Figure S1

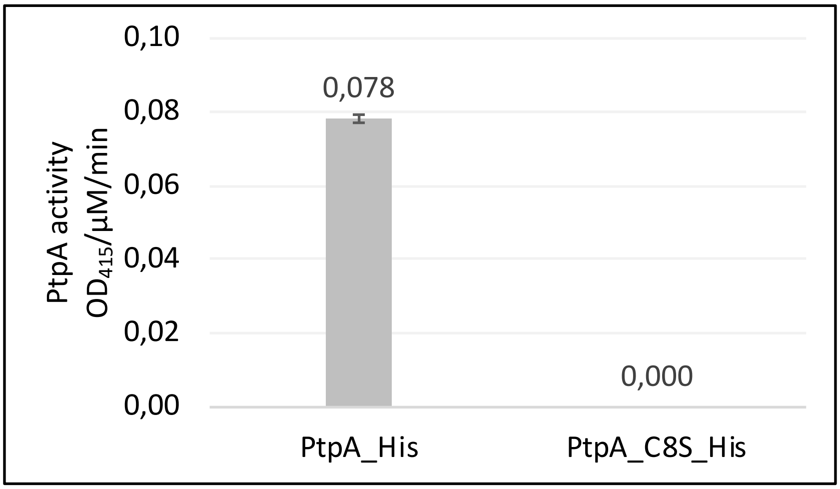
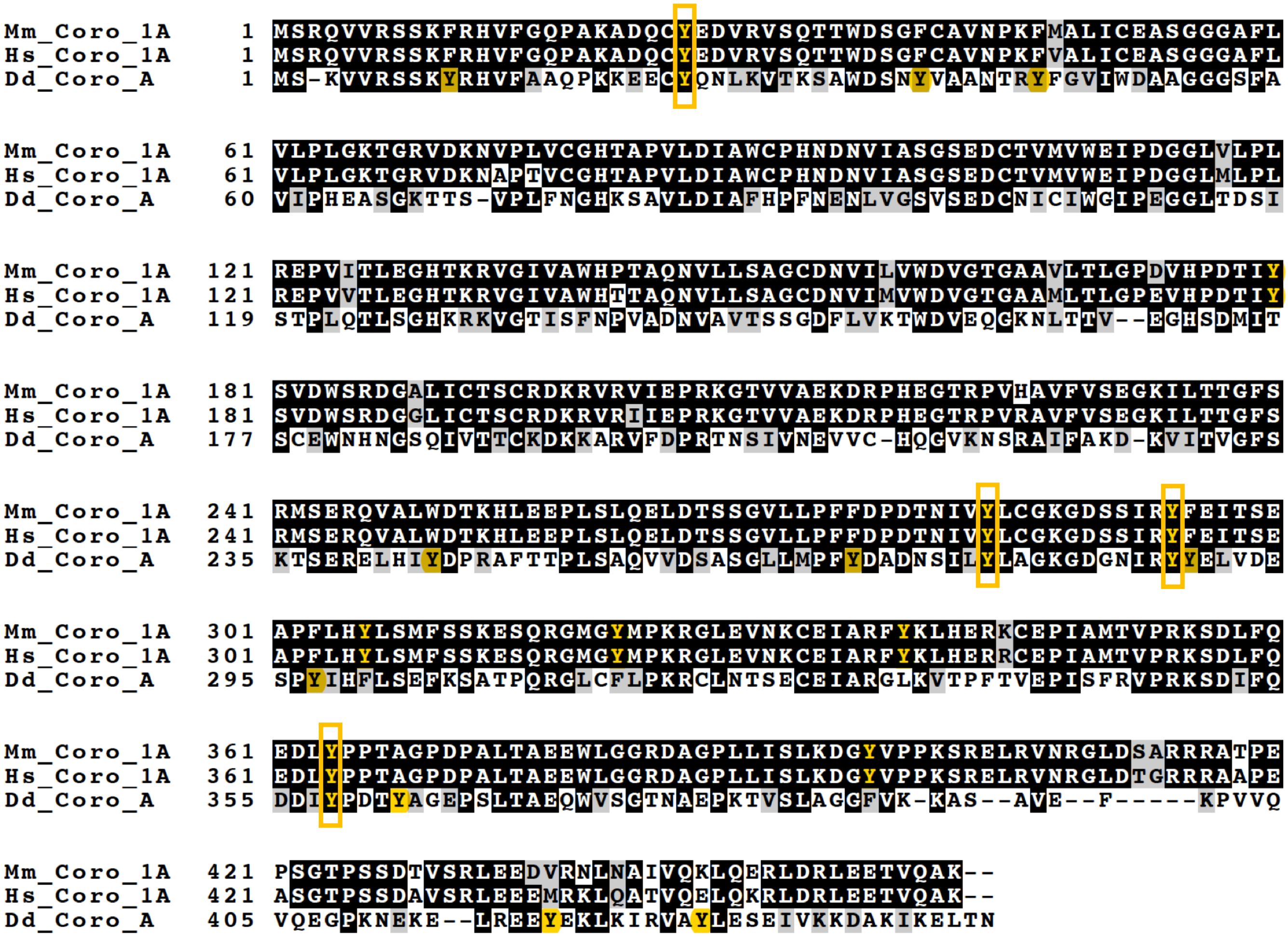


Figure S1: Phosphatase activity of PtpA and derivatives. PtpA$_{\text{\_His}}$ or PtpA_C8S$_{\text{\_His}}$ were used to test their phosphatase activity by using *p*-nitrophenylphosphate (pNPP) as a substrate as previously described by Brelle *et al.* (2016). The assay was performed in triplicate. The PtpA_C8S activity is null.

*Brelle, S., Baronian, G., Huc-Brandt, S., Zaki, L. G., Cohen-Gonsaud, M., Bischoff, M., and Molle, V. (2016) Phosphorylation-mediated regulation of the Staphylococcus aureus secreted tyrosine phosphatase PtpA. Biochem Biophys Res Commun **469**, 619-625*

Figure S2



```
Mm_Coro_1A     1 MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFMALICEASGGGAFL
Hs_Coro_1A     1 MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFVALICEASGGGAFL
Dd_Coro_A      1 MS-KVVRSSKYRHVFAAQPKKEECYQNLKVTKSAWDSNYVAANTRYFGVIWDAAGGGSFA

Mm_Coro_1A    61 VLPLGKTGRVDKNVPLVCGHTAPVLDIAWCPHNDNVIASGSEDCTVMVWEIPDGGLVLPL
Hs_Coro_1A    61 VLPLGKTGRVDKNAPTVCGHTAPVLDIAWCPHNDNVIASGSEDCTVMVWEIPDGGLMLPL
Dd_Coro_A     60 VIPHEASGKTTS-VPLFNGHKSAVLDIAFHPFNENLVGSVSEDCNICIWGIPEGGLTDSI

Mm_Coro_1A   121 REPVITLEGHTKRVGIVAWHPTAQNVLLSAGCDNVILVWDVGTGAAVLTLGPDVHPDTIY
Hs_Coro_1A   121 REPVVTLEGHTKRVGIVAWHTTAQNVLLSAGCDNVIMVWDVGTGAAMLTLGPEVHPDTIY
Dd_Coro_A    119 STPLQTLSGHKRKVGTISFNPVADNVAVTSSGDFLVKTWDVEQGKNLTTV--EGHSDMIT

Mm_Coro_1A   181 SVDWSRDGALICTSCRDKRVRVIEPRKGTVVAEKDRPHEGTRPVHAVFVSEGKILTTGFS
Hs_Coro_1A   181 SVDWSRDGGLICTSCRDKRVRIIEPRKGTVVAEKDRPHEGTRPVRAVFVSEGKILTTGFS
Dd_Coro_A    177 SCEWNHNGSQIVTTCKDKKARVFDPRTNSIVNEVVC-HQGVKNSRAIFAKD-KVITVGFS

Mm_Coro_1A   241 RMSERQVALWDTKHLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSE
Hs_Coro_1A   241 RMSERQVALWDTKHLEEPLSLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSE
Dd_Coro_A    235 KTSERELHIYDPRAFTTPLSAQVVDSASGLLMPFYDADNSILYLAGKGDGNIRYYELVDE

Mm_Coro_1A   301 APFLHYLSMFSSKESQRGMGYMPKRGLEVNKCEIARFYKLHERKCEPIAMTVPRKSDLFQ
Hs_Coro_1A   301 APFLHYLSMFSSKESQRGMGYMPKRGLEVNKCEIARFYKLHERRCEPIAMTVPRKSDLFQ
Dd_Coro_A    295 SPYIHFLSEFKSATPQRGLCFLPKRCLNTSECEIARGLKVTPFTVEPISFRVPRKSDIFQ

Mm_Coro_1A   361 EDLYPPTAGPDPALTAEEWLGGRDAGPLLISLKDGYVPPKSRELRVNRGLDSARRRATPE
Hs_Coro_1A   361 EDLYPPTAGPDPALTAEEWLGGRDAGPLLISLKDGYVPPKSRELRVNRGLDTGRRRAAPE
Dd_Coro_A    355 DDIYPDTYAGEPSLTAEQWVSGTNAEPKTVSLAGGFVK-KAS--AVE--F-----KPVVQ

Mm_Coro_1A   421 PSGTPSSDTVSRLEEDVRNLNAIVQKLQERLDRLEETVQAK--
Hs_Coro_1A   421 ASGTPSSDAVSRLEEEMRKLQATVQELQKRLDRLEETVQAK--
Dd_Coro_A    405 VQEGPKNEKE--LREEYEKLKIRVAYLESEIVKKDAKIKELTN
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Figure S2: Sequence alignment of Coronin 1A proteins. Sequences were aligned using ClustalW program. Alignments are shaded using the BOXSHADE server. Sequence designations and NCBI GI numbers are as follows: Mm_Coro-1A from Murine macrophages, GI O89053; Hs_Coro-1A from Homo sapiens, GI P31146; and Dd_Coro-A from *Dictyostelium discoideum*, GI P27133. Black boxes represent identical residues and grey boxes indicate similar residues. Tyrosine residue (Y) are highligted in orange. Similar tyrosine residues in all three species are framed in orange boxes.

Figure S3

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Plasmodium falciparum         ----MYNVPLIKNLYPDPS--NNLYGDLRICSRATETCGIACSAGYIAVPWQVEGGGMIG  54
Toxoplasma gondii             -MADAVDVPLIKNLYAEAW--KQQYSDLRLSTKQTESCGLAANTEYIAAPWDVGGGGVLG  57
Amphimedon queenslandica      -MAFKQRHSKFKHVKGEPFKKDNCYDNVKISKSPWDSNKSDVNGKFLAVVLESQGGGAFT  59
Caenorhabditis elegans        -MAQIVRQSKFRHVFCKPVKHESCMSDIRVTEITWDSLFCDVNPKFIAFINRG-AGGPFM  58
Anopheles darlingi            MSFRVVRSSKFRHVYGQALKREQCYDNIRVSKSSWDSTFCAVNPKFLAIIVESAGGGAFI  60
Drosophila melanogaster       MSFRVVRSSKFRHVYGQALKREQCYDNIRVSKSSWDSTFCAVNPKFLAIIVESAGGGAFI  60
Nilaparvata lugens            MSFRVVRTSKFRHVYGSSLKRDQCYDNIRVSKSSWDSTFCCVNPKFLAIIVESAGGGAFI  60
Trichogramma pretiosum        MSFRVVRSSKFRHVYGTPLKREQCYDNIRVSKSSWDSTFCAVNPKFLAIIVESAGGGAFI  60
Columba livia                 -MRRVVRQSKFRHVFGQAVKNDQCYDDIRVSRVTWDSSFCAVNPRFVAIIVDASGGGAFL  59
Gallus gallus                 -MRRVVRQSKFRHVFGQAVKNDQCYDDIRVSRVTWDSSFCAVNPRFVAIIVDASGGGAFL  59
Danio rerio                   MSRKVVRSSKFRHVFGQAVKADQCYDDIRISQMTWDSNFCSVNPKFVSMIVDASGGGAFI  60
Salmo salar                   MSRKVVRASKFRHVFGQGVKADQCYDDIRISQMTWDSNFCSVNPKFVAMIVDASGGGAFL  60
Xenopus tropicalis            MSRKVVRTSKFRHVFGQAVKADQCYDDIRVSQNTWDSNFCCVNPKFLAIVVEASGGGAFM  60
Ophiophagus hannah            MSRKVVRSSKFRHVYGQPVKGDQCYDDIRVSQMTWDGNFCSVNPQFLAIVVEASGGGAFL  60
Python bivittatus             MSRKVVRSSKFRHVYGQPVKADQCYDDIRVSQMTWDGNFCSVNPQFLAIVVEASGGGAFL  60
Chrysemys picta bellii        MSRKVVRSSKFRHVFGQPAKADQCYDDVRISQTTWDSSFCSVNPKFLAMIVEASGGGAFM  60
Mus musculus                  MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFMALICEASGGGAFL  60
Pteropus alecto               MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFVALICEASGGGAFL  60
Trichechus manatus            MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFVALICEASGGGAFL  60
Homo sapiens                  MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFVALICEASGGGAFL  60
Macaca nemestrina             MSRQVVRSSKFRHVFGQPAKADQCYEDVRVSQTTWDSGFCAVNPKFVALICEASGGGAFL  60
Dictyostelium discoideum      -MSKVVRSSKYRHVFAAQPKKEECYQNLKVTKSAWDSNYVAANTRYFGVIWDAAGGGSFA  59
Entamoeba histolytica         MSYRFIRTSKYRHVFGTEFKNDQQYNGTKMTNSAWDSNIIVCGYKHFSMIWDVAGGGAFA  60
Saccharomyces cerevisiae      MSGKFVRASKYRHVFGQAAKKELQYEKLKVTNNAWDSNLLKTNGKFIAVNWNASGGGAFA  60
Penicillium camemberti        MSGRFVRSSKYRHVFGRSTRKDQCYDNLRVSRNAWDTNLLKVNPKHIAVNWEAGGGGAFA  60

Plasmodium falciparum         TTS-PL-TTITLDNAASPLLPHYDESVGMIYLIGKGDGNCRYYQYSQGS--IRKVDEYKS  305
Toxoplasma gondii             FDK-PV-YHAEIDRGSSPLYPIFDETTGMLYVCGKGDSSCRYYQYHGGT--LRSVDAYRS  308
Amphimedon queenslandica      LSS-SL-ATETLDNGSGTIFSFFDEDTKMVYFIGKGDGQMRYYEILDESPYVQQLSMYQH  310
Caenorhabditis elegans        LST-PI-VEEELDTSNGVVFPFYDEDSGLVYLVGKGDCAIRYYEVNNDAPYVHYINTYTT  307
Anopheles darlingi            LGD-PI-VMVELDTSNGVMFPLYDPDTNLIYLCGKGDSVIRYFEVTPEQPFVHYINQFQT  340
Drosophila melanogaster       LNE-PI-VMVELDTSNGVMFPLYDADTNMIYLCGKGDSVIRYFEVTPEPPFVHYINTFQT  309
Nilaparvata lugens            LTE-PI-VMVELDTSNGVMFPLYDPDTNLVYLCGKGDSVIRYFEITAELPFVHYINTFQT  309
Trichogramma pretiosum        LAE-PI-TMLELDTSNGVMFPLYDPDTNLVYLCGKGDSVIRYFEITPEPPFVHYINTFQT  309
Columba livia                 MEE-PI-ALHEMDTSNGVLLPFYDPDTNIIYLCGKGDSSIRYFEITDESPYVHYLNTFSS  310
Gallus gallus                 MEE-PI-ALHEMDTSNGVLLPFYDPDTNIIYLCGKGDSSIRYFEITDESPYVHYLNTFSS  310
Danio rerio                   FGE-PL-TLQELDTSSGVLLPFFDPDTGIVYLCGKGDSSIRYFEVTDEAPYVHYLSMYSS  311
Salmo salar                   FGE-PL-TLQELDTSSGVLLPFFDPDTGIVYLCGKGDSSIRYFEVTDEAPYVHYLSMYSS  311
Xenopus tropicalis            LGE-PL-TLQELDTSSGVLIPFFDPDTNVVYLCGKGDSSIRYFEVTDEPPYVHYLSLYSS  310
Ophiophagus hannah            PEE-PL-TLQELDTSSGVLLPYYDPDTNVVYLTGKGDSSIRYFELTGEAPYVHYLSMFTS  312
Python bivittatus             PEE-PL-TLQELDTSSGVLLPYYDPDTNVVYLTGKGDSSIRYFELTGEAPYVHYLSMFTS  312
Chrysemys picta bellii        LEE-PM-NLQELDTSSGVLLPHYDPDTSMVYLCGKGDSSIRYFEVTPEAPYLHFLSLFSS  311
Mus musculus                  LEE-PL-SLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSEAPFLHYLSMFSS  312
Pteropus alecto               LEE-PL-SLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSEAPFLHYLSMFSS  312
Trichechus manatus            LEE-PL-SLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSEAPFLHFLSMFSS  312
Homo sapiens                  LEE-PL-SLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSEAPFLHYLSMFSS  312
Macaca nemestrina             LEE-PL-SLQELDTSSGVLLPFFDPDTNIVYLCGKGDSSIRYFEITSEAPFLHYLSMFSS  312
Dictyostelium discoideum      FTT-PL-SAQVVDSASGLLMPFYDADNSILYLAGKGDGNIRYYELVDESPYIHFLSEFKS  306
Entamoeba histolytica         LES-PL-CRHTVDNQSGVLMPFYDPDLSLLYLGGKGDSTISYFEIVHKKPYFYSLNTFRG  309
Saccharomyces cerevisiae      IEKGDLGGFYTVDQSSGILMPFYDEGNKILYLVGKGDGNIRYYEFQNDE--LFELSEFQS  318
Penicillium camemberti        V-REPINGFKTLDSISGVCMPFWDDGTNMLYLAGRGDGNIRYFELENDK--FEFLSEHKS  316

Plasmodium falciparum         CLPFRSFGFLPKRMCDVYKCEIGRVYKNGNNTDIRPISFYVPRKNSSIFQEDLYPPIIMR  365
Toxoplasma gondii             SVPIKNFCFIPKLAVDQMRAEIGRMLKQENGNVLQPISFIVPRKNQDVFQADLYPPAPDV  368
Amphimedon queenslandica      SLPQIGVCSMPKRFLDHKACEVMRFFKLHNKGMVEPIQMIVPRK-SGMFQEDIFPPCYAG  369
Caenorhabditis elegans        NEPQRAVGFQSKRGMSSEENEINRIYKLTTKGVVDILQFFVPRK-SDLFQHDLYPDTRST  366
Anopheles darlingi            PDSQRAIGMMPKRGCDVSTCEVARFYRLNNSGLCQVISMTVPRK-SELFQEDLYPDTLAD  399
Drosophila melanogaster       TEPQRGIGLMPKRGCDVTTCEVAKFYRMNNNGLCQVISMTVPRK-SDLFQEDLYPDTLAE  368
Nilaparvata lugens            PDPQRGIGMMPKRGCDVSSCEITRFYRLNNSGLCQVITMTVPRK-SELFQEDLYPDTLGD  368
Trichogramma pretiosum        PDPQRGIGMMPKRGCDVNSCEISRFYRLNNSGFCQVVSMTVPRK-SELFQEDLYPDTPGD  368
Columba livia                 KEPQRGMGFMPKRGLDVNKCEIARFFKLHE-RKCEPIIMTVPRK-SDLFQDDLYPDTAGP  368
Gallus gallus                 KEPQRGMGFMPKRGLDVNKCEIARFFKLHE-RKCEPIIMTVPRK-SDLFQDDLYPDTAGP  368
Danio rerio                   KESQKGMGYMPKRGLEVNKCEIARFYKLHE-RKCEPVVMTVPRK-SDLFQEDLYPNTVGP  369
Salmo salar                   KESQKGMGYMPKRGLEVNKCEIARFYKLHE-RKCEPIVMTVPRK-SDLFQEDLYPDTMGP  369
Xenopus tropicalis            KESQRGMGYMPKRGLEVNKCEIARFYKLHE-RKCEPIIMTVPRK-SDLFQEDLYPDTVGP  368
Ophiophagus hannah            KESQRGGGWMPKRGLDVSKCEIARFYKLHE-RKCEPIAMTVPRK-SDLFQEDLYPDTAGP  370
Python bivittatus             KESQRGGGWMPKRGLDVSKCEIARFYKLHE-RKCEPIAMTVPRK-SDLFQEDLYPDTAGP  370
Chrysemys picta bellii        KESQRGGGWMPKRGLDVSKCEIARFYKLHE-RRCEPIAMTVPRK-SDLFQEDLYPDTAGP  369
Mus musculus                  KESQRGMGYMPKRGLEVNKCEIARFYKLHE-RKCEPIAMTVPRK-SDLFQEDLYPPTAGP  370
Pteropus alecto               KESQRGMGYMPKRGLEVNKCEIARFYKLHE-RRCEPIAMTVPRK-SDLFQEDLYPPTAGP  370
Trichechus manatus            KESQRGMGYMPKRGLEVNKCEIARFYKLHE-RRCEPIAMTVPRK-SDLFQEDLYPPTAGP  370
Homo sapiens                  KESQRGMGYMPKRGLEVNKCEIARFYKLHE-RRCEPIAMTVPRK-SDLFQEDLYPPTAGP  370
Macaca nemestrina             KESQRGMGYMPKRGLEVNKCEIARFYKLHE-RRCEPIAMTVPRK-SDLFQEDLYPPTAGP  370
Dictyostelium discoideum      ATPQRGLCFLPKRCLNTSECEIARGLKVTP-FTVEPISFRVPRK-SDIFQDDIYPDTYAG  364
Entamoeba histolytica         EKPQSGLGVIPKRLCNTTICEITKFMKIVP-DGVVPISFCVPRK-SEFFQDDIFPNTYAG  367
Saccharomyces cerevisiae      TEAQRGFAVAPKRMVNVKENEVLKGFKTVVDQRIEPVSFFVPRR-SEEFQEDIYPDAPSN  377
Penicillium camemberti        ADPQRGVAFMPKRGVNMHDNEVARAYKTVNDQYIEPVSFIVPRR-SETFQDDIYPPTVGV  375
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Figure S3: Sequence alignment of conserved tyrosine residues harboring regions of Coronin 1 proteins. Sequences were aligned using Clustal Omega. Conserved tyrosine residues are labeled in yellow, mismatches are indicated in red. Sequences corresponding to the ones dipicted in Fig. S2 are labeld in blue. Sequences were obtained from the following NCBI entries: *Amphimedon queenslandica*, XP_003382924; *Anopheles darlingi*, GI 568254291; *Caenorhabditis elegans*, GI 25150742; *Chrysemys picta bellii*, XP_005290238; *Columba livia*, GI 1307741494; *Danio rerio*, GI 41055464; *Drosophila melanogaster*, GI 21685588; *Entamoeba histolytica*, GI 1033413111; *Gallus gallus*, GI 482661642; *Homo sapiens*, GI P31146; *Macaca nemestria*, GI 795657297; *Mus musculus*, GI O89053; *Nilaparvata lugens*, XP_022202333; *Ophiophagus hannah*, GI 565307310; *Penicillium camemberti*, GI 902279349; *Plasmodium falciparum*, GI 2808641; *Pteropus alecto*, GI 586561765; *Python bivittatus*, GI 602635008; *Saccharomyces cerevisiae*, GI 151940945; *Salmo salar*, GI 223647640; *Toxoplasma gondii*, GI 53801426; *Trichechus manatus*, GI 471410223;*Trichogramma pretiosum*, XP_014222528; *Xenopus tropicalis*, GI 54262238.