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(54) **Title:** PHARMACEUTICAL FOR TREATING AND/OR PREVENTING CANCER

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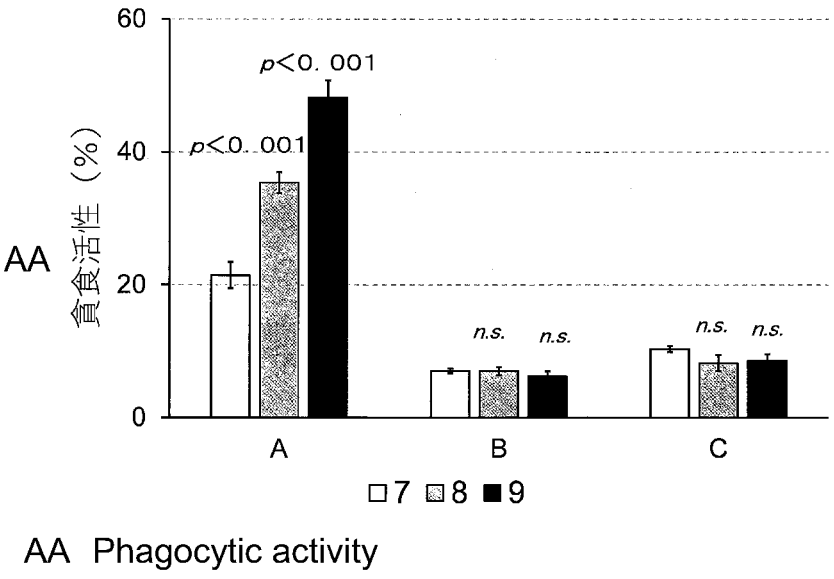
【図5】



AA Phagocytic activity

(57) **Abstract:** This pharmaceutical containing, collectively or separately as a combination, an antibody having immunological reactivity with respect to CAPRIN-1 protein or a fragment of said antibody, and an epidermal growth factor receptor (EGFR) inhibitor, is useful for treating and/or preventing cancer.

(57) 要約：ＣＡＰＲＩＮ－１タンパク質と免疫学的反応性を有する抗体又はそのフラグメントと、ＥＧＦＲ（上皮成長因子受容体）阻害剤とを、一緒に又は別々に組み合わせて含む医薬品は、癌の治療及び／又は予防に有用である。

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Description

Title of Invention: MEDICAMENT FOR TREATMENT AND/OR PREVENTION OF CANCER

Technical Field

[0001]

The present invention relates to a medicament for treatment and/or prevention of a cancer, comprising an antibody against CAPRIN-1 protein, or a fragment thereof, and an EGFR inhibitor.

Background Art

[0002]

Various antibody medicines targeting specific antigen proteins on cancer cells are applied as therapeutic agents for cancers with fewer side effects to cancer treatment because of their cancer specificity. For example, cytoplasmic-activation and proliferation-associated protein 1 (CAPRIN-1) is expressed on cell membrane surfaces of many solid cancers. Antibodies against this CAPRIN-1 protein are known to be promising in pharmaceutical uses for treatment and/or prevention of cancers (Patent Literature 1).

[0003]

In clinical practices, treatment methods using combinations of pluralities of therapeutic agents for cancer have been used as standard treatment methods in order to enhance the effectiveness of the therapeutic agents for cancers. In general, for example, breast cancer is treated by a treatment method using a combination of doxorubicin and cyclophosphamide or using a combination of a plurality of anticancer agents such as paclitaxel, trastuzumab, and pertuzumab. Therapeutic agents for cancers comprising anti-CAPRIN-1 antibodies as active ingredients have also been confirmed to have therapeutic effects on the cancers by combinations with chemotherapeutics (Patent Literature 2). However, the treatment of cancer by a combination of chemotherapeutics is not effective for every cancer to which the treatment is

applied, and few combinations of chemotherapeutics synergistically drastically enhance therapeutic effects, though some combinations additively enhance therapeutic effects.

[0004]

In addition, in recent years, development of molecular targeted therapeutics as cancer therapeutics has been vigorously promoted, and one of its targets that has attracted attention is epidermal growth factor receptor (EGFR). EGFR is a receptor-type tyrosine kinase belonging to the ERBB family and also referred to as HER1 or ErbB1. EGFR is a transmembrane glycoprotein receptor composed of three main domains: an extracellular ligand binding domain, a transmembrane domain, and an intracellular tyrosine kinase domain. EGFR is dimerized by binding of a ligand such as epidermal growth factor (EGF), transforming growth factor (TGF)-α, amphiregulin, or heparin-binding EGF-like growth factor (HB-EGF) to the EGFR ligand binding domain, and is activated by mutual phosphorylation between the two molecules (autophosphorylation) in the cytoplasmic domain. Activated EGFR is involved in the control of cell proliferation, migration, angiogenesis, metabolism and differentiation by recruiting GRB2 and SOS1 to the cell membrane and activating the downstream MAPK and PI3K/Akt/mTOR signaling pathways via RAS activation. In malignant cancer cells, EGFR is constantly activated. EGFR inhibitors exert a cancer therapeutic effect by inhibiting signaling by EGFR dimerization inhibition, ligand neutralization, ligand binding inhibition, or internalization of EGFR. However, while some malignant tumors have been affected by a breakthrough therapeutic effect with the advent of EGFR inhibitors, the acquisition of resistance to molecular targeted therapeutic drugs due to secondary mutations in EGFR and crosstalk has become a new issue, and it is necessary to develop a combination therapy to eradicate cancers (Non Patent Literatures 1 and 2).

Citation List

Patent Literature

[0005]

Patent Literature 1: WO2010/016526

Patent Literature 2: WO2011/096535

Non Patent Literature

[0006]

Non Patent Literature 1: N Engl J Med. 2005, 352(8):786-92

Non Patent Literature 2: Sci Signal. 2013, 6(294):re6

Summary of Invention

Object to be Achieved

[0007]

An object of the present invention is to provide a medicament for treatment and/or prevention of a cancer specifically expressing CAPRIN-1 protein on a cell surface.

Solution to Achieve Object

[0008]

As a result of intensive studies, the present inventors have found that a combination (combined use) of an antibody against CAPRIN-1 protein, or a fragment thereof, having an immunological reactivity with cancer cells, and an EGFR inhibitor exerts a very strong antitumor effect. On the basis of these findings, the present invention has been completed.

[0009]

Specifically, the present invention relates to the following embodiments (1) to (14):

[0010]

(1) A medicament for treatment and/or prevention of cancer, comprising an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein, and an EGFR (epidermal growth factor receptor) inhibitor together or separately in combination.

[0011]

(2) The medicament according to (1), wherein the EGFR inhibitor is Erlotinib, Zipalertinib, or PD 168393.

[0012]

(3) The medicament according to (1) or (2), wherein the antibody or the fragment thereof has an immunological reactivity with CAPRIN-1 protein having an amino acid sequence shown

by any one of the even numbered SEQ ID NOs: 2 to 30, or an amino acid sequence having 80% or more sequence identity with the amino acid sequence.

[0013]

(4) The medicament according to any of (1) to (3), wherein the antibody or the fragment thereof has an immunological reactivity with an extracellular region of CAPRIN-1 protein present on a cancer cell surface.

[0014]

(5) The medicament according to any of (1) to (4), wherein the antibody or the fragment thereof has an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having an amino acid sequence shown by any one of SEQ ID NOs: 31 to 35, 296 to 299, 308 and 309, or an amino acid sequence having 80% or more sequence identity with the amino acid sequence.

[0015]

(6) The medicament according to any of (1) to (5), wherein the antibody is a monoclonal antibody or a polyclonal antibody.

[0016]

(7) The medicament according to any of (1) to (6), wherein the antibody or the fragment thereof is any one of the following (A) to (M):

(A) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 36, 37 and 38 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 40, 41 and 42 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(B) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 44, 45 and 46 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 48, 49 and 50 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(C) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 52, 53 and 54 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 56, 57 and 58 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(D) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 60, 61 and 62 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 64, 65 and 66 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(E) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 170, 171 and 172 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 173, 174 and 175 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(F) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 176, 177 and 178 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 179, 180 and 181 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(G) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 182, 183 and 184 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 185, 186 and 187 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(H) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 188, 189 and 190 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining

regions of SEQ ID NOs: 191, 192 and 193 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(I) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 146, 147 and 148 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 149, 150 and 151 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(J) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 272, 273 and 274 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 275, 276 and 277 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(K) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 290, 291 and 292 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 293, 294 and 295 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(L) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 301, 302 and 303 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 305, 306 and 307 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein; and

(M) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 134, 135 and 136 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 137, 138 and 139 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein.

[0017]

(8) The medicament according to any of (1) to (7), wherein the antibody or the fragment thereof is any one of the following (a) to (al):

(a) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 39 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 43;

(b) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 47 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 51;

(c) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 55 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 59;

(d) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 63 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 67;

(e) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 68 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 69;

(f) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 70 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 71;

(g) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 72 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 73;

(h) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 74 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 75;

(i) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 76 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 77;

(j) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 78 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 79;

(k) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 80 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 81;

(l) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 82 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 83;

(m) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 84 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 85;

(n) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 86 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 87;

(o) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 88 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 89;

(p) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 90 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 91;

(q) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 92 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 93;

(r) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 94 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 95;

(s) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 96 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 97;

(t) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 98 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 99;

(u) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 100 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 101;

(v) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 102 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 103;

(w) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 104 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 105;

(x) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 106 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 107;

(y) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 108 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 109;

(z) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 110 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 111;

(aa) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 112 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 113;

(ab) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 114 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 115;

(ac) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 116 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 117;

(ad) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 118 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 119;

(ae) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 120 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 121;

(af) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 122 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 123;

(ag) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 124 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 125;

(ah) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 126 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 127;

(ai) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 128 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 129;

(aj) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 130 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 131;

(ak) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 132 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 133; and

(al) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 300 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 304.

[0018]

(9) The medicament according to any of (1) to (8), wherein the antibody is a human antibody, a humanized antibody, a chimeric antibody or a single chain antibody.

[0019]

(10) The medicament according to any of (1) to (9), wherein the cancer is a cancer expressing CAPRIN-1 protein on a cell membrane surface.

[0020]

(11) The medicament according to any of (1) to (10), wherein the cancer is colon cancer, lung cancer, prostate cancer, ovarian cancer, pancreatic cancer, kidney cancer, breast cancer, gastric cancer, bile duct cancer, thyroid cancer, melanoma, renal cell cancer, Hodgkin's lymphoma, head and neck cancer, mesothelioma, colorectal cancer, esophageal cancer, gastroesophageal junction cancer, hepatocellular cancer, glioblastoma, urothelial cancer, urinary bladder cancer, uterus cancer, primary central nervous system lymphoma, primary testicular lymphoma, biliary tract cancer, brain tumor, leukemia, liver cancer, sarcoma, fibrosarcoma, mastocytoma, adrenal cortex cancer, Ewing's tumor, testicle cancer, basal cell cancer, lymphoma, multiple myeloma, Paget's disease or skin cancer.

[0021]

(12) An agent increasing drug efficacy of a pharmaceutical composition for treatment and/or prevention of cancer comprising an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein as an active ingredient, wherein the agent comprises an EGFR inhibitor as an active ingredient.

[0022]

(13) An agent increasing drug efficacy of a pharmaceutical composition for treatment and/or prevention of cancer comprising an EGFR inhibitor as an active ingredient, wherein the agent comprises an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein as an active ingredient.

[0023]

(14) A method for treating and/or preventing cancer, comprising administering an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein, and an EGFR inhibitor together or separately to a subject.

Advantageous Effects of Invention

[0024]

The combination of an antibody against CAPRIN-1 protein or a fragment thereof and an EGFR inhibitor according to the present invention exerts a stronger antitumor effect than that of the antibody against CAPRIN-1 protein alone or an existing chemotherapeutic alone. In particular, although the signaling system targeted by the EGFR inhibitor is not directly related to the immune system, the present invention has the effect of increasing the phagocytic activity against cancer cells by immunocytes. Thus, the combination of the antibody or a fragment thereof against CAPRIN-1 protein and the EGFR inhibitor is effective for the treatment or prevention of cancers.

Brief Description of Drawings

[0025]

[Figure 1] Figure 1 is a diagram showing human monocytic cell (THP-1)-mediated phagocytic activity of a combination of an anti-CAPRIN-1 antibody and PD 168393 or erlotinib against a human colon cancer cell line (HCT116). Reference number 1: a test group without a drug used in combination. Reference number 2; PD 168393 combination test group (10 μM), Reference number 3; erlotinib combination test group (50 μM). The graph shows an average value of data obtained at N = 3 per sample. Error bars depict standard deviation (S.D.). As a result of conducting Student's t test, the phagocytic activity of each drug combination test group was

significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%).

[Figure 2] Figure 2 is a diagram showing human monocytic cell (THP-1)-mediated phagocytic activity of a combination of an anti-CAPRIN-1 antibody and zipalertinib (TAS6417) against a human colon cancer cell line (HCT116). Reference number 1: a test group without a drug used in combination. Reference number 2; zipalertinib (TAS6417) combination test group (20 μM), Reference number 3; zipalertinib (TAS6417) combination test group (40 μM). The graph shows an average value of data obtained at N = 3 per sample. Error bars depict standard deviation (S.D.). As a result of conducting Student's t test, the phagocytic activity of each drug combination test group was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%).

[Figure 3] Figure 3 is a diagram showing human monocytic cell (THP-1)-mediated phagocytic activity of a combination of an anti-CAPRIN-1 antibody and PD 168393 or erlotinib against a human colon cancer cell line (HCT116). Reference number 1: a test group without a drug used in combination. Reference number 2; PD 168393 combination test group (10 μM), Reference number 3; erlotinib combination test group (50 μM). Reference number A; control IgG antibody treatment group; Reference number B; anti-CAPRIN-1 antibody treatment group. The graph shows an average value of data obtained at N = 3 per sample. Error bars depict standard deviation (S.D.). As a result of conducting Dunnett's test, the phagocytic activity of each drug combination test group was significantly higher than that of the test group without a drug used in combination, in the anti-CAPRIN-1 antibody treatment group ($p < 0.001$, respectively; significance level: 5%).

[Figure 4] Figure 4 is a diagram showing human monocytic cell (THP-1)-mediated phagocytic activity of a combination of an anti-CAPRIN-1 antibody and zipalertinib (TAS6417) against a human colon cancer cell line (HCT116). Reference number 1: a test group without a drug used in combination. Reference number 2; zipalertinib (TAS6417) combination test group (20 μM), Reference number 3; zipalertinib (TAS6417) combination test group (40 μM). Reference number A; control IgG antibody treatment group; Reference number B; anti-CAPRIN-1 antibody treatment group. The graph shows an average value of data obtained at N = 3 per

sample. Error bars depict standard deviation (S.D.). As a result of conducting Dunnett's test, the phagocytic activity of each drug combination test group was significantly higher than that of the test group without a drug used in combination, in the anti-CAPRIN-1 antibody treatment group ($p < 0.001$, respectively; significance level: 5%).

[Figure 5] Figure 5 is a diagram showing human monocytic cell (THP-1)-mediated phagocytic activity of anti-CAPRIN-1 antibody, anti-CD20 antibody or anti-HER-2 antibody each alone, or a combination of each of these antibodies and PD 168393 or zipalertinib (TAS6417), against a human colon cancer cell line (HCT116). Reference number 7: a test group without a drug used in combination. Reference number 8; PD 168393 combination test group (10 μM), Reference number 9; zipalertinib (TAS6417) combination test group (40 μM). A; anti-CAPRIN-1 antibody test group (1 μM), B; anti-CD20 antibody test group (1 μM), C; anti-HER-2 antibody test group (1 μM). The graph shows an average value of data obtained at N = 3 per sample. Error bars depict standard deviation (S.D.). As a result of conducting Dunnett's test, the phagocytic activity of each drug combination test group was significantly higher than that of the test group without a drug used in combination, in the anti-CAPRIN-1 antibody test group ($p < 0.001$, respectively; significance level: 5%). In the anti-CD20 antibody or anti-HER-2 antibody test group, there was no significant change in the phagocytic activity of each drug combination test group compared to the test group without a drug used in combination. n.s.; Not Significant.

[Figure 6] Figure 6 is a diagram showing human monocytic cell (THP-1)-mediated phagocytic activity of an anti-CAPRIN-1 antibody alone, or a combination of the anti-CAPRIN-1 antibody and PD 168393, zipalertinib (TAS6417) or cisplatin, against a human colon cancer cell line (HCT116). Reference number 10: a test group without a drug used in combination. Reference number 11; PD 168393 combination test group (10 μM), Reference number 12; zipalertinib (TAS6417) combination test group (40 μM), Reference number 13; cisplatin combination test group (1 μM). The graph shows an average value of data obtained at N = 3 per sample. Error bars depict standard deviation (S.D.). Statistical test; Dunnett's test, $p < 0.001$, significance level 5%. n.s.; Not Significant.

Description of Embodiments

[0026]

The antitumor effect of the combination of an antibody against CAPRIN-1 protein or a fragment thereof (hereinafter, referred to as an "anti-CAPRIN-1 antibody") and an EGFR inhibitor, used in the present invention is preferably evaluated by examining *in vitro* the phagocytic activity against cancer cells by immunocytes in coculturing the cancer cells and the immunocytes as mentioned later. The immunocyte used in evaluating the antitumor effect *in vitro* may be any cell as long as the immunocyte is a blood cell having phagocytic activity, and preferably, is a human monocytic cell (THP-1 or U937). When an antibody binds to a cancer cell, this is recognized by an immunocyte so that the cancer cell is killed via phagocytic activity by the immunocytes. Therefore, an *in vivo* antitumor effect can be predicted by evaluating the *in vitro* antitumor effect.

[0027]

The term "combination" (or "combined use") described herein refers to simultaneous administration or addition, or administration or addition in a predetermined interval of the anti-CAPRIN-1 antibody and the EGFR inhibitor as independent active ingredients to the same organism or cell. The interval may be simultaneous administration or may be 30 minutes later, 1 hour later, 3 hours later, 6 hours later, 12 hours later, 1 day later, 2 days later, 3 days later, 5 days later, 7 days later, 2 weeks later, 3 weeks later, or 4 weeks later. During one of the anti-CAPRIN-1 antibody or the EGFR inhibitor exhibits its antitumor effect, the other can be administered or added.

[0028]

The term "comprising together or separately in combination" described herein refers to comprising a plurality of drugs in a form that allows the drugs to be administered simultaneously or separately to a patient. The form may be, for example, the form of a so-called mixed formulation in which a plurality of drugs are mixed, or may be the form of a so-called kit formulation (pharmaceutical kit) comprising a plurality of drugs as individual formulations. The form also encompasses the form of a kit formulation comprising a plurality of drugs in any combination in two or more of formulations.

[0029]

Such a kit formulation according to the present invention may be, for example, a kit formulation comprising: a formulation (or a pharmaceutical composition) comprising the anti-CAPRIN-1 antibody and a formulation (or a pharmaceutical composition) comprising the EGFR inhibitor.

[0030]

The anti-CAPRIN-1 antibody according to the present invention may be a monoclonal antibody or a polyclonal antibody and is preferably a monoclonal antibody. The antibody of the present invention may be any type of antibody as long as it can exhibit antitumor effect. The antibody is a recombinant antibody, a human antibody, a humanized antibody, a chimeric antibody, or a non-human animal antibody.

[0031]

Subjects being subjected to treatment and/or prevention of cancer according to the present invention are mammals such as primates, pet animals, livestock animals, or sport animals and preferably dogs and cats, and more preferably humans.

[0032]

Medicaments comprising an anti-CAPRIN-1 antibody and an EGFR inhibitor as active ingredients, and methods for treating and/or preventing cancers, related to the present invention, will be explained below.

[0033]

<Anti-CAPRIN-1 antibody>

Among CAPRIN-1 proteins having an amino acid sequence shown by any one of the even numbered SEQ ID NOs: 2 to 30, which are specific examples of antigens having an immunological reactivity with the anti-CAPRIN-1 antibody used in the present invention, the amino acid sequences shown by SEQ ID NOs: 6, 8, 10, 12 and 14 are amino acid sequences of canine CAPRIN-1 proteins; the amino acid sequences shown by SEQ ID NOs: 2 and 4 are amino acid sequences of human CAPRIN-1 proteins; the amino acid sequence shown by SEQ ID NO: 16 is an amino acid sequence of a bovine CAPRIN-1 protein; the amino acid sequence shown by SEQ ID NO: 18 is an amino acid sequence of a horse CAPRIN-1 protein; the amino acid

sequences shown by SEQ ID NOs: 20, 22, 24, 26 and 28 are amino acid sequences of mouse CAPRIN-1 proteins; and the amino acid sequence shown by SEQ ID NO: 30 is an amino acid sequence of a chicken CAPRIN-1 protein.

[0034]

The anti-CAPRIN-1 antibody used in the present invention may have an immunological reactivity with a CAPRIN-1 protein variant having 80% or more, preferably 90% or more, more preferably 95% or more, and further preferably 99% or more sequence identity to the amino acid sequence shown by any one of the even numbered SEQ ID NOs: 2 to 30. The term "% sequence identity" as used herein means a percentage (%) of the number of identical amino acids (or nucleotides) to the total number of amino acids (or nucleotides) in the case that two sequences are aligned such that maximum similarity can be achieved with or without introduction of gaps.

[0035]

In the present invention, the anti-CAPRIN-1 antibody refers to an antibody or a fragment (antigen binding fragment) thereof having an immunological reactivity with a full-length CAPRIN-1 protein or a fragment thereof. The term "immunological reactivity" used herein indicates the characteristics of an antibody specifically binding *in vivo* to CAPRIN-1 protein or a partial polypeptide thereof.

[0036]

The anti-CAPRIN-1 antibody used in the present invention may be a monoclonal antibody or a polyclonal antibody.

[0037]

Polyclonal antibodies having an immunological reactivity with a full-length CAPRIN-1 protein or a fragment thereof (anti-CAPRIN-1 polyclonal antibodies) can be obtained, for example, in a manner described below. Serum is obtained after mice, human antibody-producing mice, rats, rabbits, chickens, or the like are immunized using a naturally occurring CAPRIN-1 protein or the protein fused with GST or the like, or a partial peptide thereof. The obtained serum is purified via ammonium sulfate precipitation, protein A, protein G, DEAE ion-

exchange columns, affinity columns to which a CAPRIN-1 protein or a partial peptide thereof is coupled, or the like.

[0038]

Nucleotide sequences and amino acid sequences of CAPRIN-1 and homologs thereof used in the immunization can be obtained by, for example, accessing the website of GenBank (NCBI, USA) and using the BLAST or FASTA algorithm (Karlin and Altschul, Proc. Natl. Acad. Sci. USA, 90: 5873-5877, 1993; and Altschul et al., Nucleic Acids Res. 25: 3389-3402, 1997). Methods for producing CAPRIN-1 protein can be obtained with reference to WO2014/012479 or may employ cells or the like expressing CAPRIN-1 protein.

[0039]

Monoclonal antibodies having an immunological reactivity with a full-length CAPRIN-1 protein or a fragment thereof (anti-CAPRIN-1 monoclonal antibodies) can be obtained, for example, in a manner described below. Breast cancer cells SK-BR-3 expressing CAPRIN-1, a full-length CAPRIN-1 protein or a fragment thereof, or the like is administered to mice for immunization. Splenocytes separated from the mice are fused with myeloma cells. Clones capable of producing anti-CAPRIN-1 monoclonal antibodies can be selected from the obtained fusion cells (hybridomas) to obtain these antibodies. The antibodies produced from the selected hybridomas can be obtained in the same way as the aforementioned method for purifying polyclonal antibodies.

[0040]

The antibody used in the present invention includes human antibodies, humanized antibodies, chimeric antibodies, non-human animal antibodies and single chain antibodies.

[0041]

For human antibodies, human lymphocytes infected with EB virus are sensitized with a protein, protein-expressing cells, or a lysate thereof. The sensitized lymphocytes are fused with human-derived myeloma cells such as U266 cells. Antibodies having an immunological reactivity with a full-length CAPRIN-1 protein or a fragment thereof can be obtained from the obtained fusion cells.

[0042]

A humanized antibody is a modified antibody, and it is sometimes referred to as a reshaped human antibody. It is known that a humanized antibody is constructed by transplanting complementarity determining regions of an immunized animal-derived antibody into complementarity determining regions of a human antibody. In addition, a general gene recombinant technique therefor is well known. Specifically, a DNA sequence designed in a manner that allows complementarity determining regions of mouse or rabbit antibody to be ligated to human antibody framework regions is synthesized by the PCR method using several oligonucleotides prepared in such a manner that the oligonucleotides have portions overlapping each other at an end of each thereof. A humanized antibody can be obtained by ligating the above obtained DNA to DNA encoding a human antibody constant region, incorporating the resultant into an expression vector, and introducing the vector into a host for antibody production (see EP-A-239400 and WO96/02576). Framework regions of human antibody ligated to each other via complementarity determining regions are selected on the assumption that complementarity determining regions can form a good antigen binding site. If necessary, amino acids in framework regions of an antibody variable region may be substituted in such a manner that complementarity determining regions in a reshaped human antibody form an appropriate antigen binding site (Sato K. et al., Cancer Research 1993, 53:851-856). In addition, the framework regions may be substituted with framework regions from a different human antibody (see WO99/51743).

[0043]

In general, antibodies are heteromultimeric glycoproteins each comprising at least two heavy chains and two light chains. Antibodies each comprise two identical light chains and two identical heavy chains. Each heavy chain has a heavy-chain variable region at one end thereof, to which some constant regions are bound in series. Each light chain has a light-chain variable region at one end thereof to which some constant regions are bound in series. Variable regions have specific variable regions, which are called complementarity determining regions (CDRs) and impart binding specificity to an antibody. A relatively conserved portion in a variable region is called a framework region (FR). A complete heavy-chain or light-chain variable region comprises 4 FRs connected to each other via 3 CDRs (CDR1 to CDR3).

[0044]

Sequences of human-derived heavy-chain and light-chain constant regions and variable regions can be obtained from, for example, NCBI (USA; GenBank, UniGene, etc.). For example, for a human IgG1 heavy-chain constant region, see registration No. J00228; for a human IgG2 heavy-chain constant region, see registration No. J00230; for a human light chain κ constant region, see sequences such as registration Nos. V00557, X64135, and X64133; and for a human light chain λ constant region, see sequences such as registration Nos. X64132 and X64134.

[0045]

A chimeric antibody is an antibody produced by combining sequences from different animals. An example thereof is an antibody consisting of mouse antibody heavy-chain and light-chain variable regions and human antibody heavy-chain and light-chain constant regions. Such a chimeric antibody can be produced by a known method. For example, it can be obtained by ligating DNA encoding an antibody V region to DNA encoding a human antibody C region, incorporating the resultant into an expression vector, and introducing the vector into a host for antibody production.

[0046]

Non-human animal antibodies are obtained by immunizing non-human animals with sensitizing antigens according to a known method or by intraperitoneally, intracutaneously, or subcutaneously injecting sensitizing antigens into animals such as mice as a general method. For injecting sensitizing antigens, an appropriate amount of various adjuvants including CFA (Freund's complete adjuvant) is mixed therewith and the mixture is administered to animals several times. After immunization of animals and confirmation of an anti-CAPRIN-1 antibody contained in serum, the serum is obtained and the non-human animal antibody can be obtained by purification via ammonium sulfate precipitation, protein A, protein G, DEAE ion-exchange columns, affinity columns to which a CAPRIN-1 protein or a partial peptide thereof is coupled, or the like, as mentioned above. In the case of obtaining monoclonal antibodies from non-human animals, a monoclonal antibody is obtained by collecting immunocytes from the immunized animals and subjecting them to cell fusion with myeloma cells. The cell fusion of

immunocytes with myeloma cells can be carried out according to a known method (see Kohler, G. and Milstein, C. Methods Enzymol. (1981) 73, 3-46).

[0047]

The antibody used in the present invention can also be obtained as a gene recombinant antibody produced by cloning an antibody gene from a hybridoma, incorporating the clone into an adequate vector, introducing the vector into a host, and producing the antibody by using a gene recombinant technique (see Carl, A.K. Borrebaeck, James, W. Larrick, THERAPEUTIC MONOCLONAL ANTIBODIES, Published in the United Kingdom by MACMILLAN PUBLISHERS LTD, 1990).

[0048]

Amino acids in a variable region (e.g., FR) or a constant region in the anti-CAPRIN-1 antibody used in the present invention may be substituted with different amino acids. The amino acid substitution is a substitution of 1 or more, for example, less than 15, less than 10, not more than 8, not more than 6, not more than 5, not more than 4, not more than 3, or not more than 2 amino acids, preferably 1 to 9 amino acids. A substituted antibody should have characteristics of specifically binding to the antigen and binding affinity for the antigen equivalent to or more than those of an unsubstituted antibody and should be an antibody that causes no rejection when applied to humans. The amino acid substitution is preferably a conservative amino acid substitution, which is a substitution between amino acids having similar characteristics in terms of charge, side chains, polarity, aromaticity, and the like. For example, characteristically similar amino acids can be classified into the following types: basic amino acids (arginine, lysine, and histidine); acidic amino acids (aspartic acid and glutamic acid); uncharged polar amino acids (glycine, asparagine, glutamine, serine, threonine, cysteine, and tyrosine); nonpolar amino acids (leucine, isoleucine, alanine, valine, proline, phenylalanine, tryptophan, and methionine); branched-chain amino acids (threonine, valine, isoleucine); and aromatic amino acids (phenylalanine, tyrosine, tryptophan, and histidine).

[0049]

The anti-CAPRIN-1 antibody used in the present invention is expected to have a stronger antitumor effect when having higher binding affinity for CAPRIN-1 protein on cancer cell

surfaces. Association constant (affinity constant) Ka (kon/koff) is preferably at least 10^7 M^{-1}, at least 10^8 M^{-1}, at least 5×10^8 M^{-1}, at least 10^9 M^{-1}, at least 5×10^9 M^{-1}, at least 10^{10} M^{-1}, at least 5×10^{10} M^{-1}, at least 10^{11} M^{-1}, at least 5×10^{11} M^{-1}, at least 10^{12} M^{-1}, or at least 10^{13} M^{-1}.

[0050]

The anti-CAPRIN-1 antibody used in the present invention may be chemically modified. Examples of such an antibody modifier can include antibodies bound to various molecules such as polyethylene glycol (PEG) and antitumor compounds (for example, antitumor agents listed below). Regarding antibody modifiers of the present invention, substances that bind to an antibody are not limited. Such an antibody modifier can be obtained by chemically modifying an obtained antibody. Methods of such modification have been already established in the field related to the present invention.

[0051]

The binding strength of the anti-CAPRIN-1 antibody used in the present invention against effector cells can be improved by substituting 1, 2 or several amino acids in the heavy-chain constant region of the antibody or by removing fucose bound to N-acetylglucosamine in a N-glycoside-linked sugar chain bound to the heavy-chain constant region. The anti-CAPRIN-1 antibody described above may have the amino acid substitution alone or may be a composition with an antibody bound to fucose.

[0052]

Antibodies in which 1, 2 or several amino acids in the heavy-chain constant region have been substituted can be produced with reference to, for example, WO2004/063351, WO2011/120135, U.S. Patent No. 8388955, WO2011/005481, U.S. Patent No. 6737056, and WO2005/063351.

[0053]

Antibodies in which fucose bound to N-acetylglucosamine in a N-glycoside-linked sugar chain in the heavy-chain constant region has been removed, or producing cells thereof can be produced with reference to U.S. Patent No. 6602684, EP Patent No. 1914244, and U.S. Patent No. 7579170. Compositions of antibodies in which fucose bound to N-acetylglucosamine in a N-glycoside-linked sugar chain bound to the heavy-chain constant region has been removed,

with antibodies bound to fucose, or producing cells thereof can be produced with reference to, for example, U.S. Patent No. 8642292.

[0054]

The anti-CAPRIN-1 polyclonal antibody and the anti-CAPRIN-1 monoclonal antibody used in the present invention, methods for producing or purifying antibodies and methods for producing a CAPRIN-1 protein or partial polypeptide thereof used in immunization can be obtained with reference to WO2010/016526, WO2011/096517, WO2011/096528, WO2011/096519, WO2011/096533, WO2011/096534, WO2011/096535, WO2013/018886, WO2013/018894, WO2013/018892, WO2013/018891, WO2013/018889, WO2013/018883, WO2013/125636, WO2013/125654, WO2013/125630, WO2013/125640, WO2013/147169, WO2013/147176 and WO2015/020212.

[0055]

Specific examples of the anti-CAPRIN-1 antibody according to the present invention include anti-CAPRIN-1 antibodies described in WO2010/016526, WO2011/096517, WO2011/096528, WO2011/096519, WO2011/096533, WO2011/096534, WO2011/096535, WO2013/018886, WO2013/018894, WO2013/018892, WO2013/018891, WO2013/018889, WO2013/018883, WO2013/125636, WO2013/125654, WO2013/125630, WO2013/125640, WO2013/147169, WO2013/147176 and WO2015/020212 mentioned above. Preferred examples of the anti-CAPRIN-1 antibody include the following.

[0056]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein having the amino acid sequence shown by SEQ ID NO: 2 or SEQ ID NO: 4 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, further preferably 95% or more, and still further preferably 99% or more) sequence identity to the amino acid sequence.

[0057]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 31 or an amino acid sequence having 80% or more (preferably 85% or

more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 36, 37 and 38 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 40, 41 and 42 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 140, 141 and 142 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 143, 144 and 145 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, or an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 164, 165 and 166 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 167, 168 and 169 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 39 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 43, an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 70 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 71, or an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 78 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 79.

[0058]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 33 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain

variable region comprising complementarity determining regions of SEQ ID NOs: 60, 61 and 62 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 64, 65 and 66 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 63 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 67.

[0059]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 32 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 52, 53 and 54 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 56, 57 and 58 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 55 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 59.

[0060]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 34 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 170, 171 and 172 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 173, 174 and 175 (CDR1, CDR2 and

CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, or an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 176, 177 and 178 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 179, 180 and 181 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 80 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 81, or an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 82 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 83.

[0061]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 35 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 182, 183 and 184 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 185, 186 and 187 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, or an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 188, 189 and 190 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 191, 192 and 193 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 84 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 85, or an antibody or a fragment thereof comprising a heavy-chain variable region

comprising the amino acid sequence of SEQ ID NO: 86 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 87.

[0062]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 44, 45 and 46 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 48, 49 and 50 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 47 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 51.

[0063]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 296 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 146, 147 and 148 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 149, 150 and 151 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 72 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 73.

[0064]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 297 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to

the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 272, 273 and 274 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 275, 276 and 277 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 114 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 115.

[0065]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 298 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 290, 291 and 292 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 293, 294 and 295 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 120 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 121.

[0066]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 299 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 301, 302 and 303 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising

complementarity determining regions of SEQ ID NOs: 305, 306 and 307 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 300 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 304.

[0067]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 308 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 134, 135 and 136 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 137, 138 and 139 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 68 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 69.

[0068]

An antibody or a fragment thereof having an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having the amino acid sequence shown by SEQ ID NO: 309 or an amino acid sequence having 80% or more (preferably 85% or more, more preferably 90% or more, and further preferably 95% or more) sequence identity to the amino acid sequence, preferably an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 134, 135 and 136 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 137, 138 and 139 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein, and more preferably an antibody or a fragment thereof comprising a heavy-chain variable region

comprising the amino acid sequence of SEQ ID NO: 68 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 69.

[0069]

In addition, the following anti-CAPRIN-1 antibodies are also preferably used.

[0070]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 68 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 69.

[0071]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 70 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 71.

[0072]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 72 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 73.

[0073]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 74 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 75.

[0074]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 76 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 77.

[0075]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 78 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 79.

[0076]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 80 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 81.

[0077]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 82 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 83.

[0078]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 84 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 85.

[0079]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 86 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 87.

[0080]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 88 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 89.

[0081]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 90 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 91.

[0082]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 92 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 93.

[0083]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 94 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 95.

[0084]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 96 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 97.

[0085]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 98 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 99.

[0086]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 100 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 101.

[0087]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 102 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 103.

[0088]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 104 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 105.

[0089]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 106 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 107.

[0090]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 108 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 109.

[0091]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 110 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 111.

[0092]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 112 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 113.

[0093]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 114 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 115.

[0094]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 116 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 117.

[0095]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 118 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 119.

[0096]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 120 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 121.

[0097]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 122 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 123.

[0098]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 124 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 125.

[0099]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 126 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 127.

[0100]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 128 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 129.

[0101]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 130 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 131.

[0102]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 132 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 133.

[0103]

An antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 300 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 304.

[0104]

In Examples mentioned later, the polyclonal antibody or the monoclonal antibody against a full-length CAPRIN-1 protein or a polypeptide of a portion of a region expressed on cell membrane surfaces of cancer cells was confirmed to exhibit reactivity with cell membrane surfaces of a plurality of human cancer cells. Furthermore, results indicating the response in human cancer patients were obtained, and a marked antitumor effect was obtained by which a tumor completely disappeared at some cancer sites.

[0105]

<EGFR inhibitor>

The EGFR inhibitor is a drug having the action of inhibiting the activity of epidermal growth factor receptor (EGFR) mentioned below in detail.

[0106]

EGFR is a receptor-type tyrosine kinase belonging to the ERBB family and also referred to as HER1 or ErbB1. EGFR is a transmembrane glycoprotein receptor composed of three main domains: an extracellular ligand binding domain, a transmembrane domain, and an intracellular tyrosine kinase domain. EGFR is dimerized by binding of a ligand such as EGF, TGF-α, amphiregulin, or heparin-binding EGF-like growth factor (HB-EGF) to the EGFR ligand binding domain, and is activated by mutual phosphorylation between the two molecules (autophosphorylation) in the cytoplasmic domain. Activated EGFR is involved in the control of cell proliferation, migration, angiogenesis, metabolism and differentiation by recruiting GRB2 and SOS1 to the cell membrane and activating the downstream MAPK and PI3K/Akt/mTOR signaling pathways via RAS activation. EGFR is expressed in many cells, and the signaling pathway thereof plays an important role in regulating cell differentiation, development, proliferation, and maintenance in normal tissues. However, when gene amplification, gene mutation, or structural change occurs in EGFR, EGFR becomes involved in carcinogenesis, and cancer proliferation, infiltration, and metastasis. EGFR is overexpressed in many solid cancers and is involved in the malignancy and prognosis of cancer.

[0107]

EGFR inhibitors are known to exert a cancer therapeutic effect by inhibiting signaling pathways by EGFR dimerization inhibition, ligand neutralization, ligand binding inhibition,

internalization of EGFR or the like, whereas the present invention can increase the drug efficacy of cancer immunotherapy itself, specifically, the phagocytic activity against cancer cells by immunocytes as shown in the Examples herein. Since the signaling pathway activated by EGFR is not directly related to the immune system, the increase of the drug efficacy of cancer immunotherapy itself by the present invention is a new finding that cannot be expected from the technical level of a person skilled in the art at present.

[0108]

Specific examples of the EGFR inhibitor include afatinib (BIBW2992), alflutinib (AST2818), allitinib, almonertinib (HS-10296), avitinib (AC0010), befotertinib, brigatinib (AP26113), canertinib (CI-1033), dacomitinib (PF-00299804), dosimertinib, epertinib, epitinib, erlotinib (OSI-774), gefitinib (ZD1839), icotinib (BPI-2009H), lapatinib (GW-572016), lazertinib, lifirafenib (BGB-283), mavelertinib, mobocertinib (TAK788), naquotinib (ASP8273), nazartinib (EGF816), neratinib (HKI-272), O-desmethyl gefitinib, olafertinib, olmutinib (BI 1482694), oritinib, osimertinib (AZD9291), pelitinib (EKB-569), poziotinib (HM781-36B), pyrotinib (SHR-1258), rezivertinib, rociletinib (CO-1686), sapitinib (AZD8931), simotinib, sunvozertinib, tarloxotinib bromide, tesevatinib, theliatinib (HMPL-309), vandetanib (ZD6474), varlitinib, zorifertinib (AZD3759), zipalertinib, cetuximab, panitumumab, necitumumab, cetuximab sarotalocan sodium, BIBX 1382 dihydrochloride, HER2-Inhibitor-1, Mutant EGFR inhibitor, EGFR Inhibitor, EGFR/ErbB-2/ErbB-4 inhibitor-2, EGFR/ErbB-2/ErbB-4 inhibitor-3, (-)-Epigallocatechin Gallate, (E)-AG 556, (E)-AG 99, (E/Z)-AG490, (Rac)-JBJ-04-125-02, (Z)-Tyrphostin A51, AC480 (BMS-599626), AEE788 (NVP-AEE788), AG 1478 hydrochloride, AG 490, AG 494, AG 555, AG 556, AG-1478 (Tyrphostin AG-1478), AG-1557, AG-18, AG-490 (Tyrphostin B42), AG-494, AG99, AP26113-analog (ALK-IN-1), ARRY-380 analog (WO2015153959A2, compound 249), ASK120067, AST-1306, AST5902 trimesylate, Astragaloside VI, AV-412, AZ5104, BAY 2476568, BDTX-189, BGB-102, BI-4020, BLU-945, BMS-599626, BMS-690514, Butein, CCT365623 hydrochloride, Cetuximab, CGP52411, CHMFL-EGFR-202, Chrysophanic Acid, Chrysophanol, CL-387785 (EKI-785), CNX-2006, CUDC-101, Cyasterone, Daphnetin, DBPR112, Delphinidin 3-glucoside chloride, DP-C-4, DPPY, DZD9008, EAI045, EBE-A22, EGFR mutant-IN-1, EGFR/BRAF-IN-1, EGFR/CSC-

IN-1, EGFR/HER2/CDK9-IN-1, EGFR/HER2/CDK9-IN-2, EGFR/HER2/CDK9-IN-3, EGFR/HER2-IN-2, EGFR/HER2-IN-3, EGFR/HER2-IN-4, EGFR/HER2-IN-5, EGFR-IN-1, EGFR-IN-1 TFA, EGFR-IN-11, EGFR-IN-12, EGFR-IN-15, EGFR-IN-16, EGFR-IN-17, EGFR-IN-18, EGFR-IN-2, EGFR-IN-21, EGFR-IN-22, EGFR-IN-23, EGFR-IN-24, EGFR-IN-25, EGFR-IN-27, EGFR-IN-28, EGFR-IN-29, EGFR-IN-30, EGFR-IN-31, EGFR-IN-32, EGFR-IN-33, EGFR-IN-34, EGFR-IN-35, EGFR-IN-36, EGFR-IN-37, EGFR-IN-38, EGFR-IN-39, EGFR-IN-40, EGFR-IN-42, EGFR-IN-43, EGFR-IN-44, EGFR-IN-45, EGFR-IN-46, EGFR-IN-47, EGFR-IN-48, EGFR-IN-49, EGFR-IN-5, EGFR-IN-51, EGFR-IN-52, EGFR-IN-53, EGFR-IN-54, EGFR-IN-55, EGFR-IN-56, EGFR-IN-57, EGFR-IN-58, EGFR-IN-61, EGFR-IN-62, EGFR-IN-64, EGFR-IN-67, EGFR-IN-68, EGFR-IN-7, EGFR-IN-8, EGFR-IN-9, EMI1, EMI48, EMI56, Falnidamol, Genistein (NPI 031L), Genistein-d4, GW 583340 dihydrochloride, H-9 Dihydrochloride, HER2-IN-7 (WO2019214634A1, compound 23), HKI 357, HSP90-IN-13, Iressa, JBJ-02-112-05, JBJ-03-142-02, JBJ-09-063, JCN037, JND3229, JNJ 28871063 hydrochloride, Khellin, Lavendustin A, Lavendustin C, LDC0496, Licochalcone D, Lidocaine hydrochloride, Matuzumab, Methyl 2,5-dihydroxycinnamate, MS 154, MS 39, MS9427, MTX-211, Mutated EGFR-IN-1, Mutated EGFR-IN-2, Mutated EGFR-IN-3, Nimotuzumab, Norcantharidin, NRC-2694, NSC114126, NSC381467, NSC81111, OSI-420, pan-HER-IN-1, pan-HER-IN-2, Panitumumab, PD 158780, PD 174265, PD-089828, PD153035, PD158780, PD-161570, PD168393, PDE5-IN-3, PDZ1i, PF-06459988, PF-6274484, PKI-166, PP 3, PROTAC EGFR degrader 2, PROTAC EGFR degrader 3, PROTAC EGFR degrader 4, PROTAC EGFR degrader 6, PROTAC EGFR degrader 7, RG13022, RG14620, SJF 1521, SJF 1528, SU5214, Sulforaphene, TAK-285, Tarlox-TKI, TAS0728, Tephrosin, TQB3804 (EGFR-IN-7), Tyrphostin 23, Tyrphostin 25, Tyrphostin 8, Tyrphostin 9, Tyrphostin A51, Tyrphostin AG 112, Tyrphostin AG 528, Tyrphostin AG 879, Tyrphostin AG30, Tyrphostin AG-528, VEGFR-IN-1, WHI-P154, WHI-P180, WZ3146, WZ4002, WZ8040, ZD-4190, β-hydroxyisovalerylshikonin, and pharmaceutically acceptable (known) salts or (known) derivatives thereof.

[0109]

Among these EGFR inhibitors, it is preferable that the EGFR inhibitor is afatinib, alflutinib, allitinib, almonertinib, avitinib, befotertinib, brigatinib, canertinib, dacomitinib, dosimertinib, epertinib, epitinib, erlotinib, gefitinib, icotinib, lapatinib, lazertinib, lifirafenib, mavelertinib, mobocertinib, naquotinib, nazartinib, neratinib, olafertinib, olmutinib, oritinib, osimertinib, pelitinib, poziotinib, pyrotinib, rezivertinib, rociletinib, sapitinib, simotinib, sunvozertinib, tarloxotinib bromide, tesevatinib, theliatinib, vandetanib, varlitinib, zorifertinib, zipalertinib, PD 168393, or a pharmaceutically acceptable (known) salt or (known) derivative thereof; it is more preferable that the EGFR inhibitor is gefitinib, cetuximab, erlotinib, panitumumab, lapatinib, vandetanib, afatinib, osimertinib, necitumumab, dacomitinib, cetuximab sarotalocan sodium, zipalertinib, PD 168393, or a pharmaceutically acceptable (known) salt or (known) derivative thereof; and it is further preferable that the EGFR inhibitor is Erlotinib, Zipalertinib, PD 168393, or a pharmaceutically acceptable (known) salt or (known) derivative thereof.

[0110]

Erlotinib (also known as OSI-774, CP358774, NSC 718781, Tarceva) selectively inhibits the tyrosine kinase activity of EGFR. The CAS number is shown by 183321-74-6, and the IUPAC name is shown by N-(3-ethynylphenyl)-6,7-bis(2-methoxyethoxy)quinazolin-4-amine. The molecular formula is $C_{22}H_{23}N_3O_4$, and the molecular weight is 393.4. Erlotinib is also used as erlotinib hydrochloride, where the CAS number is shown by 183319-69-9, and the IUPAC name is shown by N-(3-ethynylphenyl)-6,7-bis(2-methoxyethoxy)quinazolin-4-amine; hydrochloride. The molecular formula is $C_{22}H_{24}ClN_3O_4$, and the molecular weight is 429.9. Erlotinib simply described herein is a generic name for a free form and hydrochloride of erlotinib.

[0111]

Zipalertinib (also known as TAS6417, CLN-081, TPC-064) binds to the ATP binding site in the EGFR hinge region and selectively inhibits mutated EGFR. Zipalertinib is an oral drug targeted to cancers having EGFR with exon 20 insertion mutation. The CAS number is shown by 1661854-97-2, and the IUPAC name is shown by N-[(8S)-4-amino-6-methyl-5-quinolin-3-yl-8,9-dihydropyrimido[5,4-b]indolizin-8-yl]prop-2-enamide. The molecular formula is $C_{23}H_{20}N_6O$, and the molecular weight is 396.4.

[0112]

PD 168393 is an EGFR inhibitor that irreversibly alkylates Cys-773 of EGFR. The CAS number is shown by 194423-15-9, and the IUPAC name is shown by N-[4-(3-bromoanilino)quinazolin-6-yl]prop-2-enamide. The molecular formula is $C_{17}H_{13}BrN_4O$, and the molecular weight is 369.2.

[0113]

<Other drugs>

The medicament of the present invention may comprise, as an active ingredient, an antitumor agent known in literatures and the like, in addition to the anti-CAPRIN-1 antibody and the EGFR inhibitor, as long as it does not inhibit the effects as the medicament of the present invention. Specific examples of known antitumor agents include, but are not particularly limited to, 5-fluorouracil, irinotecan, oxaliplatin, carboplatin, cisplatin, nedaplatin, gemcitabine, paclitaxel, nabpaclitaxel, imiquimod, immune checkpoint inhibitors, doxorubicin, daunorubicin, cyclophosphamide, methotrexate, thiotepa, busulfan, improsulfan, piposulfan, benzodopa, carboquone, meturedopa, uredopa, altretamine, triethylenemelamine, triethylenephosphoramide, triethilenethiophosphoramide, trimethylolomelamine, bullatacin, bullatacinone, camptothecin, bryostatin, callystatin, cryptophycin 1, cryptophycin 8, dolastatin, duocarmycin, eleutherobin, pancratistatin, sarcodictyin, spongistatin, chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard, carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine, calicheamicin, dynemicin, clodronate, esperamicin, aclacinomycin, actinomycin, authramycin, azaserine, bleomycin, cactinomycin, carabicin, carminomycin, carzinophilin, chromomycin, dactinomycin, detorbicin, 6-diazo-5-oxo-L-norleucine, adriamycin, epirubicin, esorubicin, idarubicin, marcellomycin, mitomycin C, mycophenolic acid, nogalamycin, olivomycin, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin, denopterin, pteropterin, trimetrexate, fludarabine, 6-mercaptopurine, thiamiprine, thioguanine, ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, androgens such as calusterone,

dromostanolone propionate, epitiostanol, mepitiostane, testolactone, aminoglutethimide, mitotane, trilostane, frolinic acid, aceglatone, aldophosphamide glycoside, aminolevulinic acid, eniluracil, amsacrine, bestrabucil, bisantrene, defofamine, demecolcine, diaziquone, eflornithine, elliptinium acetate, epothilone, etoglucid, lentinan, lonidamine, maytansine, ansamitocine, mitoguazone, mitoxantrone, mopidanmol, nitraerine, pentostatin, phenamet, pirarubicin, losoxantrone, podophyllinic acid, 2-ethylhydrazide, procarbazine, razoxane, rhizoxin, schizophyllan, spirogermanium, tenuazonic acid, triaziquone, roridine A, anguidine, urethane, vindesine, dacarbazine, mannomustine, mitobronitol, mitolactol, pipobroman, gacytosine, docetaxel, gemcitabine, 6-thioguanine, mercaptopurine, vinblastine, etoposide, vincristine, vinorelbine, novantrone, teniposide, edatrexate, daunomycin, aminopterin, xeloda, ibandronate, difluoromethylornithine (DMFO), topoisomerase inhibitors, retinoic acid, folinic acid, and their pharmaceutically acceptable (known) salts or (known) derivatives.

[0114]

<Antitumor effect of present invention>

The antitumor effect of the combination of the anti-CAPRIN-1 antibody and the EGFR inhibitor according to the present invention can be evaluated *in vivo* or *in vitro*. The *in vivo* antitumor effect can be evaluated by administering the anti-CAPRIN-1 antibody and the EGFR inhibitor to an organism having cancer, measuring the size of a tumor after the administration, and examining the size of the cancer over time. Also, the *in vivo* antitumor effect can be evaluated by examining a survival rate of organisms. Alternatively, the *in vivo* antitumor effect may be evaluated by examining the ability to produce cytokines or chemokines. The *in vivo* antitumor effect can be further evaluated by examining prevention of cancer, prevention of metastasis or prevention of recurrence.

[0115]

The *in vitro* antitumor effect can be evaluated by examining the cytotoxic activity or phagocytic activity against cancer cells by immunocytes in coculturing the cancer cells and the immunocytes. Thus, the antitumor effect of the combination of the anti-CAPRIN-1 antibody and the EGFR inhibitor can be evaluated by adding the anti-CAPRIN-1 antibody and the EGFR inhibitor in combination to a coculture system of cancer cells and immunocytes, and examining

the cytotoxic activity or phagocytic activity against the cancer cells by the immunocytes. The immunocyte for use here may be any cell as long as the immunocyte is a blood cell having cytotoxic activity or phagocytic activity. A human NK cell is preferred for evaluating the cytotoxic activity, and a human monocytic cell (THP-1 or U937) is preferred for evaluating the phagocytic activity. When an antibody binds to a cancer cell, this is recognized by an immunocyte so that the cancer cell is killed via cytotoxic activity or phagocytic activity by the immunocyte. Therefore, an *in vivo* antitumor effect can be predicted by evaluating the *in vitro* antitumor effect.

[0116]

An ability of an anti-CAPRIN-1 antibody used in the present invention to bind to CAPRIN-1 can be determined via binding assay using, for example, ELISA, a Western blot method, immunofluorescence, or flowcytometry analysis.

[0117]

The combination of the anti-CAPRIN-1 antibody and the EGFR inhibitor of the present invention increases an *in vitro* antitumor effect as compared with the anti-CAPRIN-1 antibody alone. The rate of increase is preferably 1.5 or more times, more preferably 2 or more times, and further preferably 3 or more times.

[0118]

<Medicament for treatment and/or prevention of cancer>

A medicament of the present invention is aimed at treating and/or preventing cancer. A cancer targeted by the medicament of the present invention is not particularly limited as long as it is a cancer (cells) expressing CAPRIN-1 protein, particularly, a cancer (cells) expressing CAPRIN-1 protein on a cell membrane surface.

[0119]

The term "treatment" used herein refers to treatment of cancer based on an antitumor effect mentioned above. The term "prevention" used herein refers to not only prevention of development of cancer but also prevention of metastasis or recurrence of cancer.

[0120]

Both the terms "tumor" and "cancer" used herein refer to malignant neoplasm, and thus they are used in an exchangeable manner.

[0121]

Cancer that can be a target in the present invention is any cancer as long as the cancer expresses CAPRIN-1 protein on a cell membrane surface. The cancer is preferably colon cancer, lung cancer, prostate cancer, ovarian cancer, pancreatic cancer, kidney cancer, breast cancer, gastric cancer, bile duct cancer, thyroid cancer, melanoma, renal cell cancer, Hodgkin's lymphoma, head and neck cancer, mesothelioma, colorectal cancer, esophageal cancer, gastroesophageal junction cancer, hepatocellular cancer, glioblastoma, urothelial cancer, urinary bladder cancer, uterus cancer, primary central nervous system lymphoma, primary testicular lymphoma, biliary tract cancer, brain tumor, leukemia, liver cancer, sarcoma, fibrosarcoma, mastocytoma, adrenal cortex cancer, Ewing's tumor, testicle cancer, basal cell cancer, lymphoma, multiple myeloma, Paget's disease or skin cancer. These cancers may be primary cancers, metastatic cancers, cancers that have metastasized, cancers that have recurred, postoperative cancers, or unresectable cancers. The term melanoma is often used interchangeably with malignant melanoma.

[0122]

More specifically, examples of the cancer include, but are not limited to, for example, cutaneous T/NK-cell lymphoma, peripheral T-cell lymphoma, multiple myeloma, Bowen's disease, prickle cell cancer, extramammary Paget's disease, mycosis fungoides, Sezary's syndrome, T-cell leukemia or lymphoma having a lesion only in the skin, cutaneous B-cell lymphoma (indolent group), cutaneous T-cell lymphatic or mammary adenoma, complex mammary adenoma, malignant mixed tumor of mammary gland, intraductal papillary carcinoma of mammary gland, lung adenocarcinoma, squamous cell cancer, small cell cancer, large cell cancer, glioma which is a neuroepithelial tissue tumor, glioblastoma, neuroblastoma, ependymoma, neuronal tumor, neuroectodermal tumor, neurilemoma, neurofibromatosis, meningioma, chronic lymphocytic leukemia, lymphoma, alimentary lymphoma, gastrointestinal lymphoma, small to medium cell lymphoma, cecal cancer, ascending colon cancer, descending colon cancer, transverse colon cancer, sigmoid colon cancer, rectal cancer, ovarian epithelial

cancer, germ cell tumor, interstitial cell tumor, pancreatic duct cancer, invasive pancreatic duct cancer, adenocarcinoma of pancreatic cancer, acinar cell cancer, adenosquamous cancer, giant cell tumor, intraductal papillary mucinous tumor, mucinous cystadenocarcinoma, pancreatoblastoma, pancreatic islet cell tumor, Frantz's tumor, serous cystadenocarcinoma, solid pseudopapillary cancer, gastrinoma, glucagonoma, insulinoma, multiple endocrine neoplasia type-1 (Wermer syndrome), nonfunctional islet cell tumor, somatostatinoma, VIPoma, uterine cervical cancer, uterine body cancer, fibrosarcoma, osteosarcoma, joint sarcoma, Ewing sarcoma, Wilms's tumor, hepatoblastoma, soft tissue sarcoma, acute leukemia, chronic leukemia, spinal cord tumor, malignant soft tissue tumor, tumors of teratoma group, and head and neck cancer including hypopharynx cancer, oropharynx cancer, tongue cancer, nasopharyngeal cancer, oral cavity cancer, lip cancer, sinus cancer, voice box cancer, cancer of the renal pelvis and ureter, urinary bladder cancer, urethra cancer, testicular tumor, malignant pleural mesothelioma, malignant bone tumor, uterine body cancer, and pediatric malignant solid tumor (rhabdomyosarcoma, neuroblastoma, hepatoblastoma, medulloblastoma, nephroblastoma, retinoblastoma, central nervous system germ cell tumor, and Ewing sarcoma family of tumors). The cancer also includes a palpable cancer, a subcutaneously existing cancer, an intracutaneously existing cancer, a superficial cancer, cancer existing in the dermis, cancer existing in a non-parenchymal organ, and progressive caner which originate from the cancers described above. The cancer also includes a palpable cancer, a subcutaneously existing cancer, an intracutaneously existing cancer, a superficial cancer, cancer existing in the dermis, and cancer existing in a non-parenchymal organ, which originate from the cancers described above and have metastasized and recurred.

[0123]

A preferable subject (patient) that can be a target is a mammal and is, for example, a mammal including primates, pet animals, livestock animals, and sport animals. Humans, dogs and cats are particularly preferable.

[0124]

A medicament of the present invention can be formulated by a method known to persons skilled in the art. For instance, the medicament of the present invention can be parenterally

used in the form of a parenteral injection of: an aseptic solution comprising water or a pharmacologically acceptable non-water solution; or a suspension liquid. For each formulation or pharmaceutical composition in the medicament of the present invention, the active ingredient (at least one of the anti-CAPRIN-1 antibody and the EGFR inhibitor) may be appropriately combined with, for example, a pharmacologically acceptable carrier, medium or additive; specifically, sterilized water, physiological saline, an isotonic solution, a buffer (buffer solution, etc.), plant oil, an oily solution, an antioxidant, a solubilizer, an emulsifier, a suspension, a surfactant, a stabilizer, a fragrance, an excipient, or a binder, and preferably, may be formulated by mixing with them in a unit dosage form required for a generally acceptable pharmaceutical formulation. An amount of an active ingredient in a formulation is determined such that an appropriate dosage within an indicated range can be achieved.

[0125]

An aseptic composition for injection can be prepared in accordance with general formulation practice using a vehicle such as distilled water for injection. An aqueous solution for injection purposes includes, for example, physiological saline or isotonic solutions comprising glucose and other adjuvants such as D-sorbitol, D-mannose, D-mannitol, and sodium chloride. Such solution may be used with an appropriate dissolution aid. Such dissolution aid includes, for example, alcohols such as ethanol and polyalcohol, such as propylene glycol, polyethylene glycol, or nonion surfactants such as polysorbate 80(TM) and HCO-60. Oily liquid includes, for example, sesame oil or soybean oil. Such oily liquid may be used in combination with a dissolution aid such as benzyl benzoate or benzyl alcohol. In addition, it may be mixed with a buffering agent such as a phosphate buffer solution or a sodium acetate buffer solution, a soothing agent such as procaine hydrochloride, a stabilizer such as benzyl alcohol or phenol, or an antioxidant. In general, a formulated injection solution is introduced into an adequate ample.

[0126]

The above pharmaceutical composition is orally or parenterally administered. Preferably, it is parenterally administered. Specifically, dosage forms include injectable agents, intranasally-administered agents, transpulmonarily-administered agents, and percutaneously-

administered agents. For example, injectable agents can be systemically or locally administered via intravenous injection, intramuscular injection, intraperitoneal injection, subcutaneous injection, or intratumoral injection. The percutaneously-administered agents include, for example, agents called liniments and external medicines. The external medicines include, for example, solid agents, solutions, sprays, ointments, creams, and gels.

[0127]

The administration method can be appropriately selected depending on age, weight, gender, and symptoms of a patient. A single dose of a pharmaceutical composition comprising at least one of the anti-CAPRIN-1 antibody and the EGFR inhibitor can be selected within a range of, for example, 0.0001 mg to 1000 mg per kg of body weight as the amount of each active ingredient. Alternatively, the dose of the active ingredient can be selected within a range of, for example, 0.001 to 100000 mg per patient's body, or 0.1 mg to 300 mg or 1 mg to 30 mg per kg of patient's body weight; however, it is not necessarily limited thereto. The dose and the administration method are changed depending on patient age, weight, gender, and symptoms. However, persons skilled in the art can appropriately select the dose and the method.

[0128]

<Administration method>

Treatment and/or prevention of cancer with a medicament for treatment and/or prevention of cancer of the present invention includes various modes, in addition to administration as a medicament mentioned above. For example, respective active ingredients in a medicament of the present invention can be administered simultaneously, concurrently, or individually in a staggered manner. As a specific example, active ingredients can be administered within a time interval up to approximately 3 weeks, i.e., the second active ingredient can be administered from immediately up to approximately 3 weeks after administration of the first active ingredient. These administrations may be carried out subsequently to a surgical procedure, or a surgical procedure may be carried out between the administrations of the first and second drugs. In addition, a medicament for treatment and/or prevention of cancer of the present invention may be administered according to a plurality of administration cycles. For example, in the case of carrying out simultaneous administration of

respective active ingredients in a medicament for treatment and/or prevention of cancer of the present invention, a pharmaceutical composition comprising both active ingredients is administered once per approximately 2 days to approximately 3 weeks as one cycle. Then, this treatment cycle may be repeated, if necessary, according to the judgment of a physician in charge. Likewise, in the case of scheduling a formulation in a staggered manner, respective administration periods of individual agents are adjusted so as to span the same period. The interval between cycles can vary from 0 to 2 months. Respective doses of the active ingredients in the medicament for treatment and/or prevention of cancer of the present invention can be set in the same way as in the respective doses of the active ingredients in a pharmaceutical composition described above.

[0129]

<Pharmaceutical kit>

A medicament for treatment and/or prevention of cancer of the present invention may be in the form of a pharmaceutical kit. The pharmaceutical kit is a package for using active ingredients in the form of separate pharmaceutical compositions (formulations) in a method for treating and/or preventing cancer. The package may comprise an instruction for administering each of the active ingredients. The respective active ingredients in the pharmaceutical compositions for treatment and/or prevention of cancer contained in the pharmaceutical kit can be in the form of pharmaceutical compositions each formulated as described above such that the active ingredients can be administered together or separately. Further, the pharmaceutical kit comprises active ingredients in amounts sufficient for one or more doses such that the active ingredients can be administered according to the administration method described above.

[0130]

<Treatment and/or prevention method>

On the basis of the contents specifically described above, the present invention further provides a method for treating and/or preventing cancer, comprising administering the medicament of the present invention, or the anti-CAPRIN-1 antibody and the EGFR inhibitor according to the present invention to a subject (patient). For example, the present invention further provides a method for treating and/or preventing cancer, comprising administering the

medicament, etc. of the present invention to a subject (patient) suspected of having cancer. In this embodiment, for example, the anti-CAPRIN-1 antibody (antibody or fragment thereof) and the EGFR inhibitor according to the present invention, and an optional antitumor agent contained in the medicament can be administered simultaneously or separately to the subject (patient).

Examples

[0131]

The present invention is hereafter described in detail with reference to the following examples, although the scope of the present invention is not limited thereto.

[0132]

(Example 1) Production of anti-CAPRIN-1 antibody

One hundred (100) μg of a human CAPRIN-1 recombinant protein produced according to Example 3 of WO2010/016526 was mixed with a MPL+TDM adjuvant (Sigma) in an amount equivalent to that of the antigen protein. The mixture was used as an antigen solution per mouse. The antigen solution was administered intraperitoneally to 6-week-old Balb/c mice (Japan SLC Inc.) and then further administered 3 times and 24 times every week for completion of immunization. A spleen was removed on day 3 after the final immunization and then ground between two sterilized glass slides. Spleen cells were obtained by repeating the following procedure three times: washing with PBS (-) (Nissui), centrifuging at 1500rpm for 10 minutes, and removing supernatant. The obtained spleen cells were mixed with mouse myeloma cell SP2/0 (purchased from ATCC) at a ratio of 10 : 1. The PEG solution prepared by mixing 200 μl of RPMI1640 medium containing 10% FBS heated at 37°C and 800 μl of PEG1500 (Boehringer) was added to the cells. The solution was incubated for 5 minutes for cell fusion. Centrifugation was performed at 1700 rpm for 5 minutes to remove supernatants. Cells were suspended in 150 ml of RPMI1640 medium (HAT selective medium) containing 15% FBS, to which 2% equivalent of HAT solution (Gibco) had been added, and then seeded onto fifteen 96-well plates (Nunc) at 100 μl per well. Cells were cultured for 7 days under conditions of 37°C and 5% CO_2, so that hybridomas resulting from fusion of spleen cells to myeloma cells were

obtained. Hybridomas were selected using binding affinity to CAPRIN-1 protein of the antibody produced by the prepared hybridomas as an indicator. The CAPRIN-1 protein solution (1 μg/ml) was added at 100 μl per well of 96-well plates and then incubated at 4°C for 18 hours. After each well was washed 3 times with PBS-T, 0.5% Bovine Serum Albumin (BSA) solution (Sigma) was added at 400 μl per well, and then the plates were incubated at room temperature for 3 hours. The solution was removed and then each well was washed 3 times with 400 μl of PBS-T. Each culture supernatant of the hybridomas obtained above was added at 100 μl per well and then incubated at room temperature for 2 hours. After each well was washed 3 times with PBS-T, an HRP-labeled anti-mouse IgG (H+L) antibody (Invitrogen) diluted 5000-fold with PBS was added at 100 μl per well and then incubated at room temperature for 1 hour. After each well was washed 3 times with PBS-T, a TMB substrate solution (Thermo) was added at 100 μl per well and then incubated for 15-30 minutes, so that a color reaction was performed. After color development, 1 N sulfuric acid was added at 100 μl per well to stop the reaction. Absorbance at 450 nm and absorbance at 595 nm were measured using an absorption spectrometer. As a result, a plurality of hybridomas producing antibodies with high absorbances were selected. The selected hybridomas were added at 0.5 hybridomas per well of 96-well plates and then cultured. After 1 week, hybridomas forming single colonies in wells were observed. Cells in these wells were further cultured. Hybridomas were selected using binding affinity to CAPRIN-1 protein of the antibody produced by cloned hybridomas as an indicator. The CAPRIN-1 protein solution (1 μg/ml) was added at 100 μl per well of 96-well plates and then incubated at 4°C for 18 hours. Each well was washed 3 times with PBS-T, a 0.5% BSA solution was added at 400 μl per well, and then incubated at room temperature for 3 hours. The solution was removed and then each well was washed 3 times with 400 μl of PBS-T. Each culture supernatant of the hybridomas obtained above was added at 100 μl per well and then incubated at room temperature for 2 hours. Each well was washed 3 times with PBS-T, an HRP-labeled anti-mouse IgG (H+L) antibody (Invitrogen) diluted 5000-fold with PBS was added at 100 μl per well and then incubated at room temperature for 1 hour. Each well was washed 3 times with PBS-T, a TMB substrate solution (Thermo) was added at 100 μl per well and then incubated for 15-30 minutes, so that a color reaction was

performed. After color development, 1 N sulfuric acid was added at 100 μl per well to stop the reaction. Absorbance at 450 nm and absorbance at 595 nm were measured using an absorption spectrometer. As a result, a plurality of mouse monoclonal antibodies exerting reactivity with CAPRIN-1 protein were obtained.

[0133]

Reactivity of each monoclonal antibody with human cancer cells confirmed to express CAPRIN-1 protein on cell membrane surfaces was further confirmed by flow cytometry. A mouse IgG control antibody exhibiting no reactivity with the cancer cells was used as a negative control. As a result of confirmation, several monoclonal antibodies were obtained which had stronger fluorescence intensity against the cancer cells than that of the mouse IgG control antibody and reacted strongly with the cell membrane surfaces of the cancer cells expressing CAPRIN-1 on the cell membrane surfaces. From among them, a monoclonal antibody against CAPRIN-1 described in WO2013/125630, which was an antibody comprising the amino acid sequence of a heavy-chain variable region shown by SEQ ID NO: 114 and the amino acid sequence of a light-chain variable region shown by SEQ ID NO: 115, was selected as a monoclonal antibody exhibiting reactivity with CAPRIN-1 protein.

[0134]

CDR1 to CDR3 of the heavy-chain variable region of the antibody selected were identified. A nucleotide sequence was designed so as to be able to express a heavy-chain variable region having framework regions comprising a human antibody sequence. This nucleotide sequence was inserted to a vector for mammalian expression having an insert of a human IgG1 heavy-chain constant region. Likewise, CDR1 to CDR3 of the light-chain variable region were identified. A nucleotide sequence was designed so as to be able to express a light-chain variable region having framework regions comprising a human antibody sequence. This nucleotide sequence was inserted to a vector for mammalian expression having an insert of a human IgG1 light-chain constant region. These two recombinant expression vectors were introduced to mammalian cells according to a general method and then a culture supernatant containing humanized monoclonal antibody #1 (humanized antibody #1) against CAPRIN-1 was obtained. The amino acid sequences of heavy chain CDR1, CDR2, and CDR3 of the

humanized monoclonal antibody #1 are shown by SEQ ID NOs: 272, 273, and 274, respectively. The amino acid sequences of light chain CDR1, CDR2, and CDR3 of the humanized monoclonal antibody #1 are shown by SEQ ID NOs: 275, 276, and 277, respectively.

[0135]

The obtained culture supernatant containing the obtained humanized anti-CAPRIN-1 monoclonal antibody #1 was purified using Hitrap Protein A Sepharose FF (GE Healthcare Bio-Sciences) according to a general method, replaced with PBS (-), and filtered through a 0.22 μm filter (Millipore) for preparation of the filtrate.

[0136]

The specific reactivity of the anti-CAPRIN-1 antibody to CAPRIN-1 protein was detected and confirmed by ELISA using CAPRIN-1 protein immobilized on a plate.

[0137]

The reactivity of the anti-CAPRIN-1 antibody with cancer cells without permeation treatment of cell membranes was examined by flow cytometry to confirm that a portion of CAPRIN-1 protein was expressed on cell membrane surfaces of cancer cells as shown in Examples given below.

[0138]

It was confirmed by flow cytometry that, against all of breast cancer cells (BT-474), colon cancer cells (HT-29 and HCT116), lung cancer cells (QG56, H1650, and A549), gastric cancer cells (NCI-N87), uterus cancer cells (HEC-1-A), prostate cancer cells (22Rv1 and DU145), pancreatic cancer cells (Panc10.5), liver cancer cells (Hep3B), ovarian cancer cells (SKOV3), kidney cancer cells (Caki-2), brain tumor cells (U-87MG), urinary bladder cancer cells (T24), esophageal cancer cells (OE33), leukemia cells (OCI-AML5), lymphoma cells (Ramos), gallbladder cancer cells (TGBC14TKB), fibrosarcoma cells (HT-1080), and melanoma cells (G-361 and A375), which are human cancer cells confirmed to express CAPRIN-1 gene, and mouse kidney cancer cells (Renca) and mouse breast cancer cells (4T1) confirmed to express CAPRIN-1 gene, the humanized antibody #1 had stronger fluorescence intensity than that of a human IgG control antibody and rabbit IgG antibody serving as negative

controls exhibiting no reactivity with the cancer cells, and reacted strongly with the cell membrane surfaces of the cancer cells expressing CAPRIN-1.

[0139]

Likewise, the anti-CAPRIN-1 antibodies described in WO2010/016526, WO2011/096517, WO2011/096528, WO2011/096519, WO2011/096533, WO2011/096534, WO2011/096535, WO2013/018886, WO2013/018894, WO2013/018892, WO2013/018891, WO2013/018889, WO2013/018883, WO2013/125636, WO2013/125654, WO2013/125640, WO2013/147169, WO2013/147176 and WO2015/020212 were also confirmed to react strongly with the cancer cell membrane surfaces.

[0140]

(Example 2A) *In vitro* antitumor effect 1 of combination of anti-CAPRIN-1 antibody and PD 168393, erlotinib, or zipalertinib (TAS6417)

Antitumor effects of a combination of an anti-CAPRIN-1 antibody and an EGFR inhibitor PD 168393, erlotinib, or zipalertinib (TAS6417) were evaluated *in vitro*. The PD 168393 used was purchased from Cayman Chemical Company (Cat. No.: 21059). The erlotinib used was erlotinib hydrochloride purchased from FUJIFILM Wako Pure Chemical Corporation (Cat. No.: 057-09111). The zipalertinib (TAS6417) used was purchased from Selleck Chemicals LLC (Cat. No.: S8814).

[0141]

Specifically, in each EGFR inhibitor combination test group, the indicated drug used in combination was applied to human cancer cells, and then the cancer cells were cocultured with human monocytic cells (THP-1) in the presence of the anti-CAPRIN-1 antibody, and the antibody-mediated phagocytic activity against the cancer cells by THP-1 was evaluated.

[0142]

The human-derived cancer cells used were a colon cancer cell line HCT116. On a 6-well plate, the human-derived cancer cells were cultured for 2 days in the presence of the respective drugs used in combination, for the PD 168393 combination test group, the erlotinib combination test group, and the TAS6417 combination test groups. Specifically, PD 168393 was added at a concentration of 10 μM, erlotinib at a concentration of 50 μM, and zipalertinib

(TAS6417) at a concentration of 20 μM or 40 μM, to HCT 116. As a control, a test group without a drug used in combination, in which only the anti-CAPRIN-1 antibody was added, was established. In the control group, the cancer cells were cultured for 2 days without addition of the drug used in combination, beforehand.

[0143]

Each cancer cell line after the culture was dissociated with TrypLE Express (Thermo), and the cancer cells were stained by the addition of calcein-AM at a final concentration of 0.04 μg/mL and incubation at 37°C for 10 minutes. Next, the cells were dispensed at 5×10^3 cancer cells per well to a 96-well plate, and the anti-CAPRIN-1 antibody (final concentration: 1 μg/mL) and 1.25×10^5 THP-1 cells were added to each well, followed by culture at 37°C for 1 hours under a condition of 5% CO_2. Then, the cells were washed with PBS (phosphate buffer solution) containing 1% FBS (fetal bovine serum), and the human monocytic cells were stained through a reaction with an APC (allophycocyanin)-labeled anti-human CD45 antibody (final concentration: 0.25 μg/mL). Further, dead cells were stained with propidium iodide (PI) (final concentration: 0.1 μg/mL), followed by the measurement of fluorescence from each cell by flow cytometry. PI-positive dead cells were excluded from analysis. The human monocytic cells THP-1 recognize an antibody bound onto cancer cells and phagocytize the cancer cells. At that time, if the cancer cells have been stained with calcein-AM, the monocytic cells ingesting the cancer cells by phagocytosis also become positive to calcein-AM. Thus, the phagocytic activity in this evaluation system was calculated as the ratio (%) of APC-positive/calcein-AM-positive cells to the whole calcein-AM-positive population.

[0144]

As a result of evaluation using the anti-CAPRIN-1 antibody prepared in Example 1 (anti-CAPRIN-1 humanized antibody #1) as an anti-CAPRIN-1 antibody, phagocytic activity against cancer cells of 69% or more was observed for PD 168393 and erlotinib combination test groups, respectively, while phagocytic activity against cancer cells of 39% or less was observed against HCT116 for the test group without a drug used in combination. As a result of conducting Student's t test, the phagocytic activity of the PD 168393 and erlotinib combination test groups

was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%) (Figure 1).

[0145]

Similarly, phagocytic activity against cancer cells of 52% or more was observed for TAS6417 combination test groups, while phagocytic activity against cancer cells of 27% or less was observed against HCT116 for the test group without a drug used in combination. As a result of conducting Student's t test, the phagocytic activity of the TAS6417 combination test groups was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%) (Figure 2). Thus, the antitumor effect of the anti-CAPRIN-1 antibody on the human cancer cells was significantly increased by approximately 1.7 to 2.5 times by using the anti-CAPRIN-1 antibody in combination with PD 168393, erlotinib, or zipalertinib (TAS6417).

[0146]

Combinations of any anti-CAPRIN-1 antibody described in WO2010/016526, WO2011/096517, WO2011/096528, WO2011/096519, WO2011/096533, WO2011/096534, WO2011/096535, WO2013/018886, WO2013/018894, WO2013/018892, WO2013/018891, WO2013/018889, WO2013/018883, WO2013/125636, WO2013/125654, WO2013/125640, WO2013/147169, WO2013/147176 and WO2015/020212 and PD 168393, erlotinib, or TAS6417 exhibit similar increase in phagocytic activity against cancer cells as in the combination of the anti-CAPRIN-1 humanized antibody #1 and PD 168393, erlotinib, or zipalertinib (TAS6417) against the above human cancer cells.

[0147]

(Example 2B) *In vitro* antitumor effect 2 of combination of anti-CAPRIN-1 antibody and PD 168393, erlotinib, or zipalertinib (TAS6417)

Antitumor effects of a combination of an anti-CAPRIN-1 antibody and an EGFR inhibitor PD 168393, erlotinib, or zipalertinib (TAS6417) were evaluated *in vitro*. The PD 168393 used was purchased from Cayman Chemical Company (Cat. No.: 21059). The erlotinib used was erlotinib hydrochloride purchased from FUJIFILM Wako Pure Chemical

Corporation (Cat. No.: 057-09111). The zipalertinib (TAS6417) used was purchased from Selleck Chemicals LLC (Cat. No.: S8814).

[0148]

Specifically, in each EGFR inhibitor combination test group, the indicated drug used in combination was applied to human cancer cells, and then the cancer cells were cocultured with human monocytic cells (THP-1) in the presence of the anti-CAPRIN-1 antibody, and the antibody-mediated phagocytic activity against the cancer cells by THP-1 was evaluated. A human IgG antibody (Sigma-Aldrich Co. LLC, Cat. No.: 4506) was used as a control antibody.

[0149]

The human-derived cancer cell used was a colon cancer cell line HCT116. On a 6-well plate, the human-derived cancer cells were cultured for 2 days in the presence of the respective drugs used in combination, for the PD 168393 combination test group, the erlotinib combination test group, and the zipalertinib (TAS6417) combination test groups. Specifically, PD 168393 was added at a concentration of 10 μM, erlotinib at a concentration of 50 μM, and zipalertinib (TAS6417) at a concentration of 20 μM or 40 μM, to HCT116. As a control, a test group without a drug used in combination, in which only the anti-CAPRIN-1 antibody was added, was established. In the control group, the cancer cells were cultured for 2 days without addition of the drug used in combination, beforehand.

[0150]

Each cancer cell line after the culture was dissociated with TrypLE Express (Thermo), and the cancer cells were stained by the addition of calcein-AM at a final concentration of 0.04 μg/mL and incubation at 37°C for 10 minutes. Next, the cells were dispensed at 5×10^3 cancer cells per well to a 96-well plate, and the anti-CAPRIN-1 antibody at a final concentration of 1 μg/mL (or control IgG antibody at the same concentration) and 1.25×10^5 THP-1 cells were added to each well, followed by culture at 37°C for 1 hour under a condition of 5% CO_2. Then, the cells were washed with PBS (phosphate buffer solution) containing 1% FBS (fetal bovine serum), and the human monocytic cells were stained through a reaction with an APC (allophycocyanin)-labeled anti-human CD45 antibody (final concentration: 0.25 μg/mL). Further, dead cells were stained with propidium iodide (PI) (final concentration: 0.1 μg/mL),

followed by the measurement of fluorescence from each cell. PI-positive dead cells were excluded from analysis. The human monocytic cells THP-1 recognize an antibody bound onto cancer cells and phagocytize the cancer cells. At that time, if the cancer cells have been stained with calcein-AM, the monocytic cells ingesting the cancer cells by phagocytosis also become positive to calcein-AM. Thus, the phagocytic activity in this evaluation system was calculated as the ratio (%) of APC-positive/calcein-AM-positive cells to the whole calcein-AM-positive population.

[0151]

As a result of evaluation using the anti-CAPRIN-1 antibody prepared in Example 1 (anti-CAPRIN-1 humanized antibody #1) as an anti-CAPRIN-1 antibody, phagocytic activity against cancer cells of 69% or more was observed for PD 168393 and erlotinib combination test groups, respectively, while phagocytic activity against cancer cells of 39% or less was observed against HCT116 for the test group without a drug used in combination. As a result of conducting Dunnett's test, the phagocytic activity of the PD 168393 and erlotinib combination test groups was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%) (Figure 3).

[0152]

Similarly, phagocytic activity against cancer cells of 52% or more was observed for zipalertinib (TAS6417) combination test groups, while phagocytic activity against cancer cells of 27% or less was observed against HCT116 for the test group without a drug used in combination. As a result of conducting Dunnett's test, the phagocytic activity of the zipalertinib (TAS6417) combination test groups was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%) (Figure 4). Thus, the antitumor effect of the anti-CAPRIN-1 antibody on the human cancer cells was significantly increased by approximately 1.7 to 2.5 times by using the anti-CAPRIN-1 antibody in combination with PD 168393, erlotinib, or zipalertinib (TAS6417).

[0153]

(Example 3) *In vitro* antitumor effects of antibody alone and combination of antibody and PD 168393 or zipalertinib (TAS6417)

Antitumor effects of anti-CAPRIN-1 antibody, anti-CD20 antibody or anti-HER-2 antibody each alone, or a combination of each of these antibodies and PD 168393 or zipalertinib (TAS6417) were evaluated *in vitro*. The PD 168393 used was purchased from Cayman Chemical Company (Cat. No.: 21059). The zipalertinib (TAS6417) used was purchased from Selleck Chemicals LLC (Cat. No.: S8814). The anti-CD20 antibody ("Rituxan") and anti-HER-2 antibody ("Herceptin") used were purchased from Chugai Pharmaceutical Co., Ltd.

[0154]

Specifically, in each EGFR inhibitor combination test group, the indicated drug used in combination was applied to human cancer cells, and then the cancer cells were cocultured with human monocytic cells (THP-1) in the presence of the anti-CAPRIN-1 antibody, anti-CD20 antibody or anti-HER-2 antibody at 1 μM, and the antibody-mediated phagocytic activity against the cancer cells by THP-1 was evaluated.

[0155]

The human-derived cancer cell used was a colon cancer cell line HCT116. On a 6-well plate, the human-derived cancer cells were cultured for 2 days in the presence of the respective drugs used in combination, for the PD 168393 combination test group and the zipalertinib (TAS6417) combination test group. Specifically, PD 168393 was added at a concentration of 10 μM, and zipalertinib (TAS6417) at a concentration of 40 μM, to HCT 116. As a control, a test group without a drug used in combination, in which only the anti-CAPRIN-1 antibody, anti-CD20 antibody or anti-HER-2 antibody was added, was established. In the control group, the cancer cells were cultured for 2 days without addition of the drug used in combination, beforehand.

[0156]

Each cancer cell line after the culture was dissociated with TrypLE Express (Thermo), and the cancer cells were stained by the addition of calcein-AM at a final concentration of 0.04 μg/mL and incubation at 37°C for 10 minutes. Next, the cells were dispensed at 1×10^4 cancer cells per well to a 96-well plate, and the anti-CAPRIN-1 antibody, anti-CD20 antibody or anti-HER-2 antibody at a final concentration of 1 μg/mL and 10×10^5 THP-1 cells were added to each well, followed by culture at 37°C for 1 hour under a condition of 5% CO_2. Then, the cells

were washed with PBS (phosphate buffer solution) containing 1% FBS (fetal bovine serum), and the human monocytic cells were stained through a reaction with an APC (allophycocyanin)-labeled anti-human CD45 antibody (final concentration: 0.25 μg/mL). Further, dead cells were stained with propidium iodide (PI) (final concentration: 0.1 μg/mL), followed by the measurement of fluorescence from each cell by flow cytometry. PI-positive dead cells were excluded from analysis. The human monocytic cells THP-1 recognize an antibody bound onto cancer cells and phagocytize the cancer cells. At that time, if the cancer cells have been stained with calcein-AM, the monocytic cells ingesting the cancer cells by phagocytosis also become positive to calcein-AM. Thus, the phagocytic activity in this evaluation system was calculated as the ratio (%) of APC-positive/calcein-AM-positive cells to the whole calcein-AM-positive population.

[0157]

As a result of evaluation using the anti-CAPRIN-1 antibody prepared in Example 1 (anti-CAPRIN-1 humanized antibody #1) as an anti-CAPRIN-1 antibody, phagocytic activity against cancer cells of 35% or more was observed for PD 168393 and zipalertinib (TAS6417) combination test groups, respectively, while phagocytic activity against cancer cells of 21% or less was observed against HCT116 for the test group without a drug used in combination. As a result of conducting Dunnett's test, the phagocytic activity of the PD 168393 and zipalertinib (TAS6417) combination test groups was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%) (Figure 5).

[0158]

On the other hand, as a result of evaluation using the anti-CD20 antibody or anti-HER-2 antibody, when the anti-CD20 antibody was used, phagocytic activity against cancer cells of 6% or less was observed for PD 168393 and zipalertinib (TAS6417) combination test groups, respectively, while phagocytic activity against cancer cells of 7% or less was observed against HCT116 for the test group without a drug used in combination, thus the drug efficacy was not increased by the combination. When the anti-HER-2 antibody was used, phagocytic activity against cancer cells of 9% or less was observed for PD 168393 and zipalertinib (TAS6417) combination test groups, respectively, while phagocytic activity against cancer cells of 10% or

less was observed against HCT116 for the test group without a drug used in combination, thus the drug efficacy was not increased by the combination (Figure 5).

[0159]

From the above, it has been suggested that the increase of the anti-tumor effect by the combination of the antibody and PD 168393 or zipalertinib (TAS6417) is an anti-CAPRIN-1 antibody-specific effect.

[0160]

Combinations of any anti-CAPRIN-1 antibody described in WO2010/016526, WO2011/096517, WO2011/096528, WO2011/096519, WO2011/096533, WO2011/096534, WO2011/096535, WO2013/018886, WO2013/018894, WO2013/018892, WO2013/018891, WO2013/018889, WO2013/018883, WO2013/125636, WO2013/125654, WO2013/125640, WO2013/147169, WO2013/147176 and WO2015/020212 and each drug exhibit similar increase in phagocytic activity as in the anti-CAPRIN-1 humanized antibody #1 against the above human cancer cells.

[0161]

(Example 4) *In vitro* antitumor effect of combination of anti-CAPRIN-1 antibody and PD 168393, zipalertinib (TAS6417), or cisplatin

Antitumor effects of a combination of an anti-CAPRIN-1 antibody and PD 168393, zipalertinib (TAS6417), or cisplatin were evaluated *in vitro*. The PD 168393 used was purchased from Cayman Chemical Company (Cat. No.: 21059). The zipalertinib (TAS6417) used was purchased from Selleck Chemicals LLC (Cat. No.: S8814). The cisplatin used was purchased from Pfizer Inc.

[0162]

Specifically, in each inhibitor combination test group, the indicated drug used in combination was applied to human cancer cells, and then the cancer cells were cocultured with human monocytic cells (THP-1) in the presence of the anti-CAPRIN-1 antibody, and the antibody-mediated phagocytic activity against the cancer cells by THP-1 was evaluated.

[0163]

The human-derived cancer cell used was a colon cancer cell line HCT116. On a 6-well plate, the human-derived cancer cells were cultured for 2 days in the presence of the respective drugs used in combination, for the PD 168393 combination test group and the zipalertinib (TAS6417) combination test group. Specifically, PD 168393 was added at a concentration of 10 μM, zipalertinib (TAS6417) at a concentration of 40 μM, and cisplatin at a concentration of 1 μM, to HCT 116. As a control, a test group without a drug used in combination, in which only the anti-CAPRIN-1 antibody was added, was established. In the control group, the cancer cells were cultured for 2 days without addition of the drug used in combination, beforehand.

[0164]

Each cancer cell line after the culture was dissociated with TrypLE Express (Thermo), and the cancer cells were stained by the addition of calcein-AM at a final concentration of 0.04 μg/mL and incubation at 37°C for 10 minutes. Next, the cells were dispensed at 1×10^4 cancer cells per well to a 96-well plate, and the anti-CAPRIN-1 antibody at a final concentration of 1 μg/mL and 10×10^5 THP-1 cells were added to each well, followed by culture at 37°C for 1 hour under a condition of 5% CO_2. Then, the cells were washed with PBS (phosphate buffer solution) containing 1% FBS (fetal bovine serum), and the human monocytic cells were stained through a reaction with an APC (allophycocyanin)-labeled anti-human CD45 antibody (final concentration: 0.25 μg/mL). Further, dead cells were stained with propidium iodide (PI) (final concentration: 0.1 μg/mL), followed by the measurement of fluorescence from each cell by flow cytometry. PI-positive dead cells were excluded from analysis. The human monocytic cells THP-1 recognize an antibody bound onto cancer cells and phagocytize the cancer cells. At that time, if the cancer cells have been stained with calcein-AM, the monocytic cells ingesting the cancer cells by phagocytosis also become positive to calcein-AM. Thus, the phagocytic activity in this evaluation system was calculated as the ratio (%) of APC-positive/calcein-AM-positive cells to the whole calcein-AM-positive population.

[0165]

As a result of evaluation using the anti-CAPRIN-1 antibody prepared in Example 1 (anti-CAPRIN-1 humanized antibody #1) as an anti-CAPRIN-1 antibody, phagocytic activity against cancer cells of 35% or more was observed for PD 168393 and zipalertinib (TAS6417)

combination test groups, respectively, while phagocytic activity against cancer cells of 21% or less was observed against HCT116 for the test group without a drug used in combination. On the other hand, phagocytic activity against cancer cells of 23% or less was observed for the cisplatin combination test group. As a result of conducting Dunnett's test, the phagocytic activity of the PD 168393 and zipalertinib (TAS6417) combination test groups was significantly higher than that of the test group without a drug used in combination ($p < 0.001$, respectively; significance level: 5%), while there was no significant change in the phagocytic activity of the cisplatin combination test group compared to that of the test group without a drug used in combination (Figure 6).

[0166]

From the above, it has been suggested that the increase of anti-tumor effect by the drug combination is an EGFR inhibitor-specific effect.

[0167]

Combinations of any anti-CAPRIN-1 antibody described in WO2010/016526, WO2011/096517, WO2011/096528, WO2011/096519, WO2011/096533, WO2011/096534, WO2011/096535, WO2013/018886, WO2013/018894, WO2013/018892, WO2013/018891, WO2013/018889, WO2013/018883, WO2013/125636, WO2013/125654, WO2013/125640, WO2013/147169, WO2013/147176 and WO2015/020212 and each drug exhibit similar change in phagocytic activity as in the anti-CAPRIN-1 humanized antibody #1 against the above human cancer cells. All publications, patents and patent applications cited herein are incorporated herein by reference in their entirety.

Claims

[Claim 1]

A medicament for treatment and/or prevention of cancer, comprising an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein, and an epidermal growth factor receptor (EGFR) inhibitor together or separately in combination.

[Claim 2]

The medicament according to claim 1, wherein the EGFR inhibitor is erlotinib, zipalertinib, or PD 168393.

[Claim 3]

The medicament according to claim 1 or 2, wherein the antibody or the fragment thereof has an immunological reactivity with CAPRIN-1 protein having an amino acid sequence shown by any one of the even numbered SEQ ID NOs: 2 to 30, or an amino acid sequence having 80% or more sequence identity with the amino acid sequence.

[Claim 4]

The medicament according to any one of claims 1 to 3, wherein the antibody or the fragment thereof has an immunological reactivity with an extracellular region of CAPRIN-1 protein present on a cancer cell surface.

[Claim 5]

The medicament according to any one of claims 1 to 4, wherein the antibody or the fragment thereof has an immunological reactivity with a partial polypeptide of CAPRIN-1 protein, the partial polypeptide having an amino acid sequence shown by any one of SEQ ID NOs: 31 to 35, 296 to 299, 308 and 309, or an amino acid sequence having 80% or more sequence identity with the amino acid sequence.

[Claim 6]

The medicament according to any one of claims 1 to 5, wherein the antibody is a monoclonal antibody or a polyclonal antibody.

[Claim 7]

The medicament according to any one of claims 1 to 6, wherein the antibody or the fragment thereof is any one of the following (A) to (M):

(A) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 36, 37 and 38 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 40, 41 and 42 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(B) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 44, 45 and 46 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 48, 49 and 50 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(C) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 52, 53 and 54 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 56, 57 and 58 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(D) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 60, 61 and 62 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 64, 65 and 66 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(E) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 170, 171 and 172 (CDR1, CDR2 and

CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 173, 174 and 175 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(F) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 176, 177 and 178 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 179, 180 and 181 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(G) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 182, 183 and 184 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 185, 186 and 187 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(H) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 188, 189 and 190 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 191, 192 and 193 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(I) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 146, 147 and 148 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 149, 150 and 151 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(J) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 272, 273 and 274 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 275, 276 and 277 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(K) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 290, 291 and 292 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 293, 294 and 295 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein;

(L) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 301, 302 and 303 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 305, 306 and 307 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein; and

(M) an antibody or a fragment thereof comprising a heavy-chain variable region comprising complementarity determining regions of SEQ ID NOs: 134, 135 and 136 (CDR1, CDR2 and CDR3, respectively) and a light-chain variable region comprising complementarity determining regions of SEQ ID NOs: 137, 138 and 139 (CDR1, CDR2 and CDR3, respectively), and having an immunological reactivity with CAPRIN-1 protein.

[Claim 8]

The medicament according to any one of claims 1 to 7, wherein the antibody or the fragment thereof is any one of the following (a) to (al):

(a) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 39 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 43;

(b) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 47 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 51;

(c) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 55 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 59;

(d) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 63 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 67;

(e) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 68 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 69;

(f) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 70 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 71;

(g) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 72 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 73;

(h) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 74 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 75;

(i) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 76 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 77;

(j) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 78 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 79;

(k) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 80 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 81;

(l) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 82 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 83;

(m) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 84 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 85;

(n) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 86 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 87;

(o) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 88 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 89;

(p) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 90 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 91;

(q) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 92 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 93;

(r) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 94 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 95;

(s) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 96 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 97;

(t) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 98 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 99;

(u) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 100 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 101;

(v) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 102 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 103;

(w) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 104 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 105;

(x) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 106 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 107;

(y) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 108 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 109;

(z) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 110 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 111;

(aa) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 112 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 113;

(ab) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 114 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 115;

(ac) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 116 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 117;

(ad) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 118 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 119;

(ae) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 120 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 121;
(af) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 122 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 123;
(ag) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 124 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 125;
(ah) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 126 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 127;
(ai) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 128 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 129;
(aj) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 130 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 131;
(ak) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 132 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 133; and
(al) an antibody or a fragment thereof comprising a heavy-chain variable region comprising the amino acid sequence of SEQ ID NO: 300 and a light-chain variable region comprising the amino acid sequence of SEQ ID NO: 304.

[Claim 9]

The medicament according to any one of claims 1 to 8, wherein the antibody is a human antibody, a humanized antibody, a chimeric antibody or a single chain antibody.

[Claim 10]

The medicament according to any one of claims 1 to 9, wherein the cancer is a cancer expressing CAPRIN-1 protein on a cell membrane surface.

[Claim 11]

The medicament according to any one of claims 1 to 10, wherein the cancer is colon cancer, lung cancer, prostate cancer, ovarian cancer, pancreatic cancer, kidney cancer, breast cancer, gastric cancer, bile duct cancer, thyroid cancer, melanoma, renal cell cancer, Hodgkin's lymphoma, head and neck cancer, mesothelioma, colorectal cancer, esophageal cancer, gastroesophageal junction cancer, hepatocellular cancer, glioblastoma, urothelial cancer, urinary bladder cancer, uterus cancer, primary central nervous system lymphoma, primary testicular lymphoma, biliary tract cancer, brain tumor, leukemia, liver cancer, sarcoma, fibrosarcoma, mastocytoma, adrenal cortex cancer, Ewing's tumor, testicle cancer, basal cell cancer, lymphoma, multiple myeloma, Paget's disease or skin cancer.

[Claim 12]

An agent increasing drug efficacy of a pharmaceutical composition for treatment and/or prevention of cancer comprising an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein as an active ingredient, wherein the agent comprises an EGFR inhibitor as an active ingredient.

[Claim 13]

An agent increasing drug efficacy of a pharmaceutical composition for treatment and/or prevention of cancer comprising an EGFR inhibitor as an active ingredient, wherein the agent comprises an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein as an active ingredient.

[Claim 14]

A method for treating and/or preventing cancer, comprising administering an antibody or a fragment thereof having an immunological reactivity with CAPRIN-1 protein, and an EGFR inhibitor together or separately to a subject.

Fig. 1

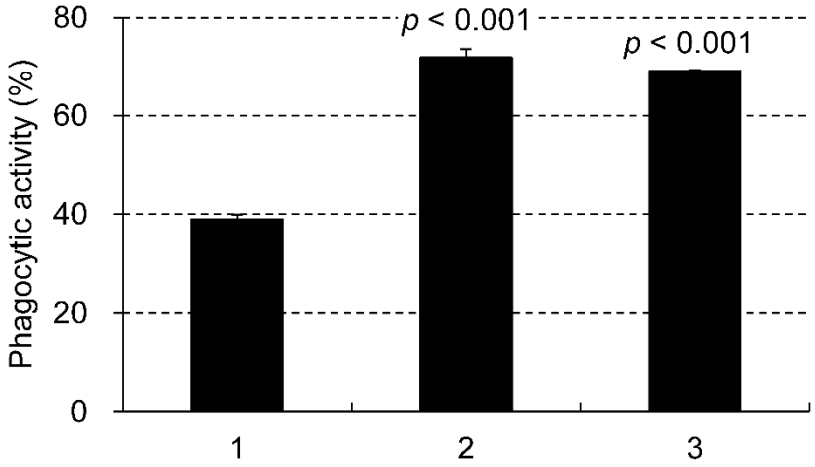


Fig. 2

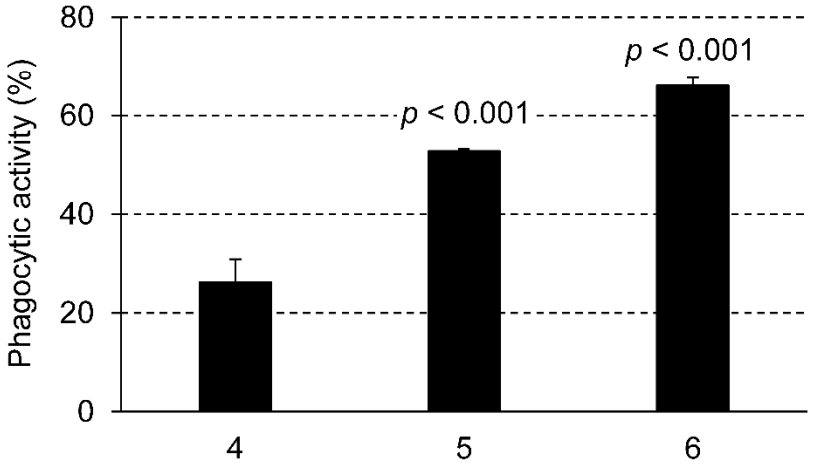


Fig. 3

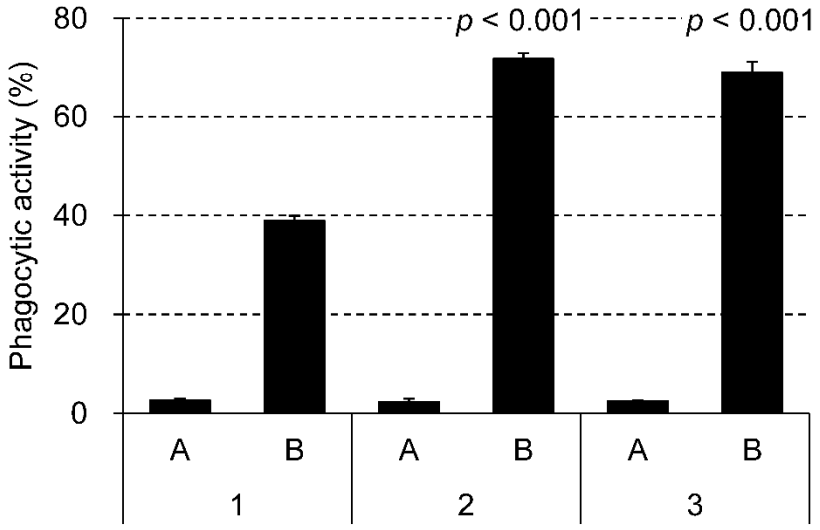


Fig. 4

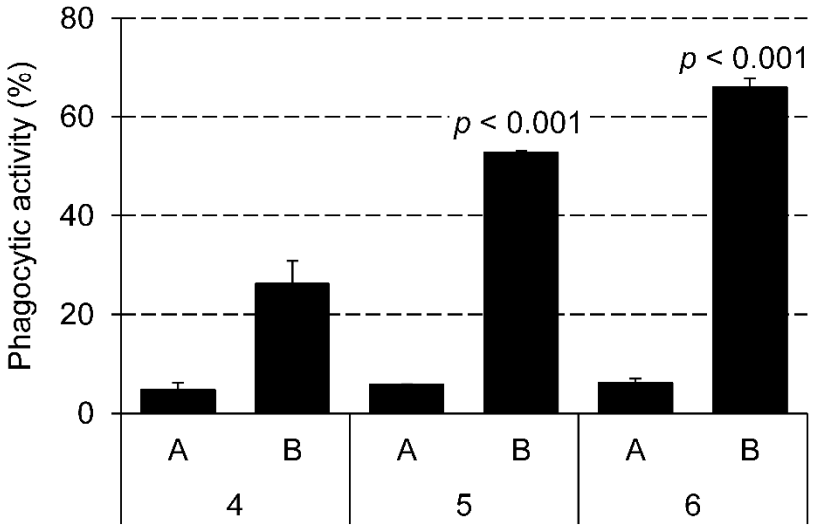


Fig. 5

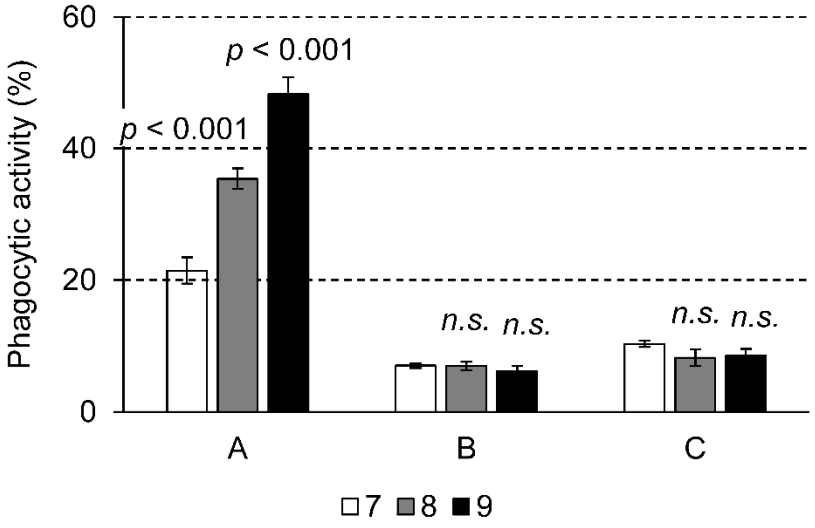
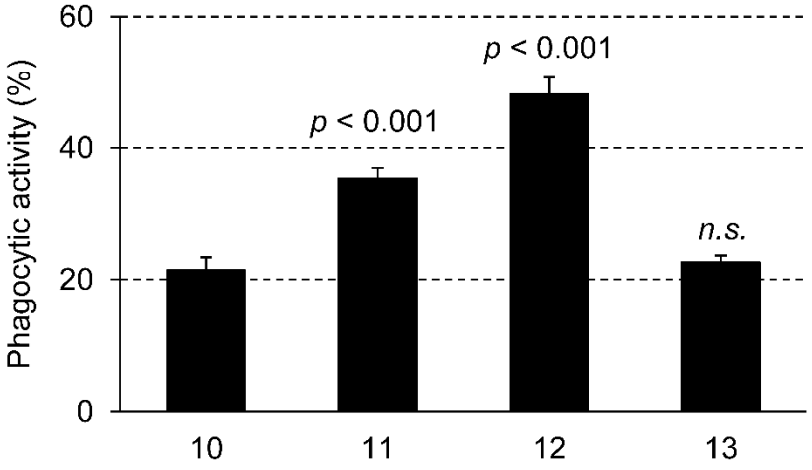


Fig. 6



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1-3	Software Name	WIPO Sequence
1-4	Software Version	2.3.0
1-5	Production Date	2023-08-02
1-6	Original free text language code	
1-7	Non English free text language code	
2	**General Information**	
2-1	Current application: IP Office	
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	22B0553WO01
2-5	Earliest priority application: IP Office	JP
2-6	Earliest priority application: Application number	2022-133049
2-7	Earliest priority application: Filing date	2022-08-24
2-8en	Applicant name	TORAY Industries, Inc.
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
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3-1-5	Residues	cagagggctg ctggctggct aagtccctcc cgctcccggc tctcgcctca ctaggagcgg 60 ctctcggtgc agcgggacag ggcgaagcgg cctgcgccca cggagcgcgc gacactgccc 120 ggaagggacc gccacccttg ccccctcagc tgcccactcg tgatttccag cggcctccgc 180 gcgcgcacga tgccctcggc caccagccac agcgggagcg gcagcaagtc gtccggaccg 240 ccaccgccgt cgggttcctc cgggagtgag gcggccgcgg gagccggggc cgccgcgccg 300 gcttctcagc accccgcaac cggcaccggc gctgtccaga ccgaggccat gaagcagatt 360 ctcggggtga tcgacaagaa acttcggaac ctggagaaga aaaagggtaa gcttgatgat 420 taccaggaac gaatgaacaa aggggaaagg cttaatcaag atcagctgga tgccgtttct 480 aagtaccagg aagtcacaaa taatttggag tttgcaaaag aattacagag gagtttcatg 540 gcactaagtc aagatattca gaaaacaata aagaagacag cacgtcggga gcagcttatg 600 agagaagaag ctgaacagaa acgtttaaaa actgtacttg agctacagta tgttttggac 660 aaattgggag atgatgaagt gcggactgac ctgaaacaag gtttgaatgg agtgccaata 720 ttgtccgaag aggagttgtc attgttggat gaattctata agctagtaga ccctgaacgg 780 gacatgagct tgaggttgaa tgaacagtat gaacatgcct ccattcacct gtgggacctg 840 ctggaaggga aggaaaaacc tgtatgtgga accacctata aagttctaaa ggaaattgtt 900 gagcgtgttt ttcagtcaaa ctactttgac agcacccaca accaccagaa tgggctgtgt 960 gaggaagaag aggcagcctc agcacctgca gttgaagacc aggtacctga agctgaacct 1020 gagccagcag aagagtacac tgagcaaagt gaagttgaat caacagagta tgtaaataga 1080 cagttcatgg cagaaacaca gttcaccagt ggtgaaaagg agcaggtaga tgagtggaca 1140 gttgaaacgg ttgaggtggt aaattcactc cagcagcaac ctcaggctgc atccccttca 1200 gtaccagagc cccactcttt gactccagtg gctcaggcag atccccttgt gagaagacag 1260 cgagtacaag accttatggc acaaatgcag ggtccctata atttcataca ggattcaatg 1320 ctggattttg aaaatcagac acttgatcct gccattgtat ctgcacagcc tatgaatcca 1380 acacaaaaca tggacatgcc ccagctggtt tgccctccag ttcattctga atctagactt 1440 gctcagccta atcaagttcc tgtacaacca gaagcgacac aggttccttt ggtatcatcc 1500 acaagtgagg ggtacacagc atctcaaccc ttgtaccagc cttctcatgc tacagagcaa 1560 cgaccacaga aggaaccaat tgatcagatt caggcaacaa tctctttaaa tacagaccag 1620 actacagcat catcatccct tcctgctgcg tctcagcctc aagtatttca ggctgggaca 1680 agcaaacctt tacatagcag tggaatcaat gtaaatgcag ctccattcca atccatgcaa 1740 acggtgttca atatgaatgc cccagttcct cctgttaatg aaccagaaac tttaaaacag 1800 caaaatcagt accaggccag ttataaccag agcttttcta gtcagcctca ccaagtagaa 1860 caaacagagc ttcagcaaga acagcttcaa acagtggttg gcacttacca tggttcccca 1920 gaccagtccc atcaagtgac tggtaaccac cagcagcctc ctcagcagaa cactggattt 1980 ccacgtagca atcagcccta ttacaatagt cgtggtgtgt ctcgtggagg ctcccgtggt 2040 gctagaggct tgatgaatgg ataccggggc cctgccaatg gattcagagg aggatatgat 2100 ggttaccgcc cttcattctc taacactcca aacagtggtt atacacagtc tcagttcagt 2160 gctccccggg attactctgg ctatcaacgg gatggatatc agcagaattt caagcgaggc 2220 tctgggcaga gtggaccacg gggagcccca cgaggtcgtg gagggccccc aagacccaac 2280 agagggatgc cgcaaatgaa cactcagcaa gtgaattaat ctgattcaca ggattatgtt 2340 taatcgccaa aaacacactg gccagtgtac cataatatgt taccagaaga gttattatct 2400 atttgttctc cctttcagga aacttattgt aaagggactg ttttcatccc ataaagacag 2460 gactacaatt gtcagctttc tattacctgg atatggaagg aaactatttt tactctgcat 2520 gttctgtcct aagcgtcatc ttgagccttg cacatgatac tcagattcct cacccttgct 2580 taggagtaaa acaatatact ttacagggtg ataataatct ccatagttat ttgaagtggc 2640 ttgaaaaagg caagattgac ttttatgaca ttggataaaa tctacaaatc agccctcgag 2700 ttattcaatg ataactgaca aactaaatta tttccctaga aaggaagatg aaaggagtgg 2760 agtgtggttt ggcagaacaa ctgcatttca cagcttttcc agttaaattg gagcactgaa 2820 cgttcagatg cataccaaat tatgcatggg tcctaatcac acatataagg ctggctacca 2880 gctttgacac agcactgttc atctggccaa acaactgtgg ttaaaaacac atgtaaaatg 2940 ctttttaaca gctgatactg tataagacaa agccaagatg caaaattagg ctttgattgg 3000 cacttttga aaaatatgca acaaatatgg gatgtaatcc ggatggccgc ttctgtactt 3060 aatgtgaaat atttagatac ctttttgaac acttaacagt ttctttgaga caatgacttt 3120

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3-2	**Sequences**	
3-2-1	Sequence Number [ID]	2
3-2-2	Molecule Type	AA
3-2-3	Length	709
3-2-4	Features	**source 1..709**
	Location/Qualifiers	mol_type=protein organism=Homo sapiens
	NonEnglishQualifier Value	
3-2-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAGAAAPASQ HPATGTGAVQ TEAMKQILGV 60 IDKKLRNLEK KKGKLDDYQE RMNKGERLNQ DQLDAVSKYQ EVTNNLEFAK ELQRSFMALS 120 QDIQKTIKKT ARREQLMREE AEQKRLKTVL ELQYVLDKLG DDEVRTDLKQ GLNGVPILSE 180 EELSLLDEFY KLVDPERDMS LRLNEQYEHA SIHLWDLLEG KEKPVCGTTY KVLKEIVERV 240 FQSNYFDSTH NHQNGLCEEE EAASAPAVED QVPEAEPEPA EEYTEQSEVE STEYVNRQFM 300 AETQFTSGEK EQVDEWTVET VEVVNSLQQQ PQAASPSVPE PHSLTPVAQA DPLVRRQRVQ 360 DLMAQMQGPY NFIQDSMLDF ENQTLDPAIV SAQPMNPTQN MDMPQLVCPP VHSESRLAQP 420 NQVPVQPEAT QVPLVSSTSE GYTASQPLYQ PSHATEQRPQ KEPIDQIQAT ISLNTDQTTA 480 SSSLPAASQP QVFQAGTSKP LHSSGINVNA APFQSMQTVF NMNAPVPPVN EPETLKQQNQ 540 YQASYNQSFS SQPHQVEQTE LQQEQLQTVV GTYHGSPDQS HQVTGNHQQP PQQNTGFPRS 600 NQPYYNSRGV SRGGSRGARG LMNGYRGPAN GFRGGYDGYR PSFSNTPNSG YTQSQFSAPR 660 DYSGYQRDGY QQNFKRGSGQ SGPRGAPRGR GGPPRPNRGM PQMNTQQVN 709
3-3	**Sequences**	
3-3-1	Sequence Number [ID]	3
3-3-2	Molecule Type	DNA
3-3-3	Length	3553
3-3-4	Features	**source 1..3553**
	Location/Qualifiers	mol_type=other DNA organism=Homo sapiens **CDS 190..2274** protein_id=311 translation=MPSATSHSGSGSKSSGPPPPSGSSGSEAAAGAGAAAPASQHPATGTGAVQTEAMKQI LGVIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQK TIKKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSLLDEFYKLV

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	NonEnglishQualifier Value	
3-3-5	Residues	cagagggctg ctggctggct aagtccctcc cgctcccggc tctcgcctca ctaggagcgg 60 ctctcggtgc agcgggacag ggcgaagcgg cctgcgccca cggagcgcgc gacactgccc 120 ggaagggacc gccacccttg ccccctcagc tgcccactcg tgatttccag cggcctccgc 180 gcgcgcacga tgccctcggc caccagccac agcgggagcg gcagcaagtc gtccggaccg 240 ccaccgccgt cgggttcctc cgggagtgag gcggccgcgg gagccggggc cgccgcgccg 300 gcttctcagc accccgcaac cggcaccggc gctgtccaga ccgaggccat gaagcagatt 360 ctcggggtga tcgacaagaa acttcggaac ctggagaaga aaaagggtaa gcttgatgat 420 taccaggaac gaatgaacaa aggggaaagg cttaatcaag atcagctgga tgccgtttct 480 aagtaccagg aagtcacaaa taatttggag tttgcaaaag aattacagag gagtttcatg 540 gcactaagtc aagatattca gaaaacaata aagaagacag cacgtcggga gcagcttatg 600 agagaagaag ctgaacagaa acgtttaaaa actgtacttg agctacagta tgttttggac 660 aaattgggag atgatgaagt gcggactgac ctgaaacaag gtttgaatgg agtgccaata 720 ttgtccgaag aggagttgtc attgttggat gaattctata agctagtaga ccctgaacgg 780 gacatgagct tgaggttgaa tgaacagtat gaacatgcct ccattcacct gtgggacctg 840 ctggaaggga aggaaaaacc tgtatgtgga accacctata aagttctaaa ggaaattgtt 900 gagcgtgttt ttcagtcaaa ctactttgac agcacccaca accaccagaa tgggctgtgt 960 gaggaagaag aggcagcctc agcacctgca gttgaagacc aggtacctga agctgaacct 1020 gagccagcag aagagtacac tgagcaaagt gaagttgaat caacagagta tgtaaataga 1080 cagttcatgg cagaaacaca gttcaccagt ggtgaaaagg agcaggtaga tgagtggaca 1140 gttgaaacgg ttgaggtggt aaattcactc cagcagcaac ctcaggctgc atccccttca 1200 gtaccagagc cccactcttt gactccagtg gctcaggcag atccccttgt gagaagacag 1260 cgagtacaag accttatggc acaaatgcag ggtccctata atttcataca ggattcaatg 1320 ctggattttg aaaatcagac acttgatcct gccattgtat ctgcacagcc tatgaatcca 1380 acacaaaaca tggacatgcc ccagctggtt tgccctccag ttcattctga atctagactt 1440 gctcagccta atcaagttcc tgtacaacca gaagcgacac aggttccttt ggtatcatcc 1500 acaagtgagg ggtacacagc atctcaaccc ttgtaccagc cttctcatgc tacagagcaa 1560 cgaccacaga aggaaccaat tgatcagatt caggcaacaa tctctttaaa tacagaccag 1620 actacagcat catcatccct tcctgctgcg tctcagcctc aagtatttca ggctgggaca 1680 agcaaacctt tacatagcag tggaatcaat gtaaatgcag ctccattcca atccatgcaa 1740 acggtgttca atatgaatgc cccagttcct cctgttaatg aaccagaaac tttaaaacag 1800 caaaatcagt accaggccag ttataaccag agcttttcta gtcagcctca ccaagtagaa 1860 caaacagagc ttcagcaaga acagcttcaa acagtggttg gcacttacca tggttcccca 1920 gaccagtccc atcaagtgac tggtaaccac cagcagcctc ctcagcagaa cactggattt 1980 ccacgtagca atcagcccta ttacaatagt cgtggtgtgt ctcgtggagg ctcccgtggt 2040 gctagaggct tgatgaatgg ataccggggc cctgccaatg gattcagagg aggatatgat 2100 ggttaccgcc cttcattctc taacactcca aacagtggtt atacacagtc tcagttcagt 2160 gctccccggg attactctgg ctatcaacgg gatggatatc agcagaattt caagcgaggc 2220 tctgggcaga gtggaccacg gggagcccca cgaggtaata ttttgtggtg gtgatcctag 2280 ctcctaagtg gagcttctgt tctggccttg gaagagctgt taatagtctg catgttagga 2340 atacatttat cctttccaga cttgttgcta gggattaaat gaaatgctct gtttctaaaa 2400 cttaatcttg gacccaaatt ttaatttttg aatgatttaa ttttccctgt tactatataa 2460 actgtcttga aaactagaac atattctctt ctcagaaaaa gtgtttttcc aactgaaaat 2520 tatttttcag gtcctaaaac ctgctaaatg tttttaggaa gtacttactg aaacattttt 2580 gtaagacatt tttggaatga gattgaacat ttatataaat ttattattcc tctttcattt 2640 ttttgaaaca tgcctattat attttagggc cagacaccct ttaatggccg gataagccat 2700 agttaacatt tagagaacca tttagaagtg atagaactaa tggaatttgc aatgccttt 2760 ggacctctat tagtgatata aatatcaagt tatttctgac ttttaaacaa aactcccaaa 2820 ttcctaactt attgagctat acttaaaaaa aattacaggt ttagagagtt ttttgttttt 2880 cttttactgt tggaaaacta cttcccattt tggcaggaag ttaacctatt taacaattag 2940 agctagcatt tcatgtagtc tgaaattcta aatggttctc tgatttgagg gaggttaaac 3000 atcaaacagg tttcctctat tggccataac atgtataaaa tgtgtgttaa ggaggaatta 3060 caacgtactt tgatttgaat actagtagaa actggccagg aaaaaggtac atttttctaa 3120 aaattaatgg atcacttggg aattactgac ttgactagaa gtatcaaagg atgtttgcat 3180 gtgaatgtgg gttatgttct ttcccacctt gtagcatatt cgatgaaagt tgagttaact 3240 gatagctaaa aatctgtttt aacagcatgt aaaaagttat tttatctgtt aaaagtcatt 3300 atacagtttt gaatgttatg tagtttcttt ttaacagttt aggtaataag gtctgttttc 3360 attctggtgc ttttattaat tttgatagta tgatgttact tactactgaa atgtaagcta 3420 gagtgtacac tagaatgtaa gctccatgag agcaggtacc ttgtctgtct tctctgctgt 3480 atctattccc aacgcttgat gatggtgcct ggcacatagt aggcactcaa taaatatttg 3540 ttgaatgaat gaa 3553
3-4	**Sequences**	
3-4-1	Sequence Number [ID]	4
3-4-2	Molecule Type	AA
3-4-3	Length	694
3-4-4	Features	**source 1..694**

	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-4-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAGAAAPASQ HPATGTGAVQ TEAMKQILGV 60 IDKKLRNLEK KKGKLDDYQE RMNKGERLNQ DQLDAVSKYQ EVTNNLEFAK ELQRSFMALS 120 QDIQKTIKKT ARREQLMREE AEQKRLKTVL ELQYVLDKLG DDEVRTDLKQ GLNGVPILSE 180 EELSLLDEFY KLVDPERDMS LRLNEQYEHA SIHLWDLLEG KEKPVCGTTY KVLKEIVERV 240 FQSNYFDSTH NHQNGLCEEE EAASAPAVED QVPEAEPEPA EEYTEQSEVE STEYVNRQFM 300 AETQFTSGEK EQVDEWTVET VEVVNSLQQQ PQAASPSVPE PHSLTPVAQA DPLVRRQRVQ 360 DLMAQMQGPY NFIQDSMLDF ENQTLDPAIV SAQPMNPTQN MDMPQLVCPP VHSESRLAQP 420 NQVPVQPEAT QVPLVSSTSE GYTASQPLYQ PSHATEQRPQ KEPIDQIQAT ISLNTDQTTA 480 SSSLPAASQP QVFQAGTSKP LHSSGINVNA APFQSMQTVF NMNAPVPPVN EPETLKQQNQ 540 YQASYNQSFS SQPHQVEQTE LQQEQLQTVV GTYHGSPDQS HQVTGNHQQP PQQNTGFPRS 600 NQPYYNSRGV SRGGSRGARG LMNGYRGPAN GFRGGYDGYR PSFSNTPNSG YTQSQFSAPR 660 DYSGYQRDGY QQNFKRGSGQ SGPRGAPRGN ILWW 694
3-5	**Sequences**	
3-5-1	Sequence Number [ID]	5
3-5-2	Molecule Type	DNA
3-5-3	Length	1605
3-5-4	Features	**source 1..1605**
	Location/Qualifiers	mol_type=other DNA
		organism=Canis familiaris
		CDS 46..1392
		protein_id=312
		translation=MALSQDIQKTIKKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLN GVPILSEEELSLLDEFYKLADPERDMSLRLNEQYEHASIHLWDLLEGKEKSVCGTTYKALKEIVERVF QSNYFDSTHNHQNGLCEEEEAASAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGE KEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSM LDFENQTLDPAIVSAQPMNPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTSEGYTAS QPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPF QSMQTVFNMNAPVPPVNEPETLKQQNQYQASYNQSFSSQPHQVEQTEGCRK
	NonEnglishQualifier Value	
3-5-5	Residues	gtcacaaata acttggagtt tgcaaaagaa ttacagagga gtttcatggc attaagtcaa 60 gatattcaga aaacaataaa gaagactgca cgtcgggagc agcttatgag agaggaagcg 120 gaacaaaaac gtttaaaaac tgtacttgag ctccagtatg ttttggacaa attgggagat 180 gatgaagtga gaactgacct gaagcaaggt ttgaatggag tgccaatatt gtctgaagaa 240 gaattgtcgt tgttggatga attctacaaa ttagcagacc ctgaacggga catgagcttg 300 aggttgaatg agcagtatga acatgcttcc attcacctgt gggacttgct ggaaggaaag 360 gaaaagtctg tatgtggaac aacctataaa gcactaaagg aaattgttga gcgtgttttc 420 cagtcaaatt actttgacag cactcacaac caccagaatg ggctatgtga ggaagaagag 480 gcagcctcag cacctacagt tgaagaccag gtagctgaag ctgagcctga gccagcagaa 540 gaatacactg aacaaagtga agttgaatca acagagtatg taaatagaca atttatggca 600 gaaacacagt tcagcagtgg tgaaaaggag caggtagatg agtggacggt cgaaacagtg 660 gaggtggtga attcactcca gcagcaacct caggctgcgt ctccttcagt accagagccc 720 cactctttga ctccggtggc tcaggcagat ccccttgtga gaagacagcg agtccaggac 780 cttatggcgc agatgcaggg gccctataat ttcatacagg attcaatgct ggattttgaa 840 aaccagacac tcgatcctgc cattgtatct gcacagccta tgaatccgac acaaaacatg 900 gacatgcccc agctggtttg ccctccagtt cattctgaat ctagacttgc tcaacctaat 960 caagttcctg tacaaccaga agctacacag gttcctttgg tttcatccac aagtgagggg 1020 tatacagcat ctcaaccctt gtaccagcct tctcatgcta cagagcaacg accacaaaag 1080 gaaccaattg accagattca ggcaacaatc tctttaaata cagaccagac tacagcgtca 1140 tcatcccttc cggctgcttc tcagcctcag gtattccagg ctgggacaag caaaccatta 1200 catagcagtg gaatcaatgt aaatgcagct ccattccaat ccatgcaaac ggtgttcaat 1260 atgaatgccc cagttcctcc tgttaatgaa ccagaaactt tgaaacaaca aaatcagtac 1320 caggccagtt ataaccagag cttttctagt cagcctcacc aagtagaaca aacagaggga 1380 tgccgcaaat gaacactcag caagtgaatt aatctgattc acaggattat gtttaaacgc 1440 caaaaacaca ctggccagtg taccataata tgttaccaga agagttatta tctatttgtt 1500 ctccctttca ggaaacttat tgtaaaggga ctgttttcat cccataaaga caggactaca 1560 attgtcagct ttatattacc tggaaaaaaa aaaaaaaaaa aaaaa 1605
3-6	**Sequences**	
3-6-1	Sequence Number [ID]	6
3-6-2	Molecule Type	AA
3-6-3	Length	448
3-6-4	Features	**source 1..448**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-6-5	Residues	MALSQDIQKT IKKTARREQL MREEAEQKRL KTVLELQYVL DKLGDDEVRT DLKQGLNGVP 60 ILSEEELSLL DEFYKLADPE RDMSLRLNEQ YEHASIHLWD LLEGKEKSVC GTTYKALKEI 120 VERVFQSNYF DSTHNHQNGL CEEEEAASAP TVEDQVAEAE PEPAEEYTEQ SEVESTEYVN 180 RQFMAETQFS SGEKEQVDEW TVETVEVVNS LQQQPQAASP SVPEPHSLTP VAQADPLVRR 240 QRVQDLMAQM QGPYNFIQDS MLDFENQTLD PAIVSAQPMN PTQNMDMPQL VCPPVHSESR 300

		LAQPNQVPVQ PEATQVPLVS STSEGYTASQ PLYQPSHATE QRPQKEPIDQ IQATISLNTD 360 QTTASSSLPA ASQPQVFQAG TSKPLHSSGI NVNAAPFQSM QTVFNMNAPV PPVNEPETLK 420 QQNQYQASYN QSFSSQPHQV EQTEGCRK 448
3-7	**Sequences**	
3-7-1	Sequence Number [ID]	7
3-7-2	Molecule Type	DNA
3-7-3	Length	4154
3-7-4	Features	**source 1..4154**
	Location/Qualifiers	mol_type=other DNA organism=Canis familiaris **CDS 1..2154** protein_id=313 translation=MPSATSLSGSGSKSSGPPPPSGSSGSEAAAAAGAAGAAGAGAAAPASQHPATGTGAV QTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFM ALSQDIQKTIKKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSL LDEFYKLADPERDMSLRLNEQYEHASIHLWDLLEGKEKSVCGTTYKALKEIVERVFQSNYFDSTHNHQ NGLCEEEEAASAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETV EVVNSLQQQPQAASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAI VSAQPMNPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQ RPQKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAP VPPVNEPETLKQQNQYQASYNQSFSSQPHQVEQTDLQQEQLQTVVGTYHGSQDQPHQVTGNHQQPPQQ NTGFPRSSQPYYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAPRD YSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQMNTQQVN
	NonEnglishQualifier Value	
3-7-5	Residues	atgccgtcgg ccaccagcct cagcggaagc ggcagcaagt cgtcgggccc gccgcccccg 60 tcgggttcct ccgggagcga ggcggcggcg gcggcggggg cggcgggggc ggcgggggcc 120 ggggcggctg cgcccgcctc ccagcacccc gcgaccggca ccggcgctgt ccagaccgag 180 gccatgaagc agatcctcgg ggtgatcgac aagaaactcc ggaacctgga gaagaaaaag 240 ggcaagcttg atgattacca ggaacgaatg aacaaagggg aaaggcttaa tcaagatcag 300 ctggatgccg tatctaagta ccaggaagtc acaaataact tggagtttgc aaaagaatta 360 cagaggagtt tcatggcatt aagtcaagat attcagaaaa caataaagaa gactgcacgt 420 cgggagcagc ttatgagaga ggaagcggaa caaaaacgtt taaaaactgt acttgagctc 480 cagtatgttt tggacaaatt gggagatgat gaagtgagaa ctgacctgaa gcaaggtttg 540 aatggagtgc caatattgtc tgaagaagaa ttgtcgttgt tggatgaatt ctacaaatta 600 gcagaccctg aacgggacat gagcttgagg ttgaatgagc agtatgaaca tgcttccatt 660 cacctgtggg acttgctgga aggaaaggaa aagtctgtat gtggaacaac ctataaagca 720 ctaaaggaaa ttgttgagcg tgttttccag tcaaattact ttgacagcac tcacaaccac 780 cagaatgggc tatgtgagga agaagaggca gcctcagcac ctacagttga agaccaggta 840 gctgaagctg agcctgagcc agcagaagaa tacactgaac aaagtgaagt tgaatcaaca 900 gagtatgtaa atagacaatt tatggcagaa acacagttca gcagtggtga aaaggagcag 960 gtagatgagt ggacggtcga aacagtggag gtggtgaatt cactccagca gcaacctcag 1020 gctgcgtctc cttcagtacc agagccccac tctttgactc cggtggctca ggcagatccc 1080 cttgtgagaa gacagcgagt ccaggacctt atggcgcaga tgcaggggcc ctataatttc 1140 atacaggatt caatgctgga ttttgaaaac cagacactcg atcctgccat tgtatctgca 1200 cagcctatga atccgacaca aaacatggac atgccccagc tggtttgccc tccagttcat 1260 tctgaatcta gacttgctca acctaatcaa gttcctgtac aaccagaagc tacacaggtt 1320 cctttggttt catccacaag tgaggggtat acagcatctc aacccttgta ccagccttct 1380 catgctacag agcaacgacc acaaaaggaa ccaattgacc agattcaggc aacaatctct 1440 ttaaatacag accagactac agcgtcatca tcccttccgg ctgcttctca gcctcaggta 1500 ttccaggctg ggacaagcaa accattacat agcagtggaa tcaatgtaaa tgcagctcca 1560 ttccaatcca tgcaaacggt gttcaatatg aatgccccag ttcctcctgt taatgaacca 1620 gaaactttga aacaacaaaa tcagtaccag gccagttata accagagctt ttctagtcag 1680 cctcaccaag tagaacaaac agaccttcag caagaacagc ttcaaacagt ggttggcact 1740 taccatggtt cccaggacca gccccaccaa gtgactggta accatcagca gcctccccag 1800 cagaacactg gatttccacg tagcagtcag ccctattaca atagtcgtgg tgtgtctcgt 1860 ggtggttccc gtggtgctag aggcttaatg aatggataca ggggccctgc caatggattc 1920 agaggaggat atgatggtta ccgcccttca ttctctaaca ctccaaacag tggttataca 1980 cagtctcagt tcagtgctcc ccgggactac tctggctatc agcgggatgg atatcagcag 2040 aatttcaagc gaggctctgg gcagagtgga ccacggggag ccccacgagg tcgtggaggg 2100 cccccaagac ccaacagagg gatgccgcaa atgaacactc agcaagtgaa ttaatctgat 2160 tcacaggatt atgtttaaac gccaaaaaca cactggccag tgtaccataa tatgttacca 2220 gaagagttat tatctatttg ttctcccttt caggaaactt attgtaaagg gactgttttc 2280 atcccataaa gacaggacta caattgtcag ctttatatta cctggatatg gaaggaaact 2340 atttttattc tgcatgttct tcctaagcgt catcttgagc cttgcacatg atactcagat 2400 tcctcaccct tgcttaggag taaaacataa tacactttac agggtgatat ctccatagtt 2460 atttgaagtg gcttggaaaa agcaagatta acttctgaca ttggataaaa atcaacaaat 2520 cagccctaga gttattcaaa tggtaattga caaaaactaa aatatttccc ttcgagaagg 2580 agtggaatgt ggtttggcag aacaactgca tttcacagct tttccggtta aattggagca 2640 ctaaacgttt agatgcatac caaattatgc atgggccctt aatataaaag gctggctacc 2700 agctttgaca cagcactatt catcctctgg ccaaacaact gtggttaaac aacacatgta 2760 aattgctttt taacagctga tactataata agacaaagcc aaaatgcaaa aattgggctt 2820 tgattggcac tttttgaaaa atatgcaaca aatatgggat gtaatctgga tggccgcttc 2880 tgtacttaat gtgaagtatt tagatacctt tttgaacact taacagtttc ttctgacaat 2940

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3-8	**Sequences**	
3-8-1	Sequence Number [ID]	8
3-8-2	Molecule Type	AA
3-8-3	Length	717
3-8-4	Features	**source 1..717**
	Location/Qualifiers	mol_type=protein organism=Canis familiaris
	NonEnglishQualifier Value	
3-8-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 717
3-9	**Sequences**	
3-9-1	Sequence Number [ID]	9
3-9-2	Molecule Type	DNA
3-9-3	Length	4939
3-9-4	Features	**source 1..4939**
	Location/Qualifiers	mol_type=other DNA organism=Canis familiaris **CDS 1..2109** protein_id=314 translation=MPSATSLSGSGSKSSGPPPPSGSSGSEAAAAAGAAGAAGAGAAAPASQHPATGTGAV QTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFM ALSQDIQKTIKKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSL LDEFYKLADPERDMSLRLNEQYEHASIHLWDLLEGKEKSVCGTTYKALKEIVERVFQSNYFDSTHNHQ NGLCEEEEAASAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETV EVVNSLQQQPQAASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAI VSAQPMNPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQ RPQKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAP VPPVNEPETLKQQNQYQASYNQSFSSQPHQVEQTDLQQEQLQTVVGTYHGSQDQPHQVTGNHQQPPQQ NTGFPRSSQPYYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAPRD YSGYQRDGYQQNFKRGSGQSGPRGAPRGNILWW
	NonEnglishQualifier Value	
3-9-5	Residues	atgccgtcgg ccaccagcct cagcggaagc ggcagcaagt cgtcgggccc gccgcccccg 60 tcgggttcct ccgggagcga ggcggcggcg gcggcggggg cggcgggggc ggcgggggcc 120 ggggcggctg cgcccgcctc ccagcacccc gcgaccggca ccggcgctgt ccagaccgag 180 gccatgaagc agatcctcgg ggtgatcgac aagaaactcc ggaacctgga gaagaaaaag 240 ggcaagcttg atgattacca ggaacgaatg aacaaagggg aaaggcttaa tcaagatcag 300 ctggatgccg tatctaagta ccaggaagtc acaaataact tggagtttgc aaaagaatta 360 cagaggagtt tcatggcatt aagtcaagat attcagaaaa caataaagaa gactgcacgt 420 cgggagcagc ttatgagaga ggaagcggaa caaaaacgtt taaaaactgt acttgagctc 480 cagtatgttt tggacaaatt gggagatgat gaagtgagaa ctgacctgaa gcaaggtttg 540 aatggagtgc caatattgtc tgaagaagaa ttgtcgttgt tggatgaatt ctacaaatta 600

		gcagaccctg aacgggacat gagcttgagg ttgaatgagc agtatgaaca tgcttccatt 660 cacctgtggg acttgctgga aggaaaggaa aagtctgtat gtggaacaac ctataaagca 720 ctaaaggaaa ttgttgagcg tgttttccag tcaaattact ttgacagcac tcacaaccac 780 cagaatgggc tatgtgagga agaagaggca gcctcagcac ctacagttga agaccaggta 840 gctgaagctg agcctgagcc agcagaagaa tacactgaac aaagtgaagt tgaatcaaca 900 gagtatgtaa atagacaatt tatggcagaa acacagttca gcagtggtga aaaggagcag 960 gtagatgagt ggacggtcga aacagtggag gtggtgaatt cactccagca gcaacctcag 1020 gctgcgtctc cttcagtacc agagccccac tctttgactc cggtggctca ggcagatccc 1080 cttgtgagaa gacagcgagt ccaggacctt atggcgcaga tgcaggggcc ctataatttc 1140 atacaggatt caatgctgga ttttgaaaac cagacactcg atcctgccat tgtatctgca 1200 cagcctatga atccgacaca aaacatggac atgccccagc tggtttgccc tccagttcat 1260 tctgaatcta gacttgctca acctaatcaa gttcctgtac aaccagaagc tacacaggtt 1320 cctttggttt catccacaag tgaggggtat acagcatctc aacccttgta ccagccttct 1380 catgctacag agcaacgacc acaaaaggaa ccaattgacc agattcaggc aacaatctct 1440 ttaaatacag 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3-10	**Sequences**	
3-10-1	Sequence Number [ID]	10

3-10-2	Molecule Type	AA
3-10-3	Length	702
3-10-4	Features	**source 1..702**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-10-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRDGYQQ NFKRGSGQSG PRGAPRGNIL WW 702
3-11	**Sequences**	
3-11-1	Sequence Number [ID]	11
3-11-2	Molecule Type	DNA
3-11-3	Length	3306
3-11-4	Features	**source 1..3306**
	Location/Qualifiers	mol_type=other DNA
		organism=Canis familiaris
		CDS 1..2040
		protein_id=315
		translation=MPSATSLSGSGSKSSGPPPPSGSSGSEAAAAAGAAGAAGAGAAAPASQHPATGTGAV QTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFM ALSQDIQKTIKKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSL LDEFYKLADPERDMSLRLNEQYEHASIHLWDLLEGKEKSVCGTTYKALKEIVERVFQSNYFDSTHNHQ NGLCEEEEAASAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETV EVVNSLQQQPQAASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAI VSAQPMNPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQ RPQKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAP VPPVNEPETLKQQNQYQASYNQSFSSQPHQVEQTDLQQEQLQTVVGTYHGSQDQPHQVTGNHQQPPQQ NTGFPRSSQPYYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAPRD YSGYQRGCRK
	NonEnglishQualifier Value	
3-11-5	Residues	atgccgtcgg ccaccagcct cagcggaagc ggcagcaagt cgtcgggccc gccgcccccg 60 tcgggttcct ccgggagcga ggcggcggcg gcggcggggg cggcgggggc ggcgggggcc 120 ggggcggctg cgcccgcctc ccagcacccc gcgaccggca ccggcgctgt ccagaccgag 180 gccatgaagc agatcctcgg ggtgatcgac aagaaactcc ggaacctgga gaagaaaaag 240 ggcaagcttg atgattacca ggaacgaatg aacaaagggg aaaggcttaa tcaagatcag 300 ctggatgccg tatctaagta ccaggaagtc acaaataact tggagtttgc aaaagaatta 360 cagaggagtt tcatggcatt aagtcaagat attcagaaaa caataaagaa gactgcacgt 420 cgggagcagc ttatgagaga ggaagcggaa caaaaacgtt taaaaactgt acttgagctc 480 cagtatgttt tggacaaatt gggagatgat gaagtgagaa ctgacctgaa gcaaggtttg 540 aatggagtgc caatattgtc tgaagaagaa ttgtcgttgt tggatgaatt ctacaaatta 600 gcagaccctg aacgggacat gagcttgagg ttgaatgagc agtatgaaca tgcttccatt 660 cacctgtggg acttgctgga aggaaaggaa aagtctgtat gtggaacaac ctataaagca 720 ctaaaggaaa ttgttgagcg tgttttccag tcaaattact ttgacagcac tcacaaccac 780 cagaatgggc tatgtgagga agaagaggca gcctcagcac ctacagttga agaccaggta 840 gctgaagctg agcctgagcc agcagaagaa tacactgaac aaagtgaagt tgaatcaaca 900 gagtatgtaa atagacaatt tatggcagaa acacagttca gcagtggtga aaaggagcag 960 gtagatgagt ggacggtcga aacagtggag gtggtgaatt cactccagca gcaacctcag 1020 gctgcgtctc cttcagtacc agagccccac tctttgactc cggtggctca ggcagatccc 1080 cttgtgagaa gacagcgagt ccaggacctt atggcgcaga tgcaggggcc ctataatttc 1140 atacaggatt caatgctgga ttttgaaaac cagacactcg atcctgccat tgtatctgca 1200 cagcctatga atccgacaca aaacatggac atgccccagc tggtttgccc tccagttcat 1260 tctgaatcta gacttgctca acctaatcaa gttcctgtac aaccagaagc tacacaggtt 1320 cctttggttt catccacaag tgaggggtat acagcatctc aacccttgta ccagccttct 1380 catgctacag agcaacgacc acaaaaggaa ccaattgacc agattcaggc aacaatctct 1440 ttaaatacag accagactac agcgtcatca tcccttccgg ctgcttctca gcctcaggta 1500 ttccaggctg ggacaagcaa accattacat agcagtggaa tcaatgtaaa tgcagctcca 1560 ttccaatcca tgcaaacggt gttcaatatg aatgccccag ttcctcctgt taatgaacca 1620 gaaactttga aacaacaaaa tcagtaccag gccagttata accagagctt ttctagtcag 1680 cctcaccaag tagaacaaac agaccttcag caagaacagc ttcaaacagt ggttggcact 1740 taccatggtt cccaggacca gccccaccaa gtgactggta accatcagca gcctccccag 1800 cagaacactg gatttccacg tagcagtcag ccctattaca atagtcgtgg tgtgtctcgt 1860 ggtggttccc gtggtgctag aggcttaatg aatggataca ggggccctgc caatggattc 1920 agaggaggat atgatggtta ccgcccttca ttctctaaca ctccaaacag tggttataca 1980 cagtctcagt tcagtgctcc ccgggactac tctggctatc agcggggatg ccgcaaatga 2040

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3-12	**Sequences**	
3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	AA
3-12-3	Length	679
3-12-4	Features	**source 1..679**
	Location/Qualifiers	mol_type=protein organism=Canis familiaris
	NonEnglishQualifier Value	
3-12-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRGCRK 679
3-13	**Sequences**	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	DNA
3-13-3	Length	2281
3-13-4	Features	**source 1..2281**
	Location/Qualifiers	mol_type=other DNA organism=Canis familiaris **CDS 1..2154** protein_id=316 translation=MPSATSLSGSGSKSSGPPPPSGSSGSEAAAAAGAAGAAGAGAAAPASQHPATGTGAV QTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFM ALSQDIQKTIKKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSL LDEFYKLADPERDMSLRLNEQYEHASIHLWDLLEGKEKSVCGTTYKALKEIVERVFQSNYFDSTHNHQ NGLCEEEEAASAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETV EVVNSLQQQPQAASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAI VSAQPMNPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQ RPQKEPIDQIQATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAP VPPVNEPETLKQQNQYQASYNQSFSSQPHQVEQTDLQQEQLQTVVGTYHGSQDQPHQVTGNHQQPPQQ NTGFPRSSQPYYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAPRD YSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQMNTQQVN
	NonEnglishQualifier Value	
3-13-5	Residues	atgccgtcgg ccaccagcct cagcggaagc ggcagcaagt cgtcgggccc gccgcccccg 60 tcgggttcct ccgggagcga ggcggcggcg gcggcggggg cggcgggggc ggcgggggcc 120 ggggcggctg cgcccgcctc ccagcacccc gcgaccggca ccggcgctgt ccagaccgag 180 gccatgaagc agatcctcgg ggtgatcgac aagaaactcc ggaacctgga gaagaaaaag 240 ggcaagcttg atgattacca ggaacgaatg aacaaagggg aaaggcttaa tcaagatcag 300 ctggatgccg tatctaagta ccaggaagtc acaaataact tggagtttgc aaaagaatta 360 cagaggagtt tcatggcatt aagtcaagat attcagaaaa caataaagaa gactgcacgt 420 cgggagcagc ttatgagaga ggaagcggaa caaaaacgtt taaaaactgt acttgagctc 480 cagtatgttt tggacaaatt gggagatgat gaagtgagaa ctgacctgaa gcaaggtttg 540

		aatggagtgc caatattgtc tgaagaagaa ttgtcgttgt tggatgaatt ctacaaatta 600 gcagaccctg aacgggacat gagcttgagg ttgaatgagc agtatgaaca tgcttccatt 660 cacctgtggg acttgctgga aggaaaggaa aagtctgtat gtggaacaac ctataaagca 720 ctaaaggaaa ttgttgagcg tgttttccag tcaaattact ttgacagcac tcacaaccac 780 cagaatgggc tatgtgagga agaagaggca gcctcagcac ctacagttga agaccaggta 840 gctgaagctg agcctgagcc agcagaagaa tacactgaac aaagtgaagt tgaatcaaca 900 gagtatgtaa atagacaatt tatggcagaa acacagttca gcagtggtga aaaggagcag 960 gtagatgagt ggacggtcga aacagtggag gtggtgaatt cactccagca gcaacctcag 1020 gctgcgtctc cttcagtacc agagccccac tctttgactc cggtggctca ggcagatccc 1080 cttgtgagaa gacagcgagt ccaggacctt atggcgcaga tgcaggggcc ctataatttc 1140 atacaggatt caatgctgga ttttgaaaac cagacactcg atcctgccat tgtatctgca 1200 cagcctatga atccgacaca aaacatggac atgccccagc tggtttgccc tccagttcat 1260 tctgaatcta gacttgctca acctaatcaa gttcctgtac aaccagaagc tacacaggtt 1320 cctttggttt catccacaag tgaggggtat acagcatctc aacccttgta ccagccttct 1380 catgctacag agcaacgacc acaaaaggaa ccaattgacc agattcaggc aacaatctct 1440 ttaaatacag accagactac agcgtcatca tcccttccgg ctgcttctca gcctcaggta 1500 ttccaggctg ggacaagcaa accattacat agcagtggaa tcaatgtaaa tgcagctcca 1560 ttccaatcca tgcaaacggt gttcaatatg aatgccccag ttcctcctgt taatgaacca 1620 gaaactttga aacaacaaaa tcagtaccag gccagttata accagagctt ttctagtcag 1680 cctcaccaag tagaacaaac agaccttcag caagaacagc ttcaaacagt ggttggcact 1740 taccatggtt cccaggacca gccccaccaa gtgactggta accatcagca gcctccccag 1800 cagaacactg gatttccacg tagcagtcag ccctattaca atagtcgtgg tgtgtctcgt 1860 ggtggttccc gtggtgctag aggcttaatg aatggataca ggggccctgc caatggattc 1920 agaggaggat atgatggtta ccgcccttca ttctctaaca ctccaaacag tggttataca 1980 cagtctcagt tcagtgctcc ccgggactac tctggctatc agcgggatgg atatcagcag 2040 aatttcaagc gaggctctgg gcagagtgga ccacggggag ccccacgagg tcgtggaggg 2100 cccccaagac ccaacagagg gatgccgcaa atgaacactc agcaagtgaa ttaatctgat 2160 tcacaggatt atgtttaaac gccaaaaaca cactggccag tgtaccataa tatgttacca 2220 gaagagttat tatctatttg gactgttttc atcccataaa gacaggacta caattgtcag 2280 c 2281
3-14	**Sequences**	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	AA
3-14-3	Length	717
3-14-4	Features	**source 1..717**
	Location/Qualifiers	mol_type=protein organism=Canis familiaris
	NonEnglishQualifier Value	
3-14-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 717
3-15	**Sequences**	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	DNA
3-15-3	Length	3386
3-15-4	Features	**source 1..3386**
	Location/Qualifiers	mol_type=other DNA organism=Bos taurus **CDS 82..2208** protein_id=317 translation=MPSATSHSGSGSKSSGPPPPSGSSGNEAGAGAAAPASQHPMTGTGAVQTEAMKQILG VIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTI KKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGVPILSEEELSLLDEFYKLADP ERDMSLRLNEQYEHASIHLWDLLEGKEKPVCGTTYKALKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPTVEDQAAEAEPEPVEEYTEQNEVESTEYVNRQFMAETQFSSGEKEQVDDWTVETVEVVNSLQQQP QAASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPMNPAQ NMDIPQLVCPPVHSESRLAQPNQVSVQPEATQVPLVSSTSEGYTASQPLYQPSHATDQRPQKEPIDQI QATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPVNEPETL KQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVGTYHGSQDQPHQVTGNHQQPPQQNTGFPRSNQ YYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSTNTPNSGYTQSQFSAPRDYSGYQRDG QQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQMNTQQVN
	NonEnglishQualifier Value	
3-15-5	Residues	cgcgtctcgc cccgtccacc gattgactcg ccgctcttgt ccttcctccc gctctttctt 60

		ctctcccctt acggtttcaa gatgccttcg gccaccagcc acagcggaag cggcagcaag 120 tcgtccggac cgccaccgcc gtcgggttcc tccgggaatg aggcgggggc cggggccgcc 180 gcgccggctt cccaacaccc catgaccggc accggggctg tccagaccga ggccatgaag 240 cagattctcg gggtgatcga caagaaactt cggaacctgg agaagaaaaa gggcaagctt 300 gatgattatc aggaacgaat gaacaaaggg gaaaggctta atcaagatca gctggatgcc 360 gtgtctaagt accaggaagt cacaaataac ttggagtttg caaaagaatt acagaggagt 420 ttcatggcat taagccaaga tattcagaaa acaataaaga agacagcacg tcgggagcag 480 cttatgagag aggaagctga acagaaacgt ttaaaaacag tacttgagct gcagtatgtt 540 ttggacaaac taggagatga tgaagtgaga actgacctga agcaaggttt gaatggagtg 600 ccaatattgt ctgaagagga gttgtcgttg ttagatgagt tctacaaatt agcagaccct 660 gaacgagaca tgagcttgag gttgaatgag cagtatgaac atgcctccat tcacctgtgg 720 gacttgctgg aaggaaagga aaaacctgta tgtggaacaa cttataaagc tctaaaggaa 780 attgttgagc gtgttttcca gtcaaactac tttgacagca cccacaacca ccagaatggt 840 ctgtgtgagg aagaggaggc agcctcagca cctacagttg aagaccaggc agctgaagct 900 gaacctgagc cagtggaaga atatactgaa caaaatgagg ttgaatcaac agagtatgta 960 aatagacaat ttatggcaga aacacagttc agcagtggtg aaaaggagca ggtagatgat 1020 tggacagttg aaacagttga ggtggtaaat tcactccagc agcaacctca ggctgcatct 1080 ccttcagtac cagaacccca ctctttgacc ccagtggctc aagccgatcc cctcgtgaga 1140 agacagcgag tacaggacct tatggcacaa atgcaggggc cctataattt catacaggat 1200 tcaatgttgg attttgaaaa ccagacactt gatcctgcca ttgtatctgc acagccgatg 1260 aatccagcac agaacatgga catccccag ctggtttgcc ctccagttca ttctgaatct 1320 agacttgctc aacctaatca agtttctgta cagccagaag ctacacaggt tcctttggtt 1380 tcatccacaa gtgagggata tacagcatct caacccttgt accaaccttc tcatgctact 1440 gaccaacgac cacaaaagga accgattgat cagattcagg cgacgatctc tttaaataca 1500 gaccagacta cagcatcatc atcccttcct gctgcttctc agcctcaagt gttccaggct 1560 gggacaagca aacctttaca tagcagtgga atcaatgtaa atgcagctcc attccaatcc 1620 atgcaaacgg tattcaatat gaatgcccca gttcctcctg ttaatgaacc agaaacttta 1680 aaacagcaaa atcagtacca ggccagttac aaccagagct tttccagtca gcctcaccaa 1740 gtagaacaaa cagagcttca gcaagaacag cttcaaacag tggttggcac ttatcatggt 1800 tctcaggacc agccccatca agtgactggt aaccaccagc agcctcctca gcagaacact 1860 ggatttccac gtagcaatca gccctattac aacagtcgtg gtgtgtctcg tggaggttcc 1920 cgtggtgcta gaggcttgat gaatggatac agaggacctg ctaatggatt cagaggagga 1980 tatgatggtt accgcccttc attctctact aacactccaa acagtggtta tacacaatct 2040 caattcagtg ctccccggga ctactctggc tatcagcggg atggatatca gcagaatttc 2100 aagcgaggct ctgggcagag tggaccacgg ggagccccac gaggtcgtgg agggccccca 2160 agacccaaca gagggatgcc gcaaatgaac actcagcaag tgaattaatc tgattcacag 2220 gattatgttt aatcgccaaa aacacactgg ccagtgtacc ataatatgtt accagaagag 2280 ttattatcta tttgttctcc ctttcaggaa acttattgta aagggactgt tttcatccca 2340 taaagacagg actacaattg tcagctttat attacctgga tatggaagga aactattttt 2400 actctgcatg ttctgtccta agcgtcatct tgagccttgc acatgatact cagattcctc 2460 acccttgctt aggagtaaaa cataatatac tttaatgggg tgatatctcc atagttattt 2520 gaagtggctt ggataaagca agactgactt ctgacattgg ataaaatcta caaatcagcc 2580 ctagagtcat tcagtggtaa ctgacaaaac taaaatattt cccttgaaag gaagatggaa 2640 ggagtggagt gtggtttggc agaacaactg catttcacag cttttccact taaattggag 2700 cactgaacat ttagatgcat accgaattat gcatgggccc taatcacaca gacaaggctg 2760 gtgccagcct taggcttgac acggcagtgt tcaccctctg gccagacgac tgtggttcaa 2820 gacacatgta aattgctttt taacagctga tactgtataa gacaaagcca aaatgcaaaa 2880 ttaggctttg attggcactt ttcgaaaaat atgcaacaat taagggatat aatctggatg 2940 gccgcttctg tacttaatgt gaaatattta gataccttc aaacacttaa cagtttcttt 3000 gacaatgagt tttgtaagga ttggtagtaa atatcattcc ttatgacgta cattgtctgt 3060 cactaatcct tggatcttgc tgtattgtca cctaaattgg tacaggtact gatgaaaatc 3120 taatggataa tcataacact cttggttaca tgtttttcct gcagcctgaa agtttttata 3180 agaaaaagac atcaaatgcc tgctgctgcc acccttttaa attgctatct tttgaaaagc 3240 accagtatgt gttttagatt gatttcccta ttttagggaa atgacagtca gtagtttcac 3300 ttctgatggt ataagcaaac aaataaaaca tgtttataaa aaaaaaaaaa aaaaaaaaaa 3360 aaaaaaaaaa aaaaaaaaaa aaaaaa 3386
3-16	**Sequences**	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	AA
3-16-3	Length	708
3-16-4	Features	**source 1..708**
	Location/Qualifiers	mol_type=protein organism=Bos taurus
	NonEnglishQualifier Value	
3-16-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGNEAGA GAAAPASQHP MTGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL NGVPILSEEE 180 LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQA AEAEPEPVEE YTEQNEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDDWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPAQNMD IPQLVCPPVH SESRLAQPNQ 420 VSVQPEATQV PLVSSTSEGY TASQPLYQPS HATDQRPQKE PIDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP ETLKQQNQYQ 540 ASYNQSFSSQ PHQVEQTELQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ QNTGFPRSNQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSTNTPNSGY TQSQFSAPRD 660

		YSGYQRDGYQ QNFKRGSGQS GPRGAPRGRG GPPRPNRGMP QMNTQQVN 708
3-17	**Sequences**	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	DNA
3-17-3	Length	3150
3-17-4	Features	**source 1..3150**
	Location/Qualifiers	mol_type=other DNA organism=Equus caballus **CDS 1..1917** protein_id=318 translation=MEGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTI KKTARREQLMREEAEQKRLKTVLELQYVLDKLGDEEVRTDLKQGLNGVPILSEEELSLLDEFYKLADP VRDMSLRLNEQYEHASIHLWDLLEGKEKSVCGTTYKALREIVERVFQSNYFDSTHNHQNGLCEEEEAT SAPTAEDQGAEAEPEPAEEYTEQSEVESTEYVNRQFMAEAQFSGEKEQVDEWTVETVEVVNSLQQQPQ AASPSVPEPHSLTPVAQADPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPMNFAQN MDMPQLVCPPVHAESRLAQPNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQRPQKEPTDQIQ ATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPVNEPETLK QQNQYQASYNQSFSSPPHQVEQTELPQEQLQTVVGTYHASQDQPHQVTGNHQQPPQQNTGFPRSSQPY YNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAPRDYSGYQRDGYQ NFKRGSGQSGPRGAPRGRGGPPRPNRGMPQMNTQQVN
	NonEnglishQualifier Value	
3-17-5	Residues	atggagggca agctcgatga ttaccaagag cgaatgaaca aaggagaaag gcttaatcag 60 gatcagctgg atgctgtgtc taagtaccag gaagtcacaa ataacttgga gtttgcgaaa 120 gaattgcaga ggagtttcat ggcgttgagt caggatattc agaaaacaat aaagaagacg 180 gcacgtcggg agcagcttat gagagaagaa gctgaacaga aacgtttaaa aactgtactt 240 gagctgcagt atgttttgga caaattggga gatgaagaag tgcgaactga cctgaaacaa 300 ggtttgaatg gagtgccaat actctctgaa gaagagttgt cgctgttgga tgagttctac 360 aagttagcag accctgtacg ggacatgagc ttgaggttga atgagcagta tgagcatgcc 420 tccattcacc tgtgggactt gctggaaggg aaggaaaaat ctgtctgtgg aacaacctat 480 aaagctctga gggaaattgt tgagcgtgtt ttccagtcca actactttga cagcacccac 540 aaccaccaga atgggctctg tgaggaggaa gaggctacct cagctccaac agctgaagac 600 cagggagctg aagctgaacc tgagccagca gaagaataca ctgaacaaag tgaagttgaa 660 tcaacagagt atgtaaatag acagtttatg gcagaagcgc agttcagtgg tgagaaggag 720 caggtggatg agtggacagt cgagacggtc gaggtggtaa attcactcca gcagcaacct 780 caggctgcat ctccttcagt accggagccc cactctttga ctccagtggc tcaggcagat 840 ccccttgtga gaagacagcg agtacaggac cttatggcgc aaatgcaggg gccctataat 900 ttcatacagg attcaatgct ggattttgaa aaccagacac ttgatcctgc cattgtatct 960 gcacagccta tgaatccagc acagaatatg gacatgcccc agctggtttg ccctccagtt 1020 catgctgaat ctagacttgc tcaacctaat caagttcctg tacaaccaga agctacacag 1080 gttcctttgg tttcatccac aagtgagggg tatacagcat ctcagccctt gtaccagcct 1140 tctcatgcta cagagcaacg accgcaaaag gaaccgactg accagatcca ggcaacaatc 1200 tctttaaata cagaccagac tacagcatca tcatcccttc ctgctgcttc tcagcctcag 1260 gtgttccagg ctgggacaag caaaccttta cacagcagtg ggatcaatgt aaatgcagcg 1320 ccattccagt ccatgcaaac ggtgttcaac atgaatgccc cggttcctcc tgttaatgaa 1380 ccagaaactt taaaacagca aaatcagtac caggccagct ataaccagag cttttccagt 1440 ccgcctcacc aagtagagca gacagagctt ccgcaagagc agcttcagac ggtggttggt 1500 acttaccatg cttcccaaga ccagccccat caagtgaccg gtaaccacca gcagcctccc 1560 cagcagaaca ctgggtttcc acgtagcagt cagccctatt acaacagtcg tggtgtgtct 1620 cgtggaggct cccgtggtgc tagaggcttg atgaatggat acaggggccc tgccaatgga 1680 ttcagaggag gatatgatgg ttaccgccct tcgttctcta acactccaaa cagcggttac 1740 acacagtctc agttcagtgc tccccgggac tactctggct atcagcggga tggatatcag 1800 cagaatttca agcgaggctc tgggcagagt ggaccccggg gagccccacg aggtcgtgga 1860 gggcccccaa gacccaacag agggatgccg caaatgaaca ctcagcaagt gaattaatct 1920 gattcacagg attatcttta atcgccaaaa cacactggcc agtgtaccat aatatgttac 1980 cagaagagtt attatctatt tgttctccct ttcaggaaac ttattgtaaa gggactgttt 2040 tcatcccata aagacaggac tacagttgtc agctttatat tacctggata tggaaggaaa 2100 ctatttttac tctgcatgtt ctgtcctaag cgtcatcttg agccttgcac atgatactca 2160 gattcctttc ccttgcttag gagtaaaaca taatatactt tatggggtga taatatctcc 2220 atagttattt gaagtggctt ggaaaaagca agattgactt ttgacattgg ataaaatcta 2280 caaatcagcc ctagagtttc atggtcattc acaaaactaa aatatttccc ttgaaaggaa 2340 gatggaagga ctggagtgtg gtttggcaga acaactgcat ttcacagctt ttcctattaa 2400 attggagcac tgaatgttaa atgcatacca aattatgcat gggcccttaa tcacacatac 2460 atggctacca gctttgacac agcactattc atcctctggc caaacgactg tggttaaaaa 2520 cacgtgtaaa ttgcttttta acagctgata ctgtaaaaga caaagctaaa atgcaaaatt 2580 aggctttcat tggcactttt cgaaaaatat gcaacaaatt tgggatgtaa tctggatggc 2640 cacttctgta cttaatgtga agtatttaga taccttttg aacacttaac agtttcttcg 2700 acaatgactt ttgtaaggat tggtagtata tatcattcct tatgacatac attgtctgtt 2760 gctaatcctt ggatcttgct gtattgtcac ctaaattggt acaggtactg atgaaaatct 2820 ctcatggata aacctaacac tcttcgtcac atgtttttcc tgcagcctga aggtttttaa 2880 aaggaaaaga tatcaaatgc ctgctgctac cacccttta aattgctatc ttttgaaaag 2940 caccagtatg tgtttttaga ttgatttccc tattttaggg aaatgacagt cagtagtttc 3000 agttctgatg gtataagcaa agcaaataaa acgtgtttat aaaagttgta tcttgaaaca 3060 ctggtgttca acagctagca gcttctgtgg ttcacccct gccttgttag tgttacccat 3120

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3-18	**Sequences**	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	AA
3-18-3	Length	638
3-18-4	Features	**source 1..638**
	Location/Qualifiers	mol_type=protein organism=Equus caballus
	NonEnglishQualifier Value	
3-18-5	Residues	MEGKLDDYQE RMNKGERLNQ DQLDAVSKYQ EVTNNLEFAK ELQRSFMALS QDIQKTIKKT 60 ARREQLMREE AEQKRLKTVL ELQYVLDKLG DEEVRTDLKQ GLNGVPILSE EELSLLDEFY 120 KLADPVRDMS LRLNEQYEHA SIHLWDLLEG KEKSVCGTTY KALREIVERV FQSNYFDSTH 180 NHQNGLCEEE EATSAPTAED QGAEAEPEPA EEYTEQSEVE STEYVNRQFM AEAQFSGEKE 240 QVDEWTVETV EVVNSLQQQP QAASPSVPEP HSLTPVAQAD PLVRRQRVQD LMAQMQGPYN 300 FIQDSMLDFE NQTLDPAIVS AQPMNPAQNM DMPQLVCPPV HAESRLAQPN QVPVQPEATQ 360 VPLVSSTSEG YTASQPLYQP SHATEQRPQK EPTDQIQATI SLNTDQTTAS SSLPAASQPQ 420 VFQAGTSKPL HSSGINVNAA PFQSMQTVFN MNAPVPPVNE PETLKQQNQY QASYNQSFSS 480 PPHQVEQTEL PQEQLQTVVG TYHASQDQPH QVTGNHQQPP QQNTGFPRSS QPYYNSRGVS 540 RGGSRGARGL MNGYRGPANG FRGGYDGYRP SFSNTPNSGY TQSQFSAPRD YSGYQRDGYQ 600 QNFKRGSGQS GPRGAPRGRG GPPRPNRGMP QMNTQQVN 638
3-19	**Sequences**	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	DNA
3-19-3	Length	6181
3-19-4	Features	**source 1..6181**
	Location/Qualifiers	mol_type=other DNA organism=Mus musculus **CDS 179..2302** protein_id=319 translation=MPSATSHSGSGSKSSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMKQILG VIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTI KKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDDVRTDLKQGLSGVPILSEEELSLLDEFYKLVDP ERDMSLRLNEQYEHASIHLWDLLEGKEKPVCGTTYKALKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETVEVVNSLQQQP QAASPSVPEPHSLTPVAQSDPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPMNPTQ NMDMPQLVCPQVHSESRLAQSNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQRPQKEPMDQI QATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPANEPETL KQQSQYQATYNQSFSSQPHQVEQTELQQDQLQTVVGTYHGSQDQPHQVPGNHQQPPQQNTGFPRSSQP YYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYSQSQFTAPRDYSGYQRDGYQ QNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQMNTQQVN
	NonEnglishQualifier Value	
3-19-5	Residues	gctggctggc taagtccctc ccgcgccggc tcttgtccca ctaggagcag ctcagagccg 60 cggggacagg gcgaagcggc ctgcgcccac ggagcgcacg tctctgttct caacgcagca 120 ccacccttgc ccccctcggc tgcccactcc agacgtccag cggctccgcg cgcgcacgat 180 gccctcggcc accagccaca gcggaagcgg cagcaaatcg tcgggaccgc cgccgccgtc 240 cggttcctcc gggagtgagg cggcggccgg ggcagctgcg ccggcttctc agcatccggc 300 aaccggcacc ggcgccgtcc agaccgaggc catgaagcag attctcggcg taatcgacaa 360 gaaacttcgg aacctggaga agaaaaaggg taaacttgat gattaccagg aacgaatgaa 420 taaaggggaa aggctcaatc aagaccagct ggatgccgta tctaagtacc aggaagtcac 480 aaataatttg gagtttgcaa aggaattaca gaggagtttc atggcattaa gtcaagatat 540 tcagaaaaca ataaagaaga cagcacgtcg ggaacagctt atgagagaag aagcagaaca 600 gaagcgctta aaaactgtac ttgagttaca gtatgtattg gataagctgg gagatgatga 660 tgtgagaaca gatctgaaac aaggtttgag tggagtgcca atattgtctg aggaggagtt 720 gtcattgctg gatgagttct acaagctcgt agatcctgag cgtgacatga gtttaaggtt 780 aaatgagcag tatgaacatg cctcaattca cttgtgggat ttgctggaag ggaaagaaaa 840 gcctgtgtgt ggaacaacct ataaagctct aaaggaaatt gttgagcgtg ttttccagtc 900 aaactacttt gatagcactc acaatcatca aaatgggttg tgtgaggagg aagaggcggc 960 ttcagcgccc acagtggagg accaggtagc tgaagctgaa cctgagccag cggaagaata 1020 cacagagcaa agtgaggttg aatcaacaga gtatgtcaat aggcagttca tggcagaaac 1080 acagttcagc agtggtgaga aggagcaagt ggatgagtgg acagttgaaa cagttgaggt 1140 tgtaaactca ctccagcagc aacctcaggc tgcgtcccct tcagtcccag agccccactc 1200 tttgactcca gtggctcagt cagatccact tgtgagaagg cagcgtgtac aagatcttat 1260 ggcacaaatg caagggccct ataatttcat acaggattca atgttggatt ttgaaaatca 1320 gacgcttgat cctgccattg tatccgcaca gcctatgaac cctacccaga acatggatat 1380 gcctcagctg gtttgccctc aggttcattc tgaatctaga cttgcccaat ctaatcaagt 1440 tcctgtacaa ccagaagcca cacaggttcc tttggtttca tccacaagtg aggggtatac 1500 agcatctcag cccttgtacc agccatctca tgctacggag cagcggccgc agaaagagcc 1560 aatggatcag attcaggcaa caatatcttt gaatacagac cagactacag catcctcatc 1620 ccttcctgct gcttctcagc ctcaagtgtt ccaggctggg acaagtaaac ctttgcacag 1680 cagtggaatc aatgtaaatg cagctccatt ccagtccatg caaacggtgt tcaatatgaa 1740 tgctccagtc cctcctgcta atgaaccaga aacgttaaaa caacagagtc agtaccaggc 1800 cacttataac cagagttttt ccagtcagcc tcaccaagtg gaacaaacag agcttcaaca 1860

		agaccaactg caaacggtgg ttggcactta ccatggatcc caggaccagc ctcatcaagt 1920 gcctggtaac caccagcaac ccccacagca gaacactggc tttccacgta gcagtcagcc 1980 ttattacaac agtcgtgggg tatctcgagg agggtctcgt ggtgccagag gcttgatgaa 2040 tggatacagg ggccctgcca atggatttag aggaggatat gatggttacc gcccttcatt 2100 ctcgaacact ccaaacagtg gttattcaca gtctcagttc actgctcccc gggactactc 2160 tggttaccag cgggatggat atcagcagaa tttcaagcga ggctctgggc agagtggacc 2220 acggggagcc ccacgaggtc gtggagggcc cccaagaccc aacagaggga tgccgcaaat 2280 gaacactcag caagtgaatt aatgtgatac acaggattat gtttaatcgc caaaaacaca 2340 ctggccagtg taccataata tgttaccaga agagttatta tctatttgtt ctccctttca 2400 ggaaacttat tgtaaaggga ctgttttcat cccataaaga caggactgca attgtcagct 2460 ttacattacc tggatatgga aggaaactat ttttattctg catgttctgt cctaagcgtc 2520 atcttgagcc ttgcacacaa tacaatactc agattcctca cccttgctta ggagtaaaac 2580 attatatact tatggggtga taatatctcc atagttagtt gaagtggctt ggaaaaaaaa 2640 tgcaagattg aatttttgac cttggataaa atctacaatc agccctagaa ctattcagtg 2700 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gctattgaag gttttaaaat ggtgtgtatt gttttttttt gggggggggg tggccagaat 6120 agtgggtcat ctaataaaac tgccatttaa aagatcaaaa aaaaaaaaaa aaaaaaaaaa 6180 a 6181
3-20	**Sequences**	
3-20-1	Sequence Number [ID]	20

3-20-2	Molecule Type	AA
3-20-3	Length	707
3-20-4	Features	**source 1..707**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-20-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 707
3-21	**Sequences**	
3-21-1	Sequence Number [ID]	21
3-21-2	Molecule Type	DNA
3-21-3	Length	6141
3-21-4	Features	**source 1..6141**
	Location/Qualifiers	mol_type=other DNA
		organism=Mus musculus
		CDS 139..2262
		protein_id=320
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	NonEnglishQualifier Value	
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3-23	**Sequences**	
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3-23-2	Molecule Type	DNA
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3-23-4	Features	**source 1..6114**
	Location/Qualifiers	mol_type=other DNA organism=Mus musculus **CDS 139..2235** protein_id=321 translation=MPSATSHSGSGSKSSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMKQILG VIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTI KKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDDVRTDLKQGLSGVPILSEEELSLLDEFYKLVDP ERDMSLRLNEQYEHASIHLWDLLEGKEKPVCGTTYKALKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETVEVVNSLQQQP QAASPSVPEPHSLTPVAQSDPLVRRQRVQDLMAQMQGPYNFIQTLDPAIVSAQPMNPTQNMDMPQLVC PQVHSESRLAQSNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQRPQKEPMDQIQATISLNTD QTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPANEPETLKQQSQYQAT YNQSFSSQPHQVEQTELQQDQLQTVVGTYHGSQDQPHQVPGNHQQPPQQNTGFPRSSQPYYNSRGVSP GGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYSQSQFTAPRDYSGYQRDGYQQNFKRGSG SGPRGAPRGRGGPPRPNRGMPQMNTQQVN
	NonEnglishQualifier Value	
3-23-5	Residues	cccaccgcgc gcgcgcgtag ccgcctgccc gcccgcccgc tgcgcgtttt gtcccgcgtc 60 tctccccgtc cgtctcctga cttgctggtc ttgtccttcc ctcccgcttt tttcctctcc 120 tctcttctcg gtctaaagat gccctcggcc accagccaca gcggaagcgg cagcaaatcg 180 tcgggaccgc cgccgccgtc cggttcctcc gggagtgagg cggcggccgg ggcagctgcg 240 ccggcttctc agcatccggc aaccggcacc ggcgccgtcc agaccgaggc catgaagcag 300 attctcggcg taatcgacaa gaaacttcgg aacctggaga agaaaaaggg taaacttgat 360 gattaccagg aacgaatgaa taaaggggaa aggctcaatc aagaccagct ggatgccgta 420 tctaagtacc aggaagtcac aaataatttg gagtttgcaa aggaattaca gaggagtttc 480 atggcattaa gtcaagatat tcagaaaaca ataaagaaga cagcacgtcg ggaacagctt 540 atgagagaag aagcagaaca gaagcgctta aaaactgtac ttgagttaca gtatgtattg 600 gataagctgg gagatgatga tgtgagaaca gatctgaaac aaggtttgag tggagtgcca 660 atattgtctg aggaggagtt gtcattgctg gatgagttct acaagctcgt agatcctgag 720 cgtgacatga gtttaaggtt aaatgagcag tatgaacatg cctcaattca cttgtgggat 780 ttgctggaag ggaaagaaaa gcctgtgtgt ggaacaacct ataaagctct aaaggaaatt 840 gttgagcgtg ttttccagtc aaactacttt gatagcactc acaatcatca aaatgggttg 900 tgtgaggagg aagaggcggc ttcagcgccc acagtggagg accaggtagc tgaagctgaa 960 cctgagccag cggaagaata cacagagcaa agtgaggttg aatcaacaga gtatgtcaat 1020 aggcagttca tggcagaaac acagttcagc agtggtgaga aggagcaagt ggatgagtgg 1080 acagttgaaa cagttgaggt tgtaaactca ctccagcagc aacctcaggc tgcgtcccct 1140 tcagtcccag agccccactc tttgactcca gtggctcagt cagatccact tgtgagaagg 1200 cagcgtgtac aagatcttat ggcacaaatg caagggccct ataatttcat acagacgctt 1260 gatcctgcca ttgtatccgc acagcctatg aaccctaccc agaacatgga tatgcctcag 1320 ctggtttgcc ctcaggttca ttctgaatct agacttgccc aatctaatca agttcctgta 1380 caaccagaag ccacacaggt tcctttggtt tcatccacaa gtgaggggta tacagcatct 1440 cagcccttgt accagccatc tcatgctacg gagcagcggc cgcagaaaga gccaatggat 1500 cagattcagg caacaatatc tttgaataca gaccagacta cagcatcctc atcccttcct 1560 gctgcttctc agcctcaagt gttccaggct gggacaagta aacctttgca cagcagtgga 1620 atcaatgtaa atgcagctcc attccagtcc atgcaaacgg tgttcaatat gaatgctcca 1680 gtccctcctg ctaatgaacc agaaacgtta aaacaacaga gtcagtacca ggccacttat 1740 aaccagagtt tttccagtca gcctcaccaa gtggaacaaa cagagcttca acaagaccaa 1800 ctgcaaacgg tggttggcac ttaccatgga tcccaggacc agcctcatca agtgcctggt 1860 aaccaccagc aacccccaca gcagaacact ggctttccac gtagcagtca gccttattac 1920 aacagtcgtg gggtatctcg aggagggtct cgtggtgcca gaggcttgat gaatggatac 1980 aggggccctg ccaatggatt tagaggagga tatgatggtt accgcccttc attctcgaac 2040 actccaaaca gtggttattc acagtctcag ttcactgctc cccgggacta ctctggttac 2100 cagcgggatg gatatcagca gaatttcaag cgaggctctg ggcagagtgg accacgggga 2160 gccccacgag gtcgtggagg gccccaaga cccaacagag ggatgccgca aatgaacact 2220 cagcaagtga attaatgtga tacacaggat tatgtttaat cgccaaaaac acactggcca 2280

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3-24	**Sequences**	
3-24-1	Sequence Number [ID]	24
3-24-2	Molecule Type	AA
3-24-3	Length	698
3-24-4	Features	**source 1..698**
	Location/Qualifiers	mol_type=protein organism=Mus musculus
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3-24-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180

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3-25	**Sequences**	
3-25-1	Sequence Number [ID]	25
3-25-2	Molecule Type	DNA
3-25-3	Length	3548
3-25-4	Features	**source 1..3548**
	Location/Qualifiers	mol_type=other DNA organism=Mus musculus **CDS 179..2257** protein_id=322 translation=MPSATSHSGSGSKSSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMKQILG VIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTI KKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDDVRTDLKQGLSGVPILSEEELSLLDEFYKLVDP ERDMSLRLNEQYEHASIHLWDLLEGKEKPVCGTTYKALKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETVEVVNSLQQQP QAASPSVPEPHSLTPVAQSDPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPMNPTQ NMDMPQLVCPQVHSESRLAQSNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQRPQKEPMDQI QATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPANEPETL KQQSQYQATYNQSFSSQPHQVEQTELQQDQLQTVVGTYHGSQDQPHQVPGNHQQPPQQNTGFPRSSQP YYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYSQSQFTAPRDYSGYQRDGYQ QNFKRGSGQSGPRGAPRGNILWW
	NonEnglishQualifier Value	
3-25-5	Residues	gctggctggc taagtccctc ccgcgccggc tcttgtccca ctaggagcag ctcagagccg 60 cggggacagg gcgaagcggc ctgcgcccac ggagcgcacg tctctgttct caacgcagca 120 ccacccttgc ccccctcggc tgcccactcc agacgtccag cggctccgcg cgcgcacgat 180 gccctcggcc accagccaca gcggaagcgg cagcaaatcg tcgggaccgc cgccgccgtc 240 cggttcctcc gggagtgagg cggcggccgg ggcagctgcg ccggcttctc agcatccggc 300 aaccggcacc ggcgccgtcc agaccgaggc catgaagcag attctcggcg taatcgacaa 360 gaaacttcgg aacctggaga agaaaaaggg taaacttgat gattaccagg aacgaatgaa 420 taaaggggaa aggctcaatc aagaccagct ggatgccgta tctaagtacc aggaagtcac 480 aaataatttg gagtttgcaa aggaattaca gaggagtttc atggcattaa gtcaagatat 540 tcagaaaaca ataaagaaga cagcacgtcg ggaacagctt atgagagaag aagcagaaca 600 gaagcgctta aaaactgtac ttgagttaca gtatgtattg gataagctgg gagatgatga 660 tgtgagaaca gatctgaaac aaggtttgag tggagtgcca atattgtctg aggaggagtt 720 gtcattgctg gatgagttct acaagctcgt agatcctgag cgtgacatga gtttaaggtt 780 aaatgagcag tatgaacatg cctcaattca cttgtgggat ttgctggaag ggaaagaaaa 840 gcctgtgtgt ggaacaacct ataaagctct aaaggaaatt gttgagcgtg ttttccagtc 900 aaactacttt gatagcactc acaatcatca aaatgggttg tgtgaggagg aagaggcggc 960 ttcagcgccc acagtggagg accaggtagc tgaagctgaa cctgagccag cggaagaata 1020 cacagagcaa agtgaggttg aatcaacaga gtatgtcaat aggcagttca tggcagaaac 1080 acagttcagc agtggtgaga aggagcaagt ggatgagtgg acagttgaaa cagttgaggt 1140 tgtaaactca ctccagcagc aacctcaggc tgcgtcccct tcagtcccag agccccactc 1200 tttgactcca gtggctcagt cagatccact tgtgagaagg cagcgtgtac aagatcttat 1260 ggcacaaatg caagggccct ataatttcat acaggattca atgttggatt ttgaaaatca 1320 gacgcttgat cctgccattg tatccgcaca gcctatgaac cctacccaga acatggatat 1380 gcctcagctg gtttgccctc aggttcattc tgaatctaga cttgcccaat ctaatcaagt 1440 tcctgtacaa ccagaagcca cacaggttcc tttggtttca tccacaagtg aggggtatac 1500 agcatctcag cccttgtacc agccatctca tgctacggag cagcggccgc agaaagagcc 1560 aatggatcag attcaggcaa caatatcttt gaatacagac cagactacag catcctcatc 1620 ccttcctgct gcttctcagc ctcaagtgtt ccaggctggg acaagtaaac ctttgcacag 1680 cagtggaatc aatgtaaatg cagctccatt ccagtccatg caaacggtgt tcaatatgaa 1740 tgctccagtc cctcctgcta atgaaccaga aacgttaaaa caacagagtc agtaccaggc 1800 cacttataac cagagttttt ccagtcagcc tcaccaagtg gaacaaacag agcttcaaca 1860 agaccaactg caaacggtgg ttggcactta ccatggatcc caggaccagc ctcatcaagt 1920 gcctggtaac caccagcaac ccccacagca gaacactggc tttccacgta gcagtcagcc 1980 ttattacaac agtcgtgggg tatctcgagg agggtctcgt ggtgccagag gcttgatgaa 2040 tggatacagg ggccctgcca atggatttag aggaggatat gatggttacc gcccttcatt 2100 ctcgaacact ccaaacagtg gttattcaca gtctcagttc actgctcccc gggactactc 2160 tggttaccag cgggatggat atcagcagaa tttcaagcga ggctctgggc agagtggacc 2220 acggggagcc ccacgaggta atatattgtg gtggtgatcc tagctcctat gtggagcttc 2280 tgttctggcc ttggaagaac tgttcatagt ccgcatgtag gttacatgtt aggaatacat 2340 ttatcttttc cagacttgtt gctaaagatt aaatgaaatg ctctgtttct aaaatttcat 2400 cttgaatcca aattttaatt tttgaatgac tttccctgct gttgtcttca aaatcagaac 2460 attttctctg cctcagaaaa gcgtttttcc aactggaaat ttatttttca ggtcttaaaa 2520 cctgctaaat gtttttagga agtacctact gaaacttttt gtaagacatt tttggaacga 2580

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3-26	**Sequences**	
3-26-1	Sequence Number [ID]	26
3-26-2	Molecule Type	AA
3-26-3	Length	692
3-26-4	Features	**source 1..692**
	Location/Qualifiers	mol_type=protein organism=Mus musculus
	NonEnglishQualifier Value	
3-26-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGNIL WW 692
3-27	**Sequences**	
3-27-1	Sequence Number [ID]	27
3-27-2	Molecule Type	DNA
3-27-3	Length	3508
3-27-4	Features	**source 1..3508**
	Location/Qualifiers	mol_type=other DNA organism=Mus musculus **CDS 139..2217** protein_id=323 translation=MPSATSHSGSGSKSSGPPPPSGSSGSEAAAGAAAPASQHPATGTGAVQTEAMKQILG VIDKKLRNLEKKKGKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTI KKTARREQLMREEAEQKRLKTVLELQYVLDKLGDDDVRTDLKQGLSGVPILSEEELSLLDEFYKLVDP ERDMSLRLNEQYEHASIHLWDLLEGKEKPVCGTTYKALKEIVERVFQSNYFDSTHNHQNGLCEEEEAA SAPTVEDQVAEAEPEPAEEYTEQSEVESTEYVNRQFMAETQFSSGEKEQVDEWTVETVEVVNSLQQQP QAASPSVPEPHSLTPVAQSDPLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPMNPTQ NMDMPQLVCPQVHSESRLAQSNQVPVQPEATQVPLVSSTSEGYTASQPLYQPSHATEQRPQKEPMDQI QATISLNTDQTTASSSLPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPANEPETL KQQSQYQATYNQSFSSQPHQVEQTELQQDQLQTVVGTYHGSQDQPHQVPGNHQQPPQQNTGFPRSSQ YYNSRGVSRGGSRGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYSQSQFTAPRDYSGYQRDGY QNFKRGSGQSGPRGAPRGNILWW
	NonEnglishQualifier Value	
3-27-5	Residues	cccaccgcgc gcgcgcgtag ccgcctgccc gcccgcccgc tgcgcgtttt gtcccgcgtc 60 tctccccgtc cgtctcctga cttgctggtc ttgtccttcc ctcccgcttt tttcctctcc 120 tctcttctcg gtctaaagat gccctcggcc accagccaca gcggaagcgg cagcaaatcg 180 tcgggaccgc cgccgccgtc cggttcctcc gggagtgagg cggcggccgg ggcagctgcg 240 ccggcttctc agcatccggc aaccggcacc ggcgccgtcc agaccgaggc catgaagcag 300 attctcggcg taatcgacaa gaaacttcgg aacctggaga agaaaaaggg taaacttgat 360 gattaccagg aacgaatgaa taaaggggaa aggctcaatc aagaccagct ggatgccgta 420 tctaagtacc aggaagtcac aaataatttg gagtttgcaa aggaattaca gaggagtttc 480 atggcattaa gtcaagatat tcagaaaaca ataaagaaga cagcacgtcg ggaacagctt 540 atgagagaag aagcagaaca gaagcgctta aaaactgtac ttgagttaca gtatgtattg 600 gataagctgg gagatgatga tgtgagaaca gatctgaaac aaggtttgag tggagtgcca 660 atattgtctg aggaggagtt gtcattgctg gatgagttct acaagctcgt agatcctgag 720 cgtgacatga gtttaaggtt aaatgagcag tatgaacatg cctcaattca cttgtgggat 780 ttgctggaag ggaaagaaaa gcctgtgtgt ggaacaacct ataaagctct aaaggaaatt 840

		gttgagcgtg ttttccagtc aaactacttt gatagcactc acaatcatca aaatgggttg 900 tgtgaggagg aagaggcggc ttcagcgccc acagtggagg accaggtagc tgaagctgaa 960 cctgagccag cggaagaata cacagagcaa agtgaggttg aatcaacaga gtatgtcaat 1020 aggcagttca tggcagaaac acagttcagc agtggtgaga aggagcaagt ggatgagtgg 1080 acagttgaaa cagttgaggt tgtaaactca ctccagcagc aacctcaggc tgcgtcccct 1140 tcagtcccag agccccactc tttgactcca gtggctcagt cagatccact tgtgagaagg 1200 cagcgtgtac aagatcttat ggcacaaatg caagggccct ataatttcat acaggattca 1260 atgttggatt ttgaaaatca gacgcttgat cctgccattg tatccgcaca gcctatgaac 1320 cctacccaga acatggatat gcctcagctg gtttgccctc aggttcattc tgaatctaga 1380 cttgcccaat ctaatcaagt tcctgtacaa ccagaagcca cacaggttcc tttggtttca 1440 tccacaagtg aggggtatac agcatctcag cccttgtacc agccatctca tgctacggag 1500 cagcggccgc agaaagagcc aatggatcag attcaggcaa caatatcttt gaatacagac 1560 cagactacag catcctcatc ccttcctgct gcttctcagc ctcaagtgtt ccaggctggg 1620 acaagtaaac ctttgcacag cagtggaatc aatgtaaatg cagctccatt ccagtccatg 1680 caaacggtgt tcaatatgaa tgctccagtc cctcctgcta atgaaccaga aacgttaaaa 1740 caacagagtc agtaccaggc cacttataac cagagttttt ccagtcagcc tcaccaagtg 1800 gaacaaacag agcttcaaca agaccaactg caaacggtgg ttggcactta ccatggatcc 1860 caggaccagc ctcatcaagt gcctggtaac caccagcaac ccccacagca gaacactggc 1920 tttccacgta gcagtcagcc ttattacaac agtcgtgggg tatctcgagg agggtctcgt 1980 ggtgccagag gcttgatgaa tggatacagg ggccctgcca atggatttag aggaggatat 2040 gatggttacc gcccttcatt ctcgaacact ccaaacagtg gttattcaca gtctcagttc 2100 actgctcccc gggactactc tggttaccag cgggatggat atcagcagaa tttcaagcga 2160 ggctctgggc agagtggacc acggggagcc ccacgaggta atatattgtg gtggtgatcc 2220 tagctcctat gtggagcttc tgttctggcc ttggaagaac tgttcatagt ccgcatgtag 2280 gttacatgtt aggaatacat ttatcttttc cagacttgtt gctaaagatt aaatgaaatg 2340 ctctgtttct aaaatttcat cttgaatcca aattttaatt tttgaatgac tttccctgct 2400 gttgtcttca aaatcagaac attttctctg cctcagaaaa gcgtttttcc aactggaaat 2460 ttatttttca ggtcttaaaa cctgctaaat gtttttagga agtacctact gaaacttttt 2520 gtaagacatt tttggaacga gcttgaacat ttatataaat ttattaccct ctttgatttt 2580 tgaaacatgc atattatatt taggctgaga agcccttcaa atggccagat aagccacagt 2640 tttagctaga gaaccattta gaattgacat aactaatcta aacttgaaca cttttaggac 2700 caatgttagt gttctaaata ccaacatatt tctgatgttt aaacagatct cccaaattct 2760 taggaccttg atgtcattaa aatttagaat gacaagctta agaggcttta gtttcatttg 2820 tttttcaagt aatgaaaaat aatttcttac atgggcagat agttaatttg ttgaacaatt 2880 acaggtagca tttcatgtaa tctgatgttc taaatggttc tcttattgaa ggaggttaaa 2940 gaattaggtt tcttacagtt tttggctggc catgacatgt ataaaatgta tattaaggag 3000 gaattataaa gtactttaat ttgaatgcta gtggcaattg atcattaaga aagtacttta 3060 aagcaaaagg ttaatgggtc atctgggaaa aatactgaag tatcaaaggt atttgcatgt 3120 gaatgtgggt tatgttcttc tatcccacct tgtagcatat tctatgaaag ttgagttaaa 3180 tgatagctaa aatatctgtt tcaacagcat gtaaaaagtt attttaactg ttacaagtca 3240 ttatacaatt ttgaatgttc tgtagtttct ttttaacagt ttaggtacaa aggtctgttt 3300 tcattctggt gctttttatt aattttgata gtatgatgtc acttcctatt gaaatgtaag 3360 ctagcgtgta ccttagaatg tgagctccat gagagcaggt accttgtttg tcttcactgc 3420 tgtatctatt cccaacgcct catgacagtg cctggcacat agtaggcact caataaatac 3480 ttgttgaatg aatgaaaaaa aaaaaaaa 3508
3-28	**Sequences**	
3-28-1	Sequence Number [ID]	28
3-28-2	Molecule Type	AA
3-28-3	Length	692
3-28-4	Features	**source 1..692**
	Location/Qualifiers	mol_type=protein organism=Mus musculus
	NonEnglishQualifier Value	
3-28-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGNIL WW 692
3-29	**Sequences**	
3-29-1	Sequence Number [ID]	29
3-29-2	Molecule Type	DNA
3-29-3	Length	2109
3-29-4	Features	**source 1..2109**
	Location/Qualifiers	mol_type=other DNA organism=Gallus gallus **CDS 1..2109** protein_id=324

		translation=MPSATNGTMASSSGKAGPGGNEQAPAAAAAAPQASGGSITSVQTEAMKQILGVIDKK LRNLEKKKSKLDDYQERMNKGERLNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTAR REQLMREEAEQKRLKTVLELQFILDKLGDDEVRSDLKQGSNGVPVLTEEELTMLDEFYKLVYPERDMN MRLNEQYEQASVHLWDLLEGKEKPVCGTTYKALKEVVERILQTSYFDSTHNHQNGLCEEEEAAPTPAV EDTVAEAEPDPAEEFTEPTEVESTEYVNRQFMAETQFSSSEKEQVDEWTVETVEVVNSLQQQTQATSP PVPEPHTLTTVAQADPLVRRQRVQDLMAQMQGPYNFMQDSMLEFENQTLDPAIVSAQPMNPAQNLDMP QMVCPPVHTESRLAQPNQVPVQPEATQVPLVSSTSEGYTASQPMYQPSHTTEQRPQKESIDQIQASMS LNADQTPSSSSLPTASQPQVFQAGSSKPLHSSGINVNAAPFQSMQTVFNMNAPVPPVNEPEALKQQNQ YQASYNQSFSNQPHQVEQSDLQQEQLQTVVGTYHGSPDQTHQVAGNHQQPPQQNTGFPRNSQPYYNSF GVSRGGSRGTRGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQPQFNAPRDYSNYQRDGYQQNFKR GSGQSGPRGAPRGRGGPPRPNRGMPQMNAQQVN
	NonEnglishQualifier Value	
3-29-5	Residues	atgccctcgg ctaccaacgg caccatggcg agcagcagcg ggaaggcggg cccgggcggc 60 aacgagcagg ccccggcggc ggcagcggcg gccccgcagg cgtcgggcgg cagcatcacc 120 tcggttcaga ccgaggccat gaagcagatc ttgggagtga tcgacaaaaa gctccgcaac 180 ctcgagaaga aaaagagcaa acttgacgat taccaggaac gaatgaacaa gggggaacgt 240 ctaaatcaag atcaactgga tgcagtgtca aaataccagg aagtgacaaa taacctggaa 300 ttcgctaaag aactgcagag gagctttatg gcactgagcc aagatatcca gaaaacaata 360 aaaaagacgg ctcgcaggga gcagctgatg agagaagagg ctgagcagaa gcgtttaaag 420 actgtgctag agctgcagtt cattttggac aagttgggtg acgatgaagt gcgcagtgac 480 ttgaaacaag gatcaaatgg agtaccggta ctgacagagg aggaactgac aatgctggat 540 gaattttaca agctagttta ccctgaaagg gacatgaaca tgaggttgaa tgagcagtat 600 gagcaagcat ctgttcacct gtgggactta ctggaaggga aggaaaaacc cgtttgtgga 660 acaacctata aagccctgaa ggaggttgtt gaacgtattc ttcaaactag ttactttgat 720 agcacccata accatcagaa cgggttatgt gaggaagaag aggcagcacc cacacctgca 780 gtagaagaca ctgtagcaga agctgagcct gatccagcag aagaatttac tgaacctact 840 gaagttgaat cgactgagta tgtaaacaga caattcatgg cagagactca gttcagcagt 900 agtgagaagg aacaggtaga tgagtggaca gttgaaacgg ttgaggttgt aaattcactg 960 cagcaacaaa cacaagctac atctcctcca gttcctgaac ctcatacact cactactgtg 1020 gctcaagcag atcctcttgt tagaagacag agagtacagg accttatggc ccagatgcag 1080 ggtccatata acttcatgca ggactctatg ctggagtttg agaaccagac acttgatcct 1140 gccattgtat ctgcacagcc catgaatcca gcacagaatt tggacatgcc gcaaatggtc 1200 tgccctccag ttcatactga gtcaagactt gcccagccta atcaagttcc tgtgcaacca 1260 gaagctacgc aggttccctt ggtttcatct acaagtgagg gatatacagc ctcccagccc 1320 atgtatcagc cttctcatac cacagagcaa cggccacaga aggaatccat tgaccagatt 1380 caggcttcaa tgtcactgaa tgcagaccag accccgtcat catcatcact tcccactgca 1440 tcccagccgc aagttttcca agctggatct agcaaacctt tgcatagcag cggaatcaat 1500 gttaatgcag ctccattcca atccatgcaa acagtattca acatgaatgc acctgttcct 1560 cctgttaatg agccagaagc ccttaagcaa caaaatcagt accaggccag ttacaaccag 1620 agtttctcca atcagccaca ccaagtagaa caatcagatc ttcagcaaga acagctccag 1680 acagtggttg gtacttacca tggttctccg gaccagaccc atcaagtggc aggaaaccac 1740 cagcaacctc cccagcagaa tactggattt ccacgcaaca gtcagcctta ttacaacagt 1800 cggggagtgt ctcgtggtgg atcacgtggg actcgtggat tgatgaatgg ttacagggga 1860 cctgcaaatg gatttagagg aggatatgat ggctaccgtc cttcattttc caacactccg 1920 aacagtggtt acacgcagcc ccaatttaat gctcctcgag attattcaaa ctaccagcgg 1980 gatggatatc agcagaactt caaacgtggt tctggacaaa gtgggcctcg gggagctcct 2040 cgaggtcgtg gagggccccc aagaccaaac agagggatgc ctcaaatgaa cgctcagcaa 2100 gtgaattaa 2109
3-30	**Sequences**	
3-30-1	Sequence Number [ID]	30
3-30-2	Molecule Type	AA
3-30-3	Length	702
3-30-4	Features	**source 1..702**
	Location/Qualifiers	mol_type=protein organism=Gallus gallus
	NonEnglishQualifier Value	
3-30-5	Residues	MPSATNGTMA SSSGKAGPGG NEQAPAAAAA APQASGGSIT SVQTEAMKQI LGVIDKKLRN 60 LEKKKSKLDD YQERMNKGER LNQDQLDAVS KYQEVTNNLE FAKELQRSFM ALSQDIQKTI 120 KKTARREQLM REEAEQKRLK TVLELQFILD KLGDDEVRSD LKQGSNGVPV LTEEELTMLD 180 EFYKLVYPER DMNMRLNEQY EQASVHLWDL LEGKEKPVCG TTYKALKEVV ERILQTSYFD 240 STHNHQNGLC EEEEAAPTPA VEDTVAEAEP DPAEEFTEPT EVESTEYVNR QFMAETQFSS 300 SEKEQVDEWT VETVEVVNSL QQQTQATSPP VPEPHTLTTV AQADPLVRRQ RVQDLMAQMQ 360 GPYNFMQDSM LEFENQTLDP AIVSAQPMNP AQNLDMPQMV CPPVHTESRL AQPNQVPVQP 420 EATQVPLVSS TSEGYTASQP MYQPSHTTEQ RPQKESIDQI QASMSLNADQ TPSSSSLPTA 480 SQPQVFQAGS SKPLHSSGIN VNAAPFQSMQ TVFNMNAPVP PVNEPEALKQ QNQYQASYNQ 540 SFSNQPHQVE QSDLQQEQLQ TVVGTYHGSP DQTHQVAGNH QQPPQQNTGF PRNSQPYYNS 600 RGVSRGGSRG TRGLMNGYRG PANGFRGGYD GYRPSFSNTP NSGYTQPQFN APRDYSNYQR 660 DGYQQNFKRG SGQSGPRGAP RGRGGPPRPN RGMPQMNAQQ VN 702
3-31	**Sequences**	
3-31-1	Sequence Number [ID]	31
3-31-2	Molecule Type	AA
3-31-3	Length	63
3-31-4	Features	**source 1..63**

	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-31-5	Residues	EEYTEQSEVE STEYVNRQFM AETQFTSGEK EQVDEWTVET VEVVNSLQQQ PQAASPSVPE	60
		PHS	63
3-32	**Sequences**		
3-32-1	Sequence Number [ID]	32	
3-32-2	Molecule Type	AA	
3-32-3	Length	18	
3-32-4	Features	**source 1..18**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-32-5	Residues	VFNMNAPVPP VNEPETLK	18
3-33	**Sequences**		
3-33-1	Sequence Number [ID]	33	
3-33-2	Molecule Type	AA	
3-33-3	Length	16	
3-33-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-33-5	Residues	ATQVPLVSST SEGYTA	16
3-34	**Sequences**		
3-34-1	Sequence Number [ID]	34	
3-34-2	Molecule Type	AA	
3-34-3	Length	25	
3-34-4	Features	**source 1..25**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-34-5	Residues	QILGVIDKKL RNLEKKKGKL DDYQE	25
3-35	**Sequences**		
3-35-1	Sequence Number [ID]	35	
3-35-2	Molecule Type	AA	
3-35-3	Length	23	
3-35-4	Features	**source 1..23**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-35-5	Residues	PRGRGGPPRP NRGMPQMNTQ QVN	23
3-36	**Sequences**		
3-36-1	Sequence Number [ID]	36	
3-36-2	Molecule Type	AA	
3-36-3	Length	5	
3-36-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-36-5	Residues	SYQMN	5
3-37	**Sequences**		
3-37-1	Sequence Number [ID]	37	
3-37-2	Molecule Type	AA	
3-37-3	Length	17	
3-37-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-37-5	Residues	AINKFGNSTG HGAAVKG	17
3-38	**Sequences**		
3-38-1	Sequence Number [ID]	38	
3-38-2	Molecule Type	AA	
3-38-3	Length	19	
3-38-4	Features	**source 1..19**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-38-5	Residues	HAYGYCGSGT WCAAGEIDA	19

3-39	**Sequences**	
3-39-1	Sequence Number [ID]	39
3-39-2	Molecule Type	AA
3-39-3	Length	128
3-39-4	Features	**source 1..128**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-39-5	Residues	AVTLDESGGG LQMSRGGLSL VCKASGFDFS SYQMNWIRQA PGKGLEFVAA INKFGNSTGH 60 GAAVKGRVTI SRDNGQSTVR LQLNNLRAED TAIYFCTKHA YGYCGSGTWC AAGEIDAWGH 120 GTEVIVSS 128
3-40	**Sequences**	
3-40-1	Sequence Number [ID]	40
3-40-2	Molecule Type	AA
3-40-3	Length	9
3-40-4	Features	**source 1..9**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-40-5	Residues	SGGGSYSYG 9
3-41	**Sequences**	
3-41-1	Sequence Number [ID]	41
3-41-2	Molecule Type	AA
3-41-3	Length	7
3-41-4	Features	**source 1..7**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-41-5	Residues	NNKRPSD 7
3-42	**Sequences**	
3-42-1	Sequence Number [ID]	42
3-42-2	Molecule Type	AA
3-42-3	Length	10
3-42-4	Features	**source 1..10**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-42-5	Residues	SGDSTDTAVF 10
3-43	**Sequences**	
3-43-1	Sequence Number [ID]	43
3-43-2	Molecule Type	AA
3-43-3	Length	108
3-43-4	Features	**source 1..108**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-43-5	Residues	QAASTQPSSV SANPGETVEI TCSGGGSYSY GWFQQKSPGS APVTVIYYNN KRPSDIPSRF 60 SGSKSGSTGT LTITGVQADD EAVYYCGSGD STDTAVFGAG TTLTVLGQ 108
3-44	**Sequences**	
3-44-1	Sequence Number [ID]	44
3-44-2	Molecule Type	AA
3-44-3	Length	5
3-44-4	Features	**source 1..5**
	Location/Qualifiers	mol_type=protein
		organism=Oryctolagus cuniculus
	NonEnglishQualifier Value	
3-44-5	Residues	SHSLG 5
3-45	**Sequences**	
3-45-1	Sequence Number [ID]	45
3-45-2	Molecule Type	AA
3-45-3	Length	16
3-45-4	Features	**source 1..16**
	Location/Qualifiers	mol_type=protein
		organism=Oryctolagus cuniculus
	NonEnglishQualifier Value	
3-45-5	Residues	DIRSGGSAYY ANWAKG 16
3-46	**Sequences**	
3-46-1	Sequence Number [ID]	46

3-46-2	Molecule Type	AA	
3-46-3	Length	13	
3-46-4	Features	**source 1..13**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-46-5	Residues	TNGPSDLTNR LDL	13
3-47	**Sequences**		
3-47-1	Sequence Number [ID]	47	
3-47-2	Molecule Type	AA	
3-47-3	Length	121	
3-47-4	Features	**source 1..121**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-47-5	Residues	EQSLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA	60
		NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRTNG PSDLTNRLDL WGQGTLVTVS	120
		S	121
3-48	**Sequences**		
3-48-1	Sequence Number [ID]	48	
3-48-2	Molecule Type	AA	
3-48-3	Length	13	
3-48-4	Features	**source 1..13**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-48-5	Residues	QASQSLYNNE NLA	13
3-49	**Sequences**		
3-49-1	Sequence Number [ID]	49	
3-49-2	Molecule Type	AA	
3-49-3	Length	7	
3-49-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-49-5	Residues	GASTLAS	7
3-50	**Sequences**		
3-50-1	Sequence Number [ID]	50	
3-50-2	Molecule Type	AA	
3-50-3	Length	13	
3-50-4	Features	**source 1..13**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-50-5	Residues	LGEFSCGSAD CFA	13
3-51	**Sequences**		
3-51-1	Sequence Number [ID]	51	
3-51-2	Molecule Type	AA	
3-51-3	Length	112	
3-51-4	Features	**source 1..112**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-51-5	Residues	QVLTQSPSSL SASVGDRVTI NCQASQSLYN NENLAWFQQK PGKVPKRLIY GASTLASGVS	60
		SRFSGSGSGT EFTLTISSLQ CEDFAIYYCL GEFSCGSADC FAFGGGTKVE IK	112
3-52	**Sequences**		
3-52-1	Sequence Number [ID]	52	
3-52-2	Molecule Type	AA	
3-52-3	Length	4	
3-52-4	Features	**source 1..4**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-52-5	Residues	FDMG	4
3-53	**Sequences**		
3-53-1	Sequence Number [ID]	53	
3-53-2	Molecule Type	AA	
3-53-3	Length	17	

3-53-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-53-5	Residues	QINDAGSRTW YATAVKG	17
3-54	**Sequences**		
3-54-1	Sequence Number [ID]	54	
3-54-2	Molecule Type	AA	
3-54-3	Length	12	
3-54-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-54-5	Residues	GSGYVGAGAI DA	12
3-55	**Sequences**		
3-55-1	Sequence Number [ID]	55	
3-55-2	Molecule Type	AA	
3-55-3	Length	120	
3-55-4	Features	**source 1..120**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-55-5	Residues	AVTLDESGGG LQTPGGGLSL VCKASGFTFS SFDMGWVRQA PGKGLEFVAQ INDAGSRTWY 60 ATAVKGRATI SRDNGQTTVR LQLNNLRAED TGTYYCTRGS GYVGAGAIDA WGHGTEVIVS 120	
3-56	**Sequences**		
3-56-1	Sequence Number [ID]	56	
3-56-2	Molecule Type	AA	
3-56-3	Length	8	
3-56-4	Features	**source 1..8**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-56-5	Residues	SGGSGYYG	8
3-57	**Sequences**		
3-57-1	Sequence Number [ID]	57	
3-57-2	Molecule Type	AA	
3-57-3	Length	7	
3-57-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-57-5	Residues	NDKRPSD	7
3-58	**Sequences**		
3-58-1	Sequence Number [ID]	58	
3-58-2	Molecule Type	AA	
3-58-3	Length	10	
3-58-4	Features	**source 1..10**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-58-5	Residues	RYDSTDSGIF	10
3-59	**Sequences**		
3-59-1	Sequence Number [ID]	59	
3-59-2	Molecule Type	AA	
3-59-3	Length	105	
3-59-4	Features	**source 1..105**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-59-5	Residues	AALTQPSSVS ANPGETVKIT CSGGSGYYGW YQQQKSPGSA PVTVIYQNDK RPSDIPSRFS 60 GSGSGSTNTL TITGVQAEDE AVYFCGRYDS TDSGIFGAGT TLTVL 105	
3-60	**Sequences**		
3-60-1	Sequence Number [ID]	60	
3-60-2	Molecule Type	AA	
3-60-3	Length	6	
3-60-4	Features	**source 1..6**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	

	NonEnglishQualifier Value		
3-60-5	Residues	GSYYMS	6
3-61	**Sequences**		
3-61-1	Sequence Number [ID]	61	
3-61-2	Molecule Type	AA	
3-61-3	Length	17	
3-61-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-61-5	Residues	YIYIGDGVTA YANWAKG	17
3-62	**Sequences**		
3-62-1	Sequence Number [ID]	62	
3-62-2	Molecule Type	AA	
3-62-3	Length	4	
3-62-4	Features	**source 1..4**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-62-5	Residues	GNKL	4
3-63	**Sequences**		
3-63-1	Sequence Number [ID]	63	
3-63-2	Molecule Type	AA	
3-63-3	Length	112	
3-63-4	Features	**source 1..112**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-63-5	Residues	QSLEESGGDL VKPGASLTLT CTASGFSFSG SYYMSWVRQA PGKGLEWIAY IYIGDGVTAY	60
		ANWAKGRFTI SKASSTTVTL QMTSLTAADT ATYFCARGNK LWGPGTLVTV SS	112
3-64	**Sequences**		
3-64-1	Sequence Number [ID]	64	
3-64-2	Molecule Type	AA	
3-64-3	Length	11	
3-64-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-64-5	Residues	QASQSISSYL A	11
3-65	**Sequences**		
3-65-1	Sequence Number [ID]	65	
3-65-2	Molecule Type	AA	
3-65-3	Length	7	
3-65-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-65-5	Residues	DASNLDS	7
3-66	**Sequences**		
3-66-1	Sequence Number [ID]	66	
3-66-2	Molecule Type	AA	
3-66-3	Length	14	
3-66-4	Features	**source 1..14**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-66-5	Residues	QCTAVSSATI YGNA	14
3-67	**Sequences**		
3-67-1	Sequence Number [ID]	67	
3-67-2	Molecule Type	AA	
3-67-3	Length	112	
3-67-4	Features	**source 1..112**	
	Location/Qualifiers	mol_type=protein	
		organism=Oryctolagus cuniculus	
	NonEnglishQualifier Value		
3-67-5	Residues	DVVMTQTPAS VEAAVGGTVT IKCQASQSIS SYLAWYQQKP GQPPKRLIYD ASNLDSGVPS	60
		RFKGSGSGTD FTITISDLEC ADAATYYCQC TAVSSATIYG NAFGGGTEVV VK	112
3-68	**Sequences**		

3-68-1	Sequence Number [ID]	68
3-68-2	Molecule Type	AA
3-68-3	Length	127
3-68-4	Features	**source 1..127**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-68-5	Residues	AVTLDESGGG LQTPGGALSL VCKASGFTFS GYDMLWVRQA PGKGLEWVAG IGSTGGGTDY 60 GAAVKGRATI SRDNGQSTVR LQLNNLRAED TATYYCAKVA GGCNSGYCRD SPGSIDAWGH 120 GTEVIVS 127
3-69	**Sequences**	
3-69-1	Sequence Number [ID]	69
3-69-2	Molecule Type	AA
3-69-3	Length	107
3-69-4	Features	**source 1..107**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-69-5	Residues	AVTQQPASVS ANPGETVKIT CSGGGSRNYY GWYQQKSPGS VPVTVIYYDD QRPSNIPSRF 60 SGALSGSTST LTITGVQADD EAVYFCGSAD SNTYEGSFGA GTTLTVL 107
3-70	**Sequences**	
3-70-1	Sequence Number [ID]	70
3-70-2	Molecule Type	AA
3-70-3	Length	148
3-70-4	Features	**source 1..148**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-70-5	Residues	MEWSGVFIFL LSGTAGVLSE VQLHQFGAEL VKPGASVKIS CKASGYTFTD YNMDWVKQSH 60 GKSLEWIGDI NPNYDSTSYN QKFKGKATLT VDKSSSTAYM ELRSLTSEDT AVYYCARSRS 120 YDYEGFAYWG QGTLVTVSAA KTTPPSVY 148
3-71	**Sequences**	
3-71-1	Sequence Number [ID]	71
3-71-2	Molecule Type	AA
3-71-3	Length	105
3-71-4	Features	**source 1..105**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-71-5	Residues	GLFCSVERCH YQLQSSQNLL SIVNRYHYMS GNPPKLLVYP ALLIYEASIT KSCVPDRFTR 60 SGSGTNFTLT INFVHADDLI FYYCQHNRGS FLPSSSVQVP RRRSN 105
3-72	**Sequences**	
3-72-1	Sequence Number [ID]	72
3-72-2	Molecule Type	AA
3-72-3	Length	109
3-72-4	Features	**source 1..109**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-72-5	Residues	PRASLGVSET LLCTSGFTFT DYYMSWVRQP PGKALEWLGF IRNKANGYTT EYSASVKGRF 60 TISRDNSQSI LYLQMNTLRA EDSATYYCAR ANWAFDYWGQ GTTVTVSSK 109
3-73	**Sequences**	
3-73-1	Sequence Number [ID]	73
3-73-2	Molecule Type	AA
3-73-3	Length	94
3-73-4	Features	**source 1..94**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-73-5	Residues	SGDRVSLSCR ASQSISNYLH WYQQKSHESP RLLIKYASQS ISGIPSRFSG SGSGTDFTLS 60 INSVETEDFG MYFCQQSNSW PYTFGGGTKL EIKQ 94
3-74	**Sequences**	
3-74-1	Sequence Number [ID]	74
3-74-2	Molecule Type	AA
3-74-3	Length	118
3-74-4	Features	**source 1..118**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	

3-74-5	Residues	AAELVRPGTS VKVSCKASGY AFTNYLIVWI KQRPGQGLEW IGVISPGSGG TNYNEKFKGK 60 AILTADKSSS TAYMQLSSLT SDEFAVYFCA REKIYDDYYE GYFDVWGAGP RHLLASLS 118
3-75	**Sequences**	
3-75-1	Sequence Number [ID]	75
3-75-2	Molecule Type	AA
3-75-3	Length	107
3-75-4	Features	**source 1..107**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-75-5	Residues	GTRCDIRLTQ TTSSLSASLG DRVTISCSAS LGIGNYLNWY QQKPDGTVKL LIYYTSNLHS 60 GVPSRFSGSG SGTDYSLTIS NLEPEDIATY YCQHYSKLPL TFGAGPS 107
3-76	**Sequences**	
3-76-1	Sequence Number [ID]	76
3-76-2	Molecule Type	AA
3-76-3	Length	113
3-76-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-76-5	Residues	GAELVRSGAS VKMSCKASGY SFTDYNMYWV KQTPGQGLEW IGYIYPGNGG TNYNQKFKGK 60 ATLTADTSSS TAYMQISSLT SEDSAVYFCA RDYDDGGYAM DYWGQGTTVT VSS 113
3-77	**Sequences**	
3-77-1	Sequence Number [ID]	77
3-77-2	Molecule Type	AA
3-77-3	Length	117
3-77-4	Features	**source 1..117**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-77-5	Residues	LLLWLTGARC DIQMTQSPAS LSASVGETVT ITCRASGNIH NYLTWYQQKQ GKSPQLLVYN 60 AKTLADGVPS RFSGSGSGTQ YSLKINRLQP EDFGSYYCQH FWNIPWTFGG GTKLNSR 117
3-78	**Sequences**	
3-78-1	Sequence Number [ID]	78
3-78-2	Molecule Type	AA
3-78-3	Length	114
3-78-4	Features	**source 1..114**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-78-5	Residues	DAELVKPGAS VKISCKASGY TFTDHSIHWV QQKPEQGLEW IGYISPGNGN IKYNEKFKGK 60 ATLTADKSSS TAYMQLNSLT SEDSAVYFCK RSLGRGGPYY FDYWGQGTTV TVSS 114
3-79	**Sequences**	
3-79-1	Sequence Number [ID]	79
3-79-2	Molecule Type	AA
3-79-3	Length	108
3-79-4	Features	**source 1..108**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-79-5	Residues	DIVLTQAAPS LPVTPGESVS ISCRSSKSLL HSNGNTYLYW FLQRPGQSPQ LLIYRMSNLA 60 SGVPDRFSGS GSGTAFTLRI SRVEAEDVGV YYCMQHREYP VTFGSGPN 108
3-80	**Sequences**	
3-80-1	Sequence Number [ID]	80
3-80-2	Molecule Type	AA
3-80-3	Length	111
3-80-4	Features	**source 1..111**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-80-5	Residues	QVQLQQSGAE LMKPGASVKI SCKATGYTFS SYWIEWVKQR PGHGLEWIGE ILPGSGSTNY 60 NEKFKGKATF TADTSSNTAY MQLSSLTSED SAVYYCASYY WYFDVWAQDH V 111
3-81	**Sequences**	
3-81-1	Sequence Number [ID]	81
3-81-2	Molecule Type	AA
3-81-3	Length	109
3-81-4	Features	**source 1..109**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus

	NonEnglishQualifier Value	
3-81-5	Residues	IVMTQAAFSN PVTLGTSASI SCRSSKNLLH SNGITYLYWY LQRPGQSPQL LIYRVSNLAS 60 GVPNRFSGSE SGTDFTLRIS RVEAEDVGVY YCAQLLELPY TSEGTKRWE 109
3-82	**Sequences**	
3-82-1	Sequence Number [ID]	82
3-82-2	Molecule Type	AA
3-82-3	Length	109
3-82-4	Features	**source 1..109**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-82-5	Residues	GGGLVKPGGS LKLSCAASGF AFSSYDMSWI RQTPEKRLEW VAYISSGAGS TYYPDTVKGR 60 FTVSRDNAKN TLYLQMSSLK SEDTAMYYCA RHFYRFDYWG QGTTVTVSS 109
3-83	**Sequences**	
3-83-1	Sequence Number [ID]	83
3-83-2	Molecule Type	AA
3-83-3	Length	113
3-83-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-83-5	Residues	LLLCVSGAPG SIVMTQTPKF LLVSAGDRIT ITCKASQSVS NDVAWYQQKP GQSPKLLIYY 60 ASNRYTGVPD RFTGSGYGTD FTFTISTVQA EDLAVYFCQQ DDRFPLTFGA GPS 113
3-84	**Sequences**	
3-84-1	Sequence Number [ID]	84
3-84-2	Molecule Type	AA
3-84-3	Length	112
3-84-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-84-5	Residues	QIQLVQSGPE LKKPGETVKI SCKASGYTFT NYGMNWVKQA PGKGLKWMGW INTYTGEPTY 60 ADDFKGRFAF SLETSASTAY LQINNLKNED TATYFCATGA WFAYWAKDSS RH 112
3-85	**Sequences**	
3-85-1	Sequence Number [ID]	85
3-85-2	Molecule Type	AA
3-85-3	Length	107
3-85-4	Features	**source 1..107**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-85-5	Residues	GVEGDIVMTQ SHKFMSTSVG DRVSITCKAS QDVGTAVAWY QQKPGQSPKL LIYWASTRHT 60 GVPDRFTGSG SGTDFTLTIS NVQSEDLADY FCQQYSSYPL TFGAGPS 107
3-86	**Sequences**	
3-86-1	Sequence Number [ID]	86
3-86-2	Molecule Type	AA
3-86-3	Length	118
3-86-4	Features	**source 1..118**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-86-5	Residues	GGGLVQPGGS MKVSCVASGF SFIDFWMNWV RQSPEKGLEW VAEIRLKSNN YATHYAESVK 60 GRFTISRDDS KSSVYLQMNN LRPEDTGIYY CTSLFYYYDG TSGFAYWGQG TTVTVLLK 118
3-87	**Sequences**	
3-87-1	Sequence Number [ID]	87
3-87-2	Molecule Type	AA
3-87-3	Length	109
3-87-4	Features	**source 1..109**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-87-5	Residues	DIVMTQSPSS LTVTAGEKVT MHCKSSQSLL NSGDQKNYLT WYQQKPGQPP KLLIYWASTR 60 ESGVPDRFTG SGSGTDFTLT ISSVQAEDLA VYYCQNDYDY PLTFGAGPS 109
3-88	**Sequences**	
3-88-1	Sequence Number [ID]	88
3-88-2	Molecule Type	AA
3-88-3	Length	148
3-88-4	Features	**source 1..148**
	Location/Qualifiers	mol_type=protein

		organism=Mus musculus
	NonEnglishQualifier Value	
3-88-5	Residues	MEWSGVFIFL LSGTAGVLSE VQLHQFGAEL VKPGASVKIS CKASGYTFTD YNMDWVKQSH 60 GKSLEWIGDI NPNYDSTSYN QKFKGKATLT VDKSSSTAYM ELRSLTSEDT AVYYCARSRS 120 YDYEGFAYWG QGTLVTVSAA KTTPPSVY 148
3-89	**Sequences**	
3-89-1	Sequence Number [ID]	89
3-89-2	Molecule Type	AA
3-89-3	Length	139
3-89-4	Features	**source 1..139**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-89-5	Residues	MSVLTQVLGL LLLWLTGARC DIQMTQSPAS LSASVGETVT ITCRASGNIH NYLAWYQQKQ 60 GKSPQLLVYN AKTLADGVPS RFSGSGSGTQ YSLKINSLQP EDFGSYYCQH FWSTLTFGAG 120 TKLELKRADA APTVSNPYD 139
3-90	**Sequences**	
3-90-1	Sequence Number [ID]	90
3-90-2	Molecule Type	AA
3-90-3	Length	100
3-90-4	Features	**source 1..100**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-90-5	Residues	DILQASGYSF TGYTMNWVKQ SHGKNLEWIG LINPYNGGTS YNQKFKGKAT LTVDKSSSTA 60 YMELLSLTSE DSAVYYCARW GVWSAMDYWG QGTTVTVSSK 100
3-91	**Sequences**	
3-91-1	Sequence Number [ID]	91
3-91-2	Molecule Type	AA
3-91-3	Length	90
3-91-4	Features	**source 1..90**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-91-5	Residues	DRVSITCKAS QNVRTAVAWY QQKPRQSPKA LIYLASNRDT GLPDRFPGRG SGTDFTLNIT 60 NVQSEDLEDY FCLQHCNYPN EFRGCTKVPI 90
3-92	**Sequences**	
3-92-1	Sequence Number [ID]	92
3-92-2	Molecule Type	AA
3-92-3	Length	116
3-92-4	Features	**source 1..116**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-92-5	Residues	LQESGAELAR PGASVKLSCK ASGYTFTSYW MQWVKQRPGQ GLEWIGAIYP GDGDTRYTQK 60 FKGKATLTAD KSSSTAYMQL SSLASEDSAV YYCARGEYGN YFAYWGQGTT VTVSSN 116
3-93	**Sequences**	
3-93-1	Sequence Number [ID]	93
3-93-2	Molecule Type	AA
3-93-3	Length	100
3-93-4	Features	**source 1..100**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-93-5	Residues	TSDASLGERV TITCKASQDI NSYLSWFQQK PGKSPKTLIY RANRLVDGVP SRFSGSGSGQ 60 DYSLTISSLE YEDMGIYYCL QYDEFPLTFG GGTKLEIKQK 100
3-94	**Sequences**	
3-94-1	Sequence Number [ID]	94
3-94-2	Molecule Type	AA
3-94-3	Length	108
3-94-4	Features	**source 1..108**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-94-5	Residues	AWLSQLSCTA SGFNIKDTYM HWVKQRPEQG LEWIGRIDPA NGNTKYDPKF QGKATITADT 60 SSNTAYLQLS SLTSEDTAVY YCARPIHYYY GSSLAYWGQG TTVTVSSK 108
3-95	**Sequences**	
3-95-1	Sequence Number [ID]	95
3-95-2	Molecule Type	AA

3-95-3	Length	104
3-95-4	Features	**source 1..104**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-95-5	Residues	EFHAVSLGQR ATISCRASES VDSYGNSFMH WYQQKPGQPP KLLIYRASNL ESGIPARFSG 60 SGSRTDFTLT INPVEADDVA TYYCQQSNED PGRSEVVPSW RSNK 104
3-96	**Sequences**	
3-96-1	Sequence Number [ID]	96
3-96-2	Molecule Type	AA
3-96-3	Length	109
3-96-4	Features	**source 1..109**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-96-5	Residues	PRASLGVSET LLCTSGFTFT DYYMSWVRQP PGKALEWLGF IRNKANGYTT EYSASVKGRF 60 TISRDNSQSI LYLQMNTLRA EDSATYYCAR ANWAFDYWGQ GTTVTVSSK 109
3-97	**Sequences**	
3-97-1	Sequence Number [ID]	97
3-97-2	Molecule Type	AA
3-97-3	Length	94
3-97-4	Features	**source 1..94**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-97-5	Residues	SGDRVSLSCR ASQSISNYLH WYQQKSHESP RLLIKYASQS ISGIPSRFSG SGSGTDFTLS 60 INSVETEDFG MYFCQQSNSW PYTFGGGTKL EIKQ 94
3-98	**Sequences**	
3-98-1	Sequence Number [ID]	98
3-98-2	Molecule Type	AA
3-98-3	Length	111
3-98-4	Features	**source 1..111**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-98-5	Residues	PACLPGGSLR LSCATSGFTF TDYYMSWVRQ PPGKALEWLG FIRNKANGYT TEYSASVKGR 60 FTISRDNSQS ILYLQMNTLR AEDSATYYCA RAPLLYYAMD YWGQGTTVTV S 111
3-99	**Sequences**	
3-99-1	Sequence Number [ID]	99
3-99-2	Molecule Type	AA
3-99-3	Length	102
3-99-4	Features	**source 1..102**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-99-5	Residues	RLPFYSLEQR ATISYRASKN VSTSGYSYMH WNQQKPGQPP KLLIYLVSNL ESGVPARFSG 60 SGSGTDFTLN IHPVEEEDAA TYYCQHIREL TRSELVPSWK SN 102
3-100	**Sequences**	
3-100-1	Sequence Number [ID]	100
3-100-2	Molecule Type	AA
3-100-3	Length	101
3-100-4	Features	**source 1..101**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-100-5	Residues	VSCKASGYTF TSYWMHWVKQ RPGQGLEWIG MIDPSNSETR LNQKFKDKAT LNVDKSSNTA 60 YMQLSSLTSE DSAVYYCARG LRHYWYFDVW GQGTTVTVSS K 101
3-101	**Sequences**	
3-101-1	Sequence Number [ID]	101
3-101-2	Molecule Type	AA
3-101-3	Length	99
3-101-4	Features	**source 1..99**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-101-5	Residues	TILWREGPFS YRASKSVSTS GYSYMHWNQQ KPGQPPRLLI YLVSNLESGV PARFSGSGSG 60 TDFTLNIHPV EEEDAATYYC QHIRELTRSE EVPSWRSNK 99
3-102	**Sequences**	
3-102-1	Sequence Number [ID]	102

3-102-2	Molecule Type	AA
3-102-3	Length	110
3-102-4	Features	**source 1..110**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-102-5	Residues	GGGLVKPGGS LKLSCAASGF TFSSYGMSWV RQTPEKRLEW VATISSGGSY TYYPDSVKGR 60 FTISRDNAKN TLYLQMSSLR SEDTAMYYCA SLASYYFDYW GQGTTLTVSS 110
3-103	**Sequences**	
3-103-1	Sequence Number [ID]	103
3-103-2	Molecule Type	AA
3-103-3	Length	113
3-103-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-103-5	Residues	GARCDVQMIQ SPSSLSASLG DIVTMTCQAS QGTSINLNWF QQKPGKAPKL LIYGASSLED 60 GVPSRFSGSC FGTDFTLTIS SLEDEDMATY FCLQHSYLPP LTFGAGTKLE LKR 113
3-104	**Sequences**	
3-104-1	Sequence Number [ID]	104
3-104-2	Molecule Type	AA
3-104-3	Length	111
3-104-4	Features	**source 1..111**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-104-5	Residues	GPGLVQPSQS LSITCTVSGF SLTTYDLHWV RQSPGKGLEW LGVIWSGGST DYNAAFISRL 60 SISKDNSKSQ VFFKMNSLQA NDTAIYYCAR NYGYSAWFAY WGQGTLVTVS A 111
3-105	**Sequences**	
3-105-1	Sequence Number [ID]	105
3-105-2	Molecule Type	AA
3-105-3	Length	118
3-105-4	Features	**source 1..118**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-105-5	Residues	PASSSDVLMT QTPLSLPVSL GDQASISCRS SQSIVHSNGN TYLEWYLQKP GQSPKLLIYK 60 VSNRFSGVPD RFSGSGSGTD FTLKISRVEA EDLGVYYCFQ GSHVPLTFGA GTKLELKR 118
3-106	**Sequences**	
3-106-1	Sequence Number [ID]	106
3-106-2	Molecule Type	AA
3-106-3	Length	114
3-106-4	Features	**source 1..114**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-106-5	Residues	GFELKKPGET VKISCKASGY TFTAYSMHWV KQTPGKGLKW LGWINTETGE PTYTDDFKGR 60 FTFSLETSAR IAYLQINDLK NEDTATYFCA RRIYYFGRGG FDYWGQGTTV TVSS 114
3-107	**Sequences**	
3-107-1	Sequence Number [ID]	107
3-107-2	Molecule Type	AA
3-107-3	Length	118
3-107-4	Features	**source 1..118**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-107-5	Residues	PASSSDVLMT QTPLSLPVRL GDQSSISCRS SQSIVHSNGN TYLEWYLQKP GQSPKLLIYK 60 VSNRFSGVPD RFSGSGSGTD FTLKISRVEP EDLGVYYCFQ GSHVPYTSEG DQAEIKLA 118
3-108	**Sequences**	
3-108-1	Sequence Number [ID]	108
3-108-2	Molecule Type	AA
3-108-3	Length	114
3-108-4	Features	**source 1..114**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-108-5	Residues	GGGLVQPGGS MRLSCVASGF TFSNSWFNWV RQSPEKGLEW VAEIRLTSDN YAIYYAESVK 60 GRFTISRDDS KSSVYLQMNN LRAEDTGIYY CTRPETARAT FAYWGQGTTV TVSS 114
3-109	**Sequences**	

3-109-1	Sequence Number [ID]	109
3-109-2	Molecule Type	AA
3-109-3	Length	118
3-109-4	Features	**source 1..118**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-109-5	Residues	PASTSDVLMT QTPLSLPVSL GDQASISCRS SQSIVHSNGN TYLEWYLQKP GQSPKVLIYK 60 VFNRFSGVPD RFSGSGSGTD FTLKISRVEA EDLGVYYCFQ GSHVPRTFGG GTKLNQTG 118
3-110	**Sequences**	
3-110-1	Sequence Number [ID]	110
3-110-2	Molecule Type	AA
3-110-3	Length	111
3-110-4	Features	**source 1..111**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-110-5	Residues	GPDLVKPGAS VKISCKASGY SFTAYYMHWV KQSHGKSLEW IGRVNPNNGG TTYNQKFKGK 60 AILTVDKSSS TAYMELRSLT FEDSAVYYCA RRIYYGYFDY WGQGTTVTVS S 111
3-111	**Sequences**	
3-111-1	Sequence Number [ID]	111
3-111-2	Molecule Type	AA
3-111-3	Length	104
3-111-4	Features	**source 1..104**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-111-5	Residues	AFFAVSLGQR ATISCKASQS VDYDGDSYMN WYQQKPGQPP KLLIYVASNL ESGVPARFSG 60 SGSGTDFTLN IHPVEEEDAA TYYCQQSNED PYTFGGGTKL EIKQ 104
3-112	**Sequences**	
3-112-1	Sequence Number [ID]	112
3-112-2	Molecule Type	AA
3-112-3	Length	106
3-112-4	Features	**source 1..106**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-112-5	Residues	GAELVKPGAS VKLSCTASGL NIRDIYMHWV KQRPEQGLEW IGKIDPANGN TKYDPKFQGK 60 ATITADTSSN TAYVQLSSLT SEDTAVYYCA GTGDYWGQGT TVTVSS 106
3-113	**Sequences**	
3-113-1	Sequence Number [ID]	113
3-113-2	Molecule Type	AA
3-113-3	Length	112
3-113-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-113-5	Residues	GTCGDIVMSQ SPSSLAVSAG EKVTMSCKSS QSLLNSRTRK NYLAWVQHKP GQSPRLLIYW 60 ASTRESGVPD RFTGSGSGTD FTLTISSVQA EDLAVYYCRQ SYNLVTFGAG PS 112
3-114	**Sequences**	
3-114-1	Sequence Number [ID]	114
3-114-2	Molecule Type	AA
3-114-3	Length	112
3-114-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-114-5	Residues	GPELVKPGAS VKMSCKASGY TFTSYVMHWV KQKPGQGLEW IGYINPYNDG TKYNEKFKGK 60 ATLTSDKSSS TAYMELSSLT SEDSAVYYCA RRYYYGSSGG YFDVWAQDHV RT 112
3-115	**Sequences**	
3-115-1	Sequence Number [ID]	115
3-115-2	Molecule Type	AA
3-115-3	Length	108
3-115-4	Features	**source 1..108**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-115-5	Residues	DVQITQSPSY LAASPGETIT INCRASKSIS KYLAWYQEKP GKTNKLLIYS GSTLQSGIPS 60 RFSGSGSGTD FTLTISSLEP EDFAMYYCQQ HNEYPYTFGG GTKLEIKR 108

3-116	**Sequences**	
3-116-1	Sequence Number [ID]	116
3-116-2	Molecule Type	AA
3-116-3	Length	113
3-116-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-116-5	Residues	GPELVKPGAS VKISCKASGY SFTGYFMNWV MQSHGKSLEW IGRINPYNGD TFYNQKFKGK 60 ATLTVDKSSS TAHMELRSLA SEDSAVYYCA RRIHYYYGSS YYAMDYWGQE PHH 113
3-117	**Sequences**	
3-117-1	Sequence Number [ID]	117
3-117-2	Molecule Type	AA
3-117-3	Length	108
3-117-4	Features	**source 1..108**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-117-5	Residues	DVQITQSPSY LAASPGETIT INCRASKSIS KYLAWYQEKP GKTNKLLIYS GSTLQSGIPS 60 RFSGSGSGTD FTLTISSLEP EDFAMYYCQQ HNEYPWTFGG GTKLEIKR 108
3-118	**Sequences**	
3-118-1	Sequence Number [ID]	118
3-118-2	Molecule Type	AA
3-118-3	Length	113
3-118-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-118-5	Residues	GAGLVKPGAS VKLSCKASGY TFTEYIIHWV KQRSGQGLEW IGWFYPGSGS IKYNEKFKDK 60 ATLTADKSSS TVYMELSRLT SEDSAVYFCA RHEVYYDYDK SMLWTTGVKN LIR 113
3-119	**Sequences**	
3-119-1	Sequence Number [ID]	119
3-119-2	Molecule Type	AA
3-119-3	Length	108
3-119-4	Features	**source 1..108**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-119-5	Residues	SPSSLAVSVG EKVTMSCKSS QSLLYSSNQK NYLAWYQQKP GQSPKLLIYW ASTRESGVPD 60 RFTGSGSGTD FTLTISSVKA EDLAVYYCQQ YYSYPYTFGG GTKLEIKR 108
3-120	**Sequences**	
3-120-1	Sequence Number [ID]	120
3-120-2	Molecule Type	AA
3-120-3	Length	113
3-120-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-120-5	Residues	GAELVRPGTS VKVSCKASVY AFTNYLIEWV KQRPGQGLEW IGVINPKSGG TKYNEKFRGK 60 ATLTADKSSS TAYMQLSSLT SGDSAVYFCA ITGTDYWGQG TTLTVSSAKT TPP 113
3-121	**Sequences**	
3-121-1	Sequence Number [ID]	121
3-121-2	Molecule Type	AA
3-121-3	Length	113
3-121-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-121-5	Residues	QGTRCDIQMT QTTSSLSASL GDRVTISCSA SQGINNYLNW YQQKPDGTVK LLIYYTSSLR 60 SGVPSRFSGS GSGTDYSLTI SNLEPEDVAT YYCQQYSKLP RTFGGGTKLE IKR 113
3-122	**Sequences**	
3-122-1	Sequence Number [ID]	122
3-122-2	Molecule Type	AA
3-122-3	Length	121
3-122-4	Features	**source 1..121**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-122-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA 60

		NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRTNG PSDLTNRLDL WGQGTLVTVS 120 S 121
3-123	**Sequences**	
3-123-1	Sequence Number [ID]	123
3-123-2	Molecule Type	AA
3-123-3	Length	112
3-123-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-123-5	Residues	QVLTQSPSSL SASVGDRVTI NCQASQSLYN NENLAWFQQK PGKVPKRLIY GASTLASGVS 60 SRFSGSGSGT EFTLTISSLQ CEDFAIYYCL GEFSCGSADC FAFGGGTKVE IK 112
3-124	**Sequences**	
3-124-1	Sequence Number [ID]	124
3-124-2	Molecule Type	AA
3-124-3	Length	121
3-124-4	Features	**source 1..121**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-124-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA 60 NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYFCTRTNG PSDLTNRLDL WGQGTLVTVS 120 S 121
3-125	**Sequences**	
3-125-1	Sequence Number [ID]	125
3-125-2	Molecule Type	AA
3-125-3	Length	112
3-125-4	Features	**source 1..112**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-125-5	Residues	QVLTQSPSSL SASVGDRVTI NCQASQSLYN NENLAWFQQK PGKVPKRLIY GASTLASGVS 60 SRFSGSGSGT EFTLTISSLQ CEDFAIYYCL GEFSCGSADC FAFGGGTKVE IK 112
3-126	**Sequences**	
3-126-1	Sequence Number [ID]	126
3-126-2	Molecule Type	AA
3-126-3	Length	121
3-126-4	Features	**source 1..121**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-126-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA 60 NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRTNG PSDLTNRLDL WGQGTLVTVS 120 S 121
3-127	**Sequences**	
3-127-1	Sequence Number [ID]	127
3-127-2	Molecule Type	AA
3-127-3	Length	113
3-127-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-127-5	Residues	EQVLTQSPSS LSASVGDRVT INCQASQSLY NNENLAWFQQ KPGKVPKRLI YGASTLASGV 60 SSRFSGSGSG TEFTLTISNL QPEDFAIYYC LGEFSCGSAD CFAFGGGTKV EIK 113
3-128	**Sequences**	
3-128-1	Sequence Number [ID]	128
3-128-2	Molecule Type	AA
3-128-3	Length	121
3-128-4	Features	**source 1..121**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-128-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA 60 NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYFCTRTNG PSDLTNRLDL WGQGTLVTVS 120 S 121
3-129	**Sequences**	
3-129-1	Sequence Number [ID]	129
3-129-2	Molecule Type	AA
3-129-3	Length	113
3-129-4	Features	**source 1..113**

	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-129-5	Residues	EIVLTQSPSS LSASVGDRVT INCQASQSLY NNENLAWFQQ KPGKVPKRLI YGASTLASGV 60 SSRFSGSGSG TEFTLTISNL QPEDFATYYC LGEFSCGSAD CFAFGGGTKV EIK 113
3-130	**Sequences**	
3-130-1	Sequence Number [ID]	130
3-130-2	Molecule Type	AA
3-130-3	Length	121
3-130-4	Features	**source 1..121**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-130-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA 60 NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRTNG PSDLTNRLDL WGQGTLVTVS 120 S 121
3-131	**Sequences**	
3-131-1	Sequence Number [ID]	131
3-131-2	Molecule Type	AA
3-131-3	Length	113
3-131-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-131-5	Residues	EIVLTQSPSS LSASVGDRVT INCQASQSLY NNENLAWFQQ KPGKVPKRLI YGASTLASGV 60 SSRFSGSGSG TEFTLTISNL QPEDFATYYC LGEFSCGSAD CFAFGGGTKV EIK 113
3-132	**Sequences**	
3-132-1	Sequence Number [ID]	132
3-132-2	Molecule Type	AA
3-132-3	Length	121
3-132-4	Features	**source 1..121**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-132-5	Residues	EVQLVESGGG LVQPGGSLRL SCAASGFSLS SHSLGWVRQA PGKGLEWIGD IRSGGSAYYA 60 NWAKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYFCTRTNG PSDLTNRLDL WGQGTLVTVS 120 S 121
3-133	**Sequences**	
3-133-1	Sequence Number [ID]	133
3-133-2	Molecule Type	AA
3-133-3	Length	113
3-133-4	Features	**source 1..113**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-133-5	Residues	EQVLTQSPSS LSASVGDRVT INCQASQSLY NNENLAWFQQ KPGKVPKRLI YGASTLASGV 60 SSRFSGSGSG TEFTLTISNL QPEDFAIYYC LGEFSCGSAD CFAFGGGTKV EIK 113
3-134	**Sequences**	
3-134-1	Sequence Number [ID]	134
3-134-2	Molecule Type	AA
3-134-3	Length	5
3-134-4	Features	**source 1..5**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-134-5	Residues	GYDML 5
3-135	**Sequences**	
3-135-1	Sequence Number [ID]	135
3-135-2	Molecule Type	AA
3-135-3	Length	17
3-135-4	Features	**source 1..17**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-135-5	Residues	GIGSTGGGTD YGAAVKG 17
3-136	**Sequences**	
3-136-1	Sequence Number [ID]	136
3-136-2	Molecule Type	AA
3-136-3	Length	19

3-136-4	Features	**source 1..19**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-136-5	Residues	VAGGCNSGYC RDSPGSIDA	19
3-137	**Sequences**		
3-137-1	Sequence Number [ID]	137	
3-137-2	Molecule Type	AA	
3-137-3	Length	10	
3-137-4	Features	**source 1..10**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-137-5	Residues	SGGGSRNYYG	10
3-138	**Sequences**		
3-138-1	Sequence Number [ID]	138	
3-138-2	Molecule Type	AA	
3-138-3	Length	7	
3-138-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-138-5	Residues	DDQRPSN	7
3-139	**Sequences**		
3-139-1	Sequence Number [ID]	139	
3-139-2	Molecule Type	AA	
3-139-3	Length	11	
3-139-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Gallus gallus	
	NonEnglishQualifier Value		
3-139-5	Residues	SADSNTYEGS F	11
3-140	**Sequences**		
3-140-1	Sequence Number [ID]	140	
3-140-2	Molecule Type	AA	
3-140-3	Length	5	
3-140-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-140-5	Residues	DYNMD	5
3-141	**Sequences**		
3-141-1	Sequence Number [ID]	141	
3-141-2	Molecule Type	AA	
3-141-3	Length	17	
3-141-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-141-5	Residues	DINPNYDSTS YNQKFKG	17
3-142	**Sequences**		
3-142-1	Sequence Number [ID]	142	
3-142-2	Molecule Type	AA	
3-142-3	Length	11	
3-142-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-142-5	Residues	SRSYDYEGFA Y	11
3-143	**Sequences**		
3-143-1	Sequence Number [ID]	143	
3-143-2	Molecule Type	AA	
3-143-3	Length	11	
3-143-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-143-5	Residues	LSIVNRYHYM S	11

3-144	**Sequences**		
3-144-1	Sequence Number [ID]	144	
3-144-2	Molecule Type	AA	
3-144-3	Length	6	
3-144-4	Features	**source 1..6**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-144-5	Residues	EASITK	6
3-145	**Sequences**		
3-145-1	Sequence Number [ID]	145	
3-145-2	Molecule Type	AA	
3-145-3	Length	9	
3-145-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-145-5	Residues	QHNRGSFLP	9
3-146	**Sequences**		
3-146-1	Sequence Number [ID]	146	
3-146-2	Molecule Type	AA	
3-146-3	Length	5	
3-146-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-146-5	Residues	DYYMS	5
3-147	**Sequences**		
3-147-1	Sequence Number [ID]	147	
3-147-2	Molecule Type	AA	
3-147-3	Length	17	
3-147-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-147-5	Residues	RNKANGYTTE YSASVKG	17
3-148	**Sequences**		
3-148-1	Sequence Number [ID]	148	
3-148-2	Molecule Type	AA	
3-148-3	Length	9	
3-148-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-148-5	Residues	ARANWAFDY	9
3-149	**Sequences**		
3-149-1	Sequence Number [ID]	149	
3-149-2	Molecule Type	AA	
3-149-3	Length	11	
3-149-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-149-5	Residues	RASQSISNYL H	11
3-150	**Sequences**		
3-150-1	Sequence Number [ID]	150	
3-150-2	Molecule Type	AA	
3-150-3	Length	7	
3-150-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-150-5	Residues	YASQSIS	7
3-151	**Sequences**		
3-151-1	Sequence Number [ID]	151	
3-151-2	Molecule Type	AA	
3-151-3	Length	7	
3-151-4	Features	**source 1..7**	

	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-151-5	Residues	YASQSIS	7
3-152	**Sequences**		
3-152-1	Sequence Number [ID]	152	
3-152-2	Molecule Type	AA	
3-152-3	Length	5	
3-152-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-152-5	Residues	NYLIV	5
3-153	**Sequences**		
3-153-1	Sequence Number [ID]	153	
3-153-2	Molecule Type	AA	
3-153-3	Length	17	
3-153-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-153-5	Residues	VISPGSGGTN YNEKFKG	17
3-154	**Sequences**		
3-154-1	Sequence Number [ID]	154	
3-154-2	Molecule Type	AA	
3-154-3	Length	11	
3-154-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-154-5	Residues	EKIYDDYYEG Y	11
3-155	**Sequences**		
3-155-1	Sequence Number [ID]	155	
3-155-2	Molecule Type	AA	
3-155-3	Length	15	
3-155-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-155-5	Residues	TISCSASLGI GNYLN	15
3-156	**Sequences**		
3-156-1	Sequence Number [ID]	156	
3-156-2	Molecule Type	AA	
3-156-3	Length	7	
3-156-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-156-5	Residues	TSNLHSG	7
3-157	**Sequences**		
3-157-1	Sequence Number [ID]	157	
3-157-2	Molecule Type	AA	
3-157-3	Length	9	
3-157-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-157-5	Residues	HYSKLPLTF	9
3-158	**Sequences**		
3-158-1	Sequence Number [ID]	158	
3-158-2	Molecule Type	AA	
3-158-3	Length	5	
3-158-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-158-5	Residues	DYNMY	5
3-159	**Sequences**		

3-159-1	Sequence Number [ID]	159	
3-159-2	Molecule Type	AA	
3-159-3	Length	17	
3-159-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-159-5	Residues	YIYPGNGGTN YNQKFKG	17
3-160	**Sequences**		
3-160-1	Sequence Number [ID]	160	
3-160-2	Molecule Type	AA	
3-160-3	Length	11	
3-160-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-160-5	Residues	DYDDGGYAMD Y	11
3-161	**Sequences**		
3-161-1	Sequence Number [ID]	161	
3-161-2	Molecule Type	AA	
3-161-3	Length	15	
3-161-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-161-5	Residues	SVGETVTITC RASGN	15
3-162	**Sequences**		
3-162-1	Sequence Number [ID]	162	
3-162-2	Molecule Type	AA	
3-162-3	Length	7	
3-162-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-162-5	Residues	NAKTLAD	7
3-163	**Sequences**		
3-163-1	Sequence Number [ID]	163	
3-163-2	Molecule Type	AA	
3-163-3	Length	9	
3-163-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-163-5	Residues	QHFWNIPWT	9
3-164	**Sequences**		
3-164-1	Sequence Number [ID]	164	
3-164-2	Molecule Type	AA	
3-164-3	Length	5	
3-164-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-164-5	Residues	DHSIH	5
3-165	**Sequences**		
3-165-1	Sequence Number [ID]	165	
3-165-2	Molecule Type	AA	
3-165-3	Length	17	
3-165-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-165-5	Residues	YISPGNGNIK YNEKFKG	17
3-166	**Sequences**		
3-166-1	Sequence Number [ID]	166	
3-166-2	Molecule Type	AA	
3-166-3	Length	12	
3-166-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	

		organism=Mus musculus	
	NonEnglishQualifier Value		
3-166-5	Residues	SLGRGGPYYF DY	12
3-167	**Sequences**		
3-167-1	Sequence Number [ID]	167	
3-167-2	Molecule Type	AA	
3-167-3	Length	16	
3-167-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-167-5	Residues	RSSKSLLHSN GNTYLY	16
3-168	**Sequences**		
3-168-1	Sequence Number [ID]	168	
3-168-2	Molecule Type	AA	
3-168-3	Length	7	
3-168-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-168-5	Residues	RMSNLAS	7
3-169	**Sequences**		
3-169-1	Sequence Number [ID]	169	
3-169-2	Molecule Type	AA	
3-169-3	Length	9	
3-169-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-169-5	Residues	MQHREYPVT	9
3-170	**Sequences**		
3-170-1	Sequence Number [ID]	170	
3-170-2	Molecule Type	AA	
3-170-3	Length	5	
3-170-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-170-5	Residues	SYWIE	5
3-171	**Sequences**		
3-171-1	Sequence Number [ID]	171	
3-171-2	Molecule Type	AA	
3-171-3	Length	17	
3-171-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-171-5	Residues	EILPGSGSTN YNEKFKG	17
3-172	**Sequences**		
3-172-1	Sequence Number [ID]	172	
3-172-2	Molecule Type	AA	
3-172-3	Length	11	
3-172-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-172-5	Residues	YYWYFDVWAQ D	11
3-173	**Sequences**		
3-173-1	Sequence Number [ID]	173	
3-173-2	Molecule Type	AA	
3-173-3	Length	15	
3-173-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-173-5	Residues	SSKNLLHSNG ITYLY	15
3-174	**Sequences**		
3-174-1	Sequence Number [ID]	174	

3-174-2	Molecule Type	AA	
3-174-3	Length	7	
3-174-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-174-5	Residues	RVSNLAS	7
3-175	**Sequences**		
3-175-1	Sequence Number [ID]	175	
3-175-2	Molecule Type	AA	
3-175-3	Length	9	
3-175-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-175-5	Residues	AQLLELPYT	9
3-176	**Sequences**		
3-176-1	Sequence Number [ID]	176	
3-176-2	Molecule Type	AA	
3-176-3	Length	5	
3-176-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-176-5	Residues	SYDMS	5
3-177	**Sequences**		
3-177-1	Sequence Number [ID]	177	
3-177-2	Molecule Type	AA	
3-177-3	Length	17	
3-177-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-177-5	Residues	YISSGAGSTY YPDTVKG	17
3-178	**Sequences**		
3-178-1	Sequence Number [ID]	178	
3-178-2	Molecule Type	AA	
3-178-3	Length	11	
3-178-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-178-5	Residues	HFYRFDYWGQ G	11
3-179	**Sequences**		
3-179-1	Sequence Number [ID]	179	
3-179-2	Molecule Type	AA	
3-179-3	Length	15	
3-179-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-179-5	Residues	SAGDRITITC KASQS	15
3-180	**Sequences**		
3-180-1	Sequence Number [ID]	180	
3-180-2	Molecule Type	AA	
3-180-3	Length	7	
3-180-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-180-5	Residues	YASNRYT	7
3-181	**Sequences**		
3-181-1	Sequence Number [ID]	181	
3-181-2	Molecule Type	AA	
3-181-3	Length	9	
3-181-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	

	NonEnglishQualifier Value		
3-181-5	Residues	QQDDRFPLT	9
3-182	**Sequences**		
3-182-1	Sequence Number [ID]	182	
3-182-2	Molecule Type	AA	
3-182-3	Length	5	
3-182-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-182-5	Residues	NYGMN	5
3-183	**Sequences**		
3-183-1	Sequence Number [ID]	183	
3-183-2	Molecule Type	AA	
3-183-3	Length	17	
3-183-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-183-5	Residues	WINTYTGEPT YADDFKG	17
3-184	**Sequences**		
3-184-1	Sequence Number [ID]	184	
3-184-2	Molecule Type	AA	
3-184-3	Length	11	
3-184-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-184-5	Residues	GAWFAYWAKD S	11
3-185	**Sequences**		
3-185-1	Sequence Number [ID]	185	
3-185-2	Molecule Type	AA	
3-185-3	Length	15	
3-185-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-185-5	Residues	SITCKASQDV GTAVA	15
3-186	**Sequences**		
3-186-1	Sequence Number [ID]	186	
3-186-2	Molecule Type	AA	
3-186-3	Length	7	
3-186-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-186-5	Residues	WASTRHT	7
3-187	**Sequences**		
3-187-1	Sequence Number [ID]	187	
3-187-2	Molecule Type	AA	
3-187-3	Length	9	
3-187-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-187-5	Residues	QQYSSYPLT	9
3-188	**Sequences**		
3-188-1	Sequence Number [ID]	188	
3-188-2	Molecule Type	AA	
3-188-3	Length	5	
3-188-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-188-5	Residues	DFWMN	5
3-189	**Sequences**		
3-189-1	Sequence Number [ID]	189	
3-189-2	Molecule Type	AA	

3-189-3	Length	19	
3-189-4	Features	**source 1..19**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-189-5	Residues	EIRLKSNNYA THYAESVKG	19
3-190	**Sequences**		
3-190-1	Sequence Number [ID]	190	
3-190-2	Molecule Type	AA	
3-190-3	Length	13	
3-190-4	Features	**source 1..13**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-190-5	Residues	LFYYYDGTSG FAY	13
3-191	**Sequences**		
3-191-1	Sequence Number [ID]	191	
3-191-2	Molecule Type	AA	
3-191-3	Length	17	
3-191-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-191-5	Residues	KSSQSLLNSG DQKNYLT	17
3-192	**Sequences**		
3-192-1	Sequence Number [ID]	192	
3-192-2	Molecule Type	AA	
3-192-3	Length	7	
3-192-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-192-5	Residues	WASTRES	7
3-193	**Sequences**		
3-193-1	Sequence Number [ID]	193	
3-193-2	Molecule Type	AA	
3-193-3	Length	9	
3-193-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-193-5	Residues	QNDYDYPLT	9
3-194	**Sequences**		
3-194-1	Sequence Number [ID]	194	
3-194-2	Molecule Type	AA	
3-194-3	Length	5	
3-194-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-194-5	Residues	DYNMD	5
3-195	**Sequences**		
3-195-1	Sequence Number [ID]	195	
3-195-2	Molecule Type	AA	
3-195-3	Length	17	
3-195-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-195-5	Residues	DINPNYDSTS YNQKFKG	17
3-196	**Sequences**		
3-196-1	Sequence Number [ID]	196	
3-196-2	Molecule Type	AA	
3-196-3	Length	11	
3-196-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		

3-196-5	Residues	SRSYDYEGFA Y	11
3-197	**Sequences**		
3-197-1	Sequence Number [ID]	197	
3-197-2	Molecule Type	AA	
3-197-3	Length	11	
3-197-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-197-5	Residues	RASGNIHNYL A	11
3-198	**Sequences**		
3-198-1	Sequence Number [ID]	198	
3-198-2	Molecule Type	AA	
3-198-3	Length	7	
3-198-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-198-5	Residues	NAKTLAD	7
3-199	**Sequences**		
3-199-1	Sequence Number [ID]	199	
3-199-2	Molecule Type	AA	
3-199-3	Length	8	
3-199-4	Features	**source 1..8**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-199-5	Residues	QHFWSTLT	8
3-200	**Sequences**		
3-200-1	Sequence Number [ID]	200	
3-200-2	Molecule Type	AA	
3-200-3	Length	5	
3-200-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-200-5	Residues	GYTMN	5
3-201	**Sequences**		
3-201-1	Sequence Number [ID]	201	
3-201-2	Molecule Type	AA	
3-201-3	Length	16	
3-201-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-201-5	Residues	NPYNGGTSYN QKFKGK	16
3-202	**Sequences**		
3-202-1	Sequence Number [ID]	202	
3-202-2	Molecule Type	AA	
3-202-3	Length	9	
3-202-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-202-5	Residues	WGVWSAMDY	9
3-203	**Sequences**		
3-203-1	Sequence Number [ID]	203	
3-203-2	Molecule Type	AA	
3-203-3	Length	11	
3-203-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-203-5	Residues	KASQNVRTAV A	11
3-204	**Sequences**		
3-204-1	Sequence Number [ID]	204	
3-204-2	Molecule Type	AA	
3-204-3	Length	7	

3-204-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-204-5	Residues	LASNRDT	7
3-205	**Sequences**		
3-205-1	Sequence Number [ID]	205	
3-205-2	Molecule Type	AA	
3-205-3	Length	9	
3-205-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-205-5	Residues	LQHCNYPNE	9
3-206	**Sequences**		
3-206-1	Sequence Number [ID]	206	
3-206-2	Molecule Type	AA	
3-206-3	Length	5	
3-206-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-206-5	Residues	SYWMQ	5
3-207	**Sequences**		
3-207-1	Sequence Number [ID]	207	
3-207-2	Molecule Type	AA	
3-207-3	Length	17	
3-207-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-207-5	Residues	AIYPGDGDTR YTQKFKG	17
3-208	**Sequences**		
3-208-1	Sequence Number [ID]	208	
3-208-2	Molecule Type	AA	
3-208-3	Length	11	
3-208-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-208-5	Residues	ARGEYGNYFA Y	11
3-209	**Sequences**		
3-209-1	Sequence Number [ID]	209	
3-209-2	Molecule Type	AA	
3-209-3	Length	11	
3-209-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-209-5	Residues	KASQDINSYL S	11
3-210	**Sequences**		
3-210-1	Sequence Number [ID]	210	
3-210-2	Molecule Type	AA	
3-210-3	Length	7	
3-210-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-210-5	Residues	RANRLVD	7
3-211	**Sequences**		
3-211-1	Sequence Number [ID]	211	
3-211-2	Molecule Type	AA	
3-211-3	Length	9	
3-211-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-211-5	Residues	LQYDEFPLT	9

3-212	**Sequences**		
3-212-1	Sequence Number [ID]	212	
3-212-2	Molecule Type	AA	
3-212-3	Length	5	
3-212-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-212-5	Residues	DTYMH	5
3-213	**Sequences**		
3-213-1	Sequence Number [ID]	213	
3-213-2	Molecule Type	AA	
3-213-3	Length	17	
3-213-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-213-5	Residues	RIDPANGNTK YDPKFQG	17
3-214	**Sequences**		
3-214-1	Sequence Number [ID]	214	
3-214-2	Molecule Type	AA	
3-214-3	Length	14	
3-214-4	Features	**source 1..14**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-214-5	Residues	ARPIHYYYGS SLAY	14
3-215	**Sequences**		
3-215-1	Sequence Number [ID]	215	
3-215-2	Molecule Type	AA	
3-215-3	Length	11	
3-215-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-215-5	Residues	SVDSYGNSFM H	11
3-216	**Sequences**		
3-216-1	Sequence Number [ID]	216	
3-216-2	Molecule Type	AA	
3-216-3	Length	7	
3-216-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-216-5	Residues	RASNLES	7
3-217	**Sequences**		
3-217-1	Sequence Number [ID]	217	
3-217-2	Molecule Type	AA	
3-217-3	Length	9	
3-217-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-217-5	Residues	QQSNEDPGR	9
3-218	**Sequences**		
3-218-1	Sequence Number [ID]	218	
3-218-2	Molecule Type	AA	
3-218-3	Length	5	
3-218-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-218-5	Residues	DYYMS	5
3-219	**Sequences**		
3-219-1	Sequence Number [ID]	219	
3-219-2	Molecule Type	AA	
3-219-3	Length	17	
3-219-4	Features	**source 1..17**	

	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-219-5	Residues	RNKANGYTTE YSASVKG	17
3-220	**Sequences**		
3-220-1	Sequence Number [ID]	220	
3-220-2	Molecule Type	AA	
3-220-3	Length	9	
3-220-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-220-5	Residues	ARANWAFDY	9
3-221	**Sequences**		
3-221-1	Sequence Number [ID]	221	
3-221-2	Molecule Type	AA	
3-221-3	Length	11	
3-221-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-221-5	Residues	RASQSISNYL H	11
3-222	**Sequences**		
3-222-1	Sequence Number [ID]	222	
3-222-2	Molecule Type	AA	
3-222-3	Length	7	
3-222-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-222-5	Residues	YASQSIS	7
3-223	**Sequences**		
3-223-1	Sequence Number [ID]	223	
3-223-2	Molecule Type	AA	
3-223-3	Length	9	
3-223-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-223-5	Residues	QQSNSWPYT	9
3-224	**Sequences**		
3-224-1	Sequence Number [ID]	224	
3-224-2	Molecule Type	AA	
3-224-3	Length	5	
3-224-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-224-5	Residues	DYYMS	5
3-225	**Sequences**		
3-225-1	Sequence Number [ID]	225	
3-225-2	Molecule Type	AA	
3-225-3	Length	17	
3-225-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-225-5	Residues	RNKANGYTTE YSASVKG	17
3-226	**Sequences**		
3-226-1	Sequence Number [ID]	226	
3-226-2	Molecule Type	AA	
3-226-3	Length	12	
3-226-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-226-5	Residues	ARAPLLYYAM DY	12
3-227	**Sequences**		

3-227-1	Sequence Number [ID]	227	
3-227-2	Molecule Type	AA	
3-227-3	Length	11	
3-227-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-227-5	Residues	NVSTSGYSYM H	11
3-228	**Sequences**		
3-228-1	Sequence Number [ID]	228	
3-228-2	Molecule Type	AA	
3-228-3	Length	7	
3-228-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-228-5	Residues	LVSNLES	7
3-229	**Sequences**		
3-229-1	Sequence Number [ID]	229	
3-229-2	Molecule Type	AA	
3-229-3	Length	8	
3-229-4	Features	**source 1..8**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-229-5	Residues	QHIRELTR	8
3-230	**Sequences**		
3-230-1	Sequence Number [ID]	230	
3-230-2	Molecule Type	AA	
3-230-3	Length	5	
3-230-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-230-5	Residues	SYWMH	5
3-231	**Sequences**		
3-231-1	Sequence Number [ID]	231	
3-231-2	Molecule Type	AA	
3-231-3	Length	17	
3-231-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-231-5	Residues	MIDPSNSETR LNQKFKD	17
3-232	**Sequences**		
3-232-1	Sequence Number [ID]	232	
3-232-2	Molecule Type	AA	
3-232-3	Length	12	
3-232-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-232-5	Residues	ARGLRHYWYF DV	12
3-233	**Sequences**		
3-233-1	Sequence Number [ID]	233	
3-233-2	Molecule Type	AA	
3-233-3	Length	11	
3-233-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-233-5	Residues	SVSTSGYSYM H	11
3-234	**Sequences**		
3-234-1	Sequence Number [ID]	234	
3-234-2	Molecule Type	AA	
3-234-3	Length	7	
3-234-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	

		organism=Mus musculus	
	NonEnglishQualifier Value		
3-234-5	Residues	LVSNLES	7
3-235	**Sequences**		
3-235-1	Sequence Number [ID]	235	
3-235-2	Molecule Type	AA	
3-235-3	Length	9	
3-235-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-235-5	Residues	QHIRELTRS	9
3-236	**Sequences**		
3-236-1	Sequence Number [ID]	236	
3-236-2	Molecule Type	AA	
3-236-3	Length	5	
3-236-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-236-5	Residues	SYGMS	5
3-237	**Sequences**		
3-237-1	Sequence Number [ID]	237	
3-237-2	Molecule Type	AA	
3-237-3	Length	14	
3-237-4	Features	**source 1..14**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-237-5	Residues	WVRQTPEKRL EWVA	14
3-238	**Sequences**		
3-238-1	Sequence Number [ID]	238	
3-238-2	Molecule Type	AA	
3-238-3	Length	11	
3-238-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-238-5	Residues	LASYYFDYWG Q	11
3-239	**Sequences**		
3-239-1	Sequence Number [ID]	239	
3-239-2	Molecule Type	AA	
3-239-3	Length	15	
3-239-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-239-5	Residues	TMTCQASQGT SINLN	15
3-240	**Sequences**		
3-240-1	Sequence Number [ID]	240	
3-240-2	Molecule Type	AA	
3-240-3	Length	7	
3-240-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-240-5	Residues	GASSLED	7
3-241	**Sequences**		
3-241-1	Sequence Number [ID]	241	
3-241-2	Molecule Type	AA	
3-241-3	Length	11	
3-241-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-241-5	Residues	LQHSYLPPLT F	11
3-242	**Sequences**		
3-242-1	Sequence Number [ID]	242	

3-242-2	Molecule Type	AA	
3-242-3	Length	5	
3-242-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-242-5	Residues	TYDLH	5
3-243	**Sequences**		
3-243-1	Sequence Number [ID]	243	
3-243-2	Molecule Type	AA	
3-243-3	Length	16	
3-243-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-243-5	Residues	VIWSGGSTDY NAAFIS	16
3-244	**Sequences**		
3-244-1	Sequence Number [ID]	244	
3-244-2	Molecule Type	AA	
3-244-3	Length	11	
3-244-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-244-5	Residues	NYGYSAWFAY W	11
3-245	**Sequences**		
3-245-1	Sequence Number [ID]	245	
3-245-2	Molecule Type	AA	
3-245-3	Length	15	
3-245-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-245-5	Residues	ASISCRSSQS IVHSN	15
3-246	**Sequences**		
3-246-1	Sequence Number [ID]	246	
3-246-2	Molecule Type	AA	
3-246-3	Length	7	
3-246-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-246-5	Residues	KVSNRFS	7
3-247	**Sequences**		
3-247-1	Sequence Number [ID]	247	
3-247-2	Molecule Type	AA	
3-247-3	Length	9	
3-247-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-247-5	Residues	FQGSHVPLT	9
3-248	**Sequences**		
3-248-1	Sequence Number [ID]	248	
3-248-2	Molecule Type	AA	
3-248-3	Length	5	
3-248-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-248-5	Residues	AYSMH	5
3-249	**Sequences**		
3-249-1	Sequence Number [ID]	249	
3-249-2	Molecule Type	AA	
3-249-3	Length	17	
3-249-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	

	NonEnglishQualifier Value		
3-249-5	Residues	WINTETGEPT YTDDFKG	17
3-250	**Sequences**		
3-250-1	Sequence Number [ID]	250	
3-250-2	Molecule Type	AA	
3-250-3	Length	11	
3-250-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-250-5	Residues	RIYYFGRGGF D	11
3-251	**Sequences**		
3-251-1	Sequence Number [ID]	251	
3-251-2	Molecule Type	AA	
3-251-3	Length	15	
3-251-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-251-5	Residues	SSISCRSSQS IVHSN	15
3-252	**Sequences**		
3-252-1	Sequence Number [ID]	252	
3-252-2	Molecule Type	AA	
3-252-3	Length	7	
3-252-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-252-5	Residues	KVSNRFS	7
3-253	**Sequences**		
3-253-1	Sequence Number [ID]	253	
3-253-2	Molecule Type	AA	
3-253-3	Length	9	
3-253-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-253-5	Residues	FQGSHVPYT	9
3-254	**Sequences**		
3-254-1	Sequence Number [ID]	254	
3-254-2	Molecule Type	AA	
3-254-3	Length	5	
3-254-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-254-5	Residues	NSWFN	5
3-255	**Sequences**		
3-255-1	Sequence Number [ID]	255	
3-255-2	Molecule Type	AA	
3-255-3	Length	19	
3-255-4	Features	**source 1..19**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-255-5	Residues	EIRLTSDNYA IYYAESVKG	19
3-256	**Sequences**		
3-256-1	Sequence Number [ID]	256	
3-256-2	Molecule Type	AA	
3-256-3	Length	11	
3-256-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-256-5	Residues	PETARATFAY W	11
3-257	**Sequences**		
3-257-1	Sequence Number [ID]	257	
3-257-2	Molecule Type	AA	

3-257-3	Length	15	
3-257-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-257-5	Residues	ASISCRSSQS IVHSN	15
3-258	**Sequences**		
3-258-1	Sequence Number [ID]	258	
3-258-2	Molecule Type	AA	
3-258-3	Length	7	
3-258-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-258-5	Residues	KVFNRFS	7
3-259	**Sequences**		
3-259-1	Sequence Number [ID]	259	
3-259-2	Molecule Type	AA	
3-259-3	Length	9	
3-259-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-259-5	Residues	FQGSHVPRT	9
3-260	**Sequences**		
3-260-1	Sequence Number [ID]	260	
3-260-2	Molecule Type	AA	
3-260-3	Length	5	
3-260-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-260-5	Residues	AYYMH	5
3-261	**Sequences**		
3-261-1	Sequence Number [ID]	261	
3-261-2	Molecule Type	AA	
3-261-3	Length	17	
3-261-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-261-5	Residues	RVNPNNGGTT YNQKFKG	17
3-262	**Sequences**		
3-262-1	Sequence Number [ID]	262	
3-262-2	Molecule Type	AA	
3-262-3	Length	11	
3-262-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-262-5	Residues	RIYYGYFDYW G	11
3-263	**Sequences**		
3-263-1	Sequence Number [ID]	263	
3-263-2	Molecule Type	AA	
3-263-3	Length	15	
3-263-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-263-5	Residues	KASQSVDYDG DSYMN	15
3-264	**Sequences**		
3-264-1	Sequence Number [ID]	264	
3-264-2	Molecule Type	AA	
3-264-3	Length	7	
3-264-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		

3-264-5	Residues	VASNLES	7
3-265	**Sequences**		
3-265-1	Sequence Number [ID]	265	
3-265-2	Molecule Type	AA	
3-265-3	Length	9	
3-265-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-265-5	Residues	QQSNEDPYT	9
3-266	**Sequences**		
3-266-1	Sequence Number [ID]	266	
3-266-2	Molecule Type	AA	
3-266-3	Length	4	
3-266-4	Features	**source 1..4**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-266-5	Residues	DIYM	4
3-267	**Sequences**		
3-267-1	Sequence Number [ID]	267	
3-267-2	Molecule Type	AA	
3-267-3	Length	17	
3-267-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-267-5	Residues	KIDPANGNTK YDPKFQG	17
3-268	**Sequences**		
3-268-1	Sequence Number [ID]	268	
3-268-2	Molecule Type	AA	
3-268-3	Length	11	
3-268-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-268-5	Residues	TGDYWGQGTT V	11
3-269	**Sequences**		
3-269-1	Sequence Number [ID]	269	
3-269-2	Molecule Type	AA	
3-269-3	Length	15	
3-269-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-269-5	Residues	TMSCKSSQSL LNSRT	15
3-270	**Sequences**		
3-270-1	Sequence Number [ID]	270	
3-270-2	Molecule Type	AA	
3-270-3	Length	7	
3-270-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-270-5	Residues	WASTRES	7
3-271	**Sequences**		
3-271-1	Sequence Number [ID]	271	
3-271-2	Molecule Type	AA	
3-271-3	Length	9	
3-271-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-271-5	Residues	RQSYNLVTF	9
3-272	**Sequences**		
3-272-1	Sequence Number [ID]	272	
3-272-2	Molecule Type	AA	
3-272-3	Length	5	

3-272-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-272-5	Residues	SYVMH	5
3-273	**Sequences**		
3-273-1	Sequence Number [ID]	273	
3-273-2	Molecule Type	AA	
3-273-3	Length	17	
3-273-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-273-5	Residues	YINPYNDGTK YNEKFKG	17
3-274	**Sequences**		
3-274-1	Sequence Number [ID]	274	
3-274-2	Molecule Type	AA	
3-274-3	Length	11	
3-274-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-274-5	Residues	RYYYGSSGGY F	11
3-275	**Sequences**		
3-275-1	Sequence Number [ID]	275	
3-275-2	Molecule Type	AA	
3-275-3	Length	15	
3-275-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-275-5	Residues	RASKSISKYL AWYQE	15
3-276	**Sequences**		
3-276-1	Sequence Number [ID]	276	
3-276-2	Molecule Type	AA	
3-276-3	Length	7	
3-276-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-276-5	Residues	SGSTLQS	7
3-277	**Sequences**		
3-277-1	Sequence Number [ID]	277	
3-277-2	Molecule Type	AA	
3-277-3	Length	9	
3-277-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-277-5	Residues	QQHNEYPYT	9
3-278	**Sequences**		
3-278-1	Sequence Number [ID]	278	
3-278-2	Molecule Type	AA	
3-278-3	Length	5	
3-278-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-278-5	Residues	GYFMN	5
3-279	**Sequences**		
3-279-1	Sequence Number [ID]	279	
3-279-2	Molecule Type	AA	
3-279-3	Length	17	
3-279-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-279-5	Residues	RINPYNGDTF YNQKFKG	17

3-280	**Sequences**		
3-280-1	Sequence Number [ID]	280	
3-280-2	Molecule Type	AA	
3-280-3	Length	11	
3-280-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-280-5	Residues	RIHYYYGSSY Y	11
3-281	**Sequences**		
3-281-1	Sequence Number [ID]	281	
3-281-2	Molecule Type	AA	
3-281-3	Length	15	
3-281-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-281-5	Residues	RASKSISKYL AWYQE	15
3-282	**Sequences**		
3-282-1	Sequence Number [ID]	282	
3-282-2	Molecule Type	AA	
3-282-3	Length	7	
3-282-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-282-5	Residues	SGSTLQS	7
3-283	**Sequences**		
3-283-1	Sequence Number [ID]	283	
3-283-2	Molecule Type	AA	
3-283-3	Length	9	
3-283-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-283-5	Residues	QQHNEYPWT	9
3-284	**Sequences**		
3-284-1	Sequence Number [ID]	284	
3-284-2	Molecule Type	AA	
3-284-3	Length	5	
3-284-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-284-5	Residues	EYIIH	5
3-285	**Sequences**		
3-285-1	Sequence Number [ID]	285	
3-285-2	Molecule Type	AA	
3-285-3	Length	17	
3-285-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-285-5	Residues	WFYPGSGSIK YNEKFKD	17
3-286	**Sequences**		
3-286-1	Sequence Number [ID]	286	
3-286-2	Molecule Type	AA	
3-286-3	Length	11	
3-286-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-286-5	Residues	HEVYYDYDKS M	11
3-287	**Sequences**		
3-287-1	Sequence Number [ID]	287	
3-287-2	Molecule Type	AA	
3-287-3	Length	15	
3-287-4	Features	**source 1..15**	

	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-287-5	Residues	LYSSNQKNYL AWYQQ	15
3-288	**Sequences**		
3-288-1	Sequence Number [ID]	288	
3-288-2	Molecule Type	AA	
3-288-3	Length	7	
3-288-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-288-5	Residues	WASTRES	7
3-289	**Sequences**		
3-289-1	Sequence Number [ID]	289	
3-289-2	Molecule Type	AA	
3-289-3	Length	9	
3-289-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-289-5	Residues	QQYYSYPYT	9
3-290	**Sequences**		
3-290-1	Sequence Number [ID]	290	
3-290-2	Molecule Type	AA	
3-290-3	Length	5	
3-290-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-290-5	Residues	NYLIE	5
3-291	**Sequences**		
3-291-1	Sequence Number [ID]	291	
3-291-2	Molecule Type	AA	
3-291-3	Length	19	
3-291-4	Features	**source 1..19**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-291-5	Residues	VINPKSGGTK YNEKFRGKA	19
3-292	**Sequences**		
3-292-1	Sequence Number [ID]	292	
3-292-2	Molecule Type	AA	
3-292-3	Length	11	
3-292-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-292-5	Residues	TGTDYWGQGT T	11
3-293	**Sequences**		
3-293-1	Sequence Number [ID]	293	
3-293-2	Molecule Type	AA	
3-293-3	Length	10	
3-293-4	Features	**source 1..10**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-293-5	Residues	VTISCSASQG	10
3-294	**Sequences**		
3-294-1	Sequence Number [ID]	294	
3-294-2	Molecule Type	AA	
3-294-3	Length	7	
3-294-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-294-5	Residues	YTSSLRS	7
3-295	**Sequences**		

3-295-1	Sequence Number [ID]	295	
3-295-2	Molecule Type	AA	
3-295-3	Length	9	
3-295-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-295-5	Residues	QQYSKLPRT	9
3-296	**Sequences**		
3-296-1	Sequence Number [ID]	296	
3-296-2	Molecule Type	AA	
3-296-3	Length	12	
3-296-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-296-5	Residues	FTSGEKEQVD EW	12
3-297	**Sequences**		
3-297-1	Sequence Number [ID]	297	
3-297-2	Molecule Type	AA	
3-297-3	Length	16	
3-297-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-297-5	Residues	AEQKRLKTVL ELQYVL	16
3-298	**Sequences**		
3-298-1	Sequence Number [ID]	298	
3-298-2	Molecule Type	AA	
3-298-3	Length	16	
3-298-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-298-5	Residues	VERVFQSNYF DSTHNH	16
3-299	**Sequences**		
3-299-1	Sequence Number [ID]	299	
3-299-2	Molecule Type	AA	
3-299-3	Length	16	
3-299-4	Features	**source 1..16**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-299-5	Residues	FQSMQTVFNM NAPVPP	16
3-300	**Sequences**		
3-300-1	Sequence Number [ID]	300	
3-300-2	Molecule Type	AA	
3-300-3	Length	5	
3-300-4	Features	**source 1..5**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-300-5	Residues	TNAMN	5
3-301	**Sequences**		
3-301-1	Sequence Number [ID]	301	
3-301-2	Molecule Type	AA	
3-301-3	Length	17	
3-301-4	Features	**source 1..17**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-301-5	Residues	RIRSKSNNYA TYYADSV	17
3-302	**Sequences**		
3-302-1	Sequence Number [ID]	302	
3-302-2	Molecule Type	AA	
3-302-3	Length	11	
3-302-4	Features	**source 1..11**	
	Location/Qualifiers	mol_type=protein	

		organism=Mus musculus	
	NonEnglishQualifier Value		
3-302-5	Residues	DWDGFLYFDY W	11
3-303	**Sequences**		
3-303-1	Sequence Number [ID]	303	
3-303-2	Molecule Type	AA	
3-303-3	Length	112	
3-303-4	Features	**source 1..112**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-303-5	Residues	GGGLVQPKGS LKLSCAASGF TFNTNAMNWV RQAPGKGLEW VARIRSKSNN YATYYADSVK	60
		DRFTISRDDS QSMLYLQMNN LKTEDTAMYY CVRDWDGFLY FDYWAKHHLT LF	112
3-304	**Sequences**		
3-304-1	Sequence Number [ID]	304	
3-304-2	Molecule Type	AA	
3-304-3	Length	15	
3-304-4	Features	**source 1..15**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-304-5	Residues	SVSTSGYSYM HWNQQ	15
3-305	**Sequences**		
3-305-1	Sequence Number [ID]	305	
3-305-2	Molecule Type	AA	
3-305-3	Length	7	
3-305-4	Features	**source 1..7**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-305-5	Residues	LVSNLES	7
3-306	**Sequences**		
3-306-1	Sequence Number [ID]	306	
3-306-2	Molecule Type	AA	
3-306-3	Length	9	
3-306-4	Features	**source 1..9**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-306-5	Residues	QHIRELTRS	9
3-307	**Sequences**		
3-307-1	Sequence Number [ID]	307	
3-307-2	Molecule Type	AA	
3-307-3	Length	104	
3-307-4	Features	**source 1..104**	
	Location/Qualifiers	mol_type=protein	
		organism=Mus musculus	
	NonEnglishQualifier Value		
3-307-5	Residues	TQSPASLAVS LGQRATISYR ASKSVSTSGY SYMHWNQQKP GQPPRLLIYL VSNLESGVPA	60
		RFSGSGSGTD FTLNIHPVEE EDAATYYCQH IRELTRSEGG PSWK	104
3-308	**Sequences**		
3-308-1	Sequence Number [ID]	308	
3-308-2	Molecule Type	AA	
3-308-3	Length	14	
3-308-4	Features	**source 1..14**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-308-5	Residues	PPVNEPETLK QQNQ	14
3-309	**Sequences**		
3-309-1	Sequence Number [ID]	309	
3-309-2	Molecule Type	AA	
3-309-3	Length	12	
3-309-4	Features	**source 1..12**	
	Location/Qualifiers	mol_type=protein	
		organism=Homo sapiens	
	NonEnglishQualifier Value		
3-309-5	Residues	ETLKQQNQYQ AS	12

3-310	**Sequences**	
3-310-1	Sequence Number [ID]	310
3-310-2	Molecule Type	AA
3-310-3	Length	709
3-310-4	Features	**source 1..709**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-310-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAGAAAPASQ HPATGTGAVQ TEAMKQILGV 60 IDKKLRNLEK KKGKLDDYQE RMNKGERLNQ DQLDAVSKYQ EVTNNLEFAK ELQRSFMALS 120 QDIQKTIKKT ARREQLMREE AEQKRLKTVL ELQYVLDKLG DDEVRTDLKQ GLNGVPILSE 180 EELSLLDEFY KLVDPERDMS LRLNEQYEHA SIHLWDLLEG KEKPVCGTTY KVLKEIVERV 240 FQSNYFDSTH NHQNGLCEEE EAASAPAVED QVPEAEPEPA EEYTEQSEVE STEYVNRQFM 300 AETQFTSGEK EQVDEWTVET VEVVNSLQQQ PQAASPSVPE PHSLTPVAQA DPLVRRQRVQ 360 DLMAQMQGPY NFIQDSMLDF ENQTLDPAIV SAQPMNPTQN MDMPQLVCPP VHSESRLAQP 420 NQVPVQPEAT QVPLVSSTSE GYTASQPLYQ PSHATEQRPQ KEPIDQIQAT ISLNTDQTTA 480 SSSLPAASQP QVFQAGTSKP LHSSGINVNA APFQSMQTVF NMNAPVPPVN EPETLKQQNQ 540 YQASYNQSFS SQPHQVEQTE LQQEQLQTVV GTYHGSPDQS HQVTGNHQQP PQQNTGFPRS 600 NQPYYNSRGV SRGGSRGARG LMNGYRGPAN GFRGGYDGYR PSFSNTPNSG YTQSQFSAPR 660 DYSGYQRDGY QQNFKRGSGQ SGPRGAPRGR GGPPRPNRGM PQMNTQQVN 709
3-311	**Sequences**	
3-311-1	Sequence Number [ID]	311
3-311-2	Molecule Type	AA
3-311-3	Length	694
3-311-4	Features	**source 1..694**
	Location/Qualifiers	mol_type=protein
		organism=Homo sapiens
	NonEnglishQualifier Value	
3-311-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAGAAAPASQ HPATGTGAVQ TEAMKQILGV 60 IDKKLRNLEK KKGKLDDYQE RMNKGERLNQ DQLDAVSKYQ EVTNNLEFAK ELQRSFMALS 120 QDIQKTIKKT ARREQLMREE AEQKRLKTVL ELQYVLDKLG DDEVRTDLKQ GLNGVPILSE 180 EELSLLDEFY KLVDPERDMS LRLNEQYEHA SIHLWDLLEG KEKPVCGTTY KVLKEIVERV 240 FQSNYFDSTH NHQNGLCEEE EAASAPAVED QVPEAEPEPA EEYTEQSEVE STEYVNRQFM 300 AETQFTSGEK EQVDEWTVET VEVVNSLQQQ PQAASPSVPE PHSLTPVAQA DPLVRRQRVQ 360 DLMAQMQGPY NFIQDSMLDF ENQTLDPAIV SAQPMNPTQN MDMPQLVCPP VHSESRLAQP 420 NQVPVQPEAT QVPLVSSTSE GYTASQPLYQ PSHATEQRPQ KEPIDQIQAT ISLNTDQTTA 480 SSSLPAASQP QVFQAGTSKP LHSSGINVNA APFQSMQTVF NMNAPVPPVN EPETLKQQNQ 540 YQASYNQSFS SQPHQVEQTE LQQEQLQTVV GTYHGSPDQS HQVTGNHQQP PQQNTGFPRS 600 NQPYYNSRGV SRGGSRGARG LMNGYRGPAN GFRGGYDGYR PSFSNTPNSG YTQSQFSAPR 660 DYSGYQRDGY QQNFKRGSGQ SGPRGAPRGN ILWW 694
3-312	**Sequences**	
3-312-1	Sequence Number [ID]	312
3-312-2	Molecule Type	AA
3-312-3	Length	448
3-312-4	Features	**source 1..448**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-312-5	Residues	MALSQDIQKT IKKTARREQL MREEAEQKRL KTVLELQYVL DKLGDDEVRT DLKQGLNGVP 60 ILSEEELSLL DEFYKLADPE RDMSLRLNEQ YEHASIHLWD LLEGKEKSVC GTTYKALKEI 120 VERVFQSNYF DSTHNHQNGL CEEEEAASAP TVEDQVAEAE PEPAEEYTEQ SEVESTEYVN 180 RQFMAETQFS SGEKEQVDEW TVETVEVVNS LQQQPQAASP SVPEPHSLTP VAQADPLVRR 240 QRVQDLMAQM QGPYNFIQDS MLDFENQTLD PAIVSAQPMN PTQNMDMPQL VCPPVHSESR 300 LAQPNQVPVQ PEATQVPLVS STSEGYTASQ PLYQPSHATE QRPQKEPIDQ IQATISLNTD 360 QTTASSSLPA ASQPQVFQAG TSKPLHSSGI NVNAAPFQSM QTVFNMNAPV PPVNEPETLK 420 QQNQYQASYN QSFSSQPHQV EQTEGCRK 448
3-313	**Sequences**	
3-313-1	Sequence Number [ID]	313
3-313-2	Molecule Type	AA
3-313-3	Length	717
3-313-4	Features	**source 1..717**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-313-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480

		LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 717
3-314	**Sequences**	
3-314-1	Sequence Number [ID]	314
3-314-2	Molecule Type	AA
3-314-3	Length	702
3-314-4	Features	**source 1..702**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-314-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRDGYQQ NFKRGSGQSG PRGAPRGNIL WW 702
3-315	**Sequences**	
3-315-1	Sequence Number [ID]	315
3-315-2	Molecule Type	AA
3-315-3	Length	679
3-315-4	Features	**source 1..679**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-315-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRGCRK 679
3-316	**Sequences**	
3-316-1	Sequence Number [ID]	316
3-316-2	Molecule Type	AA
3-316-3	Length	717
3-316-4	Features	**source 1..717**
	Location/Qualifiers	mol_type=protein
		organism=Canis familiaris
	NonEnglishQualifier Value	
3-316-5	Residues	MPSATSLSGS GSKSSGPPPP SGSSGSEAAA AAGAAGAAGA GAAAPASQHP ATGTGAVQTE 60 AMKQILGVID KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL 120 QRSFMALSQD IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL 180 NGVPILSEEE LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KSVCGTTYKA 240 LKEIVERVFQ SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST 300 EYVNRQFMAE TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP 360 LVRRQRVQDL MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPPVH 420 SESRLAQPNQ VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PIDQIQATIS 480 LNTDQTTASS SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP 540 ETLKQQNQYQ ASYNQSFSSQ PHQVEQTDLQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ 600 QNTGFPRSSQ PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYT 660 QSQFSAPRDY SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 717
3-317	**Sequences**	
3-317-1	Sequence Number [ID]	317
3-317-2	Molecule Type	AA
3-317-3	Length	708
3-317-4	Features	**source 1..708**
	Location/Qualifiers	mol_type=protein
		organism=Bos taurus
	NonEnglishQualifier Value	

3-317-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGNEAGA GAAAPASQHP MTGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD EVRTDLKQGL NGVPILSEEE 180 LSLLDEFYKL ADPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQA AEAEPEPVEE YTEQNEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDDWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQADP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPAQNMD IPQLVCPPVH SESRLAQPNQ 420 VSVQPEATQV PLVSSTSEGY TASQPLYQPS HATDQRPQKE PIDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPVNEP ETLKQQNQYQ 540 ASYNQSFSSQ PHQVEQTELQ QEQLQTVVGT YHGSQDQPHQ VTGNHQQPPQ QNTGFPRSNQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSTNTPNSGY TQSQFSAPRD 660 YSGYQRDGYQ QNFKRGSGQS GPRGAPRGRG GPPRPNRGMP QMNTQQVN 708
3-318	**Sequences**	
3-318-1	Sequence Number [ID]	318
3-318-2	Molecule Type	AA
3-318-3	Length	638
3-318-4	Features	**source 1..638**
	Location/Qualifiers	mol_type=protein organism=Equus caballus
	NonEnglishQualifier Value	
3-318-5	Residues	MEGKLDDYQE RMNKGERLNQ DQLDAVSKYQ EVTNNLEFAK ELQRSFMALS QDIQKTIKKT 60 ARREQLMREE AEQKRLKTVL ELQYVLDKLG DEEVRTDLKQ GLNGVPILSE EELSLLDEFY 120 KLADPVRDMS LRLNEQYEHA SIHLWDLLEG KEKSVCGTTY KALREIVERV FQSNYFDSTH 180 NHQNGLCEEE EATSAPTAED QGAEAEPEPA EEYTEQSEVE STEYVNRQFM AEAQFSGEKE 240 QVDEWTVETV EVVNSLQQQP QAASPSVPEP HSLTPVAQAD PLVRRQRVQD LMAQMQGPYN 300 FIQDSMLDFE NQTLDPAIVS AQPMNPAQNM DMPQLVCPPV HAESRLAQPN QVPVQPEATQ 360 VPLVSSTSEG YTASQPLYQP SHATEQRPQK EPTDQIQATI SLNTDQTTAS SSLPAASQPQ 420 VFQAGTSKPL HSSGINVNAA PFQSMQTVFN MNAPVPPVNE PETLKQQNQY QASYNQSFSS 480 PPHQVEQTEL PQEQLQTVVG TYHASQDQPH QVTGNHQQPP QQNTGFPRSS QPYYNSRGVS 540 RGGSRGARGL MNGYRGPANG FRGGYDGYRP SFSNTPNSGY TQSQFSAPRD YSGYQRDGYQ 600 QNFKRGSGQS GPRGAPRGRG GPPRPNRGMP QMNTQQVN 638
3-319	**Sequences**	
3-319-1	Sequence Number [ID]	319
3-319-2	Molecule Type	AA
3-319-3	Length	707
3-319-4	Features	**source 1..707**
	Location/Qualifiers	mol_type=protein organism=Mus musculus
	NonEnglishQualifier Value	
3-319-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 707
3-320	**Sequences**	
3-320-1	Sequence Number [ID]	320
3-320-2	Molecule Type	AA
3-320-3	Length	707
3-320-4	Features	**source 1..707**
	Location/Qualifiers	mol_type=protein organism=Mus musculus
	NonEnglishQualifier Value	
3-320-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGRGG PPRPNRGMPQ MNTQQVN 707
3-321	**Sequences**	
3-321-1	Sequence Number [ID]	321

3-321-2	Molecule Type	AA
3-321-3	Length	698
3-321-4	Features	**source 1..698**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-321-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQTLDPAIVS AQPMNPTQNM DMPQLVCPQV HSESRLAQSN QVPVQPEATQ 420 VPLVSSTSEG YTASQPLYQP SHATEQRPQK EPMDQIQATI SLNTDQTTAS SSLPAASQPQ 480 VFQAGTSKPL HSSGINVNAA PFQSMQTVFN MNAPVPPANE PETLKQQSQY QATYNQSFSS 540 QPHQVEQTEL QQDQLQTVVG TYHGSQDQPH QVPGNHQQPP QQNTGFPRSS QPYYNSRGVS 600 RGGSRGARGL MNGYRGPANG FRGGYDGYRP SFSNTPNSGY SQSQFTAPRD YSGYQRDGYQ 660 QNFKRGSGQS GPRGAPRGRG GPPRPNRGMP QMNTQQVN 698
3-322	**Sequences**	
3-322-1	Sequence Number [ID]	322
3-322-2	Molecule Type	AA
3-322-3	Length	692
3-322-4	Features	**source 1..692**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-322-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGNIL WW 692
3-323	**Sequences**	
3-323-1	Sequence Number [ID]	323
3-323-2	Molecule Type	AA
3-323-3	Length	692
3-323-4	Features	**source 1..692**
	Location/Qualifiers	mol_type=protein
		organism=Mus musculus
	NonEnglishQualifier Value	
3-323-5	Residues	MPSATSHSGS GSKSSGPPPP SGSSGSEAAA GAAAPASQHP ATGTGAVQTE AMKQILGVID 60 KKLRNLEKKK GKLDDYQERM NKGERLNQDQ LDAVSKYQEV TNNLEFAKEL QRSFMALSQD 120 IQKTIKKTAR REQLMREEAE QKRLKTVLEL QYVLDKLGDD DVRTDLKQGL SGVPILSEEE 180 LSLLDEFYKL VDPERDMSLR LNEQYEHASI HLWDLLEGKE KPVCGTTYKA LKEIVERVFQ 240 SNYFDSTHNH QNGLCEEEEA ASAPTVEDQV AEAEPEPAEE YTEQSEVEST EYVNRQFMAE 300 TQFSSGEKEQ VDEWTVETVE VVNSLQQQPQ AASPSVPEPH SLTPVAQSDP LVRRQRVQDL 360 MAQMQGPYNF IQDSMLDFEN QTLDPAIVSA QPMNPTQNMD MPQLVCPQVH SESRLAQSNQ 420 VPVQPEATQV PLVSSTSEGY TASQPLYQPS HATEQRPQKE PMDQIQATIS LNTDQTTASS 480 SLPAASQPQV FQAGTSKPLH SSGINVNAAP FQSMQTVFNM NAPVPPANEP ETLKQQSQYQ 540 ATYNQSFSSQ PHQVEQTELQ QDQLQTVVGT YHGSQDQPHQ VPGNHQQPPQ QNTGFPRSSQ 600 PYYNSRGVSR GGSRGARGLM NGYRGPANGF RGGYDGYRPS FSNTPNSGYS QSQFTAPRDY 660 SGYQRDGYQQ NFKRGSGQSG PRGAPRGNIL WW 692
3-324	**Sequences**	
3-324-1	Sequence Number [ID]	324
3-324-2	Molecule Type	AA
3-324-3	Length	702
3-324-4	Features	**source 1..702**
	Location/Qualifiers	mol_type=protein
		organism=Gallus gallus
	NonEnglishQualifier Value	
3-324-5	Residues	MPSATNGTMA SSSGKAGPGG NEQAPAAAAA APQASGGSIT SVQTEAMKQI LGVIDKKLRN 60 LEKKKSKLDD YQERMNKGER LNQDQLDAVS KYQEVTNNLE FAKELQRSFM ALSQDIQKTI 120 KKTARREQLM REEAEQKRLK TVLELQFILD KLGDDEVRSD LKQGSNGVPV LTEEELTMLD 180 EFYKLVYPER DMNMRLNEQY EQASVHLWDL LEGKEKPVCG TTYKALKEVV ERILQTSYFD 240 STHNHQNGLC EEEEAAPTPA VEDTVAEAEP DPAEEFTEPT EVESTEYVNR QFMAETQFSS 300 SEKEQVDEWT VETVEVVNSL QQQTQATSPP VPEPHTLTTV AQADPLVRRQ RVQDLMAQMQ 360

		GPYNFMQDSM LEFENQTLDP AIVSAQPMNP AQNLDMPQMV CPPVHTESRL AQPNQVPVQP	420
		EATQVPLVSS TSEGYTASQP MYQPSHTTEQ RPQKESIDQI QASMSLNADQ TPSSSSLPTA	480
		SQPQVFQAGS SKPLHSSGIN VNAAPFQSMQ TVFNMNAPVP PVNEPEALKQ QNQYQASYNQ	540
		SFSNQPHQVE QSDLQQEQLQ TVVGTYHGSP DQTHQVAGNH QQPPQQNTGF PRNSQPYYNS	600
		RGVSRGGSRG TRGLMNGYRG PANGFRGGYD GYRPSFSNTP NSGYTQPQFN APRDYSNYQR	660
		DGYQQNFKRG SGQSGPRGAP RGRGGPPRPN RGMPQMNAQQ VN	702