



COPA (NM_004371.4) - cDNA + Protein - 2024-05-17

GTCGCTGACG TGGAGGCGTC CGAAGGGCAG CAGGGTGTGT CGGGGCTCGG -31

ATTAAGACAT CGGAGTCGGA GACCTGAGAG ATGTTAACCA AATTCGAGAC 20

MetLeuThrL ysPheGluTh 7

CAAGAGCGCG CGGGTCAAAG GGCTCAGCTT TCACCCCAA AGACCTTGGA 70

rLysSerAla ArgValLysG lyLeuSerPh eHisProLys ArgProTrpI 24

TCCTGACTAG TTTACATAAT GGGGTCATCC AGTTATGGGA CTATCGGATG 120

leLeuThrSe rLeuHisAsn GlyValIleG lnLeuTrpAs pTyrArgMet 40

TGCACTCTCA TTGACAAGTT TGATGAACAT GATGGTCCAG TGCGAGGCAT 170 p.G56S

CysThrLeuI leAspLysPh eAspGluHis AspGlyProV alArgGlyIl 57

TGACTTCCAT AAGCAGCAGC CACTGTTCGT CTCTGGAGGA GATGACTATA 220

eAspPheHis LysGlnGlnP roLeuPheVa lSerGlyGly AspAspTyrL 74

AGATTAAGGT TTGGAATTAC AAGCTTCGGC GCTGTCTTTT CACATTGCTT 270

ysIleLysVa lTrpAsnTyr LysLeuArgA rgCysLeuPh eThrLeuLeu 90

GGGCACTTAG ATTATATTCG CACCACGTTT TTTCATCATG AATATCCCTG 320

GlyHisLeuA spTyrIleAr gThrThrPhe PheHisHisG luTyrProTr 107

GATTCTGAGT GCCTCCGATG ATCAGACCAT CCGAGTGTGG AACTGGCAAT 370

pIleLeuSer AlaSerAspA spGlnThrIl eArgValTrp AsnTrpGlnS 124

CTAGAACCTG TGTTTGTGTG TTAACAGGGC ACAACCATTA TGTGATGTGT 420

erArgThrCy sValCysVal LeuThrGlyH isAsnHisTy rValMetCys 140

GCTCAGTTCC ACCCCACAGA AGACTTGGTA GTATCAGCCA GCCTGGACCA 470

AlaGlnPheH isProThrGl uAspLeuVal ValSerAlaS erLeuAspGl 157

GA CTGTGCGC GTTTGGGATA TTTCTGGTCT GAGGAAAAAA AACCTGTCCC 520

nThrValArg ValTrpAspI leSerGlyLe uArgLysLys AsnLeuSerP 174

CTGGTGCGGT GGAATCGGAT GTGAGAGGAA TAACTGGGGT TGATCTATTT 570

roGlyAlaVa lGluSerAsp ValArgGlyI leThrGlyVa lAspLeuPhe 190

GGA ACTACAG ATGCAGTGGT GAAGC A TGTA CTAGAGGGTC ACGATCGTGG 620 [p.H199R](#)

GlyThrThrA spAlaValVa lLysHisVal LeuGluGlyH isAspArgGl 207

AGTAAACTGG G C TGCCTTCC ACCCCACTAT GCCCCTTATT GTATCTGGGG 670 [p.A211V](#)

yValAsnTrp AlaAlaPheH isProThrMe tProLeuIle ValSerGlyA 224

CAGATGAT C G TCAAGTGAAG ATCTGGC G CA TGAATGAATC AAAGGCATGG 720 [p.R227C](#) [p.K230N](#) [p.R233H](#) [p.R233L](#) [p.K238E](#) [p.A239P](#) [p.W240R](#) [p.W240L](#) [p.W240S](#)

laAspAspAr gGlnValLys IleTrpArgM etAsnGluSe rLysAlaTrp 240

GAGG I TGATA CCTGCCGGGG CCATTACAAC AATGTATCTT GTGCCGTCTT 770 [p.E241K](#) [p.E241A](#) [p.V242G](#) [p.D243N](#) [p.D243G](#)

GluValAspT hrCysArgGl yHisTyrAsn AsnValSerC ysAlaValPh 257

CCACCCTCGC CAAGAGT I GA TCCTCAGCAA TTCTGAGGAC AAGAGTATTC 820 [L263S](#)

eHisProArg GlnGluLeuI leLeuSerAs nSerGluAsp LysSerIleA 274

GAGTCTGGGA TATGTCTAAG CGGACTGGGG TTCAGACTTT CCGCAGAGAC 870 [p.R281W](#) [p.Q285H](#)
rgValTrpAs pMetSerLys ArgThrGlyV alGlnThrPh eArgArgAsp 290

CATGATCGTT TCTGGGTCCT AGCTGCTCAC CCTAACCTTA ACCTCTTTGC 920
HisAspArgP heTrpValLe uAlaAlaHis ProAsnLeuA snLeuPheAl 307

AGCAGGCCAT GATGGTGGTA TGATTGTGTT TAAGCTGGAA CGGGAACGGC 970
aAlaGlyHis AspGlyGlyM etIleValPh eLysLeuGlu ArgGluArgP 324

CAGCCTATGC TGTTCATGGC AATATGCTAC ACTATGTCAA GGACCGATTC 1020 [p.R339Q](#)
roAlaTyrAl aValHisGly AsnMetLeuH isTyrVally sAspArgPhe 340

TTACGACAGC TGGATTTCAA CAGCTCCAAA GATGTAGCTG TGATGCAGTT 1070
LeuArgGlnL euAspPheAs nSerSerLys AspValAlaV alMetGlnLe 357

GCGGAGTGGT TCCAAGTTTC CAGTATTCAA TATGTCATAC AATCCAGCAG 1120 [p.Y370S](#)
uArgSerGly SerLysPheP roValPheAs nMetSerTyr AsnProAlaG 374

AAAATGCAGT CCTGCTTTGT ACAAGAGCTA GCAATCTAGA GAATAGTACC 1170
luAsnAlaVa lLeuLeuCys ThrArgAlaS erAsnLeuGl uAsnSerThr 390

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TyrAspLeuT yrThrIlePr oLysAspAla AspSerGlnA snProAspAl 407

GCCTGAAGGG AAACGATCCT CAGGCCTGAC AGCCGTTTGG GTCGCTCGAA 1270 [p.P408S](#)
aProGluGly LysArgSerS erGlyLeuTh rAlaValTrp ValAlaArgA 424

ATCGGTTTGC TGTCTAGAT CGGATGCATT CGCTTCTGAT CAAGAATCTG 1320
snArgPheAl aValLeuAsp ArgMetHisS erLeuLeuIl eLysAsnLeu 440

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LysAsnGluI leThrLysLy sValGlnVal ProAsnCysA spGluIlePh 457

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eTyrAlaGly ThrGlyAsnL euLeuLeuAr gAspAlaAsp SerIleThrL 474

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euPheAspVa lGlnGlnLys ArgThrLeuA laSerValLy sIleSerLys 490

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ValLysTyrV alIleTrpSe rAlaAspMet SerHisValA laLeuLeuAl 507

CAAACACGCC ATTGTGATCT GTAACCGCAA ACTGGATGCT TTATGTAACA 1570 [p.D519Y](#)
aLysHisAla IleValIleC ysAsnArgLy sLeuAspAla LeuCysAsnI 524

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nIleGluIle AlaLeuGluA laAlaLysAl aLeuAspAsp LysAsnCysT 674

GGGAAAAGCT GGGAGAAGTG GCCCTGCTGC AGGGGAACCA CCAGATTGTG 2070

rpGluLysLe uGlyGluVal AlaLeuLeuG lnGlyAsnHi sGlnIleVal 690

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euLysGluTh rPheAspPro GluLysGluT hrIleProAs pIleAspPro 790

AATGCCAAGC TGCTCCAGCC ACCTGCACCT ATCATGCCAT TGGATACCA 2420 [p.Asn807Thr](#)

AsnAlaLysL euLeuGlnPr oProAlaPro IleMetProL euAspThrAs 807

TTGGCCTTTA TTGACTGTAT CCAAAGGATT TTTTGAAGGC ACCATTGCCA 2470

nTrpProLeu LeuThrValS erLysGlyPh ePheGluGly ThrIleAlaS 824

GCAAAGGGAA GGAGGAGCA CTGGCTGCTG ACATTGACAT TGACACTGTT 2520 [p.G828E](#)

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GGTACAGAGG GCTGGGGAGA GGATGCAGAG CTGCAGTTGG ATGAAGATGG 2570 [G844D](#)

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CACCAACTCT TAATCATCTC CCATTTTCCT TAGACATTTA AATTTCAAGG *745

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