

COPA (NM_004371.4) - cDNA - 2026-11-23

GTCGCTGACG TGGAGGCGTC CGAAGGGCAG CAGGGTGTGT CGGGGCTCGG -31

ATTAAGACAT CGGAGTCGGA GACCTGAGAG ATGTTAACCA AATTCGAGAC 20

CAAGAGCGCG CGGGTCAAAG GGCTCAGCTT TCACCCCAAA AGACCTTGGA 70

TCCTGACTAG TTTACATAAT GGGGTCATCC AGTTATGGGA CTATCGGATG 120

TGCACTCTCA TTGACAAGTT TGATGAACAT GATGGTCCAG TGCGAGGCAT 170 p.G56S

TGACTTCCAT AAGCAGCAGC CACTGTTCGT CTCTGGAGGA GATGACTATA 220

AGATTAAGGT TTGGAATTAC AAGCTTCGGC GCTGTCTTTT CACATTGCTT 270

GGGCACTTAG ATTATATTCG CACCACGTTT TTTCATCATG AATATCCCTG 320

GATTCTGAGT GCCTCCGATG ATCAGACCAT CCGAGTGTGG AACTGGCAAT 370

CTAGAACCTG TGTTTGTGTG TTAACAGGGC ACAACCATTA TGTGATGTGT 420

GCTCAGTTCC ACCCCACAGA AGACTTGGTA GTATCAGCCA GCCTGGACCA 470

GACTGTGCGC GTTTGGGATA TTTCTGGTCT GAGGAAAAAA AACCTGTCCC 520

CTGGTGCGGT GGAATCGGAT GTGAGAGGAA TAACTGGGGT TGATCTATTT 570

GGAACTACAG ATGCAGTGGT GAAGCATGTA CTAGAGGGTC ACGATCGTGG 620 p.H199R L201P

AGTAAACTGG GCTGCCTTCC ACCCCACTAT GCCCCTTATT GTATCTGGGG 670 p.A211V

CAGATGATCG TCAAGTGAAG ATCTGGCGCA TGAATGAATC AAAGGCATGG 720 p.R227C p.K230N R233C p.R233H p.R233L p.K238E p.A239P p.W240R p.W240L p.W240S

GAGGTTGATA CCTGCCGGGG CCATTACAAC AATGTATCTT GTGCCGTCTT 770 p.E241K p.E241A E241D p.V242G p.D243N p.D243G G247D

CCACCCTCGC CAAGAGTTGA TCCTCAGCAA TTCTGAGGAC AAGAGTATTC 820 H258R L263S

GAGTCTGGGA TATGTCTAAG CGGACTGGGG TTCAGACTTT CCGCAGAGAC 870 p.R281W p.Q285H

CATGATCGTT TCTGGGTCCT AGCTGCTCAC CCTAACCTTA ACCTCTTTGC 920

AGCAGGCCAT GATGGTGGTA TGATTGTGTT TAAGCTGGAA CGGGAACGGC 970

CAGCCTATGC TGTTCATGGC AATATGCTAC ACTATGTCAA GGACCGATTC 1020 p.R339Q

TTACGACAGC TGGATTTCAA CAGCTCCAAA GATGTAGCTG TGATGCAGTT 1070

GCGGAGTGGT TCCAAGTTTC CAGTATTCAA TATGTCATAC AATCCAGCAG 1120 R358W p.Y370S

AAAATGCAGT CCTGCTTTGT ACAAGAGCTA GCAATCTAGA GAATAGTACC 1170

TATGACCTGT ACACCATCCC TAAAGATGCT GACTCCCAGA ATCCTGATGC 1220

GCCTGAAGGG AAACGATCCT CAGGCCTGAC AGCCGTTTGG GTCGCTCGAA 1270 p.P408S

ATCGGTTTGC TGTCCTAGAT CGGATGCATT CGCTTCTGAT CAAGAATCTG 1320

AAGAATGAGA TCACCAAAAA GGTACAGGTG CCCAACTGTG ATGAGATCTT 1370

CTATGCTGGC ACAGGCAATC TCCTGCTTCG AGATGCGGAC TCTATCACAC 1420

TCTTTGACGT ACAGCAGAAG CGGACTCTGG CATCTGTGAA GATTTCTAAA 1470

GTGAAATACG TTATCTGGTC AGCAGACATG TCACATGTAG CACTACTAGC 1520

CAAACACGCC ATTGTGATCT GTAACCGCAA ACTGGATGCT TTATGTAACA 1570 p.D519Y

TTCATGAGAA CATTCGTGTC AAGAGTGGGG CCTGGGATGA GAGTGGGGTA 1620 S532I

TTTATCTATA CCACAAGCAA CCACATCAAA TATGCTGTCA CCACTGGGGA 1670

CCACGGGATC ATTCGAACTC TGGATTTACC CATCTATGTC ACACGGGTGA 1720

AGGGCAACAA TGTATACTGC CTAGACAGGG AGTGTCGTCC CCGGGTACTC 1770

ACCATTGATC CCACTGAGTT CAAATTCAAG CTGGCCCTGA TCAACAGAAA 1820

ATATGATGAG GTACTGCACA TGGTGAGGAA TGCCAAACTA GTTGGCCAGT 1870

CTATTATTGC TTATCTCCAG AAGAAGGGCT ATCCTGAAGT GGCACTGCAT 1920

TTTGTCAAGG ATGAGAAAAC TCGCTTTAGT CTGGCACTGG AGTGTGGAAA 1970

CATTGAGATT GCTCTGGAAG CAGCCAAAGC ACTGGATGAC AAGAACTGCT 2020

GGGAAAAGCT GGGAGAAGTG GCCCTGCTGC AGGGGAACCA CCAGATTGTG 2070 G678E

GAAATGTGCT ATCAGCGTAC CAAAAACTTT GACAAACTTT CCTTCCTGTA 2120 Y694C T697I

TCTTATCACT GGCAACTTAG AAAAACTTCG CAAGATGATG AAGATTGCTG 2170

AGATCAGAAA GGACATGAGT GGCCACTATC AGAATGCCCT ATACCTGGGT 2220

GATGTGTCAG AGCGTGTGCG GATCCTGAAG AACTGTGGAC AGAAGTCCCT 2270 R745H

GGCCTATCTC ACAGCTGCTA CCCATGGCTT AGATGAAGAA GCTGAGAGCC 2320

TAAAGGAGAC ATTTGACCCA GAGAAGGAGA CAATCCCAGA CATTGACCCT 2370 T777I

AATGCCAAGC TGCTCCAGCC ACCTGCACCT ATCATGCCAT TGGATACCAA 2420 p.Asn807Thr

TTGGCCTTTA TTGACTGTAT CCAAAGGATT TTTTGAAGGC ACCATTGCCA 2470

GCAAAGGGAA GGGAGGAGCA CTGGCTGCTG ACATTGACAT TGACACTGTT 2520 p.G828E

GGTACAGAGG GCTGGGGAGA GGATGCAGAG CTGCAGTTGG ATGAAGATGG 2570 G844D

GTTTGTGGAG GCTACAGAAG GTTTGGGGGA TGATGCTCTT GGCAAGGGAC 2620

AGGAAGAAGG AGGTGGCTGG GATGTAGAAG AAGATCTGGA GCTCCCTCCT 2670

GAGCTGGATA TATCCCCTGG GGCAGCTGGT GGGGCTGAAG ATGGTTTCTT 2720

TGTGCCCCCA ACCAAGGGAA CAAGTCCAAC TCAGATCTGG TGTAATAACT 2770

CTCAGCTTCC AGTTGATCAC ATCCTGGCAG GCTCTTTCGA AACAGCCATG 2820

CGGCTCCTTC ATGACCAAGT AGGGGTAATC CAGTTTGGCC CCTACAAGCA 2870

ACTGTTCCTA CAGACATACG CCCGAGGCCG CACAACCTAT CAGGCTCTGC 2920

CCTGCCTACC CTCCATGTAT GGCTATCCTA ATCGCAACTG GAAGGATGCA 2970

GGGCTGAAGA ATGGTGTACC AGCTGTGGGC CTGAAGCTTA ATGACCTCAT 3020

CCAACGGTTG CAGCTGTGCT ACCAGCTCAC CACAGTTGGC AAATTTGAGG 3070 p.C1013S

AGGCTGTGGA AAAATTCCGT TCCATCCTTC TCAGTGTGCC ACTTCTTGTT 3120

GTGGACAATA AACAAGAGAT TGCAGAGGCC CAGCAGCTCA TCACCATTTG 3170

CCGTGAGTAC ATTGTGGGTT TGTCCGTGGA GACAGAAAGG AAGAAGCTGC 3220 p.R1058C

CCAAAGAGAC TCTAGAACAG CAGAAGCGCA TCTGTGAGAT GGCAGCCTAT 3270

TTCACCCACT CAAACCTGCA GCCTGTGCAC ATGATCCTGG TGCTGCGTAC 3320

AGCCCTCAAT CTGTTCTTCA AGCTCAAGAA CTTCAAGACA GCTGCCACCT 3370

TTGCTCGGCG CCTACTAGAA CTCGGGCCCA AGCCTGAGGT GGCCCAACAG 3420

ACCCGAAAAA TCCTGTCTGC CTGTGAGAAG AATCCCACAG ATGCCTACCA 3470 p.R1142X

GCTCAATTAT GACATGCACA ACCCCTTTGA CATTTGTGCT GCATCATATC 3520

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TGCTATTCCC CTGAGTTCAA AGGTCAAATC TGCAGGGTCA CCACAGTGAC 3620

AGAGATTGGC AAAGATGTGA TTGGTTTAAG GATCAGTCCT CTGCAGTTTC 3670

GCTAAGGCCC CCTTTGTGTG CATGGGTCAG TCACCATATG TTCCCCCCAG *45

AGAATGTGTC TATATCCTCC TTCTAACAGC ACCTTCCCCC TGCAGCTACT *95

CTTCAGATCT GGCTCTCTGT ACCCTAAAAC CTAGTATCTT TTTCTCTTCT *145

ATGGAAAATC CGAAGGTCTA AACTTGACTT TTTTGAGGTC TTCTCAACTT *195

GACTACAGTT GTGCTCATAA TTGTCCTTGC CTTTCCAGCT TAATTATTTT *245

AAGGAACAAA TGAAAACTCT GGGCTGGGTG GAGTGGCTCA TACCTGTAAT *295

CCCAGCACTT TGGGAGGCTA CGGTGGGCAG ATCATCTGAG GCCAGGAGTT *345

CGAGACCTGC CTGGCCAACA TGGCAACACC CCGTCTCTAA TAAAAATATA *395

AAAATTAGCC TGGCATGGTA GCATGCGCCT ATAGTCCCAG CTGCTCAGGA *445

GGCTGAGGCA TGAGAATCGC TTGAACCTAG GAGGTGGAGG TTGCATTCAA *495

CTGAGATCAT ACCACTTCAT TCCAGCCTGG GTGACAGAGC AAGACTCTGT *545

CTCAAAAAAA AAAAAAAGGA AAACTCTGTG ATGGACATTT GTTTAGTAAA *595

TCCCTTCAGT ATTTATCCCT CCTTTCCCCA CAGCAGCTTT CTTTCCTGTC *645

AACTAGAAAG GAGCAGGATG TAATAAATAC ATTTTGGTGT GACTAGGCCA *695

CACCAACTCT TAATCATCTC CCATTTTCCT TAGACATTTA AATTTCAAGG *745

CAGGTACCCT CTGTGTACTC AGAAATTTGA AGAAGTTATT TGGTTTTCCA *795

AAATGCACAC TGCGGGTTAT TGATTTGTTC TTTACAACTA TTGTTCTCAT *845

ATTTCTCACA CTAAATAAAT CTCTATGAGA GCTTCTTGAC TTGGCCATTT *895

ATTTCTTGGA CACTCTCATG TTCTTGTTCA CCCATGCAGG CACCCCACCA *945

AAGTACATAT CTTCCTTCCA GTAATAATTT TTAATTACAA AATAAACATC *995

CACTATTGGA AAAAAAAAAA AAAAGCTAGC CGGGCATGGT GGTGGGTGCC *1045

TGTAATCCCA GCTACTCTGG AGGCTGAGGC AGAGGATTGC TTGAACCCGG *1095

GAGGCGGAGG TTGCAGTAAG CTGAGATCGC GCCACCGCAC TCCAGCCTGG *1145

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TTGCTAATTA TAGCAATATT TATTGAGCAC CTGCCATGTG ACTGTCACTG *1345

TTCTAGATAT TTTACATGTA ATATACAGAT AAAAGAATAG TACTTTATAT *1395

ATATTACAAT GATACAATGA TTACATTAAC AATACAATAT TTTGCTTGTC *1445

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ATAAGTACTT TTTTGCGTGT TAAATTCATG TTTTCAATAA ATAATAAATG *1545

CATATAGTTG AAAAATCA

