TABLE S2. **Features of recombinant proteins.**

Protein	**Molecular Mass**	**Oligomeric status** [(b)]	**Putative activity**	**Organism**	**Solubility** [(c)]
CpxP	19.7	dimer	Inhibitor of the CpxA kinase	*E. coli*	soluble
ClpP1	22.5	tetradecamer	peptidase	*M. tuberculosis*	soluble
ClpP2	22.9	tetradecamer	peptidase	*M. tuberculosis*	partly soluble
GFP	27.4	monomer	Green Fluorescence Protein	*Aequorea victoria*	partly soluble
PA28α	28	monomer and heptamer	Proteasome activator	*Rat*	soluble
PAN (Proteasome Activating Nucleotidase)	50	hexamer	ATPase	*Methanococcus jannaschii*	soluble
Nemo	51.8	dimer and trimer	ubiquitin binding	*Mouse*	-

[a] Molecular masses were calculated according to the amino acid composition of the recombinant protein and are given in kDa.

[b] The tetradecameric structure of ClpP1 and ClpP2 in solution is deduced from that of their ClpP homolog in *E. coli* (6). The hexameric structure of PAN was determined by size exclusion chromatography (7) and electron microscopy (5). The monomer–heptamer equilibrium self-association of PA28α was determined by analytical ultracentrifugation (2) and crystallography analysis (3). Nemo was found to self-associate into a trimer by gel filtration and analytical ultracentrifugation (1) but its IKK binding domain is a dimer as seen by gel filtration, analytical ultracentrifugation, and X-ray crystallography (4).

[c] The solubility status was followed in the BL21(DE3) cells based on the presence of the protein in the soluble fraction after a centrifugation at 14,000 g.

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