Length of CAE-final1: 2373 bp; Listed from: 1 to: 2373;
Translated from: 1 to: 2371 (whole region);
Genetic Code used: Universal; Fri, Mar 4, 2005 10:36AM

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Frame 1 Met Ala Asn Ser Tyr Asn Ala Tyr Val Ala Asn Gly Ser Gln Thr Ala Phe
        ATG GCG AAC AGC TAT AAT GCT TAC GTG GCG AAC GGT TCA CAG ACC GCA TTC
                  9         18         27         36         45

Leu Val Thr Phe Glu Gln Arg Val Phe Thr Glu Ile Gln Val Tyr Leu Asn Ser Glu
CTC GTC ACG TTC GAG CAG CGC GTG TTC ACT GAG ATT CAG GTG TAC CTC AAC TCC GAA
         60         69         78         87         96        105

Leu Gln Thr Glu Gly Tyr Thr Tyr Asn Ser Val Thr Lys Gln Ile Ile Phe Asp Thr
CTC CAG ACG GAA GGG TAC ACC TAC AAC TCT GTG ACC AAA CAG ATT ATC TTC GAC ACC
        117        126        135        144        153        162

Ala Pro Leu Ala Gly Val Ile Val Arg Leu Gln Arg Tyr Thr Ser Glu Val Leu Leu
GCC CCG CTC GCC GGG GTG ATT GTC CGA CTC CAA CGC TAC ACC TCT GAG GTT CTG CTG
        174        183        192        201        210        219

Asn Lys Phe Gly Gln Asp Ala Ala Phe Thr Gly Gln Asn Leu Asp Glu Asn Phe Glu
AAC AAG TTT GGC CAA GAC GCT GCC TTC ACC GGG CAG AAC CTT GAC GAG AAC TTT GAG
        231        240        249        258        267        276

Gln Ile Leu Phe Lys Ala Glu Glu Thr Gln Glu Ala Trp Leu Ala Pro Leu Asp Arg
CAG ATT CTG TTC AAG GCT GAG GAA ACT CAG GAA GCA TGG CTC GCG CCA CTT GAC CGC
        288        297        306        315        324        333

Ala Val Arg Val Pro Asn Ser Glu Val Ser Ile Asn Ala Leu Pro Asn Val Ala Gly
GCC GTC CGT GTT CCG AAC TCC GAA GTC TCC ATC AAC GCA TTA CCG AAC GTC GCT GGC
        345        354        363        372        381        390

Arg Arg Asn Lys Ala Leu Gly Phe Asp Ser Asn Gly Gln Pro Phe Met Ile Pro Leu
CGC CGC AAC AAG GCA CTG GGC TTT GAC AGC AAT GGT CAG CCG TTC ATG ATT CCT CTG
        402        411        420        429        438        447

Val Asp Ile Pro Asp Ser Ala Leu Ala Ile Ala Leu Ala Met Ala Asp Gly Gly Lys
GTC GAT ATC CCG GAC TCC GCG CTG GCG ATT GCT CTG GCA ATG GCT GAC GGC GGT AAG
        459        468        477        486        495        504

Trp Ile Gly Thr Leu Gly Gly Gly Thr Phe Leu Asp Arg Gln Asp Thr Val Cys Leu
TGG ATT GGT ACT CTC GGC GGG GGC ACG TTC CTC GAC CGT CAG GAT ACC GTC TGC CTG
        516        525        534        543        552        561
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FIG. 1A

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Ser Glu Phe Thr Asn Asn Thr Gly Tyr Ala Ser Val Ala Ala Ala Val Gln Ala Cys
TCC GAG TTC ACC AAC AAC ACT GGG TAC GCC TCT GTC GCC GCT GCG GTG CAG GCT TGC
        573         582         591         600         609         618

Phe Asp Tyr Ala Lys Ala Asn Gly Lys Val Val Asp Ala Arg Gly Trp Glu Gly Thr
TTC GAC TAT GCG AAA GCC AAC GGC AAG GTC GTT GAC GCT CGC GGC TGG GAA GGT ACG
        630         639         648         657         666         675

Val Asp Ser Thr Val Leu Met Asp Gly Ile Glu Val Val Gly Gly Thr Trp His Gly
GTG GAT TCC ACT GTG CTG ATG GAC GGT ATT GAG GTC GTC GGC GGT ACG TGG CAC GGC
        687         696         705         714         723         732

Lys Ala Asp Ile Arg Leu Leu Asn ser Thr Phe Arg Asn Phe Val Ala Ser Thr Val
AAG GCT GAC ATT CGC CTG CTG AAC TCC ACC TTC CGC AAC TTC GTG GCC TCT ACT GTC
        744         753         762         771         780         789

Arg Val Ala Tyr Trp Gly Gly Glu Val Arg Ile Ala Asp Tyr Glu Phe Thr Ser Ala
CGT GTC GCC TAC TGG GGC GGC GAG GTG CGT ATT GCT GAC TAT GAG TTC ACC AGC GCA
        801         810         819         828         837         846

Pro Ser Asn Ser Lys Val Thr Ser Ile Leu Phe Gln Gly Asn Ile Ala Gly Gly Ser
CCG AGC AAC TCC AAG GTT ACG TCT ATC CTG TTC CAA GGC AAC ATC GCC GGG GGC AGC
        858         867         876         885         894         903

Tyr Val Ile Glu Asn Gly Ile His Arg Asn Gly Lys Phe Gly Ile Leu Gln Gln Gly
TAC GTC ATT GAG AAC GGT ATC CAC CGC AAT GGT AAG TTC GGT ATT CTC CAA CAG GGT
        915         924         933         942         951         960

Thr Gly Glu Ala Ile Thr Asn Gly Val Ile Arg Gly Ile Thr Met Met Asp Met Gln
ACT GGC GAG GCT ATC ACC AAC GGC GTT ATC CGT GGC ATC ACC ATG ATG GAT ATG CAG
        972         981         990         999        1008        1017

Gly Asp Gly Ile Glu Met Asn Val Ile Asn Lys His Tyr Asp Gly Gly Leu Leu Ile
GGT GAC GGT ATC GAG ATG AAC GTA ATC AAC AAG CAC TAT GAT GGT GGC CTG CTG ATT
       1029        1038        1047        1056        1065        1074

Glu Asn Ile Phe Leu Glu Asn Ile Asp Gly Thr Asn Ala Pro Ile Pro Leu Ser Asn
GAG AAC ATC TTC CTT GAG AAC ATC GAC GGC ACC AAC GCG CCT ATC CCA CTG TCC AAC
       1086        1095        1104        1113        1122        1131

Trp Gly Ile Gly Ile Gly Ile Ala Gly Gln Gly Pro Phe Gly Trp Asp Ala Ala Glu
TGG GGC ATT GGT ATC GGT ATC GCT GGT CAA GGC CCG TTC GGT TGG GAT GCT GCT GAG
       1143        1152        1161        1170        1179        1188
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FIG. 1B

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Thr Gln Tyr Ala Lys Asn Val Thr Val Arg Asn Val His Ala Pro Arg Gly Val Arg
ACG CAG TAT GCG AAG AAC GTC ACT GTC CGT AAC GTC CAT GCT CCG CGT GGT GTG CGT
      1200        1209        1218        1227        1236        1245

Gln Val Val His Phe Glu Val Thr Arg Asp Ser Thr Cys Glu Asn Val Val Ala Asn
CAG GTC GTC CAC TTC GAG GTT ACG CGT GAC AGC ACC TGC GAG AAC GTA GTG GCC AAC
      1257        1266        1275        1284        1293        1302

Pro Asp Leu Ser Val Ser Ile Gly Thr Gly Leu Thr Ala Ala Gly Val Ile Thr Tyr
CCT GAC CTG TCC GTC TCC ATT GGT ACT GGC CTG ACT GCC GCT GGT GTA ATC ACG TAC
      1314        1323        1332        1341        1350        1359

Gly Cys Lys Arg Met Thr Ile Asp Gly Val Val Gly Glu Pro Met Asn Thr Gly Ala
GGC TGC AAG CGC ATG ACC ATT GAC GGT GTA GTC GGT GAG CCT ATG AAC ACC GGA GCA
      1371        1380        1389        1398        1407        1416

Thr Ser Pro Asn Asp Ile Arg Ile Val Met Leu Glu Trp Gly Ala Asn Gln Ala Gly
ACC TCT CCG AAC GAT ATT CGT ATC GTG ATG TTG GAG TGG GGT GCG AAC CAA GCA GGT
      1428        1437        1446        1455        1464        1473

Ala Gly Gly Thr Pro Gly Ala Ala Cys Pro Ser Phe Asp Met Thr Val Arg Asn Val
GCT GGC GGT ACG CCG GGT GCA GCT TGC CCA TCG TTC GAC ATG ACC GTG CGT AAC GTG
      1485        1494        1503        1512        1521        1530

Gln Thr Arg Thr Gly Arg Phe Tyr Ala Gly Val Gly Ser Asp Asp Asp Asn Thr Asn
CAG ACC CGT ACC GGG CGC TTC TAT GCT GGT GTC GGC TCC GAC GAT GAC AAC ACC AAC
      1542        1551        1560        1569        1578        1587

Thr Tyr His Leu Glu Asn Ile His Cys Tyr Lys Met Thr Leu Phe Gly Val Ala Thr
ACA TAT CAC CTT GAA AAC ATT CAC TGT TAC AAG ATG ACG CTG TTT GGT GTG GCA ACT
      1599        1608        1617        1626        1635        1644

Leu Leu Asn Met Thr Asn Val Thr Gly Val Val Phe Asp Ala Val Gly Asp Asp Ser
CTG CTG AAC ATG ACC AAC GTG ACT GGT GTG GTG TTC GAC GCT GTA GGC GAT GAC TCC
      1656        1665        1674        1683        1692        1701

Ser Gly Gly Thr Ser Ser Asn Gly Leu Tyr Pro Arg Lys Lys Thr Val Leu Asn Met
AGC GGC GGT ACG TCC TCC AAC GGT CTG TAC CCG CGT AAG AAG ACT GTT CTC AAC ATG
      1713        1722        1731        1740        1749        1758

Val Asn Val Asn Phe Tyr Gly Pro Gly Met Thr Glu Gly Ala Leu Tyr Ser Lys Ala
GTG AAC GTG AAC TTC TAC GGG CCG GGC ATG ACC GAG GGT GCG CTG TAC AGT AAG GCT
      1770        1779        1788        1797        1806        1815
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FIG. 1C

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Arg Tyr Ser Asp Ile Ser Thr Leu Asn Ser Asn Val Arg Ala Ile Pro Tyr Thr Asn
CGC TAC TCG GAT ATC AGC ACG CTG AAC TCC AAC GTG CGT GCT ATC CCG TAC ACC AAC
      1827       1836       1845       1854       1863       1872

Ile Gln Gly Asn Val Gly Val Ile Leu Ser Pro Val Asn Arg Met Tyr Thr Leu Pro
ATC CAA GGT AAC GTG GGT GTC ATC CTG TCT CCG GTC AAC CGC ATG TAC ACG CTG CCG
      1884       1893       1902       1911       1920       1929

Asn Ala Leu Ala Thr Leu Asp Gly Asn Glu Phe Pro Thr Gly Lys Glu Phe Cys Glu
AAC GCC CTC GCT ACC CTT GAC GGT AAT GAG TTC CCC ACC GGG AAA GAG TTC TGC GAA
      1941       1950       1959       1968       1977       1986

Gly Thr Val Leu Phe Lys Thr Asp Gly Ser Gly Gly Asn Phe Ile Val Thr Arg Phe
GGT ACT GTG CTG TTC AAG ACC GAT GGC TCC GGT GGC AAC TTC ATC GTG ACC CGG TTC
      1998       2007       2016       2025       2034       2043

Gly Ala Tyr Ile Pro Asp Asp Gly Asn Asn Phe Lys Val Arg Ala Ala Ala Ala Gly
GGT GCG TAC ATC CCG GAT GAC GGT AAC AAC TTC AAG GTG CGT GCT GCT GCC GCT GGC
      2055       2064       2073       2082       2091       2100

Gln Thr Tyr Leu Glu Gln Asn Leu Thr Pro Ala Gly Thr Gln Ala Ser Thr Ser Trp
CAG ACG TAT CTG GAG CAG AAC CTG ACT CCG GCT GGT ACT CAG GCT TCC ACC TCG TGG
      2112       2121       2130       2139       2148       2157

Leu Tyr His Lys Pro Ile Ser Ala Gly Thr Arg Leu Asn Val Pro Gly Ala Gly Pro
CTG TAC CAT AAG CCA ATC TCT GCT GGT ACT CGA CTC AAT GTT CCG GGT GCC GGG CCG
      2169       2178       2187       2196       2205       2214

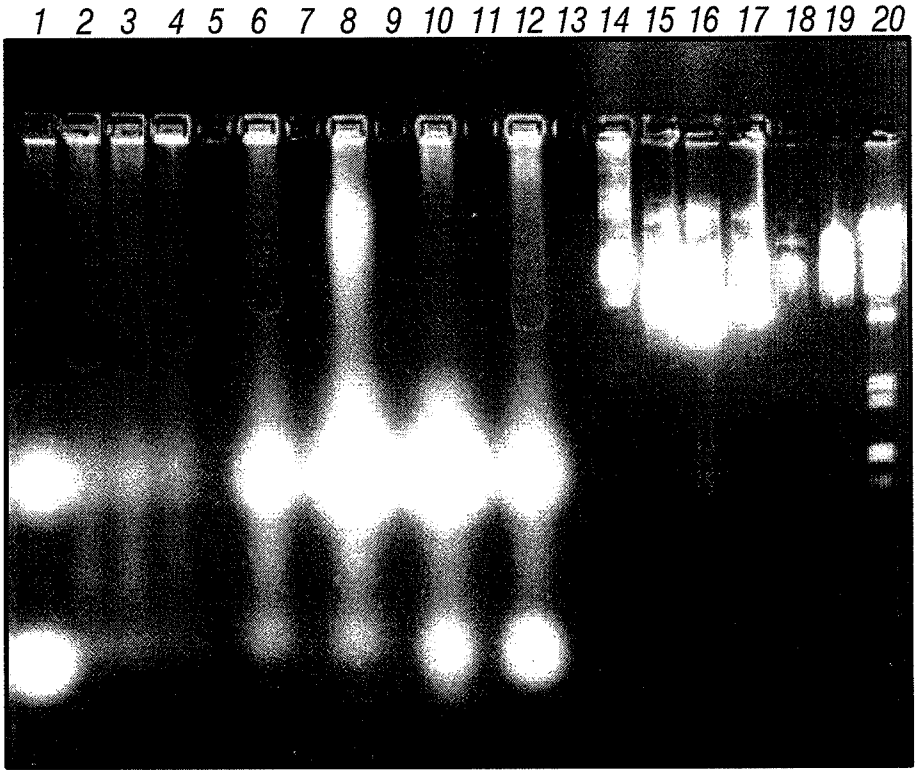
Ser Gly Gly Thr Leu Thr Val Thr Val Val Arg Ala Pro Tyr Gln Val Asp Asn Asn
AGC GGC GGT ACG CTC ACT GTG ACG GTG GTG CGT GCT CCG TAT CAG GTG GAC AAC AAC
      2226       2235       2244       2253       2262       2271

Ile Gly Asn Pro Val Arg Ile Asp Ile Thr Pro Ala Ile Val Thr Ala Ile Pro Ala
ATC GGA AAC CCG GTA CGC ATC GAC ATT ACC CCG GCC ATT GTG ACG GCA ATC CCT GCG
      2283       2292       2301       2310       2319       2328

Gly Thr Gln Leu Ala Ala Thr Tyr Pro Val Ala Try Ile TER
GGA ACG CAG CTC GCC GCT ACC TAC CCG GTG GCT TAC ATC TAA
      2340       2349       2358       2367
```

FIG. 1D

Fig. 2



Lane#	Sample
1	Laboratory Grade plasmid DNA, Prep A labeled with DTAF
2	GMP Grade DNA, Company #2 labeled with DTAF
3	GMP Grade DNA, Company #1 labeled with DTAF
4	Clinical Grade DNA, Company #1 labeled with DTAF
5	No Sample Loaded
6	Qiagen Endotoxin free DNA, Prep A Labeled with DTAF
7	No Sample Loaded
8	Detoxified LPS, Sigma, labeled with DTAF
9	No Sample Loaded
10	LPS, Sigma, labeled with DTAF
11	No Sample Loaded
12	Laboratory Grade plasmid DNA, Prep B labeled with DTAF
13	No Sample Loaded
14	Laboratory Grade plasmid DNA, Prep A labeled with EtBr
15	GMP Grade DNA, Company #2 labeled with EtBr
16	GMP Grade DNA, Company #1 labeled with EtBr
17	Clinical Grade DNA, Company #1 labeled with EtBr
18	Laboratory Grade plasmid DNA, Prep B labeled with EtBr
19	Qiagen Endotoxin free DNA, Prep A Labeled with EtBr
20	Mixture of high and low DNA molecular weight markers labeled with EtBr

Fig. 3

SEQ ID NO: 1 - - CAE Full-length Protein Sequence

MANSYNAYVANGSQTAFLVTFEQRVFTEIQVYLNSELQTEGYTYNSVTKQIIFDTAPLAGVIVRLQRYTSEVLLNKFGQDAAFTGQNLDE
NFEQILFKAEETQEAWLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFL
DRQDTVCLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVA
YWGGEVRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGL
LIENIFLENIDGTNAPIPLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLT
AAGVITYGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYH
LENIHCYKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAI
PYTNIQGNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLT
PAGTQASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 4

SEQ ID NO: 2 - - CAE Truncated Protein Sequence

LAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFLDRQDTVCLSEFTNNT
GYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVAYWGGEVRIADYEFTS
APSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGLLIENIFLENIDGTNAPI
PLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLTAAGVITYGCKRMTID
GVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYHLENIHCYKMTLFGVA
TLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAIPYTNIQGNVGVILSPV
NRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLTPAGTQASTSWLYHKP
ISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 5

SEQ ID NO: 3 - - HIS-Tagged CAE Full-length Protein Sequence

MGHHHHHHMANSYNAYVANGSQTAFLVTFEQRVFTEIQVYLNSELQTEGYTYNSVTKQIIFDTAPLAGVIVRLQRYTSEVLLNKFGQDA
AFTGQNLDENFEQILFKAEETQEAWLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWI
GTLGGGTFLDRQDTVCLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRN
FVASTVRVAYWGGEVRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNV
INKHYDGGLLIENIFLENIDGTNAPIPLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDL
SVSIGTGLTAAGVITYGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSD
DDNTNTYHLENIHCYKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDIST
LNSNVRAIPYTNIQGNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQ
TYLEQNLTPAGTQASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 6

SEQ ID NO: 4 - - HIS-Tagged CAE Truncated Protein Sequence

MGHHHHHHLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFLDRQDTV
CLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVAYWGGE
VRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGLLIENIFL
ENIDGTNAPIPLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLTAAGVIT
YGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYHLENIHC
YKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAIPYTNIQ
GNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLTPAGTQ
ASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYI

Fig. 7

SEQ ID NO: 5 - - FLAG®-Tagged CAE Full-length Protein Sequence

MANSYNAYVANGSQTAFLVTFEQRVFTEIQVYLNSELQTEGYTYNSVTKQIIFDTAPLAGVIVRLQRYTSEVLLNKFGQDAAFTGQNLDE
NFEQILFKAEETQEAWLAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFL
DRQDTVCLSEFTNNTGYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVA
YWGGEVRIADYEFTSAPSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGL
LIENIFLENIDGTNAPIPLSNWGIGIGIAGQGGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLT
AAGVITYGCKRMTIDGVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYH
LENIHCYKMTLFGVATLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAI
PYTNIQGNVGVILSPVNRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLT
PAGTQASTSWLYHKPISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYIDYKDDDDK

Fig. 8

SEQ ID NO: 6 - - FLAG®-Tagged CAE Truncated Protein Sequence

LAPLDRAVRVPNSEVSINALPNVAGRRNKALGFDSNGQPFMIPLVDIPDSALAIALAMADGGKWIGTLGGGTFLDRQDTVCLSEFTNNT
GYASVAAAVQACFDYAKANGKVVDARGWEGTVDSTVLMDGIEVVGGTWHGKADIRLLNSTFRNFVASTVRVAYWGGEVRIADYEFTS
APSNSKVTSILFQGNIAGGSYVIENGIHRNGKFGILQQGTGEAITNGVIRGITMMDMQGDGIEMNVINKHYDGGLLIENIFLENIDGTNAPI
PLSNWGIGIGIAGQGPFGWDAAETQYAKNVTVRNVHAPRGVRQVVHFEVTRDSTCENVVANPDLSVSIGTGLTAAGVITYGCKRMTID
GVVGEPMNTGATSPNDIRIVMLEWGANQAGAGGTPGAACPSFDMTVRNVQTRTGRFYAGVGSDDDNTNTYHLENIHCYKMTLFGVA
TLLNMTNVTGVVFDAVGDDSSGGTSSNGLYPRKKTVLNMVNVNFYGPGMTEGALYSKARYSDISTLNSNVRAIPYTNIQGNVGVILSPV
NRMYTLPNALATLDGNEFPTGKEFCEGTVLFKTDGSGGNFIVTRFGAYIPDDGNNFKVRAAAAGQTYLEQNLTPAGTQASTSWLYHKP
ISAGTRLNVPGAGPSGGTLTVTVVRAPYQVDNNIGNPVRIDITPAIVTAIPAGTQLAATYPVAYIDYKDDDDK

Fig. 9

SEQ ID NO: 7 - - CAE Full-Length DNA Coding Sequence

ATGGCGAACA GCTATAATGC TTACGTGGCG AACGGTTCAC AGACCGCATT CCTCGTCACG TTCGAGCAGC GCGTGTTCAC
TGAGATTCAG GTGTACCTCA ACTCCGAACT CCAGACGGAA GGGTACACCT ACAACTCTGT GACCAAACAG ATTATCTTCG
ACACCGCCCC GCTCGCCGGG GTGATTGTCC GACTCCAACG CTACACCTCT GAGGTTCTGC TGAACAAGTT GGCCAAGAC
GCTGCCTTCA CCGGGCAGAA CCTTGACGAG AACTTTGAGC AGATTCTGTT CAAGGCTGAG GAAACTCAGG AAGCATGGCT
CGCGCCACTT GACCGCGCCG TCCGTGTTCC GAACTCCGAA GTCTCCATCA ACGCATTACC GAACGTCGCT GCCGCCGCA
ACAAGGCACT GGGCTTTGAC AGCAATGGTC AGCCGTTCAT GATTCCTCTG GTCGATATCC CGGACTCCGC GCTGGCGATT
GCTCTGGCAA TGGCTGACGG CGGTAAGTGG ATTGGTACTC TCGGCGGGGG CACGTTCCTC GACCGTCAGG ATACCGTCTG
CCTGTCCGAG TTCACCAACA ACACTGGGTA CGCCTCTGTC GCCGCTGCGG TGCAGGCTTG CTTCGACTAT GCGAAAGCCA
ACGGCAAGGT CGTTGACGCT CGCGGCTGGG AAGGTACGGT GGATTCCACT GTGCTGATGG ACGGTATTGA GGTCGTCGGC
GGTACGTGGC ACGGCAAGGC TGACATTCGC CTGCTGAACT CCACCTTCCG CAACTTCGTG GCCTCTACTG TCCGTGTCGC
CTACTGGGGC GGCGAGGTGC GTATTGCTGA CTATGAGTTC ACCAGCGCAC CGAGCAACTC CAAGGTTACG TCTATCCTGT
TCCAAGGCAA CATCGCCGGG GGCAGCTACG TCATTGAGAA CGGTATCCAC CGCAATGGTA AGTTCGGTAT TCTCCAACAG
GGTACTGGCG AGGCTATCAC CAACGGCGTT ATCCGTGGCA TCACCATGAT GGATATGCAG GGTGACGGTA TCGAGATGAA
CGTAATCAAC AAGCACTATG ATGGTGGCCT GCTGATTGAG AACATCTTCC TTGAGAACAT CGACGGCACC AACGCGCCTA
TCCCACTGTC CAACTGGGGC ATTGGTATCG GTATCGCTGG TCAAGGCCCG TTCGGTTGGG ATGCTGCTGA GACGCAGTAT
GCGAAGAACG TCACTGTCCG TAACGTCCAT GCTCCGCGTG GTGTGCGTCA GGTCGTCCAC TTCGAGGTTA CGCGTGACAG
CACCTGCGAG AACGTAGTGG CCAACCCTGA CCTGTCCGTC TCCATTGGTA CTGGCCTGAC TGCCGCTGGT GTAATCACGT
ACGGCTGCAA GCGCATGACC ATTGACGGTG TAGTCGGTGA GCCTATGAAC ACCGGAGCAA CCTCTCCGAA CGATATTCGT
ATCGTGATGT TGGAGTGGGG TGCGAACCAA GCAGGTGCTG GCGGTACGCC GGGTGCAGCT TGCCCATCGT TCGACATGAC
CGTGCGTAAC GTGCAGACCC GTACCGGGCG CTTCTATGCT GGTGTCGGCT CCGACGATGA CAACACCAAC ACATATCACC
TTGAAAACAT TCACTGTTAC AAGATGACGC TGTTTGGTGT GGCAACTCTG CTGAACATGA CCAACGTGAC TGGTGTGGTG
TTCGACGCTG TAGGCGATGA CTCCAGCGGC GGTACGTCCT CCAACGGTCT GTACCCGCGT AAGAAGACTG TTCTCAACAT
GGTGAACGTG AACTTCTACG GGCCGGGCAT GACCGAGGGT GCGCTGTACA GTAAGGCTCG CTACTCGGAT ATCAGCACGC
TGAACTCCAA CGTGCGTGCT ATCCCGTACA CCAACATCCA AGGTAACGTG GGTGTCATCC TGTCTCCGGT CAACCGCATG
TACACGCTGC CGAACGCCCT CGCTACCCTT GACGGTAATG AGTTCCCCAC CGGGAAAGAG TTCTGCGAAG GTACTGTGCT
GTTCAAGACC GATGGCTCCG GTGGCAACTT CATCGTGACC CGGTTCGGTG CGTACATCCC GGATGACGGT AACAACTTCA
AGGTGCGTGC TGCTGCCGCT GGCCAGACGT ATCTGGAGCA GAACCTGACT CCGGCTGGTA CTCAGGCTTC CACCTCGTGG
CTGTACCATA AGCCAATCTC TGCTGGTACT CGACTCAATG TTCCGGGTGC CGGGCCGAGC GGCGGTACGC TCACTGTGAC
GGTGGTGCGT GCTCCGTATC AGGTGGACAA CAACATCGGA AACCCGGTAC GCATCGACAT TACCCCGGCC ATTGTGACGG
CAATCCCTGC GGGAACGCAG CTCGCCGCTA CCTACCCGGT GGCTTACATC TAA

Fig. 10

SEQ ID NO: 8 - - CAE Truncated DNA Coding Sequence

CTCGCGCCAC TTGACCGCGC CGTCCGTGTT CCGAACTCCG AAGTCTCCAT CAACGCATTA CCGAACGTCG CTGGCCGCCG
CAACAAGGCA CTGGGCTTTG ACAGCAATGG TCAGCCGTTC ATGATTCCTC TGGTCGATAT CCCGGACTCC GCGCTGGCGA
TTGCTCTGGC AATGGCTGAC GGCGGTAAGT GGATTGGTAC TCTCGGCGGG GGCACGTTCC TCGACCGTCA GGATACCGTC
TGCCTGTCCG AGTTCACCAA CAACACTGGG TACGCCTCTG TCGCCGCTGC GGTGCAGGCT TGCTTCGACT ATGCGAAAGC
CAACGGCAAG GTCGTTGACG CTCGCGGCTG GGAAGGTACG GTGGATTCCA CTGTGCTGAT GGACGGTATT GAGGTCGTCG
GCGGTACGTG GCACGGCAAG GCTGACATTC GCCTGCTGAA CTCCACCTTC CGCAACTTCG TGGCCTCTAC TGTCCGTGTC
GCCTACTGGG GCGGCGAGGT GCGTATTGCT GACTATGAGT TCACCAGCGC ACCGAGCAAC TCCAAGGTTA CGTCTATCCT
GTTCCAAGGC AACATCGCCG GGGGCAGCTA CGTCATTGAG AACGGTATCC ACCGCAATGG TAAGTTCGGT ATTCTCCAAC
AGGGTACTGG CGAGGCTATC ACCAACGGCG TTATCCGTGG CATCACCATG ATGGATATGC AGGGTGACGG TATCGAGATG
AACGTAATCA ACAAGCACTA TGATGGTGGC CTGCTGATTG AGAACATCTT CCTTGAGAAC ATCGACGGCA CCAACGCGCC
TATCCCACTG TCCAACTGGG GCATTGGTAT CGGTATCGCT GGTCAAGGCC CGTTCGGTTG GGATGCTGCT GAGACGCAGT
ATGCGAAGAA CGTCACTGTC CGTAACGTCC ATGCTCCGCG TGGTGTGCGT CAGGTCGTCC ACTTCGAGGT TACGCGTGAC
AGCACCTGCG AGAACGTAGT GGCCAACCCT GACCTGTCCG TCTCCATTGG TACTGGCCTG ACTGCCGCTG GTGTAATCAC
GTACGGCTGC AAGCGCATGA CCATTGACGG TGTAGTCGGT GAGCCTATGA ACACCGGAGC AACCTCTCCG AACGATATTC
GTATCGTGAT GTTGGAGTGG GGTGCGAACC AAGCAGGTGC TGGCGGTACG CCGGGTGCAG CTTGCCCATC GTTCGACATG
ACCGTGCGTA ACGTGCAGAC CCGTACCGGG CGCTTCTATG CTGGTGTCGG CTCCGACGAT GACAACACCA ACACATATCA
CCTTGAAAAC ATTCACTGTT ACAAGATGAC GCTGTTTGGT GTGGCAACTC TGCTGAACAT GACCAACGTG ACTGGTGTGG
TGTTCGACGC TGTAGGCGAT GACTCCAGCG GCGGTACGTC CTCCAACGGT CTGTACCCGC GTAAGAAGAC TGTTCTCAAC
ATGGTGAACG TGAACTTCTA CGGGCCGGGC ATGACCGAGG GTGCGCTGTA CAGTAAGGCT CGCTACTCGG ATATCAGCAC
GCTGAACTCC AACGTGCGTG CTATCCCGTA CACCAACATC CAAGGTAACG TGGGTGTCAT CCTGTCTCCG GTCAACCGCA
TGTACACGCT GCCGAACGCC CTCGCTACCC TTGACGGTAA TGAGTTCCCC ACCGGGAAAG AGTTCTGCGA AGGTACTGTG
CTGTTCAAGA CCGATGGCTC CGGTGGCAAC TTCATCGTGA CCCGGTTCGG TGCGTACATC CCGGATGACG GTAACAACTT
CAAGGTGCGT GCTGCTGCCG CTGGCCAGAC GTATCTGGAG CAGAACCTGA CTCCGGCTGG TACTCAGGCT TCCACCTCGT
GGCTGTACCA TAAGCCAATC TCTGCTGGTA CTCGACTCAA TGTTCCGGGT GCCGGGCCGA GCGGCGGTAC GCTCACTGTG
ACGGTGGTGC GTGCTCCGTA TCAGGTGGAC AACAACATCG GAAACCCGGT ACGCATCGAC ATTACCCCGG CCATTGTGAC
GGCAATCCCT GCGGGAACGC AGCTCGCCGC TACCTACCCG GTGGCTTACA TCTAA

Fig. 11

SEQ ID NO: 9 - - CAE Fragment

ANSYNAYVANGSQTA

SEQ ID NO: 10 - - CAE Fragment

LLEQGTGEALTDGVLR

SEQ ID NO: 11 - - CAE Fragment

VPNSEVSLNALPNVQR

SEQ ID NO: 12 - - CAE Fragment

LADYEFTSAPSNSK

SEQ ID NO: 13 - - CAE Fragment

YSDLSTLN

SEQ ID NO: 14 - - CAE Fragment

QLLFDTAPLA

SEQ ID NO: 15 - - CAE Fragment

APYQVDDNL

SEQ ID NO: 16 - - CAE Fragment

FGAYLPDD

SEQ ID NO: 17 - - CAE Fragment

LGTLGG

Fig. 12

TOXICITY MEASUREMENTS *

DNA Type	DNA Amount	# of Mice Injected	# of Dead Mice at 18 hours Post-Injection	# of Dead Mice at 1 Week Post-Injection
Super Clean	100 µg	10	0	0
Super Clean	50 µg	10	0	0
Qiagen EndoFree	100 µg	10	10	N/A
Qiagen EndoFree	50 µg	10	0	0

* Experiments performed in Balb/c mice using PDX-1 shRNA Super Clean DNA versus PDX-1 shRNA Qiagen EndoFree DNA

Fig. 13

TOXICITY MEASUREMENTS *

DNA Type	DNA Amount	# of Mice Injected	# of Dead Mice at 18 hours Post-Injection	# of Dead Mice at 3 Weeks Post-Injection
Super Clean	100 µg	20	0	0
Super Clean	40 µg	20	0	0
Qiagen EndoFree	100 µg	5	5	N/A
Qiagen EndoFree	40 µg	5	5	N/A

* Experiments performed in SCID mice using the CAE enzyme method for Super Clean DNA production

Fig. 14

TOXICITY MEASUREMENTS *

DNA Type	DNA Amount	# of Mice Injected	# of Dead Mice at 18 hours Post-Injection	# of Dead Mice at 3 Weeks Post-Injection
Super Clean	100 µg	60	0	0
Qiagen EndoFree	100 µg	5	5	N/A

* Experiments performed in PANC-1 tumor-bearing SCID mice using the CAE enzyme method for Super Clean DNA production