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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	lcl Query_1844041
Description	None ...
Molecule type	dna
Query Length	1541

Descriptions

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Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
Dermochelys coriacea voucher CRI006922 mitochondrion, complete genome	Dermochelys coriacea	1923	1923	77%	0.0	94.65%	16501	MF460363.1
Dermochelys coriacea isolate CGG-03 mitochondrion, partial genome	Dermochelys coriacea	1923	1923	77%	0.0	94.65%	16680	JX454992.1
Dermochelys coriacea isolate 9790 mitochondrion, partial genome	Dermochelys coriacea	1923	1923	77%	0.0	94.65%	16380	JX454973.1
Dermochelys coriacea isolate 5718 mitochondrion, partial genome	Dermochelys coriacea	1923	1923	77%	0.0	94.65%	16420	JX454969.1
Dermochelys coriacea isolate 88903 mitochondrion, partial genome	Dermochelys coriacea	1908	1908	77%	0.0	94.31%	16366	JX454989.1
Dermochelys coriacea voucher DC-COI-AP1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	Dermochelys coriacea	1452	1452	53%	0.0	98.53%	815	GQ152876.1
Dermochelys coriacea cytochrome c oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Dermochelys coriacea	1421	1421	52%	0.0	98.50%	798	KU883273.1
Eretmochelys imbricata isolate E13 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16582	PQ276118.1
Eretmochelys imbricata isolate E12 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16572	PQ276117.1
Eretmochelys imbricata isolate E11 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16581	PQ276116.1
Eretmochelys imbricata isolate E10 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16573	PQ276115.1
Eretmochelys imbricata isolate E9 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16580	PQ276114.1
Eretmochelys imbricata isolate E8 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16581	PQ276113.1
Eretmochelys imbricata isolate E7 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16581	PQ276112.1
Eretmochelys imbricata isolate E6 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16590	PQ276111.1
Eretmochelys imbricata isolate E5 mitochondrion, complete genome	Eretmochelys imbricata	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
Eretmochelys imbricata isolate E4 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16581	PQ276109.1
Eretmochelys imbricata isolate E1 mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16590	PQ276106.1
Eretmochelys imbricata isolate rErelmb1 genome assembly, organelle: mitochondrion	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16779	OZ223910.1
Eretmochelys imbricata mitochondrion, complete genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16386	KP221806.1
Eretmochelys imbricata isolate 61392 mitochondrion, partial genome	Eretmochelys imbricata	1347	1347	83%	0.0	84.71%	16349	JX454980.1
Eretmochelys imbricata isolate E3 mitochondrion, complete genome	Eretmochelys imbricata	1341	1341	83%	0.0	84.63%	16591	PQ276108.1
Eretmochelys imbricata isolate E2 mitochondrion, complete genome	Eretmochelys imbricata	1341	1341	83%	0.0	84.63%	16582	PQ276107.1
Eretmochelys imbricata isolate 5787 mitochondrion, partial genome	Eretmochelys imbricata	1341	1341	83%	0.0	84.63%	16354	JX454970.1
Natator depressus isolate rNatDep1 genome assembly, organelle: mitochondrion	Natator depressus	1336	1336	83%	0.0	84.53%	16559	OZ223967.1
Eretmochelys imbricata isolate Cc-C-2 mitochondrion, complete genome	Eretmochelys imbricata	1336	1336	83%	0.0	84.56%	16498	MF571906.1
Eretmochelys imbricata isolate 72489 mitochondrion, partial genome	Eretmochelys imbricata	1336	1336	83%	0.0	84.56%	16347	JX454986.1
Natator depressa haplogroup Au (X) mitochondrion, complete genome	Natator depressus	1330	1330	83%	0.0	84.45%	16281	NC_018550.1
Eretmochelys imbricata mitochondrion, complete genome	Eretmochelys imbricata	1330	1330	83%	0.0	84.48%	16478	NC_012398.1
Chelonia mydas isolate 28666 mitochondrion, complete genome	Chelonia mydas	1308	1308	83%	0.0	84.08%	16435	JX454976.1
Chelonia mydas isolate CGG-01Cmyd mitochondrion, complete genome	Chelonia mydas	1291	1291	83%	0.0	83.85%	16495	JX454990.1
Chelonia mydas isolate 54903 mitochondrion, partial genome	Chelonia mydas	1291	1291	83%	0.0	83.85%	16435	JX454978.1
Chelonia mydas isolate 13768	Chelonia mydas	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
mitochondrion, complete genome								
Chelonia mydas isolate Sample ID 9277 mitochondrion, complete genome	Chelonia mydas	1291	1291	83%	0.0	83.85%	16440	JX454972.1
Chelonia mydas isolate 8855 mitochondrion, complete genome	Chelonia mydas	1291	1291	83%	0.0	83.85%	16435	JX454971.1
Chelonia mydas mitochondrion, partial genome	Chelonia mydas	1291	1291	83%	0.0	83.85%	16350	JQ026233.1
Chelonia mydas mitochondrion, complete genome	Chelonia mydas	1291	1291	83%	0.0	83.85%	16497	NC_000886.1
Chelonia mydas mitochondrion, partial genome	Chelonia mydas	1286	1286	83%	0.0	83.77%	16350	JQ034420.1
Caretta caretta isolate 87410 mitochondrion, complete genome	Caretta caretta	1275	1275	83%	0.0	83.67%	16411	JX454988.1
Caretta caretta isolate 46603 mitochondrion, complete genome	Caretta caretta	1275	1275	83%	0.0	83.67%	16399	JX454977.1
Caretta caretta isolate Cc-C-4 mitochondrion, complete genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16446	MF579505.1
Caretta caretta isolate Cc-C-3 mitochondrion, complete genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16461	MF579504.1
Caretta caretta isolate Cc-C-1 mitochondrion, complete genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16633	MF554690.1
Caretta caretta isolate SIC25 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166644.1
Caretta caretta isolate SIC21 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166640.1
Caretta caretta isolate SIC20 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166639.1
Caretta caretta isolate SIC15 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166634.1
Caretta caretta isolate SIC14 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166633.1
Caretta caretta isolate SIC02 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166622.1
Caretta caretta isolate LIN01 mitochondrion, partial genome	Caretta caretta	1271	1271	83%	0.0	83.61%	16541	OR166619.1
Caretta caretta isolate CAL1370	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
mitochondrion, complete genome								
Lepidochelys kempii isolate 27 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16483	MN136056.1
Lepidochelys kempii isolate 1 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16438	MN136055.1
Lepidochelys kempii isolate BR1 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16406	MN136054.1
Lepidochelys kempii isolate 14 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16443	MN136053.1
Lepidochelys kempii isolate 16 mitochondrion, complete genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16444	MN136052.1
Lepidochelys kempii isolate 68091 mitochondrion, partial genome	Lepidochelys kempii	1256	1256	77%	0.0	84.78%	16386	JX454982.1
Lepidochelys kempii isolate 23 mitochondrion, complete genome	Lepidochelys kempii	1254	1254	77%	0.0	84.73%	16433	MN136061.1
Lepidochelys kempii isolate 68090 mitochondrion, partial genome	Lepidochelys kempii	1253	1253	77%	0.0	84.70%	16382	JX454981.1
Dermochelys coriacea voucher ZSI/ANRC/M/29790 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	Dermochelys coriacea	1249	1249	46%	0.0	98.30%	705	PQ069769.1
Lepidochelys olivacea isolate rLepOli2 genome assembly, organelle: mitochondrion	Lepidochelys olivacea	1232	1232	83%	0.0	83.06%	16732	OZ223140.1
Lepidochelys olivacea voucher CLP:OR1 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	Lepidochelys olivacea	1232	1232	83%	0.0	83.06%	1545	PQ459488.1
Lepidochelys olivacea isolate CGG-01LoI mitochondrion, complete genome	Lepidochelys olivacea	1232	1232	83%	0.0	83.06%	16718	NC_028634.1
Lepidochelys olivacea isolate 78920 mitochondrion, partial genome	Lepidochelys olivacea	1232	1232	83%	0.0	83.06%	16387	JX454987.1
Lepidochelys olivacea isolate 55352 mitochondrion, partial genome	Lepidochelys olivacea	1232	1232	83%	0.0	83.06%	16379	JX454979.1
Eretmochelys imbricata voucher CLP:GT1 cytochrome c	Eretmochelys imbricata	1214	1214	62%	0.0	89.35%	1000	PQ459491.1

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
oxidase subunit I (COX1) gene, partial cds; mitochondrial								
Chelonoidis alburyorum mitochondrion genomic DNA containing trnF-trnT region, specimen voucher GT-3, FS 234 (MTD18987)	Chelonoidis alburyorum	1206	1206	79%	0.0	83.55%	15349	LR968547.1
Chelonoidis alburyorum mitochondrion genomic DNA containing trnF-trnT region, specimen voucher GT-3, FS82 (MTD18982)	Chelonoidis alburyorum	1206	1206	79%	0.0	83.55%	15339	LR968543.1
Stigmochelys pardalis mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher MTD T 16076	Stigmochelys pardalis	1194	1194	72%	0.0	85.29%	15358	LR697082.1
Geochelone elegans mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher MTD T 6057	Geochelone elegans	1194	1194	80%	0.0	83.13%	15320	LR697072.1
Geochelone elegans mitochondrion, complete genome	Geochelone elegans	1194	1194	80%	0.0	83.13%	16446	NC_041096.1
Psammobates pardalis mitochondrion, complete genome	Stigmochelys pardalis	1194	1194	72%	0.0	85.29%	19403	NC_007694.1
Dermochelys coriacea voucher ZSI/ANRC/M/29790 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	Dermochelys coriacea	1171	1171	43%	0.0	98.19%	663	PQ216296.1
Cylindraspis triserrata mitochondrion genomic DNA containing trnF-trnT (including all 13 CDS) region, specimen voucher BMNH R3992	Cylindraspis triserrata	1151	1151	72%	0.0	84.64%	15335	LR697065.1
Cylindraspis triserrata mitochondrion genomic DNA containing from tRNA-Phe (partial) to tRNA-Thr (partial) region, specimen voucher NHMUK 1876.10.28.4	Cylindraspis triserrata	1151	1151	72%	0.0	84.64%	15382	OW244303.1
Trachemys decussata angusta mitochondrion genomic DNA containing from tRNA-Phe	Trachemys decussata angusta	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
(complete) to control region (partial) region, specimen voucher MTD-T 20622								
Mauremys japonica mitochondrial DNA, complete sequence	Mauremys japonica	1140	1140	72%	0.0	84.44%	16443	AP019397.1
Mauremys japonica mitochondrion, complete genome	Mauremys japonica	1140	1140	72%	0.0	84.44%	16443	NC_016951.1
Dermochelys coriacea voucher ZSI/ANRC/M/29791 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	Dermochelys coriacea	1127	1127	41%	0.0	98.12%	639	PQ069775.1
Chrysemys picta bellii mitochondrion, complete genome	Chrysemys picta bellii	1116	1116	72%	0.0	84.10%	16875	NC_023890.1
Dermochelys coriacea voucher USNM:Herp:544382 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	Dermochelys coriacea	1085	1085	39%	0.0	98.52%	607	MH273769.1
Dermochelys coriacea voucher ZSI/ANRC/M/29791 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial	Dermochelys coriacea	1077	1077	40%	0.0	98.04%	612	PQ216299.1

Graphic Summary

Query	Count
SELECT * FROM table1	1450
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SELECT * FROM table3	1350
SELECT * FROM table4	1300
SELECT * FROM table5	1250
SELECT * FROM table6	1200
SELECT * FROM table7	1150
SELECT * FROM table8	1100
SELECT * FROM table9	1050
SELECT * FROM table10	1000
SELECT * FROM table11	950
SELECT * FROM table12	900
SELECT * FROM table13	850
SELECT * FROM table14	800
SELECT * FROM table15	750
SELECT * FROM table16	700
SELECT * FROM table17	650
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SELECT * FROM table24	300
SELECT * FROM table25	250
SELECT * FROM table26	200
SELECT * FROM table27	150
SELECT * FROM table28	100
SELECT * FROM table29	50
SELECT * FROM table30	20
SELECT * FROM table31	10
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SELECT * FROM table34	1
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SELECT * FROM table93	0
SELECT * FROM table94	0
SELECT * FROM table95	0
SELECT * FROM table96	0
SELECT * FROM table97	0
SELECT * FROM table98	0
SELECT * FROM table99	0
SELECT * FROM table100	0

Score	Expect	Identities	Gaps	Strand	Frame
1923 bits(1041)	0.0()	1132/1196(95%)	3/1196(0%)	Plus/Plus	
Query 11	CTCGCTGA	ttttttt	CTACTAATCATAAAGACATTGGCAC	CCTATACCTAATTTTGGGG	70

Sbjct	5414	CTCGCTGATTTTTTCTACTAATCATAAAGACATTGGCACCCCTATACCTAATTTTTGGGG	5473
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC	130
Sbjct	5474	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC	5533
Query	131	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA	190
Sbjct	5534	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA	5593
Query	191	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTTC	250
Sbjct	5594	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTTC	5653
Query	251	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGNN	310
Sbjct	5654	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGAC	5713
Query	311	NNNNNNCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	370
Sbjct	5714	TTTTACCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	5773
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	430
Sbjct	5774	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	5833
Query	431	ACCTAACTATCTTTTTCTCTGCACCTAGCTGGTGTTTCATCAATTTTAGGAGCTATT-ACT	489
Sbjct	5834	ACCTAACTATCTTTTTCTCTGCACCTAGCTGGTGTTTCATCAATTTTAGGAGCTATTAAC	5893
Query	490	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	549
Sbjct	5894	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	5953
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	609
Sbjct	5954	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	6013
Query	610	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	669
Sbjct	6014	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	6073
Query	670	GAGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTTGGCCATCCAGAAGTAT	729
Sbjct	6074	GAGGAGGAGACCCAATCCTATACCAACCTATTCTGATTCTTTGGCCATCCAGAAGTAT	6133
Query	730	ACATCCTAATTCTACCAGGATTTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6134	ACATCCTAATTCTACCAGGATTTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6193
Query	790	AAAAAGAACCATTTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCGG	849
Sbjct	6194	AAAAAGAACCATTTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCGG	6253
Query	850	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	909
Sbjct	6254	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	6313
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAN	969
Sbjct	6314	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAC	6373
Query	970	NNNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	1029
Sbjct	6374	TAGCAACCCCTTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	6433
Query	1030	TTATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACTCATCACTAG	1089
Sbjct	6434	TTATTTTCCTATTTACTATTGGTGGATTAAACAGGTATTGTACTAGCCAACTCATCACTAG	6493
Query	1090	ACATCGTACTACACGACAGTACTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6494	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTTCCATTATGTT-CTATCAATA	6552
Query	1149	GGAGCTGTATTTGCCATCATAGGAGGCTTCATTCAGTATTTCCCCTATTCTCAGG	1204
Sbjct	6553	GGAGCTGTATTTGCCATCATAGCAGGATTTACTCACTGATTCCCTCTCTTCACAGG	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	CTCGCTGAtttttt	CTACTAATCATAAAGACATTGGCACCC	TATACCTAATTTTTGGGG		70
Sbjct 5414	CTCGCTGATTTTTT	CTACTAATCATAAAGACATTGGCACCC	TATACCTAATTTTTGGGG		5473
Query 71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				130
Sbjct 5474	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				5533
Query 131	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				190

Sbjct	5534	CGGGAACCCCTCCTAGGAGATGACCAAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA	5593
Query	191	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTTC	250
Sbjct	5594	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTTC	5653
Query	251	CCCTTATAATTGGAGACCAGACATGGCATTCCCACGAATAAACAACATAAGCTTTTGNN	310
Sbjct	5654	CCCTTATAATTGGAGACCAGACATGGCATTCCCACGAATAAACAACATAAGCTTTTGAC	5713
Query	311	NNNNNNCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	370
Sbjct	5714	TTTTACCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	5773
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	430
Sbjct	5774	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	5833
Query	431	ACCTAACTATCTTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATT-ACT	489
Sbjct	5834	ACCTAACTATCTTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATTAACT	5893
Query	490	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	549
Sbjct	5894	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	5953
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	609
Sbjct	5954	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	6013
Query	610	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	669
Sbjct	6014	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	6073
Query	670	GAGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTTGGCCATCCAGAAGTAT	729
Sbjct	6074	GAGGAGGAGACCCAATCCTATACCAACACCTATTCTGATTCTTTGGCCATCCAGAAGTAT	6133
Query	730	ACATCCTAATTCTACCAGGATTGGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6134	ACATCCTAATTCTACCAGGATTGGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6193
Query	790	AAAAAGAACCATTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCCCTGG	849
Sbjct	6194	AAAAAGAACCATTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCCCTGG	6253
Query	850	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACAGGAGCTT	909
Sbjct	6254	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACAGGAGCTT	6313
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAN	969
Sbjct	6314	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAC	6373
Query	970	NNNNNNNNNNNNNNNAGGAATAATTAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	1029
Sbjct	6374	TAGCAACCCTTCACGGAGGAATAATTAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	6433
Query	1030	TTATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6434	TTATTTTCCTATTTACTATTGGTGGATTAACAGGTATTGTACTAGCCAACTCATCACTAG	6493
Query	1090	ACATCGTACTACACGACACGTACTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6494	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTTCCATTATGTT-CTATCAATA	6552
Query	1149	GGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCTATTCTCAGG	1204
Sbjct	6553	GGAGCTGTATTTGCCATCATAGCAGGATTTACTCACTGATTCCTCTCTTCACAGG	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()	1132/1196(95%)	3/1196(0%)	Plus/Plus	
Query 11	CTCGCTGAtttttt	CTACTAATCATAAAGACATTGGCACCC	TATACCTAATTTT	GGGG	70
Sbjct 5397	CTCGCTGATTTTTT	CTACTAATCATAAAGACATTGGCACCC	TATACCTAATTTT	GGGG	5456
Query 71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				130
Sbjct 5457	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				5516
Query 131	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				190
Sbjct 5517	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				5576
Query 191	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTTC				250
Sbjct 5577	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTTC				5636
Query 251	CCCTTATAATTGGAGACCAGACATGGCATTCCCACGAATAAACAACATAAGCTTTTGNN				310

Sbjct	5637	CCCTTATAAATTGGAGCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGAC	5696
Query	311	NNNNNNCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	370
Sbjct	5697	TTTTACCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA	5756
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	430
Sbjct	5757	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	5816
Query	431	ACCTAACTATCTTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATT-ACT	489
Sbjct	5817	ACCTAACTATCTTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATTA ACT	5876
Query	490	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	549
Sbjct	5877	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	5936
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	609
Sbjct	5937	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	5996
Query	610	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	669
Sbjct	5997	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	6056
Query	670	GAGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTTGGCCATCCAGAAGTAT	729
Sbjct	6057	GAGGAGGAGACCCAATCCTATACCAACACCTATTCTGATTCTTTGGCCATCCAGAAGTAT	6116
Query	730	ACATCCTAATTCTACCAGGATTGGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6117	ACATCCTAATTCTACCAGGATTGGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6176
Query	790	AAAAAGAACCATTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCTGG	849
Sbjct	6177	AAAAAGAACCATTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCTGG	6236
Query	850	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	909
Sbjct	6237	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	6296
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAN	969
Sbjct	6297	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAC	6356
Query	970	NNNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	1029
Sbjct	6357	TAGCAACCCTTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	6416
Query	1030	TTATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6417	TTATTTTCCTATTTACTATTGGTGGATTAACAGGTATTGTACTAGCCAACTCATCACTAG	6476
Query	1090	ACATCGTACTACACGACAGTACTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6477	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTTCCATTATGTT-CTATCAATA	6535
Query	1149	GGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGG	1204
Sbjct	6536	GGAGCTGTATTTGCCATCATAGCAGGATTTACTCACTGATTCCCTCTCTTCACAGG	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	CTCGCTGAtttttt	CTACTAATCATAAAGACATTGGCACCCTATACCTAATTTTGGGG			70
Sbjct 5414	CTCGCTGATTTTTT	CTACTAATCATAAAGACATTGGCACCCTATACCTAATTTTGGGG			5473
Query 71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				130
Sbjct 5474	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				5533
Query 131	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				190
Sbjct 5534	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				5593
Query 191	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTG TTC				250
Sbjct 5594	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTG TTC				5653
Query 251	CCCTTATAAATTGGAGCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGNN				310
Sbjct 5654	CCCTTATAAATTGGAGCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGAC				5713
Query 311	NNNNNNCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA				370
Sbjct 5714	TTTTACCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA				5773
Query 371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG				430

Sbjct	5774	CAGGCTGAACAGTCTATCTCCACCTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG	5833
Query	431	ACCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATT-ACT	489
Sbjct	5834	ACCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATTA	5893
Query	490	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	549
Sbjct	5894	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	5953
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	609
Sbjct	5954	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	6013
Query	610	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	669
Sbjct	6014	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	6073
Query	670	GAGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTTGGCCATCCAGAAGTAT	729
Sbjct	6074	GAGGAGGAGACCCAATCCTATACCAACACCTATTCTGATTCTTTGGCCATCCAGAAGTAT	6133
Query	730	ACATCCTAATTCTACCAGGATTGGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6134	ACATCCTAATTCTACCAGGATTGGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6193
Query	790	AAAAAGAACCATTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCTGG	849
Sbjct	6194	AAAAAGAACCATTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCTGG	6253
Query	850	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	909
Sbjct	6254	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	6313
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAN	969
Sbjct	6314	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAC	6373
Query	970	NNNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	1029
Sbjct	6374	TAGCAACCCTTCACGGAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	6433
Query	1030	TTATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6434	TTATTTTCCTATTTACTATTGGTGGATTAACAGGTATTGTACTAGCCAACTCATCACTAG	6493
Query	1090	ACATCGTACTACACGACACGTACTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6494	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTTCCATTATGTT-CTATCAATA	6552
Query	1149	GGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCTATTCTCAGG	1204
Sbjct	6553	GGAGCTGTATTTGCCATCATAGCAGGATTTACTCACTGATTCCTCTCTTCACAGG	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()	1128/1196(94%)	3/1196(0%)	Plus/Plus	
Query	11	CTCGCTGAttttttTCTACTAATCATAAAAGACATTGGCACCCCTATACCTAATTTTTGGGG				70
Sbjct	5410	CTCGCTGATTTTTTCTACTAATCATAAAAGACATTGGCACCCCTATACCTAATTTTTGGGG				5469
Query	71	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				130
Sbjct	5470	CCTGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAAC				5529
Query	131	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				190
Sbjct	5530	CGGGAACCCCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCA				5589
Query	191	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAACTGACTTGTTT				250
Sbjct	5590	TTATAATCTTCTTCATAGTTATACCAGTTATAATCGGCGGTTTCGGAACTGACTTGTTT				5649
Query	251	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTTGN				310
Sbjct	5650	CCCTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACACATAAGCTTTTGAC				5709
Query	311	NNNNNNCTCCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA				370
Sbjct	5710	TTTTACTCCTCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAA				5769
Query	371	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG				430
Sbjct	5770	CAGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAG				5829
Query	431	ACCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATT-ACT				489
Sbjct	5830	ACCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATTA				5889
Query	490	TCATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTAT				549

Sbjct	5890	TCATTACTACAGCAATCAACATAAAAAATCTCCAGCTATATCACAATACCAAACACCATTAT	5949
Query	550	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	609
Sbjct	5950	TTGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTG	6009
Query	610	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	669
Sbjct	6010	CAGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAG	6069
Query	670	GAGGAGGAGACCCAATCCTATACCAATGCTATTCTGATTCTTTGGCCATCCAGAAGTAT	729
Sbjct	6070	GAGGAGGAGACCCAATCCTATACCAACCTATTCTGATTCTTTGGCCATCCAGAAGTAT	6129
Query	730	ACATCCTAATTCTACCAGGATTTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	789
Sbjct	6130	ACATCCTAATTCTACCAGGATTTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTA	6189
Query	790	AAAAAGAACCATTGTTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCTGG	849
Sbjct	6190	AAAAAGAACCATTGTTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTCTGG	6249
Query	850	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	909
Sbjct	6250	GTTTTATCGTTTGAGCCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTT	6309
Query	910	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAN	969
Sbjct	6310	ACTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGAC	6369
Query	970	NNNNNNNNNNNNNNNAGGAATAATTAAATGAGATGCTGCTATACTCTGAGCCCTTGGGT	1029
Sbjct	6370	TAGCAACCCTTCACGGAGGAATAATTAAATGAGATGCTGCNNNNCTCTGAGCCCTTGGGT	6429
Query	1030	TTATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAG	1089
Sbjct	6430	TTATTTTCCTATTTACTATTGGTGGATTAACAGGTATTGTACTAGCCAACTCATCACTAG	6489
Query	1090	ACATCGTACTACACGACAGTACTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATA	1148
Sbjct	6490	ACATCGTACTACATGACACCTACTATGTAGTAGCACATTTCCATTATGTT-CTATCAATA	6548
Query	1149	GGAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCCTATTCTCAGG	1204
Sbjct	6549	GGAGCTGTATTTGCCATCATAGCAGGATTTACTCACTGATTCCTCTCTTCACAGG	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	tCTACTAATCATAAAGACATTGGCACCCTATACCTAATTTTTGGGGCCTGAGCAGGAATA				84
Sbjct 1	TCTACTAATCATAAAGACATTGGCACCCTATACCTAATTTTTGGGGCCTGAGCAGGAATA				60
Query 85	GTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAACCGGGAACCTCCTA				144
Sbjct 61	GTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAACCGGGAACCTCCTA				120
Query 145	GGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCATTATAATCTTCTTC				204
Sbjct 121	GGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCATTATAATCTTCTTC				180
Query 205	ATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTCCTTATAATTGGA				264
Sbjct 181	ATAGTTATACCAGTTATAATCGGCGGTTTCGGAAACTGACTTGTTCCTTATAATTGGA				240
Query 265	GCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGNNNNNNNNCTCCCTCA				324
Sbjct 241	GCACCAGACATGGCATTCCCACGAATAAAACAACATAAGCTTTTGACTTTTACCTCCCTCA				300
Query 325	CTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTGAACAGTC				384
Sbjct 301	CTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTGAACAGTC				360
Query 385	TATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAGACCTAACTATCTTT				444
Sbjct 361	TATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAGACCTAACTATCTTT				420
Query 445	TCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATT-ACTTCATTACTACAGCA				503
Sbjct 421	TCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTATTAACCTCATTACTACAGCA				480
Query 504	ATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTATTTGTATGATCTGTA				563
Sbjct 481	ATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTATTTGTATGATCTGTA				540
Query 564	TTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTGCAGGAATCACCATA				623
Sbjct 541	TTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTGCAGGAATCACCATA				600
Query 624	CTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAGGAGGAGAGACCCA				683

Sbjct 601 CTACTTACAGATCGAAACCTAAACACAAACCTTTTGGATCCTTCAGGAGGAGGAGACCCA 660

Query 684 ATCCTATACCAAATGCTATTCTGATTCTTTGGCCATCCAGAAGTATACATCCTAATTCTA 743

Sbjct 661 ATCCTATACCAACACCTATTCTGATTCTTTGGCCATCCAGAAGTATACATCCTAATTCTA 720

Query 744 CCAGGATTTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAAAAAAGAACCATT 803

Sbjct 721 CCAGGATTTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAAAAAAGAACCATT 780

Query 804 GGTTACATAGGAATAGTTTGAGCAATAATATCCAT 838

Sbjct 781 GGTTACATAGGAATAGTTTGAGCAATAATATCCAT 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	CATTGGCACCCTATACCTAATTTTGGGGCCTGAGCAGGAATAGTAGGCACAGCACTCAG	101			
Sbjct 1	CATTGGCACCCTATACCTAATTTTGGGGCCTGAGCAGGAATAGTAGGCACAGCACTCAG	60			
Query 102	CCTATTAATCCGTGCAGAACTAAGCCAACCGGAACCCTCCTAGGAGATGACCAAATTTA	161			
Sbjct 61	CCTATTAATCCGTGCAGAACTAAGCCAACCGGAACCCTCCTAGGAGATGACCAAATTTA	120			
Query 162	CAATGTCATCGTTACAGCCCATGCCTTCATTATAATCTTCTTCATAGTTATACCAGTTAT	221			
Sbjct 121	CAATGTCATCGTTACAGCCCATGCCTTCATTATAATCTTCTTCATAGTTATACCAGTTAT	180			
Query 222	AATCGGCGGTTTCGGAAACTGACTTGTCCCCTTATAATTGGAGCACCAGACATGGCATT	281			
Sbjct 181	AATCGGCGGTTTCGGAAACTGACTTGTCCCCTTATAATTGGAGCACCAGACATGGCATT	240			
Query 282	CCCACGAATAAAACAACATAAGCTTTTGNNNNNNNCTCCCTCACTGTTACTACTTCTAGC	341			
Sbjct 241	CCCACGAATAAAACAACATAAGCTTTTGACTTTTACCTCCCTCACTGTTACTACTTCTAGC	300			
Query 342	ATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTGAACAGTCTATCCTCCACTAGCTGG	401			
Sbjct 301	ATCATCAGGAATTGAAGCAGGTGCAGGAACAGGCTGAACAGTCTATCCTCCACTAGCTGG	360			
Query 402	AAACCTAGCCCACGCTGGTGCTTCTGTAGACCTAACTATCTTTTCTCTGCACCTAGCTGG	461			
Sbjct 361	AAACCTAGCCCACGCTGGTGCTTCTGTAGACCTAACTATCTTTTCTCTGCACCTAGCTGG	420			
Query 462	TGTTTCATCAATTTTAGGAGCTATT-ACTTCATTACTACAGCAATCAACATAAAATCTCC	520			
Sbjct 421	TGTTTCATCAATTTTAGGAGCTATTAACCTCATTACTACAGCAATCAACATAAAATCTCC	480			
Query 521	AGCTATATCACAAATACCAAACACCATTATTTGTATGATCTGTATTAATTACAGCCGTTCT	580			
Sbjct 481	AGCTATATCACAAATACCAAACACCATTATTTGTATGATCTGTATTAATTACAGCCGTTCT	540			
Query 581	ATTATTACTCTCATTGCCAGTACTAGCTGCAGGAATCACCATACTACTTACAGATCGAAA	640			
Sbjct 541	ATTATTACTCTCATTGCCAGTACTAGCTGCAGGAATCACCATACTACTTACAGATCGAAA	600			
Query 641	CCTAAACACAACCTTTTTTGATCCTTCAGGAGGAGGAGACCCAATCCTATACCAAATGCT	700			
Sbjct 601	CCTAAACACAACCTTTTTTGATCCTTCAGGAGGAGGAGACCCAATCCTATACCAAACCT	660			
Query 701	ATTCTGATTCTTTGGCCATCCAGAAGTATACATCCTAATTCTACCAGGATTTCGGCATAAT	760			
Sbjct 661	ATTCTGATTCTTTGGCCATCCAGAAGTATACATCCTAATTCTACCAGGATTTCGGCATAAT	720			
Query 761	CTCACATATCGTCACCTATTATGCTGGTAAAAAAGAACCATTGTTTACATAGGAATAGT	820			
Sbjct 721	CTCACATATCGTCACCTATTATGCTGGTAAAAAAGAACCATTGTTTACATAGGAATAGT	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	CGCTGAttttttCTACTAATCATAAAGACATTGGCACCTATACCTAATTTTGGGGCC	72			
Sbjct 5405	CGTTGATTCTTTTCTACCAACCATAAAGACATTGGCACCTATACTTGATCTTTGGAGCA	5464			

Query	73	TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAACCG	132
Sbjct	5465	TGAGCAGGAATAGTAGGCACAGCACTCAGTCTATTAATCCGTGCAGAACTAAGCCAACCA	5524
Query	133	GGAACCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCATT	192
Sbjct	5525	GGAACTCTCCTAGGAGATGACCAAATTTATAATGTTATCGTTACAGCCCATGCCTTCATT	5584
Query	193	ATAATCTTCTTCATAGTTATACCAAGTTATAATCGGCGGTTTCGAAACTGACTTGTTCCC	252
Sbjct	5585	ATAATCTTTTTTATAGTTATACCAATTATAATTTGGCGGTTTCGAAACTGACTTGTTCCA	5644
Query	253	CTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACAAACATAAGCTTTTGNNNN	312
Sbjct	5645	CTAATAATTGGAGCACCAGACATAGCATTTCACGTATAAACAAACATAAGCTTTTG-ACT	5703
Query	313	NNNNTCCCTC-TCAGTGTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAAC	371
Sbjct	5704	CCTACCCCCATCACTACTACTACTAGCATCATCAGGAATTGAAGCAGGAGCAGGTAC	5763
Query	372	AGGCTGAACAGTCTATCCTCCACTAGCTGGAACCTAGCCACGCTGGTGCTTCTGTAGA	431
Sbjct	5764	AGGCTGAACAGTATATCCCCATTAGCCGGAACCTAGCTCACGCTGGCGCTTCAGTAGA	5823
Query	432	CCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTAT-TACTT	490
Sbjct	5824	CCTAACTATCTTTTCCTCCACCTAGCTGGCGTATCCTCAATCTTAGGCGCTATCAACTT	5883
Query	491	CATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTATT	550
Sbjct	5884	CATTACTACAGCAATCAACATAAAATCCCCTGCCATATCACAATACCAAACACCCTTATT	5943
Query	551	TGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTGC	610
Sbjct	5944	CGTATGATCTGTACTAATTACAGCTGTTCTATTACTACTCTCACTACCAGTACTTGCTGC	6003
Query	611	AGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAGG	670
Sbjct	6004	AGGCATTACCATACTACTTACAGACCGAAATCTAAACACAACCTTCTTTGATCCCTCAGG	6063
Query	671	AGGAGGAGACCCAATCCTATACCAAATGCTATTCTGATTCTTTGGCCATCCAGAAGTATA	730
Sbjct	6064	AGGAGGAGACCCAATCCTATATCAACACCTATTCTGATTCTTTGGTCATCCTGAAGTATA	6123
Query	731	CATCCTAATTTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAA	790
Sbjct	6124	CATCTTAATCCTTCCAGGATTTGGCATAATCTCCCACATCGTCACCTATTACTCTGGTAA	6183
Query	791	AAAAGAACCATTTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCCTGGG	850
Sbjct	6184	AAAAGAACCATTTCGGCTACATAGGAATAGTTTGAGCAATAATATCAATTGGTTTCCTGGG	6243
Query	851	TTTTATCGTTTGAGCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTTA	910
Sbjct	6244	CTTCATCGTATGAGCTCACCACATATTCACCGTTGGAATAGACGTAGATACACGAGCTTA	6303
Query	911	CTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGANN	970
Sbjct	6304	TTTCACATCCGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTATTACAGCTGATT	6363
Query	971	NNNNNNNNNNNNNAGGAATAATTAATAGAGATGCTGCTATACTCTGAGCCCTTGGGTT	1030
Sbjct	6364	AGCCACTCTACACGGTGAATAATTAATAGAGATGCTGCCATACTCTGAGCCCTAGGTTT	6423
Query	1031	TATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAGA	1090
Sbjct	6424	CATCTTCCTCTTCACTATTGGCGGATTAACAGGTATTGTATTAGCCAACTCATCACTAGA	6483
Query	1091	CATCGTACTACAGACACGTACTACGTTGTAGC-CNNNNNNNNNNNNNCTATCAATAG	1149
Sbjct	6484	CATTGTATTACAGTACTTATTATGTAGTGGCACACTTCCACTATGTT-CTTTCAATAG	6542
Query	1150	GAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCTATTCTCAGGCTACA	1209
Sbjct	6543	GAGCCGTATTTGCCATCATAGCAGGATTTACCCACTGATTCCTCTTTTCACAGGATATT	6602
Query	1210	CCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAA	1269
Sbjct	6603	CACTACACCAAACCTGAACAAAAGTACATTTTGGAGTAATATTACAGGCGTTAACATAA	6662
Query	1270	CTTTCTTCCACAACACTTTCT	1291
Sbjct	6663	CCTTCTTCCCTCAACA-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	CGCTGATtttttttCTACTAATCATAAAGACATTGGCACCTATACCTAATTTTTGGGGCC				72
Sbjct 5404	CGTTGATTCTTTTCTACCAACCATAAAGACATTGGCACCTATACTTGATCTTTGGAGCA				5463

Query	73	TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAACCG	132
Sbjct	5464	TGAGCAGGAATAGTAGGCACAGCACTCAGTCTATTAATCCGTGCAGAACTAAGCCAACCA	5523
Query	133	GGAACCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCATT	192
Sbjct	5524	GGAACCTCCTAGGAGATGACCAAATTTATAATGTTATCGTTACAGCCCATGCCTTCATT	5583
Query	193	ATAATCTTCTTCATAGTTATACCAAGTTATAATCGGCGGTTTCGAAACTGACTTGTTCCC	252
Sbjct	5584	ATAATCTTTTTTATAGTTATACCAATTATAATTTGGCGGTTTCGAAACTGACTTGTTCCA	5643
Query	253	CTTATAATTGGAGCACCAGACATGGCATTCCCACGAATAAACAAACATAAGCTTTTGNNNN	312
Sbjct	5644	CTAATAATTGGAGCACCAGACATAGCATTTCACGTATAAACAAACATAAGCTTTTG-ACT	5702
Query	313	NNNNTCCCC-TCACTGTTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAAC	371
Sbjct	5703	CCTACCCCCATCACTACTACTACTAGCATCATCAGGAATTGAAGCAGGAGCAGGTAC	5762
Query	372	AGGCTGAACAGTCTATCCTCCACTAGCTGGAACCTAGCCACGCTGGTGCTTCTGTAGA	431
Sbjct	5763	AGGCTGAACAGTATATCCCCATTAGCCGGAACCTAGCTCACGCTGGCGCTTCAGTAGA	5822
Query	432	CCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTAT-TACTT	490
Sbjct	5823	CCTAACTATCTTTTCCTCCACCTAGCTGGCGTATCCTCAATCTTAGGCGCTATCAACTT	5882
Query	491	CATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAAACACCATTATT	550
Sbjct	5883	CATTACTACAGCAATCAACATAAAATCCCCTGCCATATCACAATACCAAAACACCCTTATT	5942
Query	551	TGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTGC	610
Sbjct	5943	CGTATGATCTGTACTAATTACAGCTGTTCTATTACTACTCTCACTACCAGTACTTGCTGC	6002
Query	611	AGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAGG	670
Sbjct	6003	AGGCATTACCATACTACTTACAGACCGAAATCTAAACACAACCTTCTTTGATCCCTCAGG	6062
Query	671	AGGAGGAGACCCAATCCTATACCAAATGCTATTCTGATTCTTTGGCCATCCAGAAGTATA	730
Sbjct	6063	AGGAGGAGACCCAATCCTATATCAACACCTATTCTGATTCTTTGGTCATCCTGAAGTATA	6122
Query	731	CATCCTAATTTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAA	790
Sbjct	6123	CATCTTAATCCTTCCAGGATTTGGCATAATCTCCCACATCGTCACCTATTACTCTGGTAA	6182
Query	791	AAAAGAACCATTTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCTGGG	850
Sbjct	6183	AAAAGAACCATTTCGGCTACATAGGAATAGTTTGAGCAATAATATCAATTGGTTTCTGGG	6242
Query	851	TTTTATCGTTTGAGCCACCATATATTTACTGTTGGAATAGACGTAGACACACGAGCTTA	910
Sbjct	6243	CTTCATCGTATGAGCTCACCACATATTCACCGTTGGAATAGACGTAGATACACGAGCTTA	6302
Query	911	CTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGANN	970
Sbjct	6303	TTTCACATCCGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTATTACGCTGATT	6362
Query	971	NNNNNNNNNNNNNNAGGAATAATTAATAGAGATGCTGCTATACTCTGAGCCCTTGGGTT	1030
Sbjct	6363	AGCCACTCTACACGGTGAATAATTAATAGAGATGCTGCCATACTCTGAGCCCTAGGTTT	6422
Query	1031	TATTTTCTTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAGA	1090
Sbjct	6423	CATCTTCTCTTCACTATTGGCGGATTAACAGGTATTGTATTAGCCAACTCATCACTAGA	6482
Query	1091	CATCGTACTACAGCACGTAAGTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATAG	1149
Sbjct	6483	CATTGTATTACAGTACTTATTATGTAGTGGCACACTTCCACTATGTT-CTTTCAATAG	6541
Query	1150	GAGCTGTATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCTATTCTCAGGCTACA	1209
Sbjct	6542	GAGCGGTATTTGCCATCATAGCAGGATTTACCCACTGATTCCTCTTTTCACAGGATATT	6601
Query	1210	CCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAA	1269
Sbjct	6602	CACTACACCAAACCTGAACAAAAGTACATTTTGGAGTAATATTACAGGCGTTAACATAA	6661
Query	1270	CTTTCTTCCACAACACTTTTCT	1291
Sbjct	6662	CCTTCTTCCCTCAACA-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	CGCTGATtttttttCTACTAATCATAAAGACATTGGCACCTATACCTAATTTTTGGGGCC				72
Sbjct 5405	CGTTGATTCTTTTCTACCAACCATAAAAGACATTGGCACCTATACTTGATCTTTGGGGCA				5464

Query 73 TGAGCAGGAATAGTAGGCACAGCACTCAGCCTATTAATCCGTGCAGAACTAAGCCAACCG 132

Sbjct 5465 TGAGCAGGAATAGTAGGCACAGCACTCAGTCTATTAATCCGTGCAGAACTAAGCCAACCA 5524

Query 133 GGAACCTCCTAGGAGATGACCAAATTTACAATGTCATCGTTACAGCCCATGCCTTCATT 192

Sbjct 5525 GGAACTCTCCTAGGAGATGACCAAATTTATAATGTTATCGTTACAGCCCATGCTTTCATT 5584

Query 193 ATAATCTTCTTCATAGTTATACCAAGTTATAATCGGCGGTTTCGAAACTGACTTGTTCCC 252

Sbjct 5585 ATAATCTTTTTTATAGTTATACCAATTATAATTTGGCGGTTTCGAAACTGACTTGTTCCA 5644

Query 253 CTTATAATTTGGAGCACCAGACATGGCATTCCCACGAATAAACAAACATAAGCTTTTGNNNN 312

Sbjct 5645 CTAATAATTTGGAGCACCAGACATAGCATTTCACGTATAAACAAACATAAGCTTTTG-ACT 5703

Query 313 NNNNCTCCC-TCAGTGTACTACTTCTAGCATCATCAGGAATTGAAGCAGGTGCAGGAAC 371

Sbjct 5704 CCTACCCCCATCACTATTACTACTACTAGCATCATCAGGAATTGAAGCAGGAGCAGGTAC 5763

Query 372 AGGCTGAACAGTCTATCCTCCACTAGCTGGAAACCTAGCCCACGCTGGTGCTTCTGTAGA 431

Sbjct 5764 AGGCTGAACAGTATATCCCCATTAGCCGGAACCTAGCCCACGCTGGCGCTTCAGTAGA 5823

Query 432 CCTAACTATCTTTTCTCTGCACCTAGCTGGTGTTCATCAATTTTAGGAGCTAT-TACTT 490

Sbjct 5824 CCTAACTATCTTTTCCTCCACCTAGCTGGCGTATCCTCAATCTTAGGCGCTATCAACTT 5883

Query 491 CATTACTACAGCAATCAACATAAAATCTCCAGCTATATCACAATACCAAACACCATTATT 550

Sbjct 5884 CATTACTACAGCAATCAACATAAAATCCCCTGCCATATCACAATACCAAACACCCTTATT 5943

Query 551 TGTATGATCTGTATTAATTACAGCCGTTCTATTATTACTCTCATTGCCAGTACTAGCTGC 610

Sbjct 5944 CGTATGATCTGTACTAATTACAGCTGTTCTATTACTACTCTCGCTACCAGTACTTGCTGC 6003

Query 611 AGGAATCACCATACTACTTACAGATCGAAACCTAAACACAACCTTTTTTGATCCTTCAGG 670

Sbjct 6004 AGGCATTACCATACTACTTACAGACCGAAATCTAAACACAACCTTCTTTGATCCCTCAGG 6063

Query 671 AGGAGGAGACCCAATCCTATACCAAATGCTATTCTGATTCTTTGGCCATCCAGAAGTATA 730

Sbjct 6064 GGGAGGAGACCCAATCCTATATCAACACCTATTCTGATTCTTTGGTCATCCTGAAGTATA 6123

Query 731 CATCCTAATTTCTACCAGGATTCGGCATAATCTCACATATCGTCACCTATTATGCTGGTAA 790

Sbjct 6124 CATCTTAATCCTTCCAGGATTTGGCATAATCTCCCACATCGTCACCTATTACTCTGGTAA 6183

Query 791 AAAAGAACCATTTGGTTACATAGGAATAGTTTGAGCAATAATATCCATTGGATTCCTGGG 850

Sbjct 6184 AAAAGAACCATTTCGGCTACATAGGAATAGTTTGAGCAATAATATCAATTGGTTTCCTGGG 6243

Query 851 TTTTATCGTTTGAGCCCACTATATTTACTGTTGGAATAGACGTAGACACACGAGCTTA 910

Sbjct 6244 CTTTCATCGTATGAGCTCACCACATATTCACCGTTGGAATAGACGTAGATACACGAGCTTA 6303

Query 911 CTTTACATCAGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTGTTTAGCTGANN 970

Sbjct 6304 TTTCACATCTGCAACAATAATTATTGCCATCCCAACAGGAGTAAAAGTATTACGCTGATT 6363

Query 971 NNNNNNNNNNNNNNAGGAATAATTAATAGATGCTGCTATACTCTGAGCCCTTGGGTT 1030

Sbjct 6364 AGCCACTCTACATGGTGAATAATTAATAGAGCGCTGCCATACTCTGAGCCCTAGGTTT 6423

Query 1031 TATTTTCCTATTTACTATTGGTGGCCTGACTGGCATTGTATTAGCAAACCTCATCACTAGA 1090

Sbjct 6424 CATCTTCCTCTTCACTATTGGCGGATTAACAGGTATTGTATTAGCAAACCTCATCACTAGA 6483

Query 1091 CATCGTACTACAGACACGTACTACGTTGTAGC-CNNNNNNNNNNNNNNCTATCAATAG 1149

Sbjct 6484 CATTGTATTACAGTACTTATTATGTAGTGGCACACTTCCACTATGTT-CTTTCAATAG 6542

Query 1150 GAGCTGTATTTGCCATCATAGGAGGCTTCATCACTGATTTCCCTATTCTCAGGCTACA 1209

Sbjct 6543 GGGCCGTATTTGCCATCATAGCAGGATTTACTCACTGATTCCTCTTTTCACAGGATATT 6602

Query 1210 CCCTAGACCAAACCTACGCCAAAATCCATTTCACTATCATATTCATCGGCGTAAATCTAA 1269

Sbjct 6603 CACTACACCAAACCTGAACAAAAGTACATTTTGGAGTAATATTTACAGGCGTTAACATAA 6662

Query 1270 CTTTCTTCCACAACACTTTCT 1291

Sbjct 6663 CCTTCTTCCCTCAACA-TTTCT 6683

Taxonomy

Reports

◦ Lineage

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

.. Dermochelys coriacea	turtles	1923	12	Dermochelys coriacea hits
.. Eretmochelys imbricata	turtles	1347	22	Eretmochelys imbricata hits
.. Natator depressus	turtles	1336	3	Natator depressus hits
.. Chelonia mydas	turtles	1308	11	Chelonia mydas hits
.. Caretta caretta	turtles	1275	75	Caretta caretta hits
.. Lepidochelys kempii	turtles	1256	12	Lepidochelys kempii hits
.. Lepidochelys olivacea	turtles	1232	6	Lepidochelys olivacea hits
.. Chelonoidis alburyorum	turtles	1206	2	Chelonoidis alburyorum hits
.. Stigmochelys pardalis	turtles	1194	3	Stigmochelys pardalis hits
.. Geochelone elegans	turtles	1194	3	Geochelone elegans hits
.. Cylindraspis triserrata	turtles	1151	2	Cylindraspis triserrata hits
.. Trachemys decussata angusta	turtles	1144	1	Trachemys decussata angusta hits
.. Mauremys japonica	turtles	1140	3	Mauremys japonica hits
.. Chrysemys picta bellii	turtles	1116	2	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 rErelmb1 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
<u>Caretta caretta isolate CAL1112 mitochondrion, partial genome</u>	1271	0.0	<u>OR166599</u>
<u>Caretta caretta isolate CAL1201 mitochondrion, partial genome</u>	1271	0.0	<u>OR166602</u>
<u>Caretta caretta isolate CAL1315 mitochondrion, partial genome</u>	1271	0.0	<u>OR166605</u>
<u>Caretta caretta isolate CAL1320 mitochondrion, partial genome</u>	1271	0.0	<u>OR166607</u>
<u>Caretta caretta isolate CAL1328 mitochondrion, partial genome</u>	1271	0.0	<u>OR166612</u>
<u>Caretta caretta isolate CAL1346 mitochondrion, partial genome</u>	1271	0.0	<u>OR166614</u>
<u>Caretta caretta isolate LIN02 mitochondrion, partial genome</u>	1271	0.0	<u>OR166620</u>
<u>Caretta caretta isolate SIC05 mitochondrion, partial genome</u>	1271	0.0	<u>OR166624</u>
<u>Caretta caretta isolate SIC07 mitochondrion, partial genome</u>	1271	0.0	<u>OR166626</u>
<u>Caretta caretta isolate SIC22 mitochondrion, partial genome</u>	1271	0.0	<u>OR166641</u>
<u>Caretta caretta isolate LAT04 mitochondrion, partial genome</u>	1271	0.0	<u>OR166598</u>
<u>Caretta caretta isolate TUS05 mitochondrion, partial genome</u>	1271	0.0	<u>OR166594</u>
<u>Caretta caretta isolate TUS04 mitochondrion, partial genome</u>	1271	0.0	<u>OR166592</u>
<u>Caretta caretta isolate TUS04.2 mitochondrion, partial genome</u>	1271	0.0	<u>OR166593</u>
<u>Caretta caretta isolate SIC10 mitochondrion, partial genome</u>	1271	0.0	<u>OR166629</u>
<u>Caretta caretta isolate TUS03 mitochondrion, partial genome</u>	1271	0.0	<u>OR166590</u>
<u>Caretta caretta isolate TUS03.2 mitochondrion, partial genome</u>	1271	0.0	<u>OR166591</u>
<u>Caretta caretta isolate CAL1303 mitochondrion, partial genome</u>	1271	0.0	<u>OR166604</u>
<u>Caretta caretta isolate SIC11 mitochondrion, partial genome</u>	1271	0.0	<u>OR166630</u>
<u>Caretta caretta isolate ADR03 mitochondrion, partial genome</u>	1271	0.0	<u>OR166584</u>
<u>Caretta caretta isolate ADR02 mitochondrion, partial genome</u>	1271	0.0	<u>OR166583</u>
<u>Caretta caretta isolate ADR01 mitochondrion, partial genome</u>	1271	0.0	<u>OR166582</u>
<u>Caretta caretta isolate ADR04 mitochondrion, partial genome</u>	1271	0.0	<u>OR166585</u>
<u>Caretta caretta isolate TUS01 mitochondrion, partial genome</u>	1271	0.0	<u>OR166586</u>
<u>Caretta caretta isolate TUS01.2 mitochondrion, partial genome</u>	1271	0.0	<u>OR166587</u>
<u>Caretta caretta isolate TUS02 mitochondrion, partial genome</u>	1271	0.0	<u>OR166588</u>
<u>Caretta caretta isolate TUS02.2 mitochondrion, partial genome</u>	1271	0.0	<u>OR166589</u>
<u>Caretta caretta isolate LAT01 mitochondrion, partial genome</u>	1271	0.0	<u>OR166595</u>
<u>Caretta caretta isolate LAT02 mitochondrion, partial genome</u>	1271	0.0	<u>OR166596</u>
<u>Caretta caretta isolate LAT03 mitochondrion, partial genome</u>	1271	0.0	<u>OR166597</u>
<u>Caretta caretta isolate CAL1137 mitochondrion, partial genome</u>	1271	0.0	<u>OR166601</u>
<u>Caretta caretta isolate CAL1319 mitochondrion, partial genome</u>	1271	0.0	<u>OR166606</u>
<u>Caretta caretta isolate CAL1335 mitochondrion, partial genome</u>	1271	0.0	<u>OR166613</u>
<u>Caretta caretta isolate CAL1362 mitochondrion, partial genome</u>	1271	0.0	<u>OR166615</u>
<u>Caretta caretta isolate SIC01 mitochondrion, partial genome</u>	1271	0.0	<u>OR166621</u>
<u>Caretta caretta isolate SIC03 mitochondrion, partial genome</u>	1271	0.0	<u>OR166623</u>
<u>Caretta caretta isolate SIC06 mitochondrion, partial genome</u>	1271	0.0	<u>OR166625</u>
<u>Caretta caretta isolate SIC08 mitochondrion, partial genome</u>	1271	0.0	<u>OR166627</u>
<u>Caretta caretta isolate SIC09 mitochondrion, partial genome</u>	1271	0.0	<u>OR166628</u>
<u>Caretta caretta isolate SIC12 mitochondrion, partial genome</u>	1271	0.0	<u>OR166631</u>
<u>Caretta caretta isolate SIC13 mitochondrion, partial genome</u>	1271	0.0	<u>OR166632</u>
<u>Caretta caretta isolate SIC16 mitochondrion, partial genome</u>	1271	0.0	<u>OR166635</u>
<u>Caretta caretta isolate SIC17 mitochondrion, partial genome</u>	1271	0.0	<u>OR166636</u>
<u>Caretta caretta isolate SIC18 mitochondrion, partial genome</u>	1271	0.0	<u>OR166637</u>
<u>Caretta caretta isolate SIC19 mitochondrion, partial genome</u>	1271	0.0	<u>OR166638</u>
<u>Caretta caretta isolate SIC23 mitochondrion, partial genome</u>	1271	0.0	<u>OR166642</u>
<u>Caretta caretta isolate SIC24 mitochondrion, partial genome</u>	1271	0.0	<u>OR166643</u>

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]			

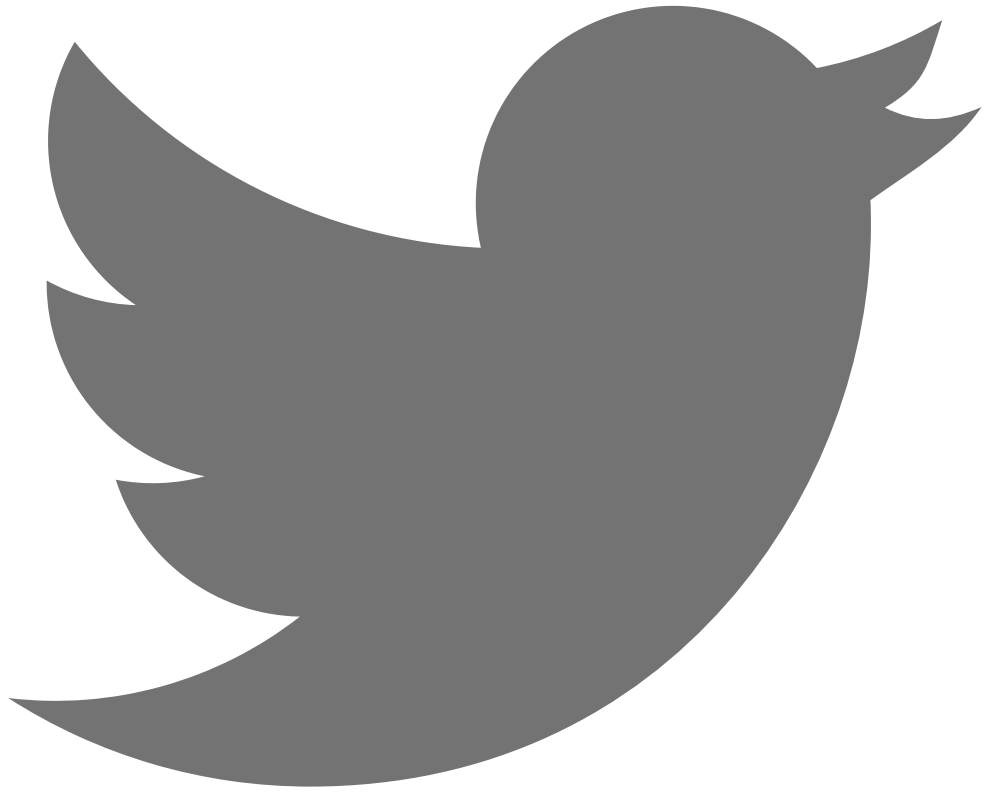
Description	Score	E value	Accession
<u>Trachemys decussata angusta mitochondrion genomic DNA containing from tRNA-Phe (complete) to control region (partial) region, specimen voucher MTD-T 20622</u>	1144	0.0	OX453476
Mauremys japonica (Japanese pond turtle) [turtles]			
<u>Mauremys japonica mitochondrial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

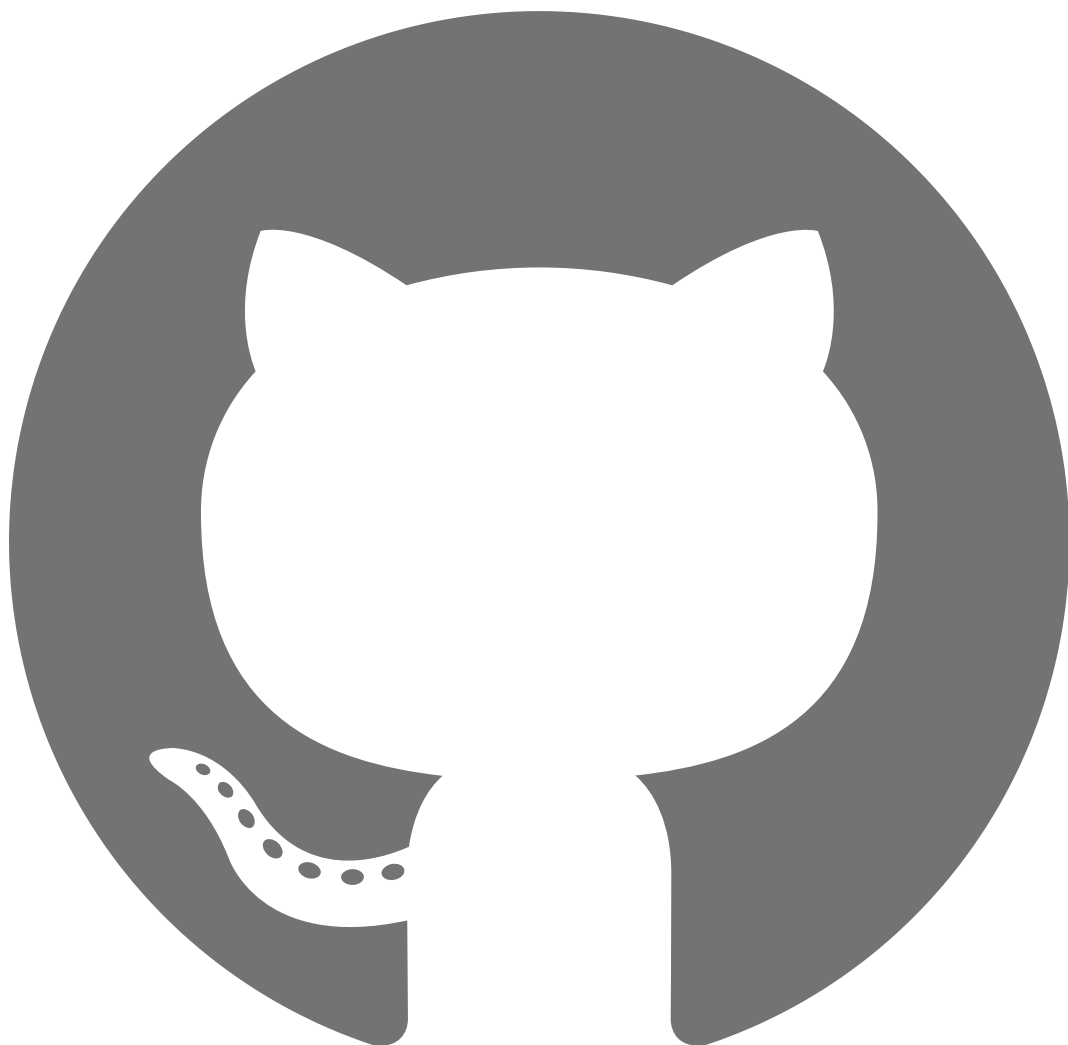
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