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BLAST® >> **blastn suite** >> results for RID-KE6WVD1K014

Job Title	Nucleotide Sequence ...
RID	KE6WVD1K014 Search expires on 12-10 01:40 am
Program	BLASTN
Database	nt
Query ID	Icl Query_1844041
Description	None ...
Molecule type	dna
Query Length	1541

Descriptions

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>Dermochelys coriacea voucher CRI006922 mitochondrial, complete genome</u>	<u>Dermochelys coriacea</u>	1923	1923	77%	0.0	94.65%	16501	MF460363.1
<u>Dermochelys coriacea isolate CGG-03 mitochondrial, partial genome</u>	<u>Dermochelys coriacea</u>	1923	1923	77%	0.0	94.65%	16680	JX454992.1
<u>Dermochelys coriacea isolate 9790 mitochondrial, partial genome</u>	<u>Dermochelys coriacea</u>	1923	1923	77%	0.0	94.65%	16380	JX454973.1
<u>Dermochelys coriacea isolate 5718 mitochondrial, partial genome</u>	<u>Dermochelys coriacea</u>	1923	1923	77%	0.0	94.65%	16420	JX454969.1
<u>Dermochelys coriacea isolate 88903 mitochondrial, partial genome</u>	<u>Dermochelys coriacea</u>	1908	1908	77%	0.0	94.31%	16366	JX454989.1
<u>Dermochelys coriacea voucher DC-COI-AP1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial</u>	<u>Dermochelys coriacea</u>	1452	1452	53%	0.0	98.53%	815	GQ152876.1
<u>Dermochelys coriacea cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial</u>	<u>Dermochelys coriacea</u>	1421	1421	52%	0.0	98.50%	798	KU883273.1
<u>Eretmochelys imbricata isolate E13 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16582	PQ276118.1
<u>Eretmochelys imbricata isolate E12 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16572	PQ276117.1
<u>Eretmochelys imbricata isolate E11 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16581	PQ276116.1
<u>Eretmochelys imbricata isolate E10 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16573	PQ276115.1
<u>Eretmochelys imbricata isolate E9 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16580	PQ276114.1
<u>Eretmochelys imbricata isolate E8 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16581	PQ276113.1
<u>Eretmochelys imbricata isolate E7 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16581	PQ276112.1
<u>Eretmochelys imbricata isolate E6 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16590	PQ276111.1
<u>Eretmochelys imbricata isolate E5 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16572	PQ276110.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>Eretmochelys imbricata isolate E4 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16581	PQ276109.1
<u>Eretmochelys imbricata isolate E1 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16590	PQ276106.1
<u>Eretmochelys imbricata isolate rErelmb1 genome assembly, organelle: mitochondrial</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16779	OZ223910.1
<u>Eretmochelys imbricata mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16386	KP221806.1
<u>Eretmochelys imbricata isolate 61392 mitochondrial, partial genome</u>	<u>Eretmochelys imbricata</u>	1347	1347	83%	0.0	84.71%	16349	JX454980.1
<u>Eretmochelys imbricata isolate E3 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1341	1341	83%	0.0	84.63%	16591	PQ276108.1
<u>Eretmochelys imbricata isolate E2 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1341	1341	83%	0.0	84.63%	16582	PQ276107.1
<u>Eretmochelys imbricata isolate 5787 mitochondrial, partial genome</u>	<u>Eretmochelys imbricata</u>	1341	1341	83%	0.0	84.63%	16354	JX454970.1
<u>Natator depressus isolate rNatDep1 genome assembly, organelle: mitochondrial</u>	<u>Natator depressus</u>	1336	1336	83%	0.0	84.53%	16559	OZ223967.1
<u>Eretmochelys imbricata isolate C-C-2 mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1336	1336	83%	0.0	84.56%	16498	MF571906.1
<u>Eretmochelys imbricata isolate 72489 mitochondrial, partial genome</u>	<u>Eretmochelys imbricata</u>	1336	1336	83%	0.0	84.56%	16347	JX454986.1
<u>Natator depressus haplogroup Au (X) mitochondrial, complete genome</u>	<u>Natator depressus</u>	1330	1330	83%	0.0	84.45%	16281	NC_018550.1
<u>Eretmochelys imbricata mitochondrial, complete genome</u>	<u>Eretmochelys imbricata</u>	1330	1330	83%	0.0	84.48%	16478	NC_012398.1
<u>Chelonia mydas isolate 28666 mitochondrial, complete genome</u>	<u>Chelonia mydas</u>	1308	1308	83%	0.0	84.08%	16435	JX454976.1
<u>Chelonia mydas isolate CGG-01Cmyd mitochondrial, complete genome</u>	<u>Chelonia mydas</u>	1291	1291	83%	0.0	83.85%	16495	JX454990.1
<u>Chelonia mydas isolate 54903 mitochondrial, partial genome</u>	<u>Chelonia mydas</u>	1291	1291	83%	0.0	83.85%	16435	JX454978.1
<u>Chelonia mydas isolate 13768</u>	<u>Chelonia mydas</u>	1291	1291	83%	0.0	83.85%	16435	JX454974.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>mitochondrion, complete genome</u>								
<u>Chelonia mydas isolate Sample ID 9277 mitochondrion, complete genome</u>	Chelonia mydas	1291	1291	83%	0.0	83.85%	16440	JX454972.1
<u>Chelonia mydas isolate 8855 mitochondrion, complete genome</u>	Chelonia mydas	1291	1291	83%	0.0	83.85%	16435	JX454971.1
<u>Chelonia mydas mitochondrion, partial genome</u>	Chelonia mydas	1291	1291	83%	0.0	83.85%	16350	JQ026233.1
<u>Chelonia mydas mitochondrion, complete genome</u>	Chelonia mydas	1291	1291	83%	0.0	83.85%	16497	NC_000886.1
<u>Chelonia mydas mitochondrion, partial genome</u>	Chelonia mydas	1286	1286	83%	0.0	83.77%	16350	JQ034420.1
<u>Caretta caretta isolate 87410 mitochondrion, complete genome</u>	Caretta caretta	1275	1275	83%	0.0	83.67%	16411	JX454988.1
<u>Caretta caretta isolate 46603 mitochondrion, complete genome</u>	Caretta caretta	1275	1275	83%	0.0	83.67%	16399	JX454977.1
<u>Caretta caretta isolate Cc-C-4 mitochondrion, complete genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16446	MF579505.1
<u>Caretta caretta isolate Cc-C-3 mitochondrion, complete genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16461	MF579504.1
<u>Caretta caretta isolate Cc-C-1 mitochondrion, complete genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16633	MF554690.1
<u>Caretta caretta isolate SIC25 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166644.1
<u>Caretta caretta isolate SIC21 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166640.1
<u>Caretta caretta isolate SIC20 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166639.1
<u>Caretta caretta isolate SIC15 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166634.1
<u>Caretta caretta isolate SIC14 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166633.1
<u>Caretta caretta isolate SIC02 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166622.1
<u>Caretta caretta isolate LIN01 mitochondrion, partial genome</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166619.1
<u>Caretta caretta isolate CAL1370</u>	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166616.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
mitochondrion, partial genome								
Caretta caretta isolate CAL1124 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166600.1
Caretta caretta isolate CAL1112 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166599.1
Caretta caretta isolate LAT04 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166598.1
Caretta caretta isolate TUS05 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166594.1
Caretta caretta isolate TUS04 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166592.1
Caretta caretta isolate TUS03 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166590.1
Caretta caretta isolate ADR03 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166584.1
Caretta caretta isolate ADR02 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166583.1
Caretta caretta isolate ADR01 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166582.1
Caretta caretta mitochondrion, complete genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16549	OR775090.1
Caretta caretta mitochondrion, complete genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16362	KP256531.1
Caretta caretta isolate 69611 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16337	JX454984.1
Caretta caretta isolate 69599 mitochondrion, complete genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16454	JX454983.1
Caretta caretta complete mitochondrial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16737	FR694649.1
Lepidochelys kempii isolate 6 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16464	MN136060.1
Lepidochelys kempii isolate 13 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16443	MN136059.1
Lepidochelys kempii isolate 3 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16443	MN136058.1
Lepidochelys kempii isolate MT1	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16372	MN136057.1

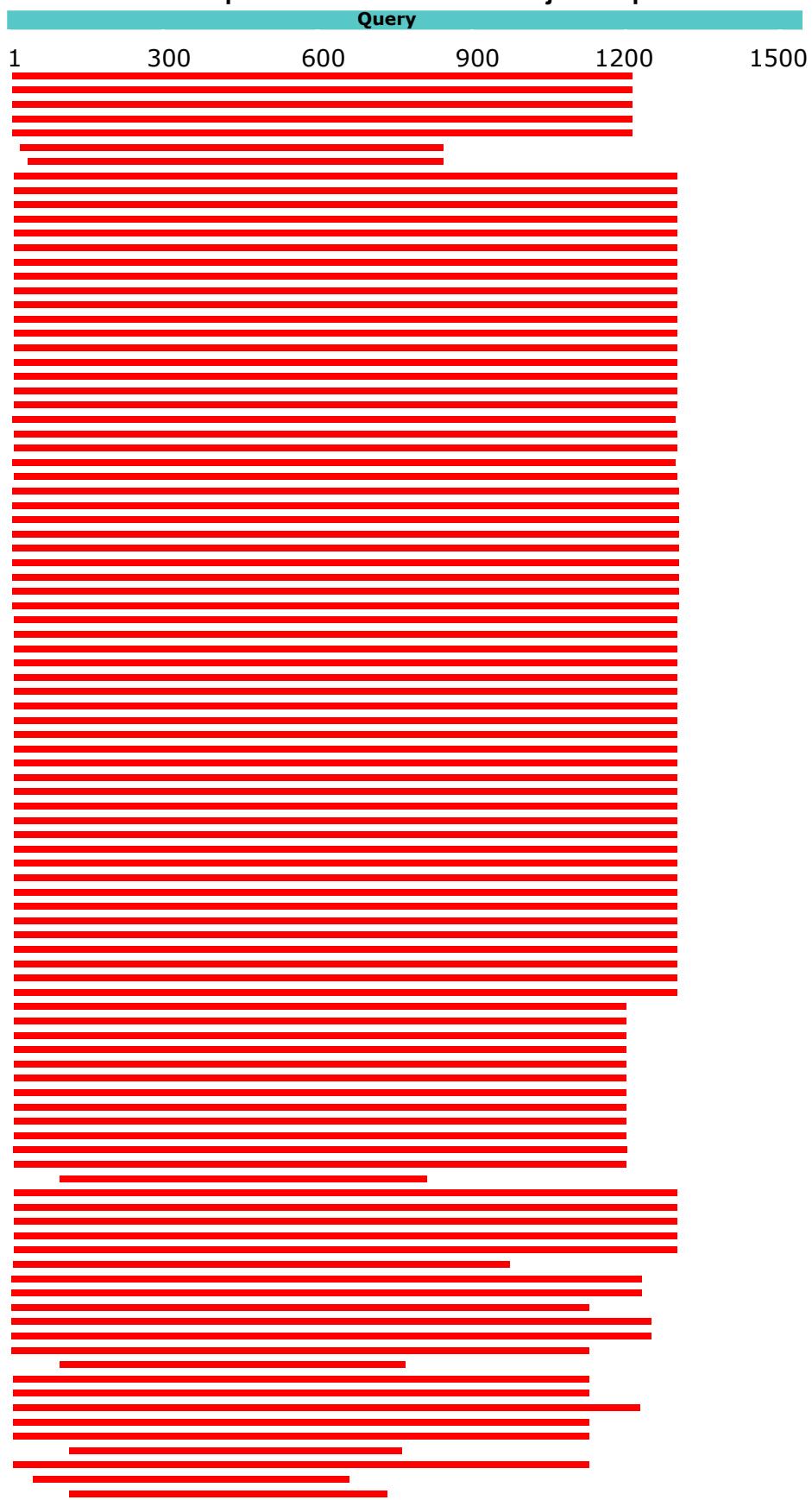
Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>mitochondrion, complete genome</u>								
<u>Lepidochelys kempii isolate 27</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys kempii</u>	1256	1256	77%	0.0	84.78%	16483	<u>MN136056.1</u>
<u>Lepidochelys kempii isolate 1</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys kempii</u>	1256	1256	77%	0.0	84.78%	16438	<u>MN136055.1</u>
<u>Lepidochelys kempii isolate BR1</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys kempii</u>	1256	1256	77%	0.0	84.78%	16406	<u>MN136054.1</u>
<u>Lepidochelys kempii isolate 14</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys kempii</u>	1256	1256	77%	0.0	84.78%	16443	<u>MN136053.1</u>
<u>Lepidochelys kempii isolate 16</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys kempii</u>	1256	1256	77%	0.0	84.78%	16444	<u>MN136052.1</u>
<u>Lepidochelys kempii isolate 68091</u> <u>mitochondrion, partial genome</u>	<u>Lepidochelys kempii</u>	1256	1256	77%	0.0	84.78%	16386	<u>JX454982.1</u>
<u>Lepidochelys kempii isolate 23</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys kempii</u>	1254	1254	77%	0.0	84.73%	16433	<u>MN136061.1</u>
<u>Lepidochelys kempii isolate 68090</u> <u>mitochondrion, partial genome</u>	<u>Lepidochelys kempii</u>	1253	1253	77%	0.0	84.70%	16382	<u>JX454981.1</u>
<u>Dermochelys coriacea voucher</u> <u>ZSI/ANRC/M/29790</u> <u>cytochrome c oxidase subunit I</u> <u>(COX1) gene, partial cds; mitochondrial</u>	<u>Dermochelys coriacea</u>	1249	1249	46%	0.0	98.30%	705	<u>PQ069769.1</u>
<u>Lepidochelys olivacea isolate rLepOli2 genome assembly, organelle:</u> <u>mitochondrion</u>	<u>Lepidochelys olivacea</u>	1232	1232	83%	0.0	83.06%	16732	<u>OZ223140.1</u>
<u>Lepidochelys olivacea voucher</u> <u>CLP:OR1</u> <u>cytochrome c oxidase subunit I</u> <u>(COX1).gene,partial cds; mitochondrial</u>	<u>Lepidochelys olivacea</u>	1232	1232	83%	0.0	83.06%	1545	<u>PQ459488.1</u>
<u>Lepidochelys olivacea isolate CGG-01Lol</u> <u>mitochondrion, complete genome</u>	<u>Lepidochelys olivacea</u>	1232	1232	83%	0.0	83.06%	16718	<u>NC_028634.1</u>
<u>Lepidochelys olivacea isolate 78920</u> <u>mitochondrion, partial genome</u>	<u>Lepidochelys olivacea</u>	1232	1232	83%	0.0	83.06%	16387	<u>JX454987.1</u>
<u>Lepidochelys olivacea isolate 55352</u> <u>mitochondrion, partial genome</u>	<u>Lepidochelys olivacea</u>	1232	1232	83%	0.0	83.06%	16379	<u>JX454979.1</u>
<u>Eretmochelys imbricata voucher</u> <u>CLP:GT1</u> <u>cytochrome c</u>	<u>Eretmochelys imbricata</u>	1214	1214	62%	0.0	89.35%	1000	<u>PQ459491.1</u>

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>oxidase subunit I (COX1).gene.,partial cds; mitochondrial Chelonoidis alburyorum mitochondrion genomic DNA containing trnF-trnT region, specimen voucher GT-3, FS 234 (MTD18987)</u>	<u>Chelonoidis alburyorum</u>	1206	1206	79%	0.0	83.55%	15349	LR968547.1
<u>Chelonoidis alburyorum mitochondrion genomic DNA containing trnF-trnT region, specimen voucher GT-3, FS82 (MTD18982)</u>	<u>Chelonoidis alburyorum</u>	1206	1206	79%	0.0	83.55%	15339	LR968543.1
<u>Stigmochelys pardalis mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher MTD T 16076</u>	<u>Stigmochelys pardalis</u>	1194	1194	72%	0.0	85.29%	15358	LR697082.1
<u>Geochelone elegans mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher MTD T 6057</u>	<u>Geochelone elegans</u>	1194	1194	80%	0.0	83.13%	15320	LR697072.1
<u>Geochelone elegans mitochondrion, complete genome Psammobates pardalis mitochondrion, complete genome</u>	<u>Geochelone elegans</u>	1194	1194	80%	0.0	83.13%	16446	NC_041096.1
<u>Dermochelys coriacea voucher ZSI/ANRC/M/29790 cytochrome c oxidase subunit I (COX1).gene.,partial cds; mitochondrial Cylindraspis triserrata mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher BMNH R3992</u>	<u>Dermochelys coriacea</u>	1171	1171	43%	0.0	98.19%	663	PQ216296.1
<u>Cylindraspis triserrata mitochondrion genomic DNA containing from tRNA-Phe (partial) to tRNA-Thr (partial) region, specimen voucher NHMUK 1876.10.28.4</u>	<u>Cylindraspis triserrata</u>	1151	1151	72%	0.0	84.64%	15335	LR697065.1
<u>Cylindraspis triserrata mitochondrion genomic DNA containing from tRNA-Phe (partial) to tRNA-Thr (partial) region, specimen voucher NHMUK 1876.10.28.4</u>	<u>Cylindraspis triserrata</u>	1151	1151	72%	0.0	84.64%	15382	OW244303.1
<u>Trachemys decussata angusta mitochondrion genomic DNA containing from tRNA-Phe</u>	<u>Trachemys decussata angusta</u>	1144	1144	79%	0.0	82.69%	16568	OX453476.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<u>(complete) to control region (partial)</u> <u>region, specimen voucher MTD-T 20622</u>								
<u>Mauremys japonica mitochondrial DNA, complete sequence</u>	<u>Mauremys japonica</u>	1140	1140	72%	0.0	84.44%	16443	AP019397.1
<u>Mauremys japonica mitochondrion, complete genome</u>	<u>Mauremys japonica</u>	1140	1140	72%	0.0	84.44%	16443	NC_016951.1
<u>Dermochelys coriacea voucher ZSI/ANRC/M/29791 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial</u>	<u>Dermochelys coriacea</u>	1127	1127	41%	0.0	98.12%	639	PQ069775.1
<u>Chrysemys picta bellii mitochondrion, complete genome</u>	<u>Chrysemys picta bellii</u>	1116	1116	72%	0.0	84.10%	16875	NC_023890.1
<u>Dermochelys coriacea voucher USNM:Herp:544382 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial</u>	<u>Dermochelys coriacea</u>	1085	1085	39%	0.0	98.52%	607	MH273769.1
<u>Dermochelys coriacea voucher ZSI/ANRC/M/29791 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial</u>	<u>Dermochelys coriacea</u>	1077	1077	40%	0.0	98.04%	612	PQ216299.1

Graphic Summary

Distribution of the top 100 Blast Hits on 100 subject sequences



Alignments

Alignment view CDS feature

Dermochelys coriacea voucher CRI006922 mitochondrion, complete genome

Sequence ID: **MF460363.1** Length: 16501 Number of Matches: 1

Range 1: 5414 to 6608

Score	Expect	Identities	Gaps	Strand	Frame
1923 bits(1041)	0.0()	1132/1196(95%)	3/1196(0%)	Plus/Plus	
Query 11	CTCGCTGAtttttt	CTACTAATCATAAAGACATTGGCACCCATACCTAATTGGGG	70		

Sbjct	5414	CTCGCTGATTTTCTACTAATCATAAAGACATTGGCACCCCTATACCTAATTTGGGG	5473
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC	130
Sbjct	5474	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC	5533
Query	131	CGGGAACCCCTCTAGGAGATGACCAAATTACAATGTCATCGTTACAGCCCAGCCTCA	190
Sbjct	5534	CGGGAACCCCTCTAGGAGATGACCAAATTACAATGTCATCGTTACAGCCCAGCCTCA	5593
Query	191	TTATAATCTCTCATAGTTATACCAAGTTATAATCGCGGTTTGGAAACTGACTTGTTC	250
Sbjct	5594	TTATAATCTCTCATAGTTATACCAAGTTATAATCGCGGTTTGGAAACTGACTTGTTC	5653
Query	251	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTGNN	310
Sbjct	5654	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTGAC	5713
Query	311	NNNNNNCTCCCTCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	370
Sbjct	5714	TTTACCTCCCTCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	5773
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAG	430
Sbjct	5774	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAG	5833
Query	431	ACCTAACTATCTTTCTGACCTAGCTGGTGTTCATCAATTAGGAGCTATT-ACT	489
Sbjct	5834	ACCTAACTATCTTTCTGACCTAGCTGGTGTTCATCAATTAGGAGCTATTAACT	5893
Query	490	TCATTACTACAGCAATCACATAAACTCCAGCTATATCACAAATACCAAACACCATTAT	549
Sbjct	5894	TCATTACTACAGCAATCACATAAACTCCAGCTATATCACAAATACCAAACACCATTAT	5953
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTACTCTCATGCCAGTAGCTG	609
Sbjct	5954	TTGTATGATCTGTATTAATTACAGCCGTTCTATTACTCTCATGCCAGTAGCTG	6013
Query	610	CAGGAATCACCATACTACAGATCGAAACCTAAACACAACCCCTTTGATCCTTCAG	669
Sbjct	6014	CAGGAATCACCATACTACAGATCGAAACCTAAACACAACCCCTTTGATCCTTCAG	6073
Query	670	GAGGAGGAGACCAATCCTATACCAAAATGCTATTCTGATTCTTGGCCATCCAGAAGTAT	729
Sbjct	6074	GAGGAGGAGACCAATCCTATACCAACACCTATTCTGATTCTTGGCCATCCAGAAGTAT	6133
Query	730	ACATCCTAATTCTACCAGGATTCCGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6134	ACATCCTAATTCTACCAGGATTCCGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6193
Query	790	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	849
Sbjct	6194	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	6253
Query	850	GTTTATCGTTGAGCCACCATATATTACTGTTGAATAGACGTAGACACACGAGCTT	909
Sbjct	6254	GTTTATCGTTGAGCCACCATATATTACTGTTGAATAGACGTAGACACACGAGCTT	6313
Query	910	ACTTACATCAGCAACAATAATTATTGCCATCCACAGGAGTAAAGTGTAGCTGAN	969
Sbjct	6314	ACTTACATCAGCAACAATAATTATTGCCATCCACAGGAGTAAAGTGTAGCTGAC	6373
Query	970	NNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	1029
Sbjct	6374	TAGCAACCCTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	6433
Query	1030	TTATTTCCATTACTATTGGTGGCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6434	TTATTTCCATTACTATTGGTGGATTACAGGTATTGTACTAGCCAACCTCATCACTAG	6493
Query	1090	ACATCGTACTACACGACACGTACTACGTTGTAGC-CNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6494	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTCCATTATGTT-CTATCAATA	6552
Query	1149	GGAGCTGTATTCGCATCATAGGAGGCTTCACTCACTGATTCCCTATTCTCAGG	1204
Sbjct	6553	GGAGCTGTATTCGCATCATAGCAGGTTACTCACTGATTCCCTCTTCAACAGG	6608

Dermochelys coriacea isolate CGG-03 mitochondrion, partial genome

Sequence ID: **JX454992.1** Length: 16680 Number of Matches: 1

Range 1: 5414 to 6608

Score	Expect	Identities	Gaps	Strand	Frame
1923 bits(1041)	0.0()	1132/1196(95%)	3/1196(0%)	Plus/Plus	
Query	11	CTCGCTGAtttttCTACTAATCATAAAGACATTGGCACCCCTATACCTAATTTGGGG	70		
Sbjct	5414	CTCGCTGATTTTCTACTAATCATAAAGACATTGGCACCCCTATACCTAATTTGGGG	5473		
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC	130		
Sbjct	5474	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC	5533		
Query	131	CGGGAACCCCTCTAGGAGATGACCAAATTACAATGTCATCGTTACAGCCCAGCCTCA	190		

Sbjct	5534	CGGGAACCCCTCCTAGGAGATGACCAAAATTACAATGTACCGTTACAGCCCCATGCCCTCA	5593
Query	191	TTATAATCTCTCATAGTTATACCAGTTATAATCGGCGGTTCGGAAACTGACTTGTTC	250
Sbjct	5594	TTATAATCTCTCATAGTTATACCAGTTATAATCGGCGGTTCGGAAACTGACTTGTTC	5653
Query	251	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTGNN	310
Sbjct	5654	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTGAC	5713
Query	311	NNNNNNCTCCCTCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	370
Sbjct	5714	TTTACCTCCCTCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	5773
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAG	430
Sbjct	5774	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAG	5833
Query	431	ACCTAACTATCTTCTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATT-ACT	489
Sbjct	5834	ACCTAACTATCTTCTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATTAACT	5893
Query	490	TCATTACTACAGCAATCAACATAAAATCTCAGCTATATCACAATACCAAACACCATTAT	549
Sbjct	5894	TCATTACTACAGCAATCAACATAAAATCTCAGCTATATCACAATACCAAACACCATTAT	5953
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTACTCTCATTGCCAGTAGCTG	609
Sbjct	5954	TTGTATGATCTGTATTAATTACAGCCGTTCTATTACTCTCATTGCCAGTAGCTG	6013
Query	610	CAGGAATCACCATACTACTACAGATCGAACCTAAACACAAACCTTTTGATCCTTCAG	669
Sbjct	6014	CAGGAATCACCATACTACTACAGATCGAACCTAAACACAAACCTTTTGATCCTTCAG	6073
Query	670	GAGGAGGAGACCCAATCCATACCAACACCTATTCTGATTCTGGCCATCCAGAAGTAT	729
Sbjct	6074	GAGGAGGAGACCCAATCCATACCAACACCTATTCTGATTCTGGCCATCCAGAAGTAT	6133
Query	730	ACATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGA	789
Sbjct	6134	ACATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGA	6193
Query	790	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	849
Sbjct	6194	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	6253
Query	850	GTTTTATCGTTGAGCCACCATAATTACTGTTGAATAGACGTAGACACACGAGCTT	909
Sbjct	6254	GTTTTATCGTTGAGCCACCATAATTACTGTTGAATAGACGTAGACACACGAGCTT	6313
Query	910	ACTTACATCAGCAACAATAATTATGCCATCCAACAGGAGTAAAAGTGTAGCTGAN	969
Sbjct	6314	ACTTACATCAGCAACAATAATTATGCCATCCAACAGGAGTAAAAGTGTAGCTGAC	6373
Query	970	NNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	1029
Sbjct	6374	TAGCAACCCTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	6433
Query	1030	TTATTTCCATTACTATTGGTGGCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6434	TTATTTCCATTACTATTGGTGGATTAAACAGGTATTGACTAGCCAACCTCATCACTAG	6493
Query	1090	ACATCGTACTACACGACACGTACTACGTTGAGC-CNNNNNNNNNNNNNATCAATA	1148
Sbjct	6494	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTCCATTATGTT-CTATCAATA	6552
Query	1149	GGAGCTGTATTCGCATCATAGGAGGCTTCATTCACTGATTCCCTATTCTCAGG	1204
Sbjct	6553	GGAGCTGTATTCGCATCATAGCAGGATTACTCACTGATTCCCTCTTCACAGG	6608

Dermochelys coriacea isolate 9790 mitochondrion, partial genome

Sequence ID: **JX454973.1** Length: 16380 Number of Matches: 1

Range 1: 5397 to 6591

Score	Expect	Identities	Gaps	Strand	Frame
1923 bits(1041)	0.0(0)	1132/1196(95%)	3/1196(0%)	Plus/Plus	
Query	11	CTCGCTGAttttttCTACTAATCATAAAGACATTGGCACCCATACCTAATTGGGG		70	
Sbjct	5397	CTCGCTGATTTTTCTACTAATCATAAAGACATTGGCACCCATACCTAATTGGGG		5456	
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGCAGAACTAAC		130	
Sbjct	5457	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGCAGAACTAAC		5516	
Query	131	CGGGAACCCCTCCTAGGAGATGACCAAAATTACAATGTACCGTTACAGCCCCATGCC		190	
Sbjct	5517	CGGGAACCCCTCCTAGGAGATGACCAAAATTACAATGTACCGTTACAGCCCCATGCC		5576	
Query	191	TTATAATCTCTCATAGTTATACCAGTTATAATCGGCGGTTCGGAAACTGACTTGTTC		250	
Sbjct	5577	TTATAATCTCTCATAGTTATACCAGTTATAATCGGCGGTTCGGAAACTGACTTGTTC		5636	
Query	251	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTGNN		310	

Sbjct	5637	CCCTTATAATTGGAGCACAGACATGGCATTCACCGAATAAACACATAAGCTTTGAC	5696
Query	311	NNNNNNCTCCCTCACTGTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	370
Sbjct	5697	TTTACCTCCCTCACTGTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	5756
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAG	430
Sbjct	5757	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAG	5816
Query	431	ACCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATT-ACT	489
Sbjct	5817	ACCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATTAAC	5876
Query	490	TCATTACTACAGCAATCAACATAAAATCTCAGCTATATCACAATACCAAACACCATTAT	549
Sbjct	5877	TCATTACTACAGCAATCAACATAAAATCTCAGCTATATCACAATACCAAACACCATTAT	5936
Query	550	TTGTATGATCTGATTAATTACAGCCCTCTATTATTACTCTCATTGCCAGTAGCTG	609
Sbjct	5937	TTGTATGATCTGATTAATTACAGCCCTCTATTATTACTCTCATTGCCAGTAGCTG	5996
Query	610	CAGGAATCACCATACTACTACAGATCGAAACCTAAACACAACCTTTTGATCCTTCAG	669
Sbjct	5997	CAGGAATCACCATACTACTACAGATCGAAACCTAAACACAACCTTTTGATCCTTCAG	6056
Query	670	GAGGAGGAGACCCAATCCATACCAAAATGCTATTCTGATTCTTGGCCATCCAGAAGTAT	729
Sbjct	6057	GAGGAGGAGACCCAATCCATACCAACACCTATTCTGATTCTTGGCCATCCAGAAGTAT	6116
Query	730	ACATCCTAATTCTACCAGGATTCCGGATAATCTCACATATCGTCACCTATTGCTGGTA	789
Sbjct	6117	ACATCCTAATTCTACCAGGATTCCGGATAATCTCACATATCGTCACCTATTGCTGGTA	6176
Query	790	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATTCATTGGATTCCCTGG	849
Sbjct	6177	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATTCATTGGATTCCCTGG	6236
Query	850	GTTTTATCGTTGAGCCACCATATATTACTGTTGAATAGACGTAGACACAGAGCTT	909
Sbjct	6237	GTTTTATCGTTGAGCCACCATATATTACTGTTGAATAGACGTAGACACAGAGCTT	6296
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCAAACAGGAGTAAAGTGTAGCTGAN	969
Sbjct	6297	ACTTTACATCAGCAACAATAATTATTGCCATCCAAACAGGAGTAAAGTGTAGCTGAC	6356
Query	970	NNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	1029
Sbjct	6357	TAGCAACCCTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	6416
Query	1030	TTATTTCCATTACTATTGGTGGCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6417	TTATTTCCATTACTATTGGTGGATTAACAGGTATTGACTAGCCAACCTCATCACTAG	6476
Query	1090	ACATCGTACTACACGACACGTAACGTTGTAGC-CNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6477	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTCCATTATGTT-CTATCAATA	6535
Query	1149	GGAGCTGTATTGCCATCATAGGAGGCTTCATTCACTGATTCCCTATTCTCAGG	1204
Sbjct	6536	GGAGCTGTATTGCCATCATAGCAGGATTACTCACTGATTCCCTCTTCACAGG	6591

Dermochelys coriacea isolate 5718 mitochondrion, partial genome

Sequence ID: **JX454969.1** Length: 16420 Number of Matches: 1

Range 1: 5414 to 6608

Score	Expect	Identities	Gaps	Strand	Frame
1923 bits(1041)	0.0()	1132/1196(95%)	3/1196(0%)	Plus/Plus	
Query	11	CTCGCTGAttttttCTACTAATCATAAAAGACATTGGCACCTATACCTAATTGGGG		70	
Sbjct	5414	CTCGCTGATTTTTCTACTAATCATAAAAGACATTGGCACCTATACCTAATTGGGG		5473	
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCGTCAGAACTAAC		130	
Sbjct	5474	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCGTCAGAACTAAC		5533	
Query	131	CGGGAACCCCTCTAGGAGATGACCAATTACAATGTCATCGTACAGCCATGCC		190	
Sbjct	5534	CGGGAACCCCTCTAGGAGATGACCAATTACAATGTCATCGTACAGCCATGCC		5593	
Query	191	TTATAATCTCTCATAGTTATACCAAGTTATAATCGCGGTTGGAAACTGACTG		250	
Sbjct	5594	TTATAATCTCTCATAGTTATACCAAGTTATAATCGCGGTTGGAAACTGACTG		5653	
Query	251	CCCTTATAATTGGAGCACAGACATGGCATTCACCGAATAAACACATAAGCTT		310	
Sbjct	5654	CCCTTATAATTGGAGCACAGACATGGCATTCACCGAATAAACACATAAGCTT		5713	
Query	311	NNNNNNCTCCCTCACTGTACTACTTCTAGCATCATCAGGAATTGAAGCAGGT		370	
Sbjct	5714	TTTACCTCCCTCACTGTACTACTTCTAGCATCATCAGGAATTGAAGCAGGT		5773	
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTG		430	

Sbjct	5774	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGGCCACGCTGGTGCTCTGTAG	5833
Query	431	ACCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATT-ACT	489
Sbjct	5834	ACCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATTAACT	5893
Query	490	TCATTACTACAGCAATCACATAAACTCCAGCTATATCACAAATACCAAACACCATTAT	549
Sbjct	5894	TCATTACTACAGCAATCACATAAACTCCAGCTATATCACAAATACCAAACACCATTAT	5953
Query	550	TTGTATGATCTGTATTAATTACAGCGCTCTATTACTCTCATGCCAGTAGCTG	609
Sbjct	5954	TTGTATGATCTGTATTAATTACAGCGCTCTATTACTCTCATGCCAGTAGCTG	6013
Query	610	CAGGAATCACCATACTACTACAGATCGAAACCTAAACACAACCTTTGATCCTTCAG	669
Sbjct	6014	CAGGAATCACCATACTACTACAGATCGAAACCTAAACACAACCTTTGATCCTTCAG	6073
Query	670	GAGGAGGAGACCAATCCTATACCAAATGCTATTCTGATTCTTGGCATCCAGAAGTAT	729
Sbjct	6074	GAGGAGGAGACCAATCCTATACCAAACACCTATTCTGATTCTTGGCATCCAGAAGTAT	6133
Query	730	ACATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTACCTATTATGCTGGTA	789
Sbjct	6134	ACATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTACCTATTATGCTGGTA	6193
Query	790	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	849
Sbjct	6194	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	6253
Query	850	GTTTTATCGTTGAGCCCACCATATATTACTGTTGAATAGACGTTAGACACACGGAGCTT	909
Sbjct	6254	GTTTTATCGTTGAGCCCACCATATATTACTGTTGAATAGACGTTAGACACACGGAGCTT	6313
Query	910	ACTTACATCAGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTGTAGCTGAN	969
Sbjct	6314	ACTTACATCAGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTGTAGCTGAN	6373
Query	970	NNNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	1029
Sbjct	6374	TAGCAACCCTTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	6433
Query	1030	TTATTTCCATTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACACTCATCACTAG	1089
Sbjct	6434	TTATTTCCATTACTATTGGTGGATTACAGGTATTGACTAGCCAACACTCATCACTAG	6493
Query	1090	ACATCGTACTACACGACACGTTAGCTACCGTGTAGC-CNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6494	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTCCATTATGTT-CTATCAATA	6552
Query	1149	GGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTCCCTATTCTCAGG	1204
Sbjct	6553	GGAGCTGTATTTGCCATCATAGCAGGATTACTCACTGATTCCCTCTTCAACAGG	6608

Dermochelys coriacea isolate 88903 mitochondrion, partial genome

Sequence ID: **JX454989.1** Length: 16366 Number of Matches: 1

Range 1: 5410 to 6604

Score	Expect	Identities	Gaps	Strand	Frame
1908 bits(1033)	0.0(0)	1128/1196(94%)	3/1196(0%)	Plus/Plus	
Query	11	CTCGCTGAttttttCTACTAATCATAAAGACATTGGCACCTATACCTAATTGGGG		70	
Sbjct	5410	CTCGCTGATTTTTCTACTAATCATAAAGACATTGGCACCTATACCTAATTGGGG		5469	
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAC		130	
Sbjct	5470	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAC		5529	
Query	131	CGGGAACCCCTCTAGGAGATGACCAATTACAATGTACCGTTACAGCCATGCCCTCA		190	
Sbjct	5530	CGGGAACCCCTCTAGGAGATGACCAATTACAATGTACCGTTACAGCCATGCCCTCA		5589	
Query	191	TTATAATCTCTCATAGTTATACCAGTTATAATCGCGGTTGGAAACTGACTGTTTC		250	
Sbjct	5590	TTATAATCTCTCATAGTTATACCAGTTATAATCGCGGTTGGAAACTGACTGTTTC		5649	
Query	251	CCCTTATAATTGGAGCACAGACATGGCATTCCACGAATAAACACATAAGCTTTGNN		310	
Sbjct	5650	CCCTTATAATTGGAGCACAGACATGGCATTCCACGAATAAACACATAAGCTTTGAC		5709	
Query	311	NNNNNNCTCCCTACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA		370	
Sbjct	5710	TTTACCTCCCTACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA		5769	
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGGCCACGCTGGTGCTCTGTAG		430	
Sbjct	5770	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGGCCACGCTGGTGCTCTGTAG		5829	
Query	431	ACCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATT-ACT		489	
Sbjct	5830	ACCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTATTAACT		5889	
Query	490	TCATTACTACAGCAATCACATAAACTCCAGCTATATCACAAATACCAAACACCATTAT		549	

Sbjct	5890	TCATTACTACAGCAATCACATAAAATCTCCAGCTATATCACAATACCAAAACACCATTAT	5949
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTACTCTCATTGCCAGTAGCTG	609
Sbjct	5950	TTGTATGATCTGTATTAATTACAGCCGTTCTATTACTCTCATTGCCAGTAGCTG	6009
Query	610	CAGGAATCACCATACTACTTACAGATCGAAACCTAACACAAACCTTTTGATCCTTCAG	669
Sbjct	6010	CAGGAATCACCATACTACTTACAGATCGAAACCTAACACAAACCTTTTGATCCTTCAG	6069
Query	670	GAGGAGGAGACCCAATCTATACCAAATGCTATTCTGATTCTGCATCCAGAAGTAT	729
Sbjct	6070	GAGGAGGAGACCCAATCTATACCAAACACCTATTCTGATTCTGCATCCAGAAGTAT	6129
Query	730	ACATCCTAATTCTACCAGGATTGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6130	ACATCCTAATTCTACCAGGATTGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6189
Query	790	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	849
Sbjct	6190	AAAAAGAACCATTTGGTACATAGGAATAGTTGAGCAATAATATCCATTGGATTCTGG	6249
Query	850	GTTTTATCGTTGAGCCCACCATATTTACTGTTGAATAGACGTAGACACACGAGCTT	909
Sbjct	6250	GTTTTATCGTTGAGCCCACCATATTTACTGTTGAATAGACGTAGACACACGAGCTT	6309
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCAAACAGGAGTAAAAGTGTAGCTGAN	969
Sbjct	6310	ACTTTACATCAGCAACAATAATTATTGCCATCCAAACAGGAGTAAAAGTGTAGCTGAC	6369
Query	970	NNNNNNNNNNNNNNAGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGT	1029
Sbjct	6370	TAGCAACCCTCACGGAGGAATAATTAAATGAGATGCTGCNNNCTGAGCCCTGGGT	6429
Query	1030	TTATTTCCATTACTATTGGTGGCTGACTGGCATTGTATTAGCAAACACTCACTAG	1089
Sbjct	6430	TTATTTCCATTACTATTGGTGGATTAACAGGTATTGACTAGCCAACACTCACTAG	6489
Query	1090	ACATCGTACTACGACACGTAACGGTTGAGC-CNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6490	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTATGTT-CTATCAATA	6548
Query	1149	GGAGCTGTATTGCCATCATAGGAGGCTTCACTGATTCCCTATTCTCAGG	1204
Sbjct	6549	GGAGCTGTATTGCCATCATAGCAGGTTACTCACTGATTCCCTCTTCACAGG	6604

Dermochelys coriacea voucher DC-COI-AP1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial

Sequence ID: **GQ152876.1** Length: 815 Number of Matches: 1

Range 1: 1 to 815

Score	Expect	Identities	Gaps	Strand	Frame
1452 bits(786)	0.0()	803/815(99%)	1/815(0%)	Plus/Plus	
Query	25	tCTACTAATCATAAAGACATTGGCACCCCTACCTAATTGGGGCCTGAGCAGGAATA	84		
Sbjct	1	TCTACTAATCATAAAGACATTGGCACCCCTACCTAATTGGGGCCTGAGCAGGAATA	60		
Query	85	GTAAGGCACAGCACTCAGCCATTAAATCCGTGCAGAACTAACGCCAACGGGAACCCCTCTA	144		
Sbjct	61	GTAAGGCACAGCACTCAGCCATTAAATCCGTGCAGAACTAACGCCAACGGGAACCCCTCTA	120		
Query	145	GGAGATGACCAAAATTACAATGTCATCGTTACAGCCATGCCCTATTATAATCTCTTC	204		
Sbjct	121	GGAGATGACCAAAATTACAATGTCATCGTTACAGCCATGCCCTATTATAATCTCTTC	180		
Query	205	ATAGTTATACCAAGTTATAATCGGCGGTTCGGAAACTGACTTGTCCCCCTATAATTGGA	264		
Sbjct	181	ATAGTTATACCAAGTTATAATCGGCGGTTCGGAAACTGACTTGTCCCCCTATAATTGGA	240		
Query	265	GCACCAGACATGGCATTCCACGAATAAACACATAAGTTGNNNNNNNCTCCCTCA	324		
Sbjct	241	GCACCAGACATGGCATTCCACGAATAAACACATAAGTTGACTTTACCTCCCTCA	300		
Query	325	CTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTAACAGTC	384		
Sbjct	301	CTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTAACAGTC	360		
Query	385	TATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAGACCTAACTATCTT	444		
Sbjct	361	TATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAGACCTAACTATCTT	420		
Query	445	TCTCTGCACCTAGCTGGTCTTCAATTAGGAGCTATT-ACCTCATTACTACAGCA	503		
Sbjct	421	TCTCTGCACCTAGCTGGTCTTCAATTAGGAGCTATTACCTACTACAGCA	480		
Query	504	ATCAACATAAAATCTCAGCTATATCACAAATACCAAACACCATTATTGTATGATCTGA	563		
Sbjct	481	ATCAACATAAAATCTCAGCTATATCACAAATACCAAACACCATTATTGTATGATCTGA	540		
Query	564	TTAATTACAGCCGTTCTATTACTCTCATTGCCAGTAGCTGCAGGAATCACCATA	623		
Sbjct	541	TTAATTACAGCCGTTCTATTACTCTCATTGCCAGTAGCTGCAGGAATCACCATA	600		
Query	624	CTACTTACAGATCGAAACCTAAACACAACCTTTTGATCCTTCAGGAGGAGACCCA	683		

Sbjct	601	CTACTTACAGATCGAACCTAAACACAACCCCTTTGATCCTTCAGGAGGAGACCCA	660
Query	684	ATCCTATACCAAAATGCTATTCTGATTCTTGGCCATCCAGAAGTATACTACATCCTAATTCTA	743
Sbjct	661	ATCCTATACCAACACCTATTCTGATTCTTGGCCATCCAGAAGTATACTACATCCTAATTCTA	720
Query	744	CCAGGATTGGCATAATCTCACATATCGTCACCTATTATGCTGGAAAAAGAACCATTT	803
Sbjct	721	CCAGGATTGGCATAATCTCACATATCGTCACCTATTATGCTGGAAAAAGAACCATTT	780
Query	804	GGTTACATAGGAATAGTTGAGCAATAATATCCAT	838
Sbjct	781	GGTTACATAGGAATAGTTGAGCAATAATATCCAT	815

Dermochelys coriacea cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial

Sequence ID: **KU883273.1** Length: 798 Number of Matches: 1

Range 1: 1 to 798

Score	Expect	Identities	Gaps	Strand	Frame
1421 bits(769)	0.0()	786/798(98%)	1/798(0%)	Plus/Plus	
Query	42	CATTGGCACCTATACTTAATTGGGGCTGAGCAGGAATAGTAGGCACAGCACTCAG			101
Sbjct	1	CATTGGCACCTATACTTAATTGGGGCTGAGCAGGAATAGTAGGCACAGCACTCAG			60
Query	102	CCTATTAAATCCGTGCAGAACTAAGCCAACCGGGAACCCCTCTAGGAGATGACCAAATTAA			161
Sbjct	61	CCTATTAAATCCGTGCAGAACTAAGCCAACCGGGAACCCCTCTAGGAGATGACCAAATTAA			120
Query	162	CAATGTCATCGTTACAGCCATGCCTTCATTATAATCTTCTCATAGTTATACAGTTAT			221
Sbjct	121	CAATGTCATCGTTACAGCCATGCCTTCATTATAATCTTCTCATAGTTATACAGTTAT			180
Query	222	AATCGGCGGTTTCGGAAACTGACTTGTCCCCCTATAATTGGAGCACAGACATGGCATT			281
Sbjct	181	AATCGGCGGTTTCGGAAACTGACTTGTCCCCCTATAATTGGAGCACAGACATGGCATT			240
Query	282	CCCACGAATAAAACAACATAAGCTTGNNNNNNNNCTCCCTCACTGTTACTACTCTAGC			341
Sbjct	241	CCCACGAATAAAACAACATAAGCTTGTACCTCCCTCACTGTTACTACTCTAGC			300
Query	342	ATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTGAACAGTCTATCCTCCACTAGCTGG			401
Sbjct	301	ATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTGAACAGTCTATCCTCCACTAGCTGG			360
Query	402	AAACCTAGCCCACGCTGGTCTGTAGACCTAACTATCTTCTCTGCACCTAGCTGG			461
Sbjct	361	AAACCTAGCCCACGCTGGTCTGTAGACCTAACTATCTTCTCTGCACCTAGCTGG			420
Query	462	TGTTTCATCAATTAGGAGCTATT-ACTTCTTACAGCAATCAACATAAAATCTCC			520
Sbjct	421	TGTTTCATCAATTAGGAGCTATTAACTTCTTACAGCAATCAACATAAAATCTCC			480
Query	521	AGCTATATCACAAACACCATTATTGTATGATCTGTATTAATTACAGCCGTCT			580
Sbjct	481	AGCTATATCACAAACACCATTATTGTATGATCTGTATTAATTACAGCCGTCT			540
Query	581	ATTATTACTCTCATTGCCAGTACTAGCTGCAGGAATCACCATACTTACAGATCGAAA			640
Sbjct	541	ATTATTACTCTCATTGCCAGTACTAGCTGCAGGAATCACCATACTTACAGATCGAAA			600
Query	641	CCTAAACACAACCTTTGATCCTTCAGGAGGAGACCAATCCTATACCAAATGCT			700
Sbjct	601	CCTAAACACAACCTTTGATCCTTCAGGAGGAGACCAATCCTATACCAAACACCT			660
Query	701	ATTCTGATTCTTGGCCATCCAGAAGTATACTACATCCTAATTCTACCAAGGATTCGGCATAAT			760
Sbjct	661	ATTCTGATTCTTGGCCATCCAGAAGTATACTACATCCTAATTCTACCAAGGATTCGGCATAAT			720
Query	761	CTCACATATCGTCACCTATTATGCTGGAAAAAGAACCATTTGGTTACATAGGAATAGT			820
Sbjct	721	CTCACATATCGTCACCTATTATGCTGGAAAAAGAACCATTTGGTTACATAGGAATAGT			780
Query	821	TTGAGCAATAATATCCAT	838		
Sbjct	781	TTGAGCAATAATATCCAT	798		

Eretmochelys imbricata isolate E13 mitochondrion, complete genome

Sequence ID: **PQ276118.1** Length: 16582 Number of Matches: 1

Range 1: 5405 to 6683

Score	Expect	Identities	Gaps	Strand	Frame
1347 bits(729)	0.0()	1086/1282(85%)	6/1282(0%)	Plus/Plus	
Query	13	CGCTGAtttttCTACTAATCATAAAGACATTGGCACCCATACTCTAATTGGGGCC			72
Sbjct	5405	CGTTGATTCTTCTACCAACCATAAAGACATTGGCACCCATACTTGATCTTGGAGCA			5464

Query 73 TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGCAGAACTAAGCCAACCG 132
 Sbjct 5465 TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGCAGAACTAAGCCAACCA 5524
 Query 133 GGAACCCTCCTAGGAGATGACCAAATTACAATGTCATCGTTACAGCCCATGCCCTCATT 192
 Sbjct 5525 GGAACTCTCCTAGGAGATGACCAAATTATAATGTTACGTTACAGCCCATGCCCTCATT 5584
 Query 193 ATAATCTTCTCATAGTTACCACTAGTATAATCGGCGGTTCGGAAACTGACTGTTCCC 252
 Sbjct 5585 ATAATCTTTTATAGTTACCAATTATAATTGGCGGTTCGGAAACTGACTGTTCCA 5644
 Query 253 CTTATAATTGGAGCACAGACATGGCATTCCCACGAATAAACACATAAGCTTGNNNN 312
 Sbjct 5645 CTAATAATTGGAGCACAGACATAGCATTCCACGTATAAACACATAAGCTTG-ACT 5703
 Query 313 NNNNCTCCC-TCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAAC 371
 Sbjct 5704 CCTACCCCCATCACTACTACTACTAGCATCATCAGGAATTGAAGCAGGAGCAGGTAC 5763
 Query 372 AGGCTGAACAGCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAGA 431
 Sbjct 5764 AGGCTGAACAGTATATCCCCATTAGCCGGAAACCTAGCTCACGCTGGCGCTTCAGTAGA 5823
 Query 432 CCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTAT-TACTT 490
 Sbjct 5824 CCTAACTATCTTCCCTCACCTAGCTGGGTATCCTCAATCTAGGCGTATCAACTT 5883
 Query 491 CATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAACACCATTATT 550
 Sbjct 5884 CATTACTACAGCAATCAACATAAAATCCCTGCCATATCACAATACCAACACCCTTATT 5943
 Query 551 TGTATGATCTGTATTAAATTACAGCCGTTCTATTACTCTCATGCCAGTAGCTGC 610
 Sbjct 5944 CGTATGATCTGACTAATTACAGCTGGTCTATTACTACTCTCACTACAGTACTTGCTGC 6003
 Query 611 AGGAATCACCATACTACTACAGATCGAAACCTAAACACAACCTTTTGATCCCTCAGG 670
 Sbjct 6004 AGGCATTACCATACTACTACAGACCGAAATCTAAACACAACCTCTTTGATCCCTCAGG 6063
 Query 671 AGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTGCCATCCAGAAGTATA 730
 Sbjct 6064 AGGAGGAGACCCAATCCTATACCAACCTATTCTGATTCTTGCTATCCTGAAGTATA 6123
 Query 731 CATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAA 790
 Sbjct 6124 CATCTTAATCCTCCAGGATTGGCATAATCTCCACATCGTCACCTATTACTCTGGTAA 6183
 Query 791 AAAAGAACCATTTGGTACAGGAATAGTTGAGCAATAATATCCATTGGATTCTGGGG 850
 Sbjct 6184 AAAAGAACCATTCGGCTACATAGGAATAGTTGAGCAATAATATCAATTGGTTCTGGGG 6243
 Query 851 TTTTATCGTTGAGCCCACCATATTTACTGTTGGAATAGACGTAGACACACGAGCTTA 910
 Sbjct 6244 CTTCATCGTATGAGCTACCACATATTACCGTTGGAATAGACGTAGACACGAGCTTA 6303
 Query 911 CTTTACATCAGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTGTGANN 970
 Sbjct 6304 TTTCACATCCGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTATTAGCTGATT 6363
 Query 971 NNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGTT 1030
 Sbjct 6364 AGCCACTCTACACGGTGGAAATAATTAAATGAGATGCTGCCACTCTGAGCCCTAGGTT 6423
 Query 1031 TATTTCCCTATTACTATTGGTGGCCTGACTGGCATGTTATTAGCAAACCTCATCACTAGA 1090
 Sbjct 6424 CATCTCCTCTTCACTATTGGCGGATTACAGGTATTGTATTAGCAACTCATCACTAGA 6483
 Query 1091 CATCGTACTACACGACACGTACTACGTTGAGC-CNNNNNNNNNNNNNCTATCAATAG 1149
 Sbjct 6484 CATTGTATTACGATACTTATTATGAGTGGCACACTCCACTATGTT-CTTCAATAG 6542
 Query 1150 GAGCTGTATTGCCATCATAGGAGGCTCATTCACTGATTCCCTATTCTCAGGCTACA 1209
 Sbjct 6543 GAGCCGTATTGCCATCATAGCAGGATTACCCACTGATTCCCTTTTACAGGATATT 6602
 Query 1210 CCCTAGACCAAAACCTACGCCAAAATCCATTCACTATCATATTCATGGCGTAATCTAA 1269
 Sbjct 6603 CACTACACCAAACCTGAACAAAAGTACATTGGAGTAATTACAGGCGTAAACATAA 6662
 Query 1270 CTTTCTTCCCACAAACTTTCT 1291
 Sbjct 6663 CTTTCTTCCCTCAACA-TTTCT 6683

Eretmochelys imbricata isolate E12 mitochondrion, complete genome

Sequence ID: **PQ276117.1** Length: 16572 Number of Matches: 1

Range 1: 5404 to 6682

Score	Expect	Identities	Gaps	Strand	Frame
1347 bits(729)	0.0()	1086/1282(85%)	6/1282(0%)	Plus/Plus	
Query 13 CGCTGAttttttCTACTAATCATAAAGACATTGGCACCCATACCTAATTGGGGCC 72					
Sbjct 5404 CGTTGATTCTTTCTACCAACCATAAGACATTGGCACCCATACCTGATCTTGGAGCA 5463					

Query 73 TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGAGAACTAAGCCAACCG 132
 Sbjct 5464 TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGAGAACTAAGCCAACCA 5523
 Query 133 GGAACCCTCCTAGGAGATGACCAAATTACAATGTCATCGTTACAGCCCATGCCCTCATT 192
 Sbjct 5524 GGAACTCTCCTAGGAGATGACCAAATTATAATGTTACGTTACAGCCCATGCTTCATT 5583
 Query 193 ATAATCTTCTCATAGTTACCAAGTTATAATCGGCGGTTCGGAAACTGACTGTTCCC 252
 Sbjct 5584 ATAATCTTTTATAGTTACCAATTATAATTGGCGGTTCGGAAACTGACTGTTCCA 5643
 Query 253 CTTATAATTGGAGCACAGACATGGCATTCCCACGAATAAACACATAAGCTTGNNNN 312
 Sbjct 5644 CTAATAATTGGAGCACAGACATAGCATTCCACGTATAAACACATAAGCTTG-ACT 5702
 Query 313 NNNNCTCCC-TCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAAC 371
 Sbjct 5703 CCTACCCCCATCACTACTACTACTAGCATCATCAGGAATTGAAGCAGGAGCAGGTAC 5762
 Query 372 AGGCTGAACAGCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAGA 431
 Sbjct 5763 AGGCTGAACAGTATATCCCCATTAGCCGGAAACCTAGCTCACGCTGGCGCTTCAGTAGA 5822
 Query 432 CCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTAT-TACTT 490
 Sbjct 5823 CCTAACTATCTTCCCTCACCTAGCTGGGTATCCTCAATCTAGGCGTATCAACTT 5882
 Query 491 CATTACTACAGCAATCAACATAAAATCTCAGCTATATCACAATACCAACACCATTATT 550
 Sbjct 5883 CATTACTACAGCAATCAACATAAAATCCCTGCCATATCACAATACCAACACCCTTATT 5942
 Query 551 TGTATGATCTGTATTAAATTACAGCCGTTCTATTACTCTCATGCCAGTAGCTGC 610
 Sbjct 5943 CGTATGATCTGACTAATTACAGCTGGTCTATTACTACTCTCACTACAGTACTGCTGC 6002
 Query 611 AGGAATCACCAACTACTACAGATCGAAACCTAAACACAACCTTTTGATCCCTCAGG 670
 Sbjct 6003 AGGCATTACCAACTACTACAGACCGAAATCTAAACACAACCTCTTTGATCCCTCAGG 6062
 Query 671 AGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTGCCATCCAGAAGTATA 730
 Sbjct 6063 AGGAGGAGACCCAATCCTATACCAACCTATTCTGATTCTTGCTATCCTGAAGTATA 6122
 Query 731 CATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAA 790
 Sbjct 6123 CATCTTAATCCTCCAGGATTGGCATAATCTCCACATCGTCACCTATTACTCTGGTAA 6182
 Query 791 AAAAGAACCATTTGGTACAGGAATAGTTGAGCAATAATATCCATTGGATTCTGGGG 850
 Sbjct 6183 AAAAGAACCATTCGGCTACAGGAATAGTTGAGCAATAATATCAATTGGTTCTGGGG 6242
 Query 851 TTTTATCGTTGAGCCCACCATATTTACTGTTGGAATAGACGTAGACACACGAGCTTA 910
 Sbjct 6243 CTTCATCGTATGAGCTACCACATATTACCGTTGGAATAGACGTAGACACGAGCTTA 6302
 Query 911 CTTTACATCAGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTGTGANN 970
 Sbjct 6303 TTTCACATCCGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTATTAGCTGATT 6362
 Query 971 NNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGTT 1030
 Sbjct 6363 AGCCACTCTACACGGTGGAAATAATTAAATGAGATGCTGCCACTCTGAGCCCTAGGTT 6422
 Query 1031 TATTTCCCTATTACTATTGGTGGCCTGACTGGCATGTTATTAGCAAACTCATCACTAGA 1090
 Sbjct 6423 CATCTCCTCTTCACTATTGGCGGATTACAGGTATTGTATTAGCAACTCATCACTAGA 6482
 Query 1091 CATCGTACTACACGACACGTACTACGTTGAGC-CNNNNNNNNNNNNNCTATCAATAG 1149
 Sbjct 6483 CATTGTATTACGATACTTATTATGAGTGGCACACTCCACTATGTT-CTTCAATAG 6541
 Query 1150 GAGCTGTATTGCCATCATAGGAGGCTCATTCACTGATTCCCTATTCTCAGGCTACA 1209
 Sbjct 6542 GAGCCGTATTGCCATCATAGCAGGATTACCCACTGATTCCCTTTTACAGGATATT 6601
 Query 1210 CCCTAGACCAAAACCTACGCCAAAATCCATTCACTATCATATTACGGCGTAATCTAA 1269
 Sbjct 6602 CACTACACCAAACCTGAACAAAAGTACATTGGAGTAATTACAGGCGTAAACATAA 6661
 Query 1270 CTTTCTTCCCACAAACTTTCT 1291
 Sbjct 6662 CTTTCTTCCCTCAACA-TTTCT 6682

Eretmochelys imbricata isolate E11 mitochondrion, complete genome

Sequence ID: **PQ276116.1** Length: 16581 Number of Matches: 1

Range 1: 5405 to 6683

Score	Expect	Identities	Gaps	Strand	Frame
1347 bits(729)	0.0()	1086/1282(85%)	6/1282(0%)	Plus/Plus	
Query 13 CGCTGAttttttCTACTAATCATAAAGACATTGGCACCCATACCTAATTGGGGCC 72					
Sbjct 5405 CGTTGATTCTTTCTACCAACCATAAGACATTGGCACCCATACCTGATCTTGGGGCA 5464					

Query	73	TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAAATCCGTGCAGAACTAAGCCAACCG	132
Sbjct	5465	TGAGCAGGAATAGTAGGCACAGCACTCAGCTATTAAATCCGTGCAGAACTAAGCCAACCA	5524
Query	133	GGAACCCTCCTAGGAGATGCCAAATTACAATGTCATCGTTACAGCCCAGCCTTCATT	192
Sbjct	5525	GGAACTCTCCTAGGAGATGCCAAATTATAATGTTACGTTACAGCCCAGCCTTCATT	5584
Query	193	ATAATCTTCTCATAGTTACCAAGTTATAATCGGCGGTTCGGAAACTGACTGTTCCC	252
Sbjct	5585	ATAATCTTTTATAGTTACCAATTATAATTGGCGGTTCGGAAACTGACTGTTCCA	5644
Query	253	CTTATAATTGGAGCACAGACATGGCATTCCCACGAATAAACACATAAGCTTGNNNN	312
Sbjct	5645	CTAATAATTGGAGCACAGACATAGCATTCCACGTATAAACACATAAGCTTG-ACT	5703
Query	313	NNNNCTCCC-TCACTGTTACTACTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAAC	371
Sbjct	5704	CCTACCCCCATCACTATTACTACTAGCATCATCAGGAATTGAAGCAGGAGCAGGTAC	5763
Query	372	AGGCTGAACAGCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTCTGTAGA	431
Sbjct	5764	AGGCTGAACAGTATATCCCCATTAGCCGGAAACCTAGCCCACGCTGGCGCTTCAGTAGA	5823
Query	432	CCTAACTATCTTCTGCACCTAGCTGGTGTTCATCAATTAGGAGCTAT-TACTT	490
Sbjct	5824	CCTAACTATCTTCCACCTAGCTGGGTATCCTCAATCTAGGCGTATCAACTT	5883
Query	491	CATTACTACAGCAATCAACATAAAATCTCAGCTATATCACAATACCAAACACCATTATT	550
Sbjct	5884	CATTACTACAGCAATCAACATAAAATCCCTGCCATATCACAATACCAAACACCCTTATT	5943
Query	551	TGTATGATCTGTATTAAATTACAGCCGTTCTATTACTCTCATGCCAGTAGCTGC	610
Sbjct	5944	CGTATGATCTGACTAATTACAGCTGGTCTATTACTACTCTCGTACCAAGTACTGCTGC	6003
Query	611	AGGAATCACCATACTACTACAGATCGAAACCTAAACACAACCTTTTGATCCTTCAGG	670
Sbjct	6004	AGGCATTACCATACTACTACAGACCGAAATCTAACACACAACCTCTTTGATCCTTCAGG	6063
Query	671	AGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTGCCATCCAGAAGTATA	730
Sbjct	6064	GGGAGGAGACCCAATCCTATATCAACACCTATTCTGATTCTTGTCATCCTGAAGTATA	6123
Query	731	CATCCTAATTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAA	790
Sbjct	6124	CATCTTAATCCTCCAGGATTGGCATAATCTCCACATCGTCACCTATTACTCTGGTAA	6183
Query	791	AAAAGAACCATTTGGTACAGGAATAGTTGAGCAATAATATCATTGGATTCTGG	850
Sbjct	6184	AAAAGAACCATTCGGCTACAGGAATAGTTGAGCAATAATATCAATTGGTTCTGGG	6243
Query	851	TTTATCGTTGAGCCCACCATATTTACTGTTGGAATAGACGTAGACACACGAGCTTA	910
Sbjct	6244	CTTCATCGTATGAGCTACCACATATTACCGTTGGAATAGACGTAGACACGAGCTTA	6303
Query	911	CTTTACATCAGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTGTGANN	970
Sbjct	6304	TTTCACATCTGCAACAATAATTATTGCCATCCAACAGGAGTAAAGTATTAGCTGATT	6363
Query	971	NNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTGGGTT	1030
Sbjct	6364	AGCCACTCTACATGGTGAATAATTAAATGAGACGCTGCCACTCTGAGCCCTAGGTT	6423
Query	1031	TATTTCCCTATTACTATTGGTGGCCTGACTGGCATGTTATTAGCAAACCTCATCACTAGA	1090
Sbjct	6424	CATCTCCTCTTCACTATTGGCGGATTACAGGTATTGTATTAGCAACTCATCACTAGA	6483
Query	1091	CATCGTACTACAGACACGTACTACGTTGAG-CNNNNNNNNNNNNNCTATCAATAG	1149
Sbjct	6484	CATTGTATTACGATACTTATTATGAGTGGCACACTCCACTATGTT-CTTCAATAG	6542
Query	1150	GAGCTGTATTGCCATCAGGAGGCTCATTCACTGATTCCCTATTCTCAGGCTACA	1209
Sbjct	6543	GGGCCGTATTGCCATCAGCAGGATTACTCACTGATTCCCTTTTACAGGATATT	6602
Query	1210	CCCTAGACCAAAACCTACGCCAAAATCCATTCACTATCATATTACGGCTAAATCTAA	1269
Sbjct	6603	CACTACACCAAACCTGAACAAAAGTACATTGGAGTAATTACAGGCTAACATAA	6662
Query	1270	CTTTCTTCCCACAACTTCT	1291
Sbjct	6663	CCTTCTTCCCTCAACA-TTTCT	6683

Taxonomy

Reports

- Lineage

Organism	Blast Name	Score	Number of Hits	Description
Durocryptodira	turtles	157		
Chelonioidea	turtles	141		

..Dermochelys coriacea	turtles	1923	<u>12</u>	Dermochelys coriacea hits
..Eretmochelys imbricata	turtles	1347	<u>22</u>	Eretmochelys imbricata hits
..Natator depressus	turtles	1336	<u>3</u>	Natator depressus hits
..Chelonia mydas	turtles	1308	<u>11</u>	Chelonia mydas hits
..Caretta caretta	turtles	1275	<u>75</u>	Caretta caretta hits
..Lepidochelys kempii	turtles	1256	<u>12</u>	Lepidochelys kempii hits
..Lepidochelys olivacea	turtles	1232	<u>6</u>	Lepidochelys olivacea hits
.Chelonoidis alburyorum	turtles	1206	<u>2</u>	Chelonoidis alburyorum hits
.Stigmochelys pardalis	turtles	1194	<u>3</u>	Stigmochelys pardalis hits
.Geochelone elegans	turtles	1194	<u>3</u>	Geochelone elegans hits
.Cylindraspis triserrata	turtles	1151	<u>2</u>	Cylindraspis triserrata hits
.Trachemys decussata angusta	turtles	1144	<u>1</u>	Trachemys decussata angusta hits
.Mauremys japonica	turtles	1140	<u>3</u>	Mauremys japonica hits
.Chrysemys picta bellii	turtles	1116	<u>2</u>	Chrysemys picta bellii hits

- Organism

Description		Score	E value	Accession
Dermochelys coriacea (leatherback sea turtle) [turtles]				
Dermochelys coriacea voucher CRI006922 mitochondrion, complete genome		1923	0.0	MF460363
Dermochelys coriacea isolate CGG-03 mitochondrion, partial genome		1923	0.0	JX454992
Dermochelys coriacea isolate 9790 mitochondrion, partial genome		1923	0.0	JX454973
Dermochelys coriacea isolate 5718 mitochondrion, partial genome		1923	0.0	JX454969
Dermochelys coriacea isolate 88903 mitochondrion, partial genome		1908	0.0	JX454989
Dermochelys coriacea voucher DC-COI-AP1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial		1452	0.0	GQ152876
Dermochelys coriacea cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial		1421	0.0	KU883273
Dermochelys coriacea voucher ZSI/ANRC/M/29790 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial		1249	0.0	PQ069769
Dermochelys coriacea voucher ZSI/ANRC/M/29790 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial		1171	0.0	PQ216296
Dermochelys coriacea voucher ZSI/ANRC/M/29791 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial		1127	0.0	PQ069775
Dermochelys coriacea voucher USNM:Herp:544382 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial		1085	0.0	MH273769
Dermochelys coriacea voucher ZSI/ANRC/M/29791 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial		1077	0.0	PQ216299
Eretmochelys imbricata (hawksbill sea turtle) [turtles]				
Eretmochelys imbricata isolate E13 mitochondrion, complete genome		1347	0.0	PQ276118
Eretmochelys imbricata isolate E12 mitochondrion, complete genome		1347	0.0	PQ276117
Eretmochelys imbricata isolate E11 mitochondrion, complete genome		1347	0.0	PQ276116
Eretmochelys imbricata isolate E10 mitochondrion, complete genome		1347	0.0	PQ276115
Eretmochelys imbricata isolate E9 mitochondrion, complete genome		1347	0.0	PQ276114
Eretmochelys imbricata isolate E8 mitochondrion, complete genome		1347	0.0	PQ276113
Eretmochelys imbricata isolate E7 mitochondrion, complete genome		1347	0.0	PQ276112
Eretmochelys imbricata isolate E6 mitochondrion, complete genome		1347	0.0	PQ276111
Eretmochelys imbricata isolate E5 mitochondrion, complete genome		1347	0.0	PQ276110
Eretmochelys imbricata isolate E4 mitochondrion, complete genome		1347	0.0	PQ276109
Eretmochelys imbricata isolate E1 mitochondrion, complete genome		1347	0.0	PQ276106
Eretmochelys imbricata isolate rEreimb1 genome assembly, organelle: mitochondrion		1347	0.0	OZ223910
Eretmochelys imbricata mitochondrion, complete genome		1347	0.0	KP221806
Eretmochelys imbricata isolate 61392 mitochondrion, partial genome		1347	0.0	JX454980

Description	Score	E value	Accession
Eretmochelys imbricata isolate E3 mitochondrion, complete genome	1341	0.0	PQ276108
Eretmochelys imbricata isolate E2 mitochondrion, complete genome	1341	0.0	PQ276107
Eretmochelys imbricata isolate 5787 mitochondrion, partial genome	1341	0.0	JX454970
Eretmochelys imbricata isolate Cc-C-2 mitochondrion, complete genome	1336	0.0	MF571906
Eretmochelys imbricata isolate 72489 mitochondrion, partial genome	1336	0.0	JX454986
Eretmochelys imbricata mitochondrion, complete genome	1330	0.0	NC_012398
Eretmochelys imbricata mitochondrion, complete genome	1330	0.0	DQ533485
Eretmochelys imbricata voucher CLP:GT1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	1214	0.0	PQ459491
Natator depressus (flatback sea turtle) [turtles]			
Natator depressus isolate rNatDep1 genome assembly, organelle: mitochondrion	1336	0.0	OZ223967
Natator depressa haplogroup Au (X) mitochondrion, complete genome	1330	0.0	NC_018550
Natator depressa isolate 21684 mitochondrion, complete genome	1330	0.0	JX454975
Chelonia mydas (Green sea turtle) [turtles]			
Chelonia mydas isolate 28666 mitochondrion, complete genome	1308	0.0	JX454976
Chelonia mydas isolate 71270 mitochondrion, partial genome	1308	0.0	JX454985
Chelonia mydas isolate CGG-01Cmyd mitochondrion, complete genome	1291	0.0	JX454990
Chelonia mydas isolate 54903 mitochondrion, partial genome	1291	0.0	JX454978
Chelonia mydas isolate 13768 mitochondrion, complete genome	1291	0.0	JX454974
Chelonia mydas isolate Sample ID 9277 mitochondrion, complete genome	1291	0.0	JX454972
Chelonia mydas isolate 8855 mitochondrion, complete genome	1291	0.0	JX454971
Chelonia mydas mitochondrion, partial genome	1291	0.0	JQ026233
Chelonia mydas mitochondrion, complete genome	1291	0.0	NC_000886
Chelonia mydas mitochondrial DNA, complete genome	1291	0.0	AB012104
Chelonia mydas mitochondrion, partial genome	1286	0.0	JQ034420
Caretta caretta (loggerhead turtle) [turtles]			
Caretta caretta isolate 87410 mitochondrion, complete genome	1275	0.0	JX454988
Caretta caretta isolate 46603 mitochondrion, complete genome	1275	0.0	JX454977
Caretta caretta isolate Cc-C-4 mitochondrion, complete genome	1271	0.0	MF579505
Caretta caretta isolate Cc-C-3 mitochondrion, complete genome	1271	0.0	MF579504
Caretta caretta isolate Cc-C-1 mitochondrion, complete genome	1271	0.0	MF554690
Caretta caretta isolate SIC25 mitochondrion, partial genome	1271	0.0	OR166644
Caretta caretta isolate SIC21 mitochondrion, partial genome	1271	0.0	OR166640
Caretta caretta isolate SIC20 mitochondrion, partial genome	1271	0.0	OR166639
Caretta caretta isolate SIC15 mitochondrion, partial genome	1271	0.0	OR166634
Caretta caretta isolate SIC14 mitochondrion, partial genome	1271	0.0	OR166633
Caretta caretta isolate SIC02 mitochondrion, partial genome	1271	0.0	OR166622
Caretta caretta isolate LIN01 mitochondrion, partial genome	1271	0.0	OR166619
Caretta caretta isolate CAL1370 mitochondrion, partial genome	1271	0.0	OR166616
Caretta caretta isolate CAL1124 mitochondrion, partial genome	1271	0.0	OR166600
Caretta caretta isolate CAL1234 mitochondrion, partial genome	1271	0.0	OR166603
Caretta caretta isolate CAL1321 mitochondrion, partial genome	1271	0.0	OR166608
Caretta caretta isolate CAL1323 mitochondrion, partial genome	1271	0.0	OR166609
Caretta caretta isolate CAL1323.2 mitochondrion, partial genome	1271	0.0	OR166610
Caretta caretta isolate CAL1325 mitochondrion, partial genome	1271	0.0	OR166611
Caretta caretta isolate CAL1384 mitochondrion, partial genome	1271	0.0	OR166617
Caretta caretta isolate CAL1385 mitochondrion, partial genome	1271	0.0	OR166618

Description	Score	E value	Accession
Caretta caretta isolate CAL1112 mitochondrion, partial genome	1271	0.0	OR166599
Caretta caretta isolate CAL1201 mitochondrion, partial genome	1271	0.0	OR166602
Caretta caretta isolate CAL1315 mitochondrion, partial genome	1271	0.0	OR166605
Caretta caretta isolate CAL1320 mitochondrion, partial genome	1271	0.0	OR166607
Caretta caretta isolate CAL1328 mitochondrion, partial genome	1271	0.0	OR166612
Caretta caretta isolate CAL1346 mitochondrion, partial genome	1271	0.0	OR166614
Caretta caretta isolate LIN02 mitochondrion, partial genome	1271	0.0	OR166620
Caretta caretta isolate SIC05 mitochondrion, partial genome	1271	0.0	OR166624
Caretta caretta isolate SIC07 mitochondrion, partial genome	1271	0.0	OR166626
Caretta caretta isolate SIC22 mitochondrion, partial genome	1271	0.0	OR166641
Caretta caretta isolate LAT04 mitochondrion, partial genome	1271	0.0	OR166598
Caretta caretta isolate TUS05 mitochondrion, partial genome	1271	0.0	OR166594
Caretta caretta isolate TUS04 mitochondrion, partial genome	1271	0.0	OR166592
Caretta caretta isolate TUS04.2 mitochondrion, partial genome	1271	0.0	OR166593
Caretta caretta isolate SIC10 mitochondrion, partial genome	1271	0.0	OR166629
Caretta caretta isolate TUS03 mitochondrion, partial genome	1271	0.0	OR166590
Caretta caretta isolate TUS03.2 mitochondrion, partial genome	1271	0.0	OR166591
Caretta caretta isolate CAL1303 mitochondrion, partial genome	1271	0.0	OR166604
Caretta caretta isolate SIC11 mitochondrion, partial genome	1271	0.0	OR166630
Caretta caretta isolate ADR03 mitochondrion, partial genome	1271	0.0	OR166584
Caretta caretta isolate ADR02 mitochondrion, partial genome	1271	0.0	OR166583
Caretta caretta isolate ADR01 mitochondrion, partial genome	1271	0.0	OR166582
Caretta caretta isolate ADR04 mitochondrion, partial genome	1271	0.0	OR166585
Caretta caretta isolate TUS01 mitochondrion, partial genome	1271	0.0	OR166586
Caretta caretta isolate TUS01.2 mitochondrion, partial genome	1271	0.0	OR166587
Caretta caretta isolate TUS02 mitochondrion, partial genome	1271	0.0	OR166588
Caretta caretta isolate TUS02.2 mitochondrion, partial genome	1271	0.0	OR166589
Caretta caretta isolate LAT01 mitochondrion, partial genome	1271	0.0	OR166595
Caretta caretta isolate LAT02 mitochondrion, partial genome	1271	0.0	OR166596
Caretta caretta isolate LAT03 mitochondrion, partial genome	1271	0.0	OR166597
Caretta caretta isolate CAL1137 mitochondrion, partial genome	1271	0.0	OR166601
Caretta caretta isolate CAL1319 mitochondrion, partial genome	1271	0.0	OR166606
Caretta caretta isolate CAL1335 mitochondrion, partial genome	1271	0.0	OR166613
Caretta caretta isolate CAL1362 mitochondrion, partial genome	1271	0.0	OR166615
Caretta caretta isolate SIC01 mitochondrion, partial genome	1271	0.0	OR166621
Caretta caretta isolate SIC03 mitochondrion, partial genome	1271	0.0	OR166623
Caretta caretta isolate SIC06 mitochondrion, partial genome	1271	0.0	OR166625
Caretta caretta isolate SIC08 mitochondrion, partial genome	1271	0.0	OR166627
Caretta caretta isolate SIC09 mitochondrion, partial genome	1271	0.0	OR166628
Caretta caretta isolate SIC12 mitochondrion, partial genome	1271	0.0	OR166631
Caretta caretta isolate SIC13 mitochondrion, partial genome	1271	0.0	OR166632
Caretta caretta isolate SIC16 mitochondrion, partial genome	1271	0.0	OR166635
Caretta caretta isolate SIC17 mitochondrion, partial genome	1271	0.0	OR166636
Caretta caretta isolate SIC18 mitochondrion, partial genome	1271	0.0	OR166637
Caretta caretta isolate SIC19 mitochondrion, partial genome	1271	0.0	OR166638
Caretta caretta isolate SIC23 mitochondrion, partial genome	1271	0.0	OR166642
Caretta caretta isolate SIC24 mitochondrion, partial genome	1271	0.0	OR166643

Description		Score	E value	Accession
Caretta caretta isolate SIC26 mitochondrion, partial genome		1271	0.0	OR166645
Caretta caretta isolate SIC27 mitochondrion, partial genome		1271	0.0	OR166646
Caretta caretta mitochondrion, complete genome		1271	0.0	OR775090
Caretta caretta mitochondrion, complete genome		1271	0.0	KP256531
Caretta caretta isolate 69611 mitochondrion, partial genome		1271	0.0	JX454984
Caretta caretta isolate 69599 mitochondrion, complete genome		1271	0.0	JX454983
Caretta caretta complete mitochondrial genome		1271	0.0	FR694649
Lepidochelys kempii (Atlantic ridley) [turtles]				
Lepidochelys kempii isolate 6 mitochondrion, complete genome		1256	0.0	MN136060
Lepidochelys kempii isolate 13 mitochondrion, complete genome		1256	0.0	MN136059
Lepidochelys kempii isolate 3 mitochondrion, complete genome		1256	0.0	MN136058
Lepidochelys kempii isolate MT1 mitochondrion, complete genome		1256	0.0	MN136057
Lepidochelys kempii isolate 27 mitochondrion, complete genome		1256	0.0	MN136056
Lepidochelys kempii isolate 1 mitochondrion, complete genome		1256	0.0	MN136055
Lepidochelys kempii isolate BR1 mitochondrion, complete genome		1256	0.0	MN136054
Lepidochelys kempii isolate 14 mitochondrion, complete genome		1256	0.0	MN136053
Lepidochelys kempii isolate 16 mitochondrion, complete genome		1256	0.0	MN136052
Lepidochelys kempii isolate 68091 mitochondrion, partial genome		1256	0.0	JX454982
Lepidochelys kempii isolate 23 mitochondrion, complete genome		1254	0.0	MN136061
Lepidochelys kempii isolate 68090 mitochondrion, partial genome		1253	0.0	JX454981
Lepidochelys olivacea (Pacific ridley) [turtles]				
Lepidochelys olivacea isolate rLepOli2 genome assembly, organelle: mitochondrion		1232	0.0	OZ223140
Lepidochelys olivacea voucher CLP:OR1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial		1232	0.0	PQ459488
Lepidochelys olivacea isolate CGG-01Lol mitochondrion, complete genome		1232	0.0	NC_028634
Lepidochelys olivacea isolate CGG-01Lol mitochondrion, complete genome		1232	0.0	JX454991
Lepidochelys olivacea isolate 78920 mitochondrion, partial genome		1232	0.0	JX454987
Lepidochelys olivacea isolate 55352 mitochondrion, partial genome		1232	0.0	JX454979
Chelonoidis alburyorum (Albury's tortoise) [turtles]				
Chelonoidis alburyorum mitochondrion genomic DNA containing trnF-trnT region, specimen voucher GT-3, FS 234 (MTD18987)		1206	0.0	LR968547
Chelonoidis alburyorum mitochondrion genomic DNA containing trnF-trnT region, specimen voucher GT-3, FS82 (MTD18982)		1206	0.0	LR968543
Stigmochelys pardalis (leopard tortoise) [turtles]				
Stigmochelys pardalis mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher MTD T 16076		1194	0.0	LR697082
Psammobates pardalis mitochondrion, complete genome		1194	0.0	NC_007694
Geochelone pardalis voucher MVZ 241333 mitochondrion, complete genome		1194	0.0	DQ080041
Geochelone elegans (star tortoise) [turtles]				
Geochelone elegans mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher MTD T 6057		1194	0.0	LR697072
Geochelone elegans mitochondrion, complete genome		1194	0.0	NC_041096
Geochelone elegans mitochondrion, complete genome		1194	0.0	MH459393
Cylindraspis triserrata (Mauritius giant flat-shelled tortoise) [turtles]				
Cylindraspis triserrata mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher BMNH R3992		1151	0.0	LR697065
Cylindraspis triserrata mitochondrion genomic DNA containing from tRNA-Phe (partial) to tRNA-Thr (partial) region, specimen voucher NHMUK 1876.10.28.4		1151	0.0	OW244303
Trachemys decussata angusta [turtles]				

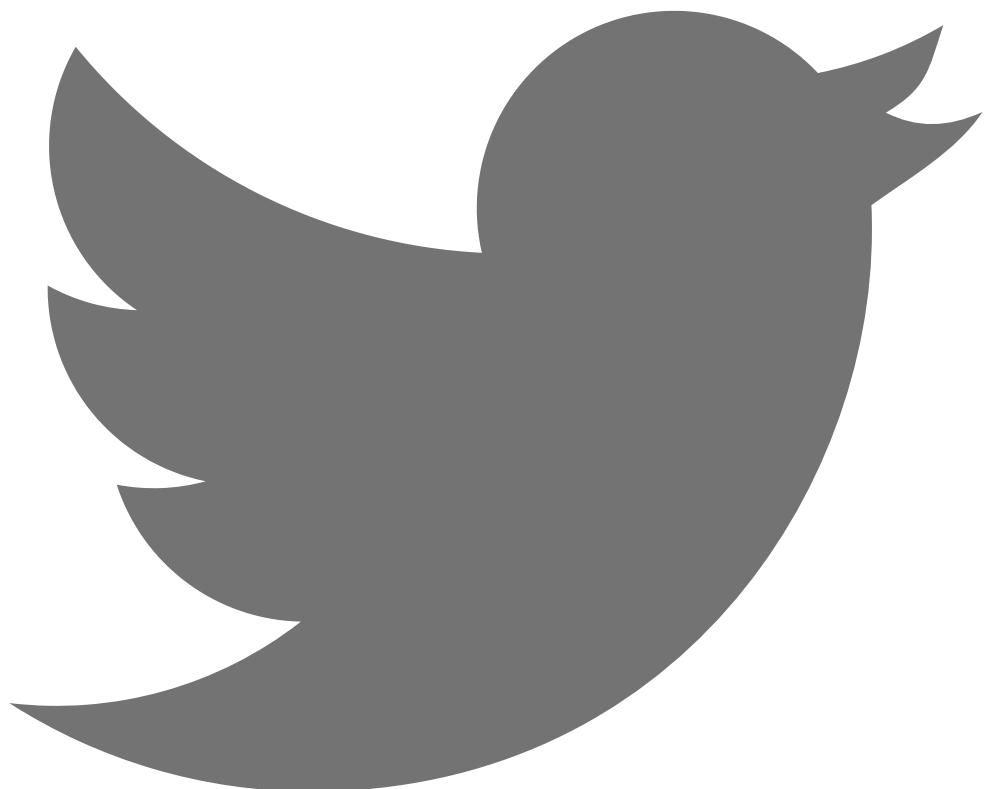
Description		Score	E value	Accession
Trachemys decussata angusta mitochondrion genomic DNA containing from tRNA-Phe (complete) to control region (partial) region, specimen voucher MTD-T 20622		1144	0.0	OX453476
Mauremys japonica (Japanese pond turtle)	[turtles]			
Mauremys japonica mitochondrial DNA, complete sequence		1140	0.0	AP019397
Mauremys japonica mitochondrion, complete genome		1140	0.0	NC_016951
Mauremys japonica mitochondrion, complete genome		1140	0.0	GU938833
Chrysemys picta bellii (western painted turtle)	[turtles]			
Chrysemys picta bellii mitochondrion, complete genome		1116	0.0	NC_023890
Chrysemys picta bellii mitochondrion, complete genome		1116	0.0	KF874616

- **Taxonomy**

Taxonomy	Number of hits	Number of Organisms	Description
Durocryptodira	157	14	
.. Chelonioidea	141	7	
... Dermochelys coriacea	12	1	Dermochelys coriacea hits
... Cheloniidae	129	6	
... Eretmochelys imbricata	22	1	Eretmochelys imbricata hits
... Natator depressus	3	1	Natator depressus hits
... Chelonia mydas	11	1	Chelonia mydas hits
... Caretta caretta	75	1	Caretta caretta hits
... Lepidochelys	18	2	
.... Lepidochelys kempii	12	1	Lepidochelys kempii hits
.... Lepidochelys olivacea	6	1	Lepidochelys olivacea hits
.. Testudinoidea	16	7	
.. Testudinidae	10	4	
... Chelonoidis alburyorum	2	1	Chelonoidis alburyorum hits
... Stigmochelys pardalis	3	1	Stigmochelys pardalis hits
... Geochelone elegans	3	1	Geochelone elegans hits
... Cylindraspis triserrata	2	1	Cylindraspis triserrata hits
.. Emydidae	3	2	
... Trachemys decussata angusta	1	1	Trachemys decussata angusta hits
... Chrysemys picta bellii	2	1	Chrysemys picta bellii hits
.. Mauremys japonica	3	1	Mauremys japonica hits

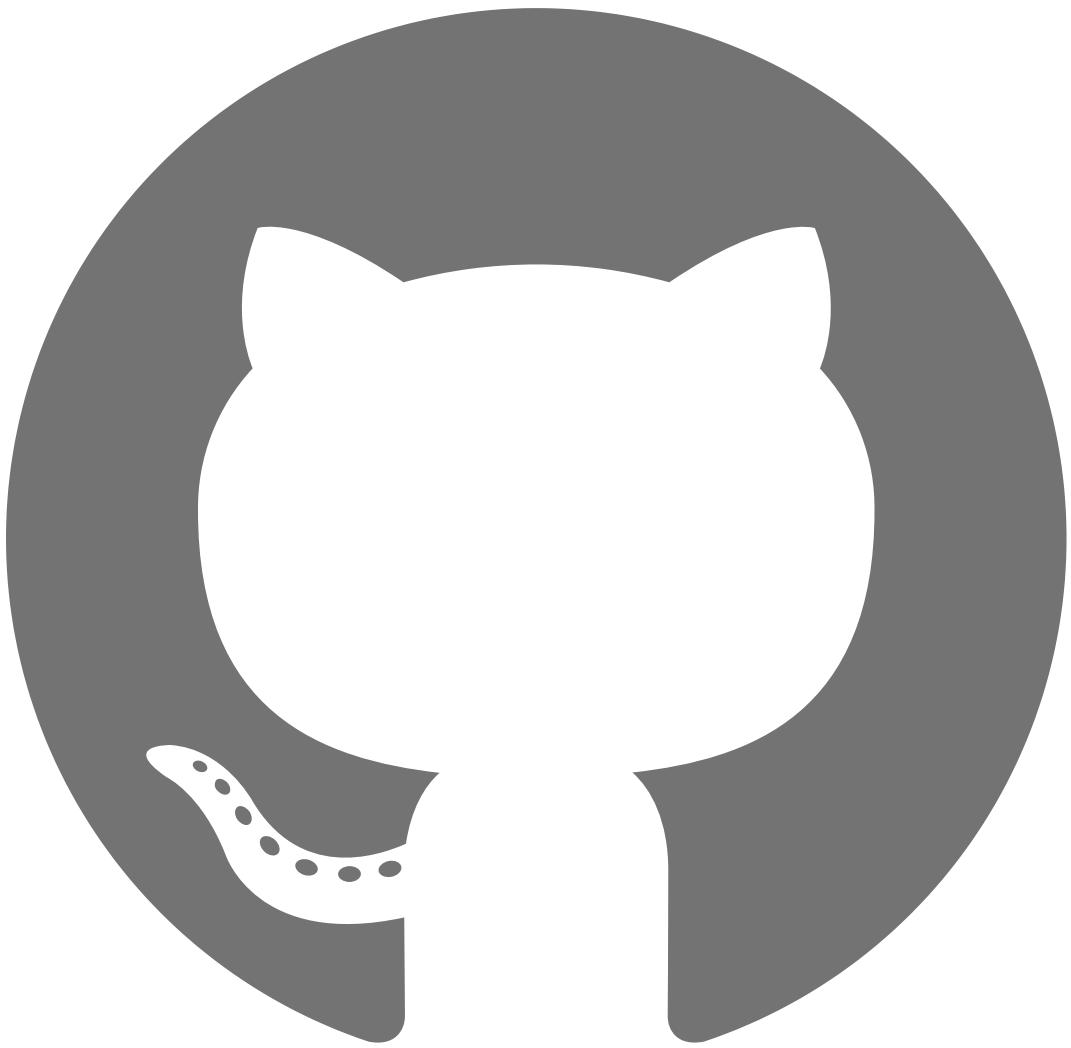
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