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BLAST® > **blastn suite** > results for RID-KE6UZT21014

Job Title	Nucleotide Sequence ...
RID	KE6UZT21014 Search expires on 12-10 01:39 am
Program	BLASTN
Database	nt
Query ID	Icl Query_6557803
Description	None ...
Molecule type	dna
Query Length	1551

Descriptions

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

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

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>mitochondrion, complete genome</u>								
<u>Eubalaena glacialis isolate Egl08Feb09B_gDNA mitochondrial, complete genome</u>	<u>Eubalaena glacialis</u>	1884	2454	93%	0.0	97.32%	16387	<u>OP205183.1</u>
<u>Eubalaena australis isolate Eaus0550m_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1884	2454	93%	0.0	97.32%	16385	<u>OP205174.1</u>
<u>Eubalaena australis isolate Eaus06GNJ_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1884	2454	93%	0.0	97.32%	16386	<u>OP205169.1</u>
<u>Eubalaena glacialis isolate Eg#1014 'Staccato' cytochrome oxidase subunit I.(cox1) gene, complete cds; mitochondrial</u>	<u>Eubalaena glacialis</u>	1884	2458	93%	0.0	97.32%	1551	<u>DQ095154.1</u>
<u>Eubalaena glacialis isolate Egl21Feb07B mitochondrial, complete genome</u>	<u>Eubalaena glacialis</u>	1879	2449	93%	0.0	97.23%	16387	<u>OP205188.1</u>
<u>Eubalaena glacialis isolate Egl20Feb07B mitochondrial, complete genome</u>	<u>Eubalaena glacialis</u>	1879	2452	93%	0.0	97.23%	16387	<u>OP205186.1</u>
<u>Eubalaena glacialis isolate Egl02Feb09D mitochondrial, complete genome</u>	<u>Eubalaena glacialis</u>	1879	2452	93%	0.0	97.23%	16387	<u>OP205181.1</u>
<u>Eubalaena australis isolate Eaus06132m_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1879	2452	93%	0.0	97.23%	16385	<u>OP205177.1</u>
<u>Eubalaena australis isolate Eaus09AI105_AI mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1879	2443	93%	0.0	97.23%	16386	<u>OP205172.1</u>
<u>Eubalaena australis isolate Eaus06GNA_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1879	2449	93%	0.0	97.23%	16386	<u>OP205168.1</u>
<u>Eubalaena australis isolate EA123 cytochrome oxidase subunit I.(cox1).gene, complete cds; mitochondrial</u>	<u>Eubalaena australis</u>	1879	2452	93%	0.0	97.23%	1551	<u>DQ095155.1</u>
<u>Eubalaena australis isolate Eaus06138m_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1873	2437	93%	0.0	97.14%	16386	<u>OP205178.1</u>
<u>Eubalaena australis isolate Eaus0587m_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1868	2437	93%	0.0	97.05%	16387	<u>OP205175.1</u>
<u>Eubalaena glacialis mitochondrial, complete genome</u>	<u>Eubalaena glacialis</u>	1862	2436	93%	0.0	96.96%	16386	<u>NC_037444.1</u>
<u>Eubalaena australis isolate Eaus06129m_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1862	2432	93%	0.0	96.96%	16386	<u>OP205176.1</u>
<u>Eubalaena australis isolate Eaus058SA_Arg mitochondrial, complete genome</u>	<u>Eubalaena australis</u>	1862	2436	93%	0.0	96.96%	16386	<u>OP205173.1</u>
<u>Eubalaena australis isolate Eaus07AI065_AI</u>	<u>Eubalaena australis</u>	1862	2436	93%	0.0	96.96%	16386	<u>OP205170.1</u>

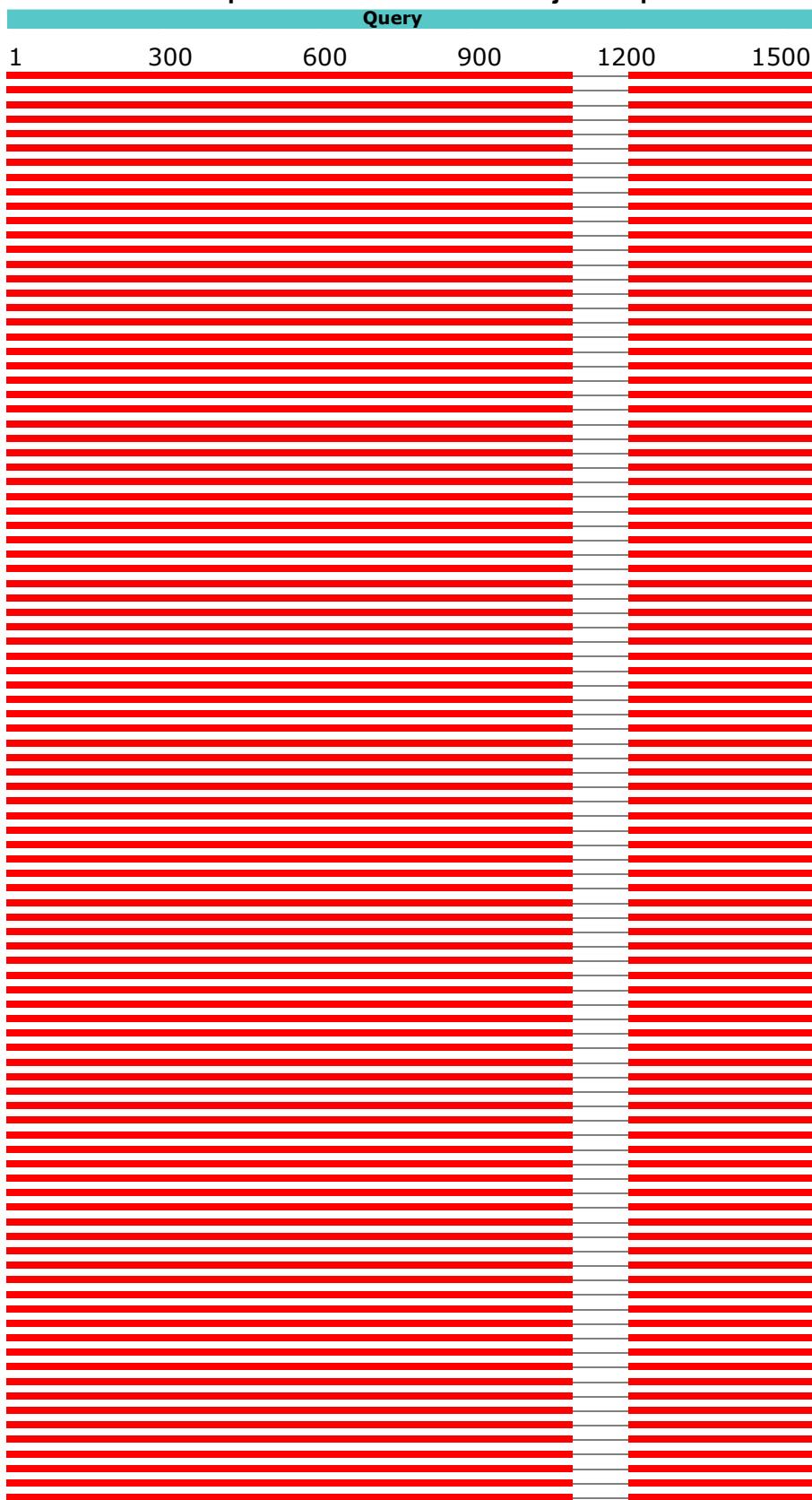
Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>mitochondrion, complete genome</u>								
<u>Eubalaena australis isolate Eaus06A1_Arg mitochondrion, complete genome</u>	<u>Eubalaena australis</u>	1862	2436	93%	0.0	96.96%	16386	<u>OP205167.1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

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

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

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	ATGTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTAA				60
Sbjct 5361	ATGTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATATTAA				5420
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCTAAGCTTATAATTGCGCTGAA				120

Sbjct	5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCCTAAGCTTATTAAATCGCGCTGAA	5480
Query	121	CTAGGTCAAGCCTGGCACACTAACATCGGAGACGATCAAGTCTACAACGCTACTAGTAACAGCC	180
Sbjct	5481	CTAGGTCAAGCCTGGCACACTAACATCGGAGACGATCAAGTCTACAACGCTACTAGTAACAGCC	5540
Query	181	CACGCCCTTGTAATAATCTCTTCATAGTAATAACCCATTATAATCGGTGGATTGGAAAC	240
Sbjct	5541	CACGCCCTTGTAATAATCTCTTCATAGTAATAACCCATTATAATCGGTGGATTGGAAAC	5600
Query	241	TGACTAGTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA	300
Sbjct	5601	TGACTAGTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA	5660
Query	301	AGCTTCTGACTACTCCCTCCTCTTCTACTACTAAAGCATCCTCAATGGTCNNNNNN	360
Sbjct	5661	AGCTTCTGACTACTCCCTCCTCTTCTACTACTAAAGCATCCTCAATGGTCGAAGCC	5720
Query	361	NNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA	420
Sbjct	5721	GGTGCAGGCACAGGCTGAACGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA	5780
Query	421	GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA	480
Sbjct	5781	GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA	5840
Query	481	GCCATTAACTTATCACAACTATCATTAAACATAAAACACCTGCCATAACCAAATACCAA	540
Sbjct	5841	GCCATTAACTTATCACAACTATCATTAAACATAAAACACCTGCCATAACCAAATACCAA	5900
Query	541	ACACCTTTTCGTATGATCAGTCCTAGTTACAGCACTGCTGCTCTACTATCACTACCT	600
Sbjct	5901	ACACCTTTTCGTATGATCAGTCCTAGTTACAGCACTGCTGCTCTACTATCACTACCT	5960
Query	601	GTCCTAGCAGCTGGAATCACCATGCTATTAACGTGACCGAAACCTAAACAACTTTCTTC	660
Sbjct	5961	GTCCTAGCAGCTGGAATCACCATGCTATTAACGTGACCGAAACCTAAACAACTTTCTTC	6020
Query	661	GACCCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC	720
Sbjct	6021	GACCCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC	6080
Query	721	CCTGAAGTATATATCTTAATCCTCCCTGGGTCGGAATAATTACACATTGTGACTTAT	780
Sbjct	6081	CCTGAAGTATATATCTTAATCCTCCCTGGGTCGGAATAATTACACATTGTGACTTAT	6140
Query	781	TACTCAGGaaaaaaaaGATCCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	840
Sbjct	6141	TACTCAGGaaaaaaaaAGAACCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	6200
Query	841	GGATTCTTAGGCTTCATCGTATGGGACACCACATATTACAGTAGGAATAGACGTTGAC	900
Sbjct	6201	GGATTCTTAGGCTTCATCGTATGGGACACCACATATTACAGTAGGAATAGACGTTGAC	6260
Query	901	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAAGTC	960
Sbjct	6261	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAAGTC	6320
Query	961	TTCAGTTGATAGCAACACTCCACGGAGGCAACATTAAATGNTCTCTGCCCTAAATATGA	1020
Sbjct	6321	TTCAGTTGATAGCAACACTCCACGGAGGCAACATTAAATGATCTCTGCCCTAAATATGA	6380
Query	1021	GCCCTAGGCTNNNNNNNNNTTCACAGTAGGTGGCTAACAGGCATCGTCCTGGCCAAC	1080
Sbjct	6381	GCCCTAGGCTCATCTCCCTTACAGTAGGTGGCTAACAGGCATCGTCCTGGCCAAC	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	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAAATTCACTTATAATCAT			1250
Sbjct	6551	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAAATTCACTTATAATCAT			6610
Query	1251	ATTCGTAGCGTAAACCTAACATTCTCCCACANNNNNNNNNNNNNNNNNATACC			1310
Sbjct	6611	ATTCGTAGCGTAAACCTAACATTCTCCCACAAACACTTCTAGGTCTATCCGTATACC			6670
Query	1311	TCGACGATACTCCGACTATCCAGACGCCAACAAATGAAATACTATCTCATCAATAGG			1370
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCCAACAAATGAAATACTATCTCATCAATAGG			6730
Query	1371	CTCATTCTCATCTAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTGCG			1430
Sbjct	6731	CTCATTCTCATCTAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTNGC			6790
Query	1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTACTNNCCTGAATGATTAAACGG			1490
Sbjct	6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTACTAACCTGAATGATTAAACGG			6850
Query	1491	ATGTCCCCACCATACCACATTCGAAGAACCCGATACATCAACCCAAAATGATCAAG			1550
Sbjct	6851	ATGTCCCCACCATACCACATTCGAAGAACCCGATACATCAACCCAAAATGATCAAG			6910
Query	1551	A 1551			

Sbjct 6911 A 6911

Eubalaena japonica isolate SWFSC_MMASTR_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	ATGTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATTTA			60	
Sbjct 5361	ATGTTCATAAACCGCTGACTATTCTCAACCAACCACAAAGACATTGGCACCTTATTTA			5420	
Query 61	TTATTTGGCCCTGAGCAGGAATAGTAGGCCTAGGCTAACGTTATTAAATTGGCGCTGAA			120	
Sbjct 5421	TTATTTGGCCCTGAGCAGGAATAGTAGGCCTAGGCTAACGTTATTAAATTGGCGCTGAA			5480	
Query 121	CTAGGTCAAGCCTGGCACACTAACGAGACGATCAAGTCTACAACGTAAGTAAACAGCC			180	
Sbjct 5481	CTAGGTCAAGCCTGGCACACTAACGAGACGATCAAGTCTACAACGTAAGTAAACAGCC			5540	
Query 181	CACGCCCTTGTAATAATCTCTCATAGTAATAACCCATTATAATCGTGGATTGGAAAC			240	
Sbjct 5541	CACGCCCTTGTAATAATCTCTCATAGTAATAACCCATTATAATCGTGGATTGGAAAC			5600	
Query 241	TGACTAGTTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA			300	
Sbjct 5601	TGACTAGTTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA			5660	
Query 301	AGCTTCTGACTACTCCCTCCTTCTTCTACTACTAAATAGCATCCTCAATGGTCNNNNNN			360	
Sbjct 5661	AGCTTCTGACTACTCCCTCCTTCTTCTACTACTAAATAGCATCCTCAATGGTCAGCC			5720	
Query 361	NNNNNNNGCACAGGCTNAACTGTATATCCCCCTAGCCGAAACCTAGCACATGCAGGA			420	
Sbjct 5721	GGTGCAGGCACAGGCTGAACGTATATCCCCCTAGCCGAAACCTAGCACATGCAGGA			5780	
Query 421	GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA			480	
Sbjct 5781	GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA			5840	
Query 481	GCCATTAACTTATCACAACATATCATTAAACATAAAAACACCTGCCATAACCAAATACCAA			540	
Sbjct 5841	GCCATTAACTTATCACAACATATCATTAAACATAAAAACACCTGCCATAACCAAATACCAA			5900	
Query 541	ACACCTCTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCACTATCACTACCT			600	
Sbjct 5901	ACACCTCTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCACTATCACTACCT			5960	
Query 601	GTCCTAGCAGCTGGAATCACCAGTGTATTAACGTGACCGAAACCTAAACACTTTCTTC			660	
Sbjct 5961	GTCCTAGCAGCTGGAATCACCAGTGTATTAACGTGACCGAAACCTAAACACTTTCTTC			6020	
Query 661	GACCCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC			720	
Sbjct 6021	GACCCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC			6080	
Query 721	CCTGAAGTATATATCTTAATCCTCCCTGGGTCGGAATAATTACACATTGTGACTTAT			780	
Sbjct 6081	CCTGAAGTATATATCTTAATCCTCCCTGGGTCGGAATAATTACACATTGTGACTTAT			6140	
Query 781	TACTCAGGaaaaaaaGATCCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC			840	
Sbjct 6141	TACTCAGGaaaaaaaGAAACCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC			6200	
Query 841	GGATTCTTAGGCTTCATCGTATGGCACACCACATATTACAGTAGGAATAGACGTTGAC			900	
Sbjct 6201	GGATTCTTAGGCTTCATCGTATGGCACACCACATATTACAGTAGGAATAGACGTTGAC			6260	
Query 901	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAGTC			960	
Sbjct 6261	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAGTC			6320	
Query 961	TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGNTCTCTGCCCTAAATATGA			1020	
Sbjct 6321	TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGATCTCTGCCCTAAATATGA			6380	
Query 1021	GCCCTAGGCTNNNNNNNNNTTCACAGTAGGTGGCTAACAGGCATCGCCTGGCCAAC			1080	
Sbjct 6381	GCCCTAGGCTTCATCTCCTTTACAGTAGGTGGCTAACAGGCATCGCCTGGCCAAC			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	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAATTCACTTATAATCAT			1250	

Sbjct	6551	CCCGCTATTCTCAGGGTACAGCCTAACATCAACATGAACAAAATTCACTTATAATCAT	6610
Query	1251	ATTCGTAGGCGTAAACCTAACATTCTCCCACANNNNNNNNNNNNNNNNATACC	1310
Sbjct	6611	ATTCGTAGGCGTAAACCTAACATTCTCCCACAAACACTCTTAGGCTATCGGTATACC	6670
Query	1311	TCGACGATACTCCGACTATCCAGACGCCACACAATATGAAATACTATCTCATCAATAGG	1370
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCCACACAATATGAAATACTATCTCATCAATAGG	6730
Query	1371	CTCATTCTCATCTCATTAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTGC	1430
Sbjct	6731	CTCATTCTCATCTCATTAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTNGC	6790
Query	1431	ATCCAACGAGAAGTACTAGCAGTAGACCTCACCTACTNNCCTGAATGATTAAACGG	1490
Sbjct	6791	ATCCAACGAGAAGTACTAGCAGTAGACCTCACCTACTAACCTGAATGATTAAACGG	6850
Query	1491	ATGTCCCCCACCATACCACACATTGAAGAACCCGATACATCAACCCAAATGATCAAG	1550
Sbjct	6851	ATGTCCCCCACCATACCACACATTGAAGAACCCGATACATCAACCCAAATGATCAAG	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	ATGTTCATAAACCGCTGACTATTCTAACCAACCACAAAGACATTGGCACCTTATATTAA				60
Sbjct 5361	ATGTTCATAAACCGCTGACTATTCTAACCAACCACAAAGACATTGGCACCTTATATTAA				5420
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCTTAAGCTTATTAAATTGGCGCTGAA				120
Sbjct 5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCACTGGCTTAAGCTTATTAAATTGGCGCTGAA				5480
Query 121	CTAGGTCAGCCTGGCACACTAACGGAGACGATCAAGTCTACACCGTACTAGTAACAGCC				180
Sbjct 5481	CTAGGTCAGCCTGGCACACTAACGGAGACGATCAAGTCTACACCGTACTAGTAACAGCC				5540
Query 181	CACGCCCTTGTAATAATCTCTCATAGTAATAACCCATTATAATCGGTGGATTGGAAAC				240
Sbjct 5541	CACGCCCTTGTAATAATCTCTCATAGTAATAACCCATTATAATCGGTGGATTGGAAAC				5600
Query 241	TGACTAGTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA				300
Sbjct 5601	TGACTAGTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA				5660
Query 301	AGCTTCTGACTACTCCCTCCTTTCTACTACTAACAGCATCCTCAATGGTCNNNNNN				360
Sbjct 5661	AGCTTCTGACTACTCCCTCCTTTCTACTACTAACAGCATCCTCAATGGTCGAAGCC				5720
Query 361	NNNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA				420
Sbjct 5721	GGTGCAGGCACAGGCTGAACGTGATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA				5780
Query 421	GCTTCAGTCGACCTTACCAATTTCCTCTACACCTAGCTGGGTATCCTCTATCCTCGGA				480
Sbjct 5781	GCTTCAGTCGACCTTACCAATTTCCTCTACACCTAGCTGGGTATCCTCTATCCTCGGA				5840
Query 481	GCCATTAACTTATCACAACATCATTAAACATAAAACACCTGCCATAACCCAAATACCAA				540
Sbjct 5841	GCCATTAACTTATCACAACATCATTAAACATAAAACACCTGCCATAACCCAAATACCAA				5900
Query 541	ACACCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCTACTATCACTACCT				600
Sbjct 5901	ACACCTTTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCTACTATCACTACCT				5960
Query 601	GTCCTAGCAGCTGGAAATCACCAGCTATTAAACTGACCGAAACCTAAACACTTTCTC				660
Sbjct 5961	GTCCTAGCAGCTGGAAATCACCAGCTATTAAACTGACCGAAACCTAAACACTTTCTC				6020
Query 661	GACCCCTGCAGGTGGAGGAGACCAATCCTGTATCAACACCTATTCTGATTTGGTCAC				720
Sbjct 6021	GACCCCTGCAGGTGGAGGAGACCAATCCTGTATCAACACCTATTCTGATTTGGTCAC				6080
Query 721	CCTGAAGTATATCTTAATCCTCCCTGGGTCGGAAATAATTACACATTGTGACTTAT				780
Sbjct 6081	CCTGAAGTATATCTTAATCCTCCCTGGGTCGGAAATAATTACACATTGTGACTTAT				6140
Query 781	TACTCAGGaaaaaaaaGATCCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC				840
Sbjct 6141	TACTCAGGaaaaaaaaGACCTTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC				6200
Query 841	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTACAGTAGGAATAGACGTTGAC				900
Sbjct 6201	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTACAGTAGGAATAGACGTTGAC				6260
Query 901	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAGTC				960
Sbjct 6261	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAGTC				6320

Query 961 TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAATGNTCTCCTGCCCTAATATGA 1020
 Sbjct 6321 TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAATGATCTCCTGCCCTAATATGA 6380
 Query 1021 GCCCTAGGCTNNNNNNNNNTTACAGTAGGTGGCTAACAGGCATCGTCCTGCCAAC 1080
 Sbjct 6381 GCCCTAGGCTTCATCTCCCTTCACAGTAGGTGGCTAACAGGCATCGTCCTGCCAAC 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	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAAATTCACTTATAATCAT				1250
Sbjct 6551	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAAATTCACTTATAATCAT				6610
Query 1251	ATTCGTAGGCGTAAACCTAACATTCTCCCACANNNNNNNNNNNNNNNNATACC				1310
Sbjct 6611	ATTCGTAGGCGTAAACCTAACATTCTCCCACAAACACTCTTAGGTCTATCCGTATACC				6670
Query 1311	TCGACGATACTCCGACTATCCAGACGCCAACAAATGAAATACTATCTCATCAATAGG				1370
Sbjct 6671	TCGACGATACTCCGACTATCCAGACGCCAACAAATGAAATACTATCTCATCAATAGG				6730
Query 1371	CTCATTCTCATCTCATTAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTGCG				1430
Sbjct 6731	CTCATTCTCATCTCATTAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTGCG				6790
Query 1431	ATCCAACGAGAAGTACTAGCAGTAGACCTCACCTACTNNCCTGAATGATTAAACGG				1490
Sbjct 6791	ATCCAACGAGAAGTACTAGCAGTAGACCTCACCTACTAACCTTGAATGATTAAACGG				6850
Query 1491	ATGTCCCCACCATACCACACATTGAAGAACCCGCATACATCAACCCAAAATGATCAAG				1550
Sbjct 6851	ATGTCCCCACCATACCACACATTGAAGAACCCGCATACATCAACCCAAAATGATCAAG				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	ATGTTCATAAACCGCTGACTATTCTAACCAACCACAAAGACATTGGCACCTTATTTA				60
Sbjct 5361	ATGTTCATAAACCGCTGACTATTCTAACCAACCACAAAGACATTGGCACCTTATTTA				5420
Query 61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCCTAGGGCTAACGTTATTAAATTGGCGCTGAA				120
Sbjct 5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCCTAGGGCTAACGTTATTAAATTGGCGCTGAA				5480
Query 121	CTAGGTCAAGCCTGGCACACTAACCGAGACGATCAAGTCTACAACGCTACTAGTAACAGCC				180
Sbjct 5481	CTAGGTCAAGCCTGGCACACTAACCGAGACGATCAAGTCTACAACGCTACTAGTAACAGCC				5540
Query 181	CACGCCCTTGTAATAATCTCTCATAGTAATACCCATTATAATCGGTGGATTGGAAAC				240
Sbjct 5541	CACGCCCTTGTAATAATCTCTCATAGTAATACCCATTATAATCGGTGGATTGGAAAC				5600
Query 241	TGACTAGTTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA				300
Sbjct 5601	TGACTAGTTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA				5660
Query 301	AGCTTCTGACTACTCCCTCCTTCCACTACTAACGATCCTCAATGGTCNNNNNN				360
Sbjct 5661	AGCTTCTGACTACTCCCTCCTTCCACTACTAACGATCCTCAATGGTCGAAGCC				5720
Query 361	NNNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA				420
Sbjct 5721	GGTGCAGGCACAGGCTGAACGTGATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA				5780
Query 421	GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTATCCTCGGA				480
Sbjct 5781	GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTATCCTCGGA				5840
Query 481	GCCATTAACTTATCACAACTATCATTAAACATAAAACACCTGCCATAACCAATACCAA				540
Sbjct 5841	GCCATTAACTTATCACAACTATCATTAAACATAAAACACCTGCCATAACCAATACCAA				5900
Query 541	ACACCTCTTCGTTGATCAGTCCTAGTTACAGCAGTGCTGCTCCACTACTACCT				600
Sbjct 5901	ACACCTCTTCGTTGATCAGTCCTAGTTACAGCAGTGCTGCTCCACTACTACCT				5960
Query 601	GTCCTAGCAGCTGGAATCACCATGCTATTAACTGACCGAAACCTAAACACTTCTTC				660

Sbjct	5961	GTCCTAGCAGCTGGAATCACCATGCTATTAACTGACCGAACCTAAATACAACCTTCTTC	6020
Query	661	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC	720
Sbjct	6021	GACCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC	6080
Query	721	CCTGAAGTATATCTTAATCCTCCCTGGGTCGGAATAATTACACATTGTGACTTAT	780
Sbjct	6081	CCTGAAGTATATCTTAATCCTCCCTGGGTCGGAATAATTACACATTGTGACTTAT	6140
Query	781	TACTCAGGaaaaaaaaaaaaGATCCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	840
Sbjct	6141	TACTCAGGAAAAAAAAGAACCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC	6200
Query	841	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTACAGTAGGAATAGACGTTGAC	900
Sbjct	6201	GGATTCTTAGGCTTCATCGTATGGGCACACCACATATTACAGTAGGAATAGACGTTGAC	6260
Query	901	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAAGTC	960
Sbjct	6261	ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAAGTC	6320
Query	961	TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGNTCTCCGCCCTAATATGA	1020
Sbjct	6321	TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGATCTCCGCCCTAATATGA	6380
Query	1021	GCCCTAGGCTTNNNNNNNNNTTACAGTAGGTGGCTAACAGGCATCGCCTGGCCAAC	1080
Sbjct	6381	GCCCTAGGCTTCATCTCCCTTTACAGTAGGTGGCTAACAGGCATCGCCTGGCCAAC	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	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAATTCACTTATAATCAT			1250
Sbjct	6551	CCCGCTATTCTCAGGGTACACGCTTAACATCAACATGAACAAAATTCACTTATAATCAT			6610
Query	1251	ATTCGTAGGCCTAACCTAACATTCTCCCACANNNNNNNNNNNNNNNATACC			1310
Sbjct	6611	ATTCGTAGGCCTAACCTAACATTCTCCCACAAACACTTCTAGGTCTATCGGTATACC			6670
Query	1311	TCGACGATACTCCGACTATCCAGACGCCAACAAATGAAATACTATCTCATCAATAGG			1370
Sbjct	6671	TCGACGATACTCCGACTATCCAGACGCCAACAAATGAAATACTATCTCATCAATAGG			6730
Query	1371	CTCATTCTCATCTCATTAAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTG			1430
Sbjct	6731	CTCATTCTCATCTCATTAAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTG			6790
Query	1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNNCCTGAATGATTAAACGG			1490
Sbjct	6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTGAATGATTAAACGG			6850
Query	1491	ATGTCCCCACCATACCACACATTGAAGAACCCGATACATCAACCCAAATGATCAAG			1550
Sbjct	6851	ATGTCCCCACCATACCACACATTGAAGAACCCGATACATCAACCCAAATGATCAAG			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	ATGTTCATAAACCGCTGACTATTCTCAACCAACCAACAAAGACATTGGCACCTTATTTA			60
Sbjct	5361	ATGTTCATAAACCGCTGACTATTCTCAACCAACCAACAAAGACATTGGCACCTTATTTA			5420
Query	61	TTATTTGGCGCCTGAGCAGGAATAGTAGGCCTAACGCTTATTAAATTGGCGCTGAA			120
Sbjct	5421	TTATTTGGCGCCTGAGCAGGAATAGTAGGCCTAACGCTTATTAAATTGGCGCTGAA			5480
Query	121	CTAGGTCAAGCCTGGCACACTAACCGAGACGATCAAGTCTACACGCTACTAGTAACAGCC			180
Sbjct	5481	CTAGGTCAAGCCTGGCACACTAACCGAGACGATCAAGTCTACACGCTACTAGTAACAGCC			5540
Query	181	CACGCCCTTGTAATAATCTCTCATAGTAATAACCCATTATAATCGGTGGATTGGAAAC			240
Sbjct	5541	CACGCCCTTGTAATAATCTCTCATAGTAATAACCCATTATAATCGGTGGATTGGAAAC			5600
Query	241	TGACTAGTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA			300
Sbjct	5601	TGACTAGTCCCTTAATAATTGGAGCACCTGACATGGCTTCCCCGTATAAATAATATA			5660

Query 301 AGCTTCTGACTACTCCCTCCTTCTACTAACTAAGCATCCTCAATGGTCNNNNNN 360
 Sbjct 5661 AGCTTCTGACTACTCCCTCCTTCTACTAACTAAGCATCCTCAATGGTCAGGCC 5720
 Query 361 NNNNNNGGCACAGGCTNAACTGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA 420
 Sbjct 5721 GGTGCAGGCACAGGCTGAACGTATATCCCCCTCTAGCCGAAACCTAGCACATGCAGGA 5780
 Query 421 GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA 480
 Sbjct 5781 GCTTCAGTCGACCTTACCATTTCTCTACACCTAGCTGGCGTATCCTCTATCCTCGGA 5840
 Query 481 GCCATTAACTTATCACAACATCATTAAACATAAAAACACCTGCCATAACCCAATACCAA 540
 Sbjct 5841 GCCATTAACTTATCACAACATCATTAAACATAAAAACACCTGCCATAACCCAATACCAA 5900
 Query 541 ACACCTCTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT 600
 Sbjct 5901 ACACCTCTTCGTATGATCAGTCCTAGTTACAGCAGTGCTGCTCCTACTATCACTACCT 5960
 Query 601 GTCCTAGCAGCTGGAATCACCAGTCTATTAACTGACCGAAACCTAAACACTTTCTTC 660
 Sbjct 5961 GTCCTAGCAGCTGGAATCACCAGTCTATTAACTGACCGAAACCTAAACACTTTCTTC 6020
 Query 661 GACCCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC 720
 Sbjct 6021 GACCCCTGCAGGTGGAGGAGACCCAATCCTGTATCAACACCTATTCTGATTTTGGTCAC 6080
 Query 721 CCTGAAGTATATATCTTAATCCTCCCTGGGTCGGAATAATTTCACACATTGTGACTTAT 780
 Sbjct 6081 CCTGAAGTATATATCTTAATCCTCCCTGGGTCGGAATAATTTCACACATTGTGACTTAT 6140
 Query 781 TACTCAGGaaaaaaaGATCCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC 840
 Sbjct 6141 TACTCAGGaaaaaaaAGAACCTTCGGCTATATAGGAATAGTCTGAGCTATGGTATCTATC 6200
 Query 841 GGATTCTTAGGCTTCATCGTATGGGACACCACATATTACAGTAGGAATAGACGTTGAC 900
 Sbjct 6201 GGATTCTTAGGCTTCATCGTATGGGACACCACATATTACAGTAGGAATAGACGTTGAC 6260
 Query 901 ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAGTC 960
 Sbjct 6261 ACACGAGCATACTTCACATCAGCCACTATAATCATGCCATCCCTACAGGGTAAAGTC 6320
 Query 961 TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGNTCTCTGCCCTAATATGA 1020
 Sbjct 6321 TTCAGTTGATTAGCAACACTCCACGGAGGCAACATTAAATGATCTCTGCCCTAATATGA 6380
 Query 1021 GCCCTAGGCTNNNNNNNNNTTCACAGTAGGTGGCTAACAGGCATCGCCTGGCCAAC 1080
 Sbjct 6381 GCCCTAGGCTTCATCTCCCTTACAGTAGGTGGCTAACAGGCATCGCCTGGCCAAC 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	CCCGCTATTCTCAGGGTACACGCTTAACCTAACATGAACAAAAATTCACTTATAATCAT				1250
Sbjct 6551	CCCGCTATTCTCAGGGTACACGCTTAACCTAACATGAACAAAAATTCACTTATAATCAT				6610
Query 1251	ATTCGTAGGCGTAAACCTAACATTCTCCCACANNNNNNNNNNNNNNNATACC				1310
Sbjct 6611	ATTCGTAGGCGTAAACCTAACATTCTCCCACAAACACTTCTAGGTCTATCCGTATACC				6670
Query 1311	TCGACGATACTCCGACTATCCAGCAGCCTACACAATATGAAATACTATCTCATCAATAGG				1370
Sbjct 6671	TCGACGATACTCCGACTATCCAGCAGCCTACACAATATGAAATACTATCTCATCAATAGG				6730
Query 1371	CTCATTCTCATCTCATTAAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTGCG				1430
Sbjct 6731	CTCATTCTCATCTCATTAAACAGCAGTTACTAATAATTTCATCATCTGAGAAGCATTGCG				6790
Query 1431	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTNNCCTGAATGATTAACCGG				1490
Sbjct 6791	ATCCAAACGAGAAGTACTAGCAGTAGACCTCACCTCTACTAACCTGAATGATTAACCGG				6850
Query 1491	ATGTCCCCCACCACACATTCGAAGAACCCGCATACATCAACCCAAAATGATCAAG				1550
Sbjct 6851	ATGTCCCCCACCACACATTCGAAGAACCCGCATACATCAACCCAAAATGATCAAG				6910
Query 1551	A 1551				
Sbjct 6911	A 6911				

Taxonomy

Reports

- Lineage

Organism	Blast Name	Score	Number of Hits	Description
Balaenidae	whales & dolphins	112		
.Eubalaena	whales & dolphins	63		
..Eubalaena japonica	whales & dolphins	1912	29	Eubalaena japonica hits
..Eubalaena glacialis	whales & dolphins	1884	15	Eubalaena glacialis hits
..Eubalaena australis	whales & dolphins	1884	19	Eubalaena australis hits
.Balaena mysticetus	whales & dolphins	1746	49	Balaena mysticetus hits

◦ Organism

Description		Score	E value	Accession
Eubalaena japonica (North Pacific right whale)	[whales & dolphins]			
Eubalaena japonica isolate SWFSC_MMASTR_44460 mitochondrion, complete genome		1912	0.0	OP205215
Eubalaena japonica isolate SWFSC_MMASTR_43855 mitochondrion, complete genome		1912	0.0	OP205204
Eubalaena japonica isolate SWFSC_MMASTR_28432 mitochondrion, complete genome		1912	0.0	OP205199
Eubalaena japonica isolate SWFSC_MMASTR_13192 mitochondrion, complete genome		1912	0.0	OP205194
Eubalaena japonica isolate SWFSC_MMASTR_43864 mitochondrion, complete genome		1912	0.0	OP205209
Eubalaena japonica isolate SWFSC_MMASTR_7966 mitochondrion, complete genome		1912	0.0	OP205193
Eubalaena japonica mitochondrion, complete genome		1912	0.0	NC_006931
Eubalaena japonica mitochondrial DNA, complete genome		1912	0.0	AP006474
Eubalaena japonica isolate SWFSC_MMASTR_43863 mitochondrion, complete genome		1912	0.0	OP205208
Eubalaena japonica isolate SWFSC_MMASTR_44461 mitochondrion, complete genome		1912	0.0	OP205216
Eubalaena japonica isolate SWFSC_MMASTR_43867 mitochondrion, complete genome		1906	0.0	OP205212
Eubalaena japonica isolate SWFSC_MMASTR_43866 mitochondrion, complete genome		1906	0.0	OP205211
Eubalaena japonica isolate SWFSC_MMASTR_43858 mitochondrion, complete genome		1906	0.0	OP205206
Eubalaena japonica isolate SWFSC_MMASTR_43853 mitochondrion, complete genome		1906	0.0	OP205203
Eubalaena japonica isolate SWFSC_MMASTR_43851 mitochondrion, complete genome		1906	0.0	OP205202
Eubalaena japonica isolate SWFSC_MMASTR_43871 mitochondrion, complete genome		1906	0.0	OP205214
Eubalaena japonica isolate SWFSC_MMASTR_43860 mitochondrion, complete genome		1901	0.0	OP205207
Eubalaena japonica isolate SWFSC_MMASTR_43850 mitochondrion, complete genome		1901	0.0	OP205201
Eubalaena japonica isolate SWFSC_MMASTR_43849 mitochondrion, complete genome		1901	0.0	OP205200
Eubalaena japonica isolate SWFSC_MMASTR_7963 mitochondrion, complete genome		1901	0.0	OP205192
Eubalaena japonica isolate SWFSC_MMASTR_62934 mitochondrion, complete genome		1895	0.0	OP205218
Eubalaena japonica isolate SWFSC_MMASTR_43870 mitochondrion, complete genome		1895	0.0	OP205213
Eubalaena japonica isolate SWFSC_MMASTR_43865 mitochondrion, complete genome		1895	0.0	OP205210
Eubalaena japonica isolate SWFSC_MMASTR_43856 mitochondrion, complete genome		1895	0.0	OP205205
Eubalaena japonica isolate SWFSC_MMASTR_28430 mitochondrion, complete genome		1895	0.0	OP205198
Eubalaena japonica isolate SWFSC_MMASTR_28428 mitochondrion, complete genome		1895	0.0	OP205197
Eubalaena japonica isolate SWFSC_MMASTR_53766 mitochondrion, complete genome		1890	0.0	OP205217
Eubalaena japonica isolate SWFSC_MMASTR_23634 mitochondrion, complete genome		1890	0.0	OP205196
Eubalaena japonica isolate SWFSC_MMASTR_23631 mitochondrion, complete genome		1890	0.0	OP205195
Eubalaena glacialis (North Atlantic right whale)	[whales & dolphins]			
Eubalaena glacialis mitochondrion, complete genome		1884	0.0	MF459656
Eubalaena glacialis isolate Egl02Feb09F mitochondrion, complete genome		1884	0.0	OP205182
Eubalaena glacialis isolate SWFSC_MMASTR_28311 mitochondrion, complete genome		1884	0.0	OP205191
Eubalaena glacialis isolate SWFSC_MMASTR_15112 mitochondrion, complete genome		1884	0.0	OP205190
Eubalaena glacialis isolate SWFSC_MMASTR_4977 mitochondrion, complete genome		1884	0.0	OP205189
Eubalaena glacialis isolate Egl20Feb10B mitochondrion, complete genome		1884	0.0	OP205187
Eubalaena glacialis isolate Egl17Feb07A mitochondrion, complete genome		1884	0.0	OP205185
Eubalaena glacialis isolate Egl10Jan08G mitochondrion, complete genome		1884	0.0	OP205184

Description		Score	E value	Accession
Eubalaena glacialis isolate Egl08Feb09B_gDNA mitochondrion, complete genome		1884	0.0	OP205183
Eubalaena glacialis isolate Eg#1014 'Staccato' cytochrome oxidase subunit I (cox1).gene, complete cds; mitochondrial		1884	0.0	DQ095154
Eubalaena glacialis isolate Egl21Feb07B mitochondrion, complete genome		1879	0.0	OP205188
Eubalaena glacialis isolate Egl20Feb07B mitochondrion, complete genome		1879	0.0	OP205186
Eubalaena glacialis isolate Egl02Feb09D mitochondrion, complete genome		1879	0.0	OP205181
Eubalaena glacialis mitochondrion, complete genome		1862	0.0	NC_037444
Eubalaena glacialis mitochondrion, complete genome		1862	0.0	MF409247
Eubalaena australis (southern right whale)	[whales & dolphins]			
Eubalaena australis isolate Eaus0550m_Arg mitochondrion, complete genome		1884	0.0	OP205174
Eubalaena australis isolate Eaus06GNJ_Arg mitochondrion, complete genome		1884	0.0	OP205169
Eubalaena australis isolate Eaus06132m_Arg mitochondrion, complete genome		1879	0.0	OP205177
Eubalaena australis isolate Eaus09AI105_Al mitochondrion, complete genome		1879	0.0	OP205172
Eubalaena australis isolate Eaus06GNA_Arg mitochondrion, complete genome		1879	0.0	OP205168
Eubalaena australis isolate EA123 cytochrome oxidase subunit I (cox1).gene, complete cds; mitochondrial		1879	0.0	DQ095155
Eubalaena australis isolate Eaus06138m_Arg mitochondrion, complete genome		1873	0.0	OP205178
Eubalaena australis isolate Eaus0587m_Arg mitochondrion, complete genome		1868	0.0	OP205175
Eubalaena australis isolate Eaus06129m_Arg mitochondrion, complete genome		1862	0.0	OP205176
Eubalaena australis isolate Eaus058SA_Arg mitochondrion, complete genome		1862	0.0	OP205173
Eubalaena australis isolate Eaus07AI065_Al mitochondrion, complete genome		1862	0.0	OP205170
Eubalaena australis isolate Eaus06A1_Arg mitochondrion, complete genome		1862	0.0	OP205167
Eubalaena australis isolate Eaus03K1_Arg mitochondrion, complete genome		1862	0.0	OP205166
Eubalaena australis isolate Eaus08AI081_Al mitochondrion, complete genome		1862	0.0	OP205171
Eubalaena australis isolate Eaus06144m_Arg mitochondrion, complete genome		1862	0.0	OP205179
Eubalaena australis mitochondrion, complete genome		1862	0.0	NC_006930
Eubalaena australis mitochondrial DNA, complete genome		1862	0.0	AP006473
Eubalaena australis isolate Eaus_AP006474 mitochondrion, complete genome		1862	0.0	OP205180
Eubalaena australis isolate EA604 cytochrome oxidase subunit I (cox1).gene, complete cds; mitochondrial		1857	0.0	DQ095156
Balaena mysticetus (bowhead whale)	[whales & dolphins]			
Balaena mysticetus voucher NHMO-DMA-43197 mitochondrion, complete genome		1746	0.0	MN145938
Balaena mysticetus isolate SWFSC LAB ID 50790 mitochondrion, complete genome		1746	0.0	MZ618258
Balaena mysticetus voucher NHMO-DMA-43194 mitochondrion, complete genome		1740	0.0	MN124685
Balaena mysticetus voucher PMO 234.423 mitochondrion, complete genome		1740	0.0	MN159085
Balaena mysticetus voucher NHMO-DMA-43206 mitochondrion, complete genome		1740	0.0	MN159084
Balaena mysticetus voucher PMO 234.429 mitochondrion, complete genome		1740	0.0	MN159082
Balaena mysticetus voucher PMO 234.522 mitochondrion, complete genome		1740	0.0	MN159081
Balaena mysticetus voucher PMO 234.573 mitochondrion, complete genome		1740	0.0	MN159080
Balaena mysticetus voucher NHMO-DMA-43191 mitochondrion, complete genome		1740	0.0	MN145939
Balaena mysticetus voucher NHMO-DMA-43195 mitochondrion, complete genome		1740	0.0	MN145937
Balaena mysticetus isolate QT3_Oeqertassussuk mitochondrion, partial genome		1740	0.0	MH198022
Balaena mysticetus isolate H mitochondrion, complete genome		1740	0.0	KY026773
Balaena mysticetus isolate I mitochondrion, complete genome		1740	0.0	KY026772
Balaena mysticetus isolate F mitochondrion, complete genome		1740	0.0	KY026771
Balaena mysticetus isolate E mitochondrion, complete genome		1740	0.0	KY026770
Balaena mysticetus isolate D mitochondrion, complete genome		1740	0.0	KY026769
Balaena mysticetus isolate C mitochondrion, complete genome		1740	0.0	KY026768
Balaena mysticetus isolate B mitochondrion, complete genome		1740	0.0	KY026767

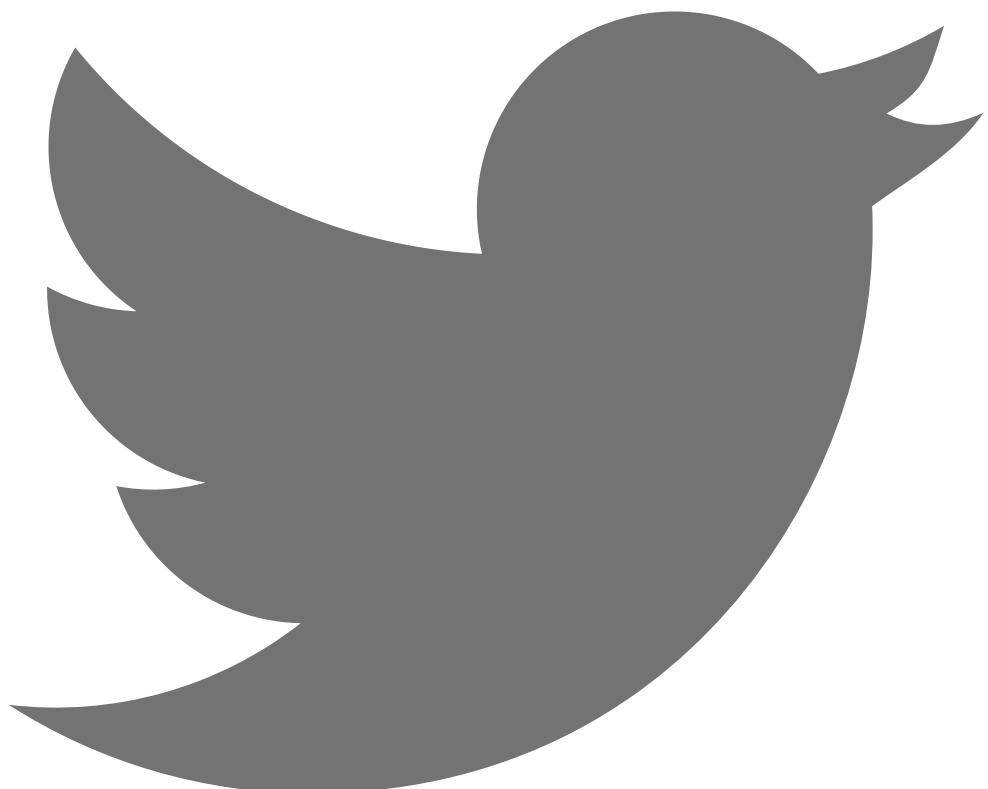
Description	Score	E value	Accession
Balaena mysticetus isolate A mitochondrion, complete genome	1740	0.0	KY026766
Balaena mysticetus isolate SWFSC LAB ID 112407 mitochondrion, complete genome	1740	0.0	MZ618260
Balaena mysticetus isolate SWFSC LAB ID 50788 mitochondrion, complete genome	1740	0.0	MZ618257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

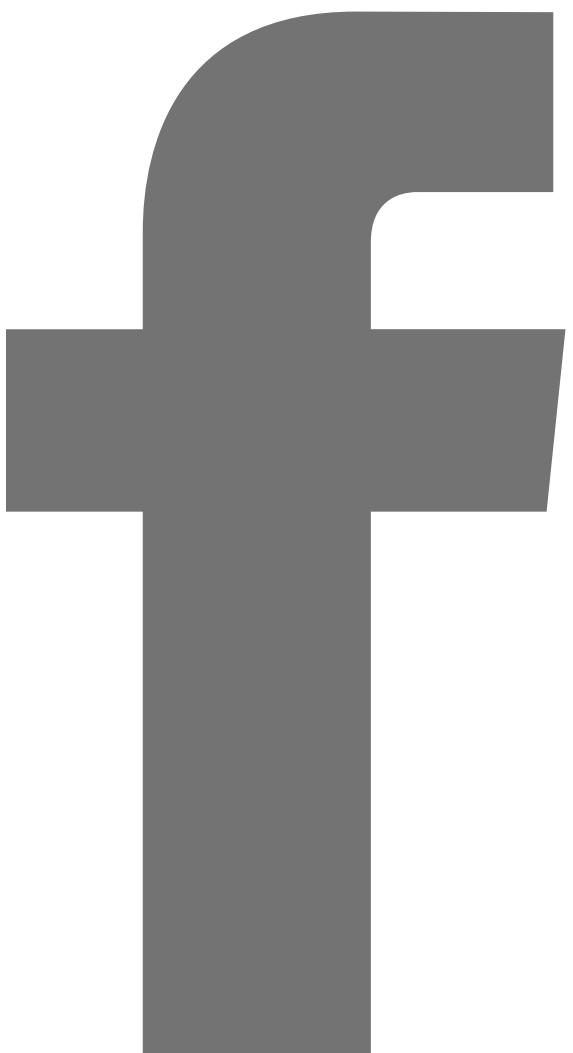
- **Taxonomy**

Taxonomy	Number of hits	Number of Organisms	Description
Balaenidae	112	4	
. Eubalaena	63	3	
.. Eubalaena japonica	29	1	Eubalaena japonica hits
.. Eubalaena glacialis	15	1	Eubalaena glacialis hits
.. Eubalaena australis	19	1	Eubalaena australis hits
. Balaena mysticetus	49	1	Balaena mysticetus hits

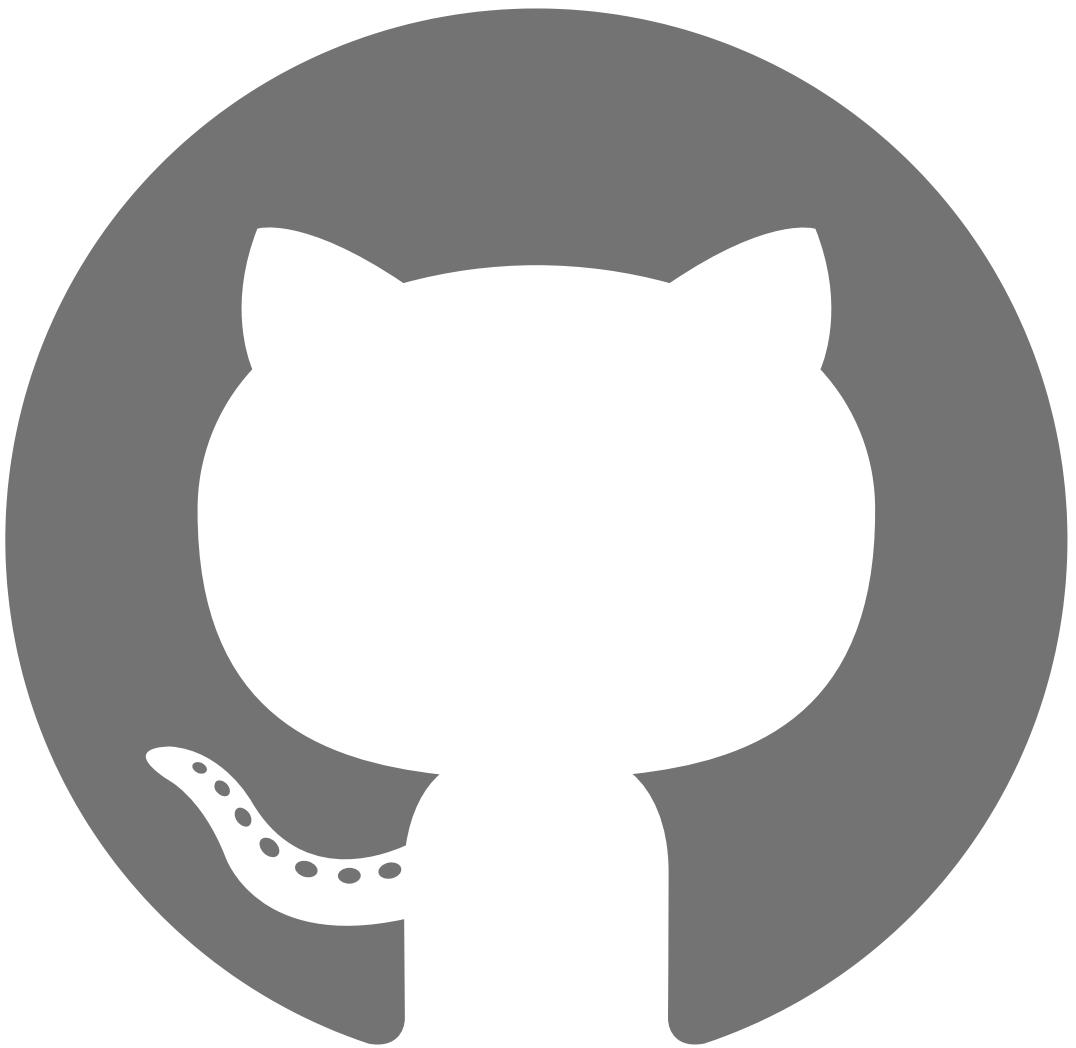
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