Supporting Information

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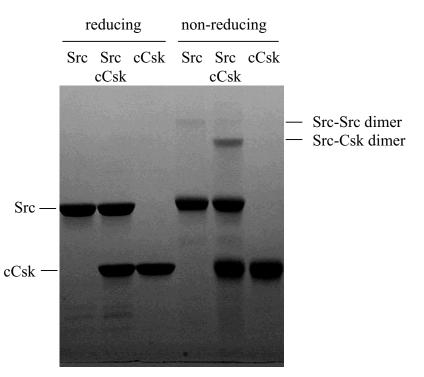


Fig. S1. Dimer formation between Src and catalytic domain of Csk. Src can form either a disulfide homodimer or a disulfide heterodimer with Csk. To determine which dimer is preferred, Src (10 μ g), the catalytic domain of Csk (cCsk, 10 μ g) or both (10 μ g each) were mixed in the presence of 1 mM DTT in 50 mM Tris (pH 8.0). The mixtures were then desalted on Sephdex G25 columns that were equilibrated with 0.1 mM H₂O₂ in 50 mM Tris (pH 8.0). The protein fractions were analyzed by SDS/PAGE under either reducing (20 mL/mL β -mercaptoethanol) or nonreducing (no β -mercaptoethanol) conditions. Under the reducing condition, no dimer was detectable in Src, cCsk, or the mixture. Under the nonreducing condition, a Src homodimer was visible in Src and the Src--CcSk mixture. Significantly more Src--CCSk heterodimer than Src-Src homodimer was detected even under the nonreducing condition. The catalytic domain of Csk, instead of full-length Csk, was used for this study so that the Src--Src homodimer and Src-CSk heterodimer could be distinguished by size. It is noted that the extent of Src dimer formation under these experimental conditions was not as prevalent as Src dimer formation when Src was directly purified under nonreducing conditions. It could be caused by interference by disulfide coupling between Src and DTT or incomplete removal of DTT.

Family	Kinase	Gly loop
Src	Src	GQGCFG
	Yes	GQGCFG
	Fgr	GTGCFG
	Blk	GSGQFG
	Brk	GSGYFG
	Frk	GSGQFG
	Fyn	GNGQFG
	Hck	GAGQFG
	Lck	GAGQFG
	Lyn	GAGQFG
FGFR	FGFR1	GEGCFG
	FGFR2	GEGCFG
	FGFR3	GEGCFG
	FGFR4	GEGCFG
Csk	Csk	GKGEFG
	Chk	GEGEFG
Ack	Ack	GDGSFG
	Tnk1	GSGCFG

Table S1. Comparison of the amino acid sequences in the Gly loop in selected families of PTKs

The Cys residues at the position equivalent to Src Cys277 are in bold. None of the other PTKs in the human kinome contain a Cys residue in this loop.

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