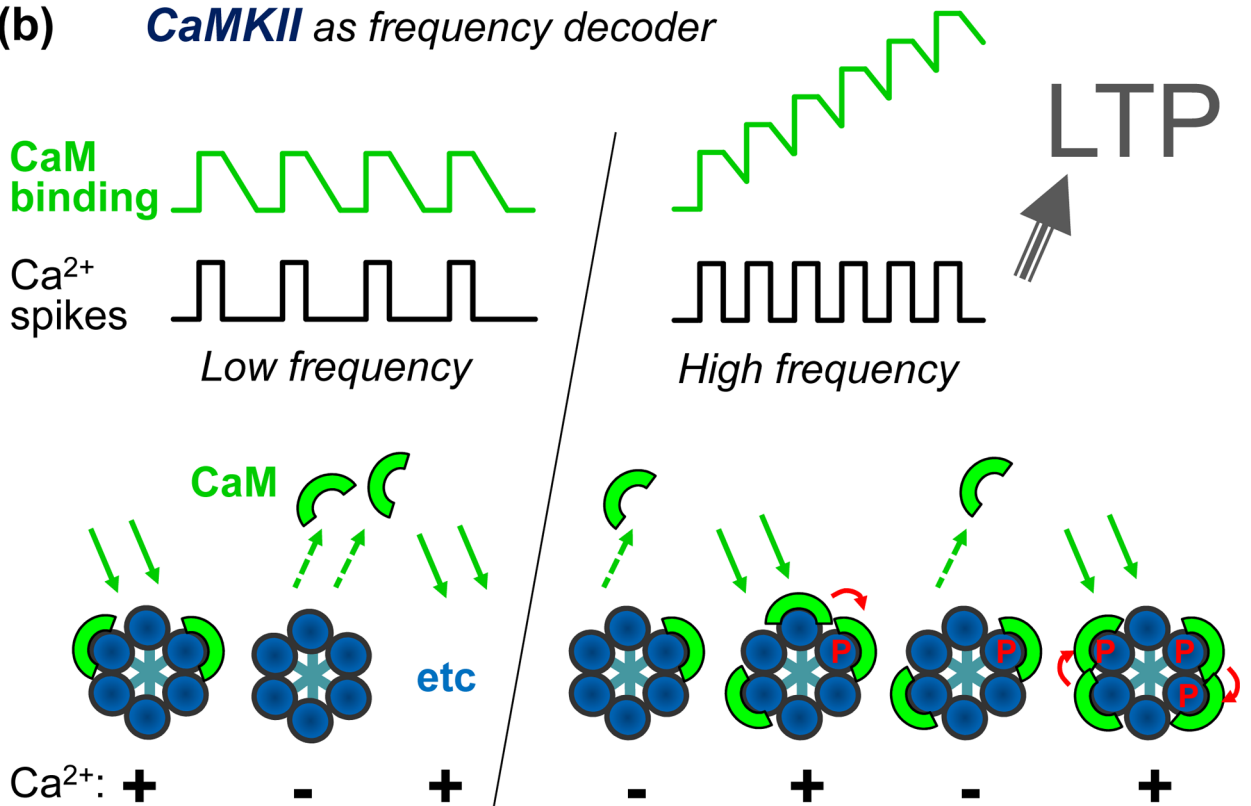


Figure 2.

Levels of CaMKII activity in response to different forms of regulation. (i) Naïve CaMKII shows only low basal activity (~0.1% of maximum), but is fully activated by Ca²⁺/CaM-stimulation [2]. This is accompanied by rapid T286-autophosphorylation; when T286-autophosphorylation is prevented by T286A mutation, the activity level remains slightly lower [58]. After T286-autophosphorylation, CaMKII remains partially active even after dissociation of Ca²⁺/CaM (autonomous), but this autonomous activity is significantly further stimulated by Ca²⁺/CaM [29]. (ii) T305/306-autophosphorylation of T286-phosphorylated CaMKII prevents Ca²⁺/CaM binding and thus further stimulation of the autonomous activity. (iii) Autonomous activity can also be induced by GluN2B binding [61] or by C280/M281 oxidation [30]; like T286-autophosphorylation, both mechanisms require an initial Ca²⁺/CaM-stimulus [30, 61]. The levels of “autonomy” (the ratio of autonomous over maximal CaM-stimulated activity) after GluN2B binding or oxidation are estimated adjustments (based on conditions in the original reports that overestimate autonomy, either by use of an autonomy-favoring substrate [29, 61] or by conditions resulting in unusually low rates of stimulated activity [30]). The activity estimates shown are based on an adapted compilation from [29, 30, 58, 61].

(a) *CaMKII stimulation and T286-autophosphorylation***(b) *CaMKII as frequency decoder*****Figure 3.**

Schematic representations of frequency detection by CaMKII autophosphorylation at T286. (a) Ca^{2+} /CaM-binding separately stimulates each individual subunit of a CaMKII holoenzyme (only 6 of the 12 subunits shown in the schematic model). However, T286 autophosphorylation requires binding of two CaM molecules to two neighboring subunit, one to activate the subunit acting as kinase, the other to expose T286 for phosphorylation (see also Fig. 1e) on the neighboring subunit acting as substrate in this intra-holoenzyme inter-subunit reaction [82, 83]. Phospho-T286 generates Ca^{2+} -independent “autonomous” activity (that can be further stimulated by Ca^{2+} /CaM; see Fig. 2). It can likely also substitute for the kinase-directed function of CaM in further autophosphorylation, but it cannot

substitute for the substrate-directed function of CaM [83]. (b) A simple model for frequency detection by T286 autophosphorylation. During submaximal Ca^{2+} -spikes, some CaM molecules bind to some subunits of a CaMKII holoenzyme, and then dissociate during the spike interval, and so on. However, at higher frequencies, with the spike interval in the range of the CaM dissociation time, additional CaM molecules accumulate before all of the initial CaM molecules dissociate. This increases the chance of CaM binding to neighboring subunit and thus autophosphorylation at T286. Such a frequency-dependent response was found in biochemical studies [40, 47], and suggestively correlates with the requirements for LTP induction, which is favored by HFS and has been shown to depend on CaMKII autonomy [26, 27].

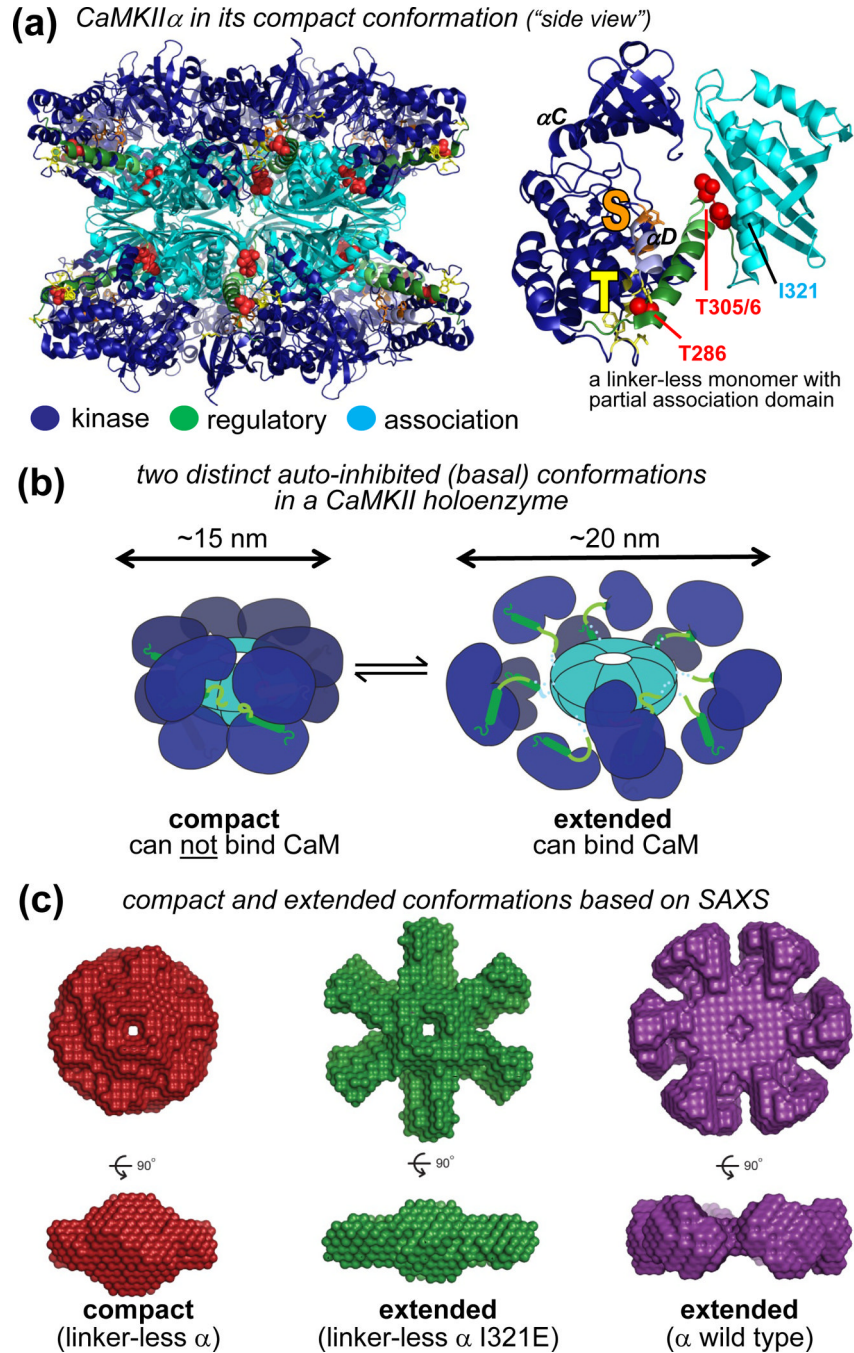


Figure 4. Two distinct inactive conformations of the *CaMKII* holoenzyme: compact and extended. (a) The only current holoenzyme crystal structure (in a compact conformation) with accurate kinase domain positioning (left; PDB1 3SOA) [31] was derived from a monomeric linker-less *CaMKII α* with a partial association domain (right; PDB 3SOA) [31], together with the known structure of the association domain assembly [32, 44, 46]. (b) In a compact conformation, the kinase domains fold back to the association domains, leaving the CaM-binding regulatory domain inaccessible to stimulation (as depicted in the crystal structure in panel a) [31]. In an extended conformation, the kinase domains protrude further outward, making the regulatory domains accessible (compare to the model depicted in Fig. 1b). CaM-

binding to the extended conformation may, in turn, also favor transition of neighboring subunits to this CaM-binding competent extended conformation [31]. (c) Small-angle X-ray scattering (SAXS) analysis indicates that the I321E mutation in a linker-less CaMKII α that interferes with the interaction of the kinase domain with the association domain causes a transition from a compact (i) to an extended conformation (ii) [31]. This mutation reduces cooperativity of activation by CaM not only for linker-less but also for full-length CaMKII α (wild type, iii), at least under molecular crowding conditions that mimic cellular protein concentrations [31]. In SAXS analysis (without molecular crowding) the major CaMKII α isoform was found in the extended conformation [31]. All panels are adapted, with permission, from [31].

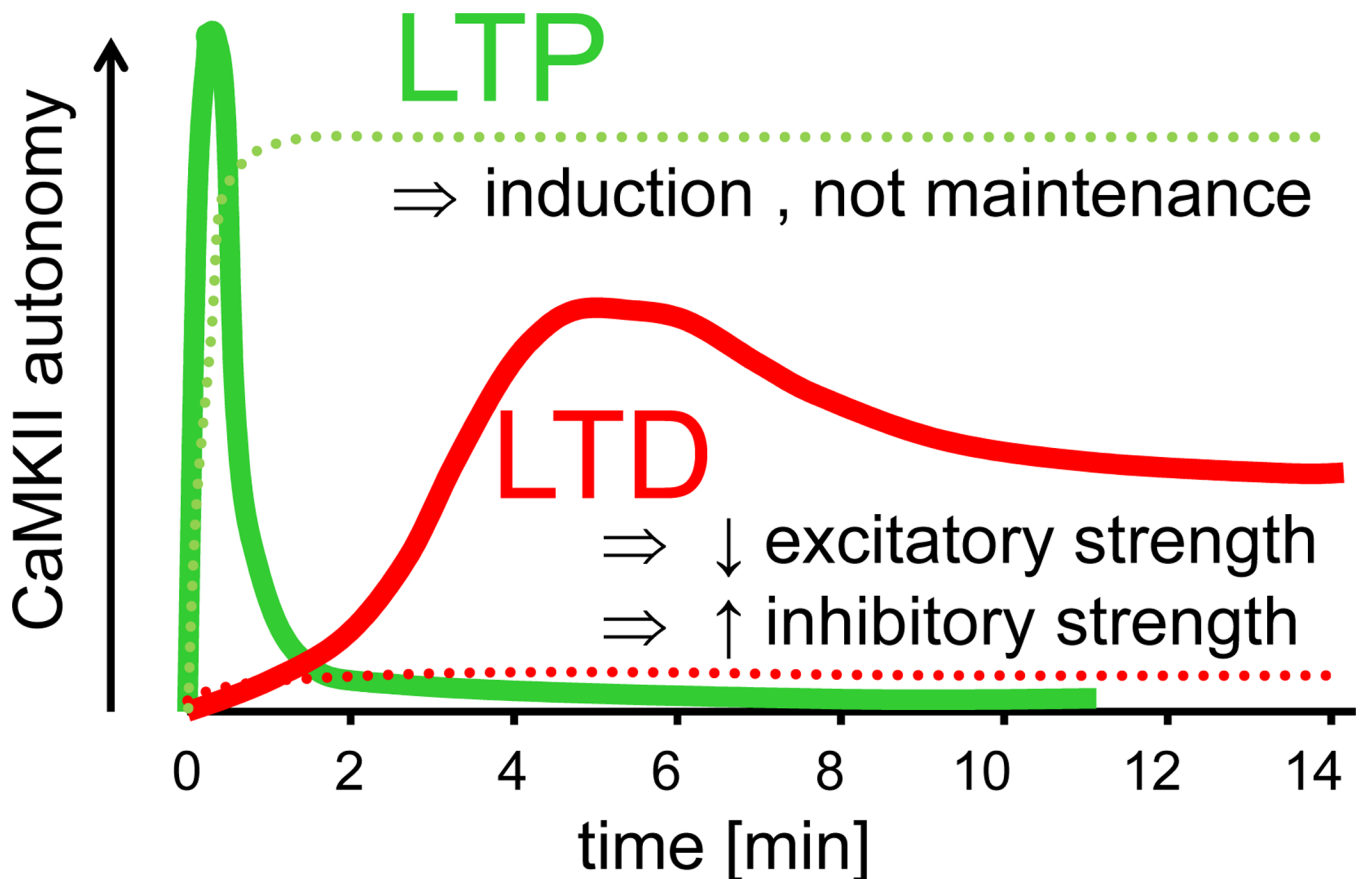


Figure 5.

Schematic diagram illustrating the time course of CaMKII autonomy after LTP (green) versus LTD (red) stimuli. The time course of CaMKII autonomy according to recent studies (solid lines) [23, 25, 28, 143] differs from the “traditional” perception (dotted lines) [139], but is consistent with a role of CaMKII T286 phosphorylation in LTP induction rather than maintenance [27], as well as with newly discovered functions in mechanisms induced by excitatory LTD-stimuli in hippocampal pyramidal neurons (depression of excitatory synapses [23] and potentiation of inhibitory synapses [25]). After LTP, the rapid activation of CaMKII in spines was found to decay with two time-constants (6 sec and 45 sec) [28], with the slower time-constant that is consistent with the decay of autonomy found in a previous biochemical study [143] illustrated here. The recent LTD-related studies assessed T286 phosphorylation after mGluR [23] or NMDAR [25] dependent LTD-stimuli, but found very similar time courses (with a peak at 5 min followed by persistence at a lower level, as illustrated here). The illustration represents an adapted compilation of the results of several studies [23, 25, 28, 139, 143]. The similarities between the two more recent studies related to LTP [28, 143] and LTD [23, 25] provide good estimates of the respective time course (as shown), however, a direct comparison between the absolute levels of peak autonomy after LTP versus LTD has not yet been made (and the relative peak levels shown are arbitrary).

Table 1
Manipulations that affect CaMKII function and their effects on hippocampal LTP and learning

(or) Protein/residue	Manipulation (or modification)	Biochemical effect (of the manipulation or the native residue)	Hippocampal LTP	Spatial Learning	Refs
CaMKII α	Inhibition	no activity	impaired	impaired	[5, 27]
	KO	no α isoform protein	impaired	impaired	[6, 22]
K42		<i>Required for ATP binding</i>	N/A	N/A	
S314	R or M	ATP binding impaired	impaired	impaired	[145]
	(Phosphorylation)	<i>Phos together with T305/306, but unknown function</i>	N/A	N/A	[70, 71]
T253	(Phosphorylation)	<i>Phos. enhances PSD association</i>	N/A	N/A	[146]
T286	(Phosphorylation)	<i>phos. generates autonomy; fast reaction (~12 sec⁻¹)</i>	N/A	N/A	[2, 29][75]
	A	no phos.; autonomy impaired	impaired	impaired	[26]
T305/306	D (regulated overexpression)	phos. mimic; constitutively autonomous	impaired	impaired	[147]
	(Phosphorylation)	<i>Phos. prevents stimulation by CaM; slow reaction</i>	N/A	N/A	[70-72]
CaMKII β	A/V or A/A	no phos.; always stimutable	facilitated	impaired "unlearning"	[127]
	D	phos mimic; no stimulation	impaired	impaired	[127]
GluN2B (T286)	(β -A303R)	prevents CaM binding; no stimulation	normal	normal	[89]
	KO	no β isoform protein	impaired	impaired	[89]
	L1298A/R1300Q or R1300Q/S1303D	impairs CaMKII binding to its major site on GluN2B	impaired	impaired	[93, 94]