Supporting Material

Figure S1: SDS-PAGE showing results of limited tryptic digest of αCaN in the absence and presence of CaM. The αCaN is protected from digestion by addition of CaM.

Figure S2: Deuterium uptake curves for RD-AID-CT peptides determined by HXMS. Different structured regions display distinct exchange kinetics. The horizontal dashed lines, where present, shows totally deuterated control exchange level, ^ denotes peptides used in the heat map, * indicates uptake curves constructed from incomplete data sets, δ shows ambiguous (isobaric) peptide assignment (see Table S1). Error bars were determined from two independent data sets.

Table S1: Ambiguous (isobaric) RD-AID-CT peptide assignments as indicated in Figure S6.

Residue Numbers	Sequence
377-412	LGSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSV
378-413	GSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVL
375-413	DELGSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVL
379-416	SEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVLREE
380-417	EEDGFDGATAAARKEVIRNKIRAIGKMARVFSVLREES
381-418	EDGFDGATAAARKEVIRNKIRAIGKMARVFSVLREESE
418-449	ESVLTLKGLTPTGMLPSGVLSGGKQTLQSATV
419-450	SVLTLKGLTPTGMLPSGVLSGGKQTLQSATVE
421-431	LTLKGLTPTGM
422-432	TLKGLTPTGML
421-495	LTLKGLTPTGMLPSGVLSGGKQTLQSATVEAIEADEAIKGFSPQHKITSF EEAKGLDRINERMPPRRDAMPSDAN
422-496	TLKGLTPTGMLPSGVLSGGKQTLQSATVEAIEADEAIKGFSPQHKITSFE EAKGLDRINERMPPRRDAMPSDANL
421-443	LTLKGLTPTGMLPSGVLSGGKQT
422-444	TLKGLTPTGMLPSGVLSGGKQTL
422-447	TLKGLTPTGMLPSGVLSGGKQTLQSA
423-448	LKGLTPTGMLPSGVLSGGKQTLQSAT

Residue Numbers	Sequence
450-455	EAIEAD
451-456	AIEADE
452-457	IEADEA
453-458	EADEAI
454-470	ADEAIKGFSPQHKITSF
460-476	GFSPQHKITSFEEAKGL
456-470	EAIKGFSPQHKITSF
457-471	AIKGFSPQHKITSFE
456-471	EAIKGFSPQHKITSFE
457-472	AIKGFSPQHKITSFEE
458-473	IKGFSPQHKITSFEEA
461-476	FSPQHKITSFEEAKGL