Query: Human Rhodopsin mRNA (NCBI Reference Sequence: NM\_000539.3)

Felis catus breed mixed c405900897.Contig1b00, whole genome shotgun sequence

Sequence ID: [ACBE01063208.1](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208)Length: 24657Number of Matches: 6

Range 1: 13277 to 14467[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/ACBE01063208.1?report=genbank&log$=nuclalign&blast_rank=1&RID=VPVV5GCA015&from=13277&to=14467)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208.1?report=graph&rid=VPVV5GCA015%5bACBE01063208.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=13218:14526&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1: **Exon 5 and 3'UTR** | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 715 bits(792) | 0.0 | 911/1253(73%) | 111/1253(8%) | Plus/Plus |

Query 1029 CAGTTCCGGAACTGCATGCTCACCACCATCTGCTGCGGCAAGAACCCACTGGGTGACGAT 1088

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Sbjct 13277 CAGTTCCGGAACTGCATGCTCACTACCCTCTGCTGTGGCAAGAACCCACTGGGTGATGAC 13336

Query 1089 GAGGCCTCTGCTACCGTGTCCAAGACGGAGACGAGCCAGGTGGCCCCGGCC**TAA**GACCTG 1148

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Sbjct 13337 GAGGCCTCCACCACCGCCTCCAAGACGGAGACCAGCCAGGTGGCACCGGCC**TAA**GCCCTG 13396

Query 1149 CCTAGGACTCTGTGGCCGACTATAGGCGTCTCCCATCCCCTACACCTTCCCCCAGCCACA 1208

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Sbjct 13397 CCAAGGACTCTATGGTCAACTGTAGGAGTCTCCCATTCCCTATGCCTACCCCCAGCCACA 13456

Query 1209 GCCATCCCACCAGGAGCAGCGCCTGTGCAGAATGAACGAAGTCACATAGGCTCCTTAAtt 1268

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Sbjct 13457 GCTGCCCCACCAGGAGCCAGGTCTGTTG-----GAACCAGGTTGCGCAGACTCCTTGAGT 13511

Query 1269 ttttttttttttttAAGAAATAATTAATGAGGCTCCTCACTCACCTGGGACAGCCTGAGA 1328

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Sbjct 13512 TAAAAAAAAA----AAAAAAAAAAAAAAAAG-------AATAACGAGAGAAAAA-TGAGG 13559

Query 1329 AGGGACATCCACCAAG-ACCTACTGATCTGGAGTCCCACGTTCCCCAAGGCCAGCGGGAT 1387

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Sbjct 13560 CTCCCCACTCGACAAGTATGGCCCGATCTGGAGTCCTGAGTTCCCAGGGGCTGGTGGGAT 13619

Query 1388 GTGTGCCCCTCCTCCTCCCAACTCATCTTTCAGGAACACGAGGATTCTTGCTTTCTGGAA 1447

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Sbjct 13620 CTCTGCCCCTCCTCTCCCCAACTCATGTCTCAGGAACACAAGAACTCTTGCTCCCTGGAA 13679

Query 1448 AAGTGTCCCAGCTTAGGGATAAGTGTCTAGCACAGAATGGGGCACACAGTAGGTGCTTAA 1507

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Sbjct 13680 AAGTGTCCCAGCTTAGGGATAAGTGTATAGCACAGAGTGGGGCACACAGTAGGTGCTTAA 13739

Query 1508 TAAATGCTGGATGGATGCAGGAAG----------------GAATGGAGGAATGAATGGGA 1551

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Sbjct 13740 TAAATGCTAGATGGATGAAGGAAGGAACGAATGGGGGAATGAATGAAGGAATGAATGGGC 13799

Query 1552 AGGGAGAACATATCTATCCTCTCAGACCCTCGCAGCAGCAGCAACTCATACTTGGCTAAT 1611

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Sbjct 13800 AGGGAGAGCATATCTACCCTCTCAAAAC--CACCTTAGCTGCAGCTCACCCTCGGCTGAT 13857

Query 1612 GATATGGAGCAGTTGTTTTTCCCTCCCTGGGCCTCACTTTCTTCTCCTATAAAATGGAAA 1671

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Sbjct 13858 GTCCTTGAACAG-----TTTCCCTCCCTGGGCCTCACTTTCTTCCCCCAGAAAATGGAAA 13912

Query 1672 TCCCAGATCCCTGGTCCTGCCGACACGCAGCTACTGAGAAGACCAAAAGAG--------- 1722

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Sbjct 13913 CCCCAAATCCTTGGTCCTGCCAACGCATGGCTGCTGTGAAGATCAAATGAGATTTTGATC 13972

Query 1723 --------gtg------tgtgtgtgtctatgtgtgtgtTTCAGCACTTTGTAAATAGCAA 1768

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Sbjct 13973 TCATATATGTGTGTATATGTGTGTGTGTGTGAGTGTGTGTAAGCACTTTGTAAATGGTAA 14032

Query 1769 GAAGCTGTACAGATTCTAGTTAATGTTGTGAATAACATCAATTAATGTAACTAGTTAATT 1828

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Sbjct 14033 GGAGCTGTACAGATTGTAGTTAACATTATGAATAACACCAATTAATATAA----TTAACT 14088

Query 1829 ACTATGATTATCACCTCCTGATAGTGAACATTTTGAGATTGGGCATTCAGATGATGGGGT 1888

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Sbjct 14089 AATATGATCATCTCTTCTTGATAGTGACCATTTTGAGACTGGGCA---AGGCCCTGAG-- 14143

Query 1889 TTCACCCAACCTTGGGGCAGG-TTTTTAAAAATTAGCTAGGCATCAAGGCCAGACCAGGG 1947

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Sbjct 14144 --CATCCAGCCT--CAGCAGGTTTTTTTTAAATTTACCAGATGTCAAGGCCAGACCAGGG 14199

Query 1948 CTGGGGGTTGGGCTGTAGGCAGGGACAGTCACAGGAATGCAGAATGCAGTCATCAGACCT 2007

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Sbjct 14200 CTGGTGGTCGGTCTGCAGAGAGGGACAGTCAAGGGAATGCAGAATACAGTCATCTGGACT 14259

Query 2008 GAAAAAACAACACTGGGGGAGGGGGACGGTGAAGGCCAAGTTCCCAATGAGGGTGAGATT 2067

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Sbjct 14260 GAAAAAACAAC------GTCAGGGGAC--TGCAGTC--TGGGACCAA------------- 14296

Query 2068 GGGCCTGGGGTCTCACCCCTAGTGTGGGGCCCCAGGTCCCGTGCCTCCCCTTCCCAATGT 2127

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Sbjct 14297 -GGCCCAGGGTCTCACCTCTGACGTGAACTCCCAGGCCCGGTGCCTCCCCTTCCTCATGC 14355

Query 2128 GGCCTATGGAGAGACAGGCCTTTCTCTCAGCCTCTGGAAGCCACCTGCTCTTTTGCTCTA 2187

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Sbjct 14356 AGCCTAGGGAGAGACAGGCCTTTCTCTCAGCTTCTGCAAACTACCTGCCCTCCTTC-CCA 14414

Query 2188 GCACCTGGGTCCCAGCA--TCTAG---AGCATGGAGC---CTCTAGAAGCCAT 2232

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Sbjct 14415 GCCCCTAGGCCACAGCAACTCTAGGCCAGCATGGAGCTGGGCCTAGAAGCCAT 14467

Range 2: 7550 to 8008[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/ACBE01063208.1?report=genbank&log$=nuclalign&blast_rank=1&RID=VPVV5GCA015&from=7550&to=8008)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208.1?report=graph&rid=VPVV5GCA015%5bACBE01063208.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=7528:8030&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp220609449_1)

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| Alignment statistics for match #2: **Exon 1 and 5'UTR** | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 658 bits(729) | 0.0 | 422/459(92%) | 1/459(0%) | Plus/Plus |

Query 1 AGAGTCATCCAGCTGGAGCCCTGAGTGGCTGAGCTCAGGCCTTCGCAGCATTCTTGGGTG 60

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Sbjct 7550 AGAGTCGTCCAGCCAGAGCCCTGGGTGGCCAAGCTCAGGCCTCAGCAGCACTCTTGGGTC 7609

Query 61 GGAGCAGCCAC-GGGTCAGCCACAAGGGCCACAGCC**ATG**AATGGCACAGAAGGCCCTAAC 119

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Sbjct 7610 TGAGCCGCCCCCGGGGCAGCCACCAGGACCACAGCC**ATG**AACGGGACGGAGGGCCCGAAC 7669

Query 120 TTCTACGTGCCCTTCTCCAATGCGACGGGTGTGGTACGCAGCCCCTTCGAGTACCCACAG 179

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Sbjct 7670 TTCTACGTGCCCTTCTCCAACAAAACGGGTGTGGTACGCAGCCCCTTCGAGTACCCACAG 7729

Query 180 TACTACCTGGCTGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTTCTGCTGATC 239

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Sbjct 7730 TACTACCTGGCTGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTCCTGCTCATC 7789

Query 240 GTGCTGGGCTTCCCCATCAACTTCCTCACGCTCTACGTCACCGTCCAGCACAAGAAGCTG 299

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Sbjct 7790 GTGCTTGGCTTCCCCATCAACTTCCTCACGCTCTACGTCACGGTCCAGCACAAGAAGCTG 7849

Query 300 CGCACGCCTCTCAACTACATCCTGCTCAACCTAGCCGTGGCTGACCTCTTCATGGTCCTA 359

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Sbjct 7850 CGCACGCCTCTCAACTACATCCTGCTCAACCTGGCCGTGGCTGACCTCTTCATGGTCTTC 7909

Query 360 GGTGGCTTCACCAGCACCCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACA 419

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Sbjct 7910 GGTGGCTTCACCACCACCCTCTACACCTCTCTGCATGGATACTTTGTCTTTGGGCCCACA 7969

Query 420 GGATGCAATTTGGAGGGCTTCTTTGCCACCCTGGGCGGT 458

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Sbjct 7970 GGATGCAATTTGGAGGGCTTCTTTGCCACACTGGGCGGT 8008

Range 3: 12173 to 12414[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/ACBE01063208.1?report=genbank&log$=nuclalign&blast_rank=1&RID=VPVV5GCA015&from=12173&to=12414)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208.1?report=graph&rid=VPVV5GCA015%5bACBE01063208.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=12161:12426&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp220609449_1)

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| Alignment statistics for match #3: **Exon 4** | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 356 bits(394) | 6e-95 | 224/242(93%) | 0/242(0%) | Plus/Plus |

Query 790 AGGCCGCTGCCCAGCAGCAGGAGTCAGCCACCACACAGAAGGCAGAGAAGGAGGTCACCC 849

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Sbjct 12173 AGGCGGCAGCCCAGCAGCAGGAGTCAGCCACCACCCAGAAGGCTGAGAAGGAGGTCACTC 12232

Query 850 GCATGGTCATCATCATGGTCATCGCTTTCCTGATCTGCTGGGTGCCCTACGCCAGCGTGG 909

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Sbjct 12233 GCATGGTCATCATCATGGTCATTGCTTTCCTGATCTGTTGGGTGCCCTACGCCAGCGTGG 12292

Query 910 CATTCTACATCTTCACCCACCAGGGCTCCAACTTCGGTCCCATCTTCATGACCATCCCAG 969

|||||||||||||||||||||||||||||||||| || |||||||||||||| |||| |

Sbjct 12293 CATTCTACATCTTCACCCACCAGGGCTCCAACTTTGGCCCCATCTTCATGACACTCCCGG 12352

Query 970 CGTTCTTTGCCAAGAGCGCCGCCATCTACAACCCTGTCATCTATATCATGATGAACAAGC 1029

||||||| |||||| | || |||||||||||||||||||||| ||||||||||||||||

Sbjct 12353 CGTTCTTCGCCAAGTCCTCCTCCATCTACAACCCTGTCATCTACATCATGATGAACAAGC 12412

Query 1030 AG 1031

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Sbjct 12413 AG 12414

Range 4: 14533 to 15066[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/ACBE01063208.1?report=genbank&log$=nuclalign&blast_rank=1&RID=VPVV5GCA015&from=14533&to=15066)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208.1?report=graph&rid=VPVV5GCA015%5bACBE01063208.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=14507:15092&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp220609449_1)

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| Alignment statistics for match #4: **Exon 5 part 2 (3'UTR only)**? | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 354 bits(392) | 2e-94 | 421/557(76%) | 33/557(5%) | Plus/Plus |

Query 2222 CTAGAAGCCATGCTCACCCGCCCACATTTAATTAACAGCTGAGTCCCTGATGTCATCCTT 2281 overlap with 3' end of previous section of Exon 5

||||||||||| ||||| ||||||||||||| || ||||||||||| || | ||||

Sbjct 14533 CTAGAAGCCATATTCACCTGCCCACATTTAATGAAGAGCTGAGTCCCCAGTGGAACCCTT 14592

Query 2282 ATCTCGAAGAGCTTAGAAACAAAGAGTGGGAAATTCCACTGGGCCTACCTTCCTTGGGGA 2341

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Sbjct 14593 TTCTCAAAGATCTCAGAAACAAAAAGTGGGAAATTCAGATGGGCCCATCTTCCCTGGGGA 14652

Query 2342 TGTTCATGGGCCCCAGTTTCCAGTTTCCCTTGCCAGACAAGCCCATCTTCAGCAGTTGCT 2401

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Sbjct 14653 TGTTCACAGATCCCAGAGTTGAGCA-CCCTTGCTGGGTAAGCCTGTTTTTAGTAGCTCC- 14710

Query 2402 AGTCCATTCTCCATTCTGGAGAATC--TGCTCCAAAAAGCTGGCCACATCTCTGAGGTGT 2459

|||||||||||||||||||| | || |||| |||| |||| | |||| ||| |

Sbjct 14711 AGTCCATTCTCCATTCTGGAAAGTCCTTGCTGCAAA--GCTGATGGGAACTCTAGGGTAT 14768

Query 2460 CAGAATTAAGCTGCCTCAGTAACTGCTCCCCCTTCTCCATATAAGCAAAGCCAGAAGCTC 2519

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Sbjct 14769 CAGAATTGTGCTGCTTGCATAACTGC---CCCTCCTCCACGTAACCAAGACCAGAAGCTC 14825

Query 2520 TAGCTTTACCCAGCTCTGCCTGGAGACTAAGGCAAATTGGGCCATTAAAAGCTCAGCTCC 2579

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Sbjct 14826 TAACTCTTCCCAGCTCTGCCTGGAGACT-AGGCAAATCGGGGCATTAAAAGCTCAGCTCC 14884

Query 2580 TAT-GTTGGTATTAACGGTGGTGGGTTTTGTTGCTTTCA--CACTCTATCCACAGGATAG 2636

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Sbjct 14885 TATACTTGGTGTTAAGGGTGGTGGTTTTTGTTGCTCTCAAGCTCTTTCTCTGCAGGATGG 14944

Query 2637 ATTGAAACT-GCCAG---CTTCCACCTGATCCCTGACCCTGGGATGGCTGGATTGAGCAA 2692

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Sbjct 14945 ATTGAAATTGGGCAGTAATTTCCACCTGATCTCTAACCCTGGGAT-GCTGGGTT------ 14997

Query 2693 TGAGCAGAGCCAAGCAGCACAGAGTCCCCTG-GGGCTAGAGGTGGAGGAGGCAGTCCTGG 2751

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Sbjct 14998 TG------GGCAACCAG--CAGGGCCCCCTGCGGGTGTGGGGTGGAGGGAGCAGGCCCGG 15049

Query 2752 GAATGGGAAAAACCCCA 2768

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Sbjct 15050 GAATGAGAAAAGCCCCA 15066

Range 5: 10460 to 10632[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/ACBE01063208.1?report=genbank&log$=nuclalign&blast_rank=1&RID=VPVV5GCA015&from=10460&to=10632)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208.1?report=graph&rid=VPVV5GCA015%5bACBE01063208.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=10452:10640&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp220609449_1)

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| Alignment statistics for match #5: **Exon 2** | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 263 bits(291) | 1e-66 | 162/173(94%) | 0/173(0%) | Plus/Plus |

Query 456 GGTGAAATTGCCCTGTGGTCCTTGGTGGTCCTGGCCATCGAGCGGTACGTGGTGGTGTGT 515

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Sbjct 10460 GGTGAAATTGCCCTGTGGTCTTTGGTGGTCCTGGCCATTGAGCGGTACGTGGTGGTGTGT 10519

Query 516 AAGCCCATGAGCAACTTCCGCTTCGGGGAGAACCATGCCATCATGGGCGTTGCCTTCACC 575

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Sbjct 10520 AAGCCCATGAGCAACTTCCGCTTTGGGGAGAACCATGCCATAATGGGCGTCGCCTTCACC 10579

Query 576 TGGGTCATGGCGCTGGCCTGCGCCGCACCCCCACTCGCCGGCTGGTCCAGGTA 628

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Sbjct 10580 TGGGTCATGGCACTGGCCTGCGCTGCACCCCCCCTCGTTGGTTGGTCCAGGTA 10632

Range 6: 11896 to 12069[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/ACBE01063208.1?report=genbank&log$=nuclalign&blast_rank=1&RID=VPVV5GCA015&from=11896&to=12069)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208.1?report=graph&rid=VPVV5GCA015%5bACBE01063208.1%5d&tracks=%5bkey:sequence_track,name:Sequence,display_name:Sequence,id:STD1,category:Sequence,annots:Sequence,ShowLabel:true%5d%5bkey:gene_model_track,CDSProductFeats:false%5d%5bkey:alignment_track,name:other%20alignments,annots:NG%20Alignments|Refseq%20Alignments|Gnomon%20Alignments|Unnamed,shown:false%5d&v=11888:12077&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp220609449_1)

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| Alignment statistics for match #6: **Exon 3** | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 232 bits(256) | 2e-57 | 157/175(90%) | 1/175(0%) | Plus/Plus |

Query 618 TGGTCCAGGTACATCCCCGAGGGCCTGCAGTGCTCGTGTGGAATCGACTACTACACGCTC 677

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Sbjct 11896 TGGTC-AGGTACATCCCTGAAGGCATGCAGTGTTCATGCGGGATCGACTACTACACACTC 11954

Query 678 AAGCCGGAGGTCAACAACGAGTCTTTTGTCATCTACATGTTCGTGGTCCACTTCACCATC 737

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Sbjct 11955 AAGCCAGAGGTCAACAACGAGTCCTTTGTCATCTACATGTTCGTGGTCCACTTCACCATC 12014

Query 738 CCCATGATTATCATCTTTTTCTGCTATGGGCAGCTCGTCTTCACCGTCAAGGAGG 792

|||||||| ||||||| || ||||| |||||||| |||||||| ||||||||||

Sbjct 12015 CCCATGATCGTCATCTTCTTTTGCTACGGGCAGCTTGTCTTCACAGTCAAGGAGG 12069

Repeat in the sequence on either side of an insert? ?

14221 gggacagtca agggaatgca gaatacagtc atctggactg aaaaaacaac gtcaggggac

14281 tgcagtctgg gaccaaggcc cagggtctca cctctgacgt gaactcccag gcccggtgcc

14341 tccccttcct catgcagcct agggagagac aggcctttct ctcagcttct gcaaactacc

14401 tgccctcctt cccagcccct aggccacagc aactctaggc cagcatgg**ag ctgggcctag**

14461 **aagccat**atg ctaggctaga ctctaggcca gcatggacat atgctaggcc agcaactcta

14521 ggccagcatg **agctagaagc cat** attcacc tgcccacatt taatgaagag ctgagtcccc

14581 agtggaaccc ttttctcaaa gatctcagaa acaaaaagtg ggaaattcag atgggcccat

14641 cttccctggg gatgttcaca gatcccagag ttgagcaccc ttgctgggta agcctgtttt

14701 tagtagctcc agtccattct ccattctgga aagtccttgc tgcaaagctg atgggaactc

14761 tagggtatca gaattgtgct gcttgcataa ctgcccctcc tccacgtaac caagaccaga

Intron between Exons 3 and 4

12001 tccacttcac catccccatg atcgtcatct tcttttgcta cgggcagctt gtcttcacag

12061 tcaaggaggt **atggacctgt gttgggtgct ggggacacat acattggttg ggttgagcct**

**12121 ggcctctgtc ccaaaggagc cacagtctgg acagcagacc ctgtgtcctt acag**gcggca

12181 gcccagcagc aggagtcagc caccacccag aaggctgaga aggaggtcac tcgcatggtc