Query sequence: human rhodopsin mRNA

Gallus gallus gene for rhodopsin, complete cds

Sequence ID: [D00702.1](https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast_rank=4&RID=VZ616JWT015)Length: 4285Number of Matches: 5

Related Information

[Gene](https://www.ncbi.nlm.nih.gov/gene?term=D00702%5bNucleotide%20Accession%5d&RID=VZ616JWT015&log$=genealign&blast_rank=4)-associated gene details

Range 1: 684 to 1056[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast_rank=4&RID=VZ616JWT015&from=684&to=1056)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/D00702.1?report=graph&rid=VZ616JWT015%5bD00702.1%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=666:1074&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1: **Exon 1** |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 371 bits(411) | 3e-100 | 306/373(82%) | 0/373(0%) | Plus/Plus |

Query 88 CCACAGCC**ATG**AATGGCACAGAAGGCCCTAACTTCTACGTGCCCTTCTCCAATGCGACGG 147

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Sbjct 684 CCGCAGCCATGAACGGGACGGAAGGCCAAGACTTCTACGTGCCCATGTCCAACAAGACCG 743

Query 148 GTGTGGTACGCAGCCCCTTCGAGTACCCACAGTACTACCTGGCTGAGCCATGGCAGTTCT 207

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Sbjct 744 GGGTGGTGCGGAGCCCCTTCGAGTACCCCCAGTACTACCTGGCTGAGCCCTGGAAGTTCT 803

Query 208 CCATGCTGGCCGCCTACATGTTTCTGCTGATCGTGCTGGGCTTCCCCATCAACTTCCTCA 267

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Sbjct 804 CGGCGCTGGCTGCCTACATGTTCATGCTGATCCTGCTCGGCTTCCCCGTCAACTTCCTCA 863

Query 268 CGCTCTACGTCACCGTCCAGCACAAGAAGCTGCGCACGCCTCTCAACTACATCCTGCTCA 327

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Sbjct 864 CGCTGTACGTCACCATCCAGCACAAGAAACTCCGGACGCCTCTAAACTACATCCTCCTGA 923

Query 328 ACCTAGCCGTGGCTGACCTCTTCATGGTCCTAGGTGGCTTCACCAGCACCCTCTACACCT 387

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Sbjct 924 ACCTGGTGGTCGCCGACCTCTTTATGGTCTTTGGAGGCTTCACGACCACCATGTACACCT 983

Query 388 CTCTGCATGGATACTTCGTCTTCGGGCCCACAGGATGCAATTTGGAGGGCTTCTTTGCCA 447

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Sbjct 984 CGATGAACGGGTACTTTGTCTTTGGAGTAACAGGGTGCTACATCGAGGGCTTCTTTGCTA 1043

Query 448 CCCTGGGCGGTGA 460

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Sbjct 1044 CGCTGGGCGGTGA 1056

Range 2: 2425 to 2666[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast_rank=4&RID=VZ616JWT015&from=2425&to=2666)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/D00702.1?report=graph&rid=VZ616JWT015%5bD00702.1%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=2413:2678&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp222856_1)

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| Alignment statistics for match #2: Exon 4 |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 315 bits(349) | 2e-83 | 215/242(89%) | 0/242(0%) | Plus/Plus |

Query 790 AGGCCGCTGCCCAGCAGCAGGAGTCAGCCACCACACAGAAGGCAGAGAAGGAGGTCACCC 849

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Sbjct 2425 AGGCTGCCGCCCAGCAGCAGGAGTCTGCCACCACCCAGAAGGCAGAGAAGGAAGTGACCC 2484

Query 850 GCATGGTCATCATCATGGTCATCGCTTTCCTGATCTGCTGGGTGCCCTACGCCAGCGTGG 909

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Sbjct 2485 GCATGGTGATCATCATGGTCATCGCCTTCCTCATCTGCTGGGTTCCCTACGCCAGCGTCG 2544

Query 910 CATTCTACATCTTCACCCACCAGGGCTCCAACTTCGGTCCCATCTTCATGACCATCCCAG 969

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Sbjct 2545 CTTTCTACATCTTCACCAACCAGGGCTCAGACTTTGGACCCATCTTCATGACCATCCCGG 2604

Query 970 CGTTCTTTGCCAAGAGCGCCGCCATCTACAACCCTGTCATCTATATCATGATGAACAAGC 1029

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Sbjct 2605 CATTCTTTGCCAAGAGCTCTGCCATCTACAATCCTGTGATCTACATCGTAATGAACAAAC 2664

Query 1030 AG 1031

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Sbjct 2665 AG 2666

Range 3: 2128 to 2297[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast_rank=4&RID=VZ616JWT015&from=2128&to=2297)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/D00702.1?report=graph&rid=VZ616JWT015%5bD00702.1%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=2120:2305&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp222856_1)

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| Alignment statistics for match #3: Exon 3 |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 213 bits(235) | 2e-52 | 149/170(88%) | 0/170(0%) | Plus/Plus |

Query 623 CAGGTACATCCCCGAGGGCCTGCAGTGCTCGTGTGGAATCGACTACTACACGCTCAAGCC 682

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Sbjct 2128 CAGGTACATCCCCGAGGGCATGCAGTGCTCGTGTGGGATCGACTACTACACGCTGAAGCC 2187

Query 683 GGAGGTCAACAACGAGTCTTTTGTCATCTACATGTTCGTGGTCCACTTCACCATCCCCAT 742

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Sbjct 2188 GGAGATCAACAACGAATCCTTTGTCATCTACATGTTCGTGGTCCACTTCATGATCCCACT 2247

Query 743 GATTATCATCTTTTTCTGCTATGGGCAGCTCGTCTTCACCGTCAAGGAGG 792

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

Sbjct 2248 GGCCGTCATCTTCTTCTGCTATGGGAACCTGGTCTGCACTGTGAAGGAGG 2297

Range 4: 1886 to 2058[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast_rank=4&RID=VZ616JWT015&from=1886&to=2058)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/D00702.1?report=graph&rid=VZ616JWT015%5bD00702.1%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=1878:2066&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp222856_1)

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| Alignment statistics for match #4: Exon 2 |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 182 bits(201) | 3e-43 | 144/173(83%) | 0/173(0%) | Plus/Plus |

Query 456 GGTGAAATTGCCCTGTGGTCCTTGGTGGTCCTGGCCATCGAGCGGTACGTGGTGGTGTGT 515

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Sbjct 1886 GGTGAAATCGCTCTCTGGTCACTCGTCGTCCTGGCCGTGGAACGATATGTGGTGGTCTGT 1945

Query 516 AAGCCCATGAGCAACTTCCGCTTCGGGGAGAACCATGCCATCATGGGCGTTGCCTTCACC 575

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Sbjct 1946 AAGCCCATGAGCAACTTCCGCTTCGGGGAGAACCACGCCATCATGGGGGTCGCGTTCTCC 2005

Query 576 TGGGTCATGGCGCTGGCCTGCGCCGCACCCCCACTCGCCGGCTGGTCCAGGTA 628

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Sbjct 2006 TGGATCATGGCCATGGCCTGCGCAGCCCCCCCGCTGTTCGGCTGGTCACGGTA 2058

Range 5: 3540 to 3611[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast_rank=4&RID=VZ616JWT015&from=3540&to=3611)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/D00702.1?report=graph&rid=VZ616JWT015%5bD00702.1%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=3537:3614&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp222856_1)

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| Alignment statistics for match #5: Exon 5 |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 81.5 bits(89) | 7e-13 | 61/72(85%) | 0/72(0%) | Plus/Plus |

Query 1029 CAGTTCCGGAACTGCATGCTCACCACCATCTGCTGCGGCAAGAACCCACTGGGTGACGAT 1088

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Sbjct 3540 CAGTTCCGTAACTGCATGATCACAACCCTCTGCTGCGGCAAGAACCCGCTGGGCGATGAG 3599

Query 1089 GAGGCCTCTGCT 1100

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Sbjct 3600 GACACGTCTGCT 3611

Gallus mRNA exons: https://www.ncbi.nlm.nih.gov/nucleotide/D00702.1?report=genbank&log$=nuclalign&blast\_rank=4&RID=VZ616JWT015

Exon 1. atgaacggg acggaaggcc aagacttcta

 721 cgtgcccatg tccaacaaga ccggggtggt gcggagcccc ttcgagtacc cccagtacta

 781 cctggctgag ccctggaagt tctcggcgct ggctgcctac atgttcatgc tgatcctgct

 841 cggcttcccc gtcaacttcc tcacgctgta cgtcaccatc cagcacaaga aactccggac

 901 gcctctaaac tacatcctcc tgaacctggt ggtcgccgac ctctttatgg tctttggagg

 961 cttcacgacc accatgtaca cctcgatgaa cgggtacttt gtctttggag taacagggtg

 1021 ctacatcgag ggcttctttg ctacgctggg cg

Exon 2 gtga aatcgctctc tggtcactcg tcgtcctggc

 1921 cgtggaacga tatgtggtgg tctgtaagcc catgagcaac ttccgcttcg gggagaacca

 1981 cgccatcatg ggggtcgcgt tctcctggat catggccatg gcctgcgcag cccccccgct

 2041 gttcggctgg tcacg

Exon 3 gtacatcccc gagggcatgc agtgctcgtg

 2161 tgggatcgac tactacacgc tgaagccgga gatcaacaac gaatcctttg tcatctacat

 2221 gttcgtggtc cacttcatga tcccactggc cgtcatcttc ttctgctatg ggaacctggt

 2281 ctgcactgtg aaggag

Exon 4. gctg ccgcccagca gcaggagtct gccaccaccc

 2461 agaaggcaga gaaggaagtg acccgcatgg tgatcatcat ggtcatcgcc ttcctcatct

 2521 gctgggttcc ctacgccagc gtcgctttct acatcttcac caaccagggc tcagactttg

 2581 gacccatctt catgaccatc ccggcattct ttgccaagag ctctgccatc tacaatcctg

 2641 tgatctacat cgtaatgaac aaacag

Exons 5. ttccgtaa ctgcatgatc acaaccctct gctgcggcaa gaacccgctg ggcgatgagg

 3601 acacgtctgc tggaaagaca gagacctcct ccgtctccac cagccaggtg tcccctgcat

 3661 ag