



C-Src Kinase Inhibition: A Promising Route in Kidney Cancer Treatment Simon Duri, Xixi Hong, Joseph Lustig, Aleksandra Porebska

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Abstract: C-Src is involved in a number of signaling pathways that ultimately lead to angiogenesis. Recently derived data leads to deduction that the most important consequence of increased c-Src activity is promotion of an agressive phenotype in multiple human tumors. Based on that information, inhibition of c-Src kinase is essential and might be considered a treatment of cancer. There are currently a number of drug molecules targeting c-Src which are in clinical trials. These include Bosutinib which has been shown to significantly reduce the renal growth in cystic bpk mouse models. Drug design can be accomplished with the aid of a number of computer software programs. These help in mapping the active site of the target molecule, which will then be used as a template for possible drug molecules. Minimum energy structures of these molecules can be obtained from programs like Spartan. However, experimental work to establish actual binding constants, solubility and toxicity of chosen drug molecules will have to be carried out.

C-Src kinase is a non receptor tyrosine kinase, encoded by the c-Src (cellular-Src) gene (Src pronounced "sarc", which is short for sarcoma, a cancer type which derives from changed connective tissue cells). C-Src protein acts as a signal transduction inhibitor that is a critical component of multiple signaling pathways that control cell growth, proliferation, invasion, and apoptosis [1, 2]. One of the signaling pathways that c-Src is involved in is the VEGF (Vascular Endothelial Growth Factor) pathway, shown below:



Figure 1: Involment of c-Src in the VEGF pathway. Source: SABiosciences, ProteinLounge.com

Phosphorylation of proteins by kinases is important in signal transduction and at PN21 and the heart, spleen, pancreas, stomach, and thymus were periodically harvested regulation of other cellular activities such as cell division. In some cases, the protein at PN21 to evaluate possible toxicity of vehicle or SKI-606. kinase will mutate so the kinase is always active, causing the cell to grow The active site of c-Src has different residues leading to different types of interactions with uncontrollably [3]. Therefore, inhibition of c-Src can be used as a way of regulating ligands. These interactions include H bonds, pi – cationic interactions and hydrophobic cell growth, ultimately resulting in cancer treatment. Imatinib and Bosutinib are interactions. These interactions are kept in mind when designing potential drug molecules to some examples of drug compounds that inhibit the autophosphorylation of c-Src, target c-Src. resulting in inhibition of cell growth and apoptosis [4].

As illustrated below, in the inactive form of c-Src, Tyr527 is phosphorylated and binds to the SH2 domain, Tyr416 is dephosphorylated, and the SH3 domain is engaged with the SH2 kinase linker. C-Src is activated by dephosphorylation of Tyr527 which leads to an "open" conformation, allowing autophosphorylation of Tyr416 and interaction of c-Src with substrates.



Source: Rucchi N et al, Anti-cancer agents in Med Chem, 2008, 8, 342

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The inhibition of c-Src has been shown to result in considerable reduction of renal growth in cystic *bpk* mice. The *bpk* mouse model is one of several PKD (Polycystic Kidney Disease) mouse models genetically modified to have a desired phenotype. In this case bpk means BALB/c polycystic kidneys, which means that BALB/c, a laboratory-bred strain of house mouse, was transformed to get the polycystic kidney disease phenotype [5]. Figure 3 below illustrates some of the experimental results.



As illustrated in (A), Lane 3, large cystic kidneys from *bpk* mice correlate with increased expression of active Src (pY418) (B, lane 3) when compared with age-matched BALB/c (wild-type control) kidneys (A, lanes 1 and 2) and corresponding Src (pY418) activity (B, lanes 1 and 2). AS illustrated in (B), Lane 4, reduction in renal Src activity with SKI-606 treatment (compared with lane 3) results in significant reduction in cystic kidney size

as shown in (A), Lane 4. Src (pY418)

MW≈60kD

β-actin MW≈40kD

Evaluation of c-Src as a drug target for different compounds can be performed in mice as

was done for the above experiment. *Bpk* (cystic) and BALB/c pups received SKI-606 (Bosutinib) at 30 mg/kg per day by i.p., starting at PN7 (postnatal day 7). Animals were treated from PN7 to PN20 (14 doses). The kidney and liver tissues were routinely harvested



Figure 4: 2D active site of c-Src showing the amino acid residues.

Potential drug molecules Figure 6: 3D active site of c-Src were designed using the known inhibitor AZD0530 as The results on the size of kidneys in mice clearly show the a starting point. Computer effectiveness of targeting c-Src in cancer treatment. Various generations of the ligands were created using Spartan ligands that can be used as potential drugs. Insertion of these software. Minimum energy ligands in the protein active site and visualization of possible 3D structures were determined using the as Discovery Studio Visualizer are very useful in optimizing the Hartree-Fock method and 3structures of the possible drug molecules. However, experimental 21G as the basis set. The 3D work will still have to be done to determine such parameters like ligands were docked in the binding constants and toxicity of those molecules that would have active site of c-Src using been selected. **Discovery Studio Visualizer** There are already a number of drug molecules targeting c-Src. software. Improvements and However, in an effort to widen the drug bank, it will be interesting optimizations of the ligand to determine the binding affinities of some of the 7 ligands above. structures were done based Toxicity experiments with the above ligands is also an important on how the ligands were step In widening potential drug molecules targeting c-Src. fitting into the active site.

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Figure 5: Some of the ligands designed as possible drug molecules targeting c-Src.

The interactions of Ligand 7 in the active site of c-Src are shown in the 3D view below with Ligand 7 docked in the active site .



software packages are available now that can be used in designing interactions with amino acid residues using software packages such