

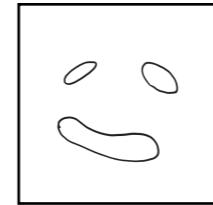
## 統合データベース講習会 AJACS番町1

# 塩基配列解析およびゲノム編集のための データベース・ウェブツール

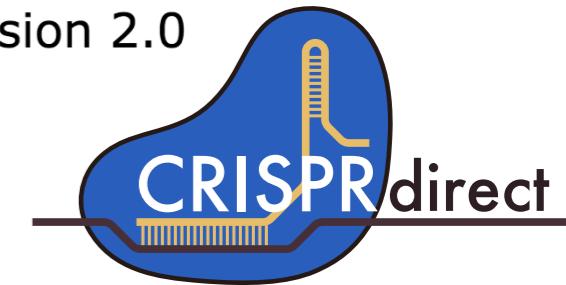
2018年 8月29日  
ライフサイエンス統合データベースセンター (DBCLS)  
**内藤雄樹**

- 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 =

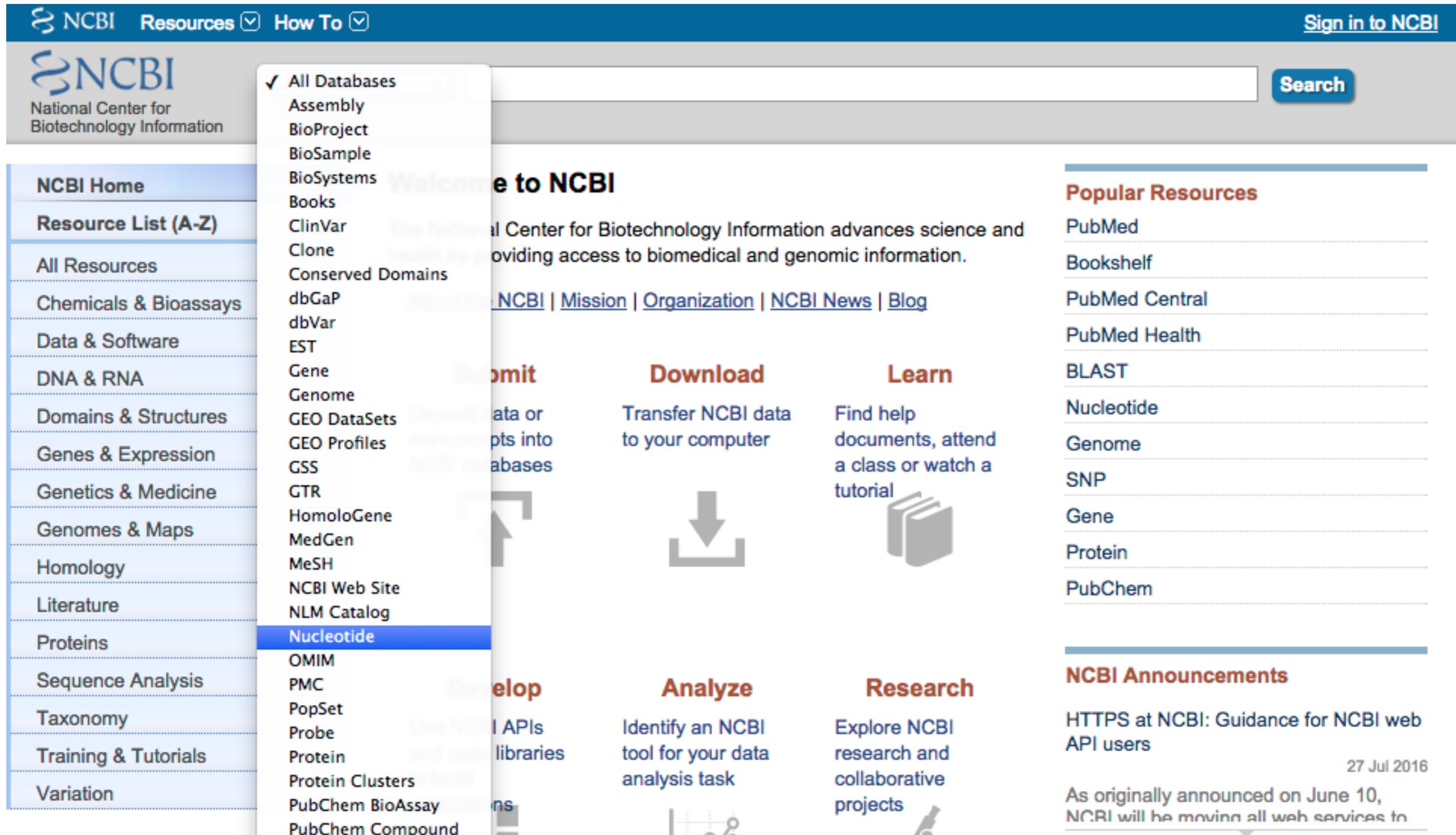


DBCLS  
Database Center  
for Life Science

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 sidebar on the left containing links for 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, and Variation. A dropdown menu under 'All Databases' lists: 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. The main content area features sections for Welcome, About NCBI, Mission, Organization, NCBI News, Blog, Submit, Download, Learn, Analyze, and Research. A search bar at the top right includes a 'Search' button and a 'Sign in to NCBI' link. 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' section at the bottom right discusses HTTPS at NCBI and a move to a new location.

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

Welcome to NCBI

NCBI advances science and providing access to biomedical and genomic information.

[NCBI](#) | [Mission](#) | [Organization](#) | [NCBI News](#) | [Blog](#)

**Submit**

Transfer NCBI data to your computer

**Download**

Find help documents, attend a class or watch a tutorial

**Analyze**

Identify an NCBI tool for your data analysis task

**Learn**

**Research**

**Popular Resources**

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

**NCBI Announcements**

HTTPS at NCBI: Guidance for NCBI web API users

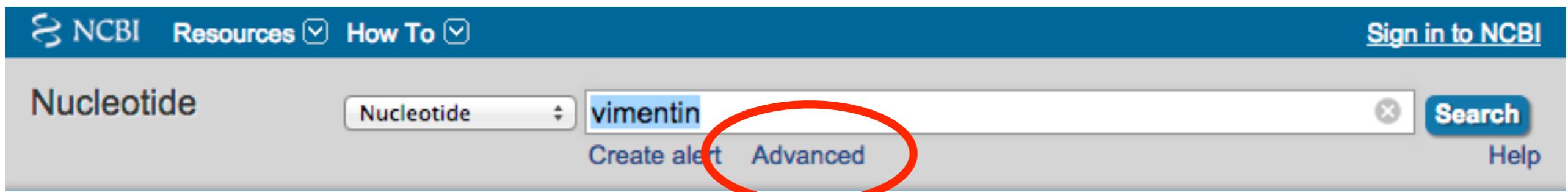
As originally announced on June 10, NCBI will be moving all web services to

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。

- 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)

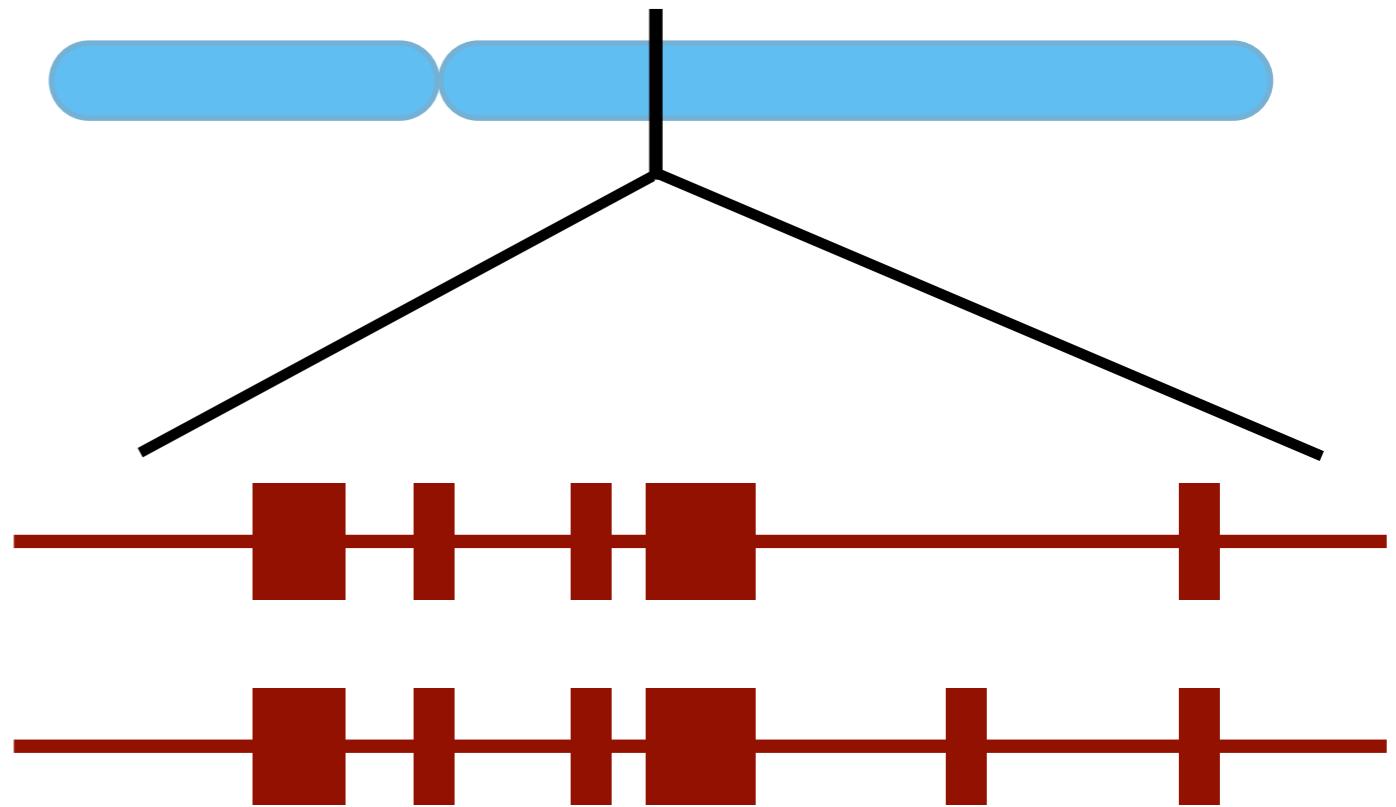
RefSeq ID:

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

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[旧バージョン](#)

GGRNA

ver.2

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。[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

PICTURES

GALLERY

IMAGE

PICTURE

GALLERY

# 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



Tissue PICTURES  
GALLERY



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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

&lt;p

# 塩基配列を検索

統合遺伝子検索

**GGRNA**

ver.2



GALLERY



TODD

PICTURES

GALLERY

TODD

PICTURES</p

# 塩基配列を検索

統合遺伝子検索

**GGRNA**

ver.2



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[旧バージョン](#)

caagaaga

検索

Homo sapiens (human)



2018-06-25 04:44:38, GGRNA : RefSeq release 88 (May, 2018)

## 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

tttaccttctgtataaggactgtgctaaaattgcagacactaggaccatgtctggcaataatgcttagcagagtacaca

caagaaga aaagtaacagca  
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 //

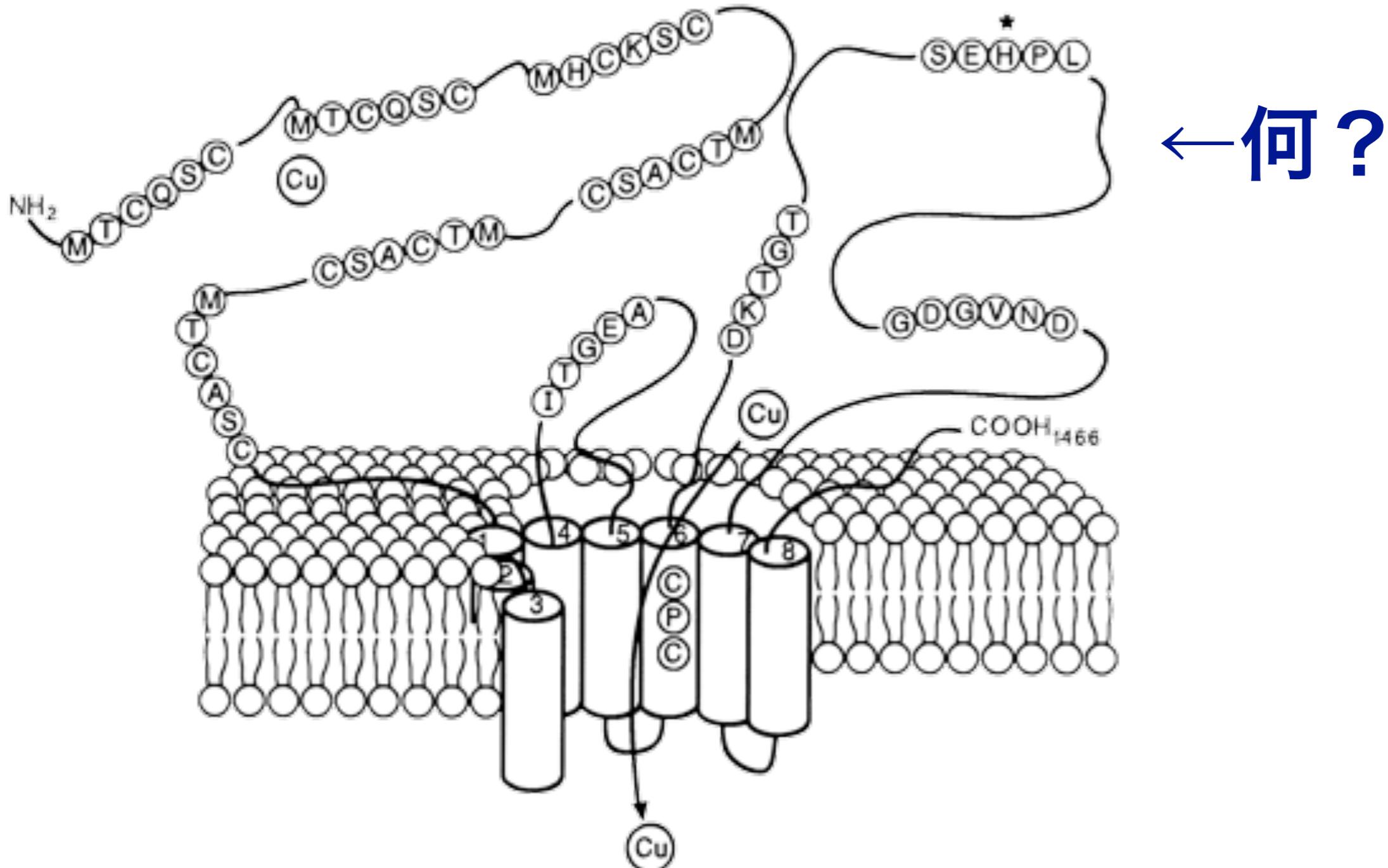
ggttgccaaatgggtttggctttcc caagaaga gactagcccattgtcaccaatgcagagctggaaatgttaaggcagaatgaaaggagaaaagcacgtcctgagcac  
 aagataactcgaaacttcaatcatatctcaggtaacttggagaagaaagcaacacctgagtcactgagcaacgttcttgttgc...  
 position 35

NR\_120624.1 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

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

agagtccagggtgtattgtcatcaccccccaagatctgtcaaaggtaatcagctcatgaggacacagaacttcagttcatgcagatgtgtggaggtggggacagctgttattttctgggaatata  
 aggtttcaatcaaggaaattnaatatctttccccaccactaaacaaacctttcaatcacttggaaaatcttacaggcaatccatgtggccacaaatgtttcatcatcattaaatcttcaat

# 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)



2018-06-25 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  
LVWWIVIGFIDFGVVQKYFPNPNKHISQTEVIIRFAFQTTSITVLCIACPCSLGLATPTAVMVGTVAAQNGILIKGGKPLEMAHKIKTVMDKTGTITHGVPRVMRVLLGD  
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  
LVWWIVIGFIDFGVVQKYFPNPNKHISQTEVIIRFAFQTTSITVLCIACPCSLGLATPTAVMVGTVAAQNGILIKGGKPLEMAHKIKTVMDKTGTITHGVPRVMRVLLGD  
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・・・

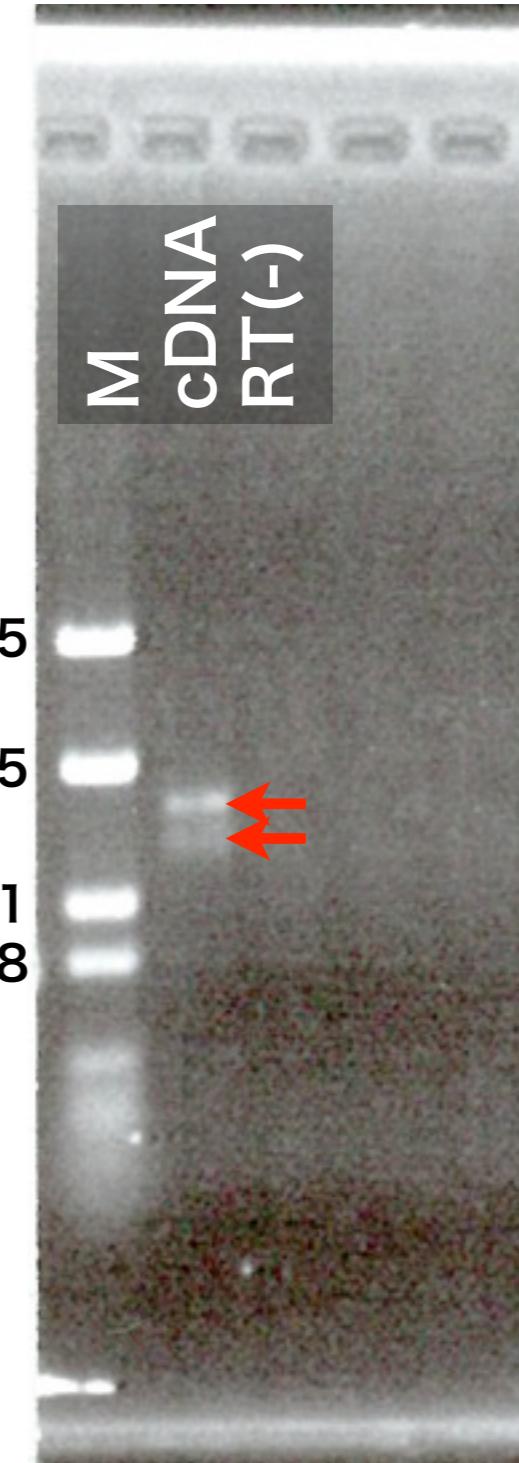
primer-F:

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)  
tgaaaaaaattcaggacttgggctgagcgccgcgaattcaatcgaaaatgaagcggaagcaggcgagtcgcagggccatcttgcaccaatcaga**agctcattactttatcagtgc**aagatgcacccacaaag  
aaagagttgttattaaccccaacggaaatccgaggctgcacccatctgcacgactatgcacgtgtcccaaggccctgtctataatttcttgaatgtgcccgagctacactggaaatcctcatccctgactttgtta  
aacagacctctgaagagaagccccaaagacagtgaagaactcgagttaccacatcagcatcgaggactcgccggctacgagctgaccagcaaggctggcttgtccatatcagatcctccacgagtgccta  
**aaccagaagagtgaatacgtcat**ggcgtgtggcaagcacacagtgcgcgggtggtaagaacaagagagtggaaagc  
agttagcctcacagaagatdttcactgtgcacccatg...  
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. \(4536 bp\)](#)  
gaagcggaaggcggagtccgagaggccatcttgcgcaga **agctcattactttatcgatgc** agatgcacccacaagaaagatgttattaaccccaacggaaatccgaggctgcacccgc  
cgagtacatgcagcgtgtctcaaggccgcgtctataatttcttgaatgtgagaacccaagttagccttgggcctcggtgaccattgtatgggtgacttacggatctggactgc  
agaataaagctgcccggactacactggaaatccatccctgactttgttaaacagacacctgaaagagaagccaaagacagtgaagaactcgagttaccatcagcatcgaggactcgccggctacgagctg  
ggcaaggcacacagtgcgcgtgtgtataaaaaacacagat...  
**position 1892 2371** **2371 - 1892 = 479**  
Synonym: C22orf12; DGCR8; Gyr; pasha  
NM\_022720.6 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

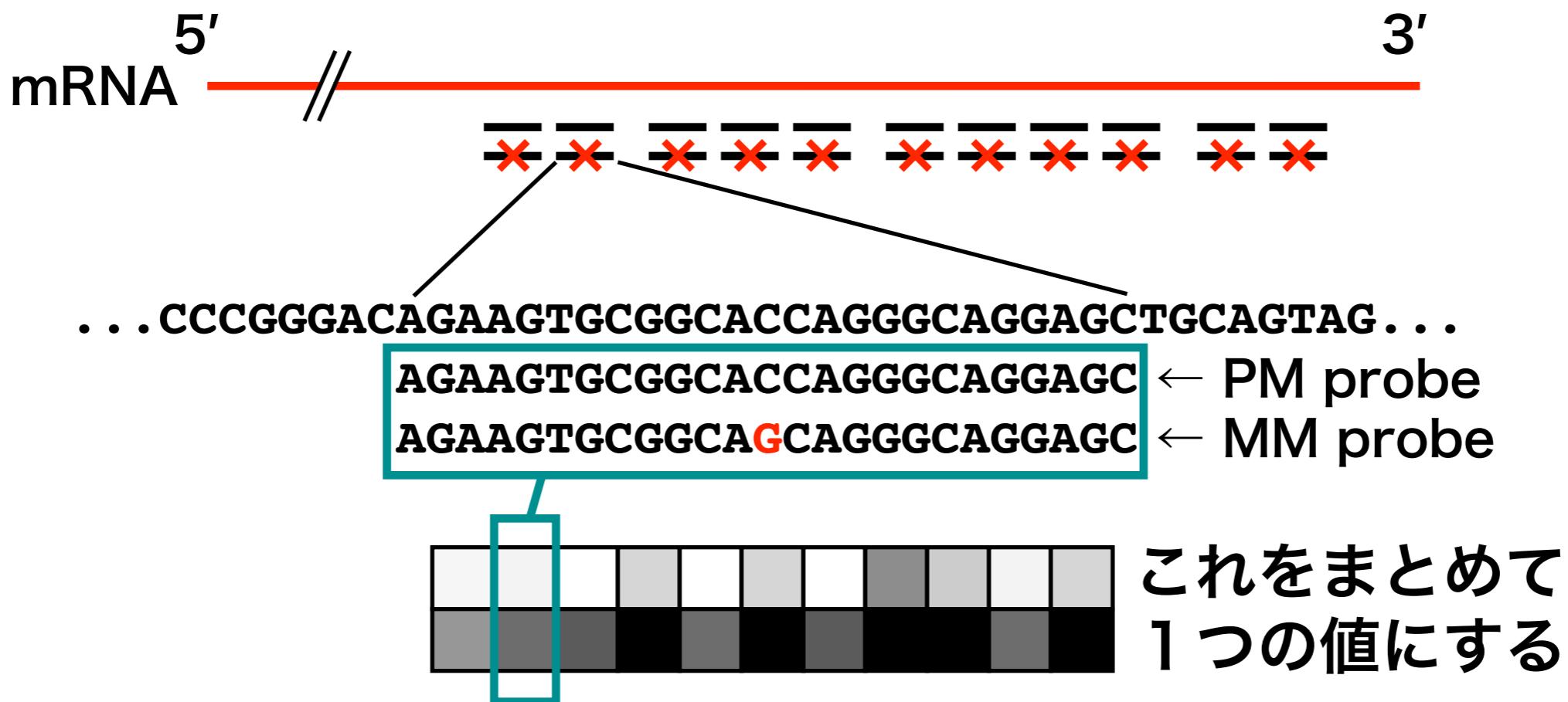
## Data Export:

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

**GGRNA**

ver.2



IMAGE  
GALLERY

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

[旧バージョン](#)

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:AGATCACTCCCAGATCACCAGGTCA \(2\)](#)
- [seq:AGAAAGTGCAGCACCCAGGGCAGGAGC \(2\)](#)
- [seq:ACGGCAGTAAGCACAAGAAAGATT \(2\)](#)
- [seq:AATGTCACCGCACACCAGGCAGTGG \(2\)](#)
- [seq:AAAATGTGCCGGGTGTACTGGTGCA \(2\)](#)
- **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)

cagccgcaccccacccaaagagctctgagcaaggaggctgtcgccccggcggagaaccggctggactggcaagcacggctggcccagtgcagcaggagggggccctgaggcatggatggacagtctgg  
 gccaaggccaccccccggacacaaggatgcggcaccaggcaggagctgcagtagtacctcccccgtctccagcctggctcccagatcactccagatcaccaggtacccccattcttaggc  
 ggcaccctcacacaccaggctgtggtccaacggcccccacccaaatgtcaccgcacaccaggcaggatgggacacggcagtaagcacaagaaagattttttttaagctaaaccaggccagg  
 gcggtggctcatgcctgtatccaggctgtttgggaggctgaggtggaggattgtttgagaccgcctgggtgacacagcaagacccatctccacaaaacgtttttaaaatgtgcgggtgtactgg  
 acacccatgtcatcccaggtaacccaaagaagctgaggcaagaggatcacttgagcccagaaggtcgaggctgcaggagctgtgatcacactg...

**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](#)

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

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  
**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 06:20:32, 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  
GCCGCCAGCCACTTATATGTATTTTTAATTCACTGACAACATTGAGTAGAAAAGATAATTTTTTTGAGACAG

« « | 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

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  
TTTCACATGCACTACCTGCCTGCTGTCCTTCACTGACAACATTTCAGGGTCTCGCAAGGCATGGAATACAATG

[chr1:197463616-197463630](#) ▼197463616  
AATGATCTTACTGTTAACACTGCACTTATTCACTGACAACATTACTTAAAGAAAAGAGATTATGATTGGATAAA

[chr2:30898313-30898327](#) ▼30898313  
GCCCCCAGCCACTTATATGTATTTTAAATTCACTGACAACATTGAGTAGAAAAGATAATTTTTTTTTGA

[chr2:163535086-163535100](#) ▼163535086  
TGAGAAAGAGGACACCCTAACGAAATTATGGCTTCACTGACAACATTAGAGAACATATCAAACGAATATTCA

[chr3:117135824-117135838](#) ▼117135824  
TCCCCCTAGCAAATCAATTCAACTTCTGTTATTCACTGACAACATTGTTTTTCACTGGCTGCAGCTTTCACAA

chr1:128011007-128011021

▼128011007

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**

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  
ATACTAGAATTAAAAGCAAATGTCTTTATTCACTGACAACATAATCATCTATAAAGAAAATCCTACAT

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

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

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

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

chr1:6720805-6720804

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**

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  
AGCAGTACTCAAGATCACCTTTTTAAAGTTCACTG-CAACATT~~CAGT~~AGATGAAAAATGTGTAGCTGTAATTCAATTGA

[chr1:106947513-106947532](#) ▼106947513  
TAGAAAACATACCAACATAAAGAAGCAATCTTTCACTG~~CACAA~~-ATTGAGTA~~T~~AAAATTAAACCGTTGAAAGGGTCATTA

[chr2:30898313-30898332](#) ▼30898313  
GCCCCCAGCCACTTATATGTATTTTAAATTCACTGACAACATTGAGTA~~G~~AAAAGATAATTTTTTTGAGACAG

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

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

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

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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) ip31.1 1q12 1q41 1q43 44

Scale chr1: 5 bases hg19  
---> T T 77,930,955 C A C T G 77,930,960 C A A C A T T C A G 77,930,965 T A G 77,930,970 A  
UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

AK5 AK5 RefSeq Genes

Publications: Sequences in Scientific Articles

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

AK5

100 Layered H3K27Ac

DNase Clusters

Txn Factor ChIP 4.88

100 Vert. Cons -4.5

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	T	C	A	G	C
Chicken																			
X_tropicalis																			
Zebrafish																			
Lamprey																			

Common SNPs(147)

Multiz Alignments of 100 Vertebrates

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

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

- 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

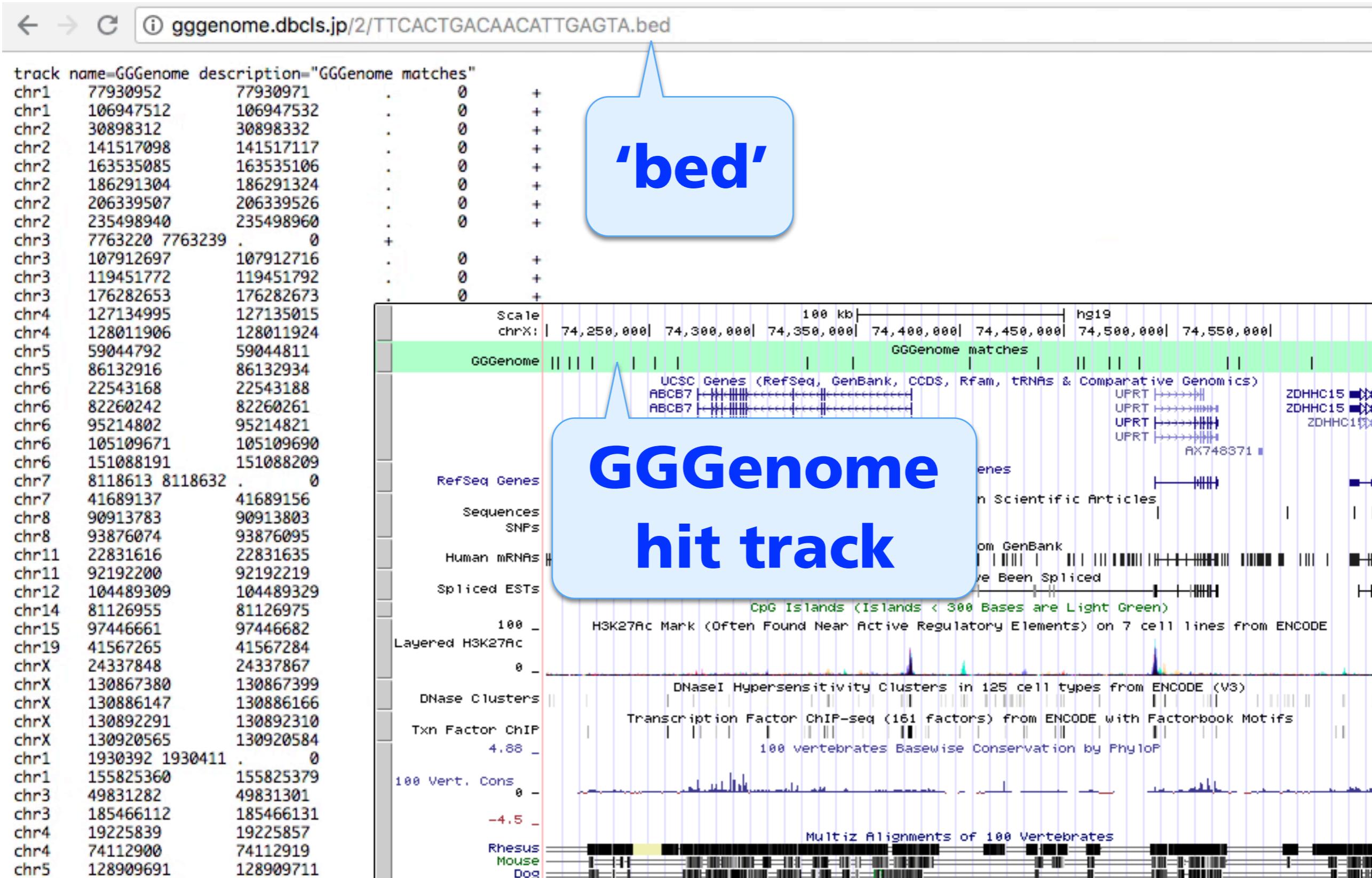
②最大ミスマッチ・  
挿入欠失 = 2 で

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 ☆

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

コメント 共有

=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	caatcaccctcacccttttatatgc	<a href="http://GGGenome.dbcls.jp/rice/caatcaccctcacccttttatatgc.txt">http://GGGenome.dbcls.jp/rice/caatcaccctcacccttttatatgc.txt</a>	=ImportData(D2)	chr01	+	27707	27
3	YN001-R	ccgctgtgaac		chr01 - 28071 28092				
4	YN002-F	tgatccaata		ATATTGTTGGTACCGAGTA				
5	YN002-R	catgcaaggta		27971 28192	chr01	-	28071	28
6	YN003-F	acgtactgtgg						
7	YN003-R	acccaaccta						
8	YN004-F	atcagattccggccggccg						
9	YN004-R	ggagagatctgggtggggag						
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/>

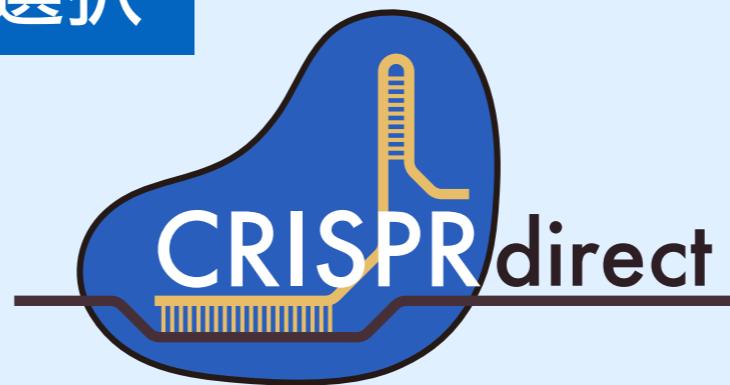
- **ゲノムを高速に検索可能**  
350種の生物種（うち植物は80種）に対応
- **短い塩基配列の検索に強い**  
ミスマッチや挿入欠失が多くても見落としのない検索
- **他のツールから呼び出すことができる（REST API）**  
Googleスプレッドシートの ImportData() 関数  
Excel 2013以降の WEBSERVICE() 関数  
R、Ruby、Galaxy、ゲノムブラウザ・・・
- **無償で自由に利用可能**  
商用利用であっても無償。  
利用記録は当センターにおいて機密扱い。

# 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

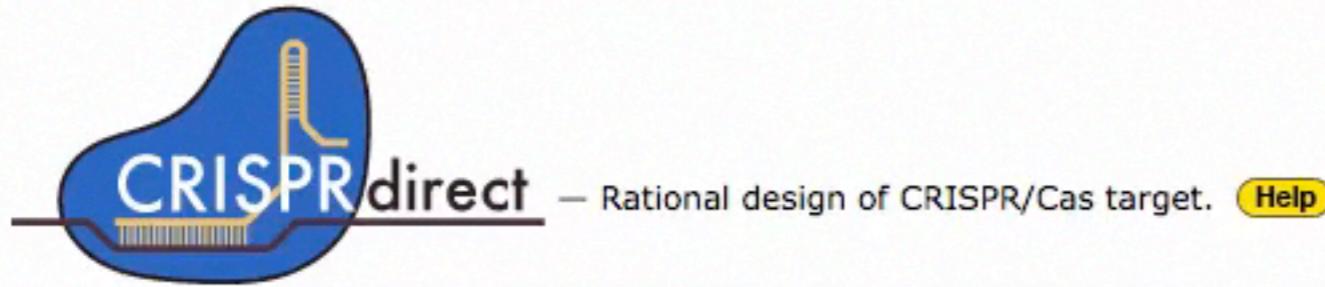


wordが完全一致せず  
BLASTで検索できない



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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: NGG (e.g. NGG, NRG) ?

PAM

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

オフターゲット検索のための  
生物種 を選択

What's 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: ?

```
agtgcaccccccgttcgcctcgctcgagctcgcgttactttacaccgcccggccgagctctccagactccggaggaggaaagcg  
atcggttacacgtacgcctcgtaaggcagaaggcagaacatctgaagaatggctgacgaggatattcaacctatttgtgtgcgacaatg  
gcactggaatggtaaaggcagggtttgctggatgtatgcaccaaggccgtttcccttagcattgttagggagaccacgtcacacc  
ggtgtcatggttgggatggccaaaaggatgcctatgtgggtatgaagctcaggcaaaaagggtatcctgactctaaagtaccc  
aattgaacatgaaattgtcaataactggatgacatggagaaaatatggcaccacaccttctacaatgagcttcgtgtgcacctg  
aagatcaccctgtattactaactgaagccctctcaatcccaaagccaaacagagagaagatgacacagatcatgtttgagaccttc  
aattgcccagcaatgtatgtcgaatccaggctgttatccttgt
```

or upload

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:

- 2017-06-19 African wild rice (Oryza barthii) genome, Obart\_v1.0 (Apr, 2014)
- 2017-06-05 African wild rice (Oryza brachyantha) genome, Oryza\_brachyantha.v1.4b (May, 2011)
- 2017-02-17 African wild rice (Oryza glaberrima) genome, AGI1.1 (May, 2011)
- 2017-01-23 Brazilian wild rice (Oryza glumaepatula) genome, ALNU02000000 (Aug, 2013)
- 2016-12-14 Longstamen rice (Oryza longistaminata) genome, v0117-2013Aug (Aug, 2013)
- 2016-09-05 Australian wild rice (Oryza meridionalis) genome, Oryza\_meridionalis\_v1.3 (Oct, 2014)
- 2016-08-30 Indian wild rice (Oryza nivara) genome, AWHD00000000 (Aug, 2013)
- 2016-06-14 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	-	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	+	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

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

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 <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	-	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	-	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	-	ccaaactccggaggaggaggacg [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	+	caacccatttgtgtgcgacaaatgg [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]

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				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	-	cctcgtaaggcagaaggcagaaca [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	+	caaccttattgtgtgcacaa[tgg] [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	cctatttgtgtgcacaaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	atttgtgtgcacaaatggcac[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]

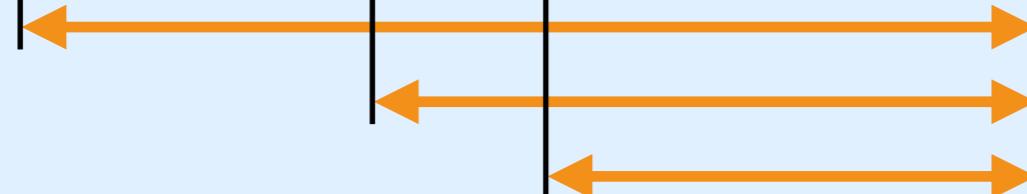
Showing 1 to 20 of 71 entries

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

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]
<b>10 - 32</b>	-	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]
<b>56 - 78</b>	-	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]
<b>154 - 176</b>	-	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]

Showing 1 to 20 of 71 entries

First Previous 1 2 3 4 Next Last

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]
<b>10 - 32</b>	-	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	-	ccggccggccggagctctccaga [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]	15 [detail]	2679 [detail]
56 - 78	+	ccggccggagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
<b>56 - 78</b>	-	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	-	ccggccggaggaggaggaggcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggccggaggaggaggatcgttac [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	+	caacccatttgtgtgcgacaaatggc [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
<b>154 - 176</b>	-	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



— 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

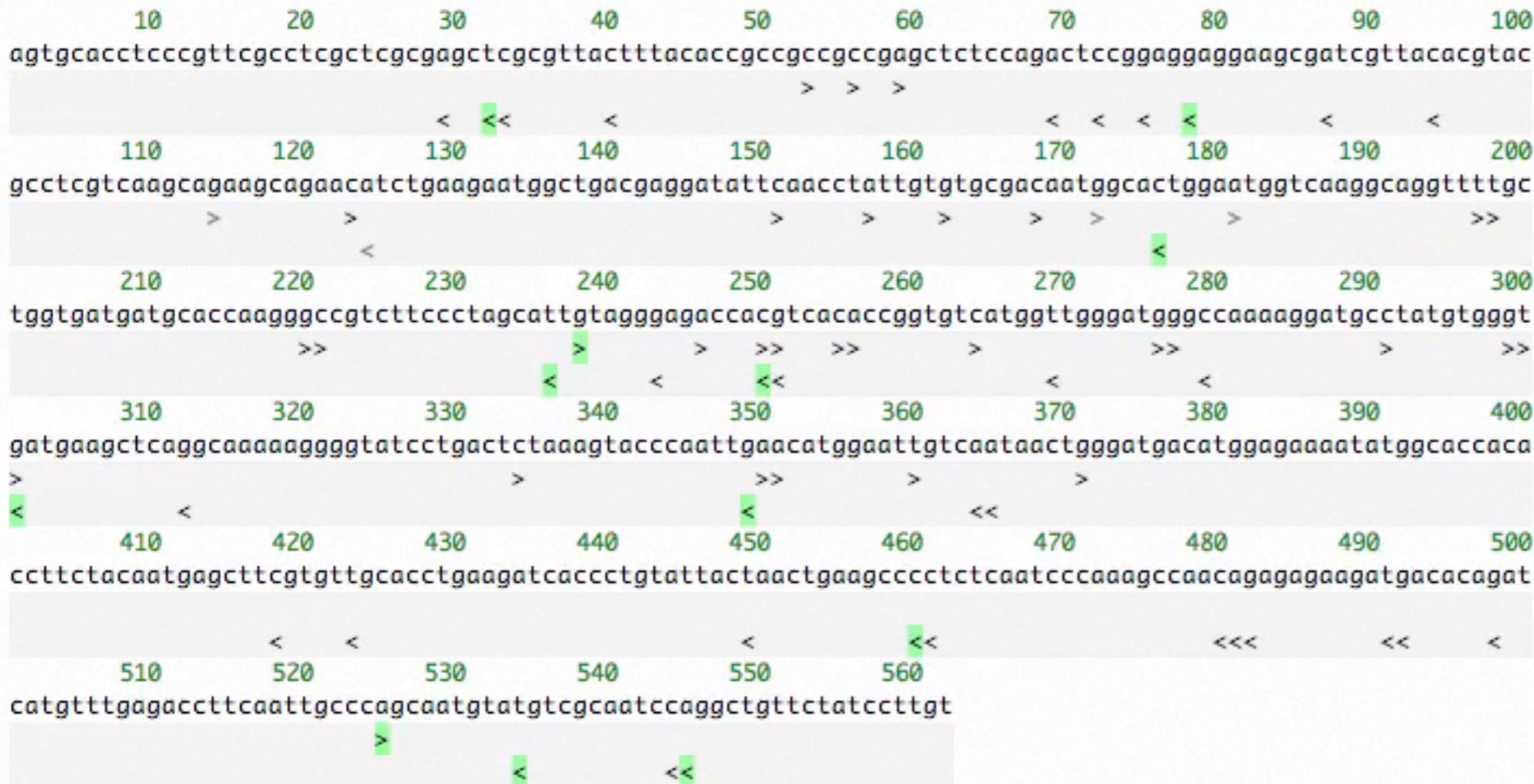
# CRISPRdirect によるガイド RNA 設計

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

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.

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

### **Data Export:**

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◆	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	Aegilops tauschii	<a href="#">ASM34733v1 (Dec, 2013)</a>
AMTR1.0	EnsemblPlants	Plant	A. trichopoda	アムボレラ・トリコポダ	Amborella trichopoda	<a href="#">AMTR1.0 (Jan, 2014)</a>
Araly_v.1.0	EnsemblPlants	Plant	Lyre-leaved rock-cress	シロイヌナズナ属	Arabidopsis lyrata	<a href="#">v.1.0 (Dec, 2008)</a>
TAIR10_en	EnsemblPlants	Plant	Thale cress	シロイヌナズナ	Arabidopsis thaliana	<a href="#">TAIR10 (Sep, 2010)</a>
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	<a href="#">v1.0 (Jan, 2009)</a>
Braol_v2.1	EnsemblPlants	Plant	Wild cabbage	ヤセイカンラン, ワイルドキャベツ	Brassica oleracea	<a href="#">v2.1</a>
IVFCAASv1	EnsemblPlants	Plant	Chinese cabbage	ハクサイ, サントウサイ	Brassica rapa ssp. pekinensis	<a href="#">IVFCAASv1 (Aug, 2009)</a>
Chlre_v3.1	EnsemblPlants	Plant	Green algae	クラミドモナス	Chlamydomonas reinhardtii	<a href="#">v3.1 (Nov, 2007)</a>
ASM9120v1	EnsemblPlants	Plant	Red alga	シアニディオシゾン	Cyanidioschyzon merolae	<a href="#">ASM9120v1 (Nov, 2008)</a>
Soybn_V1.0	EnsemblPlants	Plant	Soybean	ダイズ	Glycine max	<a href="#">V1.0 (Jan, 2010)</a>



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