



An official website of the United States government

## Here's how you know



### The .gov means it's official.

Federal government websites often end in .gov or .mil. Before sharing sensitive information, make sure you're on a federal government site.



**The site is secure.**

The **https://** ensures that you are connecting to the official website and that any information you provide is encrypted and transmitted securely.  
[Access keys](#) [NCBI Homepage](#) [MyNCBI Homepage](#) [Main Content](#) [Main Navigation](#)

## **BLAST®** >> **blastn suite** >> results for RID-KE6VHPRD016

---

Job Title	<a href="#">Nucleotide Sequence ...</a>
RID	<a href="#">KE6VHPRD016</a> Search expires on 12-10 01:39 am
Program	BLASTN
Database	nt
Query ID	Icl Query_6575757
Description	<a href="#">None ...</a>
Molecule type	dna
Query Length	1548

### **Descriptions**

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

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

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

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

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

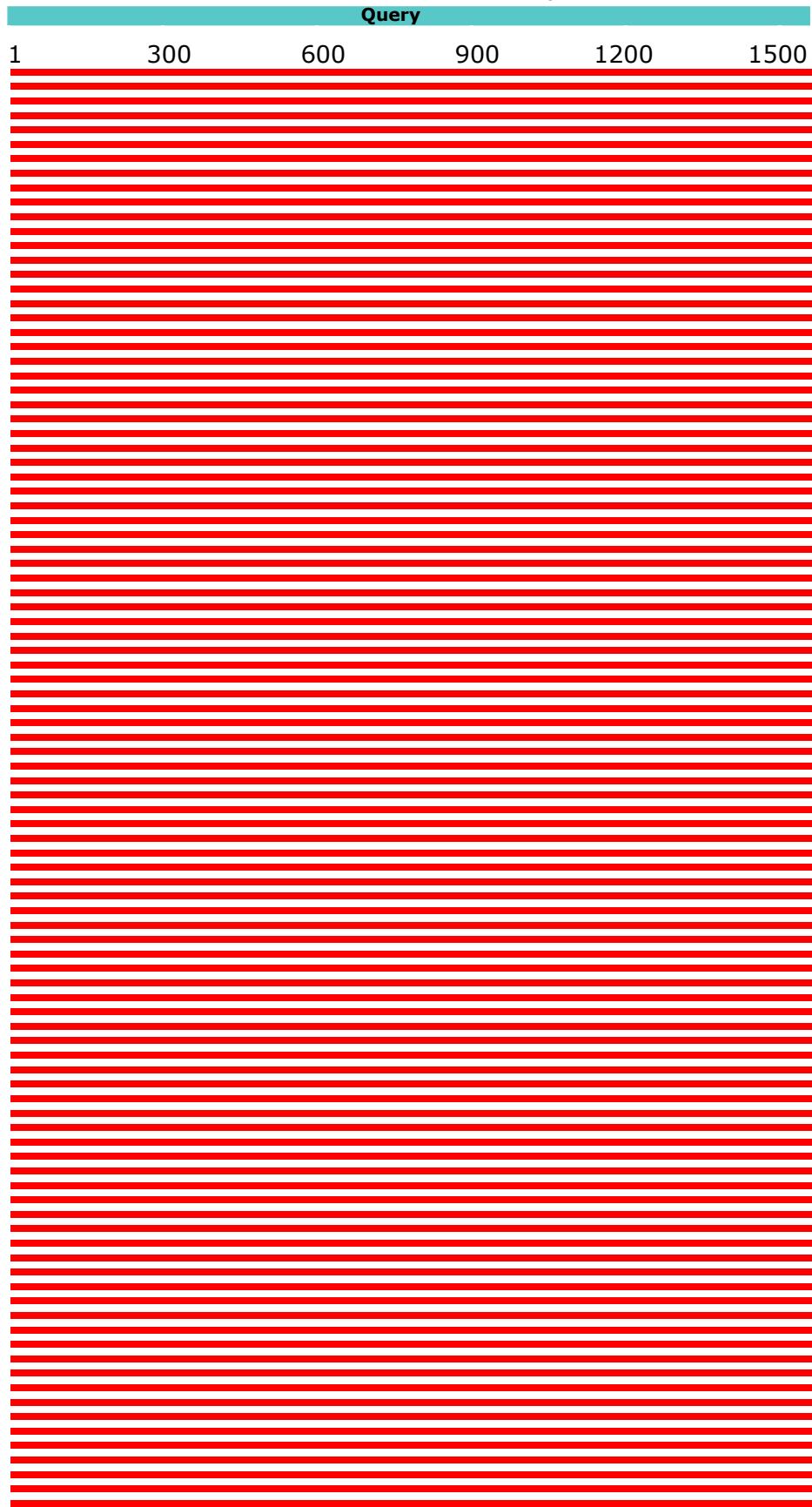
Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
S_20_01743 mitochondrion, complete genome								
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01734 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554151.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01705 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554148.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01699 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16387	<a href="#">QQ554147.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01612 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554144.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01597 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16387	<a href="#">QQ554143.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01594 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554142.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01590 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554141.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01580 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16387	<a href="#">QQ554140.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01574 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554139.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01567 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16387	<a href="#">QQ554138.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01562 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16387	<a href="#">QQ554137.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01555 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16387	<a href="#">QQ554135.1</a>
<u>Delphinapterus</u> <u>leucas</u> isolate S_20_01553 mitochondrion, complete genome	<u>Delphinapterus</u> <u>leucas</u>	2259	2259	100%	0.0	91.85%	16386	<a href="#">QQ554134.1</a>

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

Description ▾	Scientific Name ▾	Max Score ▾	Total Score ▾	Query Cover ▾	E value ▾	Per. Ident ▾	Acc. Len ▾	Accession
S_20_01463 <u>mitochondrion,</u> <u>complete genome</u>								
<u>Delphinapterus</u> <u>leucas isolate</u>	<u>Delphinapterus</u> <u>leucas</u>	2252	2252	100%	0.0	91.72%	16386	<a href="#">OQ554236.1</a>
S_20_03538 <u>mitochondrion,</u> <u>complete genome</u>								

## Graphic Summary

Distribution of the top 100 Blast Hits on 100 subject sequences



# Alignments

Alignment view **Pairwise**  CDS feature

Delphinapterus leucas isolate S\_20\_01444 mitochondrion, complete genome

Sequence ID: **OQ554110.1** Length: 16387 Number of Matches: 1

Range 1: 5370 to 6915

Score	Expect	Identities	Gaps	Strand	Frame
2265 bits(1226)	0.0(0)	1421/1546(92%)	3/1546(0%)	Plus/Plus	
Query 6	CATAAACCGATGACTATTCTTACCAATCACAAGGACATTGGCACCTATACYTAATT				65
Sbjct 5370	CATAAACCGATGACTATTCTTACCAATCACAAGGACATTGGCACCTATACYTAATT				5429
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAAAGCTTATTAAATTCTGTGCTGAATTAGG				125
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAAAGCTTATTCTGTGCTGAATTAGG				5489
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC				185
Sbjct 5490	CCAACCTGGCTACTTATTGGAGACGACCAAATYTATAACGTACTAGTAACAGCCCCACGC				5549
Query 186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT				245
Sbjct 5550	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT				5609
Query 246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT				305
Sbjct 5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT				5669
Query 306	TTGACTACTTCCTCCTCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC				365
Sbjct 5670	TTGACTGCTTCCTCCTCTTCCACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC				5729
Query 366	AGGCACAGGNTGNACTGTATATNCNNTTAGCAGGAAATCTAGCACATGCAGGAGCCTC				425
Sbjct 5730	AGGCACAGGCTGAACGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGAGCCTC				5789
Query 426	AGTCGACCTKACTATTTCTCTACATTTGCCCGTATCTCAATCCTCGGAGCTAT				485
Sbjct 5790	AGTCGACCTACTATTTCTCTACATCTAGCCGGTATCTCAATCCTCGGGCTAT				5849
Query 486	CAACTTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAAAACACC				545
Sbjct 5850	CAACTTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAAAACACC				5909
Query 546	TTTATTCTGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTACTACCTGTCCT				605
Sbjct 5910	TTTATTCTGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTACTACCTGTCCT				5969
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC				662
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCCTTTCGACCC				6029
Query 663	GGCAGGAGGAGGGACCCAGTCCTATATCACACACYTRTTCTGATTTTTGGTCACCCCGA				722
Sbjct 6030	TGCAGGAGGAGGCACCCAGTCCTATATCACACACCTATTCTGATTTTTGGTCACCCCGA				6089
Query 723	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACTTACTAYTC				782
Sbjct 6090	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTACTC				6149
Query 783	GGGaaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT				842
Sbjct 6150	GGGaaaaaaaaaGAACCCCTTGGATATATAGGATGGTGTGGCTATAATTCTATTGGTT				6209
Query 843	CCTGGGTTTCATTGTATGAGCTCACCATATATTACAGTCGGAATAGACGTTGACACACG				902
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTACAGTCGGAATAGACGTAGACACACG				6269
Query 903	AGCATATTCACATCAGTACCAATTATTGCTATTCCCTACAGGRGTAAGACGTTGACACACG				962
Sbjct 6270	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGGTAAAGACGTTGACACACG				6329
Query 963	CTGACTGGCAACCTCCACCGAGGAATANNNNNNNNNNNNNNNCTAATATGAGCCCT				1022
Sbjct 6330	CTGACTGGCAACACTCCACCGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT				6389
Query 1023	AGGCTTATYTCCTATTACAGTAGGAGGCTAACCGGTATTACCTAGCCAACTCATC				1082
Sbjct 6390	AGGCTTATYTCCTATTACAGTAGGAGGCTAACCGGTATTACCTAGCCAACTCATC				6449
Query 1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGTACTCTC				1142
Sbjct 6450	CTTAGACGTACCTCCACGACACATATTATGTAGTCGACACTCCACTATGTGCTTC				6509
Query 1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGTCAGTATTTCAGGTTAGGAGGTT				1202
Sbjct 6510	AATAGGGCTGTCTCGCCATCATAGGAGGTTCGCCACTGATTCCCACATTTTCAGG				6569
Query 1203	GTATACACTCAATTCAACATGGACAAAACCACTAATCGTAATCATANNNNNNNNNRAA				1262
Sbjct 6570	TTATACACTCAATTCAACATGGACAAAACCACTAATCGTAATCATATTCTGTAGGTGAA				6629

Query	1263	CGTGACATTCTTCCACARCACTTCTGGTCTATCTGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCACACACTTCCTCGTTATCTGAATACCCGTGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCCTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRRTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTGAGAAGCATTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCACTGTACATTAACCCAAAAAGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCACTGTACATTAACCCAAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYTACTATT		65	
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGACTTATATCTACTATT		5429	
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTTATTAAATTCTGTGCTGAATTAGG		125	
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTTATTCTGTGCTGAATTAGG		5489	
Query	126	CCAACCTGGCACACTTATGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC		185	
Sbjct	5490	CCAACCTGGCTCACTTATGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC		5549	
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT		245	
Sbjct	5550	CTTCGTGATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT		5609	
Query	246	WGTCCTTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCTAAATAACATAAGCTT		305	
Sbjct	5610	TGTCCTTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCTAAATAACATAAGCTT		5669	
Query	306	TTGACTACTCTCCTCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC		365	
Sbjct	5670	TTGACTGCTCCTCTTCCACTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC		5729	
Query	366	AGGCACAGGNGNACTGTATATNCNCNTTCTAGCAGGAAATCTAGCACATGCAGGGCCTC		425	
Sbjct	5730	AGGCACAGGCTGAACTGTGTACCCCCCTCTAGCAGGAAATCTAGCACATGCAGGGCCTC		5789	
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGCGTATCTCAATCCTCGGAGCTAT		485	
Sbjct	5790	AGTCGACCTKACTATTTCTCTACATCTAGCCGGCGTATCTCAATCCTCGGGGCTAT		5849	
Query	486	CAACTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAAATACCAAAACACC		545	
Sbjct	5850	CAACTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAAATACCAAAACACC		5909	
Query	546	TTTATTCGTATGATCAGCTTAATTACAGCAATCTACTCTATTACTACCTACCTGTCT		605	
Sbjct	5910	TTTATTCGTATGATCAGCTTAATTACAGCAGTCTACTCTATTACTACCTACCTGTCT		5969	
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC		662	
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTCGACCC		6029	
Query	663	GGCAGGAGGAGGCACCCAGTCCTATATCAACACYTRTTCTGATTTTTGGTCACCCCGA		722	
Sbjct	6030	TGCAGGAGGAGGCACCCAGTCCTATATCAACACCTATTCTGATTTTTGGTCACCCCGA		6089	
Query	723	AGTATATATCCTAATTCTACCCGGTTGGGATAATCTCACATATCGTAACCTACTAYTC		782	
Sbjct	6090	AGTATATATCTAATTCTACCCGGTTGGGATAATCTCACATATCGTAACCTACTACTC		6149	
Query	783	GGGaaaaaaaaaGAACCYTTGGATATATGGGGATRGTGTGGCTATAGTTCTATTGGTT		842	
Sbjct	6150	GGGaaaaaaaaAGAGCCCTTGGATATATAGGGATGGTGTGGCTATAATTCTATTGGTT		6209	
Query	843	CCTGGGTTTCATTGTATGAGCTCACCATAATTACAGTCGGAATAGACGTTGACACACG		902	
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTCACCATAATTACAGTCGGAATAGACGTTGACACACG		6269	
Query	903	AGCATATTCACATCAGTACCCATAATTGCTATTCTACAGGRGTAAGTCTTTAG		962	
Sbjct	6270	AGCATATTCACATCAGTACCCATAATTGCTATTCTACAGGRGTAAGTCTTTAG		6329	
Query	963	CTGACTGGCAACCCCTCCACGGAGGAAATANNNNNNNNNNNNNNCTAATATGAGCCCT		1022	
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAAATATAATGATCTCCAGCCCTAATATGAGCCCT		6389	

Query	1023	AGGCTTTATYTTCTATTACACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTCCTATTACACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTCATCCTCCACGACACATATTATGTAGTCGCACACTCCACTATGTGCTTC	6509
Query	1143	AATRGGAGGCTGTCTTGCATCATAGGAGGCTTCGCACTGATTYCCACTATTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTTCGCATCATAGGAGGTTCTGCACTGATTCCCACATTTTCAAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGTAAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACACACTTCCTCGTTATCTGAATACCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGTTACACAACATGAAACACCATTCAATAGGCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTACACAACATGAAACACCATTCAATAGGCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGG	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATGAGAAGCATTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGAGTAGATCTCACCCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAACAGCATACATYACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAACAGTGTACATTAACCCAAAAGTGCAAGA	6915

### Delphinapterus leucas isolate S\_20\_04130 mitochondrion, complete genome

Sequence ID: **Q554323.1** 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	CATAAACCGATGACTATTCTTACCAATCACAAGGACATTGGCACCCCTATACYTACTATT			65
Sbjct	5370	CATAAACCGATGACTATTCTTACCAATCACAAGGACATTGGCACCTATATCTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTAAATTCTGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTGTAAATTCTGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC			185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCCACGC			5549
Query	186	CTTCGTAATAATCTTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT			245
Sbjct	5550	CTTCGTAATAATCTTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT			5609
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTAAATAACATAAGCTT			305
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTAAATAACATAAGCTT			5669
Query	306	TTGACTACTTCCTCCTTCCCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC			365
Sbjct	5670	TTGACTGCTCCCTCTTCCCTACTACTAATAGCATCCTCAATAGTTGAAGCCGGCGC			5729
Query	366	AGGCACAGGNTGNACTGTATATNCNCNTTAGCAGGAAATCTAGCACATGCAGGAGCCTC			425
Sbjct	5730	AGGCACAGGCTGAAGTGTACCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC			5789
Query	426	AGTCGACCTKACTATTCTCTACATTTRGCCGGCTATCTCAATCCTGGAGCTAT			485
Sbjct	5790	AGTCGACCTACTATTCTCTACATCTAGCCGGCTATCTCAATCCTGGGGCTAT			5849
Query	486	CAACTTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAAAACACC			545
Sbjct	5850	CAACTTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAAAACACC			5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATTCTACTTCTATTACTACCTGTCCT			605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTACTCCATTATCACTACCTGTCCT			5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC			662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTCGACCC			6029
Query	663	GGCAGGAGGAGGCGACCCAGTCCTATATCAACACYRTTCTGATTTTTGGTCACCCCGA			722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCCTATATCAACACCTATTCTGATTTTTGGTCACCCCGA			6089
Query	723	AGTATATATCCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTAYTC			782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTCGGGATAATCTCACATATCGTAACCTACTTC			6149

Query	783	GGGaaaaaaaaGAACCYTTGGATATATGGGATRGTCGGCTATAGTTCTATTGGTTT	842
Sbjct	6150	GGGAAAAAAAGAGCCCTTGGATATATAGGATGGTGTGGCTATAATTCTATTGGTTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	6269
Query	903	AGCATATTTCACATCAGCTACCATAATTATTGCTATTCTACAGGRGTAAAGCTTTAG	962
Sbjct	6270	AGCATATTTCACATCAGCTACCATAATTATTGCTATTCCACAGGGTAAAGCTTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACCGAGGAAATANNNNNNNNNNNNNCTAATATGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACCGAGGAAATTAAATGATCTCAGCCCTAATATGCCCT	6389
Query	1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTTCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTCCACTATGTGCTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGCACTGATTYCCACTATTCAGG	1202
Sbjct	6510	AATAGGGCTGCTTCGCCATCATAGGAGGTTCGCACTGATCCCCTAATTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACCTCAATTGTAATCATANNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACCTCAATTGTAATCATATTGTAAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCGCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACAACACTTCCTCGGTTATCTGAATACCCGCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATCTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCCGGGTAGATCTCACCCATACAAACCTCGAGTGATTAACCGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCACTGTACATTAACCCAAAAGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCACTGTACATTAACCCAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT		5429	
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTATTAAATTGCTGAATTAGG		125	
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTATTAAATTGCTGAATTAGG		5489	
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC		185	
Sbjct	5490	CCAACCTGGCTACCTATTGGAGACGACCAAATTATAACGTAACAGCCCCACGC		5549	
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT		245	
Sbjct	5550	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT		5609	
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT		305	
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT		5669	
Query	306	TTGACTACTCCTCCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC		365	
Sbjct	5670	TTGACTGCTCCTCCTTCCACTACTAAATAGCATCTCAATAGTTGAAGCCGGCGC		5729	
Query	366	AGGCACAGGNTGNACTGTATATNCNCNTTAGCAGGAACTAGCACATGCAGGAGCCTC		425	
Sbjct	5730	AGGCACAGGNTGNACTGTATATNCNCNTTAGCAGGAACTAGCACATGCAGGAGCCTC		5789	
Query	426	AGTCGACCTKACTATTCTCTACATTTRGCCGGTATCTCAATCCTCGAGCTAT		485	
Sbjct	5790	AGTCGACCTKACTATTCTCTACATCTAGCCGGTATCTCAATCCTCGAGCTAT		5849	
Query	486	CAACTCATTACAACATTAAACATAAAACCACCCGCTATAACCAATACCAACACC		545	
Sbjct	5850	CAACTCATTACAACATTAAACATAAAACCACCCGCTATAACCAATACCAACACC		5909	

Query	546	TTTATTCTGATGACTAGCTTAATTACAGCAATCTACTTCTATTATCACTACCTGTCCT	605
Sbjct	5910	TTTATTCTGATGACTAGCTTAATTACAGCACTTACTCCTATTATCACTACCTGTCCT	5969
Query	606	AGCAGCCGAATTACCATGCTACTAAGCTGAAACCTAACACAACC---TTGACCC	662
Sbjct	5970	AGCAGCCGAATTACCATGCTACTAAGCTGAAACCTAACACAACCCTTCGACCC	6029
Query	663	GGCAGGAGGAGGCAGCCAGTCCTATCAACACYRTTGTGATTTTGTCACCCGA	722
Sbjct	6030	TGCAGGAGGAGGCAGCCAGTCCTATCAACACCTATTCTGATTTTGTCACCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGTCGGATAATCTCACATATCGTAACCTACTAC	6149
Query	783	GGGaaaaaaaaGAACCYTTGGATATGGGATRGTTGTCAGCTATAGTTCTATTGGTT	842
Sbjct	6150	GGGaaaaaaaaAGAGCCCTTGGATATAGGGATGGTGTGGCTATAATTCTATTGGTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATTTACAGTCGGAAAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATTTACAGTCGGAAAGACGTTGACACACG	6269
Query	903	AGCATATTCACATCAGTACCAATTGCTATTCCACAGGRGTAAGTCTTAG	962
Sbjct	6270	AGCATATTCACATCAGTACCAATTGCTATTCCACAGGGTAAGTCTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTATYTTCTATTACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTATTCCTATTACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTTGACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTATCCACGACACATATTATGTTGACACTCCACTATGCTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTCGCACTGATTYCCACTATTTCAGG	1202
Sbjct	6510	AATAGGGGCTGTCTGCCATCATAGGAGGTTCTGCACTGATTCCCACATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNRAA	1262
Sbjct	6570	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGTTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGGAAATACCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACAAACACTTCTCGGTTATCTGGAAATACCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATAACTAATARTCTTCATTATCTGAGAAGCRGTCGATCCAACGAGAGGT	1442
Sbjct	6750	AAACAGCAGTCATAACTTATAGTCTTCATTATGAGAAGCATTGCACTCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGTNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCCGGGTAGATCTCACCCATACAAACCTCGAGTGTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAAGCATACTYACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAAGTGTACATTAACCCAAAAGTGCAAGA	6915

### Delphinapterus leucas isolate S\_20\_04108 mitochondrial 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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYTACTATT			65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTTATCTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTAAATTGTCGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTGTCGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTAGTAACAGCTCACGC			185
Sbjct	5490	CCAACCTGGCTACTTATTGGAGACGACCAAATTATAACGACTAGTAACAGCCCCACGC			5549
Query	186	CTTCGTAATAATCTTCTTATAGTAATGCTTATTATAATTGGGGGTTGGAAACTGACT			245
Sbjct	5550	CTTCGTAATAATCTTCTTATAGTAATGCTTATTATAATTGGAGGGTTGGAAACTGACT			5609
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT			305
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT			5669

Query	306	TTGACTACTCCCTCTTCCCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC	365
Sbjct	5670	TTGACTGCTCCCTCTTCCCTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729
Query	366	AGGCACAGGNNTGNACTGTATATNCNCNTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425
Sbjct	5730	AGGCACAGGCTGAACGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGCTATCTCAATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTTACTATTTCTCTACATCTAGCCGGCTATCTCAATCCTCGGAGCTAT	5849
Query	486	CAACTTCATTACAACATTATAAACATAAAACCACCCGCTATAACCCAATACCAAACACC	545
Sbjct	5850	CAACTTCATTACAACATTATAAACATAAAACCACCCGCTATAACCCAATACCAAACACC	5909
Query	546	TTTATTCGTATGATCAGCTTAATTACAGCAATCTTACTTCTATTACACTACCTGTCCT	605
Sbjct	5910	TTTATTCGTATGATCAGCTTAATTACAGCAGTCTACTCCTATTACACTACCTGTCCT	5969
Query	606	AGCAGCCGGAAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TCGACCC	662
Sbjct	5970	AGCAGCCGGAAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTGACCC	6029
Query	663	GGCAGGAGGAGGCGACCCAGTCCTATATCAACACYRTTCTGATTTTGTCACCCGA	722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCCTATATCAACACCTATTCTGATTTTGTCACCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT	842
Sbjct	6150	GGGAAAAAAAGAGCCCTTGGATATATAGGGATGGTGTGGCTATAATTCTATTGGTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGGAATAGACGTTGACACACG	6269
Query	903	AGCATATTCACATCAGTACCAATTATTGCTATTCTACAGGRGTAAGCTTTAG	962
Sbjct	6270	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGGTAAGCTTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACGGAGGAAATANNNNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACCGAGGAAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTATYTTCCATTACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTATTTCTATTACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGACACTCCACTATGTGTTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGTCACGTATTYCCACTATTTCAGG	1202
Sbjct	6510	AATAGGGCTGTCTGCCATCATAGGAGGTTCGTCCACTGATTCCCACATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACACTCAATCGTAATCATANNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACACTCAATCGTAATCATATTCTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACACACTTCCTCGGTTATCTGAATACCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTTTCTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTTTCTCATCTCACT	6749
Query	1383	RACAGCAGTCATAATARTCTTCATTATCTGAGAAGCRTTCGATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATCTGAGAAGCATTTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGTNAAACNGATGTCCTCCACCAT	1502
Sbjct	6810	GTCCGCGGTAGATCTACCCATACAAACCTCGAGTGTAAACGGATGTCCTCCACCAT	6869
Query	1503	TCATACATTGAAGAACCAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAACAGTGTACATTAACCCAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYACTATT				65
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYACTATT				5429

Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCCTAACGCTATTAAATTCTGTGCTGAATTAGG	125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCCTAACGCTTAAATTCTGTGCTGAATTAGG	5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATTGTTAGTAACAGCTACGC	185
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC	5549
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT	245
Sbjct	5550	CTTCGTATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT	5609
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT	305
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT	5669
Query	306	TTGACTACTCCCTCTTCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC	365
Sbjct	5670	TTGACTGCTCCCTCTTCTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729
Query	366	AGGCACAGGNNTGNACTGTATATNCNCNTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425
Sbjct	5730	AGGCACAGGCTGAACGTGTACCCCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGTATCTCAATCCTGGAGCTAT	485
Sbjct	5790	AGTCGACCTACTATTTCTCTACATCTAGCCGGTATCTCAATCCTGGGGCTAT	5849
Query	486	CAACTTCATTACAACATTATTAAACATAAAACCACCCGCTATAACCCAATACCAAAACACC	545
Sbjct	5850	CAACTTCATTACAACATTATTAAACATAAAACCACCCGCTATAACCCAATACCAAAACACC	5909
Query	546	TTTATTCTGATGATCAGCTTAATTACAGCAATCTACTTCTATTATCACTACCTGTCCT	605
Sbjct	5910	TTTATTCTGATGATCAGCTTAATTACAGCAGTCTACTCTTATTACACTACCTGTCCT	5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTCGACCC	6029
Query	663	GGCAGGAGGAGGCACCCAGTCCTATATCAACACYTRTTCTGATTTTTGGTACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGCACCCAGTCCTATATCAACACCTATTCTGATTTTTGGTACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACTTACTAYTC	782
Sbjct	6090	AGTATATATCCTAATTCTACCCGGCTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaaaGAACCYTTGGATATATGGGGATRGTTGTTGGCTATAGTTCTATTGGTT	842
Sbjct	6150	GGGaaaaaaaaAGAGCCCTTGGATATATAGGGATGGTGTGGCTATAATTCTATTGGTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTAGACACACG	6269
Query	903	AGCATATTCACATCAGCTACCATATAATTGCTATTCCACAGGRGTAAAAGCTTTAG	962
Sbjct	6270	AGCATATTCACATCAGCTACCATATAATTGCTATTCCACAGGGTAAAAGCTTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAATATTAAATGATCTCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTATYTTCCATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTATTTCTATTACACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTCCACTATGTGTTTC	6509
Query	1143	AATRGGAGCTGCTTGCATCATAGGAGGCTCGCACTGATTYCCACTATTTCAAGG	1202
Sbjct	6510	AATAGGGGCTGCTTCGCCATCATAGGAGGTTCTGCACTGATTCCCACATTTCAAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACCTAACGCTAATCATANNNNNNNNNNRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACCTAACGCTAATCATATTCTGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTGGCTATCTGGAATACCCCGCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACAAACACTTCCTCGGTTATCTGGAATACCCCGCGATATTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCATCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCATCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRRTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATGTAGAAGCATTGCACTCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGTNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGGCGTAGATCTCACCCATACAAACCTCGAGTGTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAACAGTGTACATTAACCCAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTTATCTACTATT				5429
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAAGCTTAAATTCTGTGCTGAATTAGG				125
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAAGCTTAAATTCTGTGCTGAATTAGG				5489
Query 126	CCAACCTGGCACACTTATGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC				185
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC				5549
Query 186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT				245
Sbjct 5550	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT				5609
Query 246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT				305
Sbjct 5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT				5669
Query 306	TTGACTACTCCTCCTTCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC				365
Sbjct 5670	TTGACTGCTCCTCCTTCTACTACTAAATAGCATCTCAATAGTTGAAGCCGGCGC				5729
Query 366	AGGCACAGGNTGNACTGTATATNCNCNTTACAGGAAATCTAGCACATGCAGGAGCCTC				425
Sbjct 5730	AGGCACAGGCTGAACGTGTACCCCCCTCTAGCAGGAAATCTAGCACATGCAGGAGCCTC				5789
Query 426	AGTCGACCTKACTATTCTCTACATTTRGCCGGTATCTCAATCCTCGGAGCTAT				485
Sbjct 5790	AGTCGACCTTACTATTCTCTACATCTAGCCGGTATCTCAATCCTCGGGCTAT				5849
Query 486	CAACTTCATTACAACATTATAACATAAAACCACCGCTATAACCCAATACCAACACC				545
Sbjct 5850	CAACTTCATTACAACATTATAACATAAAACCACCGCTATAACCCAATACCAACACC				5909
Query 546	TTTATTCGTATGATCAGCTTAATTACAGCAATCTACTTCTATTACTACACTGTCCT				605
Sbjct 5910	TTTATTCGTATGATCAGCTTAATTACAGCAGTCTACTCCTATTACTACACTGTCCT				5969
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC				662
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTCGACCC				6029
Query 663	GGCAGGAGGAGGCCACCCAGTCCTATATCACACACYTRTTCTGATTTTGTCACCCGA				722
Sbjct 6030	TGCAGGAGGAGGCACCCAGTCCTATATCACACACCTATTCTGATTTTGTCACCCGA				6089
Query 723	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTAYTC				782
Sbjct 6090	AGTATATATCCTAATTCTACCCGGTCGGGATAATCTCACATATCGTAACCTACTACTC				6149
Query 783	GGGaaaaaaaaaGAACCYTTGGATATATGGGATRGTTGTTGGCTATAGTTCTATTGGTT				842
Sbjct 6150	GGGaaaaaaaaAGAGCCCTTGGATATATAGGATGGTGTGGCTATAATTCTATTGGTT				6209
Query 843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG				902
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG				6269
Query 903	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGRGTAAGCTTTAG				962
Sbjct 6270	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGGTAAGCTTTAG				6329
Query 963	CTGACTGGCAACCCCTCCACCGAGGAATANNNNNNNNNNNNNNCTAATATGAGCCCT				1022
Sbjct 6330	CTGACTGGCAACACTCCACCGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT				6389
Query 1023	AGGCTTATYTTCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC				1082
Sbjct 6390	AGGCTTATTCCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC				6449
Query 1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGACTCTC				1142
Sbjct 6450	CTTAGACGTCATCCTCCACGACACATATTATGTAGTCGACACTCCACTATGCTTTC				6509
Query 1143	AATRGGAGCTGTTGCCATAGGAGGCTCGCCACTGATTYCCACTATTTCAAGG				1202
Sbjct 6510	AATAGGGCTGCTTCGCCATAGGAGGTTCGTCCACTGATCCCACATTTCAGG				6569
Query 1203	GTATACACTCAATTCAACATGGACAAAACCTAATCGTAATCATANNNNNNNNNRAA				1262
Sbjct 6570	TTATACACTCAATTCAACATGGACAAAACCTAATCGTAATCATATTCTGTAGGTGTGAA				6629
Query 1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCCGYCGATATTCTGA				1322
Sbjct 6630	TGTAACATTCTTCCACAAACACTTCCTCGGTTATCTGAATACCCCGTCGATACTCTGA				6689
Query 1323	TTACCCAGACGCTTACACAAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT				1382

Sbjct	6690	TTACCCAGACGCCAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATAACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCCGGGTAGATCTCACCCATACAAACCTCGAGTGATTAACCGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAAGAACCAAGCATACTYAAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAAGAACCAAGTGTACATTAACCCAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCATACYACTATT			65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTTATATCTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTATTAAATTCTGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTTGTAAATTCTGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC			185
Sbjct	5490	CCAACCTGGCTACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC			5549
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT			245
Sbjct	5550	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT			5609
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCTAAATAACATAAGCTT			305
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCTAAATAACATAAGCTT			5669
Query	306	TTGACTACTCCCTCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC			365
Sbjct	5670	TTGACTGCTCCCTCTTCCACTACTAATAGCATCTCAATAGTTGAAGCCGGCGC			5729
Query	366	AGGCACAGGNTGNACTGTATATNCNCNTTAGCAGGAAACTAGCACATGCAGGAGCCTC			425
Sbjct	5730	AGGCACAGGNTGAACGTGTACCCCCCTCTAGCAGGAAACTAGCACATGCAGGAGCCTC			5789
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGTATCTCAATCCTGGAGCTAT			485
Sbjct	5790	AGTCGACCTACTATTTCTCTACATCTAGCCGGGTATCTCAATCCTGGGGCTAT			5849
Query	486	CAACTTCATTACAACATTATAACATAAAACCACCCGTATAACCAATACCAACACC			545
Sbjct	5850	CAACTTCATTACAACATTATAACATAAAACCACCGTATAACCAATACCAACACC			5909
Query	546	TTTATTCTGATGACTAGCTTAATTACAGCAATCTACTTCTATTATCACTACCTGTCCT			605
Sbjct	5910	TTTATTCTGATGACTAGCTTAATTACAGCAGTCTACTCTATTATCACTACCTGTCCT			5969
Query	606	AGCAGCCGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC			662
Sbjct	5970	AGCAGCCGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTCGACCC			6029
Query	663	GGCAGGAGGAGGCGACCCAGTCCTATCAACACYTRTTGTGATTTTTGGTCACCCCGA			722
Sbjct	6030	TGCAGGAGGAGGCGACCCAGTCCTATCAACACCTATTGATTTTTGGTCACCCCGA			6089
Query	723	AGTATATATCCTAATTCTACCGGTTGGATAATCTCACATATCGTAACCTACTAYTC			782
Sbjct	6090	AGTATATATCCTAATTCTACCGGTTGGATAATCTCACATATCGTAACCTACTACTC			6149
Query	783	GGGaaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT			842
Sbjct	6150	GGGaaaaaaaaaAGAGCCCTTGGATATATGGGATGGTGTGGCTATAATTCTATTGGTT			6209
Query	843	CCTGGGTTCTATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG			902
Sbjct	6210	CCTAGGTTCTATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG			6269
Query	903	AGCATATTCACATCAGTACCAATTATTGCTATTCCCTACAGGRGTAAAAGTCTTAG			962
Sbjct	6270	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGGTAAAAGTCTTAG			6329
Query	963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNNNCTAATATGAGCCCT			1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT			6389
Query	1023	AGGCTTTATYTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC			1082
Sbjct	6390	AGGCTTTATTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC			6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGAGTTGCACATTCCACTATGACTCTC			1142

Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGAGTCGCACACTTCCACTATGCTTC	6509
Query	1143	AATRGAGCTGTCTTGCCATCATAGGAGGCTTCGTCCACTGATTYCCACTATTTCA	1202
Sbjct	6510	AATAGGGGCTGTCTCGCCATCATAGGAGGTTCGTCCACTGATTCCCACATTTCA	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGCTAGGTGT	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCGCGATATTCTG	1322
Sbjct	6630	TGTAACATTCTTCCACAACACTTCCTCGTTATCTGAATACCCGCGATACTCTG	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCCAACACATGAAACACCATTCAATAGGCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATAACTAARTCTTCATTATCTGAGAAGCRRTCGCATCCAAACGAGAGG	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTGAGAAGCATTCGATCCAAACGAGAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCCATACAAACCTCGAGTGATTAACCGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAAGCTGACATTAACCCAAAAGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAAGCTGACATTAACCCAAAAGTGCAAGA	6915

### Delphinapterus leucas isolate S\_20\_04088 mitochondrial, complete genome

Sequence ID: **OQ554312.1** 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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCATACYTA	65		
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACTATT	5429		
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTAAATTGCTGCTGAATTAGG	125		
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTGCTGCTGAATTAGG	5489		
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTAGTAACAGCTCACGC	185		
Sbjct	5490	CCAACCTGGCTACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC	5549		
Query	186	CTTCGTAATACTCTTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT	245		
Sbjct	5550	CTTCGTAATACTCTTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT	5609		
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT	305		
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT	5669		
Query	306	TTGACTACTCCCTCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCG	365		
Sbjct	5670	TTGACTGCTCCCTCTTCCACTAAATAGCATCCTCAATAGTTGAAGCCGGCG	5729		
Query	366	AGGCACAGGNTGNACTGTATNCNCNTTACAGGAAATCTAGCACATGCAGGAGCCTC	425		
Sbjct	5730	AGGCACAGGCTGAACGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789		
Query	426	AGTCGACCTKACTATTCTCTACATTTTRGCCGGCTATCTCAATCCTCGGAGCTAT	485		
Sbjct	5790	AGTCGACCTACTATTCTCTACATCTAGCCGGCTATCTCAATCCTCGGGCTAT	5849		
Query	486	CAACTTCATTACAACATTAAACATAAAACCAACCGCTATAACCCAATACCAAAACACC	545		
Sbjct	5850	CAACTTCATTACAACATTAAACATAAAACCAACCGCTATAACCCAATACCAAAACACC	5909		
Query	546	TTTATTGCTATGATCAGCTTAATTACAGCAATTACTCTATTACACTACCTGTCCT	605		
Sbjct	5910	TTTATTGCTATGATCAGCTTAATTACAGCAATTACTCTATTACACTACCTGTCCT	5969		
Query	606	AGCAGCCGGATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC	662		
Sbjct	5970	AGCAGCCGGATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTCGACCC	6029		
Query	663	GGCAGGAGGAGCGACCCAGTCCTATATCAACACYTRTTCTGATTTTGGTCACCCGA	722		
Sbjct	6030	TGCAGGAGGAGCGACCCAGTCCTATATCAACACCTATTGATTTTGGTCACCCGA	6089		
Query	723	AGTATATATCCTAATTCTACCCGGTTCGGATAATCTCACATATCGTAACCTACTAYTC	782		
Sbjct	6090	AGTATATATTCTAATTCTACCCGGCTCGGATAATCTCACATATCGTAACCTACTACTC	6149		
Query	783	GGGaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT	842		
Sbjct	6150	GGGaaaaaaaaAGAGCCCTTGGATATAGGGATGGTGTGGCTATAATTCTATTGGTT	6209		
Query	843	CCTGGTTTCATTGTATGAGCTACCATATATTACAGTCGGAATAGACGTTGACACACG	902		

Sbjct	6210	CCTAGGTTTACATGTATGAGCTACCATATATTACAGTCGAATAGACGTAGACACAGC	6269
Query	903	AGCATATTCACATCAGCTACCATAATTGCTATTCTACAGGRGTAAGACTTTAG	962
Sbjct	6270	AGCATATTCACATCAGCTACCATAATTGCTATTCCACAGGGTAAAGCTTTAG	6329
Query	963	CTGACTGGCAACCTCCACGGAGGAATANNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACCGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTCCTATTACACAGTAGGAGGCTTAACCGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTCCTATTACAGTAGGAGGCTTAACCGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTCATCCTCACGACACATATTATGAGTCGCACACTCCACTATGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGTCCTGATTYCCACTATTTCAGG	1202
Sbjct	6510	AATAGGGGCTGCTTCGCCATCATAGGAGGTTCGTCCACTGATCCCCTAATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACCTCAATCGTAATCATANNNNNNNNRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACCTCAATCGTAATCATATTCTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTGGTCTATCTGAATACCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACACACTTCCTCGTTATCTGAATACCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCATCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCATCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAACGRTTCGATCCAAACGAGAGGT	1442
Sbjct	6750	ACAGCAGTCATACTTATAGTCTTCATTATGAGAACGATTTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGGTAGATCTCACCCATACAAACCTCGAGTGATTAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAACAGTGTACATTAACCCAAAAGGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTTATATCTACTATT		5429	
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTAAATCGTGTGAATTAGG		125	
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTGTAAATCGTGTGAATTAGG		5489	
Query	126	CCAACCTGGCACACTTATGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC		185	
Sbjct	5490	CCAACCTGGCTCACTTATGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC		5549	
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT		245	
Sbjct	5550	CTTCGTAATAATCTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT		5609	
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTGCTAAATAACATAAGCTT		305	
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTGCTAAATAACATAAGCTT		5669	
Query	306	TTGACTACTCCCTCTTCCCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC		365	
Sbjct	5670	TTGACTGCTCCCTCTTCCCTACTACTAATAGCATCTCAATAGTTGAAGCCGGCGC		5729	
Query	366	AGGCACAGGNTGNACTGTATATNCNCNTTAGCAGGAACTAGCACATGCAGGAGCCTC		425	
Sbjct	5730	AGGCACAGGCTGAAGTGTGACCCCCCTCTAGCAGGAACTAGCACATGCAGGAGCCTC		5789	
Query	426	AGTCGACCTKACTATTCTCTACATTTRGCCGGCTATCTCAATCCTCGGAGCTAT		485	
Sbjct	5790	AGTCGACCTACTATTCTCTACATCTAGCCGGCTATCTCAATCCTCGGGCTAT		5849	
Query	486	CAACTTCATTACAACATTATAACATAAAACCAACCGCTATAACCCAATACCAAAACCC		545	
Sbjct	5850	CAACTTCATTACAACATTATAACATAAAACCAACCGCTATAACCCAATACCAAAACCC		5909	
Query	546	TTTATTCTGATGTCAGTCTTAATTACAGCAATCTACTTCTATTACACTACCTGCTCT		605	
Sbjct	5910	TTTATTCTGATGTCAGTCTTAATTACAGCACTACTCCTATTACACTACCTGCTCT		5969	
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC		662	

Sbjct	5970	AGCAGCCGAAATTACCATGCTACTAAGTCGAACTAACACAACCTTTGCACCC	6029
Query	663	GGCAGGAGGAGCGACCCAGTCCTATCAACACYTRTTCTGATTTTGGTCACCCGA	722
Sbjct	6030	TGCAGGAGGAGCGACCCAGTCCTATCAACACCTATTCTGATTTTGGTCACCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaGAACCYTTGGATATATGGGATRGTTGTGGCTATAGTTCTATTGGTT	842
Sbjct	6150	GGGAAAAAAAAGAGCCCTTGGATATATAGGATGGTGTGGCTATAATTCTATTGGTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	6269
Query	903	AGCATATTCACATCAGCTACCATAATTATTGCTATTCCCTACAGGRGTAAGCTTTAG	962
Sbjct	6270	AGCATATTCACATCAGCTACCATAATTATTGCTATTCCACAGGGTAAGCTTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACCGAGGAATANNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACCGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTATYTTCCATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTATTTCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTCTCCACGACACATATTATGAGTTGCACACTCCACTATGCTTTC	6509
Query	1143	AATRGGAGCTGCTTGCCATCATAGGAGGCTCGTCCACTGATTYCCACTATTTCAGG	1202
Sbjct	6510	AATAGGGGCTGCTTCGCCATCATAGGAGGTTCTGCACTGATCCCCTAATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAACCTCAATTGTAATCATANNNNNNNNTRA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAACCTCAATTGTAATCATATTGTAAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACAACACTTCCTCGGTTATCTGAATACCCGTGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTATCTGAGAAGCRTTCGATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATGAGAAGCATTTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGTATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCCATACAAACCTCGAGTGTATTAACCGATGTCCTCCACCATA	6869
Query	1503	TCATACATTCAAGAACCAACAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTCAAGAACCAACAGTGTACATTAACCCAAAAGGTGCAAGA	6915

### Delphinapterus leucas isolate S\_20\_04076 mitochondrion, complete genome

Sequence ID: **QQ554310.1** 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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCATACYTA	TATT	65	
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTTATCTACTATT		5429	
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTTATTAAATTCTGCTGAATTAGG		125	
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCTAACGCTTATTCTGCTGAATTAGG		5489	
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTAGTAACAGCTCACGC		185	
Sbjct	5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCCACGC		5549	
Query	186	CTTCGTAATAATCTTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT		245	
Sbjct	5550	CTTCGTAATAATCTTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT		5609	
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCAAATAACATAAGCTT		305	
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAAATAACATAAGCTT		5669	
Query	306	TTGACTACTCCCTTCTTCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC		365	
Sbjct	5670	TTGACTGCTCCCTTCTTCTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC		5729	
Query	366	AGGCACAGGNTGNACTGTATATNCNCNTTACAGGAAATCTAGCACATGCAGGAGCCTC		425	

Sbjct	5730	AGGCACAGGCTGAACCTGTACCCCCCTCTAGCAGGAAATCTAGCACATGCAGGGCCTC	5789
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGTATCTCAATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTACTATTTCTCTACATCTAGCCGGTATCTCAATCCTCGGGCTAT	5849
Query	486	CAACTCATACAACATTAAACATAAAACCACCCGCTATAACCCAATACCAAACACC	545
Sbjct	5850	CAACTCATACAACATTAAACATAAAACCACCCGCTATAACCCAATACCAAACACC	5909
Query	546	TTTATTCTGATGATCAGCTTAATTACAGCAATCTACTCTATTACTACACCTGTCT	605
Sbjct	5910	TTTATTCTGATGATCAGCTTAATTACAGCAGTCTACTCTATTACTACACCTGTCT	5969
Query	606	AGCAGCCGAATTACCATGCTACTAAGTGAAACCTAACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGAATTACCATGCTACTAAGTGAAACCTAACACAACCCTTTGACCC	6029
Query	663	GGCAGGAGGAGGCGACCCAGTCCTATATCAACACYRTTCTGATTTTGGTACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGGACCCAGTCCTATATCAACACCTATTCTGATTTTGGTACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTAYTC	782
Sbjct	6090	AGTATATATTCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaaaGAACCYTTGGATATATGGGATRGTTGTTGGCTATAGTTCTATTGGTT	842
Sbjct	6150	GGGAAAAAAAGAGCCCTTGGATATATAGGGATGGTGTGGCTATAATTCTATTGGTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG	6269
Query	903	AGCATATTCACATCAGTACCATATAATTGCTATTCTACAGGRGTAAGTCTTAG	962
Sbjct	6270	AGCATATTCACATCAGTACCATATAATTGCTATTCCACAGGGTAAAGTCTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACGGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTATYTTCTTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTATTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTCCACTATGTGTTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATAGGAGGCTCGCACTGATTYCCACTATTTCAAGG	1202
Sbjct	6510	AATAGGGCTGTCTGCCATAGGAGGTTCTGCACTGATCCCACATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTATCTGAATACCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACACACTTCCTCGTTATCTGAATACCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGTTACACAAACATGAAACACCATTCAATAGGCTTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTACACAAACATGAAACACCATTCAATAGGCTTTCATCTCACT	6749
Query	1383	RACAGCAGTCATAATARTCTTCATTATCTGAGAAGCRCTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTATGAGAAGCATTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGATNAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGGTAGATCTCACCCATACAAACCTCGAGTGATTAAACGGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAAGAACCAACAGCATACATYACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAAGAACCAACAGTGTACATTAACCCAAAAGTGCAAGA	6915

### Delphinapterus leucas isolate S\_20\_04063 mitochondrial 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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYTAATT			65
Sbjct	5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATATCTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTAACTCGTGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTGTAACTCGTGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAATYTATAATGTTAGTAACAGCTCACGC			185

Sbjct	5490	CCAACCTGGCTCACTTATGGAGACGACCAAATTATAACGTACTAGTAACAGCCACGC	5549
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCATTATAATTGGGGGTTGGAAACTGACT	245
Sbjct	5550	CTTCGTGATAATCTCTTATAGTAATGCCATTATAATTGGAGGGTTGGAAACTGACT	5609
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTAAATAACATAAGCTT	305
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCAATAACATAAGCTT	5669
Query	306	TTGACTACTCCTCCTTCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC	365
Sbjct	5670	TTGACTGCTCCTCCTTCTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC	5729
Query	366	AGGCACAGGNTGNACTGTATATNCNCTTAGCAGGAAATCTAGCACATGCAGGAGCCTC	425
Sbjct	5730	AGGCACAGGCTGAACGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGAGCCTC	5789
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGCGTATCTTCATCCTCGGAGCTAT	485
Sbjct	5790	AGTCGACCTACTATTTCTCTACATCTAGCCGGCGTATCTTCATCCTCGGGCTAT	5849
Query	486	CAACTTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAAAACACC	545
Sbjct	5850	CAACTTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAAAACACC	5909
Query	546	TTTATTCGTATGATCAGTCTTAATTACAGCAATCTTACTTCTATTACTACCTGTCCT	605
Sbjct	5910	TTTATTCGTATGATCAGTCTTAATTACAGCAGTCTTACTCCTATTACTACCTGTCCT	5969
Query	606	AGCAGCCGAATTACCATGCTACTAACTGATCGAAACCTAACACACAACC---TTCGACCC	662
Sbjct	5970	AGCAGCCGAATTACCATGCTACTAACTGATCGAAACCTAACACACAACCTTTCGACCC	6029
Query	663	GGCAGGAGGAGGCACCCAGTCCTATATCAACACYRTTCTGATTTTGGTCACCCCGA	722
Sbjct	6030	TGCAGGAGGAGGCACCCAGTCCTATATCAACACCTATTCTGATTTTGGTCACCCCGA	6089
Query	723	AGTATATATCCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACTTACTAYTC	782
Sbjct	6090	AGTATATATCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTACTC	6149
Query	783	GGGaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT	842
Sbjct	6150	GGGaaaaaaaaAGAGCCCTTGGATATATAGGGATGGTGTGGCTATAATTCTATTGGTT	6209
Query	843	CCTGGGTTTCATTGTATGAGCTCACCATATATTACAGTCGGAATAGACGTTGACACACG	902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTACAGTCGGAATAGACGTAGACACACG	6269
Query	903	AGCATATTCACATCAGTACCAATTATTGCTATTCTACAGGRGTAAGTCTTAG	962
Sbjct	6270	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGGTAAGTCTTAG	6329
Query	963	CTGACTGGCAACCCCTCACGGAGGAATANNNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACCGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTATYTCCTATTACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTATTCCTATTACAGTAGGAGGCTAACCGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGACACTCCACTATGCTTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGTCACGTATTYCCACTATTTCAGG	1202
Sbjct	6510	AATAGGGCTGTCTGCCATCATAGGAGGTTCGCACTGATTCCCACATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGTAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCACARCACTTCTCGGTCTATCTGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCACACACTTCCTCGGTTATCTGAATACCCCGTCGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTCATTATCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTCATTATCTGAGAAGCATTTGCATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATACAAACCTCGAGTGTNAACNGATGTCTCCACCATA	1502
Sbjct	6810	GTCCGCGGTAGATCTCACCCATACAAACCTCGAGTGTAAACGGATGTCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAAGCATACATTAACCCAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCCTATACYTACTATT				5429
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCCTAAGCTTATTAAATTCTGTGCTGAATTAGG				125
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCCTAAGCTTATTCTGTGCTGAATTAGG				5489
Query 126	CCAACCTGGCACACTTATGGAGACGACCAAATYATAATGTTTAGTAACAGCTCACGC				185
Sbjct 5490	CCAACCTGGCTCACTTATGGAGACGACCAAATTTAAACGTACTAGTAACAGCCCACGC				5549
Query 186	CTTCGTAATAATCTTCTTATAGTAATGCCTATTATAATTGGGGGTTGGAAACTGACT				245
Sbjct 5550	CTTCGTAATAATCTTCTTATAGTAATGCCTATTATAATTGGAGGGTTGGAAACTGACT				5609
Query 246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCTAAATAACATAAGCTT				305
Sbjct 5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCTAAATAACATAAGCTT				5669
Query 306	TTGACTACTTCCCTCTTCCCTACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC				365
Sbjct 5670	TTGACTGCTCCTCTTCCCTACTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC				5729
Query 366	AGGCACAGGNTGNACTGTATATNCNCNTTACAGGAAATCTAGCACATGCAGGGCCTC				425
Sbjct 5730	AGGCACAGGCTGAACGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGGCCTC				5789
Query 426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGGTATCTCAATCCTCGGAGCTAT				485
Sbjct 5790	AGTCGACCTKACTATTTCTCTACATCTAGCCGGGTATCTCAATCCTCGGGGCTAT				5849
Query 486	CAACTTCATTACAACATTATAACATAAAACCACCCGTATAACCCAATACCAACACC				545
Sbjct 5850	CAACTTCATTACAACATTATAACATAAAACCACCCGTATAACCCAATACCAACACC				5909
Query 546	TTTATTCGTATGATCAGCTTAATTACAGCAATCTACTTCTATTACTACCTGTCCT				605
Sbjct 5910	TTTATTCGTATGATCAGCTTAATTACAGCAGTCTACTCCTATTACTACCTGTCCT				5969
Query 606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC				662
Sbjct 5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTGACCC				6029
Query 663	GGCAGGAGGAGGCACCCAGTCCTATCAACACYRTTCTGATTTTGTCACCCGA				722
Sbjct 6030	TGCAGGAGGAGGCACCCAGTCCTATCAACACCTATTCTGATTTTGTCACCCGA				6089
Query 723	AGTATATATCCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTAYTC				782
Sbjct 6090	AGTATATATTCTAATTCTACCCGGTTGGATAATCTCACATATCGTAACCTACTACTC				6149
Query 783	GGGaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT				842
Sbjct 6150	GGGaaaaaaaaAGACGCCCTTGGATATATAGGATGGTGTGGCTATAATTCTATTGGTT				6209
Query 843	CCTGGGTTTCATTGATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG				902
Sbjct 6210	CCTAGGTTTCATTGATGAGCTACCATATATTACAGTCGAATAGACGTTGACACACG				6269
Query 903	AGCATATTCACATCAGTACCAATTATTGCTATTCTACAGGRGTAAGACGTTGACACACG				962
Sbjct 6270	AGCATATTCACATCAGTACCAATTATTGCTATTCCACAGGGTAAGACGTTGACACACG				6329
Query 963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNNNCTAATATGAGCCCT				1022
Sbjct 6330	CTGACTGGCAACACTCCACGGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT				6389
Query 1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC				1082
Sbjct 6390	AGGCTTTATTCCTATTACAGTAGGAGGCTTAACCGGTATTATCCTAGCCAACTCATC				6449
Query 1083	CCTAGACATYATTCTCCACGACACATAYTATGTTGACATTCCACTATGACTCTC				1142
Sbjct 6450	CTTAGACGTATCTCCACGACACATATTATGTTGACACTCCACTATGCTTTC				6509
Query 1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGTCACGTATTGACTATTTCACT				1202
Sbjct 6510	AATAGGGGCTGTCTCGCCATCATAGGAGGTTGTCACGTACTCCACTATTTCACT				6569
Query 1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNRAA				1262
Sbjct 6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGTTGAA				6629
Query 1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCGYCGATATTCTGA				1322
Sbjct 6630	TGTAACATTCTTCCACAAACACTTCCTCGGTTATCTGAATACCCGTGACTCTGA				6689
Query 1323	TTACCCAGACGCTTACACAACATGAAACACCAATTCAATAGGCTTTCTCACT				1382
Sbjct 6690	TTACCCAGACGCTTACACAACATGAAACACCAATTCAATAGGCTTTCTCACT				6749
Query 1383	RACAGCAGTCATACTAATARTCTTCAATTCTGAGAAGCRTCAGTCCAAACGAGAGGT				1442

Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTGGAGAACGATTCACAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCGGCGTAGACTCACCCATACAAACCTCGAGTGATTAACCGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCGAGCATACATYACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCGAGTGTACATTAACCCAAAAGTGCAAGA	6915

### Delphinapterus leucas isolate S\_20\_04029 mitochondrion, complete genome

Sequence ID: **Q0554303.1** 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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCATACYTACTATT				65
Sbjct 5370	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCCATACYTACTATT				5429
Query 66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCAACGCTTATTAAATTCTGTGCTGAATTAGG				125
Sbjct 5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCCAACGCTTATTCTGTGCTGAATTAGG				5489
Query 126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTAGTAACAGCTCACGC				185
Sbjct 5490	CCAACCTGGCTCACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCACGC				5549
Query 186	CTTCGTAATAATCTCTTATAGTAATGCTTATTATAATTGGGGGTTGGAAACTGACT				245
Sbjct 5550	CTTCGTAATAATCTCTTATAGTAATGCTTATTATAATTGGGGGTTGGAAACTGACT				5609
Query 246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGTCTAAATAACATAAGCTT				305
Sbjct 5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGTCTAAATAACATAAGCTT				5669
Query 306	TTGACTACTTCCTCCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC				365
Sbjct 5670	TTGACTGCTTCCTCCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC				5729
Query 366	AGGCACAGGNTGNACTGTATATNCNCNTTACGAGGAAATCTAGCACATGCAGGAGCCTC				425
Sbjct 5730	AGGCACAGGCTGAACGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGAGCCTC				5789
Query 426	AGTCGACCTKACTATTCTCTACATTTRGCCGGTATCTCAATCCTGGAGCTAT				485
Sbjct 5790	AGTCGACCTKACTATTCTCTACATTCTCGTACATCTAGCCGGTATCTCAATCCTGGGGCTAT				5849
Query 486	CAACTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAACACC				545
Sbjct 5850	CAACTCATTACAACATTATAACATAAAACCACCCGCTATAACCCAATACCAACACC				5909
Query 546	TTTATTTCGTATGATCAGCTTAATTACAGCAATCTACTTCTATTACTACCTGTCTT				605
Sbjct 5910	TTTATTTCGTATGATCAGCTTAATTACAGCACTTACTCTATTACTACCTACCTGTCTT				5969
Query 606	AGCAGCCGAAATTACCATGCTACTAACTGATCGAACCTAAACACAACC---TTCGACCC				662
Sbjct 5970	AGCAGCCGAAATTACCATGCTACTAACTGATCGAACCTAAACACAACCTTTTCGACCC				6029
Query 663	GGCAGGAGGAGGCACCCAGTCCTATCAACACYRTTCTGATTTTGGTCACCCCGA				722
Sbjct 6030	TGCAGGAGGAGGCACCCAGTCCTATCAACACCTATTCTGATTTTGGTCACCCCGA				6089
Query 723	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTAYTC				782
Sbjct 6090	AGTATATATCCTAATTCTACCCGGTTCGGGATAATCTCACATATCGTAACCTACTACTC				6149
Query 783	GGGaaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT				842
Sbjct 6150	GGGAAAAAAAGACCCCTTGGATATATAGGGATGGTGTGGCTATAATTCTATTGGTT				6209
Query 843	CCTGGGTTTCATTGTATGAGCTCACCATATATTACAGTCGGAATAGACGTTGACACACG				902
Sbjct 6210	CCTAGGTTTCATTGTATGAGCTCACCATATATTACAGTCGGAATAGACGTTGACACACG				6269
Query 903	AGCATATTCACATCAGTACCATATTGCTATTCTACAGGRGTAAAAGTCTTAG				962
Sbjct 6270	AGCATATTCACATCAGTACCATATTGCTATTCTACAGGRGTAAAAGTCTTAG				6329
Query 963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNNNNCTAATATGAGCCCT				1022
Sbjct 6330	CTGACTGGCAACACTCCACGGAGGAATATTAAATGATCTCCAGGCCCTAATATGAGCCCT				6389
Query 1023	AGGCTTTATYTTCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC				1082
Sbjct 6390	AGGCTTTATYTTCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC				6449
Query 1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGTA				1142
Sbjct 6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGACACTTCCACTATGTCCTTC				6509
Query 1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTCGCACTGATTYCCACTATTTCA				1202

Sbjct	6510	AATAGGGGCTGTCTCGCCATCATAGGAGGTTCGCCACTGATCCCACATTTCAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATANNNNNNNNTRA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTGTAATCATATTGTAGGTGT	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCCGYCGATATTCTG	1322
Sbjct	6630	TGTAACATTCTTCCACAACACTTCCTCGGTTATCTGAATACCCCGTCGATACTCTG	6689
Query	1323	TTACCCAGACGCTTACACAAACATGAAACACCATTCTCAATAGGCTTTCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAAACATGAAACACCATTCTCAATAGGCTTTCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCAATTCTGAGAAGCRTTCGCATCCAAACGAGAG	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCAATTGAGAAGCATTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATAACAAACCTCGAGTGATNAAACNGATGTCCTCCACC	1502
Sbjct	6810	GTCCGGTAGATCTCACCCATACAAACCTCGAGTGATTAACGGATGTCCTCCACC	6869
Query	1503	TCATACATTGAGAACCAAGCAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAGAACCAAGTGTACATTAACCCAAAAGTGCAAGA	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	CATAAACCGATGACTATTCTCTACCAATCACAAGGACATTGGCACCTATACYTACTATT			5429
Query	66	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTAAATTCTGCTGAATTAGG			125
Sbjct	5430	TGGTGCCTGAGCAGGAATAGTAGGCACCGGCTAACGCTTATTCTGCTGAATTAGG			5489
Query	126	CCAACCTGGCACACTTATTGGAGACGACCAAATYTATAATGTTTAGTAACAGCTCACGC			185
Sbjct	5490	CCAACCTGGCTACTTATTGGAGACGACCAAATTATAACGTACTAGTAACAGCCCCACGC			5549
Query	186	CTTCGTAATAATCTCTTATAGTAATGCCATTATAATTGGGGGTTGGAAACTGACT			245
Sbjct	5550	CTTCGTAATAATCTCTTATAGTAATGCCATTATAATTGGGGGTTGGAAACTGACT			5609
Query	246	WGTCCCTTAATAATCGGAGCCCCGAYATGGCTTCCCTCGCTAAATAACATAAGCTT			305
Sbjct	5610	TGTCCCTTAATAATCGGAGCCCCGACATGGCTTCCCTCGCTAAATAACATAAGCTT			5669
Query	306	TTGACTACTCCCTCCTTCCACTATTAAATAGCGTCTCAATAGTTGAAGCCGGCGC			365
Sbjct	5670	TTGACTGCTCCCTCCTTCCACTACTAAATAGCATCCTCAATAGTTGAAGCCGGCGC			5729
Query	366	AGGCACAGGNTGNACTGTATNCNCNTTAGCAGGAAATCTAGCACATGCAGGAGCCTC			425
Sbjct	5730	AGGCACAGGCTGAAGTGTACCCCCCTAGCAGGAAATCTAGCACATGCAGGAGCCTC			5789
Query	426	AGTCGACCTKACTATTTCTCTACATTTRGCCGGCTATCTCAATCCTCGGAGCTAT			485
Sbjct	5790	AGTCGACCTACTATTTCTCTACATCTAGCCGGCTATCTCAATCCTCGGGCTAT			5849
Query	486	CAACTTCATTACAACATTAAACATAAAACCACCCGCTATAACCCAAATACCAAAACACC			545
Sbjct	5850	CAACTTCATTACAACATTAAACATAAAACCACCCGCTATAACCCAAATACCAAAACACC			5909
Query	546	TTTATTCTGATGACTAGCTTAATTACAGCAATTCTACTTCTATTACTACCTGTCCT			605
Sbjct	5910	TTTATTCTGATGACTAGCTTAATTACAGCAATTCTACTTCTATTACTACCTGTCCT			5969
Query	606	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACC---TTCGACCC			662
Sbjct	5970	AGCAGCCGGAATTACCATGCTACTAACTGATCGAAACCTAAACACAACCTTTTCGACCC			6029
Query	663	GGCAGGAGGAGGCACCCAGTCCTATATCAACACYRTTCTGATTTTGGTCACCCCGA			722
Sbjct	6030	TGCAGGAGGAGGCACCCAGTCCTATATCAACACCTATTCTGATTTTGGTCACCCCGA			6089
Query	723	AGTATATATCCTAATTCTACCCGGTTTGGGATAATCTCACATATCGTAACCTACTAYTC			782
Sbjct	6090	AGTATATATCCTAATTCTACCCGGTTTGGGATAATCTCACATATCGTAACCTACTTC			6149
Query	783	GGGaaaaaaaaGAACCYTTGGATATATGGGATRGTGTGGCTATAGTTCTATTGGTT			842
Sbjct	6150	GGGaaaaaaaaAGAGCCCTTGGATATATGGGATGGTGTGGCTATAATTCTATTGGTT			6209
Query	843	CCTGGGTTTCATTGTATGAGCTACCATATATTACAGTCGGAATAGACGTTGACACACG			902
Sbjct	6210	CCTAGGTTTCATTGTATGAGCTACCATATATTACAGTCGGAATAGACGTTGACACACG			6269
Query	903	AGCATATTCACATCAGCTACCATATTGCTATTCTACAGGRGTAAGTCTTTAG			962

Sbjct	6270	AGCATATTACATCAGCTACCATAATTGCTATTCCCACAGGGTAAAGCTTTAG	6329
Query	963	CTGACTGGCAACCCCTCCACGGAGGAATANNNNNNNNNNNNCTAATATGAGCCCT	1022
Sbjct	6330	CTGACTGGCAACACTCCACCGAGGAATATTAAATGATCTCCAGCCCTAATATGAGCCCT	6389
Query	1023	AGGCTTTATYTCCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	1082
Sbjct	6390	AGGCTTTATTCCTATTACAGTAGGAGGCTAACCGGTATTATCCTAGCCAACTCATC	6449
Query	1083	CCTAGACATYATTCTCCACGACACATAYTATGTAGTTGCACATTCCACTATGTACTCTC	1142
Sbjct	6450	CTTAGACGTATCCTCCACGACACATATTATGTAGTCGCACACTCCACTATGTGCTTC	6509
Query	1143	AATRGGAGCTGTCTTGCCATCATAGGAGGCTTCGTCACGTATTYCCACTATTCAGG	1202
Sbjct	6510	AATAGGGCTGTCTCGCCATCATAGGAGGTTCGTCCACTGATTCCCACATTTCAAGG	6569
Query	1203	GTATACACTCAATTCAACATGGACAAAAACTCAATTCTGAATCATANNNNNNNNNTRAA	1262
Sbjct	6570	TTATACACTCAATTCAACATGGACAAAAACTCAATTCTGAATCATATTCTGAAGGTGTGAA	6629
Query	1263	CGTGACATTCTTCCACARCACTTCTCGGTCTATCTGAATACCCCGYCGATATTCTGA	1322
Sbjct	6630	TGTAACATTCTTCCACAACACTTCCTCGGTTATCTGAATACCCGTGATACTCTGA	6689
Query	1323	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	1382
Sbjct	6690	TTACCCAGACGCTTACACAACATGAAACACCATTCTCATCAATAGGCTCTTCATCTCACT	6749
Query	1383	RACAGCAGTCATACTAATARTCTTCATTCTGAGAAGCRTTCGCATCCAAACGAGAGGT	1442
Sbjct	6750	AACAGCAGTCATACTTATAGTCTTCATTCTGAGAAGCATTGATCCAAACGAGAAGT	6809
Query	1443	ATTAACAGTGGATCTCATCTATAACAAACCTCGAGTGATNAAACNGATGTCCTCCACCATA	1502
Sbjct	6810	GTCCCGGGTAGATCTCACCCATACAAACCTCGAGTGATTAACCGATGTCCTCCACCATA	6869
Query	1503	TCATACATTGAAGAACCAAGCATACATYAACCCAAAAGGTGCAAGA	1548
Sbjct	6870	TCATACATTGAAGAACCAAGGTGACATTAACCCAAAAGTGCAAGA	6915

## Taxonomy

### Reports

- Lineage

Organism	Blast Name	Score	Number of Hits	Description
<a href="#">Delphinapterus leucas</a>	<a href="#">whales &amp; dolphins</a>	2265	100	<a href="#">Delphinapterus leucas hits</a>

- Organism

Description	Score	E value	Accession
Delphinapterus leucas (beluga whale) [whales & dolphins]			
<a href="#">Delphinapterus leucas isolate S_20_01444 mitochondrion, complete genome</a>	2265	0.0	<a href="#">Q554110</a>
<a href="#">Delphinapterus leucas isolate DL0776 mitochondrion, complete genome</a>	2265	0.0	<a href="#">MW316132</a>
<a href="#">Delphinapterus leucas isolate S_20_04130 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554323</a>
<a href="#">Delphinapterus leucas isolate S_20_04119 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554319</a>
<a href="#">Delphinapterus leucas isolate S_20_04108 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554317</a>
<a href="#">Delphinapterus leucas isolate S_20_04103 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554316</a>
<a href="#">Delphinapterus leucas isolate S_20_04096 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554315</a>
<a href="#">Delphinapterus leucas isolate S_20_04091 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554313</a>
<a href="#">Delphinapterus leucas isolate S_20_04088 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554312</a>
<a href="#">Delphinapterus leucas isolate S_20_04087 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554311</a>
<a href="#">Delphinapterus leucas isolate S_20_04076 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554310</a>
<a href="#">Delphinapterus leucas isolate S_20_04063 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554309</a>
<a href="#">Delphinapterus leucas isolate S_20_04048 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554307</a>
<a href="#">Delphinapterus leucas isolate S_20_04029 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554303</a>
<a href="#">Delphinapterus leucas isolate S_20_03996 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554297</a>
<a href="#">Delphinapterus leucas isolate S_20_03992 mitochondrion, complete genome</a>	2259	0.0	<a href="#">Q554296</a>



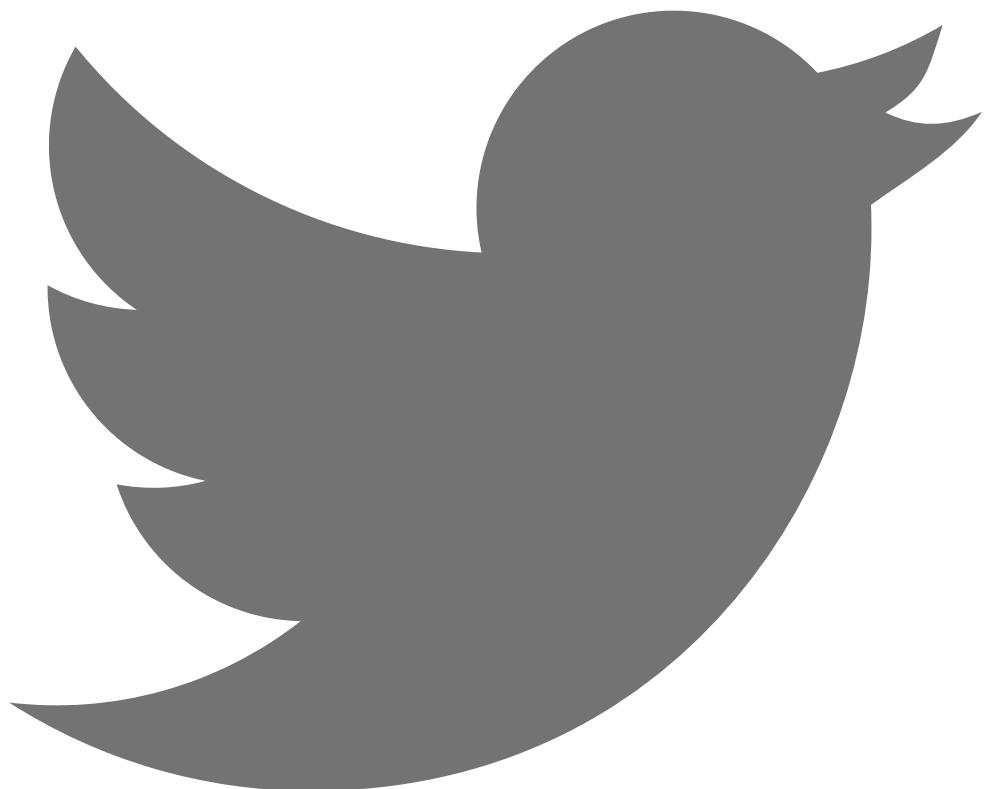
Description	Score	E value	Accession
<a href="#">Delphinapterus leucas isolate S_20_02016 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554178</a>
<a href="#">Delphinapterus leucas isolate S_20_01998 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554177</a>
<a href="#">Delphinapterus leucas isolate S_20_01968 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554176</a>
<a href="#">Delphinapterus leucas isolate S_20_01935 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554175</a>
<a href="#">Delphinapterus leucas isolate S_20_01883 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554173</a>
<a href="#">Delphinapterus leucas isolate S_20_01750 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554155</a>
<a href="#">Delphinapterus leucas isolate S_20_01743 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554153</a>
<a href="#">Delphinapterus leucas isolate S_20_01734 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554151</a>
<a href="#">Delphinapterus leucas isolate S_20_01705 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554148</a>
<a href="#">Delphinapterus leucas isolate S_20_01699 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554147</a>
<a href="#">Delphinapterus leucas isolate S_20_01612 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554144</a>
<a href="#">Delphinapterus leucas isolate S_20_01597 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554143</a>
<a href="#">Delphinapterus leucas isolate S_20_01594 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554142</a>
<a href="#">Delphinapterus leucas isolate S_20_01590 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554141</a>
<a href="#">Delphinapterus leucas isolate S_20_01580 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554140</a>
<a href="#">Delphinapterus leucas isolate S_20_01574 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554139</a>
<a href="#">Delphinapterus leucas isolate S_20_01567 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554138</a>
<a href="#">Delphinapterus leucas isolate S_20_01562 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554137</a>
<a href="#">Delphinapterus leucas isolate S_20_01555 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554135</a>
<a href="#">Delphinapterus leucas isolate S_20_01553 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554134</a>
<a href="#">Delphinapterus leucas isolate S_20_01546 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554132</a>
<a href="#">Delphinapterus leucas isolate S_20_01539 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554131</a>
<a href="#">Delphinapterus leucas isolate S_20_01530 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554130</a>
<a href="#">Delphinapterus leucas isolate S_20_01516 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554128</a>
<a href="#">Delphinapterus leucas isolate S_20_01514 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554127</a>
<a href="#">Delphinapterus leucas isolate S_20_01507 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554125</a>
<a href="#">Delphinapterus leucas isolate S_20_01494 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554124</a>
<a href="#">Delphinapterus leucas isolate S_20_01489 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554123</a>
<a href="#">Delphinapterus leucas isolate S_20_01487 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554122</a>
<a href="#">Delphinapterus leucas isolate S_20_01486 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554121</a>
<a href="#">Delphinapterus leucas isolate S_20_01482 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554120</a>
<a href="#">Delphinapterus leucas isolate S_20_01480 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554119</a>
<a href="#">Delphinapterus leucas isolate S_20_01466 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554116</a>
<a href="#">Delphinapterus leucas isolate S_20_01465 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554115</a>
<a href="#">Delphinapterus leucas isolate S_20_01463 mitochondrion, complete genome</a>	2259	0.0	<a href="#">QQ554114</a>
<a href="#">Delphinapterus leucas isolate S_20_03538 mitochondrion, complete genome</a>	2252	0.0	<a href="#">QQ554236</a>

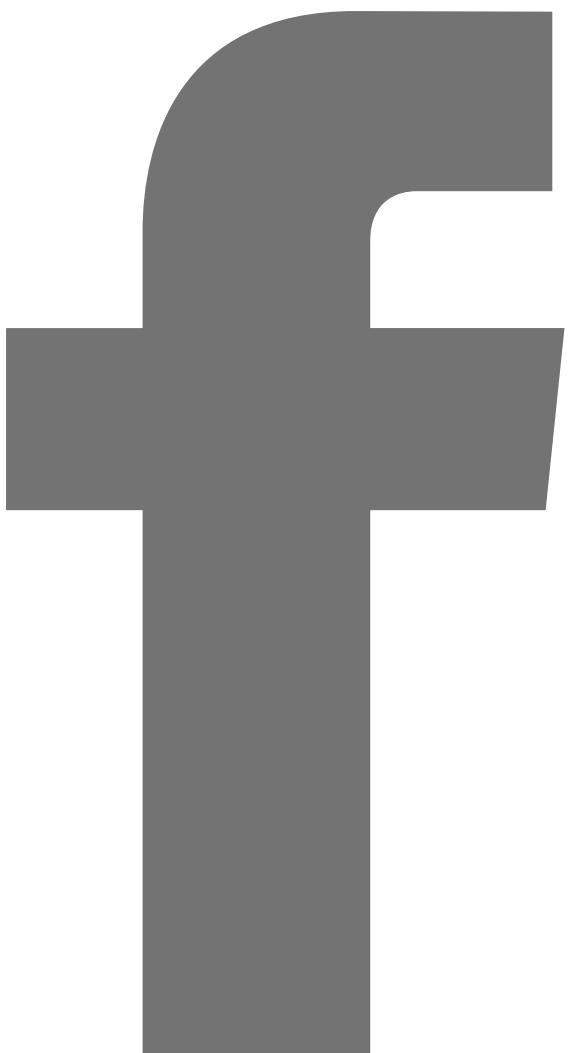
- **Taxonomy**

Taxonomy	Number of hits	Number of Organisms	Description
<a href="#">Delphinapterus leucas</a>	100	1	<a href="#">Delphinapterus leucas hits</a>

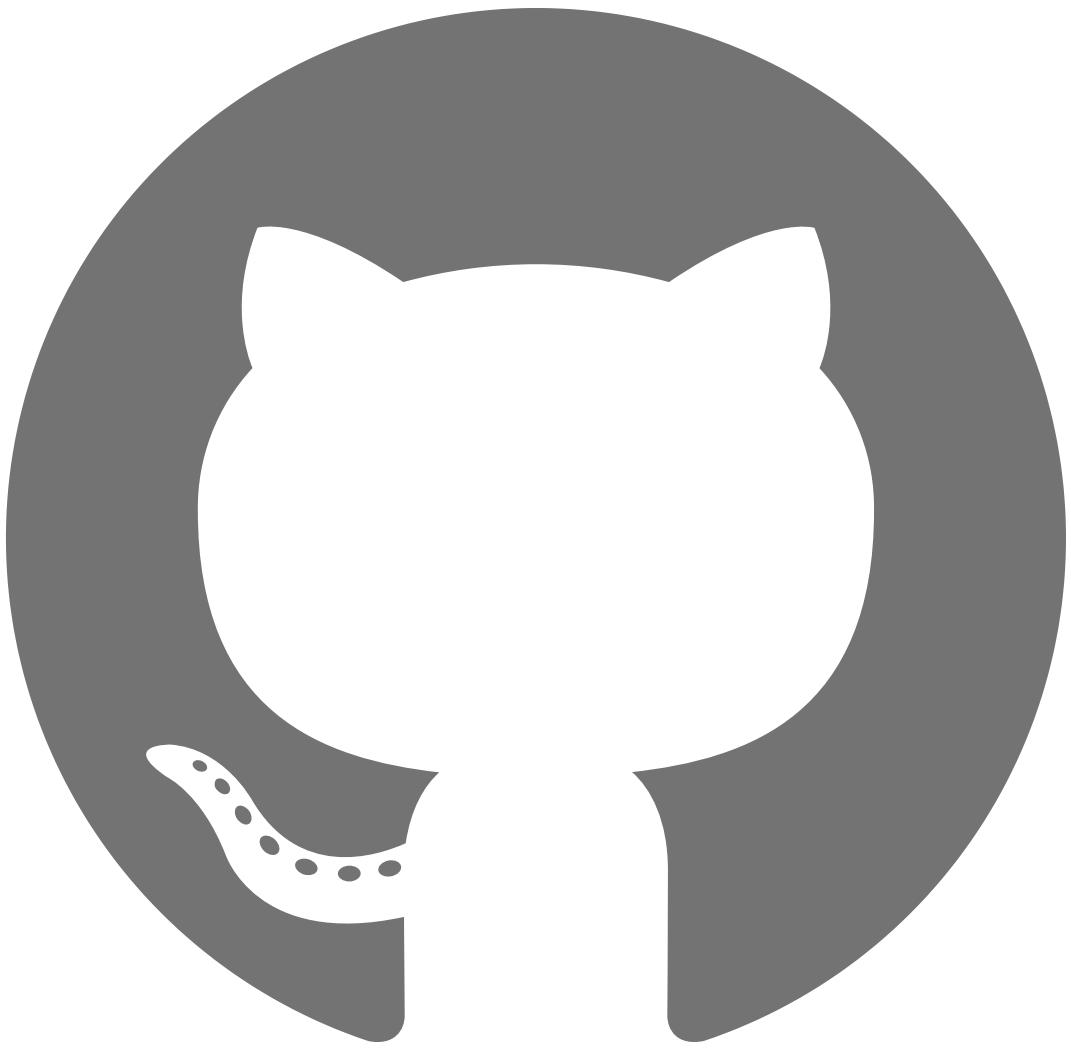
Top

Follow NCBI











Connect with NLM

National Library of Medicine  
8600 Rockville Pike  
Bethesda, MD 20894

[Web Policies](#)  
[FOIA](#)  
[HHS Vulnerability Disclosure](#)

[Help](#)  
[Accessibility](#)  
[Careers](#)

- [NLM](#)
- [NIH](#)
- [HHS](#)
- [USA.gov](#)