Table S1. $\mathrm{K}_{\mathrm{d}}$ values of $\mathrm{Ca}^{2+}$ binding to CBD12 mutants.

| Protein | Maximal Binding Capacity ( $\mathrm{mol} / \mathrm{mol}$ ) | Microscopic $\mathrm{K}_{\mathrm{d}}$ Values ( $\mu \mathrm{M}$ ) |
| :---: | :---: | :---: |
| WT | $6.1 \pm 0.04$ | $\begin{gathered} 0.03 \pm 0.003,0.04 \pm 0.001,0.1 \pm 0.42, \\ 2.0 \pm 0.6,37.3 \pm 13.4,107.9 \pm 7.5 \\ \hline \end{gathered}$ |
| H501A | $5.5 \pm 0.08$ | $\begin{aligned} & 0.03 \pm 0.02,0.07 \pm 0.01,0.9 \pm 0.5, \\ & 2.8 \pm 1.1,14.2 \pm 7.9,136.7 \pm 16.7 \end{aligned}$ |
| A502P | $6.0 \pm 0.2$ | $\begin{aligned} & 0.04 \pm 0.02,0.08 \pm 0.02,1.4 \pm 0.7, \\ & 6.3 \pm 1.8,48.3 \pm 24.9,64.0 \pm 24.7 \end{aligned}$ |
| G503A | $3.1 \pm 0.3$ | $\begin{gathered} 0.11 \pm 0.01,0.12 \pm 0.02,4.6 \pm 1.9, \\ 31.2 \pm 1.5 \end{gathered}$ |
| G503P | $3.7 \pm 0.1$ | $\begin{gathered} 0.13 \pm 0.03,0.62 \pm 0.08,1.9 \pm 0.7, \\ 3.9 \pm 0.9 \\ \hline \end{gathered}$ |
| I504A | $5.8 \pm 0.2$ | $\begin{gathered} 0.03 \pm 0.01,0.12 \pm 0.01,0.31 \pm 0.08 \\ 2.7 \pm 1.0,13.0 \pm 7.4,50.9 \pm 11.7 \end{gathered}$ |
| I504P | $4.0 \pm 0.1$ | $\begin{gathered} 0.24 \pm 0.07, \\ , 0.58 \pm 0.14,1.0 \pm 0.1, \\ 1.6 \pm 0.2 \end{gathered}$ |
| F505A | $4.9 \pm 0.2$ | $\begin{gathered} 0.12 \pm 0.02,0.37 \pm 0.15,1.9 \pm 0.3, \\ 72.6 \pm 13.7,99.7 \pm 11.8 \end{gathered}$ |
| F505P | $3.7 \pm 0.1$ | $\begin{gathered} 0.14 \pm 0.04,0.42 \pm 0.14,0.63 \pm 0.14, \\ 3.18 \pm 0.95 \end{gathered}$ |
| T506A | $6.0 \pm 0.1$ | $\begin{gathered} 0.01 \pm 0.003,0.06 \pm 0.02,1.4 \pm 0.5, \\ 3.2 \pm 0.5,9.8 \pm 2.5,22.3 \pm 2.6 \end{gathered}$ |
| T506P | $3.0 \pm 0.1$ | $0.16 \pm 0.06,0.39 \pm 0.17,5.2 \pm 2.0$ |

Equilibrium ${ }^{45} \mathrm{Ca}^{2+}$ binding was measured as described in "Materials and methods". The $\mathrm{Ca}^{2+}$-titration curves were fit to Adair equation for the appropriate number of sites. "Best fit" was obtained according to the $\chi^{2}$ weighting criteria. Values are presented as mean $\pm \operatorname{SEM}$ ( $\mathrm{n}=3$ for all the preparations).

Table S2. $\mathrm{Ca}^{2+}$ off-rates and amplitudes values of CBD12 mutants.

| Protein | Number of <br> exponents | Amplitudes (\%) |  | Rate constants (s $\mathrm{s}^{-1}$ ) |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | $A_{f}$ | $A_{s}$ | $k_{f}$ | $k_{s}$ |  |
| WT | 2 | $43.7 \pm 0.5$ | $56.3 \pm 0.5$ | $5.3 \pm 0.8$ | $0.6 \pm 0.02$ |  |
| H501A | 2 | $47.1 \pm 3.7$ | $52.9 \pm 3.7$ | $4.1 \pm 1.0$ | $0.9 \pm 0.1$ |  |
| A502P | 2 | $52.2 \pm 0.4$ | $47.8 \pm 0.4$ | $6.4 \pm 0.4$ | $1.1 \pm 0.03$ |  |
|  |  | $A_{r}$ | $A_{f}$ | $A_{s}$ | $k_{r}$ | $k_{f}$ |
| I504A | 3 | $28.2 \pm 1.7$ | $44.6 \pm 3.9$ | $27.2 \pm 3.6$ | $122.9 \pm 12.5$ | $1.8 \pm 0.3$ |
| F505A | 3 | $27.6 \pm 3.9$ | $43.3 \pm 3.2$ | $29.1 \pm 0.8$ | $96.6 \pm 14.5$ | $14.9 \pm 3.8$ |
| T506A | 3 | $17.5 \pm 0.6$ | $41.1 \pm 0.9$ | $41.4 \pm 0.8$ | $116.7 \pm 8.3$ | $2.0 \pm 0.1$ |

Traces were fit to double or triple exponential equations, as indicated, and are presented as mean $\pm \operatorname{SEM}(\mathrm{n}=6)$.

## Supplementary Figure Legend

Figure S1. ${ }^{45} \mathbf{C a}^{2+}$ titration curves of isolated CBD1 and CBD2. Curves were fitted with the following parameters: For CBD1, capacity $=4$ ions/protein and the $K_{d} S$ are $0.1,0.2,2,196 \mu \mathrm{M}$. For CBD2, capacity $=2$ ions $/$ protein and the $\mathrm{K}_{\mathrm{d}} \mathrm{S}$ are 8.5 and 47 $\mu \mathrm{M}$.

Figure S1


