

Supplementary information for:

Metal transport mechanism of the cation diffusion facilitator (CDF) protein family – structural perspective on human CDF (ZnT)-related diseases

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hZnT1
TtCzrB
MgMamM
hZnT-8
AtMTP1
hZnT-10
EcYiiP
hZnT-2
hZnT-3

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MgMamM
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hZnT-3

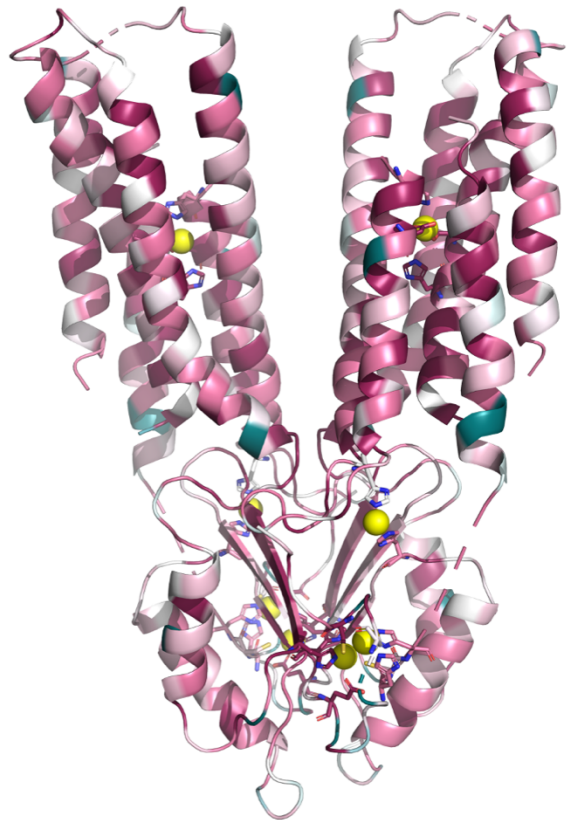
hZnT1
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hZnT1
TtCzrB
MgMamM
hZnT-8
AtMTP1
hZnT-10
EcYiiP
hZnT-2
hZnT-3

← Extended N-terminal
 ← Extended His-rich loop
 hZnT-8 TM helices
 ● A/S_{TM} site
 ● S_{IF} site
 ● B site
 ● S_{CDs} site
 ● C site



1 2 3 4 5 6 7 8 9
 Variable Average Conserved
 ☒ - Insufficient data

Figure S1. Sequence conservation between bacterial (*Escherichia coli* YiiP, *Thermus thermophilus* CzcB and *Magnetospirillum gryphiswaldense* MSR-1 MamM), plant (*Arabidopsis thaliana* MTP1) and human (ZnT-1, ZnT-2, ZnT-3, ZnT-8 and ZnT-10) CDF proteins. Multiple sequence alignment was calculated by ClustalO¹. Conservation scores and colored structure were produced by ConSurf server^{2,3} and PyMol version 2.3.5 (Schrödinger, LLC); scale of conservation ranges from dark blue (variable positions) to dark red (highly conserved positions); yellow coded residues refer to incomplete data (calculation for these sites were performed on less than 10% of the sequences). Functional regions are marked as colored arrays, human ZnT-8 transmembrane helices as cylinders and metal binding sites in human ZnT-8 and *E. coli* YiiP as colored spheres. Human ZnT-8 structure (PDB code 6XPE⁴) is presented and colored by ConSurf conservation scores, with metal binding residues presented as sticks and zinc ions in yellow spheres.

Supplemental references

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