

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
<input type="checkbox"/>	pyridoxal kinase [Plasmodium falciparum 3D7]	209	348	100%	3e-63	100.00%	<a href="#">XP_966146.1</a>
<input type="checkbox"/>	pyridoxine kinase [Plasmodium falciparum IGH-CR14]	164	164	92%	7e-46	89.19%	<a href="#">KNG73950.1</a>
<input type="checkbox"/>	hypothetical protein PFHG_00578 [Plasmodium falciparum HB3]	160	258	100%	2e-44	86.09%	<a href="#">KOB58829.1</a>
<input type="checkbox"/>	hypothetical protein PFDG_04483 [Plasmodium falciparum Dd2]	159	257	100%	3e-44	86.09%	<a href="#">KOB88033.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium gaboni]	159	466	100%	6e-44	83.76%	<a href="#">SOV12284.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium sp. DRC-Itaito]	143	279	99%	4e-38	79.44%	<a href="#">SOV21668.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium reichenowi]	137	527	100%	7e-36	79.63%	<a href="#">SOV77504.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium gaboni]	135	398	95%	4e-35	79.00%	<a href="#">XP_018642797.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium sp. gorilla clade G2]	135	260	99%	5e-35	67.54%	<a href="#">XP_028537308.1</a>
<input type="checkbox"/>	Beta-ketoacyl synthase [Beauveria brongniartii RCEF 3172]	135	4732	100%	3e-34	73.11%	<a href="#">QAA50030.1</a>
<input type="checkbox"/>	hypothetical protein PENFLA_c125G03904 [Penicillium flavigenum]	124	492	100%	2e-33	50.00%	<a href="#">OQE08728.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium reichenowi]	125	125	81%	2e-31	78.57%	<a href="#">CDO63349.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium falciparum Palo Alto/Uganda]	124	308	90%	2e-31	89.16%	<a href="#">ETW53186.1</a>
<input type="checkbox"/>	hypothetical protein DUI87_24655 [Hirundo rustica rustica]	115	342	100%	1e-30	42.86%	<a href="#">RMB98441.1</a>
<input type="checkbox"/>	PREDICTED: keratin-associated protein 6-2-like [Octopus bimaculoides]	119	1474	100%	1e-30	35.83%	<a href="#">XP_014785252.1</a>
<input type="checkbox"/>	Compactin diketide synthase mokB [Beauveria bassiana]	121	528	100%	2e-29	62.18%	<a href="#">PMB69322.1</a>
<input type="checkbox"/>	Lovastatin nonaketide synthase [Beauveria bassiana D1-5]	120	410	100%	4e-29	61.67%	<a href="#">KGQ12279.1</a>
<input type="checkbox"/>	hypothetical protein BB8028_0003g08250 [Beauveria bassiana]	119	566	100%	8e-29	63.03%	<a href="#">PQK12208.1</a>
<input type="checkbox"/>	Beta-ketoacyl synthase [Cordyceps confragosa RCEF 1005]	116	851	100%	1e-27	62.18%	<a href="#">QAA78033.1</a>
<input type="checkbox"/>	hypothetical protein EN45_062540 [Penicillium chrysogenum]	108	428	99%	1e-27	49.53%	<a href="#">KZN87693.1</a>
<input type="checkbox"/>	hypothetical protein EN45_063710 [Penicillium chrysogenum]	106	422	100%	9e-27	50.00%	<a href="#">KZN87810.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium falciparum Santa Lucia]	112	461	100%	1e-26	87.34%	<a href="#">EUT89866.1</a>
<input type="checkbox"/>	hypothetical protein LLEC1_05370 [Cordyceps confragosa]	113	953	100%	2e-26	58.82%	<a href="#">QAR01380.1</a>
<input type="checkbox"/>	putative membrane protein [Plasmodium reichenowi]	110	1061	100%	1e-25	41.53%	<a href="#">XP_012764852.2</a>
<input type="checkbox"/>	hypothetical protein LOTGIDRAFT_164889 [Lottia gigantea]	104	708	100%	7e-25	40.16%	<a href="#">XP_009059650.1</a>
<input type="checkbox"/>	conserved Plasmodium protein, unknown function [Plasmodium falciparum 3D7]	108	833	97%	9e-25	44.80%	<a href="#">XP_002808861.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium reichenowi]	107	211	87%	9e-25	77.38%	<a href="#">XP_012761977.2</a>
<input type="checkbox"/>	Plasmodium exported protein (hyp4), unknown function [Plasmodium reichenowi]	105	555	100%	2e-24	49.57%	<a href="#">SOV75054.1</a>
<input type="checkbox"/>	hypothetical protein TSACC_21742 [Terrimicrobium sacchariphilum]	98.2	648	99%	5e-24	66.29%	<a href="#">GAT33328.1</a>
<input type="checkbox"/>	N-acetyl-D-glucosamine kinase-like [Panaeus vannamei]	105	600	95%	7e-24	69.39%	<a href="#">XP_027208985.1</a>
<input type="checkbox"/>	Beta-ketoacyl synthase [Cordyceps fumosorosea ARSEF 2679]	105	567	100%	1e-23	58.54%	<a href="#">XP_018705471.1</a>
<input type="checkbox"/>	hypothetical protein PFHG_02530 [Plasmodium falciparum HB3]	104	201	97%	2e-23	44.00%	<a href="#">KOB60798.1</a>
<input type="checkbox"/>	conserved Plasmodium membrane protein, unknown function [Plasmodium reichenowi]	104	583	100%	3e-23	50.81%	<a href="#">SOV79843.1</a>
<input type="checkbox"/>	splicing factor U2af large subunit A-like [Nilaparvata lugens]	99.4	2582	100%	4e-23	42.50%	<a href="#">XP_022198530.1</a>
<input type="checkbox"/>	hypothetical protein PFMG_01564 [Plasmodium falciparum IGH-CR14]	102	297	97%	7e-23	44.00%	<a href="#">KNG75333.1</a>
<input type="checkbox"/>	pyridoxal kinase [Plasmodium sp. gorilla clade G3]	101	474	96%	7e-23	67.09%	<a href="#">SOV74700.1</a>
<input type="checkbox"/>	Beta-ketoacyl synthase [Cordyceps militaris]	102	781	100%	1e-22	57.98%	<a href="#">ATY60574.1</a>
<input type="checkbox"/>	polyketide synthase, putative [Cordyceps militaris CM01]	102	444	99%	1e-22	58.82%	<a href="#">XP_006667589.1</a>
<input type="checkbox"/>	hypothetical protein, conserved [Plasmodium vivax]	101	733	97%	2e-22	70.37%	<a href="#">XP_001608467.1</a>
<input type="checkbox"/>	hypothetical protein EDD98_3099 [Streptomyces sp. PanSC19]	99.4	1573	100%	2e-22	44.17%	<a href="#">ROQ34065.1</a>
<input type="checkbox"/>	conserved Plasmodium protein, unknown function [Plasmodium knowlesi strain H]	100	293	100%	5e-22	42.50%	<a href="#">SBO23952.1</a>
<input type="checkbox"/>	conserved Plasmodium protein, unknown function [Plasmodium gaboni]	100	375	100%	5e-22	62.07%	<a href="#">SOV15009.1</a>
<input type="checkbox"/>	lovastatin nonaketide synthase [Nannizzia gypsea CBS 118893]	100	318	91%	6e-22	59.26%	<a href="#">XP_003170591.1</a>
<input type="checkbox"/>	conserved Plasmodium protein, unknown function [Plasmodium sp. gorilla clade G3]	99.8	425	98%	9e-22	58.06%	<a href="#">SOV73987.1</a>
<input type="checkbox"/>	exported protein family 3 [Plasmodium reichenowi]	97.1	253	100%	1e-21	49.09%	<a href="#">CDO62230.1</a>

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

