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BLAST[®] >> **blastn suite** >> **results for RID-KE6VHPRD016**

Job Title	Nucleotide Sequence ...
RID	KE6VHPRD016 Search expires on 12-10 01:39 am
Program	BLASTN
Database	nt
Query ID	lcl Query_6575757
Description	None ...
Molecule type	dna
Query Length	1548

Descriptions

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Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
Delphinapterus leucas isolate S_20_01444 mitochondrion, complete genome	Delphinapterus leucas	2265	2265	100%	0.0	91.91%	16387	OQ554110.1
Delphinapterus leucas isolate DL0776 mitochondrion, complete genome	Delphinapterus leucas	2265	2265	100%	0.0	91.91%	16386	MW316132.1
Delphinapterus leucas isolate S_20_04130 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554323.1
Delphinapterus leucas isolate S_20_04119 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554319.1
Delphinapterus leucas isolate S_20_04108 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554317.1
Delphinapterus leucas isolate S_20_04103 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554316.1
Delphinapterus leucas isolate S_20_04096 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554315.1
Delphinapterus leucas isolate S_20_04091 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554313.1
Delphinapterus leucas isolate S_20_04088 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554312.1
Delphinapterus leucas isolate S_20_04087 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554311.1
Delphinapterus leucas isolate S_20_04076 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554310.1
Delphinapterus leucas isolate S_20_04063 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554309.1
Delphinapterus leucas isolate S_20_04048 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554307.1
Delphinapterus leucas isolate S_20_04029 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554303.1
Delphinapterus leucas isolate	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554297.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
S_20_03996 mitochondrion, complete genome								
Delphinapterus leucas isolate S_20_03992 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554296.1
Delphinapterus leucas isolate S_20_03971 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554294.1
Delphinapterus leucas isolate S_20_03969 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554293.1
Delphinapterus leucas isolate S_20_03968 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554292.1
Delphinapterus leucas isolate S_20_03965 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554291.1
Delphinapterus leucas isolate S_20_03952 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554289.1
Delphinapterus leucas isolate S_20_03951 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554288.1
Delphinapterus leucas isolate S_20_03849 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554284.1
Delphinapterus leucas isolate S_20_03846 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554283.1
Delphinapterus leucas isolate S_20_03836 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554282.1
Delphinapterus leucas isolate S_20_03832 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554281.1
Delphinapterus leucas isolate S_20_03830 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554280.1
Delphinapterus leucas isolate S_20_03827 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554279.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
Delphinapterus leucas isolate S_20_03825 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554278.1
Delphinapterus leucas isolate S_20_03822 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554277.1
Delphinapterus leucas isolate S_20_03816 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554276.1
Delphinapterus leucas isolate S_20_03803 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554275.1
Delphinapterus leucas isolate S_20_03785 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554273.1
Delphinapterus leucas isolate S_20_03769 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554272.1
Delphinapterus leucas isolate S_20_03764 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554271.1
Delphinapterus leucas isolate S_20_03754 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554267.1
Delphinapterus leucas isolate S_20_03753 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554266.1
Delphinapterus leucas isolate S_20_03743 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554262.1
Delphinapterus leucas isolate S_20_03742 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554261.1
Delphinapterus leucas isolate S_20_03731 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554259.1
Delphinapterus leucas isolate S_20_03707 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554253.1
Delphinapterus leucas isolate S_20_03681 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554251.1
Delphinapterus leucas isolate	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554250.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
S_20_03678 mitochondrion, complete genome								
Delphinapterus leucas isolate S_20_03644 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554243.1
Delphinapterus leucas isolate S_20_03642 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554242.1
Delphinapterus leucas isolate S_20_03551 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554240.1
Delphinapterus leucas isolate S_20_03522 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554230.1
Delphinapterus leucas isolate S_20_03503 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554223.1
Delphinapterus leucas isolate S_20_03497 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554222.1
Delphinapterus leucas isolate S_20_03496 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554221.1
Delphinapterus leucas isolate S_20_03471 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554219.1
Delphinapterus leucas isolate S_20_03466 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554218.1
Delphinapterus leucas isolate S_20_03439 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554211.1
Delphinapterus leucas isolate S_20_03438 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554210.1
Delphinapterus leucas isolate S_20_03385 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554203.1
Delphinapterus leucas isolate S_20_03257 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554202.1

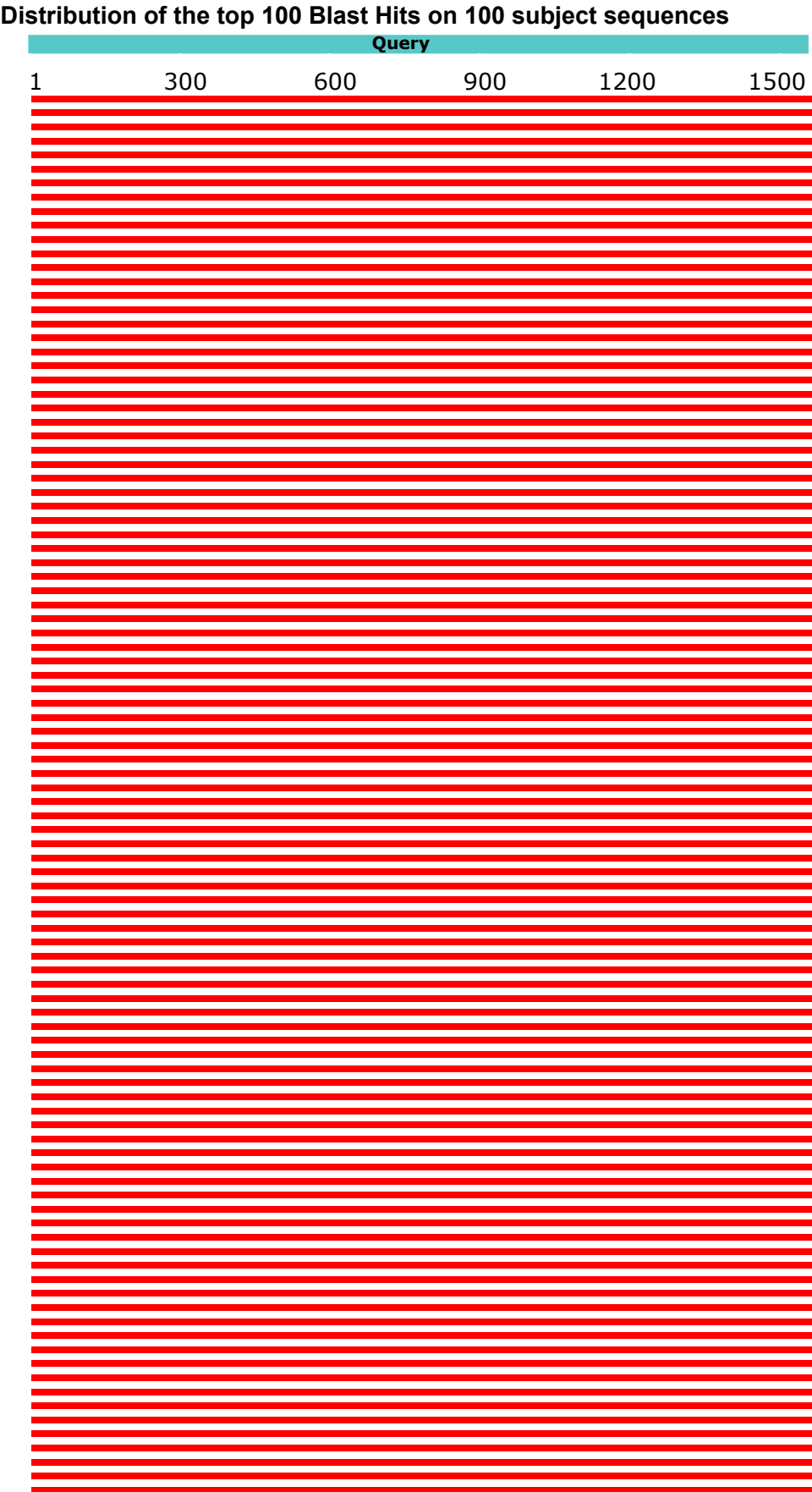
Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
Delphinapterus leucas isolate S_20_02952 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554198.1
Delphinapterus leucas isolate S_20_02925 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554196.1
Delphinapterus leucas isolate S_20_02719 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554189.1
Delphinapterus leucas isolate S_20_02539 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554188.1
Delphinapterus leucas isolate S_20_02537 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554187.1
Delphinapterus leucas isolate S_20_02329 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554185.1
Delphinapterus leucas isolate S_20_02328 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554184.1
Delphinapterus leucas isolate S_20_02024 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554180.1
Delphinapterus leucas isolate S_20_02016 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554178.1
Delphinapterus leucas isolate S_20_01998 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554177.1
Delphinapterus leucas isolate S_20_01968 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554176.1
Delphinapterus leucas isolate S_20_01935 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554175.1
Delphinapterus leucas isolate S_20_01883 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554173.1
Delphinapterus leucas isolate S_20_01750 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554155.1
Delphinapterus leucas isolate	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554153.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
S_20_01743 mitochondrion, complete genome								
Delphinapterus leucas isolate S_20_01734 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554151.1
Delphinapterus leucas isolate S_20_01705 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554148.1
Delphinapterus leucas isolate S_20_01699 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554147.1
Delphinapterus leucas isolate S_20_01612 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554144.1
Delphinapterus leucas isolate S_20_01597 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554143.1
Delphinapterus leucas isolate S_20_01594 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554142.1
Delphinapterus leucas isolate S_20_01590 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554141.1
Delphinapterus leucas isolate S_20_01580 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554140.1
Delphinapterus leucas isolate S_20_01574 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554139.1
Delphinapterus leucas isolate S_20_01567 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554138.1
Delphinapterus leucas isolate S_20_01562 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554137.1
Delphinapterus leucas isolate S_20_01555 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554135.1
Delphinapterus leucas isolate S_20_01553 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554134.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
Delphinapterus leucas isolate S_20_01546 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554132.1
Delphinapterus leucas isolate S_20_01539 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554131.1
Delphinapterus leucas isolate S_20_01530 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554130.1
Delphinapterus leucas isolate S_20_01516 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554128.1
Delphinapterus leucas isolate S_20_01514 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554127.1
Delphinapterus leucas isolate S_20_01507 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554125.1
Delphinapterus leucas isolate S_20_01494 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554124.1
Delphinapterus leucas isolate S_20_01489 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554123.1
Delphinapterus leucas isolate S_20_01487 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554122.1
Delphinapterus leucas isolate S_20_01486 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554121.1
Delphinapterus leucas isolate S_20_01482 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554120.1
Delphinapterus leucas isolate S_20_01480 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554119.1
Delphinapterus leucas isolate S_20_01466 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554116.1
Delphinapterus leucas isolate S_20_01465 mitochondrion, complete genome	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16386	OQ554115.1
Delphinapterus leucas isolate	Delphinapterus leucas	2259	2259	100%	0.0	91.85%	16387	OQ554114.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
S_20_01463 mitochondrion, complete genome								
Delphinapterus leucas isolate S_20_03538 mitochondrion, complete genome	Delphinapterus leucas	2252	2252	100%	0.0	91.72%	16386	OQ554236.1

Graphic Summary



Alignments

Alignment view

Pairwise

▼

☐ CDS feature

Restore defaults

Delphinapterus leucas isolate S_20_01444 mitochondrion, complete genome

Sequence ID: **Q0554110.1** Length: 16387 Number of Matches: 1

Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2265 bits(1226)	0.0()	1421/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCTATACYTACTATT				65
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT				5429
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG				125
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG				5489
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC				185
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC				5549
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGGTTTGAAACTGACT				245
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT				5609
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT				305
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT				5669
Query 306	TTGACTACTTCCTCCTTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC				365
Sbjct 5670	TTGACTGCTTCCTCCTTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC				5729
Query 366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC				425
Sbjct 5730	AGGCACAGGCTGAACGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC				5789
Query 426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT				485
Sbjct 5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT				5849
Query 486	CAACTTCATTACAACATATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC				545
Sbjct 5850	CAACTTCATTACAACATATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC				5909
Query 546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT				605
Sbjct 5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT				5969
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC				662
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC				6029
Query 663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTCTGATTTTTTGGTCACCCCGA				722
Sbjct 6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA				6089
Query 723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC				782
Sbjct 6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC				6149
Query 783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGGGCTATAGTTTCTATTGGTTT				842
Sbjct 6150	GGGAAAAAAGAACCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT				6209
Query 843	CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG				902
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG				6269
Query 903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCACAGGRGTAAAAGTCTTTAG				962
Sbjct 6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCCACAGGGGTAAAAGTCTTTAG				6329
Query 963	CTGACTGGCAACCCTCCACGAGGAAATANNNNNNNNNNNNNNNCCTAATATGAGCCCT				1022
Sbjct 6330	CTGACTGGCAACACTCCACGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT				6389
Query 1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC				1082
Sbjct 6390	AGGCTTTATTTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC				6449
Query 1083	CCTAGACATYATTCTCCACGACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC				1142
Sbjct 6450	CTTAGACGTATCCTCCACGACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC				6509
Query 1143	AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG				1202
Sbjct 6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTACTATTTTCAGG				6569
Query 1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNNTRAA				1262
Sbjct 6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA				6629

Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCATAACAAACCTCGAGTGATTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGGAAGAACAGGTACATTAACCCAAAAGTGCAAGA	6915

Delphinapterus leucas isolate DL0776 mitochondrion, complete genome
Sequence ID: **MW316132.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2265 bits(1226)	0.0()	1421/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCAAGCTTATTAATTCGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCAAGCTTGTTAATTCGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCACGC	5549			
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGGTTTGAAACTGACT	245			
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609			
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305			
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669			
Query 306	TTGACTACTTCCTCCTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365			
Sbjct 5670	TTGACTGCTTCCTCCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729			
Query 366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425			
Sbjct 5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789			
Query 426	AGTCGACCTKACTATTTTCTCTCTACATTTTRGCCGGCGTATCTTCAATCCTCGGAGCTAT	485			
Sbjct 5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849			
Query 486	CAACTTCATTACAACATATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	545			
Sbjct 5850	CAACTTCATTACAACATATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	5909			
Query 546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605			
Sbjct 5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969			
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662			
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029			
Query 663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA	722			
Sbjct 6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089			
Query 723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782			
Sbjct 6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149			
Query 783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT	842			
Sbjct 6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209			
Query 843	CCTGGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTTGACACACG	902			
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269			
Query 903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCTACAGGRGTAAAAGTCTTTAG	962			
Sbjct 6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCCACAGGGGTAAAAGTCTTTAG	6329			
Query 963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT	1022			
Sbjct 6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389			

Query	1023	AGGCTTTATYTTCTATTTCACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTTCTATTTCACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTCATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGTGTCTTCGCATCATAGGAGGTTTCGTCCACTGATTCCTCACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCCTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATTTGAGAAGCATTTCGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCAGTAGATCTCACCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGGAAGAACAGGTACATTAACCCAAAAGTGCAAGA	6915

Delphinapterus leucas isolate S_20_04130 mitochondrion, complete genome

Sequence ID: **OQ554323.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCTGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCTGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC	5549			
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT	245			
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609			
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305			
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669			
Query 306	TTGACTACTTCCTCCTTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365			
Sbjct 5670	TTGACTGCTTCCTCCTTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729			
Query 366	AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425			
Sbjct 5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789			
Query 426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485			
Sbjct 5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849			
Query 486	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	545			
Sbjct 5850	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	5909			
Query 546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605			
Sbjct 5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969			
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662			
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029			
Query 663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCGA	722			
Sbjct 6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCGA	6089			
Query 723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782			
Sbjct 6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149			

Query	783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTTGGGCTATAGTTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCTACAGGRGTAAGTCTTTAG	962
Sbjct	6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCACAGGGGTAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTCATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCATCATAGGAGGTTTCGTCCACTGATTCCCACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCACAACACTTCCTCGGTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCCTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACAGCATATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTTGAAGAACAGGTACATTAACCCAAAAGTGCAAGA	6915

Delphinapterus leucas isolate S_20_04119 mitochondrion, complete genome

Sequence ID: **OQ554319.1** Length: 16386 Number of Matches: 1

Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query	6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65		
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429		
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCCTAAGCTTATTAATTCGTGCTGAATTAGG	125		
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489		
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185		
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC	5549		
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT	245		
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609		
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305		
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669		
Query	306	TTGACTACTTCTCTCTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365		
Sbjct	5670	TTGACTGCTTCTCTCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729		
Query	366	AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425		
Sbjct	5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789		
Query	426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485		
Sbjct	5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGCTAT	5849		
Query	486	CAACTTCATTACAACATATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	545		
Sbjct	5850	CAACTTCATTACAACATATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	5909		

Query 546 TTTATTTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT 605
Sbjct 5910 TTTATTTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT 5969
Query 606 AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC 662
Sbjct 5970 AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC 6029
Query 663 GGCAGGAGGAGGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA 722
Sbjct 6030 TGCAGGAGGAGGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA 6089
Query 723 AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC 782
Sbjct 6090 AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC 6149
Query 783 GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT 842
Sbjct 6150 GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTCTATTGGTTT 6209
Query 843 CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG 902
Sbjct 6210 CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG 6269
Query 903 AGCATATTTACATCAGCTACCATAATTATTGCTATTCTACAGGRGTAAAAGTCTTTAG 962
Sbjct 6270 AGCATATTTACATCAGCTACCATAATTATTGCTATTCCCACAGGGGTAAAAGTCTTTAG 6329
Query 963 CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT 1022
Sbjct 6330 CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT 6389
Query 1023 AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC 1082
Sbjct 6390 AGGCTTTATTTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC 6449
Query 1083 CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC 1142
Sbjct 6450 CTTAGACGTCATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC 6509
Query 1143 AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG 1202
Sbjct 6510 AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTACTATTTTCAGG 6569
Query 1203 GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA 1262
Sbjct 6570 TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA 6629
Query 1263 CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA 1322
Sbjct 6630 TGTAACATTCTTTCCACAACACTTCCTCGGTTATCTGGAATACCCCGTCGATACTCTGA 6689
Query 1323 TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 1382
Sbjct 6690 TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 6749
Query 1383 RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT 1442
Sbjct 6750 AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTTCATCCAAACGAGAAGT 6809
Query 1443 ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA 1502
Sbjct 6810 GTCCGCGGTAGATCTCACCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA 6869
Query 1503 TCATACATTGGAAGAACCAGCATACATYAACCCAAAAGGTGCAAGA 1548
Sbjct 6870 TCATACATTGGAAGAACCAGGTACATTAACCCAAAAGGTGCAAGA 6915

Delphinapterus leucas isolate S_20_04108 mitochondrion, complete genome
Sequence ID: **OQ554317.1** Length: 16387 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCACGC	5549			
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT	245			
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609			
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305			
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669			

Query 306 TTGACTACTTCCTCCTTCTTTCCCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC 365
Sbjct 5670 TTGACTGCTTCCTCCTTCTTTCCCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC 5729
Query 366 AGGCACAGGNTGNACTGTATATNCNCNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC 425
Sbjct 5730 AGGCACAGGCTGAACGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC 5789
Query 426 AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT 485
Sbjct 5790 AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT 5849
Query 486 CAACTTCATTACAACATATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC 545
Sbjct 5850 CAACTTCATTACAACATATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC 5909
Query 546 TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT 605
Sbjct 5910 TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT 5969
Query 606 AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC 662
Sbjct 5970 AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC 6029
Query 663 GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCGA 722
Sbjct 6030 TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCGA 6089
Query 723 AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC 782
Sbjct 6090 AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC 6149
Query 783 GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT 842
Sbjct 6150 GGGAAAAAAGAGCCCTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT 6209
Query 843 CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG 902
Sbjct 6210 CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG 6269
Query 903 AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG 962
Sbjct 6270 AGCATATTTACATCAGCTACCATAATTATTGCTATTCACAGGGGTAAAAGTCTTTAG 6329
Query 963 CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT 1022
Sbjct 6330 CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT 6389
Query 1023 AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC 1082
Sbjct 6390 AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC 6449
Query 1083 CCTAGACATYATTCTCCACGACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC 1142
Sbjct 6450 CTTAGACGTATCCTCCACGACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC 6509
Query 1143 AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG 1202
Sbjct 6510 AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTACTATTTTCAGG 6569
Query 1203 GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA 1262
Sbjct 6570 TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA 6629
Query 1263 CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA 1322
Sbjct 6630 TGTAACATTCTTTCCACAACACTTCCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA 6689
Query 1323 TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 1382
Sbjct 6690 TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 6749
Query 1383 RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT 1442
Sbjct 6750 AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT 6809
Query 1443 ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA 1502
Sbjct 6810 GTCCGCGGTAGATCTCACCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA 6869
Query 1503 TCATACATTGGAAGAACAGCATACATYAACCCAAAAGGTGCAAGA 1548
Sbjct 6870 TCATACATTGGAAGAACAGGTACATTAACCCAAAAGGTGCAAGA 6915

Delphinapterus leucas isolate S_20_04103 mitochondrion, complete genome
Sequence ID: **OQ554316.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score		Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)		0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query	6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT				65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT				5429

Query	66	TGGTGCCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125
Sbjct	5430	TGGTGCCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCACGC	5549
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT	245
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669
Query	306	TTGACTACTTCCTCCTTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365
Sbjct	5670	TTGACTGCTTCCTCCTTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729
Query	366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425
Sbjct	5730	AGGCACAGGCTGAACGTGTATCCCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849
Query	486	CAACTTCATTACAACATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC	545
Sbjct	5850	CAACTTCATTACAACATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC	5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029
Query	663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGGGCTATAGTTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG	962
Sbjct	6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCACAGGGGTAAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCCTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCCGGTAGATCTCACCATACAAACCTCGAGTGATTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACCAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTTGAAGAACCAGGTACATTAACCCAAAAGGTGCAAGA	6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	

Query	6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC	5549
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGGTTTGAAACTGACT	245
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669
Query	306	TTGACTACTTCCTCCTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365
Sbjct	5670	TTGACTGCTTCCTCCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729
Query	366	AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425
Sbjct	5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTTTCTCTCTACATTTTRGCCGGCGTATCTTCAATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTTACTATTTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGCTAT	5849
Query	486	CAACTTCATTACAACCTATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	545
Sbjct	5850	CAACTTCATTACAACCTATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	5909
Query	546	TTTATTTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605
Sbjct	5910	TTTATTTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029
Query	663	GGCAGGAGGAGGGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGGGCTATAGTTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG	962
Sbjct	6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCACACAGGGGTAAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCCACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382

Sbjct	6690	TTACCCAGACGCCTACACAACATGAAACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTACCCATACAAACCTCGAGTGATTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACCCAGCATACATYAACCCAAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGGAAGAACCCAGTGACATTAACCCAAAAAGTGCAAGA	6915

Delphinapterus leucas isolate S_20_04091 mitochondrion, complete genome

Sequence ID: **OQ554313.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6		CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCTATACYTACTATT			65
Sbjct 5370		CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT			5429
Query 66		TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG			125
Sbjct 5430		TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG			5489
Query 126		CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC			185
Sbjct 5490		CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC			5549
Query 186		CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT			245
Sbjct 5550		CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT			5609
Query 246		WGTCCTTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT			305
Sbjct 5610		TGTCCTTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT			5669
Query 306		TTGACTACTTCCTCCTTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC			365
Sbjct 5670		TTGACTGCTTCCTCCTTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC			5729
Query 366		AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC			425
Sbjct 5730		AGGCACAGGCTGAACGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC			5789
Query 426		AGTCGACCTKACTATTTTCTCTCTACATTTTRGCCGGGTATCTTCAATCCTCGGAGCTAT			485
Sbjct 5790		AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGGTATCTTCAATCCTCGGGGTAT			5849
Query 486		CAACTTCATTACAACCTATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC			545
Sbjct 5850		CAACTTCATTACAACCTATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC			5909
Query 546		TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT			605
Sbjct 5910		TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT			5969
Query 606		AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC			662
Sbjct 5970		AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC			6029
Query 663		GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTCTGATTTTTTGGTCACCCGA			722
Sbjct 6030		TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCGA			6089
Query 723		AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC			782
Sbjct 6090		AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC			6149
Query 783		GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT			842
Sbjct 6150		GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT			6209
Query 843		CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG			902
Sbjct 6210		CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG			6269
Query 903		AGCATATTTACATCAGCTACCATAATTATTGCTATTCCACAGGRGTAAAAGTCTTTAG			962
Sbjct 6270		AGCATATTTACATCAGCTACCATAATTATTGCTATTCCCACAGGGGTAAAAGTCTTTAG			6329
Query 963		CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCATAATGAGCCCT			1022
Sbjct 6330		CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT			6389
Query 1023		AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC			1082
Sbjct 6390		AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC			6449
Query 1083		CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC			1142

Sbjct	6450	CTTAGACGTCATCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTTTGCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATTTGAGAAGCATTTCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCATAACAAACCTCGAGTGATTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACCAGCATACATYAACCCAAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGGAAGAACCAGGTACATTAACCCAAAAAGTGAAGA	6915

Delphinapterus leucas isolate S_20_04088 mitochondrion, complete genome

Sequence ID: **Q0554312.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC	5549			
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGGTTTGAAACTGACT	245			
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609			
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305			
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669			
Query 306	TTGACTACTTCCTCCTCTTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365			
Sbjct 5670	TTGACTGCTTCCTCCTCTTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729			
Query 366	AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425			
Sbjct 5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789			
Query 426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485			
Sbjct 5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849			
Query 486	CAACTTCATTACAACATATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC	545			
Sbjct 5850	CAACTTCATTACAACATATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC	5909			
Query 546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605			
Sbjct 5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969			
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662			
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029			
Query 663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA	722			
Sbjct 6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089			
Query 723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782			
Sbjct 6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149			
Query 783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGGGCTATAGTTTCTATTGGTTT	842			
Sbjct 6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209			
Query 843	CCTGGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTTGACACACG	902			

Sbjct	6210	CCTAGGTTTTCATTGTATGAGCTCACCATAATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTTCACATCAGCTACCATAATTATTGCTATTCCCTACAGGRGTAAAAGTCTTTAG	962
Sbjct	6270	AGCATATTTTCACATCAGCTACCATAATTATTGCTATTCCCACAGGGGTAAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCCACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTCTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCTCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATTTGAGAAGCATTGTCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCATAACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACCAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGGAAGAACCAGTGATTAACCCAAAAGGTGCAAGA	6915

Delphinapterus leucas isolate S_20_04087 mitochondrion, complete genome

Sequence ID: **OQ554311.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query	6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYTACTATT			65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC			185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC			5549
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGGTTTGGAAGCTGACT			245
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGGAAGCTGACT			5609
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT			305
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT			5669
Query	306	TTGACTACTTCCTCCTCTTTCTACTATTAAATAGCGTCTTCAATAGTTGAAGCCGGCGC			365
Sbjct	5670	TTGACTGCTTCCTCCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC			5729
Query	366	AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC			425
Sbjct	5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC			5789
Query	426	AGTCGACCTKACTATTTTCTCTCTACATTTTRGCCGGCGTATCTTCAATCCTCGGAGCTAT			485
Sbjct	5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT			5849
Query	486	CAACTTCATTACAACCTATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC			545
Sbjct	5850	CAACTTCATTACAACCTATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC			5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT			605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT			5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC			662

Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029
Query	663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTTCACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG	962
Sbjct	6270	AGCATATTTTCACATCAGCTACCATAATTATTGCTATTCACAGGGGTAAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTCACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCTCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTGTCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCATAACAAACCTCGAGTGATTAAACGGATGCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACCCAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTTGAAGAACCCAGGTACATTAACCCAAAAGTGCAAGA	6915

Delphinapterus leucas isolate S_20_04076 mitochondrion, complete genome

Sequence ID: **OQ554310.1** Length: 16386 Number of Matches: 1

Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query	6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCTATACYTACTATT			65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC			185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCCACGC			5549
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGGTTTGAAACTGACT			245
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT			5609
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT			305
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT			5669
Query	306	TTGACTACTTCCTCCTCTTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC			365
Sbjct	5670	TTGACTGCTTCCTCCTCTTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC			5729
Query	366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC			425

Sbjct	5730	AGGCACAGGCTGAACCTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849
Query	486	CAACTTCATTACAACCTATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC	545
Sbjct	5850	CAACTTCATTACAACCTATTATTAACATAAAACCACCCGCTATAACCCAATACCAAACACC	5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029
Query	663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTCTGATTTTTTGGTCACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaGAACCYTTTGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAGAGCCCTTTTGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCTACAGGRGTAAAAGTCTTTAG	962
Sbjct	6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCCACAGGGGTAAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTCACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTATCTGGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTGTCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTACCCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACAGGTGTACATTAACCCAAAAGTGAAGA	6915

Delphinapterus leucas isolate S_20_04063 mitochondrion, complete genome

Sequence ID: **OQ554309.1** Length: 16386 Number of Matches: 1

Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			

Sbjct	5490	CCAACCTGGCTCATTATTGGAGACGACCAAAATTTATAACGTACTAGTAACAGCCCACGC	5549
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAAATTGGGGGTTTGAAACTGACT	245
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAAATTGGAGGGTTTGAAACTGACT	5609
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669
Query	306	TTGACTACTTCCTCCTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365
Sbjct	5670	TTGACTGCTTCCTCCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729
Query	366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425
Sbjct	5730	AGGCACAGGCTGAACGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849
Query	486	CAACTTCATTACAACCTATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC	545
Sbjct	5850	CAACTTCATTACAACCTATTATTAACATAAAACACCCGCTATAACCCAATACCAAACACC	5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029
Query	663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG	962
Sbjct	6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGGGTAAAAGTCTTTAG	6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509
Query	1143	AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCTACTATTTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTATCTGGAATACCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTACCCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGGAAGAACAGGTACATTAACCCAAAAGTGCAAGA	6915

Score		Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)		0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query	6	CATAAACCGATGACTATTCTCTACCAATCACAAAGGACATTGGCACCCTATACYTACTATT				65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAAGGACATTGGCACTTTATATCTACTATT				5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG				125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG				5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC				185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCACGC				5549
Query	186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT				245
Sbjct	5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT				5609
Query	246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT				305
Sbjct	5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT				5669
Query	306	TTGACTACTTCCTCCTCTTTCTACTATTAAATAGCGTCTTCAATAGTTGAAGCCGGCGC				365
Sbjct	5670	TTGACTGCTTCCTCCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC				5729
Query	366	AGGCACAGGNTGNACTGTATATNCNNTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC				425
Sbjct	5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC				5789
Query	426	AGTCGACCTKACTATTTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT				485
Sbjct	5790	AGTCGACCTTACTATTTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGCTAT				5849
Query	486	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC				545
Sbjct	5850	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC				5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT				605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT				5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC				662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC				6029
Query	663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCGA				722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCGA				6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC				782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC				6149
Query	783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGTGGGCTATAGTTTCTATTGGTTT				842
Sbjct	6150	GGGAAAAAAGAGCCCTTGGATATATAGGGATGGTGTGGGCTATAATTCTATTGGTTT				6209
Query	843	CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG				902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG				6269
Query	903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG				962
Sbjct	6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCACAGGGGTAAAAGTCTTTAG				6329
Query	963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNCCTAATATGAGCCCT				1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT				6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC				1082
Sbjct	6390	AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC				6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC				1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC				6509
Query	1143	AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG				1202
Sbjct	6510	AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCCACTATTTTCAGG				6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTCGTAATCATANNNNNNNNNTRAA				1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA				6629
Query	1263	CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA				1322
Sbjct	6630	TGTAACATTCTTTCCACAACACTTCCTCGGTTTATCTGGAATACCCCGTCGATACTCTGA				6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT				1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT				6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT				1442

Sbjct	6750	AACAGCAGTCATCTTATAGTCTTATTGAGAAAGCATTGTCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCCTACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGGAAGAACCAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTTGAAGAACCAGGTACATTAACCCAAAAGTGAAGA	6915

Delphinapterus leucas isolate S_20_04029 mitochondrion, complete genome
Sequence ID: **OQ554303.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCACGC	5549			
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT	245			
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609			
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305			
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669			
Query 306	TTGACTACTTCCTCCTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365			
Sbjct 5670	TTGACTGCTTCCTCCTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729			
Query 366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425			
Sbjct 5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789			
Query 426	AGTCGACCTKACTATTTTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485			
Sbjct 5790	AGTCGACCTTACTATTTTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849			
Query 486	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	545			
Sbjct 5850	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	5909			
Query 546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605			
Sbjct 5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969			
Query 606	AGCAGCCGGAATTACCATGCTACTAAGTATCGAAACCTAAACACAACC---TTCGACCC	662			
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAAGTATCGAAACCTAAACACAACCTTTTTCGACCC	6029			
Query 663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCGA	722			
Sbjct 6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCGA	6089			
Query 723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782			
Sbjct 6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149			
Query 783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGGGCTATAGTTTCTATTGGTTT	842			
Sbjct 6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTTCTATTGGTTT	6209			
Query 843	CCTGGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTTGACACACG	902			
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269			
Query 903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG	962			
Sbjct 6270	AGCATATTTACATCAGCTACCATAATTATTGCTATTCACAGGGGTAAAAGTCTTTAG	6329			
Query 963	CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCTAATATGAGCCCT	1022			
Sbjct 6330	CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT	6389			
Query 1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082			
Sbjct 6390	AGGCTTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449			
Query 1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC	1142			
Sbjct 6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC	6509			
Query 1143	AATRGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG	1202			

Sbjct 6510 AATAGGGGCTGTCTTCGCCATCATAGGAGTTTCGTCCACTGATTCCCACTATTTTCAGG 6569

Query 1203 GTATACACTCAATTCAACATGGACAAAAACTCAATTCGTAATCATANNNNNNNNTRAA 1262

Sbjct 6570 TTATACACTCAATTCAACATGGACAAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA 6629

Query 1263 CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCCGYCGATATTCTGA 1322

Sbjct 6630 TGTAACATTCTTTCCACAACACTTCCTCGGTTATCTGGAATACCCCGTCGATACTCTGA 6689

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Sbjct 6690 TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 6749

Query 1383 RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT 1442

Sbjct 6750 AACAGCAGTCATACTTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT 6809

Query 1443 ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA 1502

Sbjct 6810 GTCCGCGGTAGATCTCACCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA 6869

Query 1503 TCATACATTGGAAGAACCCAGCATACATYAACCCAAAAGGTGCAAGA 1548

Sbjct 6870 TCATACATTTGAAGAACCCAGGTACATTAACCCAAAAGTGAAGA 6915

Delphinapterus leucas isolate S_20_03996 mitochondrion, complete genome

Sequence ID: **OQ554297.1** Length: 16386 Number of Matches: 1
Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2259 bits(1223)	0.0()	1420/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT	65			
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACTTTATATCTACTATT	5429			
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTATTAATTCGTGCTGAATTAGG	125			
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAAGCTTGTTAATTCGTGCTGAATTAGG	5489			
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTTAGTAACAGCTCACGC	185			
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTTATAACGTACTAGTAACAGCCACGC	5549			
Query 186	CTTCGTAATAATCTTCTTTATAGTAATGCCTATTATAATTGGGGGTTTGAAACTGACT	245			
Sbjct 5550	CTTCGTGATAATCTTCTTTATAGTAATGCCTATTATAATTGGAGGGTTTGAAACTGACT	5609			
Query 246	WGTCCCTTTAATAATCGGAGCCCCGAYATGGCTTTCCTCGTCTAAATAACATAAGCTT	305			
Sbjct 5610	TGTCCCTTTAATAATCGGAGCCCCGACATGGCTTTCCTCGTCTAAATAACATAAGCTT	5669			
Query 306	TTGACTACTTCCTCCTTCTTTCTACTATTAATAGCGTCTTCAATAGTTGAAGCCGGCGC	365			
Sbjct 5670	TTGACTGCTTCCTCCTTCTTTCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729			
Query 366	AGGCACAGGNTGNACTGTATATNCNCTTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425			
Sbjct 5730	AGGCACAGGCTGAAGTGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789			
Query 426	AGTCGACCTKACTATTTTCTCTCTACATTTTGCCGGCGTATCTTCAATCCTCGGAGCTAT	485			
Sbjct 5790	AGTCGACCTTACTATTTTCTCTCTACATCTAGCCGGCGTATCTTCAATCCTCGGGGCTAT	5849			
Query 486	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	545			
Sbjct 5850	CAACTTCATTACAACATTATTAACATAAAACCACCGCTATAACCCAATACCAAACACC	5909			
Query 546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTATCACTACCTGTCCT	605			
Sbjct 5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTATCACTACCTGTCCT	5969			
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662			
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTTCGACCC	6029			
Query 663	GGCAGGAGGAGGCGACCCAGTCTATATCAACACYTRTTCTGATTTTTTGGTCACCCGA	722			
Sbjct 6030	TGCAGGAGGAGGCGACCCAGTCTATATCAACACCTATTCTGATTTTTTGGTCACCCGA	6089			
Query 723	AGTATATATCCTAATTCTACCCGGTTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782			
Sbjct 6090	AGTATATATTCTAATTCTACCCGGCTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149			
Query 783	GGGaaaaaaaGAACCYTTTGGATATATGGGGATRGTTGGGCTATAGTTTCTATTGGTTT	842			
Sbjct 6150	GGGAAAAAAGAGCCCTTTGGATATATAGGGATGGTGTGGGCTATAATTCTATTGGTTT	6209			
Query 843	CCTGGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTTGACACACG	902			
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTTACAGTCGGAATAGACGTAGACACACG	6269			
Query 903	AGCATATTTACATCAGCTACCATAATTATTGCTATTCCTACAGGRGTAAAAGTCTTTAG	962			

Sbjct 6270 AGCATATTTACATCAGCTACCATAAATTATTGCTATTCCACAGGGGTAAAAAGTCTTTAG 6329

Query 963 CTGACTGGCAACCCTCCACGGAGGAAATANNNNNNNNNNNNNNCCCTAATATGAGCCCT 1022

Sbjct 6330 CTGACTGGCAACACTCCACGGAGGAAATATTAATGATCTCCAGCCCTAATATGAGCCCT 6389

Query 1023 AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC 1082

Sbjct 6390 AGGCTTTATTTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC 6449

Query 1083 CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTTCCACTATGTACTCTC 1142

Sbjct 6450 CTTAGACGTCATCCTCCACGACACATATTATGTAGTCGCACACTTCCACTATGTGCTTTC 6509

Query 1143 AATRGGAGCTGTCTTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTTCAGG 1202

Sbjct 6510 AATAGGGGCTGTCTTCGCCATCATAGGAGGTTTCGTCCACTGATTCCCACTATTTTCAGG 6569

Query 1203 GTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATANNNNNNNNNTRAA 1262

Sbjct 6570 TTATACACTCAATTCAACATGGACAAAACTCAATTCGTAATCATATTCGTAGGTGTGAA 6629

Query 1263 CGTGACATTCTTTCCACARCACTTTCTCGGTCTATCTGGAATACCCGYCGATATTCTGA 1322

Sbjct 6630 TGTAACATTCTTTCCACAACACTTCCTCGGTTTATCTGGAATACCCGTCGATACTCTGA 6689

Query 1323 TTACCCAGACGCTTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 1382

Sbjct 6690 TTACCCAGACGCCTACACAACATGAAACACCATTTTCATCAATAGGCTCTTTCATCTCACT 6749

Query 1383 RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT 1442

Sbjct 6750 AACAGCAGTCATACTATAGTCTTCATTATTTGAGAAGCATTTGCATCCAAACGAGAAGT 6809

Query 1443 ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA 1502

Sbjct 6810 GTCCGCGGTAGATCTCACCATACAAACCTCGAGTGATTAAACGGATGTCCTCCACCATA 6869

Query 1503 TCATACATTGGAAGAACCAGCATACATYAACCCAAAAGGTGCAAGA 1548

Sbjct 6870 TCATACATTTGAAGAACCAGTGATTAACCCAAAAGGTGCAAGA 6915

Taxonomy

Reports

◦ Lineage

Organism	Blast Name	Score	Number of Hits	Description
Delphinapterus leucas	whales & dolphins	2265	100	Delphinapterus leucas hits

◦ Organism

Description	Score	E value	Accession
Delphinapterus leucas (beluga whale) [whales & dolphins]			
Delphinapterus leucas isolate S_20_01444 mitochondrion, complete genome	2265	0.0	OQ554110
Delphinapterus leucas isolate DL0776 mitochondrion, complete genome	2265	0.0	MW316132
Delphinapterus leucas isolate S_20_04130 mitochondrion, complete genome	2259	0.0	OQ554323
Delphinapterus leucas isolate S_20_04119 mitochondrion, complete genome	2259	0.0	OQ554319
Delphinapterus leucas isolate S_20_04108 mitochondrion, complete genome	2259	0.0	OQ554317
Delphinapterus leucas isolate S_20_04103 mitochondrion, complete genome	2259	0.0	OQ554316
Delphinapterus leucas isolate S_20_04096 mitochondrion, complete genome	2259	0.0	OQ554315
Delphinapterus leucas isolate S_20_04091 mitochondrion, complete genome	2259	0.0	OQ554313
Delphinapterus leucas isolate S_20_04088 mitochondrion, complete genome	2259	0.0	OQ554312
Delphinapterus leucas isolate S_20_04087 mitochondrion, complete genome	2259	0.0	OQ554311
Delphinapterus leucas isolate S_20_04076 mitochondrion, complete genome	2259	0.0	OQ554310
Delphinapterus leucas isolate S_20_04063 mitochondrion, complete genome	2259	0.0	OQ554309
Delphinapterus leucas isolate S_20_04048 mitochondrion, complete genome	2259	0.0	OQ554307
Delphinapterus leucas isolate S_20_04029 mitochondrion, complete genome	2259	0.0	OQ554303
Delphinapterus leucas isolate S_20_03996 mitochondrion, complete genome	2259	0.0	OQ554297
Delphinapterus leucas isolate S_20_03992 mitochondrion, complete genome	2259	0.0	OQ554296

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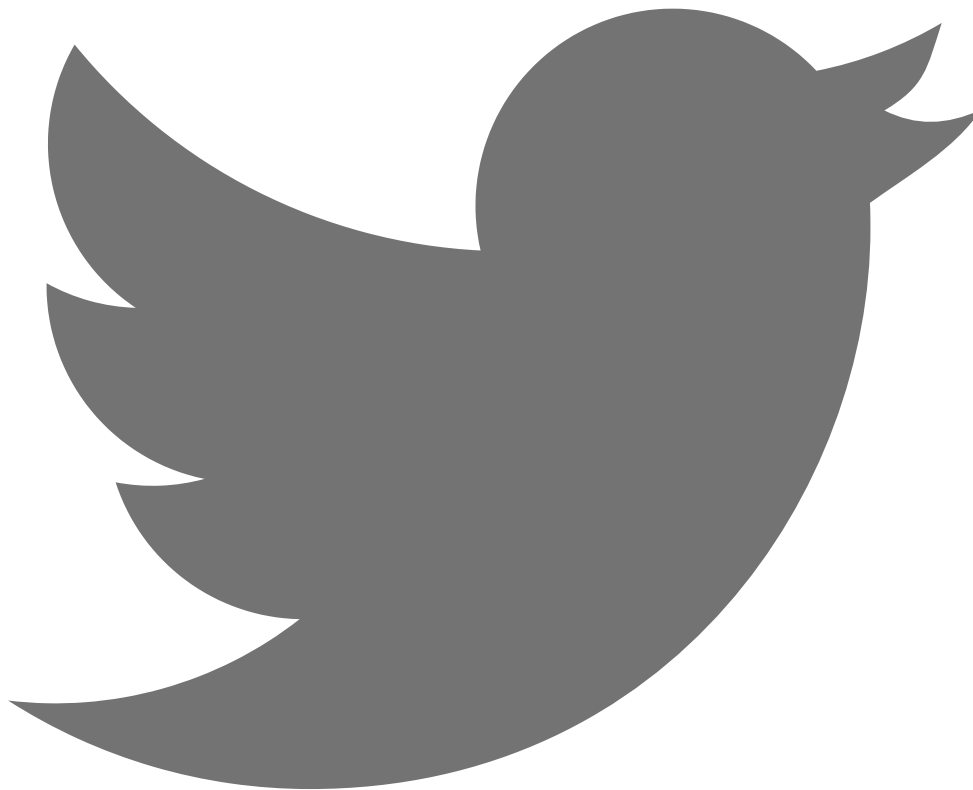
Description	Score	E value	Accession
Delphinapterus leucas isolate S_20_02016 mitochondrion, complete genome	2259	0.0	OQ554178
Delphinapterus leucas isolate S_20_01998 mitochondrion, complete genome	2259	0.0	OQ554177
Delphinapterus leucas isolate S_20_01968 mitochondrion, complete genome	2259	0.0	OQ554176
Delphinapterus leucas isolate S_20_01935 mitochondrion, complete genome	2259	0.0	OQ554175
Delphinapterus leucas isolate S_20_01883 mitochondrion, complete genome	2259	0.0	OQ554173
Delphinapterus leucas isolate S_20_01750 mitochondrion, complete genome	2259	0.0	OQ554155
Delphinapterus leucas isolate S_20_01743 mitochondrion, complete genome	2259	0.0	OQ554153
Delphinapterus leucas isolate S_20_01734 mitochondrion, complete genome	2259	0.0	OQ554151
Delphinapterus leucas isolate S_20_01705 mitochondrion, complete genome	2259	0.0	OQ554148
Delphinapterus leucas isolate S_20_01699 mitochondrion, complete genome	2259	0.0	OQ554147
Delphinapterus leucas isolate S_20_01612 mitochondrion, complete genome	2259	0.0	OQ554144
Delphinapterus leucas isolate S_20_01597 mitochondrion, complete genome	2259	0.0	OQ554143
Delphinapterus leucas isolate S_20_01594 mitochondrion, complete genome	2259	0.0	OQ554142
Delphinapterus leucas isolate S_20_01590 mitochondrion, complete genome	2259	0.0	OQ554141
Delphinapterus leucas isolate S_20_01580 mitochondrion, complete genome	2259	0.0	OQ554140
Delphinapterus leucas isolate S_20_01574 mitochondrion, complete genome	2259	0.0	OQ554139
Delphinapterus leucas isolate S_20_01567 mitochondrion, complete genome	2259	0.0	OQ554138
Delphinapterus leucas isolate S_20_01562 mitochondrion, complete genome	2259	0.0	OQ554137
Delphinapterus leucas isolate S_20_01555 mitochondrion, complete genome	2259	0.0	OQ554135
Delphinapterus leucas isolate S_20_01553 mitochondrion, complete genome	2259	0.0	OQ554134
Delphinapterus leucas isolate S_20_01546 mitochondrion, complete genome	2259	0.0	OQ554132
Delphinapterus leucas isolate S_20_01539 mitochondrion, complete genome	2259	0.0	OQ554131
Delphinapterus leucas isolate S_20_01530 mitochondrion, complete genome	2259	0.0	OQ554130
Delphinapterus leucas isolate S_20_01516 mitochondrion, complete genome	2259	0.0	OQ554128
Delphinapterus leucas isolate S_20_01514 mitochondrion, complete genome	2259	0.0	OQ554127
Delphinapterus leucas isolate S_20_01507 mitochondrion, complete genome	2259	0.0	OQ554125
Delphinapterus leucas isolate S_20_01494 mitochondrion, complete genome	2259	0.0	OQ554124
Delphinapterus leucas isolate S_20_01489 mitochondrion, complete genome	2259	0.0	OQ554123
Delphinapterus leucas isolate S_20_01487 mitochondrion, complete genome	2259	0.0	OQ554122
Delphinapterus leucas isolate S_20_01486 mitochondrion, complete genome	2259	0.0	OQ554121
Delphinapterus leucas isolate S_20_01482 mitochondrion, complete genome	2259	0.0	OQ554120
Delphinapterus leucas isolate S_20_01480 mitochondrion, complete genome	2259	0.0	OQ554119
Delphinapterus leucas isolate S_20_01466 mitochondrion, complete genome	2259	0.0	OQ554116
Delphinapterus leucas isolate S_20_01465 mitochondrion, complete genome	2259	0.0	OQ554115
Delphinapterus leucas isolate S_20_01463 mitochondrion, complete genome	2259	0.0	OQ554114
Delphinapterus leucas isolate S_20_03538 mitochondrion, complete genome	2252	0.0	OQ554236

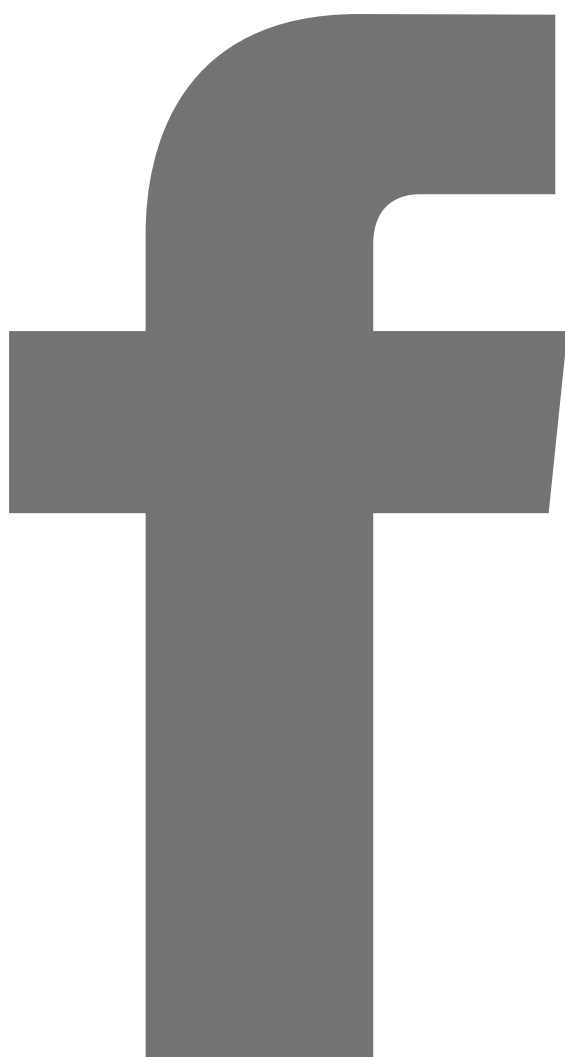
◦ **Taxonomy**

Taxonomy	Number of hits	Number of Organisms	Description
Delphinapterus leucas	100	1	Delphinapterus leucas hits

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