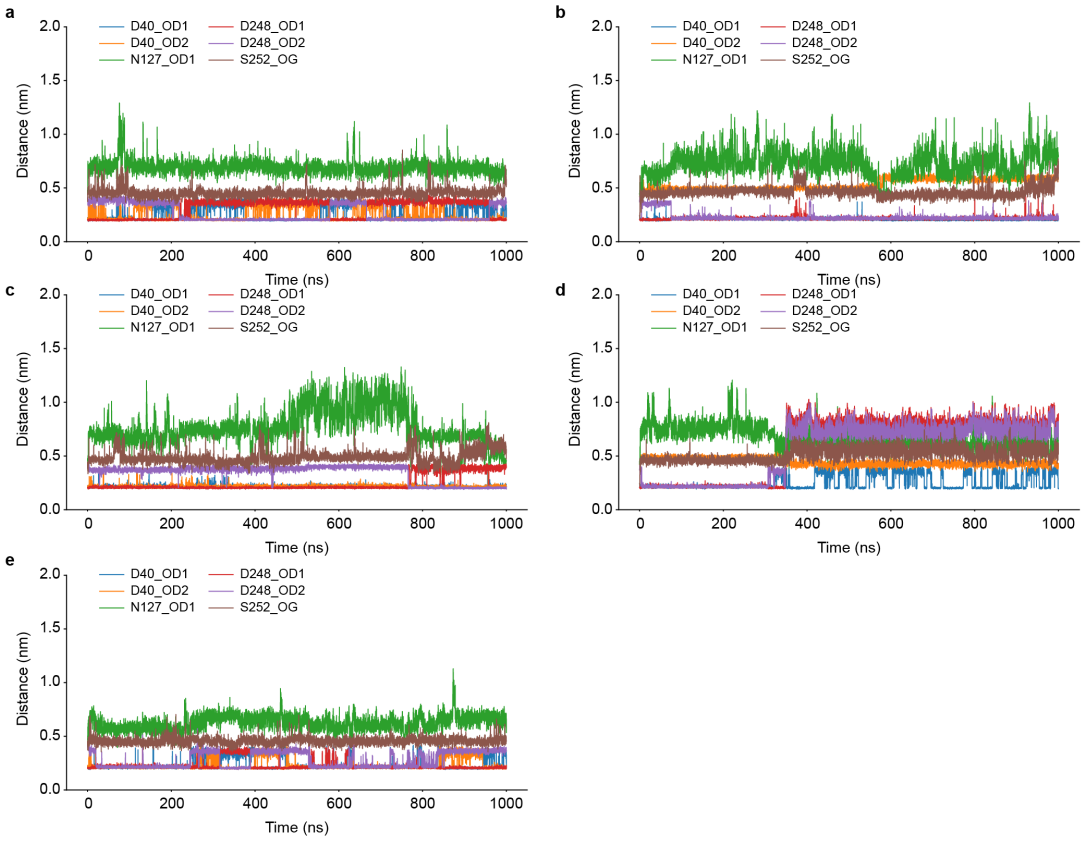
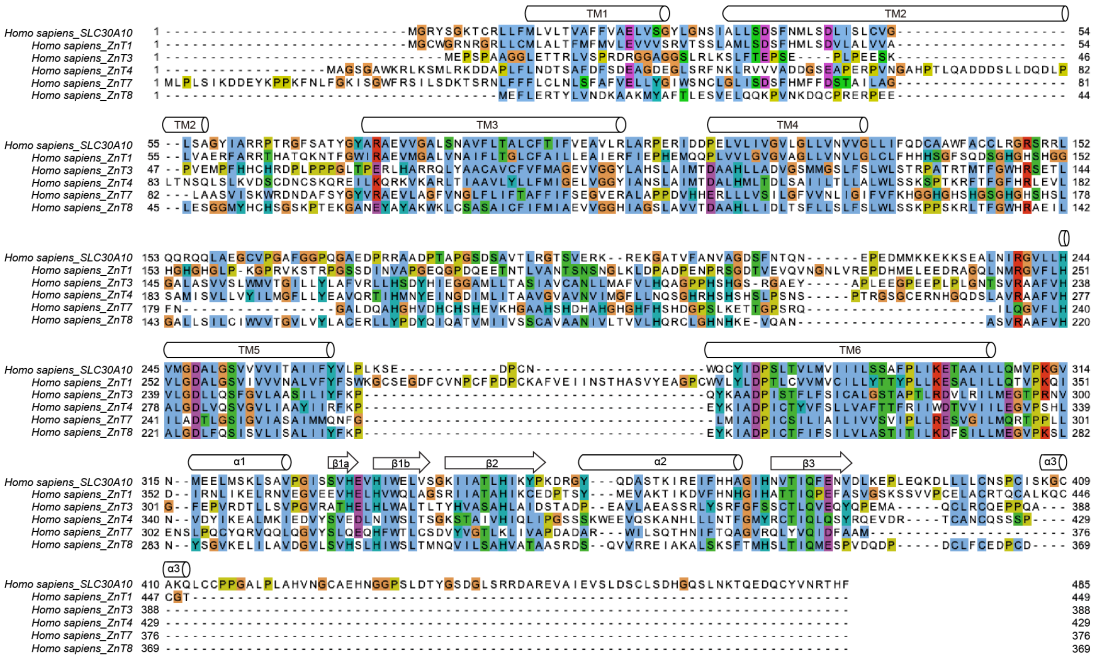


Supplementary Figure 1. MD simulation analysis of Mn^{2+}-bound hSLC30A10.
Time-dependent variation of the distance between Mn^{2+} and the coordinating residue atoms in molecular simulations of SLC30A10 over a 1000 ns time scale, in three replicas. **a-b**, Replicate 1 for each protomer of a Mn^{2+} -bound SLC30A10 dimer. **c-d**, Replicate 2 for each protomer of a Mn^{2+} -bound SLC30A10 dimer. **e**, Replicate 3 for one protomer of a Mn^{2+} -bound SLC30A10 dimer. The other protomer is shown in Fig. 3d.



Supplementary Figure 2. Sequence alignment of SLC30A10, ZnT1, ZnT3, ZnT4, ZnT7 and ZnT8. Secondary structural elements are labelled on the top of the sequences. Multiple Sequence Alignment was performed by ClustalW.

Supplementary Table 1. System for Molecular Dynamics simulations.

Molecule	Number of Molecules
SLC30A10	1
Mn^{2+}	2
POPC	2551
Na^{+}	88
Cl^{-}	84
Water	31002
Total atoms	135149

Supplementary Table 2. SLC30A10 gene mutations and blood Mn level of patients.

SLC30A10 mutation	Blood Mn level	Reference
p.Asp40Ala	3200 nM (NR<320)	[1]
p.Leu26Pro	3245 nM (NR<320)	[1]
p.Leu26Pro	3120 nM (NR<320)	[1]
p.Leu26Pro	2750 nM (NR<320)	[1]
p.Leu89Pro	2109 nM (NR<320)	[2]
p.Leu89Pro	1636 nM (NR<320)	[2]
p.Leu89Pro	1600 nM (NR<320)	[2]
p.Gly120Asp	2808 nM (NR<320)	[3]
p.Gly120Asp	2056 nM (NR<320)	[3]
p.His336Tyr	3000 nM (NR<320)	[4]
p.His336Tyr	14972.6 nM (NR<320)	[5]
p.His336Tyr	1511 nM (NR<320)	[5]
p.Leu349Pro	2366 nM (NR<320)	[2]
p.Ser41del	3310 nM (NR<320)	[1]
p.Val98_Phe134del	1145 nM (NR<320)	[2]
p.Ala105_Pro107del	N/A	[2]
p.Ala105_Pro107del	3285 nM (NR<320)	[2]
p.Val256del	3272 nM (NR<320)	[2]
p.Ile260del	3125 nM (NR<320)	[1]
p.Ile260del	3300 nM (NR<320)	[1]
p.Tyr30*	2980 nM (NR<320)	[1]
p.Gln154*	42 μg/L (NR 0.3-1.8)	[6]
p.Gly165Alafs*27	19.5 μg/L (NR 0.3-1.8)	[6]
p.Gly165Alafs*27	23.9 μg/L (NR 0.3-1.8)	[6]
p.Gly165Alafs*27	29.5 μg/L (NR 0.3-1.8)	[6]
p.Ala166Glnfs*7	9.8 μg/L (NR 0.3-1.8)	[6]
p.Phe167Ser, Pro170Leufs*22	231.6 nmol/l NR(<32.8)	[7]
p.Phe167Ser, Pro170Leufs*22	2626 nM NR(183–352)	[7]
p.Thr196Profs*17	3480 nM (NR<320)	[2]
p.Gln308*	N/A	[2]
p.Gln308*	3114 nM (NR<320)	[2]
p.Leu397Thrfs*15	1946 nM (NR<320)	[8]
p.Gln412Argfs*26	104.0 mcg/l NR(3.0–8.0)	[7]
p.Gln412Argfs*26	106 mcg/l NR(3.0–8.0)	[7]
c.957 + 1G >C (splice site mutation)	2900 nM (NR<320)	[1]
c.957 + 1G>C (splice site mutation)	3340 nM (NR<320)	[1]
deletion of exons 1 and 2	6180 nM (NR<320)	[2]
deletion of exons 1 and 2	3767 nM (NR<320)	[2]
deletion of exons 1 and 2	5096 nM (NR<320)	[2]
deletion of exons 1 and 2	6370 nM (NR<320)	[2]

NR: normal range; N/A: not available.

Supplementary Table 3. qRT-PCR primers.

Primer	Forward Primer (5'-3')	Reverse Primer (5'-3')
GAPDH	CAAATTCCATGGCACCGTCA	GACTCCACGACGTACTCAGC
SLC30A10-1	GAGATGGGCCGCTACTCTG	CAGGTCGGAGAGCATGTTGA
SLC30A10-2	GCTCTTCATGCTGGTGCTCA	CAGGTCGGAGAGCATGTTGA
FPN	AAAATCCCTGGGCCCCTTTT	GTCATGACACTAGGCGACCC
SPCA1	AACCCGAGTGCAGTTTCGAT	GCTTGCAACTTCACTGACTGG
TMEM165	GGCCCGGGTCGAGAAAATA	TCAGGCGGTTATAGCGCATT
ATP13A2	CTGTCCAGGTGCAGACTGAG	AGAGGTAATACCGCAGCACC
SLC39A8	GTTTCACCGCGGACCTGT	GTAGCCGAGGGGAGCGATA
SLC39A14	GATGCTAGAGCCGCAGAAGG	CCATAAGCCAAGCAGGGTCA
DMT1	GGTTGCGGAGCTGGTAAGAA	CCCAGGGGACTGTGAAAGAG
TRF1	GGACGCGCTAGTGTTCTTCT	CATCTACTTGCCGAGCCAGG

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