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BLAST ® » **blastn suite** » **results for RID-KE6W70XT016**

Job Title	Nucleotide Sequence ...
RID	KE6W70XT016 Search expires on 12-10 01:40 am
Program	BLASTN
Database	nt
Query ID	lcl|Query_1829605
Description	None ...
Molecule type	dna
Query Length	1415

Descriptions

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Thunnus thynnus mitochondrion, complete genome	Thunnus thynnus	571	1103	57%	4e-157	89.17%	16529	KF906720.1
Thunnus thynnus isolate DM353 mitochondrion, complete genome	Thunnus thynnus	571	1103	57%	4e-157	89.17%	16527	MT410869.1
Thunnus thynnus voucher TT02-2312 mitochondrion, complete genome	Thunnus thynnus	571	1103	57%	4e-157	89.17%	16526	JN086149.1
Thunnus thynnus mitochondrion, complete genome	Thunnus thynnus	571	1103	57%	4e-157	89.17%	16527	NC_014052.1
Thunnus thynnus thynnus mitochondrion, complete genome	Thunnus thynnus thynnus	571	1103	57%	4e-157	89.17%	16526	NC_004901.2
Thunnus thynnus thynnus mitochondrial DNA, complete genome	Thunnus thynnus thynnus	571	1103	57%	4e-157	89.17%	16526	AB097669.1
Thunnus maccoyii isolate LGM079 mitochondrion, complete genome	Thunnus maccoyii	564	1085	57%	6e-155	88.89%	16524	PV069719.1
Thunnus maccoyii genome assembly, organelle: mitochondrion	Thunnus maccoyii	564	1085	57%	6e-155	88.89%	16525	OU343215.1
Thunnus maccoyii voucher TM02-2313 mitochondrion, complete genome	Thunnus maccoyii	564	1085	57%	6e-155	88.89%	16527	JN086150.1
Thunnus albacares voucher ECSFRI-HQJQY01 mitochondrion, complete genome	Thunnus albacares	555	1070	57%	4e-152	88.41%	16528	KP259550.1
Thunnus albacares mitochondrion, complete genome	Thunnus albacares	555	1065	57%	4e-152	88.41%	16528	KM588080.1
Thunnus tonggol cytochrome c oxidase subunit I gene, complete cds; mitochondrial	Thunnus tonggol	555	929	52%	4e-152	88.41%	1551	GU799568.1
Thunnus obesus cytochrome c oxidase subunit I gene, complete cds; mitochondrial	Thunnus obesus	555	1070	57%	4e-152	88.41%	1551	GU799567.1
Thunnus maccoyii mitochondrion, complete genome	Thunnus maccoyii	551	1067	57%	5e-151	87.88%	16527	NC_014101.1
Thunnus atlanticus mitochondrion, complete genome	Thunnus atlanticus	549	1044	57%	2e-150	88.16%	16528	KU955344.1
Thunnus atlanticus mitochondrion, complete genome	Thunnus atlanticus	549	1050	57%	2e-150	88.16%	16528	KU955343.1
Thunnus albacares voucher Se3 mitochondrion, complete genome	Thunnus albacares	549	1065	57%	2e-150	88.16%	16527	KT724724.1
Thunnus atlanticus voucher Talt-UNAL-001 mitochondrion, complete genome	Thunnus atlanticus	549	1050	57%	2e-150	88.16%	16528	NC_025519.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Thunnus albacares genome assembly, organelle: mitochondrion	Thunnus albacares	549	1065	57%	2e-150	88.16%	16530	OU607616.1
Thunnus albacares voucher TY02-2316 mitochondrion, complete genome	Thunnus albacares	549	1065	57%	2e-150	88.16%	16528	JN086153.1
Thunnus obesus cytochrome oxidase subunit I (COX I) gene, complete cds; mitochondrial	Thunnus obesus	549	1076	57%	2e-150	88.16%	1559	HM071005.1
Thunnus albacares mitochondrion, complete genome	Thunnus albacares	549	1065	57%	2e-150	88.16%	16527	NC_014061.1
Thunnus obesus mitochondrion, complete genome	Thunnus obesus	544	1059	57%	8e-149	87.91%	16524	KY400011.1
Thunnus obesus voucher TO02-2315 mitochondrion, complete genome	Thunnus obesus	544	1065	57%	8e-149	87.91%	16528	JN086152.1
Thunnus albacares cytochrome oxidase subunit I (COX I) gene, complete cds; mitochondrial	Thunnus albacares	544	1043	57%	8e-149	87.91%	1559	HM071006.1
Thunnus obesus mitochondrion, complete genome	Thunnus obesus	544	1061	57%	8e-149	87.91%	16528	NC_014059.1
Thunnus maccoyii mitochondrion, complete genome	Thunnus maccoyii	542	1057	57%	3e-148	87.88%	16529	KF925362.1
Thunnus tonggol voucher USNM 445333 mitochondrion, complete genome	Thunnus tonggol	538	1048	57%	4e-147	87.66%	16529	MW232431.1
Thunnus tonggol voucher USNM 445302 mitochondrion, complete genome	Thunnus tonggol	538	1048	57%	4e-147	87.66%	16529	MW232430.1
Thunnus tonggol mitochondrion, complete genome	Thunnus tonggol	532	1043	57%	2e-145	87.41%	16528	NC_020673.1
Thunnus tonggol voucher TL02-2317 mitochondrion, complete genome	Thunnus tonggol	532	1043	57%	2e-145	87.41%	16527	JN086154.1
Thunnus alalunga isolate PS003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	531	531	28%	6e-145	87.37%	526	KR023728.1
Thunnus alalunga isolate PS002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	531	531	28%	6e-145	87.37%	526	KR023727.1
Thunnus alalunga isolate PS001 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	531	531	28%	6e-145	87.37%	526	KR023726.1
Thunnus alalunga isolate MED005	Thunnus alalunga	531	531	28%	6e-145	87.37%	526	KR023718.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial								
Thunnus alalunga isolate AN007 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	525	525	28%	3e-143	87.12%	513	KR023732.1
Thunnus alalunga isolate AN002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	525	525	28%	3e-143	87.28%	500	KR023731.1
Thunnus alalunga isolate PN046 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	525	525	28%	3e-143	87.12%	526	KR023723.1
Thunnus alalunga mitochondrion, complete genome	Thunnus alalunga	525	1043	57%	3e-143	87.12%	16527	NC_005317.1
Thunnus thynnus genome assembly, organelle: mitochondrion	Thunnus thynnus	520	1037	57%	1e-141	86.87%	16527	OZ004756.1
Thunnus alalunga voucher ECSFRI-CQJQY01 mitochondrion, complete genome	Thunnus alalunga	520	1037	57%	1e-141	86.87%	16527	KP259549.1
Thunnus alalunga isolate PS005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023730.1
Thunnus alalunga isolate PS004 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023729.1
Thunnus alalunga isolate PN049 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023725.1
Thunnus alalunga isolate PN048 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023724.1
Thunnus alalunga isolate MED032 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023722.1
Thunnus alalunga isolate MED031 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023721.1
Thunnus alalunga isolate MED024 cytochrome c	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023720.1

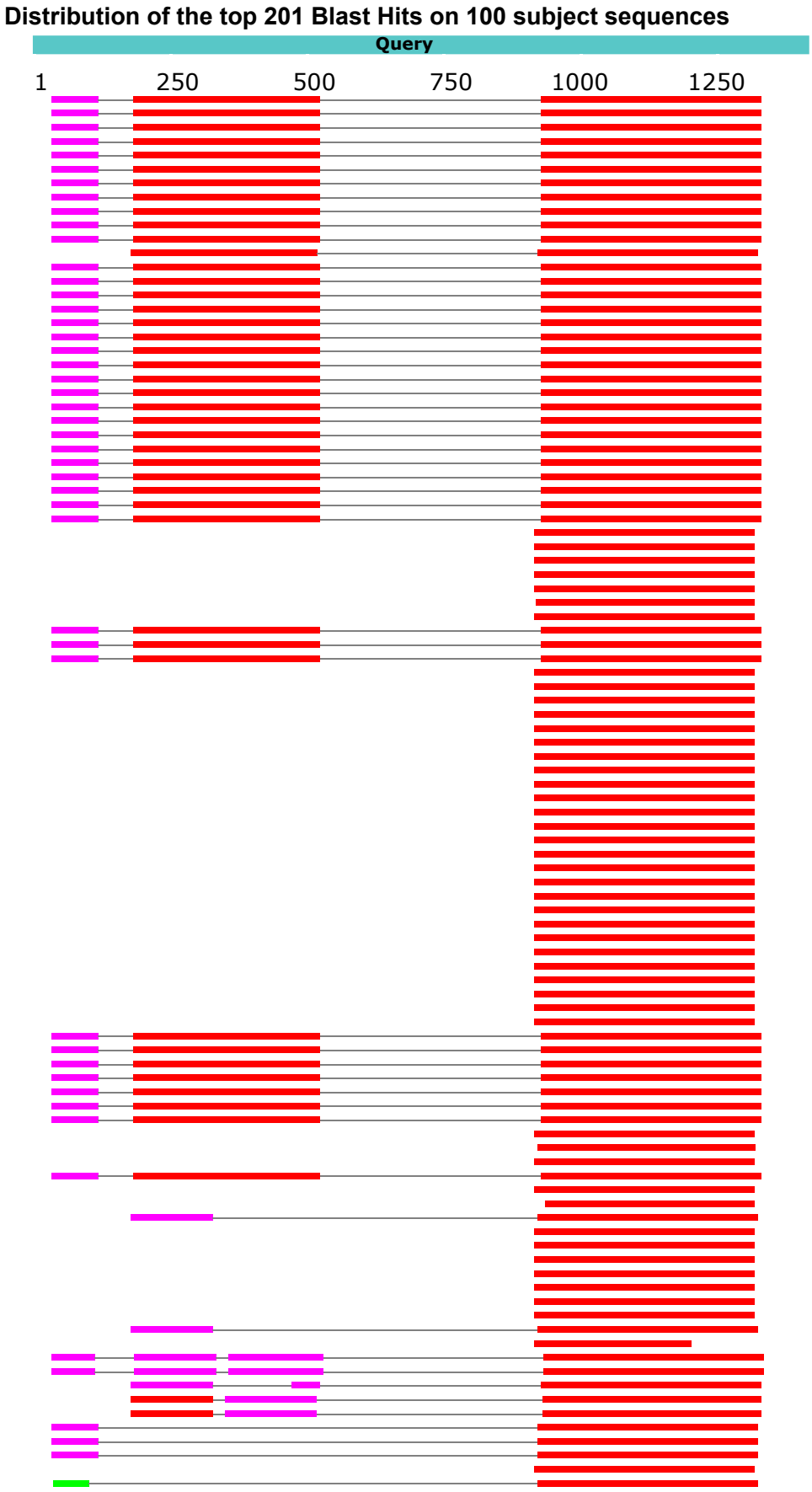
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
oxidase subunit I (COI) gene, partial cds; mitochondrial								
Thunnus alalunga isolate MED019 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023719.1
Thunnus alalunga isolate IN006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	521	KR023717.1
Thunnus alalunga isolate IN005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023716.1
Thunnus alalunga isolate IN004 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023715.1
Thunnus alalunga isolate IN003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023714.1
Thunnus alalunga isolate AS010 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023711.1
Thunnus alalunga isolate AS009 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023710.1
Thunnus alalunga isolate AS008 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023709.1
Thunnus alalunga isolate AS006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023707.1
Thunnus alalunga isolate AS003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023706.1
Thunnus alalunga isolate AS002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023705.1
Thunnus alalunga isolate AN012 cytochrome c oxidase subunit I	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023704.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
(COI) gene, partial cds; mitochondrial								
Thunnus alalunga isolate AN011 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023703.1
Thunnus alalunga isolate AN010 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	524	KR023702.1
Thunnus alalunga isolate AN009 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	520	KR023701.1
Thunnus alalunga isolate AN008 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023700.1
Thunnus alalunga isolate AN006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023699.1
Thunnus alalunga isolate AN005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023698.1
Thunnus alalunga isolate AN004 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	520	520	28%	1e-141	86.87%	526	KR023697.1
Thunnus alalunga voucher TA02-2314 mitochondrion, complete genome	Thunnus alalunga	520	1037	57%	1e-141	86.87%	16527	JN086151.1
Thunnus orientalis isolate LGM084 mitochondrion, complete genome	Thunnus orientalis	518	1030	57%	5e-141	86.84%	16550	PV069720.1
Thunnus orientalis mitochondrial DNA, complete genome	Thunnus orientalis	518	1030	57%	5e-141	86.84%	16527	LC377898.1
Thunnus thynnus mitochondrial DNA, complete genome	Thunnus thynnus	518	1035	57%	5e-141	86.84%	16528	AP006034.1
Thunnus orientalis mitochondrion, complete genome	Thunnus orientalis	518	1035	57%	5e-141	86.84%	16529	KF906721.1
Thunnus orientalis mitochondrion, complete genome	Thunnus orientalis	518	1035	57%	5e-141	86.84%	16527	GU256524.1
Thunnus orientalis mitochondrion, complete genome	Thunnus orientalis	518	1035	57%	5e-141	86.84%	16527	NC_008455.1
Thunnus alalunga isolate IN001 cytochrome c oxidase subunit I	Thunnus alalunga	514	514	28%	6e-140	86.62%	526	KR023712.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
(COI) gene, partial cds; mitochondrial								
Thunnus alalunga isolate AS007 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	514	514	28%	6e-140	86.92%	498	KR023708.1
Thunnus alalunga isolate AN003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	514	514	28%	6e-140	86.62%	526	KR023696.1
Thunnus alalunga mitochondrion, complete genome	Thunnus alalunga	514	1031	57%	6e-140	86.62%	16527	GU256526.1
Thunnus alalunga isolate IN002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	510	510	28%	8e-139	86.11%	526	KR023713.1
Thunnus alalunga isolate MED006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	Thunnus alalunga	490	490	27%	1e-132	86.47%	484	KR023733.1
Auxis rochei mitochondrion, complete genome	Auxis rochei	431	624	38%	6e-115	82.83%	16501	NC_005313.1
Auxis rochei mitochondrion, complete genome	Auxis rochei	414	414	28%	6e-110	82.07%	16505	MK548578.1
Auxis rochei voucher USNM:FISH:424772 mitochondrion, complete genome	Auxis rochei	414	414	28%	6e-110	82.07%	16505	PX070027.1
Auxis rochei mitochondrion, complete genome	Auxis rochei	414	414	28%	6e-110	82.07%	16505	KM651784.1
Auxis rochei voucher USNM 424772 mitochondrion, complete genome	Auxis rochei	414	414	28%	6e-110	82.07%	16509	MW232425.1
Auxis rochei voucher USNM 403146 mitochondrion, complete genome	Auxis rochei	414	414	28%	6e-110	82.07%	16505	MW232421.1
Auxis rochei mitochondrial DNA, complete genome, haplotype:II Ecuadorian	Auxis rochei	414	414	28%	6e-110	82.07%	16503	AB105165.1
Auxis rochei mitochondrial DNA, complete genome, haplotype:II Mediterranean	Auxis rochei	414	414	28%	6e-110	82.07%	16503	AB103468.1
Auxis rochei voucher ECSFRI-YDJ01 mitochondrion, complete genome	Auxis rochei	409	602	38%	3e-108	81.82%	16505	KP259548.1
Thunnus albacares isolate JJ7:18 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial	Thunnus albacares	381	381	20%	6e-100	87.54%	648	DQ874757.1
Sarda sarda voucher USNM:FISH:477716	Sarda sarda	374	822	55%	1e-97	80.25%	16504	PX070013.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
mitochondrion, complete genome								
Sarda sarda mitochondrion, complete genome	Sarda sarda	374	822	55%	1e-97	80.25%	16503	PP033005.1
Sarda sarda isolate DM366 mitochondrion, complete genome	Sarda sarda	374	655	41%	1e-97	80.25%	16506	NC_052756.1
Sarda orientalis mitochondrial DNA, complete sequence, specimen_voucher: NSMT:P:110211	Sarda orientalis	363	703	49%	2e-94	79.90%	16502	AP012949.1
Sarda orientalis voucher USNM 445533 mitochondrion, complete genome	Sarda orientalis	363	703	49%	2e-94	79.90%	16502	NC_060588.1
Scomberomorus guttatus mitochondrion, complete genome	Scomberomorus guttatus	350	463	34%	2e-90	79.09%	16562	PP437201.1
Scomberomorus niphonius mitochondrion, complete genome	Scomberomorus niphonius	348	467	34%	7e-90	79.04%	16646	NC_016420.1
Scomberomorus niphonius mitochondrion, complete genome	Scomberomorus niphonius	342	462	34%	3e-88	78.79%	16646	KY228987.1
Gymnocanthus herzensteini mitochondrion, complete genome	Gymnocanthus herzensteini	340	340	28%	1e-87	78.79%	16691	NC_034651.1
Istiophorus platypterus isolate SFA31 mitochondrion, complete genome	Istiophorus platypterus	339	417	32%	4e-87	78.59%	16522	OP404122.1

Graphic Summary



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

Thunnus thynnus mitochondrion, complete genome

Sequence ID: **KF906720.1** Length: 16529 Number of Matches: 3

Range 1: 6525 to 6921

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	4e-157()	354/397(89%)	0/397(0%)	Plus/Plus	

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Query  914  TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCNNNNCATCGTTCTACACGACAC  973
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Sbjct  6525  TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCTAGACATCGTTCTACACGACAC  6584

Query  974   CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  1033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6585  CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  6644

Query  1034  NNNNNNNNTCGTACACTGATTCCCACTATTCACAGGATACACCCTNNNNNNNACATGAAC  1093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6645  TGCCGCCTTCGTACACTGATTCCCACTATTCACAGGATACACCCTTCACAGCACATGAAC  6704

Query  1094  TAAAATCCACTTCGGAGTCATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  1153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6705  TAAAATCCACTTCGGAGTAATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  6764

Query  1154  CCTAGGACNNNNNNNNNNNCCTCGACGGTATTCAGACTACCCAGACGCCTACACCATTTG  1213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6765  CCTAGGACTAGCAGGAATGCCTCGACGGTATTCAGACTACCCAGACGCCTACACCCTTTG  6824

Query  1214  AAACNNNNNNNNNNNTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  1273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6825  AAACACAATTTCCTCTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  6884

Query  1274  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  1310
              |||||||||||||||||||||||||||||||||||||
Sbjct  6885  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  6921
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Range 2: 5654 to 5987

Score	Expect	Identities	Gaps	Strand	Frame
390 bits(211)	1e-102()	273/334(82%)	0/334(0%)	Plus/Plus	

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Query  180   CCCATGCCTTCGTAATGAGTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5654  CCCATGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  5713

Query  240   ACTGANNNNNTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  299
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Sbjct  5714  ACTGACTTATTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  5773

Query  300   TGAGCTTCTGACTCCTTCCCCCTTNNNNNNNNNNNNNNNNNNNNNTCAGGAGTTGAGG  359
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5774  TGAGCTTCTGACTCCTTCCCCCTTCTTTCCTTCTGCTCCTAGCTTCTTCAGGAGTTGAGG  5833

Query  360   CNNNNNCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCNNNNNNNNTAGCCCACGCAG  419
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5834  CTGGAGCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCCGGCAACCTAGCCCACGCAG  5893

Query  420   GGGCATCAGTTGACCTAACTATTTTCTCNNNnnnnnnnnNNNNNNNNTCCTCAATTCTTG  479
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5894  GGGCATCAGTTGACCTAACTATTTTCTCACTTCACTTAGCGGGGGTTTCCTCAATTCTTG  5953

Query  480   GGGCAATTAACTTCATCACAACAATTATCAATAT  513
              |||||||||||||||||||||||||||||||||
Sbjct  5954  GGGCAATTAACTTCATCACAACAATTATCAATAT  5987
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Range 3: 5510 to 5588

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	1e-27()	79/80(99%)	1/80(1%)	Plus/Plus	

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Query  35    ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  94
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Sbjct  5510  ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  5569

Query  95    CCTTAAGCTNTGCTCATCCG  114
             ||||||||| ||||||||||
Sbjct  5570  CCTTAAGCT-TGCTCATCCG  5588
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Thunnus thynnus isolate DM353 mitochondrion, complete genome

Sequence ID: **MT410869.1** Length: 16527 Number of Matches: 3

Range 1: 6525 to 6921

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	4e-157()	354/397(89%)	0/397(0%)	Plus/Plus	

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Query  914   TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCNNNNCATCGTTCTACACGACAC  973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6525  TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCTAGACATCGTTCTACACGACAC  6584

Query  974   CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  1033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6585  CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  6644

Query  1034  NNNNNNNNTCGTACACTGATTCCCACTATTCACAGGATACACCCTNNNNNNNACATGAAC  1093
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6645  TGCCGCCTTCGTACACTGATTCCCACTATTCACAGGATACACCCTTCACAGCACATGAAC  6704

Query  1094  TAAAATCCACTTCGGAGTCATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  1153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct  6705  TAAAATCCACTTCGGAGTAATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  6764

Query  1154  CCTAGGACNNNNNNNNNNNCCTCGACGGTATTCAGACTACCCAGACGCCTACACCATTTG  1213
              ||||||||           ||||||||||||||||||||||||||||||||||||||||||
Sbjct  6765  CCTAGGACTAGCAGGAATGCCTCGACGGTATTCAGACTACCCAGACGCCTACACCCTTTG  6824

Query  1214  AAACNNNNNNNNNNNTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  1273
              |||||          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6825  AAACACAATTTCCTCTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  6884

Query  1274  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  1310
              |||||||||||||||||||||||||||||||||||||
Sbjct  6885  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  6921
```

Range 2: 5654 to 5987

Score	Expect	Identities	Gaps	Strand	Frame
390 bits(211)	1e-102()	273/334(82%)	0/334(0%)	Plus/Plus	

```
Query  180   CCCATGCCTTCGTAATGAGTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5654  CCCATGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  5713

Query  240   ACTGANNNNNTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  299
              |||||     ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5714  ACTGACTTATTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  5773

Query  300   TGAGCTTCTGACTCCTTCCCCCTTNNNNNNNNNNNNNNNNNNNNNTCAGGAGTTGAGG  359
              ||||||||||||||||||||||||                     ||||||||||||
Sbjct  5774  TGAGCTTCTGACTCCTTCCCCCTTCTTTCCTTCTGCTCCTAGCTTCTTCAGGAGTTGAGG  5833

Query  360   CNNNNNCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCNNNNNNNNNTAGCCCACGCAG  419
              |     ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5834  CTGGAGCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCCGGCAACCTAGCCCACGCAG  5893

Query  420   GGGCATCAGTTGACCTAACTATTTTCTCNNNnnnnnnnnNNNNNNNNTCCTCAATTCTTG  479
              ||||||||||||||||||||||||||||||                ||||||||||||
Sbjct  5894  GGGCATCAGTTGACCTAACTATTTTCTCACTTCACTTAGCGGGGGTTTCCTCAATTCTTG  5953

Query  480   GGGCAATTAACTTCATCACAACAATTATCAATAT  513
              |||||||||||||||||||||||||||||||||
Sbjct  5954  GGGCAATTAACTTCATCACAACAATTATCAATAT  5987
```

Range 3: 5510 to 5588

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	1e-27()	79/80(99%)	1/80(1%)	Plus/Plus	

```
Query  35    ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  94
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5510  ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  5569

Query  95    CCTTAAGCTNTGCTCATCCG  114
             |||||||||| ||||||||||
Sbjct  5570  CCTTAAGCT-TGCTCATCCG  5588
```

Thunnus thynnus voucher TT02-2312 mitochondrion, complete genome

Sequence ID: **JN086149.1** Length: 16526 Number of Matches: 3

Range 1: 6525 to 6921

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	4e-157()	354/397(89%)	0/397(0%)	Plus/Plus	

```
Query  914   TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCNNNNCATCGTTCTACACGACAC  973
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6525  TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCTAGACATCGTTCTACACGACAC  6584

Query  974   CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  1033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6585  CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  6644

Query  1034  NNNNNNNNTCGTACACTGATTCCCACTATTCACAGGATACACCCTNNNNNNNACATGAAC  1093
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6645  TGCCGCCTTCGTACACTGATTCCCACTATTCACAGGATACACCCTTCACAGCACATGAAC  6704

Query  1094  TAAAATCCACTTCGGAGTCATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  1153
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  6705  TAAAATCCACTTCGGAGTAATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  6764

Query  1154  CCTAGGACNNNNNNNNNNNCCTCGACGGTATTCAGACTACCCAGACGCCTACACCATTTG  1213
              ||||||||           ||||||||||||||||||||||||||||||||||||||||||
Sbjct  6765  CCTAGGACTAGCAGGAATGCCTCGACGGTATTCAGACTACCCAGACGCCTACACCCTTTG  6824

Query  1214  AAACNNNNNNNNNNNTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  1273
              |||||          ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6825  AAACACAATTTCCTCTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  6884
```

```
Query  1274  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  1310
              |||||||||||||||||||||||||||||||||||||
Sbjct  6885  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  6921
```

Range 2: 5654 to 5987

Score	Expect	Identities	Gaps	Strand	Frame
390 bits(211)	1e-102()	273/334(82%)	0/334(0%)	Plus/Plus	

```
Query  180   CCCATGCCTTCGTAATGAGTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  239
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  5654  CCCATGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  5713

Query  240   ACTGANNNNNTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  299
              |||||      ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5714  ACTGACTTATTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  5773

Query  300   TGAGCTTCTGACTCCTTCCCCCTTNNNNNNNNNNNNNNNNNNNNNTCAGGAGTTGAGG  359
              |||||||||||||||||||||||                     ||||||||||||
Sbjct  5774  TGAGCTTCTGACTCCTTCCCCCTTCTTTCCTTCTGCTCCTAGCTTCTTCAGGAGTTGAGG  5833

Query  360   CNNNNNCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCNNNNNNNNTAGCCCACGCAG  419
              |     ||||||||||||||||||||||||||||||||||     ||||||||||||
Sbjct  5834  CTGGAGCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCCGGCAACCTAGCCCACGCAG  5893

Query  420   GGGCATCAGTTGACCTAACTATTTTCTCNNNnnnnnnnnNNNNNNNNTCCTCAATTCTTG  479
              |||||||||||||||||||||||||||||||||||||||     ||||||||||||||
Sbjct  5894  GGGCATCAGTTGACCTAACTATTTTCTCACTTCACTTAGCGGGGGTTTCCTCAATTCTTG  5953

Query  480   GGGCAATTAACTTCATCACAACAATTATCAATAT  513
              |||||||||||||||||||||||||||||||||
Sbjct  5954  GGGCAATTAACTTCATCACAACAATTATCAATAT  5987
```

Range 3: 5510 to 5588

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	1e-27()	79/80(99%)	1/80(1%)	Plus/Plus	

```
Query  35    ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  94
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  5510  ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  5569

Query  95    CCTTAAGCTNTGCTCATCCG  114
             |||||||||| ||||||||||
Sbjct  5570  CCTTAAGCT-TGCTCATCCG  5588
```

Thunnus thynnus mitochondrion, complete genome

Sequence ID: **NC_014052.1** Length: 16527 Number of Matches: 3

Range 1: 7390 to 7786

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	4e-157()	354/397(89%)	0/397(0%)	Plus/Plus	

```
Query  914   TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCNNNNCATCGTTCTACACGACAC  973
              |||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Sbjct  7390  TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCTAGACATCGTTCTACACGACAC  7449

Query  974   CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  1033
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7450  CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  7509

Query  1034  NNNNNNNNTCGTACACTGATTCCCACTATTCACAGGATACACCCTNNNNNNNACATGAAC  1093
              |||||||||||||||||||||||||||||||||||||||||||    ||||||||||||
Sbjct  7510  TGCCGCCTTCGTACACTGATTCCCACTATTCACAGGATACACCCTTCACAGCACATGAAC  7569

Query  1094  TAAAATCCACTTCGGAGTCATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  1153
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  7570  TAAAATCCACTTCGGAGTAATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  7629

Query  1154  CCTAGGACNNNNNNNNNNNCCTCGACGGTATTCAGACTACCCAGACGCCTACACCATTTG  1213
              ||||||||           ||||||||||||||||||||||||||||||||||||||||
Sbjct  7630  CCTAGGACTAGCAGGAATGCCTCGACGGTATTCAGACTACCCAGACGCCTACACCCTTTG  7689

Query  1214  AAACNNNNNNNNNNNTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  1273
              |||||           ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  7690  AAACACAATTTCCTCTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  7749

Query  1274  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  1310
              |||||||||||||||||||||||||||||||||||||
Sbjct  7750  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  7786
```

Range 2: 6519 to 6852

Score	Expect	Identities	Gaps	Strand	Frame

390 bits(211)	1e-102()	273/334(82%)	0/334(0%)	Plus/Plus

```
Query  180   CCCATGCCTTCGTAATGAGTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  239
Sbjct  6519  CCCATGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  6578

Query  240   ACTGANNNNNTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  299
Sbjct  6579  ACTGACTTATTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  6638

Query  300   TGAGCTTCTGACTCCTTCCCCCTTNNNNNNNNNNNNNNNNNNNNNTCAGGAGTTGAGG  359
Sbjct  6639  TGAGCTTCTGACTCCTTCCCCCTTCTTTCCTTCTGCTCCTAGCTTCTTCAGGAGTTGAGG  6698

Query  360   CNNNNNCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCNNNNNNNNNTAGCCCACGCAG  419
Sbjct  6699  CTGGAGCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCCGGCAACCTAGCCCACGCAG  6758

Query  420   GGGCATCAGTTGACCTAACTATTTTCTCNNNnnnnnnnnNNNNNNNNTCCTCAATTCTTG  479
Sbjct  6759  GGGCATCAGTTGACCTAACTATTTTCTCACTTCACTTAGCGGGGGTTTCCTCAATTCTTG  6818

Query  480   GGGCAATTAACTTCATCACAACAATTATCAATAT  513
Sbjct  6819  GGGCAATTAACTTCATCACAACAATTATCAATAT  6852
```

Range 3: 6375 to 6453

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	1e-27()	79/80(99%)	1/80(1%)	Plus/Plus	

```
Query  35    ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  94
Sbjct  6375  ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  6434

Query  95    CCTTAAGCTNTGCTCATCCG  114
Sbjct  6435  CCTTAAGCT-TGCTCATCCG  6453
```

Thunnus thynnus thynnus mitochondrion, complete genome

Sequence ID: **NC_004901.2** Length: 16526 Number of Matches: 3

Range 1: 6524 to 6920

Score	Expect	Identities	Gaps	Strand	Frame
571 bits(309)	4e-157()	354/397(89%)	0/397(0%)	Plus/Plus	

```
Query  914   TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCNNNNCATCGTTCTACACGACAC  973
Sbjct  6524  TGGAGGGCTAACAGGTATTGTCCTGGCCAATTCATCTCTAGACATCGTTCTACACGACAC  6583

Query  974   CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  1033
Sbjct  6584  CTACTACGTAGTAGCCCACTTCCACTACGTACTATCTATGGGAGCTGTATTCGCCATTGT  6643

Query  1034  NNNNNNNNTCGTACACTGATTCCCACTATTCACAGGATACACCCTNNNNNNNACATGAAC  1093
Sbjct  6644  TGCCGCCTTCGTACACTGATTCCCACTATTCACAGGATACACCCTTCACAGCACATGAAC  6703

Query  1094  TAAAATCCACTTCGGAGTCATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  1153
Sbjct  6704  TAAAATCCACTTCGGAGTAATGTTTGTAGGTGTCAACCTTACATTCTTCCCACAGCACTT  6763

Query  1154  CCTAGGACNNNNNNNNNNNCCTCGACGGTATTCAGACTACCCAGACGCCTACACCATTTG  1213
Sbjct  6764  CCTAGGACTAGCAGGAATGCCTCGACGGTATTCAGACTACCCAGACGCCTACACCCTTTG  6823

Query  1214  AAACNNNNNNNNNNNTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  1273
Sbjct  6824  AAACACAATTTCCTCTATTGGATCCCTTATCTCCCTAGTAGCAGTAATTATGTTCCTATT  6883

Query  1274  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  1310
Sbjct  6884  TATTATTTGAGAAGCTTTCGCTGCCAAACGTGAAGTA  6920
```

Range 2: 5653 to 5986

Score	Expect	Identities	Gaps	Strand	Frame
390 bits(211)	1e-102()	273/334(82%)	0/334(0%)	Plus/Plus	

```
Query  180   CCCATGCCTTCGTAATGAGTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  239
Sbjct  5653  CCCATGCCTTCGTAATGATTTTCTTTATAGTAATACCAATTATGATTGGAGGATTTGGAA  5712

Query  240   ACTGANNNNNTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  299
Sbjct  5713  ACTGACTTATTCCTCTAATGATCGGAGCCCCCGACATGGCATTCCCACGAATGAACAACA  5772
```

```
Query  300   TGAGCTTCTGACTCCTTCCCCCTTNNNNNNNNNNNNNNNNNNNNNNTCAGGAGTTGAGG  359
Sbjct  5773  TGAGCTTCTGACTCCTTCCCCCTTCTTTCCTTCTGCTCCTAGCTTCTTCAGGAGTTGAGG  5832
Query  360   CNNNNNCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCNNNNNNNNNTAGCCCACGCAG  419
Sbjct  5833  CTGGAGCCGGAACCGGTTGAACAGTCTACCCTCCCCTTGCCGGCAACCTAGCCCACGCAG  5892
Query  420   GGGCATCAGTTGACCTAACTATTTTCTCNNNnnnnnnnnNNNNNNNNTCCTCAATTCTTG  479
Sbjct  5893  GGGCATCAGTTGACCTAACTATTTTCTCACTTCACTTAGCAGGGGTTTCCTCAATTCTTG  5952
Query  480   GGGCAATTAACTTCATCACAACAATTATCAATAT  513
Sbjct  5953  GGGCAATTAACTTCATCACAACAATTATCAATAT  5986
```

Range 3: 5509 to 5587

Score	Expect	Identities	Gaps	Strand	Frame
141 bits(76)	1e-27()	79/80(99%)	1/80(1%)	Plus/Plus	

```
Query  35    ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  94
Sbjct  5509  ATAAAGACATCGGCACCCTCTATCTAGTATTCGGTGCATGAGCTGGAATAGTTGGCACGG  5568
Query  95    CCTTAAGCTNTGCTCATCCG  114
Sbjct  5569  CCTTAAGCT-TGCTCATCCG  5587
```

Taxonomy

Reports

- ## Lineage

Organism	Blast Name	Score	Number of Hits	Description
Percomorphaceae	ray-finned fishes		114	
.Scombrinae	ray-finned fishes		111	
..Thunnini	ray-finned fishes		100	
...Thunnus	ray-finned fishes		90	
....Thunnus thynnus	ray-finned fishes	571	7	Thunnus thynnus hits
....Thunnus thynnus thynnus	ray-finned fishes	571	3	Thunnus thynnus thynnus hits
....Thunnus maccoyii	ray-finned fishes	564	6	Thunnus maccoyii hits
....Thunnus albacares	ray-finned fishes	555	9	Thunnus albacares hits
....Thunnus tonggol	ray-finned fishes	555	6	Thunnus tonggol hits
....Thunnus obesus	ray-finned fishes	555	6	Thunnus obesus hits
....Thunnus atlanticus	ray-finned fishes	549	4	Thunnus atlanticus hits
....Thunnus alalunga	ray-finned fishes	531	43	Thunnus alalunga hits
....Thunnus orientalis	ray-finned fishes	518	6	Thunnus orientalis hits
...Auxis rochei	ray-finned fishes	431	10	Auxis rochei hits
..Sarda sarda	ray-finned fishes	374	4	Sarda sarda hits
..Sarda orientalis	ray-finned fishes	363	3	Sarda orientalis hits
..Scomberomorus guttatus	ray-finned fishes	350	1	Scomberomorus guttatus hits
..Scomberomorus niphonius	ray-finned fishes	348	3	Scomberomorus niphonius hits
.Gymnocanthus herzensteini	ray-finned fishes	340	2	Gymnocanthus herzensteini hits
.Istiophorus platypterus	ray-finned fishes	339	1	Istiophorus platypterus hits

- ## Organism

Description		Score	E value	Accession
Thunnus thynnus (Atlantic bluefin tuna)	[ray-finned fishes]			

Description	Score	E value	Accession
Thunnus thynnus mitochondrion, complete genome	571	4e-157	KF906720
Thunnus thynnus isolate DM353 mitochondrion, complete genome	571	4e-157	MT410869
Thunnus thynnus voucher TT02-2312 mitochondrion, complete genome	571	4e-157	JN086149
Thunnus thynnus mitochondrion, complete genome	571	4e-157	NC_014052
Thunnus thynnus mitochondrion, complete genome	571	4e-157	GU256522
Thunnus thynnus genome assembly, organelle: mitochondrion	520	1e-141	OZ004756
Thunnus thynnus mitochondrial DNA, complete genome	518	5e-141	AP006034
Thunnus thynnus thynnus [ray-finned fishes]			
Thunnus thynnus thynnus mitochondrion, complete genome	571	4e-157	NC_004901
Thunnus thynnus thynnus mitochondrion, complete genome	571	4e-157	AY302574
Thunnus thynnus thynnus mitochondrial DNA, complete genome	571	4e-157	AB097669
Thunnus maccoyii (southern bluefin tuna) [ray-finned fishes]			
Thunnus maccoyii isolate LGM079 mitochondrion, complete genome	564	6e-155	PV069719
Thunnus maccoyii genome assembly, organelle: mitochondrion	564	6e-155	OU343215
Thunnus maccoyii voucher TM02-2313 mitochondrion, complete genome	564	6e-155	JN086150
Thunnus maccoyii mitochondrion, complete genome	551	5e-151	NC_014101
Thunnus maccoyii mitochondrion, complete genome	551	5e-151	GU256523
Thunnus maccoyii mitochondrion, complete genome	542	3e-148	KF925362
Thunnus albacares (yellowfin tuna) [ray-finned fishes]			
Thunnus albacares voucher ECSFRI-HQJQY01 mitochondrion, complete genome	555	4e-152	KP259550
Thunnus albacares mitochondrion, complete genome	555	4e-152	KM588080
Thunnus albacares voucher Se3 mitochondrion, complete genome	549	2e-150	KT724724
Thunnus albacares genome assembly, organelle: mitochondrion	549	2e-150	OU607616
Thunnus albacares voucher TY02-2316 mitochondrion, complete genome	549	2e-150	JN086153
Thunnus albacares mitochondrion, complete genome	549	2e-150	NC_014061
Thunnus albacares mitochondrion, complete genome	549	2e-150	GU256528
Thunnus albacares cytochrome oxidase subunit I (COX I) gene, complete cds; mitochondrial	544	8e-149	HM071006
Thunnus albacares isolate JJ7:18 cytochrome oxidase subunit 1 (COX1) gene, partial cds; mitochondrial	381	6e-100	DQ874757
Thunnus tonggol (longtail tuna) [ray-finned fishes]			
Thunnus tonggol cytochrome c oxidase subunit I gene, complete cds; mitochondrial	555	4e-152	GU799568
Thunnus tonggol voucher USNM 445333 mitochondrion, complete genome	538	4e-147	MW232431
Thunnus tonggol voucher USNM 445302 mitochondrion, complete genome	538	4e-147	MW232430
Thunnus tonggol mitochondrion, complete genome	532	2e-145	NC_020673
Thunnus tonggol mitochondrion, complete genome	532	2e-145	HQ425780
Thunnus tonggol voucher TL02-2317 mitochondrion, complete genome	532	2e-145	JN086154
Thunnus obesus (bigeye tuna) [ray-finned fishes]			
Thunnus obesus cytochrome c oxidase subunit I gene, complete cds; mitochondrial	555	4e-152	GU799567
Thunnus obesus cytochrome oxidase subunit I (COX I) gene, complete cds; mitochondrial	549	2e-150	HM071005
Thunnus obesus mitochondrion, complete genome	544	8e-149	KY400011
Thunnus obesus voucher TO02-2315 mitochondrion, complete genome	544	8e-149	JN086152
Thunnus obesus mitochondrion, complete genome	544	8e-149	NC_014059
Thunnus obesus mitochondrion, complete genome	544	8e-149	GU256525
Thunnus atlanticus (blackfin tuna) [ray-finned fishes]			
Thunnus atlanticus mitochondrion, complete genome	549	2e-150	KU955344
Thunnus atlanticus mitochondrion, complete genome	549	2e-150	KU955343
Thunnus atlanticus voucher Talt-UNAL-001 mitochondrion, complete genome	549	2e-150	NC_025519

Description	Score	E value	Accession
Thunnus atlanticus voucher Talt-UNAL-001 mitochondrion, complete genome	549	2e-150	KM405517
Thunnus alalunga (albacore) [ray-finned fishes]			
Thunnus alalunga isolate PS003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	531	6e-145	KR023728
Thunnus alalunga isolate PS002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	531	6e-145	KR023727
Thunnus alalunga isolate PS001 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	531	6e-145	KR023726
Thunnus alalunga isolate MED005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	531	6e-145	KR023718
Thunnus alalunga isolate AN007 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	525	3e-143	KR023732
Thunnus alalunga isolate AN002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	525	3e-143	KR023731
Thunnus alalunga isolate PN046 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	525	3e-143	KR023723
Thunnus alalunga mitochondrion, complete genome	525	3e-143	NC_005317
Thunnus alalunga mitochondrial DNA, complete genome	525	3e-143	AB101291
Thunnus alalunga voucher ECSFRI-CQJQY01 mitochondrion, complete genome	520	1e-141	KP259549
Thunnus alalunga isolate PS005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023730
Thunnus alalunga isolate PS004 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023729
Thunnus alalunga isolate PN049 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023725
Thunnus alalunga isolate PN048 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023724
Thunnus alalunga isolate MED032 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023722
Thunnus alalunga isolate MED031 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023721
Thunnus alalunga isolate MED024 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023720
Thunnus alalunga isolate MED019 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023719
Thunnus alalunga isolate IN006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023717
Thunnus alalunga isolate IN005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023716
Thunnus alalunga isolate IN004 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023715
Thunnus alalunga isolate IN003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023714
Thunnus alalunga isolate AS010 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023711
Thunnus alalunga isolate AS009 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023710
Thunnus alalunga isolate AS008 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023709
Thunnus alalunga isolate AS006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023707
Thunnus alalunga isolate AS003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023706
Thunnus alalunga isolate AS002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023705
Thunnus alalunga isolate AN012 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023704

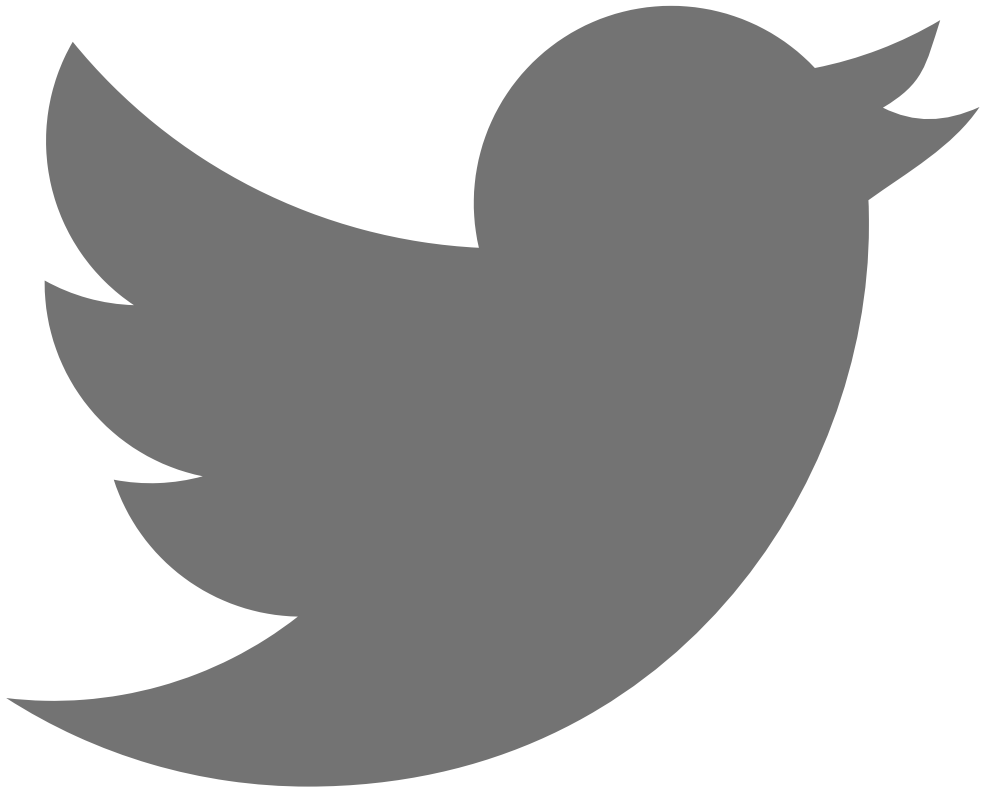
Description	Score	E value	Accession
Thunnus alalunga isolate AN011 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023703
Thunnus alalunga isolate AN010 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023702
Thunnus alalunga isolate AN009 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023701
Thunnus alalunga isolate AN008 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023700
Thunnus alalunga isolate AN006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023699
Thunnus alalunga isolate AN005 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023698
Thunnus alalunga isolate AN004 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	520	1e-141	KR023697
Thunnus alalunga voucher TA02-2314 mitochondrion, complete genome	520	1e-141	JN086151
Thunnus alalunga isolate IN001 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	514	6e-140	KR023712
Thunnus alalunga isolate AS007 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	514	6e-140	KR023708
Thunnus alalunga isolate AN003 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	514	6e-140	KR023696
Thunnus alalunga mitochondrion, complete genome	514	6e-140	GU256526
Thunnus alalunga isolate IN002 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	510	8e-139	KR023713
Thunnus alalunga isolate MED006 cytochrome c oxidase subunit I (COI) gene, partial cds; mitochondrial	490	1e-132	KR023733
Thunnus orientalis (Pacific bluefin tuna) [ray-finned fishes]			
Thunnus orientalis isolate LGM084 mitochondrion, complete genome	518	5e-141	PV069720
Thunnus orientalis mitochondrial DNA, complete genome	518	5e-141	LC377898
Thunnus orientalis mitochondrion, complete genome	518	5e-141	KF906721
Thunnus orientalis mitochondrion, complete genome	518	5e-141	GU256524
Thunnus orientalis mitochondrion, complete genome	518	5e-141	NC_008455
Thunnus orientalis mitochondrial DNA, complete genome	518	5e-141	AB185022
Auxis rochei [ray-finned fishes]			
Auxis rochei mitochondrion, complete genome	431	6e-115	NC_005313
Auxis rochei mitochondrial DNA, complete genome, haplotype:I	431	6e-115	AB103467
Auxis rochei mitochondrion, complete genome	414	6e-110	MK548578
Auxis rochei voucher USNM:FISH:424772 mitochondrion, complete genome	414	6e-110	PX070027
Auxis rochei mitochondrion, complete genome	414	6e-110	KM651784
Auxis rochei voucher USNM 424772 mitochondrion, complete genome	414	6e-110	MW232425
Auxis rochei voucher USNM 403146 mitochondrion, complete genome	414	6e-110	MW232421
Auxis rochei mitochondrial DNA, complete genome, haplotype:II Ecuadorian	414	6e-110	AB105165
Auxis rochei mitochondrial DNA, complete genome, haplotype:II Mediterranean	414	6e-110	AB103468
Auxis rochei voucher ECSFRI-YDJ01 mitochondrion, complete genome	409	3e-108	KP259548
Sarda sarda (Atlantic bonito) [ray-finned fishes]			
Sarda sarda voucher USNM:FISH:477716 mitochondrion, complete genome	374	1e-97	PX070013
Sarda sarda mitochondrion, complete genome	374	1e-97	PP033005
Sarda sarda isolate DM366 mitochondrion, complete genome	374	1e-97	NC_052756
Sarda sarda isolate DM366 mitochondrion, complete genome	374	1e-97	MT410877
Sarda orientalis (striped bonito) [ray-finned fishes]			
Sarda orientalis mitochondrial DNA, complete sequence, specimen_voucher: NSMT:P:110211	363	2e-94	AP012949
Sarda orientalis voucher USNM 445533 mitochondrion, complete genome	363	2e-94	NC_060588

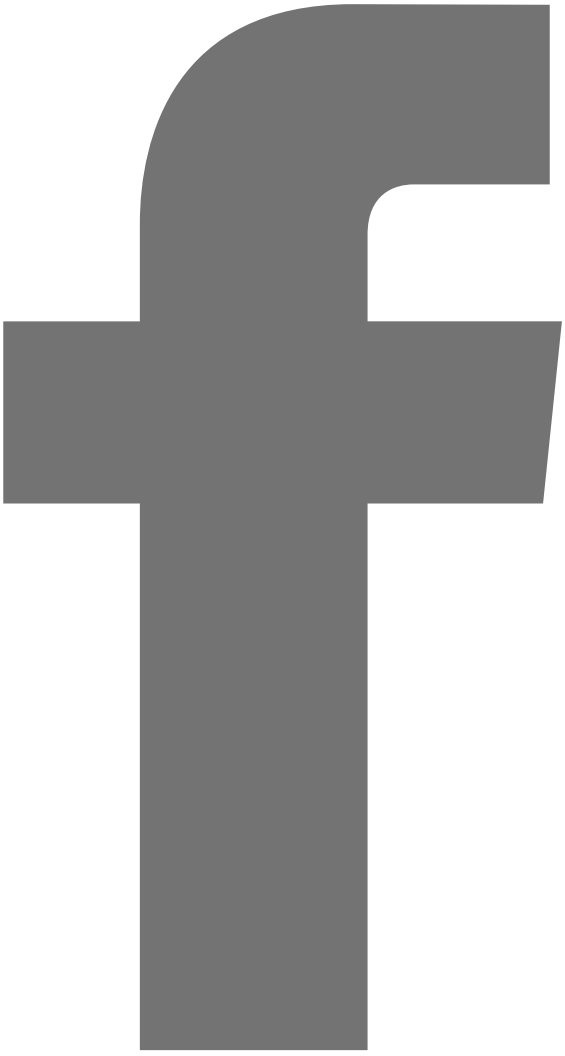
Description	Score	E value	Accession
Sarda orientalis voucher USNM 445533 mitochondrion, complete genome Scomberomorus guttatus (Indo-Pacific king mackerel) [ray-finned fishes]	363	2e-94	MW232432
Scomberomorus guttatus mitochondrion, complete genome Scomberomorus niphonius (Japanese Spanish mackerel) [ray-finned fishes]	350	2e-90	PP437201
Scomberomorus niphonius mitochondrion, complete genome	348	7e-90	NC_016420
Scomberomorus niphonius mitochondrion, complete genome	348	7e-90	GU109281
Scomberomorus niphonius mitochondrion, complete genome Gymnocanthus herzensteini [ray-finned fishes]	342	3e-88	KY228987
Gymnocanthus herzensteini mitochondrion, complete genome	340	1e-87	NC_034651
Gymnocanthus herzensteini mitochondrion, complete genome Istiophorus platypterus (Indo-Pacific sailfish) [ray-finned fishes]	340	1e-87	KX148474
Istiophorus platypterus isolate SFA31 mitochondrion, complete genome	339	4e-87	OP404122

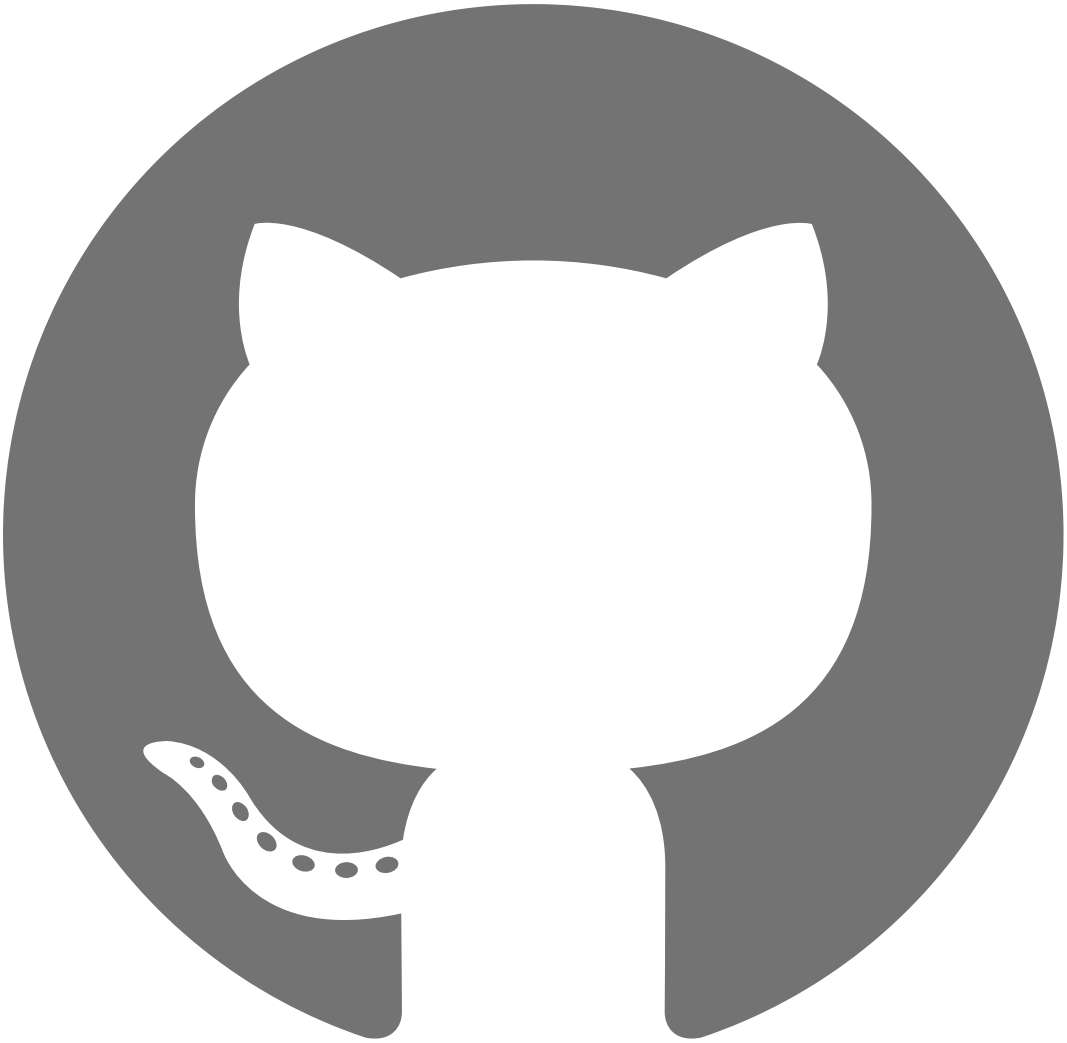
- ## Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
Percomorphaceae	114	16	
. Scombrinae	111	14	
.. Thunnini	100	10	
... Thunnus	90	9	
.... Thunnus thynnus	7	2	**Thunnus thynnus hits**
..... Thunnus thynnus thynnus	3	1	**Thunnus thynnus thynnus hits**
.... Thunnus maccoyii	6	1	**Thunnus maccoyii hits**
.... Thunnus albacares	9	1	**Thunnus albacares hits**
.... Thunnus tonggol	6	1	**Thunnus tonggol hits**
.... Thunnus obesus	6	1	**Thunnus obesus hits**
.... Thunnus atlanticus	4	1	**Thunnus atlanticus hits**
.... Thunnus alalunga	43	1	**Thunnus alalunga hits**
.... Thunnus orientalis	6	1	**Thunnus orientalis hits**
... Auxis rochei	10	1	**Auxis rochei hits**
.. Sarda	7	2	
... Sarda sarda	4	1	**Sarda sarda hits**
... Sarda orientalis	3	1	**Sarda orientalis hits**
.. Scomberomorus	4	2	
... Scomberomorus guttatus	1	1	**Scomberomorus guttatus hits**
... Scomberomorus niphonius	3	1	**Scomberomorus niphonius hits**
. Gymnocanthus herzensteini	2	1	**Gymnocanthus herzensteini hits**
. Istiophorus platypterus	1	1	**Istiophorus platypterus hits**

Top







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