



HAL
open science

Structural recognition mechanisms between human Src homology domain 3 (SH3) and ALG-2-interacting protein X (Alix)

Xiaoli Shi, Stéphane Betzi, Adrien Lugari, Sandrine Opi, Audrey Restouin, Isabelle Parrot, Jean Martinez, Pascale Zimmermann, Patrick Lecine, Mingdon Huang, et al.

► To cite this version:

Xiaoli Shi, Stéphane Betzi, Adrien Lugari, Sandrine Opi, Audrey Restouin, et al.. Structural recognition mechanisms between human Src homology domain 3 (SH3) and ALG-2-interacting protein X (Alix). *FEBS Letters*, 2012, 586, pp.1759-1764. 10.1016/j.febslet.2012.05.017 . hal-00717171

HAL Id: hal-00717171

<https://hal.science/hal-00717171>

Submitted on 19 Sep 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Published in final edited form as:

FEBS Lett. 2012 June 21; 586(13): 1759–1764. doi:10.1016/j.febslet.2012.05.017.

Structural recognition mechanisms between human Src Homology domain 3 (SH3) and ALG-2-Interacting protein X (Alix)

Xiaoli Shi^{1,2}, Stephane Betzi¹, Adrien Lugari¹, Sandrine Opi¹, Audrey Restouin¹, Isabelle Parrot³, Jean Martinez³, Pascale Zimmermann¹, Patrick Lecine⁴, Mingdong Huang², Stefan T. Arold^{5,*}, Yves Collette^{1,*}, and Xavier Morelli^{1,*}

¹CNRS UMR 7258, INSERM U 1068, Centre de Recherche en Cancérologie de Marseille, Marseille F-13009, France; Institut Paoli-Calmettes, Marseille F-13009, France; and Aix-Marseille Université, Marseille, France

²State Key Laboratory of Structural Chemistry, Fujian Institute of Research on the Structure of Matter, Chinese Academy of Sciences, 155 Yang Qiao Xi Lu, Fuzhou, Fujian 350002, China

³Institut des Biomolécules Max Mousseron (IBMM), UMR 5247 CNRS–Université Montpellier 1–Université Montpellier 2, cc17-03, Place Eugène Bataillon, 34095 Montpellier Cedex 5, France

⁴Baylor Institute for Immunology Research, INSERM UMR899, 3434 Live Oak Street, Dallas, TX 75024, USA

⁵Department of Biochemistry and Molecular Biology, Unit 1000, The University of Texas MD Anderson Cancer Center, 1515 Holcombe Boulevard, Houston, TX 77030-4009, USA

Abstract

The functions of Src family kinases are tightly regulated through Src Homology (SH) domain-mediated protein-protein interactions. We previously reported the biophysical characteristics of the Apoptosis-Linked Gene 2-Interacting protein X (Alix) in complex with the Haemopoietic cell kinase (Hck) SH3 domain. In the current study, we have combined ITC, NMR, SAXS and molecular modeling to determine a 3D model of the complex. We demonstrate that Hck SH3 recognizes an extended linear prolin-rich region of Alix. This particular binding mode enables Hck SH3 to sense a specific non-canonical residue situated in the SH3 RT-loop of the kinase. The resulting model helps clarify the mechanistic insights of Alix-Hck interaction.

Keywords

apoptosis-linked gene 2-interacting protein X (Alix); protein-protein interaction; Src homology 3 domain (SH3 domain); Src family kinase (SFK); NMR; SAXS

© 2012 Federation of European Biochemical Societies. Published by Elsevier B.V. All rights reserved

³Correspondence should be addressed to: X.M. (morelli@ifr88.cnrs-mrs.fr), Tel: +33 491 164 501; FAX: +33 491 164 540, Y.C. (yves.collette@inserm.fr, Tel: +33 491 75 84 08; FAX: + 33 491 26 03 64) or S.T.A. (starold@mdanderson.org), Tel: +1 713 792 6059; FAX: +1 713 792 0855.

*These authors contributed equally to this work as senior authors.

Publisher's Disclaimer: This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final citable form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

SUPPORTING INFORMATION Three figures and Materials and Methods.

1. INTRODUCTION

Alix [ALG-2 (apoptosis-linked gene 2)-interacting protein X] is an adapter protein involved in normal and pathological cellular processes, including regulation of apoptosis, cytoskeletal dynamics, cell surface receptor internalization, endosomal sorting processes and virus budding from infected cell membranes [1–7]. These diverse functions appear to involve binding to various viral and cellular proteins (for review, refer to [8]), including kinases such as the Src tyrosine kinase which has been implicated in the ability of Alix to regulate cell surface receptor internalization and cell adhesion [9].

Crystal structures have revealed that human Alix is composed of three domains involved in multiple and diverse protein interactions: the N-terminal Bro1 domain (residues 1–358), that binds to ESCRT-I/III proteins [7,10], a central V domain (residues 362–702) that is formed by two three-helix bundles disposed in a “V” shape; and a C-terminal PRR (proline-rich region; residues 703–868) that is not present in the available crystal structures, that serves as a docking site for a number of proteins, including TSG101 and Src-homology (SH)3 domain-containing proteins [10,11].

We previously identified Alix as a novel Hematopoietic cell kinase (Hck) SH3-binding protein by yeast two-hybrid screening using the SH3 domains of Src Family Kinases (SFKs) [12]. Identification of Src-related Hck as a novel Alix binding partner was particularly relevant given the implication of Hck in similar cellular and pathological functions, including adhesion, actin polymerization, and HIV-1 infection (for review, see [13]). We demonstrated that Alix binds to and activates Hck, and delineated the proline-rich (PxxP) motif of the Alix PRR involved in binding to Hck-SH3. In the same study, we demonstrated that Alix residues outside of the PxxP motif enhanced affinity and also possibly specificity for Hck-SH3, which was reminiscent of the tertiary binding mode used by the viral protein Nef-HIV-1 [14–16]. Interactions outside the PxxP motif are thought to enhance affinity and specificity for SH3 domains (for review, refer to [17]) as demonstrated by the high affinity binding of the viral Nef protein to Hck SH3 domain which implicates a well-defined hydrophobic pocket formed by two α -helices of Nef [14]. In addition to the canonical PXXP motif, this pocket provides a three-dimensional ‘tertiary’ binding surface which has not been described so far for cellular proteins. We thus investigated in the current research, on the mode of binding of Alix to Hck-SH3 domain by combining ITC, NMR, SAXS and molecular modeling experiments and compared it to that of HIV-1 Nef.

2. MATERIAL AND METHODS

2.1 DNA Construction

Human Alix recombinant construct (ALIX_{V+PRR}) consisting of residues 362–760 was prepared as previously described [12]. Wild-type Fyn-SH3 (Fyn_(WT)-SH3) and Fyn_(R96I)-SH3 sequences were amplified from pGEX-Fyn_(WT) and pGEX-Fyn_(R96I) plasmid constructs, respectively, and cloned into pET42a expression vectors using NdeI and XhoI restriction sites. Each construct was verified by DNA sequencing.

2.2 Yeast Two-Hybrid (Y2H)Screen

Two independent yeast two-hybrid (Y2H) were performed in parallel, using the human Hck- or Fyn_(R96I)-SH3 domain as a bait. Y2H system is based on the protocol described by Walhout *et al.* [18] as described in Materials and Methods in the Supporting Information.

2.3 Protein Expression

Human Alix recombinant construct (ALIX_{V+PRR}) was expressed with an N-terminal His₆-Smt3 fusion tag in *E. coli* strain BL21 (DE3). The different SH3 recombinant proteins (Fyn_(WT)-SH3, Fyn_(R96I)-SH3, and Hck-SH3) were similarly expressed as 6xHis C-terminal fusion proteins in *E. coli* BL21 (DE3). The different recombinant proteins (ALIX_{V+PRR} and SH3 protein) were expressed and purified as described in Materials and Methods in the Supporting Information.

2.4 Isothermal Titration Calorimetry (ITC)

ITC was used to evaluate the thermodynamics parameters of the binding between ALIX_{PI} peptide and Fyn_(WT)-SH3 or Fyn_(R96I)-SH3. Titrations were carried out at 25°C on a MicroCal ITC200 microcalorimeter (GE Healthcare, Piscataway, NJ). Experiments and data analysis were performed as described in Materials and Methods in the Supporting Information.

2.5 NMR Spectroscopy

To further elucidate the interaction mode between the SH3 domains and ALIX_{V+PRR}, ¹H-¹⁵N heteronuclear single quantum coherence (HSQC) experiments were performed as described in Materials and Methods in the Supporting Information.

2.6 Small-Angle X-Ray Scattering (SAXS) Analysis

Data used for the SAXS analysis of the complex between Fyn_(R96I) and ALIX_{V+PRR} were collected at the SWING beamline of the SOLEIL synchrotron in Paris, France, as described in more details in Materials and Methods in the Supporting Information.

2.7 Peptide docking studies

Docking of Alix peptide onto Fyn_(R96I)-SH3 and Fyn_(WT)-SH3 mutants was performed using the high-resolution modeling protocol provided by FlexPepDock [19]. The Fyn Fyn_(R96I)-SH3:HIV-1 Nef crystal structure (PDB ID 1EFN [14]) was used as a template for Fyn_(R96I)-SH3. Fyn_(WT)-SH3 was obtained by replacing I96 with an arginine (in its most common rotamer). The initial Alix peptide structure was obtained by computationally mutating and extending the Nef PXXP motif from the pdb template. FlexPepDock was set up to produce 300 low resolution and 300 high resolution structures. Produced models reached peptide backbone r.m.s.d. of more than 10 Å compared to the initial peptide structure, showing that the flexible docking procedure was not only exploring local minima.

3. RESULTS AND DISCUSSION

3.1 Isoleucine 92 from the Haemopoietic cell kinase RT-loop is involved in the specific recognition of ALIX_{V+PRR}

The so-called “tertiary” mode of recognition used by HIV-1 Nef to selectively target SH3 domains is provided by the folded core domain of the protein [14,16]. In addition to binding mediated by the PPII helix, an isoleucine residue from the RT loop of the Hck SH3 domain (I92) inserts into a well-defined hydrophobic pocket formed by two α-helices of Nef. The corresponding residue in Fyn SH3 RT loop is an arginine (R96) which leads to a low affinity binding to Nef ($K_d > 20 \mu\text{M}$), whereas its substitution by an isoleucine (R96I) converts the Fyn SH3 domain from a low to a high affinity ($K_d \approx 0.4 \mu\text{M}$) binding partner for Nef [15]. This selective mode of recognition mediated by HIV-1 Nef was reproduced in a yeast two hybrid assay, as shown in supplementary Figure S1A. Co-transformation of cells with Nef resulted in β-Galactosidase production and yeast outgrowth on media lacking uracil for Hck-SH3 and Fyn_(R96I)-SH3 as baits, but not for Fyn_(WT)-SH3. These results were confirmed

using the *lacZ* and *his3* reporters for Nef:Hck-SH3 and Nef:Fyn_(WT)-SH3 (because Fyn_(R96I)-SH3 alone was able to transactivate the *lacZ* and *his3*, Fyn_(R96I)-SH3 could not be used with these reporter systems). In contrast to HIV-1 Nef, the Src-associated in mitosis 68 kDa (SAM68) protein interacted with comparable strength with every SH3 domain, indicating that the architecture of the SAM68 binding site cannot produce a Nef-like SH3 selection of the RT-loop amino acid position 96 (negative control).

Next, we analyzed the interaction between these SH3 domains and an Alix fragment encoded by one Alix clone, called IIIA9, obtained in a yeast two hybrid screening using the Hck SH3 domain as bait [12]. This Alix fragment contained the Hck-interacting proline-rich region (PRR) as well as part of the Alix V domain (alignment details in supplementary Figure S1C), suggesting that these two regions of the Alix V domain contribute to Hck SH3 binding, which was reminiscent of the Nef binding mode of action (supplementary Figure S1B).

To confirm the “Nef-like” binding selectivity for the RT-loop position 92 *in vitro*, we carried out GST pull-down experiments followed by SDS-PAGE and Coomassie blue staining. These experiments illustrate the binding of an Alix fragment encoding for the V domain and the SH3-binding PRR motif (Alix_{V+PRR}) to Hck-SH3-GST and Fyn_(R96I)-SH3-GST but not to Fyn_(WT)-SH3-GST (supplementary Figure S2). Thus, the recombinant ALIX_{V+PRR} could differentiate SH3 domains according to their amino acids at position 92 (or 96 for Fyn), displaying a “Nef-like” selectivity *in vitro*.

3.2 Molecular recognition mode does not involve a 3D fingerprint but rather demonstrates an extended linear pattern

Next, we asked whether the ALIX_{V+PRR}-SH3 binding site was demonstrating a structurally similar binding site to the one observed for HIV-1 Nef protein. For Nef, the tertiary SH3 recognition binding site is formed by the Nef PRR and part of the folded Nef core domain [14,16]. In contrast, sequence analysis and secondary structure prediction indicates that the Alix PRR is located within an unstructured region, 35 residues away from the folded V domain (supplementary Figure S3). The location of the Alix PRR in an unstructured region is consistent with our previous SAXS data for apo-ALIX_{V+PRR} [12]. We, and others, previously published ITC experiments indicating that the affinity and thermodynamic parameters of the Nef/Hck-SH3 interaction were dramatically different from those of the interaction between Hck-SH3 and the Nef PRR peptide [15,20]. Similarly, previous ITC experiments for the Alix/Hck-SH3 complex demonstrated that a peptide containing the minimal Alix PxxP consensus motif (ALIX_{PI}, residues 737 to 760) did not fully reproduce the binding characteristics of ALIX_{V+PRR} toward Hck-SH3; however, inclusion of residues N-terminal to the PxxP consensus motif in the peptide sequence almost completely restored the binding characteristics of ALIX_{V+PRR} [12]. In the present study, we demonstrate that the isolated peptide ALIX_{PI} is also capable of distinguishing between Fyn_(WT)-SH3 ($K_d = 160 \pm 30 \mu\text{M}$) and Fyn_(R96I)-SH3 ($K_d = 54 \pm 10 \mu\text{M}$), and that ALIX_{PI} binds to each SH3 domain with K_d 's similar to those observed with ALIX_{V+PRR} (please refer to Figure 1A and B for the peptide ALIX_{PI} in complex with Fyn_(WT)-SH3 or Fyn_(R96I)-SH3 experiments, to compare with [12] for the peptide ALIX_{PI} or ALIX_{V+PRR} in complex with Hck-SH3 experiment). These results suggest that if a tertiary ‘Nef-like’ binding occurs, its thermodynamic fingerprint is weak. Also, our previous NMR studies failed to show a significant difference between the imprints of ALIX_{V+PRR} and the Alix PRR peptide on Hck-SH3, and hence they failed to reveal a clear indicator of a tertiary 3D binding site [12]. Therefore, we used NMR to investigate whether the imprint of ALIX_{V+PRR} on the different SH3 domains varies with their origin or affinity.

NMR HSQC experiments with ^{15}N -labelled Hck-SH3, Fyn_(WT)-SH3, and Fyn_(R96I)-SH3 in the presence of 1 equivalent of unlabelled ALIX_{V+PRR} showed that the chemical shifts induced by ALIX_{V+PRR} mapped to almost the same residues on the surfaces of all SH3 domains, including the low-affinity Fyn_(WT)-SH3 domain (Figure 2A–C). For all SH3 domains tested, markedly affected residues were distributed over four regions of the SH3 domain—the RT loop, the nSrc loop, the 3₁₀ helix, and the canonical hydrophobic grooves (Figure 2A)—in agreement with the results of our previous study of ALIX_{V+PRR} binding to Hck-SH3 [12]. Of note, the intensity of the chemical shift increased remarkably, as expected, with the K_d observed (using strictly the same, 1 equivalent amount of ALIX_{V+PRR} in all experiments). Although the imprints are similar globally, subtle differences can be observed in the surface area of the residues involved in the recognition process; for example, the nSrc loop seems to be more involved in the Hck-SH3–ALIX_{V+PRR} interaction than in the Fyn_(R96I)-SH3–ALIX_{V+PRR} interaction (Figure 2A–C). Nonetheless, the overall interaction mode is similar enough for all SH3 proteins to indicate a structurally similar engagement of all three SH3 domains by ALIX_{V+PRR}. Also, the extent of the binding surface on SH3 domains is compatible with an ALIX_{V+PRR} binding mode that has a linear “peptide-like” interaction rather than a ‘Nef-like’ 3D interaction.

3.3 Molecular model of the SH3-ALIX_{V+PRR} complex

To corroborate that the PRR in ALIX_{V+PRR} does not join the V domain to form a ‘Nef-like’ tertiary SH3 binding site upon SH3 engagement, we used SAXS. Ensemble Optimization Method (EOM) reconstructions showed that the PRR-bound Fyn_(R96I)-SH3 was highly flexible and had a large, variable distance from the V domain core (Figure 3 A–B). The maximum diameter (D_m) calculated from the SAXS data for Fyn_(R96I)-SH3-bound ALIX_{V+PRR} ($D_m = 190 \pm 10 \text{ \AA}$) was the same as the D_m value we measured previously for apo-ALIX_{V+PRR} [12]. These results argue against a model in which the SH3 binding motif in the flexible region C-terminal to the Alix V domain folds back onto the V domain to form a combined tertiary SH3 site.

Together, our data indicate that Alix achieves a ‘Nef-like’ RT-loop selection through a linear “peptide-like” binding mode rather than through a ‘Nef-like’ tertiary SH3 recognition mode. Hence, the observed differences in the Y2H and K_d , especially between Fyn_(WT)-SH3 and Fyn_(R96I)-SH3, must be explained by differences in the interaction between the Alix PRR sequence and the SH3 RT loops. All attempts to crystallize Fyn_(R96I)-SH3 in a complex with Alix PRR failed, because all crystals packing involve homologous interactions between PxxP-motif binding sites of the SH3 domain. We therefore used the high-resolution docking and refinement protocol FlexPepDock [19] to model SH3–peptide complexes. FlexPepDock is implemented within the ROSETTA framework, which has proven its high accuracy in several landmark modeling successes. The obtained Fyn_(R96I)-SH3/ALIX_{P1} and Fyn_(WT)-SH3/ALIX_{P1} structures provide a possible explanation for how a linear sequence can distinguish between R96 and I96. These structures show that in addition to the canonical interaction between Fyn D100 and Alix R757, the I96 of Fyn_(R96I)-SH3 may establish favorable hydrophobic interactions with ALIX_{P1} prolines 754, 758–759 (Figure 3C). These favorable proximity of hydrophobic residues is not possible with R96 of Fyn_(WT)-SH3. In addition, the proximity of the positive charge of R96 may also decrease the strength of an interaction between Fyn E94 and ALIX_{P1} K751. E94 is conserved in Hck-SH3, and FlexPepDock analysis suggests that this E94–ALIX_{P1} K751 interaction is conserved in Hck (data not shown). Our docking analysis also provides a possible explanation for our previous observation that the minimal Alix PxxP consensus does not fully reproduce the binding of ALIX_{V+PRR} [12], by suggesting that Alix M747 (which was not included in the minimal Alix PxxP peptide) engages a hydrophobic interaction with an apolar pocket formed by Fyn-SH3 L90 and Y91.

3. CONCLUSION

Our results indicate that ALIX achieves a 'Nef-like' RT-loop selection through an extended linear "peptide-like" binding mode rather than through a 'Nef-like' tertiary SH3 recognition mode. Our binding studies and computational modeling analysis suggest a molecular basis for how the extended linear interaction of ALIX with Hck-SH3 is capable of reproducing the 3D 'tertiary' binding mode of HIV-1 Nef without a 3D organization. Together with the observation that linear SH3-binding motifs can bind to SH3 domains with similar affinities than does HIV-1 Nef [21], this opens the question why Nef uses a costly three-dimensional framework for SH3 binding if a much simpler linear recognition motif achieves the same affinity and specificity.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

We thank Olivier Bornet for performing the NMR recording experiments, Marielle Beauzan for bacterial expression, Dieter Vermeire for Biacore support, Karen Muller for editorial assistance, Pascal Verdié for peptide synthesis and Javier Perez for support and setup of the SAXS beamline at the SOLEIL synchrotron in Paris, France.

FUNDING This work was supported by the Centre National de la Recherche Scientifique (CNRS); the Institut National de la Santé et de la Recherche Médicale (INSERM); the Agence Nationale de Recherche sur le SIDA et les hépatites virales (ANRS); the Ministry of Science and Technology, China [grant numbers 2007CB914304; 2006AA02A313]; the National Natural Science Foundation of China (NSFC) [grant numbers 30800181; 30625011]; the Research Foundation Flanders (FWO); the concerted action programme of the Katholieke Universiteit Leuven; and the National Institutes of Health (MD Anderson's Cancer Center Support) [grant number CA016672]. S.O. and A.L. were fellows of the ANRS, and X.S. was a fellow of the 'Ambassade de France en Chine'.

ABBREVIATIONS

ALG-2	apoptosis-linked-gene-2
Alix	ALG-2 interacting protein X
EOM	ensemble optimization method
GST	glutathione S-transferase
Hck	haemopoietic
HSQC	heteronuclear single quantum coherence
ITC	isothermal titration calorimetry
PDB	Protein Data Bank
PPII	polyproline type II
PRR	proline-rich region
SAXS	small-angle X-ray scattering
SFKs	Src family of non-receptor protein tyrosine kinases

REFERENCES

- [1]. Chatellard-Causse C, Blot B, Cristina N, Torch S, Missotten M, Sadoul R. Alix (ALG-2-interacting protein X), a protein involved in apoptosis, binds to endophilins and induces cytoplasmic vacuolization. *J Biol Chem.* 2002; 277:29108–15. [PubMed: 12034747]

- [2]. Pan S, et al. Involvement of the conserved adaptor protein Alix in actin cytoskeleton assembly. *J Biol Chem.* 2006; 281:34640–50. [PubMed: 16966331]
- [3]. Schmidt MH, Hoeller D, Yu J, Furnari FB, Cavenee WK, Dikic I, Bögler O. Alix/AIP1 antagonizes epidermal growth factor receptor downregulation by the Cbl-SETA/CIN85 complex. *Mol Cell Biol.* 2004; 24:8981–93. [PubMed: 15456872]
- [4]. Katoh K, Shibata H, Suzuki H, Nara A, Ishidoh K, Kominami E, Yoshimori T, Maki M. The ALG-2-interacting protein Alix associates with CHMP4b, a human homologue of yeast Snf7 that is involved in multivesicular body sorting. *J Biol Chem.* 2003; 278:39104–13. [PubMed: 12860994]
- [5]. Matsuo H, et al. Role of LBPA and Alix in multivesicular liposome formation and endosome organization. *Science.* 2004; 303:531–4. [PubMed: 14739459]
- [6]. Trioulier Y, Torch S, Blot B, Cristina N, Chatellard-Causse C, Verna JM, Sadoul R. Alix, a protein regulating endosomal trafficking, is involved in neuronal death. *J Biol Chem.* 2004; 279:2046–52. [PubMed: 14585841]
- [7]. Strack B, Calistri A, Craig S, Popova E, Göttinger HG. AIP1/ALIX is a binding partner for HIV-1 p6 and EIAV p9 functioning in virus budding. *Cell.* 2003; 114:689–99. [PubMed: 14505569]
- [8]. Odorizzi G. The multiple personalities of Alix. *J Cell Sci.* 2006; 119:3025–32. [PubMed: 16868030]
- [9]. Schmidt MH, Dikic I, Bögler O. Src phosphorylation of Alix/AIP1 modulates its interaction with binding partners and antagonizes its activities. *J Biol Chem.* 2005; 280:3414–25. [PubMed: 15557335]
- [10]. Lee S, Joshi A, Nagashima K, Freed EO, Hurley JH. Structural basis for viral late-domain binding to Alix. *Nat Struct Mol Biol.* 2007; 14:194–9. [PubMed: 17277784]
- [11]. Fisher RD, Chung HY, Zhai Q, Robinson H, Sundquist WI, Hill CP. Structural and biochemical studies of ALIX/AIP1 and its role in retrovirus budding. *Cell.* 2007; 128:841–52. [PubMed: 17350572]
- [12]. Shi X, et al. Identification and biophysical assessment of the molecular recognition mechanisms between the human haemopoietic cell kinase Src homology domain 3 and ALG-2-interacting protein X. *Biochem J.* 2010; 431:93–102. [PubMed: 20670214]
- [13]. Guiet R, Poincloux R, Castandet J, Marois L, Labrousse A, Le Cabec V, Maridonneau-Parini I. Hematopoietic cell kinase (Hck) isoforms and phagocyte duties - from signaling and actin reorganization to migration and phagocytosis. *Eur J Cell Biol.* 2008; 87:527–42. [PubMed: 18538446]
- [14]. Lee CH, Saksela K, Mirza UA, Chait BT, Kuriyan J. Crystal structure of the conserved core of HIV-1 Nef complexed with a Src family SH3 domain. *Cell.* 1996; 85:931–42. [PubMed: 8681387]
- [15]. Lee CH, Leung B, Lemmon MA, Zheng J, Cowburn D, Kuriyan J, Saksela K. A single amino acid in the SH3 domain of Hck determines its high affinity and specificity in binding to HIV-1 Nef protein. *EMBO J.* 1995; 14:5006–15. [PubMed: 7588629]
- [16]. Arold S, Franken P, Strub MP, Hoh F, Benichou S, Benarous R, Dumas C. The crystal structure of HIV-1 Nef protein bound to the Fyn kinase SH3 domain suggests a role for this complex in altered T cell receptor signaling. *Structure.* 1997; 5:1361–72. [PubMed: 9351809]
- [17]. Li SS. Specificity and versatility of SH3 and other proline-recognition domains: structural basis and implications for cellular signal transduction. *Biochem J.* 2005; 390:641–53. [PubMed: 16134966]
- [18]. Walhout AJ, Vidal M. High-throughput yeast two-hybrid assays for large-scale protein interaction mapping. *Methods.* 2001; 24:297–306. [PubMed: 11403578]
- [19]. London N, Raveh B, Cohen E, Fathi G, Schueler-Furman O. Rosetta FlexPepDock web server--high resolution modeling of peptide-protein interactions. *Nucleic Acids Res.* 2011; 39:W249–53. [PubMed: 21622962]
- [20]. Arold S, O'Brien R, Franken P, Strub MP, Hoh F, Dumas C, Ladbury JE. RT loop flexibility enhances the specificity of Src family SH3 domains for HIV-1 Nef. *Biochemistry.* 1998; 37:14683–91. [PubMed: 9778343]

- [21]. Ladbury JE, Arold ST. Energetics of Src homology domain interactions in receptor tyrosine kinase-mediated signaling. *Methods Enzymol.* 2011; 488:147–83. [PubMed: 21195228]
- [22]. Grzesiek S, et al. The solution structure of HIV-1 Nef reveals an unexpected fold and permits delineation of the binding surface for the SH3 domain of Hck tyrosine protein kinase. *Nat Struct Biol.* 1996; 3:340–5. [PubMed: 8599760]

- Alix achieves a specific SH3 domains RT-loop selection
- This selection is made through an extended linear 'peptide-like' binding mode
- The proline rich region does not join the V domain to form a tertiary binding site

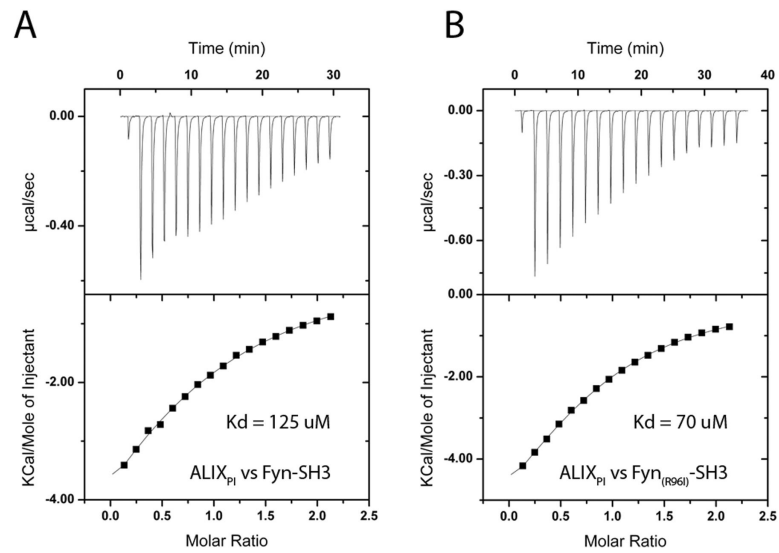


Figure 1. (A–B) Experimental ITC binding curves for the interaction between ALIX_{PI} and (A) Fyn_(wt)-SH3, (B) Fyn_(R96I)-SH3. Top panel: Raw ITC data from an experiment. Bottom panel: Nonlinear least-squares fit of the data from the top panel after blank subtraction.

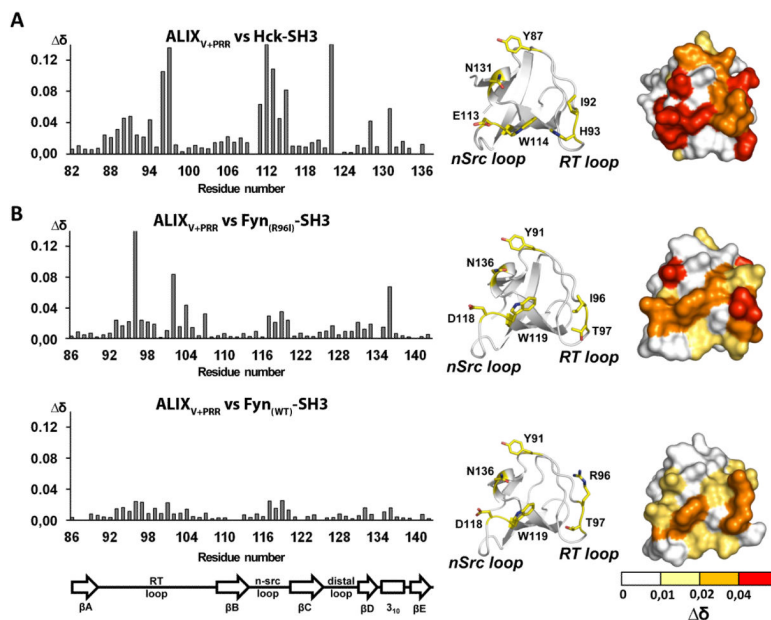


Figure 2.

Mapping of the SH3 domains' atomic recognition surfaces in the presence of ALIX_{V+PRR} by heteronuclear NMR. (A–C) Left: SH3 residues' chemical shifts observed for (A) Hck-SH3, (B) Fyn_(R96I)-SH3, and (C) Fyn_(WT)-SH3 in the presence of 1 equivalent of ALIX_{V+PRR}, shown as histograms. The relative variations of ¹H and ¹⁵N were calculated according to Grzesiek *et al.* [22]. Center: Ribbon representation of the different SH3 domains with important interacting residues in yellow for (A) Hck-SH3, (B) Fyn_(R96I)-SH3, and (C) Fyn_(WT)-SH3 (PDB entries 1BU1, 1EFN, and 1AVZ, respectively). Right: Corresponding chemical shifts of the SH3 proteins in the presence of 1 equivalent of ALIX_{V+PRR}, shown as a surface representation onto the SH3 domain structures. Small chemical shift variations are represented in yellow, larger shifts in orange, and the largest in red.

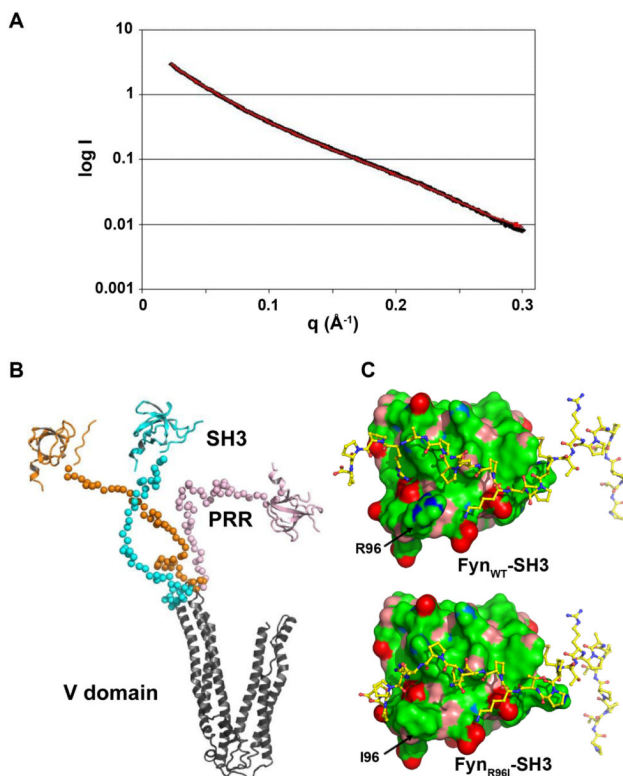


Figure 3.

SAXS model of ALIX_{V+PRR} complexed to Fyn_(R96I)-SH3. (A) Fit of EOM SAXS ensemble model (red) to data (black). (B) Three representative structural models taken from an ensemble of 15 structures produced by EOM on the basis of SAXS data, superimposed on their Alix V domain (black ribbon). ALIX_{V+PRR}-bound Fyn_(R96I)-SH3 (represented as secondary structures) and flexible residues (represented as spheres) linking the Alix PRR to the V domain have a different color for each model. (C) Alix peptide/Fyn_(R96I)-SH3 (top) and Alix peptide/Fyn_(WT)-SH3 (bottom) 3D interaction models obtained from Flexpepdock. SH3 domains are oriented as in Figure 2. SH3 surfaces are colored according to blue, positively charged atoms; red, negatively charged atoms; green, hydrophobic atoms; salmon, polar oxygens; light blue, polar nitrogens; yellow, sulfur. The Alix peptide is shown as a stick model.