

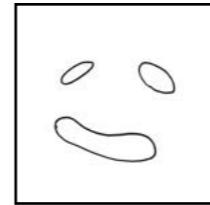
統合データベース講習会 AJACSオンライン2

塩基配列解析のための データベース・ウェブツール

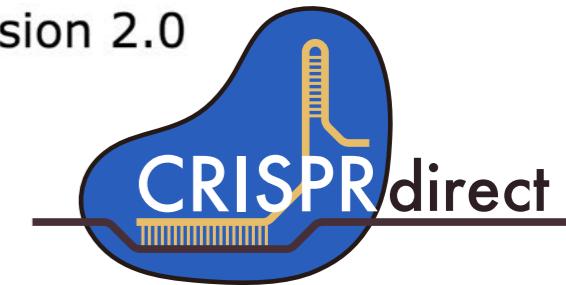
2020年10月14日
ライフサイエンス統合データベースセンター (DBCLS)
内藤雄樹

● 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

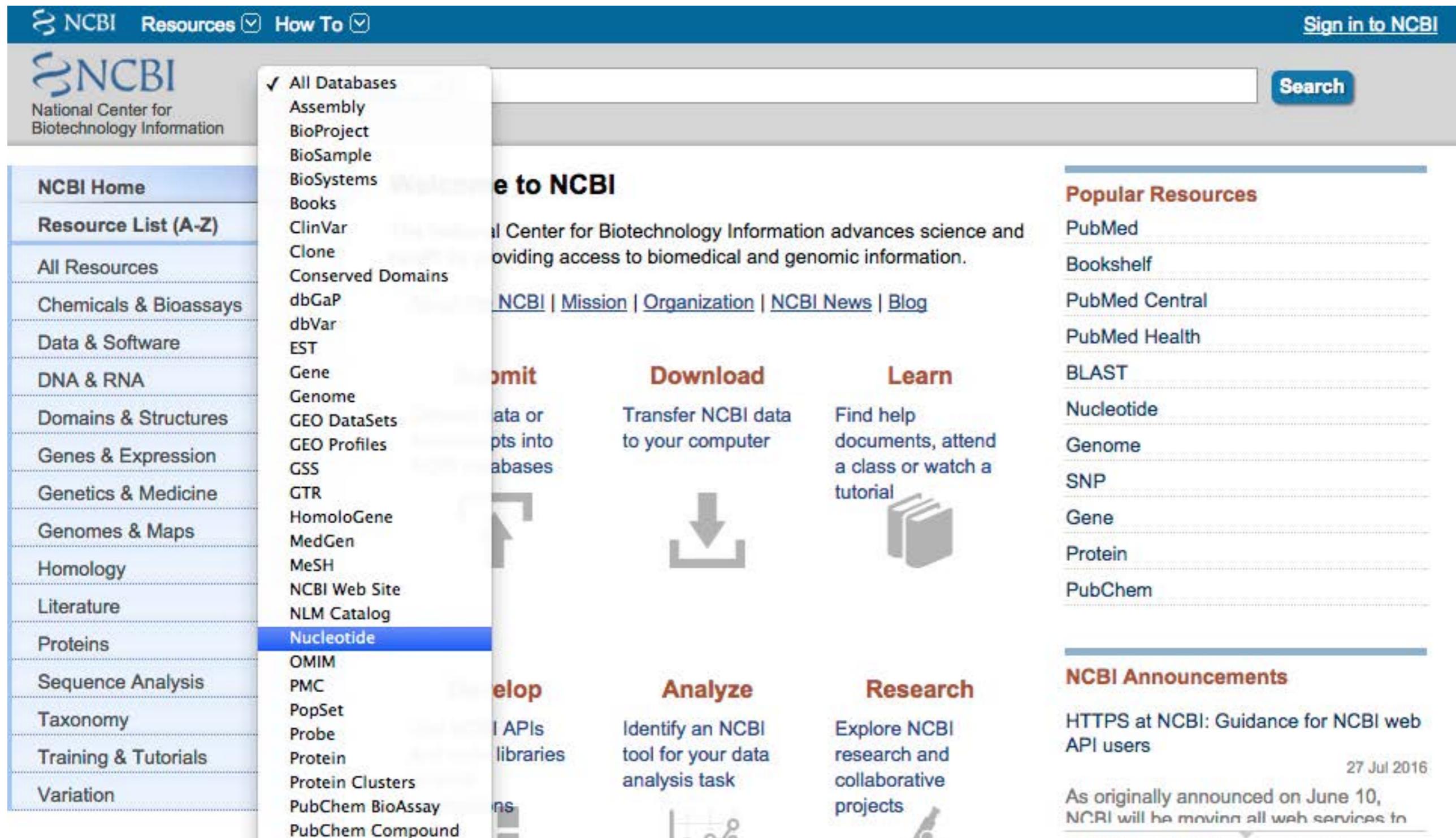
Database Center for Life Science =



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



The screenshot shows the NCBI homepage with a blue header bar containing the NCBI logo, a search bar, and links for "Resources" and "How To". On the left, there's a sidebar with a "NCBI Home" section and a "Resource List (A-Z)" section. The "Resource List" section is expanded, showing categories like 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, and PubChem Compound. A dropdown menu for "All Databases" is open. The main content area features sections for "Welcome to NCBI", "Submit", "Download", "Learn", "Analyze", and "Research". A "Popular Resources" sidebar on the right lists PubMed, Bookshelf, PubMed Central, PubMed Health, BLAST, Nucleotide, Genome, SNP, Gene, Protein, and PubChem. A "NCBI Announcements" sidebar at the bottom right discusses HTTPS and a move of services.

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

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NLM Catalog

Nucleotide

OMIM

PMC

PopSet

Probe

Protein

Protein Clusters

PubChem BioAssay

PubChem Compound

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PubMed Health

BLAST

Nucleotide

Genome

SNP

Gene

Protein

PubChem

NCBI Announcements

HTTPS at NCBI: Guidance for NCBI web API users

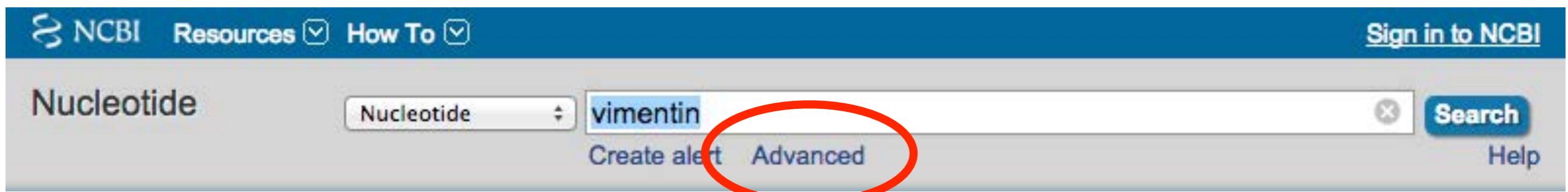
As originally announced on June 10, NCBI will be moving all web services to

27 Jul 2016

● 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。

- 国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)

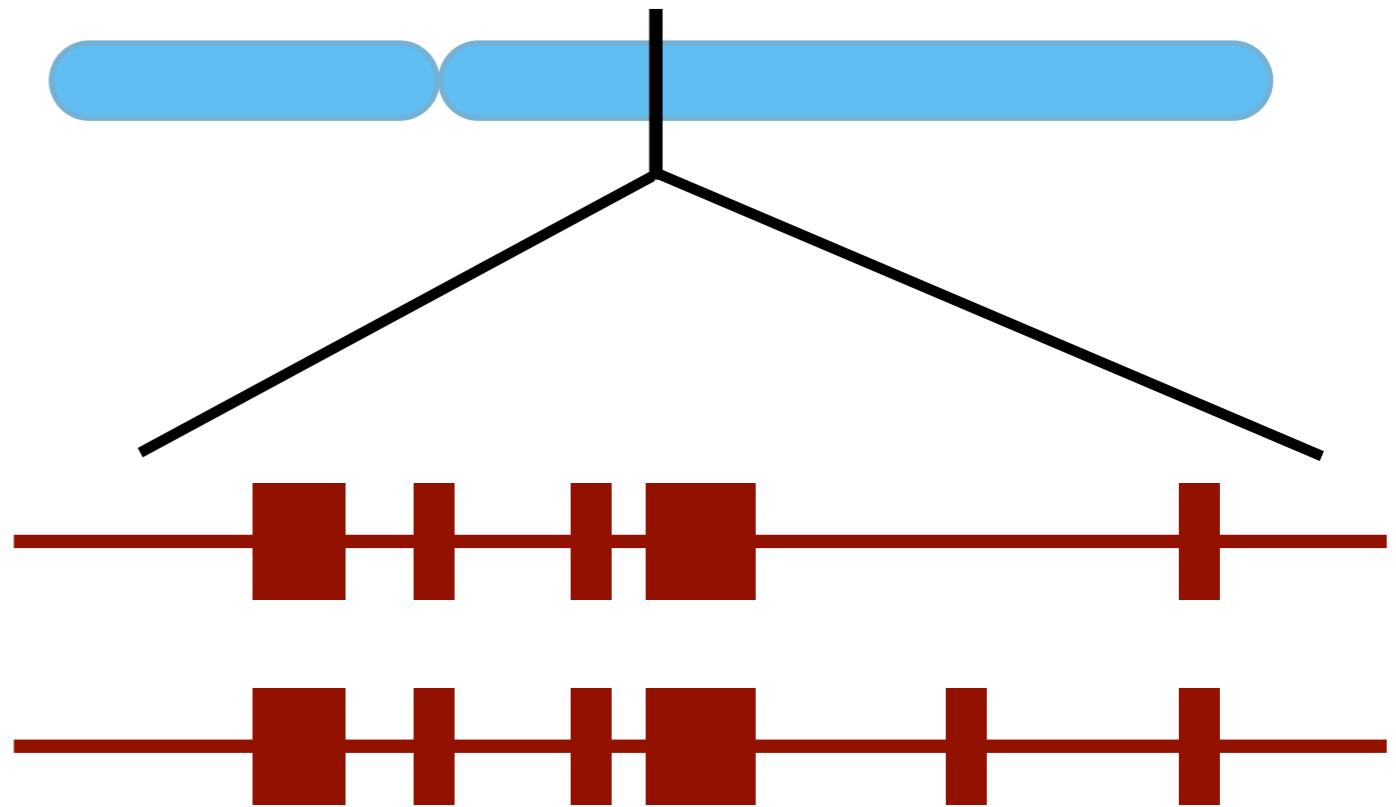
RefSeq ID:

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

[Help](#) | [Advanced search](#) | [English](#) | [旧バージョン](#)

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 **GGenome** 《グゲゲノム》へ
 - ヒトゲノムの検索例：<http://GGenome.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](#)

遺伝子名を検索

統合遺伝子検索

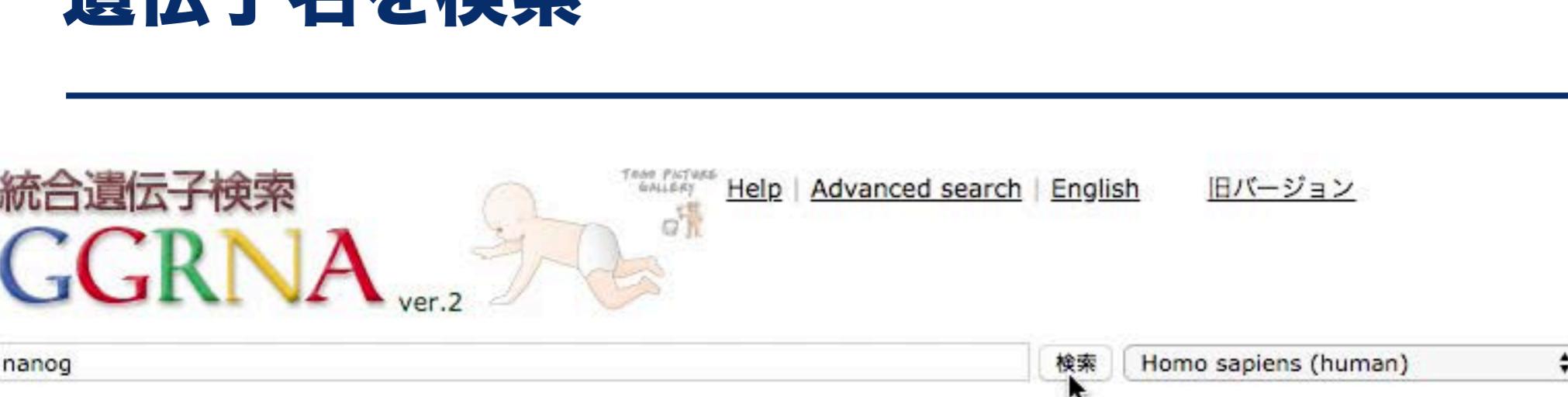
GGRNA ver.2

TRIM PICTURES GALLERY

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nanog

Homo sapiens (human)



2018-06-25 12:03:29, GGRNA : RefSeq release 88 (May, 2018)

Summary:

- [nanog \(50\)](#)
- [INTERSECTION \(50\)](#)

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。

RefSeqの転写産物

- mRNA (NM_, XM_)
- ncRNA (NR_, XR_)

[Homo sapiens Nanog homeobox retrogene P8 \(NANOGP8\), mRNA.](#) (1999 bp)

LOCUS NM_001355281 1999 bp mRNA linear PRI 01-MAY-2018 DEFINITION Homo sapiens **Nanog** homeobox retrogene P8 (**NANOGP8**), mRNA. ACCESSION NM_001355281 VERSION NM_001355281.1 KEYWORDS RefSeq. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo. REFERENCE COMMENT VALIDATED REFSEQ: This record has undergone validation or preliminary review. The reference sequence was derived from AC021231.8. Summary: This gene represents a transcribed retrogene of...

Synonym: **NANOGP1**; PNB

[NM_001355281.1 - Homo sapiens \(human\) - NCBI - UCSC - RefEx\(expression\)](#)

[Homo sapiens Nanog homeobox \(NANOG\), transcript variant 2, mRNA.](#) (2055 bp)

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 COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from DC425336.1, AY578089.1, AC006517.46 and AI656990.1. On Jul 10, 2014...

[NM_001297698.1 - Homo sapiens \(human\) - NCBI - UCSC - RefEx\(expression\)](#)

[Homo sapiens Nanog homeobox \(NANOG\), transcript variant 1, mRNA.](#) (2103 bp)

LOCUS NM_024865 2103 bp mRNA linear PRI 07-MAY-2018 DEFINITION Homo sapiens **Nanog** homeobox (**NANOG**), transcript variant 1, mRNA. ACCESSION NM_024865 VERSION NM_024865.3 KEYWORDS RefSeq. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae;

遺伝子名を検索

Gene & transcript search
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[Previous release \(v1\)](#)

GGRNA

ver.2

2018-06-25 12:03:36, GGRNA.v2 : RefSeq release 88 (May, 2018)

LOCUS NM_001355281 **1999 bp** mRNA linear PRI 01-MAY-2018
DEFINITION Homo sapiens **Nanog** homeobox retrogene P8 (**NANOGP8**), mRNA.
ACCESSION NM_001355281
VERSION NM_001355281.1
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 1999)
AUTHORS Wang R, Bhattacharya R, Ye X, Fan F, Boulbes DR, Xia L and Ellis LM.
TITLE Endothelial cells activate the cancer stem cell-associated **NANOGP8** pathway in colorectal cancer cells in a paracrine fashion
JOURNAL Mol Oncol 11 (8), 1023-1034 (2017)
PUBMED 28453235
REMARK GeneRIF: studies demonstrated a paracrine role for endothelial cells in regulating the cancer stem cells phenotype and chemoresistance in colorectal cancer cells by AKT-mediated induction of **NANOGP8**.
REFERENCE 2 (bases 1 to 1999)
AUTHORS Wang B, Chen Q, Cao Y, Ma X, Yin C, Jia Y, Zang A and Fan W.
TITLE LGR5 Is a Gastric Cancer Stem Cell Marker Associated with Stemness and the EMT Signature Genes **NANOG**, **NANOGP8**, PRRX1, TWIST1, and BMI1
JOURNAL PLoS ONE 11 (12), e0168904 (2016)
PUBMED 28033430
REMARK GeneRIF: LGR5-expressing fraction of CD54+ cells represents gastric cancer CSCs, in which LGR5 is closely associated with stemness and EMT core genes
Publication Status: Online-Only
REFERENCE 3 (bases 1 to 1999)
AUTHORS Kawamura N, Niimura K, Nagano H, Yamaguchi S, Nonomura N and Kaneda

Accession番号を検索

統合遺伝子検索

GGRNA ver.2

Help | Advanced search | English | 旧バージョン

NM_003380  Homo sapiens (human) ▲

2018-06-26 04:45:48, 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

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](#)

統合遺伝子検索

GGRNA



TESS PASTORE
GALLERY

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旧バージョン

caagaagagattgc



Homo sapiens (human)

4

2018-06-26 04:46:08, GGRNA : RefSeq release 88 (May, 2018)

Summary:

- seq:caagaagagattgc (10)
 - **INTERSECTION (10)**

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: Homo sapiens vimentin (VIM), transcript variant X1, mRNA. (1873 bp)

tcctgtggccgagctcgacgactaaggccaaggcaagtgcgcctggggaccttacgaggaggatgcggagctgcggcaggtaaccacaaagccgcgtcaggatgg
gcgcgacaacctggccgaggacatcatgcgcctccggagaaattcaggagatgttcagagagaggaagccgaaaacaccctgcaatcttcagacaggatgttacaatgcgtctggcacgtttgac
cttgaacgc当地ggaaatcttg**caagaagagattgc**cttttgaagaaaactccacgaagagggaaatccaggagctgcaggtcagattcaggaacagcatgtccaaatcgatgtggatgtttccaaggcctgacc
tcacggctgccctgcgtacgtcagcaatatgaaagtgtggctgccaagaacctgcaggaggcagaagaatggtacaaatccaagttgctgacctctgaggctgccaaccggaacaatgacgccctgcgc
caggcaaaagcaggagtcactqagtatccggagacagggtcagtcacctgtqaag...

position 832

[XM_006717500.2 - Homo sapiens \(human\) - NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

Homo sapiens vimentin (VIM), mRNA. (2195 bp)

tcctgctggccgagctcgacgcagctaaggccaaggcaagtgcgcctggggacctctacgaggaggatgcggagctgcggcggcagggtggaccagctaaccacaaagcccgcgtcagggtgg
gcgcgacaacctggccgaggacatcatgcgcctccggagaaattgcaggaggatgcttcagagagaggaagccgaaaacaccctgcaatcttcagacaggatgttgcataatgcgtctggcacgtttgac
cttgaacgc当地有三个不同的序列，它们在不同的位置上具有不同的碱基组成。第一个序列从第1位到第10位，第二个序列从第11位到第20位，第三个序列从第21位到第30位。

position 1144

NM_003380.4 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

PREDICTED: Homo sapiens dedicator of cytokinesis 5 (DOCK5), transcript variant X8, mRNA. (9068 bp)

aaggctcggaagtctggatccctacttccgagcctggatcccaga taaggatcttgc cctccctgcaacaccgagtgcccttagacagctgtgcctgagaactgcctccagccgggtcctcattccatgggctccctg
ctoactocatttcttoatcttggatatgtttaccanccccaaaaccatcatottcttccaaaaaaotcttctttqataqaattttqanqccatoccacccctccatccacatqnaattccqaaatcaatcaatcacqccctg

塩基配列を検索

統合遺伝子検索 GGRNA ver.2

caagaagagat 検索 Homo sapiens (human) ◀

TEEN PICTURE GALLERY Help | Advanced search | English 旧バージョン



Summary:

- seq:caagaagagat (465)
 - **INTERSECTION** (465)

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 family with sequence similarity 90 member A27, pseudogene \(FAM90A27P\)](#), non-coding RNA. (496 bp)

TITLE The DNA sequence and biology of human chromosome 19 JOURNAL Nature 428 (6982), 529-535 (2004) PUBMED 15057824

position 179

NR_046365.1 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

[Homo sapiens SUZ RNA binding domain containing 1 pseudogene \(LOC100130075\)](#), non-coding RNA. (1058 bp)

caccagcaacggtgtggtcagcagccccaaagtccgctagcaggcccgcctccagtcaagtccctggcacagtggaaagccgagtacaccgagggccaggaaagcgatctgggcagcgccaaccggaggagaa
gcaggagaaaaccatctcgataggcttcctgtatcttccctcaggccaaccaggatctccataaccgcagaagacagcagacagccaaataatgtgatcagacagcctctgggtcctgatgggtcacacggctca
aacagcgcagataaatgcagg**caagaagagat**ggcgactgcccgtcaacgcgtcctgggtcgccaaagggtgcactaccgtggcagacagctggacttgagcagcggaaacttgacttacttgcttg
tgatccccgttgcctccggccactgtgaccttgaatcccatgcactgtgaccccttctcccttccactgtgattggcactttgacaaggactgtcccaagtcaatggaaaggaaaaagggtgagggttaggag
aaqottqqqqqaacccaccaattactcaqagaqtcaqacaqqqc...

position 499

NR_073494.1 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

[Homo sapiens long intergenic non-protein coding RNA 2136 \(LINC02136\), long non-coding RNA.](#) (529 bp)

塩基配列を検索

統合遺伝子検索 GGRNA ver.2

Image of a crawling baby and text "IMAGE GALLERY".

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caagaaga Homo sapiens (human)

Summary:

- seq:caagaaga (32288)
 - **INTERSECTION (32288)**

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 microRNA 1248 (MIR1248), microRNA. (106 bp)

Jones S, Grocock RJ, van Dongen S, Bateman A and Enright AJ. TITLE miRBase: microRNA sequences, targets and gene nomenclature JOURNAL Nucleic Acids Res. 34 (DATABASE ISSUE), D140-D144 (2006) PUBMED 16381832

tttaccttcttgtataaggactgtctaaaattgcagacacttaggaccatgtctggcaataatgctagcagagtacaca**caagaaga**aaagtaaacagca

position 87

Synonym: hsa-mir-1248; mir-1248; MIRN1248

NR_031650.1 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

Homo sapiens uncharacterized LOC101927523 (LOC101927523), long non-coding RNA. (1014 bp)

g" /replace="t" /db_xref="dbSNP:1420081411" variation complement(1011) /gene="LOC101927523" /replace="c" /replace="t" /db_xref="dbSNP:1047866110" variation complement(1013) /gene="LOC101927523" /replace="a" /replace="c" /db_xref="dbSNP:1243001703" ORIGIN //

ggttgccaatgtttggcttccaaagaagagactagcccattgtcaccaatgcagagctggaaatgttaaggcagaatgaaaggagaaaagcacgtcctgaggcaccaagaagaagataactcgaaatgttggaaagaaacacacctgagtcattgcactgagcaacgttgcgttgcgatattgataaatctccaggcttcaacaaggggagtgcgagaataggaaactcattcaaatatctcaggtgacaagaaggatttgcgttgggttgc...

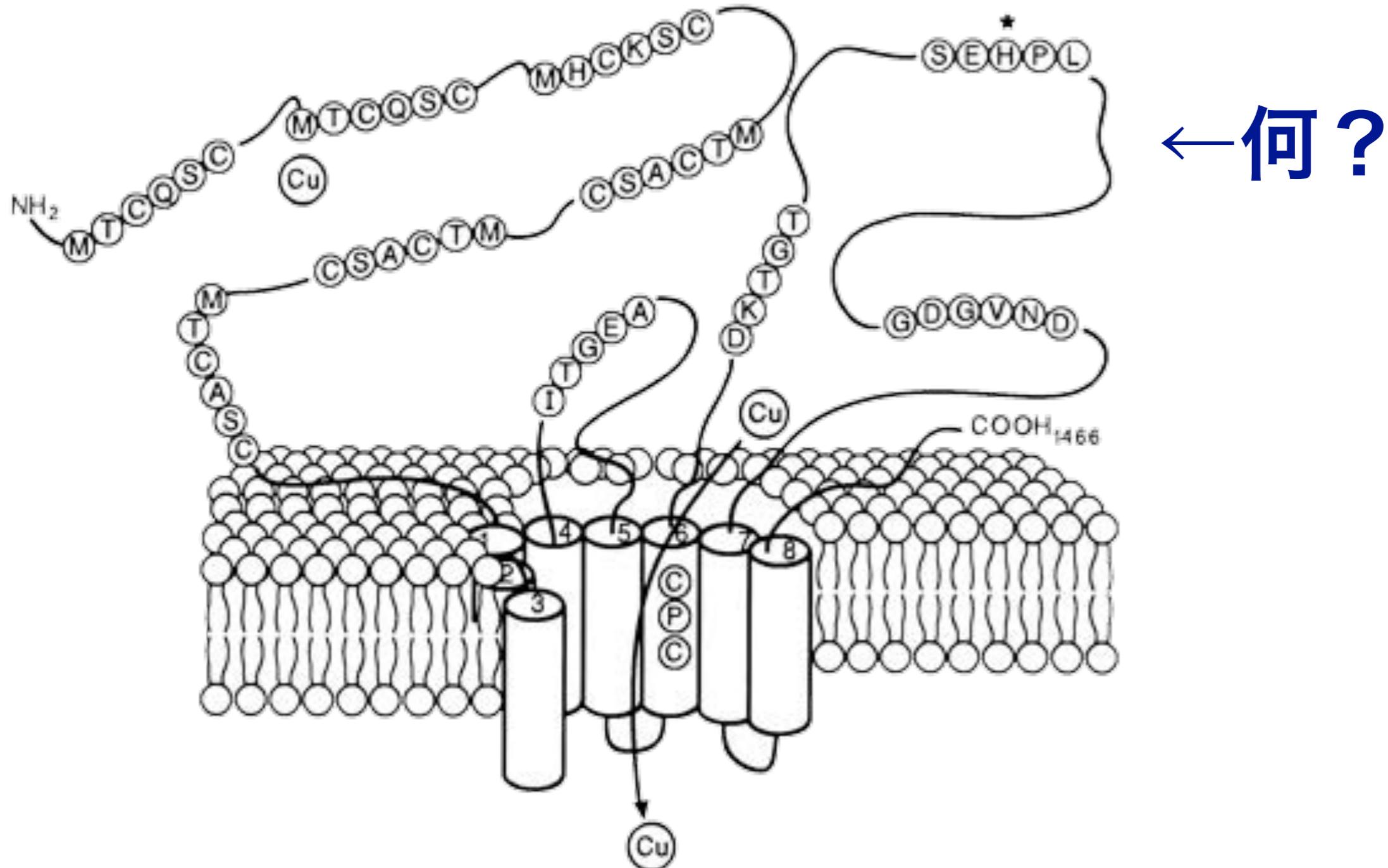
position 35

NR_120624.1 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

Homo sapiens HLA-DQB1 antisense RNA 1 (HLA-DQB1-AS1), long non-coding RNA. (552 bp)

agagtccagggtgtattgtcatcaccccccaagatctgtgcaaaggtaatcagctcatgaggacacagaacttcagcttgcagatgtgtggaggtggaaacagctgttattctctggaaatataaag
ggttcaatcaggaaaatttgtatgtatctcttccgaccactaocanccctttcactgtcactgtaaaaatcttacagocactgtggccaccatcatgttgttgcacaaatgttgttgcacatcatccttaatgttgttgc

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 ver.2

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[旧バージョン](#)

SEHPL MTCQSC

検索

Zoo (All organisms in RefSeq)

2018-06-26 05:19:49, 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**VKSIEDRISSLKGIVSMKVSLEQGSATVKYVPSVVSQQVCHQIGDMGFEASIAEGKAAS
WPSRSLPAQEAVVCLRVEG**MTCQSC**VGSIEGKVRKLQGVVRVKVSLSNQEAVITYQPYLIQPEDLRDHVNNDMGFEAAIKNKVAPLSLG...RFSGYFVPLIIIMSTLTVWIV
IGFIDFGVVQKYFPNPNKHISQTEVIIRFAFQTTSITVLCIACPCSLGLATPTAVMVGTVAAQNGILIKGGKPLEMAHKIKTVMFDTGTITHGVPRVMRVLLGDVATLPLRKV
LAVVGTAEAS**SEHPL**GVAVTKYCKEELGETLGYCTDFQAVPGCGIGCKVSNVEGILAHSERPLSAPASHLNEAGNLPAEKDAAPQTFSVLIGNREWLRNGLTISSDVSDA
MTDHEMKGQTAILVAIDGMLCGMIAIADAVKQEAALAVHTLQSMGVDVWL..."

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**VKSIEDRISSLKGIVSMKVSLEQGSATVKYVPSVVSQQVCHQIGDMGFEASIAEGKAAS
WPSRSLPAQEAVVCLRVEG**MTCQSC**VGSIEGKVRKLQGVVRVKVSLSNQEAVITYQPYLIQPEDLRDHVNNDMGFEAAIKNKVAPLSLG...RFSGYFVPLIIIMSTLTVWIV
IGFIDFGVVQKYFPNPNKHISQTEVIIRFAFQTTSITVLCIACPCSLGLATPTAVMVGTVAAQNGILIKGGKPLEMAHKIKTVMFDTGTITHGVPRVMRVLLGDVATLPLRKV
LAVVGTAEAS**SEHPL**GVAVTKYCKEELGETLGYCTDFQAVPGCGIGCKVSNVEGILAHSERPLSAPASHLNEAGNLPAEKDAAPQTFSVLIGNREWLRNGLTISSDVSDA
MTDHEMKGQTAILVAIDGMLCGMIAIADAVKQEAALAVHTLQSMGVDVWL..."

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・・・

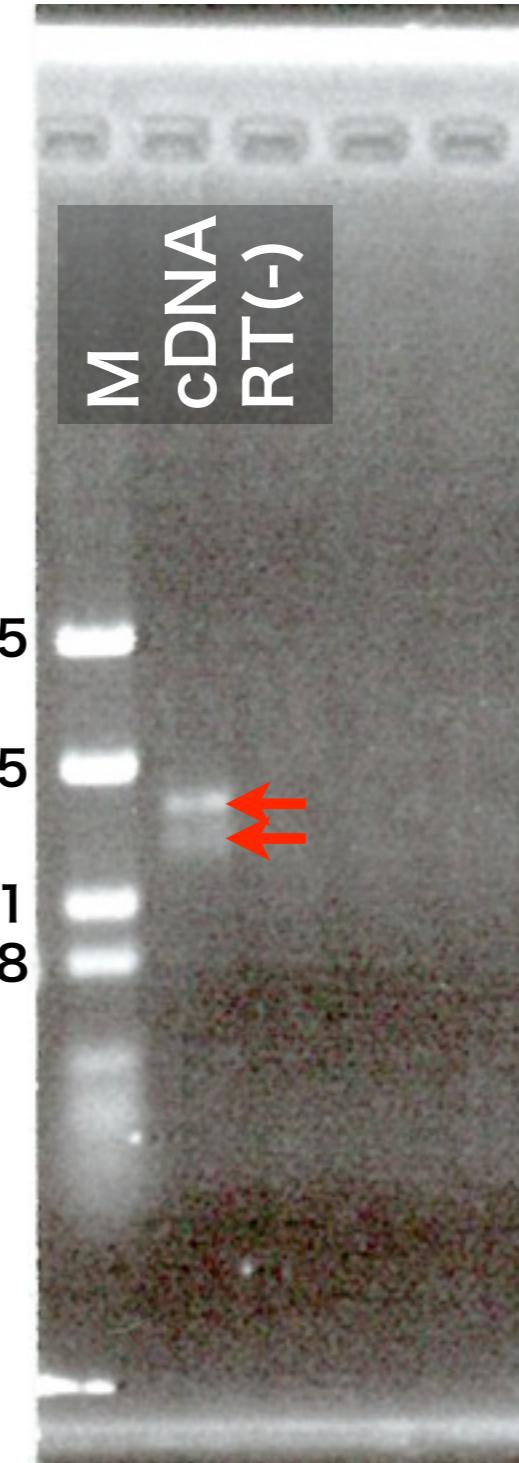
primer-F:

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:tqacqtattcactcttctqggtt (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)
tgaaaaaaattcaggacttggctgagcggcgcaattcaatcggaaatgaagcggaaagcaggcgagtcgcggccatcttgcgcggccatcaga**agctcattactttatcagtgc**aagatgcacccacaaag
aaagagtttgttattaaccccaacggaaatccgaggctgcacccatgcacggttgcgcgttgcctcaaggccctgtctataatttgcgcggccatcactggaaatccctcatccctgactttgtta
aacagacctctgaagagaagccaaagacagtgaagaactcgagtatttaaccacatcagcatcgaggactcgccggctacgagctgaccagcaaggctggctttgtccatcatcagatccacgagtgccta
aaccagaagagtgaatacgtcatggcgtgtggcaagcacacagtgcgcgggtggtaagaacaagagagtggaaagc
agtttagcctcacagaagatttcaactgtggccatcgtggaaagc
position 1892 2272 **2272 - 1892 = 380**
Synonym: C22orf12; DGCR8; Gyr; pasma
NM_001190326.1 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

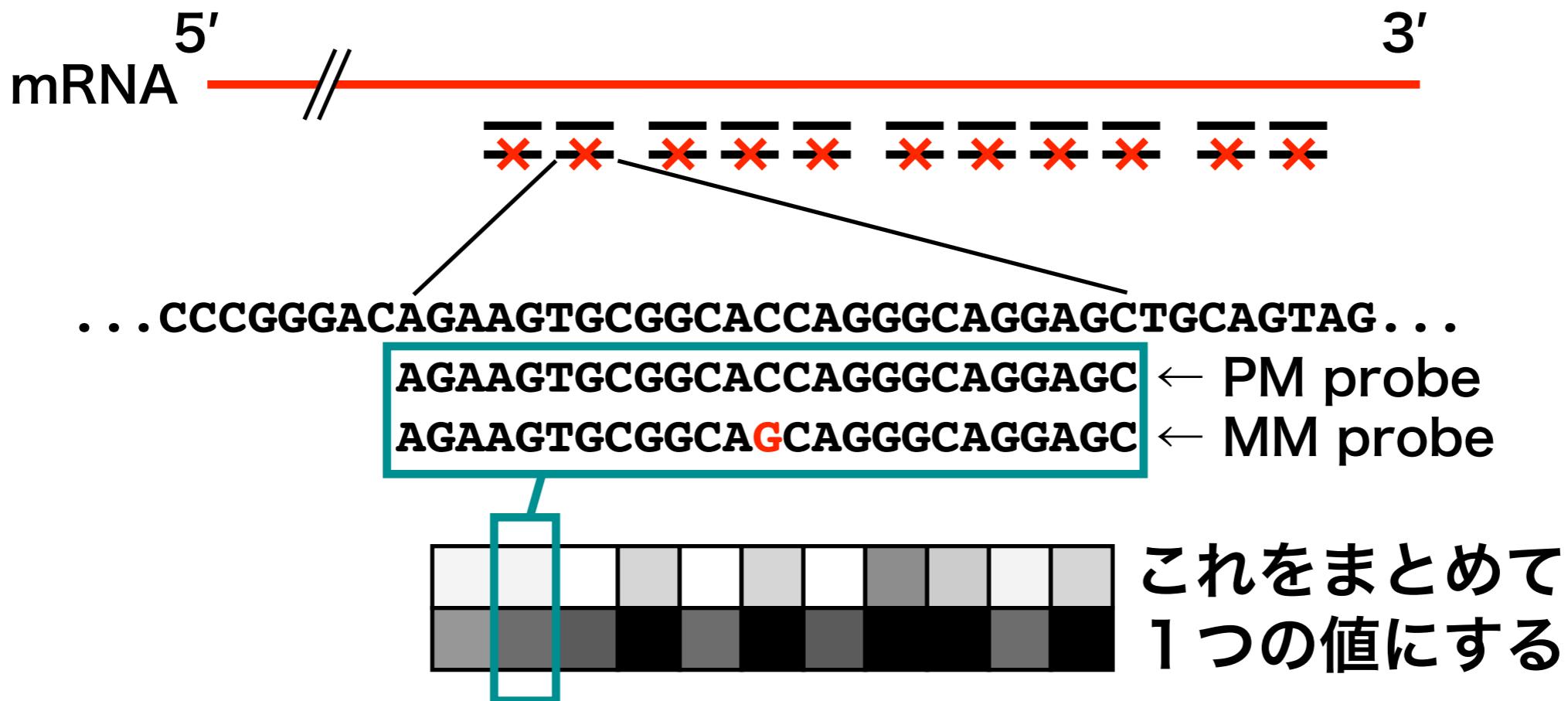
Homo sapiens DGCR8 microprocessor complex subunit (DGCR8), transcript variant 1, mRNA. (4536 bp)
gaagcggaagcaggcgaggccatcttgcgcaga **agctcattactttatcagtgca** agatgcacccacaagaaagagttgttattaaccccaacggaaatccgaggtctgcacccgc
cgagtacatgcagcgtgtcctaaggccgcgtctataatttcttgaatgtgagaacccaagtgagcccccgggcctcggtgaccattgtatgggtgacttacggatctggaaactgc
agaataaaagctgcccggactacactggaaatccatccctgactttgttaaacagacctctgaagagaagccccaaagacagtgaagaactcgagtatTTAACCATCAGCATCG
GGCAAGCACACAGTGCACGAGTCCTTAAAGAAACCATGGGATGGGTGACACGTCTATCAAGTTGAAGTGTTCTGGAAA **aaccagaagagtgaatacgtcat** ggcgtgt
ggcaagcaca...
position 1892 2371 **2371 - 1892 = 479**
Synonym: C22orf12; DGCR8; Gyr1; 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](#)

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

GGRNA ver.2

Tissue PICTURES GALLERY

Help | Advanced search | English | 日バージョン

1552311_a_at

検索

Homo sapiens (human)

2013-12-05 21:34:57, GGRNA : RefSeq release 62 (Nov, 2013)

Summary:

- [seq:TCTCCACAAACGTTTAAAATGTG \(2\)](#)
- [seq:GGGACACGGCAGTAAGCACAAGAAA \(2\)](#)
- [seq:GGCAGGAGCTGCAGTAGCTACCCCTC \(2\)](#)
- [seq:GCATGGATGGGACAGTCTGGGCCA \(2\)](#)
- [seq:ATGTGCCGGTGTACTGGTGCACAC \(2\)](#)
- [seq:AGGTCACCCCCTCTAGGCGGCAC \(2\)](#)
- [seq:AGATCACTCCCAGATCACCAAGGTCA \(2\)](#)
- [seq:AGAAGTGGGCACCAGGGCAGGAGC \(2\)](#)
- [seq:ACGGCAGTAAGCACAAGAAAGATT \(2\)](#)
- [seq:AATGTCACCGCACACCAGGCAGTGG \(2\)](#)
- [seq:AAAATGTGCCGGTGTACTGGTGCA \(2\)](#)
- **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 retina and anterior neural fold homeobox 2 \(RAX2\), mRNA.](#) (2190 bp)

```
cagccgcacggccaaaggactctgagcaaggaggctgcggggccgagaaccgcgtggactggcaagcacggctggccagtgcagcaggagggggccctgaggcatggatggacagtctggccacgc  
ccacctccgggacagaagtgcggcaccaggcaggactgcagtagctaccctccccgtctccagcctggctccccagatcactcccagatcaccaggtcacccatcttaggcggcacccacaca  
ccagtcctgtggccaacgccccccatcaccaatgtcaccgcacaccaggcagtgggacacggcagtaagcacaagaagattttttttaaagctaaaccaggccaggtgcggctcatgcctgta  
atcccagtgtttgggaggctgaggtggaggattgtgagaccagcctgggtgacacagcaagacccatctccacaaaacgtttttaaatgtgccgggtgtactggtgacacactgtcatccagctaccaag  
aagctgaggcaagaggatcacttgagccagaaggctcgaggctgcaggagctgtgatcacactg...
```

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)

マイクロアレイのプローブID

<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](#)

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

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。あまり大きいとしほうする。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

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GGGenome

TTCACTGACAACATTGAGTA

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 06:20:32, 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
GCCCGCAGCCACTTATATGTATTTTAATTCACTGACAACATTGAGTAGAAAAGATAATTTTTTTGAGACAG

◀◀ | 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 : 0 (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
AATGATCTTACTGTTAACACTGCACT**TTA**TTC**ACTGACAACATT**ACTTAAAGAAAAGAGATTATGATTGGATAAA

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

[chr2:163535086-163535100](#) ▼163535086
TGAGAAAGAGGACACC**CTAAGAATTATGGC**TTC**ACTGACAACATT**AGAGAACATATCAAACGAATATT

[chr3:117135824-117135838](#) ▼117135824
TCCCCTAGCAA**ATCAATTCAACTTCTGTT**A**TTC**ACTGACAACATTGTTTTCTACTGGCTGCAGCTTTCACAA

chr4:128011007-128011021

ゲ ゲ ゲ
GGGenome による塩基配列検索



超絶高速ゲノム配列検索

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GGGenome

TTCACTGACA

検索

Human genome, GRCh37/hg19 (Feb, 2009)



許容するミスマッチ/ギャップの数 : 0 (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
ATACTAGAATTTAAAAGCAAATGTCTTTATTCACTGACAACATAATCATCTATAAAGAAAATCCTACAT

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

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

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

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

chr1:6720825-6720824

ゲ ゲ ゲ
GGGenome による塩基配列検索



超絶高速ゲノム配列検索

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GGGenome

TTCACTGACAACATTGAGTA

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 06:21:13, 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
AGCAGTACTCAAGATCACCTTTTAAAGTTCACTG-CAACATT~~CAGTA~~GATGAAAAATGTGTAGCTGTAATTCAATTGA

[chr1:106947513-106947532](#) ▼106947513
TAGAAAACATACCACATAAAGAAGCAATCTTCACTG~~CACAA~~-ATTGAGTA~~TAAA~~TTAACCCGTTGAAAGGGTCATTA

[chr2:30898313-30898332](#) ▼30898313
GCCCCCAGCCACTTATATGTATTTTAAATTCACTGACAACATTGAGTA~~GAAAAGATA~~ATTTTTTTTTGAGACAG

[chr2:141517099-141517116](#) ▼141517099
TTTATTTCTTAACACAGCCTTGATAAAATTCACTGAC-ACATTGAGT-TAGCCATAGTGTGTAATGGGAGACTGCCA

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

chr2:186201205-186201224

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UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr1:77,930,953-77,930,971 19 bp. enter position, gene symbol, HGVS or search terms go

chr1 (p31.1) | 1p31.1 | 1q12 | 1q41 | 1q43.44

Scale: hg19
chr1: 77,930,953 - 77,930,960 - 77,930,965 - 77,930,970

UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

AK5 RefSeq Genes

Publications: Sequences in Scientific Articles

Gene Expression in 53 tissues from GTEx RNA-seq of 8555 samples (570 donors)

AK5 H3K27Ac Mark (Often Found Near Active Regulatory Elements) on 7 cell lines from ENCODE

DNase Clusters

Txn Factor ChIP

100 Vertebrates Basewise Conservation by PhyloP

Multiz Alignments of 100 Vertebrates

Gaps

Human T T C A C T G C A A C A T T C A G T A
Rhesus T T C A C T G C A A C G T T C A G C A
Mouse = = = = = = = = = = = = = = = = = = =
Dog C T C G C T G C A A C T T T C A G T A
Elephant C T C A C T G C A A T C T T C A G C C
X_tropicalis C T C A C T G C A A T C T T C A G C C
Zebrafish C T C A C T G C A A T C T T C A G C C
Lamprey C T C A C T G C A A T C T T C A G C C

Common SNPs(147)

Simple Nucleotide Polymorphisms (dbSNP 147) Found in >= 1% of Samples

Database of Genomic Variants: Structural Variation (CNV, Inversion, In/del)

● 分割統治法



● 接尾辞配列 (suffix array) + FM-index

● インデックスをSSDに置くことにより高速化

漏れのない検索を高速に実行

- 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

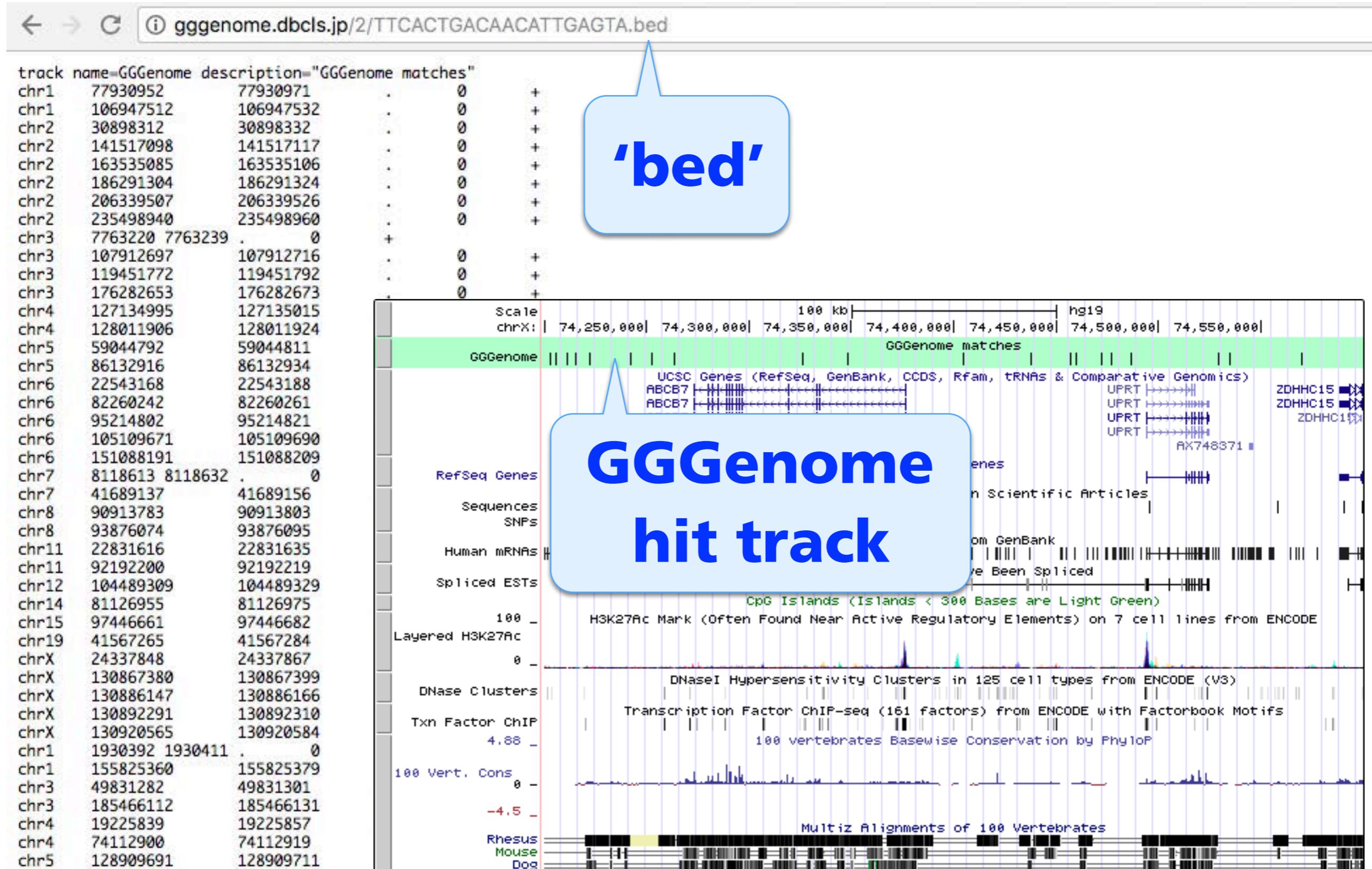
← → ⌂ ⓘ ggggenome.dbcls.jp/2/TTCACTGACAACATTGAGTA.txt

```
# [ GGGenome | 2018-07-08 04:33:37 ]
# database: Human genome, GRCh37/hg19 (Feb, 2009)
# query: TTCACTGACAACATTGAGTA
# count: 36
# query: TACTCAATGTTTCAGTGAA
# count: 33
# name strand start end snippet snippet_pos snippe
chr1 + 77930953 77930971
TCATGAAATGGAAGTGTGCCACTTCAGGGCCTGTAAAGAGATAATGCTGATGCCAGGCCA
AGTCTGTTCTGAGTTACCATGGCAACTGCTCAATTAAAGTAAAAAAATGAAAAATA
||||| - I-----X--- 18 1 0 1
chr1 + 106947513 106947532
TCATCTGGCTATATGTCCTATGTTGATAACATCAAACACGGAAAGTATAGGAAATAACATAGAAAACATACCACATAAGAAGCAATCTTCACTGCACAAATTGAGTATAAAATTAAACCGTTGAAAGGGTCATTATAT
ATGAGGAGCAGAAAGACAAGTGGAGTATAAGAAAATGGCTTAAAGTCAAACTGCCT 106947413 106947632
||||||||| - D - I 19 0 1 1
chr2 + 30898513 30898532
TTGATCTCCTGACCTCGTGTACCCACCTGCCTCCCCAAAGTGGGGATTACAGGCGTGAGCCACCGCCCCAGCCACTTATGTATTTAAATTCACTGACAACATTGAGTAGAAAAGATAATTTTTTTGAGACAGAGT
TGGTGCCTAGGGGGACTGCAGTGGCACAACTTGCTCACTGCAACCTCCACCTCCGTG 30898213 30898432
||||||||| - D - I 20 0 0 0
chr2 + 141517099 14
AATTTCACTAAAATTAAATAATAAAAGGAA
CTGATTTGTTCTTGTGAGCACCATTGCA
||||||||| - I
chr2 + 163535086 16
CTCATGGTGAATCCACACATATTGGACAGAGGG
TGTGGATTTGCTTAGAGTCATGAGAGTAAGA
||||| - D - X= 19
chr2 + 186291305 18
CCCATCATACCAATATCATTATCTCATCTTCCA
TTTTTTGAGCAGGCTCTATAATAACAAACTGA
||||||||| - D
chr2 + 206339508 20
ATGAATCAAAGGCTTGAACATATTGCCAACAT
GAAAAATAGTACTGTATCATTACATTGAACTT
||||||||| - I - X= 18
chr2 + 235498941 23
CTTGAAGGGGCCAGGTGGCAGACAGATAGTTCA
GGACCTATTAGAGCCTGGCTATGTTAGGAAATGCAGGGAGGGTCAAAGAACCGG
||||| - I - D 19 0 1 1
chr3 + 7763221 7763239
CAGAGATGTGCATGGATAGCTTGGTTGAGTCAGCTGGTAGTTCTCCAGTCTTCACTGATCAGTCAGACATAGATCAATTCTCACTGCAAAATTGAGTAGTGAATAAAACTTACTTCAGCTAACCTAAC
TTCTAGCACTAATCACTAGATATCCAATTAAACAAATGAATAAAATATAAA 7763121 7763339
||||| - X - 18 1 0 1
chr3 + 107912698 107912716
```

'txt'

TTCA-ACAG	"query"	7	"match"
- I -	"align"	1	"mis"
TTCACACGG	"sbjct"	1	"del"
====D==X=	"edit"	0	"ins"

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

The screenshot shows a Google Sheets interface with the following details:

- Title:** GGGenome primer search
- Toolbar:** Includes File, Edit, View, Insert, Format, Data, Tools, Help, and a message about saving changes.
- Formulas Bar:** Shows =ImportData(D2)
- Table Structure:** The table has columns A through I. Columns A, B, C, D, and E are explicitly labeled with headers. Column E contains the formula =ImportData(D2).

	A	B	C	D	E	F	G	H	I
1	Primer name	(1) Sequence	(2) GGGenome URL		(3) ImportDATA function	name	strand	start	end
2	YN001-F	caatcaccctcaccctttatatgc	http://GGGenome.dbcls.jp/rice/caatcaccctcaccctttatatgc.txt		=ImportData(D2)	chr01	+	27707	27
3	YN001-R	ccgctgtgaac		chr01 - 28071 28092 ATATTGTTGGTACGAGTA 27971 28192	chr01	-	28071	28	
4	YN002-F	tgatccaaata							
5	YN002-R	catgcaaggta							
6	YN003-F	acgtactgtgg							
7	YN003-R	acccaaccta							
8	YN004-F	atcagattccggccggccg							
9	YN004-R	ggagagatctggttggggag							
- Callout Boxes:**
 - A blue callout box points to the formula =ImportData(D2) in cell E2, with the text '= ImportData(D2)' inside.
 - A larger blue callout box at the bottom points to the column header 'PCRプライマー配列' (PCR Primer Array).

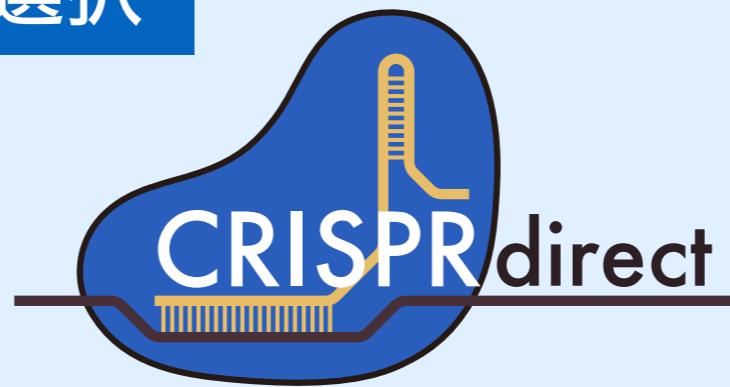
表計算ソフトから GGGenome 検索

<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。

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

CRISPRdirect によるガイド RNA 設計

 — Rational design of CRISPR/Cas target. [Help](#)

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

[retrieve sequence](#)

or Paste a nucleotide sequence: [?](#)

Accession番号

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](#)

PAM

**オフターゲット検索のための
生物種 を選択**

Whats' new:

- 2017-06-19 Added 8 species - List

CRISPRdirect によるガイド RNA 設計

retrieve sequence

or Paste a nucleotide sequence: ?

```
agtgcaccccggttcgcctcgcgagctcgctttacaccggccgcccggactctccagactccggaggagaagcg  
atcggttacacgtacgcctcgtaaggcagaaggcagaacatctgaagaatggctgacgaggatattcaacctatttgtgtgcgacaatg  
gcactggaaatggtaaaggcagggtttgctggatgtatgcaccaaggccgtttcccttagcattgttagggagaccacgtcacacc  
ggtgtcatggttgggatgggccaaggatgcctatgtgggtatgtgaagctcaggaaaaagggtatcctgactctaaagtaccc  
aattgaacatggaaattgtcaataactgggatgacatggagaaaatatggcaccacacccttacaatgagcttcgtgtgcacctg  
aagatcaccctgtattactaactgaagccccctcaatcccaaagccaaacagagagaagatgacacagatcatgtttgagaccttc  
aattgcccagcaatgtatgtcgcaatccaggctgttatccctgt
```

数文字ほど入力すると
生物種を検索 できる

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

Specificity check: rice

design

What's new:

- 2017-06-15 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	-	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	-	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	-	ccggccgagctctccagactccggagg [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	+	catctgaagaatggctgacggagg [gRNA]	50.00 %	69.80 °C	-		1 [detail]	2 [detail]	1388 [detail]
151 - 173	+	caacccatttgtgtgcgacaaatggc [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 - end	target sequence	sequence information				number of target sites		
		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 %				1 [detail]	1 [detail]	276 [detail]
11 - 33	ccgttccgcctcgctcgcgagctc [gRNA]	70.00 %				4 [detail]	4 [detail]	911 [detail]
18 - 40	cctcgctcgcgagctcgctttac [gRNA]	70.00 %				4 [detail]	4 [detail]	1072 [detail]
47 - 69	ccggccggccgagctctccaga [gRNA]	75.00 %				305 [detail]	305 [detail]	79033 [detail]
50 - 72	ccggccggagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	ccggccggagctctccagactcgg [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 75	ccggagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 78	ccgagctctccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	ccgagctctccagactccggagg [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	ccggaggaggaaagcgatcgttac [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	caaccttattgtgtcgacaaatggc [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	attgtgtcgacaaatggcacatgg [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

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		
start	- end		GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	12mer +PAM	8mer +PAM
7 - 29	-	cctcccggttcgcctcgctcgac [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cccgtttcgccctcgctcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccgttccgcctcgctcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgagctcggttac [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	+	ccggccggagctctccagactc [cg] [gRNA]	70.00 %	80.41 °C	-	SacI	1 [det]		
53 - 75	-	ccggccggagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [det]		
56 - 78	+	ccggccggagctctccagactccgg [agg] [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	+	agctctccagactccggagg [agg] [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	+	gaaggcagaacatctgaagaa [tgg] [gRNA]	40.00 %	65.99 °C	-		0 [det]	7 [det]	1117 [detail]
123 - 145	+	catctgaagaatggctgacg [agg] [gRNA]	50.00 %	69.80 °C	-		1 [det]	2 [det]	1388 [detail]
151 - 173	+	caaccttattgtgtcgacaa [tgg] [gRNA]	45.00 %	69.15 °C	-		1 [det]	3 [det]	303 [detail]
154 - 176	-	cctattgtgtcgacaaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [det]	1 [det]	667 [detail]
157 - 179	+	atttgtgtcgacaaatggcac [tgg] [gRNA]	50.00 %	72.27 °C	-		1 [det]	2 [det]	499 [detail]
162 - 184	+	gtgcgacaaatggcactggaa [tgg] [gRNA]	55.00 %	74.69 °C	-		1 [det]	6 [det]	677 [detail]

Showing 1 to 20 of 71 entries

First Previous 1 2 3 4 Next Last

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				restriction sites	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	cctcccggttcgcctcgctcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]	
10 - 32	cctcccggttcgcctcgctcgca [gRNA]				NruI	1 [detail]	1 [detail]	276 [detail]	
11 - 33	cctcccggttcgcctcgctcgca [gRNA]				NruI SacI	1 [detail]	4 [detail]	911 [detail]	
18 - 40	cctcccggttcgcctcgctcgca [gRNA]				NruI SacI	1 [detail]	4 [detail]	1072 [detail]	
47 - 69	cctcccggttcgcctcgctcgca [gRNA]				SacI	1 [detail]	305 [detail]	79033 [detail]	
50 - 72	cctcccggttcgcctcgctcgca [gRNA]				SacI	1 [detail]	37 [detail]	3555 [detail]	
53 - 75	cctcccggttcgcctcgctcgca [gRNA]				SacI	1 [detail]	3 [detail]	175 [detail]	
53 - 75	cctcccggttcgcctcgctcgca [gRNA]				SacI	1 [detail]	15 [detail]	2679 [detail]	
56 - 78	cctcccggttcgcctcgctcgca [gRNA]				BspEI SacI	1 [detail]	4 [detail]	793 [detail]	
56 - 78	cctcccggttcgcctcgctcgca [gRNA]				BspEI SacI	1 [detail]	1 [detail]	1295 [detail]	
59 - 81	cctcccggttcgcctcgctcgca [gRNA]				BspEI	1 [detail]	2 [detail]	608 [detail]	
65 - 87	cctcccggttcgcctcgctcgca [gRNA]				BspEI	1 [detail]	6 [detail]	375 [detail]	
72 - 94	cctcccggttcgcctcgctcgca [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]	
102 - 124	cctcccggttcgcctcgctcgca [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	caacctattgtgtgcgacaa tgg [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	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]	

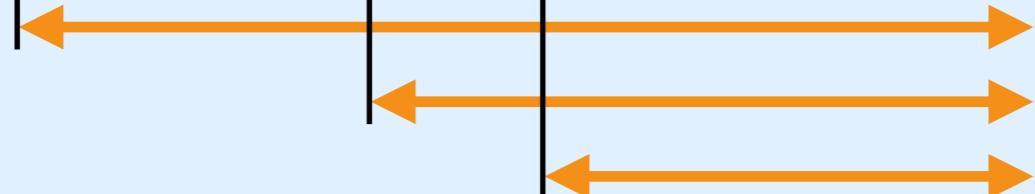
Showing 1 to 20 of 71 entries

First Previous **1** 2 3 4 Next Last

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

Search		Sequence	Sequence Information			sites	Off-target sites		8mer + PAM
Start	End		Length	GC% of 20mer	Tm of 20mer		+PAM	+PAM	
7 - 29	-	cctcccgttcgcctcgctcgcg [gRNA]	23mer	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail] 370 [detail]
10 - 32	-	cccggttgcgcctcgctcgcgagct [gRNA]	23mer	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail] 276 [detail]
11 - 33	-	ccgtttcgcgcctcgctcgcgagctc [gRNA]	23mer	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail] 911 [detail]
18 - 40	-	cctcgctcgcgagctcgctttac [gRNA]	23mer	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail] 1072 [detail]
47 - 69	-	ccggccggccgagctctccaga [gRNA]	23mer	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail] 79033 [detail]
50 - 72	-	ccggccggagctctccagactc [gRNA]	23mer	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail] 3555 [detail]
53 - 75	+	ccggccggagctctccagactc [cg] [gRNA]	23mer	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail] 175 [detail]
53 - 75	-	ccggagctctccagactccgg [gRNA]	23mer	70.00 %	80.27 °C	-	SacI	1 [detail]	1 [detail] 2679 [detail]
56 - 78	+	ccgagctctccagactccgg [agg] [gRNA]	23mer	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	1 [detail] 1 [detail]
56 - 78	-	ccgagctctccagactccggagg [gRNA]	23mer	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail] 1 [detail]
59 - 81	+	agctctccagactccggagg [agg] [gRNA]	23mer	65.00 %	79.68 °C	-	BspEI	1 [detail]	1 [detail] 1 [detail]
65 - 87	-	ccaaactccggaggaggaaagcga [gRNA]	23mer	65.00 %	78.93 °C	-	BspEI	1 [detail]	1 [detail] 1 [detail]
72 - 94	-	ccggaggaggaaagcgatcgttac [gRNA]	23mer	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail] 3180 [detail]
102 - 124	-	cctcggtcaaggcagaaggcagaaca [gRNA]	23mer	50.00 %	71.33 °C	-		0 [detail]	3 [detail] 588 [detail]
114 - 136	+	gaaggcagaacatctgaagaa [tgg] [gRNA]	23mer	40.00 %	65.99 °C	-		0 [detail]	7 [detail] 1117 [detail]
123 - 145	+	catctgaagaatggctgacg [agg] [gRNA]	23mer	50.00 %	69.80 °C	-		1 [detail]	2 [detail] 1388 [detail]
151 - 173	+	caaccttattgtgtcgacaa [tgg] [gRNA]	23mer	45.00 %	69.15 °C	-		1 [detail]	3 [detail] 303 [detail]
154 - 176	-	cctattgtgtcgacaaatggcac [gRNA]	23mer	50.00 %	72.27 °C	-		1 [detail]	1 [detail] 667 [detail]
157 - 179	+	atttgtgtcgacaaatggcac [tgg] [gRNA]	23mer	50.00 %	72.27 °C	-		1 [detail]	2 [detail] 499 [detail]
162 - 184	+	gtgcgacaaatggcactggaa [tgg] [gRNA]	23mer	55.00 %	74.69 °C	-		1 [detail]	6 [detail] 677 [detail]

Showing 1 to 20 of 71 entries

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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

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- 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

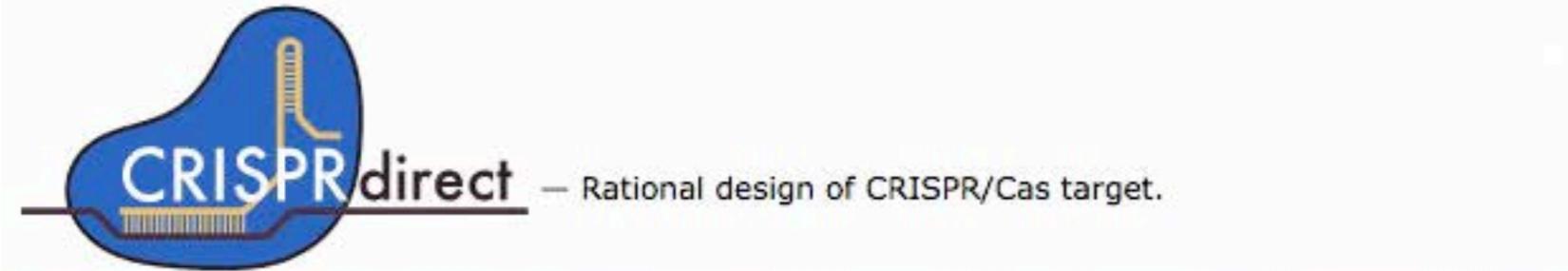
position		target sequence	sequence information				number of target sites		
start - end	-	20mer+PAM (total 23mer)	GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	2mer +PAM	8mer +PAM
7 - 29	-	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	[detail]	370 [detail]
10 - 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	-	ccggccggaggaggaggacgca [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggccggaggaggacgatcggtac [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	+	catctgaagaatggctgacgg [gRNA]	50.00 %	69.80 °C	-		1 [detail]	2 [detail]	1388 [detail]
151 - 173	+	caacccatttgtgtgcgacaaatggc [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

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Graphical View:

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

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:

- CCNcccattcgccctcgactcgaa (1)
- tcacqaqcqaaaaacqaaacqgggNGG (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
CCAACGAGGCCAGGTGAGCTCTCCCCCTCCCCCGATTCGCTCGCTTCGCGACCGAGTTCACTTGAGCTGGGTTGCACTGAC

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGCTCGCGAGCGAGGCGAACGGGAGGTGCACTGCTGGTGGACGGACGAAGA

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGCTCGCGAGCGAGGCGAACGGGAGGTGCACTGCTGGTGGACGGACGAAGA

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGCTCGCGAGCGAGGCGAACGGGAGGTGCACTGCTGGTGGACGGACGAAGA

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGCTCGCGAGCGAGGCGAACGGGAGGAGTGCACTGCTGGTGGACGGACGAAGA

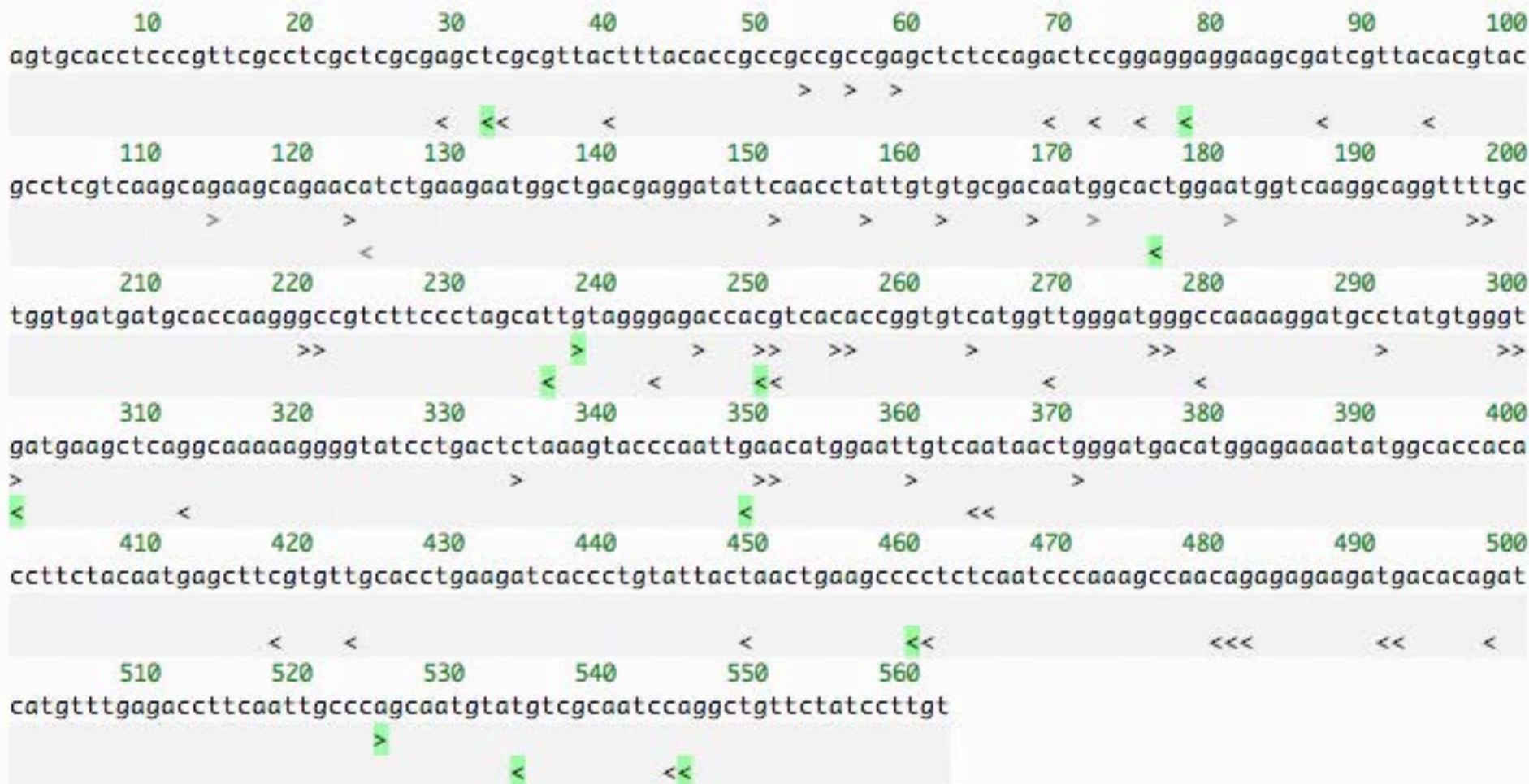
CRISPRdirect によるガイド RNA 設計

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

First Previous 1 2 3 4 Next Last

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
catgtttgagaccttcaattgcccgccatgttatgttcgcataatccaggctgttctatccttgt
 >
 < <<

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_(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	-	cctcccggttcgcctcgctcgca	75	83.48	0	Nrul	1	5	370				
8	10	32	-	cccggtcgccctcgctcgagct	70	81.73	0	Nrul	1	1	276				
9	11	33	-	ccggtcgccctcgctcgagctc	70	81.09	0	Nrul,Sacl	1	4	911				
10	18	40	-	cctcgctcgcgagctcgctttac	70	80.24	0	Nrul,Sacl	1	4	1072				
11	47	69	-	ccggccggcccgagcttccaga	75	84.25	0	Sacl	1	305	79033				
12	50	72	-	ccggccggcggactctccagactc	70	80.41	0	Sacl	1	37	3555				
13	53	75	+	ccggccggactctccagactccgg	70	80.41	0	Sacl	1	3	175				
14	53	75	-	ccggccggactctccagactccgg	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	-	ccagactccggaggaggaaagcga	65	78.93	0	BspEI	1	6	375				
19	72	94	-	ccggaggaggaaggcgatcgttac	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。

(生物種の追加について)

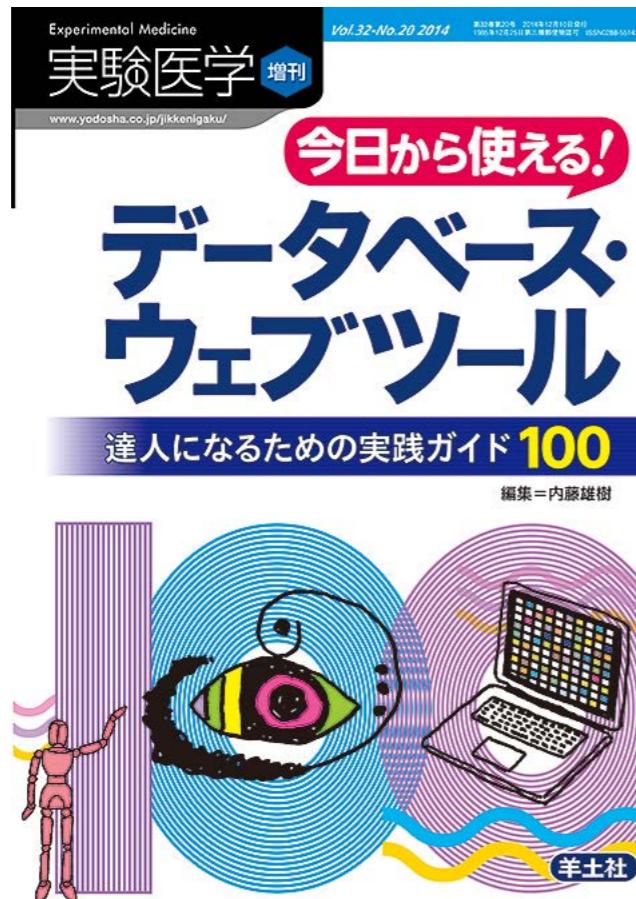
ゲノムが公開されていれば対応します。
ゲノム配列の所在、生物種に関する情報
をご連絡ください（項目はヘルプページ
の一覧を参照）

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	Aegilops tauschii	ASM34733v1 (Dec, 2013)
AMTR1.0	EnsemblPlants	Plant	A. trichopoda	アムボレラ・トリコポダ	Amborella trichopoda	AMTR1.0 (Jan, 2014)
Araly v.1.0	EnsemblPlants	Plant	Lyre-leaved rock-cress	シロイヌナズナ属	Arabidopsis lyrata	v.1.0 (Dec, 2008)
TAIR10_en	EnsemblPlants	Plant	Thale cress	シロイヌナズナ	Arabidopsis thaliana	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	Brachypodium distachyon	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	Brassica oleracea	v2.1
IVFCAASv1	EnsemblPlants	Plant	Chinese cabbage	ハクサイ, サントウサイ	Brassica rapa ssp. pekinensis	IVFCAASv1 (Aug, 2009)
Chlre v3.1	EnsemblPlants	Plant	Green algae	クラミドモナス	Chlamydomonas reinhardtii	v3.1 (Nov, 2007)
ASM9120v1	EnsemblPlants	Plant	Red alga	シアニディオシゾン	Cyanidioschyzon merolae	ASM9120v1 (Nov, 2008)
Soybn V1.0	EnsemblPlants	Plant	Soybean	ダイズ	Glycine max	V1.0 (Jan, 2010)



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