



F Root mean square deviation (RMSD, Å) values for structural alignments of *Ec* SufE (PDB id: 1MZG) with homology models of *Pf* SufE and SufE-like domains of apicomplexan MnmA orthologs

<i>Pf</i> SufE	0.664
<i>Pf</i> MnmA	0.311
<i>Bm</i> MnmA	1.200
<i>Ta</i> MnmA	0.450
<i>Tg</i> MnmA	1.203
<i>Et</i> MnmA	1.066

G *Pf* MnmA
SufE-like domain (residues 146–380)

INDVQKIYDEVNNIKDKEQKINYLMEQCSSLCKENYFPPILNLNKAYRNKRIDEFNKGKNKIFYINE
VGKNIWYKYVNR**C**DEILFMAIDIQIDEDQRRNSIKDVHVDVHDDNIKTCTLIKDDKHFEKYKDIHN
DNILKNILPLDKKIDSIKNMLNHKYMKKKKCIITIDAYSNNLILYCFLYLILKHINKMYLYSFMNI
QIKEITAKLKEFLDLHFNVHHIIDYIHEYIYNFLMSY

H Percentage (%) sequence identity of SufE-like domains

	<i>Ec</i> SufE	<i>Pf</i> SufE	<i>Pf</i> MnmA	<i>Bm</i> MnmA	<i>Ta</i> MnmA	<i>Tg</i> MnmA	<i>Et</i> MnmA
<i>Ec</i> SufE		43.84	20.51	14.39	20.62	13.39	10.88
<i>Pf</i> SufE	43.84		27.59	10.88	20.71	13.77	13.07
<i>Pf</i> MnmA	20.51	27.59		16.52	35.48	18.5	15.04
<i>Bm</i> MnmA	14.39	10.88	16.52		20.83	24.02	22.9
<i>Ta</i> MnmA	20.62	20.71	35.48	20.83		19.92	16.23
<i>Tg</i> MnmA	13.39	13.77	18.5	24.02	19.92		27.07
<i>Et</i> MnmA	10.88	13.07	15.04	22.9	16.23	27.07	