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SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO



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Act. 444 RESPUESTAREQUE Folios: 73

s Sanitarios

Señor

JEFE DIVISIÓN DE NUEVAS CREACIONES

SUPERINTENDENCIA DE INDUSTRIA Y COMERCIO

E. S. D.

REF: EXPEDIENTE: 04-088188

**TITULO: "JUEGO DE PRIMERS Y PROCEDIMIENTO PARA
DETECTAR UN MARCADOR DE SEXO
MASCULINO..."**

ACTUACIÓN: RESPUESTA A EXAMEN DE PATENTABILIDAD

TM

CARLOS ORLANDO MAYA RODRÍGUEZ, mayor de edad, vecino de esta ciudad, identificado con la Cédula de Ciudadanía No.17.117.818 expedida en Bogotá, Abogado titulado en ejercicio y portador de la Tarjeta Profesional No. 17.402 del Consejo Superior de la Judicatura, obrando en calidad de apoderado de la UNIVERSIDAD TECNOLÓGICA DE PEREIRA, según poder debidamente conferido y legalizado, adjunto a las diligencias administrativas de la referencia.

Encontrándome dentro del término legal comparezco para responder el oficio de Requerimiento No. 13716 del Examen emanado de esa Oficina, **del cual pedimos prorroga** y fundamento en el Artículo 45 de la Decisión 486 de 2.000 de C.A.N, damos respuesta en los siguientes términos.

1. De la solicitud de Patente

1.1. Con respecto a la solicitud del contrato de acceso a recursos genéticos solicitado por su despacho, hacemos la siguiente aclaración:

Carrera 13 A No. 28-38 Mz 2 Bufette 245 Parque Central Bavaria
Tel. (57 1) 341 9841 - FAX (57 1) 336 8592 - Cel. (315) 317 1181
E-mails: consultas@tmtamayo.net, carlos.tamayo@tmtamayo.net
www.tmtamayo.com / Bogotá D.C., COLOMBIA, S.A.

COL 12010 Carlos Tamayo & Asociados
10000 NW 25 TH ST UNIT 1
MIAMI, FL 33172-2204
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El requerimiento del contrato de acceso se hace de acuerdo con el Art. 26
Literal h) de la decisión 486 de 2000 de la CAN.

Art. 26

"Artículo 26.- La solicitud para obtener una patente de invención se presentará ante la oficina nacional competente y deberá contener lo siguiente:

(...)

h) De ser el caso, la copia del contrato de acceso, cuando los productos o procedimientos cuya patente se solicita han sido obtenidos o desarrollados a partir de recursos genéticos o de sus productos derivados de los que cualquiera de los Países Miembros es país de origen;

En este caso los primers sintéticos sobre los que se TMsolicita la patente, no están dentro de las categorías que menciona el artículo en citado, debido a que dichos primers, son sintéticos. Los primers sintéticos no son resultado de una extracción genética; por el contrario son generados a partir de compuestos químicos, los que se fabrican en el sintetizador de oligos y no se extraen directamente de fuentes naturales como las plantas.

En la Decisión 391 de 1996 sobre "régimen común sobre acceso a los Recurso Genéticos" Art. 1 Define (...)

"RECURSOS GENETICOS: Todo material de naturaleza biológica que contenga información genética de valor o utilidad real o potencial".

PRODUCTO DERIVADO Moléculas, combinación o mezcla de moléculas naturales, incluyendo extractos crudos de organismos vivos o muertos de origen biológico, proveniente de metabolismos de seres vivos"



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Los Primers sintéticos no se encuentran en la categoría de recursos genéticos porque no son de naturaleza biológica, son de naturaleza química.

Los Primers sintéticos no entran dentro de la categoría de los productos derivados porque sus moléculas o combinaciones de moléculas no son de origen biológico natural.

Por lo anterior, solicitamos, no requerir, el contrato de acceso por no encuadrar dentro del Art. 26 Literal h) de la Decisión 486 de la CAN

Sin embargo informamos a su despacho que se han realizado los trámites necesarios para la obtención de este contrato de acceso, por lo que aportamos:

- Certificación de grupos Étnicos
- Solicitud de contrato de acceso
- Carta a la C.V.C.
- Respuesta de la C.V.C.

A la fecha el documento de contrato de acceso se encuentra en trámite, dado que para obtener esta certificación es necesario:

- 1.- DAS.- Pasado Judicial
- 2.- Subdirección de Inteligencia del Ejército
- 3.- Instituto Agustin Codazzi para las coordenadas y Mapa
- 4.- Ministerio del Interior, Certificación de Comunidades
- 5.- Ministerio de Ambiente, Vivienda, para el Formulario de Solicitud



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6.- Permiso de la C.V.C.

2- Para atender lo objetado por el señor examinador respecto de la Reivindicación 1 la que considera que no es patentable, hacemos la siguiente aclaración:

La reivindicación 1 hace referencia a un juego de Primers, pero este juego de primers son artificiales y se sintetizan utilizando productos químicos, luego los primers no se presentan como se encuentran en la naturaleza.

Por lo anterior se presenta una nueva reivindicación 1 en la que se ha esta aclaración, cumpliendo a sí con lo establecido en el artículo 15 literal b) de la Decisión 486 de la CAN, ya que este artículo considera:

"Artículo 15.- No se considerarán invenciones:

(...)

"b) El todo o parte de seres vivos tal como se encuentran en la naturaleza, los procesos biológicos naturales, el material biológico existente en la naturaleza o aquel que pueda ser aislado, inclusive genoma o germoplasma de cualquier ser vivo natural "subrayado fuera de texto, para destacar".

Por lo anterior, anexamos las pruebas de alineamiento de los primers sintéticos Vs. Secuencia blanco, donde varia desde 72% al 95% la alineación con lo cual se demuestra que los primers son obtenidos por síntesis química.

3 **Presentamos un nuevo Titulo**



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"JUEGO DE PRIMERS ARTIFICIALES SINTÉTICOS Y PROCEDIMIENTO PARA DETECTAR UN MARCADOR DE SEXO MASCULINO EN PLANTAS DE BORORO"

4.- Determinación del estado de la Técnica

Respecto del documento D1 US4683195 y documento D1 US6180345 no afectan el nivel inventivo de la presente solicitud, por las siguientes razones:

- D1: Divulga el proceso PCR y el diseño de cebadores según la secuencia blanco, a diferencia de la solicitud en estudio, que reclama un par de primer artificiales sintetizados a partir de producto químicos y el proceso estandarizado que involucra dichos primers sintéticos.
- D2.- Enseña la aplicación de técnicas de biología molecular, entre ellas PCR, diseño de primers, identificación de la secuencia blanco para determinación del sexo de la papaya, mientras que la presente solicitud, reclama un juego de primers artificiales sintetizados a partir de productos químicos y el proceso estandarizado que involucra dichos primers sintéticos, para determinar el sexo del borojó.

Con las anteriores aclaraciones a la reivindicación 1, estamos presentando:

- Nuevo capítulo descriptivo
- Nuevo capítulo reivindicatorio
- Nuevos dibujos.

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www.tmtamayo.com / Bogotá D.C., COLOMBIA, S.A.

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Lo anteriores, con un contenido que no excede el alcance de la solicitud inicial.

Por lo aquí expuesto, ruego a usted dar por subsanado dicho requerimiento, sin perjuicio de lo cual desde ya nos acogemos a lo dispuesto por el inciso segundo del artículo 45 de la decisión 486 de la Comunidad Andina de Naciones que a la letra dice: "(...) Cuando la oficina nacional competente estimare que ello es necesario para los fines del examen de patentabilidad, podrá notificar al solicitante dos o más veces (...)"

NOTIFICACIONES

Mi poderdante y yo recibiremos notificaciones en la Secretaría de su Despacho o en mi Oficina de Abogado ubicada en la Carrera 13A No. 28-38 Ofc. 246 MZ. 2 Parque Central Bavaria de la ciudad de Bogotá D.C.

Del señor Jefe


CARLOS ORLANDO MAYA RODRIGUEZ

No. 17.117.818 expedida en Bogotá

T.P No. 17.402 del C.S.J.

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*Corporación Autónoma
Regional del Valle del Cauca*

Buenaventura, 06 de enero de 2009

0751-05-00043-2009

Doctor
Álvaro H. Alegria
Director
Universidad Tecnológica de Pereira
Centro de Biología Molecular y Biotecnología
Apartado Aéreo O@7
Tej. CONM.3137300- FAX: 3213206. Pereira (Ris)

Cordial saludo

De acuerdo con la información suministrada a la corporación, en oficio radicada el 11 de diciembre de 2008 en la ciudad de Cali, en el cual solicita un contrato de acceso a recursos genéticos y donde se manifiesta sobre los trabajos de investigación que se viene adelantando por parte de la universidad desde el año 2002 en la planta dioica del borojo (*Borojoa patinoi*, cuatrocasas) tendiente a la estabilización de métodos moleculares que permitan identificar el sexo del borojo en plántulas antes de la siembra en cultivos.

Quiero informarles que las actas de acuerdos, elaborada en actividades relacionadas con comunidades negra producto de permisos de investigación a realizarse en estos territorios, se debe realizara mediante la elaboración de una consulta previa, el cual es garante el Ministerio de el Interior y es quien certifica la presencia de comunidades negras en el sector, considerando que anexo al documento de solicitud se encuentra un acta de acuerdo elaborada en el año 2002 entre el consejo comunitario de sabaleta y la universidad tecnológica, por consiguiente de acuerdo con el decreto numero 309 de 2000 del Ministerio del Medio Ambiente los permisos de investigación con acceso a recursos genéticos son competencia del Ministerio de Ambiente, Vivienda y Desarrollo Territorial.

Atentam

MARIELLA HIN ROZA HINOJO
Directora Ambiental Regional Pacifico Oeste
Buenaventura
cvc

Proyecto: Fernex Hinojosa
elaboró: Fernex Hinojosa



OFI09-6647-DAI-0220

Bogotá D.C., 09 de Marzo de 2009

Doctor

CARLOS MAYA RODRIGUEZ

T.P. No. 17.402 del Consejo Superior de la Judicatura

TM TAMAYO & ASOCIADOS

Bogotá

Asunto: Certificación de presencia de grupos étnicos en la Inspección de Policía de Zabaletas en jurisdicción del municipio de Buenaventura, departamento del Valle del Cauca, para la solicitud de Patente de invención denominada "Proceso y Obtención de marcadores moleculares para determinar el sexo en Plantas de Borojó".

Apreciado Dr. Maya:

Atendiendo su solicitud, radicada en esta Dirección el 4 de marzo de 2009, donde solicita certificación de presencia de grupos étnicas para la solicitud de patente de invención denominada "Proceso y obtención de marcadores moleculares para determinar el sexo en Plantas de Borojó", me permito informar lo siguiente:

Revisadas las bases de datos institucionales aportadas por la Dirección para Comunidades Negras, Afrocolombianas, Raizales y Palenqueras sobre comunidades negras **SE REGISTRA** el Consejo Comunitario de la Comunidad negra de Zabaletas, Bogotá y La Loma en jurisdicción del municipio de Buenaventura, departamento del Valle del Cauca.

Revisadas las bases de datos institucionales aportadas por la Dirección de Asuntos Indígenas, Minorías y Rom, del DANE, Asociaciones de Cabildos y/o Autoridades Tradicionales y los reconocimientos emanados de dicha Dirección **SE REGISTRAN** comunidades indígenas en el municipio de Buenaventura, pero no se tiene información exacta de la presencia de dichas comunidades en la Inspección de Zabaletas en jurisdicción del municipio de Buenaventura.

Por lo anterior, se requerirá realizar una verificación en terreno para determinar los grupos étnicos existentes en dicha zona, para lo cual se debe coordinar con el Grupo de Consulta previa del Ministerio del Interior y de Justicia.

Atentamente,

CLAUDIA TERESA CACERES DOMINGUEZ

Coordinadora Grupo de Consulta Previa.

Ministerio del Interior y de Justicia.

Elaboró: Myriam E. Sierra-Martha Rocío Vanegas Rad Ext09-8936/04/03/09

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CONSEJO REGIONAL DE ECONOMIA INTEGRADOS
REGIONAL PACIFICO
SABALETAS
BUENAVENTURA

Sabaletas, 13 de Septiembre de 2002.

Doctor
GUSTAVO ADOLFO RENGIFO
Director
CVC Regional Pacifico
Buenaventura

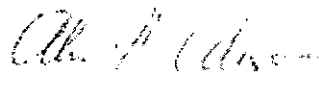
Cordial saludo.

Por medio de la presente le hacemos llegar el Acta de Acuerdos entre el Consejo Comunitario y la Universidad Tecnológica de Pereira UTP, el cual adelanta una investigación para determinar el sexo de la especie de *Borojoa patinot*, mediante el uso de marcadores moleculares.

Esta investigación no generará ningún daño o deterioro al medio ambiente, pero si arrojará resultados que nos servirán para el adelantamiento en el desarrollo de nuestras comunidades.

Atentamente,


NEPOMUCENO CAICEDO A.
Representante Legal
Consejo Comunitario de Sabaletas


ALVARO H. ALEGRIA
Investigador
Universidad Tecnológica de Pereira

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ANEXO

**SOLICITUD DE ACCESO
A RECURSOS GENETICOS**

IDENTIFICACION

I. SOLICITANTE O REPRESENTANTE LEGAL

I.1. IDENTIFICACION

Nombre o Razón Social Universidad Tecnológica de Pereira U.T.P.
Apoderado: Carlos Orlando Mayu Rodriguez
Nacionalidad Colombiana
Documento de Identidad
Domicilio Legal Vereda la Julita - Pereira
Teléfono 313 7300 Fax 321 3206 Correo Elect. rector@utp.edu.co

II. RESPONSABLE TECNICO DEL PROYECTO

1. IDENTIFICACION

Nombre o Razón Social Alvaro Hernan Alegria Soto
.....
Nacionalidad Colombiana
Documento de Identidad 6.067.110
Domicilio Legal Vereda la Julita - Pereira
Teléfono 321 5393 Fax 321 5393 Correo Elect. cambiotepe@utp.edu.co

2. ACTIVIDADES DE ACCESO REALIZADAS EN LOS ULTIMOS 5 AÑOS DEL RESPONSABLE TECNICO

AÑO	ACTIVIDAD	PAIS	CONTRAPARTE
2003	Recoleccion Hojas Jovenes de Borojo en Sabaleto	Colombia	

3. CURRICULUM DE ESTUDIOS DEL RESPONSABLE TECNICO

AÑO	ESTUDIOS SUPERIORES (ESPECIALIDAD)	GRADO	INSTITUCION	LUGAR
1968	Bioguinica y Biologia Molecular	PhD	Harvard U.	E.E.U.U.
1967	Investigacion	Fellow	Yeshiva U.	E.E.U.U.
1966	Master en B. Mol	Master	Harvard U.	E.E.U.U.
1956	Medico Cirujano	Medico	U. del Valle	Cali - Valle

4. PUBLICACIONES DEL RESPONSABLE TECNICO (Tres más importantes)

TITULO	AÑO	REVISTA / LIBRO
DNA Finger Printing AFIP	2006	Journal Of insect Science Vol. 6 pag 30
Determinacion de Sexo en Borojo	2004	Revista de Biotecnologia Vol. VI(2) 9-14
Ident. de Marcadores Moleculares en Insectos	2006	Revista Actualidades Biologicas 28(84) 7-15

5. EXPERIENCIAS DEL RESPONSABLE TECNICO (Actividad realizada en los últimos 5 años)

AÑO	ACTIVIDAD O CARGO	CANTIDAD	PAIS
2009	Director Cenbiotep desde 1995		Colombia
2009	Director Maestría en Biología Molecular y Biotecnología desde el 2003		

6. GRUPO DE TRABAJO A CARGO DE LA ACTIVIDAD DE ACCESO

DOMICILIO	NOMBRE	ESPECIALIDAD	GRADO ACADEM.
U. Tecnológica de Pereira	Alvaro H. Alegria	Biología Molecular	PhD
U. Tecnológica de Pereira	Duvernay Garibay	Biología Molecular	MSc
U. Tecnológica de Pereira	Lucero Rengifo	Biología Molecular	MSc
U. Tecnológica de Pereira	Enrique Aguilar	Biología	BSc

III. DATOS DEL PROVEEDOR DEL RECURSO

1. IDENTIFICACION

Nombre o Razón Social Consejo Comunitario de la Comunidad Negra de Zabaletas

Documento de Identidad Nit: 835.000.846-3

Domicilio Zabaletas

Teléfono Fax Correo Elect.

IV. DATOS DE LA PERSONA O ENTIDAD NACIONAL DE APOYO CIENTIFICO O CULTURAL

1. IDENTIFICACION

Nombre o Razón Social Nepamuceno Caicedo A.

Domicilio Legal Zabaletas

Teléfono Fax Correo Elect.

V. PROPUESTA DE PROYECTO

1. TÍTULO
2. JUSTIFICACION, OBJETIVOS Y LITERATURA TECNICA
3. AREA DE APLICACIÓN
4. TIPO DE ACTIVIDAD Y USOS QUE SE DARÁ AL RECURSO
5. LISTA DE REFERENCIA DE RECURSOS GENÉTICOS, PRODUCTOS DERIVADOS Y COMPONENTES INTANGIBLES ASOCIADOS, A LOS QUE SE PRETENDE ACCEDER (NOMBRE CIENTÍFICO, NOMBRE VULGAR Y NÚMERO DE MUESTRAS)
6. LOCALIZACION DE LAS AREAS DE ACCESO Y DE REALIZACION DE LAS ACTIVIDADES DE ACCESO (COORDENADAS)

a) DE RECOLECCION

b) UBICACION DEL AREA DE ACCESO

In Situ ☐ Ex Situ ☐ Coordinada ☐

Detalle:

c) LUGAR DE PROCESAMIENTO Y/O USO DEL MATERIAL GENETICO, LOCALIZACIÓN

- EN CASO DE RECURSOS EX SITU SE INCLUIRÁ LA INFORMACION RÉLEVANTE SOBRE EL CENTRO DE COMERCIALIZACION EX SITU.

7. CRONOGRAMA INDICATIVO

ACTIVIDADES	TIEMPO	LUGAR	METODOLOGIA *
EXPLORACION			
RECOLECCION			
EXTRACCION			
MANEJO			
INVESTIGACION			

Duración aproximada: _____

* Tipo y tamaño de la muestra, diseño de muestreo y tipo de caracterización.

8. MATERIALES Y MÉTODOS

9. PROCEDIMIENTO DE EXPLORACION Y RECOLECCION

10. MANEJO DE LA MUESTRA

11. EVENTUALES RESULTADOS ESPERADOS

12. PRESUPUESTO INICIAL

13. OTROS

VI. CARTA DE ACEPTACION EN PRINCIPIO O CONTRATO DEL PROVEEDOR DE LOS RECURSOS BIOLÓGICOS, DE LOS RECURSOS GENÉTICOS O DEL COMPONENTE INTANGIBLE

VII. CARTA DE COMPROMISO DE LA PERSONA O ENTIDAD NACIONAL DE APOYO

VIII. DECLARACION JURADA O AFFIDAVIT DEL SOLICITANTE, CONSIGNANDO LA VERACIDAD DE LOS DATOS ANOTADOS EN LA SOLICITUD.

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PATENTE DE INVENCION

JUEGO DE PRIMERS ARTIFICIALES SINTÉTICOS Y PROCEDIMIENTO PARA DETECTAR UN MARCADOR DE SEXO MASCULINO EN PLANTAS DE BOROJO

ESFERA TECNOLÓGICA

Proveer un juego de Primers o iniciadores artificiales sintéticos producidos a través de síntesis química de 20 y 22 pares de bases para diagnosticar el sexo en plantas de borojo conforme a la técnica de la reacción en cadena de la polimerasa PCR.

Esta invención se ubica en el área de la Biotecnología.

ESTADO DE LA TÉCNICA

Existe el documento US4683195 "Process For Amplifying, Detecting And/Or Cloning Nucleic Acid Sequences" con fecha de publicación 28 de julio de 1987 que divulga el proceso de PCR que corresponde a las características de una PCR convencional.

Existe el documento US6180345 "Process For Simultaneous Preparation Of Sex Specific And Gender-Neutral Semisynthetic Amplicon Useful For Sex Determination" con fecha de publicación 30 de enero de 2001, que enseña la aplicación de técnicas de biología molecular entre las que se cuenta el PCR para determinar el sexo en Papaya.

La presente solicitud de patente de invención pretende determinar el sexo a edad temprana en Borojo por medio de un juego de Primers.

Las plantas femeninas de muchas especies dioicas son de valor comercial por la producción de frutos, tales como papaya y kiwi o de semillas como pistacho, nuez moscada, pimienta negra, por lo que se prefieren en altas proporciones en un cultivo (Parasnis et al 2000, Ainsworth, 2000). Sin embargo en muchas especies dioicas el sexo no es revelado sino hasta alcanzar la madurez cuando aparecen las flores, lo cual puede tomar de meses a años. Unas pocas especies dioicas contienen cromosomas heteromórficos como *Silene*, *Rumex* y *Humulus*, lo que permite identificar su sexo citológicamente (Negrutiu et al, 2001). Sin embargo, muchas de las especies dioicas carecen de cromosomas sexuales diferentes morfológicamente, lo que ha generado un interés por desarrollar estrategias de identificación del sexo de plantas dioicas a través de marcadores moleculares. Las técnicas basadas en PCR (Reacción en Cadena de la Polimerasa) han sido de gran utilidad y han sido explotadas para detectar diferencias entre plantas masculinas y femeninas a nivel molecular. Existen en vegetales varios marcadores moleculares ligados al sexo generados ya sea a través de estudios de mapeo genético (Spada et al, 1998, Liu et al, 2004) o de investigaciones encaminadas a encontrar marcadores ligados al sexo de especies agrónomicamente importantes, por ejemplo se han usado microsatélites para identificar diferencias específicas de sexo en papaya, *Carica papaya* (Parasnis et al, 1999), AFLP para la identificación de marcadores ligados al sexo de *Dioscorea tokoro* (Terauchi y Kahl, 1999) de espárrago *Asparagus officinalis* (Reamon-Büttner et al, 1999) y patrones de bandas RAPD ligados al sexo de marihuana *Cannabis sativa* L. (Mandolino et al, 2002), de álamo *Salix viminalis* L. (Alstrom-Rapaport et al, 1998) de *Atriplex garrettii* (Ruas et al, 1998) y de *Silene latifolia* (Nakao et al, 2002). En especies como papaya y kiwi el diagnóstico del sexo puede realizarse desde estados tempranos de desarrollo de la planta gracias al diseño

iniciadores de PCR a partir de marcadores moleculares (Parasnis et al, 2000, Deputy et al, 2002, Gill et al, 1998).

REVELACIÓN DE LA INVENCION

La presente solicitud de patente de invención se relaciona con un método de protocolo para identificar el sexo de especies vegetales, particularmente el borojo, planta nativa del Chocó en Colombia a través de marcadores moleculares asociados al sexo de dicha especie vegetal.

Un objetivo del modelo propuesto es proveer marcadores moleculares específicos a partir de una secuencia de nucleótidos que permita el diseño de iniciadores para determinar el sexo de la planta o especies vegetales en edad temprana mediante la reacción en cadena de la polimerasa que aquí llamaremos PCR.

Otro objetivo es igualmente proveer una secuencia de 210 bases del marcador AFLPE/M-CAA

El principal objetivo es proveer un juego de Primers o secuencia de los iniciadores artificiales sintéticos producidos a través de síntesis química de 20 y 22 pares de bases para diagnosticar el sexo en plantas de borojo conforme a la técnica de la reacción en cadena de la polimerasa PCR.

Los primers son sintéticos utilizando compuestos químicos denominados deoxinucleótidos y son: guanina (G), adenina (A), Citosina (C) y Timina (T), con los cuales se hacen los primers en una máquina conocida como sintetizador de oligos, y no se extraen directamente de fuentes naturales como las plantas.

El borojó es una especie originaria del departamento del Chocó (Colombia) perteneciente a la tribu Gardenieae, género Magnoliopsida, orden Rubiales, familia Rubiaceae.

especie Borojoa Patinoi Cuatrecasas (Cuatrecasas, 1948). Hace parte de los ecosistemas de vega de río a lo largo del Pacífico colombiano, es endémico de esta región, ampliamente cultivado encontrándose desde Bahía Solano (Chocó) hasta el río Naya (límites de Valle y Cauca), aunque actualmente está diseminada en todo el territorio colombiano incluyendo la Amazonía y la zona cafetera, ya que se adapta desde los 0 a los 500 m.s.n.m, pero en condiciones óptimas, requiere precipitaciones mayores a 400 mm y una temperatura media de 26 °C. Los sitios de producción comercial de la fruta son el Chocó (zona del Atrato, Loró y Bajo San Juan) y el Valle del Cauca (región del Bajo Anchicayá y el Bajo Calima (Buenaventura) (Constantino et al, 2000).

El borojó hace parte del pequeño grupo de plantas que florecen y que son sexualmente dimórficas, las plantas dioicas. Los árboles machos no productores de frutos, no se diferencian fenotípicamente de las hembras antes de la floración, las inflorescencias masculinas son terminales, en racimo, color blanco crema y las flores femeninas son solitarias, terminales y también color blanco crema. El fruto es una baya que en sus primeros estadios es verde claro y al madurar se torna pardo rojizo, tiene un mesocarpo carnoso con sabor aromático y muy perfumado, tiene propiedades alimenticias por poseer aminoácidos esenciales y es fuente de calcio, hierro, fósforo y vitamina C. Posee metabolitos secundarios de gran interés como modelos químicos para nuevas drogas. Además posee propiedades que le atribuye la medicina tradicional y popular como diurético, cicatrizante, afrodisíaco y antitumoral (Gentry, 1982, 1988). Teniendo en cuenta estas propiedades, la expectativa de mercadeo alrededor de la fruta de borojó en el ámbito nacional e internacional es prometedora, la proyección comercial muestra una rentabilidad superior o igual a la de ciertos cultivos comerciales de la zona

andina e interandina. La producción bajo condiciones naturales con técnicas del saber tradicional es de 5 a 12 frutos árbol/año durante los primeros 5 años y de 12 a 30 frutos árbol/año para el resto del período de utilidad (Mosquera y Arenas, 1995)

Problema técnico que se solucionó

Uno de las dificultades que presenta el cultivo del borojó es poder reconocer el sexo de las plantas antes de la floración, aspecto que sería muy ventajoso a la hora de establecer un cultivo. Pero no existe un método basado en características como formas, tamaños, apariencia de la planta, hoja o fruto para distinguir las plantas femeninas de las masculinas antes de que estas florezcan. Cuando se establece un cultivo sin conocer el sexo de las plantas, es probable que cuando florezcan aproximadamente la mitad resulten machos y esto representa un costo en espacio, tiempo y dinero debido, a que estos árboles machos no van a producir frutos. Si se puede determinar el sexo de plantas de borojó en edad temprana, se puede diseñar el cultivo y determinar cuántas plantas masculinas serán suficientes para polinizar las plantas femeninas, esto permitiría establecer cultivos comerciales más productivos. Se evitará de esta manera sembrar plantas macho improductivas con la consiguiente pérdida de tiempo, espacio de sembrado y recursos, aunque algunas sean necesarias para los procesos de fertilización.

Nosotros obtuvimos dos marcadores moleculares específicos para plantas masculinas de *Borojoa patinoi* C. obtenidos mediante AFLP, determinamos la secuencia de nucleótidos de uno de ellos y estamos trabajando para obtener la secuencia del segundo marcador. A partir de la secuencia de nucleótidos ya obtenida diseñamos iniciadores artificiales sintéticos producidos a través de

síntesis química para determinar el sexo de las plantas en edad temprana mediante PCR.

Breve descripción de las figuras

La descripción para el procedimiento de la presente invención se acompaña de las siguientes foto -figuras a saber:

- La figura o foto 1 corresponde al marcador AFLP E-ACC/M-CAA asociado al sexo de plantas de borojo, en donde la flecha indica la banda específica para planta masculina;
- La figura o foto 2 corresponde al marcador asociado al sexo en plantas de borojo , en donde la flecha indica la banda específica para plantas masculinas , siendo marcador AFLP E-ACC/M-CAT;
- La figura o foto 3 presenta el diagnostico de sexo en plántulas de borojo mediante PCR. en donde la presencia de banda superior corresponde a plantas macho no productoras de frutos y la banda inferior corresponde a dimeros de iniciadores;
- La figura o foto 4 presenta el diagnostico de sexo de plantas de borojo adultas mediante PCR en donde la presencia de banda corresponde a plantas macho.
- La figura 5 representa la gráfica de alineamiento de Primers sintéticos 20 pares vs. secuencia blanco,
- La figura 6 representa la gráfica de alineamiento de Primers sintéticos 20 pares vs. secuencia blanco.

MEJOR MANERA DE REALIZAR LA INVENCION

Al hacer el examen de alineamiento (BLAST) de los primers artificiales sintéticos de 20 letras y 22 letras con la secuencia blanco, el alineamiento no es perfecto varía del 80% al 95%; debido a que la síntesis de los primers es química, es decir que se hicieron utilizando una máquina y con compuestos químicos.

No es una síntesis biológica porque la planta no fabrica los primers, la maquina con la que se fabrica los primers es un sintetizador de nucleotidos.

Los primers no hacen parte del Genoma de la planta, al cotejar con el genoma de la planta no alinean al 100%, tal como se demuestra en los exámenes de alineamiento de los primers con la secuencia blanco, con un nucleótido diferente la alineación es menor al 100% y en este caso varía entre el 72% y 95%.

Los primers son sintéticos utilizando compuestos químicos denominados deoxinucleotidos y son: guanina (G), adenina (A), Citosina (C) y Timina (T), con los cuales se hacen los primers en una máquina conocida como sintetizador de oligos, y no se extraen directamente de fuentes naturales como las plantas.

La invención se basa en procedimientos conforme al siguiente protocolo de etapas:

1 Extracción de ADN:

Para realizar la extracción de ADN el protocolo consiste en:

1. Macerar el material vegetal (hojas tiernas) con nitrógeno líquido.
2. Incubar 100 mg de cada muestra con 1.5 ml de buffer de extracción a 65 °C durante 60 minutos, mezclando ocasionalmente por inversión.
3. Completar volumen a 2 ml con cloroformo: alcohol isoamílico 24 : 1 y mezclar por inversión.
4. Centrifugar durante 10 minutos a 10.000 rpm a 4 °C. Separar fase acuosa en otro tubo.
5. Repetir el paso 3 y 4.
6. Repetir el paso 3 y 4.
7. Adicionar a la fase acuosa 2/3 del volumen de isopropanol frío.

8. Después de incubar 2 horas a -20°C , centrifugar a 10.000 rpm durante 10 minutos a 4°C .
9. Lavar el precipitado con 1 ml de etanol al 76% y 10 mM de acetato de amonio, incubar 20 minutos a 4°C .
10. Centrifugar durante 5 minutos a 10.000 rpm a 4°C .
11. Descartar sobrenadante, dejar secar el precipitado y resuspender en 200 μl de buffer TE (Tris 100 mM, EDTA 10 mM).
12. Adicionar 2.5 μl de RNasa A (10 mg/ml), e incubar durante 30 minutos a 37°C .
13. Precipitar con 400 μl de etanol absoluto y 20 μl de acetato de sodio 3 M, dejar a -20°C durante 30 minutos.
14. Centrifugar a 12000 rpm durante 15 minutos a 4°C .
15. Lavar el precipitado con etanol al 70 %, dejar secar y resuspender en 200 μl de TE.

E.2 Reacciones de AFLPs:

Se usó el estuche comercial AFLP Analysis System I" de Invitrogen

- Las reacciones de digestión enzimática con EcoRI/MseI, la ligación de adaptadores y la reacción de preamplificación se realizaron con 300 ng de ADN iniciales, pero a la mitad del volumen recomendado en las especificaciones del estuche comercial.

- Las diluciones se modificaron como se describe en el siguiente protocolo:

1. Se digirieren 300 ng de ADN con 1,25 U de EcoRI y de MseI, en tampón 5X en un volumen total de 12.5 μl a 37°C por 2 horas.
2. Después de inactivar las endonucleasas a 70°C por 15 minutos, se realiza la ligación de los adaptadores, usando 12 μl de la solución para ligación de adaptadores EcoRI/MseI y 0.5 U de T4 ADN ligasa a 20°C durante 2 horas.

3. Esta mezcla se diluye 10 veces para la reacción de PCR+1, la que se hace en un volumen de 25 μ l y contiene 20 μ l de la mezcla de cebadores para preamplificación, 2.5 μ l de tampón 10X PCR con Mg, 2.5 U de Taq ADN polimerasa y 2.5 μ l de ADN diluido del paso anterior.

4. El programa de temperaturas es: 20 ciclos de 94°C por 30 seg, 56°C por 60 seg y 72°C por 60 seg.

5. Para la amplificación selectiva (PCR+3), el producto del PCR+1 se diluye 25 veces, y se hace una mezcla de 2 μ l de tampón 10X PCR con Mg, 7.9 μ l de agua ultrapura, 0.5 U de Taq ADN polimerasa, 4.5 μ l de la mezcla cebador MseI/dNTPs, 0.5 μ l de cebador EcoRI y 5 μ l de ADN preamplificado y diluido, en un volumen final de 20 μ l. Los cebadores EcoRI y MseI que presentaron una banda específica para plantas de sexo masculino fueron: E AAC – M CAA y E ACC – M CAT

6. El programa de temperaturas es: a) 1 ciclo a 94°C por 30 seg; 65 °C por 30 seg y 72°C por 60 seg; b) 13 ciclos en los que la temperatura de alineamiento bajó 0.7 °C en cada ciclo; c) 23 ciclos a: 94°C por 30 seg, 56°C por 30 seg y 72°C por 60 seg.

E.3. Separación electroforética de los productos de la reacción de AFLP

Se realiza una electroforesis en TBE 1X para separar los productos del PCR+3 en un gel de poliacrilamida al 6% y 7 M de urea preparado también en TBE 1X:

1. Uno de los vidrios se trata con Sigmacote (Sigma), lo que facilita separar el gel del vidrio después de la corrida electroforética.

2. Paralelamente, el otro vidrio se trata con BindSilane (Promega), reactivo que favorece la unión del gel sobre el vidrio y permite realizar la tinción de plata sobre éste.

3. Los productos de PCR+3 se diluyen a la mitad con tampón de carga (95% de formamida, 1 mg mL⁻¹ de xilen

cianol, 1 mg mL⁻¹ de azul de bromofenol y 10 mM EDTA) y se denaturan durante 3 min a 96°C.

4. Se colocan en hielo inmediatamente, y se mantienen allí hasta servir en el gel.

5. El gel se pre-corre sólo con tampón de carga en algunos pozos, por 25 min antes de cargar las muestras.

6. La corrida se realiza a 87 W por 2,0 a 2,5 h o hasta 5 cm antes de caer el xilen cianol desde el gel.

7. Para visualizar las bandas de ADN en el gel se tiñe con nitrato de plata siguiendo las instrucciones del estuche comercial "Silver Sequence DNA Staining Reagents" de Promega.

E.4 Secuenciación de los marcadores

El marcador asociado a sexo de la combinación E-AAC / M-CAA se purificó a partir de tres muestras directamente del gel de acrilamida teñido con nitrato de plata. El método de purificación fue el siguiente:

- Adicionar 10 µl de TE o agua sobre la banda en gel teñido con nitrato de plata.
- cortar la banda con bisturí y picarla bien
- colocar en un eppendorf
- Adicionar 20 µl de TE o agua
- Colocar 5 minutos en agua hirviendo
- Centrifugar 2 minutos a 8000 rpm
- Tomar 10 µl de sobrenadante y hacer PCR con las mismas condiciones de los pasos 5 y 6 de la reacción de AFLP.

El producto de PCR se analiza en una electroforesis de poliacrilamida al 12 % y se purifica nuevamente usando el protocolo mismo protocolo anterior. Se realiza la reacción de secuenciación a partir del producto purificado, siguiendo las instrucciones del manual del estuche comercial "Silver Sequence DNA Sequencing Reagents" de Promega, de la siguiente manera:

1. Se prepara una reacción que contiene: 10.8 µl de H₂O, 10 µl de "DNA sequencing 5X buffer", 10 µl de producto purificado de PCR, 1.2 de cebador y 2 µl de Taq polimerasa. Esta mezcla se reparte entre cuatro tubos, adicionando 8 µl a cada uno y que contienen 4 µl de ddATP, ddCTP, ddGTP y ddTTP respectivamente.
2. El programa de amplificación es el siguiente: 95 °C 2 min, 50 ciclos a 95 °C 30 seg, 60 °C 30 seg y 70°C 90 seg.

El resultado se observó en un gel de acrilamida al 6% y 7 M de úrea, a partir del cual se realizaron las lecturas de las secuencias. La secuencia concenso fue:

5'-

gcaaataaaattttgttgatgattgttgatcattccaaagttgaagtaaaaaatcagc
tgctagcaaatgtaatctgataagtatcatctttgatcattgatgttccctgttctgt
gacggataaacaatagaatgcttttctgttttcatttcttcatttatgatgccatcagtt
ctttgcaatttgtttggttggttactcaggactca - 3'

E.5 Diseño de iniciadores para PCR

Usando el programa Gene Runner versión 3.0 se diseñaron dos iniciadores para simplificar la técnica de identificación de sexo de plantas de borojó a un PCR.

BM1a: 5'- TGTTGATGATTGTTGTCATTCC- 3'

BM1b: 5'- AAATTGCAAAGAACTGATGG - 3'

E.6 Reacciones de PCR

Las reacciones de PCR se realizaron de la siguiente manera: 7.53 µl de H₂O, 1.5 µl de buffer10X, 0.9 µl de MgCl₂ 25 mM, 0.3 µl de una mezcla de dNTPs 2.5 mM, 0.88 µl de iniciador 1a, 0.79 µl de iniciador 1b, 0.1 µl de Taq DNA polimerasa y 3 µl de ADN.

Los productos de amplificación se observaron en geles de agarosa al 2 %.

EXAMEN DE ALINEAMIENTO (BLAST) DE LOS PRIMERS SINTÉTICOS CON LA SECUENCIA BLANCO

Al hacer el examen de alineamiento (BLAST) de los primers artificiales sintéticos de 20 letras y 22 letras con la secuencia blanco, el alineamiento no es perfecto varía del 72% al 95%; debido a que la síntesis de los primers es química, es decir que se hicieron utilizando una máquina y con compuestos químicos.

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BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save](#) [Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (22 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

icll4194

Description

None

Molecule type

nucleic acid

Query Length

22

Database Name

nr

Description

All GenBank+EMBL+DBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ (iteration)

References

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs". Nucleic Acids Res. 25:3389-3402.
Other reports: [Source](#) [Summary](#) [Taxonomy reports](#) [\[Distance tree of results\]](#)

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Database

Posted date	Dec 10, 2008 6:42 PM
Number of letters	250,069,024
Number of sequences	7,821,680
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Length adjustment	18
Effective length of query	4
Effective length of database	25409278784
Effective search space	101637115136
Effective search space used	101637115136

 [Designing or Testing PCR Primers?](#) Try your s

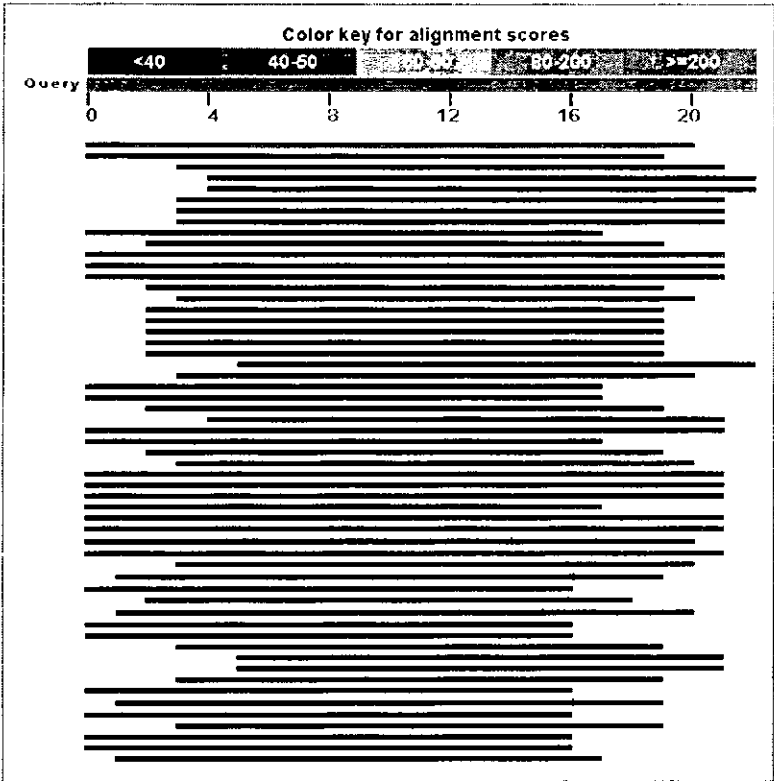
Query Summary

Distribution of 111 Blast Hits on the Query Sequence

28
1001

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



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Full Reports

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

Accession	Sequence	Length	Score	E-value	Ident	Gap	Start	End	Frame	Annotations
AY721982.1	Borojoa patinoi APLP molecular marker genomic sequence	40.1	40.1	90%	0.084	100%				
AC079945.21	Homo sapiens 3 BAC RP11-569D3 (Roswell Park Cancer Institute Human BAC Library) complete sequence	38.2	38.2	86%	0.13	100%				
XM_002000067.1	Drosophila melanogaster C122714 (DmoglC122714), mRNA	36.2	36.2	81%	1.3	100%				G
XM_001610598.1	Rabiesia bovis seryl-tRNA synthetase, putative (BBOV_IV007240) partial mRNA	36.2	36.2	81%	1.3	100%				G
CP000764.1	Bacillus cereus subsp. cytotoxus NVH 391-98, complete genome	36.2	66.4	81%	1.3	100%				
AC162884.4	Mus musculus chromosome 5, clone RP24-169E23, complete sequence	36.2	36.2	81%	1.2	100%				
AL512638.5	Human DNA sequence from clone RP4-663N10 on chromosome 1. Contains the 5' end of the NCPB gene for nerve growth factor (beta polypeptide), the 3' end of a novel gene, a renin (REN) pseudogene and one CpG island, complete sequence	36.2	36.2	81%	1.2	100%				
AC101685.9	Mus musculus chromosome 5, clone RP23-187K3, complete sequence	36.2	36.2	81%	1.3	100%				
CR380959.2	Candida glabrata strain CRS138 chromosome M complete sequence	34.2	34.2	77%	5.2	100%				
NG_008340.1	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), and DNA fragmentation factor, 45kDa, alpha polypeptide (DFFA), on chromosome 1	34.2	34.2	77%	5.2	100%				
XM_001990506.1	Drosophila grimshawi CH18188 (Dgri1CH18188), mRNA	34.2	34.2	95%	5.2	95%				G
AP009853.1	Lotus japonicus genomic DNA, chromosome 1, clone: LjT07G07, TM1730b, complete sequence	34.2	34.2	95%	5.2	95%				
AP007306.2	Lotus japonicus genomic DNA, chromosome 2, clone: LjT20J15, TM1492, complete sequence	34.2	34.2	95%	5.2	95%				
AC152349.12	Medicago truncatula clone mth2-52p10, complete sequence	34.2	34.2	77%	5.2	100%				
XM_001430565.1	Paramecium tetraurelia hypothetical protein (GSPAT90033057001) partial mRNA	34.2	34.2	77%	5.2	100%				G
XM_001304113.1	Trichomonas vaginalis G3 surface antigen BspA-like (TVAC_287080) partial mRNA	34.2	34.2	77%	5.2	100%				G
XM_001304112.1	Trichomonas vaginalis G3 surface antigen BspA-like (TVAC_287070) partial mRNA	34.2	34.2	77%	5.2	100%				G
AC150393.2	Branchiostoma floridae clone CH302-13E12, complete sequence	34.2	34.2	77%	5.2	100%				
AC149306.9	Medicago truncatula clone mth2-88b8, complete sequence	34.2	34.2	77%	5.2	100%				
CP000117.1	Anabaena variabilis ATCC 29413, complete genome	34.2	34.2	77%	5.2	100%				
AC141639.3	Mus musculus BAC clone RP23-354J7 from chromosome 18, complete sequence	34.2	34.2	77%	5.2	100%				
AC123055.3	Mus musculus BAC clone RP24-267D17 from chromosome 3, complete sequence	34.2	34.2	77%	5.2	100%				
AC098882.3	Mus musculus BAC clone RP23-122D13 from 12, complete sequence	34.2	34.2	77%	5.2	100%				
AC159294.2	Mus musculus BAC clone RP23-287I15 from chromosome 12, complete sequence	34.2	34.2	77%	5.2	100%				
AL591403.10	Human DNA sequence from clone RP11-108G8 on chromosome 1. Contains part of the PEX14 gene for peroxisomal biogenesis factor 14, complete sequence	34.2	34.2	77%	5.2	100%				
CR751224.20	Zebrafish DNA sequence from clone DKEY-241F21 in linkage group 22. Contains the calr gene for calreticulin, the trhl gene for trhl protein and the gene for a novel protein similar to vertebrate RAD23 homolog B (S. cerevisiae) (acc:123349), complete sequence	34.2	34.2	77%	5.2	100%				
AC090220.13	Homo sapiens chromosome 18, clone RP11-712P20, complete sequence	34.2	34.2	95%	5.2	95%				
XM_449757.1	Candida glabrata CRS138 hypothetical protein (CAGL0M09493g) partial mRNA	34.2	34.2	77%	5.2	100%				G
AF411806.1	Lycopersicon esculentum BAC clone Clemson_id 307, partial sequence	34.2	34.2	77%	5.2	100%				
AC122713.2	Homo sapiens chromosome 5 clone RP11-39H3, complete sequence	34.2	34.2	77%	5.2	100%				
AC026462.5	Homo sapiens chromosome 16 clone RP11-297L17, complete sequence	34.2	34.2	95%	5.2	95%				
AC007340.8	Homo sapiens chromosome 16 clone RP11-35805, complete sequence	34.2	34.2	95%	5.2	95%				
AB023036.1	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB19	34.2	34.2	95%	5.2	95%				E
AC092534.4	Homo sapiens BAC clone RP13-629D7 from 2, complete sequence	34.2	34.2	77%	5.2	100%				
AP004488.1	Lotus japonicus genomic DNA, chromosome 2, clone: LjT02F05, TM0020, complete sequence	34.2	34.2	95%	5.2	95%				
AC139355.8	Medicago truncatula clone mth2-3603, complete sequence	34.2	34.2	95%	5.2	95%				
BX001038.6	Zebrafish DNA sequence from clone CH211-12M10 in linkage	34.2	62.4	90%	5.2	100%				

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	group 19 Contains the 3' end of the gene for a novel protein similar to vertebrate odz and odd Oz/ten-m homolog 2 (Drosophila) (ODZ2), complete sequence								
AC169177.4	Medicago truncatula chromosome 7 clone mth2-1p4, complete sequence	34.2	34.2	95%	5.2	95%			
AC135237.6	Mus musculus BAC clone RP23-306F11 from chromosome 3, complete sequence	34.2	34.2	77%	5.2	100%			
FM180568.1	Escherichia coli O127:H6 E2348/69 complete genome, strain R2348/69	32.2	62.4	81%	20	100%			
NG_009005.1	Homo sapiens ankyrin 2, neuronal (ANK2) on chromosome 4	32.2	32.2	72%	20	100%			
NM_069908.5	Caenorhabditis elegans hypothetical protein (B0001.7) mRNA, complete cds	32.2	32.2	72%	20	100%			G
AM920427.1	Penicillium chrysogenum Wisconsin 54-1255 complete genome, contig Pc90c12	32.2	60.5	86%	20	100%			
EU263801.1	Nesiararchus nasutus isolate NES2 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	32.2	32.2	72%	20	100%			
EU263800.1	Nesiararchus nasutus isolate NES1 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	32.2	32.2	72%	20	100%			
AC171619.9	Medicago truncatula clone mth2-160a1, complete sequence	32.2	32.2	72%	20	100%			
AB435541.1	Aspergillus oryzae Aodshp gene for succinate dehydrogenase iron-sulfur subunit, carboxin resistant mutation form, complete cds, strain: CR14	32.2	32.2	72%	20	100%			
AB435540.1	Aspergillus oryzae Aodshp gene for succinate dehydrogenase iron-sulfur subunit, carboxin resistant mutation form, complete cds, strain: CR9	32.2	32.2	72%	20	100%			
AP009240.1	Escherichia coli SE11 DNA, complete genome	32.2	32.2	72%	20	100%			
AC225830.3	Pan troglodytes BAC clone CH251-61K15 from chromosome 7, complete sequence	32.2	32.2	72%	20	100%			
CP001164.1	Escherichia coli O157:H7 str. EC4115, complete genome	32.2	62.4	81%	20	100%			
EU697538.1	Haemulon melanurum cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial	32.2	32.2	72%	20	100%			
CU695221.7	Zebrafish DNA sequence from clone CH73-308M11 in linkage group 3, complete sequence	32.2	32.2	72%	20	100%			
EU870371.1	Spinacia oleracea phospholipase C (plc) mRNA, complete cds	32.2	32.2	72%	20	100%			
XM_002061364.1	Drosophila willistoni GK20745 (Dmir\GK20745), mRNA	32.2	32.2	72%	20	100%			G
XM_002053001.1	Drosophila virilis GJ23660 (Dvir\GJ23660), mRNA	32.2	32.2	72%	20	100%			G
XM_002004765.1	Drosophila mojavensis GI19393 (Dmoj\GI19393), mRNA	32.2	32.2	72%	20	100%			G
XM_001996606.1	Drosophila grimshawi GH22517 (Dgri\GH22517), mRNA	32.2	32.2	72%	20	100%			G
XM_001991839.1	Drosophila grimshawi CH11829 (Dgri\CH11829), mRNA	32.2	32.2	72%	20	100%			G
XM_001983867.1	Drosophila grimshawi CH15311 (Dgri\CH15311), mRNA	32.2	32.2	72%	20	100%			G
NW_001263840.1	Dictyostelium discoideum AX4 chromosome 4 DDB0232607.02, whole genome shotgun sequence	32.2	32.2	72%	20	100%			
NW_001263736.1	Dictyostelium discoideum AX4 chromosome 6 DDB0232839.02, whole genome shotgun sequence	32.2	60.5	72%	20	100%			
NW_001263690.1	Dictyostelium discoideum AX4 chromosome 6 DDB0232985.02, whole genome shotgun sequence	32.2	32.2	72%	20	100%			
XM_001895817.1	Brugia malayi hypothetical protein partial mRNA	32.2	32.2	72%	20	100%			G
CP000970.1	Escherichia coli SMS-3-5, complete genome	32.2	32.2	72%	20	100%			
CP000948.1	Escherichia coli str. K12 substr. DH10B, complete genome	32.2	60.5	86%	20	100%			
AC212783.3	Homo sapiens FOSMID clone ABC10-44680300N13 from chromosome 9, complete sequence	32.2	32.2	72%	20	100%			
XM_001816927.1	Aspergillus oryzae FIB40 hypothetical protein partial mRNA	32.2	32.2	72%	20	100%			G
CP000946.1	Escherichia coli ATCC 8739, complete genome	32.2	60.5	86%	20	100%			
AB353133.1	Escherichia coli O55:H6 DNA for O55-antigen biosynthesis gene clusters and their flanking regions, strain: ICC219	32.2	60.5	86%	20	100%			
AB353132.1	Escherichia coli O55:H7 DNA for O55-antigen biosynthesis gene clusters and their flanking regions, strain: WC416	32.2	32.2	72%	20	100%			
AB353131.1	Escherichia coli O55:H7 DNA for O55-antigen biosynthesis gene clusters and their flanking regions, strain: TB182A	32.2	32.2	72%	20	100%			
CP000924.1	Thermoanaerobacter pseudethanolicus ATCC 33223, complete genome	32.2	32.2	72%	20	100%			
CP000923.1	Thermoanaerobacter sp. X514, complete genome	32.2	32.2	72%	20	100%			
CU366904.1	Aphanomyces euteiches cDNA	32.2	32.2	90%	20	95%			
CU359699.1	Aphanomyces euteiches cDNA	32.2	32.2	90%	20	95%			
CU359669.1	Aphanomyces euteiches cDNA	32.2	32.2	90%	20	95%			
EU194551.1	Sus scrofa aquaporin 9 (AQP9) mRNA, complete cds	32.2	32.2	72%	20	100%			UG
AC203446.12	Salmo salar BAC CH214-363E24 (Children's Hospital Oakland Research Institute Atlantic Salmon BAC Library) complete sequence	32.2	32.2	72%	20	100%			
EU294510.1	Snowshoe hare virus segment small, complete sequence	32.2	32.2	72%	20	100%			
AC206007.4	Pongo abelii BAC clone CH276-384E20 from chromosome unknown, complete sequence	32.2	32.2	72%	20	100%			
NM_001112684.1	Sus scrofa aquaporin 9 (AQP9), mRNA >gb EU220427.1 Sus	32.2	32.2	72%	20	100%			UG

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	scrofa aquaporin 9 mRNA, complete cds								
EF609476.1	Taractichthys longipinnis voucher BM-A1077 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	32.2	32.2	72%	20	100%			
EF452871.1	Rasbora cf. bankanensis CTOL508 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial	32.2	32.2	72%	20	100%			
AC209582.2	Pongo abelii BAC clone CH276-170A3 from chromosome 16, complete sequence	32.2	32.2	72%	20	100%			
CP000800.1	Escherichia coli E24377A, complete genome	32.2	32.2	72%	20	100%			
CP000802.1	Escherichia coli HS, complete genome	32.2	60.5	86%	20	100%			
AC200440.2	Pongo abelii BAC clone CH276-229E22 from chromosome 19, complete sequence	32.2	32.2	72%	20	100%			
CR954185.3	Medicago truncatula chromosome 5 clone mth4-20m5, COMPLETE SEQUENCE	32.2	32.2	72%	20	100%			
AC202694.6	Rhesus Macaque BAC CH250-420G21 (1) complete sequence	32.2	32.2	72%	20	100%			
CP000698.1	Geobacter uranireducens Rf4, complete genome	32.2	60.5	100%	20	100%			
AC091173.10	Homo sapiens chromosome 8, clone RP11-280G9, complete sequence	32.2	32.2	72%	20	100%			
AC003989.1	Homo sapiens BAC clone CTE-7J15 from 7, complete sequence	32.2	32.2	72%	20	100%			
AC007030.3	Homo sapiens PAC clone RP5-111214 from 7, complete sequence	32.2	32.2	72%	20	100%			
AC142290.1	Pan troglodytes EAC clone RP43-180M6 from chromosome 7, complete sequence	32.2	32.2	72%	20	100%			
AC087269.5	Homo sapiens chromosome 8, clone RP11-211C9, complete sequence	32.2	32.2	72%	20	100%			
AC016136.21	Homo sapiens 12 BAC RP11-1036M20 (Roswell Park Cancer Institute Human BAC Library) complete sequence	32.2	32.2	72%	20	100%			
AC109486.2	Homo sapiens chromosome 5 clone RP11-546M4, complete sequence	32.2	32.2	72%	20	100%			
AC010229.7	Homo sapiens chromosome 5 clone CTC-312N19, complete sequence	32.2	32.2	72%	20	100%			
BA000041.2	Pan troglodytes DNA, major histocompatibility complex class I region	32.2	60.5	95%	20	100%			

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13

 Designing or Testing PCR Primers? Try your s

Alignments: **Select All**  selected sequences Distance from all results

>gb|AY721982.1|  Borjoia patinoi AFLP molecular marker genomic sequence
Length=292

Score = 40.1 bits (20), Expect = 0.084
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1 TGTTCATGATTGTTGTCATT 20
Sbjct 84 TGTTCATGATTGTTGTCATT 103

>gb|AC079945.21|  Homo sapiens 3 BAC RP11-689D3 (Roswell Park Cancer Institute
Human BAC Library) complete sequence
Length=149249

Score = 38.2 bits (19), Expect = 0.33
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGTCATT 19
Sbjct 60321 TGTTCATGATTGTTGTCATT 60303

>ref|XM_002000067.1|  Drosophila mojavensis GI22714 (Dmoj\GI22714), mRNA
Length=1083

GENE ID: 6574045 Dmoj\GI22714 | GI22714 gene product from transcript GI22714-RA
[Drosophila mojavensis] (10 or fewer PubMed links)

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCATTG 21
Sbjct 1028 TGATGATTGTTGTCATTG 1011

>ref|XM_001610598.1|  Babesia bovis seryl-tRNA synthetase, putative (BBOV_IV007240)
partial mRNA
Length=1509

GENE ID: 5478882 BBOV_IV007240 | seryl-tRNA synthetase (Babesia bovis T2Bo)

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Minus

Query 5 GATGATTGTTGTCATTGC 22
Sbjct 847 GATGATTGTTGTCATTGC 830

>gb|CP000764.1|  Bacillus cereus subsp. cytotoxis NVH 391-98, complete genome
Length=4067024

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features in this part of subject sequence:
phosphate ABC transporter, inner membrane subunit PatC

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Minus

Query 5 GATGATTGTTGTCATTGC 22
Sbjct 3046945 GATGATTGTTGTCATTGC 3046928

Features in this part of subject sequence:
conserved hypothetical protein

Score = 30.2 bits (15), Expect = 81
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 6 ATGATTGTTGTCATT 20
Sbjct 3415103 ATGATTGTTGTCATT 3415089

33
1/1

>gb|AC162884.4|  Mus musculus chromosome 5, clone RP24-169E23, complete sequence
Length=158942

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCATTG 21
|||||
Sbjct 21990 TGATGATTGTTGTCATTG 22007

>emb|AL512638.5|  Human DNA sequence from clone RP4-663N10 on chromosome 1 Contains the 5' end of the NGFB gene for nerve growth factor (beta polypeptide), the 3' end of a novel gene, a renin (REN) pseudogene and one CpG island, complete sequence
Length=177066

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCATTG 21
|||||
Sbjct 121049 TGATGATTGTTGTCATTG 121032

>gb|AC101685.9|  Mus musculus chromosome 5, clone RP23-187K3, complete sequence
Length=185522

Score = 36.2 bits (18), Expect = 1.3
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCATTG 21
|||||
Sbjct 61933 TGATGATTGTTGTCATTG 61916

>emb|CR380959.2|  Candida glabrata strain CBS138 chromosome M complete sequence
Length=1402899

Features in this part of subject sequence:
unnamed protein product

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 TGTTCATGATTGTTGTC 17
|||||
Sbjct 944270 TGTTCATGATTGTTGTC 944286

>ref|NG_008340.1|  Homo sapiens peroxisomal biogenesis factor 14 (PEX14); and DNA fragmentation factor, 45kDa, alpha polypeptide (DFFA), on chromosome 1
Length=162813

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCAT 19
|||||
Sbjct 76208 TTGATGATTGTTGTCAT 76192

>ref|XM_001990506.1|  Drosophila grimshawi GH18188 (Dgri\GH18188), mRNA
Length=3609

GENE ID: 6564447 Dgri\GH18188 | GH18188 gene product from transcript GH18188-RA [Drosophila grimshawi] (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 5.2
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGTCATTG 21
|||||
Sbjct 1667 TGTTCATGATTGTTGTTATTG 1647

>dbj|AP009853.1|  Lotus japonicus genomic DNA, chromosome 1, clone: LjT07G07, TM1730b, complete sequence
Length=52231

Score = 34.2 bits (17), Expect = 5.2
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGTCATTG 21
|||||
Sbjct 29449 TGTTCATGATTGTTGTCATTG 29429

>dbj|AP007306.2|  Lotus japonicus genomic DNA, chromosome 2, clone: LjT20J15, TM1492, complete sequence
Length=123684

Score = 34.2 bits (17), Expect = 5.2
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGTCATTG 21
 Sbjct 26853 TGTGATGATTGTTGTCATTG 26833

>gb|AC152349.12| **E** Medicago truncatula clone mth2-52p10, complete sequence
 length=105424

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 3 TTGATGATTGTTGTCAT 19
 Sbjct 20993 TTGATGATTGTTGTCAT 31009

>ref|XM_001430565.1| **G** Paramecium tetraurelia hypothetical protein (GSPATT00033057001)
 partial mRNA
 length=769

GENE ID: 5016386 GSPATT00033057001 | hypothetical protein
 [Paramecium tetraurelia strain d4-2]

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 4 TGATGATTGTTGTCATT 20
 Sbjct 62 TGATGATTGTTGTCATT 46

>ref|XM_001304113.1| **G** Trichomonas vaginalis G3 surface antigen BspA-like (TVAG_287080)
 partial mRNA
 length=2106

GENE ID: 4748877 TVAG_287080 | surface antigen BspA-like
 [Trichomonas vaginalis G3] (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCAT 19
 Sbjct 17 TTGATGATTGTTGTCAT 1

>ref|XM_001304112.1| **G** Trichomonas vaginalis G3 surface antigen BspA-like (TVAG_287070)
 partial mRNA
 length=2487

GENE ID: 4748876 TVAG_287070 | surface antigen BspA-like
 [Trichomonas vaginalis G3] (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCAT 19
 Sbjct 362 TTGATGATTGTTGTCAT 346

>gb|AC150393.2| **D** Branchiostoma floridae clone CH302-13E12, complete sequence
 length=207808

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCAT 19
 Sbjct 2802 TTGATGATTGTTGTCAT 2786

>gb|AC149306.9| **D** Medicago truncatula clone mth2-88b8, complete sequence
 length=89880

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCAT 19
 Sbjct 31394 TTGATGATTGTTGTCAT 31378

>gb|CP000117.1| **D** Anabaena variabilis ATCC 29413, complete genome
 length=6365727

Features flanking this part of subject sequence:
 377 bp at 5' side: NAD-dependent epimerase/dehydratase
 191 bp at 3' side: heterocyst formation protein HetP-like

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 3 TTGATGATTGTTGTCAT 19
 Sbjct 1208402 TTGATGATTGTTGTCAT 1208418

>gb|AC141639.3|  Mus musculus BAC clone RP23-354J7 from chromosome 18, complete sequence
Length=216358

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 6 ATGATTGTTGTCATTGC 22
|||||
Sbjct 114886 ATGATTGTTGTCATTGC 114870

>gb|AC123055.3|  Mus musculus BAC clone RP24-267D17 from chromosome 3, complete sequence
Length=187223

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCATT 20
|||||
Sbjct 27562 TGATGATTGTTGTCATT 27578

>gb|AC098882.3|  Mus musculus BAC clone RP23-122D13 from 12, complete sequence
Length=223130

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGTC 17
|||||
Sbjct 189461 TGTGATGATTGTTGTC 189445

>gb|AC159294.2|  Mus musculus BAC clone RP23-287I15 from chromosome 12, complete sequence
Length=226841

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query J TGTGATGATTGTTGTC 17
|||||
Sbjct 4956 TGTGATGATTGTTGTC 4940

>emb|AL591403.10|  Human DNA sequence from clone RP11-108G8 on chromosome 1 Contains part of the PEX14 gene for peroxisomal biogenesis factor 14, complete sequence
Length=97687

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCAT 19
|||||
Sbjct 50422 TTGATGATTGTTGTCAT 50406

>emb|CR751224.20|  Zebrafish DNA sequence from clone DKEY-241P21 in linkage group 22 Contains the calr gene for calreticulin, the trhl gene for trhl protein and the gene for a novel protein similar to vertebrate RAD23 homolog B (S. cerevisiae) (zgc:123349), complete sequence
Length=151612

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 5 GATGATTGTTGTCATTG 21
|||||
Sbjct 132079 GATGATTGTTGTCATTG 132095

>gb|AC090220.13|  Homo sapiens chromosome 18, clone RP11-712P20, complete sequence
Length=194234

Score = 34.2 bits (17), Expect = 5.2
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Plus

Query 1 TGTGATGATTGTTGTCATTG 21
|||||
Sbjct 145229 TGTGATGATTGTTGTCATTG 145249

>ref|XM_449757.1|  Candida glabrata CBS138 hypothetical protein (CAGL0M09493g) partial mRNA
Length=2127

GENE ID: 2891321 CAGL0M09493g | hypothetical protein [Candida glabrata CBS 138]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

36
117

Query 1 TGTGATGATTGTTGTC 17
 |||||
 Sbjct 1367 TGTGATGATTGTTGTC 1383

>gb|AF411806.1|  Lycopersicon esculentum BAC clone Clemson_Id 207, partial sequence
 Length=61382

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 3 TTGATGATTGTTGTCAT 19
 |||||
 Sbjct 39536 TTGATGATTGTTGTCAT 39552

>gb|AC122713.2|  Homo sapiens chromosome 5 clone RP11-39H3, complete sequence
 Length=149006

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 4 TGATGATTGTTGTCATT 20
 |||||
 Sbjct 55599 TGATGATTGTTGTCATT 55615

>gb|AC026462.5|  Homo sapiens chromosome 16 clone RP11-297L17, complete sequence
 Length=179640

Score = 34.2 bits (17), Expect = 5.2
 Identities = 20/21 (95%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 1 TGTGATGATTGTTGTCATTG 21
 |||||
 Sbjct 167710 TGTGATGATTGTTGTCATTG 167730

>gb|AC007340.8|  Homo sapiens chromosome 16 clone RP11-35805, complete sequence
 Length=172833

Score = 34.2 bits (17), Expect = 5.2
 Identities = 20/21 (95%), Gaps = 0/21 (0%)
 Strand=Plus/Minus

Query 1 TGTGATGATTGTTGTCATTG 21
 |||||
 Sbjct 166808 TGTGATGATTGTTGTCATTG 166788

>dbj|AB023036.1|  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19
 Length=20349

Score = 34.2 bits (17), Expect = 5.2
 Identities = 20/21 (95%), Gaps = 0/21 (0%)
 Strand=Plus/Minus

Query 1 TGTGATGATTGTTGTCATTG 21
 |||||
 Sbjct 81098 TGTGATGATTGTTGTCATTG 81078

>gb|AC092534.4|  Homo sapiens BAC clone RP13-629D7 from 2, complete sequence
 Length=33235

Score = 34.2 bits (17), Expect = 5.2
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 TGTGATGATTGTTGTC 17
 |||||
 Sbjct 2009 TGTGATGATTGTTGTC 2025

>dbj|AP004488.1|  Lotus japonicus genomic DNA, chromosome 2, clone: LjT02F05, TM0020,
 complete sequence
 Length=80920

Score = 34.2 bits (17), Expect = 5.2
 Identities = 20/21 (95%), Gaps = 0/21 (0%)
 Strand=Plus/Minus

Query 1 TGTGATGATTGTTGTCATTG 21
 |||||
 Sbjct 2095 TGTGATGATTGTTGTCATTG 2075

>gb|AC139355.8|  Medicago truncatula clone mth2-3603, complete sequence
 Length=108135

Score = 34.2 bits (17), Expect = 5.2
 Identities = 20/21 (95%), Gaps = 0/21 (0%)
 Strand=Plus/Plus

Query 1 TGTGATGATTGTTGTCATTG 21
 |||||
 Sbjct 22585 TGTGATGATTGTTGTCATTG 22605

>emb|BX001038.5|  Zebrafish DNA sequence from clone CU211-12M10 in linkage group
 19 Contains the 3' end of the gene for a novel protein similar

34
118

to vertebrate odz and odd Oz/ten-m homolog 2 (Drosophila)
(ODZ2), complete sequence
Length=180659

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCATT 20
|||||
Sbjct 45424 TGATGATTGTTGTCATT 45440

Score = 28.2 bits (14), Expect = 319
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTT 14
|||||
Sbjct 62390 TGTTCATGATTGTT 62377

>gb|AC169177.4|  Medicago truncatula chromosome 7 clone mth2-1p4, complete sequence
Length=124443

Score = 34.2 bits (17), Expect = 5.2
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGTCATTG 21
|||||
Sbjct 13120 TGTTCATGATTGTTGTCATTG 13100

>gb|AC135237.6|  Mus musculus BAC clone RP23-306F11 from chromosome 3, complete sequence
Length=199436

Score = 34.2 bits (17), Expect = 5.2
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCATT 20
|||||
Sbjct 155817 TGATGATTGTTGTCATT 155833

>emb|FM180568.1|  Escherichia coli 0127:H6 E2348/69 complete genome, strain E2348/69
Length=4965553

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features flanking this part of subject sequence:
2036 bp at 5' side: transposase of ISEc13
978 bp at 3' side: 3-methyl-adenine DNA glycosylase II

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 2267685 TGATGATTGTTGTCAT 2267670

Features in this part of subject sequence:
T3SS structure protein EscS

Score = 36.2 bits (15), Expect = 81
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 GTTGATGATTGTTGT 16
|||||
Sbjct 4130874 GTTGATGATTGTTGT 4130888

>ref|NG_009006.1|  Homo sapiens ankyrin 2, neuronal (ANK2) on chromosome 4
Length=572658

Features in this part of subject sequence:
ankyrin 2 isoform 3

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGT 16
|||||
Sbjct 472136 TGTTCATGATTGTTGT 472121

>ref|NM_069908.5|  Caenorhabditis elegans hypothetical protein (B0001.7) mRNA, complete cds
Length=2378

GENE ID: 178165 B0001.7 | hypothetical protein [Caenorhabditis elegans]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 20

38
119

Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCA 18
|||||
Sbjct 134 TTGATGATTGTTGTCA 119

>emb|AM920427.1|  Penicillium chrysogenum Wisconsin 54-1255 complete genome, contig
Pc00c12
Length=3288431

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features in this part of subject sequence:
Pc12g12230

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 5 GATGATTGTTGTCATT 20
|||||
Sbjct 2940111 GATGATTGTTGTCATT 2940126

Features in this part of subject sequence:
Pc12g00460

Score = 28.2 bits (14), Expect = 319
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 2 GTTGATGATTGTTG 15
|||||
Sbjct 101916 GTTGATGATTGTTG 101903

>gb|EU263801.1| Nesiarchus nasutus isolate NES2 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Length=937

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGT 16
|||||
Sbjct 314 TGTGATGATTGTTGT 299

>gb|EU263800.1| Nesiarchus nasutus isolate NES1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Length=944

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGT 16
|||||
Sbjct 314 TGTGATGATTGTTGT 299

>gb|AC171619.9|  Medicago truncatula clone mth2-160a1, complete sequence
Length=114238

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 95866 TGATGATTGTTGTCAT 95881

>dbj|AB435541.1| Aspergillus oryzae Aosh1p gene for succinate dehydrogenase iron-sulfur subunit, carboxin resistant mutation form, complete cds, strain: CR14
Length=2729

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 6 ATGATTGTTGTCATTG 21
|||||
Sbjct 2438 ATGATTGTTGTCATTG 2423

>dbj|AB435540.1| Aspergillus oryzae Aosh1p gene for succinate dehydrogenase iron-sulfur subunit, carboxin resistant mutation form, complete cds, strain: CR9
Length=2729

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 6 ATGATTGTTGTCATTG 21
|||||
Sbjct 2438 ATGATTGTTGTCATTG 2423

>dbj|AP009240.1|  Escherichia coli SE11 DNA, complete genome
Length=4887515

29

Features in this part of subject sequence:
conserved hypothetical protein

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 2401401 TGATGATTGTTGTCAT 2401386

>gb|AC225830.3|  Pan troglodytes BAC clone CH251-61K15 from chromosome 7, complete
sequence
Length=178757

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTGATGATTGTTGT 16
|||||
Sbjct 156782 TGTGATGATTGTTGT 156797

>gb|CP001164.1|  Escherichia coli O157:H7 str. EC4115, complete genome
Length=5572075

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features flanking this part of subject sequence:
2753 bp at 5' side: uridine kinase
969 bp at 3' side: DNA-3-methyladenine glycosylase 2

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 2786398 TGATGATTGTTGTCAT 2786383

Features in this part of subject sequence:
EscS protein

Score = 30.2 bits (15), Expect = 81
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 2 GTTGATGATTGTTGT 16
|||||
Sbjct 4720212 GTTGATGATTGTTGT 4720226

>gb|EU697538.1| Haemulon melanurum cytochrome oxidase subunit I (COI) gene, partial
cds; mitochondrial
Length=652

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGT 16
|||||
Sbjct 461 TGTGATGATTGTTGT 446

>emb|CU695221.7|  Zebrafish DNA sequence from clone CH73-308M11 in linkage group
3, complete sequence
Length=87846

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 23802 TGATGATTGTTGTCAT 23817

>gb|EU870371.1| Spinacia oleracea phospholipase C (plc) mRNA, complete cds
Length=2313

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGT 16
|||||
Sbjct 62 TGTGATGATTGTTGT 47

>ref|XM_002061364.1|  Drosophila willistoni GK20745 (Dwil\GK20745), mRNA
Length=2226

GENE ID: 6638294 Dwil\GK20745 | GK20745 gene product from transcript GK20745-PA
(Drosophila willistoni) (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTGATGATTGTTGT 16

40
121

Sbjct 2129 TGTTCATGATTGTTGT 2114

>ref|XM_002053001.1| **G** Drosophila virilis GJ23660 (Dvir\GJ23660), mRNA
Length=5481
GENE ID: 6631141 Dvir\GJ23660 | GJ23660 gene product from transcript GJ23660-RA
[Drosophila virilis] (10 or fewer PubMed links)
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 2 GTTGATGATTGTTGT 17
Sbjct 5016 GTTGATGATTGTTGT 5031

>ref|XM_002004765.1| **G** Drosophila mojavensis GI19393 (Dmoj\GI19393), mRNA
Length=7299
GENE ID: 6578902 Dmoj\GI19393 | GI19393 gene product from transcript GI19393-RA
[Drosophila mojavensis] (10 or fewer PubMed links)
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGT 16
Sbjct 1031 TGTTCATGATTGTTGT 1016

>ref|XM_001996606.1| **G** Drosophila grimshawi GH22517 (Dgri\GH22517), mRNA
Length=1713
GENE ID: 6570428 Dgri\GH22517 | GH22517 gene product from transcript GH22517-RA
[Drosophila grimshawi] (10 or fewer PubMed links)
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTTGT 16
Sbjct 1043 TGTTCATGATTGTTGT 1028

>ref|XM_001991839.1| **G** Drosophila grimshawi GH11829 (Dgri\GH11829), mRNA
Length=771
GENE ID: 6565309 Dgri\GH11829 | GH11829 gene product from transcript GH11829-RA
[Drosophila grimshawi] (10 or fewer PubMed links)
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 7 TGATTGTTGTCATTGC 22
Sbjct 110 TGATTGTTGTCATTGC 95

>ref|XM_001983867.1| **G** Drosophila grimshawi GH15311 (Dgri\GH15311), mRNA
Length=2145
GENE ID: 6556631 Dgri\GH15311 | GH15311 gene product from transcript GH15311-RA
[Drosophila grimshawi] (10 or fewer PubMed links)
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 GTTGATGATTGTTGT 16
Sbjct 1475 GTTGATGATTGTTGT 1460

>ref|NW_001263840.1| **D** Dictyostelium discoideum AX4 chromosome 4 DDB0232607.02, whole
genome shotgun sequence
Length=285333

Features in this part of subject sequence:
hypothetical protein
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 GTTGATGATTGTTGT 16
Sbjct 275356 GTTGATGATTGTTGT 275371

>ref|NW_001263736.1| **D** Dictyostelium discoideum AX4 chromosome 6 DDB0232839.02, whole
genome shotgun sequence
Length=599037

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features in this part of subject sequence:
gelsolin-related protein

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

```

Query    1      TGTTCGATGATTGTTGT 16
          |||||
Sbjct    481544 TGTTCGATGATTGTTGT 481559

```

Features in this part of subject sequence:
hypothetical protein

Score = 28.2 bits (14), Expect = 319
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query	3	TTGATGATTGTTGT	16
Subject	235028	TTGATGATTGTTGT	235041

```
>ref|NW_001263690.1| Dictyostelium discoideum AX4 chromosome 6 DDB0232885.02, whole
genome shotgun sequence
length=47451
```

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query	i	TGTTGATGATTGTTGT	16
Subject	7259	TGTTGATGATTGTTGT	7274

ref|XM_001895817.1|  *Brugia malayi* hypothetical protein partial mRNA
Length=1030

GENE ID: 6099299 Bm1 21985 | hypothetical protein [Brugia malayi]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query	1	TGTTGATGATTGTTGT	16
Sbjct	39	TGTTGATGATTGTTGT	24

```
>gb|CP000970.1| Escherichia coli SMS-3-5, complete genome
length=5068389
```

Features in this part of subject sequence:
sensory box-containing diguanylate cyclase

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

```

Query    4          TGATGATTGTTGTCAT  19
          |||||
Sbjct  1009235  TGATGATTGTTGTCAT  1009250

```

```
>gb|CP000948.1| Escherichia coli str. K12 substr. DH10B, complete genome
length=4685137
```

Sort alignments for this subject sequence by:

E value	Score	Percent identity	Query start position	Subject start position
---------	-------	------------------	----------------------	------------------------

Features in this part of subject sequence:
predicted diguanylate cyclase, GGDEF domain signalling pr...

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```

Query 4      TGATGATTGTTGTCAT 19
             |||||
Sbjct. 2234747 TGATGATTGTTGTCAT 2234732

```

Features in this part of subject sequence:
predicted transporter

Score = 28.2 bits (14), Expect = 319
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query	1	TGTTGATGATTGTT	14
Shjet	3807081	TGTTGATGATTGTT	3807088

```
>gb|AC212783.3| Homo sapiens FOSMID clone ABC10-44680300N13 from chromosome 9,
complete sequence
length=41117
```

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTGTGATGATTGTTGT 16

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

11/12/2008

```
>gb|CP000924.1|  Thermoanaerobacter pseudethanolicus ATCC 33223, complete genome
length=2362816
```

Features in this part of subject sequence:
Tfp pilus assembly protein Pile-like protein

<http://blast.ncbi.nlm.nih.gov/Blast.cgi>

11/12/2008

43
12X

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 7 TGATTGTTGTCATTGC 22
Sbjct 1133211 TGATTGTTGTCATTGC 1133226

>gb|CP000923.1|  Thermoanaerobacter sp. X514, complete genome
Length=2457259

Features in this part of subject sequence:
Tfp pilus assembly protein Pile-like protein

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 7 TGATTGTTGTCATTGC 22
Sbjct 1539663 TGATTGTTGTCATTGC 1539678

>emb|CU366904.1| Aphanomyces euteiches cDNA
Length=864

Score = 32.2 bits (16), Expect = 20
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCATTGC 22
Sbjct 93 TTGATGATTGTTTTCATTGC 74

>emb|CU359699.1| Aphanomyces euteiches cDNA
Length=811

Score = 32.2 bits (16), Expect = 20
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCATTGC 22
Sbjct 176 TTGATGATTGTTTTCATTGC 157

>emb|CU359669.1| Aphanomyces euteiches cDNA
Length=842

Score = 32.2 bits (16), Expect = 20
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 3 TTGATGATTGTTGTCATTGC 22
Sbjct 464 TTGATGATTGTTTTCATTGC 445

>gb|EU194551.1|  Sus scrofa aquaporin 9 (AQP9) mRNA, complete cds
Length=1261

GENE ID: 100127153 AQP9 | aquaporin 9 [Sus scrofa] (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 7 TGATTGTTGTCATTGC 22
Sbjct 781 TGATTGTTGTCATTGC 796

>gb|AC203446.12|  Salmo salar BAC CH2i4-363E24 (Children's Hospital Oakland Research Institute Atlantic Salmon BAC Library) complete sequence
Length=215491

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 7 TGATTGTTGTCATTGC 22
Sbjct 60413 TGATTGTTGTCATTGC 60398

>gb|EU294510.1| Snowshoe hare virus segment small, complete sequence
Length=892

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 GTTGATGATTGTTGTC 17
Sbjct 407 GTTGATGATTGTTGTC 392

>gb|AC206007.4|  Pongo abelii BAC clone CH276-384E20 from chromosome unknown,
complete sequence
Length=216892

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

44
125

Query 1 TGTTCGATGATTGTTGT 16
|||||
Sbjct 168118 TGTTCGATGATTGTTGT 168103

>ref|NM_001112684.1| **UG** Sus scrofa aquaporin 9 (AQP9). mRNA
gb|EU220427.1| **UG** Sus scrofa aquaporin 9 mRNA, complete cds
Length=904

GENE ID: 100127153 AQP9 | aquaporin 9 [Sus scrofa] (10 or fewer PubMed links)
Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 7 TGATTGTTGTCATTGC 22
|||||
Sbjct 600 TGATTGTTGTCATTGC 615

>gb|EF609476.1| Taractichthys longipinnis voucher BW-A1077 cytochrome oxidase subunit 1 (COI) gene, partial cds; mitochondrial
Length=655

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTTCGATGATTGTTGT 16
|||||
Sbjct 461 TGTTCGATGATTGTTGT 446

>gb|EF452871.1| Rasbora cf. bankanensis CTOL508 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial
Length=676

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 TGTTCGATGATTGTTGT 16
|||||
Sbjct 474 TGTTCGATGATTGTTGT 459

>gb|AC209582.2| **D** Pongo abelii BAC clone CH276-170A3 from chromosome 16, complete sequence
Length=197664

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTCGATGATTGTTGT 16
|||||
Sbjct 39779 TGTTCGATGATTGTTGT 39794

>gb|CP000800.1| **D** Escherichia coli E24377A, complete genome
Length=4979619

Features in this part of subject sequence:
sensory box-containing diguanylate cyclase

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 2328820 TGATGATTGTTGTCAT 2328805

>gb|CP000802.1| **D** Escherichia coli HS, complete genome
Length=4643538

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features flanking this part of subject sequence:
2752 bp at 5' side: uridine kinase
977 bp at 3' side: DNA-3-methyladenine glycosylase 2

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 2189957 TGATGATTGTTGTCAT 2189942

Features in this part of subject sequence:
major facilitator family transporter

Score = 28.2 bits (14), Expect = 319
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 1 TGTTCGATGATTGTT 14
|||||
Sbjct 3740784 TGTTCGATGATTGTT 3740771

45
120

>gb|AC200440.2|  Pongo abelii BAC clone CH276-229E22 from chromosome 19, complete sequence
Length=187160

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTCATGATTGTTGT 16
|||||
Sbjct 158173 TGTTCATGATTGTTGT 158188

>emb|CR954185.3|  Medicago truncatula chromosome 5 clone mth4-20m5, COMPLETE SEQUENCE
Length=210707

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 4 TGATGATTGTTGTCAT 19
|||||
Sbjct 159273 TGATGATTGTTGTCAT 159288

>gb|AC202694.6|  Rhesus Macaque BAC CH250-420G21 () complete sequence
Length=152690

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 2 GTTGATGATTGTTGTC 17
|||||
Sbjct 100424 GTTGATGATTGTTGTC 100439

>gb|CP000698.1|  Geobacter uraniireducens Rf4, complete genome
Length=5136364

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features in this part of subject sequence:
hypothetical protein

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 7 TGATTGTTGTCATTGC 22
|||||
Sbjct 2002650 TGATTGTTGTCATTGC 2002635

Features flanking this part of subject sequence:
510 bp at 5' side: **hypothetical protein**
209 bp at 3' side: **hypothetical protein**

Score = 28.2 bits (14), Expect = 319
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 1 TGTTCATGATTGTT 14
|||||
Sbjct 4406333 TGTTCATGATTGTT 4406320

>gb|AC091173.10|  Homo sapiens chromosome 8, clone RP11-280G9, complete sequence
Length=142265

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTCATGATTGTTGT 16
|||||
Sbjct 4479 TGTTCATGATTGTTGT 4494

>gb|AC003989.1|  Homo sapiens BAC clone CTB-7J15 from 7, complete sequence
Length=118103

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTCATGATTGTTGT 16
|||||
Sbjct 110629 TGTTCATGATTGTTGT 110644

>gb|AC007030.3|  Homo sapiens PAC clone RPS-111214 from 7, complete sequence
Length=117853

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTCATGATTGTTGT 16
|||||
Sbjct 104538 TGTTCATGATTGTTGT 104553

46
127

>gb|AC142290.1|  Pan troglodytes BAC clone RP43-160M6 from chromosome 7, complete sequence
Length=234045

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTGATGATTGTTGT 16
|||||
Sbjct 178654 TGTTGATGATTGTTGT 178669

>gb|AC087269.5|  Homo sapiens chromosome 8, clone RP11-211C9, complete sequence
Length=187924

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTGATGATTGTTGT 16
|||||
Sbjct 129049 TGTTGATGATTGTTGT 129064

>gb|AC016136.21|  Homo sapiens 12 BAC RP11-1036M20 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=176704

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTGATGATTGTTGT 16
|||||
Sbjct 114770 TGTTGATGATTGTTGT 114785

>gb|AC109486.2|  Homo sapiens chromosome 5 clone RP11-546M4, complete sequence
Length=202405

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 5 GATGATTGTTGTCAAT 20
|||||
Sbjct 57610 GATGATTGTTGTCAAT 57625

>gb|AC010229.7|  Homo sapiens chromosome 5 clone CTC-312N19, complete sequence
Length=70523

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTGATGATTGTTGT 16
|||||
Sbjct 28401 TGTTGATGATTGTTGT 28416

>dbj|BA000041.2|  Pan troglodytes DNA, major histocompatibility complex class I region
Length=1750601

Features flanking this part of subject sequence:
22995 bp at 5' side: HCGV
72147 bp at 3' side: hypothetical protein

Score = 32.2 bits (16), Expect = 20
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 TGTTGATGATTGTTGT 16
|||||
Sbjct 1439900 TGTTGATGATTGTTGT 1439915

Select All (6) selected sequences Distance tree of results

138

BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search](#) [Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (20 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|15412

Description

None

Molecule type

nucleic acid

Query Length

20

Database Name

nr

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Program

BLASTN 2.2.19+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997). "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs". Nucleic Acids Res. 25:3389-3402. Other reports: [Search Summary](#) [[Taxonomy reports](#)] [[Distance tree of results](#)]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Database

Posted date	Dec 10, 2008 6:42 PM
Number of letters	250,069,024
Number of sequences	7,821,680
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

Results Statistics

Length adjustment	18
Effective length of query	2
Effective length of database	25409278784
Effective search space	50818557568
Effective search space used	50818557568

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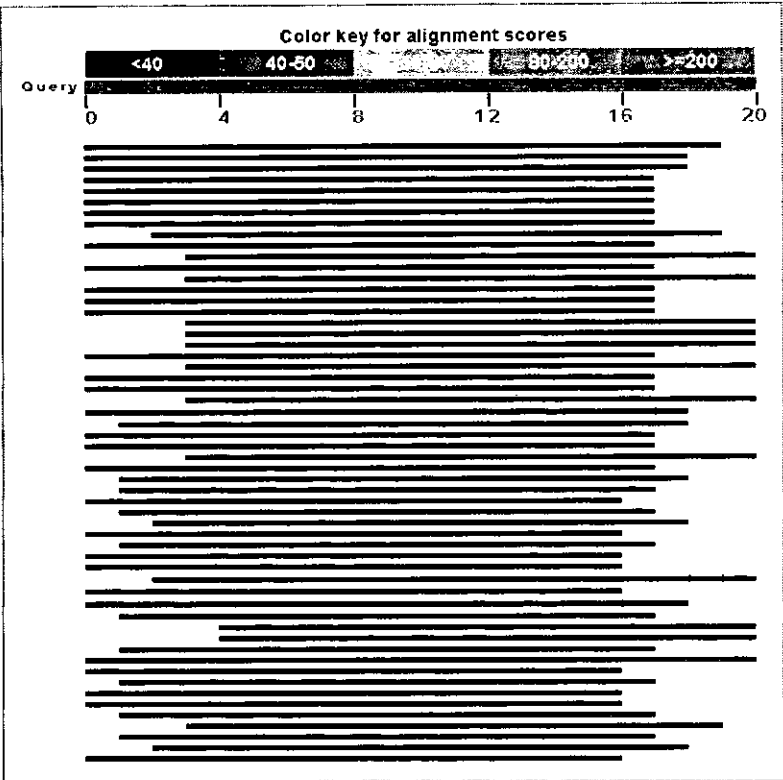
Graphic Summary

Distribution of 120 Blast Hits on the Query Sequence

43
18

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top. Clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



44
29

Descriptions

Legend for links to other resources: **U** UniGene **G** GEO **G** Gene **S** Structure **M** Map Viewer

Sequences producing significant alignments:

(Click headers to sort columns)

CU329670.1	Schizosaccharomyces pombe chromosome I	38.2	207	95%	0.17	100%	
XM_608880.1	Plasmodium berghei strain ANKA hypothetical protein (PB300712.00.0) partial mRNA	36.2	36.2	90%	0.65	100%	G
XM_720897.1	Plasmodium yoelii yoelii str. 17XNL CCAMT-box DNA binding protein subunit B (PY05521) partial mRNA	36.2	36.2	90%	0.65	100%	G
NM_001106110.2	Rattus norvegicus doublecortin domain containing 2 (Dcdc2), mRNA	34.2	34.2	85%	2.6	100%	U G
AM437208.2	Vitis vinifera contig VV79X007262.2, whole genome shotgun sequence	34.2	34.2	85%	2.6	100%	
AM442592.2	Vitis vinifera contig VV78X237640.4, whole genome shotgun sequence	34.2	34.2	85%	2.6	100%	
AC193648.3	Gallus gallus BAC clone CH261-104F4 from chromosome 2, complete sequence	34.2	60.5	85%	2.6	100%	
AC196590.7	Rhesus Macaque BAC CH250-202D9 () complete sequence	34.2	34.2	85%	2.6	100%	
AM481562.1	Vitis vinifera, whole genome shotgun sequence, contig VV78X069585.4, clone ENTAV 115	34.2	34.2	85%	2.6	100%	
AM438043.1	Vitis vinifera contig VV78X086428.2, whole genome shotgun sequence	34.2	34.2	85%	2.6	100%	
NM_001007122.2	Homo sapiens fibronectin type III and SPRY domain containing 2 (FSD2), mRNA >gb BC130569.1 Homo sapiens fibronectin type III and SPRY domain containing 2, mRNA (cDNA clone MGC:163441 IMAGE:40146600), complete cds	34.2	34.2	85%	2.6	100%	U G
AC192771.2	Rhesus Macaque BAC CH250-438D19 () complete sequence	34.2	34.2	85%	2.6	100%	
XR_024654.1	PREDICTED: Pan troglodytes similar to SPRY domain containing 1 (LOC453595), mRNA	34.2	34.2	85%	2.6	100%	G
AC142507.13	Medicago truncatula clone mth2-30h19, complete sequence	34.2	34.2	85%	2.6	100%	
AC100734.4	Mus musculus chromosome 15, clone RP24-316L11, complete sequence	34.2	34.2	85%	2.6	100%	
AC125220.3	Mus musculus BAC clone RP23-70H20 from 15, complete sequence	34.2	34.2	85%	2.6	100%	
AC134099.2	Homo sapiens 3 BAC RP11-221B6 (Roswell Park Cancer Institute Human BAC Library) complete sequence	34.2	34.2	85%	2.6	100%	
AK122875.1	Homo sapiens cDNA FLJ16510 fis, clone HEART1000132, highly similar to Homo sapiens hypothetical protein LOC123722 (LOC123722), mRNA	34.2	34.2	85%	2.6	100%	U G
AC105339.9	Homo sapiens chromosome 15, clone RP11-752G15, complete sequence	34.2	34.2	85%	2.6	100%	
AC161347.2	Mus musculus chromosome 15, clone RP23-273M5, complete sequence	34.2	34.2	85%	2.6	100%	
AC044907.16	Homo sapiens chromosome 15, clone RP11-127F21, complete sequence	34.2	34.2	85%	2.6	100%	
BX950859.12	Zebrafish DNA sequence from clone CH211-134M1 in linkage group 11, complete sequence	34.2	34.2	85%	2.6	100%	
AL592522.12	Mouse DNA sequence from clone RP23-210M6 on chromosome 11 Contains the Olfr222 and Olfr223 genes for olfactory receptor 222 and 223, a high mobility group box 1 (Hmgb1) pseudogene, the Cias1 gene for cold autoinflammatory syndrome 1 homolog (human), a novel gene (4933439C10Rik), the gene for a novel protein (D130067D09), a ribosomal protein L18 (Rpl18) pseudogene, an ariadne homolog 2 (Drosophila) (Arih2) pseudogene, the gene for a novel zinc finger domain-containing protein, the 3' end of the gene for a novel protein and one CpG island, complete sequence	34.2	34.2	85%	2.6	100%	
AC096561.1	Homo sapiens BAC clone RP11-257D7 from 2, complete sequence	34.2	34.2	85%	2.6	100%	
BX005135.5	Zebrafish DNA sequence from clone CH211-89P16 in linkage group 11, complete sequence	34.2	60.5	90%	2.6	100%	
AP001684.1	Homo sapiens genomic DNA, chromosome 21q, section 28/105	34.2	34.2	85%	2.6	100%	G
AC142096.25	Medicago truncatula clone mth2-6m16, complete sequence	34.2	66.7	85%	2.6	100%	
M80517.1	Epstein-Barr virus, artifactual joining of B95-8 complete genome and the sequences from Raji of the large deletion found in B95-8	34.2	34.2	85%	2.6	100%	
AL833295.1	Homo sapiens mRNA; cDNA DKFZp451H129 (from clone DKFZp451H129)	34.2	34.2	85%	2.6	100%	U G
M11924.1	Epstein-Barr virus B95-8, 12kb short unique region	34.2	34.2	85%	2.6	100%	
AP000705.2	Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:B745D19, LL56-APP region, complete sequence	34.2	34.2	85%	2.6	100%	
NC_009013.1	Homo sapiens component of oligomeric golgi complex 8 (COG8) on chromosome 16	32.2	32.2	80%	10	100%	
AC231672.1	Solanum tuberosum chromosome 11 clone RH186L12, complete sequence	32.2	32.2	80%	10	100%	
XM_002072183.1	Drosophila willistoni GK22446 (Dwil\GK22446), mRNA	32.2	32.2	80%	10	100%	G
XM_002065621.1	Drosophila willistoni GK14555 (Dwil\GK14555), mRNA	32.2	32.2	80%	10	100%	G
AC221040.4		32.2	32.2	80%	10	100%	

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132

	and a CpG island, complete sequence								
AC105750.2	Homo sapiens chromosome 3 clone RP11-776K4, complete sequence	32.2	32.2	80%	10	100%			
AC112217.2	Homo sapiens chromosome 3 clone CTD-2028L5, complete sequence	32.2	32.2	80%	10	100%			
AK036441.1	Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830108M16 product: hypothetical protein, full insert sequence	32.2	32.2	80%	10	100%			
AC106868.5	Homo sapiens BAC clone RP11-174E22 from 4, complete sequence	32.2	32.2	80%	10	100%			
AC105753.2	Homo sapiens chromosome 3 clone RP11-189A1, complete sequence	32.2	32.2	80%	10	100%			
AC007540.3	Homo sapiens 12q24.1 BAC RPC111-128P10 (Roswell Park Cancer Institute Human BAC Library) complete sequence	32.2	58.5	80%	10	100%			
AC099775.2	Homo sapiens chromosome 3 clone RP11-169G24, complete sequence	32.2	32.2	80%	10	100%			
AC044810.7	Homo sapiens chromosome 11, clone RP11-494M8, complete sequence	32.2	32.2	80%	10	100%			
AC021427.10	Homo sapiens chromosome 11, clone RP11-399N15, complete sequence	32.2	32.2	80%	10	100%			
AL513128.11	Human DNA sequence from clone RP11-301N24 on chromosome 10. Contains the 3' end of the SPAG6 gene for sperm associated antigen 6 (pf16, MGC26276, Repro-SA-1, DKF2p4341153), the 3' end of a novel gene, the 3' end of the PIP5K2A gene for phosphatidylinositol-4-phosphate 5-kinase type II alpha and two CpG islands, complete sequence	32.2	32.2	80%	10	100%			
AL162425.15	Human DNA sequence from clone RP11-523L1 on chromosome 9. Contains the TNC gene for tenascin C (hexabrachion) (TN, HXB) and a novel gene, complete sequence	32.2	32.2	80%	10	100%			
AL133472.12	Human DNA sequence from clone RP1-177C7 on chromosome 6. Contains the 5' end of the gene for a novel protein (FLL30976) and the 5' end of the KIAA0274 gene (similar to the novel protein CG17840). Contains a CpG island, complete sequence	32.2	32.2	80%	10	100%			
AC154546.2	Mus musculus BAC clone RP23-431I7 from chromosome 16, complete sequence	32.2	32.2	80%	10	100%			
AC026464.7	Homo sapiens chromosome 16 clone RP11-343C2, complete sequence	32.2	32.2	80%	10	100%			
AC175456.2	Gallus gallus BAC clone CH261-8a20 from chromosome u1, complete sequence	32.2	32.2	80%	10	100%			
AC026474.7	Homo sapiens chromosome 16 clone RP11-7005, complete sequence	32.2	32.2	80%	10	100%			
AC008756.9	Homo sapiens chromosome 16 clone CTD-3028M10, complete sequence	32.2	32.2	80%	10	100%			
AC018693.8	Homo sapiens BAC clone RP11-555N21 from 2, complete sequence	32.2	32.2	80%	10	100%			
AC151391.3	Oryctolagus cuniculus clone LB1-231P8, complete sequence	32.2	32.2	80%	10	100%			
AC009107.11	Homo sapiens chromosome 16 clone RP11-459P6, complete sequence	32.2	32.2	80%	10	100%			
AC124104.11	Mus musculus chromosome 15, clone RP24-281D14, complete sequence	32.2	32.2	80%	10	100%			
BX648070.1	Homo sapiens mRNA; cDNA DKF2p686i15210 (from clone DKF2p686i15210)	32.2	32.2	80%	10	100%			
AL592283.5	Mouse DNA sequence from clone RP23-396C23 on chromosome 4. Contains the 5' end of the Nfib gene for nuclear factor 1/B, a novel gene and a CpG island, complete sequence	32.2	32.2	80%	10	100%			
AC010679.6	Homo sapiens BAC clone RP11-128O11 from 2, complete sequence	32.2	32.2	80%	10	100%			
AC012087.10	Homo sapiens 3 BAC RP11-317L10, RP11-150K6, RP11-68D12 (Roswell Park Cancer Institute Human BAC Library) complete sequence	32.2	32.2	80%	10	100%			
AC092833.4	Homo sapiens BAC clone RP13-490C19 from 2, complete sequence	32.2	32.2	80%	10	100%			
AC153487.1	Taeniopygia guttata clone TG__Ba0319A15, complete sequence	32.2	32.2	80%	10	100%			

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133**Now** Designing or Testing PCR Primers? Try your s

Alignments Select All Get selected sequences Distance tree of results

>emb|CU329670.1| ☒ Schizosaccharomyces pombe chromosome I
 Length=5579133

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Features flanking this part of subject sequence:
 491 bp at 5' side: glutamine amidotransferase (predicted)
 177 bp at 3' side: N-acetylglucosamine-phosphate mutase (predicted)

Score = 38.2 bits (19), Expect = 0.17
 Identities = 19/19 (100%), Gaps = 0/19 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGATG 19
 |||||
 Sbjct 431385 AAATTGCAAAGAACTGATG 431367

Features in this part of subject sequence:
 microtubule-associated protein Asel (predicted)

Score = 30.2 bits (15), Expect = 40
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 1 AAATTGCAAAGAACT 15
 |||||
 Sbjct 1880380 AAATTGCAAAGAACT 1880394

Features in this part of subject sequence:
 ATP-dependent DNA helicase Hrp3

Score = 30.2 bits (15), Expect = 40
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 5 TGCAAAGAACTGATG 19
 |||||
 Sbjct 5382367 TGCAAAGAACTGATG 5382401

Features in this part of subject sequence:
 Dopey family protein

Score = 28.2 bits (14), Expect = 160
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 2 AATTGCAAAGAACT 15
 |||||
 Sbjct 494799 AATTGCAAAGAACT 494786

Features in this part of subject sequence:
 ski complex subunit Ski7 (predicted)

Score = 28.2 bits (14), Expect = 160
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 2 AATTGCAAAGAACT 15
 |||||
 Sbjct 5324425 AATTGCAAAGAACT 5324412

Features in this part of subject sequence:
 DNA polymerase zeta catalytic subunit Rev3

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 4 TTGCAAAGAACTG 16
 |||||
 Sbjct 3134217 TTGCAAAGAACTG 3134205

Features flanking this part of subject sequence:
 1537 bp at 5' side: phenylalanine-tRNA ligase beta subunit (predicted)
 87 bp at 3' side: cystathionine gamma-synthase (predicted)

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 1 AAATTGCAAAGAA 13

53
134

Sbjct 4101660  AAAATTGCAAAGAA 4101672

>ref|XM_668880.1|  Plasmodium berghei strain ANKA hypothetical protein (PB300712.00.0)
partial mRNA
Length=990

GENE ID: 3422397 PB300712.00.0 | hypothetical protein
[Plasmodium berghei strain ANKA] (10 or fewer PubMed links)

Score = 36.2 bits (18), Expect = 0.65
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGAT 18

Sbjct 136 AAATTGCAAAGAACTGAT 153

>ref|XM_720897.1|  Plasmodium yoelii yoelii str. 17XNL CCAAT-box DNA binding protein
subunit B (PY05521) partial mRNA
length=2538

GENE ID: 3791330 PY05521 | CCAAT-box DNA binding protein subunit B
[Plasmodium yoelii yoelii str. 17XNL] (10 or fewer PubMed links)

Score = 36.2 bits (18), Expect = 0.65
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGAT 18

Sbjct 136 AAATTGCAAAGAACTGAT 153

>ref|NM_001106110.2|  Rattus norvegicus doublecortin domain containing 2 (Dcdc2), mRNA
length=6788

GENE ID: 291130 Dcdc2 | doublecortin domain containing 2 [Rattus norvegicus]
(10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17

Sbjct 3832 AAATTGCAAAGAACTGA 3816

>emb|AM437208.2| Vitis vinifera contig VV79X007262.2, whole genome shotgun sequence
Length=3515

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17

Sbjct 1426 AAATTGCAAAGAACTGA 1410

>emb|AM442592.2| Vitis vinifera contig VV78X237640.4, whole genome shotgun sequence
Length=8553

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGA 17

Sbjct 5913 AAATTGCAAAGAACTGA 5929

>gb|AC193648.3|  Gallus gallus BAC clone CH261-104F4 from chromosome z, complete
sequence
Length=254320

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17

Sbjct 106765 AAATTGCAAAGAACTGA 106749

Score = 26.3 bits (13), Expect = .631
Identities = 15/17 (88%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17

Sbjct 127079 AAATTGCAAAGCACTGA 127063

>gb|AC196590.7|  Rhesus Macaque BAC CH250-202D9 () complete sequence
Length=159816

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)

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135

Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 34048 AAATTGCAAAGAACTGA 34032

>emb|AM481562.1|  Vitis vinifera, whole genome shotgun sequence, contig VV78X069585.4,
 clone ENTAV 115
 Length=77691

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGATG 19
 |||||
 Sbjct 20448 ATTGCAAAGAACTGATG 20432

>emb|AM438043.1|  Vitis vinifera contig VV78X086428.2, whole genome shotgun sequence
 Length=3842

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 1262 AAATTGCAAAGAACTGA 1246

>ref|NM_001007122.2|  Homo sapiens fibronectin type III and SPRY domain containing
 2 (FSD2), mRNA

gb|BC130569.1|  Homo sapiens fibronectin type III and SPRY domain containing
 2, mRNA (cDNA clone MGC:163441 IMAGE:40146600), complete cds
 Length=2493

GENE ID: 123722 FSD2 | fibronectin type III and SPRY domain containing 2
 (Homo sapiens) (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATGG 20
 |||||
 Sbjct 1070 TTGCAAAGAACTGATGG 1086

>gb|AC192771.2|  Rhesus Macaque BAC CH250-438D19 () complete sequence
 Length=139492

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 139231 AAATTGCAAAGAACTGA 139215

>ref|XR_024654.1|  PREDICTED: Pan troglodytes similar to SPRY domain containing
 1 (LOC453595), mRNA
 Length=6229

GENE ID: 453595 LOC453595 | similar to SPRY domain containing 1
 (Pan troglodytes)

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATGG 20
 |||||
 Sbjct 1085 TTGCAAAGAACTGATGG 1101

>gb|AC142507.13|  Medicago truncatula clone mth2-30h19, complete sequence
 Length=117666

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 37072 AAATTGCAAAGAACTGA 37056

>gb|AC100734.4|  Mus musculus chromosome 15, clone RP24-316L11, complete sequence
 Length=182088

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 90456 AAATTGCAAAGAACTGA 90472

>gb|AC125220.3|  Mus musculus BAC clone RP23-70H20 from 15, complete sequence
 Length=184933

58
136

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
|||||
Sbjct 24056 AAATTGCAAAGAACTGA 24040

>gb|AC134099.2|  Homo sapiens 3 BAC RP11-221B6 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=153726

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATGG 20
|||||
Sbjct 7179 TTGCAAAGAACTGATGC 7195

>dbj|AK122875.1|  Homo sapiens cDNA FLJ16510 fis, clone HEART1000132, highly similar to Homo sapiens hypothetical protein LOC123722 (LOC123722), mRNA
Length=2679

GENE ID: 123722 PSD2 | fibronectin type III and SPRY domain containing 2
(Homo sapiens) (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATGG 20
|||||
Sbjct 1085 TTGCAAAGAACTGATGG 1101

>gb|AC105339.9|  Homo sapiens chromosome 15, clone RP11-752G15, complete sequence
Length=175786

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATGG 20
|||||
Sbjct 20129 TTGCAAAGAACTGATGG 20145

>gb|AC161347.2|  Mus musculus chromosome 15, clone RP23-273M5, complete sequence
Length=191833

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
|||||
Sbjct 131919 AAATTGCAAAGAACTGA 131903

>gb|AC044907.16|  Homo sapiens chromosome 15, clone RP11-127F21, complete sequence
Length=170793

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 4 TTGCAAAGAACTGATGG 20
|||||
Sbjct 61736 TTGCAAAGAACTGATGG 61720

>emb|BX950859.12|  Zebrafish DNA sequence from clone CH211-134M1 in linkage group 11, complete sequence
Length=176832

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGA 17
|||||
Sbjct 2606 AAATTGCAAAGAACTGA 2622

>emb|AL592522.12|  Mouse DNA sequence from clone RP23-210M6 on chromosome 11 Contains the Olfr222 and Olfr223 genes for olfactory receptor 222 and 223, a high mobility group box 1 (Hmgb1) pseudogene, the C1asl gene for cold autoinflammatory syndrome 1 homolog (human), a novel gene (4933439C10Rik), the gene for a novel protein (D130067D09), a ribosomal protein L18 (Rpl18) pseudogene, an ariadne homolog 2 (Drosophila) (Arih2) pseudogene, the gene for a novel zinc finger domain-containing protein, the 3' end of the gene for a novel protein and one CpG island, complete sequence
Length=157300

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

86
78
15

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 115467 AAATTGCAAAGAACTGA 115483

>gb|AC096561.1| **D** Homo sapiens BAC clone RP11-257D7 from 2, complete sequence
 Length=170304

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 4 TTGCAAGAACTGATGG 20
 |||||
 Sbjct 126535 TTGCAAGAACTGATGG 126519

>emb|BX005135.5| **D** Zebrafish DNA sequence from clone CH211-89P16 in linkage group
 11, complete sequence
 Length=166622

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 24902 AAATTGCAAAGAACTGA 24886

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 6 GCAAAGAACTGAT 18
 |||||
 Sbjct 164049 GCAAAGAACTGAT 164037

>dbj|AP001684.1| **BB** Homo sapiens genomic DNA, chromosome 21q, section 28/105
 Length=340000

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGAT 18
 |||||
 Sbjct 19888 AATTGCAAAGAACTGAT 19904

>gb|AC142096.25| **D** Medicago truncatula clone mth2-6m16, complete sequence
 Length=129053

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 114585 AAATTGCAAAGAACTGA 114601

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 3 ATTGCAAAGAACT 15
 |||||
 Sbjct 23929 ATTGCAAAGAACT 23917

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 3 ATTGCAAAGAACT 15
 |||||
 Sbjct 24116 ATTGCAAAGAACT 24128

>gb|M80517.1|HS4B958RAJ **D** Epstein-Barr virus, artifactual joining of B95-8 complete genome
 and the sequences from Raji of the large deletion found
 in B95-8
 Length=184113

Score = 34.2 bits (17), Expect = 2.6
 Identities = 17/17 (100%), Gaps = 0/17 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 371 AAATTGCAAAGAACTGA 355

>emb|AL833295.1|HSM804608 **UEG** Homo sapiens mRNA; cDNA DKFZp451H129 (from clone DKFZp451H129)
 Length=6436

87
+28
138

GENE ID: 123722 FSD2 | fibronectin type III and SPRY domain containing 2
[Homo sapiens] (10 or fewer PubMed links)

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATGG 20
Sbjct 1086 TTGCAAAGAACTGATGG 1102

>gb|M11924.1|HS4SUR Epstein-Barr virus R95-8, 12kb short unique region
Length=12052

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTGA 17
Sbjct 423 AAATTGCAAAGAACTGA 467

>dbj|AP000705.2| Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:B745D19,
LL56-APP region, complete sequence
Length=145859

Score = 34.2 bits (17), Expect = 2.6
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGAT 18
Sbjct 120362 AATTGCAAAGAACTGAT 120378

>ref|NG_009013.1| Homo sapiens component of oligomeric golgi complex 8 (COG8) on
chromosome 16
Length=18003

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
Sbjct 10561 AATTGCAAAGAACTGA 10546

>gb|AC231672.1| Solanum tuberosum chromosome 11 clone RH186L12, complete sequence
Length=124595

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 115307 AAATTGCAAAGAACTG 115292

>ref|XM_002072183.1| Drosophila willistoni GK22446 (Dwil\GK22446), mRNA
Length=2160

GENE ID: 6649510 Dwil\GK22446 | GK22446 gene product from transcript GK22446-RA
[Drosophila willistoni] (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
Sbjct 152 AATTGCAAAGAACTGA 137

>ref|XM_002065621.1| Drosophila willistoni GK14555 (Dwil\GK14555), mRNA
Length=1797

GENE ID: 6642433 Dwil\GK14555 | GK14555 gene product from transcript GK14555-RA
[Drosophila willistoni] (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 3 AATTGCAAAGAACTGAT 18
Sbjct 762 AATTGCAAAGAACTGAT 777

>gb|AC221040.4| Homo sapiens FOSM1 clone ABC10-44456900K13 from chromosome unknown,
complete sequence
Length=43178

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 136 AAATTGCAAAGAACTG 121

53
125

>ref|NG_007977.1|  Homo sapiens FIG4 homolog (S. cerevisiae) (FIG4); and chromosome 6 open reading frame 199 (C6orf199), on chromosome 6
Length=141211

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
|||
Sbjct 20579 AATTGCAAAGAACTGA 20564

>gb|EU168191.1|  Heterosigma akashiwo strain CCMP 452 chloroplast, complete genome
Length=160149

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||
Sbjct 39282 AAATTGCAAAGAACTG 39297

>gb|EU168190.1|  Heterosigma akashiwo strain NIES 293 chloroplast, complete genome
Length=159370

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
|||
Sbjct 38105 AAATTGCAAAGAACTG 38090

>gb|CP000806.1|  Cyanobacteria sp. ATCC 51142 circular chromosome, complete sequence
Length=4934271

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Features in this part of subject sequence:
putative thioester reductase

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||
Sbjct 3109577 ATTGCAAAGAACTGAT 3109562

Features in this part of subject sequence:
hypothetical protein

Score = 26.3 bits (13), Expect = 631
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 8 AAAGAACTGATGG 20
|||
Sbjct 1100162 AAAGAACTGATGG 1100174

Features in this part of subject sequence:
unknown

Score = 26.3 bits (13), Expect = 631
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 4 TTGCAAAGAACTG 16
|||
Sbjct 1748605 TTGCAAAGAACTG 1748593

Features in this part of subject sequence:
unknown

Score = 26.3 bits (13), Expect = 631
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 7 CAAAGAACTGATG 19
|||
Sbjct 3378032 CAAAGAACTGATG 3378020

>gb|AC200759.2|  Gallus gallus BAC clone CH261-3808 from chromosome 2, complete sequence
Length=202190

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
|||

59
40

Sbjct 83475 AAATTGCAAAGAACTG 83460

Score = 28.2 bits (14), Expect = 160
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 2 AAATTGCAAAGAACT 15
 |||||
 Sbjct 154738 AAATTGCAAAGAACT 154725

>gb|EF657230.1|  Cucumis melo clone BAC 13J4, complete sequence
 Length=98716

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
 |||||
 Sbjct 7443 AAATTGCAAAGAACTG 7458

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 6 GCAAAGAACTGAT 18
 |||||
 Sbjct 53043 GCAAAGAACTGAT 53031

>gb|AC171166.4|  Medicago truncatula chromosome 7 BAC clone mth2-119c4, complete sequence
 Length=128666

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 2 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 75324 AAATTGCAAAGAACTGA 75309

Score = 28.2 bits (14), Expect = 160
 Identities = 14/14 (100%), Gaps = 0/14 (0%)
 Strand=Plus/Minus

Query 4 TTGCAAAGAACTGA 17
 |||||
 Sbjct 68666 TTGCAAAGAACTGA 68653

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 3 ATTGCAAAGAACT 15
 |||||
 Sbjct 69652 ATTGCAAAGAACT 69640

>emb|AM458498.2| Vitis vinifera contig VV78X001424.3, whole genome shotgun sequence
 Length=2812

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 5 TGCAAAGAACTGATGG 20
 |||||
 Sbjct 2124 TGCAAAGAACTGATGG 2109

>emb|AM425354.2|  Vitis vinifera contig VV78X102512.5, whole genome shotgun sequence
 Length=75839

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 5 TGCAAAGAACTGATGG 20
 |||||
 Sbjct 69939 TGCAAAGAACTGATGG 69924

>emb|AM480373.2|  Vitis vinifera contig VV78X173528.113, whole genome shotgun sequence
 Length=11552

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 2 AAATTGCAAAGAACTGA 17
 |||||
 Sbjct 3845 AAATTGCAAAGAACTGA 3860

60
141

>emb|AM427274.2| **D** Vitis vinifera contig VV78X210943.5, whole genome shotgun sequence
Length=23558

Score = 32.2 bits (16), Expect = 10
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTGATGG 20
Sbjct 4454 AAATAGCAAAGAACTGATGG 4473

>ref|XM_001014459.2| **UG** Tetrahymena thermophila SB210 hypothetical protein (TTHERM_00522810)
mRNA, partial cds
Length=913

GENE ID: 4505112 TTHERM_00522810 | hypothetical protein
[Tetrahymena thermophila SB210] (10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 259 AAATTGCAAAGAACTG 274

>emb|AM494955.1| **D** Leishmania braziliensis chromosome 18
Length=708397

Features flanking this part of subject sequence:
105 bp at 5' side: vacuolar ATP synthase subunit c, putative
1721 bp at 3' side: hypothetical protein, conserved

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
Sbjct 232290 AATTGCAAAGAACTGA 232275

>ref|XM_001312491.1| **G** Trichomonas vaginalis G3 hypothetical protein (TVAG_104430) partial
mRNA
Length=3681

GENE ID: 4757371 TVAG_104430 | hypothetical protein [Trichomonas vaginalis G3]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 3390 AAATTGCAAAGAACTG 3405

>gb|AC192749.2| **D** Gallus gallus BAC clone CH261-1S7J3 from chromosome 2, complete
sequence
Length=161853

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 35498 AAATTGCAAAGAACTG 35513

>emb|BX936447.21| **U** Zebrafish DNA sequence from clone DKEY-13D5 in linkage group
9 Contains the 5' end of a novel gene and one novel gene, complete
sequence
Length=196603

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
Sbjct 85084 AATTGCAAAGAACTGA 85069

>gb|EF043233.1| Tomato leaf curl New Delhi virus - [Potato] isolate Happur segment
DNA B, complete sequence
Length=2693

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATG 19
Sbjct 2248 TTGCAAAGAACTGATG 2263

>emb|CR749178.8| **D** Zebrafish DNA sequence from clone DKEY-220H13 in linkage group
21, complete sequence
Length=102340

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 92680 AATTGCAAAGAACTGA 92665

>ref|XM_001165843.1| **G** PREDICTED: Pan troglodytes hypothetical protein LOC744440 (LOC744440), mRNA
Length=5064

GENE ID: 744440 LOC744440 | hypothetical protein LOC744440 [Pan troglodytes]

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 4254 ATTGCAAAGAACTGAT 4239

>gb|AC187334.3| **D** Canis Familiaris chromosome 2, clone XX-13J11, complete sequence
Length=213652

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 162012 AAATTGCAAAGAACTG 161997

>ref|NM_001042520.1| **UG** Homo sapiens hypothetical protein MGC13057 (MGC13057), transcript variant 3, mRNA
Length=4007

GENE ID: 84281 MGC13057 | hypothetical protein MGC13057 [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 3467 ATTGCAAAGAACTGAT 3452

>ref|NM_001042521.1| **UG** Homo sapiens hypothetical protein MGC13057 (MGC13057), transcript variant 2, mRNA
Length=4019

GENE ID: 84281 MGC13057 | hypothetical protein MGC13057 [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 3479 ATTGCAAAGAACTGAT 3464

>ref|NM_001042519.1| **UGG** Homo sapiens hypothetical protein MGC13057 (MGC13057), transcript variant 1, mRNA
Length=4051

GENE ID: 84281 MGC13057 | hypothetical protein MGC13057 [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 3511 ATTGCAAAGAACTGAT 3496

>ref|NM_032321.2| **UGG** Homo sapiens hypothetical protein MGC13057 (MGC13057), transcript variant 4, mRNA
Length=3978

GENE ID: 84281 MGC13057 | hypothetical protein MGC13057 [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 3438 ATTGCAAAGAACTGAT 3423

>ref|XM_001082154.1| **UG** PREDICTED: Macaca mulatta similar to SPRY domain containing 1 (LOC693575), mRNA
Length=6117

GENE ID: 693575 LOC693575 | similar to SPRY domain containing 1

62
12/3

(Macaca mulatta)

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 5 TGCAAAGAACTGATGG 20
 |||||
 Sbjct 1089 TGCAAAGAACTGATGG 1104

>emb|CT963111.1|  Medicago truncatula chromosome 5 clone mth2-43h1, COMPLETE SEQUENCE
 Length=120939

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
 |||||
 Sbjct 30808 AAATTGCAAAGAACTG 30823

>gb|AC150387.2|  Branchiostoma floridae clone CH302-103N24, complete sequence
 Length=193376

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 3 ATTGCAAAGAACTGAT 18
 |||||
 Sbjct 99188 ATTGCAAAGAACTGAT 99203

>gb|AY721982.1| Borojoa patinoi AFLP molecular marker genomic sequence
 Length=292

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 5 TGCAAAGAACTGATGG 20
 |||||
 Sbjct 253 TGCAAAGAACTGATGG 238

>gb|AC132875.8|  Mus musculus chromosome 15, clone RP24-381023, complete sequence
 Length=185786

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
 |||||
 Sbjct 77661 AATTGCAAAGAACTGA 77646

>gb|AC165415.5|  Mus musculus chromosome 15, clone RP23-17G19, complete sequence
 Length=227254

Sort alignments for this subject sequence by:
 E value Score Percent identity
 Query start position Subject start position

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGA 17
 |||||
 Sbjct 62432 AATTGCAAAGAACTGA 62447

Score = 26.3 bits (13), Expect = 631
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAA 13
 |||||
 Sbjct 151181 AAATTGCAAAGAA 151169

>gb|AC158589.7|  Mus musculus chromosome 5, clone RP24-388A6, complete sequence
 Length=173087

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGA 17
 |||||
 Sbjct 72960 AATTGCAAAGAACTGA 72975

>gb|AC138116.4|  Mus musculus BAC clone RP24-242H5 from chromosome 15, complete sequence
 Length=164014

Score = 32.2 bits (16), Expect = 10
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
 |||||

63
148

Sbjct 157628 AAATTGCAAAGAACTG 157613

>gb|AC073318.8|  Homo sapiens BAC clone RP11-266F12 from 7, complete sequence
Length=162460

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 100815 AAATTGCAAAGAACTG 100800

Score = 26.3 bits (13), Expect = 631
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 5 TGCAAAGAACTGA 17
|||||
Sbjct 37113 TGCAAAGAACTGA 37125

>gb|AC161001.4|  Mus musculus BAC clone RP23-30A18 from chromosome 14, complete sequence
Length=215474

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 98343 AAATTGCAAAGAACTG 98350

>gb|AC151964.12|  Medicago truncatula clone mth2-47g17, complete sequence
Length=117929

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 89121 AAATTGCAAAGAACTG 89136

>gb|AC159336.13|  Mus musculus 10 BAC RP24-430N21 (Roswell Park Cancer Institute (C57BL/6J Male) Mouse BAC Library) complete sequence
Length=180454

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 50615 AATTGCAAAGAACTGA 50600

>emb|AL158166.13|  Human DNA sequence from clone RP11-4C20 on chromosome 10 Contains the gene for a novel protein (MGC32871), the 5' end of the PTPRE gene for protein tyrosine phosphatase receptor type E, a novel gene and the CLRN3 for clarin 3 and a CpG island, complete sequence
Length=111852

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 43399 AAATTGCAAAGAACTG 43414

>gb|AC105750.2|  Homo sapiens chromosome 3 clone RP11-776K4, complete sequence
Length=166478

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATG 19
|||||
Sbjct 156631 TTGCAAAGAACTGATG 156646

>gb|AC112217.2|  Homo sapiens chromosome 3 clone CTD-2028L5, complete sequence
Length=156545

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 118803 AATTGCAAAGAACTGA 118788

15

>dbj|AK036441.1| Mus musculus adult male bone cDNA, RIKEN full-length enriched library, clone:9830108M16 product:hypothetical protein, full insert sequence
Length=3811

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 4 TTGCAAAGAACTGATG 19
Sbjct 2217 TTGCAAAGAACTGATG 2202

>gb|AC106868.5| Homo sapiens BAC clone RP11-174E22 from 4, complete sequence
Length=136000

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
Sbjct 75356 AATTGCAAAGAACTGA 75341

>gb|AC105753.2| Homo sapiens chromosome 3 clone RP11-189A1, complete sequence
Length=146753

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 124606 AAATTGCAAAGAACTG 124621

>gb|AC007540.3| Homo sapiens 12q24.1 BAC RPC11-128P10 (Roswell Park Cancer Institute Human BAC Library) complete sequence
Length=174652

Sort alignments for this subject sequence by:
E value Score Percent identity
Query start position Subject start position

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 5 TGCAAAGAACTGATGG 20
Sbjct 105927 TGCAAAGAACTGATGG 105912

Score = 26.3 bits (13), Expect = 631
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 8 AAAGAACTGATGG 20
Sbjct 77582 AAAGAACTGATGG 77594

>gb|AC099775.2| Homo sapiens chromosome 3 clone RP11-169G24, complete sequence
Length=181443

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 163695 AAATTGCAAAGAACTG 163710

>gb|AC044810.7| Homo sapiens chromosome 11, clone RP11-494M8, complete sequence
Length=194297

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 51723 AAATTGCAAAGAACTG 51738

>gb|AC021427.10| Homo sapiens chromosome 11, clone RP11-399N15, complete sequence
Length=174147

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
Sbjct 113775 AAATTGCAAAGAACTG 113790

>emb|AL513128.11| Human DNA sequence from clone RP11-301N24 on chromosome 10 Contains the 3' end of the SPAG6 gene for sperm associated antigen 6 (p16, MGC26276, Repro-SA-1, DKFZp434I153), the 3' end of a novel gene, the 3' end of the PIP5K2A gene for phosphatidylinositol-4-phosphate

65
126

5-kinase type II alpha and two CpG
islands, complete sequence
length=184685

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 106214 AAATTGCAAAGAACTG 106199

>emb|AL162425.15| [E] Human DNA sequence from clone RP11-523L1 on chromosome 9 Contains
the TNC gene for tenascin C (hexabrachion) (TN, HXB) and
a novel gene, complete sequence
Length=177728

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 80760 AAATTGCAAAGAACTG 80745

>emb|AL133472.12| [E] Human DNA sequence from clone RP1-177C7 on chromosome 6 Contains
the 5' end of the gene for a novel protein (FLJ30976) and
the 5' end of the KIAA0274 gene (similar to the novel protein
CG17840). Contains a CpG island, complete sequence
Length=87434

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 34203 AATTGCAAAGAACTGA 34188

>gb|AC154546.2| [E] Mus musculus BAC clone RP23-431I7 from chromosome 16, complete
sequence
Length=180261

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 5 TGCAAAGAACTGATGG 20
|||||
Sbjct 178400 TGCAAAGAACTGATGG 178415

>gb|AC026464.7| [E] Homo sapiens chromosome 16 clone RP11-343C2, complete sequence
Length=190185

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 59183 AATTGCAAAGAACTGA 59198

>gb|AC175466.2| [E] Gallus gallus BAC clone CH261-8A20 from chromosome u1, complete
sequence
Length=233533

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 180034 AATTGCAAAGAACTGA 180049

>gb|AC026474.7| [E] Homo sapiens chromosome 16 clone RP11-7005, complete sequence
Length=196220

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 84514 AATTGCAAAGAACTGA 84499

>gb|AC008756.9| [E] Homo sapiens chromosome 16 clone CTD-3028M10, complete sequence
Length=173527

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 99861 AAATTGCAAAGAACTG 99876

66
28

>gb|AC018693.8|  Homo sapiens BAC clone RP11-555N21 from 2, complete sequence
Length=164125

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 131361 AAATTGCAAAGAACTG 131376

>gb|AC151391.3|  Oryctolagus cuniculus clone LB1-231P8, complete sequence
Length=53522

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 5 TGCAAAGAACTGATGG 20
|||||
Sbjct 38863 TGCAAAGAACTGATGC 38848

>gb|AC009107.11|  Homo sapiens chromosome 16 clone RP11-459F6, complete sequence
Length=208220

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 65634 ATTGCAAAGAACTGAT 65649

>gb|AC124104.11|  Mus musculus chromosome 15, clone RP24-281D14, complete sequence
Length=157873

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 4 TTGCAAAGAACTGATG 19
|||||
Sbjct 126313 TTGCAAAGAACTGATG 126328

>emb|BX548070.1|HSM808216  Homo sapiens mRNA; cDNA DKFZp686I15210 (from clone DKFZp686I15210)
Length=3556

GENE ID: 84281 MGC13057 | hypothetical protein MGC13057 [Homo sapiens]
(10 or fewer PubMed links)

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 3016 ATTGCAAAGAACTGAT 3001

>emb|AL592283.5|  Mouse DNA sequence from clone RP23-386C23 on chromosome 4 Contains
the 5' end of the Nfib gene for nuclear factor 1/B, a
novel gene and a CpG island, complete sequence
Length=197763

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 17436 AAATTGCAAAGAACTG 17451

>gb|AC010679.6|  Homo sapiens BAC clone RP11-128O11 from 2, complete sequence
Length=188937

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 3 ATTGCAAAGAACTGAT 18
|||||
Sbjct 126402 ATTGCAAAGAACTGAT 126387

>gb|AC012087.10|AC012087  Homo sapiens 3 BAC RP11-317L10,RP11-150K6,RP11-68D12 (Roswell
Park Cancer Institute Human BAC Library) complete sequence
Length=194635

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 2 AATTGCAAAGAACTGA 17
|||||
Sbjct 177913 AATTGCAAAGAACTGA 177928

>gb|AC092833.4|  Homo sapiens BAC clone RP13-490C19 from 2, complete sequence
Length=143506

67
148
AB

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 136825 AAATTGCAAAGAACTG 136840

>gb|AC153487.1|  Taeniopygia guttata clone TG__Ba0319A15, complete sequence
Length=136080

Score = 32.2 bits (16), Expect = 10
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1 AAATTGCAAAGAACTG 16
|||||
Sbjct 6019 AAATTGCAAAGAACTG 6034

Select All Get selected sequences Distance tree of results

68
~~198~~
199

Foto 1

Fig. 1

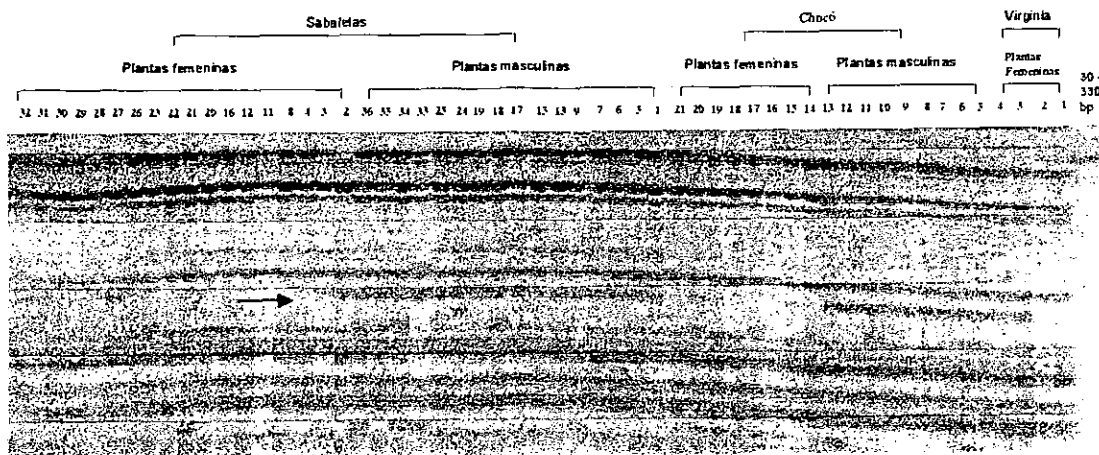


Foto 2

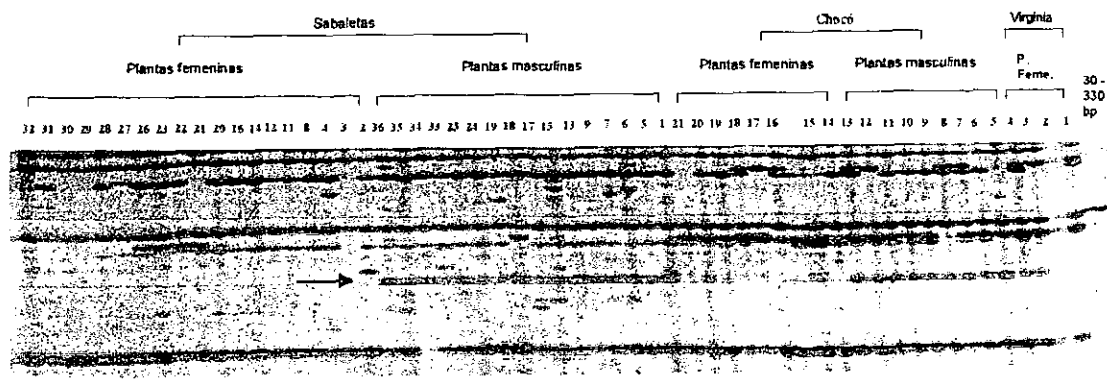


Fig. 2

Foto 3

Fig. 3

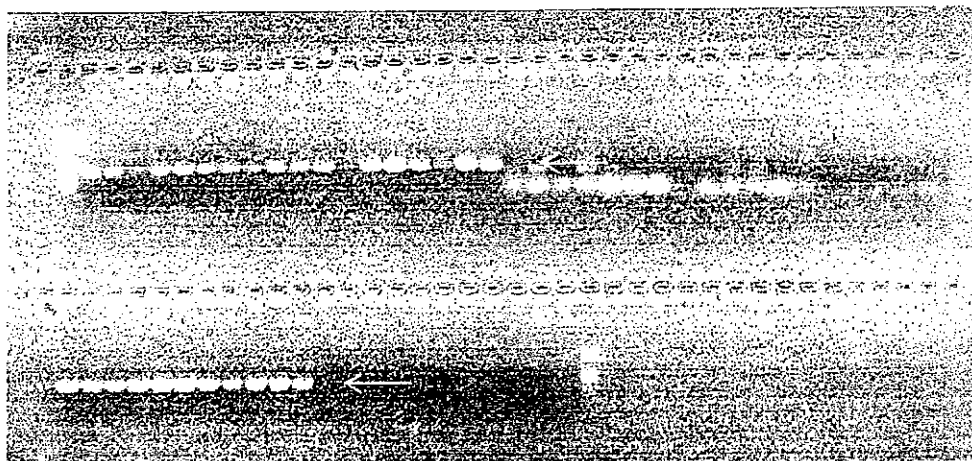


Foto 4

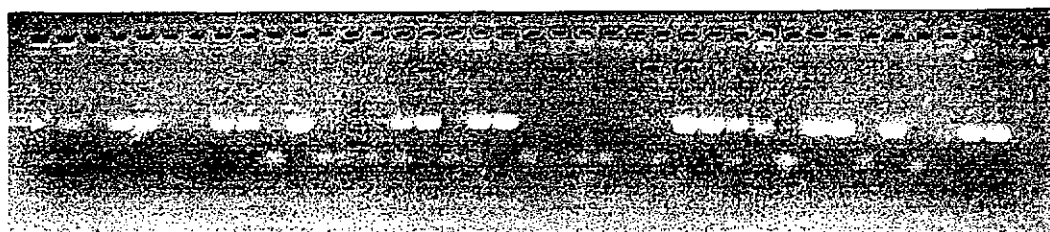


Fig. 4

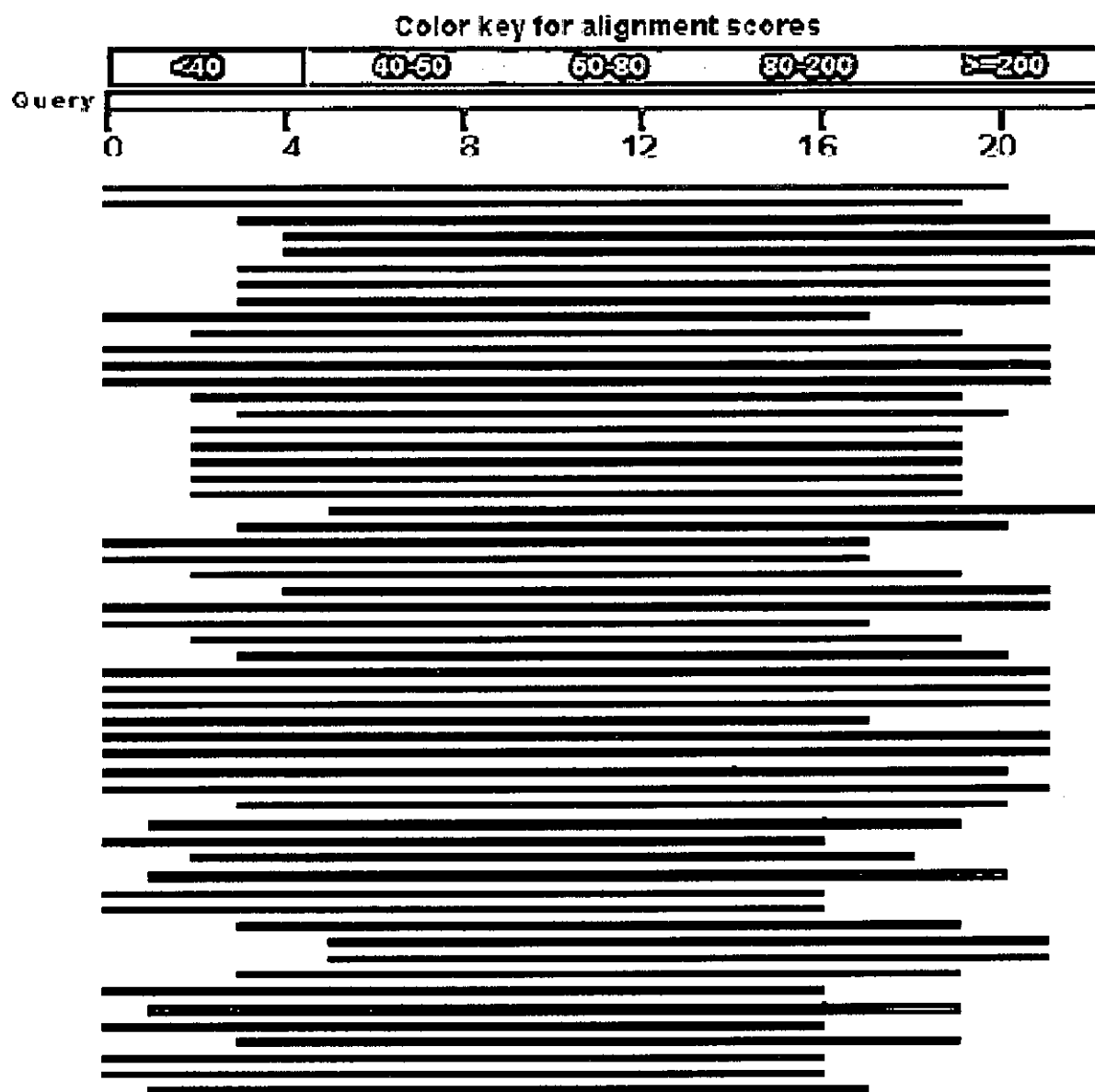


FIG. 5

7.1
52

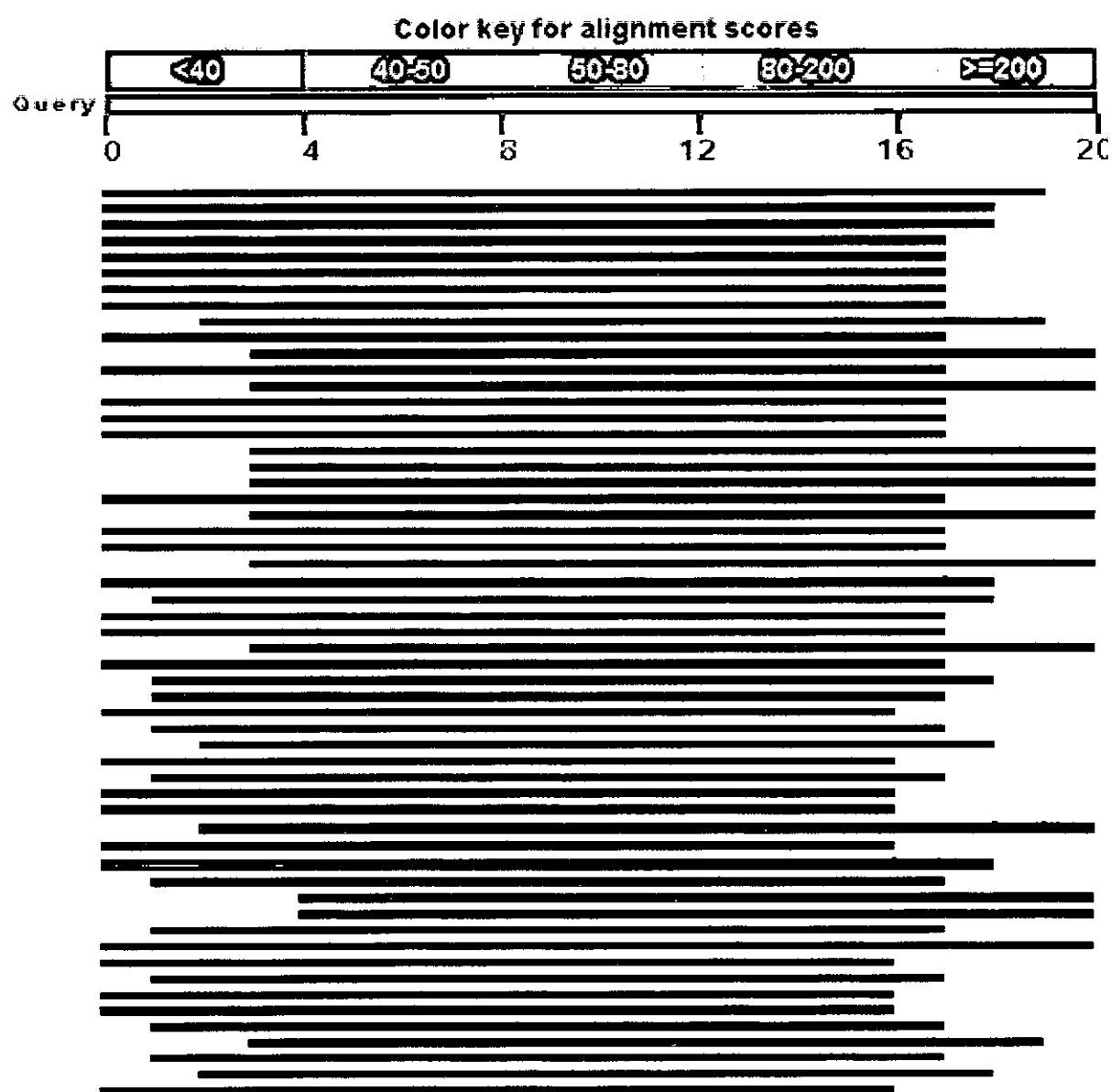


FIG. 6

REIVINDICACIONES

1. Un par de primers sintéticos caracterizado porque el par de primers se obtiene artificialmente mediante síntesis química y detecta un marcador de sexo masculino en plantas de borjón en edad temprana y tiene las secuencias:

BM1a: 5'-TGTTGATGATTGTTGTCATTCC-3'

BM1b: 5'-AAATTGCAAAGAACTGATGG - 3'

2. Un método para la determinación temprana del sexo en plantas dioicas de borjón para plantas masculinas que emplea los primers de la reivindicación 1 caracterizado por que comprende una reacción en cadena de la polimerasa usando (i) un par de primers sintéticos sexo-específicos que se unen y amplifican una secuencia blanco identificada de la planta masculina de borjón para producir un amplicón específico para plantas masculinas y (ii) un par de oligonucleótidos sintéticos que se unen específicamente y específicamente amplifican una secuencia que se encuentra en las plantas masculinas de borjón.
3. El método de acuerdo con la reivindicación 1 ó 2 donde se utilizan el primer BM1a con la secuencia 5'-TGTTGATGATTGTTGTCATTCC-3' y el primer BM1b con la secuencia 5'- AAATTGCAAAGAACTGATGG-3' específicos para plantas masculinas de borjón.

RESUMEN

La presente patente se refiere a un par de Primers sintéticos o secuencia de iniciadores 20 y 22 pares de bases para diagnosticar el sexo vegetal mediante la técnica del PCR o reacción en cadena de la Polimerasa.

Se obtiene con un procedimiento o protocolo para identificar el sexo de especies vegetales particularmente el borojo, planta nativa de Chocó en Colombia, mediante unos marcadores moleculares asociados al sexo de dicha planta. Más en particular la invención protege una secuencia de un número de bases del marcado.