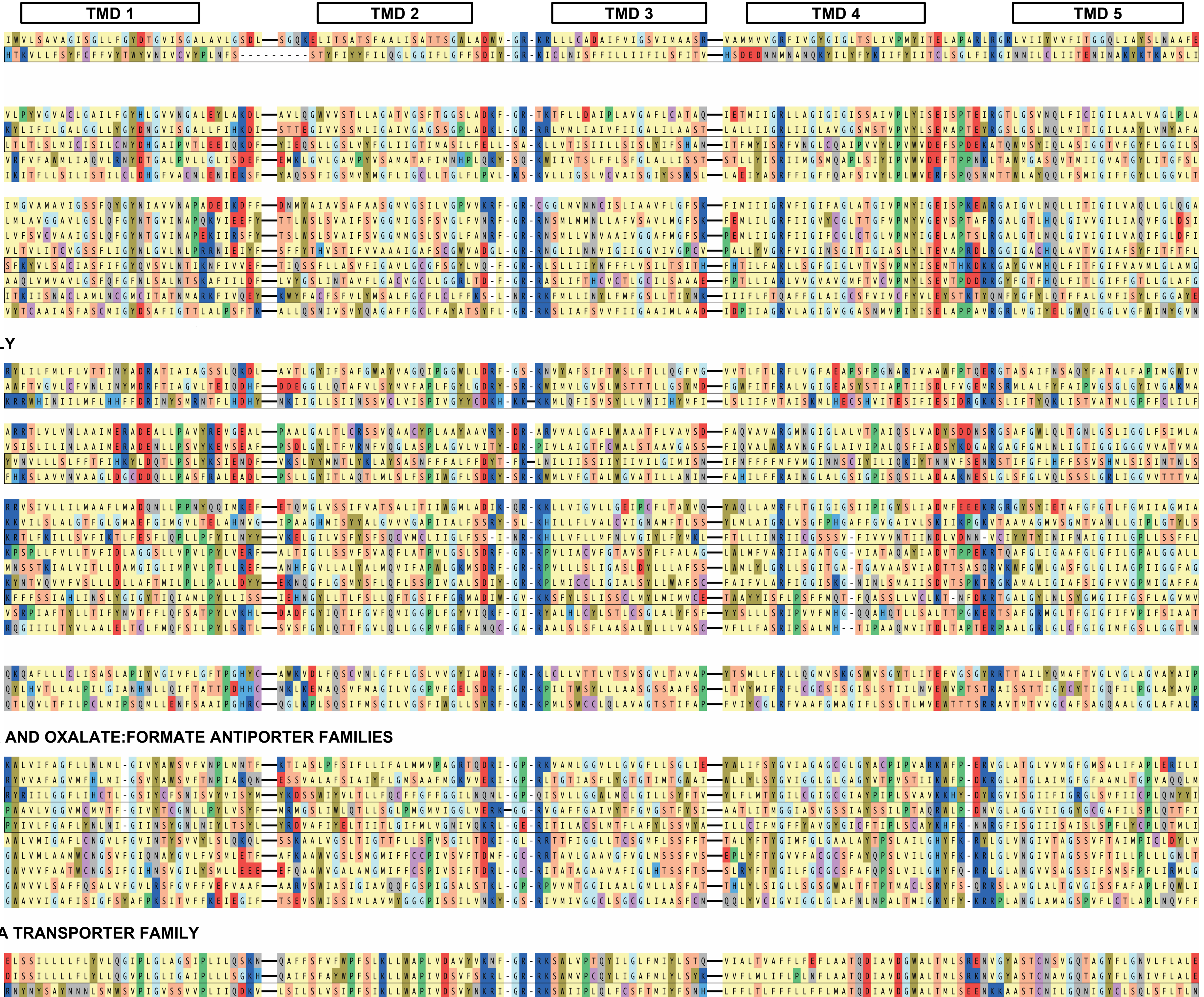
MAJOR FACILITATOR SUPERFAMILY



S. pombe 19114232 myo-inositol
PFL0170w

SUGAR PORTER FAMILY

O. europaea 15625046 plastid hexose (p)
S. epidermidis 27467165 bicyclomycin (p)
PFI0785c
C. parvum 46229527 unknown
C. parvum 46227905 unknown

H. roretzi 22759733 glucose (p)
H. sapiens 121751 glucose
X. laevis 29165704 sugar (p)
S. mansoni 1078817 glucose
PFB0210c (PfHT1)
T. gondii 21630202 glucose
PFI0955w
N. crassa 101871 quinate (p)

DRUG:H⁺ ANTIPORTER-1 FAMILY

P. putida 26990311 D-glucarate (p)
A. gambiae 31217117 unknown
PF11_0059

O. sativa 37806444 unknown
A. thaliana 15234530 unknown
PF14_0260
PFB0275w

P. furiosus 18976815 unknown
E. coli 1657592 arabinose (p)
PF14_0387
G. violaceus 35212055 tetracycline (p)
E. coli 135547 metal-tetracycline:H⁺
A. mellifera 48141033 unknown
PFE0825w
C. elegans 17539410 tumour suppressing (p)
M. musculus 6679180 organic cation (p)

ORGANIC CATION FAMILY

R. norvegicus 6981300 organic cation
M. musculus 31543719 organic anion
H. sapiens 8923870 organic anion

MONOCARBOXYLATE PORTER AND OXALATE:FORMATE ANTIPORTER FAMILIES

A. fulgidus 11497979 oxalate:formate (p)
L. lactis 7107009 oxalate:formate
PFB0465c
C. briggsae 39587811 unknown
PFI1295c
A. gambiae 21300238 unknown
R. norvegicus 20301958 aromatic amino acid
H. sapiens 5730045 monocarboxylate:H⁺ (p)
M. musculus 29336097 monocarboxylate:H⁺ (p)
H. sapiens 19923753 monocarboxylate:H⁺

PEPTIDE-ACETYL-COENZYME A TRANSPORTER FAMILY

H. sapiens 4757708 acetyl-CoA:CoA
C. elegans 17536529 acetyl-CoA:CoA (p)
PF10_0360

Additional data file 4. The alignment of the *P. falciparum* putative MFS proteins with a representative selection of MFS proteins from other organisms. The region over TMDs 1-5 of the alignment is shown. Sequences are separated into clusters of well-related sequences and are grouped as subfamilies of the MFS. *P . falciparum* sequences are boxed and the protein designators highlighted. For proteins of other organisms, the NCBI accession (gi) number and the known or putative (p) substrate specificity of the transporter are given. In some proteins, one or more of the extramembrane loop regions have been truncated and this is indicated by a solid black line. Residues are shaded as follows: positively charged, blue; negatively charged, red; hydoxyl, orange; amido, grey; proline, green; cysteine, purple; histidine, mid blue; glycine, light blue; tryptophan and tyrosine, olive green; remaining nonpolar, yellow.