

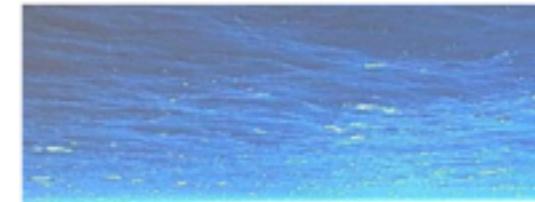
統合データベース講習会 AJACS宮崎2

塩基配列解析のための データベース・ウェブツール

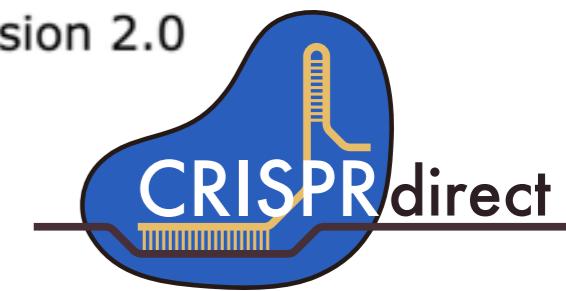
2019年 8月28日
ライフサイエンス統合データベースセンター (DBCLS)
内藤雄樹

- 内藤 雄樹 (ないとう ゆうき)

Twitter: @meso_cacase



siDirect version 2.0



- ライフサイエンス統合データベースセンター

Database Center for Life Science =



生命科学データベース研究開発のための機関
東大(柏)と三島の国立遺伝学研究所に間借り

- 遺伝子名などキーワードで探す
- 遺伝子のさまざまなIDとは？
- 塩基配列から遺伝子を探す

● NCBI トップページ

NCBI Resources How To Sign in to NCBI

NCBI National Center for Biotechnology Information

NCBI Home Resource List (A-Z) All Resources Chemicals & Bioassays Data & Software DNA & RNA Domains & Structures Genes & Expression Genetics & Medicine Genomes & Maps Homology Literature Proteins Sequence Analysis Taxonomy Training & Tutorials Variation

All Databases Assembly BioProject BioSample BioSystems Books ClinVar Clone Conserved Domains dbGaP dbVar EST Gene Genome GEO DataSets GEO Profiles GSS GTR HomoloGene MedGen MeSH NCBI Web Site NLM Catalog Nucleotide OMIM PMC PopSet Probe Protein Protein Clusters PubChem BioAssay PubChem Compound

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Analyze Identify an NCBI tool for your data analysis task

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Popular Resources

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- PubMed Central
- PubMed Health
- BLAST
- Nucleotide
- Genome
- SNP
- Gene
- Protein
- PubChem

NCBI Announcements

- HTTPS at NCBI: Guidance for NCBI web API users

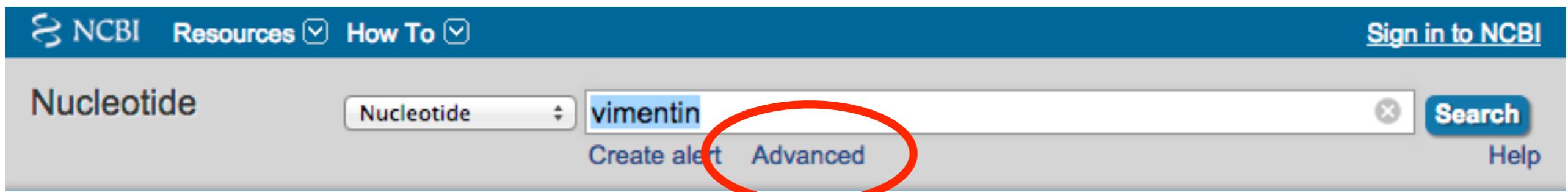
27 Jul 2016

As originally announced on June 10, NCBI will be moving all web services to

● 検索窓にキーワードを追加していく

- ... AND “*Bombyx mori*”[Organism]
- ... AND AGO1 [Gene Name]
- ... AND patent[Title]

● または、Advanced searchに行く



- Accession Number
- RefSeq ID
- Gene ID
- Symbol (遺伝子名)

- GenBank/ENA/DDBJ 国際塩基配列データベースに登録された塩基配列のID
俗にGenBankのAccession番号と呼ばれることがあるが、正確でない。
- A12345 や AB123456 の形をしている
参考：アルファベットの割り当て
→ DDBJ の Prefix Letter List
- A12345.1 のようにバージョンを表示
UTRが延長されたりエラーが修正されて A12345.2 のようにアップデートされる。

- 國際塩基配列データベースに登録された配列をもとに transcriptごとに1個登録 → RefSeqデータベース 遺伝子の百科事典のようなもの
- 選択的スプライシングで生じるvariantには別々の IDが付与されている
- NM_012345.6 の形式をしている
実用上はAccession番号の一種として扱うことができる。

- 遺伝子ごとに付与される遺伝子名と番号

| 慣用名 | Symbol | Gene ID |
|----------------------|--------|-----------|
| ヒト Argonaute 1 | AGO1 | 26523 |
| ショウジョウバエ Argonaute 1 | AGO1 | 36544 |
| カイコ Argonaute 1 | Ago1 | 100124421 |
| シロイヌナズナ Argonaute 1 | AGO1 | 841262 |

- Symbolは慣用名と一致しないこともある（ヒトp53→TP53）
- 別の生物種で同一のSymbolがついていることもある
- Gene IDは生物種と遺伝子を特定できる

ヒト Chr22 (q11)

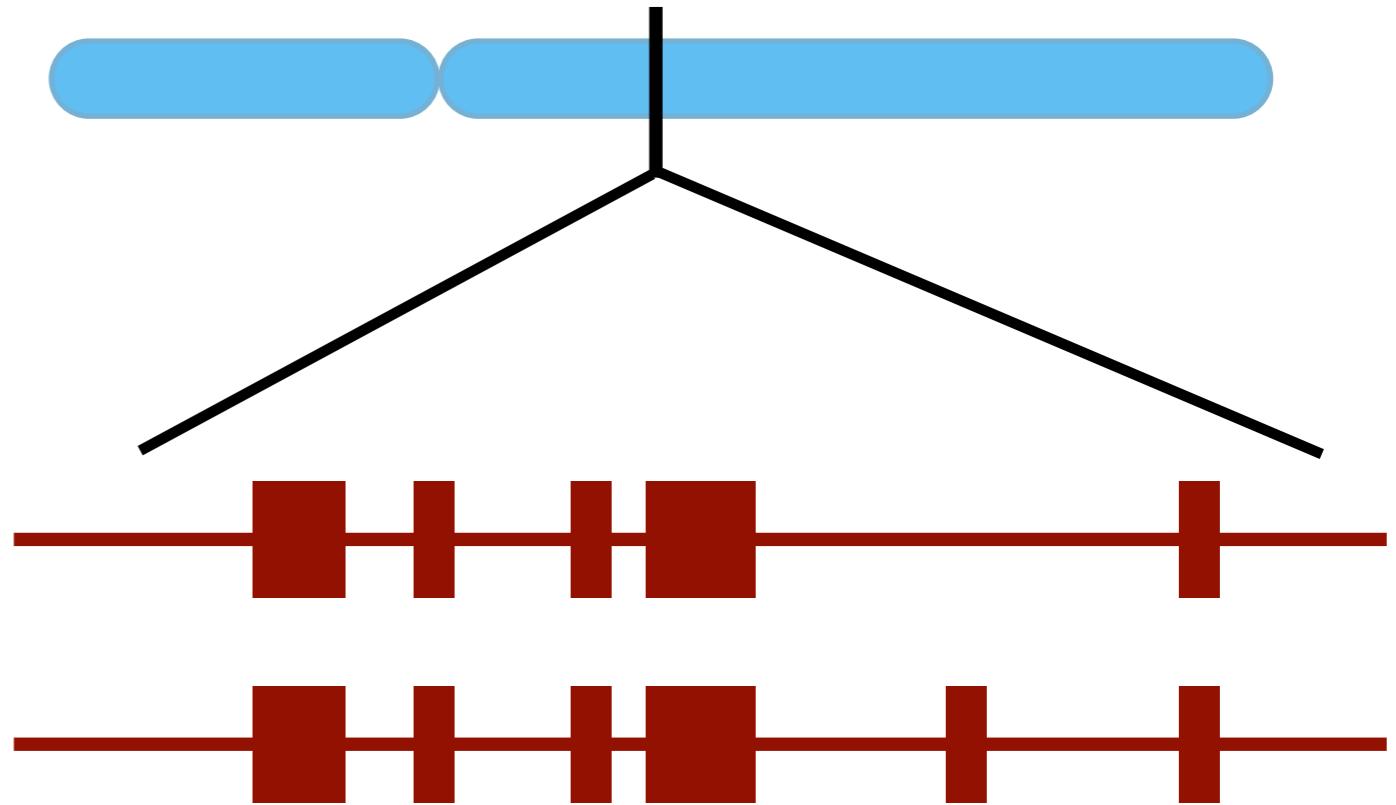
RefSeq ID:

NM_001190326

NM_022720

transcriptごと

(塩基配列ごと)



Symbol: DGCR8

Gene ID: 54487

遺伝子 (locus) ごと

● NCBI BLAST

<http://www.ncbi.nlm.nih.gov/blast/>

(または **BLAST** をググる)

● UCSC BLAT

<http://genome.ucsc.edu/> → Tools / Blat へ

(または **BLAT** をググる)

- 検索ワードが多様（遺伝子名, ID, 遺伝子機能, タンパクのドメイン名, 疾患, 塩基配列, アミノ酸配列,）

→ 入口が異なる。知らないと探せない

- BLAST 等による塩基配列の検索

→ 検索が遅い

ググる

統合遺伝子検索 GGRNA (ぐぐるな)



統合遺伝子検索

GGRNA ver.2

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検索

Zoo (All organisms in RefSeq) ▾

遺伝子をGoogleのように検索できるサイトです。 [NCBI RefSeq](#) の transcript を全文検索します。

検索例：

- ・ 「[homeobox](#)」 「[claudin](#)」 フリーワード検索
- ・ 「"RNA interference"」 ダブルクオートで囲ってフレーズ検索
- ・ 「[Argonaute "PAZ domain"](#)」 Argonaute かつ "PAZ domain" のAND検索
- ・ 「[NM_001518](#)」 「[10579](#)」 RefSeq IDやGene IDなど各種IDから検索
- ・ 「[symbol:VIM](#)」 遺伝子名(symbolまたはsynonym)から検索
- ・ 「[ref:Naito](#)」 文献情報のなかからフリーワード検索
- ・ 「[1552311_a_at](#)」 マイクロアレイのプローブIDから塩基配列を検索
- ・ 「[aa:KDEL](#)」 アミノ酸配列を検索
- ・ 「[caagaagagattg](#)」 塩基配列を検索
- ・ 「[comp:caagaagagattg](#)」 相補鎖を検索
- ・ 「[iub:aggtcannrtgacct](#)」 N, R, Y 等のあいまいな塩基を含む塩基配列を検索
- ・ [詳細な使い方](#)
- ・ ゲノム配列を検索したいときは [GGGenome](#) 《ゲゲゲノム》へ
 - ヒトゲノムの検索例：<http://GGGenome.dbcls.jp/TTCATTGACAACATT>

新着情報：

- 2018-05-30 データベースをRefSeq rel. 88 (May, 2018)に更新。
- 2015-01-13 HTTPSによる暗号化通信に対応 - <https://GGRNA.dbcls.jp/>
- 2013-07-24 ソースを公開 - [GitHub](#)
- 2013-07-08 GGRNA ver.2公開。全生物種のRefSeqを検索できます。
- 2012-05-29 下記論文の日本語による解説を「DBCLSからの成果発信」に掲載。
- 2012-05-29 GGRNAの論文がNucleic Acids Researchに掲載されました。
- [過去の新着情報](#)

統合遺伝子検索

GGRNA

ver.2



TITLE

PICTURE

GALLERY

LINK

IMAGE

PICTURE

遺伝子名を検索

Gene & transcript search
[Home](#) | [Help](#) | [Advanced search](#)
[Previous release \(v1\)](#)

GGRNA

 ver.2

2018-06-22 16:31:57, GGRNA.v2 : RefSeq release 88 (May, 2018)

LOCUS NM_001297698 2055 bp mRNA linear PRI 07-MAY-2018
DEFINITION Homo sapiens **Nanog** homeobox (**NANOG**), transcript variant 2, mRNA.
ACCESSION NM_001297698 XM_005253484
VERSION NM_001297698.1
KEYWORDS RefSeq.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2055)
AUTHORS You L, Guo X and Huang Y.
TITLE Correlation of Cancer Stem-Cell Markers OCT4, SOX2, and **NANOG** with Clinicopathological Features and Prognosis in Operative Patients with Rectal Cancer
JOURNAL Yonsei Med. J. 59 (1), 35-42 (2018)
PUBMED 29214774
REMARK GeneRIF: Rectal tumor tissue OCT4 (p<0.001), SOX2 (p=0.003), and **NANOG** (p<0.001) expressions were higher than those in adjacent tissue.
REFERENCE 2 (bases 1 to 2055)
AUTHORS Seo S, Jeon HY and Kim H.
TITLE Comparison of Cellular Transforming Activity of OCT4, **NANOG**, and SOX2 in Immortalized Astrocytes
JOURNAL DNA Cell Biol. 36 (11), 1000-1009 (2017)
PUBMED 28933914
REMARK GeneRIF: High **NANOG** expression is associated with brain neoplasms.
REFERENCE 3 (bases 1 to 2055)
AUTHORS Song KH, Choi CH, Lee HJ, Oh SJ, Woo SR, Hong SO, Noh KH, Cho H, Chung EJ, Kim JH, Chung JY, Hewitt SM, Baek S, Lee KM, Yee C, Son M, Mao CP, Wu TC and Kim TW.
TITLE HDAC1 Upregulation by **NANOG** Promotes Multidrug Resistance and a Stem-like Phenotype in Immune Edited Tumor Cells

Accession番号を検索

統合遺伝子検索

GGRNA

ver.2



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NM_003380

検索

Homo sapiens (human)



2018-06-25 04:41:25, GGRNA : RefSeq release 88 (May, 2018)

Summary:

- [refid:NM_003380 \(1\)](#)
- **INTERSECTION (1)**

Results:

検索語に色がつきます。重なると色が濃く表示されます。

[Homo sapiens vimentin \(VIM\), mRNA.](#) (2195 bp)

LOCUS **NM_003380** 2195 bp mRNA linear PRI 10-APR-2018 DEFINITION Homo sapiens vimentin (VIM), mRNA. ACCESSION **NM_003380**
 VERSION **NM_003380**.4 KEYWORDS RefSeq. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata;
 Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo. REFERENCE
 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from DA980400.1,
 BQ050765.1, BC000163.2 and T50493.1. This sequence is a reference standard in the RefSeqGene project. On Aug...

NM_003380.4 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

◀◀ | ページ / 1 | ▶▶ | C

1件中 1 - 1 を表示

Data Export:

下記より最大10000件まで検索結果を取得できます。

- タブ区切りテキスト → [表示](#) | [ダウンロード](#)
 エクセル等の表計算ソフトに直接コピペできます。
- JSON形式 → [リンク](#) | [ダウンロード](#)

塩基配列を検索

統合遺伝子検索

GGRNA

ver.2



GALLERY



TODD PICTURES



GALLERY



GALLERY



GALLERY



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GALLERY



GALLERY

GALLERY

塩基配列を検索

統合遺伝子検索

GGRNA

ver.2



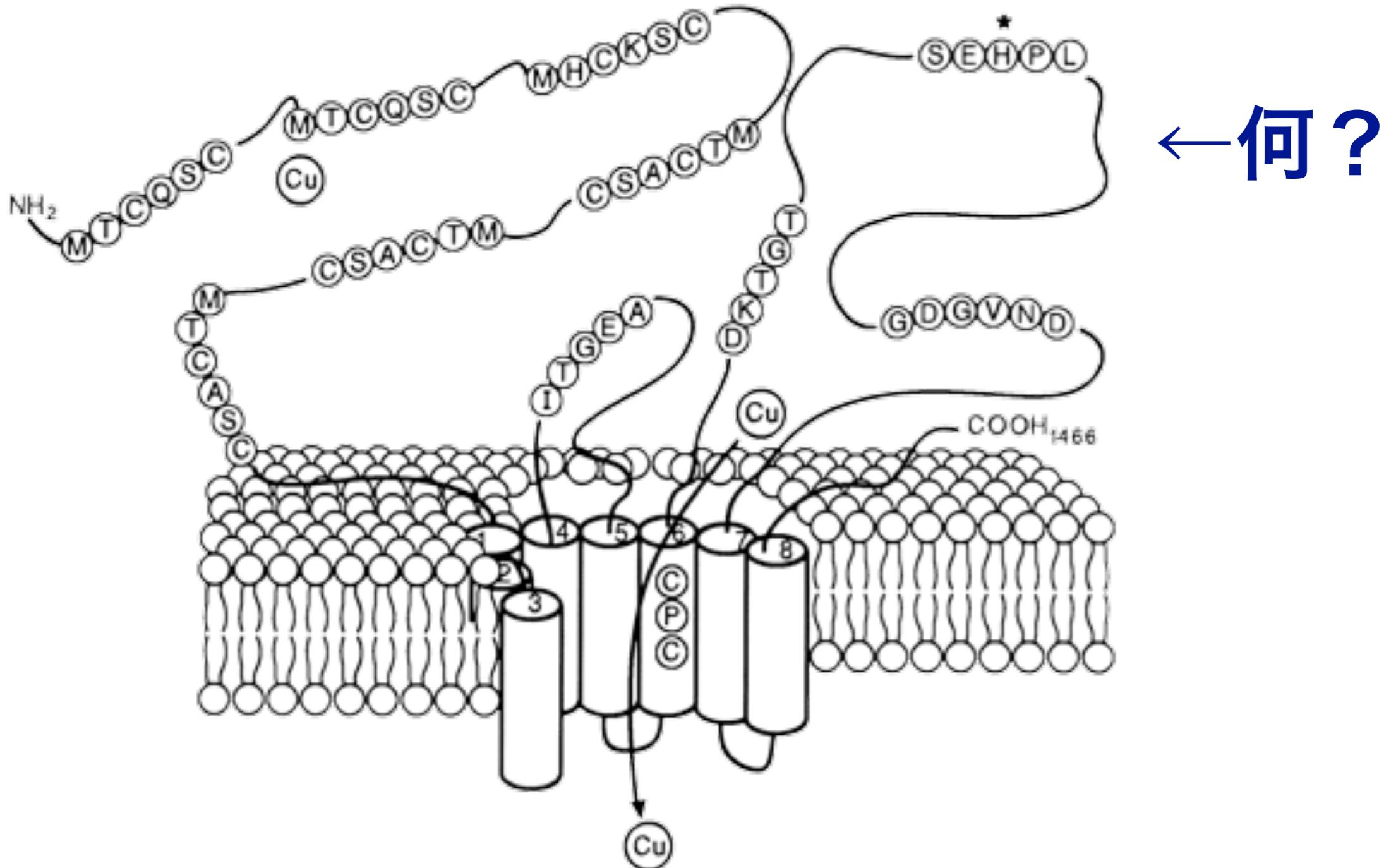
GALLERY

TODD

PICTURES

GALLERY

アミノ酸配列を検索



Schaefer et al. (1999) IV. Wilson's disease and Menkes disease.
Am. J. Physiol. Gastrointest. Liver Physiol. 276, G311-G314



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アミノ酸配列を検索

統合遺伝子検索

GGRNA
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SEHPL MTCQSC

検索

Zoo (All organisms in RefSeq)



2018-06-25 04:49:29, GGRNA : RefSeq release 88 (May, 2018)

Summary:

- [SEHPL \(8838\)](#)
- [MTCQSC \(993\)](#)
- [INTERSECTION \(555\)](#)

Results:

検索語に色がつきます。重なると色が濃く表示されます。

[PREDICTED: Macaca nemestrina ATPase copper transporting beta \(ATP7B\), transcript variant X8, mRNA.](#) (6516 bp)

copper-transporting ATPase 2 isoform X4" /protein_id="XP_011754963.1" /db_xref="GeneID:105490756"

/translation="MKKSFAFDNVGYEGGLDGLGPSSQVDTSTIRILG**MTCQSC**VKSIEDRISSLKGIVSMKVSLEQGSATVKYVPSVVSQQVCHQIGDMGFEASIAEGK
AASWPSRSLPAQEAVVKLRVEG**MTCQSC**VGSIEGKVRKLQGVVRVKVSLSNQEAVITYQPYLIQPEDLRDHVNDMGFEAAIKNKVAPLSLG...RFSGYFVPLIIIMSTLT
LVWWIVIGFIDFGVVQKYFPNPNKHISQTTEVIIRFAFQTTSITVLCIACPCSLGLATPTAVMVGTVAAQNGILIKGGKPLEMAHKIKTVMDKTGTITHGVPRVMRVLLGD
VATLPLRKVLAVVGTAEAS**SEHPL**GVAVTKYCKEELGTETLGYCTDFQAVPGCGIGCKVSNVEGILAHSERPLSAPASHLNEAGNLPAEKDAAPQTFSVLIGNREWLRR
NGLTISSDVSDAMTDHEMKGQTAILVAIDGMLCGMIAIADAVKQEAALAVHTLQSMGVDVVL..."

AA_position 35 1035

XM_011756661.2 - Macaca nemestrina (pig-tailed macaque) - [NCBI](#)

[PREDICTED: Macaca nemestrina ATPase copper transporting beta \(ATP7B\), transcript variant X10, mRNA.](#) (6827 bp)

copper-transporting ATPase 2 isoform X4" /protein_id="XP_011754965.1" /db_xref="GeneID:105490756"

/translation="MKKSFAFDNVGYEGGLDGLGPSSQVDTSTIRILG**MTCQSC**VKSIEDRISSLKGIVSMKVSLEQGSATVKYVPSVVSQQVCHQIGDMGFEASIAEGK
AASWPSRSLPAQEAVVKLRVEG**MTCQSC**VGSIEGKVRKLQGVVRVKVSLSNQEAVITYQPYLIQPEDLRDHVNDMGFEAAIKNKVAPLSLG...RFSGYFVPLIIIMSTLT
LVWWIVIGFIDFGVVQKYFPNPNKHISQTTEVIIRFAFQTTSITVLCIACPCSLGLATPTAVMVGTVAAQNGILIKGGKPLEMAHKIKTVMDKTGTITHGVPRVMRVLLGD
VATLPLRKVLAVVGTAEAS**SEHPL**GVAVTKYCKEELGTETLGYCTDFQAVPGCGIGCKVSNVEGILAHSERPLSAPASHLNEAGNLPAEKDAAPQTFSVLIGNREWLRR
NGLTISSDVSDAMTDHEMKGQTAILVAIDGMLCGMIAIADAVKQEAALAVHTLQSMGVDVVL..."

AA_position 35 1035

XM_011756663.2 - Macaca nemestrina (pig-tailed macaque) - [NCBI](#)

ある遺伝子に対して
RT-PCRをかけようとしたら
なぜかバンドが2本・・・

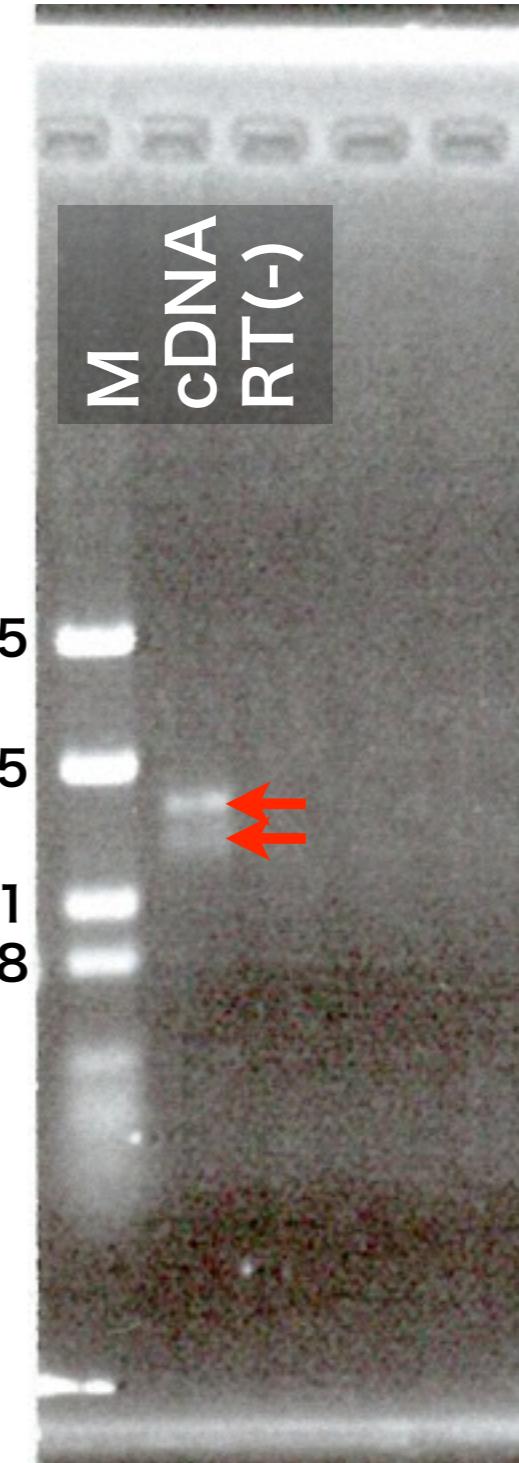
primer-F:

agctcattactttatcagtgcA

primer-R:

tgacgtattcaactcttctggtt

増幅遺伝子は何か？
予想されるバンドのサイズは？



PCRのプライマー

- seq:aqctcattactttatcaqtqca (2)
 - comp:tqacgtattcactcttctqggt (2)
 - **INTERSECTION (2)**

Results:

トップ50件を表示。検索語に色がつきます。重なると色が濃く表示されます。

[Homo sapiens DGCR8 microprocessor complex subunit \(DGCR8\), transcript variant 2, mRNA. \(4437 bp\)](#)
tgaaaaaaattcaggacttgggctgagcgccggcaattcaatcgaaaatgaagcggaagcaggcgagtcgcggccatcttgcacccatcaga **agctcattactttatcagtgc**aagatgcacccacaaag
aaagagttgttattaaccccaacggaaatccgaggctgcacccatctgcacgactatgcacgtgtccctcaaggccctgtctataatttcttgaatgtgcccgagctacactggaaatcctcatccctgactttgtta
aacagacctctgaagagaagccccaaagacagtgaagaactcgagtatttaaccacatcagcatcgaggactcgccggctacgagctgaccagcaaggctggctgtccatatcagatcctccacgagtgcctta
aaccagaagagtgaatacgtcatggcgtgtggcaagcacacagtgcgcgggtggtaagaacaagagagtggaaagc
agtttagcctcacagaagatdttcactgtgtggaaatgcacacgtctatcaagttgaagtggctctggaaaa
position 1892 2272 **2272 - 1892 = 380**
Synonym: C22orf12; DGCR8; Gyr1; psnha
NM_001190326.1 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

[Homo sapiens DGCR8 microprocessor complex subunit \(DGCR8\), transcript variant 1, mRNA. \(4536 bp\)](#)
gaagcggaaggcggagtccgagaggcccatttgcagccaatcaga **agctcattttatcagtgtca** agatgcacccacaaagaaagatgtttataaccccaacggaaatccgaggtctgcattctgca
cgagtacatgcagcgtgtcctcaaggccgcgtctataatttcttgaatgtgagaacccaagtgagccttgggcctcggtgaccattgtatgggtgacttacggatctggaaactgcaagcagaaaaacttgcga
agaataaaagctgcccggagctacactggaaatcctcatccctgactttgttaaacagacctctgaagagaagccccaaagacagtgaagaactcgagtatttaaccacatcagcatcgaggactcgcgggtctacgagctg
accaccaagactcccttttgtctccatatcagatcctccacgagtgcctaaaagaaaccatggatgggtgacacgtctatcaagttgaagtggttcctggaaa **aaccagaagagtgaatacgtcat** tggcgtgt
ggcaaggcacacagtgcgcgtgtgtataaaacaagagat...
position 1892 2371 **2371 - 1892 = 479**
Synonym: C22orf12; DGCR8; Gyr; pasha
NM_022720.3 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

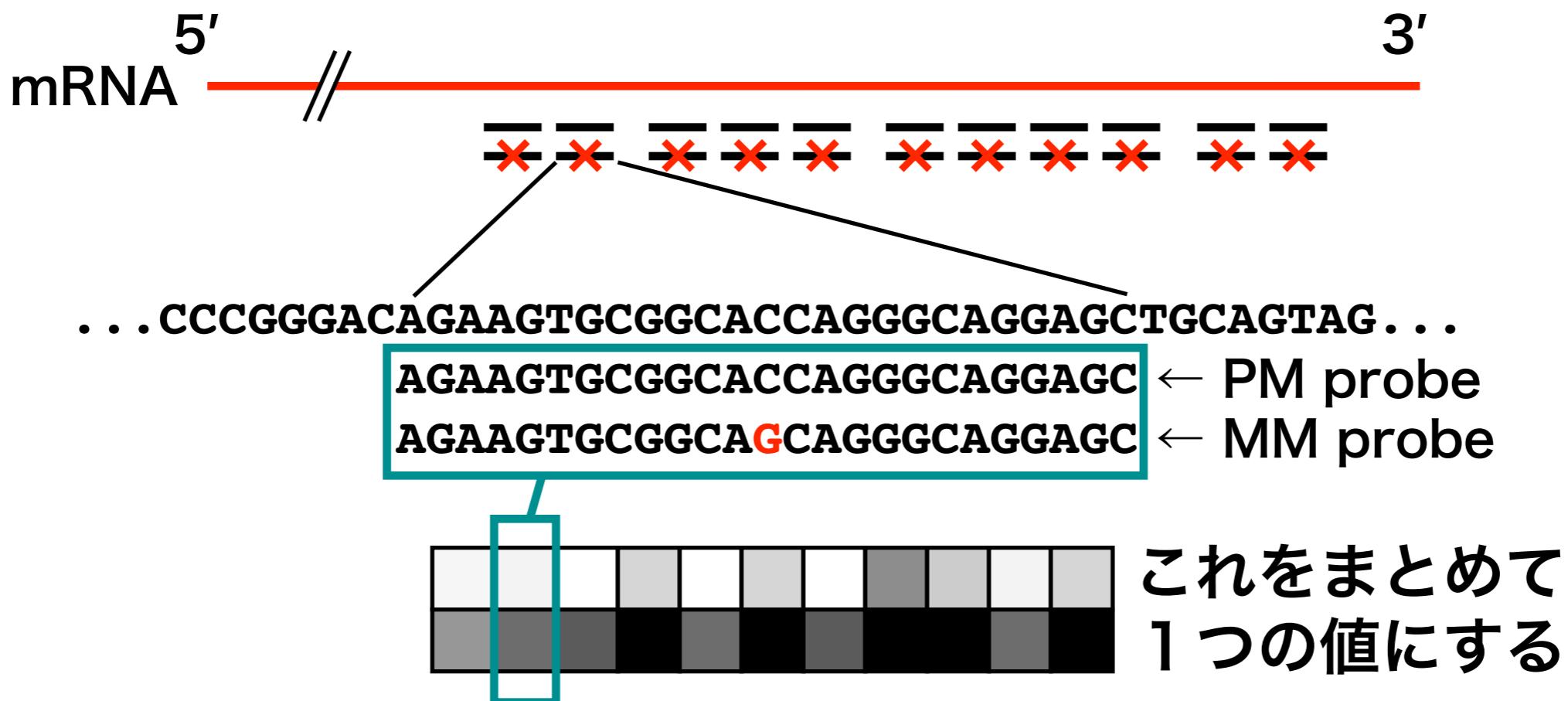
Data Export:

下記より最大10000件まで検索結果を取得できます。

- タブ区切りテキスト → [表示](#) | [ダウンロード](#)
エクセル等の表計算ソフトに直接コピペできます。
 - JSON形式 → [リンク](#) | [ダウンロード](#)

Debug Info:

Affymetrix社GeneChipマイクロアレイ
1遺伝子につき25塩基 × 11箇所のプローブ
→ 「プローブセット」 例) 1552311_a_at



マイクロアレイのプローブID

統合遺伝子検索

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IMAGE
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1552311_a_at

検索

Homo sapiens (human)



2018-06-25 06:49:15, GGRNA : RefSeq release 88 (May, 2018)

Summary:

- [seq:TCTCCACAAACGTTTTAAAATGTG \(2\)](#)
- [seq:GGGACACGGCAGTAAGCACAAGAAA \(2\)](#)
- [seq:GGCAGGAGCTGCAGTAGCTACCCCTC \(2\)](#)
- [seq:GCATGGGATGGGACAGTCTGGGCCA \(2\)](#)
- [seq:ATGTGCCGGGTGTACTGGTGCACAC \(2\)](#)
- [seq:AGGTCACCCCATCTCTAGGCAGCAC \(2\)](#)
- [seq:AGATCACTCCCAGATCACCAAGGTCA \(2\)](#)
- [seq:AGAACGTGCGGCACCAGGGCAGGAGC \(2\)](#)
- [seq:ACGGCAGTAAGCACAAGAAAGATT \(2\)](#)
- [seq:AATGTCACCGCACACCAGGGCAGTGG \(2\)](#)
- [seq:AAAAATGTGCCGGGTGTACTGGTGCA \(2\)](#)
- **INTERSECTION (2)**

Results:

検索語に色がつきます。重なると色が濃く表示されます。

[Homo sapiens retina and anterior neural fold homeobox 2 \(RAX2\), transcript variant 2, mRNA.](#) (2190 bp)

cagccgcaccccacccaaagagctcgatggggactgtcgccccggagaaccggctggactggcaaggcacggctggcccagtgcaggcaggagggggccctgaggcatggatggacagtctgg
 gccaaggccaccccccggacacaaggatgcggcaccaggcaggagctgcagtagtacctcccccgtctccagccctggctcccaatgcactcccaatgcaccaggtcacccatctctagggc
 ggcacccctcacacaccaggctctgtggtccaaacggcccccacccaaatgtcaccgcacaccaggcaggatggcagtaagcacaagaaagattttttttaagctaaaccaggccagggt
 gcgggtggctcatgcctgtatcccaatggggactgtggggaggattggctggagaccgcctgggtgacacagcaagaccatctccacaaaacgtttttaaaatgtgcgggtgtactggtgca
 acacccatgtcatcccaggatcccaagaagactgaggcaagaggatcacttgagcccagaaggtcgaggctgcaggagctgtgatcacactg...

position 1592 1634 1650 1698 1717 1783 1807 1812 1955 1972 1975

Synonym: ARMD6; CORD11; QRX; RAXL1

NM_032753.3 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

[Homo sapiens retina and anterior neural fold homeobox 2 \(RAX2\), transcript variant 1, mRNA.](#) (2428 bp)

<http://GGRNA.dbcls.jp/>

- 遺伝子をGoogleのように検索
- 検索対象はRefSeqの転写産物
 - RefSeq ID : NM_*, XM_* = mRNA
 - RefSeq ID : NR_*, XR_* = ncRNA
- さまざまなキーワードに対応
- 塩基配列、アミノ酸配列も素早く検索
 - とくに短い配列の検索が得意
- 無償で自由に利用可能
 - 商用利用であっても無償。
 - 利用記録は当センターにおいて機密扱い。

超絶高速ゲノム配列検索
GGGenome

[Help](#) | [English](#)

検索窓 | Human genome, GRCh37/hg19 (Feb, 2009) 

許容するミスマッチ/ギャップの数 : (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

検索例 :

- [[TTCATTGACAAACATT](#)] 塩基配列を検索
- [詳細な使い方](#)
- 遺伝子や転写産物のキーワード検索は **GGRNA** 《ぐぐるな》へ
 - 例) ヒトの「nanog」を検索 : <http://GGRNA.dbcls.jp/hs/nanog>

検索結果へのリンク :

- [http\[s\]://GGGenome.dbcls.jp/db/k/\[strand\]/sequence\[.format\]\[.download\]](http://GGGenome.dbcls.jp/db/k/[strand]/sequence[.format][.download])
 - **db** → hg19, mm10, dm3, ce10, TAIR10, pombe, refseq, etc. 省略時は hg19
[検索可能なデータベース一覧](#)
 - **k** → 許容するミスマッチ/ギャップの数。あまり大きいとしぼうする。省略時は 0
 - **strand** → '+' ('plus') または '-' ('minus') で特定の方向のみ検索。省略時は両方向を検索
 - **sequence** → 塩基配列。大文字・小文字は区別しない
 - **format** → html, txt, csv, bed, gff, json。省略時は html
 - **download** → URLの最後に付加すると検索結果をファイルとしてダウンロードできる
- 例1 : <http://GGGenome.dbcls.jp/TTCATTGACAAACATT>
 - ヒトゲノム **hg19** (省略可) で
 - ミスマッチ/ギャップを許容せず (省略可)
 - **TTCATTGACAAACATT** を検索し
 - **html** 形式 (省略可) で結果を返す
- 例2 : <http://GGGenome.dbcls.jp/mm10/2/+//TTCATTGACAAACATTGCGT.txt>
 - マウスゲノム **mm10** で
 - 2 ミスマッチ/ギャップまで許容して

超絶高速ゲノム配列検索 [Help](#) | [English](#)

GGGenome

TTCACTGACAACATTGAGTA Human genome, GRCh37/hg19 (Feb, 2009) 

許容するミスマッチ/ギャップの数: (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

2017-06-28 06:20:32, GGGenome : Human genome, GRCh37/hg19 (Feb, 2009)

Summary:

- [TTCACTGACAACATTGAGTA \(1\)](#)
- [TACTCAATGTTGTCAGTGAA \(0\)](#)
- **TOTAL (1)**

Results:

検索語に色がつきます (ミスマッチ・挿入欠失)。

chr2:30898313-30898332 ▼30898313
GCCCGCAGCCACTTATATGTATTTTAAATTCACTGACAACATTGAGTAGAAAAGATAATTTTTTTGAGACAG

« « | ページ / 1 | > > | C

1 件中

Data Export:

下記のフォーマットで最大100000件まで検索結果を取得できます。

- タブ区切りテキスト → [表示](#) | [ダウンロード](#)
エクセル等の表計算ソフトに直接コピペできます。
- CSV形式 → [表示](#) | [ダウンロード](#)
エクセル等の表計算ソフトにて開くことができます。

ゲ ゲ ゲ
GGGenome による塩基配列検索



超絶高速ゲノム配列検索

[Help](#) | [English](#)

GGGenome

TTCACTGACAACATT

検索

Human genome, GRCh37/hg19 (Feb, 2009)



許容するミスマッチ/ギャップの数: (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

2017-06-28 06:20:47, GGGenome : Human genome, GRCh37/hg19 (Feb, 2009)

Summary:

- [TTCACTGACAACATT \(10\)](#)
- [AATGTTGTCAGTGAA \(7\)](#)
- **TOTAL (17)**

Results:

検索語に色がつきます (ミスマッチ・挿入欠失)。

[chr1:173400829-173400843](#) ▼173400829
TTTCACATGCACTACCTGCCTGCTGTC**TTC**ACTGACAACATTTCAGGGTCTCGCAAGGCATGGAATACAATG

[chr1:197463616-197463630](#) ▼197463616
AATGATCTTACTGTTAACACTGCACTT**A**TTCACTGACAACATTACTTAAAGAAAAGAGATTATGATTGGATAAA

[chr2:30898313-30898327](#) ▼30898313
GCCCCCAGCCACTTATATGTATTTTAA**TTC**ACTGACAACATTGAGTAGAAAAGATAATTTTTTTTTGA

[chr2:163535086-163535100](#) ▼163535086
TGAGAAAGAGGACACCCTAACGAAATTATGG**TTC**ACTGACAACATTAGAGAACATATCAAACGAATATT

[chr3:117135824-117135838](#) ▼117135824
TCCCCTAGCAAATCAATTCAACTTCTGTT**A**TTCACTGACAACATTGTTTTCTACTGGCTGCAGCTTTCACAA

chr1:128011007-128011021

▼128011007

超絶高速ゲノム配列検索

[Help](#) | [English](#)

GGGenome

Human genome, GRCh37/hg19 (Feb, 2009)



許容するミスマッチ/ギャップの数 : (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

2017-06-28 06:21:00, GGGenome : Human genome, GRCh37/hg19 (Feb, 2009)

Summary:

- [TTCACTGACA \(4957\)](#)
- [TGTCAGTGAA \(5068\)](#)
- **TOTAL (10025)**

Results:

検索語に色がつきます (ミスマッチ・挿入欠失)。

[chr1:620618-620627](#) ▼620618
ATACTAGAATTAAAAGCAAATGTCTTTATTCACTGACAACATAATCATCTATAAAGAAAATCCTACAT

[chr1:728363-728372](#) ▼728363
CCCTCAGGCCACACAGCTGACGCTGTAGAGATTCACTGACATCCAGTCTGATGGACACTGTTCTCCAGCC

[chr1:1336263-1336272](#) ▼1336263
CCGCAGGGCTCTGCCACATCCCTGTCTTCCTTCACATGAAACGCAGAAAAGGCAGCTTGCCACAA

[chr1:3274566-3274575](#) ▼3274566
AGAGGCCCACTCGTGAGCCTTGCTGTGCCCTTCACATGACATGCTCGCCCCATGAGCTGAGTCTGCCTTGAC

[chr1:3783925-3783934](#) ▼3783925
CTCCGCTGCGTGTAGATACCACACTGTCTATTCACTGACACTTGGGTTGCTTCCACCTTTGGCCTGGCC

chr1:672000E-6720004

▼3783925

ゲ ゲ ゲ
GGGenome による塩基配列検索



超絶高速ゲノム配列検索
GGGenome

[Help](#) | [English](#)

TTCACTGACAACATTGAGTA Human genome, GRCh37/hg19 (Feb, 2009)

許容するミスマッチ/ギャップの数 : (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

2017-06-28 06:21:13, GGGenome : Human genome, GRCh37/hg19 (Feb, 2009)

Summary:

- [TTCACTGACAACATTGAGTA \(36\)](#)
- [TACTCAATGTTGTCAGTGAA \(33\)](#)
- **TOTAL (69)**

Results:

検索語に色がつきます (ミスマッチ・挿入欠失)。

[chr1:77930953-77930971](#) ▼77930953
AGCAGTACTCAAGATCACCTTTTTAAAGTTCACTG-CAACATT~~CAGTA~~GATGAAAAATGTGTAGCTGTAATTATTGA

[chr1:106947513-106947532](#) ▼106947513
TAGAAAACATACCAACATAAAGAACATCTTTCACTG~~CACAA~~-ATTGAGTAATAAAATTAAACCGTTGAAAGGGTCATTA

[chr2:30898313-30898332](#) ▼30898313
GCCCCCAGCCACTTATATGTATTTTTAAATTCACTGACAACATTGAGTAAGAAAGATAATTTTTTTTTGAGACAG

[chr2:141517099-141517116](#) ▼141517099
TTTATTTCTTAAACACAGCCTTGATAAAATTCACTGAC-ACATTGAGT-TAGCCATAGTGTGAATGGGAGACTGCCA

[chr2:163535086-163535103](#) ▼163535086
TGAGAAAGAGGACACCCTAAGAATTATGGTTCACTGACAACATT-AG-AGAACATATCAAACCAAACGAATATTCTGG

[chr2:186201205-186201224](#) ▼186201205

- アドレス = 検索クエリ になっている
- 結果をさまざまな形式で出力できる

検索例：

http[s]://GGGenome.dbcls.jp/hg38/2/ATAGGACCATA[.txt]

暗号化通信
に対応

①ヒトゲノム
hg38に対し

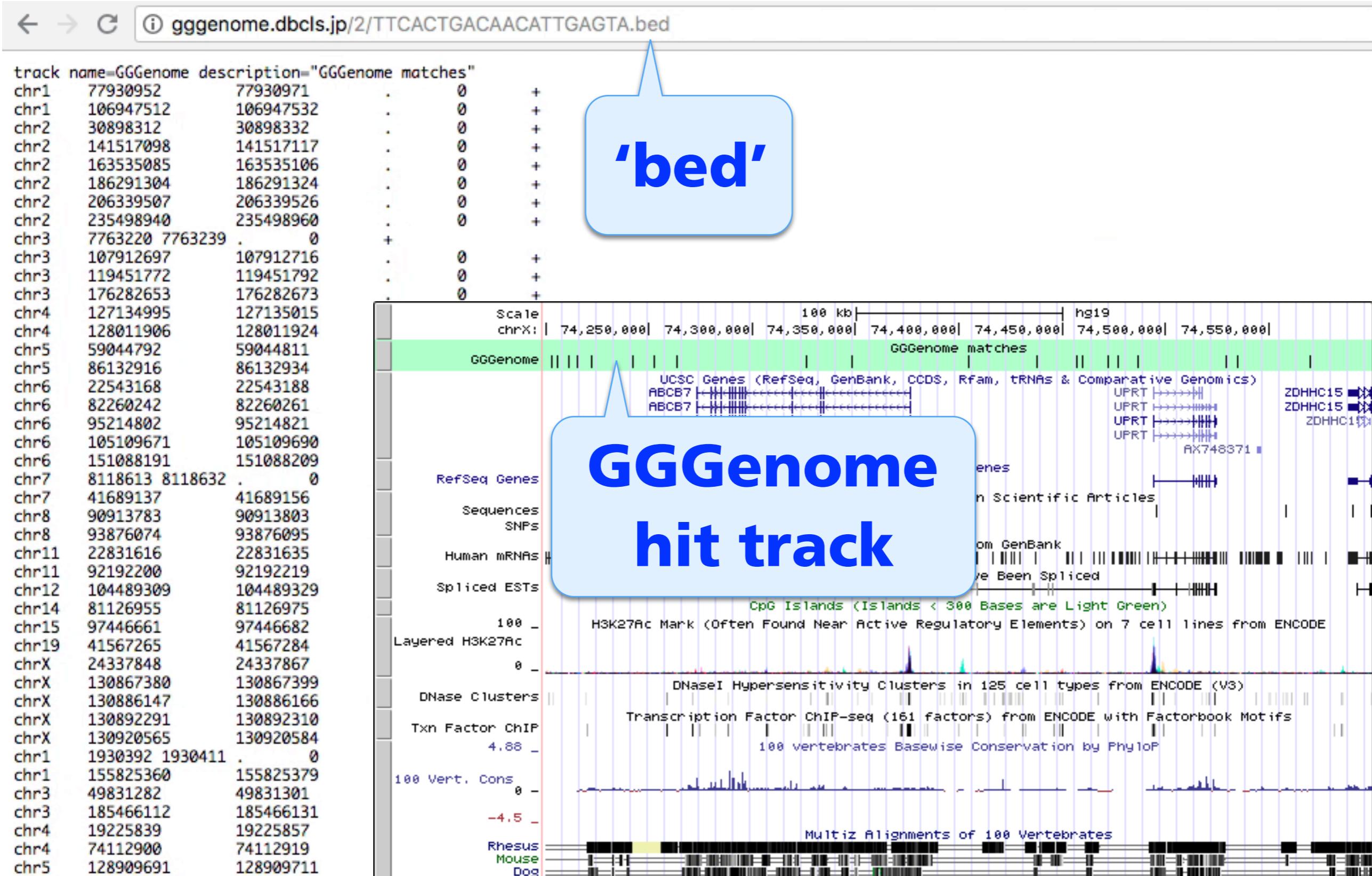
②最大ミスマッチ・
挿入欠失 = 2 で

③この配列を検索

④結果はテキスト
(txt) 形式で。

GGGenome を他のツールから呼び出す

GGGenome を他のツールから呼び出す



GGGenome を他のツールから呼び出す

← → ⌂ ⓘ ggggenome.dbcls.jp/2/TTCACTGACAACATTGAGTA.json

```
{ ...  
  • database: "Human genome, GRCh37/hg19 (Feb, 2009)",  
  • error: "none",  
  • results:  
    [ ...  
      { ...  
        • align: "||||||| ||||| ||||",  
        • del: 0,  
        • edit: "-----I-----X----",  
        • ins: 1,  
        • match: 18,  
        • mis: 1,  
        • name: "chr1",  
        • position: 77930953,  
        • position_end: 77930971,  
        • query: "TTCACTGACAACATTGAGTA",  
        • sbjct: "TTCACTG-CAACATTGAGTA",  
        • snippet: "TCATGAAATGGAAGTGCTGCCACTTCAGGGTCTGTAAAGAGATAATGCTGATGCCAGGCCAGGGAAAAAGCAGTACTCAAGATCACCTTTTAAAGTTCACTGCAAC",  
        • snippet_end: 77931071,  
        • snippet_pos: 77930853,  
        • strand: "+"  
      },  
      { ...  
        • align: "||||||| ||||| |||||",  
        • del: 1,  
        • edit: "-----D-----I-----",  
        • ins: 1,  
        • match: 19,  
        • mis: 0,  
        • name: "chr1",  
        • position: 106947513,  
        • position_end: 106947532,  
        • query: "TTCACTG-ACAACATTGAGTA",  
        • sbjct: "TTCACTGCACAA-ATTGAGTA",  
        • snippet: "TCATGAAATGGAAGTGCTGCCACTTCAGGGTCTGTAAAGAGATAATGCTGATGCCAGGCCAGGGAAAAAGCAGTACTCAAGATCACCTTTTAAAGTTCACTGCAAC",  
        • snippet_end: 106947632,  
        • snippet_pos: 106947533,  
        • strand: "+"  
      }  
    ]  
  }  
}
```

'json'

表計算ソフトから GGGenome 検索

GGGenome primer search ☆

コメント 共有

ファイル 編集 表示挿入 表示形式 データ ツール ヘルプ 変更内容をすべてドライブに保存しました

A B C D E F G H I

=ImportData(D2)

| | Primer name | (1) Sequence | (2) GGGenome URL | (3) ImportDATA function | name | strand | start | end |
|----|-------------|---------------------------|---|-------------------------|-------|--------|-------|-----|
| 1 | YN001-F | caatcaccctcacccttttatatgc | http://GGGenome.dbcls.jp/rice/caatcaccctcacccttttatatgc.txt | =ImportData(D2) | chr01 | + | 27707 | 27 |
| 2 | YN001-R | ccgctgtgaac | | chr01 - 28071 28092 | | | | |
| 3 | YN002-F | tgatccaata | | ATATTGTTGGTACCGAGTA | | | | |
| 4 | YN002-R | catgcaaggta | | 27971 28192 | | | | |
| 5 | YN003-F | acgtactgtgg | | | | | | |
| 6 | YN003-R | acccaaccta | | | | | | |
| 7 | YN004-F | atcagattccggccggccg | | | | | | |
| 8 | YN004-R | ggagagatctgggtggggag | | | | | | |
| 9 | | | | | | | | |
| 10 | | | | | | | | |
| 11 | | | | | | | | |
| 12 | | | | | | | | |
| 13 | | | | | | | | |
| 14 | | | | | | | | |
| 15 | | | | | | | | |
| 16 | | | | | | | | |
| 17 | | | | | | | | |
| 18 | | | | | | | | |
| 19 | | | | | | | | |
| 20 | | | | | | | | |
| 21 | | | | | | | | |
| 22 | | | | | | | | |
| 23 | | | | | | | | |
| 24 | | | | | | | | |

= ImportData(D2)

PCRプライマー配列

表計算ソフトから GGGenome 検索

<http://GGGenome.dbcls.jp/>

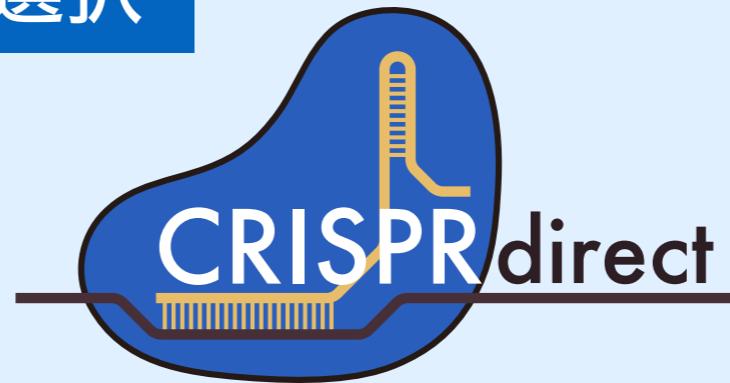
- **ゲノムを高速に検索可能**
350種の生物種（うち植物は80種）に対応
- **短い塩基配列の検索に強い**
ミスマッチや挿入欠失が多くても見落としのない検索
- **他のツールから呼び出すことができる（REST API）**
Googleスプレッドシートの ImportData() 関数
Excel 2013以降の WEBSERVICE() 関数
R、Ruby、Galaxy、ゲノムブラウザ・・・
- **無償で自由に利用可能**
商用利用であっても無償。
利用記録は当センターにおいて機密扱い。

CRISPR-Cas9 のガイド RNA 設計



PAMに隣接する配列の選択

ガイドRNA
設計支援ツール



オフターゲット配列検索

GGGenome

高速で正確な塩基配列検索ツール

GAAGGCAGTCCAGTGAAATG
| | | | | | | | | | | | | |
GAAGCAGTACAGAGAAATG

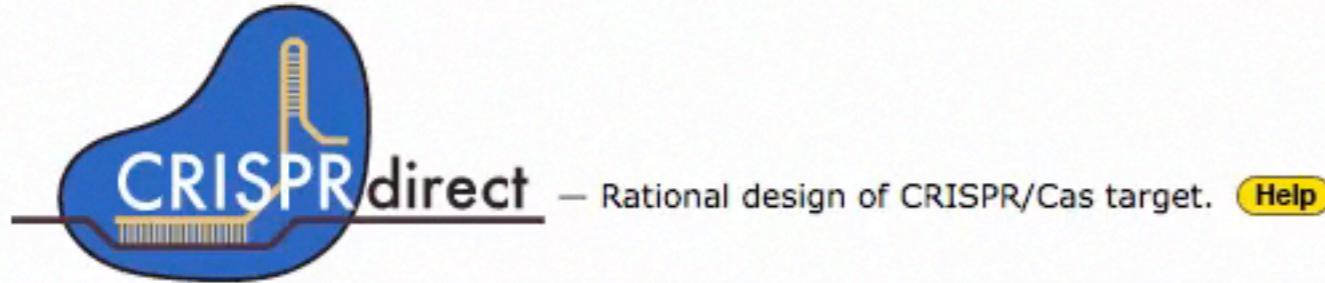


wordが完全一致せず
BLASTで検索できない



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CRISPRdirect によるガイド RNA 設計



<http://crispr.dbcls.jp/>

Enter an accession number (e.g. NM_006299) or genome location (e.g. hg19)

retrieve sequence

Accession番号

or Paste a nucleotide sequence: ?

または
塩基配列 を入力

or upload sequence file: ? ファイルを選択 選択されていません

PAM sequence requirement: (e.g. NGG, NRG) ?

Specificity check: Human (Homo sapiens) genome, GRCh37/hg19 (Feb, 2009)

design

What's new:

PAM

オフターゲット検索のための
生物種 を選択

CRISPRdirect によるガイド RNA 設計

retrieve sequence

or Paste a nucleotide sequence: ?

```
agtgcacccgggttcgcctcgctcgagctcgcttactttacaccgcccggcggagctctccagactccggaggaggaaagcg  
atcggttacacgtacgcctcgtaaggcagaaggcagaacatctgaagaatggctgacgaggatattcaacctatttgtgtgcgacaatg  
gcactggaatggtaaaggcagggtttgctggatgtatgcaccaaggccgtttcccttagcattgttagggagaccacgtcacacc  
ggtgtcatggttgggatgggccaaggatgcctatgtgggtatgtgaagctcaggcaaaaagggtatcctgactctaaagtaccc  
aattgaacatggaaattgtcaataactgggatgacatggagaaaatatggcaccacacccatcataatgagcttcgtgtgcaccc  
aagatcaccctgtattactaactgaagccccctcaatcccaaagccaaacagagagaagatgacacagatcatgtttgagaccc  
aattggccagcaatgtatgtcgcaatccaggctgttatccttgt
```

数文字ほど入力すると
生物種を検索 できる

or upload file

PAM sequence requirement: NGG (e.g. NGG, NRG) ?

Specificity check: rice ?

design

What's new:

- 2017-06-19 African wild rice (Oryza brachyantha) genome, Oryza_brachyantha.v1.4b (May, 2011)
- 2017-06-05 African wild rice (Oryza glaberrima) genome, AGI1.1 (May, 2011)
- 2017-02-17 Brazilian wild rice (Oryza glumaepatula) genome, ALNU02000000 (Aug, 2013)
- 2017-01-23 Longstamen rice (Oryza longistaminata) genome, v0117-2013Aug (Aug, 2013)
- 2016-12-14 Australian wild rice (Oryza meridionalis) genome, Oryza_meridionalis_v1.3 (Oct, 2014)
- 2016-09-05 Indian wild rice (Oryza nivara) genome, AWHD00000000 (Aug, 2013)
- 2016-08-30 Red rice (Oryza punctata) genome, AVCL00000000 (Aug, 2013)
- 2015-10-05 Brownbeard rice (Oryza rufipogon) genome, PRJEB4137 (Aug, 2013)
- 2015-01-13 Rice (Oryza sativa ssp. indica) genome, ASM465v1 (Jan, 2005)
- 2014-11-21 Rice (Oryza sativa ssp. japonica) genome, Os-Nipponbare-Reference-IRGSP-1.0 (Oct, 2011)

CRISPRdirect によるガイド RNA 設計

- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA vectors with pol III promoter.

show **highly specific** target only

Show 20 entries Search:

| position | | target sequence | sequence information | | | | number of target sites  | | |
|-----------|-------|------------------------------------|----------------------|-------------|---------------|-------------------|--|--------------|----------------|
| start | - end | 20mer+PAM (total 23mer) | GC% of 20mer | Tm of 20mer | TTTT in 20mer | restriction sites | 20mer +PAM | 12mer +PAM | 8mer +PAM |
| 7 - 29 | - | cctcccggttcgcgcctcgctcgcg [gRNA] | 75.00 % | 83.48 °C | - | NruI | 1 [detail] | 5 [detail] | 370 [detail] |
| 10 - 32 | - | cccgtttcgccctcgctcgcgagct [gRNA] | 70.00 % | 81.73 °C | - | NruI | 1 [detail] | 1 [detail] | 276 [detail] |
| 11 - 33 | - | ccgttccgcctcgctcgcgagctc [gRNA] | 70.00 % | 81.09 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 911 [detail] |
| 18 - 40 | - | cctcgctcgcgagctcgcttac [gRNA] | 70.00 % | 80.24 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 1072 [detail] |
| 47 - 69 | - | ccggccggccgagctctccaga [gRNA] | 75.00 % | 84.25 °C | - | SacI | 1 [detail] | 305 [detail] | 79033 [detail] |
| 50 - 72 | - | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 37 [detail] | 3555 [detail] |
| 53 - 75 | + | ccggccgagctctccagactcgg [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 3 [detail] | 175 [detail] |
| 53 - 75 | - | ccggccgagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | SacI | 1 [detail] | 15 [detail] | 2679 [detail] |
| 56 - 78 | + | ccggccgagctctccagactccggagg [gRNA] | 70.00 % | 80.27 °C | - | BspEI SacI | 1 [detail] | 4 [detail] | 793 [detail] |
| 56 - 78 | - | ccggccgagctctccagactccggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI SacI | 1 [detail] | 1 [detail] | 1295 [detail] |
| 59 - 81 | + | agctctccagactccggaggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI | 1 [detail] | 2 [detail] | 608 [detail] |
| 65 - 87 | - | ccaaactccggaggaggaaagcga [gRNA] | 65.00 % | 78.93 °C | - | BspEI | 1 [detail] | 6 [detail] | 375 [detail] |
| 72 - 94 | - | ccggccgagctctccagactccggagg [gRNA] | 55.00 % | 73.00 °C | - | BsiEI PvuI | 1 [detail] | 14 [detail] | 3180 [detail] |
| 102 - 124 | - | cctcggtcaaggcagaaggcagaaca [gRNA] | 50.00 % | 71.33 °C | - | | 0 [detail] | 3 [detail] | 588 [detail] |
| 114 - 136 | + | gaaggcagaacatctgaagaaatgg [gRNA] | 40.00 % | 65.99 °C | - | | 0 [detail] | 7 [detail] | 1117 [detail] |
| 123 - 145 | + | catctgaagaatggctgacgtgg [gRNA] | 50.00 % | 69.80 °C | - | | 1 [detail] | 2 [detail] | 1388 [detail] |
| 151 - 173 | + | caacccatttgtgtgcgacaaatgg [gRNA] | 45.00 % | 69.15 °C | - | | 1 [detail] | 3 [detail] | 303 [detail] |
| 154 - 176 | - | cctatttgtgtgcgacaaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 1 [detail] | 667 [detail] |
| 157 - 179 | + | atttgtgtgcgacaaatggcacatgg [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 2 [detail] | 499 [detail] |
| 162 - 184 | + | gtgcgacaaatggcactggaaatgg [gRNA] | 55.00 % | 74.69 °C | - | | 1 [detail] | 6 [detail] | 677 [detail] |

Showing 1 to 20 of 71 entries

First Previous 1 2 3 4 Next Last

Graphical View:

CRISPRdirect によるガイド RNA 設計

- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA vectors with pol III promoter.

show **highly specific** target only

Show 20 entries Search:

| position | | target sequence | sequence information | | | | number of target sites | | |
|-----------|-------|-------------------------------------|----------------------|-------------|---------------|-------------------|------------------------|--------------|----------------|
| start | - end | 20mer+PAM (total 23mer) | GC% of 20mer | Tm of 20mer | TTTT in 20mer | restriction sites | 20mer +PAM | 12mer +PAM | 8mer +PAM |
| 7 - 29 | - | cctcccggttcgcctcgctcgcg [gRNA] | 75.00 % | 83.48 °C | - | NruI | 1 [detail] | 5 [detail] | 370 [detail] |
| 10 - 32 | - | cccgtttcgccctcgctcgcgagct [gRNA] | 70.00 % | 83.41 °C | - | SacI | 1 [detail] | 1 [detail] | 276 [detail] |
| 11 - 33 | - | ccgttccgcctcgctcgcgagctc [gRNA] | 70.00 % | 83.41 °C | - | SacI | 1 [detail] | 4 [detail] | 911 [detail] |
| 18 - 40 | - | cctcgctcgcgagctcgcttac [gRNA] | 70.00 % | 83.41 °C | - | SacI | 1 [detail] | 4 [detail] | 1072 [detail] |
| 47 - 69 | - | ccggccggccgagctctccaga [gRNA] | 75.00 % | 83.41 °C | - | SacI | 1 [detail] | 305 [detail] | 79033 [detail] |
| 50 - 72 | - | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 37 [detail] | 3555 [detail] |
| 53 - 75 | + | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 3 [detail] | 175 [detail] |
| 53 - 75 | - | ccggccggagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | SacI | 1 [detail] | 15 [detail] | 2679 [detail] |
| 56 - 78 | + | ccggccggagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | BspEI SacI | 1 [detail] | 4 [detail] | 793 [detail] |
| 56 - 78 | - | ccggccggagctctccagactccggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI SacI | 1 [detail] | 1 [detail] | 1295 [detail] |
| 59 - 81 | + | agctctccagactccggaggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI | 1 [detail] | 2 [detail] | 608 [detail] |
| 65 - 87 | - | ccaaactccggaggaggaggacg [gRNA] | 65.00 % | 78.93 °C | - | BspEI | 1 [detail] | 6 [detail] | 375 [detail] |
| 72 - 94 | - | ccggaggaggaggacgatcgttac [gRNA] | 55.00 % | 73.00 °C | - | BsiEI PvuI | 1 [detail] | 14 [detail] | 3180 [detail] |
| 102 - 124 | - | cctcggtcaaggcagaaggcagaaca [gRNA] | 50.00 % | 71.33 °C | - | | 0 [detail] | 3 [detail] | 588 [detail] |
| 114 - 136 | + | gaaggcagaacatctgaagaaatgg [gRNA] | 40.00 % | 65.99 °C | - | | 0 [detail] | 7 [detail] | 1117 [detail] |
| 123 - 145 | + | catctgaagaatggctgacgtgg [gRNA] | 50.00 % | 69.80 °C | - | | 1 [detail] | 2 [detail] | 1388 [detail] |
| 151 - 173 | + | caaccttattgtgtgcgacaaatgg [gRNA] | 45.00 % | 69.15 °C | - | | 1 [detail] | 3 [detail] | 303 [detail] |
| 154 - 176 | - | cctattgtgtgcgacaaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 1 [detail] | 667 [detail] |
| 157 - 179 | + | attgtgtgcgacaaatggcacatgg [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 2 [detail] | 499 [detail] |
| 162 - 184 | + | gtgcgacaaatggcactggaaatgg [gRNA] | 55.00 % | 74.69 °C | - | | 1 [detail] | 6 [detail] | 677 [detail] |

Showing 1 to 20 of 71 entries

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標的サイトの
位置と塩基配列

CRISPRdirect によるガイド RNA 設計

- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA vectors with pol III promoter.

show **highly specific** target only

Show 20 entries

| position | | target sequence | sequence information | | | | number of target sites <small>?</small> | | |
|-----------|-------|-------------------------------------|----------------------|-------------|---------------|-------------------|---|------------|---------------|
| start | - end | 20mer+PAM (total 23mer) | GC% of 20mer | Tm of 20mer | TTTT in 20mer | restriction sites | 20mer +PAM | 12mer +PAM | 8mer +PAM |
| 7 - 29 | - | cctcccggttcgcctcgctcgcg [gRNA] | 75.00 % | 83.48 °C | - | NruI | 1 [detail] | 5 [detail] | 370 [detail] |
| 10 - 32 | - | cccgtttcgccctcgctcgcgagct [gRNA] | 70.00 % | 81.73 °C | - | NruI | 1 [detail] | 1 [detail] | 276 [detail] |
| 11 - 33 | - | ccgttccgcctcgctcgcgagctc [gRNA] | 70.00 % | 81.09 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 911 [detail] |
| 18 - 40 | - | cctcgctcgcgagctcggttac [gRNA] | 70.00 % | 80.24 °C | - | NruI SacI | 1 [det] | | |
| 47 - 69 | - | ccggccggccgagctctccaga [gRNA] | 75.00 % | 84.25 °C | - | SacI | 1 [det] | | |
| 50 - 72 | - | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [det] | | |
| 53 - 75 | + | ccggccggagctctccagactcgg [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [det] | | |
| 53 - 75 | - | ccggccggagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | SacI | 1 [det] | | |
| 56 - 78 | + | ccggccggagctctccagactccggagg [gRNA] | 70.00 % | 80.27 °C | - | BspEI SacI | 1 [det] | 4 [detail] | 793 [detail] |
| 56 - 78 | - | ccggccggagctctccagactccggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI SacI | 1 [det] | 1 [det] | 1295 [detail] |
| 59 - 81 | + | agctctccagactccggaggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI | 1 [det] | 2 [det] | 608 [detail] |
| 65 - 87 | - | ccaaactccggaggaggaaagcga [gRNA] | 65.00 % | 78.93 °C | - | BspEI | 1 [det] | 6 [det] | 375 [detail] |
| 72 - 94 | - | ccggccggagctctccagactccgg [gRNA] | 55.00 % | 73.00 °C | - | BsiEI PvuI | 1 [det] | 14 [det] | 3180 [detail] |
| 102 - 124 | - | cctcggtcaaggcagaaggcagaaca [gRNA] | 50.00 % | 71.33 °C | - | | 0 [det] | 3 [det] | 588 [detail] |
| 114 - 136 | + | gaaggcagaacatctgaagaaatgg [gRNA] | 40.00 % | 65.99 °C | - | | 0 [det] | 7 [det] | 1117 [detail] |
| 123 - 145 | + | catctgaagaatggctgacgtgg [gRNA] | 50.00 % | 69.80 °C | - | | 1 [det] | 2 [det] | 1388 [detail] |
| 151 - 173 | + | caacccatttgtgtgcgacaaatggc [gRNA] | 45.00 % | 69.15 °C | - | | 1 [det] | 3 [det] | 303 [detail] |
| 154 - 176 | - | cctatttgtgtgcgacaaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [det] | 1 [det] | 667 [detail] |
| 157 - 179 | + | atttgtgtgcgacaaatggcacatgg [gRNA] | 50.00 % | 72.27 °C | - | | 1 [det] | 2 [det] | 499 [detail] |
| 162 - 184 | + | gtgcgacaaatggcactggaaatgg [gRNA] | 55.00 % | 74.69 °C | - | | 1 [det] | 6 [det] | 677 [detail] |

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配列に関する情報
制限酵素サイト も

CRISPRdirect によるガイド RNA 設計

- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA vectors with pol III promoter.

show **highly specific** target only

Show 20 entries

| position | | target sequence | sequence information | | | | number of target sites <small>?</small> | | |
|----------------|---|------------------------------------|----------------------|----------------|------------------|----------------------|---|---------------|----------------|
| start - end | - | 20mer+PAM (total 23mer) | GC% of 20mer | Tm of 20mer | TTTT in 20mer | restriction sites | 20mer +PAM | 12mer +PAM | 8mer +PAM |
| 7 - 29 | - | cctcccggttcgcctcgctcgca [gRNA] | 75.00 % | 83.48 °C | - | NruI | 1 [detail] | 5 [detail] | 370 [detail] |
| 10 - 32 | | | | | | NruI | 1 [detail] | 1 [detail] | 276 [detail] |
| 11 - 32 | | | | | | NruI SacI | 1 [detail] | 4 [detail] | 911 [detail] |
| 18 - 40 | | | | | | NruI SacI | 1 [detail] | 4 [detail] | 1072 [detail] |
| 47 - 69 | | | | | | SacI | 1 [detail] | 305 [detail] | 79033 [detail] |
| 50 - 72 | | | | | | SacI | 1 [detail] | 37 [detail] | 3555 [detail] |
| 53 - 75 | | | | | | SacI | 1 [detail] | 3 [detail] | 175 [detail] |
| 53 - 75 | | | | | | SacI | 1 [detail] | 15 [detail] | 2679 [detail] |
| 56 - 78 | | | | | | BspEI SacI | 1 [detail] | 4 [detail] | 793 [detail] |
| 56 - 78 | | | | | | BspEI SacI | 1 [detail] | 1 [detail] | 1295 [detail] |
| 59 - 81 | | | | | | BspEI | 1 [detail] | 2 [detail] | 608 [detail] |
| 65 - 87 | | | | | | BspEI | 1 [detail] | 6 [detail] | 375 [detail] |
| 72 - 94 | - | ccggaggagaagcgatcgttac [gRNA] | 55.00 % | 73.00 °C | - | BsiEI PvuI | 1 [detail] | 14 [detail] | 3180 [detail] |
| 102 - 124 | - | cctcggtcaaggcagaaggcagaaca [gRNA] | 50.00 % | 71.33 °C | - | | 0 [detail] | 3 [detail] | 588 [detail] |
| 114 - 136 | + | gaagcagaacatctgaagaa[tgg] [gRNA] | 40.00 % | 65.99 °C | - | | 0 [detail] | 7 [detail] | 1117 [detail] |
| 123 - 145 | + | catctgaagaatggctgacg[agg] [gRNA] | 50.00 % | 69.80 °C | - | | 1 [detail] | 2 [detail] | 1388 [detail] |
| 151 - 173 | + | caaccttattgtgtgcgacaa[tgg] [gRNA] | 45.00 % | 69.15 °C | - | | 1 [detail] | 3 [detail] | 303 [detail] |
| 154 - 176 | - | cctatttgtgtgcgacaaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 1 [detail] | 667 [detail] |
| 157 - 179 | + | atttgtgtgcgacaaatggcac[tgg] [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 2 [detail] | 499 [detail] |
| 162 - 184 | + | gtgcgacaaatggcactggaa[tgg] [gRNA] | 55.00 % | 74.69 °C | - | | 1 [detail] | 6 [detail] | 677 [detail] |

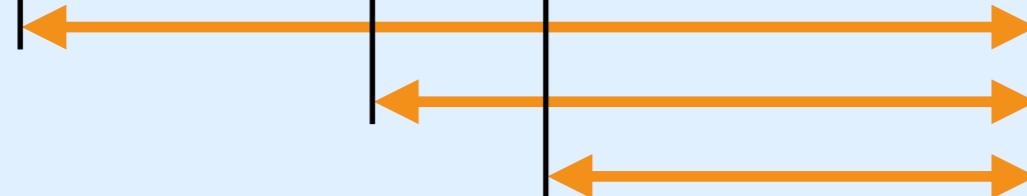
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ゲノムに何箇所あるか？

20mer PAM

NNNNNNNNNNNNNNNNNN NGG



CRISPRdirect によるガイド RNA 設計

- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA

show highly specific target only

| Site | | sequence information | | | | off-target sites | | | |
|------------------|---|-------------------------------------|-------------|---------------|-------|------------------|------------|--------------|----------------|
| | | GC% of 20mer | Tm of 20mer | TTTT in 20mer | SITES | +PAM | +PAM | 8mer +PAM | |
| - | - | cctcccggttcgcgcgtcgcgca [gRNA] | 75.00 % | 83.48 °C | - | NruI | 1 [detail] | 5 [detail] | 370 [detail] |
| 10 - 32 | - | cccgtttcgccctcgctcgcgagct [gRNA] | 70.00 % | 81.73 °C | - | NruI | 1 [detail] | 1 [detail] | 276 [detail] |
| 11 - 33 | - | ccgttgcgcctcgctcgcgagctc [gRNA] | 70.00 % | 81.09 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 911 [detail] |
| 18 - 40 | - | cctcgctcgcgagctcgcttac [gRNA] | 70.00 % | 80.24 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 1072 [detail] |
| 47 - 69 | - | ccggccggccgagctctccaga [gRNA] | 75.00 % | 84.25 °C | - | SacI | 1 [detail] | 305 [detail] | 79033 [detail] |
| 50 - 72 | - | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 37 [detail] | 3555 [detail] |
| 53 - 75 | + | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 3 [detail] | 175 [detail] |
| 53 - 75 | - | ccggccggagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | SacI | 1 [detail] | 1 [detail] | 2679 [detail] |
| 56 - 78 | + | ccggccggagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | BspEI SacI | 1 [detail] | 1 [detail] | 1 [detail] |
| 56 - 78 | - | ccggccggagctctccagactccggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI SacI | 1 [detail] | 1 [detail] | 1 [detail] |
| 59 - 81 | + | ccggccggagctctccggaggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI | 1 [detail] | 1 [detail] | 1 [detail] |
| 65 - 87 | - | ccggccggagctctccggaggagg [gRNA] | 65.00 % | 78.93 °C | - | BspEI | 1 [detail] | 1 [detail] | 1 [detail] |
| 72 - 94 | - | ccggccggagctctccggaggagg [gRNA] | 55.00 % | 73.00 °C | - | BsiEI PvuI | 1 [detail] | 14 [detail] | 3180 [detail] |
| 102 - 124 | - | ccgtcaaggcagaaggcagaaca [gRNA] | 50.00 % | 71.33 °C | - | | 0 [detail] | 3 [detail] | 588 [detail] |
| 114 - 136 | + | ccggccggagctctccggaggagg [gRNA] | 40.00 % | 65.99 °C | - | | 0 [detail] | 7 [detail] | 1117 [detail] |
| 123 - 145 | + | ccggccggagctctccggaggagg [gRNA] | 50.00 % | 69.80 °C | - | | 1 [detail] | 2 [detail] | 1388 [detail] |
| 151 - 173 | + | ccggccggagctctccggaggagg [gRNA] | 45.00 % | 69.15 °C | - | | 1 [detail] | 3 [detail] | 303 [detail] |
| 154 - 176 | - | ccgttgtgtgcgacaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 1 [detail] | 667 [detail] |
| 157 - 179 | + | ccgttgtgtgcgacaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 2 [detail] | 499 [detail] |
| 162 - 184 | + | ccgttgtgtgcgacaatggcac [gRNA] | 55.00 % | 74.69 °C | - | | 1 [detail] | 6 [detail] | 677 [detail] |

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Graphical View:

緑：おすすめ

オフターゲット
サイトが少ない

オフターゲット
サイトが多い

CRISPRdirect によるガイド RNA 設計

- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA vectors with pol III promoter.

show **highly specific** target only

Show 20 entries

| position | | target sequence | sequence information | | | | number of target sites <small>?</small> | | |
|------------------|-------|------------------------------------|----------------------|-------------|---------------|-------------------|---|--------------|----------------|
| start | - end | 20mer+PAM (total 23mer) | GC% of 20mer | Tm of 20mer | TTTT in 20mer | restriction sites | 20mer +PAM | 2mer +PAM | 8mer +PAM |
| 7 - 29 | - | cctcccggttcgcctcgctcgcgaa [gRNA] | 75.00 % | 83.48 °C | - | NruI | 1 [detail] | [detail] | 370 [detail] |
| 10 - 32 | - | cccgtttcgccctcgctcgcgagct [gRNA] | 70.00 % | 81.73 °C | - | NruI | 1 [detail] | 1 [detail] | 276 [detail] |
| 11 - 33 | - | ccgttccgcctcgctcgcgagctc [gRNA] | 70.00 % | 81.09 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 911 [detail] |
| 18 - 40 | - | cctcgctcgcgagctcgcttac [gRNA] | 70.00 % | 80.24 °C | - | NruI SacI | 1 [detail] | 4 [detail] | 1072 [detail] |
| 47 - 69 | - | ccggccggccgagctctccaga [gRNA] | 75.00 % | 84.25 °C | - | SacI | 1 [detail] | 305 [detail] | 79033 [detail] |
| 50 - 72 | - | ccggccggagctctccagactc [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 37 [detail] | 3555 [detail] |
| 53 - 75 | + | ccggccgagctctccagactcgg [gRNA] | 70.00 % | 80.41 °C | - | SacI | 1 [detail] | 3 [detail] | 175 [detail] |
| 53 - 75 | - | ccggccgagctctccagactccgg [gRNA] | 70.00 % | 80.27 °C | - | SacI | 1 [detail] | 15 [detail] | 2679 [detail] |
| 56 - 78 | + | ccggccgagctctccagactccggagg [gRNA] | 70.00 % | 80.27 °C | - | BspEI SacI | 1 [detail] | 4 [detail] | 793 [detail] |
| 56 - 78 | - | ccggccgagctctccagactccggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI SacI | 1 [detail] | 1 [detail] | 1295 [detail] |
| 59 - 81 | + | agctctccagactccggaggagg [gRNA] | 65.00 % | 79.68 °C | - | BspEI | 1 [detail] | 2 [detail] | 608 [detail] |
| 65 - 87 | - | ccggccggaggaggaggacg [gRNA] | 65.00 % | 78.93 °C | - | BspEI | 1 [detail] | 6 [detail] | 375 [detail] |
| 72 - 94 | - | ccggccgaggaggaggacgatcgttac [gRNA] | 55.00 % | 73.00 °C | - | BsiEI PvuI | 1 [detail] | 14 [detail] | 3180 [detail] |
| 102 - 124 | - | cctcggtcaaggcagaaggcagaaca [gRNA] | 50.00 % | 71.33 °C | - | | 0 [detail] | 3 [detail] | 588 [detail] |
| 114 - 136 | + | gaaggcagaacatctgaagaaatgg [gRNA] | 40.00 % | 65.99 °C | - | | 0 [detail] | 7 [detail] | 1117 [detail] |
| 123 - 145 | + | catctgaagaatggctgacggagg [gRNA] | 50.00 % | 69.80 °C | - | | 1 [detail] | 2 [detail] | 1388 [detail] |
| 151 - 173 | + | caacccatttgtgtcgacaaatggc [gRNA] | 45.00 % | 69.15 °C | - | | 1 [detail] | 3 [detail] | 303 [detail] |
| 154 - 176 | - | cctatttgtgtcgacaaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 1 [detail] | 667 [detail] |
| 157 - 179 | + | atttgtgtcgacaaatggcacatgg [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 2 [detail] | 499 [detail] |
| 162 - 184 | + | gtgcgacaaatggcactggaaatgg [gRNA] | 55.00 % | 74.69 °C | - | | 1 [detail] | 6 [detail] | 677 [detail] |

Showing 1 to 20 of 71 entries

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Graphical View:

CRISPRdirect によるガイド RNA 設計



— Rational design of CRISPR/Cas target.

0 mismatch/gap | ≤1 mismatch/gap | ≤2 mismatches/gaps | more: 2

Search for: both strand plus strand minus strand

2017-06-28 07:17:02, GGGenome : Rice genome, Os-Nipponbare-Reference-IRGSP-1.0 (Oct, 2011)

Summary:

- CCNcccattcgcctcgactcgaa (1)
- tgcgcqaaqaaaggacgaaacgggNGG (4)
- **TOTAL (5)**

Results:

Showing first 200 results for each strand of the query sequence.

Matches are highlighted with blue background. **Mismatches** and **indels** are marked in red.

[chr12:23545769-23545793](#) ▼ 23545769
CCAACGAGGCCAGGTGAGCTCTCCCCCTCCCCCGATTGCCCTCGCTTCGCGACCGAGTTCACTTGAGCTGGGTTGCACTGAC

[chr05:21504153-21504175](#) ▼ 21504153
TCGGCGGCCGGCGGTGTAAAGTAACGCGAGCTCGCGAGCGAGGCCAACGGGAGGTGCACTGCTGGTGGACGGACGAAGA

[chr05:21504153-21504175](#) ▼ 21504153
TCGGCGGCCGGCGGTGTAAAGTAACGCGAGCTCGCGAGCGAGGCCAACGGGAGGTGCACTGCTGGTGGACGGACGAAGA

[chr05:21504153-21504175](#) ▼ 21504153
TCGGCGGCCGGCGGTGTAAAGTAACGCGAGCTCGCGAGCGAGGCCAACGGGAGGTGCACTGCTGGTGGACGGACGAAGA

[chr05:21504153-21504175](#) ▼ 21504153
TCGGCGGCCGGCGGTGTAAAGTAACGCGAGCTCGCGAGCGAGGCCAACGGGAGGAGTGCACTGCTGGTGGACGGACGAAGA

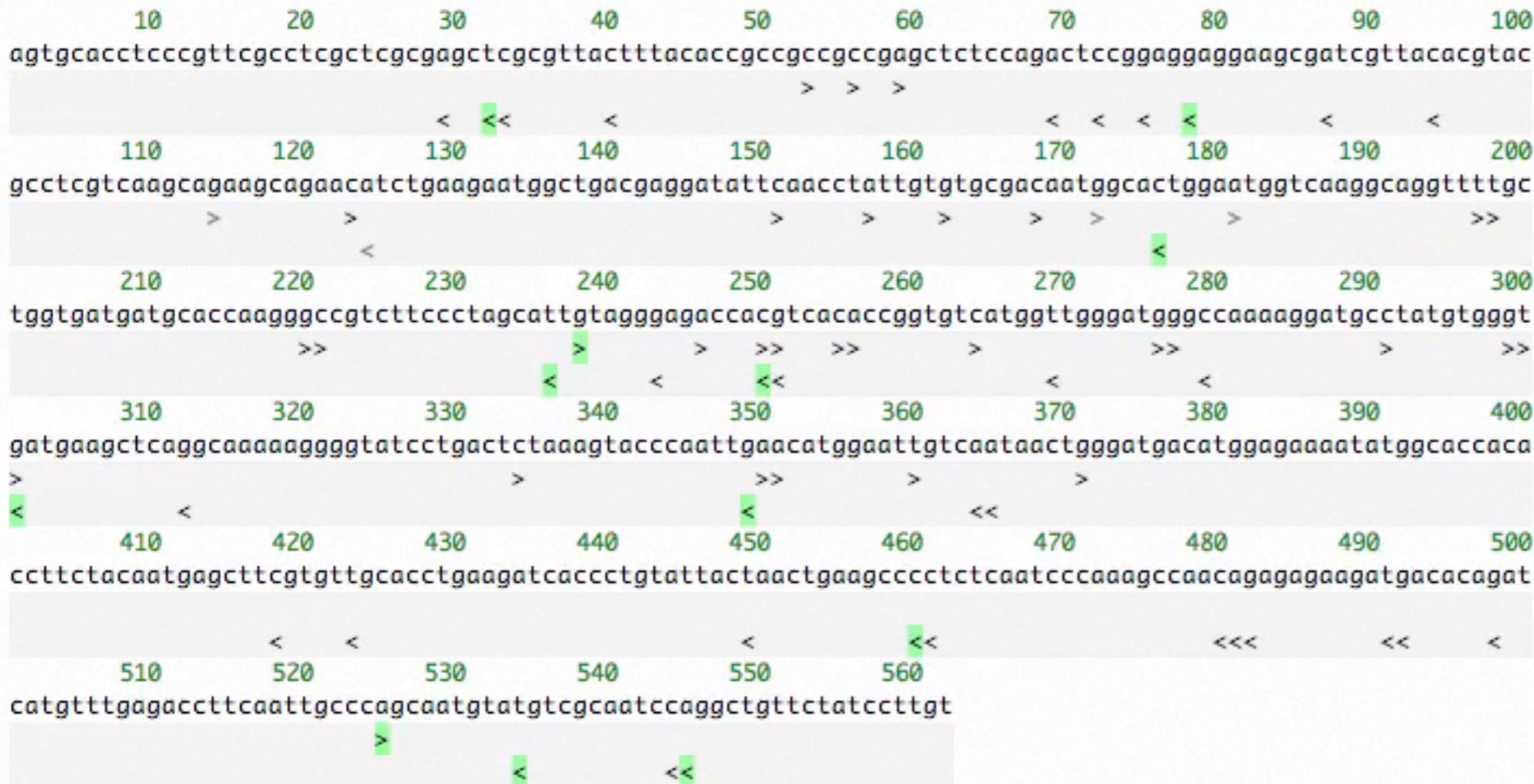
CRISPRdirect によるガイド RNA 設計

| | | | | | | | | | |
|-----------|---|-----------------------------------|---------|----------|---|--|------------|------------|--------------|
| 151 - 173 | + | caacctattgtgtcgacaa[tgg] [gRNA] | 45.00 % | 69.15 °C | - | | 1 [detail] | 3 [detail] | 303 [detail] |
| 154 - 176 | - | cctattgtgtcgacaaatggcac [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 1 [detail] | 667 [detail] |
| 157 - 179 | + | attgtgtcgacaaatggcac[tgg] [gRNA] | 50.00 % | 72.27 °C | - | | 1 [detail] | 2 [detail] | 499 [detail] |
| 162 - 184 | + | gtgcgacaaatggcactggaa[tgg] [gRNA] | 55.00 % | 74.69 °C | - | | 1 [detail] | 6 [detail] | 677 [detail] |

Showing 1 to 20 of 71 entries

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Graphical View:



Data Export:

- Tab-delimited text: [Open in new window](#) | [Download](#)
- JSON format: [Open in new window](#) | [Download](#)

Tab-delimited text can be copy-pasted into spreadsheet softwares (e.g. Excel) or text editors.

CRISPRdirect によるガイド RNA 設計

< < <
510 520 530 540 550 560
catgtttgagacaccttcaattgcccccaggcaatgttatgtcgcaatccaggctgttctatccttgt
>
< <<

Data Export:

- Tab-delimited text: [Open in new window](#) | [Download](#)
 - JSON format: [Open in new window](#) | [Download](#)

Tab-delimited text can be copy-pasted into spreadsheet softwares (e.g. Excel) or text editors.

CRISPRdirect によるガイド RNA 設計

| ◆ | A | B | C | D | E | F | G | H | I | J | K | L | M | N | O |
|----|--------------------|---|--------|---------------------------|----|-------|------|------------|-----------|-----------|----------|---|---|---|---|
| 1 | # [CRISPRdirect] | 2017-06-28 12:37:35] | | | | | | | | | | | | | |
| 2 | # sequence_name: | | | | | | | | | | | | | | |
| 3 | # pam_sequence | NGG | | | | | | | | | | | | | |
| 4 | # specificity_db | Rice (Oryza sativa ssp. japonica) genome, Os-Nipponbare-Reference-IRGSP-1.0 (Oct, 2011) | | | | | | | | | | | | | |
| 5 | # start | end | strand | sequence | GC | Tm | TTTT | RE_sites | hit_20mer | hit_12mer | hit_8mer | | | | |
| 6 | # | | | | | | | | | | | | | | |
| 7 | 7 | 29 | - | cctcccggttcgcctcgctcgcgaa | 75 | 83.48 | 0 | Nrul | 1 | 5 | 370 | | | | |
| 8 | 10 | 32 | - | cccggttcgcctcgctcgcgagct | 70 | 81.73 | 0 | Nrul | 1 | 1 | 276 | | | | |
| 9 | 11 | 33 | - | ccggttcgcctcgctcgcgagctc | 70 | 81.09 | 0 | Nrul,Sacl | 1 | 4 | 911 | | | | |
| 10 | 18 | 40 | - | cctcgctcgcgagctcgcgttac | 70 | 80.24 | 0 | Nrul,Sacl | 1 | 4 | 1072 | | | | |
| 11 | 47 | 69 | - | ccggccggcccgagctctccaga | 75 | 84.25 | 0 | Sacl | 1 | 305 | 79033 | | | | |
| 12 | 50 | 72 | - | ccggccggcgagctctccagactc | 70 | 80.41 | 0 | Sacl | 1 | 37 | 3555 | | | | |
| 13 | 53 | 75 | + | ccggccgagctctccagactccgg | 70 | 80.41 | 0 | Sacl | 1 | 3 | 175 | | | | |
| 14 | 53 | 75 | - | ccggccgagctctccagactccgg | 70 | 80.27 | 0 | Sacl | 1 | 15 | 2679 | | | | |
| 15 | 56 | 78 | + | ccgagctctccagactccggagg | 70 | 80.27 | 0 | BspEI,Sacl | 1 | 4 | 793 | | | | |
| 16 | 56 | 78 | - | ccgagctctccagactccggagg | 65 | 79.68 | 0 | BspEI,Sacl | 1 | 1 | 1295 | | | | |
| 17 | 59 | 81 | + | agctctccagactccggaggagg | 65 | 79.68 | 0 | BspEI | 1 | 2 | 608 | | | | |
| 18 | 65 | 87 | - | ccagactccggaggaggagaagc | 65 | 78.93 | 0 | BspEI | 1 | 6 | 375 | | | | |
| 19 | 72 | 94 | - | ccggaggaggaagcgatcgttac | 55 | 73 | 0 | BsiEI,Pvul | 1 | 14 | 3180 | | | | |
| 20 | 102 | 124 | - | cctcgtaaggcagaaggcagaaca | 50 | 71.33 | 0 | | 0 | 3 | 588 | | | | |
| 21 | 114 | 136 | + | gaagcagaacatctgaagaatgg | 40 | 65.99 | 0 | | 0 | 7 | 1117 | | | | |
| 22 | 123 | 145 | + | catctgaagaatggctgacgagg | 50 | 69.8 | 0 | | 1 | 2 | 1388 | | | | |
| 23 | 151 | 173 | + | caacctattgtgtcgacaatgg | 45 | 69.15 | 0 | | 1 | 3 | 303 | | | | |
| 24 | 154 | 176 | - | cctattgtgtcgacaatggcac | 50 | 72.27 | 0 | | 1 | 1 | 667 | | | | |
| 25 | 157 | 179 | + | attgtgtcgacaatggcactgg | 50 | 72.27 | 0 | | 1 | 2 | 499 | | | | |
| 26 | 162 | 184 | + | gtgcgacaatggcactggaatgg | 55 | 74.69 | 0 | | 1 | 6 | 677 | | | | |
| 27 | 168 | 190 | + | caatggcactggaatggtaagg | 50 | 72.31 | 0 | | 5 | 8 | 545 | | | | |
| 28 | 172 | 194 | + | ggcactggaatggtaaggcagg | 60 | 77.26 | 0 | | 0 | 2 | 447 | | | | |
| 29 | 181 | 203 | + | atggtaaggcagggtttgtgg | 50 | 73.64 | 1 | | 0 | 1 | 1511 | | | | |
| 30 | 197 | 219 | + | ttgctggtgatgtatgcaccaagg | 50 | 73.43 | 0 | | 1 | 4 | 553 | | | | |
| 31 | 198 | 220 | + | tgcgttgtatgtatgcaccaagg | 50 | 73.43 | 0 | | 1 | 9 | 616 | | | | |
| 32 | 214 | 236 | - | ccaaggcccgtttcccttagcat | 60 | 80.62 | 0 | | 1 | 1 | 121 | | | | |
| 33 | 220 | 242 | + | gccgtttccctagcattgtagg | 55 | 76.01 | 0 | | 1 | 2 | 796 | | | | |
| 34 | 221 | 243 | + | ccgtttccctagcattgtagg | 50 | 72.87 | 0 | | 1 | 3 | 538 | | | | |
| 35 | 221 | 243 | - | ccgtttccctagcattgtagg | 50 | 73.65 | 0 | | 1 | 6 | 1777 | | | | |

<http://crispr.dbcls.jp/>

● PAMに隣接し、特異性の高い20塩基を選択

ゲノムのほかの領域とは塩基配列が一致せず、標的とする部位とだけ完全一致する配列を選択。特にPAM近傍のseed(12塩基または8塩基) の特異性を重視。

● 大量設計にも対応

ヘルプページにてスクリプトを公開

● 多くの生物種に対応

350種の生物種に対応 (GGGenomeと同じ)

● 無償で自由に利用可能

商用利用であっても無償。

利用記録は当センターにおいて機密扱い。

ゲノムが公開されていれば対応します。
ゲノム配列の所在、生物種に関する情報
をご連絡ください（項目はヘルプページ
の一覧を参照）

検索可能なデータベース一覧(ゲノム)

Show 25 entries Search: plant

| Database | Source | Group | Species | 生物種 | Latin name | Assembly information |
|-----------------------------|---------------|-------|------------------------|------------------------|--------------------------------------|--|
| ASM34733v1 | EnsemblPlants | Plant | Tausch's goatgrass | タルホコムギ | <i>Aegilops tauschii</i> | ASM34733v1 (Dec, 2013) |
| AMTR1.0 | EnsemblPlants | Plant | <i>A. trichopoda</i> | アムボレラ・トリコポダ | <i>Amborella trichopoda</i> | AMTR1.0 (Jan, 2014) |
| Araly v.1.0 | EnsemblPlants | Plant | Lyre-leaved rock-cress | シロイヌナズナ属 | <i>Arabidopsis lyrata</i> | v.1.0 (Dec, 2008) |
| TAIR10_en | EnsemblPlants | Plant | Thale cress | シロイヌナズナ | <i>Arabidopsis thaliana</i> | TAIR10 (Sep, 2010) |
| Bradi v1.0 | EnsemblPlants | Plant | Purple false brome | セイヨウヤマカモジ, ミナトカモジグサ | <i>Brachypodium distachyon</i> | v1.0 (Jan, 2009) |
| Braol v2.1 | EnsemblPlants | Plant | Wild cabbage | ヤセイカンラン, ワイルドキャベツ | <i>Brassica oleracea</i> | v2.1 |
| IVFCAASv1 | EnsemblPlants | Plant | Chinese cabbage | ハクサイ, サントウサイ | <i>Brassica rapa ssp. pekinensis</i> | IVFCAASv1 (Aug, 2009) |
| Chlre v3.1 | EnsemblPlants | Plant | Green algae | クラミドモナス | <i>Chlamydomonas reinhardtii</i> | v3.1 (Nov, 2007) |
| ASM9120v1 | EnsemblPlants | Plant | Red alga | シアニディオシゾン | <i>Cyanidioschyzon merolae</i> | ASM9120v1 (Nov, 2008) |
| Soybn V1.0 | EnsemblPlants | Plant | Soybean | ダイズ | <i>Glycine max</i> | V1.0 (Jan, 2010) |



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