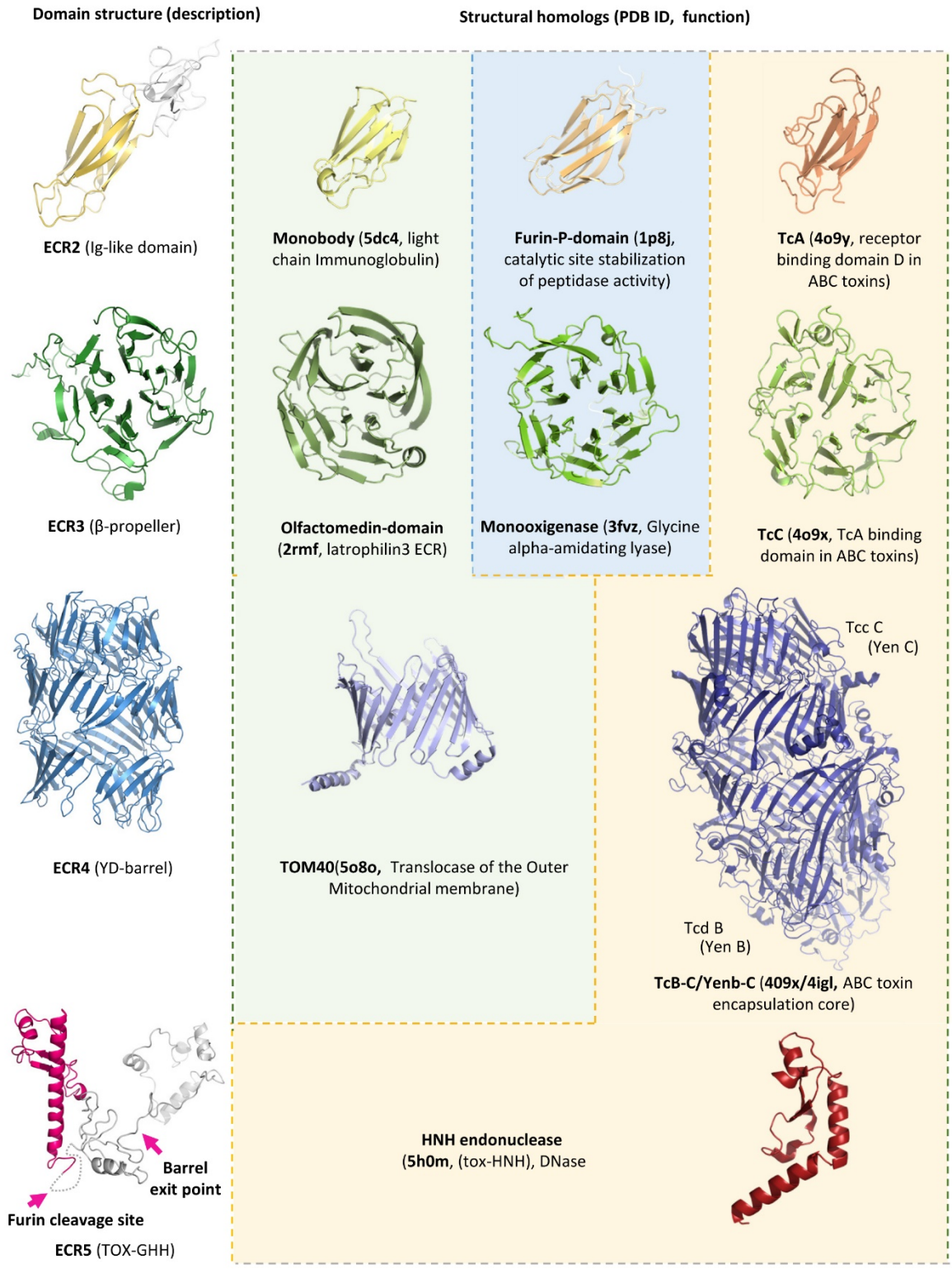
Table S1| Related to Figure 1; Data collection and Model Refinement

Data collection	
Particles	426,107
Pixel size (Å)	1.00
Defocus range	-1.4 to -2.4
Voltage (kV)	300
Electron dose (e^-/A^2)	45
Refinement	
CC map_model	0.735
Model content	
Total number of atoms	10,138
No. of protein chains	1
No. of sugar modifications	8
Model quality	
RMSD	
Bond lengths (Å) / Bond angles (°)	0.01/0.9
Ramachandran plot statistics	
Most favored (%)	90.25
Outliers (%)	0.15
Rotamer outliers (%)	0.81
C-beta deviations	0
Clashescore	19.75
B_iso_{mean}	45.07

Table S2| Related to Figures 1-2; Structural homologs of TEN2 domains



TEN2 domains are presented to the left. Domain names and numbers are indicated below the structure. Structural homologs are highlighted to the right. ABC toxin homologs are indicated by a yellow background. Homologs with protease activity, suspected to be involved in TCAP processing, in blue. Additional homologs in green. PDB ID and protein functions are indicated in parenthesis.