**Table S1**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Old gene ID****(PlasmoDB 6.0)** | **New gene ID****(PlasmoDB 8.0)** | **PEXEL motif** | **PEXEL score** | **SP** | **TMD** | **MW (kDa)** | **comments** |
|  |  |  |  |  |  |  |  |
| PB108789.00.0 | PbANKA\_010020 | RvLsE | 11.93 | + | 2 | 39.5 | Member of *P. yoelii* subtelomeric family PYST-B |
| PB108818.00.0 | PbANKA\_100030 | RvLsE | 11.86 | + | 2 | 39.9 |  |
| **PB106275.00.0** | **PbANKA\_136550** | **RiLsE** | **11.70** | **h** | **1** | **36.3** | **IBIS-1 (1)** |
| PB402722.00.0 | PbANKA\_010020 | RvLsE | 11.51 | + | 2 | 39.5 | Identical to PB108789.00.0  |
| **PB108030.00.0** | **PbANKA\_140070** | **RhLaE** | **11.17** | **h** | **2** | **20.0** | **Conserved rodent malaria protein** |
| PB106994.00.0 | PbANKA\_070070 | RiLsS | 11.04 | h | - | 24.8 |  |
| PB000439.00.0 | PbANKA\_072150 | RnLnE | 10.26 | h | 1 | 261.5 |  |
| **PB103567.00.0** | **PbANKA\_021580** | **RiLaD** | **10.08** | **+** | **2** | **29.0** | **PbCP1 paralog****Member of *P. yoelii* subtelomeric family PYST-B** |
| PB108101.00.0 | PbANKA\_104030 | RiLaD | 9.91 | + | 1 | 28.3 | Member of *P. yoelii* subtelomeric family PYST-B |
| **PB106995.00.0** | **PbANKA\_070060** | **RyLsE** | **9.84** | **+** | **1** | **26.1** |  |
| PB402966.00.0 | PbANKA\_114540 | RnLsE | 9.28 | + | - | 55.2 | Identical to PB106385.00.0 |
| **PB106385.00.0** | **PbANKA\_114540** | **RnLsE** | **9.08** | **+** | **-** | **55.2** | **Homologous to surface protein in *Borrelia burgdorferi*****Identical to PB402966.00.0 according to new annotation** |
| PB103457.00.0 | PbANKA\_124590 | RlLaE | 8.93 | + | 1 | 51.0 | Phage fibre protein superfamily |
| PB000319.03.0 | PbANKA\_120060 | RiLaS | 8.88 | h | - | 251.0 |  |
| **PB101512.00.0** | **PbANKA\_021540** | **RiLaD** | **8.79** | **+** | **1** | **23.0** | **Member of *P. yoelii* subtelomeric family PYST-B** |
| PB102673.00.0 | PbANKA\_021560 | RiLaD | 8.42 | + | 2 | 30.2 | Member of *P. yoelii* subtelomeric family PYST-B |
| **PB108495.00.0** | **PbANKA\_000080** | **RtLaD** | **8.29** | **+** | **2** | **28.6** | **PbCP1 paralog****Member of *P. yoelii* subtelomeric family PYST-B** |
| PB000565.03.0 | PbANKA\_010930 | KiLyE | 8.09 | h | 6 | 33.3 | SNARE associated Golgi protein |
| PB103476.00.0 | PbANKA\_124620 | RiLvD | 8.04 | n.a. | n.a. | n.a. | Partial annotationIdentical to PB107841.00.0 according to PlasmoDB 8.0 |
| PB107841.00.0 | PbANKA\_124620 | RiLvD | 8.04 | n.a. | n.a. | n.a. | Partial annotationIdentical to PB103476.00.0 according to PlasmoDB 8.0 |
| PB106913.00.0 | PbANKA\_010060 | RfLvE | 7.77 | + | 1 | 18.9 | Conserved rodent malaria protein |

**Table S1**

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Old gene ID****(PlasmoDB 6.0)** | **New gene ID****(PlasmoDB 8.0)** | **PEXEL motif** | **PEXEL score** | **SP** | **TMD** | **MW (kDa)** | **comments** |
|  |  |  |  |  |  |  |  |
| PB000247.02.0 | PbANKA\_143230 | KsLaS | 7.46 | + | - | 20.8 | CelTOS (cell traversal protein for ookinetes and sporozoites) |
| **PB104040.00.0** | **PbANKA\_031630** | **RiLaY** | **7.36** | **+** | **1** | **32.2** |  |
| PB402997.00.0 | PbANKA\_114660 | RtLaD | 6.97 | + | 2 | 28.3 | Member of *P. yoelii* subtelomeric family PYST-BT-SNARE protein family |
| PB101458.00.0 | PbANKA\_146500 | RsLsE | 6.59 | + | - | 97.5 | Putative PYST-C2 homologue |
| PB108856.00.0 | n.a. | RiLsE | 6.24 | n.a. | n.a. | n.a. | Partial annotation |
| PB100936.00.0 | PbANKA\_030060 | RnLaE | 5.82 | h | 1 | 72.5 |  |
| PB108171.00.0 | PbANKA\_030440 | RiLgD | 5.78 | + | 1 | 21.6 | MSP4/5 |
| PB402817.00.0 | PbANKA\_124600 | RiLaY | 5.73 | + | 1 | 26.7 | Member of *P. yoelii* subtelomeric family PYST-B |
| **PB403061.00.0** | **PbANKA\_124660** | **RiLaY** | **4.80** | **+** | **2** | **29.0** | **PbCP1****Member of *P. yoelii* subtelomeric family PYST-B** |
| PB403104.00.0 | n.a. | RiLaY | 4.79 | n.a. | n.a. | n.a. | Partial annotation |
| PB107834.00.0 | PbANKA\_000400 | RiLaY | 4.76 | + | 2 | 28.3 | Highest homology to PbCP1 (Pb400)Member of *P. yoelii* subtelomeric family PYST-B |
| PB102226.00.0 | PbANKA\_140040 | RiLeE | 4.10 | + | 1 | 30.5 | Member of *P. yoelii* subtelomeric family PYST-B |
| PB108348.00.0 | PbANKA\_122900 | RnLsE | 4.08 | h | - | 126.3 | Glycoprotein (MG2) |
| PB102443.00.0 | PbANKA\_072280 | RiLaY | 4.08 | + | 2 | 28.9 | Member of *P. yoelii* subtelomeric family PYST-B |
| PB103795.00.0 | PbANKA\_072260 | RiLeE | 4.03 | + | 1 | 29.9 | Member of *P. yoelii* subtelomeric family PYST-B |
| **PB403086.00.0** | **PbANKA\_124710** | **RiLsY** | **4.01** | **+** | **2** | **28.4** | **Member of *P. yoelii* subtelomeric family PYST-B** |

1. Ingmundson A, Nahar C, Brinkmann V, Lehmann MJ, Matuschewski K. The exported *Plasmodium berghei* protein IBIS1 delineates membranous structures in infected red blood cells. *Mol* *Microbiol.* 2012 Mar;83(6):1229-43.