ValidNESs: a database of validated leucine-rich nuclear export signals

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ValidNESs (http://validness.ym.edu.tw/) is a new database for validated leucine-rich nuclear export signal (NES)-containing proteins [1]. The disease relevance of these proteins has gained recognition in recent years. Previous studies have demonstrated that many cellular NES-containing proteins are involved in important processes such as signal transduction, cell-cycle regulation and tumor suppression. Viral NES-containing proteins, on the other hand, are often found related to viral genome trafficking. Until recently only about one third of known CRM1 cargo proteins are accessible in a single database since the last compilation in 2003 [2]. However, as of 2012 our database ValidNESs, and NESdb [3] have filled this gap. ValidNESs includes a total of 262 functional NES sites from 221 NES-containing proteins. In addition to sequence information, we provide local structural information for 52 NESs retrieved from the Protein Data Bank (PDB).

Currently two computational methods have been published to predict NESs: our NESsential [4] and a method called NetNES [5]. We have demonstrated that NESsential is the only approach capable of identifying promising NES-containing candidate proteins. Our NESsential publication has received attention, and was rated as a “must read” by the faculty of 1000 (http://f1000.com/716547838); but users needed to download and install the software themselves to make predictions with NESsential. Therefore, we have integrated a web interface to prediction by NESsential into ValidNESs, enabling valuable hints to be gained by in silico prediction.

Reference:

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