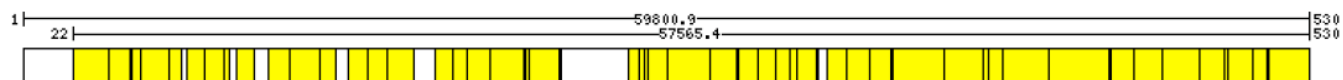
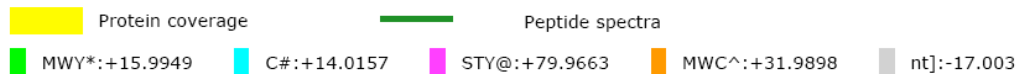


Supplementary figure 1. Detailed mass spectrometry analysis for CaMKII gamma C-1 autophosphorylation sites. The results shown are the result of a single microcapillary reverse-phase HPLC run, directly coupled to the nano-electrospray ionization source of an ion trap mass spectrometer. This instrument configuration is capable of acquiring individual sequence (MS/MS) spectra on-line at high sensitivity (<1 femtomole) for multiple peptides in the chromatographic run. These MS/MS spectra, (also referred to as CID, sequence or fragmentation spectra), are then correlated with known sequences using the algorithm Sequest developed at the Univ. of Washington and programs developed in by [17]. MS/MS peptide sequences are then reviewed for consensus with known proteins and the results manually confirmed for fidelity.

Supplementary figure 2. Sites of autophosphorylation. Sites of autophosphorylation of CaMKII gamma C-1 in the presence of $\text{Ca}^{2+}/\text{CaM}$ as determined by mass spectrometry are represented in blue with the residue number at the top. Residues described as phospho-sites in the literature and not found to be autophosphorylated here are also numbered.



Legend:



Supplementary figure 1

MATTATCTRFTDDYQLFEELGKGAF²⁶S²⁶VVRRRCVKKTSTQEYAA
KIINTKKLSARDHQKLEREARICRLLKHPNIVRLHDSISEEGFHY
LVFDLVTGGELFEDIVAREYYSEADASHCIHQILES²⁵⁴VNHHIQHDI
VHRDLKPENLLLASKCKGAAVKLADFG²⁶²LAI²⁸⁰EVQGEQQA²⁸⁷WFGF
AGTPGYLSPEVLRKDPYGKPV²⁶²DIWACGVILYILLVGYPPFWDE
DQHKLYQQIKAGAYDFPSPEWDTVTPEAKN²⁵⁴LINQML²⁸⁰TINPAKR
IT²⁶²ADQALKHPWVCQRSTVA²⁸⁰S²⁸⁰MMHRQET²⁸⁷VECLRKFNARRK²⁸⁷KLK
GAIL³⁰⁶TTML³⁰⁷VSRNFSA³¹⁵AK³¹⁹S³¹⁹LLNKKSDGGVKEPQTTVVHNATDGI
KGSTE³⁵⁰SCNTTTEDEDLKVRKQEIIKITEQLIEAINNGDFEAYTKIC
DPGLTSFEPEALGNLVEGMD³⁵⁰FHKFYFENLLSKNSKPIHTTILNPH
VHVIGEDAACIA³⁵⁰YIRLTQYIDGQGRPRTSQSEETR³⁵⁰VWHRRDGK
WLVN³⁵⁰VHYHCSGAPAAPLQ

Supplementary figure 2