An interaction map of proteasome subunits

O. Coux
CRBM-CNRS UPR 1086, 1919 route de Mende, 34293
Montpellier cedex 5, France

Despite the central role of the 26S proteasome in eukaryotic cells, many facets of its structural organization and its functioning are still poorly understood. To learn more about the interactions between its different subunits, as well as its possible functional partners in cells, we performed with Marc Vidal’s laboratory (DFCI, Boston), a systematic two-hybrid analysis using C. elegans 26S proteasome subunits as baits (Davy et al. (2001), EMBO Rep. 2, 821-828, and http://vidal.dfci.harvard.edu/Proteasome/data.htm).

A pair-wise matrix of all subunit combinations allowed to detect numerous possible intra-complex interactions, among which some were already reported by others and eight were novel. Interestingly, four new interactions were detected between two ATPases of the 19S regulatory complex and three α-subunits of the 20S proteolytic core. Possibly, these interactions participate in the association of these two complexes to form the 26S proteasome.

Proteasome subunits sequences were also used to screen a cDNA library in order to identify new interactors of the complex. Among the interactors found, most (58) have no clear connection to the proteasome, and could be either substrates or potential cofactors of this complex. Few interactors (7) could be directly or indirectly linked to proteolysis. The others (12) interacted with more than one proteasome subunit, forming ‘interaction clusters’ of potential biological interest.