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

Felis catus ops gene for opsin

Sequence ID: [AJ417432.1](https://www.ncbi.nlm.nih.gov/nucleotide/AJ417432.1?report=genbank&log$=nuclalign&blast_rank=2&RID=W5VUPBMA014)Length: 2761Number of Matches: 4

Related Information

[Gene](https://www.ncbi.nlm.nih.gov/gene?term=AJ417432%5bNucleotide%20Accession%5d&RID=W5VUPBMA014&log$=genealign&blast_rank=2)-associated gene details

Range 1: 46 to 504[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AJ417432.1?report=genbank&log$=nuclalign&blast_rank=2&RID=W5VUPBMA014&from=46&to=504)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AJ417432.1?report=graph&rid=W5VUPBMA014%5bAJ417432.1%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=24:526&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1: **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 46 AGAGTCGTCCAGCCAGAGCCCTGGGTGGCCAAGCTCAGGCCTCAGCAGCACTCTTGGGTC 105

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

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Sbjct 106 TGAGCCGCCCCCGGGGCAGCCACCAGGACCACAGCC**ATG**AACGGGACGGAGGGCCCGAAC 165

Query 120 TTCTACGTGCCCTTCTCCAATGCGACGGGTGTGGTACGCAGCCCCTTCGAGTACCCACAG 179

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Sbjct 166 TTCTACGTGCCCTTCTCCAACAAAACGGGTGTGGTACGCAGCCCCTTCGAGTACCCACAG 225

Query 180 TACTACCTGGCTGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTTCTGCTGATC 239

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Sbjct 226 TACTACCTGGCTGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTCCTGCTCATC 285

Query 240 GTGCTGGGCTTCCCCATCAACTTCCTCACGCTCTACGTCACCGTCCAGCACAAGAAGCTG 299

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Sbjct 286 GTGCTTGGCTTCCCCATCAACTTCCTCACGCTCTACGTCACGGTCCAGCACAAGAAGCTG 345

Query 300 CGCACGCCTCTCAACTACATCCTGCTCAACCTAGCCGTGGCTGACCTCTTCATGGTCCTA 359

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Sbjct 346 CGCACGCCTCTCAACTACATCCTGCTCAACCTGGCCGTGGCTGACCTCTTCATGGTCTTC 405

Query 360 GGTGGCTTCACCAGCACCCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACA 419

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Sbjct 406 GGTGGCTTCACCACCACCCTCTACACCTCTCTGCATGGATACTTTGTCTTTGGGCCCACA 465

Query 420 GGATGCAATTTGGAGGGCTTCTTTGCCACCCTGGGCGGT 458

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Sbjct 466 GGATGCAATTTGGAGGGCTTCTTTGCCACACTGGGCGGT 504

Range 2: 1410 to 1822[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AJ417432.1?report=genbank&log$=nuclalign&blast_rank=2&RID=W5VUPBMA014&from=1410&to=1822)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AJ417432.1?report=graph&rid=W5VUPBMA014%5bAJ417432.1%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=1390:1842&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp16516828_1)

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| Alignment statistics for match #2: **Exon 3 and 4?** |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 568 bits(629) | 1e-159 | 375/414(91%) | 1/414(0%) | Plus/Plus |

Query 618 TGGTCCAGGTACATCCCCGAGGGCCTGCAGTGCTCGTGTGGAATCGACTACTACACGCTC 677

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Sbjct 1410 TGGTC-AGGTACATCCCTGAAGGCATGCAGTGTTCATGCGGGATCGACTACTACACACTC 1468

Query 678 AAGCCGGAGGTCAACAACGAGTCTTTTGTCATCTACATGTTCGTGGTCCACTTCACCATC 737

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Sbjct 1469 AAGCCAGAAGTCAACAACGAGTCCTTTGTCATCTACATGTTCGTGGTCCACTTCACCATC 1528

Query 738 CCCATGATTATCATCTTTTTCTGCTATGGGCAGCTCGTCTTCACCGTCAAGGAG/GCCGCT 797

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Sbjct 1529 CCCATGATCGTCATCTTCTTTTGCTACGGGCAGCTTGTCTTCACAGTCAAGGAG/GCGGCA 1588

Query 798 GCCCAGCAGCAGGAGTCAGCCACCACACAGAAGGCAGAGAAGGAGGTCACCCGCATGGTC 857

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Sbjct 1589 GCCCAGCAGCAGGAGTCAGCCACCACCCAGAAGGCTGAGAAGGAGGTCACTCGCATGGTC 1648

Query 858 ATCATCATGGTCATCGCTTTCCTGATCTGCTGGGTGCCCTACGCCAGCGTGGCATTCTAC 917

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Sbjct 1649 ATCATCATGGTCATTGCTTTCCTGATCTGTTGGGTGCCCTACGCCAGCGTGGCATTCTAC 1708

Query 918 ATCTTCACCCACCAGGGCTCCAACTTCGGTCCCATCTTCATGACCATCCCAGCGTTCTTT 977

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Sbjct 1709 ATCTTCACCCACCAGGGGTCCAACTTTGGCCCCATCTTCATGACACTCCCGGCGTTCTTC 1768

Query 978 GCCAAGAGCGCCGCCATCTACAACCCTGTCATCTATATCATGATGAACAAGCAG 1031

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

Sbjct 1769 GCAAAGTCCTCCTCCATCTACAACCCTGTCATCTACATCATGATGAACAAGCAG 1822

Range 3: 754 to 926[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AJ417432.1?report=genbank&log$=nuclalign&blast_rank=2&RID=W5VUPBMA014&from=754&to=926)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AJ417432.1?report=graph&rid=W5VUPBMA014%5bAJ417432.1%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=746:934&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp16516828_1)

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| Alignment statistics for match #3 **Exon 2** |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 259 bits(286) | 7e-67 | 161/173(93%) | 0/173(0%) | Plus/Plus |

Query 456 GGTGAAATTGCCCTGTGGTCCTTGGTGGTCCTGGCCATCGAGCGGTACGTGGTGGTGTGT 515

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Sbjct 754 GGTGAAATTGCCCTGTGGTCTTTGGTGGTCCTGGCCATTGAGCGGTACGTGGTGGTGTGT 813

Query 516 AAGCCCATGAGCAACTTCCGCTTCGGGGAGAACCATGCCATCATGGGCGTTGCCTTCACC 575

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Sbjct 814 AAGCCCATGAGCAACTTCCGCTTTGGGGAGAACCATGCCATAATGGGCGTCGCTTTCACC 873

Query 576 TGGGTCATGGCGCTGGCCTGCGCCGCACCCCCACTCGCCGGCTGGTCCAGGTA 628

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

Sbjct 874 TGGGTCATGGCACTGGCCTGCGCTGCACCCCCCCTCGTTGGTTGGTCCAGGTA 926

Range 4: 2512 to 2705[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AJ417432.1?report=genbank&log$=nuclalign&blast_rank=2&RID=W5VUPBMA014&from=2512&to=2705)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AJ417432.1?report=graph&rid=W5VUPBMA014%5bAJ417432.1%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=2503:2714&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp16516828_1)

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| Alignment statistics for match #4: **Exon 5 and 3'UTR** |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 226 bits(250) | 4e-57 | 166/194(86%) | 0/194(0%) | Plus/Plus |

Query 1032 TTCCGGAACTGCATGCTCACCACCATCTGCTGCGGCAAGAACCCACTGGGTGACGATGAG 1091

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Sbjct 2512 TTCCGGAACTGCATGCTCACTACCCTCTGCTGTGGCAAGAACCCACTGGGTGATGACGAG 2571

Query 1092 GCCTCTGCTACCGTGTCCAAGACGGAGACGAGCCAGGTGGCCCCGGCC**TAA**GACCTGCCT 1151

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Sbjct 2572 GCTTCCACAACCGGTTCCAAGACGGAGACCAGCCAGGTGGCACCGGCC**TAA**GNCCTGCCA 2631

Query 1152 AGGACTCTGTGGCCGACTATAGGCGTCTCCCATCCCCTACACCTTCCCCCAGCCACAGCC 1211

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Sbjct 2632 AGGACTCTATGGTCAACTGTAGGAGTCTCCCATTCCCTATGCCTACCCCNAGCCACAGCT 2691

Query 1212 ATCCCACCAGGAGC 1225

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Sbjct 2692 GCCCCACCAGGAGC 2705

Cat Scaffold Sequence ID: [ACBE01063208.1](https://www.ncbi.nlm.nih.gov/nuccore/ACBE01063208)

12001 tccacttcac catccccatg atcgtcatct tcttttgcta cgggcagctt gtcttcacag

12061 tcaaggag**gt atggacctgt gttgggtgct ggggacacat acattggttg ggttgagcct**

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

12181 gcccagcagc aggagtcagc caccacccag aaggctgaga aggaggtcac tcgcatggtc

Intron between 12069 and 17124