| Description | Max Score | Total Score | Query | E value | Per. Ident | Accession |
|--|--------------|----------------|-------|------------|---------------|----------------|
| pyridoxal kinase [Plasmodium falciparum 3D7] | 209 | 348 | 100% | 3e-63 | 100.00% | XP_966146.1 |
| pyridoxine kinase [Plasmodium falciparum IGH-CR14] | 164 | 164 | 92% | 7e-46 | 89.19% | KNG73950.1 |
| hypothetical protein PFHG_00578 [Plasmodium falciparum HB3] | 160 | 258 | 100% | 2e-44 | 86.09% | KOB58829.1 |
| hypothetical protein PFDG_04483 [Plasmodium falciparum Dd2] | 159 | 257 | 100% | 3e-44 | 86.09% | KOB88033.1 |
| pyridoxal kinase [Plasmodium gaboni] | 159 | 466 | 100% | 6e-44 | 83.76% | SOV12284.1 |
| pyridoxal kinase [Plasmodium sp. DRC-Itaito] | 143 | 279 | 99% | 4e-38 | 79.44% | SOV21668.1 |
| pyridoxal kinase [Plasmodium reichenowi] | 137 | 527 | 100% | 7e-36 | 79.63% | SOV77504.1 |
| pyridoxal kinase [Plasmodium gaboni] | 135 | 398 | 95% | 4e-35 | 79.00% | XP_018642797.1 |
| pyridoxal kinase [Plasmodium sp. gorilla clade G2] | 135 | 260 | 99% | 5e-35 | 67.54% | XP_028537308.1 |
| Beta-ketoacyl synthase [Beauveria brongniartii RCEF 3172] | 135 | 4732 | 100% | 3e-34 | 73.11% | OAA50030.1 |
| hypothetical protein PENFLA_c125G03904 [Penicillium flavigenum] | 124 | 492 | 100% | 2e-33 | 50.00% | OQE08728.1 |
| pyridoxal kinase [Plasmodium reichenowi] | 125 | 125 | 81% | 2e-31 | 78.57% | CDO63349.1 |
| pyridoxal kinase [Plasmodium falciparum Palo Alto/Uganda] | 124 | 308 | 90% | 2e-31 | 89.16% | ETW53186.1 |
| hypothetical protein DUI87_24655 [Hirundo rustica rustica] | 115 | 342 | 100% | 1e-30 | 42.86% | RMB98441.1 |
| PREDICTED: keratin-associated protein 6-2-like [Octopus bimaculoides] | 119 | 1474 | 100% | 1e-30 | 35.83% | XP_014785252.1 |
| Compactin diketide synthase mokB [Beauveria bassiana] | 121 | 528 | 100% | 2e-29 | 62.18% | PMB69322.1 |
| Lovastatin nonaketide synthase [Beauveria bassiana D1-5] | 120 | 410 | 100% | 4e-29 | 61.67% | KGQ12279.1 |
| hypothetical protein BB8028_0003g08250 [Beauveria bassiana] | 119 | 566 | 100% | 8e-29 | 63.03% | PQK12208.1 |
| Beta-ketoacyl synthase [Cordyceps confragosa RCEF 1005] | 116 | 851 | 100% | 1e-27 | 62.18% | OAA78033.1 |
| hypothetical protein EN45_062540 [Penicillium chrysogenum] | 108 | 428 | 99% | 1e-27 | 49.53% | KZN87693.1 |
| hypothetical protein EN45_063710 [Penicillium chrysogenum] | 106 | 422 | 100% | 9e-27 | 50.00% | KZN87810.1 |
| pyridoxal kinase [Plasmodium falciparum Santa Lucia] | 112 | 461 | 100% | 1e-26 | 87.34% | EUT89866.1 |
| hypothetical protein LLEC1_05370 [Cordyceps confragosa] | 113 | 953 | 100% | 2e-26 | 58.82% | OAR01380.1 |
| putative membrane protein [Plasmodium reichenowi] | 110 | 1061 | 100% | 1e-25 | 41.53% | XP_012764852.2 |
| hypothetical protein LOTGIDRAFT_164889 [Lottia gigantea] | 104 | 708 | 100% | 7e-25 | 40.16% | XP_009059650.1 |
| conserved Plasmodium protein, unknown function [Plasmodium falciparum 3D7] | 108 | 833 | 97% | 9e-25 | 44.80% | XP_002808861.1 |
| pyridoxal kinase [Plasmodium reichenowi] | 107 | 211 | 87% | 9e-25 | 77.38% | XP_012761977.2 |
| Plasmodium exported protein (hyp4), unknown function [Plasmodium reichenowi] | 105 | 555 | 100% | 2e-24 | 49.57% | SOV75054.1 |
| hypothetical protein TSACC 21742 [Terrimicrobium sacchariphilum] | 98.2 | 648 | 99% | 5e-24 | 66.29% | GAT33328.1 |
| N-acetyl-D-glucosamine kinase-like [Penaeus vannamei] | 105 | 600 | 95% | 7e-24 | 69.39% | XP_027208985.1 |
| Beta-ketoacyl synthase [Cordyceps fumosorosea ARSEF 2679] | 105 | 567 | 100% | 1e-23 | 58.54% | XP_018705471.1 |
| hypothetical protein PFHG_02530 [Plasmodium falciparum HB3] | 104 | 201 | 97% | 2e-23 | 44.00% | KOB60798.1 |
| conserved Plasmodium membrane protein, unknown function [Plasmodium reichenowi] | 104 | 583 | 100% | 3e-23 | 50.81% | SOV79843.1 |
| splicing factor U2af large subunit A-like [Nilaparvata lugens] | 99.4 | 2582 | 100% | 4e-23 | 42.50% | XP_022198530.1 |
| hypothetical protein PFMG_01564 [Plasmodium falciparum IGH-CR14] | 102 | 297 | 97% | 7e-23 | 44.00% | KNG75333.1 |
| pyridoxal kinase [Plasmodium sp. gorilla clade G3] | 101 | 474 | 96% | 7e-23 | 67.09% | SOV74700.1 |
| Beta-ketoacyl synthase [Cordyceps militaris] | 102 | 781 | 100% | 1e-22 | 57.98% | ATY60574.1 |
| polyketide synthase, putative [Cordyceps militaris CM01] | 102 | 444 | 99% | 1e-22 | 58.82% | XP_006667589.1 |
| hypothetical protein, conserved [Plasmodium vivax] | 101 | 733 | 97% | 2e-22 | 70.37% | XP_001608467.1 |
| hypothetical protein EDD98_3099 [Streptomyces sp. PanSC19] | 99.4 | 1573 | 100% | 2e-22 | 44.17% | ROQ34065.1 |
| conserved Plasmodium protein, unknown function [Plasmodium knowlesi strain H] | 100 | 293 | 100% | 5e-22 | 42.50% | SBO23952.1 |
| conserved Plasmodium protein, unknown function [Plasmodium gaboni] | 100 | 375 | 100% | 5e-22 | 62.07% | SOV15009.1 |
| lovastatin nonaketide synthase [Nannizzia gypsea CBS 118893] | 100 | 318 | 91% | 6e-22 | 59.26% | XP_003170591.1 |
| conserved Plasmodium protein, unknown function [Plasmodium sp. gorilla clade G3] | 99.8 | 425 | 98% | 9e-22 | 58.06% | SOV73987.1 |
| exported protein family 3 [Plasmodium reichenowi] | 97.1 | 253 | 100% | 1e-21 | 49.09% | CDO62230.1 |

Figure S1. BLAST results of the MNXH or TNXH repeats domain alignment, commonly shown in plasmodium genome.

| Dd2 HB3 IGH-CR14 PaloAlto/Uganda PfPdxK Reichenowi SantaLucia | RRKRKIHRGKSNDNGNMNGHMNGHMNGHMNGHTNGHMNGHMNDHMNDHMN RRKRKIHRGKSNDNGNMNGHMNGHMNGHMNGHTNGHMNGHMNDHMNDHMN RRKRKIHRGKSNDNGNMNGHMNGHMNGHTNGHMNGHMNDHMNDHMN RRKRKIHRGKSNDNGNMNGHMNGHMNGHMNGHMNGHMNGHMNDHMN RRKRKIHRGKSNDNGNMNGHMNGHMNGHMNGHMNGHMNGHMNGHMN RRKRKIHRGKSNDNGNMNGYMNGYMNGHTNGHMNGHTNGHVNGHTNDHMN RRKRKIHRGKSNDNGNMNGHMNGHMNGHTNGHMNGHMNDHMN ************************************ |
|---|---|
| Dd2 HB3 IGH-CR14 PaloAlto/Uganda PfPdxK Reichenowi SantaLucia | GHMNGHTNDHMNGHTNDHMNGHTNDHMNGHTNDH GHMNGHTNDHMNGHTNDHMNGHTNDHMNGHTND |
| Dd2 HB3 IGH-CR14 PaloAlto/Uganda PfPdxK Reichenowi SantaLucia | MNDHMNGHTNDHMNDHMNGHTNDHMNDHMNGHTNSHTHGLTNGHMD MNDHMNGHTNDHMNDHMNGHTNDHMNDHMNGHTNSHTHGLTNGHMD TNDHMNGHTNDHMNDHMNGHTNDHMNDHMNGHTNSHTHGLTNGHMDDHMNGHTNDHMNDHMNGHTNDHMNDHMNGHTNSHTHGLTNGHMD TNDHMNGHTNDHMNDHMNGHTNDHMNGHTNSHTHGLTNGHMD TNGHMNGHTNDHMNGHTNDHMNGHTNSHTHGLTNGHMD ************************************ |
| Dd2 HB3 IGH-CR14 PaloAlto/Uganda PfPdxK Reichenowi SantaLucia | EPNGEHPYRLMNSNELKSSHQIIPQGKQIHEKDMLKNNILTISQGRKKDE EPNGEHPYRLMNSNELKSSHQIIPQGKQIHEKDMLKNNILTISQGRKKDE EPNGEHPYRLMNSNELKSSHQIIPQGKQIHEKDMLKNNILTISQGRKKDE EPNGEHPYRLMNSNELKSSHQIIPQGKQIHEKDMLKNNILTISQGRKKDE EPNGEHPYRLMNSNELKSSHQIIPQGKQIHEKDMLKNNILTISQGRKKDE EPNGEHPYRLINSNEHKSSHQVIPRGKQINEKGMLKNNILKISQGRKKDE EPNGEHPYRLMNSNELKSSHQVIPRGKQINEKGMLKNNILTISQGRKKDE EPNGEHPYRLMNSNELKSSHQIIPQGKQIHEKDMLKNNILTISQGRKKDE *********************************** |
| Dd2 HB3 IGH-CR14 PaloAlto/Uganda PfPdxK Reichenowi SantaLucia | ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ELYFIENIINLNFLWVCDPVMGDNGRLYVDERVVESYKKAIEYVDIITPN ************************************ |
| Dd2 HB3 IGH-CR14 PaloAlto/Uganda PfPdxK Reichenowi SantaLucia | QYETELLCGIKINEEKDVIKCLNVLLHKGVKIVIITSVNYNFDKDHLFLY QYETELLCGIKINEEKDVIKCLDVLLHKGVKIVIITSVNYNFDKDHLFLY QYETELLCGIKINEEKDVIKCLDVLLHKGVKIVIITSVNYNFDKDHLFLY QYETELLCGIKINEEKDVIKCLDVLLHKGVKIVIITSVNYNFDKDHLFLY QYETELLCGIKINEEKDVIKCLDVLLHKGVKIVIITSVNYNFDKDHLFLY QYETELLCGIKINEEKDVIKCLNVLLHKGVKIVIITSVNYNFDKDHLFLY QYETELLCGIKINEEKDVIKCLDVLLHKGVKIVIITSVNYNFDKDHLFLY |

Figure S2. Alignment of different resource plasmodial falciparum contain a common FIxxIIxL motif after the xNxH repeat motif domains, shows in the red square.