The Tyrosine Kinase c-Src Specifically Binds to the Active Integrin αIIbβ3 to Initiate Outside-in Signaling in Platelets*

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Background: β3-bound c-Src initiates outside-in signaling in platelets.

Results: After platelet stimulation, β3 binds to the c-Src SH3 domain at a site overlapping with its PPII helix binding site.

Conclusion: The interaction of c-Src with β3 requires c-Src activation to vacate the PPII helix binding site.

Significance: The mode of c-Src binding to β3 prevents c-Src-mediated signaling in circulating platelets.

It is currently believed that inactive tyrosine kinase c-Src in platelets binds to the cytoplasmic tail of the β3 integrin subunit via its SH3 domain. Although a recent NMR study supports this contention, it is likely that such binding would be precluded in inactive c-Src because an auto-inhibitory linker physically occludes the β3 tail binding site. Accordingly, we have re-examined c-Src binding to β3 by immunoprecipitation as well as NMR spectroscopy. In unstimulated platelets, we detected little to no interaction between c-Src and β3. Following platelet activation, however, c-Src was co-immunoprecipitated with β3 in a time-dependent manner and underwent progressive activation as well. We then measured chemical shift perturbations in the 15N-labeled SH3 domain induced by the C-terminal β3 peptide NITYRGT and found that the peptide interacted with the SH3 domain RT-loop and surrounding residues. A control peptide whose last three residues where replaced with those of the β1 cytoplasmic tail induced only small chemical shift perturbations on the opposite face of the SH3 domain. Next, to mimic inactive c-Src, we found that the canonical polyproline peptide RPLPPL prevented binding of the β3 peptide to the RT-loop. Under these conditions, the β3 peptide induced chemical shift perturbations similar to the negative control. We conclude that the primary interaction of c-Src with the β3 tail occurs in its activated state and at a site that overlaps with PPII binding site in its SH3 domain. Interactions of inactive c-Src with β3 are weak and insensitive to β3 tail mutations.

Platelet spreading on fibrinogen-coated surfaces and platelet-induced fibrin clot retraction are mediated by the integrin αIIbβ3 interposed between immobilized fibrinogen or fibrin and the platelet cytoskeleton and occur when αIIbβ3-initiated “outside-in” signaling causes platelet cytoskeletal contraction

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The c-Src SH3 domain also binds to the C-terminal Arg-Gly-Thr (RGT) residues of the β3 CT in an interaction that can be inhibited by proline-rich peptides selective for the SH3 domain (3). The C terminus of the β3 CT is quite different from the polyproline sequences usually recognized by SH3 domains (16, 17). Nonetheless, in a recent NMR study, Katyal et al. concluded that like polyproline helices, the CT of inactive c-Src is already occupied by the linker connecting the SH2 and kinase domains (14). Nonetheless, the interaction of c-Src with the sh3 domain of inactive c-Src (3, 20, 21).

**Experimental Procedures**

**Protein and Peptide Synthesis**—cDNAs corresponding to the human c-Src SH3 domain (residues Ala-83 to Ser-143) and the human c-Src SH4-SH3 domains (residues Met-1 to Ser-143) were cloned between the NdeI and XhoI restriction sites of the pET-28a vector (Novagen) such that they contained an N-terminal 6×His tag followed by a thrombin cleavage site. The cDNAs were then expressed overnight at 20 °C in BL21-Codon-Plus(DE3) cells (Agilent Technologies) induced with 1 mM IPTG and isolated from bacterial lysates by affinity chromatography using a HisTrap HP column (GE Healthcare) on an AKTApurifier 10 system. Following cleavage by thrombin to remove the 6×His tag, the recombinant proteins were purified by ion exchange chromatography. 7-mer peptides were purchased from Mimotopes.

**Immunoprecipitation and Immunoblotting of c-Src Bound to β3**—To measure the association of c-Src with β3 in unstimulated and stimulated platelets, human platelets obtained from blood anticoagulated at a ratio of 5:1 with ACD (sodium citrate 65 mM, citric acid 77 mM, glucose 95 mM, pH 4.4) were washed with 10 mM HEPES buffer, pH 7.35, containing 135 mM NaCl, 2.7 mM KCl, 3 mM EDTA, 1 μM PGE1, and 0.3 units/ml apyrase. The proteins were resuspended in modified Tyrode’s buffer (20 mM HEPES, pH 7.35, containing 135 mM NaCl, 2.7 mM KCl, 3 mM Na2HPO4, 5 mM glucose, 10 units/ml apyrase, and 0.1% BSA). 500-μl aliquots of the washed platelets were then stimulated with 1 unit/ml thrombin for up to 90 s and lysed with 125 μl of lysis buffer containing 1% Nonidet P-40, 50 mM Tris, 150 mM NaCl, and 1 mM EDTA. β3 and associated proteins were immunoprecipitated from lysates from equal numbers of platelets using integrin β3 (D-11) monoclonal antibody (Santa Cruz Biotechnology) and protein G magnetic beads (Millipore). The immunoprecipitated proteins were separated on 4–12% NuPAGE Bis-Tris gels (Life Technologies), transferred to nitrocellulose membranes (Life Technologies), and immunoblotted for phosphorylated c-Src residue 419 (pTyr419) with a pTyr419-specific antibody (Cell Signaling) followed by an incubation with horseradish peroxidase-conjugated anti-IgG. Protein-bound antibody was visualized using Enhanced Chemiluminescence (Amersham Biosciences). Membranes were then stripped of protein-bound antibody using Restore Western blot Stripping Buffer (Thermo Scientific), blocked with 5% nonfat dry milk (Bio-Rad) and immunoblotted again with either integrin β3 (D-11) or a c-Src-specific antibody (Cell Signaling).

**Surface Plasmon Resonance (SPR)—**All SPR experiments were performed on a Biacore 3000 (GE Healthcare). The c-Src SH4-SH3 domain protein was coupled to a CM5 SPR sensor chip using EDC/NHS. Injections of the C-terminal β3 CT peptide NITYRG and the class 1 PPII core peptide RPLPPLP (22, 23) were performed at a flow rate of 10 μl/min for 5 min in 20 mM HEPES buffer, pH 7.4, containing 150 mM NaCl. Each peptide was injected as a dilution series in concentrations ranging from 0 to 5 μM (0, 0.039, 0.078, 0.156, 0.313, 0.625, 1.25, 2.5, and 5 μM). The resulting sensograms were evaluated using
BIAsuccessful software and fitted to a 1:1 steady-state binding model.

Nuclear Magnetic Resonance (NMR) Spectroscopy—The
c-Src SH3 domain was labeled with $^{15}$N by bacterial expression
in M9 minimal media supplemented with $^{15}$N ammonium
chloride (Cambridge Isotopes). For titration of the SH3 domain
with the $\beta_3$ CT peptide NITYRGT, NMR data were collected at
20 °C on a Bruker DMX-600 spectrometer with a 5-mm $xy$-$z$-
shielded pulse-field gradient triple-resonance probe. Initially,
two NMR samples were prepared in 20 mM NaPO4 buffer, pH
6.0, containing 100 mM NaCl. One contained 1 mM $^{15}$N-labeled
SH3 domain only and the other contained 15.7 mM NITYRGT.
A series of titration experiments were then performed at
NITYRGT concentrations ranging between 5.4 mM and 15.7
mM. For titrations using the mutant $\beta_3$/β1 peptide NITYEGK
and RPLPPLP, ligands were prepared at 100 mM in 50 mM
NaPO4 buffer, pH 6.3, containing 50 mM NaCl. The stocks were
added into 0.33 mM $^{15}$N SH3 in 20 mM NaPO4 buffer, pH 6.0,
containing 100 mM NaCl at ligand concentrations of 0, 0.10,
0.30, 0.89, 1.09, 1.28, and 1.48 mM for NITYEGK, and 0, 0.02,
0.06, 0.12, 0.22, 0.42, 0.81, 1.40, and 2.17 mM for RPLPPLP,
respectively. For titration of NITYRGT in presence of RPLP-
PLP, 6 eq RPLPPLP (1.96 mM) was added into the 0.33 mM $^{15}$N
SH3 sample first, then 100 mM NITYRGT stock was added to
the sample to reach concentrations of 0, 0.10, 0.29, 0.88, 2.76,
4.58, 6.33, and 8.03 mM. Two-dimensional $^{15}$N-HSQC spectra
were recorded along $t_1(15N)$ and $t_2(1H)$, respectively, with 256
square bell window functions shifted by 90° and zero-filled
Fourier Transform, time domain data were multiplied by sine
functions of $2\pi f t$ to suppress sidebands and reduce the
magnitude of the central peak. The 2D spectra were calculated
using the method of Schumann et al. (26).

Results

c-Src Binding to $\beta_3$ in Platelets Increases Progressively follow-

ing $\alphaIIb\beta_3$ Activation—The putative $\beta_3$ CT binding site on the
SH3 domain of inactive c-Src is occupied by the linker connect-
ing the c-Src SH2 and kinase domains (13, 18). Nonetheless,
c-Src activity is stimulated after $\beta_3$ CT binding (3). Therefore,
we sought to understand how $\beta_3$ CT binding to c-Src regulates
its enzymatic activity. To begin to address this question, we
measured the time course of c-Src binding to $\beta_3$ and its subse-
cuential activation following platelet stimulation by thrombin.
Human platelets were isolated from platelet-rich plasma in the
presence of PGE1 to prevent factitious platelet activation dur-
ing the isolation procedure and were stimulated by 1 unit/ml
thrombin. The stimulated platelets were lysed with Nonidet
P-40, $\beta_3$ was immunoprecipitated from the lysates, and was
immunoblotted for c-Src and for phosphorylated c-Src residue
Tyr-419, an indicator of c-Src activation. As shown in Fig. 2,
there was little c-Src binding to $\beta_3$ in unstimulated platelets.
However, c-Src binding to $\beta_3$ was detectable within 10 s after
thrombin stimulation, reached a maximum at 30 s, and
decayed thereafter. Further, similar to the rapid and transient
c-Src activation that Clark and Brugge observed in detergent
extracts of thrombin-stimulated platelets (12), we detected the
phosphorylation of Tyr-419 of $\beta_3$-bound c-Src within 20 s fol-
lowing thrombin stimulation. Tyr-419 phosphorylation then
increased progressively, reaching a maximum at 60 s, after
which it also declined. Thus, these results indicate that the vast
majority of c-Src binding to $\beta_3$ occurs subsequent to $\alphaIIb\beta_3$
activation, after which the $\beta_3$-bound c-Src becomes enzymat-
ically active.

Measuring the Affinity of Peptide Ligands for the c-Src SH3
Domain—At a minimum, the c-Src binding site on $\alphaIIb\beta_3$
consists of the three C-terminal $\beta_3$ CT residues RGT (3). Accord-
ingly, we used SPR to compare the affinities of a $\beta_3$ C-terminal
heptapeptide NITYRGT and the canonical polyproline helix
heptapeptide RPLPPLP for a recombinant human c-Src SH3
domain immobilized on a CM5 SPR chip. As shown by the
equilibrium binding sensorgrams in Fig. 3, NITYRGT bound
weakly to the SH3 domain. Although NITYRGT binding did
not reach saturation, an estimated $K_d$ calculated using
BIAsuccessful software was 320 ± 120 mM. By contrast, RPLPPLP
binding to the SH3 domain was saturable and sub-
stantially stronger with an estimated $K_d$ of 259 ± 52 
M.

Detection of NITYRGT Binding to the c-Src SH3 Domain by
Two-dimensional NMR—To determine how the $\beta_3$ CT inter-
acts with c-Src, we turned to NMR, measuring NITYRGT bind-
ing to the c-Src SH3 domain labeled with $^{15}$N. Because our SPR
measurements indicated that NITYRGT binding to the SH3
domain was weak, we measured chemical shift perturbations
(CSP) induced by NITYRGT in the two-dimensional HSQC
spectrum of the SH3 domain, an NMR technique able to detect
and localize weak protein-protein interactions (27). CSP for
each SH3 domain residue, calculated using the relationship
$\Delta\text{ppm} = (\Delta^1H^2 + (\Delta^{15}N/5)^{1/2})$, were determined from
recorded HSQC spectra when we serially titrated NITYRGT at
concentrations up to 15.7 mM against a single 1 mM concen-
tration of the $^{15}$N-labeled c-Src SH3 domain. The interactions
appeared to be in fast exchange, as only shifts in peak location
were observed and peaks remained sharp and intense through-
out the course of the titration (Fig. 4, A and B).

The specificity of the CSP induced by NITYRGT is illustrated in
Fig. 4B, which compares the CSP of Leu-92 and Arg-98 as a
function of NITYRGT concentration. Although there were
essentially no CSP for Leu-92, there was a direct linear relation-
ship between the concentration of NITYRGT and the CSP
induced for Arg-98. Nonetheless, the titration of Arg-98 did not
reach saturation, and the majority of the NITYRGT was not
bound to the c-Src SH3 domain, even at 15.7 mM (Fig. 4C).
Under these conditions, $[\text{SH3}]_{\text{total}}$ approximates $[\text{SH3}]_{\text{free}}$ and
$[\beta_3]_{\text{total}}$ approximates $[\beta_3]_{\text{free}}$. Thus, the relationship $\Delta\text{ppm} =$
**c-Src Binding to β3 Integrin**

**A.**

<table>
<thead>
<tr>
<th>IP: β3</th>
<th>IB: β3</th>
<th>IB: c-Src</th>
<th>IB: c-Src pTyr419</th>
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**FIGURE 2.** A, time course of c-Src binding to the integrin β3 subunit and its subsequent activation after platelet stimulation by thrombin. Following the stimulation of washed human platelets by 1 unit/ml thrombin for the indicated times, platelets were lysed with 1% Nonidet P-40, β3 was immunoprecipitated (IP) from the lysates using a β3-specific monoclonal antibody, and the immunoprecipitated β3 was serially immunoblotted (IB) for β3, c-Src, and phosphorylated c-Src residue 419 (pTyr419). B, densitometry using NIH ImageJ software of the immunoblot shown in Fig. 2A demonstrating the time course of c-Src binding to the integrin β3 subunit and its subsequent activation after platelet stimulation by thrombin. The densitometry for β3-bound c-Src and for β3-bound c-Src containing phosphorylated tyrosine residue 419 (pY419) at each time point was normalized using the densitometry for the corresponding β3 band.

**B.**

<table>
<thead>
<tr>
<th>Normalized Densitometry Units</th>
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<td>Time after thrombin addition (sec)</td>
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**FIGURE 3.** Representative SPR measurements of steady state NITYRGT (A) and RPLPPLP (B) binding to the c-Src SH3 domain. Average dissociation constants ($K_d$), calculated using BIAevaluation software, from 9–12 steady state measurements, were $259 \pm 52 \mu M$ and $320 \pm 120 \mu M$ for RPLPPLP and NITYRGT, respectively.
\( \Delta \text{ppm}_{\text{max}} \times \left[ \frac{[\text{SH3}]_{\text{free}} 	imes [\beta_3]_{\text{free}}}{K_d \times [\text{SH3}]_{\text{total}}} \right] \) simplifies to \( \Delta \text{ppm} = [\beta_3]_{\text{total}} \times \left( \frac{\Delta \text{ppm}_{\text{max}}}{K_d} \right) \). The term \( \Delta \text{ppm}_{\text{max}} \) represents the change in chemical shift when the SH3 domain is fully bound by ligand. As saturation was not reached at the highest concentration, it is likely that the \( K_d \) is greater than 10 mM.

Further analysis of the NITYRGT titration results revealed fourteen SH3 domain residues [Glu-96, Ser-97, Arg-98, Thr-99, Glu-100, Thr-101, Asp-102, Leu-103, Asn-115, Asn-116, Glu-118, Ser-126, Gly-130, and Thr-132] with CSP exceeding the threshold of 2 standard deviations, indicative of specific protein-protein interaction (Fig. 4D) (27). The majority of these residues are located in the n-Src- and RT-loops, the specificity pocket, and in the region occupied by the linker connecting the SH2 and kinase domains in the compact structure of inactive c-Src (Fig. 4E). The largest CSP occurred in residues in or adjacent to the RT-loop, especially residues Arg-98 (0.25 ppm), Glu-100 (0.15 ppm), and Asp-102 (0.13 ppm). It is noteworthy that Asp-102, which forms a salt-bridge with the Arg of PPII helices (17, 28) has a significant chemical shift change, suggesting that Asp-102 also interacts with residue Arg-760 in the \( \beta_3 \) CT. On the other hand, there were minimal CSP for the aromatic residues Tyr-93, Tyr-95, Trp-122, and Tyr-139.

\textbf{Verifying the Specificity of NITYRGT Binding using the Mutant Peptide NITYEGK}—The \( \beta_1 \) integrin CT does not interact with the c-Src SH3 domain (3, 20, 21). Accordingly, to address the specificity of the interaction of NITYRGT with the SH3 domain, we repeated the NMR titration using the peptide NITYEGK in which we replaced the C-terminal three residues of NITYRGT with the corresponding residues of \( \beta_1 \). When the SH3 domain was titrated with NITYEGK, chemical shifts were perturbed for a completely different set of residues than when the titration was performed using NITYRGT (Fig. 5, A–C). There were no large CSP in or around residues 91–107, as was the case for NITYGRT; instead small, but statistically significant, CSP were seen in residues Gln-112, His-125, Ser-126, Gly-130, and Thr-132. These residues are located on the 2\textsuperscript{nd}, 3\textsuperscript{rd}, and 4\textsuperscript{th} strands of the SH3 domain, distant from the face of the SH3 domain that binds PPII ligands and NITYRGT (Fig. 5D). These results indicate that the negative control peptide

\begin{figure}
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\includegraphics[width=\textwidth]{figure4.png}
\caption{\textbf{The C-terminal \( \beta_3 \) peptide NITYRGT binds to the RT-Loop of the c-Src SH3 domain.} A, superimposition of HSQC spectra of 1 mM \( ^{15}N \)-labeled c-Src SH3 domain in the presence of 0, 5.4, 6.7, 7.5, 8.3, 9.2, 10.3, 12.6, and 15.7 mM NITYRGT. B, subspectra for c-Src SH3 domain residues Leu-92 and Arg-98 at NITYRGT concentrations of 0, 5.4, 6.7, 8.3, 9.2, 10.3, 12.6, and 15.7 mM. C, plot of CSP in ppm for residue Arg-98 as a function of NITYRGT concentration. D, CSP induced in each residue of the c-Src SH3 domain by 15.7 mM NITYRGT. The dotted line represents 2 standard deviations for CSP induced in the c-Src SH3 HSQC, determined by iteratively fitting the CSP to normal distributions as described by Schumann et al. (26). The calculated standard deviation of NITYRGT-induced CSP was 0.027 ppm. E, CSP induced by NITYRGT in the c-Src SH3 domain are color-coded by magnitude and mapped onto an NMR structure of the SH3 domain (PDB 1NLP).}
\end{figure}
NITYEGK fails to interact with the specific polypeptide binding site of the SH3 domain.

Comparing NITYRGT and PPII Peptide RPLPPLP Binding to the c-Src SH3 Domain—Because polyproline peptides selective for the c-Src SH3 domain blocked the interaction of the SH3 domain with the β3 CT in solid phase assays (3), we compared CSP induced in the c-Src SH3 domain by the class 1 PPII core peptide RPLPPLP with those induced by NITYRGT. Serial titration of RPLPPLP into a solution containing 15N-labeled SH3 caused significant CSP of up to 1 ppm in the SH3 HSQC spectra (Fig. 6A). Global fitting of CSP for Val-90, Leu-92, Val-114, Asn-115, and Ile-135, residues whose peaks were in the fast exchange mode as a function of RPLPPLP concentration and did not overlap with others, yielded a $K_d$ of 83 ± 27 μM for RPLPPLP binding to the SH3 domain binding, similar to the $K_d$ for RPLPPLP binding determined by SPR. Major CSP occurred in three regions: residues 98–103 (RT-loop), 117–122 (n-Src loop and specificity pocket including Trp-121 and Trp-122), and residues 137–138. It is noteworthy that the binding surface for RPLPPLP defined by CSP overlaps with that expected from the SH3 domain crystal structure, although negligible CSP patterns were observed for the aromatic cluster Tyr-93, Tyr-95, and Tyr-139 (Fig. 6B) (13, 17).

To directly compare the binding sites for NITYRGT and RPLPPLP on the c-Src SH3 domain, we normalized the CSP induced by each peptide by dividing the CSP for each residue by the CSP for Arg-98 whose chemical shift was perturbed by both peptides. There was extensive overlap in the CSP induced by NITYRGT and RPLPPLP (Fig. 6C). Further, the CSP for SH3 residues 83–113 were highly correlated ($R^2 = 0.87$) (Fig. 6D). Thus, both NITYRGT and RPLPPLP interact with residues located in the RT-loop of the SH3 domain, although RPLPPLP binds with substantially greater affinity.

Because of its relatively higher affinity, it is likely that RPLPPLP binding to the PPII binding site on the SH3 domain will block binding of the NITYRGT peptide. To demonstrate that this is the case, we mixed 0.33 mM 15N-labeled c-Src SH3 domain with 1.96 mM RPLPPLP (6 eq.) and serially titrated the mixture with NITYRGT at concentrations up to 8.03 mM. HSQC spectra were recorded, and CSP for each residue were calculated as described above. Under these conditions, CSP were induced by NITYRGT, but the chemical shifts for residues...
located in the RPLPPLP binding site were unperturbed (Fig. 7A). Instead, CSP was observed for residues that non-specifically interacted with NITYEGK (Fig. 7, B and C) with an essentially perfect correlation between the CSP induced by both peptides ($R^2 = 0.96$) (Fig. 7D). Thus, these results indicate that when the PPII binding site in the SH3 domain is occupied by a PPII helix, the β3 CT is unable to specifically interact with c-Src.

Discussion

αIIbβ3-mediated outside-in signaling in platelets appears to be initiated by c-Src bound to the β3 CT via its SH3 domain. However, when and how c-Src binds to β3 remains unclear, in particular since the ligand binding surface on the SH3 domain is already occupied in inactive c-Src (3) and the affinity of PPII helices for the SH3 domain is several orders of magnitude greater than that of β3. Here, we have addressed these questions, finding first that c-Src binding to β3, as well as c-Src activation, increase with time following platelet stimulation and second that the binding site for the β3 CT on the c-Src SH3 domain overlaps with the binding site for PPII helices.

Recently, Xiao et al. reported a crystal structure in which the tri-peptide RGT was bound to residues 119–122 in the n-Src loop of the c-Src SH3 domain (numbering according to UniProtKB/Swiss-Prot entry P12931) and speculated that by binding at this location, RGT might disrupt the intramolecular interaction between the SH3 domain and the linker between the SH2 and kinase domains (29). We found that both RPLPPLP and NITYRGT caused CSP in these residues, but the CSP were substantially smaller than those induced in residues 98–103 and those caused by NITYRGT were no longer present when the SH3 domain was occupied by RPLPPLP, implying that NITYRGT binding is not sufficiently strong to displace a PPII helix from the SH3 domain. Subsequently, Katyal et al. reported NMR and paramagnetic relaxation enhancement (PRE) studies that localized the β3 CT binding site in the SH3 domain to an extended interface consisting of residues in both the RT and n-Src loops, as well as an isolated interaction with Tyr-134 in the 4th β strand (18). Similar to our results, the largest CSP they detected involved residues 98–103 (numbering according to UniProtKB/Swiss-Prot entry P12931). Nevertheless, they focused their attention on residues 138–139, as well as residues 118–121 in the n-Src loop, because the PRE experiments suggested that the β3 C-terminal Thr binds in proximity to these residues. Further, in contrast to the data shown in Fig. 2, they concluded that the SH3 domain interacts constitutively with inactive αIIbβ3 because they did not detect CSP when the β3 CT was phosphorylated at tyrosine residues.

FIGURE 6. NITYRGT and the PPII core peptide RPLPPLP bind to the same region of the c-Src SH3 domain. A, CSP caused by the peptide RPLPPLP for each residue in the HSQC spectra of the 15N-labeled c-Src SH3 domain. The dotted line represents 2 standard deviations for RPLPPLP-induced CSP. The calculated standard deviation of RPLPPLP-induced CSP was 0.100 ppm. B, magnitude of CSP are color-coded and mapped onto an NMR structure of the c-Src SH3 domain (PDB 1NLP). C, superimposition of normalized CSP for RPLPPLP (blue) and NITYRGT (red, taken from Fig. 4). CSP were normalized by dividing the maximal CSP for each residue by the maximal CSP for Arg-98, a residue whose chemical shift was most perturbed by each peptide. D, correlation between the normalized CSP induced in c-Src SH3 domain residues 83–113 by NITYRGT and RPLPPLP ($R^2 = 0.87$).
747 and 759, phosphorylations that occur subsequent to αIIbβ3 activation (30).

Our SPR and NMR measurements of β3 CT binding to the c-Src SH3 domain indicated that the interaction is substantially weaker than had been reported previously when c-Src SH3 binding was measured to the β3 CT immobilized on a solid support. One possible explanation for this discrepancy is that we used the seven C-terminal β3 residues for our measurements, whereas the entire β3 CT was immobilized for the solid-state measurements (3). Nonetheless, it appears that the C-terminal β3 residues are sufficient to mediate binding to the SH3 domain (3, 18). A second possibility is that the increased affinity was a reflection of an increased avidity of dimeric GST-SH3 fusion proteins (3, 31). But the third and most likely possibility is that additional interactions contribute to the interaction of β3 with c-Src under physiologic conditions and were absent in our measurements. For example, sequences in the β3 CT adjacent to those essential for c-Src binding also recognize members of the kindlin and filamin protein families, and these proteins could cooperate to enhance c-Src binding. Further, we recently found that in solution, the β3 CT has weak affinity for the talin-1 FERM domain, whereas appending it to acidic phospholipids increased its affinity for the FERM domain by three orders of magnitude (19). Since all Src family kinases are myristoylated (32, 33) and c-Src contains a conserved patch of positively-charged Arg and Lys residues that are necessary for its binding to bilayers containing negatively-charged phospholipids (34), it is possible that the interaction of c-Src with β3 is a ternary interaction in which protein-lipid interactions play an important role. Lastly, in the presence of membranes, c-Src binding to β3 would be restricted to a 2-dimensional surface where binding partners have much higher probability of collision than in 3-dimensional space.

We found that the β3 CT peptide NITYRGRT binds to a site on the RT-loop of c-Src SH3 domain that includes residues 98–103 and that can also be occupied by the canonical polyproline II helical peptide RPLPPLP, although RPLPPLP binds to the site with significantly greater affinity (22, 23). CSP for acidic residues located in the RT-loop were particularly sensitive to the presence of NITYRGRT and were not present when we

![Figure 7](image-url)
replaced the C-terminal residues of NITYRGT with EGK. Thus, it is likely that the conserved Arg-760 makes an important contribution to NITYRGT binding, perhaps by forming a salt-bridge with SH3 domain residue Asp-102. We also detected overlapping CSP for NITYRGT and RPLPPLP for more C-terminal SH3 domain residues, but the magnitude of the CSP induced by NITYRGT were quite small, implying that the predominant binding site for CT encompasses SH3 domain residues 98–103 (27). This contrasts with PPII helices like RPLPPLP whose binding interface on the SH3 domain is much more extensive (17) and likely responsible for their substantially greater affinity for SH3 domain binding.

The model shown in Fig. 8, based on the results described above, illustrates the behavior of c-Src in unstimulated and stimulated platelets. In unstimulated platelets, inactive c-Src does not interact with inactive αIIbβ3 when the PPII helix binding on the SH3 domain is occupied. However, the very high concentrations of both proteins in platelets, as well as interactions with other partner proteins and with membranes would tend to co-localize c-Src to the vicinity of the SH3 domain (10, 34).

FIGURE 8. A proposed mechanism for αIIbβ3-mediated c-Src activation. In circulating platelets, where both αIIbβ3 and c-Src are present in their inactive conformations, there is no specific interaction between the β3 CT and c-Src. When platelets are stimulated, αIIbβ3 is activated, c-Src is extended, and the β3 CT is able to interact with the PPII helix binding surface of the c-Src SH3 domain that is no longer occupied by the linker between the SH2 and kinase domains. Activated αIIbβ3 then oligomerizes, enabling the trans-autophosphorylation of Tyr-419 responsible for c-Src activation.

activated αIIbβ3 then oligomerizes, enabling the trans-autophosphorylation of Tyr-419 in the activation loop of the c-Src kinase domain, the completion of c-Src activation, and the initiation of outside-in platelet signaling.

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