

<u>Description</u>	<u>Scientific Name</u>	<u>Query Cover</u>	<u>Per. Ident</u>	<u>Acc. Len</u>	Accession
Homo sapiens nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Homo sapiens	100%	100.00%	4360	NM_005746.3
PREDICTED: Pan troglodytes nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Pan troglodytes	99%	98.43%	5147	XM_016945642.2
PREDICTED: Pan troglodytes nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Pan troglodytes	99%	98.43%	4602	XM_016945641.1
PREDICTED: Gorilla gorilla gorilla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Gorilla gorilla gorilla	100%	98.39%	4603	XM_004046013.3
PREDICTED: Gorilla gorilla gorilla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Gorilla gorilla gorilla	98%	98.37%	5093	XM_019031136.2
PREDICTED: Pongo abelii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pongo abelii	100%	96.97%	4487	XM_009235897.2
PREDICTED: Nomascus leucogenys nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Nomascus leucogenys	100%	96.74%	5217	XM_003268147.3
PREDICTED: Hylobates moloch nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Hylobates moloch	100%	96.49%	5233	XM_032761351.1
PREDICTED: Rhinopithecus roxellana nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Rhinopithecus roxellana	99%	95.19%	4607	XM_010380669.2

PREDICTED: Trachypithecus francoisi nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Trachypithecus francoisi	100%	95.08%	4608	XM_033194871.1
PREDICTED: Papio anubis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Papio anubis	100%	94.74%	5182	XM_009203633.4
PREDICTED: Papio anubis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Papio anubis	100%	94.74%	4637	XM_021936153.2
PREDICTED: Theropithecus gelada nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Theropithecus gelada	100%	94.72%	4646	XM_025378096.1
PREDICTED: Theropithecus gelada nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Theropithecus gelada	99%	94.72%	5109	XM_025378097.1
PREDICTED: Ptilinopus tephrosceles nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ptilinopus tephroscele	100%	94.84%	4612	XM_023183070.1
PREDICTED: Cercocebus atys nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Cercocebus atys	100%	94.61%	5175	XM_012054608.1
PREDICTED: Cercocebus atys nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Cercocebus atys	100%	94.61%	4637	XM_012054607.1
PREDICTED: Rhinopithecus bieti nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Rhinopithecus bieti	99%	94.94%	4518	XM_017874677.1
PREDICTED: Macaca fascicularis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Macaca fascicularis	100%	94.39%	5114	XM_015447907.1

PREDICTED: Macaca fascicularis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Macaca fascicularis	100%	94.39%	4638	XM_005550471.2
PREDICTED: Macaca mulatta nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Macaca mulatta	100%	94.33%	5188	XM_015134666.2
PREDICTED: Macaca mulatta nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Macaca mulatta	100%	94.33%	4643	XM_015134665.2
PREDICTED: Pan troglodytes nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Pan troglodytes	93%	98.34%	4325	XM_016945643.1
PREDICTED: Chlorocebus sabaues nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Chlorocebus sabaues	100%	94.23%	4639	XM_007982516.2
PREDICTED: Callithrix jacchus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Callithrix jacchus	99%	93.43%	4580	XM_002751724.4
PREDICTED: Sapajus apella nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Sapajus apella	99%	93.23%	4558	XM_032276321.1
PREDICTED: Cebus imitator nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Cebus imitator	99%	93.09%	4559	XM_017515439.1
PREDICTED: Aotus nancymaae nicotinamide phosphoribosyltransferase (LOC105720296), partial mRNA	Aotus nancymaae	92%	92.21%	4102	XM_021673269.1
PREDICTED: Galeopterus variegatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Galeopterus variegatus	99%	88.57%	4638	XM_008567863.1

PREDICTED: Galeopterus variegatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Galeopterus variegatus	98%	88.49%	4515	XM_008567870.1
PREDICTED: Microcebus murinus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Microcebus murinus	99%	87.94%	4625	XM_012746431.1
PREDICTED: Galeopterus variegatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Galeopterus variegatus	96%	88.44%	4468	XM_008567859.1
PREDICTED: Hipposideros armiger nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Hipposideros armiger	99%	86.64%	4569	XM_019660160.1
PREDICTED: Galeopterus variegatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X5, mRNA	Galeopterus variegatus	95%	88.16%	4578	XM_008567876.1
PREDICTED: Pteropus alecto nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pteropus alecto	100%	85.91%	4492	XM_006925370.3
PREDICTED: Carlito syrichta nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Carlito syrichta	96%	87.14%	4235	XM_021719452.1
PREDICTED: Pteropus vampyrus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pteropus vampyrus	100%	85.84%	4502	XM_011372509.2
PREDICTED: Monodon monoceros nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Monodon monoceros	99%	85.58%	5179	XM_029233596.1
PREDICTED: Lipotes vexillifer nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Lipotes vexillifer	99%	85.55%	4994	XM_007453335.1

PREDICTED: <i>Zalophus californianus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Zalophus californianus	99%	85.90%	4556	XM_027575084.1
PREDICTED: <i>Eumetopias jubatus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Eumetopias jubatus	99%	85.85%	4568	XM_028120338.1
PREDICTED: <i>Callorhinus ursinus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Callorhinus ursinus	99%	85.80%	7270	XM_025872714.1
PREDICTED: <i>Leptonychotes weddellii</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Leptonychotes weddellii	100%	85.66%	4423	XM_031026881.1
PREDICTED: <i>Physeter catodon</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X5, mRNA	Physeter catodon	99%	85.47%	5025	XM_024115955.1
PREDICTED: <i>Pteropus giganteus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pteropus giganteus	98%	85.85%	4438	XM_039849466.1
PREDICTED: <i>Phoca vitulina</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Phoca vitulina	99%	85.57%	4963	XM_032402359.1
PREDICTED: <i>Halichoerus grypus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Halichoerus grypus	99%	85.54%	4420	XM_036109058.1
PREDICTED: <i>Neomonachus schauinslandi</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Neomonachus schauinsl	100%	85.58%	4579	XM_021682932.1
PREDICTED: <i>Mirounga leonina</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Mirounga leonina	100%	85.40%	4929	XM_035020371.1

PREDICTED: Rousettus aegyptiacus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Rousettus aegyptiacus	100%	85.44%	4458	XM_016145871.2
PREDICTED: Tupaia chinensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Tupaia chinensis	98%	85.89%	4620	XM_006149171.3
PREDICTED: Canis lupus dingo nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Canis lupus dingo	99%	85.33%	4573	XM_025449478.2
PREDICTED: Canis lupus familiaris nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Canis lupus familiaris	99%	85.30%	4535	XM_038423805.1
PREDICTED: Canis lupus familiaris nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Canis lupus familiaris	99%	85.30%	4535	XM_038454081.1
PREDICTED: Trichechus manatus latirostris nicotinamide phosphoribosyltransferase (LOC101355029), transcript variant X1, mRNA	Trichechus manatus latir	99%	85.48%	9837	XM_004382605.3
PREDICTED: Enhydra lutris kenyoni nicotinamide phosphoribosyltransferase (LOC111155324), mRNA	Enhydra lutris kenyoni	99%	85.19%	4587	XM_022515465.1
PREDICTED: Lontra canadensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Lontra canadensis	99%	85.22%	4495	XM_032873363.1
PREDICTED: Panthera pardus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Panthera pardus	99%	85.19%	4716	XM_019451197.1
PREDICTED: Felis catus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Felis catus	99%	84.88%	4490	XM_011280328.3

PREDICTED: Acinonyx jubatus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Acinonyx jubatus	99%	84.84%	4417	XM_027071685.1
PREDICTED: Equus caballus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Equus caballus	99%	84.72%	4466	XM_023638876.1
PREDICTED: Mustela erminea nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Mustela erminea	98%	85.07%	6497	XM_032305830.1
PREDICTED: Suricata suricatta nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Suricata suricatta	99%	84.90%	4532	XM_029927315.1
PREDICTED: Choloepus didactylus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Choloepus didactylus	99%	84.86%	4503	XM_037836405.1
PREDICTED: Lynx canadensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Lynx canadensis	99%	84.54%	4383	XM_030307779.2
PREDICTED: Vulpes vulpes nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Vulpes vulpes	96%	84.92%	4511	XM_025984071.1
PREDICTED: Equus asinus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Equus asinus	96%	85.05%	4350	XM_014831824.1
PREDICTED: Choloepus didactylus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Choloepus didactylus	98%	84.76%	4632	XM_037836406.1
PREDICTED: Hyaena hyaena nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Hyaena hyaena	99%	84.07%	4387	XM_039249783.1

PREDICTED: Mustela putorius furo nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Mustela putorius furo	96%	84.77%	6713	XM_013059034.1
PREDICTED: Equus przewalskii nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Equus przewalskii	96%	84.37%	4347	XM_008527396.1
PREDICTED: Panthera tigris altaica nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Panthera tigris altaica	96%	84.79%	4615	XM_007083970.2
PREDICTED: Heterocephalus glaber nicotinamide phosphoribosyltransferase (Nampt), mRNA	Heterocephalus glaber	100%	83.59%	4424	XM_004839676.3
PREDICTED: Hyaena hyaena nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Hyaena hyaena	98%	83.90%	4608	XM_039249784.1
PREDICTED: Manis javanica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Manis javanica	98%	83.70%	4522	XM_017679882.2
PREDICTED: Manis pentadactyla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Manis pentadactyla	94%	84.56%	4296	XM_036892490.1
PREDICTED: Eptesicus fuscus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Eptesicus fuscus	99%	82.67%	4388	XM_008149991.2
PREDICTED: Choloepus didactylus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Choloepus didactylus	96%	83.97%	4195	XM_037836408.1
PREDICTED: Manis pentadactyla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Manis pentadactyla	93%	84.50%	4281	XM_036892491.1

PREDICTED: Physeter catodon nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Physeter catodon	88%	85.16%	4052	XM_028490185.1
PREDICTED: Manis javanica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Manis javanica	96%	83.64%	4397	XM_017679898.2
PREDICTED: Macaca nemestrina nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Macaca nemestrina	63%	95.44%	3551	XM_024790884.1
PREDICTED: Macaca nemestrina nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Macaca nemestrina	63%	95.44%	3006	XM_011730467.2
PREDICTED: Manis pentadactyla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X5, mRNA	Manis pentadactyla	90%	84.47%	4157	XM_036892494.1
PREDICTED: Manis javanica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Manis javanica	96%	83.21%	4493	XM_017679890.2
PREDICTED: Manis pentadactyla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Manis pentadactyla	90%	83.98%	4252	XM_036892493.1
PREDICTED: Ursus arctos horribilis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ursus arctos horribilis	96%	87.21%	5443	XM_026503589.1
PREDICTED: Saimiri boliviensis boliviensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Saimiri boliviensis boliviensis	59%	94.21%	2879	XM_010344323.2
PREDICTED: Sturnira hondurensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Sturnira hondurensis	98%	87.33%	4927	XM_037057045.1

PREDICTED: Ceratotherium simum simum nicotinamide phosphoribosyltransferase (LOC101406745), transcript variant X1, mRNA	Ceratotherium simum si	62%	92.24%	2828	XM_004439295.2
PREDICTED: Dipodomys ordii nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Dipodomys ordii	90%	89.87%	4290	XM_013034734.1
PREDICTED: Trichechus manatus latirostris nicotinamide phosphoribosyltransferase (LOC101355029), transcript variant X3, mRNA	Trichechus manatus latir	96%	84.09%	9678	XM_023737057.1
PREDICTED: Artibeus jamaicensis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Artibeus jamaicensis	94%	90.38%	4862	XM_037150485.1
PREDICTED: Chinchilla lanigera nicotinamide phosphoribosyltransferase (Nampt), mRNA	Chinchilla lanigera	97%	86.65%	4386	XM_013510535.1
PREDICTED: Rhinolophus ferrumequinum nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Rhinolophus ferrumequi	59%	92.71%	2865	XM_033088522.1
PREDICTED: Talpa occidentalis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Talpa occidentalis	59%	94.01%	2644	XM_037511469.1
PREDICTED: Odobenus rosmarus divergens nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Odobenus rosmarus dive	59%	92.60%	2783	XM_012566903.1
PREDICTED: Ursus maritimus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ursus maritimus	92%	86.89%	4339	XM_008703620.1
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Myotis lucifugus	89%	90.52%	4402	XM_006085386.3

PREDICTED: Phyllostomus discolor nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Phyllostomus discolor	59%	92.63%	2852	XM_028525138.2
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Myotis lucifugus	89%	89.57%	4434	XM_023751078.1
PREDICTED: Otolemur garnettii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Otolemur garnettii	58%	92.37%	2756	XM_012812119.2
PREDICTED: Castor canadensis nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Castor canadensis	59%	91.76%	2763	XM_020186436.1
PREDICTED: Molossus molossus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Molossus molossus	58%	92.08%	2591	XM_036246636.1
PREDICTED: Oryctolagus cuniculus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Oryctolagus cuniculus	95%	89.00%	4283	XM_002712033.3
PREDICTED: Fukomys damarensis nicotinamide phosphoribosyltransferase (Nampt), mRNA	Fukomys damarensis	58%	92.56%	2629	XM_033756754.1
PREDICTED: Pan paniscus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Pan paniscus	48%	99.62%	2559	XM_034964751.1
PREDICTED: Neomonachus schauinslandi nicotinamide phosphoribosyltransferase pseudogene (LOC110593898), misc RNA	Neomonachus schauinsl	56%	92.92%	2655	XR_002481177.1
PREDICTED: Myotis myotis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Myotis myotis	59%	91.00%	2676	XM_036327545.1

PREDICTED: Pipistrellus kuhlii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Pipistrellus kuhlii	59%	90.72%	2694	XM_036429711.1
PREDICTED: Loxodonta africana nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Loxodonta africana	59%	90.47%	2691	XM_023544521.1
PREDICTED: Jaculus jaculus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Jaculus jaculus	59%	90.64%	2704	XM_004652881.1
PREDICTED: Ailuropoda melanoleuca nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ailuropoda melanoleuca	56%	92.92%	2504	XM_011233147.2
PREDICTED: Pan paniscus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Pan paniscus	48%	98.13%	2273	XM_034964752.1
PREDICTED: Pan paniscus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Pan paniscus	48%	98.13%	2590	XM_034964750.1
PREDICTED: Loxodonta africana nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Loxodonta africana	59%	90.17%	2697	XM_010587346.2
PREDICTED: Erinaceus europaeus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Erinaceus europaeus	58%	90.85%	2736	XM_007526968.2
PREDICTED: Myotis brandtii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Myotis brandtii	56%	91.99%	2600	XM_014537028.1
PREDICTED: Galeopterus variegatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X6, mRNA	Galeopterus variegatus	93%	85.28%	4327	XM_008567881.1

PREDICTED: Myotis davidii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Myotis davidii	56%	91.51%	2580	XM_015571210.1
PREDICTED: Mastomys coucha nicotinamide phosphoribosyltransferase (Nampt), mRNA	Mastomys coucha	91%	84.22%	4622	XM_031355710.1
PREDICTED: Eptesicus fuscus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Eptesicus fuscus	96%	80.93%	4230	XM_028158852.1
PREDICTED: Peromyscus maniculatus bairdii nicotinamide phosphoribosyltransferase (Nampt), mRNA	Peromyscus maniculatus	75%	84.20%	3426	XM_006989531.2
PREDICTED: Cavia porcellus nicotinamide phosphoribosyltransferase (Nampt), partial mRNA	Cavia porcellus	82%	90.63%	4030	XM_023565106.1
PREDICTED: Onychomys torridus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Onychomys torridus	66%	89.25%	3518	XM_036206081.1
PREDICTED: Cricetulus griseus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Cricetulus griseus	88%	84.42%	4365	XM_027417008.2
PREDICTED: Cricetulus griseus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Cricetulus griseus	88%	84.42%	4363	XM_007649529.4
PREDICTED: Mus caroli nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Mus caroli	83%	83.69%	4329	XM_021179359.2
PREDICTED: Grammomys surdaster nicotinamide phosphoribosyltransferase (Nampt), mRNA	Grammomys surdaster	90%	83.67%	4571	XM_028768789.1

Mus musculus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Mus musculus	91%	83.66%	4547	NM_021524.2
PREDICTED: Meriones unguiculatus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Meriones unguiculatus	59%	88.86%	2821	XM_021645891.1
PREDICTED: Peromyscus leucopus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Peromyscus leucopus	59%	89.24%	2650	XM_028891743.2
PREDICTED: Pan paniscus nicotinamide phosphoribosyltransferase-like (LOC100972580), mRNA	Pan paniscus	44%	99.03%	2172	XM_034929796.1
PREDICTED: Pan troglodytes nicotinamide phosphoribosyltransferase pseudogene (LOC741031), misc_RNA	Pan troglodytes	44%	98.62%	2041	XR_682615.1
PREDICTED: Propithecus coquereli nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Propithecus coquereli	50%	93.10%	2621	XM_012650328.1
PREDICTED: Arvicanthis niloticus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Arvicanthis niloticus	59%	88.08%	2803	XM_034514067.1
PREDICTED: Mus pahari nicotinamide phosphoribosyltransferase (Nampt), mRNA	Mus pahari	58%	88.46%	3038	XM_021201732.2
PREDICTED: Rattus rattus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Rattus rattus	77%	87.67%	4541	XM_032907624.1
PREDICTED: Mus caroli nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Mus caroli	80%	83.41%	4199	XM_029484514.1

PREDICTED: Trichechus manatus latirostris nicotinamide phosphoribosyltransferase (LOC101355029), transcript variant X2, mRNA	Trichechus manatus latir	97%	82.49%	9717	XM_023737056.1
Arvicola amphibius nicotinamide phosphoribosyltransferase (Nampt), mRNA	Arvicola amphibius	80%	86.21%	4474	XM_038335810.1
PREDICTED: Odobenus rosmarus divergens nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Odobenus rosmarus dive	48%	94.10%	2232	XM_004413120.1
PREDICTED: Condylura cristata nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Condylura cristata	48%	94.01%	2276	XM_004676923.2
PREDICTED: Mesocricetus auratus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Mesocricetus auratus	75%	86.34%	4198	XM_021230722.1
PREDICTED: Mesocricetus auratus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Mesocricetus auratus	75%	86.34%	4549	XM_013117829.2
Rattus norvegicus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Rattus norvegicus	58%	87.76%	2590	NM_177928.3
PREDICTED: Miniopterus natalensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Miniopterus natalensis	47%	92.66%	2279	XM_016204749.1
PREDICTED: Desmodus rotundus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Desmodus rotundus	48%	93.14%	2217	XM_024558567.1
PREDICTED: Orycteropus afer afer nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Orycteropus afer afer	48%	93.08%	2123	XM_007944436.1

PREDICTED: Phascolarctos cinereus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Phascolarctos cinereus	71%	86.99%	4372	XM_020984577.1
PREDICTED: Vombatus ursinus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Vombatus ursinus	74%	86.86%	4403	XM_027838689.1
PREDICTED: Rattus norvegicus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Rattus norvegicus	73%	87.70%	4343	XM_039111890.1
PREDICTED: Sarcophilus harrisi nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Sarcophilus harrisi	73%	86.18%	4412	XM_031938752.1
PREDICTED: Trichosurus vulpecula nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Trichosurus vulpecula	71%	87.04%	4589	XM_036759591.1
PREDICTED: Monodelphis domestica nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Monodelphis domestica	70%	86.80%	4300	XM_007504106.1
PREDICTED: Manis javanica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Manis javanica	97%	80.42%	4438	XM_037003611.1
PREDICTED: Equus caballus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Equus caballus	96%	80.86%	4328	XM_023638877.1
PREDICTED: Puma concolor nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Puma concolor	44%	92.22%	2395	XM_025929801.1
PREDICTED: Zalophus californianus nicotinamide phosphoribosyltransferase-like (LOC113939659), mRNA	Zalophus californianus	45%	90.91%	2037	XM_035724624.1

PREDICTED: Callithrix jacchus actin-related protein 2/3 complex subunit 5-like protein (LOC108588234), misc RNA	Callithrix jacchus	44%	93.19%	3220	XR_001907101.2
PREDICTED: Manis pentadactyla nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Manis pentadactyla	91%	81.03%	4178	XM_036892492.1
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Myotis lucifugus	86%	88.28%	4273	XM_023751079.1
PREDICTED: Neophocaena asiaeorientalis asiaeorientalis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Neophocaena asiaeorientalis	99%	81.96%	4635	XM_024760867.1
PREDICTED: Lagenorhynchus obliquidens nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Lagenorhynchus obliquidens	95%	81.91%	4291	XM_027123893.1
PREDICTED: Lagenorhynchus obliquidens nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Lagenorhynchus obliquidens	98%	81.91%	4920	XM_027123892.1
PREDICTED: Lagenorhynchus obliquidens nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Lagenorhynchus obliquidens	99%	81.91%	5390	XM_027123891.1
PREDICTED: Tursiops truncatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Tursiops truncatus	99%	81.88%	5392	XM_033862896.1
PREDICTED: Orcinus orca nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Orcinus orca	98%	81.88%	4907	XM_033439101.1
PREDICTED: Orcinus orca nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Orcinus orca	99%	81.88%	4851	XM_004263362.2

PREDICTED: Orcinus orca nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Orcinus orca	99%	81.88%	4962	XM_033439092.1
PREDICTED: Delphinapterus leucas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Delphinapterus leucas	95%	81.91%	4291	XM_030761467.1
PREDICTED: Delphinapterus leucas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Delphinapterus leucas	98%	81.91%	4367	XM_022554333.2
PREDICTED: Globicephala melas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Globicephala melas	95%	81.87%	4304	XM_030834392.1
PREDICTED: Globicephala melas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Globicephala melas	98%	81.87%	4929	XM_030834391.1
PREDICTED: Globicephala melas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Globicephala melas	99%	81.87%	5399	XM_030834390.1
PREDICTED: Phocoena sinus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Phocoena sinus	99%	81.60%	4623	XM_032642788.1
PREDICTED: Balaenoptera musculus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Balaenoptera musculus	99%	81.57%	4680	XM_036863843.1
PREDICTED: Balaenoptera musculus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Balaenoptera musculus	99%	81.57%	5058	XM_036863842.1
PREDICTED: Pipistrellus kuhlii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Pipistrellus kuhlii	56%	90.37%	2536	XM_036429713.1

PREDICTED: Myotis myotis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Myotis myotis	56%	90.18%	2517	XM_036327547.1
PREDICTED: Peromyscus leucopus nicotinamide phosphoribosyltransferase-like (LOC114688826), mRNA	Peromyscus leucopus	46%	88.98%	2060	XM_037202193.1
PREDICTED: Aotus nancymae nicotinamide phosphoribosyltransferase-like (LOC110568769), mRNA	Aotus nancymae	36%	96.71%	1861	XM_021673169.1
PREDICTED: Marmota flaviventris nicotinamide phosphoribosyltransferase (Nampt), mRNA	Marmota flaviventris	99%	81.36%	4442	XM_034635668.1
PREDICTED: Octodon degus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Octodon degus	41%	91.56%	1988	XM_004634990.1
PREDICTED: Camelus ferus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Camelus ferus	99%	81.02%	4659	XM_032484208.1
PREDICTED: Camelus dromedarius nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Camelus dromedarius	99%	81.02%	4652	XM_031454695.1
PREDICTED: Camelus bactrianus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Camelus bactrianus	99%	80.95%	4815	XM_010946702.1
PREDICTED: Eptesicus fuscus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Eptesicus fuscus	96%	78.37%	4249	XM_028158841.1
PREDICTED: Vicugna pacos nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Vicugna pacos	99%	80.68%	4651	XM_031679788.1

PREDICTED: Castor canadensis nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Castor canadensis	96%	78.76%	6212	XM_020186438.1
PREDICTED: Urocitellus parryii nicotinamide phosphoribosyltransferase (Nampt), mRNA	Urocitellus parryii	36%	95.29%	1669	XM_026395750.1
PREDICTED: Physeter catodon nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, misc RNA	Physeter catodon	36%	95.76%	2031	XR_003679952.1
PREDICTED: Delphinapterus leucas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, misc RNA	Delphinapterus leucas	36%	95.23%	7883	XR_002642121.2
PREDICTED: Delphinapterus leucas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, misc RNA	Delphinapterus leucas	36%	95.23%	1900	XR_002642120.2
PREDICTED: Phocoena sinus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, misc RNA	Phocoena sinus	36%	95.17%	5233	XR_004351397.1
PREDICTED: Nannospalax galili nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Nannospalax galili	39%	91.01%	1813	XM_008830730.3
PREDICTED: Microtus ochrogaster nicotinamide phosphoribosyltransferase (Nampt), mRNA	Microtus ochrogaster	44%	88.10%	2246	XM_026778837.1
PREDICTED: Bubalus bubalis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Bubalus bubalis	99%	94.34%	4483	XM_006042817.2
PREDICTED: Bos indicus x Bos taurus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Bos indicus x Bos taurus	99%	94.28%	5032	XM_027539678.1

PREDICTED: Bos indicus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Bos indicus	99%	94.28%	4617	XM_019958670.1
PREDICTED: Ovis aries nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ovis aries	99%	94.28%	4396	XM_004007842.4
Bos taurus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Bos taurus	99%	94.22%	5048	NM_001244141.1
PREDICTED: Physeter catodon nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, misc RNA	Physeter catodon	36%	93.62%	3311	XR_003679951.1
PREDICTED: Physeter catodon nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, misc RNA	Physeter catodon	36%	93.62%	3401	XR_003679950.1
PREDICTED: Capra hircus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Capra hircus	99%	94.19%	5046	XM_018047232.1
PREDICTED: Colobus angolensis palliatus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Colobus angolensis palliatus	33%	97.40%	1706	XM_011956870.1
PREDICTED: Tursiops truncatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Tursiops truncatus	58%	95.04%	3190	XM_033862897.1
PREDICTED: Odocoileus virginianus texanus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Odocoileus virginianus texanus	99%	93.77%	5021	XM_020893508.1
PREDICTED: Nannospalax galili nicotinamide phosphoribosyltransferase (Nampt), transcript variant X1, mRNA	Nannospalax galili	39%	88.86%	1857	XM_029562330.1

PREDICTED: Sus scrofa uncharacterized LOC110255500 (LOC110255500), ncRNA	Sus scrofa	66%	79.05%	14819	XR_002335906.1
PREDICTED: Sus scrofa nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Sus scrofa	99%	79.05%	4780	XM_021102257.1
PREDICTED: Mandrillus leucophaeus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Mandrillus leucophaeus	33%	96.78%	1789	XM_011986391.1
Sus scrofa nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Sus scrofa	51%	95.23%	2322	NM_001031793.2
PREDICTED: Ictidomys tridecemlineatus nicotinamide phosphoribosyltransferase (Nampt), mRNA	Ictidomys tridecemlineatus	36%	92.80%	1668	XM_021722429.1
PREDICTED: Macaca mulatta uncharacterized LOC114674283 (LOC114674283), ncRNA	Macaca mulatta	42%	87.98%	5434	XR_003725303.1
PREDICTED: Bison bison bison nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Bison bison bison	96%	78.95%	4977	XM_010841499.1
PREDICTED: Chrysemys picta bellii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Chrysemys picta bellii	67%	81.64%	4368	XM_005292365.3
PREDICTED: Mauremys reevesii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Mauremys reevesii	67%	81.63%	4533	XM_039517034.1
PREDICTED: Trachemys scripta elegans nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Trachemys scripta elegans	56%	81.68%	3237	XM_034766564.1

PREDICTED: Bos indicus x Bos taurus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, misc RNA	Bos indicus x Bos taurus	99%	78.80%	5141	XR_003510789.1
PREDICTED: Bos indicus x Bos taurus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Bos indicus x Bos taurus	96%	78.80%	4891	XM_027539679.1
PREDICTED: Meriones unguiculatus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X4, mRNA	Meriones unguiculatus	43%	88.09%	2034	XM_021645894.1
PREDICTED: Meriones unguiculatus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X3, mRNA	Meriones unguiculatus	43%	88.09%	2155	XM_021645893.1
PREDICTED: Meriones unguiculatus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Meriones unguiculatus	46%	88.09%	2092	XM_021645892.1
PREDICTED: Monodon monoceros nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Monodon monoceros	33%	95.69%	2455	XM_029233595.1
PREDICTED: Bos taurus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Bos taurus	96%	78.79%	4471	XM_010804167.2
PREDICTED: Apteryx rowi nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Apteryx rowi	66%	81.58%	4386	XM_026059010.1
PREDICTED: Chelonia mydas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Chelonia mydas	62%	81.27%	4335	XM_037889149.1
PREDICTED: Terrapene carolina triunguis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Terrapene carolina triun	67%	81.31%	4304	XM_024208494.3

PREDICTED: Dromaius novaehollandiae nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Dromaius novaehollandi	66%	81.42%	4386	XM_026097637.1
Dermochelys coriacea nicotinamide phosphoribosyltransferase transcript variant X2 (NAMPT), mRNA	Dermochelys coriacea	61%	81.44%	4524	XM_038401003.1
PREDICTED: Marmota marmota marmota nicotinamide phosphoribosyltransferase (Nampt), partial mRNA	Marmota marmota marm	74%	95.57%	3414	XM_015488207.1
PREDICTED: Balaenoptera acutorostrata scammoni nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Balaenoptera acutorostr	56%	95.37%	2672	XM_007180899.1
PREDICTED: Cygnus atratus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Cygnus atratus	66%	81.01%	4395	XM_035549374.1
PREDICTED: Chelonia mydas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Chelonia mydas	62%	80.70%	4353	XM_037889148.1
PREDICTED: Aquila chrysaetos chrysaetos nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Aquila chrysaetos chrysa	58%	81.09%	4389	XM_030014466.1
PREDICTED: Gopherus evgoodei nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Gopherus evgoodei	66%	81.20%	4347	XM_030551044.1
PREDICTED: Sorex araneus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Sorex araneus	33%	94.44%	1476	XM_004602114.1
PREDICTED: Apteryx rowi nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Apteryx rowi	66%	81.43%	4423	XM_026059011.1

PREDICTED: Apteryx australis mantelli nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Apteryx mantelli mantel	54%	81.43%	3477	XM_013943612.1
PREDICTED: Neopelma chrysocephalum nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Neopelma chrysocephal	55%	80.99%	4382	XM_027679341.1
PREDICTED: Chelonoidis abingdonii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Chelonoidis abingdonii	56%	81.14%	2856	XM_032787317.1
PREDICTED: Tyto alba alba nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Tyto alba alba	66%	80.94%	4589	XM_032996250.1
PREDICTED: Nothoprocta perdicaria nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Nothoprocta perdicaria	55%	81.02%	3431	XM_026046355.1
PREDICTED: Galeopterus variegatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Galeopterus variegatus	31%	96.93%	1752	XM_008567861.1
PREDICTED: Corvus moneduloides nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Corvus moneduloides	55%	80.89%	4391	XM_032106282.1
PREDICTED: Calypte anna nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Calypte anna	55%	80.99%	3833	XM_030463201.1
PREDICTED: Corvus cornix cornix nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Corvus cornix cornix	55%	80.81%	4382	XM_039570902.1
PREDICTED: Oxyura jamaicensis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Oxyura jamaicensis	55%	80.77%	3548	XM_035332709.1

PREDICTED: Trachemys scripta elegans nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Trachemys scripta elegans	56%	80.16%	3285	XM_034766549.1
PREDICTED: Gavialis gangeticus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Gavialis gangeticus	65%	81.00%	4313	XM_019509420.1
PREDICTED: Corapipo altera nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Corapipo altera	55%	80.89%	4411	XM_027639640.1
PREDICTED: Empidonax traillii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Empidonax traillii	55%	80.76%	4414	XM_027890082.1
PREDICTED: Aythya fuligula nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Aythya fuligula	55%	80.70%	3529	XM_032190781.1
PREDICTED: Anas platyrhynchos nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Anas platyrhynchos	66%	80.70%	4396	XM_027459202.2
PREDICTED: Eumetopias jubatus nicotinamide phosphoribosyltransferase pseudogene (LOC114216300), misc_RNA	Eumetopias jubatus	34%	93.31%	1578	XR_003610748.1
Dermochelys coriacea isolate rDerCor1 chromosome 1	Dermochelys coriacea	61%	81.30%	5543	XR_005292811.1
Dermochelys coriacea nicotinamide phosphoribosyltransferase transcript variant X1 (NAMPT), mRNA	Dermochelys coriacea	61%	81.30%	4619	XM_038400994.1
PREDICTED: Camarhynchus parvulus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Camarhynchus parvulus	55%	80.72%	3563	XM_030960238.1

PREDICTED: Aquila chrysaetos chrysaetos nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Aquila chrysaetos chrysa	58%	80.50%	4407	XM_030014465.1
PREDICTED: Chiroxiphia lanceolata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Chiroxiphia lanceolata	55%	80.80%	4409	XM_032687697.1
PREDICTED: Alligator mississippiensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Alligator mississippiensis	55%	80.85%	3473	XM_006276629.3
PREDICTED: Gopherus evgoodei nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Gopherus evgoodei	66%	80.62%	4365	XM_030550968.1
PREDICTED: Falco peregrinus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Falco peregrinus	61%	80.61%	4372	XM_005243486.3
PREDICTED: Bos mutus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Bos mutus	44%	94.49%	2034	XM_005901436.2
PREDICTED: Strigops habroptila nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Strigops habroptila	55%	80.52%	3642	XM_030479528.1
PREDICTED: Falco rusticolus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Falco rusticolus	61%	80.55%	4374	XM_037388040.1
PREDICTED: Parus major nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Parus major	55%	80.70%	4381	XM_015628424.3
PREDICTED: Serinus canaria nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Serinus canaria	55%	80.53%	4396	XM_030238008.1

PREDICTED: Lepidothrix coronata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Lepidothrix coronata	55%	80.74%	3811	XM_017811493.1
PREDICTED: Neopelma chrysocephalum nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Neopelma chrysocephalum	55%	80.41%	4400	XM_027679339.1
PREDICTED: Pseudopodoces humilis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Pseudopodoces humilis	55%	80.60%	4373	XM_005526000.2
PREDICTED: Chelonoidis abingdonii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Chelonoidis abingdonii	56%	80.56%	2874	XM_032787316.1
PREDICTED: Melopsittacus undulatus nicotinamide phosphoribosyltransferase (LOC101869767), mRNA	Melopsittacus undulatus	55%	80.61%	4308	XM_034062864.1
PREDICTED: Struthio camelus australis nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Struthio camelus australis	56%	80.83%	4384	XM_009666003.1
PREDICTED: Dasypus novemcinctus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Dasypus novemcinctus	33%	94.05%	1637	XM_004467551.3
PREDICTED: Haliaeetus leucocephalus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Haliaeetus leucocephalus	54%	81.02%	3435	XM_010581092.1
PREDICTED: Corvus moneduloides nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Corvus moneduloides	55%	80.30%	4410	XM_032106281.1
PREDICTED: Calypte anna nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Calypte anna	55%	80.41%	3851	XM_030463194.1

PREDICTED: Pipra filicauda nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Pipra filicauda	55%	80.66%	4425	XM_027751813.2
PREDICTED: Catharus ustulatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Catharus ustulatus	55%	80.52%	4373	XM_033058152.1
PREDICTED: Haliaeetus albicilla nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Haliaeetus albicilla	54%	80.98%	3435	XM_009915952.1
PREDICTED: Charadrius vociferus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Charadrius vociferus	54%	81.11%	3678	XM_009883548.1
PREDICTED: Gopherus evgoodei nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Gopherus evgoodei	66%	81.09%	4499	XM_030550877.1
PREDICTED: Chelonia mydas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Chelonia mydas	60%	80.82%	4571	XM_037889151.1
PREDICTED: Chelonia mydas nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Chelonia mydas	60%	80.82%	4347	XM_037889150.1
PREDICTED: Anser cygnoides domesticus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Anser cygnoides domest	54%	80.81%	3439	XM_013190754.1
PREDICTED: Corvus cornix cornix nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Corvus cornix cornix	55%	80.23%	4401	XM_039570900.1
PREDICTED: Passer montanus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Passer montanus	55%	80.52%	4374	XM_039723689.1

PREDICTED: <i>Molothrus ater</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Molothrus ater	55%	80.48%	4367	XM_036400949.1
PREDICTED: <i>Oxyura jamaicensis</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Oxyura jamaicensis	55%	80.19%	3566	XM_035332701.1
PREDICTED: <i>Anser cygnoides domesticus</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Anser cygnoides domest	54%	80.80%	3529	XM_013190752.1
PREDICTED: <i>Gavia stellata</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Gavia stellata	54%	80.85%	3556	XM_009817195.1
PREDICTED: <i>Trachemys scripta elegans</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Trachemys scripta elega	56%	79.51%	3307	XM_034766557.1
PREDICTED: <i>Crocodylus porosus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Crocodylus porosus	66%	80.61%	4302	XM_019543559.1
PREDICTED: <i>Opisthocomus hoazin</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Opisthocomus hoazin	54%	80.87%	3577	XM_009933780.1
PREDICTED: <i>Phalacrocorax carbo</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Phalacrocorax carbo	54%	80.75%	3535	XM_009504128.1
PREDICTED: <i>Corapipo altera</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Corapipo altera	55%	80.30%	4429	XM_027639638.1
PREDICTED: <i>Empidonax traillii</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Empidonax traillii	55%	80.18%	4432	XM_027890081.1

PREDICTED: Aythya fuligula nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Aythya fuligula	55%	80.12%	3547	XM_032190771.1
PREDICTED: Anas platyrhynchos nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Anas platyrhynchos	66%	80.12%	4414	XM_027459200.2
PREDICTED: Nipponia nippon nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Nipponia nippon	54%	80.60%	3505	XM_009462970.1
PREDICTED: Pygoscelis adeliae nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pygoscelis adeliae	58%	80.70%	4322	XM_009328370.1
PREDICTED: Alligator sinensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Alligator sinensis	65%	80.86%	4260	XM_025207378.1
PREDICTED: Chiroxiphia lanceolata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Chiroxiphia lanceolata	55%	80.22%	4427	XM_032687695.1
PREDICTED: Merops nubicus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Merops nubicus	54%	80.99%	3410	XM_008942729.1
PREDICTED: Numida meleagris nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Numida meleagris	58%	80.49%	4655	XM_021384581.1
PREDICTED: Falco peregrinus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Falco peregrinus	61%	80.03%	4391	XM_027795358.1
PREDICTED: Sturnus vulgaris nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Sturnus vulgaris	55%	80.28%	4369	XM_014869004.1

PREDICTED: Strigops habroptila nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Strigops habroptila	55%	79.94%	3660	XM_030479527.1
PREDICTED: Pterocles gutturalis nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Pterocles gutturalis	54%	80.63%	3385	XM_010082091.1
PREDICTED: Falco rusticolus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Falco rusticolus	61%	79.97%	4393	XM_037388039.1
PREDICTED: Parus major nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Parus major	55%	80.12%	4400	XM_015628423.3
PREDICTED: Serinus canaria nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Serinus canaria	55%	79.95%	4414	XM_030238007.1
PREDICTED: Lepidothrix coronata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Lepidothrix coronata	55%	80.16%	3829	XM_017811492.1
PREDICTED: Pseudopodoces humilis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Pseudopodoces humilis	55%	80.02%	4391	XM_014255185.1
PREDICTED: Fulmarus glacialis nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Fulmarus glacialis	54%	80.57%	3405	XM_009585326.1
PREDICTED: Leptosomus discolor nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Leptosomus discolor	54%	80.63%	3511	XM_009960924.1
PREDICTED: Lonchura striata domestica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Lonchura striata domest	55%	80.39%	4386	XM_021534670.2

PREDICTED: Pelecanus crispus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Pelecanus crispus	54%	80.60%	3405	XM_009480267.1
PREDICTED: Tauraco erythrolophus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Tauraco erythrolophus	54%	80.57%	3405	XM_009987169.1
PREDICTED: Nestor notabilis nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Nestor notabilis	54%	80.57%	3397	XM_010024427.1
PREDICTED: Pipra filicauda nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Pipra filicauda	55%	80.08%	4446	XM_027751812.2
PREDICTED: Egretta garzetta nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Egretta garzetta	53%	80.83%	2440	XM_009636073.2
PREDICTED: Catharus ustulatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Catharus ustulatus	55%	79.94%	4391	XM_033058151.1
PREDICTED: Pelodiscus sinensis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pelodiscus sinensis	56%	80.35%	3407	XM_006137565.2
PREDICTED: Phasianus colchicus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Phasianus colchicus	58%	80.38%	4538	XM_031597951.1
PREDICTED: Gopherus evgoodei nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Gopherus evgoodei	66%	80.50%	4517	XM_030550794.1
PREDICTED: Cariama cristata nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Cariama cristata	54%	80.43%	3518	XM_009697817.1

PREDICTED: Acanthisitta chloris nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Acanthisitta chloris	54%	80.71%	3401	XM_009070204.1
PREDICTED: Motacilla alba alba nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Motacilla alba alba	55%	80.20%	4388	XM_038153822.1
PREDICTED: Colius striatus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Colius striatus	54%	80.59%	2495	XM_010207340.1
PREDICTED: Taeniopygia guttata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Taeniopygia guttata	55%	80.18%	4375	XM_030291782.2
PREDICTED: Empidonax traillii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Empidonax traillii	54%	80.57%	4422	XM_027890080.1
PREDICTED: Passer montanus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Passer montanus	55%	79.94%	4392	XM_039723688.1
PREDICTED: Chlamydotis macqueenii nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Chlamydotis macqueenii	54%	80.57%	3389	XM_010121413.1
PREDICTED: Manacus vitellinus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Manacus vitellinus	54%	80.63%	4355	XM_018068044.2
PREDICTED: Coturnix japonica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Coturnix japonica	58%	80.21%	4390	XM_015849616.2
PREDICTED: Lepidothrix coronata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Lepidothrix coronata	54%	80.59%	4020	XM_017811491.1

PREDICTED: Numida meleagris nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Numida meleagris	58%	79.91%	4673	XM_021384580.1
PREDICTED: Sturnus vulgaris nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Sturnus vulgaris	55%	79.70%	4387	XM_014869003.1
PREDICTED: Phaethon lepturus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Phaethon lepturus	54%	80.47%	3406	XM_010290764.1
PREDICTED: Pipra filicauda nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Pipra filicauda	54%	80.51%	4428	XM_027751811.2
PREDICTED: Geospiza fortis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Geospiza fortis	54%	80.34%	4360	XM_031059032.1
PREDICTED: Antrostomus carolinensis nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Antrostomus carolinensi	54%	80.39%	2498	XM_010172534.1
PREDICTED: Apaloderma vittatum nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Apaloderma vittatum	54%	80.37%	2504	XM_009876301.1
PREDICTED: Calidris pugnax nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Calidris pugnax	61%	80.36%	4361	XM_014963367.1
PREDICTED: Lonchura striata domestica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Lonchura striata domest	55%	79.81%	4404	XM_021534669.2
PREDICTED: Corvus brachyrhynchos nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Corvus brachyrhynchos	54%	80.04%	4300	XM_017745889.1

PREDICTED: Athene cunicularia nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Athene cunicularia	54%	79.80%	3461	XM_026868005.1
PREDICTED: Tinamus guttatus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Tinamus guttatus	54%	80.15%	3036	XM_010220213.1
PREDICTED: Cuculus canorus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Cuculus canorus	54%	80.14%	3447	XM_009557304.1
PREDICTED: Chrysochloris asiatica nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Chrysochloris asiatica	33%	92.55%	1476	XM_006834384.1
PREDICTED: Motacilla alba alba nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Motacilla alba alba	55%	79.62%	4407	XM_038153821.1
PREDICTED: Taeniopygia guttata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Taeniopygia guttata	55%	79.60%	4393	XM_030291774.2
PREDICTED: Corapipo altera nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Corapipo altera	54%	80.11%	4381	XM_027639639.1
PREDICTED: Empidonax traillii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Empidonax traillii	54%	79.98%	4440	XM_027890079.1
PREDICTED: Manacus vitellinus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Manacus vitellinus	54%	80.07%	4288	XM_018068046.1
PREDICTED: Gallus gallus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Gallus gallus	58%	79.72%	4617	XM_015275716.2

PREDICTED: Columba livia nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Columba livia	65%	80.15%	4337	XM_021295424.1
PREDICTED: Buceros rhinoceros silvestris nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Buceros rhinoceros silve	54%	80.09%	3531	XM_010143188.1
PREDICTED: Chiroxiphia lanceolata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Chiroxiphia lanceolata	54%	80.02%	4365	XM_032687696.1
PREDICTED: Chaetura pelagica nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Chaetura pelagica	57%	80.16%	4416	XM_010003850.1
PREDICTED: Coturnix japonica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Coturnix japonica	58%	79.63%	4409	XM_015849527.2
PREDICTED: Falco cherrug nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Falco cherrug	60%	79.83%	4242	XM_027797649.1
PREDICTED: Picoides pubescens nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Dryobates pubescens	54%	80.03%	2512	XM_009902268.1
PREDICTED: Cyanistes caeruleus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Cyanistes caeruleus	54%	79.85%	4373	XM_023919020.1
PREDICTED: Lepidothrix coronata nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Lepidothrix coronata	54%	80.00%	4038	XM_017811490.1
PREDICTED: Pipra filicauda nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Pipra filicauda	54%	79.92%	4620	XM_027751810.2

PREDICTED: Phasianus colchicus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Phasianus colchicus	58%	80.17%	4729	XM_031598029.1
PREDICTED: Nannospalax galili nicotinamide phosphoribosyltransferase-like (LOC103743693), mRNA	Nannospalax galili	34%	91.91%	1485	XM_029568493.1
PREDICTED: Ficedula albicollis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ficedula albicollis	53%	80.12%	2729	XM_016303080.1
PREDICTED: Coturnix japonica nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X1, mRNA	Coturnix japonica	57%	80.08%	4336	XM_015849455.2
PREDICTED: Zonotrichia albicollis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Zonotrichia albicollis	54%	79.58%	4373	XM_005482835.1
PREDICTED: Ornithorhynchus anatinus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ornithorhynchus anatinu	60%	81.30%	4299	XM_029077685.2
PREDICTED: Elephantulus edwardii nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Elephantulus edwardii	32%	92.54%	1680	XM_006882686.1
PREDICTED: Echinops telfairi nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Echinops telfairi	32%	92.12%	1491	XM_004702780.1
PREDICTED: Octodon degus nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Octodon degus	30%	94.06%	1528	XM_023719512.1
PREDICTED: Ceratotherium simum simum nicotinamide phosphoribosyltransferase (LOC101406745), transcript variant X2, mRNA	Ceratotherium simum si	59%	90.07%	2673	XM_014794475.1

PREDICTED: Dipodomys ordii nicotinamide phosphoribosyltransferase (Nampt), transcript variant X2, mRNA	Dipodomys ordii	87%	94.06%	4161	XM_013034735.1
PREDICTED: Tursiops truncatus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, mRNA	Tursiops truncatus	55%	94.96%	2576	XM_019940600.2
PREDICTED: Artibeus jamaicensis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Artibeus jamaicensis	91%	88.01%	4721	XM_037150492.1
PREDICTED: Pipistrellus kuhlii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, misc RNA	Pipistrellus kuhlii	33%	93.27%	1721	XR_004986581.1
PREDICTED: Gopherus evgoodei nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X5, mRNA	Gopherus evgoodei	62%	79.72%	4261	XM_030551130.1
PREDICTED: Aptenodytes forsteri nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Aptenodytes forsteri	43%	83.05%	2011	XM_019474576.1
PREDICTED: Ochotona princeps nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Ochotona princeps	45%	91.83%	2539	XM_036497211.1
PREDICTED: Anolis carolinensis nicotinamide phosphoribosyltransferase (nampt), mRNA	Anolis carolinensis	45%	81.43%	3341	XM_003221538.3
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X5, mRNA	Myotis lucifugus	83%	87.16%	4141	XM_023751080.1
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X4, mRNA	Myotis lucifugus	86%	87.16%	4261	XM_014452813.2

PREDICTED: Gekko japonicus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Gekko japonicus	46%	80.43%	4247	XM_015409550.1
PREDICTED: Pogona vitticeps nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pogona vitticeps	45%	80.48%	2791	XM_020797258.1
PREDICTED: Myotis myotis nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Myotis myotis	56%	94.22%	2536	XM_036327546.1
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X7, mRNA	Myotis lucifugus	26%	94.78%	2666	XM_023751082.1
PREDICTED: Myotis lucifugus nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X6, mRNA	Myotis lucifugus	28%	94.78%	1356	XM_023751081.1
PREDICTED: Tachyglossus aculeatus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Tachyglossus aculeatus	51%	79.94%	3079	XM_038741214.1
PREDICTED: Pipistrellus kuhlii nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X2, mRNA	Pipistrellus kuhlii	56%	93.42%	2556	XM_036429712.1
PREDICTED: Podarcis muralis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Podarcis muralis	49%	80.14%	4173	XM_028747464.1
PREDICTED: Python bivittatus nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Python bivittatus	45%	79.54%	4581	XM_007440236.2
PREDICTED: Trichosurus vulpecula nicotinamide phosphoribosyltransferase-like (LOC118844560), mRNA	Trichosurus vulpecula	33%	85.42%	1467	XM_036752464.1

PREDICTED: Zootoca vivipara nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Zootoca vivipara	42%	79.38%	1997	XM_035127959.1
Gallus gallus nicotinamide phosphoribosyltransferase pseudogene 1 (NAMPTP1), mRNA	Gallus gallus	33%	84.78%	1538	NM_001030728.1
PREDICTED: Lacerta agilis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Lacerta agilis	36%	82.33%	1663	XM_033161732.1
PREDICTED: Rhinatrema bivittatum nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Rhinatrema bivittatum	44%	77.81%	3800	XM_029615471.1
PREDICTED: Meleagris gallopavo nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Meleagris gallopavo	30%	85.28%	1458	XM_031552117.1
PREDICTED: Notechis scutatus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Notechis scutatus	44%	76.16%	2828	XM_026677241.1
PREDICTED: Geotrypetes seraphini nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Geotrypetes seraphini	37%	79.49%	4025	XM_033959280.1
PREDICTED: Microcaecilia unicolor nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Microcaecilia unicolor	35%	80.52%	2956	XM_030215941.1
PREDICTED: Crotalus tigris nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Crotalus tigris	45%	75.81%	3326	XM_039354466.1
PREDICTED: Pseudonaja textilis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pseudonaja textilis	40%	79.60%	2965	XM_026701422.1

PREDICTED: <i>Thamnophis elegans</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Thamnophis elegans	41%	79.67%	2929	XM_032220997.1
PREDICTED: <i>Manis pentadactyla</i> nicotinamide phosphoribosyltransferase-like (LOC118916539), mRNA	Manis pentadactyla	24%	88.39%	1183	XM_036893586.1
PREDICTED: <i>Protobothrops mucrosquamatus</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Protobothrops mucrosq	44%	75.33%	2200	XM_015813591.1
PREDICTED: <i>Chelonia mydas</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X6, mRNA	Chelonia mydas	25%	86.51%	2990	XM_037889153.1
PREDICTED: <i>Chelonia mydas</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X5, mRNA	Chelonia mydas	25%	86.51%	2355	XM_037889152.1
PREDICTED: <i>Numida meleagris</i> nicotinamide phosphoribosyltransferase (NAMPT), transcript variant X3, misc RNA	Numida meleagris	31%	85.99%	1822	XR_002434332.1
PREDICTED: <i>Latimeria chalumnae</i> nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Latimeria chalumnae	33%	79.78%	1578	XM_006005986.2
Xenopus laevis nicotinamide phosphoribosyltransferase L homeolog (nampt.L), mRNA	Xenopus laevis	32%	79.45%	4314	NM_001096519.1
Xenopus tropicalis nicotinamide phosphoribosyltransferase (nampt), mRNA	Xenopus tropicalis	32%	79.38%	2553	NM_001011388.2
PREDICTED: <i>Eurypyga helias</i> nicotinamide phosphoribosyltransferase (LOC104502587), partial mRNA	Eurypyga helias	23%	86.34%	1032	XM_010161710.1

Xenopus laevis nicotinamide phosphoribosyltransferase S homeolog (nampt.S), mRNA	Xenopus laevis	32%	79.03%	1860	NM_001089015.1
PREDICTED: Elephantulus edwardii nicotinamide phosphoribosyltransferase-like (LOC102844384), mRNA	Elephantulus edwardii	18%	92.99%	876	XM_006894601.1
PREDICTED: Acipenser ruthenus nicotinamide phosphoribosyltransferase (LOC117419927), mRNA	Acipenser ruthenus	32%	78.49%	2786	XM_034033325.2
PREDICTED: Acipenser ruthenus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Acipenser ruthenus	32%	78.18%	2882	XM_034026961.2
PREDICTED: Balearica regulorum gibbericeps nicotinamide phosphoribosyltransferase (LOC104630251), partial mRNA	Balearica regulorum gibb	20%	87.87%	1011	XM_010298635.1
PREDICTED: Polypterus senegalus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Polypterus senegalus	32%	78.08%	4705	XM_039761189.1
PREDICTED: Nanorana parkeri nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Nanorana parkeri	33%	77.63%	1694	XM_018568627.1
PREDICTED: Rhincodon typus nicotinamide phosphoribosyltransferase (nampt), mRNA	Rhincodon typus	32%	77.72%	4634	XM_020516383.1
PREDICTED: Scyliorhinus canicula nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X1, mRNA	Scyliorhinus canicula	32%	77.75%	4347	XM_038780159.1
PREDICTED: Amblyraja radiata nicotinamide phosphoribosyltransferase (nampt), mRNA	Amblyraja radiata	33%	77.38%	4676	XM_033037662.1

PREDICTED: Mesitornis unicolor nicotinamide phosphoribosyltransferase (LOC104544690), partial mRNA	Mesitornis unicolor	20%	87.17%	912	XM_010189625.1
PREDICTED: Balearica regulorum gibbericeps nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Balearica regulorum gibr	33%	76.93%	2480	XM_010307587.1
PREDICTED: Scyliorhinus canicula nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X3, mRNA	Scyliorhinus canicula	31%	77.47%	4270	XM_038780161.1
PREDICTED: Scyliorhinus canicula nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X2, mRNA	Scyliorhinus canicula	31%	77.44%	4621	XM_038780160.1
PREDICTED: Lepisosteus oculatus nicotinamide phosphoribosyltransferase (nampt), mRNA	Lepisosteus oculatus	32%	76.82%	4153	XM_006633383.2
PREDICTED: Mesitornis unicolor nicotinamide phosphoribosyltransferase (NAMPT), partial mRNA	Mesitornis unicolor	33%	76.48%	2486	XM_010194644.1
PREDICTED: Pantherophis guttatus nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Pantherophis guttatus	30%	84.14%	1605	XM_034433674.1
PREDICTED: Erpetoichthys calabaricus nicotinamide phosphoribosyltransferase (nampt), mRNA	Erpetoichthys calabaricu	27%	79.05%	1335	XM_028809948.1
PREDICTED: Chanos chanos nicotinamide phosphoribosyltransferase (nampt), transcript variant X1, mRNA	Chanos chanos	32%	75.77%	3080	XM_030782901.1
PREDICTED: Chanos chanos nicotinamide phosphoribosyltransferase (nampt), transcript variant X2, mRNA	Chanos chanos	32%	75.70%	3077	XM_030782909.1

PREDICTED: Callorhinchus milii nicotinamide phosphoribosyltransferase (nampt), mRNA	Callorhinchus milii	31%	75.89%	1957	XM_007905146.1
PREDICTED: Xiphophorus couchianus nicotinamide phosphoribosyltransferase (nampt), mRNA	Xiphophorus couchianus	32%	75.05%	4774	XM_028044445.1
PREDICTED: Xiphophorus maculatus nicotinamide phosphoribosyltransferase (nampt), mRNA	Xiphophorus maculatus	32%	75.05%	4775	XM_005799080.3
PREDICTED: Xiphophorus hellerii nicotinamide phosphoribosyltransferase (nampt), mRNA	Xiphophorus hellerii	32%	74.84%	4781	XM_032590135.1
PREDICTED: Sturnira hondurensis nicotinamide phosphoribosyltransferase-like (LOC118977058), partial mRNA	Sturnira hondurensis	12%	100.00%	525	XM_037031819.1
PREDICTED: Seriola dumerili nicotinamide phosphoribosyltransferase (nampt), mRNA	Seriola dumerili	32%	74.63%	1581	XM_022749244.1
PREDICTED: Pangasianodon hypophthalmus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Pangasianodon hypophthalmus	32%	74.95%	3104	XM_026923262.2
PREDICTED: Sinocyclocheilus rhinoceros nicotinamide phosphoribosyltransferase-like (LOC107718548), mRNA	Sinocyclocheilus rhinoceros	32%	74.56%	2294	XM_016525662.1
PREDICTED: Sinocyclocheilus anshuiensis nicotinamide phosphoribosyltransferase-like (LOC107656408), transcript variant X2, mRNA	Sinocyclocheilus anshuiensis	32%	74.56%	2254	XM_016444270.1
PREDICTED: Sinocyclocheilus anshuiensis nicotinamide phosphoribosyltransferase-like (LOC107656408), transcript variant X1, mRNA	Sinocyclocheilus anshuiensis	32%	74.56%	2321	XM_016444269.1

PREDICTED: <i>Seriola lalandi dorsalis</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Seriola lalandi dorsalis	32%	74.56%	5447	XM_023418008.1
PREDICTED: <i>Eurypyga helias</i> nicotinamide phosphoribosyltransferase-like (LOC104507841), mRNA	Eurypyga helias	31%	75.75%	2436	XM_010149260.1
PREDICTED: <i>Aotus nancymaae</i> nicotinamide phosphoribosyltransferase (LOC105715552), partial mRNA	Aotus nancymaae	12%	97.80%	546	XM_012449973.1
PREDICTED: <i>Sinocyclocheilus anshuiensis</i> nicotinamide phosphoribosyltransferase (LOC107658946), mRNA	Sinocyclocheilus anshuiensis	32%	74.41%	2111	XM_016447680.1
PREDICTED: <i>Mastacembelus armatus</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Mastacembelus armatus	32%	74.56%	5204	XM_026326373.2
PREDICTED: <i>Sinocyclocheilus grahami</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Sinocyclocheilus grahami	32%	74.34%	2427	XM_016270303.1
PREDICTED: <i>Cyprinodon tularosa</i> nicotinamide phosphoribosyltransferase (nampt1), mRNA	Cyprinodon tularosa	32%	74.44%	2086	XM_038274719.1
PREDICTED: <i>Fundulus heteroclitus</i> nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Fundulus heteroclitus	32%	74.44%	4825	XM_012870510.3
PREDICTED: <i>Pimephales promelas</i> nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Pimephales promelas	32%	74.37%	2191	XM_039660704.1
PREDICTED: <i>Sphaeramia orbicularis</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Sphaeramia orbicularis	32%	74.18%	4732	XM_030148709.1

PREDICTED: Poecilia formosa nicotinamide phosphoribosyltransferase (nampt), mRNA	Poecilia formosa	32%	74.22%	4800	XM_007579190.2
PREDICTED: Poecilia mexicana nicotinamide phosphoribosyltransferase (LOC106905851), mRNA	Poecilia mexicana	32%	74.22%	1727	XM_014970866.1
PREDICTED: Cyprinodon variegatus nicotinamide phosphoribosyltransferase (nampt), mRNA	Cyprinodon variegatus	32%	74.30%	1722	XM_015388266.1
PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase-like (LOC113067909), mRNA	Carassius auratus	32%	74.21%	3308	XM_026240397.1
PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase (LOC113064575), mRNA	Carassius auratus	32%	74.21%	2846	XM_026235428.1
PREDICTED: Danio rerio nicotinamide phosphoribosyltransferase a (nampta), mRNA	Danio rerio	32%	74.04%	2254	XM_002661340.5
PREDICTED: Poecilia latipinna nicotinamide phosphoribosyltransferase (nampt), mRNA	Poecilia latipinna	32%	73.99%	2462	XM_015051544.1
PREDICTED: Perca fluviatilis nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Perca fluviatilis	32%	74.09%	4759	XM_039791364.1
PREDICTED: Paramormyrops kingsleyae nicotinamide phosphoribosyltransferase (nampt), mRNA	Paramormyrops kingsley	31%	74.69%	2888	XM_023838304.1
PREDICTED: Sinocyclocheilus rhinoceros nicotinamide phosphoribosyltransferase (LOC107705339), mRNA	Sinocyclocheilus rhinoceros	32%	73.99%	2346	XM_016508597.1

PREDICTED: Etheostoma cragini nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Etheostoma cragini	32%	74.11%	1823	XM_034862951.1
PREDICTED: Epinephelus lanceolatus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Epinephelus lanceolatus	32%	74.03%	5815	XM_033614689.1
PREDICTED: Echeneis naucrates nicotinamide phosphoribosyltransferase (nampt), transcript variant X1, mRNA	Echeneis naucrates	32%	74.01%	2912	XM_029495344.1
PREDICTED: Poecilia reticulata nicotinamide phosphoribosyltransferase (nampt), mRNA	Poecilia reticulata	32%	74.01%	4818	XM_008400967.2
PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase (nampt), mRNA	Cottoperca gobio	32%	74.02%	5074	XM_029461746.1
PREDICTED: Electrophorus electricus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Electrophorus electricus	31%	74.58%	2908	XM_027007526.2
PREDICTED: Perca flavescens nicotinamide phosphoribosyltransferase (nampt), mRNA	Perca flavescens	32%	74.04%	1761	XM_028570350.1
PREDICTED: Monopterus albus nicotinamide phosphoribosyltransferase (nampt), mRNA	Monopterus albus	32%	73.94%	2903	XM_020599576.1
PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase-like (LOC113047893), mRNA	Carassius auratus	32%	73.92%	3405	XM_026209262.1
PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase-like (LOC113101511), mRNA	Carassius auratus	32%	73.92%	2347	XM_026265651.1

PREDICTED: Lates calcarifer nicotinamide phosphoribosyltransferase (nampt), mRNA	Lates calcarifer	32%	74.03%	5516	XM_018685153.1
PREDICTED: Echeneis naucrates nicotinamide phosphoribosyltransferase (nampt), transcript variant X2, mRNA	Echeneis naucrates	32%	73.94%	1926	XM_029495345.1
PREDICTED: Cyprinus carpio nicotinamide phosphoribosyltransferase-like (LOC109047414), mRNA	Cyprinus carpio	30%	74.78%	1468	XM_019065134.1
Micropterus salmoides nicotinamide phosphoribosyltransferase (nampt1), mRNA	Micropterus salmoides	32%	74.18%	5307	XM_038738892.1
PREDICTED: Archocentrus centrarchus nicotinamide phosphoribosyltransferase (nampt), mRNA	Archocentrus centrarchu	32%	73.92%	4788	XM_030720143.1
PREDICTED: Ictalurus punctatus nicotinamide phosphoribosyltransferase (nampt), mRNA	Ictalurus punctatus	32%	73.91%	1718	XM_017494287.1
PREDICTED: Austrofundulus limnaeus nicotinamide phosphoribosyltransferase (nampt), mRNA	Austrofundulus limnaeu:	32%	73.81%	5292	XM_014032934.1
PREDICTED: Megalops cyprinoides nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Megalops cyprinoides	32%	73.88%	2357	XM_036517828.1
PREDICTED: Boleophthalmus pectinirostris nicotinamide phosphoribosyltransferase (nampt), transcript variant X1, mRNA	Boleophthalmus pectinir	33%	73.84%	2019	XM_020926455.1
PREDICTED: Periophthalmus magnuspinnatus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Periophthalmus magnus	33%	73.75%	5581	XM_033989155.1

PREDICTED: Cyprinus carpio nicotinamide phosphoribosyltransferase (LOC109064254), transcript variant X2, mRNA	Cyprinus carpio	32%	73.88%	1717	XM_019081251.1
PREDICTED: Cyprinus carpio nicotinamide phosphoribosyltransferase (LOC109064254), transcript variant X1, mRNA	Cyprinus carpio	32%	73.88%	1717	XM_019081250.1
PREDICTED: Etheostoma spectabile nicotinamide phosphoribosyltransferase (nampt), mRNA	Etheostoma spectabile	32%	73.82%	4577	XM_032504650.1
PREDICTED: Tachysurus fulvidraco nicotinamide phosphoribosyltransferase (nampt), mRNA	Tachysurus fulvidraco	32%	73.91%	1813	XM_027151013.1
PREDICTED: Sander lucioperca nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Sander lucioperca	32%	73.82%	3369	XM_031284811.2
PREDICTED: Astatotilapia calliptera nicotinamide phosphoribosyltransferase (nampt), mRNA	Astatotilapia calliptera	32%	73.86%	4872	XM_026146150.1
PREDICTED: Maylandia zebra nicotinamide phosphoribosyltransferase (nampt), mRNA	Maylandia zebra	32%	73.86%	4853	XM_004560903.3
PREDICTED: Haplochromis burtoni nicotinamide phosphoribosyltransferase (nampt), mRNA	Haplochromis burtoni	32%	73.86%	4848	XM_005941581.2
PREDICTED: Neolamprologus brichardi nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Neolamprologus brichardi	32%	73.86%	4800	XM_006780644.2
PREDICTED: Boleophthalmus pectinirostris nicotinamide phosphoribosyltransferase (nampt), transcript variant X2, mRNA	Boleophthalmus pectinirostris	33%	73.77%	2016	XM_020926456.1

PREDICTED: Sparus aurata nicotinamide phosphoribosyltransferase (nampt), mRNA	Sparus aurata	32%	73.71%	5067	XM_030439787.1
PREDICTED: Notolabrus celidotus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Notolabrus celidotus	31%	74.15%	3044	XM_034673471.1
PREDICTED: Hippoglossus hippoglossus nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X2, mRNA	Hippoglossus hippoglossus	32%	73.75%	1745	XM_034578112.1
PREDICTED: Hippoglossus hippoglossus nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X1, misc RNA	Hippoglossus hippoglossus	32%	73.75%	2018	XR_004613060.1
PREDICTED: Hippoglossus stenolepis nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Hippoglossus stenolepis	32%	73.75%	2091	XM_035147450.1
PREDICTED: Oreochromis niloticus nicotinamide phosphoribosyltransferase (nampt), mRNA	Oreochromis niloticus	32%	73.79%	4819	XM_003450710.5
PREDICTED: Pundamilia nyererei nicotinamide phosphoribosyltransferase (nampt), mRNA	Pundamilia nyererei	32%	73.79%	3218	XM_005725250.1
PREDICTED: Oreochromis aureus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Oreochromis aureus	32%	73.79%	4832	XM_031726509.2
PREDICTED: Ictidomys tridecemlineatus nicotinamide phosphoribosyltransferase-like (LOC101969407), mRNA	Ictidomys tridecemlineatus	26%	95.28%	1181	XM_013361033.2
PREDICTED: Nematolebias whitei nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Nematolebias whitei	32%	73.58%	2340	XM_037695925.1

PREDICTED: Anabas testudineus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Anabas testudineus	32%	73.50%	4621	XM_026362603.1
PREDICTED: Myripristis murdjan nicotinamide phosphoribosyltransferase (nampt), mRNA	Myripristis murdjan	32%	73.59%	5316	XM_030045641.1
PREDICTED: Parambassis ranga nicotinamide phosphoribosyltransferase (nampt), mRNA	Parambassis ranga	32%	73.64%	5344	XM_028425065.1
PREDICTED: Acanthopagrus latus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Acanthopagrus latus	32%	73.57%	4976	XM_037122075.1
PREDICTED: Amphiprion ocellaris nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Amphiprion ocellaris	32%	73.52%	2943	XM_023285794.2
PREDICTED: Cynoglossus semilaevis nicotinamide phosphoribosyltransferase (nampt), mRNA	Cynoglossus semilaevis	32%	73.46%	4876	XM_008315785.3
PREDICTED: Cyclopterus lumpus nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X2, mRNA	Cyclopterus lumpus	32%	73.36%	4118	XM_034526414.1
PREDICTED: Cyclopterus lumpus nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X1, mRNA	Cyclopterus lumpus	32%	73.36%	4345	XM_034526413.1
PREDICTED: Scleropages formosus nicotinamide phosphoribosyltransferase (nampt), mRNA	Scleropages formosus	31%	74.11%	1871	XM_018726343.2
PREDICTED: Anguilla anguilla nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Anguilla anguilla	32%	73.44%	3118	XM_035425287.1

PREDICTED: <i>Sebastes umbrosus</i> nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Sebastes umbrosus	32%	73.32%	2622	XM_037760757.1
PREDICTED: <i>Paramormyrops kingsleyae</i> nicotinamide phosphoribosyltransferase-like (LOC111835587), mRNA	Paramormyrops kingsley	32%	73.30%	3107	XM_023796053.1
PREDICTED: <i>Acanthochromis polyacanthus</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Acanthochromis polyaca	32%	73.38%	5234	XM_022202889.1
PREDICTED: <i>Stegastes partitus</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Stegastes partitus	32%	73.31%	3904	XM_008278892.1
PREDICTED: <i>Nothobranchius furzeri</i> nicotinamide phosphoribosyltransferase (nampt), mRNA	Nothobranchius furzeri	32%	73.24%	3844	XM_015958020.1
PREDICTED: <i>Morone saxatilis</i> nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Morone saxatilis	32%	73.31%	1660	XM_035676979.1
PREDICTED: <i>Esox lucius</i> nicotinamide phosphoribosyltransferase (LOC105029720), mRNA	Esox lucius	32%	73.36%	2112	XM_010903224.3
PREDICTED: <i>Colossoma macropomum</i> nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Colossoma macropomur	31%	73.75%	1899	XM_036577781.1
PREDICTED: <i>Scleropages formosus</i> nicotinamide phosphoribosyltransferase-like (LOC108931584), mRNA	Scleropages formosus	32%	73.08%	2855	XM_018747455.2
PREDICTED: <i>Pygocentrus nattereri</i> nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Pygocentrus nattereri	31%	73.83%	2112	XM_017686568.2

PREDICTED: Scophthalmus maximus nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X2, mRNA	Scophthalmus maximus	32%	73.11%	5006	XM_035649697.1
PREDICTED: Oryzias latipes nicotinamide phosphoribosyltransferase (nampt), mRNA	Oryzias latipes	32%	72.96%	1933	XM_023952347.1
PREDICTED: Salmo salar nicotinamide phosphoribosyltransferase (nampt), mRNA	Salmo salar	32%	73.31%	1818	XM_014125919.1
PREDICTED: Oryzias melastigma nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Oryzias melastigma	32%	72.94%	3728	XM_024287936.2
Larimichthys crocea nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Larimichthys crocea	32%	72.88%	1646	NM_001303355.1
PREDICTED: Kryptolebias marmoratus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Kryptolebias marmoratu	32%	72.81%	5237	XM_017414910.3
PREDICTED: Thalassophryne amazonica nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Thalassophryne amazoni	32%	72.82%	3122	XM_034163040.1
PREDICTED: Salmo trutta nicotinamide phosphoribosyltransferase-like (LOC115197667), transcript variant X2, mRNA	Salmo trutta	31%	73.27%	1865	XM_029759415.1
PREDICTED: Salmo trutta nicotinamide phosphoribosyltransferase-like (LOC115197667), transcript variant X1, mRNA	Salmo trutta	31%	73.27%	1923	XM_029759414.1
PREDICTED: Paralichthys olivaceus nicotinamide phosphoribosyltransferase (nampt), partial mRNA	Paralichthys olivaceus	31%	73.17%	3037	XM_020092128.1

PREDICTED: Elephantulus edwardii nicotinamide phosphoribosyltransferase-like (LOC102875946), partial mRNA	Elephantulus edwardii	12%	93.54%	543	XM_006903532.1
PREDICTED: Labrus bergylta nicotinamide phosphoribosyltransferase-like (LOC109991695), mRNA	Labrus bergylta	32%	72.59%	4840	XM_020644043.2
PREDICTED: Syngnathus acus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Syngnathus acus	31%	73.03%	3561	XM_037242560.1
PREDICTED: Salmo salar nicotinamide phosphoribosyltransferase (LOC100380855), mRNA	Salmo salar	32%	72.90%	3375	XM_014152971.1
PREDICTED: Salvelinus namaycush nicotinamide phosphoribosyltransferase-like (LOC120066497), mRNA	Salvelinus namaycush	32%	72.96%	1794	XM_039017911.1
PREDICTED: Scophthalmus maximus nicotinamide phosphoribosyltransferase 1 (nampt1), transcript variant X1, mRNA	Scophthalmus maximus	31%	73.01%	4932	XM_035649687.1
PREDICTED: Salvelinus namaycush nicotinamide phosphoribosyltransferase (LOC120032167), mRNA	Salvelinus namaycush	32%	72.83%	3225	XM_038978138.1
PREDICTED: Clupea harengus nicotinamide phosphoribosyltransferase (nampt), mRNA	Clupea harengus	32%	72.63%	3299	XM_012823546.2
PREDICTED: Oncorhynchus mykiss nicotinamide phosphoribosyltransferase (LOC110500466), mRNA	Oncorhynchus mykiss	32%	72.89%	2009	XM_021577854.2
PREDICTED: Oncorhynchus kisutch nicotinamide phosphoribosyltransferase (LOC109864323), mRNA	Oncorhynchus kisutch	32%	72.76%	4666	XM_031796981.1

PREDICTED: Salmo trutta nicotinamide phosphoribosyltransferase (LOC115180000), mRNA	Salmo trutta	32%	72.76%	3251	XM_029741834.1
PREDICTED: Oncorhynchus keta nicotinamide phosphoribosyltransferase (LOC118392341), mRNA	Oncorhynchus keta	32%	72.69%	3373	XM_035784252.1
PREDICTED: Salarias fasciatus nicotinamide phosphoribosyltransferase (nampt), mRNA	Salarias fasciatus	32%	72.46%	3386	XM_030113007.1
PREDICTED: Oncorhynchus nerka nicotinamide phosphoribosyltransferase-like (LOC115106959), mRNA	Oncorhynchus nerka	32%	72.62%	3291	XM_029630221.1
PREDICTED: Oncorhynchus tshawytscha nicotinamide phosphoribosyltransferase-like (LOC112254994), mRNA	Oncorhynchus tshawytscha	32%	72.68%	1794	XM_024428016.1
PREDICTED: Oncorhynchus tshawytscha nicotinamide phosphoribosyltransferase-like (LOC112238280), mRNA	Oncorhynchus tshawytscha	32%	72.68%	1794	XM_024406850.1
PREDICTED: Pungitius pungitius nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Pungitius pungitius	32%	72.37%	3322	XM_037460635.1
PREDICTED: Oncorhynchus keta nicotinamide phosphoribosyltransferase (LOC118373568), mRNA	Oncorhynchus keta	31%	72.85%	3343	XM_035759740.1
PREDICTED: Salvelinus alpinus nicotinamide phosphoribosyltransferase (LOC111951445), mRNA	Salvelinus alpinus	32%	72.48%	3302	XM_023969528.1
PREDICTED: Oncorhynchus nerka nicotinamide phosphoribosyltransferase-like (LOC115116225), mRNA	Oncorhynchus nerka	32%	72.47%	1832	XM_029644710.1

PREDICTED: Oncorhynchus mykiss nicotinamide phosphoribosyltransferase (LOC110490269), mRNA	Oncorhynchus mykiss	31%	72.78%	3262	XM_021563565.2
PREDICTED: Oncorhynchus kisutch nicotinamide phosphoribosyltransferase-like (LOC109896755), mRNA	Oncorhynchus kisutch	31%	72.71%	3202	XM_031831894.1
PREDICTED: Salmo trutta nicotinamide phosphoribosyltransferase-like (LOC115198747), transcript variant X2, mRNA	Salmo trutta	31%	72.71%	3174	XM_029760986.1
PREDICTED: Salmo trutta nicotinamide phosphoribosyltransferase-like (LOC115198747), transcript variant X1, mRNA	Salmo trutta	31%	72.71%	3214	XM_029760985.1
PREDICTED: Oncorhynchus tshawytscha nicotinamide phosphoribosyltransferase (LOC112214341), mRNA	Oncorhynchus tshawytscha	31%	72.71%	3235	XM_024372990.1
PREDICTED: Salmo salar nicotinamide phosphoribosyltransferase-like (LOC106609207), mRNA	Salmo salar	31%	72.71%	3209	XM_014207729.1
PREDICTED: Oncorhynchus mykiss nicotinamide phosphoribosyltransferase (LOC110500207), mRNA	Oncorhynchus mykiss	31%	72.71%	3246	XM_036957589.1
PREDICTED: Astyanax mexicanus nicotinamide phosphoribosyltransferase (nampt), mRNA	Astyanax mexicanus	31%	72.97%	1937	XM_022666577.1
PREDICTED: Gouania willdenowi nicotinamide phosphoribosyltransferase-like (LOC114465204), mRNA	Gouania willdenowi	32%	71.80%	4188	XM_028450046.1
PREDICTED: Betta splendens nicotinamide phosphoribosyltransferase (nampt), mRNA	Betta splendens	32%	72.10%	4309	XM_029162530.1

PREDICTED: Hippocampus comes nicotinamide phosphoribosyltransferase (nampt), mRNA	Hippocampus comes	31%	72.38%	1884	XM_019866028.1
PREDICTED: Oncorhynchus kisutch nicotinamide phosphoribosyltransferase-like (LOC109867082), mRNA	Oncorhynchus kisutch	32%	72.32%	2061	XM_020455999.2
PREDICTED: Oncorhynchus nerka nicotinamide phosphoribosyltransferase (LOC115133159), mRNA	Oncorhynchus nerka	31%	72.49%	3200	XM_029666099.1
PREDICTED: Esox lucius nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Esox lucius	32%	72.21%	1741	XM_010896476.5
PREDICTED: Gymnodraco acuticeps nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Gymnodraco acuticeps	32%	71.86%	4703	XM_034236772.1
PREDICTED: Trematomus bernacchii nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Trematomus bernacchii	32%	71.86%	4828	XM_034131287.1
PREDICTED: Salvelinus namaycush nicotinamide phosphoribosyltransferase-like (LOC120049894), mRNA	Salvelinus namaycush	31%	72.42%	3310	XM_038996386.1
PREDICTED: Pseudochaenichthys georgianus nicotinamide phosphoribosyltransferase 1 (nampt1), mRNA	Pseudochaenichthys gec	32%	71.72%	2562	XM_034112514.1
PREDICTED: Denticeps clupeoides nicotinamide phosphoribosyltransferase (nampt), mRNA	Denticeps clupeoides	31%	72.34%	2882	XM_028954657.1
PREDICTED: Takifugu rubripes nicotinamide phosphoribosyltransferase (nampt), mRNA	Takifugu rubripes	31%	72.13%	3309	XM_003972819.3

PREDICTED: Danio rerio uncharacterized LOC100150117 (LOC100150117), ncRNA	Danio rerio	32%	71.52%	3469	XR_001800584.2
PREDICTED: Megalops cyprinoides nicotinamide phosphoribosyltransferase-like (LOC118772037), mRNA	Megalops cyprinoides	31%	71.93%	1590	XM_036520276.1
PREDICTED: Danio rerio uncharacterized LOC557816 (LOC557816), mRNA	Danio rerio	32%	71.24%	4039	XM_021472385.1
PREDICTED: Danio rerio uncharacterized LOC100150117 (LOC100150117), ncRNA	Danio rerio	32%	71.24%	3982	XR_002459722.1
PREDICTED: Danio rerio uncharacterized LOC557816 (LOC557816), mRNA	Danio rerio	32%	71.24%	4039	XM_021479984.1
PREDICTED: Danio rerio si:dkey-145c18.2 (si:dkey-145c18.2), mRNA	Danio rerio	32%	71.17%	3228	XM_009293769.2
PREDICTED: Anguilla anguilla nicotinamide phosphoribosyltransferase-like (LOC118219008), mRNA	Anguilla anguilla	31%	71.44%	3152	XM_035401788.1
PREDICTED: Gadus morhua nicotinamide phosphoribosyltransferase (nampt), mRNA	Gadus morhua	31%	70.92%	4868	XM_030341219.1
PREDICTED: Danio rerio si:dkey-145c18.3 (si:dkey-145c18.3), mRNA	Danio rerio	32%	70.26%	3236	XM_021467940.1
PREDICTED: Aotus nancymaae nicotinamide phosphoribosyltransferase-like (LOC110568792), mRNA	Aotus nancymaae	8%	95.71%	1097	XM_021673273.1

PREDICTED: Oncorhynchus keta nicotinamide phosphoribosyltransferase-like (LOC118374842), mRNA	Oncorhynchus keta	24%	73.52%	1532	XM_035761311.1
PREDICTED: Mustela erminea nicotinamide phosphoribosyltransferase-like (LOC116571491), mRNA	Mustela erminea	9%	92.36%	481	XM_032309459.1
PREDICTED: Thamnophis sirtalis nicotinamide phosphoribosyltransferase (NAMPT), mRNA	Thamnophis sirtalis	20%	87.44%	2384	XM_014066457.1
PREDICTED: Egretta garzetta nicotinamide phosphoribosyltransferase-like (LOC104133974), partial mRNA	Egretta garzetta	9%	87.59%	543	XM_009647452.2
PREDICTED: Anarrhichthys ocellatus nicotinamide phosphoribosyltransferase-like (LOC116393360), mRNA	Anarrhichthys ocellatus	16%	72.04%	3211	XM_031865613.1
PREDICTED: Poecilia formosa nicotinamide phosphoribosyltransferase-like (LOC103129527), mRNA	Poecilia formosa	16%	71.79%	4013	XM_007540672.1
PREDICTED: Poecilia mexicana nicotinamide phosphoribosyltransferase-like (LOC106905456), mRNA	Poecilia mexicana	16%	71.65%	929	XM_014970312.1
PREDICTED: Kryptolebias marmoratus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Kryptolebias marmoratu	19%	68.98%	4832	XM_017423749.3
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X6, mRNA	Latimeria chalumnae	29%	66.33%	2502	XM_014491513.1
PREDICTED: Epinephelus lanceolatus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Epinephelus lanceolatus	29%	66.07%	2749	XM_033626909.1

PREDICTED: Sparus aurata nicotinamide phosphoribosyltransferase-like (LOC115583676), mRNA	Sparus aurata	28%	66.19%	4775	XM_030420777.1
PREDICTED: Biomphalaria glabrata nicotinamide phosphoribosyltransferase-like (LOC106074111), partial mRNA	Biomphalaria glabrata	25%	67.15%	4132	XM_013234842.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X5, mRNA	Latimeria chalumnae	28%	66.00%	2749	XM_014491512.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X4, misc RNA	Latimeria chalumnae	28%	66.00%	2365	XR_001354404.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X3, mRNA	Latimeria chalumnae	28%	66.00%	2544	XM_014491511.1
Micropterus salmoides nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Micropterus salmoides	28%	66.01%	5748	XM_038696857.1
PREDICTED: Parambassis ranga nicotinamide phosphoribosyltransferase-like (LOC114436198), mRNA	Parambassis ranga	28%	65.75%	2376	XM_028406348.1
PREDICTED: Monopterus albus nicotinamide phosphoribosyltransferase-like (LOC109951434), transcript variant X1, mRNA	Monopterus albus	28%	65.91%	3504	XM_020585942.1
PREDICTED: Larimichthys crocea nicotinamide phosphoribosyltransferase (LOC104922484), mRNA	Larimichthys crocea	28%	65.60%	5042	XM_010735316.3
PREDICTED: Acanthopagrus latus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Acanthopagrus latus	25%	66.52%	4278	XM_037102024.1

PREDICTED: Echeneis naucrates nicotinamide phosphoribosyltransferase-like (LOC115043453), mRNA	Echeneis naucrates	29%	65.68%	2608	XM_029501952.1
PREDICTED: Amblyraja radiata nicotinamide phosphoribosyltransferase-like (LOC116983075), mRNA	Amblyraja radiata	14%	69.94%	1793	XM_033036644.1
PREDICTED: Cyanistes caeruleus uncharacterized LOC111942146 (LOC111942146), ncRNA	Cyanistes caeruleus	4%	90.57%	239	XR_002870431.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X2, mRNA	Latimeria chalumnae	18%	68.04%	3811	XM_014491510.1
PREDICTED: Sinocyclocheilus grahami nicotinamide phosphoribosyltransferase-like (LOC107590551), mRNA	Sinocyclocheilus graham	9%	75.12%	1003	XM_016279360.1
PREDICTED: Amphiprion ocellaris nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Amphiprion ocellaris	28%	65.41%	5935	XM_023282555.2
PREDICTED: Paralichthys olivaceus nicotinamide phosphoribosyltransferase-like (LOC109640359), mRNA	Paralichthys olivaceus	28%	65.67%	1836	XM_020104322.1
PREDICTED: Morone saxatilis nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Morone saxatilis	28%	65.51%	3550	XM_035662398.1
PREDICTED: Meleagris gallopavo nicotinamide phosphoribosyltransferase-like (LOC104915959), mRNA	Meleagris gallopavo	6%	82.44%	338	XM_010726927.3
PREDICTED: Hippoglossus stenolepis nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Hippoglossus stenolepis	28%	65.52%	5500	XM_035152229.1

PREDICTED: Xiphophorus couchianus nicotinamide phosphoribosyltransferase-like (LOC114135936), transcript variant X1, mRNA	Xiphophorus couchianus	29%	65.31%	3411	XM_028003647.1
PREDICTED: Myripristis murdjan nicotinamide phosphoribosyltransferase-like (LOC115359797), mRNA	Myripristis murdjan	19%	67.18%	4703	XM_030052435.1
PREDICTED: Poecilia latipinna nicotinamide phosphoribosyltransferase-like (LOC106946294), transcript variant X2, mRNA	Poecilia latipinna	28%	65.48%	4078	XM_015030512.1
PREDICTED: Betta splendens nicotinamide phosphoribosyltransferase-like (LOC114855563), transcript variant X2, mRNA	Betta splendens	19%	67.09%	4218	XM_029150818.1
PREDICTED: Betta splendens nicotinamide phosphoribosyltransferase-like (LOC114855563), transcript variant X1, mRNA	Betta splendens	19%	67.09%	4358	XM_029150817.1
PREDICTED: Poecilia mexicana nicotinamide phosphoribosyltransferase-like (LOC106932544), transcript variant X2, mRNA	Poecilia mexicana	28%	65.32%	3720	XM_015011312.1
PREDICTED: Lates calcarifer nicotinamide phosphoribosyltransferase-like (LOC108873533), mRNA	Lates calcarifer	28%	65.48%	5951	XM_018661766.1
PREDICTED: Chanos chanos nicotinamide phosphoribosyltransferase-like (LOC115814688), transcript variant X2, mRNA	Chanos chanos	19%	67.45%	2288	XM_030777618.1
PREDICTED: Chanos chanos nicotinamide phosphoribosyltransferase-like (LOC115814688), transcript variant X1, mRNA	Chanos chanos	19%	67.45%	2279	XM_030777617.1
PREDICTED: Boleophthalmus pectinirostris nicotinamide phosphoribosyltransferase-like (LOC110165776), mRNA	Boleophthalmus pectinir	29%	65.64%	2171	XM_020930964.1

PREDICTED: Hippoglossus hippoglossus nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X1, mRNA	Hippoglossus hippoglossus	28%	65.36%	3413	XM_034586837.1
PREDICTED: Mastomys coucha receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X4, mRNA	Mastomys coucha	13%	75.25%	10294	XM_031359464.1
PREDICTED: Hippocampus comes nicotinamide phosphoribosyltransferase-like (LOC109514513), mRNA	Hippocampus comes	28%	65.31%	4418	XM_019867688.1
PREDICTED: Xiphophorus hellerii nicotinamide phosphoribosyltransferase-like (LOC116710812), transcript variant X1, mRNA	Xiphophorus hellerii	28%	65.14%	3442	XM_032550058.1
PREDICTED: Seriola lalandi dorsalis nicotinamide phosphoribosyltransferase-like (LOC111668643), mRNA	Seriola lalandi dorsalis	28%	65.38%	2589	XM_023424745.1
PREDICTED: Poecilia formosa nicotinamide phosphoribosyltransferase-like (LOC103150295), transcript variant X2, mRNA	Poecilia formosa	28%	65.32%	4127	XM_007569855.2
PREDICTED: Anarrhichthys ocellatus nicotinamide phosphoribosyltransferase-like (LOC116398876), mRNA	Anarrhichthys ocellatus	25%	66.28%	3421	XM_031875600.1
PREDICTED: Poecilia latipinna nicotinamide phosphoribosyltransferase-like (LOC106946294), transcript variant X1, mRNA	Poecilia latipinna	28%	65.30%	4132	XM_015030511.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X7, mRNA	Latimeria chalumnae	18%	67.58%	1551	XM_014491514.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X1, mRNA	Latimeria chalumnae	18%	67.58%	3902	XM_014491509.1

PREDICTED: Xiphophorus maculatus nicotinamide phosphoribosyltransferase-like (LOC102220339), transcript variant X1, mRNA	Xiphophorus maculatus	29%	65.00%	3270	XM_005803698.2
Cyprinodon tularosa nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Cyprinodon tularosa	19%	67.02%	2324	XM_038269068.1
PREDICTED: Seriola dumerili nicotinamide phosphoribosyltransferase-like (LOC111221675), mRNA	Seriola dumerili	28%	65.30%	4257	XM_022745168.1
PREDICTED: Poecilia mexicana nicotinamide phosphoribosyltransferase-like (LOC106932544), transcript variant X1, mRNA	Poecilia mexicana	28%	65.13%	3781	XM_015011311.1
PREDICTED: Xiphophorus couchianus nicotinamide phosphoribosyltransferase-like (LOC114135936), transcript variant X3, mRNA	Xiphophorus couchianus	25%	65.98%	3283	XM_028003649.1
PREDICTED: Xiphophorus couchianus nicotinamide phosphoribosyltransferase-like (LOC114135936), transcript variant X2, mRNA	Xiphophorus couchianus	25%	65.98%	3468	XM_028003648.1
PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase-like (LOC115008611), transcript variant X2, mRNA	Cottoperca gobio	28%	65.06%	4238	XM_029432309.1
PREDICTED: Mus musculus receptor (TNFRSF)-interacting serine-threonine kinase 1 (Ripk1), transcript variant X1, mRNA	Mus musculus	13%	74.75%	10556	XM_036157927.1
PREDICTED: Mus caroli receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X2, mRNA	Mus caroli	13%	75.19%	7954	XM_029468644.1
PREDICTED: Scyliorhinus canicula nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Scyliorhinus canicula	28%	65.23%	1846	XM_038810563.1

PREDICTED: Acipenser ruthenus nicotinamide phosphoribosyltransferase-like (LOC117972040), mRNA	Acipenser ruthenus	29%	65.10%	5037	XM_034920272.1
PREDICTED: Xiphophorus hellerii nicotinamide phosphoribosyltransferase-like (LOC116710812), transcript variant X2, mRNA	Xiphophorus hellerii	28%	65.03%	3499	XM_032550059.1
PREDICTED: Erpetoichthys calabaricus nicotinamide phosphoribosyltransferase-like (LOC114668379), mRNA	Erpetoichthys calabaricu	29%	65.26%	2869	XM_028824099.1
PREDICTED: Crassostrea virginica nicotinamide phosphoribosyltransferase-like (LOC111109680), mRNA	Crassostrea virginica	21%	66.70%	1500	XM_022445898.1
PREDICTED: Poecilia formosa nicotinamide phosphoribosyltransferase-like (LOC103150295), transcript variant X1, mRNA	Poecilia formosa	28%	65.14%	4188	XM_007569854.2
PREDICTED: Notothenia coriiceps nicotinamide phosphoribosyltransferase-like (LOC104961716), partial mRNA	Notothenia coriiceps	10%	71.97%	713	XM_010790049.1
PREDICTED: Poecilia mexicana nicotinamide phosphoribosyltransferase-like (LOC106932544), transcript variant X3, misc RNA	Poecilia mexicana	26%	65.24%	1744	XR_001421293.1
PREDICTED: Pungitius pungitius nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Pungitius pungitius	19%	66.94%	4856	XM_037490927.1
PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase-like (LOC115008611), transcript variant X4, mRNA	Cottoperca gobio	25%	65.71%	4464	XM_029432311.1
PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase-like (LOC115008611), transcript variant X3, mRNA	Cottoperca gobio	25%	65.71%	4391	XM_029432310.1

PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase-like (LOC115008611), transcript variant X1, mRNA	Cottoperca gobio	25%	65.71%	4484	XM_029432308.1
PREDICTED: Anabas testudineus nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X1, mRNA	Anabas testudineus	19%	66.79%	2116	XM_026344574.2
PREDICTED: Scleropages formosus nicotinamide phosphoribosyltransferase-like (LOC108923454), mRNA	Scleropages formosus	14%	68.58%	3187	XM_018734206.2
PREDICTED: Poecilia latipinna nicotinamide phosphoribosyltransferase-like (LOC106946294), transcript variant X3, misc_RNA	Poecilia latipinna	26%	65.33%	1738	XR_001424743.1
PREDICTED: Poecilia reticulata nicotinamide phosphoribosyltransferase-like (LOC103465472), transcript variant X1, mRNA	Poecilia reticulata	28%	64.85%	3831	XM_008410345.2
PREDICTED: Epinephelus lanceolatus nicotinamide phosphoribosyltransferase-like (LOC117250801), partial mRNA	Epinephelus lanceolatus	14%	68.79%	749	XM_033616779.1
PREDICTED: Xiphophorus maculatus nicotinamide phosphoribosyltransferase-like (LOC102220339), transcript variant X2, mRNA	Xiphophorus maculatus	28%	64.87%	3327	XM_023324974.1
PREDICTED: Polypterus senegalus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Polypterus senegalus	29%	65.18%	2677	XM_039770579.1
PREDICTED: Cyclopterus lumpus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Cyclopterus lumpus	28%	64.83%	5064	XM_034532704.1
PREDICTED: Sinocyclocheilus rhinoceros nicotinamide phosphoribosyltransferase-like (LOC107728616), mRNA	Sinocyclocheilus rhinoceros	19%	66.55%	2731	XM_016538857.1

PREDICTED: Acipenser ruthenus nicotinamide phosphoribosyltransferase-like (LOC117414206), mRNA	Acipenser ruthenus	29%	64.71%	5067	XM_034024009.2
PREDICTED: Austrofundulus limnaeus nicotinamide phosphoribosyltransferase-like (LOC106530702), mRNA	Austrofundulus limnaeu:	16%	68.33%	4835	XM_014026378.1
PREDICTED: Notothenia coriiceps nicotinamide phosphoribosyltransferase-like (LOC104961715), mRNA	Notothenia coriiceps	10%	72.40%	651	XM_010790047.1
PREDICTED: Sinocyclocheilus grahami nicotinamide phosphoribosyltransferase-like (LOC107550476), mRNA	Sinocyclocheilus graham	28%	65.04%	2473	XM_016231798.1
PREDICTED: Callorhinchus milii nicotinamide phosphoribosyltransferase-like (LOC103179768), mRNA	Callorhinchus milii	27%	64.93%	4345	XM_007895174.1
PREDICTED: Acanthochromis polyacanthus nicotinamide phosphoribosyltransferase-like (LOC110969654), mRNA	Acanthochromis polyaca	28%	64.70%	5546	XM_022219777.1
PREDICTED: Etheostoma cragini nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Etheostoma cragini	15%	68.14%	2952	XM_034868970.1
PREDICTED: Hippoglossus hippoglossus nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X2, mRNA	Hippoglossus hippogloss	24%	65.99%	3277	XM_034586838.1
PREDICTED: Sinocyclocheilus rhinoceros nicotinamide phosphoribosyltransferase-like (LOC107739284), mRNA	Sinocyclocheilus rhinoce	28%	64.80%	2483	XM_016551364.1
PREDICTED: Sinocyclocheilus grahami nicotinamide phosphoribosyltransferase-like (LOC107590159), mRNA	Sinocyclocheilus graham	19%	66.43%	2734	XM_016278775.1

Danio rerio nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Danio rerio	19%	66.75%	2025	NM_212668.2
PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase-like (LOC115008611), transcript variant X6, mRNA	Cottoperca gobio	24%	65.65%	3954	XM_029432313.1
PREDICTED: Pecten maximus nicotinamide phosphoribosyltransferase-like (LOC117330330), mRNA	Pecten maximus	26%	66.17%	5710	XM_033888536.1
PREDICTED: Anabas testudineus nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X3, mRNA	Anabas testudineus	18%	66.67%	2217	XM_026344576.2
PREDICTED: Anabas testudineus nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X2, mRNA	Anabas testudineus	18%	66.67%	2210	XM_026344575.2
PREDICTED: Sinocyclocheilus grahami nicotinamide phosphoribosyltransferase-like (LOC107579595), mRNA	Sinocyclocheilus graham	6%	77.85%	592	XM_016265408.1
PREDICTED: Denticeps clupeoides nicotinamide phosphoribosyltransferase-like (LOC114801335), mRNA	Denticeps clupeoides	14%	68.17%	3219	XM_028999484.1
PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase-like (LOC113076104), mRNA	Carassius auratus	16%	67.66%	3174	XM_026248777.1
PREDICTED: Sinocyclocheilus anshuiensis nicotinamide phosphoribosyltransferase-like (LOC107696850), mRNA	Sinocyclocheilus anshuie	28%	64.83%	2483	XM_016497376.1
PREDICTED: Poecilia latipinna nicotinamide phosphoribosyltransferase-like (LOC106946294), transcript variant X4, mRNA	Poecilia latipinna	24%	65.68%	3917	XM_015030513.1

PREDICTED: Periophthalmus magnuspinnatus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Periophthalmus magnus	19%	67.01%	2840	XM_033965979.1
PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase-like (LOC113055252), mRNA	Carassius auratus	28%	64.86%	3080	XM_026221407.1
PREDICTED: Pocillopora damicornis nicotinamide phosphoribosyltransferase-like (LOC113669070), transcript variant X2, mRNA	Pocillopora damicornis	22%	65.91%	3797	XM_027185063.1
PREDICTED: Pocillopora damicornis nicotinamide phosphoribosyltransferase-like (LOC113669070), transcript variant X1, mRNA	Pocillopora damicornis	22%	65.91%	3602	XM_027185062.1
PREDICTED: Cottoperca gobio nicotinamide phosphoribosyltransferase-like (LOC115008611), transcript variant X5, misc RNA	Cottoperca gobio	23%	65.68%	2438	XR_003832312.1
PREDICTED: Etheostoma spectabile nicotinamide phosphoribosyltransferase-like (LOC116687964), mRNA	Etheostoma spectabile	15%	67.68%	2461	XM_032513706.1
PREDICTED: Perca flavescens nicotinamide phosphoribosyltransferase-like (LOC114554450), mRNA	Perca flavescens	19%	66.11%	1979	XM_028576304.1
PREDICTED: Sphaeramia orbicularis nicotinamide phosphoribosyltransferase-like (LOC115419038), mRNA	Sphaeramia orbicularis	19%	66.35%	5191	XM_030133646.1
PREDICTED: Lepisosteus oculatus nicotinamide phosphoribosyltransferase-like (LOC102687550), mRNA	Lepisosteus oculatus	18%	66.14%	3256	XM_015347229.1
PREDICTED: Poecilia reticulata nicotinamide phosphoribosyltransferase-like (LOC103465472), transcript variant X2, mRNA	Poecilia reticulata	24%	65.47%	3899	XM_008410347.2

PREDICTED: Pimephales promelas nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Pimephales promelas	25%	65.35%	4193	XM_039673621.1
PREDICTED: Astyanax mexicanus nicotinamide phosphoribosyltransferase-like (LOC103041462), mRNA	Astyanax mexicanus	14%	67.92%	1957	XM_022682801.1
PREDICTED: Sander lucioperca nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Sander lucioperca	18%	66.22%	2303	XM_031277248.2
PREDICTED: Perca fluviatilis nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Perca fluviatilis	19%	66.15%	3284	XM_039796734.1
PREDICTED: Crassostrea gigas nicotinamide phosphoribosyltransferase (LOC105342526), mRNA	Crassostrea gigas	24%	65.57%	2049	XM_011449497.3
PREDICTED: Esox lucius nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Esox lucius	19%	66.08%	3302	XM_010881670.3
PREDICTED: Mustela erminea uncharacterized LOC116569541 (LOC116569541), ncRNA	Mustela erminea	3%	91.72%	2204	XR_004277065.1
PREDICTED: Sebastes umbrosus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Sebastes umbrosus	28%	64.52%	2136	XM_037765040.1
PREDICTED: Oryzias latipes nicotinamide phosphoribosyltransferase (LOC101156645), mRNA	Oryzias latipes	29%	64.39%	2937	XM_004068909.4
PREDICTED: Stegastes partitus nicotinamide phosphoribosyltransferase-like (LOC103375230), partial mRNA	Stegastes partitus	24%	65.45%	6430	XM_008305448.1

PREDICTED: <i>Oryzias melastigma</i> nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Oryzias melastigma	19%	65.89%	2943	XM_024270679.2
PREDICTED: <i>Gymnodraco acuticeps</i> nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Gymnodraco acuticeps	14%	68.04%	4703	XM_034233397.1
PREDICTED: <i>Salvelinus namaycush</i> nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Salvelinus namaycush	14%	67.56%	3093	XM_039008976.1
PREDICTED: <i>Oncorhynchus keta</i> nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X1, mRNA	Oncorhynchus keta	14%	67.77%	3148	XM_035777518.1
PREDICTED: <i>Scophthalmus maximus</i> nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Scophthalmus maximus	19%	65.86%	4600	XM_035631327.1
PREDICTED: <i>Stegastes partitus</i> nicotinamide phosphoribosyltransferase-like (LOC103364892), partial mRNA	Stegastes partitus	16%	67.90%	1189	XM_008292179.1
PREDICTED: <i>Oncorhynchus kisutch</i> nicotinamide phosphoribosyltransferase (LOC109896974), transcript variant X1, mRNA	Oncorhynchus kisutch	19%	66.35%	3148	XM_020491459.2
PREDICTED: <i>Mizuhopecten yessoensis</i> nicotinamide phosphoribosyltransferase-like (LOC110460388), transcript variant X2, misc RNA	Mizuhopecten yessoensi	18%	67.40%	2283	XR_002464007.1
PREDICTED: <i>Mizuhopecten yessoensis</i> nicotinamide phosphoribosyltransferase-like (LOC110460388), transcript variant X1, mRNA	Mizuhopecten yessoensi	18%	67.40%	2323	XM_021513263.1
PREDICTED: <i>Oncorhynchus kisutch</i> nicotinamide phosphoribosyltransferase (LOC109896974), transcript variant X2, mRNA	Oncorhynchus kisutch	16%	67.55%	2971	XM_031806311.1

PREDICTED: <i>Oncorhynchus mykiss</i> nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X1, mRNA	Oncorhynchus mykiss	14%	67.61%	3045	XM_021569602.2
PREDICTED: <i>Gymnodraco acuticeps</i> nicotinamide phosphoribosyltransferase-like (LOC117533183), mRNA	Gymnodraco acuticeps	7%	75.82%	667	XM_034196828.1
PREDICTED: <i>Oncorhynchus mykiss</i> nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X2, mRNA	Oncorhynchus mykiss	11%	69.66%	3162	XM_036950558.1
PREDICTED: <i>Limulus polyphemus</i> nicotinamide phosphoribosyltransferase-like (LOC106469665), mRNA	Limulus polyphemus	20%	66.00%	3489	XM_013930166.2
PREDICTED: <i>Pygocentrus nattereri</i> nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Pygocentrus nattereri	14%	66.98%	4658	XM_017711752.2
PREDICTED: <i>Oncorhynchus tshawytscha</i> nicotinamide phosphoribosyltransferase-like (LOC112219097), transcript variant X1, mRNA	Oncorhynchus tshawytscha	14%	67.45%	3135	XM_024380312.1
PREDICTED: <i>Trematomus bernacchii</i> nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Trematomus bernacchii	14%	67.38%	4744	XM_034143793.1
PREDICTED: <i>Oncorhynchus tshawytscha</i> nicotinamide phosphoribosyltransferase-like (LOC112219097), transcript variant X2, mRNA	Oncorhynchus tshawytscha	11%	69.46%	2987	XM_024380319.1
PREDICTED: <i>Stylophora pistillata</i> nicotinamide phosphoribosyltransferase-like (LOC111329663), mRNA	Stylophora pistillata	15%	67.26%	3771	XM_022934423.1
PREDICTED: <i>Oncorhynchus keta</i> nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X3, mRNA	Oncorhynchus keta	11%	69.46%	3223	XM_035777520.1

PREDICTED: Oncorhynchus keta nicotinamide phosphoribosyltransferase 2 (nampt2), transcript variant X2, mRNA	Oncorhynchus keta	11%	69.46%	3208	XM_035777519.1
PREDICTED: Oncorhynchus nerka nicotinamide phosphoribosyltransferase-like (LOC115143310), transcript variant X2, mRNA	Oncorhynchus nerka	14%	67.30%	3075	XM_029683582.1
PREDICTED: Colossoma macropomum nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Colossoma macropomur	14%	66.77%	2148	XM_036559141.1
PREDICTED: Anguilla anguilla nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Anguilla anguilla	11%	68.86%	2926	XM_035388867.1
PREDICTED: Oncorhynchus nerka nicotinamide phosphoribosyltransferase-like (LOC115143310), transcript variant X3, mRNA	Oncorhynchus nerka	11%	69.06%	2866	XM_029683583.1
PREDICTED: Oncorhynchus nerka nicotinamide phosphoribosyltransferase-like (LOC115143310), transcript variant X1, mRNA	Oncorhynchus nerka	11%	69.06%	3090	XM_029683581.1
PREDICTED: Morone saxatilis nicotinamide phosphoribosyltransferase-like (LOC118328054), mRNA	Morone saxatilis	13%	67.41%	955	XM_035661658.1
PREDICTED: Salmo salar nicotinamide phosphoribosyltransferase-like (LOC106565851), mRNA	Salmo salar	11%	68.60%	3056	XM_014133445.1
PREDICTED: Salmo trutta nicotinamide phosphoribosyltransferase-like (LOC115207669), mRNA	Salmo trutta	11%	68.92%	3167	XM_029774993.1
PREDICTED: Gouania willdenowi nicotinamide phosphoribosyltransferase-like (LOC114463542), mRNA	Gouania willdenowi	19%	65.43%	2009	XM_028447166.1

PREDICTED: Pomacea canaliculata nicotinamide phosphoribosyltransferase-like (LOC112571701), mRNA	Pomacea canaliculata	28%	64.32%	6459	XM_025250921.1
PREDICTED: Electrophorus electricus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Electrophorus electricus	9%	70.29%	3463	XM_035520486.1
PREDICTED: Limulus polyphemus nicotinamide phosphoribosyltransferase-like (LOC106469485), transcript variant X1, mRNA	Limulus polyphemus	14%	67.79%	3121	XM_022398015.1
PREDICTED: Branchiostoma floridae nicotinamide phosphoribosyltransferase-like (LOC118416121), mRNA	Branchiostoma floridae	14%	67.75%	1594	XM_035821196.1
PREDICTED: Strongylocentrotus purpuratus nicotinamide phosphoribosyltransferase (LOC577046), mRNA	Strongylocentrotus purp	17%	66.46%	6595	XM_777300.5
PREDICTED: Actinia tenebrosa nicotinamide phosphoribosyltransferase-like (LOC116308254), mRNA	Actinia tenebrosa	13%	67.26%	2288	XM_031718639.1
PREDICTED: Exaiptasia pallida nicotinamide phosphoribosyltransferase (LOC110251362), mRNA	Exaiptasia diaphana	11%	68.83%	2741	XM_021058066.2
PREDICTED: Strongylocentrotus purpuratus nicotinamide phosphoribosyltransferase-like (LOC115919496), mRNA	Strongylocentrotus purp	17%	66.33%	6585	XM_030973504.1
PREDICTED: Limulus polyphemus nicotinamide phosphoribosyltransferase-like (LOC106469485), transcript variant X2, mRNA	Limulus polyphemus	13%	67.98%	2977	XM_022398016.1
PREDICTED: Pseudochaenichthys georgianus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Pseudochaenichthys gec	13%	67.30%	4676	XM_034082219.1

PREDICTED: Branchiostoma belcheri nicotinamide phosphoribosyltransferase-like (LOC109476757), mRNA	Branchiostoma belcheri	23%	65.16%	1572	XM_019777772.1
PREDICTED: Octopus sinensis nicotinamide phosphoribosyltransferase (LOC115211035), transcript variant X2, mRNA	Octopus sinensis	24%	65.04%	1725	XM_036502124.1
PREDICTED: Octopus bimaculoides nicotinamide phosphoribosyltransferase-like (LOC106883145), mRNA	Octopus bimaculoides	22%	65.12%	1649	XM_014934043.1
PREDICTED: Monopterus albus nicotinamide phosphoribosyltransferase-like (LOC109951434), transcript variant X2, mRNA	Monopterus albus	21%	65.47%	3375	XM_020585943.1
PREDICTED: Octopus sinensis nicotinamide phosphoribosyltransferase (LOC115211035), transcript variant X1, mRNA	Octopus sinensis	22%	65.26%	1523	XM_036502123.1
PREDICTED: Asterias rubens nicotinamide phosphoribosyltransferase-like (LOC117307354), mRNA	Asterias rubens	20%	64.87%	2278	XM_033792083.1
PREDICTED: Gadus morhua nicotinamide phosphoribosyltransferase-like (LOC115557112), transcript variant X2, mRNA	Gadus morhua	19%	64.86%	2687	XM_030374699.1
PREDICTED: Clupea harengus nicotinamide phosphoribosyltransferase-like (LOC105912295), mRNA	Clupea harengus	14%	65.98%	1874	XM_012841250.2
PREDICTED: Rhinopithecus roxellana putative cyclin-Y-like protein 3 (LOC104674309), mRNA	Rhinopithecus roxellana	2%	90.40%	1344	XM_030924441.1
PREDICTED: Notolabrus celidotus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Notolabrus celidotus	14%	65.78%	4332	XM_034690859.1

PREDICTED: Piliocolobus tephrosceles vacuolar protein sorting-associated protein 35-like (LOC113220003), mRNA	Piliocolobus tephroscele	2%	90.91%	606	XM_026448580.1
PREDICTED: Saccoglossus kowalevskii nicotinamide phosphoribosyltransferase-like (LOC100370741), mRNA	Saccoglossus kowalevski	19%	64.58%	3292	XM_002741557.2
PREDICTED: Lingula anatina nicotinamide phosphoribosyltransferase (LOC106177084), mRNA	Lingula anatina	20%	65.61%	1551	XM_013559763.1
PREDICTED: Megalops cyprinoides nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Megalops cyprinoides	19%	64.22%	1777	XM_036531633.1
PREDICTED: Actinia tenebrosa nicotinamide phosphoribosyltransferase-like (LOC116302032), mRNA	Actinia tenebrosa	10%	69.06%	1969	XM_031711222.1
PREDICTED: Gadus morhua nicotinamide phosphoribosyltransferase-like (LOC115557112), transcript variant X1, mRNA	Gadus morhua	18%	64.68%	2547	XM_030374698.1
PREDICTED: Acropora millepora nicotinamide phosphoribosyltransferase-like (LOC114961592), mRNA	Acropora millepora	21%	64.54%	3896	XM_029340359.1
PREDICTED: Tachysurus fulvidraco nicotinamide phosphoribosyltransferase-like (LOC113661848), mRNA	Tachysurus fulvidraco	6%	71.24%	3290	XM_027176326.1
PREDICTED: Monodelphis domestica uncharacterized LOC107652358 (LOC107652358), ncRNA	Monodelphis domestica	4%	78.00%	7854	XR_001629846.1
PREDICTED: Amphimedon queenslandica nicotinamide phosphoribosyltransferase-like (LOC100638634), mRNA	Amphimedon queenslan	25%	64.52%	1600	XM_003384982.3

PREDICTED: Pangasianodon hypophthalmus nicotinamide phosphoribosyltransferase 2 (nampt2), mRNA	Pangasianodon hypopht	8%	70.90%	1944	XM_026935397.2
Opisthorchis viverrini hypothetical protein partial mRNA	Opisthorchis viverrini	7%	70.06%	1922	XM_009164244.1
PREDICTED: Acropora digitifera nicotinamide phosphoribosyltransferase-like (LOC107357523), mRNA	Acropora digitifera	14%	65.74%	2502	XM_015924167.1
PREDICTED: Anneissia japonica nicotinamide phosphoribosyltransferase-like (LOC117103319), mRNA	Anneissia japonica	16%	65.00%	2125	XM_033243861.1
PREDICTED: Ictalurus punctatus nicotinamide phosphoribosyltransferase-like (LOC108255025), transcript variant X1, mRNA	Ictalurus punctatus	14%	65.23%	2562	XM_017450612.1
PREDICTED: Nematostella vectensis nicotinamide phosphoribosyltransferase (LOC5502792), mRNA	Nematostella vectensis	14%	65.49%	3121	XM_032371101.1
PREDICTED: Ictalurus punctatus nicotinamide phosphoribosyltransferase-like (LOC108255025), transcript variant X3, mRNA	Ictalurus punctatus	7%	69.75%	2331	XM_017450614.1
PREDICTED: Ictalurus punctatus nicotinamide phosphoribosyltransferase-like (LOC108255025), transcript variant X2, mRNA	Ictalurus punctatus	7%	69.75%	2315	XM_017450613.1
PREDICTED: Octopus bimaculoides nicotinamide phosphoribosyltransferase-like (LOC106878595), mRNA	Octopus bimaculoides	21%	64.91%	3653	XM_014927851.1
PREDICTED: Octopus sinensis nicotinamide phosphoribosyltransferase-like (LOC115210232), mRNA	Octopus sinensis	12%	66.67%	2315	XM_036501748.1

PREDICTED: Camelus ferus uncharacterized LOC116665040 (LOC116665040), transcript variant X2, ncRNA	Camelus ferus	1%	98.73%	4133	XR_004321627.1
PREDICTED: Camelus ferus uncharacterized LOC116665040 (LOC116665040), transcript variant X1, ncRNA	Camelus ferus	1%	98.73%	4169	XR_004321626.1
PREDICTED: Camelus dromedarius uncharacterized LOC116153950 (LOC116153950), ncRNA	Camelus dromedarius	1%	98.73%	4165	XR_004137723.1
PREDICTED: Penaeus monodon nicotinamide phosphoribosyltransferase-like (LOC119593700), transcript variant X2, mRNA	Penaeus monodon	8%	68.35%	2437	XM_037942661.1
PREDICTED: Penaeus monodon nicotinamide phosphoribosyltransferase-like (LOC119593700), transcript variant X1, mRNA	Penaeus monodon	8%	68.35%	1787	XM_037942659.1
Trichoplax adhaerens hypothetical protein (TRIADDRAFT_20412), partial mRNA	Trichoplax adhaerens	19%	64.22%	1410	XM_002109351.1
PREDICTED: Anneissia japonica nicotinamide phosphoribosyltransferase-like (LOC117107008), mRNA	Anneissia japonica	12%	68.70%	2382	XM_033248524.1
Strongyloides ratti Quinolate phosphoribosyl transferase,C-terminal domain and Nicotinamide phosphoribosyl transferase family-containing protein (SRAF_X000135900) partial mRNA	Strongyloides ratti	9%	67.87%	1521	XM_024648063.1
PREDICTED: Sinocyclocheilus grahami nicotinamide phosphoribosyltransferase-like (LOC107590552), mRNA	Sinocyclocheilus graham	4%	73.27%	1091	XM_016279361.1
PREDICTED: Petromyzon marinus nicotinamide phosphoribosyltransferase-like (LOC116952276), transcript variant X1, mRNA	Petromyzon marinus	11%	66.19%	2207	XM_032971477.1

PREDICTED: Acanthaster planci nicotinamide phosphoribosyltransferase-like (LOC110982121), transcript variant X2, mRNA	Acanthaster planci	15%	65.42%	2841	XM_022240311.1
PREDICTED: Acanthaster planci nicotinamide phosphoribosyltransferase-like (LOC110982121), transcript variant X1, mRNA	Acanthaster planci	15%	65.42%	2838	XM_022240310.1
Echinococcus granulosus Nicotinamide phosphoribosyltransferase (EGR_07009), partial mRNA	Echinococcus granulosus	4%	74.47%	1770	XM_024496258.1
Loa loa pre-B cell enhancing factor partial mRNA	Loa loa	11%	66.46%	1485	XM_003144369.1
Capsaspora owczarzaki ATCC 30864 pre-B-cell colony-enhancing factor mRNA	Capsaspora owczarzaki f	8%	67.47%	1653	XM_004363896.2
PREDICTED: Penaeus vannamei nicotinamide phosphoribosyltransferase-like (LOC113828203), mRNA	Penaeus vannamei	8%	66.92%	1729	XM_027381131.1
PREDICTED: Notothenia coriiceps nicotinamide phosphoribosyltransferase-like (LOC104942131), partial mRNA	Notothenia coriiceps	10%	66.29%	997	XM_010767330.1
PREDICTED: Petromyzon marinus nicotinamide phosphoribosyltransferase-like (LOC116952276), transcript variant X2, mRNA	Petromyzon marinus	7%	67.58%	2121	XM_032971478.1
Lottia gigantea hypothetical protein partial mRNA	Lottia gigantea	26%	62.66%	1410	XM_009061104.1
PREDICTED: Oncorhynchus keta nicotinamide phosphoribosyltransferase-like (LOC118382531), mRNA	Oncorhynchus keta	6%	70.15%	606	XM_035769313.1

Schistosoma mansoni nicotinate phosphoribosyltransferase related pre-B cell enhancing factor partial mRNA	Schistosoma mansoni	11%	65.85%	1456	XM_018796432.1
Helobdella robusta hypothetical protein partial mRNA	Helobdella robusta	23%	63.37%	1371	XM_009026890.1
Schistosoma haematobium nicotinate phosphoribosyltransferase related pre-B cell enhancing factor (MS3_0019831), partial mRNA	Schistosoma haematobi	11%	66.20%	2593	XM_035733805.1
Brugia malayi Pre-B cell enhancing factor precursor partial mRNA	Brugia malayi	12%	65.32%	1497	XM_001893213.1
PREDICTED: Heterocephalus glaber uncharacterized LOC110346270 (LOC110346270), ncRNA	Heterocephalus glaber	1%	91.55%	6339	XR_002390202.1
PREDICTED: Spodoptera litura nicotinamide phosphoribosyltransferase-like (LOC111363439), mRNA	Spodoptera litura	5%	69.32%	1374	XM_022980263.1
PREDICTED: Oncorhynchus keta uncharacterized LOC118374843 (LOC118374843), ncRNA	Oncorhynchus keta	4%	71.65%	607	XR_004823687.1
PREDICTED: Amphimedon queenslandica nicotinamide phosphoribosyltransferase-like (LOC100637371), mRNA	Amphimedon queenslan	4%	71.35%	1562	XM_003384810.2
Monosiga brevicollis MX1 uncharacterized protein (MONBRDRAFT_24677), partial mRNA	Monosiga brevicollis MX	4%	69.77%	1527	XM_001744871.1
PREDICTED: Aplysia californica nicotinamide phosphoribosyltransferase (LOC101858297), mRNA	Aplysia californica	7%	68.70%	2477	XM_013086876.2

PREDICTED: Carassius auratus nicotinamide phosphoribosyltransferase-like (LOC113092089), mRNA	Carassius auratus	3%	72.37%	2412	XM_026257686.1
PREDICTED: Cyprinus carpio nicotinamide phosphoribosyltransferase-like (LOC109066351), mRNA	Cyprinus carpio	12%	64.40%	2794	XM_019083377.1
PREDICTED: Acropora digitifera nicotinamide phosphoribosyltransferase-like (LOC107357526), mRNA	Acropora digitifera	7%	66.35%	1743	XM_015924171.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X10, mRNA	Latimeria chalumnae	3%	73.13%	3072	XM_014491518.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X9, mRNA	Latimeria chalumnae	3%	73.13%	6780	XM_014491517.1
PREDICTED: Latimeria chalumnae synaptoporin (SYNPR), transcript variant X8, mRNA	Latimeria chalumnae	3%	73.13%	6865	XM_014491516.1
PREDICTED: Ixodes scapularis nicotinamide phosphoribosyltransferase (LOC8032532), mRNA	Ixodes scapularis	7%	65.30%	1529	XM_029983262.1
PREDICTED: Ixodes scapularis nicotinamide phosphoribosyltransferase-like (LOC115314655), mRNA	Ixodes scapularis	7%	65.30%	2097	XM_029973780.1
PREDICTED: Nematostella vectensis nicotinamide phosphoribosyltransferase (LOC5497614), partial mRNA	Nematostella vectensis	4%	68.29%	1016	XM_032378398.1
PREDICTED: Cyprinodon variegatus nicotinamide phosphoribosyltransferase-like (LOC107105235), partial mRNA	Cyprinodon variegatus	3%	70.73%	834	XM_015405360.1

Trichinella spiralis nicotinamide phosphoribosyltransferase (Tsp_05934) mRNA, complete cds	Trichinella spiralis	1%	82.54%	1635	XM_003380179.1
PREDICTED: Eurytemora affinis nicotinamide phosphoribosyltransferase-like (LOC111705382), mRNA	Eurytemora affinis	3%	71.22%	2517	XM_023477903.1
PREDICTED: Chlorocebus sabaesus uncharacterized LOC119618263 (LOC119618263), transcript variant X2, ncRNA	Chlorocebus sabaesus	2%	74.77%	11807	XR_005242964.1
PREDICTED: Chlorocebus sabaesus uncharacterized LOC119618263 (LOC119618263), transcript variant X1, ncRNA	Chlorocebus sabaesus	2%	74.77%	11632	XR_005242963.1
PREDICTED: Panthera pardus uncharacterized LOC109265194 (LOC109265194), ncRNA	Panthera pardus	2%	73.68%	5328	XR_002079075.1
Aureococcus anophagefferens hypothetical protein mRNA	Aureococcus anophagefi	3%	69.44%	1607	XM_009044495.1
Aureococcus anophagefferens hypothetical protein partial mRNA	Aureococcus anophagefi	3%	69.44%	1371	XM_009040446.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X17, misc RNA	Cercocebus atys	2%	73.87%	12288	XR_001010152.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X16, misc RNA	Cercocebus atys	2%	73.87%	12255	XR_001010151.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X14, misc RNA	Cercocebus atys	2%	73.87%	12470	XR_001010149.1

PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X13, misc RNA	Cercocebus atys	2%	73.87%	12145	XR_001010148.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X12, misc RNA	Cercocebus atys	2%	73.87%	11948	XR_001010147.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X11, misc RNA	Cercocebus atys	2%	73.87%	12094	XR_001010146.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X10, misc RNA	Cercocebus atys	2%	73.87%	11834	XR_001010145.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X9, misc RNA	Cercocebus atys	2%	73.87%	12067	XR_001010144.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X8, misc RNA	Cercocebus atys	2%	73.87%	12314	XR_001010143.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X7, misc RNA	Cercocebus atys	2%	73.87%	11968	XR_001010142.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X6, misc RNA	Cercocebus atys	2%	73.87%	11980	XR_001010141.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X5, misc RNA	Cercocebus atys	2%	73.87%	12065	XR_001010140.1
PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X4, misc RNA	Cercocebus atys	2%	73.87%	12333	XR_001010139.1

PREDICTED: Cercocebus atys uncharacterized LOC105572607 (LOC105572607), transcript variant X3, misc RNA	Cercocebus atys	2%	73.87%	12201	XR_001010138.1
PREDICTED: Rhinolophus ferrumequinum endosome-lysosome associated apoptosis and autophagy regulator family member 2 (ELAPOR2), mRNA	Rhinolophus ferrumequi	2%	72.41%	8116	XM_033088759.1
PREDICTED: Amphimedon queenslandica nicotinamide phosphoribosyltransferase-like (LOC109592278), partial mRNA	Amphimedon queenslan	1%	75.61%	991	XM_020007770.1
PREDICTED: Rattus norvegicus receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X10, mRNA	Rattus norvegicus	1%	84.62%	4424	XM_017600529.2
PREDICTED: Rattus norvegicus receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X8, mRNA	Rattus norvegicus	1%	84.62%	4415	XM_017600527.2
PREDICTED: Ceratotherium simum simum tubby like protein 3 (LOC101391871), transcript variant X2, mRNA	Ceratotherium simum si	1%	79.69%	2986	XM_014793973.1
PREDICTED: Ceratotherium simum simum tubby like protein 3 (LOC101391871), transcript variant X1, mRNA	Ceratotherium simum si	1%	79.69%	2921	XM_004438761.2
PREDICTED: Rattus norvegicus receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X6, mRNA	Rattus norvegicus	1%	84.31%	4858	XM_039095693.1
PREDICTED: Rattus norvegicus receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X5, mRNA	Rattus norvegicus	1%	84.31%	4689	XM_017600526.2
PREDICTED: Rattus norvegicus receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X2, mRNA	Rattus norvegicus	1%	84.31%	4680	XM_017600524.2

PREDICTED: Rattus norvegicus receptor interacting serine/threonine kinase 1 (Ripk1), transcript variant X1, mRNA	Rattus norvegicus	1%	84.31%	4845	XM_017600523.2
PREDICTED: Chlorocebus sabaeus family with sequence similarity 124 member A (FAM124A), mRNA	Chlorocebus sabaeus	2%	71.93%	4842	XM_007960444.2
PREDICTED: Phocoena sinus eukaryotic elongation factor 2 kinase (EEF2K), transcript variant X4, misc RNA	Phocoena sinus	2%	75.00%	6361	XR_004345678.1
PREDICTED: Phocoena sinus eukaryotic elongation factor 2 kinase (EEF2K), transcript variant X2, mRNA	Phocoena sinus	2%	75.00%	6370	XM_032604226.1
PREDICTED: Phocoena sinus eukaryotic elongation factor 2 kinase (EEF2K), transcript variant X1, mRNA	Phocoena sinus	2%	75.00%	6580	XM_032604225.1
PREDICTED: Otolemur garnettii autophagy related 4A cysteine peptidase (ATG4A), mRNA	Otolemur garnettii	2%	72.07%	2115	XM_012811381.2
PREDICTED: Callithrix jacchus uncharacterized LOC118149771 (LOC118149771), transcript variant X2, ncRNA	Callithrix jacchus	2%	73.04%	2363	XR_004737495.1
PREDICTED: Callithrix jacchus uncharacterized LOC118149771 (LOC118149771), transcript variant X1, ncRNA	Callithrix jacchus	2%	73.04%	2922	XR_004737494.1
PREDICTED: Lynx canadensis centlein (CNTLN), mRNA	Lynx canadensis	1%	86.36%	5404	XM_030293937.2
PREDICTED: Sparus aurata SCY1 like pseudokinase 1 (scyl1), transcript variant X2, mRNA	Sparus aurata	1%	78.87%	4131	XM_030395592.1

PREDICTED: Sparus aurata SCY1 like pseudokinase 1 (scy1), transcript variant X1, mRNA	Sparus aurata	1%	78.87%	4145	XM_030395591.1
PREDICTED: Felis catus centlein (CNTLN), transcript variant X3, mRNA	Felis catus	1%	86.36%	6430	XM_019816024.2
PREDICTED: Felis catus centlein (CNTLN), transcript variant X2, misc RNA	Felis catus	1%	86.36%	6342	XR_002148230.2
PREDICTED: Felis catus centlein (CNTLN), transcript variant X1, mRNA	Felis catus	1%	86.36%	6433	XM_011288695.3