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**BLAST**<sup>®</sup> >> **blastn suite** >> results for RID-KE6UZZ21014

Job Title	<a href="#">Nucleotide Sequence ...</a>
RID	<a href="#">KE6UZZ21014</a> Search expires on 12-10 01:39 am
Program	BLASTN
Database	nt
Query ID	Id Query_6557803
Description	<a href="#">None ...</a>
Molecule type	dna
Query Length	1551

**Descriptions**

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_44460 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1912	2487	93%	0.0	97.79%	16386	<a href="#">OP205215.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43855 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1912	2487	93%	0.0	97.79%	16386	<a href="#">OP205204.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_28432 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1912	2491	93%	0.0	97.79%	16386	<a href="#">OP205199.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_13192 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1912	2487	93%	0.0	97.79%	16386	<a href="#">OP205194.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_7966 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1912	2491	93%	0.0	97.79%	16386	<a href="#">OP205193.1</a>
<a href="#">Eubalaena japonica mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1912	2491	93%	0.0	97.79%	16386	<a href="#">NC_006931.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43867 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1906	2476	93%	0.0	97.69%	16387	<a href="#">OP205212.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43866 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1906	2476	93%	0.0	97.69%	16387	<a href="#">OP205211.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43858 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1906	2476	93%	0.0	97.69%	16387	<a href="#">OP205206.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43853 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1906	2485	93%	0.0	97.69%	16387	<a href="#">OP205203.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43851 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1906	2480	93%	0.0	97.69%	16387	<a href="#">OP205202.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43860 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1901	2476	93%	0.0	97.60%	16387	<a href="#">OP205207.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43850 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1901	2480	93%	0.0	97.60%	16387	<a href="#">OP205201.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43849 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1901	2480	93%	0.0	97.60%	16387	<a href="#">OP205200.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_7963 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1901	2480	93%	0.0	97.60%	16387	<a href="#">OP205192.1</a>

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_62934 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1895	2460	93%	0.0	97.51%	16386	<a href="#">OP205218.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43870 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1895	2460	93%	0.0	97.51%	16386	<a href="#">OP205213.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43865 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1895	2463	93%	0.0	97.51%	16386	<a href="#">OP205210.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43856 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1895	2460	93%	0.0	97.51%	16386	<a href="#">OP205205.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_28430 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1895	2460	93%	0.0	97.51%	16386	<a href="#">OP205198.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_28428 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1895	2460	93%	0.0	97.51%	16386	<a href="#">OP205197.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_53766 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1890	2454	93%	0.0	97.42%	16386	<a href="#">OP205217.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_23634 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1890	2454	93%	0.0	97.42%	16386	<a href="#">OP205196.1</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_23631 mitochondrion, complete genome</a>	<a href="#">Eubalaena japonica</a>	1890	2458	93%	0.0	97.42%	16386	<a href="#">OP205195.1</a>
<a href="#">Eubalaena glacialis mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2458	93%	0.0	97.32%	16387	<a href="#">MF459656.1</a>
<a href="#">Eubalaena glacialis isolate SWFSC_MMASTR_28311 mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2458	93%	0.0	97.32%	16387	<a href="#">OP205191.1</a>
<a href="#">Eubalaena glacialis isolate SWFSC_MMASTR_15112 mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2454	93%	0.0	97.32%	16387	<a href="#">OP205190.1</a>
<a href="#">Eubalaena glacialis isolate SWFSC_MMASTR_4977 mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2454	93%	0.0	97.32%	16387	<a href="#">OP205189.1</a>
<a href="#">Eubalaena glacialis isolate Egl20Feb10B mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2458	93%	0.0	97.32%	16387	<a href="#">OP205187.1</a>
<a href="#">Eubalaena glacialis isolate Egl17Feb07A mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2454	93%	0.0	97.32%	16387	<a href="#">OP205185.1</a>
<a href="#">Eubalaena glacialis isolate Egl10Jan08G</a>	<a href="#">Eubalaena glacialis</a>	1884	2458	93%	0.0	97.32%	16387	<a href="#">OP205184.1</a>

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">mitochondrion, complete genome</a>								
<a href="#">Eubalaena glacialis isolate Egl08Feb09B_gDNA mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1884	2454	93%	0.0	97.32%	16387	<a href="#">OP205183.1</a>
<a href="#">Eubalaena australis isolate Eaus0550m_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1884	2454	93%	0.0	97.32%	16385	<a href="#">OP205174.1</a>
<a href="#">Eubalaena australis isolate Eaus06GNJ_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1884	2454	93%	0.0	97.32%	16386	<a href="#">OP205169.1</a>
<a href="#">Eubalaena glacialis isolate Eg#1014 'Staccato' cytochrome oxidase subunit I (cox1) gene, complete cds; mitochondrial</a>	<a href="#">Eubalaena glacialis</a>	1884	2458	93%	0.0	97.32%	1551	<a href="#">DQ095154.1</a>
<a href="#">Eubalaena glacialis isolate Egl021Feb07B mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1879	2449	93%	0.0	97.23%	16387	<a href="#">OP205188.1</a>
<a href="#">Eubalaena glacialis isolate Egl020Feb07B mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1879	2452	93%	0.0	97.23%	16387	<a href="#">OP205186.1</a>
<a href="#">Eubalaena glacialis isolate Egl02Feb09D mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1879	2452	93%	0.0	97.23%	16387	<a href="#">OP205181.1</a>
<a href="#">Eubalaena australis isolate Eaus06132m_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1879	2452	93%	0.0	97.23%	16385	<a href="#">OP205177.1</a>
<a href="#">Eubalaena australis isolate Eaus09AI105_AI mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1879	2443	93%	0.0	97.23%	16386	<a href="#">OP205172.1</a>
<a href="#">Eubalaena australis isolate Eaus06GNA_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1879	2449	93%	0.0	97.23%	16386	<a href="#">OP205168.1</a>
<a href="#">Eubalaena australis isolate EA123 cytochrome oxidase subunit I (cox1) gene, complete cds; mitochondrial</a>	<a href="#">Eubalaena australis</a>	1879	2452	93%	0.0	97.23%	1551	<a href="#">DQ095155.1</a>
<a href="#">Eubalaena australis isolate Eaus06138m_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1873	2437	93%	0.0	97.14%	16386	<a href="#">OP205178.1</a>
<a href="#">Eubalaena australis isolate Eaus0587m_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1868	2437	93%	0.0	97.05%	16387	<a href="#">OP205175.1</a>
<a href="#">Eubalaena glacialis mitochondrion, complete genome</a>	<a href="#">Eubalaena glacialis</a>	1862	2436	93%	0.0	96.96%	16386	<a href="#">NC_037444.1</a>
<a href="#">Eubalaena australis isolate Eaus06129m_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1862	2432	93%	0.0	96.96%	16386	<a href="#">OP205176.1</a>
<a href="#">Eubalaena australis isolate Eaus058SA_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1862	2436	93%	0.0	96.96%	16386	<a href="#">OP205173.1</a>
<a href="#">Eubalaena australis isolate Eaus07AI065_AI</a>	<a href="#">Eubalaena australis</a>	1862	2436	93%	0.0	96.96%	16386	<a href="#">OP205170.1</a>

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">mitochondrion, complete genome</a>								
<a href="#">Eubalaena australis isolate Eaus06A1_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1862	2436	93%	0.0	96.96%	16386	<a href="#">OP205167.1</a>
<a href="#">Eubalaena australis isolate Eaus03K1_Arg mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1862	2432	93%	0.0	96.96%	16386	<a href="#">OP205166.1</a>
<a href="#">Eubalaena australis mitochondrion, complete genome</a>	<a href="#">Eubalaena australis</a>	1862	2436	93%	0.0	96.96%	16385	<a href="#">NC_006930.1</a>
<a href="#">Eubalaena australis isolate EA604 cytochrome oxidase subunit I (cox1) gene, complete cds; mitochondrial</a>	<a href="#">Eubalaena australis</a>	1857	2430	93%	0.0	96.86%	1551	<a href="#">DQ095156.1</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43197 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1746	2247	93%	0.0	95.02%	16389	<a href="#">MN145938.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50790 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1746	2247	93%	0.0	95.02%	16390	<a href="#">MZ618258.1</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43194 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2247	93%	0.0	94.93%	16389	<a href="#">MN124685.1</a>
<a href="#">Balaena mysticetus voucher PMO 234.423 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16391	<a href="#">MN159085.1</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43206 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MN159084.1</a>
<a href="#">Balaena mysticetus voucher PMO 234.429 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MN159082.1</a>
<a href="#">Balaena mysticetus voucher PMO 234.522 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MN159081.1</a>
<a href="#">Balaena mysticetus voucher PMO 234.573 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">MN159080.1</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43191 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MN145939.1</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43195 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MN145937.1</a>
<a href="#">Balaena mysticetus isolate QT3_Qeqertassussuk mitochondrion, partial genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16382	<a href="#">MH198022.1</a>
<a href="#">Balaena mysticetus isolate H mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">KY026773.1</a>
<a href="#">Balaena mysticetus isolate I mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026772.1</a>

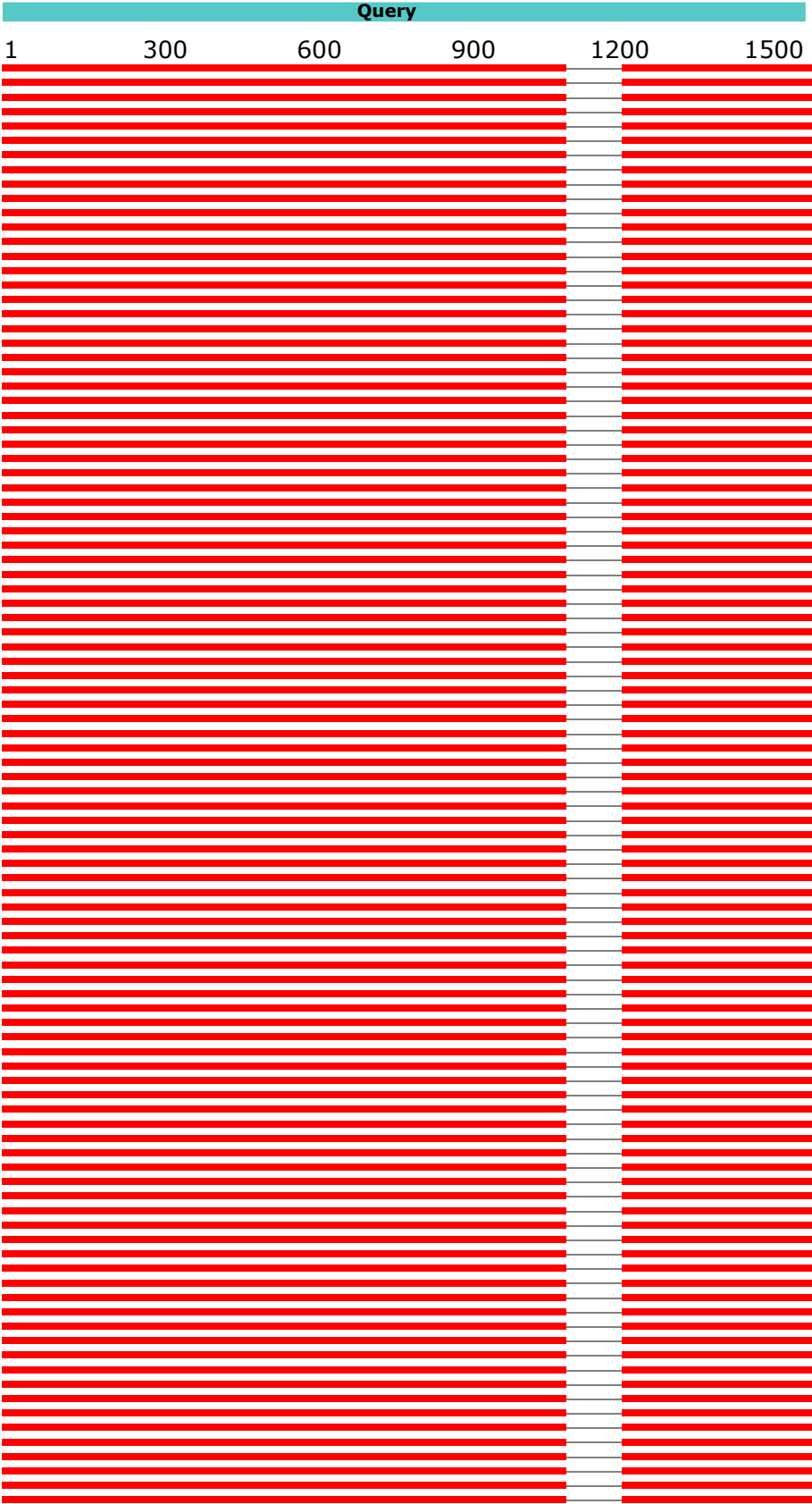
Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">Balaena mysticetus isolate F mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026771.1</a>
<a href="#">Balaena mysticetus isolate E mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026770.1</a>
<a href="#">Balaena mysticetus isolate D mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026769.1</a>
<a href="#">Balaena mysticetus isolate C mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026768.1</a>
<a href="#">Balaena mysticetus isolate B mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026767.1</a>
<a href="#">Balaena mysticetus isolate A mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">KY026766.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 112407 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2236	93%	0.0	94.93%	16390	<a href="#">MZ618260.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50788 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618257.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50787 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">MZ618256.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50785 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618254.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 44672 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618253.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 18978 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618252.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 18972 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618251.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 18971 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618250.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 17876 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618248.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 17875 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618247.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 17874 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618246.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 7095 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618245.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 7094 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MZ618244.1</a>

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<a href="#">Balaena mysticetus isolate 17-05 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">MT649195.1</a>
<a href="#">Balaena mysticetus isolate 17-08 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">MT649194.1</a>
<a href="#">Balaena mysticetus isolate 17-12 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">MT649193.1</a>
<a href="#">Balaena mysticetus isolate 17-21 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2236	93%	0.0	94.93%	16390	<a href="#">MT649192.1</a>
<a href="#">Balaena mysticetus isolate 17-20 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">MT649191.1</a>
<a href="#">Balaena mysticetus isolate 17-18 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MT649190.1</a>
<a href="#">Balaena mysticetus isolate 17-17 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MT649189.1</a>
<a href="#">Balaena mysticetus isolate 17-10 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MT649188.1</a>
<a href="#">Balaena mysticetus isolate 17-07 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MT649187.1</a>
<a href="#">Balaena mysticetus isolate 18-06 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">MT649186.1</a>
<a href="#">Balaena mysticetus mitochondrial DNA, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16389	<a href="#">AP006472.1</a>
<a href="#">Balaena mysticetus mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1740	2242	93%	0.0	94.93%	16390	<a href="#">NC_005268.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50797 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1735	2236	93%	0.0	94.83%	16390	<a href="#">MZ618259.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50786 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1735	2236	93%	0.0	94.83%	16389	<a href="#">MZ618255.1</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 1266 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1735	2236	93%	0.0	94.83%	16389	<a href="#">MZ618243.1</a>
<a href="#">Balaena mysticetus isolate 17-19 mitochondrion, complete genome</a>	<a href="#">Balaena mysticetus</a>	1735	2236	93%	0.0	94.83%	16391	<a href="#">MT649196.1</a>

Graphic Summary



Distribution of the top 200 Blast Hits on 100 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

Eubalaena japonica isolate SWFSC\_MMASTR\_44460 mitochondrion, complete genome  
Sequence ID: **OP205215.1** Length: 16386 Number of Matches: 2  
Range 1: 5361 to 6444

Score	Expect	Identities	Gaps	Strand	Frame
1912 bits(1035)	0.0()	1060/1084(98%)	0/1084(0%)	Plus/Plus	
Query 1	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA	60			
Sbjct 5361	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA	5420			
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA	120			

Sbjct	5421	TTATTTGGCGCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA	5480
Query	121	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC	180
Sbjct	5481	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC	5540
Query	181	CACGCCTTTGTAATAATCTTCTTCATAGTAATACCCATTATAATCGGTGGATTTGGAAAC	240
Sbjct	5541	CACGCCTTTGTAATAATCTTCTTCATAGTAATACCCATTATAATCGGTGGATTTGGAAAC	5600
Query	241	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA	300
Sbjct	5601	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA	5660
Query	301	AGCTTCTGACTACTCCCTCCTTCTTTCTACTACTAATAGCATCCTCAATGGTCNNNNNN	360
Sbjct	5661	AGCTTCTGACTACTCCCTCCTTCTTTCTACTACTAATAGCATCCTCAATGGTCGAAGCC	5720
Query	361	NNNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGGAACCTAGCACATGCAGGA	420
Sbjct	5721	GGTGCAGGCACAGGCTGAACTGTATATCCCCCTCTAGCCGGAACCTAGCACATGCAGGA	5780
Query	421	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA	480
Sbjct	5781	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA	5840
Query	481	GCCATTAACTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA	540
Sbjct	5841	GCCATTAACTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA	5900
Query	541	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT	600
Sbjct	5901	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT	5960
Query	601	GTCTTAGCAGCTGGAATCACCATGCTATTAAGTGACCGAAACCTAAATACAACCTTTCTTC	660
Sbjct	5961	GTCTTAGCAGCTGGAATCACCATGCTATTAAGTGACCGAAACCTAAATACAACCTTTCTTC	6020
Query	661	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC	720
Sbjct	6021	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC	6080
Query	721	CCTGAAGTATATATCTTAATCTCCCTGGGTTCGGAATAATTCACACATTGTGACTTAT	780
Sbjct	6081	CCTGAAGTATATATCTTAATCTCCCTGGGTTCGGAATAATTCACACATTGTGACTTAT	6140
Query	781	TACTCAGGaaaaaaaGATCCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	840
Sbjct	6141	TACTCAGGAAAAAAAAAGAACCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	6200
Query	841	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC	900
Sbjct	6201	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC	6260
Query	901	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC	960
Sbjct	6261	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC	6320
Query	961	TTCAGTTGATTAGCAAACTCCACGGAGGCAACATTAAATGNTCTCCTGCCCTAATATGA	1020
Sbjct	6321	TTCAGTTGATTAGCAAACTCCACGGAGGCAACATTAAATGATCTCCTGCCCTAATATGA	6380
Query	1021	GCCCTAGGCTTNNNNNNNNNTTTCACAGTAGGTGGTCTAACAGGCATCGTCTGGCCAAC	1080
Sbjct	6381	GCCCTAGGCTTCATCTTCCTTTTCACAGTAGGTGGTCTAACAGGCATCGTCTGGCCAAC	6440
Query	1081	TCAT 1084	
Sbjct	6441	TCAT 6444	

Range 2: 6551 to 6911

Score	Expect	Identities	Gaps	Strand	Frame
575 bits(311)	3e-158()	336/361(93%)	0/361(0%)	Plus/Plus	
Query	1191	CCCGCTATTCTCAGGGTACACGCTTAACTCAACATGAACAAAAATTCACTTTATAATCAT	1250		
Sbjct	6551	CCCGCTATTCTCAGGGTACACGCTTAACTCAACATGAACAAAAATTCACTTTATAATCAT	6610		
Query	1251	ATTCGTAGGCGTAAACCTAACATTCTTCCCACNNNNNNNNNNNNNNNNNNNNNATACC	1310		
Sbjct	6611	ATTCGTAGGCGTAAACCTAACATTCTTCCCACAACACTTCTTAGGTCTATCCGGTATACC	6670		
Query	1311	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG	1370		
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG	6730		
Query	1371	CTCATTCATCTCATTAAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTTCG	1430		
Sbjct	6731	CTCATTCATCTCATTAAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTNGC	6790		
Query	1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNNCCTTGAATGATTAAACGG	1490		
Sbjct	6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTTGAATGATTAAACGG	6850		
Query	1491	ATGTCCCCCACCATACCCACACATTGGAAGAACCCGCATACATCAACCCAAAATGATCAAG	1550		
Sbjct	6851	ATGTCCCCCACCATACCCACACATTGGAAGAACCCGCATACATCAACCCAAAATGATCAAG	6910		
Query	1551	A 1551			

Eubalaena japonica isolate SWFSC\_MMSTR\_43855 mitochondrion, complete genome  
Sequence ID: **OP205204.1** Length: 16386 Number of Matches: 2  
Range 1: 5361 to 6444

Score	Expect	Identities	Gaps	Strand	Frame
1912 bits(1035)	0.0()	1060/1084(98%)	0/1084(0%)	Plus/Plus	
Query 1	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA	60			
Sbjct 5361	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA	5420			
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA	120			
Sbjct 5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA	5480			
Query 121	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC	180			
Sbjct 5481	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC	5540			
Query 181	CACGCCTTTGTAATAATCTTCTCATAGTAATACCCATTATAATCGGTGGATTTGGAAC	240			
Sbjct 5541	CACGCCTTTGTAATAATCTTCTCATAGTAATACCCATTATAATCGGTGGATTTGGAAC	5600			
Query 241	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA	300			
Sbjct 5601	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA	5660			
Query 301	AGCTTCTGACTACTCCCTCCTTCTTCTACTACTAATAGCATCCTCAATGGTCNNNNN	360			
Sbjct 5661	AGCTTCTGACTACTCCCTCCTTCTTCTACTACTAATAGCATCCTCAATGGTCGAAGCC	5720			
Query 361	NNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGGAACCTAGCACATGCAGGA	420			
Sbjct 5721	GGTGCAGGCACAGGCTGAAGTGTATATCCCCCTCTAGCCGGAACCTAGCACATGCAGGA	5780			
Query 421	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA	480			
Sbjct 5781	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA	5840			
Query 481	GCCATTAACTTTATCACAACTATCATTAACATAAAACCACCTGCCATAACCCAATACCAA	540			
Sbjct 5841	GCCATTAACTTTATCACAACTATCATTAACATAAAACCACCTGCCATAACCCAATACCAA	5900			
Query 541	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT	600			
Sbjct 5901	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT	5960			
Query 601	GTCTTAGCAGCTGGAATCACCATGCTATTAAGTACCAGAAACCTAAATACAACCTTCTTC	660			
Sbjct 5961	GTCTTAGCAGCTGGAATCACCATGCTATTAAGTACCAGAAACCTAAATACAACCTTCTTC	6020			
Query 661	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC	720			
Sbjct 6021	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC	6080			
Query 721	CCTGAAGTATATATCTTAATCCTCCCTGGGTTTCGGAATAATTCACACATTGTGACTTAT	780			
Sbjct 6081	CCTGAAGTATATATCTTAATCCTCCCTGGGTTTCGGAATAATTCACACATTGTGACTTAT	6140			
Query 781	TACTCAGGaaaaaaGATCCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	840			
Sbjct 6141	TACTCAGGAAAAAAGAACCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	6200			
Query 841	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC	900			
Sbjct 6201	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC	6260			
Query 901	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC	960			
Sbjct 6261	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC	6320			
Query 961	TTCAGTTGATTAGCAAACTCCACGGAGGCAACATTAAATGNTCTCCTGCCCTAATATGA	1020			
Sbjct 6321	TTCAGTTGATTAGCAAACTCCACGGAGGCAACATTAAATGATCTCCTGCCCTAATATGA	6380			
Query 1021	GCCCTAGGCTTNNNNNNNNNTTCACAGTAGGTGGTCTAACAGGCATCGTCCTGGCCAAC	1080			
Sbjct 6381	GCCCTAGGCTTCATCTTCTTTTCACAGTAGGTGGTCTAACAGGCATCGTCCTGGCCAAC	6440			
Query 1081	TCAT 1084				
Sbjct 6441	TCAT 6444				

Range 2: 6551 to 6911

Score	Expect	Identities	Gaps	Strand	Frame
575 bits(311)	3e-158()	336/361(93%)	0/361(0%)	Plus/Plus	
Query 1191	CCCCTATTCTCAGGGTACACGCTTAAGTCAACATGAACAAAAATCACTTTATAATCAT	1250			

Sbjct	6551	CCCGCTATTCTCAGGGTACACGCTTAACCTCAACATGAACAAAAATTCACTTATAATCAT	6610
Query	1251	ATTTCGTAGGCGTAAACCTAACATTCTTCCCACANNNNNNNNNNNNNNNNNNNATACC	1310
Sbjct	6611	ATTTCGTAGGCGTAAACCTAACATTCTTCCCACAACACTTCTTAGGTCTATCCGGTATACC	6670
Query	1311	TCGACGATACTCCGACTATCCAGACGCTACACAATATGAAATACTATCTCATCAATAGG	1370
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCTACACAATATGAAATACTATCTCATCAATAGG	6730
Query	1371	CTCATTCATCTCATTAAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTGCG	1430
Sbjct	6731	CTCATTCATCTCATTAAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTNGC	6790
Query	1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNCCCTGAATGATTAAACGG	1490
Sbjct	6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTTGAATGATTAAACGG	6850
Query	1491	ATGTCCCCCACCATAACCACACATTGGAAGAACCCGCATACATCAACCCAAAAATGATCAAG	1550
Sbjct	6851	ATGTCCCCCACCATAACCACACATTGGAAGAACCCGCATACATCAACCCAAAAATGATCAAG	6910
Query	1551	A 1551	
Sbjct	6911	A 6911	

Eubalaena japonica isolate SWFSC\_MMASTR\_28432 mitochondrion, complete genome  
Sequence ID: **OP205199.1** Length: 16386 Number of Matches: 2  
Range 1: 5361 to 6444

Score	Expect	Identities	Gaps	Strand	Frame
1912 bits(1035)	0.0()	1060/1084(98%)	0/1084(0%)	Plus/Plus	
Query 1	ATGTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA				60
Sbjct 5361	ATGTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA				5420
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA				120
Sbjct 5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA				5480
Query 121	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC				180
Sbjct 5481	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC				5540
Query 181	CACGCCTTTGTAATAATCTTCTCATAGTAATACCCATTATAATCGGTGGATTGGAAAC				240
Sbjct 5541	CACGCCTTTGTAATAATCTTCTCATAGTAATACCCATTATAATCGGTGGATTGGAAAC				5600
Query 241	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA				300
Sbjct 5601	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA				5660
Query 301	AGCTTCTGACTACTCCCTCCTTCTTCTACTACTAATAGCATCCTCAATGGTCNNNNN				360
Sbjct 5661	AGCTTCTGACTACTCCCTCCTTCTTCTACTACTAATAGCATCCTCAATGGTCGAAGCC				5720
Query 361	NNNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA				420
Sbjct 5721	GGTGCAGGCACAGGCTGAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA				5780
Query 421	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA				480
Sbjct 5781	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA				5840
Query 481	GCCATTAACTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA				540
Sbjct 5841	GCCATTAACTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA				5900
Query 541	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT				600
Sbjct 5901	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT				5960
Query 601	GTCTAGCAGCTGGAATCACCATGCTATTAAGTGACCGAAACCTAAATACAACCTTCTTC				660
Sbjct 5961	GTCTAGCAGCTGGAATCACCATGCTATTAAGTGACCGAAACCTAAATACAACCTTCTTC				6020
Query 661	GACCCTGCAGGTGGAGGAGACCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC				720
Sbjct 6021	GACCCTGCAGGTGGAGGAGACCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC				6080
Query 721	CCTGAAGTATATATCTTAATCTCCCTGGGTTCGGAATAATTTACACATTGTGACTTAT				780
Sbjct 6081	CCTGAAGTATATATCTTAATCTCCCTGGGTTCGGAATAATTTACACATTGTGACTTAT				6140
Query 781	TACTCAGGaaaaaaGATCCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC				840
Sbjct 6141	TACTCAGGAAAAAAGAACCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC				6200
Query 841	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC				900
Sbjct 6201	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC				6260
Query 901	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC				960
Sbjct 6261	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC				6320

Query	961	TTT	1020
Sbjct	6321	TTT	6380
Query	1021	GCCCTAGGCTTNNNNNNNNNTTTCACAGTAGGTGGTCTAACAGGCATCGTCCTGGCCAAC	1080
Sbjct	6381	GCCCTAGGCTTCATCTTCTTTTCACAGTAGGTGGTCTAACAGGCATCGTCCTGGCCAAC	6440
Query	1081	TCAT	1084
Sbjct	6441	TCAT	6444

Range 2: 6551 to 6911

Score	Expect	Identities	Gaps	Strand	Frame
579 bits(313)	2e-159()	337/361(93%)	0/361(0%)	Plus/Plus	
Query	1191	CCCGCTATTCTCAGGGTACACGCTTAACTCAACATGAACAAAAATTCAC			1250
Sbjct	6551	CCCGCTATTCTCAGGGTACACGCTTAACTCAACATGAACAAAAATTCAC			6610
Query	1251	ATTTCGTAGGCGTAAACCTAACATTCTTCCACANNNNNNNNNNNNNNNNNATACC			1310
Sbjct	6611	ATTTCGTAGGCGTAAACCTAACATTCTTCCACAACTTCTTAGGTCTATCCGGTATACC			6670
Query	1311	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG			1370
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG			6730
Query	1371	CTCATTCATCTCATTAAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTTCGC			1430
Sbjct	6731	CTCATTCATCTCATTAAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTTCGC			6790
Query	1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNNCCTTGAATGATTAAACGG			1490
Sbjct	6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTTGAATGATTAAACGG			6850
Query	1491	ATGTCCCCCACCATACCACACATTTCGAAGAACCCGCATACATCAACCCAAAATGATCAAG			1550
Sbjct	6851	ATGTCCCCCACCATACCACACATTTCGAAGAACCCGCATACATCAACCCAAAATGATCAAG			6910
Query	1551	A			1551
Sbjct	6911	A			6911

Eubalaena japonica isolate SWFSC\_MMASTR\_13192 mitochondrion, complete genome  
Sequence ID: **OP205194.1** Length: 16386 Number of Matches: 2  
Range 1: 5361 to 6444

Score	Expect	Identities	Gaps	Strand	Frame
1912 bits(1035)	0.0()	1060/1084(98%)	0/1084(0%)	Plus/Plus	
Query	1	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA			60
Sbjct	5361	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA			5420
Query	61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA			120
Sbjct	5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA			5480
Query	121	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC			180
Sbjct	5481	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC			5540
Query	181	CACGCCTTTGTAATAATCTTCTTCATAGTAATACCCATTATAATCGGTGGATTTGGAAAC			240
Sbjct	5541	CACGCCTTTGTAATAATCTTCTTCATAGTAATACCCATTATAATCGGTGGATTTGGAAAC			5600
Query	241	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA			300
Sbjct	5601	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA			5660
Query	301	AGCTTCTGACTACTCCCTCCTTCTTTCCTACTACTAATAGCATCCTCAATGGTCNNNNN			360
Sbjct	5661	AGCTTCTGACTACTCCCTCCTTCTTTCCTACTACTAATAGCATCCTCAATGGTCGAAGCC			5720
Query	361	NNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGGAACCTAGCACATGCAGGA			420
Sbjct	5721	GGTGCAGGCACAGGCTGAACTGTATATCCCCCTCTAGCCGGAACCTAGCACATGCAGGA			5780
Query	421	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA			480
Sbjct	5781	GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA			5840
Query	481	GCCATTAACCTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA			540
Sbjct	5841	GCCATTAACCTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA			5900
Query	541	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT			600
Sbjct	5901	ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT			5960
Query	601	GTCCTAGCAGCTGGAATCACCATGCTATTAAGTACCGAAACCTAAATACAACCTTCTTC			660

Sbjct	5961	GTCCTAGCAGCTGGAATCACCATGCTATTA	6020
Query	661	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC	720
Sbjct	6021	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC	6080
Query	721	CCTGAAGTATATATCTTAATCCTCCCTGGGTT	780
Sbjct	6081	CCTGAAGTATATATCTTAATCCTCCCTGGGTT	6140
Query	781	TACTCAGGaaaaaaaGATCCTTTCCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	840
Sbjct	6141	TACTCAGGAAAAAAGAACCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	6200
Query	841	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC	900
Sbjct	6201	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC	6260
Query	901	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC	960
Sbjct	6261	ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC	6320
Query	961	TTCAGTTGATTAGCAACTCCACGGAGGCAACATTAAATGNTCTCCTGCCCTAATATGA	1020
Sbjct	6321	TTCAGTTGATTAGCAACTCCACGGAGGCAACATTAAATGATCTCCTGCCCTAATATGA	6380
Query	1021	GCCCTAGGCTTNNNNNNNNNTTTCACAGTAGGTGGTCTAACAGGCATCGTCTGGCCAAC	1080
Sbjct	6381	GCCCTAGGCTTCATCTTCCTTTTTCACAGTAGGTGGTCTAACAGGCATCGTCTGGCCAAC	6440
Query	1081	TCAT	1084
Sbjct	6441	TCAT	6444

Range 2: 6551 to 6911

Score	Expect	Identities	Gaps	Strand	Frame
575 bits(311)	3e-158()	336/361(93%)	0/361(0%)	Plus/Plus	
Query	1191	CCCGCTATTCTCAGGGTACACGCTTAACATGAACAAAAATTCAC		TTTATAATCAT	1250
Sbjct	6551	CCCGCTATTCTCAGGGTACACGCTTAACATGAACAAAAATTCAC		TTTATAATCAT	6610
Query	1251	ATTTCGTAGGCGTAAACCTAACATTCTTCCCACANNNNNNNNNNNNNNNNNNNATACC			1310
Sbjct	6611	ATTTCGTAGGCGTAAACCTAACATTCTTCCCACAACACTTCTTAGGTCTATCCGGTATACC			6670
Query	1311	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG			1370
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG			6730
Query	1371	CTCATTATCTCTATTAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTCGC			1430
Sbjct	6731	CTCATTATCTCTATTAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTNGC			6790
Query	1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNNCCTTGAATGATTAAACGG			1490
Sbjct	6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTTGAATGATTAAACGG			6850
Query	1491	ATGTCCCCCACCATAACCACACATTGGAAGAACCCGCATACATCAACCCAAAAATGATCAAG			1550
Sbjct	6851	ATGTCCCCCACCATAACCACACATTGGAAGAACCCGCATACATCAACCCAAAAATGATCAAG			6910
Query	1551	A		1551	
Sbjct	6911	A		6911	

Eubalaena japonica isolate SWFSC\_MMASTR\_7966 mitochondrion, complete genome

Sequence ID: **OP205193.1** Length: 16386 Number of Matches: 2

Range 1: 5361 to 6444

Score	Expect	Identities	Gaps	Strand	Frame
1912 bits(1035)	0.0()	1060/1084(98%)	0/1084(0%)	Plus/Plus	
Query 1	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA	60			
Sbjct 5361	ATGTTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTTA	5420			
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA	120			
Sbjct 5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCCTAAGCTTATTAATTCGCGCTGAA	5480			
Query 121	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC	180			
Sbjct 5481	CTAGGTCAGCCTGGCACACTAATCGGAGACGATCAAGTCTACAACGTACTAGTAACAGCC	5540			
Query 181	CACGCCTTTGTAATAATCTTCTTCATAGTAATACCCATTATAATCGGTGGATTTGAAAC	240			
Sbjct 5541	CACGCCTTTGTAATAATCTTCTTCATAGTAATACCCATTATAATCGGTGGATTTGAAAC	5600			
Query 241	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA	300			
Sbjct 5601	TGACTAGTTCCTTAATAATTGGAGCACCTGACATGGCTTTCCCCGTATAAATAATATA	5660			

Query 301 AGCTTCTGACTACTCCCTCCTTCTTTCCCTACTACTAATAGCATCCTCAATGGTCNNNNNN 360  
Sbjct 5661 AGCTTCTGACTACTCCCTCCTTCTTTCCCTACTACTAATAGCATCCTCAATGGTCGAAGCC 5720  
Query 361 NNNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA 420  
Sbjct 5721 GGTGCAGGCACAGGCTGAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA 5780  
Query 421 GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA 480  
Sbjct 5781 GCTTCAGTCGACCTTACCATTTTCTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA 5840  
Query 481 GCCATTAACCTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA 540  
Sbjct 5841 GCCATTAACCTTTATCACAACATCATTAACATAAAACCACCTGCCATAACCCAATACCAA 5900  
Query 541 ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT 600  
Sbjct 5901 ACACCTCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT 5960  
Query 601 GTCCTAGCAGCTGGAATCACCATGCTATTAAGTGACCGAAACCTAAATACAACCTTTCTTC 660  
Sbjct 5961 GTCCTAGCAGCTGGAATCACCATGCTATTAAGTGACCGAAACCTAAATACAACCTTTCTTC 6020  
Query 661 GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC 720  
Sbjct 6021 GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTTTGGTCAC 6080  
Query 721 CCTGAAGTATATATCTTAATCCTCCCTGGGTTTCGGAATAATTTACACATTGTGACTTAT 780  
Sbjct 6081 CCTGAAGTATATATCTTAATCCTCCCTGGGTTTCGGAATAATTTACACATTGTGACTTAT 6140  
Query 781 TACTCAGGaaaaaaaGATCCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC 840  
Sbjct 6141 TACTCAGGAAAAAAGAACCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC 6200  
Query 841 GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC 900  
Sbjct 6201 GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTTACAGTAGGAATAGACGTTGAC 6260  
Query 901 ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC 960  
Sbjct 6261 ACACGAGCATACTTCACATCAGCCACTATAATCATCGCCATCCCTACAGGGGTAAAAGTC 6320  
Query 961 TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGNTCTCCTGCCCTAATATGA 1020  
Sbjct 6321 TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGATCTCCTGCCCTAATATGA 6380  
Query 1021 GCCCTAGGCTTNNNNNNNNNTTTCACAGTAGGTGGTCTAACAGGCATCGTCTGGCCAAC 1080  
Sbjct 6381 GCCCTAGGCTTCATCTTCTTTTCACAGTAGGTGGTCTAACAGGCATCGTCTGGCCAAC 6440  
Query 1081 TCAT 1084  
Sbjct 6441 TCAT 6444

Range 2: 6551 to 6911

Score	Expect	Identities	Gaps	Strand	Frame
579 bits(313)	2e-159()	337/361(93%)	0/361(0%)	Plus/Plus	
Query 1191	CCCGCTATTCTCAGGGTACACGCTTAACTCAACATGAACAAAAATTCACTTTATAATCAT				1250
Sbjct 6551	CCCGCTATTCTCAGGGTACACGCTTAACTCAACATGAACAAAAATTCACTTTATAATCAT				6610
Query 1251	ATTCGTAGGCGTAAACCTAACATTCTTCCACANNNNNNNNNNNNNNNNNNNNATACC				1310
Sbjct 6611	ATTCGTAGGCGTAAACCTAACATTCTTCCACAACACTTCTTAGGTCTATCCGGTATACC				6670
Query 1311	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG				1370
Sbjct 6671	TCGACGATACTCCGACTATCCAGACGCCTACACAATATGAAATACTATCTCATCAATAGG				6730
Query 1371	CTCATTCATCTCATTAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTCGC				1430
Sbjct 6731	CTCATTCATCTCATTAACAGCAGTTATACTAATAATTTTCATCATCTGAGAAGCATTCGC				6790
Query 1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNNCCTTGAATGATTAAACGG				1490
Sbjct 6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTTGAATGATTAAACGG				6850
Query 1491	ATGTCCCCCACCATACCACACATTGGAAGAACCCGCATACATCAACCCAAAATGATCAAG				1550
Sbjct 6851	ATGTCCCCCACCATACCACACATTGGAAGAACCCGCATACATCAACCCAAAATGATCAAG				6910
Query 1551	A 1551				
Sbjct 6911	A 6911				

Organism	Blast Name	Score	Number of Hits	Description
<a href="#">Balaenidae</a>	<a href="#">whales &amp; dolphins</a>		<a href="#">112</a>	
<a href="#">.Eubalaena</a>	<a href="#">whales &amp; dolphins</a>		<a href="#">63</a>	
<a href="#">..Eubalaena japonica</a>	<a href="#">whales &amp; dolphins</a>	1912	<a href="#">29</a>	<a href="#">Eubalaena japonica hits</a>
<a href="#">..Eubalaena glacialis</a>	<a href="#">whales &amp; dolphins</a>	1884	<a href="#">15</a>	<a href="#">Eubalaena glacialis hits</a>
<a href="#">..Eubalaena australis</a>	<a href="#">whales &amp; dolphins</a>	1884	<a href="#">19</a>	<a href="#">Eubalaena australis hits</a>
<a href="#">.Balaena mysticetus</a>	<a href="#">whales &amp; dolphins</a>	1746	<a href="#">49</a>	<a href="#">Balaena mysticetus hits</a>

◦ **Organism**

Description	Score	E value	Accession
Eubalaena japonica (North Pacific right whale) [whales & dolphins ]			
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_44460 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205215</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43855 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205204</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_28432 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205199</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_13192 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205194</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43864 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205209</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_7966 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205193</a>
<a href="#">Eubalaena japonica mitochondrion, complete genome</a>	1912	0.0	<a href="#">NC_006931</a>
<a href="#">Eubalaena japonica mitochondrial DNA, complete genome</a>	1912	0.0	<a href="#">AP006474</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43863 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205208</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_44461 mitochondrion, complete genome</a>	1912	0.0	<a href="#">OP205216</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43867 mitochondrion, complete genome</a>	1906	0.0	<a href="#">OP205212</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43866 mitochondrion, complete genome</a>	1906	0.0	<a href="#">OP205211</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43858 mitochondrion, complete genome</a>	1906	0.0	<a href="#">OP205206</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43853 mitochondrion, complete genome</a>	1906	0.0	<a href="#">OP205203</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43851 mitochondrion, complete genome</a>	1906	0.0	<a href="#">OP205202</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43871 mitochondrion, complete genome</a>	1906	0.0	<a href="#">OP205214</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43860 mitochondrion, complete genome</a>	1901	0.0	<a href="#">OP205207</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43850 mitochondrion, complete genome</a>	1901	0.0	<a href="#">OP205201</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43849 mitochondrion, complete genome</a>	1901	0.0	<a href="#">OP205200</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_7963 mitochondrion, complete genome</a>	1901	0.0	<a href="#">OP205192</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_62934 mitochondrion, complete genome</a>	1895	0.0	<a href="#">OP205218</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43870 mitochondrion, complete genome</a>	1895	0.0	<a href="#">OP205213</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43865 mitochondrion, complete genome</a>	1895	0.0	<a href="#">OP205210</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_43856 mitochondrion, complete genome</a>	1895	0.0	<a href="#">OP205205</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_28430 mitochondrion, complete genome</a>	1895	0.0	<a href="#">OP205198</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_28428 mitochondrion, complete genome</a>	1895	0.0	<a href="#">OP205197</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_53766 mitochondrion, complete genome</a>	1890	0.0	<a href="#">OP205217</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_23634 mitochondrion, complete genome</a>	1890	0.0	<a href="#">OP205196</a>
<a href="#">Eubalaena japonica isolate SWFSC_MMASTR_23631 mitochondrion, complete genome</a>	1890	0.0	<a href="#">OP205195</a>
Eubalaena glacialis (North Atlantic right whale) [whales & dolphins ]			
<a href="#">Eubalaena glacialis mitochondrion, complete genome</a>	1884	0.0	<a href="#">MF459656</a>
<a href="#">Eubalaena glacialis isolate EglA02Feb09F mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205182</a>
<a href="#">Eubalaena glacialis isolate SWFSC_MMASTR_28311 mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205191</a>
<a href="#">Eubalaena glacialis isolate SWFSC_MMASTR_15112 mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205190</a>
<a href="#">Eubalaena glacialis isolate SWFSC_MMASTR_4977 mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205189</a>
<a href="#">Eubalaena glacialis isolate EglA20Feb10B mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205187</a>
<a href="#">Eubalaena glacialis isolate EglA17Feb07A mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205185</a>
<a href="#">Eubalaena glacialis isolate EglA10Jan08G mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205184</a>



Description	Score	E value	Accession
<a href="#">Eubalaena glacialis isolate Egla08Feb09B_gDNA mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205183</a>
<a href="#">Eubalaena glacialis isolate Eg#1014 'Staccato' cytochrome oxidase subunit I (cox1)_gene, complete cds; mitochondrial</a>	1884	0.0	<a href="#">DQ095154</a>
<a href="#">Eubalaena glacialis isolate Egla21Feb07B mitochondrion, complete genome</a>	1879	0.0	<a href="#">OP205188</a>
<a href="#">Eubalaena glacialis isolate Egla20Feb07B mitochondrion, complete genome</a>	1879	0.0	<a href="#">OP205186</a>
<a href="#">Eubalaena glacialis isolate Egla02Feb09D mitochondrion, complete genome</a>	1879	0.0	<a href="#">OP205181</a>
<a href="#">Eubalaena glacialis mitochondrion, complete genome</a>	1862	0.0	<a href="#">NC_037444</a>
<a href="#">Eubalaena glacialis mitochondrion, complete genome</a>	1862	0.0	<a href="#">MF409247</a>
Eubalaena australis (southern right whale) [whales & dolphins ]			
<a href="#">Eubalaena australis isolate Eaus0550m_Arg mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205174</a>
<a href="#">Eubalaena australis isolate Eaus06GNJ_Arg mitochondrion, complete genome</a>	1884	0.0	<a href="#">OP205169</a>
<a href="#">Eubalaena australis isolate Eaus06132m_Arg mitochondrion, complete genome</a>	1879	0.0	<a href="#">OP205177</a>
<a href="#">Eubalaena australis isolate Eaus09AI105_AI mitochondrion, complete genome</a>	1879	0.0	<a href="#">OP205172</a>
<a href="#">Eubalaena australis isolate Eaus06GNA_Arg mitochondrion, complete genome</a>	1879	0.0	<a href="#">OP205168</a>
<a href="#">Eubalaena australis isolate EA123 cytochrome oxidase subunit I (cox1)_gene, complete cds; mitochondrial</a>	1879	0.0	<a href="#">DQ095155</a>
<a href="#">Eubalaena australis isolate Eaus06138m_Arg mitochondrion, complete genome</a>	1873	0.0	<a href="#">OP205178</a>
<a href="#">Eubalaena australis isolate Eaus0587m_Arg mitochondrion, complete genome</a>	1868	0.0	<a href="#">OP205175</a>
<a href="#">Eubalaena australis isolate Eaus06129m_Arg mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205176</a>
<a href="#">Eubalaena australis isolate Eaus058SA_Arg mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205173</a>
<a href="#">Eubalaena australis isolate Eaus07AI065_AI mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205170</a>
<a href="#">Eubalaena australis isolate Eaus06A1_Arg mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205167</a>
<a href="#">Eubalaena australis isolate Eaus03K1_Arg mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205166</a>
<a href="#">Eubalaena australis isolate Eaus08AI081_AI mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205171</a>
<a href="#">Eubalaena australis isolate Eaus06144m_Arg mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205179</a>
<a href="#">Eubalaena australis mitochondrion, complete genome</a>	1862	0.0	<a href="#">NC_006930</a>
<a href="#">Eubalaena australis mitochondrial DNA, complete genome</a>	1862	0.0	<a href="#">AP006473</a>
<a href="#">Eubalaena australis isolate Eaus_AP006474 mitochondrion, complete genome</a>	1862	0.0	<a href="#">OP205180</a>
<a href="#">Eubalaena australis isolate EA604 cytochrome oxidase subunit I (cox1)_gene, complete cds; mitochondrial</a>	1857	0.0	<a href="#">DQ095156</a>
Balaena mysticetus (bowhead whale) [whales & dolphins ]			
<a href="#">Balaena mysticetus voucher NHMO-DMA-43197 mitochondrion, complete genome</a>	1746	0.0	<a href="#">MN145938</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50790 mitochondrion, complete genome</a>	1746	0.0	<a href="#">MZ618258</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43194 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN124685</a>
<a href="#">Balaena mysticetus voucher PMO 234.423 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN159085</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43206 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN159084</a>
<a href="#">Balaena mysticetus voucher PMO 234.429 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN159082</a>
<a href="#">Balaena mysticetus voucher PMO 234.522 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN159081</a>
<a href="#">Balaena mysticetus voucher PMO 234.573 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN159080</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43191 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN145939</a>
<a href="#">Balaena mysticetus voucher NHMO-DMA-43195 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MN145937</a>
<a href="#">Balaena mysticetus isolate QT3_Qeqertassussuk mitochondrion,.partial genome</a>	1740	0.0	<a href="#">MH198022</a>
<a href="#">Balaena mysticetus isolate H mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026773</a>
<a href="#">Balaena mysticetus isolate I mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026772</a>
<a href="#">Balaena mysticetus isolate F mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026771</a>
<a href="#">Balaena mysticetus isolate E mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026770</a>
<a href="#">Balaena mysticetus isolate D mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026769</a>
<a href="#">Balaena mysticetus isolate C mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026768</a>
<a href="#">Balaena mysticetus isolate B mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026767</a>

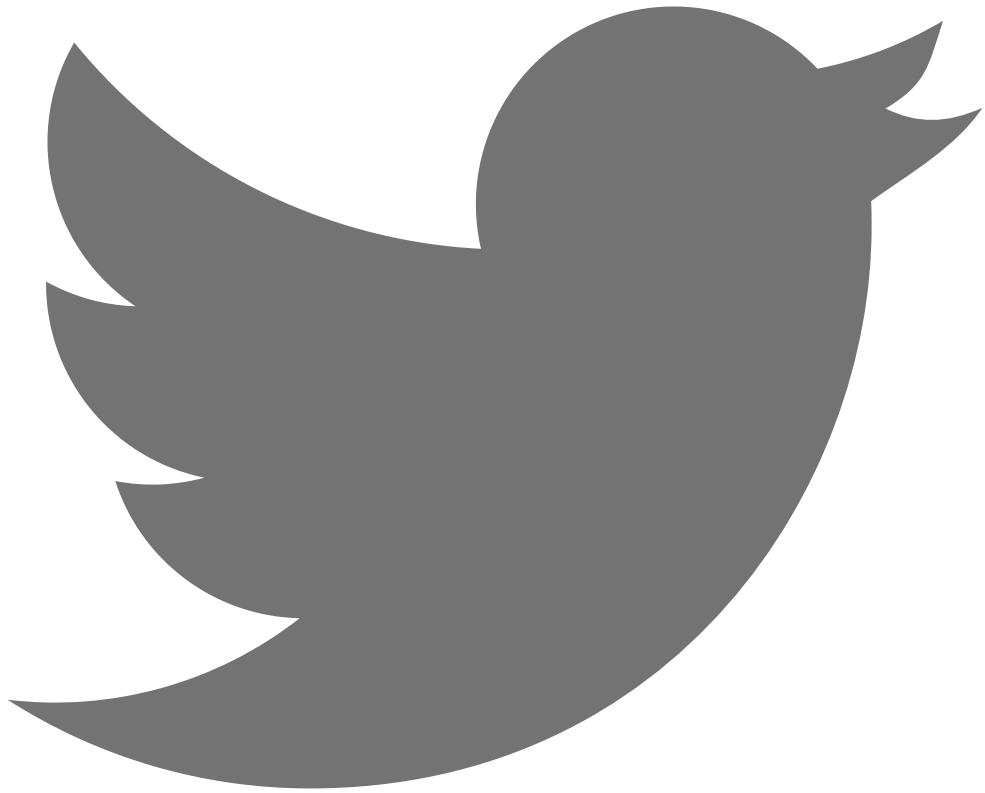
Description	Score	E value	Accession
<a href="#">Balaena mysticetus isolate A mitochondrion, complete genome</a>	1740	0.0	<a href="#">KY026766</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 112407 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618260</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50788 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618257</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50787 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618256</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50785 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618254</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 44672 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618253</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 18978 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618252</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 18972 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618251</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 18971 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618250</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 17876 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618248</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 17875 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618247</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 17874 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618246</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 7095 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618245</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 7094 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MZ618244</a>
<a href="#">Balaena mysticetus isolate 17-05 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649195</a>
<a href="#">Balaena mysticetus isolate 17-08 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649194</a>
<a href="#">Balaena mysticetus isolate 17-12 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649193</a>
<a href="#">Balaena mysticetus isolate 17-21 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649192</a>
<a href="#">Balaena mysticetus isolate 17-20 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649191</a>
<a href="#">Balaena mysticetus isolate 17-18 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649190</a>
<a href="#">Balaena mysticetus isolate 17-17 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649189</a>
<a href="#">Balaena mysticetus isolate 17-10 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649188</a>
<a href="#">Balaena mysticetus isolate 17-07 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649187</a>
<a href="#">Balaena mysticetus isolate 18-06 mitochondrion, complete genome</a>	1740	0.0	<a href="#">MT649186</a>
<a href="#">Balaena mysticetus mitochondrial DNA, complete genome</a>	1740	0.0	<a href="#">AP006472</a>
<a href="#">Balaena mysticetus mitochondrion, complete genome</a>	1740	0.0	<a href="#">NC_005268</a>
<a href="#">Balaena mysticetus complete mitochondrial genome</a>	1740	0.0	<a href="#">AJ554051</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50797 mitochondrion, complete genome</a>	1735	0.0	<a href="#">MZ618259</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 50786 mitochondrion, complete genome</a>	1735	0.0	<a href="#">MZ618255</a>
<a href="#">Balaena mysticetus isolate SWFSC LAB ID 1266 mitochondrion, complete genome</a>	1735	0.0	<a href="#">MZ618243</a>
<a href="#">Balaena mysticetus isolate 17-19 mitochondrion, complete genome</a>	1735	0.0	<a href="#">MT649196</a>

◦ Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
<a href="#">Balaenidae</a>	<a href="#">112</a>	4	
. <a href="#">Eubalaena</a>	<a href="#">63</a>	3	
.. <a href="#">Eubalaena japonica</a>	<a href="#">29</a>	1	<a href="#">Eubalaena japonica hits</a>
.. <a href="#">Eubalaena glacialis</a>	<a href="#">15</a>	1	<a href="#">Eubalaena glacialis hits</a>
.. <a href="#">Eubalaena australis</a>	<a href="#">19</a>	1	<a href="#">Eubalaena australis hits</a>
. <a href="#">Balaena mysticetus</a>	<a href="#">49</a>	1	<a href="#">Balaena mysticetus hits</a>

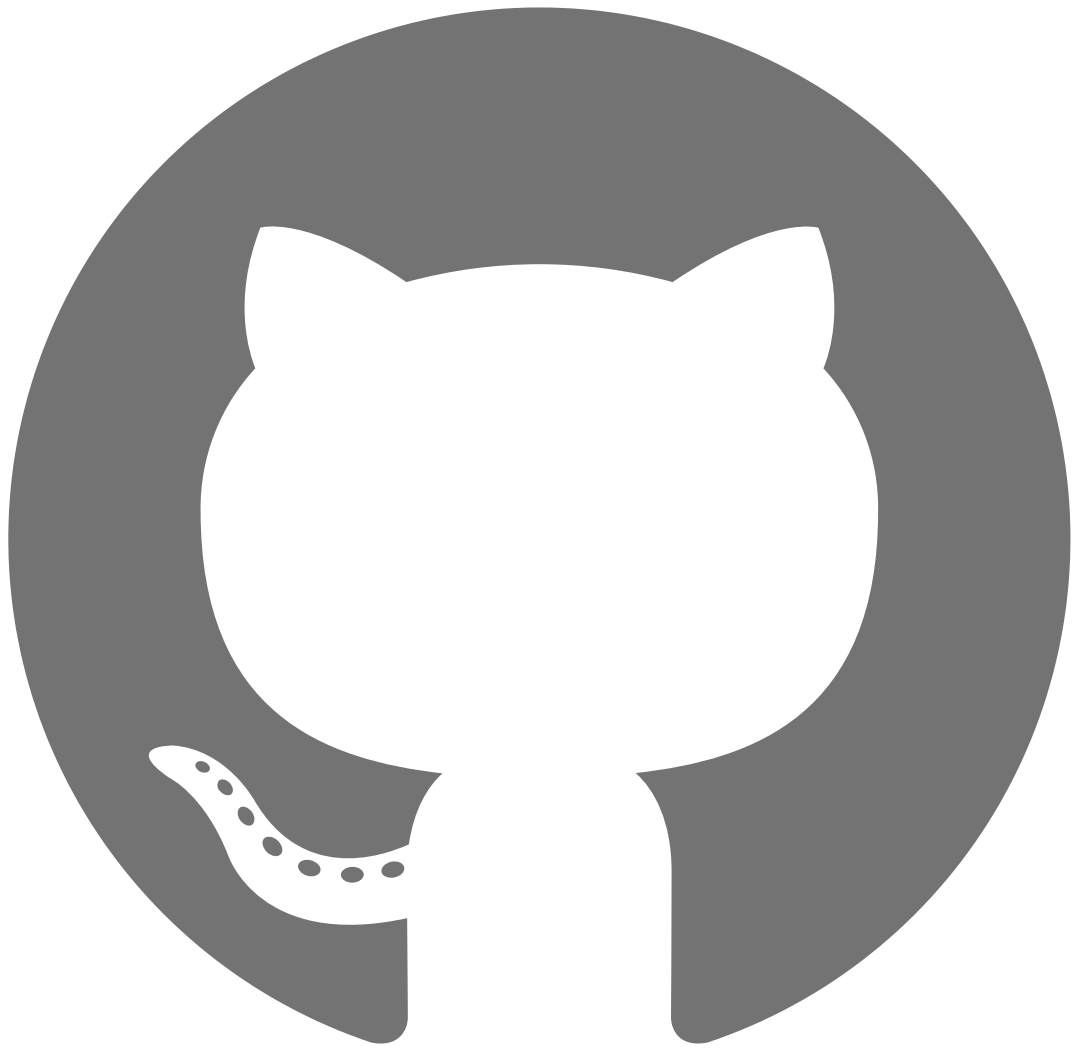
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