

| Organism | UNIPROT | sirtuin | aa's | Da | pI | Pro | Ser | Thr | Sequence of the $\beta 8$ - $\beta 9$ connector region * |
|-------------------------------------|------------|---------|------|-------|------|-----|-----|-----|--|
| Leishmania | | | | | | | | | |
| <i>Leishmania infantum</i> | Q8I6E4 | SIR2rp1 | 84 | 9014 | 4.4 | 7 | 16 | 3 | RVGGLLFRFPDDPLNTVHEDAVAKEGRSSSSQSRSPSASPRREEGGTEDSPSSP NEE VEEASTSSSSDGYGQYGDYHAHPDVCR |
| <i>Leishmania major</i> | Q25337 | SIR2rp1 | 84 | 8961 | 4.2 | 5 | 16 | 3 | RVGGLLFRFPDDPLDTHDDAVAKEGRSSSSQSRSPSASARREEGGTEDGSSSP NEEVEDASTSSSSDGYGQYGDYHAHPDVCR |
| <i>Leishmania amazonensis</i> | Q8IT90 | SIR2rp1 | 84 | 8819 | 4.8 | 5 | 15 | 2 | RVGGLLFRFPDDPLNTVHDDAVAKEGQSSSSQSRSPSASARCEKGGVEDRSSS PKEGGDEASTSGSSDGYGQYGDYHAHPDLCR |
| Leptomonas | | | | | | | | | |
| <i>Leptomonas pyrrocoris</i> | A0A0N0VI28 | SIR2rp1 | 103 | 10389 | 3.9 | 6 | 21 | 3 | RVGGSFFRFPDDDDVPSAEGLAATSSAASSSSSRLLAGDGVGADSGDGHRS AAASTAPESIAATRESNEEGREEDAASSSSSSDGYAQYGDYDVHPPLCR |
| <i>Leptomonas seymouri</i> | A0A0N1HVQ5 | SIR2** | 93 | 9562 | 3.9 | 9 | 14 | 4 | RVGGNLFRRFPDDELPMFMDAVGATGAPSSPPQPPEAAGSADGHSSATGSTP QQCTAGLLEGDVEEREVSSSSSSDGYAQYGEYSAHPDLR |
| Phytomonas | | | | | | | | | |
| <i>Phytomonas sp. isolate Hart1</i> | W6L9Z1 | SIR2** | 102 | 10835 | 4.2 | 3 | 13 | 3 | IFNLERVGGRMFYLPEDVMDEKKASGREDDSSASSAAATHAEDDGIAMNGNA AATLHGNCDFDRNALEEPLLGEVASDSSSSSEGFITEHEEALLRPVCR |
| Trypanosoma | | | | | | | | | |
| <i>Trypanosoma brucei brucei</i> | Q57V41 | SIR2rp1 | 63 | 6825 | 9.5 | 2 | 11 | 5 | RVGGRMFRFPDTRTPNFRASSYRLSTGNGNGSKISSGDSSNSSSSVDGYDQFTL AENDETVLR |
| <i>Trypanosoma cruzi</i> | Q4DP02 | SIR2** | 60 | 6214 | 7.4 | 2 | 17 | 3 | RVGGAMFRFPDTEPTLNSFSRNHTGNSHSSSSNSSSSSSSSSDGYSQFANHAA DAGGICR |
| Non kinetoplastids | | | | | | | | | |
| <i>Plasmodium falciparum</i> | Q8IE47 | SIR2A | | | | | | | Region not observed |
| <i>Toxoplasma gondii</i> | B9PMV3 | SIR2 | 9 | 962 | 11.0 | 0 | 1 | 3 | TTGLTNRIS |
| <i>Entamoeba histolytica</i> | M3S670 | SIR2** | 13 | 1515 | 9.7 | 0 | 0 | 0 | KVGKMMCYDNLGR |
| <i>Schistosoma mansoni</i> | T1VXA1 | SIRT2 | 36 | 4210 | 10.2 | 0 | 5 | 1 | YNDGSTESGLSSFIMRFMVAGFKQNYMKWGRSDNKR |
| <i>Drosophila melanogaster</i> | Q9VK34 | SIR2 | | 1751 | 5.1 | 0 | 1 | 0 | QLHHLKFDVELLGD |
| <i>Saccharomyces cerevisiae</i> | P06700 | SIR2 | 7 | 827 | 7.8 | 1 | 0 | 0 | PVKHAEF |
| <i>Saccharomyces cerevisiae</i> | P53686 | Hst2 | 12 | 1334 | 10.6 | 1 | 0 | 2 | TVGDFKANKRPT |
| <i>Homo sapiens</i> | Q96EB6 | SIRT1 | 7 | 860 | 8.0 | 2 | 0 | 0 | PLPHLHF |
| <i>Homo sapiens</i> | Q8IXJ6 | SIRT2 | 28 | 2979 | 9.6 | 1 | 2 | 0 | KAGQSDPFLGMIMGLGGGMDFDSSKAYR |
| <i>Homo sapiens</i> | Q9NTG7 | SIRT3 | 12 | 1389 | 12.4 | 2 | 1 | 0 | LVGPLAWHPRSR |

* The connector region between $\beta 8$ and $\beta 9$ strands is defined by reference to conserved flanking amino acids Glu250 and Asp263 of ScHst2 via multiple sequence alignments (e.g. equivalent to Glu243 and Asp328 in LiSIR2rp1). ** hypothetical sir2rp1 homologs of ScHst2/hSIRT2.