Query: Human rhodopsin mRNA (ref|NM\_000539.3)

Loxodonta africana isolate ISIS603380 cont3.30946, whole genome shotgun sequence

Sequence ID: [AAGU03030947.1](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947)Length: 162596Number of Matches: 6

Range 1: 34017 to 35030[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AAGU03030947.1?report=genbank&log$=nuclalign&blast_rank=1&RID=W0R9T68K015&from=34017&to=35030)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947.1?report=graph&rid=W0R9T68K015%5bAAGU03030947.1%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=33967:35080&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match

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| Alignment statistics for match #1: Exon 5a | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 554 bits(614) | 1e-154 | 764/1051(73%) | 97/1051(9%) | Plus/Minus |

Query 1029 CAGTTCCGGAACTGCATGCTCACCACCATCTGCTGCGGCAAGAACCCACTGGGTGACGAT 1088

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Sbjct 35030 CAGTTCCGGAACTGCATGCTCACCACCATCTGCTGCGGCAAGAACCCATTCGGTGAGGAA 34971

Query 1089 GAGGCCTCTGCTACCGTGTCCAAGACGGAGACGAGCCAGGTGGCCCCGGCC**TAA**GACCTG 1148

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Sbjct 34970 GAGGGCTCCACCACCGCCTCCAAGACGGAGACCAGCCAGGTGGCCCCGGCC**TAA**GCCCTA 34911

Query 1149 CCTAGGACTCTGTGGCCGACTATAGGCGTCTCCCATCCCCTACACCTTCCCCCAGCCACA 1208

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Sbjct 34910 CCGAAGGCTCTGCGCCAG-CTAGAGGAGAGGCATACCCCCCGCACCTGCCCCAAGCCATA 34852

Query 1209 GCCATCCCACCAGGAGCAGCGCCTGTGCAGAATGAACGAAGTCACATAGGCTCCTTAAtt 1268

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Sbjct 34851 GCCGCCCCACCAGCAGG-GTGCCTGTTG-----GAACCAGGCCACACAGGTTCCCTGATT 34798

Query 1269 tttttt--------ttttttttAAGAAATAATTA-------ATGAGGCTCCTCACTCACC 1313

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Sbjct 34797 TAAAAGAAGAAAAATAAAAATCATGAACTAACGAGAGAAAAATGAAGCTGCCCCCTCGGT 34738

Query 1314 TGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCACGTTCCCC 1373

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Sbjct 34737 GGGGTCAGCCTGAGGAGGGACCGC-ACCGAGACC--CCAATCTGGAGT-------TCCCA 34688

Query 1374 AAGGCCAGCGGGATGTGTGCCCCTCCTCCTCCCAACTCATCTTTCAGGAACACGAGGATT 1433

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Sbjct 34687 GGGGCTGATGGGACCTGT---CTGCCTCCTCCCTCCTCATCTCTCAGGAACACAAGGACT 34631

Query 1434 CTTGCTTTCTGGAAAAGTGTCCCAGCTTAGGGATAAGTGTCTAGCACAGAATGGGGCACA 1493

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Sbjct 34630 CTTGCTCTCTGGAAA-GTGTCCCTGCTTAGGGATAAGTGTCTAGCACAGAGAGGGGCACA 34572

Query 1494 CAGTAGGTGCTTAATAAATGCTGGATGGATGCAGGAAGGAATGGA----GGAATGAATGG 1549

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Sbjct 34571 TAGTAGGTGCTTAATAAAAGCTTGATGGATGAAGGAAGGAATGGATGGAGGAAAGAATGG 34512

Query 1550 ------GAAGGGA---GAACA---TATCTATCCTCTCAGACCC-TCGCAGCAGCAGCAAC 1596

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Sbjct 34511 AGGAACGAATGGCTGGGAAAAATCTACCTGTCCTCTCAAAAGCATCTTAGCAACAGCAGC 34452

Query 1597 TCATACTT--GGCTAA-TGATATGGAGCAGTTGTTTTTCCCTCCCTGGGCCTCACTTTCT 1653

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Sbjct 34451 TCATACTTTTGGTTATGTGACCTTGGGCAGTTGCTTT-CCCTCCG-GAGCCTCTCTTTCT 34394

Query 1654 TCTCCTATAAAATGGAAATCCCAGATCCCTGGTCCTGCCGAC-ACGCAG--CTACTGAGA 1710

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Sbjct 34393 TGCCCCATAGAACAGAAATCCCA-ATCC-TGGACCTGCCTCCTACCTAGGGCTGCTGTGA 34336

Query 1711 AGACCAAAAGAG-------gtgtgtgtgtgtct--------atgtg------tgtgtTTC 1749

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Sbjct 34335 AGATCAGATGAGATTGTGTGTGTGTGTGTGTGTGCGTGCACATGTGCACGCATGTGTGTA 34276

Query 1750 AGCACTTTGTAAATAGCAAGAAGCTGTACAGATTCTAGTTAATGTTGTGAATAACATCAA 1809

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Sbjct 34275 AGCACTTTGTAAATGATAAAGAGCTGTACAGACTGTAGTTAACGTCATGAATAATACCTA 34216

Query 1810 TTAATGTAACTAGTTAATTACTATGATTATCACCTCCTGATAGTGAACATTTTGAGATTG 1869

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Sbjct 34215 TTAATATGATTAATTAACTACTGTGATTATCTCCTCTTGATAGTGATCATTTTGAGATTG 34156

Query 1870 GGCATTCAGATGATGGGGTTTCACCCAACCTTGGGGCAGGTTTTTAAAAATTAGCTAGG- 1928

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Sbjct 34155 ACCATCCAGACAATGGGGTTTCACGCAGCCT--CAGCACGTTTTTAAAAAGTAGCTAGGT 34098

Query 1929 CATCAAGGCCAGACCAGGGCTGGGGGTTGGGCTGTAGGCAGGGACAGTCACAGGAATGCA 1988

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Sbjct 34097 GTTCAAGGCCATACCAGAACT---GGTCCGGCTGCAGGGAGGGCCAGTCAAAG------- 34048

Query 1989 GAATGCAGTCATCAGACCTGAAAAAACAACA 2019

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Sbjct 34047 GAATGCAGTCAACAAACCTGTAAAAACAGCA 34017

Range 2: 40002 to 40453[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AAGU03030947.1?report=genbank&log$=nuclalign&blast_rank=1&RID=W0R9T68K015&from=40002&to=40453)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947.1?report=graph&rid=W0R9T68K015%5bAAGU03030947.1%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=39980:40475&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp253649805_1)

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| Alignment statistics for match #2: Exon 1 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 530 bits(587) | 5e-147 | 396/458(86%) | 6/458(1%) | Plus/Minus |

Query 1 AGAGTCATCCAGCTGGAGCCCTGAGTGGCTGAGCTCAGGCCTTCGCAGCATTCTTGGGTG 60

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Sbjct 40453 AGAGTCATTT-GCTGGCGTCCTG-GTGACTGATCCCAGGCTTGGGCAGCATCTTCAGGTT 40396

Query 61 GGAGCAGCCACGGGTCAGCCACAAGGGCCACAGCC**ATG**AATGGCACAGAAGGCCCTAACT 120

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Sbjct 40395 GTAGCG--CGTGGG-CAGCCTTGAGG-CCGCAGCC**ATG**AATGGGACAGAAGGCCCGAATT 40340

Query 121 TCTACGTGCCCTTCTCCAATGCGACGGGTGTGGTACGCAGCCCCTTCGAGTACCCACAGT 180

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Sbjct 40339 TCTACGTGCCCTTCTCCAACAAGACGGGTGTGGTACGCAGCCCCTTTGAGTACCCGCAGT 40280

Query 181 ACTACCTGGCTGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTTCTGCTGATCG 240

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Sbjct 40279 ACTACCTAGCAGAGCCATGGCAGTTCTCCATGCTGGCCGCCTACATGTTCCTGCTTATCG 40220

Query 241 TGCTGGGCTTCCCCATCAACTTCCTCACGCTCTACGTCACCGTCCAGCACAAGAAGCTGC 300

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Sbjct 40219 TGCTTGGCTTCCCCATCAACTTCCTCACGCTCTACGTGACCGTGCAGCATAAGAAGCTGC 40160

Query 301 GCACGCCTCTCAACTACATCCTGCTCAACCTAGCCGTGGCTGACCTCTTCATGGTCCTAG 360

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Sbjct 40159 GCACACCACTCAACTACATCCTGCTCAACCTGGCCGTAGCCAACCATTTCATGGTCTTTG 40100

Query 361 GTGGCTTCACCAGCACCCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACAG 420

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Sbjct 40099 GCGGCTTCACCACCACCCTCTATACCTCTCTGCATGGATACTTCGTCTTCGGGTCCACTG 40040

Query 421 GATGCAATTTGGAGGGCTTCTTTGCCACCCTGGGCGGT 458

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Sbjct 40039 GATGCAACCTGGAGGGCTTCTTTGCCACCCTGGGCGGT 40002

Range 3: 35844 to 36085[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AAGU03030947.1?report=genbank&log$=nuclalign&blast_rank=1&RID=W0R9T68K015&from=35844&to=36085)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947.1?report=graph&rid=W0R9T68K015%5bAAGU03030947.1%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=35832:36097&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp253649805_1)

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| Alignment statistics for match #3: Exon 4 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 343 bits(379) | 2e-90 | 221/242(91%) | 0/242(0%) | Plus/Minus |

Query 790 AGGCCGCTGCCCAGCAGCAGGAGTCAGCCACCACACAGAAGGCAGAGAAGGAGGTCACCC 849

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Sbjct 36085 AGGCGGCTGCCCAGCAACAGGAGTCAGCCACCACCCAGAAGGCGGAGAAGGAGGTCACCC 36026

Query 850 GCATGGTCATCATCATGGTCATCGCTTTCCTGATCTGCTGGGTGCCCTACGCCAGCGTGG 909

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Sbjct 36025 GCATGGTCATCATCATGGTCATCGCGTTCCTGATCTGCTGGGTGCCCTATGCTAGCGTGG 35966

Query 910 CATTCTACATCTTCACCCACCAGGGCTCCAACTTCGGTCCCATCTTCATGACCATCCCAG 969

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Sbjct 35965 CCTTCTATATATTCACCCACCAGGGCTCTGACTTCGGGCCCATCCTCATGACCCTCCCAG 35906

Query 970 CGTTCTTTGCCAAGAGCGCCGCCATCTACAACCCTGTCATCTATATCATGATGAACAAGC 1029

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

Sbjct 35905 CGTTCTTTGCCAAGAGCTCTGCCATCTACAACCCCGTCATCTACATTATGATGAATAAGC 35846

Query 1030 AG 1031

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Sbjct 35845 AG 35844

Range 4: 33335 to 33964[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AAGU03030947.1?report=genbank&log$=nuclalign&blast_rank=1&RID=W0R9T68K015&from=33335&to=33964)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947.1?report=graph&rid=W0R9T68K015%5bAAGU03030947.1%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=33304:33995&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp253649805_1)

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| Alignment statistics for match #4: Exon 5b | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 328 bits(363) | 3e-86 | 474/657(72%) | 59/657(8%) | Plus/Minus |

Query 2144 GGCCTTTCTCTCAGCCTCTGGAAGCCACCTGCTCTTT-TGCTCTAGCACCTGGGTCCCAG 2202

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Sbjct 33964 GGCCTCTCTCTCGGCTTCTGAGAAACACCTGGTCCTTCTGCCCTAGCTCCCAGGACACAG 33905

Query 2203 CATCTA-GAGCATG----GAGCCTCTAGAAGCCATGCTCACCCGCCCACATTTAATTAAC 2257

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Sbjct 33904 CATCTCTGGGTCTGTACAGAGCTTCTAGCAGCCATGCCCATCCGCCCACATTCAATGAAG 33845

Query 2258 AGCTGAGTCCCTGATGTCATCCTTATCTCGAAGAGCTTAGAAACAAAGAGTGGGAAATTC 2317

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Sbjct 33844 AGCTGAGTCCCCGATGTCACTCTCGTCACACAGAGCTTAGAAACAAACAGTGGGAAATTT 33785

Query 2318 CACTGGGCCTACCTTCCTTGGGGATGTTCATGGGCCCCAGTTTCCAGTTTCCCTTGCCAG 2377

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Sbjct 33784 GGCTGGGCCCACCATCCCTGGGG-TGTTCA---GTTTCAGATTACAG-CTCCCATGGTAG 33730

Query 2378 ACAAGCCCAT-CTTCAGCAGTTGCTAGTCCATTCTCCATTCTGGAGAATC--TGCTCCAA 2434

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Sbjct 33729 ACAAGCCCCTGTTTCAGCAGCTAATAGTCTATTTTCCATTCTGGAGAGTCCTGGCTTCTA 33670

Query 2435 AAAGCTGGCCACATCTCTGAGGTGTCAGAATTAAGCTGCCTCAGTAACTGCTCCCCCTTC 2494

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Sbjct 33669 ------GGCC-CA------GGGAGTCAGAAGCAAGCCGCTTCCGTGTCT----CGCCTTC 33627

Query 2495 TCCATATAAGCAAAGCCAGAAGCTCTAGCTTTACCCAGCTCTGCCTGGAGACTAAGGCAA 2554

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Sbjct 33626 ----CATTACCAAAGCCAGAAGCTCTAGCTCTTCCCAGCTCTGCCCGGAGAAAAAGGCAA 33571

Query 2555 ATTGGGCCATTAAAAGCTCAGCTCCTAT-GTTGGTATTAACG-GTGGTGGGTTTTGTTGC 2612

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Sbjct 33570 ACTGGGACATTAAAAGCTCAGCTCCTATACTTTGCGTTAATGTCTAGTGGTTCTTGTGGC 33511

Query 2613 TTTCA--CACTCTATCCACAGGATAGATTGAAACT-GCCAGCTTCCACCTGATCCCTGAC 2669

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Sbjct 33510 TCTTAAGCATCTTATGTGCAGGATGAATTGAAACTGGGCTGCTTCCACCTGAGCCCTGGC 33451

Query 2670 CCTGGGATGGCTGGATTGAGCAATGAGCAGAGCCAAGCAGCACAGAGTCCCCTGGGGCTA 2729

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Sbjct 33450 CCTGGGATGCCTGGGCTGGGCAGCCAGCAGAGCAAAGCAGTCCAGAGT-TCCTGGGGAGA 33392

Query 2730 GAGG------------------TGGAGGAGGCAGTCCTGGGAATGGGAAAAACCCCA 2768

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Sbjct 33391 GTGGCGGAATGGGGTACGGGGTTGGAGGAAGCAGTCCCAGGAATGGGGAAAGCCCCA 33335

Range 5: 37690 to 37862[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AAGU03030947.1?report=genbank&log$=nuclalign&blast_rank=1&RID=W0R9T68K015&from=37690&to=37862)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947.1?report=graph&rid=W0R9T68K015%5bAAGU03030947.1%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=37682:37870&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp253649805_1)

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| Alignment statistics for match #5: Exon 2 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 250 bits(276) | 7e-63 | 159/173(92%) | 0/173(0%) | Plus/Minus |

Query 456 GGTGAAATTGCCCTGTGGTCCTTGGTGGTCCTGGCCATCGAGCGGTACGTGGTGGTGTGT 515

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Sbjct 37862 GGTGAAATCGCCCTGTGGTCGTTGGTGGTCCTGGCCATCGAGCGGTATGTGGTGGTGTGT 37803

Query 516 AAGCCCATGAGCAACTTCCGCTTCGGGGAGAACCATGCCATCATGGGCGTTGCCTTCACC 575

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Sbjct 37802 AAGCCCATGAGCAACTTCCGCTTCGGGGAGAACCACGCCATCATGGGTGTCGCCTTCACC 37743

Query 576 TGGGTCATGGCGCTGGCCTGCGCCGCACCCCCACTCGCCGGCTGGTCCAGGTA 628

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Sbjct 37742 TGGGTCATGGCTCTGGCCTGTGCTGCGCCACCCCTCGTTGGCTGGTCCAGGTA 37690

Range 6: 36212 to 36382[GenBank](https://www.ncbi.nlm.nih.gov/nucleotide/AAGU03030947.1?report=genbank&log$=nuclalign&blast_rank=1&RID=W0R9T68K015&from=36212&to=36382)[Graphics](https://www.ncbi.nlm.nih.gov/nuccore/AAGU03030947.1?report=graph&rid=W0R9T68K015%5bAAGU03030947.1%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=36204:36390&appname=ncbiblast&link_loc=fromHSP) Next Match Previous Match [First Match](https://blast.ncbi.nlm.nih.gov/Blast.cgi#hsp253649805_1)

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| Alignment statistics for match #6: Exon 3 | | | | |
| **Score** | **Expect** | **Identities** | **Gaps** | **Strand** |
| 224 bits(247) | 1e-54 | 152/171(89%) | 0/171(0%) | Plus/Minus |

Query 622 CCAGGTACATCCCCGAGGGCCTGCAGTGCTCGTGTGGAATCGACTACTACACGCTCAAGC 681

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Sbjct 36382 CCAGGTATATCCCTGAAGGCATGCAGTGCTCATGTGGGATCGACTACTACACGCTCAAGC 36323

Query 682 CGGAGGTCAACAACGAGTCTTTTGTCATCTACATGTTCGTGGTCCACTTCACCATCCCCA 741

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Sbjct 36322 CCGAGGTCAATAATGAGTCCTTCGTCATCTACATGTTTGTGGTCCACTTCACCATCCCTA 36263

Query 742 TGATTATCATCTTTTTCTGCTATGGGCAGCTCGTCTTCACCGTCAAGGAGG 792

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Sbjct 36262 TGACCATCATCTTCTTCTGCTACGGGCAGCTGGTCTTCACGGTCAAGGAGG 36212

Gap in Exon 5?

1861 ttgagattgg gcattcagat gatggggttt cacccaacct tggggcaggt ttttaaaaat

1921 tagctaggca tcaaggccag accagggctg ggggttgggc tgtaggcagg gacagtcaca

1981 ggaatgcaga atgcagtcat cagacctgaa aaaacaacac tgggggaggg ggacggtgaa

2041 ggccaagttc ccaatgaggg tgagattggg cctggggtct cacccctagt gtggggcccc

2101 aggtcccgtg cctccccttc ccaatgtggc ctatggagag acaggccttt ctctcagcct

2161 ctggaagcca cctgctcttt tgctctagca cctgggtccc agcatctaga gcatggagcc

2221 tctagaagcc atgctcaccc gcccacattt aattaacagc tgagtccctg atgtcatcct

Extra piece in the human gene? Not translated.

Present in Primates and and gappy in Euarchontoglires and Laurasiatheria. Most of the region absent in Afrotheria?