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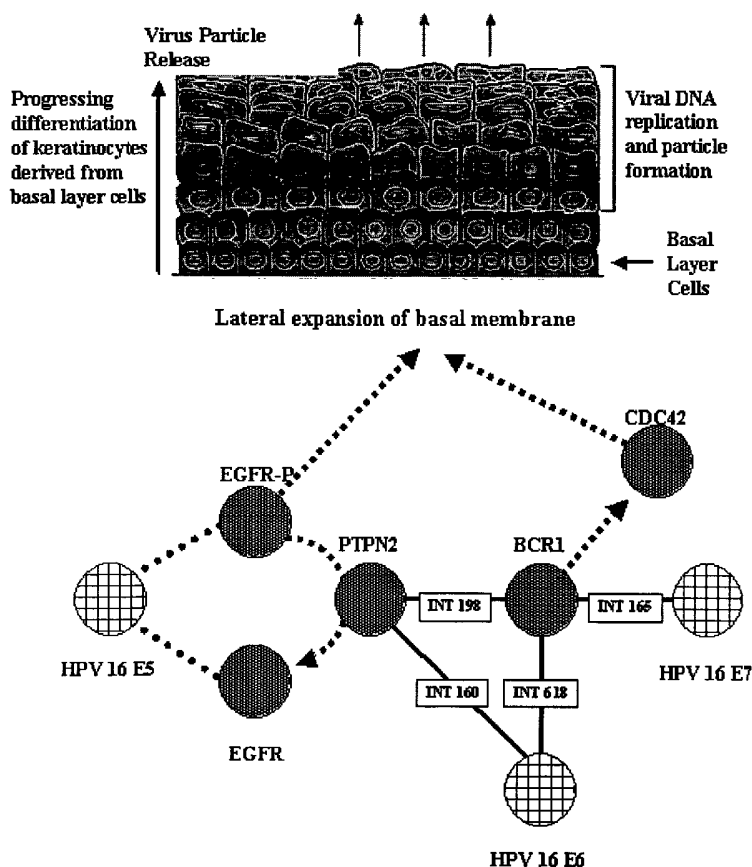
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[Continued on next page]

(54) Title: COMPLEXES AND METHODS OF USING SAME



(57) Abstract: The invention provides complexes of at least two polypeptides, and methods of using the same. Purified complexes of two polypeptides are provided, including chimeric complexes, and chimeric polypeptides and complexes thereof are also provided, as are nucleic acids encoding chimeric polypeptides and vectors and cells containing the same. Also provided are methods of identifying agents that disrupt polypeptide complexes, methods of identifying complex or polypeptide in a sample, and for removing the same, methods of determining altered expression of a polypeptide in a subject, and methods of treating/preventing disorders involving altered levels of complex or polypeptide.



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COMPLEXES AND METHODS OF USING SAME

FIELD OF THE INVENTION

The invention relates generally to polypeptides and complexes of two or more
5 polypeptides, as well as to methods of use thereof.

BACKGROUND OF THE INVENTION

Greater than seventy types of human papilloma virus (HPV) are recognized, each type associated with a specific clinical manifestation. (Principles of Internal Medicine,
10 Fauci et al, pp. 190-1100, 14th edition, McGraw Hill). It is predicted that as many as 1-2% of sexually active individuals have genital warts induced predominantly by various types of HPV. Infection may results in a spectrum of epithelial proliferative disorders ranging from common warts through genital warts to invasive cervical cancer. Currently, HPV is the most common sexually transmitted disease and is the etiological agent for 99.7% of all
15 cervical cancers including a number of other cancers such as cancer of the anogenital tract, cancer of the oral cavity, head, neck, and larynx (Walboomers, et al., J Pathol 189 (1): 12-9 (1999); Munoz, J Clin Virol 19 1-2): 1-5 (2000); Gillison, et. al., Curr Opin Oncol 13 (3): 183-8 (2001)). Cervical cancer has a very high survival rate (95% for Stage IA and 80% for Stage IIA) of five-years and is highly tractable to treatment when caught early. The
20 progression of disease is relatively slow compared to many cancers. In later stages, such as IIB, III, or IVA, the five-year survival rate drops off precipitously (65, 40, and 20 percent, respectively)(Cannistra, et al., N Engl J Med 334 (16): 1030-8 (1996))

HPV genomes are highly conserved and express only eight proteins two of which are capsid proteins (L1 and L2). The other proteins (E1, E2 and E4) are nonstructural and
25 are involved in the replication and transcription of the HPV genome. E1 is a helicase and represents the only enzyme function that encodes HPV. The remaining proteins function via protein-protein or protein-DNA interactions within the infected cell.

HPV has to facilitate its own replication within terminally differentiating (non-replicating) host cells. Important to the viral proliferation is the expression of early genes from the viral genome, E5, E6, and E7. HPV pathogenesis requires the availability of epidermal and mucosal epithelial cells that are still capable of proliferation. E5, E6 and E7 proteins are involved in the aberrant proliferation of the epithelial basal layer such that there is enhanced proliferation and lateral expansion of the basal layer (zur Hausen, Biochim Biophys Acta 1288 (2): F55-78 (1996)).

Cancer caused by HPV is due to the integration, and subsequent expression, of viral E6 and E7 proteins. E6 interacts with p53 (Werness, et al., Science 248 (4951): 76-9 (1990)). and affects the expression of the catalytic subunit of telomerase (hTERT) and Rb (Dyson et al. Science 243(4893): 934-7 (1989); Kiyono et al., Natural 396(6706): 84-8 (1998)). E6 and E7 work synergistically to transform cells (Munger, et al. J Virol 63 (10): 4417-21 (1989); McDougall, Curr Top Microbiol Immunol 186: 101-19 (1994)). E5 is not required for long-term transformation, however it is known to interact with growth factor receptors that mediate cellular proliferation, such as the epidermal growth factor receptor, the platelet-derived growth factor- β receptor, and the colony-stimulating factor-1 receptor (Hwang, et al., Virology 211(1): 227-33 (1995)). The E6 and E7 proteins of HPV maintain infected keratinocytes in a cycling undifferentiated state by blocking p53-and RB-mediated cell-cycle control pathways. US 5,532,348 describes the purification of the E6 protein and methods of blocking the inhibitory effect of E6 on tumor suppressor protein, p53. In oncogenic indications, HPV causes alteration in cyclin-cyclin-dependent kinase complexes, as a prelude to loss of genomic stability, predisposing the cell to neoplastic transformation. E6 and E7 proteins must persist in the cell for it to remain transformed (Tindle, Nature Rev Cancer 2 (1): 59-65 (2002)).

Existing diagnostic methodologies have been described in detail in Wright, et al., Jama 287 (16): 2120-9 (2002). Papanicolaou testing (Pap smear) is the front line screen for cervical cancer testing. However this methodology is limited to reproductive and anogenital screening and does not apply for screening patients for head and neck/larynx cancers. Furthermore, the methodology is not conclusive, ambiguous Pap smear results must be clarified by PCR testing for the presence of high-risk HPV strains (Schiffman, et al., J Clin Microbiol 33 (3): 545-50 (1995)). Following a positive result from PCR testing or multiple ASCUS (Atypical Squamous Cells of Undetermined Significance) results, colposcopy (visual exam of the cervical region) and possibly a biopsy are performed to

determine if premalignant or malignant lesions are present (Wright, et al., Jama 287 (16): 2120-9 (2002)).

Current therapies for HPV infection are largely ablative, ineffective and limited. Immunomodulatory cytokines show promise for the suppression of HPV transcription, for example transforming growth factor- β and interleukin-1. Retinoic acid can suppress HPV infection and may have some effect on premalignant and malignant cervical lesions. Cidovovir™, an acyclic nucleoside phosphonate, with a broad specificity for DNA viruses can suppress HPV infection as can the immunomodulatory drug Imiquimod™. Both drugs seem to act through the stimulation of cytokines (zur Hausen, Nat Rev Cancer 2 (5): 342-50 (2002)).

Other than the avoidance of contact, resolution of the disease has not been successful. Despite the current understanding of HPV infection and replication, the detection and prevention of HPV has been difficult because the nature of replication, expression, proliferation and host protein interactions are incredibly complex. Host defense responses to HPV infection are not largely understood. The ability to identify critical HPV-host protein interactions would not only help clarify how these complicated processes are regulated but could potentially identify important new therapeutic targets and diagnostic markers.

There remains a need to elucidate biochemical pathways that specifically affect the survival or condition of host cells and to determine what molecules and/or functional elements of such molecules are responsible for regulating such pathways. There is also a need for products and processes that permit the effective regulation of specific steps in such biochemical pathways. The identification of protein complexes associated with specific biological activities can be used to identify or prevent conditions associated with the absence or presence of these complexes.

SUMMARY OF THE INVENTION

The invention is based, in part, upon the identification of protein-protein interactions in and humans. Interacting proteins present in complexes according to the invention are shown in, e.g., Tables 1-7, in the second and fifth columns thereof (i.e., columns 2 and 5).

In one aspect, the invention provides a purified complex including a first interactor listed in Tables 1-7 column 2, and a second interactor recited in column 5 of Tables 1-7.

In another aspect, the invention provides an antibody which specifically binds polypeptide complexes according to the invention. The antibody preferably binds to a complex comprising one or more polypeptides with greater affinity than its affinity for either polypeptide that is not present in the complex.

5 Also provided by the invention are kits containing reagents that can specifically detect the complexes of the invention. In one embodiment, the reagent is a complex-specific antibody, while in other embodiments the reagent is an antibody specific for the first or second polypeptides of the complex.

10 In another aspect, the invention provides pharmaceutical compositions including the complexes described herein. Such compositions are formulated to be suitable for therapeutic administration in the treatment of deficiencies or diseases involving altered levels of the complexes of the invention.

In still another aspect, the invention provides methods of identifying an agent that disrupts a polypeptide complex by providing a complex described herein, contacting the
15 complex with a test agent, and detecting the presence or amount of a polypeptide in the complex.

In a further aspect, the invention provides a method for inhibiting the interaction of a protein with a ligand by contacting a complex of the protein and ligand with an agent that blocks formation of the complex. .

20 In yet another aspect, the invention provides a method of identifying a polypeptide complex in a subject by providing a biological sample from the subject and detecting, if present, the level of a complex, described herein, in the subject. In a specific embodiment, the invention encompasses a method to monitor protein interactions or formation of the protein complexes as an indicator of specific state or condition in response to treatment
25 with a drug or pharmaceutical. An aspect of this embodiment includes the use of antibodies, specific for the protein complex, as a reagent in a method to determine the relative abundance of the complex under various conditions or in specific tissues. Recombinant proteins may be expressed with "epitope" tags in order to easily monitor their expression and interactions.

30 Also provided by the invention is a method for detecting a polypeptide in a biological sample by providing a biological sample containing a first polypeptide, and contacting the sample with a second polypeptide under conditions suitable to form a polypeptide complex.

In another aspect, the invention provides a method for the detection of protein complexes used in assays to detect protein-protein interactions, wherein the interactions include full-length proteins, as well as protein fragments that interact in cell-based and *in vitro* assays. In another aspect, the identified protein complexes can be used in a diagnostic assay for determining a specific disease or pathological condition or state, as well as for detection of a predisposition to a disease or pathological condition. Included in this aspect is a method for the use of labeled or fusion proteins for detection, and/or the use of antibodies specific for the individual proteins or the protein complex. The method measures the ability of the proteins to form the complex, and includes the identification of mutations or single nucleotide polymorphisms (SNPs), which may affect the ability of the proteins to form the complex or function normally.

In a further aspect, the invention provides a method for determining altered expression of a polypeptide in a subject by providing a biological sample from the subject, measuring the level of polypeptide complex in the sample, and comparing the level of the complex in the sample to the level of complex in a reference sample with a known polypeptide expression level. The present invention includes a method to modulate or regulate a specific phenotype by modulating protein components or complexes, which occur in a related pathway. This can be achieved through modulation with a drug or antibody or antisense oligonucleotides, the activity of a protein or complex, the ability of a protein or complex to interact with its biological partner, or the elimination of a protein from a pathway or a complex. Such changes can be observed through monitoring modulation in gene expression of target genes, or the presence or absence of phenotype specific markers. Included as an embodiment of this aspect are vectors, antibodies, libraries of compounds, gene specific antisense oligonucleotides, and cell lines.

In a still further aspect, the invention provides a method of treating or preventing a disease or disorder involving altered levels of a complex described herein or a polypeptide described herein, by administering, to a subject in need thereof, a therapeutically-effective amount of at least one molecule that modulates the function of the complex or polypeptide. In one embodiment, the agent modulates the function of a polypeptide selected from the polypeptides recited in Tables 1-7, columns 2, 3, 5 or 6.

In the specification and the appended claims, the singular forms include plural referents unless the context clearly dictates otherwise. Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood

by one of ordinary skill in the art to which this invention belongs. All patents and publications cited in this specification are incorporated by reference herein in their entirety

BRIEF DESCRIPTION OF THE DRAWINGS

- 5 Figure 1 is a graphical illustration showing the interactions between human host proteins and HPV 16 E5, HPV 16 E6 and HPV 16 E7 and the relevant biological events tied to the activity of proteins involved in host cell proliferation.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

- 10 The term "pre-cancerous cervical lesions" is intended to refer to those abnormalities which clinically may be described as "pre-malignant" conditions and which may, without treatment, proceed to full malignancies.

The present invention makes possible the accurate diagnosis and treatment of infections associated with HPV. The invention further clarifies the mechanism of action or
15 biochemical pathways that lead to phenotypes indicative of a disease or abnormal condition. Preferred protein interactions include interactions described in Tables 1-7, most preferred interactions include those described in Tables 4-7. The invention further provides complexes of interacting polypeptides which have not heretofore been shown to interact directly and methods of using these complexes. In another aspect, certain interactions and
20 complexes reveal utilities for known molecules that have not previously been associated with HPV infection. In one embodiment, interactions between viral proteins and phosphatases that regulate the activity of growth factor receptors are disclosed.

Some interacting polypeptides were identified by determining which of the predicted open-reading frames (ORFs) of the yeast encode polypeptides that interact in a
25 yeast two-hybrid system. The interacting pairs were identified to include (i) interactions that place functionally unclassified proteins in a biological context, (ii) novel interactions between proteins involved in the same biological function, (iii) novel interactions that link together biological functions into larger cellular processes (iv) and identification of potential therapeutic targets and/or diagnostic markers useful in a human clinical setting.
30 In a specific embodiment, protein interactions and pathways in a natural host cell which interact with critical proteins of HPV 1a, HPV 16 or HPV 11 have been identified. The interactions provide a better understanding of the biology of HPV infection as they relate to

clinically related HPV strains. More specifically, the present invention provides elucidation of the biochemistry in the strains of virus that are known, respectively, to cause warts, non-cancerous lesions, and tumors. All interactors identified in this invention are potential diagnostic markers for HPV infection and a subset of these have additional value
5 as therapeutic targets. The interactions of the invention are listed in Tables 1 through 7 below. In one embodiment, tabular data depicted in the tables have been exemplified as in Figure 1.

Prey identified from screens of different tissues were directly tested against all baits from HPV 1, 11, and 16 directly as well as the converse test which is the basis of the one-
10 by-one matrix reaction through Pathcalling (see also U.S. Patents 6,057,101 and 6,083,693). A subset of the observed interactions was observed to be specific for each strain tested and others were observed to be conserved interactions for all the strains tested. For example, those interactions that were specific for HPV 16 were analyzed for their potential role in the development of malignancies. Those interactions that were unique to
15 low risk strains are indicative of low-risk infection and the associated consequences, such as common warts (HPV 1a) and benign cervical lesions (HPV 11). Interactions common to both HPV 11 and HPV 16 are relevant to cervical infection, while those common to HPV 1a and HPV 11 are relevant to benign response to infection. All of the above interactions, and the interactions common to any two or more HPV strains are relevant to the general
20 phenomenon of warts.

New insights into novel interactions between proteins involved in the same biological function are also provided. In one embodiment, proteins involved in inactivation of the discs large tumor (DLG) suppressor have been described in Kuhne, et al., Oncogene
30: 18(40) pp. 5487-596 (1999). The present invention describes the novel interaction
25 between proteins HPV16 E6 or E7 with DLG that is related to proteosome-mediated degradation. In another embodiment, HPV16 E6 and ubiquitin-specific protease 9 as well as HPV16 E7 and proteosome 26S subunit are novel interactions. These protein interactions may indicate their involvement in proteosome-mediated degradation.

In another aspect, the interactions described by the present invention provide new
30 insights into E6 and E7 mechanisms of action. E7 may enhance the transforming activity of E6 by binding to and inactivating downstream tumor suppressor effects of p53. Because E6 and E7 have several common interactors, concerted action on common biological pathways is indicated. E6 and E7 transforming activity may also be mediated by interactions with other candidate tumor suppressor or proteins involved in cellular

proliferation and apoptosis. Therefore, inhibition or regulation of these interactions are suitable as targets for candidate therapeutics.

In another embodiment, interaction was also identified between complexes of HPV16 E6 and TCP-1, proteasome subunit PMSC1 and syntaxin 4. The interactions have relevance to tumor suppression via protein folding, unfolding and trafficking pathways. Such interactions provide opportunities to develop tools against various pathologic situations in which signaling through these proteins via p53 which are involved in cancer

The newly identified protein-protein interactions of the present invention connect biological functions into larger cellular processes. For example, Figure 1 depicts a diagram of the protein-protein interactions and the relevant biological events tied to the activity of proteins involved in host cell proliferation described in Table A. Viral proteins are depicted as hatched circles, human proteins as closed circles, and the solid lines between the circles represent the physical interactions observed as a consequence of the yeast two-hybrid matrix assay. The broken arrow indicates the predicted direct/indirect activity of PTPN2 as an enzyme that may directly or indirectly affect signal transduction activity of EGFR in the presence of its ligand (Boonstra, Rijken et al. 1995).

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Table A.

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	Screen/Matrix/MS
160	cbe_251445	HPV 16 E6	NA	cbe_2576474	PTPN2	SMT	MatrixMating/PathCalling
165	cbe_251448	HPV 16 E7	NA	cbe_422236	BCR1	SMT	MatrixMating/PathCalling
198	cbe_422236	BCR1	SMT	cbe_2576474	PTPN2	SMT	MatrixMating
618	cbe_422236	BCR1	SMT	cbe_251445	HPV 16 E6	NA	MatrixMating

The viral life cycle of HPV has been well described in both general terms and in terms of HPV's role in cancer (zur Hausen 2002). In short, the basal layer of cells of epithelia depicted in this figure is typically infected by HPV as a result of the exposure of the cells to virus that has penetrated via microlesions. Viral proliferation, formation, and egress from the host is coordinated with the proliferation of the basal layer of cells and their differentiation into keratinocytes. As the keratinocytes mature they release the mature viral particles. Part of the viral life cycle includes the induction of the lateral proliferation of the basal layer. Under normal conditions the proliferation is in a vertical direction as indicated. The co-opting of the proliferative capacity of the basal layer of cells is essential for the successful reproduction of the virus; therefore it is essential that the virus take control of this process.

In some circumstances, co-opting of the proliferation results in a benign lesions. In other cases the results may lead to a cancer in a susceptible tissue such as the cervix.

HPV16 is well known to induce cancers of the anogenital tract as well as oral-laryngeal cancers. This highly frequent consequence of chronic HPV 16 infection is the result of the integration of two viral proto-oncogenes, HPV 16 E6 and HPV 16 E7. One or both of these proteins is capable of transforming cells independently of viral infection when transformed into cells (Munger, Phelps et al. 1989; zur Hausen 2002). HPV 16 E5 is known to play a role early in infection by interacting with epidermal growth factor receptor (EGFR) (Hwang, Nottoli et al. 1995; zur Hausen 2002). EGFR is a growth factor receptor whose activity is controlled by its phosphorylation state. Phosphorylated EGFR (EGFR-P) is the consequence of ligand binding and leads to the induction of proliferative intracellular signals (Boonstra, Rijken et al. 1995). PTPN2 is a poorly characterized protein tyrosine phosphatase that can dephosphorylate phospho-tyrosine (Johnson, Cool et al. 1993). The importance of tyrosine dephosphorylation in regulating enzymatic activity has been demonstrated for EGFR (Boonstra, Rijken et al. 1995). Breakpoint cluster region 1 protein (BCR1) is a GTPase-activating protein (GAP) for RAC1 and CDC42 and promotes the exchange of RAC or CDC42-bound GDP by GTP, thereby activating them (Ahmed, Lee et al. 1994). CDC42 is well known to affect cell polarity (Takai, Sasaki et al. 2001).

Some newly disclosed interactions (INT 160, 165, 198, and 618) provide new biological context for these proteins as well as strongly indicating a previously unanticipated functional role for HPV 16 proteins as individual entities as well as components of a complex present in active infections. A diagnostic device that measures

the presence of complexes of proteins is the basis to identify active infection as opposed to a late stage infection under which circumstances the transforming consequence of the infection is the result of the integration and aberrant expression of HPV 16 E6 and/or HPV 16 E7. HPV 16 E5 protein's role occurs early in the viral life cycle (zur Hausen 2002).

5 Novel interactions between HPV 16 and the cell polarity pathway controlled by CDC2 via the direct interactions between HPV 16 viral oncogenes E6 and E7 (INT 165 and INT 618, and indirectly via INT 160 and INT 198) indicates that agents which affect the activity of BCR1 and other GAPs or other effectors of CDC42, such as guanine nucleotide exchange factors (GEFs), or enzymes involved in the post translation modification of
10 CDC42 but not previously associated with HPV infection, are drug targets for the treatment of HPV infection. Any existing agent that affects the activity of enzymes in the CDC42-mediated polarity pathway are suitable as drugs for the treatment of HPV infection. Therefore treatment of HPV infection includes treatment modes which inhibit the ability of HPV to cause basal layer cells proliferation.

15 In one embodiment, INT 160, INT 198, and INT 165 show direct and indirect interactions between HPV 16 viral oncogenes and PTPN2. Phosphatases play a role in the signal transduction pathways necessary for cellular proliferation (Carr, Wang et al. 2002) which has been indicated as a consequence of HPV infection of the basal layer cells (zur Hausen 2002). Agents that affect the activity of PTPN2 may be used to treat HPV16
20 infection. Treatment of the infection early will reduce the chance of HPV proto-oncogene insertion into the host genome, thereby reducing the probability of tumor induction. In summary, EGFR and CDC42 play roles in cellular proliferation. HPV co-opts the activity of these pathways via novel interaction with PTPN2 and BCR1 as identified by the present invention. Therefore, clinical intervention in these pathways is to treat HPV
25 infection is encompassed by the present invention. Identification of the interactions described in Figure 1 leads to diagnosis of an active HPV infection at an early stage possible to intervene in the course of the infection and the course of the disease leading to conditions as mild as warts and as severe as tumors.

30 The complexes disclosed herein are also useful, *inter alia*, in identifying agents that modulate cellular processes in which one or more members of the complex have previously been associated. For example, many of the interacting proteins identified by INT ID numbers as shown in Tables 1 through 7, have been previously implicated *inter alia*, in cell growth, cell division, and /or DNA synthesis, protein synthesis, folding or turnover and vesicle trafficking molecules. Accordingly, new agents which modulate cell growth, cell

division, and/or DNA synthesis can be identified by evaluating the ability of a test agent to affect formation or dissolution of a complex having INT ID numbers described herein.

Complexes according to the invention can also be used in methods for identifying desired polypeptides in a biological sample by forming a complex of a first polypeptide and
5 a second polypeptide that interacts with the first polypeptide. The presence of the complex indicates that the sample contains the first polypeptide.

The complexes of the invention are useful treating, e.g., alleviating a symptom of , preventing, diagnosing, or screening for compounds to treat or prevent disorders associated with HPV invention. For example, HPV, the human papilloma virus, has been linked to
10 many cancers (e.g., cervical cancer) and intraepithelial neoplasias (commonly called dysplasias, *i.e.*, abnormal cell growth that is generally considered to be precancerous when it occurs in the female reproductive system). Although most of the research that has been done on these conditions is in the female reproductive tract (especially the cervix, but also the vulva and vagina), the virus is linked to cancers and precancerous conditions in all of
15 the following: eye, lung, skin, anus, penis, prostate, esophagus, and stomach.

Symptoms of HPV infection include for example, genital warts are growths or bumps that appear on the vulva, in or around the vagina or anus, on the cervix, or on the penis, scrotum, groin (where the genital area meets the inner thigh). They may be raised or flat, single or multiple, small or large

20 The Pap test is the major front-line test for dysplasia. During this test, cells are taken from the cervical area and examined under a microscope for abnormalities. There are two different systems for classifying dysplasia.

The Bethesda, or SIL (squamous intraepithelial lesion) System looks only at individual cells, generally from a Pap test, and classifies them according to the degree of
25 cell abnormality. These break down into:

- ASCUS (atypical squamous cells of undetermined significance) means the cells aren't quite right, but they aren't clearly dysplastic, either. This can be caused by a lot of different factors, including hormonal changes, yeast or other infections, medications, or other sources of inflammation. HPV testing is sometimes done at this point .- AGUS or AGCUS
30 (atypical glandular cells of undetermined significance) is a finding of atypical glandular cells. This is less common, but since a different type of cancer (adenocarcinoma) develops

from glandular (mainly the columnar) cells, this is usually followed up right away with more testing. Adenocarcinoma often doesn't have the extended precancerous phase that squamous cell carcinoma does.

5 - LSIL - low grade squamous intraepithelial lesion - this is also called "mild dysplasia", however, the true degree and extent of the dysplasia can only be determined upon further evaluation of the cervix itself. Since most LSIL "regresses" - that is, returns to normal without treatment, a woman with LSIL may be advised to return for another Pap test in a few months.

10 - HSIL - high grade squamous intraepithelial lesion - this type of Pap result will always be evaluated further and treated, as it detects cell changes that have progressed beyond the mild stage.

CIN system - The other major system of classifying dysplasia is called the CIN system, for cervical intraepithelial neoplasia. There are corresponding classifications for vaginal and vulvar dysplasia called VAIN and VIN. This system of classification is based both on the
15 degree of dysplasia in the individual cells (like SIL) and how far below the surface of the cervix the dysplasia goes.

- CIN I - corresponds to mild dysplasia or LSIL. Additionally, the abnormal cells are only on the very surface of the cervix. As stated under SIL, most of these will regress back to normal over time. About 11% will progress to CIN 3. Only a very small percentage of CIN
20 I leads to cancer.

- CIN 2 - corresponds to moderate dysplasia or HSIL. About half of the thickness of the epithelium is abnormal (dysplastic). Left alone, about 43% of CIN 2 will regress back to normal, and 20% will progress to CIN 3.

25 - CIN 3 - corresponds to severe dysplasia or HSIL. All or almost all of the epithelium is dysplastic. Although some CIN 3 will spontaneously regress, this is almost always treated since the next step is cancer. This is sometimes also referred to as carcinoma in situ.

These utilities, as well as additional utilities, are discussed in greater detail below
Purified Polypeptide Complexes

30 In one aspect, the invention includes a purified complex that includes two or more polypeptides. In one embodiment, the invention provides purified complexes of two or

more polypeptides. One of the polypeptides includes a polypeptide selected from the polypeptides recited in Tables 1 through 7, column 2 (referenced as cbe_SEQ ID Interactor A) and another includes a polypeptide selected from the polypeptides recited in Table 1 through 7, column 5 (referenced as cbe_SEQ ID Interactor B). In preferred embodiments the first and second polypeptides of the complex are the polypeptides enumerated in Tables 4-7. In some embodiments a first polypeptide is listed as a "bait" polypeptide and a second polypeptide is denoted as "prey" polypeptide, while in other embodiments the first polypeptide corresponds to a "prey" polypeptide and the second is a "bait" polypeptide.

By "corresponding polypeptide" is meant, with reference to Tables 1-7, the polypeptide recited in the same row, reading across from left to right or right to left, as a specific selected peptide. For example, in Table 3, in the first row, the corresponding polypeptide of cbe_251059 is cbe_2599246 (Prey 1054152). These protein pairs are designated as INT ID 137 as is indicated in Table 3. In the second row, however, the corresponding polypeptide of cbe_251059 is cbe_2789381 (Prey 775). These protein pairs are designated as INT ID 138.

Also as used herein, "protein" and "protein complex" are used synonymously with "polypeptide" and "polypeptide complex." A "purified" polypeptide, protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the polypeptide is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of polypeptide complex having less than about 30% (by dry weight) of non-complex proteins (also referred to herein as a "contaminating protein"), more preferably less than about 20% of contaminating protein, still more preferably less than about 10% of contaminating protein, and most preferably less than about 5% non-complex protein. When the polypeptide or complex is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

Table 1. HPV 1a specific interactions.

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
383	cbe_1710	QP-C	NA	cbe_251917	HPV 1a E2	NA	PathCalling
384	cbe_22607	Hs.101882	NA	cbe_251740	HPV 1a E1-E4	NA	PathCalling
385	cbe_92628	FTHP1	NA	cbe_251919	HPV 1a E6	NA	PathCalling
393	cbe_251740	HPV 1a E1-E4	NA	cbe_251740	HPV 1a E1-E4	NA	MatrixMating
394	cbe_251740	HPV 1a E1-E4	NA	cbe_251777	Prey2316	NA	PathCalling
395	cbe_251740	HPV 1a E1-E4	NA	cbe_251900	Prey2598	NA	PathCalling
396	cbe_251740	HPV 1a E1-E4	NA	cbe_1380530	RPL13	NA	PathCalling
397	cbe_251740	HPV 1a E1-E4	NA	cbe_1796502	CTNND2	NA	PathCalling
398	cbe_251740	HPV 1a E1-E4	NA	cbe_1807361	FLJ22729	NA	PathCalling
399	cbe_251740	HPV 1a E1-E4	NA	cbe_2685998	Prey2313	NA	PathCalling
400	cbe_251740	HPV 1a E1-E4	NA	cbe_2830508	Prey142356	NA	PathCalling
401	cbe_251740	HPV 1a E1-E4	NA	cbe_3478832	gbh_y14735	NA	PathCalling
402	cbe_251740	HPV 1a E1-E4	NA	cbe_3705944	TNFAIP1	NA	PathCalling
403	cbe_251740	HPV 1a E1-E4	NA	cbe_3764052	CKM	SMT	PathCalling
404	cbe_251740	HPV 1a E1-E4	NA	cbe_3833533	TRIM29	NA	PathCalling
405	cbe_251740	HPV 1a E1-E4	NA	cbe_3927174	SCP2	SMT	PathCalling
406	cbe_251740	HPV 1a E1-E4	NA	cbe_4138433	KIFAP3	NA	PathCalling
407	cbe_251740	HPV 1a E1-E4	NA	cbe_4267981	TNNC1	NA	PathCalling
408	cbe_251740	HPV 1a E1-E4	NA	cbe_4383836	KIAA0905	NA	PathCalling
409	cbe_251740	HPV 1a E1-E4	NA	cbe_4567083	Prey1207	NA	PathCalling
410	cbe_251917	HPV 1a E2	NA	cbe_251976	Prey2777	NA	MatrixMating/PathCalling
411	cbe_251917	HPV 1a E2	NA	cbe_1469980	FLJ20259	NA	MatrixMating/PathCalling
412	cbe_251917	HPV 1a E2	NA	cbe_2826346	RPS10	NA	PathCalling
413	cbe_251917	HPV 1a E2	NA	cbe_2830508	Prey142356	NA	PathCalling
414	cbe_251917	HPV 1a E2	NA	cbe_3345510	COX6C	SMT	PathCalling
415	cbe_251917	HPV 1a E2	NA	cbe_3583511	MGC3222	NA	PathCalling
416	cbe_251917	HPV 1a E2	NA	cbe_3625721	EIF2B2	NA	PathCalling
417	cbe_251917	HPV 1a E2	NA	cbe_3641816	ANKH	NA	PathCalling
418	cbe_251917	HPV 1a E2	NA	cbe_3826540	Hs.98226	NA	MatrixMating/PathCalling
419	cbe_251917	HPV 1a E2	NA	cbe_4268532	Prey1053593	NA	PathCalling
420	cbe_251917	HPV 1a E2	NA	cbe_4269834	GNB2L1	NA	MatrixMating/PathCalling
421	cbe_251917	HPV 1a E2	NA	cbe_4270118	Hs.211143	NA	PathCalling
422	cbe_251919	HPV 1a E6	NA	cbe_251929	Prey2672	NA	PathCalling
423	cbe_251919	HPV 1a E6	NA	cbe_3461331	MET	AT/PT/SMT	PathCalling

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
424	cbe_251919	HPV 1a E6	NA	cbe_3621798	XPO1	NA	PathCalling
425	cbe_251919	HPV 1a E6	NA	cbe_3665307	HK1	NA	PathCalling
426	cbe_251919	HPV 1a E6	NA	cbe_4267867	ANXA2	NA	PathCalling
427	cbe_251925	HPV 1a E7	NA	cbe_251953	Prey2724	NA	MatrixMating/PathCalling
428	cbe_251925	HPV 1a E7	NA	cbe_3753270	gbh_ac004503	NA	MatrixMating/PathCalling
429	cbe_251925	HPV 1a E7	NA	cbe_3760926	gbh_al359334	NA	MatrixMating/PathCalling
430	cbe_251925	HPV 1a E7	NA	cbe_3789063	AP2M1	NA	MatrixMating
431	cbe_251925	HPV 1a E7	NA	cbe_3810032	gbh_af142421	NA	MatrixMating/PathCalling
432	cbe_251925	HPV 1a E7	NA	cbe_3820530	PGAM1	SMT	MatrixMating/PathCalling
433	cbe_251925	HPV 1a E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating
434	cbe_251925	HPV 1a E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating/PathCalling
435	cbe_252016	HPV 1a L1	NA	cbe_4267526	HRIHFB2206	NA	MatrixMating/PathCalling
436	cbe_252016	HPV 1a L1	NA	cbe_252039	Prey2919	NA	PathCalling
437	cbe_252016	HPV 1a L1	NA	cbe_2611002	NR1H4	SMT	MatrixMating/PathCalling
438	cbe_252016	HPV 1a L1	NA	cbe_2980052	ARHC	SMT	PathCalling
439	cbe_252016	HPV 1a L1	NA	cbe_3800240	IVD	SMT	PathCalling
440	cbe_252016	HPV 1a L1	NA	cbe_4268726	NR1H2	SMT	PathCalling
441	cbe_251088	HPV 16 E2	NA	cbe_4296923	SCGB1A1	AT/PT	PathCalling
442	cbe_252041	HPV 1a L2	NA	cbe_252041	HPV 1a L2	NA	MatrixMating
443	cbe_252041	HPV 1a L2	NA	cbe_252090	Prey2820	NA	MatrixMating
444	cbe_252041	HPV 1a L2	NA	cbe_2321045	WNT2B	NA	PathCalling
445	cbe_252041	HPV 1a L2	NA	cbe_2603140	Prey146	NA	MatrixMating/PathCalling
446	cbe_252041	HPV 1a L2	NA	cbe_3222359	LOC51748	NA	PathCalling
447	cbe_252041	HPV 1a L2	NA	cbe_3456824	gbh_120086	AT	PathCalling
448	cbe_252041	HPV 1a L2	NA	cbe_3606990	Prey1053670	NA	PathCalling
449	cbe_252041	HPV 1a L2	NA	cbe_3770440	gbh_af217505	NA	MatrixMating/PathCalling
450	cbe_252041	HPV 1a L2	NA	cbe_3810791	EPHB1	NA	MatrixMating/PathCalling
451	cbe_252041	HPV 1a L2	NA	cbe_4248793	GSN	AT/PT	PathCalling
452	cbe_252041	HPV 1a L2	NA	cbe_4268470	HSPE1	NA	MatrixMating/PathCalling
453	cbe_252041	HPV 1a L2	NA	cbe_4269628	RIL	NA	MatrixMating
454	cbe_252041	HPV 1a L2	NA	cbe_4540466	PUM1	NA	MatrixMating/PathCalling

Table 2. HPV11 specific interactions

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/A/T/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/A/T/SMT/NA	PathCalling Screen and/or Matrix Assay
1	cbe_6464	Hs.19954	NA	cbe_250781	HPV 11 E2	NA	MatrixMating/PathCalling
2	cbe_244811	DGUOK	SMT	cbe_250777	HPV 11 E4	NA	MatrixMating/PathCalling
5	cbe_250777	HPV 11 E4	NA	cbe_862174	MT2A	NA	MatrixMating/PathCalling
6	cbe_250777	HPV 11 E4	NA	cbe_1699351	SCO1	NA	MatrixMating/PathCalling
7	cbe_250777	HPV 11 E4	NA	cbe_4344185	SRA1	NA	MatrixMating/PathCalling
8	cbe_250781	HPV 11 E2	NA	cbe_251821	Prey2419	NA	PathCalling
9	cbe_250781	HPV 11 E2	NA	cbe_251826	Prey2429	NA	PathCalling
10	cbe_250781	HPV 11 E2	NA	cbe_251857	Prey2492	NA	PathCalling
11	cbe_250781	HPV 11 E2	NA	cbe_251858	Prey2494	NA	PathCalling
12	cbe_250781	HPV 11 E2	NA	cbe_366279	Prey2439	NA	PathCalling
13	cbe_250781	HPV 11 E2	NA	cbe_408167	Prey2412	NA	PathCalling
14	cbe_250781	HPV 11 E2	NA	cbe_3563252	Hs.306083	NA	PathCalling
15	cbe_250781	HPV 11 E2	NA	cbe_4269472	MKG15	NA	PathCalling
16	cbe_250781	HPV 11 E2	NA	cbe_4269571	KRT8	NA	PathCalling
17	cbe_250808	HPV 11 E6	NA	cbe_250809	Prey152	NA	PathCalling
18	cbe_250808	HPV 11 E6	NA	cbe_250895	Prey343	NA	PathCalling
19	cbe_250808	HPV 11 E6	NA	cbe_250904	Prey365	NA	PathCalling
20	cbe_250808	HPV 11 E6	NA	cbe_250906	Prey370	NA	PathCalling
21	cbe_250808	HPV 11 E6	NA	cbe_250907	Prey372	NA	PathCalling
22	cbe_250808	HPV 11 E6	NA	cbe_250908	Prey375	NA	PathCalling
23	cbe_250808	HPV 11 E6	NA	cbe_250912	Prey385	NA	PathCalling
24	cbe_250808	HPV 11 E6	NA	cbe_250922	Prey409	NA	PathCalling
25	cbe_250808	HPV 11 E6	NA	cbe_250924	Prey413	NA	PathCalling

26	cbe_250808	HPV 11 E6	NA		cbe_250925	Prey415	NA	PathCalling
27	cbe_250808	HPV 11 E6	NA		cbe_2541164	GPRK5	SMT	PathCalling
28	cbe_250808	HPV 11 E6	NA		cbe_3580897	HSPA5	NA	PathCalling
29	cbe_250808	HPV 11 E6	NA		cbe_3590661	NUP214	SMT	MatrixMating/PathCalling
30	cbe_250808	HPV 11 E6	NA		cbe_3694420	ARHGEF2	NA	PathCalling
31	cbe_250808	HPV 11 E6	NA		cbe_3929669	CD164	AT/PT	PathCalling
32	cbe_250808	HPV 11 E6	NA		cbe_4175362	MAPK9	SMT	PathCalling
33	cbe_250808	HPV 11 E6	NA		cbe_4268235	KIAA0410	NA	MatrixMating/PathCalling
34	cbe_250834	HPV 11 E7	NA		cbe_250878	Prey302	NA	MatrixMating/PathCalling
35	cbe_250834	HPV 11 E7	NA		cbe_250883	Prey244	NA	MatrixMating/PathCalling
36	cbe_250834	HPV 11 E7	NA		cbe_250888	Prey228	NA	MatrixMating/PathCalling
37	cbe_250834	HPV 11 E7	NA		cbe_3056756	KIAA0440	NA	MatrixMating/PathCalling
38	cbe_250834	HPV 11 E7	NA		cbe_3454406	gbh_af252829	NA	MatrixMating/PathCalling
39	cbe_250834	HPV 11 E7	NA		cbe_3760926	gbh_al359334	NA	MatrixMating/PathCalling
40	cbe_250834	HPV 11 E7	NA		cbe_3845697	Hs.191063	NA	MatrixMating/PathCalling
41	cbe_250834	HPV 11 E7	NA		cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
42	cbe_250834	HPV 11 E7	NA		cbe_4265947	RBP4	AT/PT	MatrixMating/PathCalling
43	cbe_250834	HPV 11 E7	NA		cbe_4268935	RPL26	NA	MatrixMating/PathCalling
44	cbe_250834	HPV 11 E7	NA		cbe_4269451	gbh_af038189	NA	MatrixMating/PathCalling
45	cbe_250834	HPV 11 E7	NA		cbe_4269681	Hs.224712	NA	MatrixMating/PathCalling
46	cbe_250834	HPV 11 E7	NA		cbe_4269818	Hs.73680	NA	MatrixMating/PathCalling
47	cbe_250834	HPV 11 E7	NA		cbe_4270015	RPS26	NA	MatrixMating/PathCalling
48	cbe_250834	HPV 11 E7	NA		cbe_4270441	Prey1052970	NA	PathCalling
49	cbe_250834	HPV 11 E7	NA		cbe_4280774	ITGB4	AT/PT	MatrixMating/PathCalling
50	cbe_251663	HPV 11 E1	NA		cbe_3643627	DKFZP434I1735	NA	PathCalling
51	cbe_251663	HPV 11 E1	NA		cbe_3842044	PSMB3	NA	PathCalling
52	cbe_251663	HPV 11 E1	NA		cbe_4269915	gbh_u23460	AT/SMT	PathCalling

53	cbe_251663	HPV 11 E1	NA	cbe_4270423	Prey1053526	AT	PathCalling
99	cbe_251445	HPV 16 E6	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling

Table 3. HPV16 specific interactions

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	Screen/Matrix/MS
137	cbe_251059	HPV 16 E1-E4	NA	cbe_2599246	Prey1054152	NA	PathCalling
138	cbe_251059	HPV 16 E1-E4	NA	cbe_2789381	Prey775	NA	MatrixMating
139	cbe_251059	HPV 16 E1-E4	NA	cbe_3472582	RABIF	NA	PathCalling
140	cbe_251059	HPV 16 E1-E4	NA	cbe_3621899	pcnp	NA	PathCalling
141	cbe_251059	HPV 16 E1-E4	NA	cbe_3880186	FLJ20343	NA	MatrixMating/PathCalling
142	cbe_251059	HPV 16 E1-E4	NA	cbe_4269156	PCDH1	AT/PT	PathCalling
143	cbe_251059	HPV 16 E1-E4	NA	cbe_4269329	SP260	AT	PathCalling
144	cbe_251063	HPV 16 E1	NA	cbe_251099	Prey802	NA	MatrixMating/PathCalling
145	cbe_251063	HPV 16 E1	NA	cbe_4465094	Prey1053092	NA	PathCalling
146	cbe_251088	HPV 16 E2	NA	cbe_252041	HPV 1a L2	NA	MatrixMating
147	cbe_251088	HPV 16 E2	NA	cbe_2321057	EFEMP1	AT/PT	MatrixMating/PathCalling
148	cbe_251088	HPV 16 E2	NA	cbe_3670766	ACTC	NA	MatrixMating/PathCalling
149	cbe_251088	HPV 16 E2	NA	cbe_3922906	BSMAP	AT	PathCalling
150	cbe_251088	HPV 16 E2	NA	cbe_4268208	DAD1	AT	MatrixMating/PathCalling
151	cbe_251088	HPV 16 E2	NA	cbe_4279962	DKKL1-pending	AT/PT	PathCalling
159	cbe_251445	HPV 16 E6	NA	cbe_2253980	gbh_d38112_5	NA	MatrixMating/PathCalling
160	cbe_251445	HPV 16 E6	NA	cbe_2576474	PTPN2	SMT	MatrixMating/PathCalling
161	cbe_251445	HPV 16 E6	NA	cbe_4269405	gbh_af155653	NA	MatrixMating/PathCalling
162	cbe_251445	HPV 16 E6	NA	cbe_4269703	LOC51182	NA	MatrixMating/PathCalling

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	Screen/Matrix/MS
99	cbe_251445	HPV 16 E6	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling
163	cbe_251448	HPV 16 E7	NA	cbe_251468	Prey1628	NA	MatrixMating/PathCalling
164	cbe_251448	HPV 16 E7	NA	cbe_251502	Prey1609	NA	MatrixMating/PathCalling
165	cbe_251448	HPV 16 E7	NA	cbe_422236	BCR1	SMT	MatrixMating/PathCalling
166	cbe_251448	HPV 16 E7	NA	cbe_2693325	Prey1673	NA	MatrixMating/PathCalling
167	cbe_251448	HPV 16 E7	NA	cbe_2898065	Prey1620	NA	MatrixMating/PathCalling
168	cbe_251448	HPV 16 E7	NA	cbe_3474077	KRT4	NA	MatrixMating
169	cbe_251448	HPV 16 E7	NA	cbe_3773649	EEF1A1L14	NA	MatrixMating/PathCalling
170	cbe_251448	HPV 16 E7	NA	cbe_3787129	LOC55828	NA	MatrixMating/PathCalling
171	cbe_251448	HPV 16 E7	NA	cbe_3789063	AP2M1	NA	MatrixMating/PathCalling
172	cbe_251448	HPV 16 E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating
173	cbe_251448	HPV 16 E7	NA	cbe_3921620	MPP3	AT	MatrixMating/PathCalling
174	cbe_251448	HPV 16 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
175	cbe_251448	HPV 16 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating
176	cbe_251448	HPV 16 E7	NA	cbe_4268611	NDUFS3	SMT	MatrixMating/PathCalling
177	cbe_251448	HPV 16 E7	NA	cbe_4268684	MIZF	NA	MatrixMating/PathCalling
178	cbe_251448	HPV 16 E7	NA	cbe_4268740	ZNF-U69274	NA	MatrixMating/PathCalling
179	cbe_251448	HPV 16 E7	NA	cbe_4269658	PSMCI	NA	MatrixMating/PathCalling
180	cbe_251448	HPV 16 E7	NA	cbe_4269876	SBP2	NA	MatrixMating/PathCalling
181	cbe_251448	HPV 16 E7	NA	cbe_4270186	STX4A	AT	MatrixMating/PathCalling
182	cbe_251737	HPV 16 L2	NA	cbe_422227	Prey277610	NA	PathCalling
183	cbe_251737	HPV 16 L2	NA	cbe_422247	Prey277642	NA	PathCalling
184	cbe_251737	HPV 16 L2	NA	cbe_3056756	KIAA0440	NA	MatrixMating/PathCalling
185	cbe_251737	HPV 16 L2	NA	cbe_3473488	gbh_al121903	NA	PathCalling
186	cbe_251737	HPV 16 L2	NA	cbe_3575702	SUI1	NA	PathCalling

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	Screen/Matrix/MS
187	cbe_251737	HPV 16 L2	NA	cbe_3663966	KIAA1389	NA	PathCalling
188	cbe_251737	HPV 16 L2	NA	cbe_3849002	HSPC224	AT	PathCalling
189	cbe_251737	HPV 16 L2	NA	cbe_3884811	Hs.30289	NA	PathCalling
190	cbe_251737	HPV 16 L2	NA	cbe_4268684	MZF	NA	MatrixMating
191	cbe_251737	HPV 16 L2	NA	cbe_4270335	KIAA0276	NA	PathCalling
192	cbe_251784	HPV 16 L1	NA	cbe_251790	Prey2347	NA	PathCalling
193	cbe_251784	HPV 16 L1	NA	cbe_422204	Prey2335	NA	PathCalling
194	cbe_251784	HPV 16 L1	NA	cbe_552305	Prey2354	NA	PathCalling
195	cbe_251784	HPV 16 L1	NA	cbe_967711	Hs.201037	NA	PathCalling
196	cbe_251784	HPV 16 L1	NA	cbe_1505425	HCDI	NA	PathCalling
197	cbe_251784	HPV 16 L1	NA	cbe_4281271	CRYAB	NA	PathCalling
316	cbe_2599246	Prey1054152	NA	cbe_3929637	HPV 16 E5	AT/PT	PathCalling
618	HPV 16 E6422236	BCR1	SMT	251445	HPV 16 E6	NA	MatrixMating
317	cbe_2830508	Prey142356	NA	cbe_3929637	HPV 16 E5	AT/PT	PathCalling

Table 4. HPV1a and HPV 11 specific interactions

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
137	cbe_251059	HPV 16 E1-E4	NA	cbe_2599246	Prey1054152	NA	PathCalling
138	cbe_251059	HPV 16 E1-E4	NA	cbe_2789381	Prey775	NA	MatrixMating
139	cbe_251059	HPV 16 E1-E4	NA	cbe_3472582	RABIF	NA	PathCalling
140	cbe_251059	HPV 16 E1-E4	NA	cbe_3621899	pcnp	NA	PathCalling
141	cbe_251059	HPV 16 E1-E4	NA	cbe_3880186	FLJ20343	NA	MatrixMating/PathCalling

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
142	cbe_251059	HPV 16 E1-E4	NA	cbe_4269156	PCDH1	AT/PT	PathCalling
143	cbe_251059	HPV 16 E1-E4	NA	cbe_4269329	SP260	AT	PathCalling
144	cbe_251063	HPV 16 E1	NA	cbe_251099	Prey802	NA	MatrixMating/PathCalling
145	cbe_251063	HPV 16 E1	NA	cbe_4465094	Prey1053092	NA	PathCalling
146	cbe_251088	HPV 16 E2	NA	cbe_252041	HPV 1a L2	NA	MatrixMating
147	cbe_251088	HPV 16 E2	NA	cbe_2321057	EFEMP1	AT/PT	MatrixMating/PathCalling
148	cbe_251088	HPV 16 E2	NA	cbe_3670766	ACTC	NA	MatrixMating/PathCalling
149	cbe_251088	HPV 16 E2	NA	cbe_3922906	BSMAP	AT	PathCalling
150	cbe_251088	HPV 16 E2	NA	cbe_4268208	DAD1	AT	MatrixMating/PathCalling
151	cbe_251088	HPV 16 E2	NA	cbe_4279962	DKKL1-pending	AT/PT	PathCalling
159	cbe_251445	HPV 16 E6	NA	cbe_2253980	gbh_d38112_5	NA	MatrixMating/PathCalling
160		HPV 16 E6	NA	cbe_2576474	PTPN2	AT/SMT	MatrixMating/PathCalling
161	cbe_251445	HPV 16 E6	NA	cbe_4269405	gbh_af155653	NA	MatrixMating/PathCalling
162	cbe_251445	HPV 16 E6	NA	cbe_4269703	LOC51182	NA	MatrixMating/PathCalling
99	cbe_251445	HPV 16 E6	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling
163	cbe_251448	HPV 16 E7	NA	cbe_251468	Prey1628	NA	MatrixMating/PathCalling
164	cbe_251448	HPV 16 E7	NA	cbe_251502	Prey1609	NA	MatrixMating/PathCalling
165	cbe_251448	HPV 16 E7	NA	cbe_422236	BCR1	NA	MatrixMating/PathCalling
166	cbe_251448	HPV 16 E7	NA	cbe_2693325	Prey1673	NA	MatrixMating/PathCalling
167	cbe_251448	HPV 16 E7	NA	cbe_2898065	Prey1620	NA	MatrixMating/PathCalling
168	cbe_251448	HPV 16 E7	NA	cbe_3474077	KRT4	NA	MatrixMating
169	cbe_251448	HPV 16 E7	NA	cbe_3773649	EEF1A1L14	NA	MatrixMating/PathCalling
170	cbe_251448	HPV 16 E7	NA	cbe_3787129	LOC55828	NA	MatrixMating/PathCalling
171	cbe_251448	HPV 16 E7	NA	cbe_3789063	AP2M1	NA	MatrixMating/PathCalling
172	cbe_251448	HPV 16 E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
173	cbe_251448	HPV 16 E7	NA	cbe_3921620	MPP3	AT	MatrixMating/PathCalling
174	cbe_251448	HPV 16 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
175	cbe_251448	HPV 16 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating
176	cbe_251448	HPV 16 E7	NA	cbe_4268611	NDUFS3	SMT	MatrixMating/PathCalling
177	cbe_251448	HPV 16 E7	NA	cbe_4268684	MIZF	NA	MatrixMating/PathCalling
178	cbe_251448	HPV 16 E7	NA	cbe_4268740	ZNF-U69274	NA	MatrixMating/PathCalling
179	cbe_251448	HPV 16 E7	NA	cbe_4269658	PSMC1	NA	MatrixMating/PathCalling
180	cbe_251448	HPV 16 E7	NA	cbe_4269876	SBP2	NA	MatrixMating/PathCalling
181	cbe_251448	HPV 16 E7	NA	cbe_4270186	STX4A	AT	MatrixMating/PathCalling
182	cbe_251737	HPV 16 L2	NA	cbe_422227	Prey277610	NA	PathCalling
183	cbe_251737	HPV 16 L2	NA	cbe_422247	Prey277642	NA	PathCalling
184	cbe_251737	HPV 16 L2	NA	cbe_3056756	KIAA0440	NA	MatrixMating/PathCalling
185	cbe_251737	HPV 16 L2	NA	cbe_3473488	ggh_al121903	NA	PathCalling
186	cbe_251737	HPV 16 L2	NA	cbe_3575702	SUI1	NA	PathCalling
187	cbe_251737	HPV 16 L2	NA	cbe_3663966	KIAA1389	NA	PathCalling
188	cbe_251737	HPV 16 L2	NA	cbe_3849002	HSPC224	AT	PathCalling
189	cbe_251737	HPV 16 L2	NA	cbe_3884811	Hs.30289	NA	PathCalling
190	cbe_251737	HPV 16 L2	NA	cbe_4268684	MIZF	NA	MatrixMating
191	cbe_251737	HPV 16 L2	NA	cbe_4270335	KIAA0276	NA	PathCalling
192	cbe_251784	HPV 16 L1	NA	cbe_251790	Prey2347	NA	PathCalling
193	cbe_251784	HPV 16 L1	NA	cbe_422204	Prey2335	NA	PathCalling
194	cbe_251784	HPV 16 L1	NA	cbe_552305	Prey2354	NA	PathCalling
195	cbe_251784	HPV 16 L1	NA	cbe_967711	Hs.201037	NA	PathCalling
196	cbe_251784	HPV 16 L1	NA	cbe_1505425	HCDI	NA	PathCalling
197	cbe_251784	HPV 16 L1	NA	cbe_4281271	CRYAB	NA	PathCalling

INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
316	cbe_2599246	Prey1054152	NA	cbe_3929637	HPV 16 E5	AT/PT	PathCalling
317	cbe_2830508	Prey142356	NA	cbe_3929637	HPV 16 E5	AT/PT	PathCalling
INT ID	cbe_SEQ CG ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ CG ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	Screen/Matrix/MS
137	cbe_251059	HPV 16 E1-E4	NA	cbe_2599246	Prey1054152	NA	PathCalling
138	cbe_251059	HPV 16 E1-E4	NA	cbe_2789381	Prey775	NA	MatrixMating
139	cbe_251059	HPV 16 E1-E4	NA	cbe_3472582	RABIF	NA	PathCalling
140	cbe_251059	HPV 16 E1-E4	NA	cbe_3621899	pcnp	NA	PathCalling
141	cbe_251059	HPV 16 E1-E4	NA	cbe_3880186	FLJ20343	NA	MatrixMating/PathCalling
142	cbe_251059	HPV 16 E1-E4	NA	cbe_4269156	PCDH1	AT/PT	PathCalling
143	cbe_251059	HPV 16 E1-E4	NA	cbe_4269329	SP260	AT	PathCalling

Table 5. HPV1a and HPV 16 specific interactions

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
137	cbe_251059	HPV 16 E1-E4	NA	cbe_2599246	Prey1054152	NA	PathCalling
138	cbe_251059	HPV 16 E1-E4	NA	cbe_2789381	Prey775	NA	MatrixMating
139	cbe_251059	HPV 16 E1-E4	NA	cbe_3472582	RABIF	NA	PathCalling
140	cbe_251059	HPV 16 E1-E4	NA	cbe_3621899	pcnp	NA	PathCalling
141	cbe_251059	HPV 16 E1-E4	NA	cbe_3880186	FLJ20343	NA	MatrixMating/PathCalling
142	cbe_251059	HPV 16 E1-E4	NA	cbe_4269156	PCDH1	AT/PT	PathCalling
143	cbe_251059	HPV 16 E1-E4	NA	cbe_4269329	SP260	AT	PathCalling
144	cbe_251063	HPV 16 E1	NA	cbe_251099	Prey802	NA	MatrixMating/PathCalling
145	cbe_251063	HPV 16 E1	NA	cbe_4465094	Prey1053092	NA	PathCalling

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
146	cbe_251088	HPV 16 E2	NA	cbe_252041	HPV 1a L2	NA	MatrixMating
147	cbe_251088	HPV 16 E2	NA	cbe_2321057	EFEMP1	AT/PT	MatrixMating/PathCalling
148	cbe_251088	HPV 16 E2	NA	cbe_3670766	ACTC	NA	MatrixMating/PathCalling
149	cbe_251088	HPV 16 E2	NA	cbe_3922906	BSMAP	AT	PathCalling
150	cbe_251088	HPV 16 E2	NA	cbe_4268208	DAD1	AT	MatrixMating/PathCalling
151	cbe_251088	HPV 16 E2	NA	cbe_4279962	DKKL1-pending	AT/PT	PathCalling
159	cbe_251445	HPV 16 E6	NA	cbe_2253980	gbh_d38112_5	NA	MatrixMating/PathCalling
160	cbe_251445	HPV 16 E6	NA	cbe_2576474	PTPN2	AT/SMT	MatrixMating/PathCalling
161	cbe_251445	HPV 16 E6	NA	cbe_4269405	gbh_af155653	NA	MatrixMating/PathCalling
162	cbe_251445	HPV 16 E6	NA	cbe_4269703	LOC51182	NA	MatrixMating/PathCalling
99	cbe_251445	HPV 16 E6	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling
163	cbe_251448	HPV 16 E7	NA	cbe_251468	Prey1628	NA	MatrixMating/PathCalling
164	cbe_251448	HPV 16 E7	NA	cbe_251502	Prey1609	NA	MatrixMating/PathCalling
165	cbe_251448	HPV 16 E7	NA	cbe_422236	BCR1	NA	MatrixMating/PathCalling
166	cbe_251448	HPV 16 E7	NA	cbe_2693325	Prey1673	NA	MatrixMating/PathCalling
167	cbe_251448	HPV 16 E7	NA	cbe_2898065	Prey1620	NA	MatrixMating/PathCalling
168	cbe_251448	HPV 16 E7	NA	cbe_3474077	KRT4	NA	MatrixMating
169	cbe_251448	HPV 16 E7	NA	cbe_3773649	EEF1A1L14	NA	MatrixMating/PathCalling
170	cbe_251448	HPV 16 E7	NA	cbe_3787129	LOC55828	NA	MatrixMating/PathCalling
171	cbe_251448	HPV 16 E7	NA	cbe_3789063	AP2M1	NA	MatrixMating/PathCalling
172	cbe_251448	HPV 16 E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating
173	cbe_251448	HPV 16 E7	NA	cbe_3921620	MPP3	AT	MatrixMating/PathCalling
174	cbe_251448	HPV 16 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
175	cbe_251448	HPV 16 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating
176	cbe_251448	HPV 16 E7	NA	cbe_4268611	NDUFS3	SMT	MatrixMating/PathCalling

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
177	cbe_251448	HPV 16 E7	NA	cbe_4268684	MIZF	NA	MatrixMating/PathCalling
178	cbe_251448	HPV 16 E7	NA	cbe_4268740	ZNF-U69274	NA	MatrixMating/PathCalling
179	cbe_251448	HPV 16 E7	NA	cbe_4269658	PSMC1	NA	MatrixMating/PathCalling
180	cbe_251448	HPV 16 E7	NA	cbe_4269876	SBP2	NA	MatrixMating/PathCalling
181	cbe_251448	HPV 16 E7	NA	cbe_4270186	STX4A	AT	MatrixMating/PathCalling
383	cbe_1710	QP-C	NA	cbe_251917	HPV 1a E2	NA	PathCalling
410	cbe_251917	HPV 1a E2	NA	cbe_251976	Prey2777	NA	MatrixMating/PathCalling
411	cbe_251917	HPV 1a E2	NA	cbe_1469980	FLJ20259	NA	MatrixMating/PathCalling
412	cbe_251917	HPV 1a E2	NA	cbe_2826346	RPS10	NA	PathCalling
413	cbe_251917	HPV 1a E2	NA	cbe_2830508	Prey142356	NA	PathCalling
414	cbe_251917	HPV 1a E2	NA	cbe_3345510	COX6C	SMT	PathCalling
415	cbe_251917	HPV 1a E2	NA	cbe_3583511	MGC3222	NA	PathCalling
416	cbe_251917	HPV 1a E2	NA	cbe_3625721	EIF2B2	NA	PathCalling
417	cbe_251917	HPV 1a E2	NA	cbe_3641816	ANKH	NA	PathCalling
418	cbe_251917	HPV 1a E2	NA	cbe_3826540	Hs.98226	NA	MatrixMating/PathCalling
419	cbe_251917	HPV 1a E2	NA	cbe_4268532	Prey1053593	NA	PathCalling
420	cbe_251917	HPV 1a E2	NA	cbe_4269834	GNB2L1	NA	MatrixMating/PathCalling
421	cbe_251917	HPV 1a E2	NA	cbe_4270118	Hs.211143	NA	PathCalling
441	cbe_252041	HPV 1a L2	NA	cbe_252090	Prey2820	NA	MatrixMating
442	cbe_252041	HPV 1a L2	NA	cbe_2321045	WNT2B	NA	PathCalling
443	cbe_252041	HPV 1a L2	NA	cbe_2603140	Prey146	NA	MatrixMating/PathCalling
444	cbe_252041	HPV 1a L2	NA	cbe_3222359	LOC51748	NA	PathCalling
445	cbe_252041	HPV 1a L2	NA	cbe_3456824	gbh_120086	AT	PathCalling
446	cbe_252041	HPV 1a L2	NA	cbe_3606990	Prey1053670	NA	PathCalling
447	cbe_252041	HPV 1a L2	NA	cbe_3770440	gbh_at217505	NA	MatrixMating/PathCalling

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
448	cbe_252041	HPV 1a L2	NA	cbe_3810791	EPHB1	NA	MatrixMating/PathCalling
449	cbe_252041	HPV 1a L2	NA	cbe_4248793	GSN	AT/PT	PathCalling
450	cbe_252041	HPV 1a L2	NA	cbe_4268470	HSPE1	NA	MatrixMating/PathCalling
451	cbe_252041	HPV 1a L2	NA	cbe_4269628	RIL	NA	MatrixMating
452	cbe_252041	HPV 1a L2	NA	cbe_4340466	PUM1	NA	MatrixMating/PathCalling
576	cbe_252090	Prey2820	NA	cbe_552975	HPV 1a E1	NA	MatrixMating
579	cbe_71919	FLJ13236	NA	cbe_552975	HPV 1a E1	NA	PathCalling
580	cbe_251071	Prey734	NA	cbe_552975	HPV 1a E1	NA	MatrixMating
581	cbe_552975	HPV 1a E1	NA	cbe_3001381	IRF1	NA	MatrixMating
582	cbe_552975	HPV 1a E1	NA	cbe_3340492	TRIP	NA	MatrixMating
583	cbe_552975	HPV 1a E1	NA	cbe_3926508	TDE1	AT	PathCalling
584	cbe_552975	HPV 1a E1	NA	cbe_4269167	TLK2	SMT	MatrixMating
585	cbe_552975	HPV 1a E1	NA	cbe_4269681	Hs.224712	NA	MatrixMating
586	cbe_552975	HPV 1a E1	NA	cbe_4269703	LOC51182	NA	MatrixMating
587	cbe_552975	HPV 1a E1	NA	cbe_4269931	NDUFAB1	SMT	MatrixMating
280	cbe_2585091	SLC5A6	AT/SMT	cbe_3929637	HPV 16 E5	AT/PT	MatrixMating/PathCalling
431	cbe_251925	HPV 1a E7	NA	cbe_3810032	gbh_af142421	NA	MatrixMating/PathCalling
316	cbe_2599246	Prey1054152	NA	cbe_3929637	HPV 16 E5	AT/PT	PathCalling
317	cbe_2830508	Prey142356	NA	cbe_3929637	HPV 16 E5	AT/PT	PathCalling

Table 6. HPV 11, and HPV 16 specific interactions

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
34	cbe_250834	HPV 11 E7	NA	cbe_250878	Prey302	NA	MatrixMating/PathCalling
35	cbe_250834	HPV 11 E7	NA	cbe_250883	Prey244	NA	MatrixMating/PathCalling
36	cbe_250834	HPV 11 E7	NA	cbe_250888	Prey228	NA	MatrixMating/PathCalling
37	cbe_250834	HPV 11 E7	NA	cbe_3056756	KIAA0440	NA	MatrixMating/PathCalling
38	cbe_250834	HPV 11 E7	NA	cbe_3454406	gbh_af252829	NA	MatrixMating/PathCalling
39	cbe_250834	HPV 11 E7	NA	cbe_3760926	gbh_al359334	NA	MatrixMating/PathCalling
40	cbe_250834	HPV 11 E7	NA	cbe_3845697	Hs.191063	NA	MatrixMating/PathCalling
41	cbe_250834	HPV 11 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
42	cbe_250834	HPV 11 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating/PathCalling
43	cbe_250834	HPV 11 E7	NA	cbe_4268935	RPL26	NA	MatrixMating/PathCalling
44	cbe_250834	HPV 11 E7	NA	cbe_4269451	gbh_af038189	NA	MatrixMating/PathCalling
45	cbe_250834	HPV 11 E7	NA	cbe_4269681	Hs.224712	NA	MatrixMating/PathCalling
46	cbe_250834	HPV 11 E7	NA	cbe_4269818	Hs.73680	NA	MatrixMating/PathCalling
47	cbe_250834	HPV 11 E7	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling
48	cbe_250834	HPV 11 E7	NA	cbe_4270441	Prey1052970	NA	PathCalling
49	cbe_250834	HPV 11 E7	NA	cbe_4280774	ITGB4	AT/PT	MatrixMating/PathCalling
159	cbe_251445	HPV 16 E6	NA	cbe_2253980	gbh_d38112_5	NA	MatrixMating/PathCalling
160	cbe_251445	HPV 16 E6	NA	cbe_2576474	PTPN2	AT/SMT	MatrixMating/PathCalling
161	cbe_251445	HPV 16 E6	NA	cbe_4269405	gbh_af155653	NA	MatrixMating/PathCalling
162	cbe_251445	HPV 16 E6	NA	cbe_4269703	LOC51182	NA	MatrixMating/PathCalling
99	cbe_251445	HPV 16 E6	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling
163	cbe_251448	HPV 16 E7	NA	cbe_251468	Prey1628	NA	MatrixMating/PathCalling
164	cbe_251448	HPV 16 E7	NA	cbe_251502	Prey1609	NA	MatrixMating/PathCalling

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
165	cbe_251448	HPV 16 E7	NA	cbe_422236	BCR1	NA	MatrixMating/PathCalling
166	cbe_251448	HPV 16 E7	NA	cbe_2693325	Prey1673	NA	MatrixMating/PathCalling
167	cbe_251448	HPV 16 E7	NA	cbe_2898065	Prey1620	NA	MatrixMating/PathCalling
168	cbe_251448	HPV 16 E7	NA	cbe_3474077	KRT4	NA	MatrixMating
169	cbe_251448	HPV 16 E7	NA	cbe_3773649	EEF1A1L14	NA	MatrixMating/PathCalling
170	cbe_251448	HPV 16 E7	NA	cbe_3787129	LOC55828	NA	MatrixMating/PathCalling
171	cbe_251448	HPV 16 E7	NA	cbe_3789063	AP2M1	NA	MatrixMating/PathCalling
172	cbe_251448	HPV 16 E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating
173	cbe_251448	HPV 16 E7	NA	cbe_3921620	MPP3	AT	MatrixMating/PathCalling
174	cbe_251448	HPV 16 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
175	cbe_251448	HPV 16 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating
176	cbe_251448	HPV 16 E7	NA	cbe_4268611	NDUFS3	SMT	MatrixMating/PathCalling
177	cbe_251448	HPV 16 E7	NA	cbe_4268684	MIZF	NA	MatrixMating/PathCalling
178	cbe_251448	HPV 16 E7	NA	cbe_4268740	ZNF-U69274	NA	MatrixMating/PathCalling
179	cbe_251448	HPV 16 E7	NA	cbe_4269658	PSMC1	NA	MatrixMating/PathCalling
180	cbe_251448	HPV 16 E7	NA	cbe_4269876	SBP2	NA	MatrixMating/PathCalling
181	cbe_251448	HPV 16 E7	NA	cbe_4270186	STX4A	AT	MatrixMating/PathCalling
182	cbe_251737	HPV 16 L2	NA	cbe_422227	Prey277610	NA	PathCalling
183	cbe_251737	HPV 16 L2	NA	cbe_422247	Prey277642	NA	PathCalling
184	cbe_251737	HPV 16 L2	NA	cbe_3056756	KIAA0440	NA	MatrixMating/PathCalling
185	cbe_251737	HPV 16 L2	NA	cbe_3473488	gbh_al121903	NA	PathCalling
186	cbe_251737	HPV 16 L2	NA	cbe_3575702	SU11	NA	PathCalling
187	cbe_251737	HPV 16 L2	NA	cbe_3663966	KIAA1389	NA	PathCalling
188	cbe_251737	HPV 16 L2	NA	cbe_3849002	HSPC224	AT	PathCalling
189	cbe_251737	HPV 16 L2	NA	cbe_3884811	Hs.30289	NA	PathCalling

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
190	cbe_251737	HPV 16 L2	NA	cbe_4268684	MIZF	NA	MatrixMating
191	cbe_251737	HPV 16 L2	NA	cbe_4270335	KIAA0276	NA	PathCalling

Table 7. HPV1a, HPV 11, and HPV 16 specific interactions

INT ID	cbe_SEQ ID Interactor A	COMMON NAME INT A	PT/AT/SMT/NA	cbe_SEQ ID Interactor B	COMMON NAME INT B	PT/AT/SMT/NA	PathCalling Screen and/or Matrix Assay
34	cbe_250834	HPV 11 E7	NA	cbe_250878	Prey302	NA	MatrixMating/PathCalling
35	cbe_250834	HPV 11 E7	NA	cbe_250883	Prey244	NA	MatrixMating/PathCalling
36	cbe_250834	HPV 11 E7	NA	cbe_250888	Prey228	NA	MatrixMating/PathCalling
37	cbe_250834	HPV 11 E7	NA	cbe_3056756	KIAA0440	NA	MatrixMating/PathCalling
38	cbe_250834	HPV 11 E7	NA	cbe_3454406	gbh_af252829	NA	MatrixMating/PathCalling
39	cbe_250834	HPV 11 E7	NA	cbe_3760926	gbh_al359334	NA	MatrixMating/PathCalling
40	cbe_250834	HPV 11 E7	NA	cbe_3845697	Hs.191063	NA	MatrixMating/PathCalling
41	cbe_250834	HPV 11 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
42	cbe_250834	HPV 11 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating/PathCalling
43	cbe_250834	HPV 11 E7	NA	cbe_4268935	RPL26	NA	MatrixMating/PathCalling
44	cbe_250834	HPV 11 E7	NA	cbe_4269451	gbh_af038189	NA	MatrixMating/PathCalling
45	cbe_250834	HPV 11 E7	NA	cbe_4269681	Hs.224712	NA	MatrixMating/PathCalling
46	cbe_250834	HPV 11 E7	NA	cbe_4269818	Hs.73680	NA	MatrixMating/PathCalling
47	cbe_250834	HPV 11 E7	NA	cbe_4270015	RPS26	NA	MatrixMating/PathCalling
48	cbe_250834	HPV 11 E7	NA	cbe_4270441	Prey1052970	NA	PathCalling
49	cbe_250834	HPV 11 E7	NA	cbe_4280774	ITGB4	AT/PT	MatrixMating/PathCalling
163	cbe_251448	HPV 16 E7	NA	cbe_251468	Prey1628	NA	MatrixMating/PathCalling
164	cbe_251448	HPV 16 E7	NA	cbe_251502	Prey1609	NA	MatrixMating/PathCalling

165	cbe_251448	HPV 16 E7	NA	cbe_422236	BCR1	NA	MatrixMating/PathCalling
166	cbe_251448	HPV 16 E7	NA	cbe_2693325	Prey1673	NA	MatrixMating/PathCalling
167	cbe_251448	HPV 16 E7	NA	cbe_2898065	Prey1620	NA	MatrixMating/PathCalling
168	cbe_251448	HPV 16 E7	NA	cbe_3474077	KRT4	NA	MatrixMating
169	cbe_251448	HPV 16 E7	NA	cbe_3773649	EEF1A1L14	NA	MatrixMating/PathCalling
170	cbe_251448	HPV 16 E7	NA	cbe_3787129	LOC55828	NA	MatrixMating/PathCalling
171	cbe_251448	HPV 16 E7	NA	cbe_3789063	AP2M1	NA	MatrixMating/PathCalling
172	cbe_251448	HPV 16 E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating
173	cbe_251448	HPV 16 E7	NA	cbe_3921620	MPP3	AT	MatrixMating/PathCalling
174	cbe_251448	HPV 16 E7	NA	cbe_4260642	PTPN21	SMT	MatrixMating/PathCalling
175	cbe_251448	HPV 16 E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating
176	cbe_251448	HPV 16 E7	NA	cbe_4268611	NDUFS3	SMT	MatrixMating/PathCalling
177	cbe_251448	HPV 16 E7	NA	cbe_4268684	MIZF	NA	MatrixMating/PathCalling
178	cbe_251448	HPV 16 E7	NA	cbe_4268740	ZNF-U69274	NA	MatrixMating/PathCalling
179	cbe_251448	HPV 16 E7	NA	cbe_4269658	PSMC1	NA	MatrixMating/PathCalling
180	cbe_251448	HPV 16 E7	NA	cbe_4269876	SBP2	NA	MatrixMating/PathCalling
181	cbe_251448	HPV 16 E7	NA	cbe_4270186	STX4A	AT	MatrixMating/PathCalling
427	cbe_251925	HPV 1a E7	NA	cbe_251953	Prey2724	NA	MatrixMating/PathCalling
428	cbe_251925	HPV 1a E7	NA	cbe_3753270	gbh_ac004503	NA	MatrixMating/PathCalling
429	cbe_251925	HPV 1a E7	NA	cbe_3760926	gbh_al359334	NA	MatrixMating/PathCalling
430	cbe_251925	HPV 1a E7	NA	cbe_3789063	AP2M1	NA	MatrixMating
431	cbe_251925	HPV 1a E7	NA	cbe_3810032	gbh_af142421	NA	MatrixMating/PathCalling
432	cbe_251925	HPV 1a E7	NA	cbe_3820530	PGAM1	SMT	MatrixMating/PathCalling
309	cbe_251925	HPV 1a E7	NA	cbe_3834015	TFPI	AT/PT	MatrixMating
433	cbe_251925	HPV 1a E7	NA	cbe_4265947	RBP4	AT/PT	MatrixMating/PathCalling
434	cbe_251925	HPV 1a E7	NA	cbe_4267526	HRIHFB2206	NA	MatrixMating/PathCalling

In certain embodiments, the first polypeptide is labeled. In other embodiments, the second polypeptide is labeled, while in some embodiments, both the first and second polypeptides are labeled. Labeling can be performed using any art-recognized method for labeling polypeptides. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

The invention also includes complexes of two or more polypeptides in which at least one of the polypeptides is present as a fragment of a complex-forming polypeptide according to the invention. For example, one or more polypeptides may include an amino acid sequence sufficient to bind to its corresponding polypeptide. A binding domain of a given first polypeptide can be any number of amino acids sufficient to specifically bind to, and complex with, the corresponding second polypeptide under conditions suitable for complex formation. The binding domain can be the minimal number of amino acids required to retain binding affinity, or may be a larger fragment or derivative of the polypeptides listed in Tables 1 through 7, columns 2 and 5.

Procedures for identifying binding domains can be readily identified by one of ordinary skill in the art including the procedures described herein. For example, nucleic acid sequences containing various portions of a "bait" protein can be tested in a yeast two hybrid screening assay in combination with a nucleic acid encoding the corresponding "prey" protein.

In certain embodiments, the "bait" polypeptide of the complex are HPV derived proteins L1, L2, E2, E4, E5, E6 and E7. In some embodiments the "prey" protein of the complex are identified as cellular proliferation and transformation proteins, proteins involved in protein synthesis, folding or turnover and vesicle trafficking molecules when screened against several human prey libraries.

In other embodiments, the complexes are human ortholog complexes, chimeric complexes, or specific complexes implicated in fungal pathways, as discussed in detail below.

Polypeptides forming the complexes according to the invention can be made using techniques known in the art. For example, one or more of the polypeptides in the complex can be chemically synthesized using art-recognized methods for polypeptide synthesis. These methods are common in the art, including synthesis using a peptide synthesizer. See, *e.g.*, *Peptide Chemistry, A Practical Textbook*, Bodansky, Ed. Springer-Verlag, 1988; Merrifield, *Science* 232: 241-247 (1986); Barany, *et al*, *Intl. J. Peptide Protein Res.* 30: 705-739 (1987); Kent, *Ann. Rev. Biochem.* 57:957-989 (1988), and Kaiser, *et al*, *Science* 243: 187-198 (1989).

Alternatively, polypeptides can be made by expressing one or both polypeptides from a nucleic acid and allowing the complex to form from the expressed polypeptides. Any known nucleic acids that express the polypeptides, whether yeast or human (or chimerics of these polypeptides) can be used, as can vectors and cells expressing these polypeptides. Sequences of yeast ORFs and human polypeptides as referenced in Tables 3 and 7 are publicly available, *e.g.* at the *Saccharomyces* Genome Database (SGD) and GenBank (*see, e.g.* Hudson *et al.*, *Genome Res.* 7: 1169-1173 (1997)). If desired, the complexes can then be recovered and isolated.

Recombinant cells expressing the polypeptide, or a fragment or derivative thereof, may be obtained using methods known in the art, and individual gene product or complex may be isolated and analyzed (*See, e.g.*, *e.g.*, as described in Sambrook *et al.*, eds., *MOLECULAR CLONING: A LABORATORY MANUAL*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY*, John Wiley & Sons, New York, NY, 1993). This is achieved by assays that are based upon the physical and/or functional properties of the protein or complex. The assays can include, *e.g.*, radioactive labeling of one or more of the polypeptide complex components, followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled products. Polypeptide complex may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the proteins/protein complex). These methods can include, *e.g.*, column chromatography (*e.g.*, ion exchange, affinity, gel exclusion, reverse-phase, high pressure, fast protein liquid, etc), differential centrifugation, differential solubility, or similar methods used for the purification of proteins.

Combinatorial libraries recognized in the art may be used to provide "prey" proteins. In a preferred embodiment, a keratinocyte library, one of the cell types from tissues normally infected by HPV strains is disclosed.

Complexes Useful for Identifying HPV Infection

5 The invention further provides complexes of polypeptides useful, *inter alia*, in identifying agents that inhibit viral proliferation and cell proliferation leading to cancer.

There have been recent breakthroughs in vaccine and immunotherapy for HPV infection (Koutsky, Ault et al. 2002), these therapeutic modes are still under investigation. If these, or other new modalities of therapy prove to be successful in treating HPV infection, it will be
10 necessary to stage and monitor the progression of HPV-induced disease and the course of treatment. The tools described herein are certain to have utility for assessing the stage of disease and the success of treatment.

Protein interactions which are useful for identifying HPV infection are considered below.

Protein interactions that are unique to HPV1a may be used, for example, in a diagnostic
15 embodiment to determine if an infection by HPV is of a potentially cancer causing nature or not. An interaction that is unique to HPV 1a indicates that the infection is not of a kind that is known to cause cancer or cervical lesions. In one embodiment, an ELISA assay that uses an antibody against one of the non-viral proteins indicated in Tables 1 through 7 as a first antibody and an antibody specific for a virally encoded protein may be used to determine if an infection is
20 actively producing viral protein. Those interactions (indicated "INT ID") that correspond to the interaction between a protein encoded by the nucleotide sequence indicated by a SEQ ID for Interactor A ("SEQ ID INT A") with the protein encoded by the nucleic acid represented by a SEQ ID for Interactor B ("SEQ ID INT B"), one or both of which may have a common name (indicated "COMMON NAME INT A"; "COMMON NAME INT B") one or both of which may
25 have utility as a protein therapeutic (PT), antibody target (AT), or a small molecule target (SMT), and/or may have a therapeutic utility for in indication that may or may not directly involve the interaction of HPV1a, HPV11, HPV16, a combination of the these viruses, or members of the family of viruses they represent (those that cause warts, non-cancerous lesions, or cancerous lesions of the anal-genital tract, and/or head/neck/oral cancers or the non-cancerous
30 versions of the same and the like)(NA). In all cases the interactions have application in the diagnosis of any HPV infections and conditions induced by such infections, active or latent.

Interactions with any one or more PT, AT, SMT, and/or NA for which there exists or may be developed a molecule that therapeutically affects any one or more of the indicated proteins in an interaction with one or more HPV proteins of the strains listed or family members of such viruses may be used as a therapeutic agent for the treatment of HPV infections and/or the conditions caused directly or indirectly by HPV infection

Chimeric Polypeptides, DNA, Vectors and Recombinant Cells

In a further aspect, the invention provides a chimeric polypeptide that includes sequences of two interacting proteins according to the invention. The interacting proteins can be, *e.g.*, the interacting protein pairs disclosed in Tables 1-7, herein. Also included are chimeric polypeptides including multimers, *i.e.*, sequences from two or more pairs of interacting proteins. An example of such a chimeric polypeptide is a polypeptide that includes amino acid sequences from INT A and INT B, and from INT ID Interactor A and INT ID Interactor B. The chimeric polypeptide includes a region of a first protein covalently linked, *e.g.* via peptide bond, to a region of a second protein.

In some embodiments, the chimeric polypeptide(s) of the complex include(s) six or more amino acids of a first protein covalently linked to six or more amino acids of a second protein. In other embodiments, the chimeric polypeptide includes at least one binding domain of a first or second protein.

Preferably, the chimeric polypeptide includes a region of amino acids of the first polypeptide able to bind to a second polypeptide. Alternatively, or in addition, the chimeric polypeptide includes a region of amino acids of the second polypeptide able to bind to the first polypeptide.

Nucleic acid encoding the chimeric polypeptide, as well as vectors and cells containing these nucleic acids, are within the scope of the present invention. The chimeric polypeptides can be constructed by expressing nucleic acids encoding chimeric polypeptides using recombinant methods, described above, then recovering the chimeric polypeptides, or by chemically synthesizing the chimeric polypeptides. Host-vector systems that can be used to express chimeric polypeptides include, *e.g.*: (i) mammalian cell systems which are infected with vaccinia virus, adenovirus; (ii) insect cell systems infected with baculovirus; (iii) yeast containing yeast vectors or (iv) bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA.

Depending upon the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

The expression of the specific proteins may be controlled by any promoter/enhancer known in the art including, *e.g.*: (i) the SV40 early promoter (see *e.g.*, Bernoist & Chambon, *Nature* 290: 304-310 (1981)); (ii) the promoter contained within the 3'-terminus long terminal repeat of Rous Sarcoma Virus (see *e.g.*, Yamamoto, *et al.*, *Cell* 22: 787-797 (1980)); (iii) the Herpesvirus thymidine kinase promoter (see *e.g.*, Wagner, *et al.*, *Proc. Natl. Acad. Sci. USA* 78: 1441-1445 (1981)); (iv) the regulatory sequences of the metallothionein gene (see *e.g.*, Brinster, *et al.*, *Nature* 296: 39-42 (1982)); (v) prokaryotic expression vectors such as the β -lactamase promoter (see *e.g.*, Villa-Kamaroff, *et al.*, *Proc. Natl. Acad. Sci. USA* 75: 3727-3731 (1978)); (vi) the *tac* promoter (see *e.g.*, DeBoer, *et al.*, *Proc. Natl. Acad. Sci. USA* 80: 21-25 (1983)).

Plant promoter/enhancer sequences within plant expression vectors may also be utilized including, *e.g.*: (i) the nopaline synthetase promoter (see *e.g.*, Herrar-Estrella, *et al.*, *Nature* 303: 209-213 (1984)); (ii) the cauliflower mosaic virus 35S RNA promoter (see *e.g.*, Garder, *et al.*, *Nuc. Acids Res.* 9: 2871 (1981)) and (iii) the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (see *e.g.*, Herrera-Estrella, *et al.*, *Nature* 310: 115-120 (1984)).

Promoter/enhancer elements from yeast and other fungi (*e.g.*, the Gal4 promoter, the alcohol dehydrogenase promoter, the phosphoglycerol kinase promoter, the alkaline phosphatase promoter), as well as the following animal transcriptional control regions, which possess tissue specificity and have been used in transgenic animals, may be utilized in the production of proteins of the present invention.

Other animal transcriptional control sequences derived from animals include, *e.g.*: (i) the insulin gene control region active within pancreatic β -cells (see *e.g.*, Hanahan, *et al.*, *Nature* 315: 115-122 (1985)); (ii) the immunoglobulin gene control region active within lymphoid cells (see *e.g.*, Grosschedl, *et al.*, *Cell* 38: 647-658 (1984)); (iii) the albumin gene control region active within liver (see *e.g.*, Pinckert, *et al.*, *Genes and Devel.* 1: 268-276 (1987)); (iv) the myelin basic protein gene control region active within brain oligodendrocyte cells (see *e.g.*, Readhead, *et al.*, *Cell* 48: 703-712 (1987)); and (v) the gonadotrophin-releasing hormone gene control region active within the hypothalamus (see *e.g.*, Mason, *et al.*, *Science* 234: 1372-1378 (1986)).

The vector may include a promoter operably-linked to nucleic acid sequences which encode a chimeric polypeptide, one or more origins of replication, and optionally, one or more

selectable markers (*e.g.*, an antibiotic resistance gene). A host cell strain may be selected which modulates the expression of chimeric sequences, or modifies/processes the expressed proteins in a desired manner. Moreover, different host cells possess characteristic and specific mechanisms for the translational and post-translational processing and modification (*e.g.*, glycosylation, phosphorylation, and the like) of expressed proteins. Appropriate cell lines or host systems may thus be chosen to ensure the desired modification and processing of the foreign protein is achieved. For example, protein expression within a bacterial system can be used to produce an unglycosylated core protein; whereas expression within mammalian cells ensures "native" glycosylation of a heterologous protein.

10 **Antibodies Specific for Polypeptide Complexes**

The invention further provides antibodies and antibody fragments (such as Fab or (Fab)₂ fragments) that bind specifically to the complexes described herein. By "specifically binds" is meant an antibody that recognizes and binds to a particular polypeptide complex of the invention, but which does not substantially recognize or bind to other molecules in a sample, or to any of the polypeptides of the complex when those polypeptides are not complexed.

For example, a purified complex, or a portion, variant, or fragment thereof, can be used as an immunogen to generate antibodies that specifically bind the complex using standard techniques for polyclonal and monoclonal antibody preparation.

A full-length polypeptide complex can be used, if desired. Alternatively, the invention provides antigenic fragments of polypeptide complexes for use as immunogens. In some embodiments, the antigenic complex fragment includes at least 6, 8, 10, 15, 20, or 30 or more amino acid residues of a polypeptide. In one embodiment, epitopes encompassed by the antigenic peptide include the binding domains of the polypeptides, or are located on the surface of the protein, *e.g.*, hydrophilic regions.

If desired, peptides containing antigenic regions can be selected using hydropathy plots showing regions of hydrophilicity and hydrophobicity. These plots may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, *Proc. Nat. Acad. Sci. USA* 78:3824-3828 (1981); Kyte and Doolittle, *J. Mol. Biol.* 157:105-142 (1982).

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an

antigen binding site that specifically binds (immunoreacts with) an antigen, such as a polypeptide complex. Such antibodies include, e.g., polyclonal, monoclonal, chimeric, single chain, Fab and F(ab')₂ fragments, and an Fab expression library. In specific embodiments, antibodies to human ortholog complexes.

5 Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies. For example, for the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed
10 polypeptide complex. Alternatively, the immunogenic polypeptides or complex may be chemically synthesized, as discussed above. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, e.g., Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human
15 adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against complex can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

 The term "monoclonal antibody" or "monoclonal antibody composition", as used herein,
20 refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide complex. A monoclonal antibody composition thus typically displays a single binding affinity for a particular protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular complex, or polypeptide, any technique that provides for the production of antibody
25 molecules by continuous cell line culture may be utilized. Such techniques include, e.g., the hybridoma technique (see Kohler & Milstein, *Nature* 256: 495-497 (1975)); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, *Immunol Today* 4: 72 (1983)); and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, In: *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., (1985) pp. 77-96). If
30 desired, human monoclonal antibodies may be prepared by using human hybridomas (see Cote, *et al.*, *Proc. Natl. Acad. Sci. USA* 80: 2026-2030 (1983)) or by transforming human B-cells with

Epstein Barr Virus *in vitro* (see Cole, *et al.*, In: *Monoclonal Antibodies and Cancer Therapy*, *supra*).

Methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*, *Science* 246: 1275-1281 (1989)) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for the desired protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polypeptide or polypeptide complex may be produced by techniques known in the art including, *e.g.*: (i) an F_(ab)₂ fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_(ab)₂ fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Chimeric and humanized monoclonal antibodies against the polypeptide complexes, or polypeptides, described herein are also within the scope of the invention, and can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.*, *Science* 240: 1041-1043 (1988); Liu *et al.*, *Proc. Nat. Acad. Sci. USA* 84: 3439-3443 (1987); Liu *et al.*, *J. Immunol.* 139: 3521-3526 (1987); Sun *et al.*, *Proc. Nat. Acad. Sci. USA* 84: 214-218 (1987); Nishimura *et al.*, *Cancer Res.* 47: 999-1005 (1987); Wood *et al.*, *Nature* 314: 446-449 (1985); Shaw *et al.*, *J. Natl. Cancer Inst.* 80: 1553-1559 (1988); Morrison, *Science* 229: 1202-1207 (1985); Oi *et al.*, *BioTechniques* 4: 214 (1986); U.S. Pat. No. 5,225,539; Jones *et al.*, *Nature* 321: 552-525 (1986); Verhoevan *et al.*, *Science* 239: 1534 (1988); and Beidler *et al.*, *J. Immunol.* 141: 4053-4060 (1988).

Methods for the screening of antibodies that possess the desired specificity include, *e.g.*, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. For example, selection of antibodies that are specific to a particular domain of a polypeptide complex is facilitated by generation of hybridomas that bind to the complex, or fragment thereof, possessing such a domain.

In certain embodiments of the invention, antibodies specific for the polypeptide complexes described herein may be used in various methods, such as detection of complex, and identification of agents which disrupt complexes. These methods are described in more detail, below. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

Polypeptide complex-specific, or polypeptide-specific antibodies, can also be used to isolate complexes using standard techniques, such as affinity chromatography or immunoprecipitation. Thus, the antibodies disclosed herein can facilitate the purification of specific polypeptide complexes from cells, as well as recombinantly produced complexes expressed in host cells.

Kits

In a specific embodiment, the invention provides kits containing a reagent, for example, an antibody described above, which can specifically detect a polypeptide complex, or a constituent polypeptide, described herein. Such kits can contain, for example, reaction vessels, reagents for detecting complex in sample, and reagents for development of detected complex, *e.g.* a secondary antibody coupled to a detectable marker. The label incorporated into the anti-complex, or anti-polypeptide antibody may include, *e.g.*, a chemiluminescent, enzymatic, fluorescent, colorimetric or radioactive moiety. Kits of the present invention may be employed in diagnostic and/or clinical screening assays.

Pharmaceutical Compositions

The invention further provides pharmaceutical compositions of purified complexes suitable for administration to a subject, most preferably, a human, in the treatment of disorders involving altered levels of such complexes. Such preparations include a therapeutically-effective

amount of a complex, and a pharmaceutically acceptable carrier. As utilized herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopoeia or other generally recognized pharmacopoeia for use in animals and, more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered and includes, but is not limited to such sterile liquids as water and oils.

The therapeutic amount of a complex which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and may be determined by standard clinical techniques by those of average skill within the art. In addition, *in vitro* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the overall seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. However, suitable dosage ranges for intravenous administration of the complexes of the present invention are generally about 20-500 micrograms (μg) of active compound per kilogram (Kg) body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems. Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

Various delivery systems are known and can be used to administer a pharmaceutical preparation of a complex of the invention including, e.g.: (i) encapsulation in liposomes, microparticles, microcapsules; (ii) recombinant cells capable of expressing the polypeptides of the complex; (iii) receptor-mediated endocytosis (*see, e.g., Wu et al., J. Biol. Chem.* 262: 4429-4432 (1987)); (iv) construction of a nucleic acid encoding the polypeptides of the complex as part of a retroviral or other vector, and the like.

Methods of administration include, e.g., intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The pharmaceutical preparations of the present invention may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other

biologically-active agents. Administration can be systemic or local. In addition, it may be advantageous to administer the pharmaceutical preparation into the central nervous system by any suitable route, including intraventricular and intrathecal injection. Intraventricular injection may be facilitated by an intraventricular catheter attached to a reservoir (*e.g.*, an Ommaya reservoir). Pulmonary administration may also be employed by use of an inhaler or nebulizer, and formulation with an aerosolizing agent. It may also be desirable to administer the pharmaceutical preparation locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, by injection, by means of a catheter, by means of a suppository, or by means of an implant. In a specific embodiment, administration may be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

Alternatively, pharmaceutical preparations of the invention may be delivered in a vesicle, in particular a liposome, (*see, e.g.*, Langer, *Science* 249:1527-1533 (1990)) or via a controlled release system including, *e.g.*, a delivery pump (*see, e.g.*, Saudek, *et al.*, *New Engl. J. Med.* 321: 574 (1989) and a semi-permeable polymeric material (*see, e.g.*, Howard, *et al.*, *J. Neurosurg.* 71: 105 (1989)). Additionally, the controlled release system can be placed in proximity of the therapeutic target (*e.g.*, the brain), thus requiring only a fraction of the systemic dose. *See, e.g.*, Goodson, In: *Medical Applications of Controlled Release*, 1984 (CRC Press, Boca Raton, FL).

Screening, Diagnostic, and Therapeutic Methods

The invention further provides methods of identifying an agent which modulate formation or stability a polypeptide complex described herein. By modulate is meant to increase or decrease the rate at which the complex is assembled or disassembled, or to increase or decrease the stability of an assembled complex. Thus, an agent can be tested for its ability to disrupt a complex, or to promote formation or stability of a complex.

In one embodiment, the invention provides a method of identifying an agent that promotes disruption of a complex. The method includes providing a polypeptide complex, contacting the complex with a test agent, and detecting the presence of a polypeptide displaced from the complex. The presence of displaced polypeptide indicates the disruption of the complex by the agent. In some embodiments, the complex is a human ortholog complex, as described above, which includes "bait" and "prey" proteins selected from those recited in Tables 4 through 7. Agents which disrupt complexes of the invention may present novel modulators of

cell processes and pathways in which the complexes participate. For example, agents which disrupt complexes involving EGFR proteins, DLG, ubiquitin 9 or may be selected as potential HPV therapeutics. In another embodiment, agents which modulate the activity of BCR1, GAP or other effectors of CDC42-pathways are encompassed by the invention.

5 Any compound or other molecule (or mixture or aggregate thereof) can be used as a test agent. In some embodiments, the agent can be a small peptide, or other small molecule produced by *e.g.*, combinatorial synthetic methods known in the art. Disruption of the complex by the test agent, *e.g.* binding of the agent to the complex, can be determined using art recognized methods, *e.g.*, detection of polypeptide using polypeptide-specific antibodies, as described above. Bound
10 agents can alternatively be identified by comparing the relative electrophoretic mobility of complexes exposed to the test agent to the mobility of complexes that have not been exposed to the test agent.

Agents identified in the screening assays can be further tested for their ability to alter and/or modulate cellular functions, particularly those functions in which the complex has been
15 implicated. These functions include, *e.g.*, control of cell-cycle progression; regulation of transcription; control of intracellular signal transduction, etc., as described in detail above.

In another embodiment, the invention provides methods for inhibiting the interaction of a polypeptide with a ligand, by contacting a complex of the protein and the ligand with an agent that disrupts the complex, as described above. In certain embodiments, the polypeptides are
20 associated with protein synthesis, folding or turnover and vesicle trafficking molecules. In certain embodiments, the ligand is an interacting polypeptide, and the polypeptide and ligands are selected from those recited in Tables 1-7, preferably Tables 4-7, and most preferably interactions involving HPV 16. Inhibition of complex formation allows for modulation of cellular functions and pathways in which the targeted complexes participate.

25 In another embodiment, the invention provides a method for identifying a polypeptide complex in a subject. The method includes the steps of providing a biological sample from the subject, detecting, if present, the level of polypeptide complex. In some embodiments, the complex includes a first polypeptide (a "bait" polypeptide) selected from the polypeptides recited in Tables 4-7, column 2 or 3, and a second polypeptide ("prey" polypeptide) selected from the
30 polypeptides recited in Tables 4-7, column 5 or 6. Any suitable biological sample potentially containing the complex may be employed, *e.g.* blood, urine, cerebral-spinal fluid, plasma, skin,

etc. Complexes may be detected by, *e.g.*, using complex-specific antibodies as described above. The method provides for diagnostic screening, including in the clinical setting, using, *e.g.*, the kits described above.

In still another embodiment, the present invention provides methods for detecting a polypeptide in a biological sample, by providing a biological sample containing the polypeptide, contacting the sample with a corresponding polypeptide to form a complex under suitable conditions, and detecting the presence of the complex. A complex will form if the sample does, indeed, contain the first polypeptide. In some embodiments, the polypeptide being detecting is a “prey” protein selected from the polypeptides recited in Tables 1 through 7, columns 2 or 3, and is detected by complexing with the corresponding “bait” protein recited in Tables 1-7, column 5 or 6. Conversely, in other embodiments the polypeptide being detected is the “bait” protein. Alternatively, a yeast “bait” or “prey” ortholog may be employed to form a chimeric complex with the polypeptide in the biological sample.

In still another embodiment, the invention provides methods for removing a first polypeptide from a biological sample by contacting the biological sample with the corresponding second peptide to form a complex under conditions suitable for such formation. The complex is then removed from the sample, effectively removing the first polypeptide. As with the methods of detecting polypeptide described above, the polypeptide being removed may be either a “bait” or “prey” protein, and the second corresponding polypeptide used to remove it may be either a yeast or human ortholog polypeptide.

Methods of determining altered expression of a polypeptide in a subject, *e.g.* for diagnostic purposes, are also provided by the invention. Altered expression of proteins involved in cell processes and pathways can lead to deleterious effects in the subject. Altered expression of a polypeptide in a given pathway leads to altered formation of complexes which include the polypeptide, hence providing a means for indirect detection of the polypeptide level. The method involves providing a biological sample from a subject, measuring the level of a polypeptide complex of the invention in the sample, and comparing the level to the level of complex in a reference sample having known polypeptide expression. A higher or lower complex level in the sample versus the reference indicates altered expression of either of the polypeptides that forms the complex. The detection of altered expression of a polypeptide can be used to diagnose a given disease state, and or used to identify a subject with a predisposition for a

disease state. Any suitable reference sample may be employed, but preferably the test sample and the reference sample are derived from the same medium, *e.g.* both are urine, etc. The reference sample should be suitably representative of the level polypeptide expressed in a control population.

5 The invention further provides methods for treating or preventing a disease or disorder involving altered levels of a polypeptide complex, or polypeptide, disclosed herein, by administering to a subject a therapeutically-effective amount of at least one molecule that modulates the function of the complex. As discussed above, altered levels of polypeptide complexes described herein may be implicated in disease states resulting from a deviation in
10 normal function of the pathway in which a complex is implicated. For example, altered levels of the observed complex between E6 or E7 and DLG tumor suppressor or Ubiquitin protease 9 may be implicated in abrogation of p53 interactions. In subjects with a deleteriously high level of complex, modulation may consist, for example, by administering an agent which disrupts the complex, or an agent which does not disrupt, but down-regulates, the functional activity of the
15 complex. Alternatively, modulation in subjects with a deleteriously low level of complex may be achieved by pharmaceutical administration of complex, constituent polypeptide, or an agent which up-regulates the functional activity of complex. Pharmaceutical preparations suitable for administration of complex are described above.

 In one embodiment, a disease or disorder involving altered levels of a polypeptide
20 selected from the polypeptides recited in Tables 1 through 7 or the corresponding polypeptides in columns 2 or 5, are treated by administering a molecule that modulates the function of the polypeptide. In certain embodiments, the modulating molecule is the corresponding polypeptide, *e.g.* administering a “prey” protein corresponding to a “bait” protein modulates the latter by forming a complex with it.

25 The details of one or more embodiments of the invention are set forth in the description above. Although any methods and materials similar or equivalent to those described herein can be used in the practice of the present invention, the preferred methods and materials are now described. For example, additional interactions can be identified using other two-hybrid systems (*i.e.* using a LexA binding domain fusion or *HIS3* as a reporter gene), including variables such as
30 different protein domains or genomic activation domain libraries. Other features, objects, and advantages of the invention will be apparent from the description and from the claims.

The practice of the present invention generally employs conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See for example J. Sambrook et al., "Molecular Cloning; A Laboratory Manual" (1989); "DNA Cloning", Vol. I and II (D. N. Glover ed., 1985); "Oligonucleotide Synthesis" (M. J. Gait ed., 1984); "Nucleic Acid Hybridization" (B. D. Hames and S. J. Higgins eds., 1984); "Transcription and Translation" (B. D. Hames & S. J. Higgins eds., 1984); "Animal Cell Culture" (R. I. Freshney ed., 1986); "Immobilized Cells and Enzymes" (IRL Press, 1986); "A Practical Guide to Molecular Cloning" (B. Perbal, 1984); the series, "Methods in Enzymology" (Academic Press, Inc.); "Gene Transfer Vectors for Mammalian Cells" (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Meth. Enzymol. (1987) 154 and 155 (Wu and Grossman, and Wu eds., respectively); "Immunochemical Methods in Cell and Molecular Biology" (Academic Press, London); "Protein Purification: Principles and Practice", Third Ed. (Scopes, Springer-Verlag, N.Y., 1994); and "Handbook of Experimental Immunology", Volumes I-IV (Weir and Blackwell, eds., 1986).

The following examples are presented in order to more fully illustrate the preferred embodiments of the invention. These examples should in no way be construed as limiting the scope of the invention, as defined by the appended claims.

Example 1 SeqCalling™ Technology

cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly was included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly

represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

Example 2 Identifying Nucleic Acids and Proteins by PathCalling™

5 The sequences of the HPV proteins and interactors in this application were derived by laboratory cloning of cDNA fragments and by *in silico* prediction of the sequence as described in Example A. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, were cloned. *In silico* prediction was based on sequences available in CuraGen's proprietary sequence databases or in the public human sequence databases, and
10 provided either the full-length DNA sequence, or some portion thereof.

cDNA libraries were derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that
15 regulate gene expression, for example, growth factors, chemokines or steroids.

Preparation of yeast cells

Yeast lysates were produced as follows: 1-1.5 ml samples from a yeast culture were removed, samples were frozen on dry ice. On ice, low-salt lysis Buffer was added to the cell pellets. Glass beads were added, the cells were resuspended by a brief vortexing. The cells were
20 lysed by beating the beads for 90 sec. The lysate was placed on ice for 5 min and the beads beaten again for 90 sec. The sample were put back on ice. Once the lysate was recovered free of beads, the lysate was centrifuge at maximum speed in a microcentrifuge for 3 to 5 min at 4°C and put back on ice. 25 to 50 µl were removed from the supernatant and mixed with an equal volume of 2X Protein Sample Buffer then saved for Western analysis.

Immunoprecipitation from yeast

The lysate samples were thawed and the desired volume (based on the protein concentration) were put into a fresh microcentrifuge tube. All the samples were made into the same volume with fresh low-salt lysis Buffer. Antibody was diluted in Low-Salt Lysis Buffer (10 µl per sample) and mixed by vortexing. This was incubated on ice for 30 min.

ProteinA-Sepharose/Antibody Binding

Protein A-Sepharose beads were equilibrated with low-salt lysis Buffer by suspending the beads in low-salt Buffer, centrifuging briefly to sediment the beads and removing the supernatant. This equilibration was repeated then a wash step was performed for 2 or 3 times. The Buffer-equilibrated beads were aliquoted into fresh 0.5 ml microcentrifuge tubes making
5 sure that all the tubes had an equal amount of beads. The antibody/extract mixture was centrifuged in a microcentrifuge at full speed for 1 min at 4°C. The supernatant was recovered and added to the proteinA-Sepharose. The mixture was mixed in an end-over-end rotator for 1 to 2 hr at 4°C then centrifuged briefly in a microcentrifuge (bringing the centrifuge up to full speed and then back down). The supernatant was removed. Keeping the samples on ice as much as
10 possible, the beads were washed by adding 400 µl of bead Buffer. The beads were resuspended and centrifuged again. The supernatant was removed. The beads were resuspended in bead Buffer and the mixture transferred to a fresh tube. The old tube was rinsed with more bead-Buffer to recover residual beads to the new tube. The beads were centrifuged, the supernatant removed and the beads washed with Bead Buffer.

15 If the immunoprecipitate is only for analysis of radio-labeled proteins bound, the beads can be simply resuspended in protein sample Buffer, boiled for 90 sec and electrophoresed. If an enzymatic assay of some sort is involved, the beads should be washed in the reaction Buffer 1 or 2 times

20 In cases where interactions cannot be validated in the yeast system, the interacting proteins are tagged with different epitopes at the N or the C-terminus and expressed in appropriate mammalian cell lines by transient transfection. The cells are grown for 48-72 h, lysed, and the substrate protein is immunoprecipitated using antibody specific to the epitope and analyzed by western blotting as described for the yeast system.

25 **Example 3 Yeast 2 Hybrid analysis of interactions**

The cDNA thus derived was then directionally cloned into the appropriate two-hybrid vector (Gal4-activation domain (Gal4-AD) fusion). Such cDNA libraries as well as commercially available cDNA libraries from Clontech (Palo Alto, CA) were then transferred from E.coli into a CuraGen Corporation proprietary yeast strain (disclosed in U. S. Patents
30 6,057,101 and 6,083,693, incorporated herein by reference in their entireties).

Gal4-binding domain (Gal4-BD) fusions of a CuraGen Corporation proprietary library of human sequences was used to screen multiple Gal4-AD fusion cDNA libraries resulting in the selection of yeast hybrid diploids in each of which the Gal4-AD fusion contains an individual cDNA. Each sample was amplified using the polymerase chain reaction (PCR) using non-specific primers at the cDNA insert boundaries.

Physical clone: the cDNA fragment derived by the screening procedure is a recombinant DNA covering the entire open reading frame. The cDNA was cloned into pACT2 plasmid (Clontech) and used to make the cDNA library. The recombinant plasmid was inserted into the host and selected by the yeast hybrid diploid generated during the screening procedure by the mating of both CuraGen Corporation proprietary yeast strains N106' and YULH (U. S. Patents 6,057,101 and 6,083,693) to provide the clones.

Interaction protein pairs are added to CuraGen's PathCalling™ Protein Interaction Database. This database allows for the discovery of novel pharmaceutical drug targets by virtue of their interactions and/or presence in pathologically related signaling pathways. Protein interactions are subsequently analyzed using bioinformatic tools within GeneScape™, which provides a means of visualization of binary protein interactions, protein complex formation, as well as complete cellular signaling pathways. Specifically, the sequences, which encode proteins identified by INT ID in Tables 1 through 3 were found to interact and resulted in the formation of a protein complex within a series of complexes resulting in identification of a protein interaction. The interaction is specifically relevant to HPV pathology. The specific interactions, which constitute the specific complexes, is useful for therapeutic intervention through the use of recombinant protein or antibody therapies, small molecule drugs, or gene therapy approaches. Protein interactions, which are identified through the mining of the PathCalling™ database, can be screened *in vitro* and *in vivo* to provide expression, functional, biochemical, and phenotypic information. Assays for expression, functional, biochemical, phenotypic, diagnostic, prognostic, monitoring of HPV-induced tumors' and/or lesions' response to therapy, immunization, therapeutic immunization, immunotherapy, tumor burden monitoring, ELISA assay to determine if an infection is active or latent, and the like may be used alone or in conjunction and include, but are not limited to the following technologies; RTQ-PCR, transfection of recombinant proteins, co-immunoprecipitation and mass spectrometry, FRET, Affinity Chromatography, Immunohistochemistry or Immunocytochemistry, gene CHIP hybridizations, antisense (i.e.

knock-down, knock-up), GeneCalling experiments, and/or biochemical assays (phosphorylation, dephosphorylation, protease, etc...).

Example D Protein-Protein Interactions

- 5 The amino acid sequences of the polypeptides involved in the novel protein-protein interactions and the nucleic acid sequences of the polynucleotides which encode them are listed below.

Protein SEQ IDs:

- 10 Table 10
SEQ ID NO:1
cbe_1380530 RPL13
ribosomal protein L13
length=211
- 15 MAPSRNGMVLKPHFHKDWQRRVATWFNQ PARKIRRRKARQAKARRIAPRPASGP IIRPIVR
CPTVRYHTKVRAGRGSLEELRVAGIHKKVARTIGISVDP RRRNKSTESLQTNVQRLKEY
RSKLILFPRKPSAPKKGDSSAEELKLATQLTGPVMPVRNVYKKEKARVITEEEKNFKAFA
SLRMARANARLFGIRAKRAKEAAEQDVEKKK
- 20 Table 11
SEQ ID NO:2
cbe_1469980 FLJ20259
hypothetical protein FLJ20259
length=776
- 25 MNNSLENTISFEEYIRVKARSVPQHRMKEFLDSLASKGPEALQEFQQTATTTMVYQQGGN
CIYTDSTE VAGSLLELACPVTTSVQPQTQQEQQIQVQQPQQVQVQVQVQQSPQQVSAQLS
PQLTVHQPT EQPIQVQVQIQGQAPQSAAPSIQTPSLQSPSPSQLQAAQIQVQHVAQQI
QAAEIP EEHI PHQQIQAQLVAGQSLAGGQQIQIQTVGALSPPPSQQGSPREGERRVGTAS
VLQPVKKRKVEMPITVSYAISGQPVATVLAI PQGQQQSYVSLRPDLLTVDSAHLYSATGT
30 ITSPGTGTW T I PVYSAQPRGDPQQQSITHIAI PQEAYNAVHVSGSPTALAAVKLEDDKEK
MVGTTSVVKNSHEEVVQTLANS LFPAQFMNGNIHIPVAVQAVAGTYQNTAQTVHIWDPQQ
QPQQQT PQEQTPPPQQQQQLQVTC SAQTVQVAEVEPQSQPQSPPELLLPNSLKPEEGLE
VWKNWAQTKNAELEKDAQNRLAPIGRRLRFQEDLISSAVAE LNYGLCLMTREARNGEG
EPYDPDVLYYIFLCIQKYL FENGRVDDIFSDLYYVRFT EWLHEVLKDVQPRVTP LGYVLP
35 SHVTEEMLWECKQLGAHSPSTLLTTL MFFNTKYFLLKTV DQHMKLAFSKVLRQT KKNPSN
PKDKSTSIRYLKALGIHQ TGQKVTD DMYAEQTENPENPLRCPIKLYDFYLFKCPQSVKGR
NDTFYLTPEPVVAPNSPIWYSVQPI SREQMGQMLTRILVIREIQEAIAVANASTMH
- 40 Table 12
SEQ ID NO:3
cbe_1505425 HCDI
HCDI protein
length=319
- 45 MGWRRKRVPQRGRKAPPPQLHGNINNNLYFPIRWRDRLHWDSNPAAECQRHEVTLVSRKP
GPGRITWDELAASGLPSCDAAVNLAGENILNPLRRWNETFQKEVLGSRLETTQLLAKAIT
KAPQPPKAWVLVTGVAYYQPSLTA EYDEDS PGGDFDFSNLVTKWEAAARLP GDSTRQVV
VRSGVVLGRGGGAMGHMLLPFRLGLGGPIGSGHQFPWIHIGDLA GILTHALEANHVHGV
LNGVAPSSATNAEFAQTLGAALGRRAFIPLPSAVVQAVFGRQRAIMLLEGQKVI PQR TLA

TGYQYSFPELGAALKEIVA

Table 13

SEQ ID NO:4

cbe_1710 QP-C

low molecular mass ubiquinone-binding protein (9.5kD)

length=93

MGREFGNLTRMRHVISYSLSPFEQRAYPHVFTKGIPNVLRRIRESFFRVVPQFVVFYLIY
TWGTEEFERSKRRIQLPMKMTNEQIRIMTVPCL

Table 14

SEQ ID NO:5

cbe_1796502 CTNND2

catenin (cadherin-associated protein), delta 2 (neural plakophilin-related
arm-repeat protein)

length=1225

MFARKPPGAAPLGAMPVPDQPSASEKTSSLSPLNTSNGDGSETETTSAILASVKEQEL
QFERLTRELEAERQIVASQLERCKLGSETGSMSSMSSAEEQFQWQSQDGQKDIEDELTTG
LELVDSICIRSLQESGILDPQDYSTGERPSLLSQSALQLNSKPEGSFQYPASYHSNQTAL
GETTPSQLPARGTQARATGQSFSQGTTSRAGHLAGPEPAPPPPPPPREPFPAPSLGSAFHL
PDAPPAAAAAALYYSSSTLPAPPRGGSPLAAPQGGSPTKLQRGGSAPGATYAAPRGSSP
KQSPSRLAKSYSTSSPINIVSSAGLSPIRVTSPTTVQSTISSSPIHQLSSTIGTYATLS
PTKRLVHASEQYSKHSQELYATATLQRPGLAAGSRASYSSQHGLGPELRALQSPEHHI
DPIYEDRVYQKPPMRSLSQSQGDPLPPAHTGTYRTSTAPSSPGVDSVPLQRTGSQHGPQN
AAAAATFQRASYAAGPASNYADPYRQLQYCPVESPYSKSGPALPPEGLARSPSIDSIQK
DPREFGWRDPDELPEVIQMLQHQPFSVQSNAAAYLQHLCFGDNKIKAEIRRQGGIQLLVDL
LDHRMTEVHRSACGALRNLVYKANDDNKIALKNCGGIPALVRLLRKTTDLEIRELVTGV
LWNLS SCDALKMPIIQDALAVLTNAVIIPHSGWENSPLQDDRKIQLHSSQVLRNATGCLR
NVSSAGEEARRRMRECDGLTDALLYVIQSALGSSEIDSKTVENCVCILRNLSYRLAAETS
QQQHMGTDDEL DGLLCGEANGKDAESSGCWGKKKKKKKSQDQWDGVGPLPDCAEPPKGIQM
LWHPISIVKPYLTLLSECSNPDTLEGAAGALQNLAAAGSWKWSVYIRAAVRKEKGLPIILVEL
LRIDNDRVVCATATLRNMA LDVRNKELIGKYAMRDLVHRLPGGNNNSNTASKAMSDDTV
TAVCCTLHEVITKNMENAKALRDAGGIEKLVGISKSKGDKHSPKVVKAAASQVLNSMWQYR
DLRSLYKKDGWSQYHFASSSTIERDRQRPYSSSRTPSISPVRVSPNNRSASAPASPREM
ISLKERKTDYECTGSNATYHGAKGEHTSRKDAMTAQNTGISTLYRNSYGAPAEDIKHNQV
SAQPVPPQEPSRKDYETYQPFQNSTRYNDESFFEDQVHHRPPASEYTMHLGLKSTGNYVDF
YSAARPYSELNYETSHYPASPD SWV

Table 15

SEQ ID NO:6

cbe_1807361 FLJ22729

hypothetical protein FLJ22729

length=158

MRGIYSSSVYLEEISSIISKMPKADFYVLEKTGLSIQNSSLFPILLHFHIMEAMLYALLN
KTFAQDQGHQVLSMNRNAVKGKHFELMIGDSRTSGKELVKQFLFDSILKADPRVFFPSDKI
VHYRQMFLLSTELQRVEELYDSSLQAIAFYELAVFDSQP

Table 16

SEQ ID NO:7

cbe_2253980 Prey1135

Homo sapiens, clone MGC:14302, mRNA, complete cds.

length=24

MHYSPDASTAFSSIAHITRDVNYG

Table 17

SEQ ID NO:8

cbe_244811 DGUOK

deoxyguanosine kinase

length=189

MAAGRLFLSRLRAPFSSMAKSPLEGVSSSRGLHAGRGPRRLSIEGNIAVGKSTFVKLLTK
TYPEWHVATEP VATWQNIQAAGTQKACTA QSLGNLLDMMYREPARWSYTFQTF SFLSRLK
5 VQLEPFPEKLLQARKPVQIFERSVYSRLHF EALMNI PVLVLVDVNDDFSEEVT KQEDLMR
EVNTFVKNL

Table 18

SEQ ID NO:9

cbe_250777 HPV 11 E4

Human papillomavirus 11 E4

length=108

MVVPIIGKYVMAAQLYVLLHLYLALY EKYPLL NLLHTPPHRPPPLQCPPAPRKTACRRRL
10 GSEHVDRLTTPCVWPTSDPWTVQSTTSSLTIT TSTKEGTTVTVQLRL

Table 19

SEQ ID NO:10

cbe_250781 HPV 11 E2

Human papillomavirus 11 E2

length=367

MEAI AKRLDACQDQLLELYEENSID IHHKIMHWKCIRLESVLLHKAKQMGLSHIGLQVVP
PLTVSETKGHNAIEMQMHLESLAKTQYGV EPWTLQDTSYEMWLT PPKRCFKKQGN TVEVK
25 FDGCEDNVMEYV VVWTHIYLQDNDSWVKVTSSVDAKGIYYTCGQFKTYVNFNKEAQKYGS
TNHWEVCYGSTVICSPASVSSTVREVSIAEPTTYTPAQTTAPTVSACTTEDGVSAPPRKR
ARGPSTNNTLCVANIRSVDSTINNIVTDNY NKHQRRNNCHSAATPIVQLQGDSNCLKCFR
YRLNDKYKHLFELASSTWHWASPEAPHKNAIVTLTYSSEEQRQQFLNSVKI PPTIRHKVG
FMSLHLL

Table 20

SEQ ID NO:11

cbe_250808 HPV 11 E6

Human papillomavirus 11 E6

length=150

MESKDA TSATSIDQLCKTFNLSLHTLQIQCVFCRNALT TAEIYAYAYKNLKV VWRDNFP
35 FAACACCLELQKINQYRHFNYAAYAPTVEETNEDILKVLIRCYLCHKPLCEIEKLKHI
LGKARFIKLNNQWKGRCLHCWTTCMEDLLP

Table 21

SEQ ID NO:12

cbe_250834 HPV 11 E7

Human papillomavirus 11 E7

length=98

MHGRLVTLKDIVLDLQPPDPVGLHCYEQLEDSS EDEVKVDKQDAQPLTQHYQILTCCC
45 CDSNVRLVVECTDGDIRQLQDLLLGT LNIVCPICAPK

Table 22

SEQ ID NO:13

cbe_251059 HPV 16 E1-E4

HPV 16 E1-E4

length=92

MADPAAATKYPLLKLLGSTWPTTPPRPI PKPSPWAPKKHRLSSDQDQSQT PETPATPLS
55 CCTETQWTVLQSSLHLTAHTKDGLTVIVTLHP

Table 23

SEQ ID NO:14

cbe_251063 HPV 16 E1

Human papillomavirus 16 E1

length=649

MADPAGTNGEETGTCNGWFYVEAVVEKKTGDAISDDENENDSDTGEDLVDFIVNDNDYLT
 QAETETAHALFTAQEAQHRDAVQVLKRKYLGSPLSDISGCVDDNNISPRLKAICIEKQSR
 AAKRRLFESSEDSGYGNTTEVETQQMLQVEGRHETETPCSQYSGSGGGCSQYSSGSGGEGV
 SERHTICQTPLTNILNVLKTSNAKAAMLAKFKELYGVVSFSELVRPFKSNKSTCCDWCIAA
 FGLTPSIADSIKTLTLLQYCLYLHIQSLACSWGMVVLVRYKCGKNRETIEKLLSKLLCV
 SPMCMMEPPKLRSTAAALYWYKTGISNISEVYGDTPEWIQRQTVLQHSFNDCTFELSQM
 VQWAYDNDIVDDSEIAYKYAQLADTNSNASAFKLSNSQAKIVKDCATMCRHYKRAEKKQM
 SMSQWIKYRCRDVDDGGDWKQIVMFLRYQGVEFMSFLTALKRFLQGI PKKNCILLYGAAN
 TGKSLFGMSLMKFLQGSGVICFVNSKSHFWLQPLADAKIGMLDDATVPCWNYIDDNLRLNAL
 DGNLVSMVDVKHRPLVQLKCPPLLITSNINAGTDSRWPYLNRLVVFTFPNEFPFDENGNP
 VYELNDKNWKSFFSRTWSRLSLHEDEDKENDGDSLPTFKCVSGQNTNTL

Table 24

SEQ ID NO:15

cbe_251088 HPV 16 E2

Human papillomavirus 16 E2

length=365

METLCQRLNVCQDKILTHYENDSTDRLRDHIDYWKHMRLECAIYYKAREMGFKHINHQVVP
 TLAVSKNKALQAIELQLTLETIYNSQYSNEKWTLDVSLLEVYLTAPTGCICKKHGYTVEVQ
 FDGDICNTMHYTNWTHIYICEEASVTVEGQVDYGLYYVHEGIRTYFVQFKDDAEKYSK
 NKVWEVHAGGQVILCPTSVFSSNEVSSPEIIRQHLANHPAATHTKAVALGTEETQTTIQR
 PRSEPDGTGNPCHTTKLLHRDSVDSAPILTAFNSSHKGRINCNSNTTPIVHLKGDANTLKC
 LRYRFKKHCTLYTAVSSTWHWTGHNVKHKSIAIVTLTYDSEWQRDQFLSQVKIPKTTITVST
 GFMSI

Table 25

SEQ ID NO:16

cbe_251445 HPV 16 E6

Human papillomavirus 16 E6

length=158

MHQKRTAMFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIV
 YRDGNPYAVCDKCLKFYISKISEYRHICYSLYGTLEQQYKNKPLCDLLIRCINCQKPLCPE
 EKQRHLDDKKQRFHNIRGRWTGRCMSSCRSSRTRRETQL

Table 26

SEQ ID NO:17

cbe_251448 HPV 16 E7

Human papillomavirus 16 E7

length=98

MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIIVTFCKK
 CDSTLRLCVQSTHVDIRTLEDLLMGTGLGIVCPICSQKP

Table 27

SEQ ID NO:18

cbe_251663 HPV 11 E1

Human papillomavirus 11 E1

length=649

MADDSGTENEGSGCTGWMVEAIVEHTTGTQISEDEEEVEEDSGYDMVDFIDDRHITQNS
 VEAQALFNROEADAHYATVQDLKRKYLGS PYVSPISNVANAVESEISPRLDAIKLTTPK
 KVKRRLFETRELTDSGYGYSEVEAATQVEKHGDPENGGDGQERDTGRDIEGEGVEHREAE
 AVDDSTREHADTSGILELLKCKDIRSTLHGKFKDCFGLSFVDLIRPFKSDRTTCADWVVA
 5 GFGIHHSIADAFQKLIIEPLSLYAHIQWLTNAWGMVLLVLIRFKVNKSRCRTVARTLGTLLN
 IPENHMLIEPPKIQSGVRALYWFRGTGISNASTVIGEAPWITRQTVIEHSLADSQFKLTE
 MVQWAYDNDICEESEIAFEYAQRGDFDSNARAFNSNMQAKYVKDCAIMCRHYKHAEMKK
 MSIKQWIKYRGTKVDSVGNWKPIVQFLRHQNI EFIPFLSKLKLWLHGTPKKNCIAIVGPP
 DTGKSCFCMSLIKFLGGTVISYVNSCSHFWLQPLTDAKVALLDDATQPCWTYMDTYMRNL
 10 LDGNPMSIDRKHRALTLIKCPPLLVTNSNIDISKEEKYKYLHSRVTTFTFPNPFPPDRNGN
 AVYELSDANWKCFERLSSSLDIEDSEDEEDGSNSQAFRCVPGSVVRTL

Table 28

SEQ ID NO:19

cbe_251737 HPV 16 L2

Human papillomavirus 16 L2

length=473

MRHKRS AKRTKRASATQLYKTCQAGTCPPDIIPKVEGKTIQVQILQYGS MG VFFGGLGI
 20 GTGSGTGGR TG YIPLGTRPPTATDTLAPVRPPLTVDPVGPSPDSIVSLVEETS FIDAGAP
 TSVPSIPPDVSGFSITTSTDTTPAILDINNVTVTTHNNPTFTDPSVLQPPTPAETGGH
 FTLSSSTISTHNYEEIPMDTFIVSTNPNTVTSSTPIPGSRPVARLGLYSRTTQQVKVDP
 AFVTTPTKLITYDNPAYEGIDVDNTLYFSSNDNSINIAPDPDFLDIVALHRPALTSRRTG
 IRYSRIGNKQTLRTRSGKSIGAKVHYYYDLSTIDPAEEIELQTITPSTYTTTSHAASPTS
 25 INNGLYDIYADDFITDTSTTPVPSVPSTSLSGYIPANTTIPFGGAYNIPLVSGPDIPINI
 TDQAPSLIPIVPGSPQYTIADAGDFYLHPSYMLRKRKRRLPYFFSDVSLAA

Table 29

SEQ ID NO:20

cbe_251740 HPV 1a E1-E4

Human Papillomavirus 1a E1-E4

length=125

MADNKAPQGLLGLLYTPTTQPYPRVTPPSNRRPSTTPNSQDRGRPRRS DKDSRKHLYAD
 30 GLTDGEDPEVPEVEDEEKENQRPLGHPDLSLLRETLEVYTQRLKRDILQDLDDFCRKLGI
 HPWSV

Table 30

SEQ ID NO:21

cbe_251784 HPV 16 L1

Human papillomavirus 16 L1

length=531

MQVTFIYILVITCYENDVN VYHIFQMSLWLPSEATVYLPPVPVSKVVSTDEYVARTNIY
 YHAGTSRLLAVGHYPYFPIKKPNNKILVPKVSGLYRVFRIHLPDPNKFGFPDTSFYNP
 45 TQRLVWACVGVGVGRGQPLGVGISGHPLLNKLDDTENASAYAANAGVDNRECISMDYKQT
 QLCLIGCKPPIGEHWGKGSPCTNVA VNP GDCPPLELINTVIQDGMVHTGFGAMDFTTLQ
 ANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRRQMFVRHLFN RAGTVGENVPDD
 LYIKSGSGSTANLASSNYFPTPSGSMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVV
 DTRSTNMSLCAAISTSETTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHS
 50 NSTILEDWNFLQPPPGGTLED TYRFVTQAIACQKHTPPAPKEDDPLKKYTFWEVNLKEK
 FSADLDQFPLGRKFLQAGLKAKPKFTLGKRKATPTTSSTSTAKRKKRKL

Table 31

SEQ ID NO:22

cbe_251917 HPV 1a E2

Human Papillomavirus 1a E2

length=401

MENLSSRLDLLQEQLMNLVEQDSKLIEDQIKQWNLIRQEQVLFHFARKNGVMRIGLQAVP
SLASSQEKAKTAIEMVLHLESLKDSPYGTEDWSLQDTSRELFLAPPAGTFKKSGSTLEVT
YDNNPDNQTRHTIWNHVYYQNGDDVWRKVSSGVDAGVYYLEHDGYKNYYVLFEEASKY
5 STTGQYAVNRYGKRFTNVMSSTSSPRAAGAPAVHSDYPTLSESDTAQQSTSIDYTELPGQ
GETSQVRQRQKTPVRRRPYGRRRSRSPRGGRREGESTPSRTPGSVPSARDVGSIHHTP
QKGHSSRLRRLLEAWDPPVVCVKGANQLKCLRYRLKASTQVDFDSISTTWHWTDRKNT
ERIGSARMLVKFIDEAQREKFLERVALPRSVSVFLGQFNGS

10

Table 32

SEQ ID NO:23

cbe_251919 HPV 1a E6

Human Papillomavirus 1a E6

15

length=140

MATPIRTVRQLSESLCIPYIDVLLPCNFCNYFLSNAEKLFFDHFDLHLVWRDNLVFGCCQ
GCARTVSLLEFVLYYQESYEVPEIEEILDRPLLQIELRCVTCIKKLSVAEKLEVVSNGER
VHRVRNRLKAKCSLCRLYAI

20

Table 33

SEQ ID NO:24

cbe_251925 HPV 1a E7

Human Papillomavirus 1a E7

25

length=93

MVGEMPALKDLVLQLEPSVLDLDLYCYEEVPPDDIEEELVSPQQPYAVVASCAYCEKLVR
LTVLADHSAIRQLEELLRLSLNIVCPLCTLQRQ

30

Table 34

SEQ ID NO:25

cbe_251976 FLJ23584

hypothetical protein FLJ23584

length=234

35

MNPVPHWGEVFLLVGGEHGLASQGTTPARDHRVGISPASQQAQPESWRRRQRDKGVDPE
KAPSLTRQSQNPPLTAPLGMPSACSLPCGPAPEAAIILAGPPTALTVPKGTGLKSK
RLLLESMLRRRIIAHLKWLPRRILESYFLFNFLGSCSLTLAGARLSGLNTGQELQAQQR
YCEAQGSPPLKSPERFQVRQRPDRKSSKLPIQARALERNRPHMSEPIKHFHPA

40

Table 35

SEQ ID NO:26

cbe_252016 HPV 1a L1

Human Papillomavirus 1a L1

45

length=508

MYNVFQMAVWLPAQNKFYLPQPITRILSTDEYVTRTNLFYHATSERLLLVGHPLEISS
NQTVTIPKVSFNAFRVFRVRFADPNRFAFGDKAIFNPETERLVWGLRGIEIGRGQPLGIG
ITGHPLLNKLDAAENPTNYINTHANGDSRQNTAFDAKQTQMFLVGCTPASGEHWTSSRCF
GEQVKLGDCPRVQMIESVIEDGDMMDIGFGAMDFAALQQDKSDVPLDVVQATCKYPDYIR
50 MNHEAYGNSMFFFARREQMYTRHFFTRGGSVGDKEAVPQSLYLTADAEPRTTLATTNYVG
TPSGSMVSSDVQLFNRSYWLQRCQGQNGICWRNQLFITVGDNTRGTSLSISMKNNASTT
YSNANFNDFLRHTEEFDSLFIQVLCVKVLTPEINLAYIHTMDPNILEDWQLSVSQPPTNPL
EDQYRFLGSSLAACKPEQAPPEPQTDYPYSQYKFEVDLTERMSEQLDQFPLGRKFLYQSG
55 MTQRTATSSSTTKRKTVRVSTSAKRRRKA

Table 36

SEQ ID NO:27

cbe_252041 HPV 1a L2

Human Papillomavirus 1a L2

length=507

5 MYRLRRKRAAPKDIYPSCKISNTCPPDIQNKIEHTTIADKILQYGS LGVFLGGLGIGTAR
 GSGGRIGYTPLEGEGGVVRVATRPTPVRPTIPVETVGPSEIFPIDVVDPTGPAVIPLQDLG
 RDFPIPTVQVIAEIHPISDIPNIVASSTNEGESAILDVLRG NATIRT VSR TQYNNPSFTV
 ASTSNISAGEASTSDIVFVSNNGSGDRVVGEDIPLVELNLGLETDTSSVVQETAFFSSSTPI
 10 AERPSFRPSRFYNRRLYEQVQVQDPRFVEQPQSMVTFDNPAFEPELDEVSIIFQRDL DAL
 AQTPVPEFRDVVYLSKPTFSREPGGRLRVSR LGKSS TIRTRLGTAIGARTHFFYDLSSIA
 PEDSIELLPLGEHSQTTVISSNLGDTAFIQGETAEDDLEVISLET PQLYSEEELLD TNES
 VGENLQLTITNSEGEVSILDLTQSRVRPPFGTEDTSLHVYYPNSSKGTP IINPEESFTPL
 VIIALNNSTGDFELHPSLRKRRKRAYV

15

Table 37

SEQ ID NO:28

cbe_2685998 Prey2313

Homo sapiens, clone IMAGE:3625550, mRNA, partial cds.

20

length=361

25

AICLDYFTDPVSI GCGHNFCRCVCTQLWGGEDEEDRDEL DREEEEEEDGEEEEVEAVGAGA
 GWDTPMRDE DYEGDMEEEVEEEEEEGVFWTSGMSRSSWDNMDYVWEEDEEEDLDYYLGDM
 EEEDLRGEDEEDEEEVLEEEVEEEDLDPVTPLPPPPAPRRCTCPQCRKSFRRSFRPNLQ
 LANMVQVIRQMHTPGGRSRVTDQGICPKHQEALKLFCEVDEE AICVVCRESRSHKQHSV
 VPLEE VVQEYKAKLQGHVEPLRKHLEAVQKMKAKEERRVTELKSQMKSELA AVASEFGRL
 TRFLAEEQAGLERRLREMHEAQLGRAGAAASRLAEQAAQLSRL LAEAQERSQGGRLRLQ
 V

30

Table 38

SEQ ID NO:29

cbe_2826346 RPS10

ribosomal protein S10

length=165

35

MLMPKKNRIAIYELLFKEGVMVAKKDVHMPKHP ELADKNV PNLHVMKAMQSLKSRGYVKE
 QFAWRHFYWL TN EGIQYLRDYLHL PPEIVPATLRRSRPETGRPRPKGLEGERPARLTRG
 EADRD TYRRSAVPPGADKKA EAGAGSATEFQFRGGFGRGRGQPPQ

40

Table 39

SEQ ID NO:30

cbe_2830508 Prey292051

Homo sapiens, clone MGC:12344, mRNA, complete cds.

length=20

45

MQLKTL SLATPPRETAVINL

Table 40

SEQ ID NO:31

50

cbe_3001381 IRF1

interferon regulatory factor 1

length=325

55

MPITRMRMRPWLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKHGWDINKDACLF RSWAI
 HTGRYKAGEKEPD PKTWKANFR CAMNSLPDIEEVKDQSRNKGSSAVRVYRMLPPLTKNQR
 KERKSKSSRDAKSKAKRKSCGDSSPDTFSDGLSSSTLPDDHSSYTVPGYMQDLEVEQALT
 PALSPCAVSSTLPDWHIPVEVVPDSTSDLYNFQVSPMPSTSEATTDEDEEGKLPEDIMKL
 LEQSEWQPTNVDGKG YLLNEPGVQPTSVYGDFSCKEPEIDSPGGDIGLSLQRVFTDLKN

MDATWLDSSLTPVRLPSIQAIPCAP

Table 41

SEQ ID NO:32

cbe_3056756 KIAA0440

signal-induced proliferation-associated 1 like 1
length=1804

MTSLKRSQTERPLATDRASVVGTDGTPKVHTDDFYMRFRSQNGSLGSSVMAPVGPPRSE
GSHHITSTPGVPKMGVRARIADWPPRKENIKESSRSSQEIETSSCLDSLSSKSSPVSQGS
SVSLNSNDSAMLKSIQNTLKNKTRPSENMDSRFLMPEAYPSSPRKALRRIRQRSNSDITI
SELDVDSFDECISPTYKTGPSLHREYGSTSSIDKQGTSGESFFDLLKGYKDDKSDRGPTP
TKLSDFLITGGGKSGFSLDVIDGPISQRENLRLEKEREKPLKRRSKSETGDSSI FRKLR
NAKGEEELGKSSDLEDNRSEDSVRPWTCPKCFAYHDVQSILFDLNEAIMNRHNVIKRRNTT
TGASAAAVASLVSGPLSHSASFSSPMGSTEDLNSKGSLSMDQGDGKSNELVMSCPYFRNE
IGGEGERKISLSKSNSGSFSGCESASFESTLSSHCTNAGVAVLEVPEKNLVLHLDRVKRY
IVEHVDLGAYYYRKFYQKEHWNYFGADENLGPVAVSIRREKPDDEMKENGSPYNYRI IFR
TSELMTLRGSVLEDAI PSTAKHSTARGPLKEVLEHVPELNVQCLRLAFNTPKVTEQLM
KLDEQGLNYQQKVGIMYCKAGQSTEEEMYNESAGPAFEEFLQLLGERVRLKGFKEYRAQ
LDTKT DSTGTHSLYTTYKDYEIFHVS TMLPYTPNNKQQLLRKRHIGNDIVTIVFQEPGA
QPFSPKNIRSHFQHV FVIVRVHNP CSDSVCYSVAVTRSRDVPSFGPPI PKGVTFPKSNVF
RDFLLAKVINAENAAHKSEKFRAMATRTRQEYKDLAEKNVTNTPIDPSGKFPFISLASK
KKEKSKPYPGAELSSMGAIVWAVRAEDYNKAMELDCLLGISNEFIVLIEQETKSVFNCS
CRDVIGWTSTDTSLKIFYERGECSVSGSFINIEEIKEIVKRLQFVSKGCESVEMTLRRNG
LGQLGFHVNYEGIVADVEPYGYAWQAGLRQGSRLVEICKVAVATLSHEQMIDLLRTSVTV
KVVI I PPDDCTPRRSCSETYRMPVMEYKMNEGVS YE FKF PFRNNNKWRNASKGPHSPQ
VPSQVQSPMTSRLNAGKGDGKMPPPERAANI PRSISSDGRPLERRLSPGSDIYVTVSSMA
LARSQCRNSPSNLSSSSDTGSGVGGTYRQKSMPEGFGVSRSPASIDRQNTQSDIGSGSKS
TPSWQCRNSEDIA DQMAYSYRGPQDFNSFVLEQHEYTEPTCHLPAVSKVLP AFRESPPSGRL
MRQDPVVHLSPNKQGHSDSHYSSSHSSNTLSSNASSAHSDEKWDGDRTESELNSYNYLQ
GTSADSGIDTTSYGPSHGSTASLGAATSSPRSGPGKEKVAPLWHSSSEVISMADRTLETE
SHGLDRKTESSLSDIHSKSQAGSTPLTRENSTFSINDAASHTSTMSSRHSASPVVFTSA
RSSPKHEELHPAAPSQ LAPS FSSSSSSSSSGPRSFYPRQGATSKYLIGWKKPEGTINSVGFM
DTRKRHQSDGNEIAHTRLRASTRDLRASPKPTSKSTIEEDLKKLIDLESPTPESQSKFKF
HALSSPQSPFPSTPTSRRALHRTLSDESI YNSQREHFFT SRASLLDQALPNDVLFSS TYP
SLPKSLPLRRPSYTLGMSLSLHGEFSASDSSLTDIQETRRQPM PDPGLMPLPDTAADLDWS
NLVDAAKAYEVQRASFFAASDENHRPLSAASNSDQLEDQALAQMKPYSSSKDSSPTLASK
VDQLEGMLKMLREDLKKKEDKAHLQAEVQHLREDNLRLQEE SQNASDKLKKFTEWVFNT
IDMS

Table 42

SEQ ID NO:33

cbe_3340492 TRIP

TRAF interacting protein

length=469

MPIRALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQS FETAPSRTCPCRIQVGKRTI IN
KLFFDLAQEEENVLDREFLKNELDNVRAQLSQDKKEKRD SQVI IDTLRDTLEERNATVVS
LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEV
EEMIRDMGVQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKL RKDLFSSRSKLQTVY
SELDQAKLELKS AQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRVLVLESPAPVE
VNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYEKLCKLEKSHSPIQDVPKKICKGP
RKESQLSLGGQSCAGEPDEELVGAFPI FVRNAILGQKQPKRPRSESSCSKD VVRTGFDGL
GGRTKFIQPTDTVMIRPLPVKPKTKVKQVRVRVKTVP SLFQA KLDTFLWS

Table 43

SEQ ID NO:34

cbe_3345510 COX6C
cytochrome c oxidase subunit VIc
length=75
MAPEVLPKPRMRGLLARRLRNHMAVAFVLSLGVAALYKFRVADQRKKAYADFYRNYDVMK
5 DFEEMRKAGIFQSVK

Table 44

SEQ ID NO:35

10 cbe_3454406 gbh_af252829
Homo sapiens chromosome 8 clone BAC 495D4 map 8q24, *** SEQUENCING
length=338
MGKKQNRKTGNSKTQSTSPPPKERSSSPATDQSWMENDFDELREEGFRRSNYSELREDIQ
15 TKGKEVENFEKNLEECITRITNTEKCLKELMELKTKARELREECRSLRSQCDQLEERVSA
MEDEMNMKQEGKFKREKRIKRNEQSLQEIWDYVKRPNLRLIGVPESDAENGTKLENTLQD
IIQETFPNLARQANVQIQEIQRTPQRYSSRRATPRHIIVRFTKVEMKEKMLRAAREKGRV
TLKGKPIRLTADLSAETLQARREWGPILNILKEKNFQPRISYPAKLSFISEGEIKYFTDK
QMLTDFVTSRPALKELLKEALNMERNNRYQPLQNHAKM

Table 45

SEQ ID NO:36

cbe_3461331 MET

25 met proto-oncogene (hepatocyte growth factor receptor)
length=1408
MKAPAVLAPGILVLLFTLVQRSNGECKEALAKSEMNVNMKYQLPNFTAETPIQNVILHEH
HIFLGATNYIYVLNEEDLQKVAEYKTGPVLEHPDCFCQDCSSKANLSGGVWKDNINMAL
VVDYYDDQLISCGSVNRGTCQRHVFPNHNTADIQSEVHCIFSPQIEEPSQCPDCVVSAL
GAKVLSSVKDRFINFFVGNTINSSYFPDHPHLSISVRRLKETKDGFMFLTDQSYIDVLE
30 FRDSYPIKYVHAFESNNFIYFLTQVRETLDQAQTFHTRIIRFCSINSGLHSYMEMPLCIL
TEKRKKRSTKKEVFNIQAAVYVSKPGAQLARQIGASLNDLILFGVFAQSKPDSAEPMDRS
AMCAFPKIYVNDFFNKIVNKNVRCLQHFYGPNEHCNRTLLRNSSGCEARRDEYRTEF
TTALQRVDLFGQFSEVLLTSISTFIKGDLTIANLGTSEGRFMQVVVSRSGPSTPHVNF
LDShpVSPEVIVEHTLNQNGYTTLVITGKKITKIPLNGLGCRHFQSCSQCLSAPPFVQCGW
35 CHDKCVRSEECLSGTWTQQICLPAIYKVFPNSAPLEGGRRLTICGWDFGFRNNKFDLKK
TRVLLGNESCTLTSESTMTLKTCTVGPAMNKHFNMSIIISNGHGTQYSTFSYVDPVIT
SISPKYGPMAAGTLLTLTGNYLNSGNSRHISIGGKTCTLKSVSNSILECYTPAQTISTEF
AVKLKIDLANRETSIFSREDPIVYEIHPTKSFISTWWKEPLNIVSFLFCFASGGSTITG
VGKNLNSVSVPRMVINVHEAGRNFVACQHRNSEIICCTTPSLQQLNLQLPLKTKAFFM
40 LDGILSKYFDLIYVHNPVFKPFKEKPVMSMGNENVLEIKGNDIDPEAVKGEVLKVGKNSC
ENIHLHSEAVLCTVPNDLLKLNSELNIEWKQAISSTVLGKIVVQPDQNTGLIAGVVSIS
TALLLLLGFFLWLKKRKQIKDLGSELVRYDARVHTPHLDRLVSARSVSPTTEMVSNESVD
YRATFPEDQFPNSSQNGSCRQVQYPLTDMSPILTSGDSDISSPLLQNTVHIDLALNP
VQAVQHVVIGPSSLI VHFNEVIGRGHFGCVYHGTLLDNDGKKIHCAVKS LN RITDIGEVS
45 QFLTEGIIMKDFSHPNVLSLLGICLRSEGSPLVVLPMKHGDLRNFIRNETHNPTVKDLI
GFGQLQVAKAMKYLASKKFVHRDLAARNCMLDEKFTVKVADFGLARDMYDKEYYSVHNKTG
AKLPVKWMALESLOTQKFTTKSDVWSFGVVLWELMTRGAPPYPDVNTFDITVYLLQGRRL
LQPEYCPDPLYEVMKLCWHPKAEMRPSFSELVSRISAIFSTFIGEHYVHV NATYVNVKCV
50 APYPSLLSSEDNADDEVDRPASFWETS

Table 46

SEQ ID NO:37

cbe_3473488 gbh_al121903

55 Human DNA sequence from clone RP1-155G6 on chromosome 20 Contains
length=641
VGCNPNEVDVAIFAVDSLRLQSLMKFLEKGE LANFRFQKDFLRPF E HIMKKNRSPTIRDMAI

RCIAQMVNSQAANIRSGWKNIFAVFHQAASDHDGNIVELAFQTTCHIVTTIFQHHPAAI
 DSFQDAVKCLSEFACNAAFPDTSMELIRFCGKYVSEPRVLQEYTSDDMNVPAGDRV
 WVRGWFPILFELSCIINRCKLDVTRGLTVMFEIMKSYGHTFEKHWWQDLFRIVFRIFDN
 5 MKLPEQLSEKSEWMTTTCNHALYAICDVFTQFYEALNEVLLSDVFAQLQWCVKQDNEQLA
 RSGTNCLENLVISNGEKFSPEVWDETCNCMLDIFKTTIPHVLLTWRPVGMEEDSSEKHL
 VDLDRQSLSSIDKNPSERGQSLSNPTDDSWKGRPYANQKLFASLLIKCVVQLELIQTID
 NIVFYPATSKKEDAEHMVAAQDITLADIHIETEDQGMKYMSQHLFKLLDCLQESHFS
 SKAFNSNYEQRTVLWRAGFKGSKPNLLKQETSSLACCLRILFRMYVDENRRDSWEEIQ
 10 RLLTVCSEALAYFITVNSESHREAWTSLLLLLLTKTLKINDEKFAHASMYYPYLCEIMQ
 FDLIPELRAVLRKFFLRIGVVYKIWIPEEPSQVPAALSPVW

Table 47

SEQ ID NO:38

cbe_3474077 KRT4

keratin 4

length=534

MIARQQCVRGGPRGFSCGSAIVGGGKRGAFSSVSMSSGAGRCSSGGFGSRSLYNLRGNKS
 ISMSVAGSRQACFGGAGGFGTGGFGAGGFGAGFGTGGFGGGFGGSFSGKGGPGFPVCPA
 20 GGIQEVITINQSLTPLHVEIDPEIQKVRTEEREQIKLLNNKFASFIDKVQFLEQQNKVLE
 TKWNLQQTITTTSSKNLEPLFETYLSVLRKQLDTLGNDKGRQLQSELKTMQDSVEDFKTK
 YEEEINKRTAAENDFVVLKKDVAAYLNKVELEAKVDSLNDINFLKVLDAELSQMQTH
 VSDTSVVLSDMNNRNLDSLIIAEVRAQYEEIAQRSKAEAEALYQTKVQQLQISVDQHG
 NLKNTKSEIAELNRMIOQLRAEIEINIKKQCQTLQVSVADAEQRGENALKDAHSKRVELEA
 25 ALQQAKEELARMLREYQELMSVKLALDIEIATYRKLEGEYRMSGECQSAVSISVSGS
 TSTGGISGGLSGSGSGLSSGSGSGSGSGFGGGSVSGSSSSKIISTTTLNKRR

Table 48

SEQ ID NO:39

cbe_3563252 LOC91689

hypothetical gene supported by AL449243

length=107

MASGAARWLVLAPVRSGALRSGPSLRKGDVSAAWSGSGRSLVPSGSIIVTRSGAILPKP
 35 VKMSFGLLRVFSIVIPFLYVGTLSKNFAALLEEHDIFVPEDDDDDDD

Table 49

SEQ ID NO:40

cbe_3575702 SUI1

putative translation initiation factor

length=113

MSAIQNLHSFDPFADASKGDDLPAAGTEDIHIRIQQRNGRKTLTTVQGIADDYDKKKLV
 45 KAFKKKFACNGTVIEHPEYGEVIQLQGDQRKNICQFLVEIGLAKDDQLKVHGF

Table 50

SEQ ID NO:41

cbe_3580897 HSPA5

heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)

length=654

MKLSLVAAMLLLLSAAARAEEDKKEDVGTGVGIDLGTTYSVGVFKNGRVEIIANDQGNR
 ITPSYVAFTPEGERLIGDAAKNQLTSNPENTVFDKRLIGRTWNPVSVQDQDIKFLPFKVV
 55 EKKTYPYIQVDIGGQTKTFAPEEISAMVLTKMKETAAYLGKKVTHAVVTVPAYFNDAQ
 RQATKDAGTIAGLNVMRIINEPTAAAIAYGLDKREGEKNI LVFDLGGGTDFDVSLTIDNG
 VFEVVATNGDTHLGGEDFDQVRMEHFIKLYKKKTGKDVRKDNRAVQKLRREVEKAKRAL
 SQHQARIEIESFYEGEDFSETLTRAKFEELNMDLFRSTMKPQKVLESDLKKSIDEIV

LVGGSTRIPKIQQLVKEFFNGKEPSRGINPDEAVAYGAAGVAGVLSGDQDTGDLVLLDVC
 PLTLGIETVGGVMTKLIPRNTVVPTKKSQIFSTASDNQPTVTIKVYEGERPLTKDNHLLG
 TFDLTGIPPAPRGVPQIEVTFEIDVNGILRVTAEDKGTGNKNKITITNDQNRLTPEEIER
 MVNDAEKFAEEDKKLKERIDTRNELESYAYSLSKNQIGDKEKLGKLSSEDKETMEKAVEE
 KIEWLESHQDADIEDFKAKKKELEEIVQPIISKLYGSAGPPPTGEEDTAEKDEL

Table 51

SEQ ID NO:42

cbe_3583511 MGC3222

hypothetical protein MGC3222

length=255

VVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPAVKLRRHVEMYQWVETEEES
 REYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHNNPSAMAVESFTATAPFVQIGRF
 FLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLRVFSFYAGLSG
 DDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAEVSAPVPSYGGGTSMSF
 LPSSGYLIRSHYQGS

Table 52

SEQ ID NO:43

cbe_3590661 NUP214

nucleoporin 214kDa

length=2127

MRAAGAEGRKFAVERPGFRGQGRGRQWLLRHTEGGAMGDEMDAMI PEREMKDFQFRALK
 KVRIFDSPEELPKERSLLAVSNKYGLVFAGGASGLQIFPTKNLLIQNKPGDDPNKIVDK
 VQGLLVPMKFPIHHLALSCDNLTLACMMSSSEYGSIIAFFDVRTFSNEAKQQKRPFAHYHK
 LLKDAGGMVIDMKWNPTVPSMVAVCLADGSI AVLQVTETVKVCATLPSTVAVTSVCWSPK
 GKQLAVGKQNGTVVQYLPTLQEKKVI PCPPFYESDHPVRVLDVLWIGTYVFAIVYAAADG
 TLETSFDVVMALLPKKEEKHPEIFVNFMEPCYGSCTERQHYYLSYIEEWDLVLAASAAS
 TEVSIARQSDQINWESWLLDSSRAELPVTDKSDDSLPMGVVDYTNQVEITISDEKTL
 PPAPVLMMLSTDGVLCPFYMINQNGVKSIIKTPERLSLEGERQPKSPGSTPTTPTSSQA
 PQKLDASAAAAPASLPSSPAAPIATFSLLPAGGAPT VFSFGSSSLKSSATVTGEPPSYS
 SGSDSSKAAPGPGPSTFSFVPPSKASLAPTPAASPVAPSAASFSGSSGFKPTLESTPVP
 SVSAPNIAMKPSFPSTSAVKVNLSEKFTAAATSTPVSSSQSAPPMSPFSSASKPAASGP
 LSHPTPLSAPPSSVPLKSSVLPSPSGRSAQSSSPVPSMVQKSPRITPPAAKPGSPQAKS
 LQPAVAEKQGHQWKSDPVMAGIGEEIAHFQKELEELKARTSKACFQVGTSEEMKMLRTE
 SDDLHTFLLEIKETTESLHGDISSLKTTLLEGFAGVEEAREQNERNRDSGYLHLLYKRPL
 DPKSEAQLQEIRRLHLVQDNDVLDLEWDQHLEKQKKQRHLLVPERETLNFNTLAN
 NREIINQQRKRLNHLVDSLQQLRLYKQTSLSWSLSSAVPSQSSIHSFSDLESCLNALLKT
 TIESHTKSLPKVPKLSPMKQAQLRNFLAKRKT PPVRSTAPASLSRSAFLSQRYEDLDE
 VSSSTSSVSQSLESEDARTSCKDDEAVVQAPRHAPVVRTPSIQPSLLPHAAPFAKSHLVHG
 SSPGVMGTSVATSASKII PQGADSTMLATKTVKHGAPSPSHPI SAPQAAAAAALRRQMAS
 QAPAVNTLTSTLKNVPQVNVQELKNNPATPSTAMGSSVPYSTAKT PHPVLT PVAANQA
 KQGSLLNSLKPSTPASGQLSSGDKASGTAKI ETAVTSTPSASGQFSKPFSSPSGTGF
 NFGIITPTPSSNFTAAQGATPSTKESSQPDASFSSGGGSKPSYEAIPESSPPSGITSASNT
 TPGEPAASSSRPVAPSGTALSTTSSKLETPPSKLGELLFPSSLAGETLGSFSGLRVQAD
 DSTKPTNKASSTSLTSTQPTKTSVPSGFNFTAPPVLGKHTEPPVTSSATTTSVAPPAAT
 STSSTAVFGSLPVTSAAGSSGVSIFGGTSLSAGKTSFSGSQQTNSTVPPSAPPPTTAATP
 LPTSFPFLSFGSLSSATTPSLPMSAGRSTEEATSSALPEKPGDSEVSASAASLLEEQQS
 AQLPQAPPQTSDSVKKEPVLAQPAVSNSGTAASSTSLVALSAEATPATTGVPDARTEAVP
 PASSFSVPGQTAVTAIISSAGPVAVETSSSTPIASSTTSIVAPGPSAEAAAFGTVTSGSS
 VFAQPPAASSSSAFNQLTNNTATAPSATPVFGQVAASTAPSLFGQQTGSTASTAAATPQV
 SSSGFSSPAFGTTAPGVFGQTTFGQASVFGQSASSAASVFSFSGQPGFSSVPAFGQPASST
 PTSTSGSVFGAASSTSSSSSFSFGQSSPNTGGGLFGQSNAPAFGQSPGFGQGGSVFGGTS
 AATTTAATSGFSFCQASGFGSSNTGSVFGQAASTGGIVFGQSSSSSSGVSFGSGNTGRGG
 GFFSGLGGKPSQDAANKNPFSSASGGFGSTATSNTSNLFGNSGAKTFGGFASSSFGEQKP

TGTFSSGGGSVASQGFSSPNKTGGFGAAPVFGSPPTFGGSPGFGGVPAFGSAPAFSTSP
 LGSTGGKVFGEGTAAASAGGFGGSSNTTSFGLASQNAPTFGSLSQQTSGFGTQSSGF
 SGFGSGTGGFSFGSNNSSVQFGGWRS

5

Table 53

SEQ ID NO:44

cbe_3606990 Prey1053670

10 Homo sapiens, Similar to CG5604 gene product, clone MGC:11330, mRNA, complete
 cds.

length=81

MSSDERKAFLQFTTGCSTLPPGGLANLHPRLTVVRKVDATDASYPSVNTCVHYLKLPEYS
 SEEIMRERLLAATMEKGFHLN

15

Table 54

SEQ ID NO:45

cbe_3621798 XPO1

exportin 1 (CRM1 homolog, yeast)

20

length=1071

MPAINTMLADHAARQLLDFSQKLDINLLDNVNCCLYHGEGAQQRMAQEVLTHTLKEHPDAW
 TRVDTILEFSQNMNTKYYGLQILENVIKTRWKILPRNQCEGIKKYVVGLIIKTSSDPTCV
 EKEKVYIGKLNLMILVQILKQEWPKHWPTFISDIVGASRTSESLCQNNMVLKLLSEEVFD
 FSSGQITQVQSKHLKDSMCNEFSQIFQLCQFVMENSQNAPLVHATLETLLRFLNWIPLGY
 25 IFETKLISTLIYKFLNVPMFRNVSLKCLTEIAGVSVSQYEEQFVTLFTLTMMQLKQMLPL
 NTNIRLAYSNGKDDEQNFIQNLFLCTFLKEHDQLIEKRLNLRETLMALHYMLLVSEV
 EETEIFKICLEYWNHLAAELYRESPFSTSASPLLSGSQHFDVPPRRQLYLPMLFKVRLLM
 VSRMAKPEEVLVVENDQGEVVREFMKDTSINLYKNMRETLVYLTHLDYVDTERIMTEKL
 HNQVNGTEWSWKNLNTLCWAIGSISGAMHEEDEKRFVTVIKDLLGLCEQKRGKDNKAI
 30 ASNIMYIVQYPRFLRAHWKFLKTVVNKLFEFMHETHDGVQDMACDTFIKIAQKCRRHV
 QVQVGEVMPFIDEILNNINTIICDLQPPQVHTFYEAUGYMGAGTQDTVQEHLEKYMLL
 PNQVWDSIIQQATKNVDILKDPETVKQLGSILKTNVRACKAVGHPFVIQLGRIYLDMLNV
 YKCLSENISAAIQANGEMVTQPLIRSMRTVKRETLKLISGWVSRSDNPQMVAENFVPL
 LDAVLIDYQRNVPAAREPEVLSTMAIIVNKLGGHITAEIPQIFDAVFECTLMINKDFEE
 35 YPEHRTNFFLLLQAVNSHCFPAFLAIPPTQFKLVLDSSIWAFKHTMRNVADTGLQILFTL
 LQNVAQEEAAAQSFYQTYFCDILQHIFSVVTDTSHTAGLTMHASILAYMFNLVEEGKIST
 SLNPGNPVNNQIFLQEYVANLLKSAFPHLQDAQVKLFVTGLFSLNQDIPAFKEHLRDFLV
 QIKEFAGEDTSDLFLEEREIALRQADEEKHKRQMSVPGIFNPHEIPEEMCD

40

Table 55

SEQ ID NO:46

cbe_3621899 PCNP

PEST-containing nuclear protein

45

length=178

MADGKAGDEKPEKSQRAGAAGGPAAAAEKPVKTKTVSSSSNGGESSRSAAEKRSAAAAAD
 LPTKPTKISKFGFAIGSQTTKKASAIKLGSSSKPKETVPTLAPKTLVAAAFNEDEDESE
 PEEMPPEAKMRMKNIGRDTPTSAGPNSFNKGKHGFSNQLWERNIKSHLGNVHDQDN

50

Table 56

SEQ ID NO:47

cbe_3625721 EIF2B2

eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa

55

length=351

MPGSAAKGSELSEIESFVETLKRGGGPRSSSEEMARETLGLLRQIITDHRWSNAGELMEL
 IRREGRRMTAAQSETTVGNMVRRLVKIIREEYGRLLHGRSDESDQQESLHKLLTSGGLNE

DFSFHYAQLQSNIIIEAINELLVELEGTMENIAAQALEHIHSNEVIMTIGFSRTVEAFLKE
 AARKRKFHVIVAECAPFCQGHMAVNLSKAGIETTVMTDAAIFAVMSRVNKVIIGTKTIL
 ANGALRAVTGTHTLALAAKHSTPLIVCAPMFKLSPQFPNEEDSFHKFVAPEEVLPTFTEG
 DILEKVSVHCPVFDYVPPELITLFIISNIGGNAPSYIYRLMSELYHPDDHVL

5

Table 57

SEQ ID NO:48

cbe_3641816 ANKH a

10 nkylosis, progressive homolog (mouse)

length=492

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMK
 FFTGPMSEDFKNVGLVFNNSKRDRTKAVLCMVVAGIAAVFHTLIAYSIDLGYIINKLHHV
 DESVGSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILL
 15 HSHLECREPLILPILSLYMGALVRCTTCLGYYKNIHDIIPDRSGPELGGDATIRKMLSF
 WWPLALILATQIRSRPIVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVY
 PAFDKNPNKSLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVD
 FAFaelCVVPLRIFSFPPVPTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPY
 LGVHGATLGVGSLLAGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEE
 20 VTDIVEMREENE

Table 58

SEQ ID NO:49

25 cbe_3643627 DKFZP434I1735

DKFZP434I1735 protein

length=1590

VILHPSISVRLAAAWCLHCAVALPSYLTPLLDRCLERLTGHKSSPEAVTGFSFAVAALL
 GAVKHCPGLIPHGKGIIMTLAEDLLCSAAQNSRLSAQRTQAGWLLISALMTLGPVAVSH
 30 HLARVLLLWKCVFPASPKDLETEKSRGDSFTWQVTLLEGAGALCAIKSFVSHCGDLLTEE
 VTQRLPLPCAVDLLTQLSSILKMYGSPLKTPSVVYRQRLYELLILLPPETYEGLNLCAL
 LRELAADLTAPDIQVAASTFLLPPLCHQDDLLILSPFLQETDHRFIEEQLLLGNGVACGS
 LEYDPYSIYEKDVEGDSVPKPLPPALSVISSASKLFGVVCACHVGETQRLILEQLLDSIK
 HTKGARQQVQVLHVSSVSSFLKYVAGSKGCLGPEEMKRFALTLMVGALES PNPLLRCAA
 35 AESWARLAQMVDGAGTAGLAQVSFDKLSARDVVTRTGHSALGSLHRYLGGISSQHL
 NSCIGILYTLAQDSTSPDVQTWALHSLSLIIDSAGPLYVHVEPTLSLIIMLLNVPPTH
 AEVHQSLGRCLNALITTLGPELQGNSTSIISLRTSCLLGCAVMQDNPDCLVQAQAISCLQ
 QLHMFAPRHVNLSSLVSCLCVNLCSPYLLLRRAVLACLRQLVQREAAEVSEHAVMLAKDS
 REELTPDANIREVGLLEGALLILLDKETDERLCHDIKETLNYMLTSMAVEKLSLWLKCKD
 40 VLAASADFTAVTCVDTMQEEEGDKGDDASVLTTRRDEKSHPFTNPRWATRVFAAECVCRI
 INQCENANSAHFDIALAQEMKKRDSRNDFLVLHLADLIRMAFMAATDHSDQLRLSGLEML
 LVVIRRFATVPEPEFGHVILEQYQANVGAALRPAFTSETPPDVTAACQVCSAWIASGV
 VSDLNDLRRVHQLLVSSLTKIQAGKEALSHLYNESASTMEILAVLKAWAEVYIIAVQRHK
 NHRQPLKTTTCLEDGIRNGSCSSDGLLDLVYADLGTLSRLWLAALQDFALLTLPSEFASQ
 45 LPAEGGAFYTAETSENAKLHYNSWALILHATALWLTSTGFVVADPDEGASNLSPVTPPT
 SMCQSSSGATIKSPEDVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQALLDVP
 WPRSKIGSDQDLGIELLNVLHRVILTRESPSIQLASLEVVRQIIICAAQEHVKEKRRSAEV
 DDGAAEKETLPEFGEGKDTGGLVPGKSLVFATLELCVCILVRQLPELNPCLTGPVGVKAT
 KPQILLEDGSRVLAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAVKLPGGQLS
 50 STVAASLQALKGILSSPMARAESRTAWTDLLRSALTITLDCWDPVDETHQELDEVSLLT
 AITVFILSTSPEVTTIPCLQKRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYP
 YIYSLASCIMEKLQEIHDRKRPENTAELEIFQEGIKVLETLTVAEEHRAQLVACLLPIL
 ISFLLDENSLGSATSIMRNLHDFALQNLMOIGPQYSSVFKSLVASSPALKARLEAAIKGN
 QESVKVKIPTSKYTKSPGKNSSIQLKTSFL

55

Table 59

SEQ ID NO:50
cbe_3663966 KIAA1389
KIAA1389 protein
length=1514

5 FSTRYPLSIANYDHKAMVPFGFPEFFRCDPAISPSLHAAAQISRGEFVRISGLDYVDSAL
LMGRDRDKPFKRRLKSESVELSLFRKLRTVKSEHETFKFTSELEESRLERGIWPWNCQRC
FAHYDVQSILFNINEAMATRVNGKRKNITTGASAASQTQMPTGQTGNCEPLGSKEDLN
SKENLDADEGDGKSNLVLSCPYFRNETGGEGDRRIALSRANSSSFSSGESCSFESSLSS
10 HCTNAGVSVLEVPRENQPIHREKVKRYII EHDLDGAYYRKFFYGKEHQNYFGIDENLGP
VAVSIRREKVEDAKEKEGSQFNRYVAFRTSELTTLRGAILED AIPSTARHGTARGLPLKE
VLEYVPELSIQCLRQASNSPKVSEQLLKLDEQGLSFQHKIGILYCKAGQSTEEEMYNNE
TAGPAFEEFLDLLGQVRVLKGF SKYRAQLDNKTDSTGTHSLYTTYKDYELMFHVSTLLPY
MPNNRQQLLRKRHIGNDIVTIVFQEPGALPFTPKSIRSHFQHV FVIVKVHNPCTENVCYS
15 VGVSRSKDVPPFGPPI PKGVTFPKSAVFRD FLLAKVINAENAAHKSEKFRAMATRTRQEY
LKDLAENFVTATVDTSVKFSFITLGAKKKEKVKPRKDAHLFSIGAIMWHVIARDFGQSA
DIECLGISNEFIMLIEKDSKNVFNCSRDVIGWTSGLVSIKV FYEREGECVLLSSVDNC
AEDIREIVQRLVIVTRGCETVEMTLRRNGLGQLGFHVNFEGIVADVEPFGFAWKAGLRQG
SRLVEICKVAVATLTHEQMIDLLRTSVTVKVVI IQPHDDGSPRRGCSELCPIMVEYKLD
20 SEGTPCEYKTPFRRNTTWHRVPTPALQPLSRASPIPGTPDRLPCQQLLQQAQAAIPRSTS
FDRKLPDGTSSPSNQSSSDPGPGSGPWPRQVGYDGCQSP LLLLEHQSGPLECDGARE
REDTMEASRHPETKWHGPPSKVLGSKYKERALQKDGSKCKDSPNKLSHIGDKSCSSHSSSNT
LSSNTSSNSDDKHFGSGDLMDPELLGLTYIKGASTDSGIDTAPCMPATILGPVHLAGSRS
LIHSRAEQWADAADVSGPDDEPAKLYSVHGYASAI SAGSAAEGSMGDLSEISSHSSGSHH
25 SGSPSAHCSKSSGSLDSSKVYIVSHSSGQQVPGSMSKPYHRQGA VNKYVIGWKKSEGSP
PEEPEVTECPGMYSEMVMSTATQHQT VVGDAVAETQHVLSKEDFLKLMLPDSPLVEEGR
RKFSFYGNLSPRRSLYRTLSDSICSNRRGSSFGSSRSSVLDQALPNDILFSTTPPYHST
LPPRAHPAPSMGSLRNEFWFSDGSLSDKSKCADPGLMPLPDTATGLD WTHLVDAARAFEG
LDSDEELGLLCHHTSYLDQRVASFCTLTDMQHGDLEGAQELPLCVDPGSGKEFMDTTGE
30 RSPSPLTGKVNQLELILRQLQTDLRKEKQDKAVLQAEVQHLRQDNMRLQEESQTATAQLR
KFTWEFFTTIDKKS

Table 60

35 SEQ ID NO:51
cbe_3665307 HK1
hexokinase 1
length=905
MAKRALRDFIDKLYAMRLSDETLIDIMTRFRKEMKNGLSRDNFTATVKMLPTFVRSIP
DGSEKGD FIALDLGGSSFRILRVQVNHEKNQNVHMESEVYDTPENIVHGSGSQLFDHVAE
40 CLGDFMEKRKIKDKKLPGVFTFSFPCQQSKIDEAILITWTKRFKASGVEGADVVKLLNKA
IKKRGDYDANIVAVVNDTVGTMTCGYDDQHCEVGLI IGTGTNACYMEELRHIDLVEGDE
GRMCINTEWGAFGDDGSLEDIRTEFDREIDRGS LNPGKQLFEKMSVGMYLGEVLRLILVK
MAKEGLLFEGRITPELLTRGKFNTSDVSAIEKNKEGLHNAKEILTRLGV EPSDDDCVSVQ
45 HVCTIVSFRSANLVAATLGAILNRLRDNKGT PRLRTTVGVGDGSLYKTHPQYSRRFHKTLR
RLVPDSDVRFLLSESGSGKAAMVTAVAYRLAEQHRQIEETLAHFHLTKDMLLEVKKRMR
AEMELGLRKQTHNNAVVKMLPSFVRRTPDGTENGDFLALDLGGTNFRVLLVKIRSGKKRT
VEMHNKIYAIPIEIMQGTGEELFDHIVSCISDFLDYMGIKGPRMPLGFTFSFPCQQTSLD
AGILITWTKGFKATDCVGHVTVLLRDAIKRREEFDLDVAVVNDTVGTMTCAYEEPTC
50 EVGLIVGTGSNACYMEEMKNVEMVEGDQGMCMINMEWGAFDNGCLDDIRTHYDRLVDEY
SLNAGKQRYEKMISGMYLGEIVRNILIDFTKKGFLFRGQISETLKTRGIFETKFLSQIES
DRLALLQVRAILQQLGLNSTCDD SILVKTVCGVVSRRAAQLCGAGMAAVVDKIRENRGLD
RLNVTVGVDGTLYKLHPHFSRIMHQT VKELSPKCNVSFLLEDGSGKGAALITAVGVRLR
TEASS

55

Table 61
SEQ ID NO:52

cbe_3670766 ACTC

actin, alpha, cardiac muscle

length=377

MCDDEETALVCDNGSGLVKAGFAGDDAPRAVFPSIVGRPRHQGVMMGMGQKDSYVGDEA
 QSKRGILTLYPIEHGIITNWDDMEKIWHHTFYNELRVAPEEHPTLLTEAPLNPKANREK
 MTQIMFETFNVPAMYVAIQAVLSLYASGRRTTGIVLDSGDGVTHNVPIYEGYALPHAIMRL
 DLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKEKLCYVALDFENEMATAASSSSLEK
 SYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRKDLANNV
 LSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWIS
 KQEYDEAGPSIVHRKCF

Table 62

SEQ ID NO:53

cbe_3694420 ARHGEF2

rho/rac guanine nucleotide exchange factor (GEF) 2

length=958

MKEAKDARYTNGHLFTTISVSGMTMCYACNKSITAKEALICPTCNVTIHNRCKDTLANCT
 KVKQKQKKAALLKNNTALQSVSLRSKTTIRERPSSAIYPSDSFRQSLGSRGRSSLSLA
 KSVSTTNIAGHFNDSEPLGLRRILSQSTDLSNMNRNRTLSVESLIDEEVIYSELMSDFEMD
 EKDFAAADSWSLAVDSSFLQHKKEVMKQDVIYELIQTELHHVRTLKIMTRLFRTGMLEE
 LHLEPGVVQGLFPCVDELSDIHRFLSQLLERRRQALCPGSTRNFVIHRLGDLISQFSG
 PSAEQMCKTYSEFCSRHSKALKLYKELYARDKRFQFIRKVTRPAVLKRHGVQECILLVT
 QRITKYPLLI SRILQSHSGIEEERQDLTTALGLVKELLSNVDEGIYQLEKGARLQEIYNR
 MDPRAQTPVPKGPFGREELLRRKLIHDGCLLWKTATGRFKDVLVLLMTDVLVFLQEKDQ
 KYIFPTLDKPSVVSQNLIVRDIANQEKGMFLISAAPPEMYEVHTASRDDRSTWIRVIQQ
 SVRTCPREDFFLIETEDEAYLRRIKMELOQKDRALVELLREKVGLFAEMTHFQAEDGG
 SGMALPTLPRGLFRSESLSPRGERLLQDAIREVEGLKDLLVGPVVELLLTPREPALPLE
 PDSGGNTSPGVTANGEARTFNNGSIELCRADSDSSQRDRNGQLRSPQEEALQRLVNLYGL
 LHGLQAABAQQDTLMEARFPEGPERREKLCRANSRDGEAGRAGAAPVAPEKQATELALLQ
 RQHALLQEELRRCRRLGEERATEAGSLEARLRESEQARALLEREAEARRQLAALGQTEP
 LPAEAPWARRPVDPRRSLPAGDALYLSFNPPQPSRGTDRLDLPVTTTRSVHRNFEDRERQ
 ELGSPERLQDSSDPDTGSEEEGSSRLSPPHSPRDFTRMQDIPEETESRDGEAVASES

Table 63

SEQ ID NO:54

cbe_3705944 TNFAIP1

tumor necrosis factor, alpha-induced protein 1 (endothelial)

length=316

MSGDTCLCPASGAKPKLSGFKGGGLGNKYVQLNVGGSLYYTTVRALTRHDTMLKAMFSGR
 MEVLTDKEGWILIDRCGKHFGTILNYLRDDTITLPQNRQEIKEKMAEAKYYLIQGLVNMC
 QSALQDKKDSYQPCNIPIITSLKEEERLIESSTKPVVKLLYNRSNNKYSYTSNSDDHLL
 KNIELFDKLSLRFNGRVLFIKDVIGDEICWSFYGQGRKLAEVCCTSIYVATEKKQTKVE
 FPEARIYEETLNVLLYETPRVPDNLLEATSRSRSPSEDEETFELDRVRRRIHVKRY
 STYDDRQLGHQSTHRD

Table 64

SEQ ID NO:55

cbe_3753270 gbh_ac004503

Homo sapiens chromosome 5, P1 clone 1354A7 (LBNL H47), complete
 length=515

MALFVRLALALALALGPAATLAGPAKSPYQLVLQHSRLRGRQHGPNVCAVQKVIGTNRK
 YFTNCKQWYQRKICGKSTVISYECCPGYEKVPGEKGCPAALPLSNLYETLGVVGSTTTQL
 YTDRTKLRPEMEGPGSFTIFAPSNEAWASLPAEVLDLSVSNVNIELLNALRYHMGRRV
 LTDELKHGMTLTSMYQNSNIQIHYPNGIVTVNCARLLKADHHATNGVVHLIDKVISTIT

NNIQQIIIEIEDTFETLRAAVAASGLNTMLEGNGQYTLLAPTNEAFEKIPSETLNRILGDP
 EALRDLLNNHILKSAMCAEAI VAGLSVETLEGTTLLEVGCSDMLTINGKAIISNKDILAT
 NGVIHYIDELLIPDSAKTLFELAAESDVSTAIDLFRQAGLGNHLSGSERLTLLAPLNSVF
 KDGTTPIDAHTRNLLRNHIIKDQLASKYLYHGQTLETTLGGKKLRVVFYRNSLCIENSCIA
 5 AHDKRGRYGTLTMDRVLTPPMGTVMVDVLKGDNRF

Table 65

SEQ ID NO:56

cbe_3764052 MARK4

MAP/microtubule affinity-regulating kinase 4

length=381

MPFGNTHNKFKNLYKPEEEYPDL SKHNNHMAKVLTLELYKKLRDKETPSGFTVDDVIQTG
 VDNPGHPFIMTVGCVAGDEESYEVFKELFDPIISDRHGGYKPTDKHKTDLNHENLKGDD
 15 LDPNYVLSSRVRTGRSIRKGYTLPPHCSRGERRAVEKLSVEALNSLTGEFKGKYYPLKSMT
 EKEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKSFLVWVNEEDHLRVISM
 EKGGMKEVFRFCVGLQKIEEIFKKAGHPFMWNQHLGYVLTCPSNLGTGLRGGVHVKLA
 HLSKHPKFEEILTRLRLQKRGTGGVDTAAVGSVFDVSNADRLGSSEVEQVQLVVDGVKLM
 VEMEKKLEKGQSIDDMIPAQK
 20

Table 66

SEQ ID NO:57

cbe_3770440 gbh_af217505

Homo sapiens uncharacterized bone marrow protein BM028 mRNA,
 length=116

MWTKKDAGKKVVP CRHDWHQTGGEVTISVYAKNSLP ELSRVEANSTLLNVHIVFEGEKEF
 DQNVKLWGVIDVKRSYVTMTATKIEITMRKAEPMQWASLELPAKKQEKQKDDTTD
 30

Table 67

SEQ ID NO:58

cbe_3772244 PIGQ

phosphatidylinositol glycan, class Q

length=760

MVLKAFFPTCCVSTDSGLLVGRWVPEQSSAVVLAVLHFFPIPIQVKQLLAQVRQASQVGV
 AVLGTWCHCRQEP EESLGRFLES LGAVFPHEPWLRLCRERGGTFWSCEATHRQAPTAPGA
 PGEDQVMLIFYDQRQVLLSQLHLPTVLPDRQAGATTASTGGLAAVFDTVARSEVLF RSDR
 FDEGPVRLSHWQSEGVEASILAELARRASGPICLLLASLLSLVSAVSACRVFKLWPLSFL
 40 GSKLSTCEQLRHRLEHLTLIFSTRKAENPAQLMRKANTVASVLLDVALGLMLLSWLHGRS
 RIGHLADALVPVADHVAEELQHLLQWLMGAPAGLKMNRALDQVLGRFFLYHIHLWISYIH
 LMSPPFVEHILWHVGLSACLGLTVALSLLSDIIALLTFHIYCFYVYGARLYCLKIHGLSSL
 WRLFRGKKWNVLRQRVDSCSYDL DQLFIGTLLFTILLFLLPTTALYYLVFTLLRLLVAV
 QGLIHLLVDLINSPLYSGLRLCRPYRLADKPTALQPRGAHLPPPQLWLPPQALLGRPV
 45 PQAVPWGAHLPLEAERGQAGLRELLARLAPPHGHSQPSALPGWHQLSWRMSCALWTLLCA
 PEHGRPCYHTLGLEVIGSEQMWGWP ARLAALHHWHCLPWDPLPTCCGHHGGEHSNPRCPE
 HCPMPTLCTQVQVRVPPQQPQVEGWSPWGLPSGSALAVGVEGPCQDEPPSPRHPLAPSAE
 QHPASGGLKQSLTPVPSPGPGPSLPEPHGVYLRMFPGGEVAL
 50

Table 68

SEQ ID NO:59

cbe_3773649 EEF1A1L14

eukaryotic translation elongation factor 1 alpha 1-like 14

length=398

MQSERGITIDISLWKPFETSKYYVTIIDAPGHRDFIQNMITGTSQADCAVLIVAAGVGEFE
 AGISKNGQTREHALLAYTLGVKQLIVGVNKMDS TEPPYSQKRYEEIVKEVSTYIKKIGYN
 55

PDTVAFVPI SGWNGDNMLEPSANMPWFKGWKVTRKDGNASGTTLLEALDCILPPTRPTDK
 PLGLPLQDVYKIGGIGTVPVGRVETGVLKPGMVVTFGPVNVTTTEVKSVMHHEALGEALP
 GDNVGFNVKNVSVKDVRRGNVAGDSKNDPPMEAAGFPAQVIIILNHPGQISAGYAPVLDCH
 5 TAHIAACKFAELKEKIDRRSGKKLEDGPKFLKSGDAAIVDMVPGKPMCYESFSDYPPLGCF
 AVRDMRQTVAVGVIAVDKKAAGAGKVTKSAQKAQKAK

Table 69

SEQ ID NO:60

cbe_3787129 LOC55828

zinc finger protein ZNF140-like protein

length=478

MSQVTFSDVAIDFSHEEWACLDQAQRDLKDVVMVQNYENLVSVGLSVTKPYVIMLLEDGK
 EPWMMEKKLSKAYPFPLSHSVPASVNFSGFALFEHCSEVTEIFELSELVFWVLHFLSNS
 15 PNSTVEAFSRSKKKKKKKKKRQCFAFLIYFRLGIKMGKQGIINKEGYLYEDSPQPVTEK
 VVKQSYEFNSNKNLEYTECDTFRSTFHSKSTLSEPQNNNSAEGNSHKYDILKKNLSKKS
 IKSERINGGKKLLNSNKSAAFNQSKSLTLPQTCNREKIYTCSECGKAFGKQSILSRHWR
 IHTGEKPYECRECGKTFSHGSSLTRHQISHSGEKPYKIECGKAFSHGSSLTNHQSTHTG
 20 EKPYECMNCGKSFSRVSLLIQHLRIHTQEKRYECRICGKAFIHSSSLIHHQKSHTGEKPY
 ECRECGKAFCCSSHLTQHQRHSMKKKYECNKCLKVFSSFSFLVQHQSITHEEKPFV

Table 70

SEQ ID NO:61

cbe_3789063 AP2M1

adaptor-related protein complex 2, mu 1 subunit

length=435

MIGGLFIYNHKGVELISRVRDDIGRNAVDARVNVVIHARQQVRSPTVNIARTSFHFVVKR
 SNIWLAAVTKQNVNAAMVFEFLYKMCVMAAYFGKISEENIKNNFVLIYELLDEILDFGY
 30 PQNSETGALKTFITQQGIKSQHQTKEEQSQITSQVTGQIGWRREGIKYRRNELFLDVLES
 VNLLMSPQGGVLSAHVSGRVVMKSYLSGMPECKFGMNDKIVIEKQKGTADETSKSGKQS
 IAIDDCTFHQCVRLSKFDSERSISFIPPDGEFELMRYRTTKDIILPFRVIPLVREVGRTK
 LEVKVVIKSNFKPSLLAQKIEVRIPTPLNTSGVQVICMKGKAKYKASENAIVWKIKRMAG
 MKESQISAEIELLPTNDKKKWARPPISMNFEVPPFAPSGLKVRYLKVFEKPLNYSHDHVIK
 35 WVRVYIGRSGIYETRC

Table 71

SEQ ID NO:62

cbe_3800240 IVD

isovaleryl Coenzyme A dehydrogenase

length=423

MATATRLLGWRVASWRLRPPLAGFVSQRAHSLLPVDDAINGLSEEQRQLRQTMAKFLQEH
 LAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITAPVQYGGSGLGYLEHVLVMEIISRASG
 45 AVGLSYGAHNSLCINQLVRNGNEAQKEKYLPKLISGEYIGALAMSEPNAGSDVVSMKLKA
 EKKGNHYIILNGNKFWITNGPDADVLIYAKTDLAAVPASRGITAFIVEKGMPGFSTSKKL
 DKLGMGRSNTCELI FEDCKIPAANILGHENKGVYVLMISGLDLERLVLGGPLGLMQAVLD
 HTIPYLHVREAFGQKIGHFQLMQGKMADMYTRLMACRQYVYNVAKACDEGHCTAKDCAGV
 50 ILYSAECATQVALDGIQCFGGNGYINDFPMGRFLRDAKLYEIGAGTSEVRRRLVIGRAFNA
 DFH

Table 72

SEQ ID NO:63

be_3810032 gbh_af142421

Homo sapiens QUA KING isoform 5 (QUAKING) mRNA, complete cds.

length=337

METKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLEKLLDEEISRVKDMYNDTLNGS
TEKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVR
GKGSMRDKKKEEQNRGKPNWEHLNEDLHVLIITVEDAQNRAEIKLKRAVEEVKKLLVPAAE
GEDSLKKMQLMELAILNGTYRDANIKSPALAFSLAATAQAAPRIITGPAPVLPAPALRTP
5 TPAGPTIMPLIRIQITAVMPNGTPHPTAAIVPPGPEAGLIYTPYEYPYTLAPATSILEYP
IEPSGVLGAVATKVRHRDMRVHPYQRIVTADRAATGN

Table 73

10 SEQ ID NO:64

cbe_3810791 EPHB1

EphB1

length=984

15 MALDYLLLLLLASAVAAMEETLMDTRTATAELGWTANPASGWEEVSGYDENLNTIRTYQV
CNVFEPNQNNWLLTTFINRRGAHRIYTEMRFTVRDCSSLPNVPGSCKETFNLYYYETDSV
IATKKSafWSEAPYLKVDITAADESFSQVDFGGRMLKVNTEVRSFGPLTRNGFYLAQDY
GACMSLLSVRVFFKKCPISIVQNFAVFPETMTGAESTSLVIARGTCIPNAEEVDVPIKLYC
NGDGEWMVPIGRCTCKPGYEPENSACKACPAGTFKASQEAEGCSHCPSNSRSPAEASPI
CTCRTGYRADFDPEVACTSVPSGPRNVISIVNETSIILEWHPPRETGGRDDVTYNIIC
20 KKRADRRSCSRCDNVEFVPRQLGLTECRVSISSLWHTPYTFDIQAINGVSSKSPFPF
QHVSVNITTNQAAPSTVPIMHQVSATMRSITLSWPQPEQPNGIILDYEIRYYEKEHNEFN
SSMARSQNTARIDGLRPGMVVVQVRARTVAGYKFGSKMCFQTLTDDDYKSELREQLP
LIAGSAAAGVVFVSLVAISIVCSRKRAYSKEAVYSDKLQHYSTGRGSPGMKIYIDPFTY
EDPNEAVREFAKEIDVSFVKIEEVIGAGEFGEVYKGRLLKPGKREIYVAIKTLKAGYSEK
25 QRRDFLSEASIMQFDHPNIIIRLEGVVTKSRPVMIIITEFMENGALDSFLRQNDGQFTVIQ
LVGMLRGIAAGMKYLAEMNYVHRDLAARNILVNSNLVCKVSDFGLSRYLQDDTSDPTYTS
SLGGKIPVRWTAPEAIAYRKFTSASDVWSYGIWMVEVMSFGERPYWDMNQDVINAIEQD
YRLPPMDCPAALHQLMLDCWQKDRNSRPRFAEIVNTLDKMI RNPA SLKTVATITAVPSQ
PLLDRSIPDFTAFTTVDDWLSAIKMOVYRDSFLTAGFTSLQLVQTMTSEDLLRIGITLAG
30 HQKKILNSIHSRMVQISQSPTAMA

Table 74

35 SEQ ID NO:65

cbe_3820530 PGAM1

phosphoglycerate mutase 1 (brain)

length=254

40 MAAYKLVLIRHGESAWNLENRFSGWYDADLSPAGHEEAKRGQALRDAGYEFDICFTSVQ
KRAIRTLWTVLDAIDQMWLPPVVRTWRLNERHYGGLTGLNKAETAAXHGEAQVKIWRRSYD
VPPPPMEPDHPFYNSISKDRRYADLTEDQLPSCESLKDTIARALPFWNEEIVPQIKEGKR
VLIAAHGNSLRGIVKHLEGLSEEAIMELNLPTGIPIVYELDKNLKPIKPMQFLGDEETVR
KAMEAVAAQGKAKK

45 Table 75

SEQ ID NO:66

cbe_3825897 POLR2L

polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa

length=67

50 MIIPVRCFTCGKIVGNKWEAYLGLLQAEYTEGDALDALGLKRYCCRRMLLAHVLDLIEKLL
NYAPLEK

Table 76

55 SEQ ID NO:67

cbe_3826540 NYD-TSP1

testis-specific protein NYD-TSP1

length=430

MASSAKSAEMPTISKTLNPTDPHQEYLDPRITIALFEIGSHSPSSWGSPLFLKNSSHQV
TEQQTAKQFNLLKEIKDILKNMAGFEKITEAKELFEETNITEDVSAHKENIRGLDKIN
EMLSTNLPVSLAPEKEDNEKKQEMILETNITEDVSAHKENIRGLDKINEMLSTNLPVSLA
5 PEKEDNEKKQQMIMENQNSENTAQVFARDLVNRLEEKKVNETQQSQEKAKNRLNVQEET
MKIRNNMEQLLQEAHWSKQHTELSKLIKSYQKSQKDISETLGNNGVGFQTQPNNEVSAK
HELEEQVKKLSHDTYSLQLMAALLENECQILQQRVEILKELHHQKQGTLEKPIQINYKQ
DKKNQKPSEAKKVEYKQNKQAMKGTFWKKDRSCRSLDVCLNKKACNTQFNIHVARKALR
10 GKMRSSASSLR

Table 77

SEQ ID NO:68

cbe_3833533 TRIM29

15 tripartite motif-containing 29

length=588

MEAADASRSNGSSPEARDARSPSGPSGSLNGTKADGKDAKTTNGHGGEAAEGKSLGSAL
KPGEGRSALFAGNEWRRPIIQFVESGDDKNSNYFSMDSMEGKRSPYAGLQLGAAKKPPVT
FAEKGELRKSIFSESRRKPTVSIMEPGETRRNSYPRADTGLFSRSKSGSEEVLCDSICGNK
20 QKAVKSCLVQCASFCEHLKPHLEGAAFRDHQLLEPIRDFEARKCPVHGKTMELFCQTDQ
TCICYLCMFQEHKNHSTVTVEEAKAEKETELSLQKEQLQLKIIIEIEDEAEKWQKEKDRIK
SFTTNEKAILQNFRLDVRDLEKQKEEVRAALEQREQDAVDQVKVIMDALDERAKVLHED
KQTREQLHSISDSVLFLEQFEGALMSNYSLPPPLPTYHVLLEGEGLGQSLGNFKDDLNV
MRHVEKMKCADLSRNFIERNHMENGGDHRYVNNYTNSTFGGEWSAPDTMKRYSMYLT
25 VRTSYQPSPPGRFTKETTKQNFNNLYGTGKNYTSRVWEYSSSIQNSDNDLPVVQGSSSFS
LKGYPSLMRSQSPPKAQPQTWKSQKQTMLSHYRPFYVKNKNGIGSNEAP

Table 78

SEQ ID NO:69

cbe_3834015 TFPI

tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)

length=304

MIYTMKKVHALWASVCLLLNLAPAPLNADSEDEEHTIITDTELPPLKLMHSFCAFKADD
35 GPCKAIMKRFFFNIFTRQCEEFIYGGCEGNQNRPFESLEECKKMCTRDNANRIIKTTLQQE
KPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDGPN
GFQVDNYGTQLNAVNNSLTPQSTKVPSLFEFHGPSWCLTPADRGLCRANENRFYNSVIG
KCRPFKYSGCGNENNFSTSKQECLRACKKGFIQIRISKGLIKTKRKRKKQRVKIAEYEEIF
40 VKNM

Table 79

SEQ ID NO:70

cbe_3842044 PSMB3

45 proteasome (prosome, macropain) subunit, beta type, 3

length=205

MSIMSYNGGAVMAMKGKNCVAIAADRRFGIQAQLVTDFQKIFPMGDRLYIGLAGLATDV
QTVAQRLKFRNLNLYELKEGRQIKPYTLMSMVANLLYEKRFGPYYTEPVIAGLDPKTFKPF
ICSLDLIGCPMVTDDFVVSQCAEQMYGMCESLWEPNMDPDHLFETISQAMLNVDRAV
50 SGMGVIVHIIEDKITTRTLKARMD

Table 80

SEQ ID NO:71

55 cbe_3845697 Hs.191063

Human DNA sequence from clone RP1-63M2 on chromosome 20 Contains the gene for
CBFA2T2 (core-binding factor, runt domain, alpha subunit 2; translocated to,

2), part of a gene for a protein similar to ACTIN, the E2F1 (E2F transcription factor 1) gene, a nov
length=412

5 DRGREVSGRRSRVARRSGAFSPAAGPSPKVASVSGSRRVHRPSSLGRIAVVVDQGS GFTK
AGFAGENQPRIVLKSSSLVPSWDRPVLPAGPCELAGGVARAHPIKHGVADWEALEGLW
ERLLVGGLRVCPEQWPVLVSDSPLAPPAGRERVAELLFETLAVPACHMASTALLALCSTG
AFSGLAVEAGAGVCHATPIYAGHSWHQATFRLNVAGSTLSRYLRDLLVAANPDLLQQALP
RKAITHLKKRSCYVSLDFEGDLRDPARHHPASFSVNGCCVCLSSERFRCPEPIFQPGLL
10 GQAEQGLPALAFRALQKMPKTLRTRLADTVVLGGSTLFPGF AERLDKELEAQCRRHGYA
ALRPHLVAKHGRGMAVWTGGSMVASLHSFQRRWITRAMYQECGRLLYDVFN

Table 81

15 SEQ ID NO:72
cbe_3849002 CKLF1
chemokine-like factor 1
length=152
MDNVQPKIKHRPFCFSVKGHV KMLRLALTVTSMTFFIIAQAPEPYIVITGFEVTVILFFI
20 LLYVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVC
CLADGALIYRKLLFNPSGPYQKKPVHEKKEVL

Table 82

25 SEQ ID NO:73
cbe_3880186 FLJ20343
hypothetical protein FLJ20343
length=501
MAQPHTTSVPYFARSPAPPPPSRSGAPPQPPATLRPSRRRTRP RPADRRDAPADCAYLW
30 RILTPRRGRARRSDVGARHRACGRRDVL LSRQGPANPEGARRVVGGQERVWPAVRRGRGG
SMFRLLSWSLGRGFLRAAGRRRCRGCSARLLPGLAGGPGPEVQVPPSRVAPHGRGPGLLPL
LAALAWFSRPAAAEQ QGADGAAEDGADEAEAEI IQLLKRAKLSIMKDEPEEAELIL
HDALRLAYQTDNKKAITTYTDLMANLAFIRGQLENAEQLFKATMSYLLGGGMKQEDNAII
EISLKLASIYAAQNRQEFVAGYEF CISTLEEKIEREKELAEDIMSVEEKANTHLLLGMC
LDACARYLLFSKQPSQAQRMYEKALQISEEIQGERHPQTIVLMSDLATTLDAQGRFDEAY
35 IYMQRASDLARQINHP ELMVLSNLA AVL MHRERYTQAKEIYQEALQAKLKKDEISVQH
IREELAELSKSRPLTNSVKL

Table 83

40 SEQ ID NO:74
cbe_3884811 RCP
Rab coupling protein
length=649
MSLMVSAGRGLGAVWSPTHVQVTVLQARGLRAKGP GGTSDAYAVIQVGKEYATSVSERS
45 LGAPVWREEATFELPSLLSSGPA AATLQLTVLHRALLGLDKFLGRAEVDLRLDHRDQGR
RKTQWYKLKSKPGKKDKERGEIEVDIQFMRNNMTAS MFDLSMKDKSRNPFGLKDKIKGK
NKDSGSDTASAIIPSTTPSVSDDES SVKDKKKKSKI KTL LSKSNLQKTPLSQSMSVLPT
SKPEKVLRLRPGDFQSQWDEDDNEDESSASDVMSHKRTASTDLKQLNQVNFTLPKKEGLS
50 FLGGLRSKNDVLSRSNVCINGNHVYLEQPQPTGEIKDSSPSSSPSPKGFRKKT LFSSTEN
LAAGSWKEPAEGGGLSTD RDVSESSTKDSLKSMTLPT YRPAPLISGDLREKMAPANSEAT
KEAKESKKPESRRSSLLSMTGKKDVAKGSEGENLLTVPGREKEGMLMGVKPGEDASGPA
EDLVRRSEKDTAAVVS RQGSSSLNLFEDVQITEPEAEPE SKSEPRPPISSPRAPQTRAVKP
RLHPVKPMNATATKVANCSLGTATII SENLNNEVMKKYSPSDPAFAYAQLTHDELIQLV
55 LKQKETISKKEFQVRELEDYIDNLLVRVMEETPNILRIPTQVGKKAGKM

Table 84

SEQ ID NO:75
cbe_4138433 KIFAP3
kinesin-associated protein 3
length=792

5 MQGEDARYLKRKVKGGNIDVHPSEKALIVHYEVEATILGEMGDPMLGERKECQKIIRLKS
LNANTDITSLARKVVEECKLIHPSKLNVEVEQLLYLQNRDLSLGSKEKKEKSSKPKDPPP
FEGMEIDEVANINDMDEYIELLYEDIPDKVRGSALILQLARNPDNLEELLNLETALGALA
RVLREDWKQSVELATNIIYIFFCFSSFSQFHGLITHYKIGALCMNIIDHELKRHELWQEE
10 LSKKKKAVDEDPENQTLRKDYKTFKKYQGLVVKQEQLLRVALYLLNLAEDTRTELKMR
NKNIVHMLVKALDRDNFELLILVVSFLKKLSIFMENKNDMVEMDIVEKLVKMIPCEHEDL
LNITLRLLLNLSFDTGLRNKMVQVGLLPKLTALLGNDNYKQIAMCVLYHISMDDRFSMF
AYTDCIPQLMKMLFECSDERIDLELISFCINLAANKRNVQLICEGNLKMMLKRALKFKD
PLLMKMI RNISQHDGPTKNLFI DYVGDLAAQISNDEEEEFVIECLGTLANLTIPDLDWEL
15 VLKEYKLVYPYLKDKLKPGAAEDDLVLEVIMIGTVSMDDSCAALLAKSGIIPALIELLNA
QQEDDEFVCQIIYVFYQMVFHQATRVDIIKETQAPAYLIDLMHDKNNEIRKVCNDTLDII
AEYDEEWAKKIQSEKFRWHNSQWLEMVESRQMDSESEQYLYGDDRIEPIIHEGDILERPDL
FYNSDGLIASEGAISPDDFNDYHLQNGDVVGQHSFPGSLGMDGFGQPVGILGRPATAYGF
RPDEPYYYGYGS

20

Table 85
SEQ ID NO:76
cbe_4279962 DKKL1-pending
soggy-1 gene

25

length=242
MGEASPPAPARRHLLVLLLLLSTLVI PSAAPIHDADAQESSLGLTGLQSLQGF SRLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS
ENNVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWIIKLPRRRSH
30 QDALEGGHWLSEKRRHLQAIRDGLRKGT HKDVL EEGTESSSHSRLSPRKTHLLYILRPSR
QL

30

Table 86
SEQ ID NO:77

35

cbe_4281271 CRYAB
crystallin, alpha B
length=175
MDIAIHHPWIRRPFFPFHSPSR LFDQFFGEHLLESDFPTSTLSLSPFYLRPPSFLRAPSW
FDTGLSEMRLEKDRFSVNLDVKHFSPEELKVVLGDVIEVHGKHEERQDEHGFISREFHR
40 KYRIPADVDPLTITSSLS SDGVLTVNGPRKQVSGPERTIPITREEKPAVTAAPKK

40

Table 87
SEQ ID NO:78

45

cbe_4344185 SRA1
steroid receptor RNA activator 1
length=237
MTRCPAGQAEVEMAELYVKPGNKERGWNDDPPQFSYGLQTQAGGPRRSLLTRVAAPQDGS
PRVPASETSPGPPPMGPPPPSSKAPRSPVVGSGPASGVEPTSFVPESEARLMEDVLRPLE
50 QALED CRGHTRKQVCD DISRRLALLQE QWAGGKLSIPVKRMALLVQELSSHRWDAADDI
HRSLMVDHVTEVSQWMVGKRLIAEKRS LFSEEAA NEEKSAATAEKNHTIPGFQQAS

50

Table 88
SEQ ID NO:79
cbe_4383836 KIAA0905
yeast Sec31p homolog

55

length=1220

MKLKEVDRTAMQAWSPAQNHPIYLATGTSAAQQLDATFSTNASLEIFELDLSDPSLDMKSC
ATFSSSHRYHKLWGPYKMDSKGDVSGVLIAGGENGNIILYDPSKI IAGDKEVVIAQNDK
HTGPVRALDVNIFQTNLVASGANESIEIYIIDLNNFATPMTPGAKTQPPEDISCIAWNROV
5 QHILASASPSGRATVWDLRKNEPIIKVSDHSNRMHCSGLAWHPDVATQMVLADEDDRLPV
IQMWDLRFASSPLRVLENHARGILAIWMSMADPELLLSGCKDAKILCSNPNTGEVLYELP
TNTQWCFDIQWCPRNPVLSAASFDGRISVYSIMGGSTDGLRQKQVDKLSSTSGNLDPFPG
TGQPLPPLQIPQQTAAHSIVLPLKKPKWIRRPVGASFSFGGKLVTFENVRMPSHQGAEQ
QQQHHVFISQVVTEKEFLSRSDQLQQAQVQSQGFINYCQKKIDASQTEFEKNVWSFLKVN
10 FEDDSRGKYLELLGYRKEDLGKKIALALNKVDGANVALKDSQVAQSDGEESPAEEQLL
GEHIKEEKEESEFLPSSGGTFNISVSGDIDGLITQALLTGNFESAVDLCLHDNRMDAII
LAIAGGQELLARTQKKYFAKSQSKITRLITAVVMKNWKEIVESCDLKNWREALAAVLTYA
KPDEFSALCDLLGTRLENEGDSLLQTQACLCYICAGNVEKLVACWTKAQDGSHPHSLQDL
IEKVVILRKAVQLTQAMDTSTVGVLLAAKMSQYANLLAAQGSIAAALAFPLDNTNQPNIM
15 QLRDRLCRAQGEPEVAGHESPKIPYEKQQLPKGRPGPVAGHHQMPRVQTQQYYPHGENPPP
PGFIMHGNVNPNASGQLPTSPGHMHTQVPPYPQPPYQPAQPPYFPGTGGSSAMYRPPQPPVA
PPTSNAYPNTPYISSASSYTQGSQLYAAQHQAASSPTSSPATSFPPPPSSGASFQHGPGGA
PPSSAYALPPGTTGTLPAASELPASQRTGPNQGWNDPPALNRVPPKKKMPENFMPPVPI
TSPIMNPLGDPQSMQLQQQPSAPVPLSSQSSFPQPHLPGGQPFHGVQQPLGQTGMPPSFS
20 KPNIEGAPGAPIGNTFQHVQSLPTKKITKKPIPDEHLILKTTTFEDLIQRCLSSATDPQTK
RKLLDDASKRLEFLYDKLREQTLSPITITSLGHNIARSIETRNYSEGLTMHITHIVSTSNFSE
TSAFMPVLKVVLQANKLGV

Table 89

SEQ ID NO:80

cbe_4540466 PUM1

pumilio homolog 1 (Drosophila)

length=1186

MSVACVLKRKAVLWQDSFSPHLKHHQPQEPANPNMPVVLTSQTGSQAQPQPAANQALAAGT
30 HSSVPVGSIGVAGRSQDDAMVDYFFQRQHGEQLGGGGSGGGYNNSKRWPTGDNIHAEH
QVRSMDLNDHDFQALALEGRAMGEQLLPKKFWETDESSKDGPKGIFLGQWRDSAWGTS
DHSVSQPIMVQRRPGQSFHVNSEVNSVLSRSESGGLGVSMVEYVLSSTPGDSCLRKGGF
GPRDADSDENDKGEKKNKGTFTDGLKDLKEEGDVMKTNGLPVQNGIDADVKDFSRTPG
NCQNSANEVDLLGPNQNGSEGLAQLTSTNGAKPVEDFSNMESQSVPLDPMEHVGMEPLQF
35 DYSGTQVPVDSAAATVGLFDYNSQQQLFQRPNALAVQQLTAAQQQQYALAAHQPHIGLA
PAAFVPNPYIIISAAPPGTDPYTAGLAAAATLGPVAVPHQYYGVTPWGVYPASLFQQQAAA
AAAAATNSANQQTTPQAQQGQQQVLRGGASQRPLTPNQNGQQQTDPLVAAAANVSALAFG
QGLAAGMPGYPVLAPAAYYDQTGALVNVNAGARNLGAPVRLVAPAPVIISSSAAQAATAA
AAASANGAAGGLAGTTNGPFRPLGTQQPQQPQQPNNNLASSSFYGNNSLNSNSQSSSL
40 FSQGSAAQPANTS LGFGSSSSSLGATLGSA LGGFGTAVANSNTGSGSRRLSLTGSSDLYKRT
SSSLTPIGHSFYNGLSFSSSPGPGVMPLPSQGPQHSQTTPPSLSSHGSSSSSLNLGGLTNG
SGRYISAAPGAEAKEYRSASSASSLFSSTLFSRRLRYGMSDVMPSGRSRLLEDFRNNR
YPNLQLREIAGHIMEFSQDQHGSRFIQLKLERATPAERQLVFNEILQAAYQLMVDVFGNY
VIQKFFEFGSLEQKLALAEIRIGHVLSLALQMYGCRVIQKALEFIPSDQQNEMVRELDGH
45 VLKCVKDQNGNHVVQKCIQVQPSLQFIIDAFKQGVFALSTHPYGCRVIQRIELHCLPD
QTLPILEELHQHTEQLVQDQYGNVVIQHVLEHGRPEDKSKIVAEIRGNVLVLSQHKFASN
VVEKCVTHASRTERAVLIDEVCTMNDGPHSALYTMMDQYANYVVQKIDVAEPGQRKIV
MHKIRPHIATLRKYTYGKHILAKLEKYYMKNGVLDLGPICGPPNGII

Table 90

SEQ ID NO:81

cbe_4567083 LOC157378

hypothetical protein BC017881

length=178

MEALNTAQGARDFIYSLHSTERSCLLKEHHRFESIAIAQEKLEAPPPTPGQLRYVFIHNA
IPFIGFGFLDNAIMIVAGTHIEMSIGIILGISTMAAAALGNLVSDLAGLGLAGYVEALAS

RLGLSIPDLTPKQVDMWQTRLSTHLGKAVGVTIGCILGMFPLIFFGGGEEDEKLETKS

Table 91

SEQ ID NO:82

cbe_552975 HPV 1a E1

Human Papillomavirus 1a E1

length=612

MADNKGTENDWFLVEATDCEETLEETSLGDLDNVSCVSDLSDLLDEAPQSQGNSLELFHK
QESLESEQELNALKRKLLYSPQARSADETDIASISPRLETISITKQDKKRYRRQLFSQDD
SGLELSLLQDETENIDESTQVDQQQKEHTGEVGAAGVNILKASNIRAALLSRFKDTAGVS
FTDLTRSYKSNKTCGDWVLAVWGVRENLIDSVKELLQTHCVYIQLEHAVTEKNRFLFLL
VRFKAQKSRETVIKLITTILPVDASYILSEPPKSRVAAALFWYKRSMSTVFTWGTTL
WIAQQTLINHLQDSESPFELCKMVQWAYDNGHTEECKIAYYYAVLADEDENARAFSSNS
QAKYVKDCAQMVRHYLRAEMAQMSMSEWIFRKLDNVEGSGNWKEIVRFLRFQEVFISFM
IAFKDLLCGKPKKNCLLIFGPPNTGKSMFCTSLKLLGGKVISYCNSKSQFWLQPLADAK
IGLLDDATKPCWDYMDIYMRNALDGNITCIDLKHRAPQQIKCPPLLITSNIDVKSDTCWM
YLHSRISAFKFAHEFPFKDNGDPGFSLTDENWKSFFERFWQQLELSDQEDEGNDGKPQQS
LRLTARAANEPI

Table 92

SEQ ID NO:83

cbe_552976 HPV 11 L2

Human papillomavirus 11 L2

length=455

MKPRARRRKRSATQLYQTCKATGTCPPDVIPKVEHTTIADQILKWGSLGVFFGGLGIGT
GAGSGGRAGYIPLGSSPKPAITGGPAARPPVLVEPVAPSDPSIVSLIEESAIINAGAPEV
VPPTQGGFTITSSSETTPAILDVSVTNHTTTSVFQNPFLTPEPSVIQPPVEASGHILIS
APTITSQHVEDIPLDTFVVSSSDSGPTSSTPLPRAFFRPRVGLYSRALQQVQVTDPAFLS
TPQRLVTYDNPVYEGEDVSLQFTHESIHNAPDEAFMDIIRLHRPAITSRRGLVRFSRIGQ
RGSMTYTRSGQHIGARIHYFQDISPVTQAAEEIELHPLVAAENDTFDIYAEPFDPI PDPVQ
HSVTQSYLTSTPNTLSQSWGNTTVPLSIPSDWVQSGPDITFPTASMGTPFSPVTPALPT
GPVFITGSDFYLHPTWYFARRRRKRIPLFFTDVAA

Table 93

SEQ ID NO:84

cbe_71919 FLJ13236

hypothetical protein FLJ13236

length=341

MAKGLLVTYALWAVGGPAGLHHLYLGRDSSHALLWMLTLGGGGLGWLWEFWKLPSFVAQAN
RAQQQRQSPRGVTPPLSPIRFAAQVIVGIYFGLVALISLSSMVNFYIVALPLAVGLGVLL
VAAVGNQTSDFKNTLGSAFLTSPIFYGRPIAILPISVAASITAQRHRRYKALVASEPLSV
RLYRLGLAYLAFTGPLAYSALCNTAATLSYVAETFGSFLNWFSEFFLLGRLMEFVLLLPY
RIWRLLMGETGFNSSCFQEWAKLYEFVHSFQDEKRQLAYQVLGLSEGATNEEIHRSYQEL
VKVWHPDHNLDDQTEEAQRHFLEIQAAEVLVSQPRKPWGSRR

Nucleic Acid SEQ IDs:

Table 94

SEQ ID NO:85

cbe_1380530 RPL13

ribosomal protein L13

length=1110

ctttccgctcggtgttttctgcgaggagccgcagggccgtaggcagccatggcgccc
 agccggaatggcatggtcttgaagccccacttccacaaggactggcagcggcgcggtggcc
 acgtggttcaaccagccggccccgtaagatccgcagacgtaaggcccggaagccaaggcg
 cgccgcatcgccccgcgccccgcgtcggtcccatccggcccatcgtgcgctgccccacg
 gttcggtagcacacgaaggtgcgcgccggccgcggcttcagcctggaggagctcaggggtg
 gccggcattcacagaaggtggcccgaccatcggcatttctgtggatccgaggaggcgg
 aacaagtccacggagtccctgcaggccaacgtgcagcggctgaaggagtaccgctccaaa
 ctcatcctcttccccaggaagccctcgcccccaagaaggagacagttctgctgaagaa
 ctgaaactggccaccagctgaccggaccggtcatgcccgccggaacgtctataagaag
 gagaaagctcgagtcactgaggaagagaagaatttcaaagccttcgctagtctccgt
 atggcccgtgccaacgcccggctcttcggcatacgggcaaaaagagccaaggaagccgca
 gaacaggatgttgaaaagaaaaataaagccctctggggacttggaatcagtcggcagt
 catgctgggtctccacgtggtgtgttctggtgggaacaactgggcctgggatggggcttca
 ctgctgtgacttctcctgccaggggatttggggcttcttgaaagacagttccaagccct
 ggataatgctttactttctgtgttgaaagcactgttggtgtttgggtagtgtgactgatga
 aaacgggttttctgtggggaggttacagaggctgacttcagagtggacttgtgttttttc
 tttttaaaagaggcaaggttgggctggtgctcacagctgtaatcccagcactttgaggttg
 gctgggagttcaagaccagcctggccaacatgtcagaactactaaaaataaagaaatcag
 ccatgaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Table 95

SEQ ID NO:86

cbe_1469980 FLJ20259

hypothetical protein FLJ20259

length=3101

gagggttgaatgtaagatggcgcccaggagagctgtgaggagaaaaccctgtcggtcttgg
 agcgacgacggcagaaccaggggtccctggcggtgcggcggggcccggcggtgcagcggag
 gcggcgggcgggcgggcagtgacgtcgccggaatattagaagtcttaagaactcaggaca
 agcagcagaaatcatgcaacatggtgactggaaccctaaggactctgcaatatgaataa
 ttccctagagaacaccatctcctttgaagagtacatccgagtaaaggcacgggtctgtccc
 gcaacacaggatgaaggaatttctggactcactggcctctaagggggccagaagcccttca
 ggagttccagcagacagccaccactaccatggtgtaccaacaggggtgggaactgcatata
 cacagacagcactgaagtggctgggtcttctgctgaacttgctgtccagtaccaccag
 tgttcagccacaaacccagcaagaacagcagatccaggttcagcagccgcagcaggttca
 ggtccaggtgcaggtacagcagctctccgcaacaggtctcggtcagctctccccacaact
 caccgttcaccagcctactgagcaacccatccaggtccaggtgcagatccaaggccaggc
 accacagtcagcagccccctccattcagaccccgctctctgcagagtccagtcctcgca
 gctgcaagcagctcagatccaggtgcagcagctgcaagcagcccagcagatccaggctgc
 agaaatcccggaggagcacatcccacatcagcaaatccaggctcagctggtggctggcca
 gtctcttgctggtggtcagcagatccaaatccagaccgtgggtgccctttccccaccacc
 atcccagcaggggtcaccocgggaaggggagcgggcggttggcacggccagtgctcca
 accagtgaagaagcgcaaaagtggagatgcccatcactgtgtcctacgccatctcagggca
 gccggtggccaccgtgctggccattccacagggccagcagcagagttatgtgtctttgag
 gccagacttactgacagttagacagtgccacctgtacagtgccactgggaccattactag
 ccctacaggagaaacctggaccatccctgtttattctgccagccccggggggaccctca
 gcagcagagcattaccacattgccattccccagggaagcctacaacgcagttcacgtcag

tggctcaccacagccctggcagctgttaagctggaggatgacaaggagaagatgggtggg
 caccacatctgtagtgaaaaactcccatgaagaggtagtgcagacccttgcaaactctct
 ctttccagcacagttcatgaatggcaacatccacattccagtggtgtgcaggctgtggc
 5 aggcacgtaccagaatacggctcaaactgtccatatatgggacccccaacagcagccgca
 gcagcaaactcccaggaacagacaccaccacagcagcagcagcagcaactccaagt
 tacttgttcagctcaaactgtccaggttgcaggtgaagttgaaccacagtcacagccacagcc
 tccccagaacttctgcttccaaattctttgaagccagaagaagggttgaagtatggaa
 aaactgggcccagaccaagaatgctgaactagagaaggatgctcagaacagattggcacc
 10 cattgggaggcgccaactgctgcgattccaggaagatctcatctcctctgctgtggcaga
 gttgaattatgggctctgtctaatacgacaggggaagctcgaaatggagaagggtgaacccta
 tgaccagatgtgctctactatatttctctgtgtattcaaaagtatctttttgaaaatgg
 aagggtagatgacattttctccgactctttatgttcgggtcacggagtggctacatga
 agttctgaaggatgttcagccccgggtcactccacttggctatgtcttcccagccacgt
 gactgaggagatgctatgggagtgaagcagcttggggctcactccccctccaccttgc
 15 gaccaccctcatgttctttaataccaagtacttctattgaagacagtgaccagcacat
 gaagctggccttctccaaggtcttgcgacagacaaagaagaacccctctaataccaagga
 taaaagcacgagtatccgggtacttgaaggcccttggaaatacaccagactggccagaaagt
 tacagatgacatgtatgcagaacagacggaaaaatccagagaatccattgagatgtcccat
 caagctctatgatcttctacctcttcaaatagccccagagtgtgaaaggccggaatgacac
 20 cttttacctgacacctgagccagtggtggcccccaacagcccaatctggtactcagcca
 gcctatcagcagagagcagatgggacaaatgctgacgcggatcctggtgataagagaaat
 tcaggaggccatcgagtgcccaatgcaagcactatgcactgagatgccttggccatggc
 acaagagaaaccagccaggaaaaaccagacagactttcacactaaagaagaggcctccat
 ttttttttttcttttttttatttggtgtagttacgaagcctttcaggctgcttctgttaa
 25 aatataaaaagaaaactttgccccctttgcatcttcataaacctgctgcggcagactcctc
 agccgatggtggctctgggtttccttgagtgtcatatgtcccagaaagtgtctggctgac
 tcttttttgtctggggcctggggaaagggttggactgtgaaaagaaatgtggcccttt
 ccatcttcaagagagatggaattaatgatggatggaccctggaggggaatctcccagccg
 acttccactgggctgacagactttgctgaccacaggggaacgatgttcttttctttcttc
 30 atgatcagacataaacttagcatcttaattggaagaaaaatgaggggaacttcaattatga
 tttattaaagacaatttctattaaaaaaaaaaaaaaaaaaaaa

Table 96

35 SEQ ID NO:87
 cbe_1505425 HCDI
 HCDI protein
 length=1522
 agtcgctatgcgtgtcttgtgggtgagggagggcagaaaggagagtgctgggcgggctt
 40 agtcggagattgaggactgggaatccgcttccgggagggcactgtctagtgcacaggcaa
 cctggccttcgcctcctagcccgagaagccgaatctccctaatacctgtgacctgtgtca
 cctctgcatcgcgaggagggggataaagtggggagaagtctggtgtcagatgggatggcgc
 cggaagaggggtgccacagcggggacggaaggcgcccccaaccccaactccacgggaatata
 45 aacaatttgtattttccgatcaggtggcgggacaggcttcattgggacagccctaacc
 gctgctgaatgccagaggcacgaagtacgttgggtctccgaaagccgggcccggcgg
 atcacgtgggatgagctcgctgcacggggctgccgagctgcgatgccgcccgtcaacctg
 gccggagagaacatcctcaaccctctccgaagatggaatgaaaccttccaaaaagaggtt
 ctcggcagccgcttagagaccaaccaattgctggctaaagccatcaccaaagccccacaa
 50 ccccccaaggcctgggtcttagtcacaggtgtagcttactaccagcccagtctgactgcg
 gagtatgatgaagacagcccaggaggggactttgacttttctccaacctcgtaaccaa
 tgggaagctgcagccaggcttctggagattctacacgcaggtgggtggcgctcagggt
 gttgtgctgggcctgggggtgggtgcatggggccacatgctgctgccctttcgccctgggc
 ctggggggcccatcggtcaggccaccaattcttcccctggatacacatcggggacctg
 55 gcaggaatcctgacccatgcccttgaagcaaaccacgtgcacggggctcctgaatggagt
 gctccatcctccgccactaatgctgagtttggccagaccttgggtgctgccctgggcccgc
 cgagccttcatccctctcccagcgtgtggtgcaagctgtcttgggagacagcgtgcc
 atcatgctgctggaggccagaaggatgacccacagcgaacactggccactggctaccag

tattccttcccagagctaggggctgccttaaaggaaattgtagcctaagtaggtcgtggc
 aagggcctgaggcctgttcctcacaggcttccagggttaggcactgtgaataggctcagct
 cctctagagagctgaagccatctgggtcttagattcctctcccagtcctcttcccattg
 ttctgttgctccaccttattgtctcaaggccgtaatctcatcaggttgggacattaatct
 5 tttcaactccttgtaagatttcccagtttggttctctacatgtcctgcagctgccccac
 ttctcctttacgctgtgtagagaatgctctgcagtttaggcaataaaaaataaattgtctc
 actaaaaaaaaaaaaaaaaaaaaa

10 Table 97

SEQ ID NO:88

cbe_1710 QP-C

low molecular mass ubiquinone-binding protein (9.5kD)

length=428

15 aaaaataagtaggaagtgtcaattttaatttggttcagtttccggagggcgagctgag
 ccctggccgcgccacaatgggcccgcgagtttggaatctgacgcggatgcggcatgtga
 tcagctacagcttgccacgttcgagcagcgcgcctatccgcacgtcttcactaaaggaa
 tccccaatgttctgcgcgcgcatcgggagtccttcttccgctggtgccgcagttttag
 tgttttatcttatctacacatgggggactgaagagttcgagagatccaagaggaggatcc
 20 agctgcctatgaaaatgacaaatgagcaacgcacccggatgacgggtccctgtctctgaa
 agacctttctctggaagaggagctctgcattgtagtgtctcaaagacacaataaacttct
 atgggtctg

25 Table 98

SEQ ID NO:89

cbe_1796502 CTNND2

catenin (cadherin-associated protein), delta 2 (neural plakophilin-related
 arm-repeat protein)

length=4746

30 gccagcatcccttgtcccgcggcgggctcagacaacaaaagcggaagatgctgcagttgg
 gcaaggtcaggaccttgccctgaaagccgggcccgcgcgcaacgcctcttcccggact
 gaggagctgtcgccggcggagggtgcatgtttgaggaagccgcgggcccgcgcctt
 tgggagctatgcctgttccagaccagccttcatcagcctcagagaagacgagttccctga
 35 gccccggcttaaaccacctccaacggggatggctctgaaacagaaaccacctctgccatcc
 tcgcctcagtc aaagaacaggaattacagtttgaaaggctgaccccgagagctggaggctg
 aacggcagatcgtagccagccagctggagcgcagcaagctcggatccgagactggcagca
 tgagcagcatgagttcagcagaagagcagtttcagtgccagtcacaagatggtcaaaaag
 atatcgaagatgagcttacaacaggtctcgagctggtggactcctgtattaggtcactac
 40 aggaatcaggaatacttgaccacaggattattctacaggtgaaaggccagcctgctct
 cccagagtgcacttcagctcaattccaaacctgaagggtcttccagtatccggccagct
 accatagcaaccagaccctggccctgggggaaaccacccttcacagctcccggcccag
 gcacacaagcccagctacggggccagagcttcagccagggcacgaccagccgcgcggcc
 acctggcggggcccagaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 45 ccagcctgggcagcgccttccacctgcccagcgcgcgcgcgcgcgcgcgcgcgcgcgc
 tctactactccagctccacgctgcccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 cccagggcggttcgcccaccaagctgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc
 acgcgcgcgcgcgcgcgcgcctctcgcccagcagtcgcccagccgcctggccaagtctaca
 gcaccagctcgcccatcaacatcgtcgtgtcctcgcccggcctgtccccgatccgcgtga
 50 cctcgccccccaccgtgcagtcacccatctcctcctcgcccatccaccagctgagctcca
 cctcgggcacgtacgccacctgtcgcccaccaagcgctggtccacgcgtccgagcagt
 acagcaagcactcgaggagctgtatgccacggccacctccagaggccgggcagcctgg
 cagctggttcccagcctcatcacgcagccagcatgggcacctggggcccagagttgccccg
 cctgcagtcccagaaacaccacatagatcccatctatgaagaccgcgtctatcagaagc
 55 cccctatgaggagctcagccagagccagggggaccctctgccgcagcacacaccggca
 cctaccgcagcagcacagccccatcttccctggtgtcgactccgtccccttgacgcgca
 caggcagccagcacggcccacagaatgccgcgcgcgcgcgcgccttccagaggccagctatg

cgcgcggccagcctccaattacgcggaccctaccgacagctgcagattgtccctctg
 ttgagctccatacagcaaatccggccctgctctccgcctgaaggcaccttggccaggt
 ccccgccattgatagcattcagaaagatcccagagaatttgatggagagaccggaac
 5 tgcggaagtgattcagatggtgcagcaccagtttccctcgggtccagtctaaccggcgag
 cctacttgcaacacctctgttttgagacaacaaaattaaagccgagataaggagacaag
 gaggcatccagctcctgggtggacctgttgatcatcggtgacccaagtccaccgtagt
 cctgtggagctctgagaaacctgggtgatgggaaggccaacgatgataacaaaattgccc
 tgaaaaactgtgggtggcatcccagcactgggtgaggttactccgcaagacgactgacctgg
 10 agatccgggagctgggtcacaggagtcctttggaacctctcctcatgcatgacactcaaaa
 tgccaatcatccaggatgccctagcagtagtaccacacgcgggtgattatccccactcag
 gctgggaaaaattcgctcttcaggatgatcggaataacagctgcattcatcacaggtgc
 tgcgtaacgccaccgggtgcttaaggaatgttagttcgccggagaggaggcccgagaa
 ggatgagagagtgtgatgggttacggatgccttgctgtacgtgatccagtctgcgtgg
 ggagcagtgagatcgatagcaagaccgttgaaaactgtgtgtgcattttaaggaacctct
 15 cgtaccgggtggcggcagaaacgtctcagggacagcacatgggcacggacgagctggacg
 ggctactctgtggcgaggccaatggcaaggatgctgagagctctgggtgctggggcaaga
 agaagaagaaaaagaaatcccaagatcagtggtggagtaggacctcttcagactgtg
 ctgaaccacaaaagggtaccagatgctgtggcaccatcaatagtcaaacctaccta
 cactgctctctgagtgctcaaatccagacacgctggaagggcgaggcgccctgcaga
 20 acttggtgcaggagctggaagtggtagtatatccgagccgctgtccgaaaagaga
 aaggcctgccatcctcgtggagctgctccgaatagacaatgacctgtggtgtgcgcgg
 tggccactgcgtgcggaacatggccttgagcgtcagaaataaggagctcatcggaat
 acgcatgagagacctagtccacaggcttcaggagggaacaacagcaacaactgcaa
 gcaaggccatgtcggtgacacagtgacagctgtctgctgcacactgcacgaagtatta
 25 ccaagaacatggagaacgccaaggccttacgggatgccggtggcatcgagaagtgggtcg
 gcatctccaaaagcaaaaggagataaacactctccaaaagtgggtcaaggctgcactcagg
 tctcaacagcatgtggcagtagcagatctgaggagctctacaaaaaggatggatgggt
 cacaataccactttgtagcctcgtcttcaaccatcgagagggaccggcaaggccctact
 cctcctccgcacgcccctccatctcccctgtgcgctgtctcccaacaaccgctcagcaa
 30 gtccccagcttcacctcgggaaatgatcagcctcaaagaaaggaaaacagactacgagt
 gcaccggcagcaacgccacctaccacggagctaaaggcgaacacacttcaggaaagatg
 ccatgacagctcaaaacactggaatttcaactttgtataggaattcttatgggtgcgccg
 ctgaagacatcaaacacaaccaggtttcagcacagccagtcacacaggagccagcagaa
 aagattacgagacctaccagccatttcagaattccacaagaaattacgatgagtccttct
 35 tccaggaccaggtccaccatcgccctcccgccagcagtagacacatgcacctgggtctca
 agtccaccggcaactacgttgacttctactcagctgcccgtccctacagtgaactgaact
 atgaaacgagccactaccggcctccccgactcctgggtgtgaggagcagggcacaggc
 gctccgggaacagtgcatgtgcatgcataccacaagacatttcttctgttttgttttt
 40 tctcctgcaaattagtttggtaaagcctgttccataggaaggctgtgataaccagtaag
 gaaatattaagagctatttttagaaagctaaatgaatcgcaagttaacttggaatcagta
 gaaagctaaagtgtcctaaatatgacagtgggcagcaccttctagcgtgagctgtaaa
 gtaacgagaagtgtttatactgaacgtggttgatgggaggagagacgaggcattcgggc
 cgggtggggcgtaagggttatcgttaaagcacaagacacagaatagtttacacactgtgtgg
 45 gggacggcttctcagcgtttgtttactctcttcacgtgtgactctaggcttcaggtt
 gcattgggggttctctgtacagcaagatgttcttgccctttgttaatgcattgttgttaa
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 gtatggatttccagttttcttactttctcccagtagttttaacaaaaaaaaaaaaaa
 50 gcaggaaaaaaggaaatatttagcagtagttgttcgttctgatgtgaatttgtttgtgac
 aactaaacaaggcattcagcagtttctgacaattaacatacatcattccacactccttgt
 caacaaagtgtttttcactgcctaaaatttttagatgtagatatgtgaaatagatttttt
 catttataccagttttctttatgatgatacagtggttaaaagaaaataaattacaattgat
 ctgtca

55

Table 99
SEQ ID NO: 90

cbe_1807361 FLJ22729

hypothetical protein FLJ22729

length=1278

5 aatggaggaagactggacactactgattcaacttggagatgagcgggtctgtcctcttcac
 ggcgggagagaggtggagatgctttctgaccccgctcgagggtcatccctgtactgggcctt
 acataatttctgctgtcggaaaaaatccactacacctaagaaaattactcccaatgttac
 tttttgtgatgaaaatgcaaaggagcccgaaaatgcacttgacaagctcttctcttcaga
 acagcaggttccatcttgcattgttgaatacagcatctactaaagaacttgaagcttt
 ccgattgcttcgtggaagaaggtccatcaatatcgtagagcacagagaaaactttggggcc
 10 atttcagaatttagagagtttaataatgaatgtgccttgtttaagtataaaagtacagttca
 agtttgttaactccatactttgtccaaagactggacgggaaaaaagaaagtacccggaaaa
 ccggttcctgagaaagctcctcaaaccagacatagaaagagaaagacttaagaattgcct
 gggctcaccttgatcgtaagttgacagtgtgactggcagcaaagtgaccgttggagtt
 taatgagaggaatatactcatcatcagttctattagaagagatttctcgatcatttcaa
 15 agatgcctaaagcagattttctatgttctggaaaaaacaggactatccattcagaactcat
 ctctgtttccaatactgttacattttcatatcatggaagccatgctgtatgccttattaa
 ataaaaacttttgcccaggatgggcagcatcaggtgctgagcatgaatcgaaatgcagtgg
 ggaagcattttgaactgatgattgggtgactcccgactagtggaaaagagctagtgaagc
 agtttctcttcgattctatactgaaggcggatcctcgggtgttcttcccatcagataaaa
 20 tagttcactacagacagatgtttttatctactgaactacaaagagtagaagagctttatg
 attcattattacaagctattgccttctatgaattagcagtgttgactctcagccttaga
 attctgaggttaacgtgctaaagtataattattagctctaacgtaacaccaactgttg
 aacatccatgttattggaaaagaacacattttcagtgatttttagatgtttaaattctga
 cttttggctattaaatggtttacacaataagccaagaccaaatacaataaacattttatga
 25 gaaaaaaaaaaaaaaaaa

Table 100

SEQ ID NO:91

30 cbe_2253980 Prey1135

Homo sapiens, clone MGC:14302, mRNA, complete cds.

length=1863

35 ggcacgaggcaggggtctgtctgcgacctttacggtagtgagggttagggacgatgggaga
 gcagctttgttctgaagtgccgtcgaggattaggatcgagtttcttcgatcgtgagggc
 aattattagtggtccttagccccccagatggcatcttgaggagagagaatccacgctacg
 agaactaacatagtgacatcgagttgtccgtagccgatttgcggttacggagttgtt
 gcaagtaagaaggggaaatccgagcgttctcgcttggtttctccacgtgtgaagt
 ggaatggtagtatatctcgtgctatctctgtcaagggaagaaggagaagggaatttatt
 tgaggccctacgacgtggtgcggtggctcacgcctgtaatcccaacactttgggagggcg
 40 aggcaggcggatcatctgagatcgagagttcgagaccagcttgaccaacatggagaaacc
 ccgtctctactaaaagtacaaaattagccaggcatggtggcacatgccgtaatcccagc
 tactcgggagggtgagggcaggagagtagcttgagcccaggaggcgaggttgtggtgagc
 cgagatcgcgccattgcacagcctgggcaacgagcgaactccatctcaaaaaataaat
 aaaaatttttttaaaaaaaaaaaaaaaaaaactcgaggcaaaactaacccttaataaaat
 45 taattaaccactcatctcagacctccccaccccatccaacatctcgcgatgatgaaact
 tcggctcactccttggcgctgctgatcctccaaatcaccacaggactattcctagcca
 tgcactactcaccagacgcctcaaccgccttttcatcaatcgcccacatcactcgagacg
 taaattatggctgaatcatccgctaccttcacgccaatggcgctcaatattctttatct
 gcctcttctacacatcgggcgaggcctatattacggatcatttctctactcagaaacct
 50 gaaacatcggcattatcctcctgcttgcaactatagcaacagccttcataggctatgtcc
 tcccgtgaggccaaatatcattctgaggggcccacagtaattacaaacttactatcgcca
 tccatacattgggacagacctagttcaatgaatctgaggaggctactcagtagacagtc
 ccaccctcacacgattctttacctttcacttcatcttgccttcatatttcagccctag
 cagcactccacctcctattcttgcagaaacgggatcaaacacccccctaggaatcacct
 55 cccattccgataaaatcaccttccacccttactacacaatcaaagacgcctcggcttac
 ttctcttcttctctccttaatgacattaacactattctcaccagacctcctaggcgacc
 cagacaattataccctagccaaccccttaaacaccctccccacatcaagcccgaatgat

atttcctatttcgctacacaattctccgatccgtccctaacaaactaggaggcgctccttg
 ccctattactatccatcctcatcctagcaataatccccatcctccatataatccaaacaac
 aaagcataataatttcgcccactaagccaatcactttattgactcctagccgcagacctcc
 5 tcatcttaacctgaatcgaggacaaccagtaagctacccttttaccatcattggacaag
 tagcatccgtactatacttcacaacaatcctaatacctaatacctaactatctccctaattg
 aaaacaaaataactcaaattgggcctaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
 aaa

10 Table 101

SEQ ID NO:92

cbe_22607 Hs.101882

601276943F1 Homo sapiens cDNA, 5' end

length=796

15 ccgcggccgctcgcagcttgetggcctctcccgcgcctcacgtcggactccgtctccgcg
 gcaggaagcagcatggaagctgaggacatccaggaggagttagacctgccccatctgctg
 gactatttccaggaccccggtgtccatcgagtgcggacacaacttctgccgcggctgctg
 caccgcaacatgggcgcggggcggcaggaccgtatcccctgccccgaatgtcggcaccca
 tcggcgccccgcgcgctgcagacccaactgggcctggccaggetgactgagaagacgca
 20 gcgcggcgccctgggccccgtgccccgggctgtgcggccgccaactgggagccgctgcg
 gctcttctgcgaggacgaccagcgccagtgtgcctgggtgtgcagggagtcccaggagca
 ccagactcacgcatggcacccatcgacgaggcttcgagagctaccgggagaaacttctt
 aagtctcagcgtactctcgtggccaacgatgacgcacacgtcatgcatttacaggatgtc
 gacagtgcgaaccgccacacacgtggcaggataaacgcatacggagtacgcgaaatgag
 25 acatcacgcacggcggtttttaacagcgtggcaccacttcctgggtgaagaacgaggacct
 gtctcttccagcagcttgcaaacgaagaagcacagaccagcacgacgctgaatgacacc
 acttcacactccgtccacttcgctcctgagaccctcttaaggggggacaaccgcceccc
 tgggcgtcacacccca

30

Table 102

SEQ ID NO:93

cbe_244811 DGUOK

deoxyguanosine kinase

length=880

35 aacgggtgcgtggagcagctgagcagcgatacctagggcggaagtgtctcggcggaagt
 gatcgctgtgtgaatcgtgggtgggatggccgcgggcccgcctcttcttaagtgcgcttcg
 agcacccttcagttccatggccaagagcccactcgaggcggttccctcctccagaggcct
 gcagcgggggcgcggggccccgaaggctctccatcgaaggcaacattgctgtgggaaagt
 40 caggtttgtgaagtactcacgaaaacttaccagaatggcacgtagctacagaacctgt
 agcaacatggcagaatatccaggctgctggcaccacaaaagcctgcactgcccagctct
 tggaaacttgctggatatgatgtaccgggagccagcacgatggtcctacacattccagac
 attttctttttgagccgcctgaaagtacagctggagcccttccctgagaaactcttaca
 ggccaggaagccagtacagatctttgagaggtctgtgtacagtgacaggctccactttga
 45 ggctctgatgaacattccagtgctggtgttgatgtcaatgatgatttttctgaggaagt
 aacaaacaagaagacctcatgagagaggtaaacacctttgttaagaatctgtaaccaat
 accatgaagttcaggctgtgatctgggctccctgactttctgaagctagaaaaatgttgt
 gtctcccaaccacctttccatccccagcccctctcatccctggagcactctgccgctcaa
 gagctgggtttgttaattattgttagactttgccattgtttcttttgtacctgaagcatt
 50 ttgaaaataaagtcttacttaagttatgcttgtttttctaa

Table 103

SEQ ID NO:94

cbe_250777 HPV 11 E4

Human papillomavirus 11 E4

length=324

55

atggtagtagccaatcattgggaagtagttatggcagcacagttatatgttctcctgcat
 ctgtatctagcactgtacgagaagtagccattgctgaacctactacatacaccgacac
 agaccaccgcccctacagtgctcgccctgcaccacggaagacggcggtgctggcgccgcta
 ggaagcgagcacgtggaccgtccactaacaacaccctgtgtgtggccaacatcagatccg
 5 tggacagtacaatcaacaacatcgctactgacaattacaacaagcaccaaagaaggaaca
 actgtcacagtgacgtacgccta

Table 104

SEQ ID NO:95

cbe_250781 HPV 11 E2

Human papillomavirus 11 E2

length=1104

atggaagcaatagccaagcgtagatgctgcccaggatcagttgttagaactttatgaa
 10 gaaaacagtagttgatatacacaacacattatgcattggaaatgcatacgattggaaagt
 gtattactacacaaagcaaaacaaatgggctgagccacatcggttacaagtagtagcca
 ccattaactgtgtcagagactaaaggacataatgctattgaaatgcaaatgcatttagaa
 tccttagcaaaaactcagtagtggtgtggaaccttggacattacaggacaccagttatgaa
 atgtggctaaccaccacccaaacgggtgctttaaaaaacagggaataactgtggaggtaaaa
 20 tttgatggctgtggaagacaatgtaattggagtagtggtatggacacatatatacctgcag
 gacaacgactcatgggtaaaagtaactagttccgtagatgccaagggcatatattataca
 tgtggacaattttaaacatatattatgtaatttttaataaagaggcacaaaagtaggtagt
 accaatcattgggaagtagttatggcagcacagttatatgttctcctgcatctgtatct
 agcactgtacgagaagtagccattgctgaacctactacatacaccgacagaccacc
 25 gccctacagtgctcgccctgcaccacggaagacggcggtgctggcgccgctaggaagcga
 gcacgtggaccgtccactaacaacaccctgtgtgtggccaacatcagatccgtggacagt
 acaatcaacaacatcgctactgacaattacaacaagcaccaaagaaggaacaactgtcac
 agtgcagctacgcctatagtgaactgcaaggtgattccaattgtttaaaatgttttaga
 tatagactgaatgacaaatataaacatttgtttgaattagcatcttcaacgtggcattgg
 30 gcctcacctgaggcaccacataaaaatgcaattgttaacattaacatatagcagtgaggaa
 caacgtcagcaatttttaaacagtgtaaaaataccaccaccattaggcataaggtgggg
 tttatgtcattacattttattgtaa

Table 105

SEQ ID NO:96

cbe_250808 HPV 11 E6

Human papillomavirus 11 E6

length=453

atggaaaagttaaagtagcctccacgtctgcaacatctatagaccagttgtgcaagacgttt
 40 aatctttctttgacactctgcaaattcagtgctgttttgcaggaatgcactgaccacc
 gcagagatatatgcatatgcctataagaacctaaagggtgtgtgtggcgagacaactttccc
 tttgcagcgtgtgctgttgccttagaactgcaagggaaaattaaccaatatagacacttt
 aattatgctgcatatgcacctacagtagaagaagaaccaatgaagatattttaaaagtg
 45 ttaattcgttgttacctgtgtcacagccgttgtgtgaaatagaaaaactaaagcacata
 ttgggaaaggcacgcttcataaaaactaaataaccagtggaaggggtcggttgcctacactgc
 tggacaacatgcatggaagacttgttaccctaa

Table 106

SEQ ID NO:97

cbe_250809 Prey152

PathCalling Prey Sequence 152

length=515

cgcgcccgctcgacgagagaactagtctcgagtttttttcaagtcttttccttttttt
 55 ttctattttcctgggttgagctatttactattttatagaagagttctttatataatcaga
 aacctttgtcagctgtatgtgctgccaatgtcttctcccacaacgtgggttgccctttca

cattcttactgataacttttgataaaaagatgttcttaccattagtaaaacttattgtct
ctcctttgagtactgattttgaatatcttttaagaaatctctgccttctcccaaattatg
aagatattcttataatgttaccttataaaactttattattttactttccatatgtaaattta
5 taaatcatctgaaattgtttttgtcaaaggaatgagaaaacaaaattcttacttaaaaaa
atagcccatccacaaagtcttactgattgataatacattcggttcattcttttccattgc
actgcagtattgaatttctgtgtttctctgagaat

Table 107

SEQ ID NO:98

cbe_250834 HPV 11 E7

Human papillomavirus 11 E7

length=297

atgcatggaagacttggtaccctaaaggatatagtactagacctgcagcctcctgacct
15 gtagggttacattgctatgagcaattagaagacagctcagaagatgaggtggacaagggtg
gacaaaacagacgcacaaacctttaacacaacattaccaataactgacctgttgctgtgga
tgtgacagcaacgtccgactggttggtgagtgacagacggagacatcagacaactacaa
gaccttttgctgggcacactaaatattgtgtgtcccatctgcgcaccaaaccataa

Table 108

SEQ ID NO:99

cbe_250883 Prey244

PathCalling Prey Sequence 244

length=447

aaaaaaagaaaaagaaaattctgccttatatttccattgaataaaaactgacattccagaa
agctgcattgtgttttatcctgtggattcatcattctgtgtaccaccagaggtctgcat
agtctggtctgaaaactgctgatttaaggccgggcgcagtggtcatgcctgtaatcca
gcactttggaagggtcgaggcgggcggatcacctgaggttcaggaattcgagaccagcctg
30 gccgacatggcgaggccccaactctactaaaaatattggaaattaggcatggtggtggcg
cctgtaattccagctgctcgaggagactgagacaggagaatcgctgaaccgggaaggcgg
aggttgcaagtgcgcgagatcggtgccattgcactccagcctgggcaacaagagcaaaagt
ccatctcaaaaaaaaaaaaaaaaaaacc

Table 109

SEQ ID NO:100

cbe_250888 Prey228

PathCalling Prey Sequence 228

length=507

aacagctttttcagataagaacaaggagcatagctttttcatcacagactctgatgcttct
ggaggagatttttgagagaaagatcaggtgaacatacacaagaaaccaactcacctcat
tcaactgaaaaaggatgtagaaaatatggggaagaagaacttcagaaggttttatttgaa
caaatagattttacggagacgactggaacaagaattccaggtgttaaaaggaaacacatct
45 ttcccagttattcaataattttcaggatcagatgaaaagggagctagcctaccgagaagaa
atggtgcaacagttacaaattatcccctatgcagcaagtttgatcaggaaagaaaagctt
ggcgcccatctcagcaaaagctaaaaggtgcacagaactacttactcttgttctcttgta
agatacagcctgccatggagcacttctgacctgtttaagactgcagatcgaaagggt
50 tgggaattaaatacaaaatcaggttca

Table 110

SEQ ID NO:101

cbe_250907 Prey372

PathCalling Prey Sequence 372

length=183

gtactttgtagttttttcatccctactctctttaactggaaatatagaaattagcacattc

atgtcaaacactgtccctttctgtcatgttctggatgagcaattaatcttgtttatactg
aataaaattttatttgagttgtgaacataaaaaaaaaaaaaaaaaaaaaaaaaaaaaaccca
aaa

5

Table 111

SEQ ID NO:102

cbe_250925 Prey415

PathCalling Prey Sequence 415

10

length=448

cttagaggttagcagattgtcatatttgaatggaggatttgagctgagaagtggctgaga
gttattctgatacaaatagggtgtgcaatttttggtagtcccattcatcagcttctaaa
aaggagtagcagaaacacttgcacagcagcaggagttacttacccttcctgaatggctgc
atcttcttaaggctgttttttccctcctaaacagaaaatcatacattctgcaacaaaag
15 ctggaacatcctaaatgcctggaagcagtttagttttaaggggtgaggccaggtgcggt
ggcttggctgggcacagtggtcacacctgtaatcccagctactcaggaggctgaggcag
gagaatcacttggaccaggagggtggaggttgacagtgagccaggattgtgccactgcact
ccagctgggcggcagagtgagactctc

20

Table 112

SEQ ID NO:103

cbe_251059 HPV 16 E1-E4

HPV 16 E1-E4

25

length=276

atggctgatcctgcagcagcaacgaagtatcctctcctgaaattattaggcagcacttgg
ccaaccaccccgccgcgacccataccaaagccgtcgcttgggcaccgaagaaacacaga
cgactatccagcgaccaagatcagagccagacaccgaaacccctgccacaccactaagt
tgttgacagagactcagtggacagtgctccaatcctcactgcatttaacagctcacaca
30 aaggacggattaactgtaataagtaaacactacaccca

Table 113

SEQ ID NO:104

cbe_251063 HPV 16 E1

Human papillomavirus 16 E1

length=1947

35

atggctgatcctgcaggtaccaatggggaagagggtagcgggatgtaatggatggttttat
gttagggctgtagtggaaaaaaaaaaacaggggatgctatatcagatgacgagaacgaaaat
40 gacagtgtatcaggtgaagatttggtagattttatagtaaatgataatgattatttaaca
caggcagaaacagagacagcacatgcgttgtttactgcacaggaagcaaaacaacataga
gatgcagtacaggttctaaaacgaaagtatttgggtagtcacttagtgatattagtggg
tgtgtagacaataatattagtcctagattaaaagctatatgtatagaaaaacaaagtaga
gctgcaaaaaggagattatttgaaagcgaagacagcgggtatggcaatactgaagtggaa
45 actcagcagatgttacaggtagaagggcgccatgagactgaaacaccatgtagttagt
agtgggtggaagtgggggtggttgacgtcagtagtggaagtgggggagaggggtgtt
agtgaagacacactatatgccaaacaccacttacaatatattttaaatgtactaaaaact
agtaatgcaaaggcagcaatgttagcaaaatttaaagagttatacgggggtgagttttca
gaattagtaagaccatttaaaagtaataaatcaacgtgttgcgattgggtgtattgtcgca
50 tttggacttacaccagctatagctgacagtataaaaacactattacaacaatattgttta
tatttacacattcaaagtttagcatgttcatggggaatgggtgtgttactattagtaaga
tataaatgtggaaaaaatagagaaacaattgaaaaattgctgtctaaactattatgtgtg
tctccaatgtgtatgatgatagagcctccaaaattgcgtagtacagcagcagcattatat
tggtataaaacaggtatatcaaatattagtgaagtgtatggagacacgccagaatggata
55 caaagacaaacagattacaacatagtttaaatgattgtacatttgaattatcacagatg
gtacaatgggcctacgataatgacatagtagacgatagtgaattgcatataaatatgca
caattggcagacactaatagtaatgcaagtgcctttctaaaaagtaattcacaggcaaaa

attgtaaaggattgtgcaacaatgtgtagacattataaacgagcagaaaaaaaaacaaatg
 agtatgagtcaatggataaaaatatagatgtgatagggtagatgatggagggtgattggaag
 caaattgttatgtttttaagggtatcaagggtgtagagtttatgtcatttttaactgcatta
 aaaagatttttgcaaggcatacctaaaaaaaattgcatattactatatggtgcagctaac
 5 acaggtaaatcattatgttggtatgagtttaataaatttctgcaagggtctgtaatatgt
 tttgtaaaattctaaaagccatttttgggttacaaccattagcagatgccaaaataggatg
 ttagatgatgctacagtgccctgttggaactacatagatgacaatttaagaaatgcattg
 gatggaaatttagtttctatggatgtaaaagcatagaccattgggtacaactaaaatgccct
 ccattattaattacatctaacattaatgctggtacagattctaggtggccttatttacat
 10 aatagattggtggtgtttacatttccaatgagtttccatttgacgaaaacggaaatcca
 gtgtatgagcttaataagaaactggaaatccttttctcaaggacgtggtccagatta
 agtttgcacgaggacgaggacaaggaaaacgatggagactctttgccaacgtttaaatgt
 gtgtcaggacaaaataactaacacatta

Table 114

SEQ ID NO:105

cbe_251071 Prey734

PathCalling Prey Sequence 734

length=473

cgcggccgcgtcgaccgggttcccgaggagatgaagttcgtgtacaaagaagagcatccg
 ttcgagaagcgcgctctgagggcgagaagatccgaaagaaataccgggaccgggtgccg
 gtgatagtagaaaaggctcccaaagctcggataggagacctggacaaaagaaatacctg
 gtgccttctgatctcacagttgggtcagttctacttcttgatccggaagcgaattcatctc
 25 cgagctgaggatgccttggttttctttgtcaacaatgtcattccacccaccagtgccaca
 atgggtcagctgtaccaggaacaccatgaagaagacttctttctctacattgcctacagt
 gacgaaagtgtctacggtctgtgaagctgctgccctgagctggaggggggtctcattct
 acaaagagagaggtggcccccttctgacctctcctccttcagctcaacacac

Table 115

SEQ ID NO:106

cbe_251088 HPV 16 E2

Human papillomavirus 16 E2

length=1098

atggagactctttgccaacgtttaaatgtgtgtcaggacaaaataactaacacattatgaa
 aatgatagtacagacctacgtgaccatatagactattggaaacacatgcgcctagaatgt
 gctattttattacaaggccagagaaatgggatttaaacatattaaccaccaagtgggtgcca
 40 aactggctgtatcaaagaataaagcattacaagcaattgaaactgcaactaacgttagaa
 acaatatataactcacaatatagtaaatgaaaagtggacattacaagacgttagccttgaa
 gtgtatttaactgcaccaacaggatgtataaaaaaacatggatatacagtggaaagtgcag
 tttgatggagacatatgcaatacaatgcattatacaaactggacacatatatatattgt
 gaagaagcatcagtaactgtggtagaggggtcaagttgactattatggtttatattatgtt
 catgaaggaatacgaacatattttgtgcagtttaagatgatgcagaaaaatatagtaaa
 45 aataaagtatgggaagttcatgcgggtgggtcaggtaatattatgtcctacatctgtgtt
 agcagcaacgaagtatcctctcctgaaattattaggcagcacttgccaaccaccccgcc
 gcgaccataccaaagccgtcgcttgggcaccgaagaaacacagacgactatccagcga
 ccaagatcagagccagacaccggaaacccctgccacaccactaagttgttgacagagac
 tcastggacagtgtccaatcctcactgcatttaacagctcacacaaaggacggattaac
 50 tgaatagtaacactacaccatagtagcatttaaaagggtgatgctaatactttaaatgt
 ttaagatatagatttaaaaagcatgtacattgtatactgcagtgctgtctacatggcat
 tggacaggacataatgtaaaacataaaagtgaattgttacacttacatatgatagtga
 tggcaacgtgaccaatttttgtctcaagttaaaataccaaaaactattacagtgctact
 55 ggatttatgtctatatga

Table 116

SEQ ID NO:107

cbe_251128 Prey870

PathCalling Prey Sequence 870

length=490

5 gaggagcaatgccctgatgccctcctccttcgctctctatgggctggcttcagctaccat
ctgtacagctgcagctccaaaatctctccacagtcacacctcccactcagctccagat
cccatcactgctgccagctggatccccccgaaggaggctcagagtctacctcccaggc
ccttggccactgagctccttgagagtcctctcctcgtgccctttgcagctccaccaac
ccaaccaccagctccctcctccaagcctcacattctccacctccaggctttgatcaggca
10 cagaacgcccttccatggaatgccctccatgcctgtgtntccaacctactgaatctggg
ggactgactgcccgaatctgagacttaggtcagaaggcacctctgtgaagcctgccatga
cacattataacatgcgtcacattatagtttaccatttacacattcaaaaaaaaaaaaaa
aaaaaaaacc

15

Table 117

SEQ ID NO:108

cbe_251445 HPV 16 E6

Human papillomavirus 16 E6

length=477

20 atgcacaaaaagagaactgcaatgtttcaggacccacaggagcgacccagaaagttacca
cagttatgcacagagctgcaacaactatacatgatataatattagaatgtgtgtactgc
aagcaacagttactgagcagctgaggtatagactttgcttttcgggatttatgcatagta
tatagagatgggaatccatattgctgtatgtgataaatgtttaagttttattctaaaatt
25 agtgagtatagacattattgttatagtttgtatggaacaacattagaacagcaatacaac
aaaccgttgtgtgattttgttaattaggtgtattaactgtcaaaagccactgtgtcctgaa
gaaaagcaaaagacatctggacaaaaagcaaagattccataatataaggggtcggtggacc
ggtcgagtgtatgtcttgttgcatcatcaagaacacgtagagaaaccagctgtaa

30

Table 118

SEQ ID NO:109

cbe_251448 HPV 16 E7

Human papillomavirus 16 E7

length=297

35 atgcatggagatacacctacattgcatgaatatatgttagatttgcaaccagagacaact
gatctctactgttatgagcaattaaatgacagctcagaggaggaggatgaaatagatggt
ccagctggacaagcagaaccggacagagcccattacaatttgtaaccttttgttgcaag
tgtgactctacgcttcggttgtgcgtacaaagcacacacgtagacattcgtaactttggaa
40 gacctgttaattgggcacactaggaattgtgtgccccatctgttctcagaaaccataa

Table 119

SEQ ID NO:110

cbe_251468 Prey1628

PathCalling Prey Sequence 1628

length=486

45 gtcgacgcggccgcgggagctgatgggcagcctgcgccaccctggatcacctgactcgg
cagaagcggagggggaccttgaccagccaccaaccaggaagacaagcctggggcactg
50 accctgaagtctgaaccaggaagcaagccaaggtgcccagagagggccaggagcctgtg
aagcaagctgactttgttcgcagcaagtctttcctgataaacctgtgaagcccgctgtg
gaccggaagcagggggcacaagctcaacttcaaggaggggctgcaaagaggaatctcattg
tcccatcagaacttggtcagctctgcagtgatgatggagaaggaactgcatcagctgaag
agagccagttatgccagtacagatcagccatcctggatggaaacttgccagaaagaaatct
55 caagcttggagtgacatgccccagattataaaataggtgggcagtggtctgataaagcat
gtccac

Table 120

SEQ ID NO:111

cbe_251502 Prey1609

PathCalling Prey Sequence 1609

length=506

ttccccgcctctcggttagctccggcctcccggggcttctgggtttggagagtttgggga
gcggagacacctcccagggtcctccgcgttgaccctatttgcgagggcgggagcgggg
tgggccgacggcgaaagctccagaggtgggacctctcccttcagcagctcttctgactt
catgattctgccccctcttctcattgcaggtcacaccgacaaatctgaagcgggtttgcc
gggagtgtagccgtctccccagcctgggcccacccggtccacagggattccatttccggc
cttacactccgctccacgatctcatccaggcgtgcagctgtgcagctgctctacagact
gcagggacctgctgagacgaatccccggacgaggtgatggctggaccggcggaggaggcg
ggagccattgtcccgagagcctgtggcctctgcctccgcaggtgtcaccaagagtgacc
tacacacgagtgagcccagggcaggc

Table 121

SEQ ID NO:112

cbe_251663 HPV 11 E1

Human papillomavirus 11 E1

length=1947

atggcggacgattcaggtacagaaaatgaggggtcggggtgtacaggatggtttatggta
gaagccatagtagagcacactacaggtacacaaatcagaagatgaggaagaggaggtg
gaggacagtgggtatgacatgggtggactttattgatgacaggcatattacacaaaattct
gtggaagcacaggcattgtttaataggcaggaggcggatgctcattatgcgactgtgcag
gacctaaaacgaaagtatttaggcagtcctatgtaagtccataaagcaatgtagcta
gcagtagaaaagttagataaagtcacgggttagacgccattaaacttacaacacagccaaa
aaggtaaagcgacggctgtttgaaacacgggaattaacggacagtggtatggctattct
gaagtggaaagctgcaacgcaggttagagaaacatggcgacccggaaaatgggggagatggt
caggaaagggacacagggaggacatagagggtgagggggtggaacatagagaggcggaa
gcagtagacgacagcaccgagagcatgcagacacatcaggaatattagaattactaaa
tgtaaggatatacgatctacattacatggtaagtttaaagactgctttgggctgtcattt
gttgatttaattaggccattttaaagttagataaccacatgtgccgattgggtgggtgca
ggatttggtatcatcatagcatagcagatgcatttcaaaagtttaattgagccattaa
gtttatgacatatacaatggcttacaatgcatggggaatggtagctatttagtattaata
agggttaaagtaaataagagcagatgtaccgtggcacgtacattaggtacgttattaat
atacctgaaaatcacatgttaattgagcctcctaaaatacaaaagtggcgtagcagccctg
tattgggttaggacaggcatttcaaatgcaagtacagttataggggagggcgccggaatgg
ataacgcgccgacccgttattgaaacatagtttggtgacagtcattttaaattaactgaa
atgggtgcagtgggcatatgataatgatatttgtgaagaaagttagatagcatttgaat
gcacagcgtggagactttgactccaatgcaaggccctttttaaatagtaatatgcaggct
aaatatgtaaaagattgtgcaattatgtgcagacattataaacatgcagaaatgaaaaag
atgtctattaaacaatggattaagttaggggtactaaagttgacagtgtaggtaactgg
aagccaattgtgcagtttctaagacatcaaaacatagaatttattccatttttaagcaaa
ctaaaattatggctgcacggaacgccccaaaaaaatgtatagccattgtagggccacct
gacactgggaagtgcgtgcttttgcatgagtttaattaaagttttggggggaacagttatt
agttatgttaattcctgcagccatttctggctacagccactaacggatgcaaaagtggca
ttattggatgatgccacacaacctgttgacatatatggatacatatatgagaaacctta
ttagatggtaattcctatgagcatagatagaaaacatagagcattaacattaattaagtgt
ccaccgctactggttacatcaaatatagacattagcaaaaggagagaaatacaaatattta
catagtagagttaccacatttacatttccaaatccattcccctttgacagaaatgggaat
gcagtatatgaactatcagatgcaaaactggaaatgtttctttgaaagactgtcgtccagc
ctagacattgaggattcagaggacgaggaagatggaagcaatagccaagcgttttagatgc
gtgccaggatcagttgttagaacttta

Table 122

SEQ ID NO:113

cbe_251737 HPV 16 L2

Human papillomavirus 16 L2

length=1422

5
10
15
20
25
30

atgcgacacaaacggttctgcaaaacgcacaaaacgtgcatcggtacccaactttataaa
acatgcaaacaggcaggtacatgtccacctgacattatacctaagggtgaaggcaaaact
attgctgtacaaatattacaatatggaagtatgggtgtatTTTTTGGTGGGTtaggaatt
ggaacaggggcgggtacaggcggacgcactgggtatattccattgggaacaaggcctccc
acagctacagatacacttgctcctgtaagacccccctttaacagtagatcctgtgggccct
tctgatccttctatagtttcttttagtggaagaaactagttttattgatgctggtgcacca
acatctgtaccttccattccccagatgtatcaggatttagtattactacttcaactgat
accacacctgctatattagatattaataatactgttactactgttactacacataataat
cccactttcactgacccatctgtattgcagcctccaacacctgcagaaactggagggcat
tttacactttcatcatccactattagtagacacataattatgaagaaattcctatggataca
tttattggttagcacaacccctaacacagtaactagtagcacaccataaccagggtctcgc
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gcttttgaaccactcccactaaacttattacatatgataatcctgcatatgaaggata
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cctgactttttggatatagttgctttacatagggcagcattaacctctaggcgtactggc
attaggtacagtagaattggtaataaacaacactacgtactcgtagtggaaaatctata
gggtgctaagggtacattattattatgatttaagtactattgatcctgcagaagaaatagaa
ttacaaactataacaccttctacatatactaccacttcacatgcagcctcacctacttct
attaataatggattatatgatatttatgcagatgactttattacagatacttctacaacc
ccggtaccatctgtacctctacatctttatcagggttatattcctgcaaatacaacaatt
ccttttgggtggtgcatacaaatattccttttagtatcagggtcctgatatacccattaatata
actgaccaagctccttcatttaattcctatagttccagggtctccacaatatacaattatt
gctgatgcagggtgactttttattacatcctagtattacatggttacgaaaacgacgtaaa
cgtttaccatatttttttttcagatgtctctttggctgcctag

Table 123

SEQ ID NO:114

cbe_251740 HPV 1a E1-E4

Human Papillomavirus 1a E1-E4

length=375

35
40
45

atggcagataataaaagctccccagggtgctggggctcctgcagtacactccgactacc
caacctatccgagagtgcacccgcccagcaatcgacgtccatcgactacaccgaactcc
caggacagggggagacctcgcaggtccgacaaagacagcagaaaacacctgtacgcagac
ggccttacggacggcgaagatccagaagtcacagaggtggaggacgaagagaaggagaat
caacgcctctaggacacccggatctgtccctctgcgcgagacggttggaagtatacaca
caacgcctcaaaagggaacattcttcaagacttagacgacttctgcaggaagcttgggatc
cacccgtggtctgtg

Table 124

SEQ ID NO:115

cbe_251784 HPV 16 L1

Human papillomavirus 16 L1

length=1596

50
55

atgcagggtgactttttattacatcctagttattacatgttacgaaaacgacgtaaacgtt
taccatatttttttttcagatgtctctttggctgcctagtgggcccactgtctacttgct
cctgtcccagtatctaagggtgtaagcacggatgaatatgttgacgcacaaacatatat
tatcatgcaggaacatccagactacttgaggtggacatccctattttcctattaaaaaa
cctaacaataacaaaatattagttcctaaggtatcaggattacaatacaggggtatttaga
atacatttacctgaccccaataagtttggttttctgacacctcattttataatccagat
acacagcgggtggtttgggcctgtgtaggtgttaggttaggtcgtgggtcagccattaggt

gtgggcattagtggccatcctttattaaataaattggatgacacagaaaatgctagtgt
 tatgcagcaaatgcaggtgtggataatagagaatgtatatctatggattacaaacaaaca
 caattgtgtttaattggttgcaaacacctataggggaacactggggcaaaggatcccca
 5 tgtaccaatgttgcagtaaatccaggtgattgtccaccattagagttaataaacacagtt
 attcaggatggtgatatgggttcatactggctttggtgctatggactttactacattacag
 gctaacaaaagtgaagttccactggatatttgtacatctatttgcaaatatccagattat
 attaaaatggtgtcagaaccatattggcgacagcttattttttttatttacgaagggaacaa
 atgtttgtagacatttatttaaatagggtggtactgttgggtgaaaatgtaccagacgat
 10 ttatacattaaaggctctgggtctactgcaaattagccagttcaaattattttcctaca
 cctagtgggtctatgggttacctctgatgcccataattcaataaaccttattgggttaca
 cgagcacaggggccacataatggcatttgggtgggtaaccaactatttggttactgttgtt
 gatactacacgcagtacaaatattgtcattatgtgctgccatatctacttcagaaactaca
 tataaaaaataactttaaggagtacctacgacatggggaggaatatgatttacagttt
 atttttcaactgtgcaaaaataaccttaactgcagacgttatgacatacatattctatg
 15 aattccactattttggaggactggaattttggtctacaacctccccaggaggcacacta
 gaagatacttatagggttggtaaccaggcaattgcttgtcaaaaacatacacctccagca
 cctaaagaagatgatccccttaaaaaatacacttttgggaagttaatttaaaggaaaag
 ttttctgcagacctagatcagtttcccttaggacgcaaatttttactacaagcaggattg
 aaggccaaaccaaatttacattaggaaaacgaaaagctacaccaccacctcatctacc
 20 tctacaactgctaaccgcaaaaaaacgtaagctgtaa

Table 125

SEQ ID NO:116

25 cbe_251790 Prey2347
 PathCalling Prey Sequence 2347
 length=313

gagacaccagcactagccagcaggtgccccttcctcaggttctgagtttcagcccatg
 cgatcactcctccaagcttctaggttttaataattccaacttttccccctttgtccctca
 30 gaggtggtagctgcttccagaaattgctaccttcagatgataccacagagttctctttttg
 ctttttgagttcttcgataactagtttaattgattccttatacttagctaaccattctctat
 attaaattctctctgttaaaacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
 aaaaccaaaaaaaa

Table 126

SEQ ID NO:117

40 cbe_251821 Prey2419
 PathCalling Prey Sequence 2419
 length=439

ctgaaatgcacatacatgcttttagtgtaatgcagaatgcatttattggagaactcataaa
 catectataaaaattttcttccctgagatgcaactataaaaacttggccttattctgagaat
 gcttaacatagatttcattccatactgtaacactgattttgttgttgttgccttaaagca
 gctcagcttccctgaggtagtgttatgtctctgtggcaacaagggtgaaaatgtctagctta
 45 ttttgtcaaagtcaacaataatccacagactccagacctaataatctgtcccaatttgcc
 attttacttttagtgctccaaaaatattggcttatagaaaaacaatagggtgttttaagag
 atttacctgaatgatatagagaatgtctagatattttctggctatcaggtaaaacctacc
 cttcaagatggtagaatat

Table 127

SEQ ID NO:118

55 cbe_251826 Prey2429
 PathCalling Prey Sequence 2429
 length=553

ctttcagcagcagcggtagagcagtgaccaggcgtctccgcgatgggccccggggacttc
 cgccgctgcagagagagaatttcccaggggctccagggaactcccaggtagagcggagctt

tggttcccacctcgtcccgcgtgcgacttcttcggggacggcaggagcacggacatccag
gaggaggccctcgccgccagcccgctgctggaggacctcagacgacggctgacgcgcgcc
ttccagtggcggtgcagcgcgcgatctcgaggcgcgtgcaggaggcggcggcgccg
5 gcggcgccggaggagcagagctggacggcggttgaggccaccctggccaggctgcggcg
gagctggtggaaatgcatttccaaaaccaccagctggctagaactttactggacctaaac
atgaaagtgcagcaattgaaaaaggagatgaactggaaattacatcagactcccaaagc
ccaaaagatgatgctgccaatccggaatanagaaatgcacacgcaagggtggcgcggt
ggctcacgcctgg

10

Table 128

SEQ ID NO:119

cbe_251857 Prey2492

PathCalling Prey Sequence 2492

15

length=54

ggatcagacattcgcgggacgagatcgacccaacgagggagcgcaacctgcctc

Table 129

SEQ ID NO:120

cbe_251900 Prey2598

PathCalling Prey Sequence 2598

length=410

20

tggcgtgcggcttccgcccgcgtattgcttgccaggatggatcccggagcgcgcagagg
25 agtccctgaggagctagggaccccaaggcctttcacgcgtgcgggccagtcctcagtc
gctggagggtgggtcccacggaatcctgttagtttctaccacctcctcccccttctctgg
agctggtggagcttcagaagtcctgtggagcgtcggtgggatcagtttgtctcggtgaa
aagtaaaccttgaaagctttccagagtggtgaatcttccaccagaaaacttgatcacatc
aatatctgcagttccaatttccaaaaagaagaagtagctgattttcagctttctgtgga
30 ttctttattggaaaaagacaatgaccattcagaccagatatcaagtcaag

Table 130

SEQ ID NO:121

cbe_251917 HPV 1a E2

Human Papillomavirus 1a E2

length=1206

35

atggaaaacctcagcagtcgcttagacttactgcaagagcagctaatgaacctatatgaa
caggacagtaaatgtatagaagatcaaattaagcagtggaatctaattagacaagaacaa
40 gttcttttccatttcgccagaaaaaatgggtaatgagaattggattgcaggcagttcca
tctttagcgtcctcacaggagaaggcaaacagcagctattgaaatggtgttacatttagag
tctttaaaggactcaccttatggcacagaggattgggtcacttcaagacactagcagagag
ctgtttttggcacccccagctggcaccttcaagaagagtgccagcacacttgagggtacc
tatgacaataaacctgataatcagacaaggcacacaatttggaatcatgtgtattatcaa
45 aatggggacgatgtatggagaaaagtatccagtgggtgtgatgctgtaggagtgtactat
ttagaacacgatggctataaaaaattattatgtgtattttgctgaggaggcctctaagtac
agcacaacaggacaatatgctgtaaattacaggggtaaaagggttacaaatgttatgtct
tccactagctccccagggtgctggggctcctgcagtacactccgactaccaacccta
tccgagagtgcacccgccagcaatcgacgtccatcgactacaccgaactcccaggacag
50 ggggagacctcgagggtccgacaaagacagcagaaaacacctgtacgcagacggccttac
ggcggcggaagatccagaagtcacagaggtggaggacgaagagaaggagaatcaacgccc
tctaggacacccggatctgtcccttctgcgcgagacggttgaagtatacacacaacgcct
caaaagggacattcttcaagacttagacgacttctgcaggaagcttgggatccaccctg
gtctgtgtaaaagggggtgccaatcagcttaagtgtctcaggtacagacttaaagcatct
55 actcaagttgactttgacagcataagcaccacatggcattggacagatagaaaaaacacc
gagaggataggtagtgctagaatgttagtaaagtttattgatgaggctcaacgagagaag
tttcttgagagagttgctttgccagatcagtgctctgtgtttttgggacagtttaatggg

tcttaa

Table 131

5 SEQ ID NO:122

cbe_251919 HPV 1a E6

Human Papillomavirus 1a E6

length=423

10 atggcgacaccaatccggaccgtcagacagctttccgaaagcctctgtatcccatatatt
gatgtttttattgccttgtaatttttgtaattatttttgtctaagtctgagaagctgctt
tttgatcattttgatttgcatcttgtctggagagacaatttgggtgttggatgctgtcaa
gggtgtgctagaactgttagcctattggagtttgtttatattatcaggagtcttatgag
gtaccggaaatagaagaaattttggacagacctttattgcaaattgaactccgttgtgtt
15 acatgcataaaaaaactgagtggtgctgaaaaattggaggttgtgtcaaacggagaaaga
gtgcatagagttagaacagacttaaagcaaagtgtagtttgtgtcgcttgtatgctata
taa

Table 132

SEQ ID NO:123

20 cbe_251925 HPV 1a E7

Human Papillomavirus 1a E7

length=282

25 atgggtggcgaaatgccagcactaaaggacctggttcttcaacttgaaccaagcgtccta
gatttagatctttattgttacgaggaggtgcctcctgatgacatagaggaggagttagt
tcgcctcagcaaccttatgtgtcggttgccttctgtgcctattgagagaaactggttcga
ttgaccgtcctcgcggtacacagcgccattagacagctggaggaactccttctgcgatct
ttgaacatcggtgcccactgtgcaccctacagcgacagtaa

Table 133

SEQ ID NO:124

30 cbe_251929 Prey2672

PathCalling Prey Sequence 2672

length=408

35 gtctctacaaataataaaaaattgtctgggcatggtggcctgtgccgtagtcccagcta
ctcaggaggggtgaggtgggaggatcgcttgggcctaggaggtcaagcctgcagtgagttg
taatcacgccactgcactccagcctgggcaacacagcgagatcctatttctcctatttct
ctctgtctctctcacacacacacacacacacacacataatgtggaatgattaaa
caaagctaattaacatcgggtcacctcctttaaattttccagcaagacatgtgaaattt
40 attcttttagcctattttgaaatacatgtcatatatcattattaactatagtaccctgg
tgtgcatggatctcaaaaacttatttttctgtctaactcaaacttt

Table 134

45 SEQ ID NO:125

cbe_251953 Prey2724

PathCalling Prey Sequence 2724

length=617

50 ggccgactcccaggatccgttgcggcgcgggcgagcagccaatggcgagccccacagtct
cgcgagagtgtcaggcgctcttcgtggctgccctcttagctgctagcggagctcctcag
ggggcgggcgggagcctacaattcctagaaagaaaatcgccattccggaaacagaactg
cagttaagaccctcgaaaagatctaagatagtgatgcctataaacacctgacgaatttc
agaatgtgacaaagcgagaggatgcattatttcaaaacaaaacagaaggctaaaatttg
cagganaaaagaaaatcagtaaacgggaatcctcggaactggattgtaagcaagatttgaa
55 tgaattagaagctgaaggtatttaggctgtgataganggtacatatttcatcccacag
agaaaacataataactcgaaatttcgtgaaaaacgcaaactgtcggaatctcctcagtc
gactaatgcgcgcttgacatgcgatgtgaatgccctctgtcgggcgctgtcgctgacgcac

atctgtccgtggctcgtctatcgatatgtgtgtgttatgctgtgtctatcgcgctcgctgt
cactgtccgggtgcctt

5 Table 135
SEQ ID NO:126
cbe_251976 FLJ23584
hypothetical protein FLJ23584
length=4992

10 ggctatcctactgcagctggctgcatcagatgtgccaggcctgccctctagctcccaaca
ccatctgctgatctaagctttgcatgttgtgtgctgctgggtgcctgtgctgtgt
ggggccattccatggccctgagtgggagccagtgcagggcctgctctccagaatcacag
ctgcagggaccctcagtgtgtggcaacctgcttgtctctgectctttctggctgtggca
ggccggcactgttggcaccaggtcaccaggaccgcttcagcacaaggaatgtcatcaa
15 ggtgccactgcagaagcgggcagtgccctccatgaggtgcgaaactgtcttcaagctgac
tcctgaattcttcagtctggaaagtccagggcctagattctcaacaatgcgcacaaag
gcagagatggggataccggaggagcctccaggaatcatggggccagaacctgctctctcc
acagcaccatgtccaggccaccttcgggtgtccacacccactctgagcccatcttttg
taccacctccatttcaaacacctgtttactgcctcagaacagttcctggaaagcatggca
20 ggtgcttgggtgtctccatgatggtcagactcgccctgcttggacatgtgtcaagagat
ggagcagctgctgcttcactcacaggaagggttgggtgctgactggagcctgtcatcagtgt
gaggtctgccccacctccatgaccttaaccacctctcttccaaacttactttcagctga
gaggctgcagttctgccccagagagctcctgctgatccttcccacaaactgagaa
tgtgacttggaaagtcttggcactgtcgaccagaggcctgggaaccagggggtaaaaacc
25 agaaagcaggcagagaggatagtagagagaccaggctccaaggtgggtgaaccagacag
ggagcagacgggaggatgcttcagaaatccaggcatctggggagtagtctccagtagact
ttggaatggagggtgatgcagagactaacgtgttggagtgtgcaaaccagagactagtta
taagtgaactgatggcgagatcttgacaccagggtgggacaccaggaccggatgggag
ttgagagtgaaccaacattcaggaactagggaatagaaaccagagggaggctggagggtg
30 agaactcctctgaaacccaggcacatagggagagaaccaagaacagtttaagatgtaaaa
ttgatgcagagacccaacacctgagtgaggagaaccaggataagaatggaagtgaggatg
ctgtggagaccagacatttgagaagaaggacaagaaaggaggtggagaggaggatgggg
aagagatccaggctcaaggattggggaagcaaggccagactggagatgagaatggtgagg
agaccagacaccacagtgaggagaacaagatcagatgaaaggatgctgggatgtggaaa
35 ttcatgatggaagggggagaacaaggatcaggttggaggatcaggatgctgcacaaaccc
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ccttggattggggaaaaacaggaatgtgttggaaatgggaatgttacagagatccagacac
caaggtgggagaagcatgatcaagggtggaagtgaagaagctaaagaagaccaagcatctg
ggggagagaaccagaaacaattaaagtcatgaaattcaagtggggtggggaaataagggcc
40 tgagaagagatgaagatgctaaggaaaccagatagctaccaagaagaagctcagggaga
taagagaaggattgggtggtgatccaggcactatggtggggaaccggagacaagttagca
agtgaattttatagagaatttgagatactatgttgggagaatcagaactggattggagggt
gaacatagagcagaaattcaggcatcagagaagagagaccaaagaaaggatggatgtgag
gatggcacaatatcctggcaccggaggctgagatccaggaacaattaaaaggatgaaact
45 gatgtggagactcagagcaatgagccacttagagaagaggatggtacagacattcagtca
ctaggaggagagagggttaaagggtgaggatgataaagacaccagggaacttgggaggaaa
aatcagggtcagttaggaaatgaatttagtggaagattcacataccaaaggggaagaat
caggaacatattagaggcgaagatggtgcacataccagatatctgagtcagggaactgg
ggcaaattacaagtcaaattgatggagaaatgcattcagcagaatggaagaaagatcag
50 cagattggagggtgagaatggggcagaaattcagatacaagggaagagaaacctgagagaa
gttggagggtgaggacggtgtaaagacctgggcacctgggaaagaaacccagagtcagttt
agaatgagctcttggtagaaagatccttttatcagagtggaagagccagaagcagatggga
agtgagaatggaacagaaattcaggctccagtgagagaaaccagagagaacctggagggt
gaggacggtgtaaagactcagagacctaaagagagagaacgaggaccagttagatagtga
55 attggaggggagccattcaccaggaggaggaaactgggagctgattggaaaggatgttgca
gaaatcaggcatcagagaagagaaaccagagagaggttggaaacgaggacggtagaatg
atctggagggttaggggaaaaaactggaggcttagagcgaagaaacagactgttaaaaag

5 taaagataatggaaagaccggtttatcagagtggagaaccaggaacagggtggaggtgg
 gaatgatgaagaaattcaaatacaggggaagagaaacctgagagggaccacagctgatga
 tggtagacagagaccaggtcctgcaggagatgaccagggacagttaaagagttgaaattgc
 tgaagagatccaggtacaagggcaaggaaataagaatgacgggtggagttgaggatgttgc
 10 agaactccaggatataggaagccagagaaagtgcacagatgaggatgttggagagcctcg
 agcaccaggggagggaacaaggatctggtcagaggagaggatgctgtgagggacagctct
 ccaagtgcactgttctgggagtgagaggccacaggcaggaagcacagcctaccatggcc
 tccagccttcaactggctatggatgtgggacccgggaacaggaacaggcagtggtgtgaa
 tgggtttcatctctgccccctgtcctgagatgaatcctgtccccactggggtgaagtctt
 15 cctgctggtgggtggggaggagagcatctggccagccagggcacaaccctgccaggga
 tcatagagtggggatcagtcagcctcccagcaggcccaacctgaatcctggagaagacg
 acaaagggacaaaggggtggatccagagaagccccagcctgactcggcagtccaaaaa
 cctccgtctctgacagctcccttgggcatgccctctgctgctcctgtctccctgtgg
 cccagccccggaagctgccatcattctagcgggtcctcccacggcctcactgtcctgcc
 20 caaggggacaggcctcaagaagagcaaacgactgctcctggagtcctcatgaggaggag
 gatgacacactgaagtggggctctccccggcgatcctggagtcctatttctgtttaa
 cttcttaggatcttgcctattgaccttgcctggggcgaggctctctggactgaacacagg
 ccaggagctccaagcccagcaggaaaggtattgtgaggcccaaggctccccaccaggcct
 taagtccccagagaggttccagagggttcagcgcccagacagaaaaagctcgaaactcc
 25 tatacaagccagagctctggagaggaacagaccgcacatgtcagagcccattaaagcattt
 ccatccagcctgaaaaggccaggagagtcaggccaccagggggcgccagagaaccacagg
 agatccaggaagcgcttgctaggaccaagctcccagctcccaggacccccaggccggcag
 cggagtccaggagctggtgtggcccacaaagggctcgagagagcctcccagtgagaacagta
 ggggacaggaaaatgatcaggtcaagggctctcccagctggcagagagggctcccagcagag
 30 tgaggacttcatctctagggcagaccacgcccactggaggaaggaatgtacatcctggg
 aggcctctaagctccccagactcaaatgccagcagctcacatactggagaagaggaagcc
 tggaatctacaggggtgcagaggggctgggacagcagccttctgccattctgcagaacctg
 tcagcttcaaagggaggtccactctgcggtggcaagctgggcctgaccttctggcca
 agatgtcctggtccccacagctcgccaagcgcaagcacttggccccctaacctgagcctga
 35 gggaacctgattctactctgctccccaaagtgggtgatcctcgtgcaggggaggacagca
 tcggagatcacactgcttcacagaggatcttcagctgcaaggtcactgctgtactggg
 ccaccttcttaagacagagagtcctccagggccaggagcacctgggaacccaaatgggg
 ctccacagaatacacgagcctccaaaaagtttagtattatgaagcatctgaattttttt
 ctcttccagaatggctttaaaaagtagactcaggcccagagtcctcaggacatatcagaa
 40 aagctttgagagtgtcctgatcctgcaagcctctaataaattgggtcatttgggcaaaa
 aaaaaaaaaa

40 Table 136
 SEQ ID NO:127
 cbe_252016 HPV 1a L1
 Human Papillomavirus 1a L1
 length=1527
 45 atgtataatgtttttcagatggctgtctggttaccagcgcagaataagttctatcttctc
 cccagcccatcactagaatcctgtccactgatgaatgtgaaccagaaccaatctcttc
 taccatgcaacatctgaacgtctactgctggtcggacatcctttgtttgagatctccagt
 aatcaaactgtaactataccaaaagtgtcaccaaatgcatttagagtttttaggggtgcgt
 tttgctgatccaaatagatttgcatttggggataaggcaatttttaaccagaaacagaa
 50 agattagtttggggcctaagagggatagagataggttagaggccagccttaggtatagga
 ataacggggccacctcttttaaataggttagatgatgcagaaaatccaacaaattatatt
 aatactcatgcaaatggagattctagacaaaatactgcttttgatgcaaaacagacacaa
 atgttcctcgtcggctgtactcctgcttcagggtgaacactggacaagtgcgttgccca
 ggggaacaagtgaaacttggggactgccccagggtgcaaatgatagagtctgtcatagaa
 gatgggtgacatgatggatattgggtttggggctatggattttgctgctttacagcaagac
 55 aagtctgatgtcccttagatgtgttcaagcaacatgcaaatatcctgattatcagaa
 atgaaccatgaagcctatggcaactctatgttttttttgacagtcgagcagcaaatgtat
 accaggcacttttttactcgcggggggttcgggtgggtgataaggaggcagtcacacaaagc

ctgtattttaacagcagatgctgaaccaagaacaacttttagcaacaacaaattatgtaggc
 acaccaagtggctctatgggttcatctgatgtccaattgtttaatagatcttactggctt
 cagcgtatgtcaaggccagaataatggcatttggctggagaaaccagttattttattacagtt
 5 ggagataataccagaggaacaagtttatctatcagtatgaaaaacaatgcaagtactaca
 tattccaatgctaatttttaagatttttctaagacatactgaagaatttgatctttctttt
 atagttcagctttgtaaagtaaagtttaactcccgaaaatctagcctacattcatacaatg
 gaccctaataatttttagaggattggcaactatctgtatctcaaccacctaccaatcctcta
 gaagatcaatatagggttttagggctctccttggcagcaaaatgtccagaacaggcgctt
 10 cctgagccccagactgatccttatagtcaatataaattctgggaagtcgatctcacagaa
 aggatgtccgaacaatttagaccaatttccactaggaaggaaatttctatatcaaagtggc
 atgacacaacgtactgtactagttccaccacaaagcgcaaaacagtgcggtgatctacg
 tcagccaagcgcaggcgtaaggcttag

15 Table 137

SEQ ID NO:128

cbe_252041 HPV 1a L2

Human Papillomavirus 1a L2

length=1524

20 atgtatcgctacgtagaaaaacgcgctgccccaaagatatatcccctcatgcaaaata
 tcaaacacctgcccacctgacattcaaaataaaattgagcatacaacaattgctgataaa
 atattgcaatatggcagctctgggagtttttttgggaggttgggcattggaacagccaga
 ggctctggaggaagaattgggttatactcccctcggtaggggtggtaggggttagagttgct
 25 actcgtccaactccagtaaggcctacaatacctgtggaaacagtagggcccagtgaaatt
 tccccatagatgtttagatcctacaggccctgctgttattcccctacaagatttaggt
 agagacttccaataccaactgtgcagggtattgcagaaattcacccatttctgacata
 ccaaacattgttgcatcttcaacaaatgaaggagaatctgcatattagatgtgttacga
 gggaatgcaaccatacgcactgtttcaagaacacaatacaataacccctctttcactgtt
 gcatctacatctaataaagtgtggagaagcatcaacatcagatattgtatttgttagc
 30 aatgggttcaggtgacaggggtggtagggcgaggatatccccttggtagaattaaacttaggc
 cttgaaacagacacatctctgttgtagaagaacagcattttccagcagcacaccaatt
 gctgaaagaccctcttttaggccctcaagattctataataggcgtctatatgaacagggtg
 caagtacaagaccctagggtcggttagcagccacagtcattgggtcacttttgataatcca
 gcatttgagccagagcttgatgaggtgtctattatcttccaaagagacttagatgctctt
 35 gctcagacaccagtgccatgaatttagagatgtagtttatctgagcaagcccacattttcg
 cgggaaccagggggacgggttaaggggttagccgccttggcaaaagttcaactattcgtaca
 cgccctgggcacagcaattggcgccagaacccacttttctatgatttaagttctattgct
 ccagaagactcaattgaattattgccttttaggtgagcatagtcaacaaacagtcattagt
 tccaacttaggtgacacagcatttatacaaggtgagacagcagaggatgacttagaagtt
 40 atctctttagaacaccacaatttatattcagaagaagagcttttagacacaaacgaaagt
 gtgggcgaaaatttgcaacttactattactaactcagagggtaggggttctatactagat
 ttaacacaaagcagagtcaggccaccttttggcactgaagatactagcttgcattgtatat
 tacccaaattcttctaagggaactccaataattaatcctgaagaatcatttacaccttg
 45 gttattatagctcttaacaactcaacaggggattttgagttacatcctagtcttagaaag
 cgtcgtaaaagagcttatgtataa

Table 138

SEQ ID NO:129

50 cbe_252090 Prey2820

PathCalling Prey Sequence 2820

length=535

55 gaggcagcattccacccatgctgagagccactgggtgctcccagcttgggtctgtatcct
 cctgagcagctcccacccctgaaatgctttggagaagaaagaaggaggccatgtttg
 gaaggaatgcagcagcagggccttgggggagtcctccgcccgggtgagggctgtcattac
 cacctggaggacctagaaggcgtcagagcatcatcaacgaactgaagaaggcccagtg
 ggcagctctggggctgcatctgagccagtggtgcttggcgaaggagggtgtggattcccc

agcaccaatgaataccctgatctggaagaggagagagcaacctatccacaggaagaggac
 cgttttctcactcctggcagggcccagctgcttttggtctccctggagccccctggatcag
 gaggaggttgtgcctccaggcagctgcactctctggcctcgttcagcactgtcacagcc
 agaaggaaccccccttcacaatccctgggggatggagttggcagcgtctgaagagt

5

Table 139

SEQ ID NO:130

cbe_2685998 Prey2313

10 Homo sapiens, clone IMAGE:3625550, mRNA, partial cds.
 length=1922

gcgccatctgcctcgattacttcacggacccccgtgtccatcggtcggggcacaacttct
 gccgagtttgtgtaacccagttgtgggtggggaggatgaggaggacagagatgagttag
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 15 cggggtgggacacccccatgcgggatgaagactacgagggtgacatggaggaggaggtcg
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 tggaggaggaggacctgaggggggaggatgaggaggacgaggaggaaagtgtggaggagg
 ttgaggaagaggatctagacccccgtcaccacctgccccgcctccagcccccgagggt
 20 gcttcacatgccctcagtgccgaaagagctttcctcggcggagcttccgccccaacctgc
 agctggccaatatggtccaggtgattcggcagatgcacccaacccctggtcgaggagacc
 gcgtgaccgatcagggcatctgtcccaaacaccaagaagccctgaagctcttctgcgagg
 tagacgaagaggccatctgtgtggtgtgccgagaatccaggagccacaaacagcacagcg
 tgggtgccattggaggaggtggtgcaggagtacaaggccaaactgcaggggacagtggaac
 25 cactgaggaagcacctggaggcagtgagaaagatgaaagccaaggaggagagggcagtgga
 cagaactgaagagccagatgaagttagagctggcagcgggtggcctcggagtttgggagac
 tgacacggtttctggctgaagagcaggcagggctggaacggcgtctcagagagatgcatg
 aagcccagctggggcgtgcgggagccgcggctagtgccttgagaaacaggccgcccagc
 tcagcgcctgtggcagaggcccaggagcggagccagcaggggggtctccggctgctcc
 30 aggtgtgaagaggtacagctgcagccccagagggtctggtcccctgaccgtgccaaccc
 catagccatgacttctgacagatgccatcgtgagggaaaatgagccggatgttctgtcag
 gctgcgagagtggacctgacgtggacctgacacggctcaccggccctgatgctgtcc
 cctgaccgcccgggggtccgcctggcagagcggcggcaggaggttctgacctcccaag
 cgcttctcggccgactgctgcgtactgggggcccagggttccgctccggccggcactac
 35 tgggaggagcctaagaacacctcctggcctccagctcagccttctctcacctactatgtc
 tgtccaacagaccggccagaatttagcttacttgagagagatctggaatggtcgccatg
 attgaaaccacgcaccattacatcatcattacattaattacatcaacataaattatctt
 tcccccttccctttccagcactcaaccaaggagcaaagctcatcccacccacacccct
 ccagggtctgctcactgccaggtcctctcccctttgttcagtggagctggcttttctcc
 40 cagcccccttccatgcctttcactccatttggaagctctgagggggagcctggggacgg
 gtttgggtcccaggaggagagccttgggtataatctattttctaggagcctcttgct
 tgtcacttgagctttcgccctctgctttgatggctgaggtgaactcatgttctttggga
 aaaggggaaggcgtgctgtggaataaaatgtttatttgcttctcaaaaaaaaaaaaaaaa
 aa

45

Table 140

SEQ ID NO:131

cbe_2693325 Prey1673

50 Prey1673, 194 bp.

length=194

tgtacactgcccaatgtgggtgcagagctgagggactgagctggggcaccagggtgggc
 agattggcatgaggagagaggaggacctcaagtgggaagagaggcaaagttagcactg
 gagacaggagtggaaggaagagctgaaggattcagctcctggccagatagttgggatgat
 55 gctcttttagatct

Table 141

SEQ ID NO:132

cbe_2789381 Prey775

AL523176 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC001YA04 3 prime, mRNA

sequence (AL523176.1: 98%/1043, p=0.000000), 1498 bp.

length=1498

tactggaggggccgggtcccagcctggatgttacccaaccccatgacggaccctttcattg
 cagcgatctgcacacgtgtgggtgtttccataggacattgtcaggcacagatggctggc
 cgaagcacgtgcatttcagttttgaggctcctgtcctcaggcagtggtgactcaggccct
 10 gggagtcatgtggatgccagtagcctgggcccacagagctgctgggatgtggggggcata
 tcaagtgaagatggcaactctgatctgacgcctctgtgctcaggggccctggaggaggg
 gctactgccccttgccccttagacaacaggacagagaccagagggactgggcggcttgtc
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 15 tctccctccccagccacagatagccacagggggctttcaaaaccaggcagggccaaagcc
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 gagtggagcagaggagaagaccagactgtgcatagtccctgaggagggttagcctca
 ggtgccacagcctggttcggcctggcgccccaggacgcagcagcaaccttgggcttcct
 gcggggtgactaccttgccctccggcctgcccgttgactaactatgctctgtggttttg
 20 ttccagagaactcagattgcacagagctagactcgggcagccagagcggcgagctgagt
 aacaggggtaacacctccctgctgcccctccctctctccctctctctccctctctctt
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 tcttggtctctgttggtgacagacccccccctaagggtgctcgtttgggggctcttcagg
 cagcacctcagcctggcacccccactcccctgcacagccccaggcctcaggaccccacc
 25 cctctgaggccccaggggagccctgttcacgctggtttctccccaggacccatgagcttcc
 tggctggcctgggccttgtgtgggactggccctgctcctgtactgctatccgccagacc
 ccaagggcctgccagggacccggcgctcctcggtttctcgctgtcatcatcgacagac
 atgtcagccgctacctgctggccttctggcagatgacctaggggggctctgacagaccc
 tggaccagggcctcacctgccactcaacaaagagtcctcgagccggcccgccaagggg
 30 actgctgcttcttttctaaatgcataattttcattatttataatttgtgtaaaaaaacac
 acctcaccttacaagggtgctgaccatattaaatgttcagggtctctcaaaaaaaaaa

Table 142

SEQ ID NO:133

cbe_2826346 RPS10

ribosomal protein S10

length=598

ctccttcttttccagccccggtagccgaccctgcagccgcagagatgttgatgcctaaga
 agaaccggattgccatttatgaactcctttttaaggaggagtgatgggtggccaagaagg
 40 atgtccacatgccctaagcaccggagctggcagacaagaatgtgccaaccttcatgtca
 tgaaggccatgcagttctctcaagtcccgaggctacgtgaaggaacagtttgccctggagac
 atttctactggtagcttaccatgaggggtatccagtatctccgtgattaccttcatctgc
 ccccgagattgtgctgccaccctacgccgtagccgtccagagactggcaggcctcggc
 45 ctaaaggctctggagggtgagcgacctgcgagactcacaagaggggaagctgacagagata
 cctacagacggagtgctgtgccacctgggtgccgacaagaaagccgaggctggggctgggt
 cagcaaccgaattccagtttagaggcggatttggtcgtaggagctggtagccacctcagt
 aaaattggagaggattcttttgcattgaataaacttacagccaaaaaaccttaaaaaa

Table 143

SEQ ID NO:134

cbe_2830508 Prey292051

Homo sapiens, clone MGC:12344, mRNA, complete cds.

length=769

catcaccccataaacaatataggtttggctcctagcctttctattagctcttagtaagatta
 cacatgcaagcatccccgttccagtgagttcacctctaaatcaccacgatcaaaaggga

caagcatcaagcacgcagcaatgcagctcaaaacgcttagcctagccacacccccacggg
 aaacagcagtgattaaccttttagcaataaacgaaagttaaactaagctataactaacccca
 ggggttggtcaatttcgtgccagccaccgcggtcacacgattaacccaagtcaatagaagc
 5 cggcgtaaagagtggttttagatcacccctccccaataaagctaaaactcacctgagttg
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 10 acctcaccacctcttgctcagcctatataccgccatcttcagcaaacctgatgaaggct
 acaaagtaagcgcaagtaccacgtaaaagcgttaggtcaagggtgtagccatgaggtgg
 caagaatgggtacattttctacccagcaacaatatactctgccggc

Table 144

SEQ ID NO:135

cbe_2898065 Preyl620

Homo sapiens, DKFZP434F162 protein, clone MGC:21493 IMAGE:3871231, mRNA, complete cds.

length=2156

20 gagctgaagagacctggagccgacagacgggtgaaggccatgccgccttctgggaaagt
 ccccgaaaggagaatctgtggctacagtgtagtgggggtcctgctcctttgtgtgctca
 accatggaaaagtctcttgagcatgtcactcagcacctgcagcagcactgcatggctct
 ggggaggaggaggaagaggaagaggaggatgaccacttgaggagaattctcctgcttg
 25 tggcaggaatgtggcttttgttctctggactgttctgctgacctcatccgccatgtctac
 ttccactgctaccacccaagctgaaacagtgggggctgcaggccttgcaaagccaggct
 gaccttggcccttgcatcctggacttccagagccggaacgtcatccctgatatccctgac
 cacttctgtgtctgtgggagcactgtgagaattccttcgacaatcctgagtggtttat
 cggcatgtggaagcacacagctctgtgctgtgaatcgaagcagtcggcaaggacaaccg
 30 gtggctctgtgtggctggaaaggctgtacctgcacctcaaggaccgcagtaaaacttcga
 gagcactcccgagccatacccaggagaagtggtagcctgccccacctgtgggggcatg
 tttgccaaacaataccaagtctttagatcacatccgtcgccagacctcattggatcagcag
 cacttccagtgttctcactgttccaagagatttgccacagagcggtctattgcgggaccac
 atgcgcaaccatgtgaatcactataagtgcctctgtgtgacatgacctgcccgtgct
 35 tctcctcccgcaaccacatgcgctttcgtcacagtgaggaccggcctttaaatgtgac
 tggtgtgactacagctgcaagaattctattgacctccagaagcacctggataccacagc
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 tctatcaagtccattaccgcaaagtacatgaaggagactctgagccaaggtacaaatgt
 catgtgtgtgacaaatgcttcacacggggcaacaacctcaccgtgcaccttcgcaagaag
 40 caccagttcaagtggccctcagggcatccccgttttcggtacaaggaacatgaagatggc
 tatatcggtgcagctgggttcgctacgagagtgtagagctgacacagcaactgctgcgg
 caaccacaagaggatcgggcctgggaacgtcgctgaacgagagcagcctgcagggcatt
 attctagaaacagtgccaggggagccaggacgtgaaggaagaggaagaggagggaagggt
 agcgaagggaagcagccctctcagcctctcaggacaacccagttctgtcatccacgtggtg
 45 aatcagaccaatgcccaaggccagcaagagattgtctactatgtgctgtctgaagccca
 ggggagcctccccagtcctgagccacctcagggggcatcatggaaaagcttcaagga
 atagctgaggagccagagatccagatgggttgaggccgagagccagaccatttcttcc
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 50 attctgcagactctaaagacttccctttctgccagactacatttctgtggggagcctgag
 gactctggattctttgaggggatcctggatgtgtgttcttgttaagaggctgttatc
 aggtcttaactataacctcaagatcgtcttgacagtattaaatccttagctcacatcca
 tccccatcttctgggtccttaggcccaggatggcatgtgactgggtccctgcaagggtc
 ctttctttgtcaccagccaaggcatgataaccaagtagccatttctcttaagggttc
 55 ctctacaaccccaaggacttcatgattatcctcagggacaggattggaggcatgagcg
 tgtttattaacaagatgttttggtaataaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Table 145

SEQ ID NO:136

cbe_3001381 IRF1

interferon regulatory factor 1

length=2035

5 cgagccccgcgaaccgaggccacccggagccgtgccagtcacgcccggccgtgcccg
 cggccttaagaaccaggcaacctctgccttcttccctcttccactcggagtcgcgctccg
 cgcgccctcactgcagccctgcgtcgccgggacccctcgcgcgcgaccagccgaatcgct
 cctgcagcagagccaacatgcccatcactcggatgcgcatgagaccctggctagagatgc
 10 agattaattccaacaaatcccggggctcatctggattaataaaggaggagatgatcttcc
 agatcccatggaagcatgctgccaagcatggctgggacatcaacaaggatgcctgtttgt
 tccggagctggggcattcacacaggccgatacaaaagcaggggaaaaggagccagatccca
 agacgtggaaggccaactttcgctgtgccatgaactccctgccagatcgcaggaggtga
 aagaccagagcaggaacaagggcagctcagctgtgcgagtgtagcgatgcttccacctc
 15 tcaccaagaaccagagaaaagaaaagtggaagtccagccgagatgctaagagcaagg
 ccaagaggaagtcatgtggggattccagccctgataccttctctgatggactcagcagct
 ccactctgcctgatgaccacagcagctacacagttccaggtacatgcaggacttggagg
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 ggacatcccagtggaagttgtgcccagcagcaccagtgatctgtacaacttccaggtgt
 20 caccatgccctccacctctgaagctacaacagatgaggatgaggaagggaattacctg
 aggacatcatgaagctcttgagcagtcggagtgccagccaacaaacgtggatgggaagg
 ggtacctactcaatgaacctggagtcagcccaacctctgtctatggagactttagctgta
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 tcacagatctgaagaacatggatgccacctggctggacagcctgctgacccagtcgggt
 25 tgccctccatccaggccattccctgtgcaccgtagcagggcccctgggcccctcttattc
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 30 agagtcagtgctggtcttttctctgagccagctgcctggagagggtctcgctgtca
 ctgggtggctcctaggggaacagaccagtgacccagaaaagcataaacaccaatcccagg
 gctggctctgcactaagcgaaaattgcactaaatgaatctcgttccaaagaactaccct
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 tcggggcaatgctccctcagcctcagaggagctctaccctgctccctgctttggctgagg
 35 ggcttgggaaaaaaacttggcacttttctgtgtggatcttgccacatttctgatcagagg
 tgtacactaacatttcccccgagctcttggcctttgcatttatttatacagtgccttgc
 cggggccccaccacccctcaagccccagcagccctcaacaggcccaggagggaagtgtg
 agcgcttggtatgacttaaaattggaatgtcatctaaccattaagtcatgtgtgaaca
 40 cataaggacgtgtgtaaatatgtacatttgtcttttataaaaagtaaaattggt

Table 146

SEQ ID NO:137

cbe_3056756 KIAA0440

signal-induced proliferation-associated 1 like 1

length=6028

45 ggtgtggacgttgtctaaatttcggtagccatggcacaagaatataagaaagcatgggat
 tatggcaaccacagaatctcagtagtacaagttccattcagtttttctgaaagaaagcc
 ctctgttaaagtgaagcaaaagaaactgttggtgattataacgtttagaagttccaat
 50 tcagtgttttacaataaaagcatcatttaaccttttaaatgaaaaagattaagatctcat
 gcaactgttgtattttctggaagccattctccaaaagggaagtgcacatttaaaacacag
 atatgatggctccttgcctgcagggttaagtctacttgcctttacatcatgaccagcttg
 aaacgggtcacagacagaaaggcctcttgccactgacaggccctctgttgttgccacagac
 ggcacccccaaagtccacactgatgatttctacatgcggcgcttccgggtcccaaatggc
 55 agcttaggatcatcagttatggctcctgtaggaccccccgagtggaaggttctcaccat
 ataacctcaacccccggagtcacaaaaatgggggtaagggcaaggattgcagattggccc
 ccaagaaaggaaaacataaaagaatctagccgttcaagccaggaaatagaaacctcaagt

tgccttgatagcctgtcctccaaaagcagtcctgtgagtcagggaaagtctgttagcctc
 aattccaatgactcagccatgctgaaaagcatacagaacacgctgaaaaacaagacaaga
 ccgtcggagaacatggactccagatttctcatgcctgaagcctaccccagctccccaga
 aaagctcttcgcagaatacgcagcgaagcaacagtgatcaccataagtgaacttgat
 5 gtggatagctttgatgaatgtatctcacctacatacaagactggaccatcactgcacagg
 gaatatggtagcacatcttcaattgataaacaggggaacatctggagaaagctttttgat
 ttgttaaagggtacaaagatgacaaatctgatcgaggtccaactccaaccaagctcagt
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 10 cgttcaaaatctgaaactggagactcctctatttttcgtaaatgcgcaatgccaaagt
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 gaggcaattatgaacaggcacaatgttattaagaggagaaacaccaccactggagcttcc
 gcagctgccgtggcatccttgggtctctggacctctgtctcattcagccagttttagctcc
 15 ccaatgggcagcacagaggacctgaattccaaggaagcctcagcatggaccaggaggat
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 atgacactgagaggttcgggtcctggaggacgccattccgtcgacagccaagcactcgaca
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 25 tgcctgcggttggccttcaacacacccaaggtcacagagcagctcatgaaactggatgaa
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 cacattggaaatgatcgttaacaattgttttccaagagcctggagcacagccattcagc
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 gctgaagactacaacaaggccatggaactagactgccttttagggatctccaatgagttc
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 45 caggcaggggtgagggcagggcagtcgcctgggtggagatctgcaaggtggcggtagccact
 ctgagccatgagcagatgatcgacctcctgagaacatctgtcacgggtgaagggtgtcatc
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 gtgatggagtacaaaatgaatgaagggtgttcatacgaattcaagtttcccttccgaaat
 aataacaagtggcagaggaacgccagcaaggggcctcattcacctcaagtcctccag
 50 gtgcagagtcctatgacactcgcggctgaatgctggaaaaggagatgggaagatgcctcct
 ccagaagagcgcgcaacatccctcgaagcatctccagtgacgggcgcccactagagagg
 cggctgtctcctgggtcggacatctatgtgacgggtctcatccatggctttagcaagatcc
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 55 attgacaggcagaacacccagtcagatattgggtggcagcggaaaatccacgcctagctgg
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 tccagtagcaatactctctccagcaatgcgtcaagtgcccatagtgatgagaagtggtag
 gatggggaccgcacagaatccgaactcaacagctataactatctgcaaggcacctctgct
 5 gacagtggcattgacaccacctcttatggccccagccacggcagcacagcctcgctgggg
 gctgccacatcgtcacctcgctcagggccaggcaaggagaaagtggcaccctatggcac
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 10 accatgagctcccagacactctgccagcccagtggttttcaccagtggccggagtccact
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 cgtcatcagagcgatggcaatgaaatagcccacaccaggtgcgtgcctcaaccagagac
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 25 aagccttacagcagcagtaaaagactcctctccactctggcttctaaagtggaccagctg
 gaaggtatgctgaagatgcttcgggaagatttgaaagaaggaaaaagaagacaaagctcac
 cttcaggcgagggtgcagcacctgcgagaggacaacctgagggtacaggaggagtccag
 aacgcctcggaacagctgaagaagttcacagaatgggtcttcaacaccatagacatgagc
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 30 agcccttattccctccatagaaagcatcctcagagcaccttccctggcttctactctgc
 ccccttccgggagtgacacacacaatagttgcagatcaacaatcatcacctgcctttg
 tagaaaagaaaaacaaaaaagtaataaaaaattttaaacagtaaaataaaaagtttaact
 gctaaaaaaaaaaaaaaaaaaaaaaaaa

35

Table 147

SEQ ID NO:138

cbe_3340492 TRIP

TRAF interacting protein

40

length=2007

45

50

55

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 cccgaaaaaaaaaaaaaaaaaaaaaa

20 Table 148
 SEQ ID NO:139
 cbe_3345510 COX6C
 cytochrome c oxidase subunit VIc
 length=444

25 ctttagtcaggaaggacgttggtggttagcgtatcaaggacagtaactacc
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 gatatttgaggagatgaggaaggctgggtatcttccagagtgtaaagtaattctggaatata
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 ctttgaaaaaaaaaaaaaaaaaaaa

35 Table 149
 SEQ ID NO:140
 cbe_3454406 gbh_af252829
 Homo sapiens chromosome 8 clone BAC 495D4 map 8q24, *** SEQUENCING
 length=488

40 ccgagcagcctaactgggaggcacccccagcagaggcacactgacacctcacacggcag
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 45 gaatgattttgacgagctgagagaagaaggcttcagacgatcaaataactctgagctacg
 ggaggacattcaaaccaaaggcaaagaagttggaaactttgaaaaaatttagaagaatg
 tataactagaataaccaatacagagaagtgttaaaggagctgatggagctgaaaaccaa
 ggctcgag

50 Table 150
 SEQ ID NO:141
 cbe_3461331 MET
 met proto-oncogene (hepatocyte growth factor receptor)
 length=4620

55 cgccctcgccgcccgcggcgccccgagcgctttgtgagcagatgcggagccgagtgagg
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20

Table 151

SEQ ID NO:142

cbe_3473488 gbh_al121903

Human DNA sequence from clone RP1-155G6 on chromosome 20 Contains
 length=5694

25

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Table 152

SEQ ID NO:143

cbe_3474077 KRT4

keratin 4

length=2617

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 caaggctgaggctgaagccctgtaccagaccaaggtccagcagctccagatctcggttga
 40 ccaacctggtgacaacctgaagaacaccaagagtgaattgcagagctcaacaggatgat
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 cgtggctgatgcagagcagcgaggtgagaatgcccttaaagatgccacagcaagcgct
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 45 gctggagggcgaggagtacagaatgtctggagaatgccagagtgcctgagcatctctgt
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 55 attatccatctacatcagaaccaaactacttctccaacacccggcagcacttggccctgc
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Table 153

SEQ ID NO:144

cbe_3563252 LOC91689

hypothetical gene supported by AL449243

length=1586

5 agcgggctttcttccccgagggcgccacgagggctgggcgggtgggggtgcgggtgcccgggt
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 10 caggtccggggctctccggagcgggctagcttgaggaaagatggcgatgtctccggcgc
 atggagcggctcagggcggagcctggtagcgtcggggtcagtcacgttaccgcagcgg
 cgccattttgccccaaaccgggtgaaaatgtccttcggccttctgcgtgtgttctccattgt
 gatcccccttctctatgtcgggacactcattagcaagaactttgctgctctacttgagga
 15 acatgacattttgttccagaggatgatgatgatgactaacaggaattacagaaagg
 agaaagcactaactgaagaaatggtagtctcagtttctctgccttccctatcagcag
 aaaggctcggggaaggccctcagcctcccagtcctggtagaagcttcctgtatggtccatga
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 caaacaagcaatcaaattatgaataaacataataaataatcagccgtgcgtgactgagtga
 20 tggctgcagtttctcagtatccctagggtctagttggtagcagttgtctctgctgtccttt
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 cccttaagaaagcttcatgggctaactaaagcctcatgccattctgtgttcagtgccagt
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 25 gttctgtgatagaggatagataggttttcatctatttccctggcttataactccaaa
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 ctctgacctaccttgtctgatttttaggtcatgagacccccatttcagaagggttctgcc
 30 ccataacctgagaggaagaaatgtagacaggccttgttggacttccccactccatctgat
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 ctatccaatgaggtctccataaaaggcccaagaagacaggttttagagagctttcgagaa
 cagaacacttggctttgcaaagtggcagcctggagagaacttggaaagctccacgcccct
 tctataacctcaccctatgcattcttccagctgtatcttttgtgatctctttataataaa
 35 ccagtaaacggaaaaa

Table 154

SEQ ID NO:145

cbe_3575702 SUI1

putative translation initiation factor

length=1324

40 cggcagagcgcgcgcgaggattcagcagcctcccccttgagccccctcgcttcccagacg
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 tccaccgaggaaaaggaatcgatcgatgtccgctatccagaacctccactctttcgac
 45 ccctttgctgatgcaagtaaggggtgatgacctgcttctgctggcactgaggattatc
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 gatgattacgataaaaaagaaactagtgaaggcgtttaagaaaaagtttgctgcaatggt
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 tgatccatcagtcagtagctagctgtagagcttgcaacttaatagcagcagctgccc
 5 tggcatgtgaagtaacaaactgggttttgggttttttttcccttcagttttaatgttat
 gtgtaatgtattttaacccttattttaataaaaacttggttttcagaaaaaaaaaaaa
 aaaa

10 Table 155

SEQ ID NO:146

cbe_3580897 HSPA5

heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
length=3925

15 acagcacagacagattgacctattgggggtgtttcgcgagtgtgagaggggaagcgccgcg
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 ccgctgcaagtgcgaaattgcgctgtgctcctgtgctacggcctgtggctggactgcct
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 ctgagcgcgccgccccgaggaggaggacaagaaggaggacgtgggcacgggtggtcggc
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 gaacgtctgattggcgatgccgccaagaaccagctcacctccaaccccgagaacacgggtc
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 25 ggaggtgggcaacaaagacatttgcctcctgaagaaatttctgccatggttctcactaaa
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 5 gcatttcacagtgcccaagagtgggttttcttgaaactacttggtttcctatttccct
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 agacttcaaaaaaaaaaaaaaaaaa

Table 156

SEQ ID NO:147

cbe_3583511 MGC3222

hypothetical protein MGC3222

length=5765

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 agggagtacaccgaggatgggcaggtgaagaaggagacgaggtattcctacaacactgaa
 35 tggaggtcagaaatcatcaacagcaaaaacttcgaccgagagattggccacaataacccc
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 ggtgggtgtcccatgtgctgagatggagaaggcgccagtgctcagcactagacagggtgag
 atgtcaagtggaaatgtcaaggaggtggtaggtggtaggtggtaggtgtgaggc
 ccgggagagggtccagagctgcagctttaaattggagggtcacggcatgtggaggccaagg
 25 aagcagatgggatgtccggggagagagtatggactgaagcagctaaagaattgcagcatc
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 40 ccatgccagagcaggagccccgggtcaatttggactctgcacccccctcctcttcaggg
 gccagacttggcagcatgtgcaccaggttgggtgttaccagctcatgtcttccccacatc
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 tttct

Table 157

SEQ ID NO:148

cbe_3590661 NUP214

nucleoporin 214kDa

length=6614

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 15 ccagccagcctgtctcgatcagcctttctgtctcagagatattatgaagacttggatgaa
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 25 aagcaggggtctctaataaattcccttaagccatctgggcctacaccagcatccggtcag
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 30 tcttatgaggccatttccgaaagctcacctccctcaggaatcacatccgcatcaaacacc
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 55 cccacatccaccagtggaaagtgtctttgggtgccgcctcaagtaccagttagctccagttcc
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 ccgcatcctcagcttcttccccgagaaatgctggagcaggctgttcagaccgacgttggc
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 aaaaaaaaaaaaaa

20 Table 158

SEQ ID NO:149

cbe_3606990 Prey1053670

Homo sapiens, Similar to CG5604 gene product, clone MGC:11330, mRNA, complete cds.

25 length=1206

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 gttgtattttctttgtatattataaacatttttaacttgttgcggtttgaagtaaaaa
 45 atttccaaaatgtatgctcaacaataatcattaaaatgtttgcagcgtaaaaaaaaaaaa
 aaaaaa

Table 159

50 SEQ ID NO:150

cbe_3621798 XPO1

exportin 1 (CRM1 homolog, yeast)

length=4148

55 aggaaggaaggagcagttgggtcaatctctggtaattctatgccagcaattatgacaatgt
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 aagtagtgacacatttaaaggagcatcctgatgcttggacaagagtcgacacaattttgg

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 10 cattgtctcagatttctgaactggattcccctgggatataatttttgagaccaaattaatca
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10 aaaaaaaa

Table 160

SEQ ID NO:151

cbe_3621899 PCNP

PEST-containing nuclear protein

length=602

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20 cattaaagtaagttaaattcatgtatcgatataattaaatcatgtaagaactaagagttc
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tggttaggaatatacacaggctgcttctctggagttattaccaactaaaagacctcagcaa
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caaggaaattttatactgtatgcntttgtcngtgactatgcntttaaagatgtgtttaa
25 cggcnaattttaaaaaagttcntataccatccaaaattcnaaacacnccctaccatacc
caatctaccaangtatatgtggtgngatcccaaatgggtggaagatgcatttccttccc
cc

Table 161

SEQ ID NO:152

cbe_3625721 EIF2B2

eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa

length=1522

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55 cacaggagtcacctaataaaaaaaatccttgatactgttgccctgccttttttagtcacccc
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5

SEO ID NO:153

ankylosis, progressive homolog (mouse)

10

15

30

45

50

112

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 TcctTTaaaaaaattatagacacggttcactaaattgatttagtcagaattcctagact
 5 gaaagaacctaaacaaaaaaatTTTTaaagatataaatatatgctgtatatgttatgta
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 20 gcagaggttgtagtgagccgagatcgcgccatcgactccagcctgggtgacaagagcaa
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Table 163

25 SEQ ID NO:154

cbe_3643627 DKFZP434I1735

DKFZP434I1735 protein

length=5477

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Table 164

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KIAA1389 protein

length=5801

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55

Table 165
SEQ ID NO:156

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Table 166

SEQ ID NO:157

cbe_3670766 ACTC

actin, alpha, cardiac muscle

length=1294

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Table 167

SEQ ID NO:158

cbe_3694420 ARHGEF2

rho/rac guanine nucleotide exchange factor (GEF) 2

length=4093

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5

Table 168

SEQ ID NO:159

cbe_3705944 TNFAIP1

10 tumor necrosis factor, alpha-induced protein 1 (endothelial)
 length=3508

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15

Table 169

SEQ ID NO:160

cbe_3714119 Prey1053021

Sequence 1 from Patent WO0131003.

20

length=3331

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 25 ttcatgctgcaaagagtcctgagtagtaccactatgagtacacggcgtgtgacagcacgggtt
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Table 170

SEQ ID NO:161

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 length=2039

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5 Table 171

SEQ ID NO:162

cbe_3760926 gbh_al359334

Homo sapiens EST from clone 628609, 5' end.

length=881

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15 cgtgaagtccgtggaagcctgtggtacaaaaatgttgagccgtagatgccgtcggaaat
ggtgaaggagactcgaagtactctgaggcttgtaggagggtaaaatagagaccagtaa
aattgtaataagcagtgcttgaattatttgggttcggttggtttctattagactatggtg
agctcaggtgattgatactcctgatgcgagtaatacggatgtgtttaggagtgaggacttc
taggggatttagcgggggtgatgcctgttgggggacagtgccctcctaattgggggtagg
20 ggtaggctggagtggtgtaaaaggctcagaaaaatcctgcgaagaaaaaacttctgaggt
aataaataggattatcccgatcgaaggccttttggacaggtggtgtgtgggtggcctt
ggtatgtgctttctcgtgttacatcgcgccatcattgggtataggttagtgtgttggtta
gtaggcctagtagaggagcgttatggagtggagtgaatcacatggctaggccggaggt
cattaggagggtgagagggctcctgttacggggtcatggg

25

Table 172

SEQ ID NO:163

cbe_3764052 MARK4

30 MAP/microtubule affinity-regulating kinase 4

length=1620

tgggtcagtgacacctccaggatacagacagcccccttcagcccagcccagccaggtct
cctacaccgccaccatgccattcggtaacaccacacaagaagttcaagctgaattacaagc
ctgaggaggagtaccccgacctcagcaaacataacaaccacatggccaaggtactgacct
35 ttgaactctacaagaagctgcgggacaaggagactccatctggcttcaactgtagacgatg
tcatccagacaggagtggacaaccaggtcaccccttcatcatgaccgtgggctgcgtgg
ctggtgatgaggagtccacgaagttttcaaggaaactcttgacccccatcatctcggtac
gccacgggggctacaaaccactgacaagcacaagactgacctcaaccatgaaaacctca
aggggtggagacgacctggacctaaactacgtgctcagcagccgcgtccgcactggccgca
40 gcatcaagggtcacacgttgccccacactgctcccgtggcgagcgccggcggtggaga
agctctctgtggaagctctcaacagcctgacgggcgagttcaaagggagtagtacctc
tgaagagcatgacggagaaggagcagcagcagctcatcgatgaccttctgttcgaca
agcccggtgtccccgctgctgctggcctcaggcatggcccgcgactggcccgaccccggtg
gcatctggcacaatgacaacaagagcttctggtgtgggtgaacgaggaggatcacctcc
45 gggatcatctccatggagaaggggggcaacatgaaggaggtttccgcccgttctgcgtag
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acctgggctacgtgctcacctgcccatccaacctgggcactgggctgcgtggaggcgtgc
atgtgaagctggcgacctgagcaagcaccceaagttcgaggagatcctcaccgcctgc
gtctgcagaagaggggtacaggtggcgtggacacagctgccgtgggctcagtatttgacg
50 tgtccaagctgatcgggtgggctcgtccgaagtagaacaggtgcagctgggtgggtggtg
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55 accaatgggctccatcctctggattctggccaatgaaatatctccctggcaggggtcctct
tcttttcccagagctccaccccaaccaggagctctagttaatggagagctcccagcacac
tcggagcttgctgtttgtctccacgcaaagcgataaaataaaagcattgggtggccttaaaa

aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Table 173

5 SEQ ID NO:164

cbe_3770440 gbh_af217505

Homo sapiens uncharacterized bone marrow protein BM028 mRNA,
length=1725

10 cctcaaaaagaagaagaatgtgtcatatatcaatttggggatataagcaaatacctagtca
cagtcgttttctaaaaagtattgttttctggaaaaacctaagttttaagaatgatgccac
agcgaagtctctattttaactttttaatttgatttttttctttgttacagaagaagaca
atgatgaaattaaggattggggacctcatgtaagaatgggaggggtgttccaaaggacat
accaggggtctaggaggagtctaggaaggaagtcctgtgttatatcattctgggagtacc
15 tattttccatgaggggatgaaatactggagctgttgtagaagaaaaacttctgattttaa
tacattcttagcccaagagggtgtacaaaagggaacacatgtggactaaaaagatgc
tgggaaaaaagtgttccatgtagacatgactggcatcagactggaggtgaagtaccat
ttcagtatatgctaaaaactcactccagaacttagccgagtagaagcaaatagcacatt
gttaaattgtcatattgtatttgaaggagagaaggaatttgatcaaaatgtgaaattatg
gggtgtgattgtatgtaaagcgaagttatgtaactatgactgcaacaaagattgaaatcac
20 tatgagaaaagctgaaccgatgcagtgggcaagccttgaaactgcctgcagctaaaaagca
ggaaaaacaaaaagatgacacacagattgagtgggagatggaaggaaggctattacatt
atttccgaatttttaatactgtgtgaagtgggtggcttgcctgcgtgtaattctttgttttg
ttgttgtgttactgaatgtggcatttcagggttaacattaggttcttaaaagccaaagtc
agtttgcctttttgtgcctctcatctttctttgtgttatgtaagattgattattcattt
25 ctccctactggtaggaaccatagttgtgtcctatactgaagaggctggaaagtagccca
taaccataattgcagtatcttctttgtatttctctgttaagcaaagaaatattaaggaaca
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gaagctctgcagttttttctatgtgggatgattacttttttaaggaggatttaattctgag
30 gtagtataagtaactaaaggggaatatgaattgtttaacaaattagaatttgtttacaa
ctacttgaatttttaaatatgtcaaaacttacattacttgccaagcagtatgatgttat
aggaaacataaataagattacagaggtatcaatttgggttaaaattcaccattttataaga
ctaagcaataatcttaacaacctctttcctgaatatttaaatgtgtttgtatgggtgttat
gactaattgttactgatttagagactaagccctcttaaaacctttagttaaatataaaaa
35 gaaattatataatcttgccctccctgatggaaaactatataaaattgtagacttaaaagg
tttgtggaaatacattaggatatcagaaaactaaatataatggagttgctttatgactatt
acatgttaataaaaaatagcttaattgttttggaaaaa

40 Table 174

SEQ ID NO:165

cbe_3772244 PIGQ

phosphatidylinositol glycan, class Q

length=2878

45 cagcgagcgccgtcgtctgccccgggccccgcccacggtccccaaccccatccggaccc
cgccgcccagcgcgcgccccggaagcaccgcctcccggcatggtgctcaaggccttc
ttccccacgtgctgctctcgacggacagcgggctgctggtgggacgggtgggtgccggag
cagagcagcgccgtggtcctggcggtcctgcactttcccttcatccccatccaggtcaag
cagctcctggcccaggtgcggcaggccagccaggtgggcgtggccgtgctgggcacctgg
50 tgccactgccggcaggagcccaggagagcctgggcccgttccctggagagcctgggtgct
gtcttccccatgagccctggctgcggtgtgcccggagagaggcggcacgttctggagc
tgcgaggccaccaccggcaagcgcccactgccccgggtgccctggtgaggaccaggtc
atgctcatcttctatgaccagcgccaggtgttgctgtcacagctacacctgccaccgtc
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55 gacacggtagcacgcagtgaggtgctcttcgcagtgaccgcttgatgagggcccgctg
cggctgagccactggcagtcggagggcggtggaggccagcatcctcgcgagctggccagg
cgagcctcgggaccatttgccctgctgttgccagcctgctgtcgctggtctcagctgtc

agtgccctgccgagtggttcaagctctggccctgtccttcctcgggagcaaaactctccacg
 tgcgaacagctccggcaccggctggagcacctcacgctaattctcagtacacggaaggcg
 gagaacctgccagctgatgaggaaggccaacacgggtggcctctgtgctgctggacgtg
 5 gccctgggctcatgctgctgtcctggctccacgggagaagccgcatcgggcatctggcc
 gacgccctcggttcctgtggctgaccacgtggccgaggagctccagcatctgtgcagtgg
 ctgatgggtgctcccgccgggctcaagatgaaccgtgactggaccaggtgctgggcccgc
 ttcttcctctaccacatccacctgtggatcagctacatccacctcatgtcccccctcggtg
 gagcacatcctttggcacgtgggctctcggcctgctgggctgacgggtggcctgtcc
 ctctctcggacattatcgccctcctcacctccacatctactgcttttacgtctatgga
 10 gccaggtgtactgctgaagatccatggcctgtcctcactgtggcgtctgttcggggg
 aagaagtggaaactctctgcgcagcgcgtggactcctgttcctatgacctggaccagctg
 ttcatcgggactctgctcttcacacatcctgctcttcctcctgctaccacagccctgtac
 tacctgggtgttaccctgctccggctcctgggtgctgcgctgcaggccctgatccatctg
 ctcgaggacctcatcaactcctgcgctgtactcactgggtcttcggctctgccggccc
 15 tacaggtggcgataaaacccactgccctacagccgctgggtgcacacctaccgctccc
 cagctgtggctgccaccccaagcactcctggggcgccctgtgcgcaagctgttccttgg
 ggagctcatctacccctggaggcagagaggggacaagcaggactgagggaaactgctggct
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 agctggcgcatgtcctgtgctttgtggacgtgctgtgtgctcctgaacacggcaggccc
 20 tgctatcacaccttgggcttggaggtcattgggagtgagcagatgtgggggtggccagcc
 aggtggccgactccatcactggcactgctgccttgggaccgcttcccacctgctgc
 ggtcaccatggtggcgagcacagcaacccaggtgtccagagcactgccccatgcccacc
 ctgtgtaccaggtccagagggtccgtccaccacagcagcccaggtggagggtggtct
 ccctgggggtccccagtggtctgcctggctgtgggggtggaggaccttgccaggat
 25 gaacccccagtcacagaccctctagctccctcagccgaacagcaccctgcatctggg
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 cacggggtttatttgcggtatgttccctggagaggtcgctttgtgaagaaacatcagcag
 gctgtgagcatcgccaggtgctgtggggcgaggagcagcctcagtgcaagggcccgc
 cactgaccagccgtacctattcgtccacgggtgccccgtagcagcaggtcctgcggcaa
 30 atctgtctccctcatgggctcccagggaaggaggaagccctgctgtgcagacacctct
 gtggccccccaggagtgtagtgccctgggaggggcccgtggcactgagggcgaaagt
 cctgccagacggcacgggtctgggtgcggtgttccctgtgagcccgagtcgcttcagga
 ggggagcctgcaggtgccggtggtgaggggatgacgcgctgtgggtgggaggaggcagc
 gcccctctcagcagcaccaggactgcctgggactccctggcaacccagcaccggggaagc
 35 cgtcagctgctgtgacaataaaacctgccccgtgtctggaaaaaaaaaaaaaaaaaaaaa

Table 175

SEQ ID NO:166

40 cbe_3773649 EEF1A1L14

eukaryotic translation elongation factor 1 alpha 1-like 14
 length=2106

gtatacgaaatcataaaatctcatagatgtatcctgagtagggcggggcccgtgaaaccc
 tctgaatctgcggccaccacccggtaaggctaaataactaatcagacaccgatagtgaact
 45 agtaccgtgagggaaagggtgaaaagaacccgagaggggagtgaaatagattctgaaacca
 ttacttacaagtggctcatttacttacaagtgtcagagcacgttaaagtgtgatggcgt
 acatcttgacgtatgggcccggcgagttatgttaatatgcaagggttaagcagaaaaagcg
 gagccgtagggaaaccgaggtctgaataggcgacttttagtatattggcatatacccgaaa
 tcaggatgatctatccatgagcaggttgaagcttaggtaaaactaagtggaggaccgaacc
 50 gtagtacgctaaaaagtgcgggatggacttgtggatagtgggtgaaattccaatcgaacc
 tggagatagctgggtctcttcgaaatagctttagggctagcgtatagtattgtttaatgg
 gggtagagcagtggaatggcgccatctagctgtactgactataatcaaactccg
 aataccattaaaattaaagctatgcagtcggaacgtggtatcaccattgatatctcctgtg
 ggaaatttgagaccagcaagtactatgtgactatcattgatgccccaggacacagagact
 55 ttatccaaaacatgattacagggaacctctcaggctgactgtgctgtcctgattgttgctg
 ctgggtgttggtgaatttgaagctgggtatctccaagaatgggcagaccgagagcatgcc
 ttctggcttacacactgggtgtgaaacaactaattgtcggtgttaacaaatggattcca

ctgagccaccctacagccagaagagatatgaggaaattgttaaggaagt cagcacttaca
 ttaagaaaattgggtacaaccccgacacagtagcatattgtgccaatcttggttgaatg
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 gtaaggatggcaatgccagtggaaccacgctgcttgaggctctggactgcatcctaccac
 5 caactcgtccaactgacaagcccttgggcctgcctctccaggatgtctacaaaattggtg
 gtattgggtactgttccctgttggccgagtgagagactgggtgttctcaaaccgggtatgggtg
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 aggatgttcgtcgtggcaacgttgcctgggtgacagcaaaaatgaccaccaatggaagcag
 10 ctggcttccctgctcaggtgattatcctgaaccatccaggccaaataagcgccggctatg
 cccctgtattggattgccacacggctcacattgcatgcaagtttgctgagctgaaggaaa
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 atgctgccattgttgatatgggttccctggcaagcccatgtgtgttgagagcttctcagact
 atccaccttgggctgcttctgctgttcgtgatagagacagacagttgcgggtgggtgtca
 15 tcaaagcagtggaagaaggctgctggagctggcaaggtcaccaagtctgccagaaaag
 ctcagaaggctaaatgaatattatccctaatcctcccacccactcttaatcagtggtgg
 aagaccgggtctcagaactgtttgtttcaattgccatttaagtttagtagtaaaagactgg
 ttaatgataacaatgcatcgtaaaaccttccagaaggaaaggagaatgttttgggacac
 gttgggtttcttttttgcgtgtggcagtttttagttattagtttttaaaatcagtactttt
 20 taatggaaacaacttgacccccaaatttgtcacagaattttgggaccattaaaagggtta
 actggg

Table 176

25 SEQ ID NO:167

cbe_3787129 LOC55828

zinc finger protein ZNF140-like protein

length=2978

ggagggccctgctgaggactccggcaagtgtgggtcgcgggcgacggcggggctaaggccct
 30 gggccgcgcgcgggtttgaccacggccggggccttgggcatttccctggccttccctgttga
 gccgtgtaaacgcggggtgatgacggcgccgacctcttggcactgttgtgagagcgaagt
 gggcgcgagagcagacgccagctacagtttttttgggttatgtcgtcatgaagccggcgc
 tttcagttgtgcaaccttgaacaaatgggacactgcccattcttaagataagaacctgga
 aaggggactctgttggccatttgaaattgcagaataatgtctcaggtgacatttagtgat
 35 gtggctatagacttctctcatgaagagtgggcatgcctagattctgctcagagggactta
 tacaaggatgtgatgggtccagaattatgagaacctgggtctctgtaggtcttccgtaact
 aagccatatgtgatcatgttatttgaggatggaaaagagccctggatgatggagaaaaaa
 ctgtcaaaagcttaccatttcccttatcacactctgttccctgcttctgtgaactttgga
 ttctctgctctatttgagcattgttcagaagtcactgaaatatttgagttgtcagaacta
 40 tgtgttttctgggtgcttcatttcttatccaattctcctaattccactgtagaagctttt
 tcaagaagtataaaaaaaaaaaaaaaaaaaaaaaaaaaggcagtgctttgcttcttgata
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 tatgaagattcaccccaaccagtaacaatggaaaaagttgtaaaacaaagttatgaattt
 tcaaatcttaataagaatttggaaatatacagaatgcgacacatttagaagcacctttcat
 45 tcaaagtctactcttctgaaccacaaaacaattctgctgaagggaattcacacaaat
 gatataataagaagaatttatcaaaaaagtcagttataaaaagtgaagagaataaatggg
 ggaaagaaacttttaaatcttaataaaaagtggggcagccttcaaccagagcaaatctctt
 acccttccccagacttgtaatagagagaaaatctatacatgcagtgaatgtgggaaagcc
 tttggcaaacagtcaatcctcagtcgccactggagaattcatcacaggagagaagccctat
 50 gaatgtcgtgaatgtgggaagacttttagccatgggtcatcccttacacgacatcagata
 agccatagtggagagaaaaccttacaattgcattgaatgtgggaaggcctttagccatggc
 tcatcattactaaccatcagagcactcacacgggagagaaaaccgtatgaatgtatgaac
 tgtggaaagtcttttagtcgtgtgtcccttctcattcagcatctaagaattcatacgcaa
 gaaaaacgctatgagtgctgtatgtggaaaggccttcatcatagttcgtctctcatt
 55 caccatcagaaaagccatactggagagaagccttatgaatgtagagaatgtgggaaagct
 ttctgctgtagctcacaccttactcaacatcaagaattcacagtatgaagaaaaaatat
 gaatgcaacaaatgtctcaagggtcttttagtagcttctcatttcttgggtcaacatcagagt

attcatactgaagaaaaaccgtttgaagtttagaaatgcaggaaatccttcaaccagctt
 gaatcactgaatatgcatttgagaaatcacattagattgaaaccctacgaatgcagtata
 tgtgggaaagccttttagtcataggtcgtccctgcttcaacatcacagtattcatactgga
 gagaaaccttacgaatgtattaaatgtgggaagaccttcagctgtagttcaaacccttact
 5 gtacatcagagaattcatactggagaaaagccatataaatgtagttagtgggaaagct
 tttagcaaaggctcgaatcttactgcccataaaagagtacataatggagagaaaccaat
 agtgtggttaagtgtggaaaagccttttagatcatatgaatccctatacatgtgagaaatct
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 catcagaaaaatgtatactggggaaaagtgtgatgaagggtggtgaacatgggagactttt
 10 agcaatgatgcagatttttttattagagtttatactgtagagaaatcatatgaagtcaat
 aaatgtgggaaagcctttgtcagttatttaaccccttaattgaccntaagtatactcacact
 aggaaaaaatctgtgtacatgtagcaaatgtgggaaagactataggcaataggaatctcct
 gcaaacctctacaggagaaaaagttgtatgaatgtggaaactttagaaattgaaggaattt
 ttcagttccaagtgcaccccttattctataggaaataaactggagacaaatctcattta
 15 agagatgcagcaaagtgttactaagagtgtttatcttgccagacataagaagatgaatg
 gtagagcaacctgaaggatttagaaattacataataatctttgcagttatgctatttga
 aacaggattatataaggagagcaaataaacataagtatgcatttcttagagcagtagcttg
 cagtttcagttgagttctacttagaaattcttttagctagtgggcatgtgaagatattt
 agtcacccagaggagccagtaaatgttataatgttaaaaaattaaagctgcaaaagaaata
 20 aaatggtgttaataaaaaattttggcatctaataaaatcattttgtatatcaaaaaaaaaa
 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Table 177

25 SEQ ID NO:168
 cbe_3789063 AP2M1
 adaptor-related protein complex 2, mu 1 subunit
 length=1936
 ccgaggcagcgggcagacgagcagggggcgggcggaacatcttgggatccggagagtggcc
 30 gggccggcagacgagggggccgaggacaccaggtctgttctcagagcgatgggcccgcgga
 gactgatctgccgccatgattggaggcttattcatctataatcacaagggggaggtgctc
 atctcccaggtctaccgagatgacatcgggaggaacgcagtggtgccttccgggtcaat
 gttatccatgccggcagcaggtgcccagccccgtcaccaacattgctcgcaccagcttc
 ttccacgttaagcgggtccaacatttggctggcagcagtcaccaagcagaatgtcaacgct
 35 gccatggtcttcgaattcctctataagatgtgtgacgtgatggctgcctactttggcaag
 atcagcagggaaaacatcaagaacaattttgtgctcatatagagctgctggatgagatt
 ctagactttggctacccacagaattccgagacaggcgcgctgaaaaaccttcacacgcag
 cagggcatcaagagtcaagatcagacaaaagaagagcagtcacagatcaccagccaggta
 actgggcagattggctggcggcgagagggtatcaagatcgtcggaatgagctcttctctg
 40 gatgtgctggagagtgtgaacctgctcatgtcccacaagggcaggtgctgagtgccat
 gtgtcgggcccgggtggtgatgaagagctacctgagtgcatgcctgaatgcaagtttggg
 atgaatgacaagattgtttatgaaaagcagggcacaagcacagctgatgaaacaagcaag
 agcgggaagcaatcaattgccattgatgactgcaccttccaccagtggtgcgactcagc
 aagtttgactctgaacgcagcatcagctttatcccggccagatggagagtttgagcttatg
 45 aggtatcgcacaaccaaggacatcatccttcccttccgggtgatcccgtagtgcgagaa
 gtgggacgcacaaactggaggtcaaggtggtcatcaagtccaactttaaacctcactg
 ctggctcagaagatcgaggtgaggatcccaacccactgaacacaagcggggtgcaggtg
 atctgcatgaaggggaaggccaagtacaaggccagcgagaatgccatcgtgtggaagatc
 aagcgcagtgaggcatgaaggaatcgcagatcagcgcagagattgagcttctgcctacc
 50 aacgacaagaagaatgggctcgacccccatttccatgaactttgaggtgccattcgcg
 cctctggcctcaaggtgcgctacttgaaggtgtttgaaccgaagctgaactacagcgac
 catctgtcatcaaatgggtgcgctacattggccgcagtggtgcatttatgaaactcgctgc
 tagctgccactaggcagctagccccactccccagccaccctcctccacaggtccaggtgc
 cgctccctccccaccacacatcagtgctcctcctcctgctttgctgccttcccttg
 55 caccagcccagctcaggtctgggccaagcacattacaagtgggaccgggtggagcagccc
 ctgggctccctgggaggggagttctgaggctcctgctctccatccacctgtctgtcct
 ggcctaagccaggctctgagttctgtgaccaaagccaggtgggttcccttccctccca

cccctgtggccacagctctggagtgagggttggttggccctcacctcagagctcccc
aaaggccagtaaatggatccccggcctcagtcctactctgctttgggatagtgtgagctt
cattttgtacacgtgtgacttcgtccagttacaaaccaataaaactctgtagagtggaaa
aaaaaaaaaaaaaaaa

5

Table 178

SEQ ID NO:169

cbe_3800240 IVD

10 isoaleryl Coenzyme A dehydrogenase
length=2216

15 tttccgcagtttaggggctgctatttcaacgcagggagataaaaagaaaaaacacttgc
cttctaccccgctaaaaacactcatcctagggagcacgccagcatttgcagcgttcgggg
cagggccactcgccctggggcgttgactggctggaagctggcagggcgtcacgggtga
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ccagcgggcccactcgcttttggccgtggacgatgcaatcaatgggctaagcgaggagca
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cctgggcgtattgggcatcacagccccctgttcagtatggcggctccggcctgggctacct
ggagcatgtgctggtgatggaggagatatcccgagcttcgggagcagtggggctcagtta
cgggtgccactccaacctctgcatcaaccagcttgtacgcaatgggaatgaggccagaa
30 agagaagtatctccgaagctgatcagtggtgagtacatcgagccctggccatgagtga
gccaatgcaggctctgatgtgtctctatgaagctcaaagcggaaaagaaaggaaatca
ctacatcctgaatggcaacaagttctggatcactaatggccctgatgctgacgtcctgat
tgtctatgccaagacagatctggctgctgtgccagcttctcggggcatcacagccttcat
tgtggagaagggtatgcctggcttttagcacctctaagaagctggacaagctggggatgag
35 gggctctaacacctgtgagctaatctttgaagactgcaagattcctgctgccaacatcct
gggcatgagaataaagggtgtctacgtgctgatgagtgggctggacctggagcggctggt
gctggcggggggcctcttgggctcatgcaagcggctcctggaccacaccattccctacct
gcacgtgaggggaagcctttggccagaagatcgccacttccagttgatgcaggggaagat
ggctgacatgtacaccgcctcatggcgtgtcggcagtatgtctacaatgtcgccaaggc
35 ctgcatgagggccattgcactgctaaggactgtgcaggtgtgattctttactcagctga
gtgtgctacacaggtagccctggacggcattcagtggtttgggtggcaatggctacatcaa
tgactttcccatgggcccgtttcttcgagatgccaaagctgtatgagataggggctgggac
cagcgaggtgagggcgtggtcatcggcagagccttcaatgcagacttctactagtctg
agacccttcgcccccttttctgcacctagtggccttcttgggaagtagagatgtggcg
40 gctttccaccctgcccacagcaggccctcctgcccagctgctctgtcagccctctggc
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cctgtgccacggctagtgtgtgtgatttaaaatggactcagcaggaagcatattgtctg
gggattgttgggacaggttttgggtgactctgtgcccttgctctctaactctgagccac
ctcccagggtaggcacctgggggcatgcaggtgccacctcccagggtaggcacctgggg
45 gcatgcaggtaccacctctttctcttgggtgaggctctggcaaggagatctctctgctc
aagcacagcagaatcatggccctctccatgaattggaacttggtacaggttaagtatcc
ctaactctgaaatctgaaacacttgtggttccaagcattttggataaggcaaatcaact
ttcagtccttttctgggggaaaaaataataaacctagcctagccaggcgtggtg

50

Table 179

SEQ ID NO:170

cbe_3810032 gbh_af142421

55 Homo sapiens QUAKING isoform 5 (QUAKING) mRNA, complete cds.
length=1497

ccgggggcttctcagttttatttatcaatctatatgcataccttatgccagtcacaca
cagtgtaattactgtagctttgtagtcagttttgaaatcaagaagtatgagtccttcgt

tcttatttttcaaaattatcttggctgttctgtgtcccggtgtgtttctagataaaatttta
 ggatcatcttgtcaatttctggggatattggctgggttcttgggttacttccatgtgttc
 tctttaaatggctagactgggcttgggtttttcagtatcggttggaatctgagagggg
 5 aaatggaaacgaaggagaagccgaagccacccagattacctgatgcagctgatgaacg
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 cagaaatcaaattgaagagagcagttgaagaagtgaagaaattattggtacctgcagcag
 aaggagaagacagcctgaagaagatgcagctgatggagcttgcgattctgaatggcacct
 acagagatgccgacattaaatcaccagccctgccttttctcttgcagcaacagcccagg
 15 ctgctccaaggatcattactgggcctgcgcggttctcccaccagctgccctgcgtactc
 ctacgccagctggccctaccataatgcctttgatcagacaaatacagaccgctgtcatgc
 caaacggaaactcctcacccaactgctgcaatagtctcctccaggggcccgaagctggttaa
 tctatacacccctatgagtaccctacacattggcaccagctacatcaatccttgagtatc
 ctattgaacctagtgggtgtattaggtgcggtggctactaaagttcgaaggcacgatatgc
 20 gtgtccatccttaccaaaggattgtgaccgcagaccgagccgacccggcaactaaccta
 tgaccttctgacctctgaactcttcaccaatgatgacctgacctgcctgcctgctgat
 cagttaaactggtaatcgctttgcttgctgtcgtcagtgacgagctgaggcacttgt
 ccgttcgtcttaccatctaaccaacaaaagacaaaagaattgttgcctccaactc

Table 180

SEQ ID NO:171

cbe_3810791 EPHB1

EphB1

length=3865

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 cgcccacgcagcgctccgggaagtccggtccgggcgagagcgcgaaaggataccgagaag
 ccacccgcggagagcgcagcggcgccctgggacgcggcgctctcccgcgctgctgcctc
 35 ggcttggctctcgccctgcgggcccgtcgcccgccgatggccctggattatctactactgct
 cctcctggcatccgcagtggtgctgcatggaagaaacgttaatggacaccagaacggctac
 tgcagagctgggctggacggccaatcctgcgtccgggtgggaagaagttagtggtacga
 tgaaaacctgaacaccatccgcacctaccaggtgtgcaatgtcttcgagcccaaccagaa
 caattggctgctcaccaccttcataaccggcggggggcccacgcacatacacagagat
 40 gccttctactgtgagagactgcagcagcctccctaattgtcccaggatcctgcaaggagac
 cttaacttgtattactatgagactgactctgtcattgccaccaagaagttagccttctg
 gtctgaggccccctacctcaaagtagacaccattgctgcagatgagagcttctcccagggt
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 tcggaatgggtttttacctcgcttttcaggattatggagcctgtatgtctcttcttctgt
 ccgtgtcttcttcaaaaagtgtcccagcatttgtgcaaaattttgcagtggttccagagac
 45 tatgacaggggcagagagcacatctctggtgattgctcggggcacatgcatcccaacgc
 agaggaagtggacgtgcccataaaactctactgcaacggggatggggaatggatggtgcc
 tattgggcgatgcacctgcaagcctggctatgagcctgagaacagcgtggcatgcaaggc
 ttgccctgcaggacattcaaggccagccaggaagctgaaggctgctcccactgcccctc
 caacagccgctcccctgcagaggcgtctcccatctgcacctgtcggaccgggtattaccg
 50 agcggactttgacctccagaagtggcactgactagcgtcccatcaggtcccgcgaatgt
 tatctccactgtcaatgagacgtccatcattctggagtggcaccctccaaggagacagg
 tgggcccggatgatgtgacctacaacatcatctgcaaaaagtgcggggcagaccgcccggag
 ctgctcccgtgtgacgacaatgtggagtgtgtgccaggcagctgggcctgacggagtg
 ccgctctccatcagcagcctgtggggccacaccccctacacctttgacatccaggccat
 55 caatggagtctccagcaagagtcccttccccccacagcagctctctgtcaacatcaccac
 aaaccaagccgcccctccaccgttcccatcatgcaccaagttagtgccactatgaggag
 catcaccttgcctggtgacagccggagcagcccaatggcatcatcctggactatgagat

cccgtactatgagaaggaacacaatgagttcaactcctccatggccaggagt cagaccaa
 cacagcaaggattgatgggctgcggcctggcatggtatatgtggtacaggtgcgtgcccg
 cactgttgctggctacggcaagttcagtggaagatgtgcttccagactctgactgacga
 5 tgattacaagt cagagctgagggagcagctgcccctgattgctggctcggcagcggccgg
 ggtcgtgttcgttgtgtccttgggtggccatctctatcgtctgtagcaggaaacgggctta
 tagcaaagaggctgtgtacagcgataagctccagcattacagcacaggccgaggctcccc
 agggatgaagatctacattgaccccttcaacttatgaggatcccaacgaagctgtccggga
 gtttgccaaggagattgatgtatcttttgtgaaaattgaagaggctcatcgagcagggga
 10 gtttggaagtgtaacaagggcggttgaaaactgccaggcaagagggaaatctacgtggc
 catcaagaccctgaaggcagggtactcggagaagcagcgtcgggactttctgagtgaggc
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 15 cattctggtcaacagtaacctgggtgtgcaaggtgtccgactttggcctctcccgtacct
 ccaggatgacacctcagatcccacctacaccagctccttgggaggggaagatccctgtgag
 atggacagctccagaggccatcgctaccgcaagttcacttcagccagcgacgttggag
 ctatgggatcgtcatgtgggaagtcatgtcatttggagagagacctattgggatatgtc
 caaccaagtgtcatcaatgccatcgagcaggactaccggctgccccaccatggactg
 20 tccagctgctctacaccagctcatgtggactgttggcagaaggaccggaacagccggcc
 ccggttgcggagattgtcaacacctagataagatgatccggaaccggcaagtctcaa
 gactgtggcaaccatcacgcctgcttcccagcccctgctcgaccgctccatcccaga
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 ggacagcttccctactgctggttccctccctccagctggtcaccagatgacatcaga
 25 agacctcctgagaataggcatcaccttggcaggccatcagaagaagatcctgaacagcat
 tcattctatgagggccagataaagtcagtcaccaacggcaatggcatgagaactctgtt
 tcttgggggaaggagaggagggaaggaccagggtcaagggggaccagagggtgaccact
 gtggaatgtactggagagactggcttctcagctgaggaatgcatttccatcagtgaagaa
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 30 atgccgtgggaaccacaaatatataataataaaaaatataaaaagggtgatgttcaacagaag
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 tgttccattttcttctcaccatgacattcttttcttttctccttctgactcctccct
 gagagtcccctccttctcccacactcgtttcccttctgctcatgactcctgtagggaagt
 35 ttcttcaaacaaaaccagctcctgagctcctcagatgttgttctgtcagttgccaagga
 ctttgcctgacctgcatggggatccaaccaattcaattaatgtcttcatattgaagaag
 agatgtaccttcaattgaaaacctcgtttttcttttgtttgcatttctgcaaaaaggaa
 aaagaaccacaaattggggaattc

40

Table 181

SEQ ID NO:172

cbe_3820530 PGAM1

phosphoglycerate mutase 1 (brain)

45

length=1709

gggcggggtgccgcacccccagcccgccgcatggccgcctacaaactggtgctgatccg
 gcacggcgagagcgcatggaacctggagaaccgcttcagcggctggtacgacgcccagct
 gagcccgggggccacgaggaggcgaagcgggcgggcaggcgctacgagatgctggcta
 5 tgagtttgacatctgcttcacctcagtgacagaagagagcgatccggacctctggacagt
 gctagatgccattgatcagatgtggtgccagtggtgaggacttggcgccctcaatgagcg
 50 gcaactatgggggtctaaccgggtctcaataaagcagaaactgctgcaaagcatggtgaggc
 ccagggtgaagatctggaggcgctcctatgatgtcccaccacctccgatggagcccagcca
 tcccttctacagcaacatcagtaaggatcgaggtatgcagacctcacagaagatcagct
 accctcctgtgagagtctgaaggatactattgccagagctctgcccttctggaatgaaga
 55 aatagttcccagatcaaggaggggaacgtgtactgattgcagcccattggcaacagcct
 ccggggcatttgtcaagcatctggagggtctctctgaagaggctatcatggagctgaacct
 gccgactggtattcccattgtctatgaattggacaagaacttgaagcctatcaagcccat

gcagtttctgggggatgaagagacggtgcgcaaagccatggaagctgtggctgccaggg
 caaggccaagaagtgaaggccggcgaggatactgtcccaggagcaccctccctgcc
 cgtcttgtccctctgcccctcccacctgcacatgtcacactgaccacatctgtagacatc
 ttgagttgtagctgcagacggggaccagtggctcccattttcatttttagccattttgtcg
 5 cctgcaccactcccttcatacaatctagtcagaatagcagttctagagcacaggttctc
 agtctaagctatggaaaagctccccttatccaacagagtttaaaagtagtgacttgggtt
 tttgcgagtgtttgtttactaaggactttggggaggaacctatgctaagccatgaccagt
 gaggagaagcaacagagcctgtctgtcccatgagcggagtctgtcctctgctcttctgc
 agtcaggtcactgcctactgcctgggggctctagtcattccagtggaagacgaatgtaac
 10 ctgctgggtgatgtgacaactgtttccctccctgacccagaggatctggctctaggttgg
 gatcaatcctgaatttcggttatgtgttaatttacttttattaaaaagtatagtatatat
 aatacaaaaacaataacccttctggggtttctgtggcggttgaaatagtcccacatgtgg
 tcatcagaaatagcattcctcataccaatataggatcagctccttgacctctgaggggtc
 aggagtgttctcctgggtgtgtgtattagaatcccttccctgcttgtttcatggcagtgaaa
 15 tgcctcttggctcctgtccagtgtatctttcactgatttctgaatcatgttctagttgctt
 gaccctgccacatgggtccagtgttcatctgagcataactgtactaatcctttttccat
 atcagtataataaaggagtgtgtgcaat

20 Table 182

SEQ ID NO:173

cbe_3825897 POLR2L

polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa

length=392

25 agtctgggacgcgcccgcgccatgatcatccctgtacgtgcttcacttgtggcaagatc
 gtcggcaacaagtgggaggcttacctggggctgctgcaggccgagtacaccgagggggac
 gcgctggatgcccctgggcctgaagcgtactgctgccgcggatgctgctggcccacgtg
 gacctgatcgagaagctgctcaattatgcacccctggagaagtgaccacgctgaaaccca
 cccaccgctgtgctgacccatgggcccctgagcgtcctaccccgaattcacgaggctgagg
 30 catccgggagctggcgtaatgcctggcgcagtggtgtgtatcccatacccactctgg
 aaggaaccatccagttaaaggtctttcagaacc

35 Table 183

SEQ ID NO:174

cbe_3826540 NYD-TSP1

testis-specific protein NYD-TSP1

length=1880

40 ctttcccacccttccctcccacaaaggctgtctgagatgccaccttccacctaacaatcat
 ctcccaaattttaactccttaactttgggtctctgacttctgcttgattccacagtctccac
 ccacatttgacaaaaggaccatcacctgtccttccctggaatctctaaagttttctgcttt
 ccttctgtcctgatggccagctctgctaagtcagctgagatgccaccatctccaaaacc
 cttaacctactcctgatcctcatcaagaatatctggaccctaggattaccattgcctta
 45 ttcgaaattggatcacattccccttccctcctggggctctctcccttccctaaagaatagc
 agccatcaagttacagaacaacagactgcacagaagttaacaatctcttaaaagaatt
 aaagatattcttaaaaatatggcaggttttgaagagaagatcacagaagcaaaagaactt
 tttgaggaaaccaatattactgaggatgtgtcagcccacaaagaaaatatcagaggactt
 gacaaaatcaatgaaatgttatcaacaaacctgcctgttagtttagccccagagaaagaa
 gacaatgaaaagaacaggagatgatattggaaaccaatattactgaggatgtgtcagcc
 50 cacaagaaaatatcagaggacttgacaaaatcaatgaaatgttatcaacaaacctgcct
 gttagtttagccccagagaaagaagacaatgaaaagaacagcagatgataatggaaaac
 cagaactctgagaacaccgcacaagtttttgcaagagatttggttaaatcgtttagaagaa
 aaaaaagtccttaacgaaactcaacaaagttaggaaaaagcaaaaaacagacttaatgtt
 caagaagaactatgaaaattaggaacaacatggagcagttactacaggaagcagaacac
 55 tggagtaaacataactgagctcagtaaaactgataaaatcctatcagaaatctcagaaa
 gacataagtgaactcttggaataatggagtcggtttccaaacccagccaaataatgaa
 gtgtcggctaagcatgagctggaggaacaggtgaagaaactgagccatgacacctattca

ttgcagttgatggcagctttgctagagaatgaatgccaaatcttacagcagagtagag
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 aactataaacaggacaagaaaaatcagaagccatcagaagcaaagaaagtagaaatgtat
 aagcagaacaagcaagcaatgaagggtacattttggaaaaaagacagatcctgtagaagc
 5 ctggatgtttgtcttaataaagaaagcttgcaataccagttcaatattcatgttgcaaga
 aaagctcttaggggaaaaatgaggtcagctagcagcctaagatagaaaataccaaaagca
 gatgaaaagggtgaatccttaaaaaactacatctgttacctccaacttgtcagtcatgatc
 aatcatcaaacttgggcagatctgctggttcaaccaagaaagagctatagaataaggag
 attgacacttatattactcattacttcagcagttatgtaagtctggtctttaatgaccat
 10 tgtgtctacatcaagttcataacttttcacctttacaatctgcttgttttttttgaatt
 attagatagacagcctagagtgagaagtttaaagggtccaattaagtttaagatctaaataaa
 aaccagaatacaagggaaaaaiaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
 aaaaaaaaaaaaaaaaaaaaaa

Table 184

SEQ ID NO:175

cbe_3833533 TRIM29

tripartite motif-containing 29

length=3018

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 tgcgatggaagctgcagatgcctccaggagcaacgggtcgagcccagaagccagggatgc
 ccggagcccgtcgggccccagtgccagcctggagaatggcaccagggctgacggcaagga
 25 tgccaagaccaccaacgggcacggcggggagcagctgagggcaagagcctgggcagcgc
 cctgaagccaggggaaggtaggagcgccctgttcgagggaatgagtgccggcgacccat
 catccagtttgtcgagtcggggacgacaagaactccaactacttcagcatggactctat
 ggaaggcaagaggtcgccgtacgcagggctccagctgggggctgccaagaagccaccctg
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 caagccccacctggagggcgccgcttccgagaccaccagctgctcgagcccatccggga
 ctttgaggcccgcaagtgtcccgatggaagacgatggagctcttctgccagaccga
 35 ccagacctgcatctgctacctttgcatgttccaggagcacaagaatcatagcacctgac
 agtggaggaggccaagggcgagaaggagacggagctgtcactgcaaaaggagcagctgca
 gctcaagatcattgagattgaggatgaagctgagaagtggcagaaggagaaggaccgcat
 caagagcttcaccaccaatgagaaggccatcctggagcagaacttcggggacctggtgcg
 ggacctggagaagcaaaaggaggaagtgagggctgcgctggagcagcgggagcaggatgc
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 ggacaagcagaccgggagcagctgcatagcatcagcagactctgtgtgtttctgcagga
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 gctggagggggaggcctgggacagtcactaggcaacttcaaggacgacctgctcaatgt
 atgcatgcgccacgttgagaagatgtgcaaggcggacctgagccgttaacttcattgagag
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 gggtagtgagtgacccggacaccatgaagagatactccatgtacctgacacccaaagg
 tggggctccggacatcataccagccctcgtctcctggccgcttcaccaaggagaccacca
 gaagaatttcaacaatctctatggcaccaaaaggttaactacacctccggggtctgggagta
 ctccctcagcattcagaactctgacaatgacctgcccgtcgtccaaggcagctcctcctt
 50 ctccctgaaaggctatccctcctcatgcggagccaaagcccaaggccagccccagac
 ttggaaactctggcaagcagactatgctgtctcactaccggccattctacgtcaacaagg
 caacgggattgggtccaacgaagcccatgagctcctggcggaagggaacgaggcgccaca
 cccctgctctcctcctgacctgctgctcttgcccttctaagctactgtgcttgtctggg
 tgggaggggagcctggtcctgacctgccctctgcagccctctgccagcctcttgggggca
 55 gttccggcctctccgacttccccactggccacactccattcagactcctttcctgcttg
 tgacctcagatggtcaccatcattcctgtgctcagaggccaacccatcacaggggtgaga
 taggttggggcctgccctaaccgcagcctcctcctctcgggctggatctgggggctag

cagtgagtaccgcgatgggtatcagcctgcctctcccgccacgcctgctgtctccaggc
 ctatagacgtttctctccaaggccctatcccccaatgttggtcagcagatgcctggacagc
 acagccacccatctccattcacatggccacctcctgcttcccagaggactggccctac
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 acagccactttgagtctgtgggtccctggagggtggcttctcctgactggcaggatgacct
 tagccaagatattcctctgttccctctgctgagataaagaattcccttaacatgatataa
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 ttcagtctacactttggcattctctctggcgatggagtgtggctgggctgaccgcaaaag
 10 gtgccttacacactgccccaccctcagccgttggcccatcagaggctgcctcctccttc
 tgattacccccatgttgcatatcagggtgctcaaggattggagaggagacaaaaccagg
 agcagcacagtggggacatctccgctctcaacagccccaggcctatgggggctctggaag
 gatgggcccagcttgaggggttggggaggagacatccagcttgggctttcccttttga
 15 ataaaccattggtctgtc

Table 185

SEQ ID NO:176

cbe_3834015 TFPI

tissue factor pathway inhibitor (lipoprotein-associated coagulation inhibitor)

length=915

atgatttacacaatgaagaaagtacatgcactttgggcttctgtatgcctgctgcttaat
 cttgccccctgccccctttaatgctgattctgaggaagatgaagaacacacaattatcaca
 gatacggagtggccaccactgaaacttatgcattcattttgtgcattcaaggcggatgat
 25 ggcccatgtaaagcaatcatgaaaagatttttcttcaatattttcactcgacagtgcgaa
 gaatttatatatgggggatgtgaaggaaatcagaatcgatttgaaagtctggaagagtgc
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 aagccagatttctgcttttggagaagatcctggaatatgtcgagggttatattaccagg
 tatttttataacaatcagacaaaacagtgtgaacgtttcaagtatggtggatgcctgggc
 30 aatatgaacaattttgagacactggaagaatgcaagaacatttgtgaagatgggtccgaat
 ggtttccaggtggataattatggaacccagctcaatgctgtgaataactccctgactccg
 caatcaaccaaggttcccagcctttttgaatttcacgggtccctcatggtgtctcactcca
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 aaatgccgcccatttaagtacagtggatgtgggggaaatgaaaacaattttacttccaaa
 35 caagaatgtctgagggcatgtaaaaaaggtttcatccaaagaatatcaaaaggaggccta
 attaaaacaaaagaaaaagaaagaagcagagagtgaaaatagcatatgaagaaattttt
 gttaaaaaatatgtga

Table 186

SEQ ID NO:177

cbe_3842044 PSMB3

proteasome (prosome, macropain) subunit, beta type, 3

length=784

gagcgggttgcgcagtgaaggctagaccgggtttactggaattgctctggcgatcgagggg
 tcctagtacaccgcaatcatgtctattatgtcctataacggagggggccgtcatggccatg
 aaggggaagaactgtgtggccatcgctgcagacaggcgcttcgggatccaggcccagatg
 gtgaccacggacttccagaagatctttcccatgggtgaccggctgtacatcggctctggcc
 gggctcgccactgacgtccagacagttgccagcgcctcaagttccggctgaacctgtat
 50 gaggttgaaggaaaggtcggcagatcaaaccttataccctcatgagcatgggtggccaacctc
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 aagacctttaagcccttcatttgcctctagacctcatcggtgccccatgggtgactgat
 gactttgtggctcagtggcacctgcgcgaacaaatgtacggaatgtgtgagtcctctgg
 gagcccaacatggatccggatcacctgtttgaaaccatctccaaagccatgctgaatgct
 55 gtggaccgggatgcagtgtcaggcatgggagtcattgtccacatcatcgagaaggacaaa
 atcaccaccaggacactgaaggccgaatggactaacctgttcccagagcccacttttt
 tttcttttttgaataaaaatagcctgtctttcaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

aaaa

Table 187

5 SEQ ID NO:178
cbe_3845697 Hs.191063
Human DNA sequence from clone RP1-63M2 on chromosome 20 Contains the gene for
CBFA2T2 (core-binding factor, runt domain, alpha subunit 2; translocated to,
2), part of a gene for a protein similar to ACTIN, the E2F1 (E2F transcription
10 factor 1) gene, a nov
length=532
tttggcatggacacaagtggggcatcacctttattgccataaagttagggccctgtgggta
ggcagctggactggcattctctgaactggcagtggttggggagattcaaactgcagttca
aaatgaggggtcccatgggtcccaaataccttctcctggcccagaaagggtatgggggtga
15 cccatccagtcagctccaacctccaggaggaccctgccagctccaacacttgactcttt
agatagagagctgtcccccaacgcagtgccacccccccagctccagcctgactcagttga
acacatcgtacagcagcctggagccacactcctggtacatggcccagttatccagcggc
gctggaaggagtgagggaggccaccatggagccgcccgtccacacagccatgccacgcc
catgcttgccaccaggtggggccgcagggccgcgtagccgtgccgcccgcactgcgcct
20 ncagctccttgtccaggcgctcggcgaagccaggaaacagtggtggagccgcc

Table 188

25 SEQ ID NO:179
cbe_3849002 CKLF1
chemokine-like factor 1
length=689
gcaagagagcggaagccgagctgggcgagaagttaggggagggcggtgctccgccgcggt
ggcggttgctatcgcttcgcagaacctactcaggcagccagctgagaagagttgagggaa
30 agtgcctgctgctgggtctgcagacgcgatggataacgtgcagccgaaaataaaacatcgc
cccttctgcttcagtggtgaaaggccacgtgaagatgctgcggctggcactaactgtgaca
tctatgacctttttatcatcgcacaagccctgaaccatatattgttatcactggattt
gaagtcaccgttatcttatttttcatacttttatatgtactcagacttgatcgattaatg
aagtgggtattttggcctttgcttgatattatcaactcactggtaacaacagttatcatg
35 ctcatcgtatctgtgtggcactgataccagaaaccacaacattgacagttggtggaggg
gtgtttgcacttgtagacagcagtatgctgtccttgccgacggggcccttatttaccggaag
cttctgttcaatcccagcgggtccttaccagaaaaagcctgtgcatgaaaaaaaaagaagtt
ttgtaattttatattactttttagtttgataactaagtatataacatatcttctgtattctt
cAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
40

Table 189

45 SEQ ID NO:180
cbe_3880186 FLJ20343
hypothetical protein FLJ20343
length=2784
gatgccccgccccgcgcccatggcgagccacacacgacctcggtcccgtacttcgcgcgc
tctcctgcaccgcccgcgccatctcgctcaggagctcctccacaaccgcccgaacacta
cggccatcgcgccgcaggacacgccctccacgaccggcggaaccgcccgcgacgctccagct
50 gactgcgcctacctgtggaggatcctgacccccgcggggcagggcgagacggagtgc
gtcggggcgcgctcatcgcgctgcggacgcagggatgtcctgctcagtcgtcagggccc
gccaatccggagggcgctcggcgctggtcggggccaggagcgctctggcctgcagtgc
cgagaggacgcggcgaggcatgttcggctcctgagctggagcctgggcccagggcttc
ctgcggggccgcggggcggtgccggggctgctccgcgcgctgctcccggggctggca
55 ggaggtccggggcccgaggtgcaggtgccgccatcccagctcgcgccgcacggccggggc
ccaggcctgctgccgctgctggcagcgctcgctggttctcgaggcccgctgcggcagag
gaggaggagcagcagggagccgacggggccgctgccgaggacggggcgagcagggccgag

gcagagatcatccagctgctgaagcgagccaagttgagcattatgaaagatgagccagaa
 gaggtgagtttaattttgcatgacgctcttcgtctcgctatcagactgataacaagaag
 gccatcacttacacttatgatttgatggccaacttagcatttatacggggtcagcttgaa
 5 aatgctgaacaactttttaagcaacaatgagttacctccttgagggggcatgaagcag
 gaggacaatgcaataattgaaatttccctaaagctggccagtatctatgctgcgcagAAC
 agacaggaatttgcgtgtgctggctatgaattctgcatttcaactctagaggaaaaaatt
 gaaagagaaaaggaatttagcagaagacattatgtcagtggaagagaaagccaatacccac
 ctctcttgggcatgtgcttagacgcctgtgctcgctaccttctgttctccaagcagccg
 10 tcacaggcacaaaaggatgtatgaaaaagctctgcagatttctgaagaaatacaaggagaa
 agaccccacagaccattgtgctgtagtgacctggctactaccctggatgcacagggc
 cgctttgatgaggcctatatttatatgcaaaggcctcagatctggcaagacagataaat
 catcctgagctacacatggtagctcagtaatttagctgcagttttgatgcacagagaacga
 tatacacaaagcaaaagagatctaccaggaagcactgaagcaagcaagctgaaaaagat
 gaaatttctgtacaacacatcagggagagttggctgagctgtcaaagaaaagtagacct
 15 ttgacaaattctgtcaagctctaaatccatttttgtgtagggagaataatgtctagtaat
 gtggaagaatagctatcattcctgtctctgtggcaccgatcaatggcttaaatctgtcg
 tttttgatattcaggtttcctcaatttagccttagtgaaggaggggtgtacacactgcc
 atttttgtattttaaggaaaaatgactttcattcccaactgattatgaccttcaggat
 20 gtctgcaagtgtgctttcagttgtaacacgtgacttgggtgctgtccctgctggtctaag
 tagaactgtagattcatatgggctgggtgtcctgtgcgctgtgggtgtggtgattcagcc
 tggcatttctaccataagtttttgggtctgctgatttgcctgtcttctcttacttta
 ctttatcaatacctggcaaaactgaccagaattaccttccctcatggcaagggggattatg
 gtgaattgttgttcttatagtctgtttcatgaagcacaagtggaatttaatacataaaaag
 25 agaaaaatatcttagtttgcctaccagcatccagcatgaagttgtaagtgaggataggc
 acgtgacagtatagcaccatttgaatttaaataaaaagtgaaccatatttatctggttat
 ataaaactaaaaatgggggtgtttatatataaaaactaaaaactaagaatgatgaacctttt
 gtctgtgttatctgaacactctacttcttgcagccttagtcacacaactgagtcactct
 caagtactctttaaggacacacagcccaggctgttctgagtcagaataggccctacagg
 30 tatattttaaaactcttcgtaattctaattgtgtactgctggtatagctgaactactgacc
 tggatcttagtcctagccttttgccttttgcaatttcagtatcttcatctctaaactagg
 gaaacactgggattctttcttagctgtgggggaaggtatttgggttagatgactttgaatg
 aatagactgctgtgctgaaagagctttatcacactgtctcaaagtatgtaaagatacata
 ggtggatgctcttactgcagcagtcataatacatttttagccatttacctaaggaaaaa
 35 gacagttttctaggtaccatgaaggaagattgacctgttggatgcctgtgggggtgg
 gatgtgagtgaggactgataaactgatacttttgggtcgtatgtacatactggaagaatct
 tcataataaatgagactacacaac

Table 190

40 SEQ ID NO:181
 cbe_3884811 RCP
 Rab coupling protein
 length=2112
 45 cccgcttctggagtggttatcgtcaccatgtccctaattggtctcggtggccggggcctgg
 gggcgtgtggtccccaaaccacgtgcaggtgacggtgctgcaggcgcggggcctgcggg
 ccaagggccccgggggacagcgacgcgtacgcggtgatccaggtgggcaaggagaagt
 acgccacctccgtgtcggagcgcagcctgggcgcgcccggtgtggcgcgaggaggccacct
 tcgagctgccatcgctgctgtcctcggaccgcggcgccgccaccctgcagctcaccg
 50 tgcctgcaccgcgcgctgctcggcctcgacaagtctcctgggcgcgcgaggtggacctgc
 gggatctgcaccgcgacaggggccgcaggaagacgcagtggtataagttgaaatccaaac
 caggaagaaggacaaggagcgaggagaattgaggtgacatccagtttatgagaaaca
 acatgactgccagcatgtttgaccttctatgaaagacaagtctcggaatccatttggaa
 agctgaaggacaagatcaaggggaagaataaggacagtggtcagacaccgcctccgcca
 55 tcatccctagcacgacaccttcggtcgacagtgatgatgagctctgtggttaaagacaaga
 aaaagaaatcaaagatcaagaccttactttccaagtcaaatttgacagaagacgcctctt
 ccagtcctatgtctgtcctgccgacttcaaagccagaaaaagtgctgcttcgtcccgag
 actttcagtcacagtgaggatgaagatgacaatgaggatgagtcctcctcggcctcggtg

tcatgtctcacaagagaacagcgagtagcgatcttaagcaactgaaccagggtcaacttta
 cccttcccaagaaggaaggactttcctttcttggtggccttcggtctaagaatgatgtcc
 tttcccgctctaattgtctgcatcaatgggaaccatgtttacctggagcagccccaacca
 ccggtgagatcaaggatagcagcccgctcctcctcccatcccccaagggtttcagaaaga
 5 aaacattgttctctctacagagaacctggcggtctgggtcttggaaggagcctgctgaag
 gaggtgggctgtctactgacagggtgtctccgaatcttccaccaaggactccttgaagt
 ctatgaccttgccgacctaccgacctgccccactgatcagtggggacctcagggaaaaaa
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 ggaggtcctctttgctgtctctgatgacggggaagaaggatgtggctaaggggcagtgaag
 10 gtgaaaacctctcacgggtccagggagggaagaaggagcagctgctgaggggttaagc
 cgggggaggacgcacatcggggctgctgaagacctgtgagaagatctgagaaagatactg
 cagctgttgtctccagacagggcagctccctgaacctcttgaagatgtgcagatcacag
 aaccagaagctgagccagagctccaagtctgaaccgagacctccaatttctctccgaggg
 ctccccagaccagagctgtcaagccccgacttcatcctgtgaagccaatgaatgccacgg
 15 ccaccaaggttgctaactgcagcttggaactgccaccatcatcagtgagaacttgaaca
 atgaggtcatgatgaagaaatacagccctcggacctgcatttgcatatgcgagctga
 cccacgatgagctgattcagctggtcctcaaacagaaggaaacgataagcaagaaggagt
 tccaggtccgcgagctggaagactacattgacaacctgcttgtcagggctcatggaagaaa
 ccccaatatcctccgcacccgactcaggttggaacaaaagcaggaaagatgtaatca
 20 gcagaaaaaaacaccgagacgtttctgtgacttactttcacctgctccaggggtcaag
 gacttgcttgctgataaccagccagcagggtccgaatcaccatctccctcacatgtta
 tccggcaagagt

25 Table 191

SEQ ID NO:182

cbe_4138433 KIFAP3

kinesin-associated protein 3

length=2997

30 caagaggtgcagagcaagcgcatgcgtcgtgacggccccggcttaggcgactctgggcggg
 tctgggcccgtccagtggttttggggcacagaagctgtggaggagctggaggcttcaccg
 tggtaaccacagcgccgctgctgccccgccttgacggcctcaggactgtcatcgctctg
 ggtgtgaggggtactttggccaccgtccccggaaataaccgcgcctgcctctcaagatacc
 ccattctctccacgcccgtgccgtgccgcatgcaaggggaggacgccagatacctcaa
 35 aaggaaagttaaaggagggaatatagatgtacatccatcagaaaaagcactcattgttca
 ctatgaagtggaaagctaccattcttggagaaatgggggaccccatgttgggagaacgaaa
 agaattgtcaaaaaatcattcgacttaagagtctcaatgccaacacagatataacttcctt
 ggcaaggaaggtggttgaagaatgtaaactcattcatccttcaaaactaaatgaggtaga
 acagctgttgtactatctacagaaccgcccgtgattcattgtcaggaaaagagaaaaaga
 40 aaaaatcaagcaagcctaagatccacctccttttgaaggaatggagattgatgaagttgc
 taacattaatgacatggatgaatatattgagttattatatgaagatatcctgacaaagt
 tcgggggttctgctttgatcctgcagcttgctcgaaatcctgataacttggagaactact
 attgaatgaaactgcccttggtgcattagcaagggtcctgagagaagactggaagcaag
 tgtcgagttagctacaaacataatttacatcttttttgtttctccagcttttctcaatt
 45 tcatggacttattactcactataaaaattggagctctgtgtatgaatattattgatcatga
 gttaaaaagacatgagctttggcaagaagaactctcaagaagaagaaagctgttgatga
 agacctgaaaaccaaacttgagaaaggattatgaaaaaacctttaaaaagtaccaggg
 gcttgttggtaaaacaggaacagctattacgagttgctctttatttgcctctgaatcttgc
 tgaggatactcgtaccgaactgaaaatgaggaacaagaacatagttcacatgttggtgaa
 50 agcccttgatcgggacaattttgagctgctaatttttagttgtgtcattcttgaagaaact
 cagcatttttatggagaataaaaatgatattggtggaatggatattgttgaaaaactggt
 gaaaatgataccttgtagcatgaagacctgctgaatatcaccctccgacttttactaaa
 cctatcctttgacacaggactgaggaataagatggtacaagttggactgcttcccaagct
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 55 aagcatggatgaccgttttaaatcaatgtttgcatacactgactgtataccacagttaat
 gaagatgctgtttgaatgttcagatgaacgaattgacttggaactcatttctttctgcat
 taatcttgctgctaacaaaagaatgtacagcttatctgtgaaggaaatgggctgaagat

gctcatgaagagggtctgaagtttaaggatccattgctgatgaaaatgattagaaacat
 ttctcagcatgatggaccaactaaaaatctgtttattgattatgttggggaccttgcagc
 ccagatctctaatgatgaagaaggagggtttgtgattgaatgttgggaactcttgcaaa
 cttgaccattccagacttagactgggaattggttcttaagaatataagtgggtccata
 5 cctcaaggataaaactaaaaccaggtgctgcagaagatgatcttgttttagaagtggttat
 aatgattggaactgtatccatggatgactcttgtgctgcattgctagccaaatctggcat
 aatccctgcactcattgaattgctaaatgctcaacaagaagatgatgaatttgtgtgtca
 gataatttatgtcttctaccagatggttttccaccaagccacaagagacgtcataatcaa
 ggaaacacagggtccagcatatctcatagacctaatgcatgataagaataatgaaatccg
 10 aaaggctctgtgataatacattagatattatagcggaaatgatgaagaatgggctaagaa
 aattcagagtgaagaagtttcgctggcataaactctcagtggctggagatggtagagagtcg
 tcagatggatgagagtgcagctacttctgtatggatgatcgaattgagccatacattca
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 tgaaggagccataagtcccgatttcttcaatgattaccaccttcaaaatggagatgttgt
 15 tgggcagcattcatttcttggcagccttggaaatggatggcttggccaaccagttggcat
 tcttggacgcccctgccacagcatatggattccgcccctgatgaaccttactactatggcta
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 gttgggttaattttggatctttgcctaataatgcatgttgatgttattgtgggtctgtgt
 ttgtttttatttttatatgttgttagctgcagattaaccccagcccctctgtcttctgtt
 20 aagtacagttgatactgacattgttctactcatcaaaccacatcttgatgctaagtaacat
 ttcccatgagcctcaaaactgaatgctgaaaagctactagactggaaaacaaacactgca
 ttatgtatgttaagtgactaatttaattttcaattaaaaagcgtaaagtgaaatgaa

25 Table 192
 SEQ ID NO:183
 cbe_422204 Prey2335
 PathCalling Prey Sequence 2335
 length=394
 30 aaggaaggaaggaaggaaggaaggaaggaaggaaggaagaaagaaatcatccagcatgtccc
 tttcttctcctatgggattttaccaactgacaaattctagtgtcctgccatcaccacac
 atgtgcagcaaaagcctccacatttgcaaaatctaagtcaatctctaaaagatgcttcgag
 gaagcaccaggttcttctgtctaataaccgcagtggtcatgtgacacctccccctcccc
 caaccagttctctctgaaaactaccacccacccaccaataaagtagcatgacgtctgt
 35 ccttcagctgccaatatctacaatcaaccaacaagtcattaaaaaaaaaaaaaaaaaaaaa
 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaagaa

40 Table 193
 SEQ ID NO:184
 cbe_422227 Prey277610
 PathCalling Prey Sequence 277610
 length=140
 gtctgagtgtactgaagaggacgtcgtcacttctggaccaagccctgcccacgacgtc
 45 ctcttcagtagcacgtacccttctctcccaagtcgatccggttgaggaggccttcttac
 accttaggaatgaaatcgct

50 Table 194
 SEQ ID NO:185
 cbe_422236 BCR1
 PathCalling Prey Sequence 1759
 length=553
 55 ggcagaggggttacaactcaggttccacacctcgcttttcacagcctccgagggcagca
 gtgcacatgggggagacatctcccagaggccaaggcctccagtgtcaccgatgccctc
 tgtgaagtggggtagaactcgtcagtgaaaaggggctcgggcagctcacggaagtacag
 cttcagcatgcctgcgatggcggttcacgtccatctcgctcatcatcaccgacacgtcctt

gttatctggaaagagcatggaaatgcagcggcctccttgaagatcctgataaatgaagaa
 aagacacagagaaggatgtgacatgcctgggccgtggagcactctgagatctcatcgcg
 acaccaactgccacacctccatcccgctcctgcgcaggccggcactcactgacgttgaagc
 ctgccttcagtgcctggatgtccgtggccacccagacatgcggtagatgccacctcct
 5 ccatgcctcggcgcttgatctcctcacacactggcgacgatgtagggcacttggacctc
 tctctcctgcgga

Table 195

SEQ ID NO:186

cbe_4279962 DKKL1-pending

soggy-1 gene

length=908

aaaattcggcacgaggccgggctgtggtctagcataaaggcggagcccagaagaaggggc
 15 ggggtatgggagaagcctccccacctgcccccgcaaggcggcatctgctggtcctgctgc
 tgctcctctctaccctggatccctccgctgcagctcctatccatgatgctgacgccc
 aagagagctccttgggtctcacaggcctccagagcctactccaaggcttcagccgacttt
 tcctgaaaggtaacctgcttcggggcatagacagcttattctctgcccccatggacttcc
 20 ggggcctccctgggaactaccacaaaggagaaccaggagcaccagctggggaacaaca
 ccctctccagccacctccagatcgacaagatgaccgacaacaagacaggagaggtgctga
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 aggtacccaggatggaggagaaggaggccctggtacccatccagaaggccacggacagct
 tccacacagaactccatccccgggtggccttctggatcattaagctgccacggcgagggt
 25 cccaccaggatgcctggaggggcgccactggctcagcgagaagcgacaccgcctgcagg
 ccatccgggatggactccgcaaggggaccacaaggacgtcctagaagaggggaccgaga
 gctcctccactccaggctgtcccccgaaagacccacttactgtacatcctcaggccct
 ctcggcagctgtaggggtggggaccggggagcacctgcctgtagcccccatcagaccctg
 cccaagcaccatattgaaataaagttctttcttacatctaaaaaaaaaaaaaaaaaaaa
 30 aaaaaaaa

Table 196

SEQ ID NO:187

cbe_4281271 CRYAB

crystallin, alpha B

length=691

gacccctcacactcacctagccaccatggacatcgccatccaccacccctggatccgccc
 ccccttctttcctttccactccccagccgctctttgaccagttcttcggagagcacct
 40 gttggagtctgatcttttcccgacgtctactccctgagtccttctaccttcggccacc
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 tttcatctccaggagttccacaggaaataccggatcccagctgatgtagacctctcac
 45 cattacttcatccctgtcatctgatggggctcctcactgtgaatggaccaaggaaacaggt
 ctctggccctgagcgcaccattcccatcaccgtgaagagaagcctgctgtcaccgcagc
 cccaagaaatagatgccctttcttgaattgcattttttaaaacaagaaagtttccccac
 cagtgaatgaaagtcttgtgactagtgtgaagcttattaatgctaagggcaggcccaaa
 ttatcaagctaataaaatatcattcagcaac

Table 197

SEQ ID NO:188

cbe_4344185 SRA1

steroid receptor RNA activator 1

length=2069

ttatagcaaaatcagtgcataaaaaatccctcagtgcacctcactggatgtgagtattt
 55 gggcctgggacagggtcgggggctaaccacctgtgtgagatgagtgcttttgtgtctgtg

cttgatgttggtggctctctgtagtcacatgacagcatgggtgtgatggagatctgactt
 cattcaacaaacatatcttctaaggagttccctgtgccaggcactaagctgggcactggg
 aatgtaataaaatagtcagggtccaccttctaagactgtccgacagggaacgaacaag
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 gaactgacatctgaactgagaactgaaggaagatgagtactagttaggctaccggacgtg
 aatgtggagattgtgcagggcaatgcaagaggaggctgtagaagtcaacctggctagatc
 acagcgggtgtatgtggggcaggagcttcttgtttgaatttgctcctgagaggatgag
 gcctcctagagcactggctcctggacagcaacctccttgggtgccttgtgaccagggccc
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 ggccaagcgggaagtggagatggcggagctgtacgtgaagccgggcaacaaggaacgcggc
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 gagacttctcctgggcctcccccaatggggcctccacctccttcaagtaaggctcccagg
 tccccacgtgtggggagtggtcctgcctctggcgtggagcccacaagtttcccagtcgag
 tctgaggctcgactgatggaggatgtgctgagacctttggaacaggcattggaagactgc
 cgtggccacacaaggaagcaggtatgtgatgacatcagccgacgcctggcactgctgcag
 20 gaacagtggttgaggaaagtgtcaatacctgtaaagaagagaatggctctactggtg
 caagagcttcaagccaccgggtgggacgcagcagatgacatccaccgctccctcatggtt
 gaccatgtgactgaggtcagtcagtggttaggagttaaaagattaattgcagaaaag
 aggagtctgttttcagaggaggcagccaatgaagagaaatctgcagccacagctgagaag
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 gactgtcccactgggcctgaccacctatgagggaaagaagtcccacctgggcccagaggga
 gttcatgtgttactcataacatgcatttcaataaaaacatctctgcggtgggccttgggt
 aggagagatgaacccttccgggtgccaagctagtcccctctgggtgtcctcgactgccctgc
 tccctgtgtatctgcaaacctctgttctcccttctccattcatcaggaagggtatctgctg
 30 ggtaaagttagactactgcctaccactttttcccaaagtagactgaaagcacatcctgtg
 ctgggcccagcagctgtgtttggatgggttctatttcagcatgagaacagactcaataga
 acggggagacttttccctcaacaaaaggaaagacagtcctatttgcactgtatcaccctt
 gagatactactgttacagagattagaacc

Table 198

SEQ ID NO:189

cbe_4383836 KIAA0905

yeast Sec31p homolog

length=4129

gacgagcgtgcactaacgcaggatccggctgccgaaggtcctcgccagcaggatgaagt
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 acctagcaacaggaacatctgctcagcaattggatgcaacatttagtacgaatgcttccc
 ttgagatatttgaattagacctctctgatccatccttggtatgaaatcttgtgccacat
 45 tctcctcttctcacagggtaccacaagttgatttgggggccttataaaatggattccaaag
 gagatgtctctggagtctgattgcagggtggtgaaatggaaatattattctctatgatc
 cttctaaaattatagctggagacaaggaagttgtgattgccagaatgacaagcactg
 gccagtgagagccttggtatgtgaacattttccagactaatctggttagcttctggtgcta
 atgaatctgaaatctacatatgggatctaaataattttgcaaccccaatgacaccaggag
 50 ccaaaacacagccgccagaagatatcagctgcattgcatggaacagacaagttcagcata
 ttttagcatcagccagtcacagtgggccgggactgtatgggacttagaaaaaatgagc
 caatcatcaaagtcagtgaccatagtaacagaatgcattgttctgggttggcatggcatc
 ctgtatgtctcagatgggtccttgcctccgaggatgaccgggtaccagtgatccaga
 tgtgggtatctcgatttgcttctcctcctcacttctgtgtcctggaaaacatgccaggggga
 55 ttttggcaattgcttgagcatggcagatcctgaattgttactgagctgtggaaaagatg
 ctaagattctctgctccaatccaaacacaggagaggtgttatatgaacttcccaccaaca
 cacagtggtgcttcgatattcagtggtgtccccgaaatcctgctgtcttatcagctgctt

cgtttgatggcggtatcagtggtttattctatcatgggaggaagcacagatggtttaagac
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 agcccttctcctcggttacaattccacagcagactgctcagcatagtatagtgtgcctc
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 5 aactgggtacgtttgagaatgtcagaatgccttctcatcagggagctgagcagcagcagc
 agcagcaccatgtgttcattagtcaggttgtaacagaaaaggagttcctcagccgatcag
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 atgcttctcagactgaatttgagaaaaatgtgtggtcctttttgaaggtaaactttgagg
 atgattctcgtggaaaaatccttgaacttctaggatcacagaaaagaagatctaggaaaga
 10 agattgctttggccttgaaacaaagtggatggagccaatgtggctcttaagactctgacc
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 tctctgtcagtggggacattgatggtttaattactcaggctttgctgacgggcaattttg
 agagtgtgtgacctttgtttacatgataaccgcatggccgatgccattatattggcca
 15 tagcaggtggacaagaactcttggctcgaaccagaaaaaatacttcgcaaaatcccaaa
 gcaaaattaccaggctcatcactgcagtggtgatgaagaactggaaagagattgttgagt
 cttgtgatcttaaaaattggagagaggctttagctgcagtatgacttatgcaaagccgg
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 tctgcagactcaagcatgtctctgctatatttgtgcagggaatgtagagaaattagtgtg
 20 catgttggactaaagctcaagatggaagccaccctttgtcacttcaggatctgattgaga
 aagttgtcatcctgcgaaaagctgtgcaactcactcaagccatggacactagtactgtag
 gagtctcttggctgcgaagatgagtcagtatgccaatttgttggcagctcagggcagta
 ttgctgcagccttggttttcttctgacaacaccaaccagccaaatatcatgcagcttc
 gtgacagactttgtagagcacaggagagcctgtagcaggacatgaatcacctaaaattc
 25 cgtacgagaaacagcagctccccagggcaggcctggaccagttgctggccaccaccaga
 tgccaagagttcaaaactcaacaatattatccccatggagaaaaatcctccacctccgggtt
 tcataatgcatggaaaatgttaatccaaatgcttctggtcagcttcccacatctccaggct
 atatgcacaccagggtaccaccttatccacagccacagccttatcaaccagcccagccgt
 atcccttcggaacaggggggtcagcaatgtatcgacctcagcagcctgttgctcctcta
 30 cttcaaacgcttaccctaaccaccttacatatcttctgcttcttctatactgggcagt
 ctcagctgtacgcagcacagcaccaggcctcttcacctacctccagccctgctacttctt
 tccctcctcccccttctctggagcatccttcagcatggcggaccaggagctccaccat
 catcttcagcttatgcactgcctcctggaacaacagggtacactgcctgctgccagtgagc
 tgcttgcgtcccaaagaacaggctcctcagaatggttggaatgacctccagctttgaaca
 35 gagtacccaaaaagaagaagatgcctgaaaacttcatgcctcctgttcccatcacatcac
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 cagtaccactgtcaagccagctcttcattcccacagccacatcttccagggtggccagccct
 tccatggcgtacagcaacctcttgggtcaaacaggcatgccaccatctttttcaaagccca
 atattgaagggtccccaggggctcctatttggaataccttcagcatgtgcagctcttgcc
 40 caacaaaaaaattaccaagaaacctattccagatgagcacctcattctaaagaccacat
 ttgaggatcttattcagcgctgcctttcttcagcaacagaccctcaaaccaagaggaagc
 tagatgatgccagcaaacggttggagtttctgtatgataaaacttagggaacagacacttt
 caccaacaatcaccagtggtttacacaacattgcaaggagcattgaaactcgaaactact
 cagaaggattgaccatgcataccacatagttagcaccagcaacttcagtgcagacctctg
 45 ctttcatgccagttctcaaagttgttctcaccaggccaataagctgggtgtctaaaagg
 acagcttctcttccactcaatattgccatttttccaaagaaacatgttaaaaaaaaaaat
 tataagacatggactagtcctcattagcatgtttgcatagcaaccagtcagagcatttta
 cactatttctgctgatatactcaccttagaactgctcagaaccctgggtgctttatttttg
 ttttaattctttgttgccagtgatgattttcctattctgcaaatagtgtatttcttggtat
 50 tacacatagtaggtttcctgaagtattctgataaatgtgttttttaaaacctcaatat
 actttttagaaaaggagcatctggttatgcataaagcagagctaaaactaaatttcttcc
 atgtcctccctacttctcagtgctcaatcagattaaagtgtgtaatcct

55 Table 199
 SEQ ID NO:190
 cbe_4465094 Prey1053092

PathCalling Prey Sequence 1053092

length=452

5 TCACAAAACAAGCCTTCAGAATCAGATGAATGGAGGACCTTTTTATAGCCAGAATCCAGTT
 TCAGATACACCACCTCCACCGCCACCTGTGGAAGAACCAGTCTTTGATGAGTCTCCCCCA
 CCTCCTCCTCCTCCAGAAGATTACGAAGAGGAGGAAGCTGCTGTGGTTGAGTATAGTGAT
 CTTTATGCTGAAGAGGACCCACCGTGGGCTCCACGTTCTTACTTGGAAAAGGTTGTGGCA
 ATTTATGACTATACAAAAGACAAGGAAGATGAGCTGTCTTTTTCAGGAAGGAGCCATTATT
 TATGTCATCAAGAAGAATGACGATGTATTAATAAACAAGCAAGCTGAGTCTGAACAAATG
 GATCTTTCTGCCATCATTTGTACAATGCTGAGCTGTCTGGATTGAAATAAAATGACCATT
 10 TTTATGTATGTCAAAAAAAAAAAAAAAAAACCC

Table 200

SEQ ID NO:191

15 cbe_4540466 PUM1

pumilio homolog 1 (Drosophila)

length=5390

gggggtgaaaggtaagggggagcgagagcgccagagagagaagatcggggggctgaaatc
 catcttcatcctaccgctccgcccgtgttggtggaatgagcgttgcagtggtcttgaaga
 20 gaaaagcagtgctttggcaggactcttcagccccacctgaaacatcaccctcaagaac
 cagctaatcccaacatgcctgttgttttgacatctggaacaggggtcgcaagcgcagccac
 aaccagctgcaaatcaggctcttgcagctgggactcactccagccctgtcccaggatcta
 taggagttgcaggccgttcccaggacgacgctatggtggactacttctttcagaggcagc
 atggtgagcagcttgggggaggaggaagtggaggaggcggtataataatagcaaactc
 25 gatggcctactggggataacattcatgcagaacatcaggtgcgttccatggatgaactga
 atcatgattttcaagcacttgctctggagggaagagcgatgggagagcagctcttgccag
 gtaaaaagtgttgggaaacagatgaatccagcaaagatggacaaaaggaatattcctgg
 gtgatcaatggcgagacagtgcttggggaacatcagatcattcagtttcccagccaatca
 tgggtgcagagaagacctgggtcagagtttccatgtgaacagtgaggtcaattctgtactgt
 30 cccacgatcggagagtgggggactaggcgttagcatggtggagtatgtgttgagctcat
 ccccgggcgattcctgtctaaagaaaggaggttggcccaagggtgcagacagtgatg
 aaaacgacaaaagggtgaaaagaagaacaagggtacgtttgatggagataagctaggagatt
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 atgcagacgtcaaagattttagccgtacccctggtaattgccagaactctgctaataag
 35 tggatcttctgggtccaaaccagaatggttctgagggttagcccagctgaccagcacca
 atggtgccaagcctgtggaggatttctccaacatggagtcccagagtgctccccttggaac
 ccatggaacatgtgggcatggagcctcttcagtttgattattcaggcacgcaggtacctg
 tggactcagcagcagcaactgtgggactttttgactacaattctcaacaacagctgttcc
 aaagacctaatgcgcttgctgtccagcagttgacagctgctcagcagcagcagatgcac
 40 tggcagctgctcatcagccgcacatcggttagctcccgtgcgtttgtcccaatccat
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 cgacactaggcccagctgtgggtccctcaccagttatggagttactccctggggagtct
 accctgccagtcttttccagcagcaagctgccgctgccgctgcagcaactaattcagcta
 atcaacagaccacccacaggctcagcaaggacagcagcaggttctccgtggaggagcca
 45 gccaacgtcctttgaccccaaacagaaccagcagggacagcaaacggatccccttgtgg
 cagctgcagcagtgaaattctgcccttgcatttggacaaggctctggcagcaggtatgccag
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 50 ctggtggtcttgctggaacaacaaatggaccatttcgccccttaggaacacagcagctc
 agccccagccccagcagcagcccaataacaacctggcatccagttctttctacggcaaca
 actctctgaacagcaattcacagagcagctccctctctcccagggtctgcccagcctg
 ccaacacatccttgggatctcggaagtagcagttctctcggcgccaccctgggatccgccc
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 55 ccctgactggcagcagtgacctttataagaggacatcgagcagcttgacccccattggac
 acagttttataacggccttagcttttctcctctcctggacccgtgggcatgcctctcc
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cttcaagcttaaaccctgggaggactcacgaatggcagtggaagatacatctctgctgctc
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 gcactcttttctcttctctcgtttgcgatatggaatgtctgatgtcatgccttctggca
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 5 ttgctggacataataatggaattttcccaagaccagcatgggtccagattcattcagctga
 aactggagcgtgccacaccagctgagcgccagcttgctctcaatgaaatcctccaggctg
 cctaccaactcatgggtggatgtgtttggttaattacgtcattcagaagtcttttgaatttg
 gcagtcttgaacagaagctggctttggcagaacggattcgaggccacgtcctgtcattgg
 cactacagatgtatggctgccgtgttatccagaaagctcttgagtttattccttcagacc
 10 agcagaatgagatgggttcgggaactagatggccatgtcttgaagtgtgtgaaagatcaga
 atggcaatcacgtgggttcagaaatgcattgaatgtgtacagcccagctctttgcaattta
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 ttaccagcacacagagcagcttgtagaggatcaatatggaaattatgtaatccaacatg
 15 tactggagcacggctcgctcctgaggataaaaagcaaaattgtagcagaaatccgaggcaatg
 tacttgtatttgagtgcgcacaaatttgcaagcaatgttgtggagaagtgtgttactcacg
 cctcacgtacggagcgcgctgtgctcatcgatgaggtgtgcacatgaacgacggctccc
 acagtgccttatacaccatgatgaaggaccagtatgccaactacgtgggtccagaagatga
 ttgacgtggcggagccaggccagcggaagatcgtcatgcataagatccggccccacatcg
 20 caactcttcgtaagtacacctatggcaagcacattctggccaagctggagaagtactaca
 tgaagaacgggtgtgacttagggcccatctgtggccccctaatgggtatcatctgaggca
 gtgtcacccgctgttccctcattcccgctgacctcactggccccactggcaaatccaacca
 gcaaccagaaatgttctagtgtagagtctgagacgggcaagtgggtgtctccaggattact
 cctcctccaaaaaagggaatcaaatccacgagtggaaaagcctttgtaaatttaatttta
 25 ttacacataaacatgtactatttttttaattgactaattgccctgctgttttactgggtgt
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 tgtatctatatttcacatgtggaaactttcagggtgggtgggtttaacaaaaaaaaaagc
 tttaaaaaaaaaagaaaaaaggaaaaagggttttagctcatttgccctggcggcaagttt
 tgcaaatagctcttccccacctcctcatttttagtaaaaaacaaaaaacaacaaaaacc
 30 tgagaagtttgaattgtagttaaattgaccccaactggcatttaacactgtttataaaaa
 atatatatatatatatatataatgaaaaagggttcagagttgctaaagcttcagtt
 tgtgacattaaagtttatgaaattctaaaaaatgccttttttgagagactatattatgctga
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 35 tgtgattgtttactgcctactggatttttttctattaacattgaaaggtaaaatctgatt
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 ctaatctgtatctataatgtaccctagtagtcgaacatacttttgattgtacaattgtac
 atttgtataacctgtaatgtaaatgtggagaagtgtgaatcaacataaacacgttttttg
 40 taagaaaagagaattagccagccctgtgcattcagtgatattctcaccttttatggctg
 tagcatatagtgtgtatattgtaaatgtgaatttcaaccagaagtaatttttttcttt
 tgaaggaataaatgttctttatacagcctagttaatgtttaaaaagaaaaaatagcttg
 gttttatttgcctctagctcctcaagtatagcgagattctttctaaatgttattcaagatt
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 45 cttgtaaagtgtgaatcgcccttccctttttgtacagaagatgaactgtattttgcatttt
 gtctacttgtaagtgaatgtaacatactgtcaattttccttggttgaaatagaattgta
 acactacacgggtgtacatttccagagccttggtgtatatttccaatgaacttttttgcaag
 cacacttgtaaccatattgtgtataattaaacaaacctgtgtatgcttatgctgggcaact
 attttttgtaactcttggtgtagattgtctctaaacaatgtgtgatctttattttgaaaaa
 50 tacagaactttggaatctgaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Table 201

SEQ ID NO:192

55 cbe_4567083 LOC157378

hypothetical protein BC017881

length=2604

45

SEO ID NO:193

50 PathCalling Prev Sequence 2354

55 aaggaaaggaaggaaggaaggaaggaaggaagaaagaaatcatccagcatgtcc
tttcttctcctatgggatttaccaactgacaaattctagtgtcctgccatccccacac
atgtgcagcaaagcctccacatttgcaaaatctaagtcaatctctaaaagatgcttcgag
gaagcccccagttccttctgctaataaccgcagtggtgtcatgtgacacctccccctcccc
g

Table 203

SEQ ID NO:194

cbe_552975 HPV 1a E1

Human Papillomavirus 1a E1

length=1839

5 atggcagataataaaggtactgaaaacgattgggttttgggtggaggcgacagattgtgag
 gaaacggttagaggaaacctcacttggtagcctagataatgtttcttgtgttagcgactta
 tctgatttatttagacgaggcgccgcaaagccagggggaattccctggaattgtccacaag
 caagaatcgctggaaagcgaacaggaacttaatgctttaaaccgaaagttaactttacagt
 10 cctcaggcgagaagcgcggacgaaacagacattgctagcattagtcctagattagaaact
 atttctattacaaagcaagacaaaaaaagggtatcgaaggcaactgttttctcaggatgat
 agtgggttagagctatcgctgcttcaggatgaaactgaaaatattgatgaatcgacacag
 gtagatcaacagcagaaagaacatactggggaagttggggccgctggggtgaacattttg
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 15 ttacagacctgacgcggtcgtacaagagcaacaaaacctgtgtggagattgggttttg
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 tgttgttatattcaattggaacatgcagtaactgaaaaaatagattttttattttttattg
 gtacgatttaaagcccagaaaagttagagagactgtgataaaacttataaccacaattctt
 ccagttgatgctagctatattttgtctgagcctccaaaatcaagaagtgtggctgctgca
 20 ttatttttggtataaaagatctatgtcttcaactgtttttacatgggggtacaactttggag
 tggattgcacagcaaaccttattaatcatcagttagattccgaaagtccctttgagctt
 tgtaaaaatgggttcagtgggcctatgataatggacatacagaagagtgtaaaattgcata
 tattatgctgttttagcagatgaggatgaaaatgcaagggcatttctaagctctaattca
 caggcaaaatattgtgaaagactgtgcacaaatggtaagacactatttacgtgctgagatg
 25 gcacaaatgtctatgtcagagtggatttttagaaaactagataatgtagaagggtctggt
 aattggaaagaaattgtaagatttttaagatttcaagaagttgaatttataagctttatg
 attgcatttaaagatttggtatgtggttaagccaaagaaaaactgtttgttaatatgtgga
 cctccaaatacaggaaaatcaatgttttgtacaagtttattaaagttgttaggagggaaa
 gtgatttcatactgtaacagtaaaagtcagttttggtgagcctctggctgatgctaag
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 aaatgccacctttacttattactagtaatatattgatgttaaatcagatacctgttggatg
 tatttgcatagtagaatatcagcttttaaatgtctcatgagtttccatttaaagacaat
 ggtgatccaggattttccttaacagacgaaaattggaaatctttctttgaaagggttttg
 35 caacagttagaattaagtgaaccaagaagacgagggaaacgatggaaaacctcagcagtcg
 ctagacttactgcaagagcagctaatagaacctatatga

Table 204

SEQ ID NO:195

cbe_552976 HPV 11 L2

Human papillomavirus 11 L2

length=1368

40 atgaaacctagggcacgcagacgtaaacgtgcgtcagccacacaactatatcaaacatgc
 aaggccactggtacatgtccccagatgtaattcctaaagttgaacatactactattgca
 gatcaaatattaaaatggggaagcttaggggtttttttgggtgggttaggtattggtaca
 45 ggggctggtagtgccggtcgtgcagggtatatacccttgggaagctctcccaagcctgct
 attactggggggccagcagcagtcgccagtgcttgtggagcctgttgccttccgat
 cctccattgtgtccttaattgaggagtctgctattattaatgctggtgcacctgagggtg
 50 gtacccctacacagggtggctttactataacatcatctgaatcgactacacctgctatt
 ttagatgtgtctgttaccatcacactaccactagtgtgtttcaaaatcccctgtttaca
 gaaccgtctgtaatacacagcccaaccacctgtggaggccagtggtcacatacttatatct
 gcccacaataacatcccaacatgtagaagacattccactagacacttttgttgtatcc
 tctagtgatagtggaacctacatccagtactcctcttccctcgtgcttttctcggcctcgg
 55 gtgggtttgtatagtcgtgccttacagcaggtacaggttacggaccccgctttttgtcc
 acgccacagcagattggtaacttatgacaaccctgtctatgaaggagaagatgtaagttta
 caatttaccatgagtcctatccacaatgcacctgatgaagcatttatggatattattaga

ctacatagaccagctataacgtccagacggggtcttggtgcgttttagtcgcattgggcaa
 cgggggtccatgtacacacgcagtggaacaacataggtgcccgcatacattatcttcag
 gacatttcaccagttacacaagctgcagaggaaatagaactgcaccctctagtggctgca
 gaaaatgacacggttgatatttatgctgaaccatttgaccctatccctgaccctgtccaa
 5 cttctgtttacacagtccttatcttacctccacacctaataccctttcacaaatcgtgggt
 aataccacagtcctcattgtcaatccctagtgcactgggttggtgcagtcctgggcctgacata
 acttttctactgcactatggaacaccccttagtcctgtaactcctgctttacctaca
 ggccctgtttttattacaggttctgacttctatttgcactcctacatgggtactttgcacgc
 10 agacgccgtaaacgtattcccttattttttacagatgtggcgccctag

Table 205

SEQ ID NO:196

cbe_6464 Hs.19954

603029812F1 Homo sapiens cDNA, 5' end

length=959

ctggcgccggcgcccaactctaaccagcgcaaaatgtccctggaacaggaggaggaaacgc
 aacctggcggtcctaggacgcagagacgccgtccccgccttcattgagcccaacgtgc
 gcttctggatcacccagcgccaatcctttattcgacgatttcttcaatggacagaattat
 20 tagatcctacaaatgtgttcatttcagttgaaagtatagaaaactcgaggcaactattgt
 gcacaaatgaagatgtttccagccctgcctcggcggaaccaaaggatacaagaagcttggga
 agcggagtcttgcaacagtgcatcccgacagcagcaacctgatccccaagctttttcgac
 ctgcagcgttctgcctttcatggcgccacgggtattttgtcaatgacgccactgaaag
 ggatcaagtcctgtattttacctcaggttttctctgtgcctacatggcagcgttcaaca
 25 gcatcaatggaaacagaagttacacttgtaagccactagaaagatcattactaatggcgg
 gagccgttgcttcttcaactttcttaggagtaatccctcagtttggtccagatgaagtatg
 gcctgactggcccttggtatataaagactcttacctgtgatcttctcgtgcaagccagt
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 30 gctagccatccagaaatagtgcatgtttgggaccctcagttcttgattcctgaagttctt
 caacctaaactttttaaaggagccagttattcaggaaaaacccaggtcatgtggatttga
 aactgtcttgtaactgtcctggcatggaactgatgggtggcatttcttttaatttttcaa

Table 206

SEQ ID NO:197

cbe_71919 FLJ13236

hypothetical protein FLJ13236

length=1854

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 ggatgtccctcactgcagcctgtccgtggatgtctctgccttaagggaattggaggtgga
 45 accatccagtcctgaaggtcaacggagcgtgaagagaggagcgtgcagcttgagggtcta
 aggataactctggggccatgacagccatgagtctcacagaggacccccagacttctgtgc
 tgcgagtaaccggacttggtctgagaccttgccctagaggatggccaaggggctcctgg
 tgacctatgccctctgggctgtggggggccctgctgggctccaccacctgtacctgggaa
 gggacagccacgcccctgctctggatgctgacctggggggaggtgggctgggctggctct
 gggagtctggaagctcccaagctttgtagctcaggccaacagagcccaggacagaggc
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 ttggcatctattttggccttggtggcactgattagccttcttccatgggtcaacttctata
 ttgtggccctccactggcagttggcttaggggtcttgctgggtggctgctgttggaacc
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 55 gccgctacaaagctttgggtggcatcagagccgctcagtgctgcggctctatcgtctgggct
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 ttacagttttcaggatgagaagcgtcagctggcttaccaggttttgggcctctcagaag
 5 gggcaacaaatgaagaaatacatcggagttaccaggagctagtgaaggtctggcaccag
 accacaacctggaccagacagaggagcacagaggcacttcctggagatccaggctgcgt
 atgaagtctgagtcacccaggaagccttggggatcccggaggtgaaaagaaacttccc
 cctgaggactgactcttcttagcagagctgggcaacttgtcccaaatctagctttgcca
 cgaatggcatcccaacagagttaaagaaactgcttgcaggggctgggcgtggtggctcat
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 gaccagcagcctggccaatatgggtgaaacttcgtctctactaaaaatacaaaaaattggc
 caggagtgggtggcaggcacctgtagtccagctacttgggaggctgaggcaggagaatca
 cctgaacctgagaggcggaggttgagtgagccgagatcacgccactgcactccagcctg
 ggcaacaagagtgaactccgtctcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Table 207

SEQ ID NO:198

cbe_92628 FTHP1

ferritin, heavy polypeptide pseudogene 1

length=2083

catcaaaagaatgaagaacataagaaaaggtaactacatcagtaaatatattgctttttt
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 tacatgcagtggtcacacctataatcccagcactttgggaggctgaggtgggtggatca
 25 cttaggtcagaatgttcaagaccagcctggccaacatggtgatctttgtgtctattaaa
 aaatacaaaaaataagccaggcgtgggtggcgggcacctgtaatccagctactctaaggctg
 aggcaagagatcacttgaatccaggaggcagaggctgcagtcagccaaaattactccact
 gccctccagcctaggcaacagagtgagaatctgtctcaaaaaataaaaaataaaatc
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 gttgaagatagctctgcaataatttaaagctatataactataaacactaaagcaaccattaa
 tatagcaaaattgaaaatatgaagttaataagggaacaaaggagataaaatgtaatttta
 agaaatatacaaaataattacaaaaagacagcataatagtaaaagagaatgaacagataaa
 acaattataaaacaaacaccaagctgagagacttaaacctaatcacacgataatcacact
 35 aaatgtaaatgggtccaaatacccccatcaaaaaggagagactttcaaatagataatgaaa
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 gtggaagaatgacaaaagaagagacattcttcaccaagagtcctcgggggtttcctgcttc
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 actgcaggtgcgccagaactaccaccaggactcagaggccgcatcaaccgccagatca
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 atgcggtttgaagaactttgccaaatactttcttcaccaatctcatgaggagaggagc
 atgctgagaaactgatgaaactgcagaaccaacaagggtggctgaattttccttcaggata
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 ttggaaaaaatgtgaatcagtcactactggaactgcacaaactggccactgacaaaaat
 gacccccatttggtgtgacttcattgagacacattacctgaatgagcaggtgaaagccatc
 aaagaattgggtgaacgtgaccaacttgcaagaatgggagcaccgcaatctggcttggc
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 gtaccattccttcaataaagaaatctggtaccccccccaaaaagaatgacaaaagat
 agcacatgtgaatacaaaataaaaagtaagctactgtggctacattcatgtcagacaaagt
 aaatttcagagttagagaattattaccagtaataaatgattatttcatagtataaaggggt
 55 caattcatgaaaaagacataatcctaacctaatacaacagttcaaaataaatgcagcaa
 aaactggaaggagaaagaaacagatcctctagagtcgacctgc

OTHER EMBODIMENTS

Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims, which follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims. The choice of nucleic acid starting material, clone of interest, or library type is believed to be a matter of routine for a person of ordinary skill in the art with knowledge of the embodiments described herein. Other aspects, advantages, and modifications considered to be within the scope of the following claims. The claims presented are representative of the inventions disclosed herein. Other, unclaimed inventions are also contemplated. Applicants reserve the right to pursue such inventions in later claims.

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CLAIMS

We claim:

5

1. A purified complex comprising a first polypeptide and a second polypeptide, wherein said first polypeptide comprises an amino acid sequence of a polypeptide selected from the group consisting of the polypeptides recited in Table 1 through 7, column 2, and wherein said second polypeptide comprises an amino acid sequence of the corresponding polypeptide recited in
10 Tables 1 through 7, column 5, wherein said first polypeptide binds said second polypeptide.

2. The complex of claim 1, wherein said first polypeptide is labeled with a detectable substance.

15

3. The complex of claim 1, wherein said second polypeptide is labeled is labeled with a detectable substance.

4. A chimeric polypeptide comprising six or more amino acids of the first polypeptide of claim 1 covalently linked to six or more amino acids of the second polypeptide of claim 1.

20

5. A nucleic acid encoding the chimeric polypeptide of claim 4.

6. A vector comprising the nucleic acid of claim 5.

25

7. A cell comprising the vector of claim 8.

8. An antibody which specifically binds the complex of claim 1.

30

9. The antibody of claim 8, wherein said antibody binds to the complex of claim 1 with higher affinity than it binds to said first or second polypeptide when said polypeptides are not complexed.

10 A pharmaceutical composition comprising the complex of claim 1.

11. A kit comprising a reagent which can specifically detect the complex of claim 1.

5 12. The kit of claim 11, wherein said reagent is selected from the group consisting of an antibody specific for said complex, an antibody specific for said first polypeptide, and an antibody specific for said second polypeptide.

10 13. A method of identifying an agent which disrupts a polypeptide complex, the method comprising:
(a) providing the complex of claim 1;
(b) contacting the complex with a test agent; and
(c) detecting the presence of a polypeptide displaced from said complex,
wherein the presence of displaced polypeptide indicates said agent disrupts said complex.

15

14. A method for identifying an agent which disrupts a polypeptide complex comprising at least one HPV-associated protein or HPV interactor protein, the method comprising:
(a) providing the complex of claim 1;
(b) contacting said complex with a test agent; and
20 (c) detecting the presence of a polypeptide displaced from said complex,
wherein the presence of displaced polypeptide indicates said agent disrupts said complex.

15. A method of identifying a polypeptide complex in a subject, the method comprising:
(a) providing a biological sample from said subject; and
25 (b) detecting, if present, the polypeptide complex of claim 1 in said sample,
thereby identifying said complex.

16. A method of detecting a polypeptide in a biological sample, the method comprising:
(a) providing a biological sample comprising the first polypeptide of claim 1;

(b) contacting said biological sample with the second polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptides; and

(c) detecting the presence of a complex of said first and second polypeptide, wherein the presence of said complex indicates the presence of said first polypeptide in said sample.

17. A method of detecting a polypeptide in a biological sample, the method comprising:

(a) providing a biological sample comprising the second polypeptide of claim 1;

(b) contacting said biological sample with the first polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptides; and

(c) detecting the presence of a complex of said first and second polypeptide, wherein the presence of said complex indicates the presence of said second polypeptide in said sample.

18. A method of removing a polypeptide from a biological sample, the method comprising:

(a) providing a biological sample comprising the first polypeptide of claim 1;

(b) contacting said biological sample with the second polypeptide of claim 1 under conditions suitable for formation of a complex comprising said first and second polypeptide; and

(c) removing said complex from said sample, thereby removing said first polypeptide from said sample.

19. A method of determining altered expression of a polypeptide in a subject, the method comprising:

(a) providing a biological sample from said subject,

(b) measuring the level of the complex of claim 1 in said sample; and

(c) comparing the level of said complex from step (b) to the level of said complex in a reference sample whose level of the complex of claim 1 is known,

thereby determining whether said subject has altered expression of said first or second polypeptide.

20. A method of treating or preventing a disease or disorder involving altered levels of the complex of claim 1, the method comprising:

administering a therapeutically-effective amount of least one molecule that modulates the function of said complex to a subject in need thereof.

21. A method of screening for pre-cancerous cervical lesions comprising contacting a patient derived cervical cell with a molecule that binds specifically to HPV E6 or E7 protein, detecting binding of said molecule, thereby identifying pre-cancerous cervical lesions.

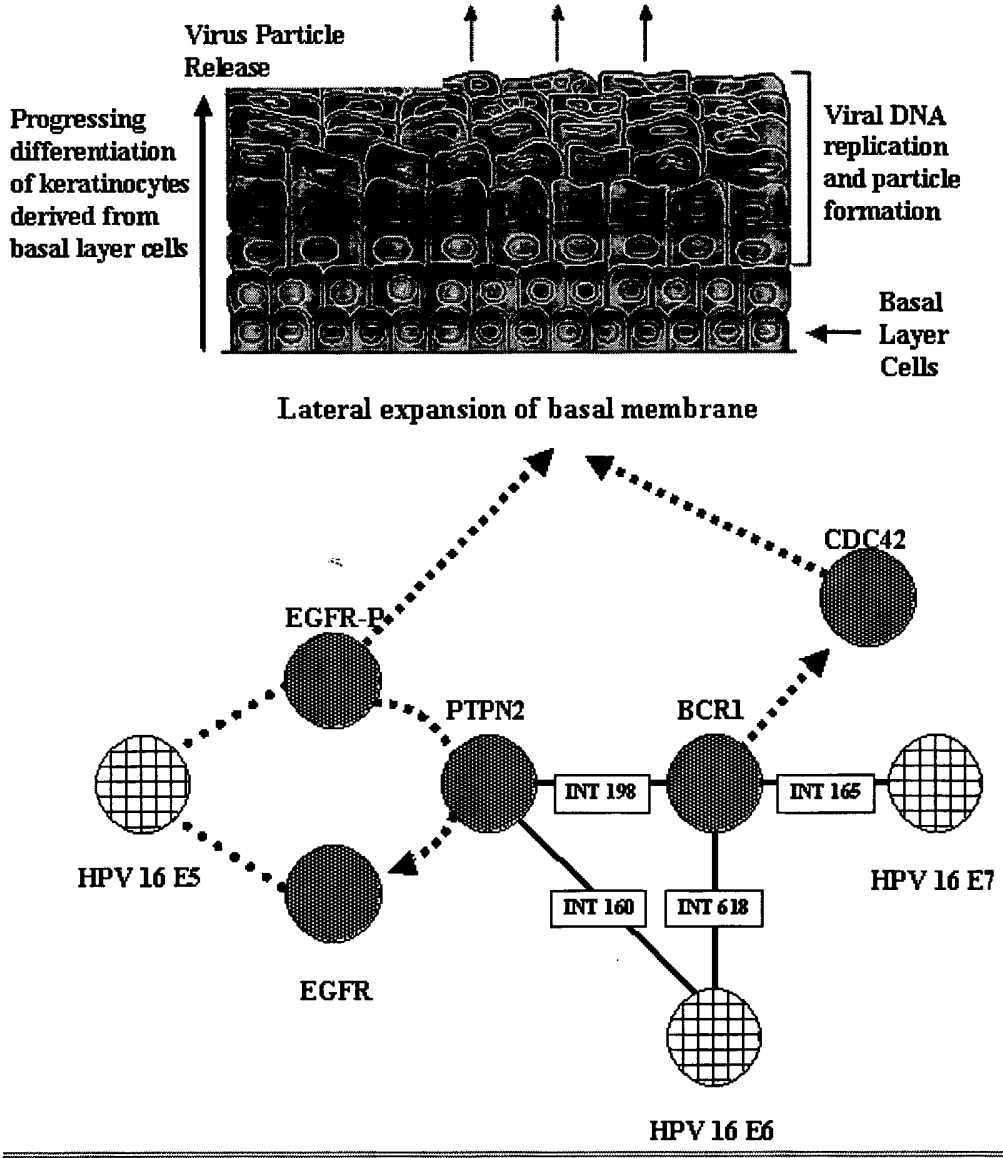
22. The method of claim 21, wherein said E6 or E7 protein are proteins from HPV types selected from the group consisting of HPV 1a, HPV 11 and HPV 16.

23. A method of classifying an HPV infection in a patient, comprising contacting a patient derived cell with a molecule that binds specifically to a subset of HPV E6 or E7 proteins, said molecule selected from a keratinocyte library, detecting binding of said molecule thereby classifying an HPV infection in said patient.

24. The method of claim 23, wherein the cell is obtained from the site of HPV infection.

25. The method of claim 23, wherein the cell is selected from head, neck, larynx, skin, anogenital, epithelial, mucosal or cervical tissue.

FIGURE 1



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