SUPPLEMENTARY MATERIAL

Mass-spectrometric analysis.

SDS PAGE gel bands containing the corresponding MJ1004 constructs were subjected to in-gel tryptic digestion according to Shevchenko *et al*. (1996) with minor modifications. The gel piece was swollen in a digestion buffer containing 50 mM NH_4HCO_3 and 12.5 ng μL^{-1} of trypsin (Roche Diagnostics) in an ice bath. After 30 minutes the supernatant was removed and discarded, 20 µL of 50 mM NH_4HCO_3 were added to the gel piece and the digestion allowed to proceed at 310 K overnight. Prior to MS analysis, sample was acidified by adding 5 µL 0.5 % TFA. 0.5 µL of digested sample was directly spotted onto the MALDI target and then mixed with 0.5 µL α-Cyano-4-hydroxycinnamic acid (CHCA) matrix solution (20 µg μL^{-1} in ACN, 0.1 % TFA, 70:30, vol/vol). Peptide mass fingerprinting was performed on a Bruker Autoflex III mass spectrometer (Bruker-Daltonics, Bremen, Germany). Positively charged ions were analyzed in reflector mode, using delayed extraction. The spectra were obtained by randomly scanning the sample surface. About 600-800 spectra were averaged to improve the signal to noise ratio. Spectra were externally calibrated resulting in a mass accuracy of <50 ppm when external calibration was performed and typically <20 ppm in the case for internal calibration. Protein identification was performed by searching in a non-redundant protein database (NCBI) using Mascot searching engine (http://matrixscience.com). The following parameters were used for database searches: missed cleavages 1, allowed modifications carbamidomethylation of cysteine (complete) and oxidation of methionine (partial).

Supplementary Table 1. Bateman module orientation found in dimeric assemblies of CBS domain containing proteins for which the crystal structure is known. H.H = *head-to-head*; H.T = *head-to-tail*.

UniProt	Organism	PDB	Bateman orientation
A9CIP4	*Agrobacterium tumefaciens*	3FHM	H.H
Q81MQ0	*Bacillus anthracis*	3LQN	H.H
O31698	*Bacillus subtilis*	1YAV	H.H
O34994	*Bacillus subtilis*	3FV6	H.H
Q7WB69	*Bordetella parapertussis*	3JTF	H.H
Q8KDJ9	*Chlorobium tepidum*	3GBY	H.H
Q183U2	*Clostridium difficile*	3LV9	H.T
Q8XIQ9	*Clostridium perfringens*	3LB2, 3L31	H.H
Q9VRD9	*Drosophila melanogaster*	3PC2, 3PC3, 3PC4	H.T
Q8FD73	*Escherichia coli CFT073*	3FNA	H.H
A6TEL6	*Klebsiella pneumoniae*	3K2V	H.H
A6TCM0	*Klebsiella pneumoniae*	3HF7	H.H
P51800	*Homo sapiens*	2PFI	H.H
P54619	*Homo sapiens*	2UV4, 2UV5, 2UV6, 2UV7	H.T
P51795	*Homo sapiens*	2J9L, 2JA3	----
Q58622	*Methanocaldococcus jannaschii*	3KH5, 3LFZ	H.H
Q57564	*Methanocaldococcus jannaschii*	3KPB, 3KPC, 3KPD	H.H
O27659	*Methanothermobacter thermautotrophicus*	1PBJ	H.T
O06186	*Mycobacterium tuberculosis*	1Y5H, 1XKF	H.H
Q82SE2	*Nitrosomonas europaea*	2RC3	H.H
Q04HE1	*Oenococcus oeni PSU*	3OCO	H.H
Q87VX8	*Pseudomonas syringae*	3LFR	H.H
Q8ZVX8	*Pyrobaculum aerophilum*	2RIF, 2RIH	H.H
P54645	*Rattus norvegicus*	2V8Q, 2V92, 2V9J	H.H
P06782	*Saccharomyces cerevisiae*	2QLV	H.H
P0A2L3	*Salmonella typhimurium LT2*	3NQR	H.H
O74536	*Schizosaccharomyces pombe*	2QR1, 2QRC, 2QRD, 2QRE	H.H
Q8EDE1	*Shewanella oneidensis*	3LHH	----
Q8EGN5	*Shewanella oneidensis*	3KXR	H.H
Q9EUQ9	*Streptococcus pneumoniae*	3K6E	H.H
P0C0H6	*Streptococcus pyogenes*	1ZFJ	H.H
Q97U20	*Sulfolobus solfataricus*	3DDJ	H.H
Q96Y20	*Sulfolobus tokodaii strain7*	2EF7	H.H
Q9WZZ4	*Thermotoga maritima*	1VR9	H.H
Q9X033	*Thermotoga maritima*	1O50	H.T
Q9HLD9	*Thermoplasma acidophilum*	1PVM, 2QH1	H.H
P21564	*Torpedo marmorata*	2D4Z	----

Reference

Shevchenko, A., Wilm, M., Vorm, O. & Mann, M. (1996). *Anal Chem*. **68**, 850–858.