

Homologous proteins in CMNR <sup>1</sup> microorganisms				Homologous proteins in mammalians <sup>2</sup>			
Organism	Protein	Identity (%)	E-value	Organism	Protein	Identity (%)	E-value
<i>C. pseudotuberculosis</i> 1002	SodC	100	3x10 <sup>-122</sup>	<i>Ovis aries</i>	Sod	36%	3x10 <sup>-15</sup>
<i>C. pseudotuberculosis</i> 258	SodC	100	3x 10 <sup>-122</sup>	<i>Bos taurus</i>	Sod1	34%	2x10 <sup>-15</sup>
<i>C. pseudotuberculosis</i> C231	SodC	100	3x10 <sup>-122</sup>	<i>Equus caballus</i>	Sod1	32%	8x10 <sup>-15</sup>
<i>C. diphtheriae</i> HC02	SodC	68	2x10 <sup>-75</sup>	<i>Mus musculus</i>	Sod1	34%	2x10 <sup>-16</sup>
<i>M. tuberculosis</i> SUMu007	SodC	43	9x10 <sup>-28</sup>	<i>Homo sapiens</i>	Sod1	34%	3x10 <sup>-16</sup>
<i>N. farcinica</i> IFM 10152	SodC	44	4x10 <sup>-35</sup>				
<i>Rhodococcus</i> sp. RHA1	SodC	49	2x10 <sup>-42</sup>				

**Additional file 3:** NCBI BLASTP searches were performed in UniprotKB database. <sup>1</sup>*Corynebacterium, Mycobacterium, Nocardia, Rhodococcus*; <sup>2</sup>*Ovis, Bos, Equus and Mus* genera, *Homo sapiens*.