**Table S1. X ray data collection and refinement statistics for human CSN6$^{\Delta C}$ crystal**

| Data collection | CSN6$^{\Delta C}$ (residues 31-211) |
|---|---|
| PDB code | 4QFT |
| Space group | $P3_121$ |
| Cell dimensions (Å) | |
| a | 96.84 |
| b | 96.84 |
| c | 48.33 |
| Maximal resolution (Å) | 1.76 |
| Observed reflections | 263,696 |
| Unique reflections | 26,172 |
| Completeness (%) | 100 |
| $R_{merge}$ [a] | 0.104 |
| Mean I/σ(I) | 14.4 |
| Highest resolution bin (Å) | 1.86-1.76 |
| Completeness (%) | 100 |
| $R_{merge}$ [a] | 0.492 |
| Mean I/σ(I) | 4.9 |
| | |
| Refinement | |
| Protein atoms | 1474 |
| Waters | 181 |
| Resolution range (Å) | 48.00-1.76 |
| $R_{conv}$ [b] (%) | 15.5 |
| $R_{free}$ [c] (%) | 20.6 |
| Mean protein B factor (Å$^2$) | 25.3 |
| Mean solvent B factor (Å$^2$) | 39.1 |
| Rms deviation bond angles (°) | 1.164 |
| Rms deviation bond length (Å) | 0.007 |
| Estimated coordinate error (Å) | 0.112 |

[a] $R_{merge} = \Sigma_h\Sigma_j |I_{h,j} - \bar{I}_h|/\Sigma_h\Sigma_j|I_{h,j}|$, where $I_{h,j}$ is the $j$th observation of reflection $h$.

[b] $R_{conv} = \Sigma_h||F_{oh}| - |F_{ch}||/\Sigma_h|F_{oh}|$, where $F_{oh}$ and $F_{ch}$ are the observed and calculated structure factor amplitudes respectively for the reflection $h$.

[c] $R_{free}$ is equivalent to $R_{conv}$ for a 5% subset of reflections not used in the refinement