

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

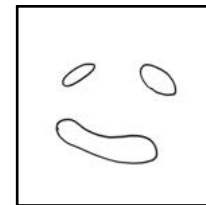
2020年10月14日

ライフサイエンス統合データベースセンター (DBCLS)

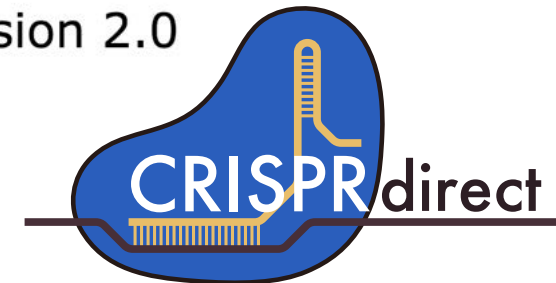
内藤雄樹

- 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 =

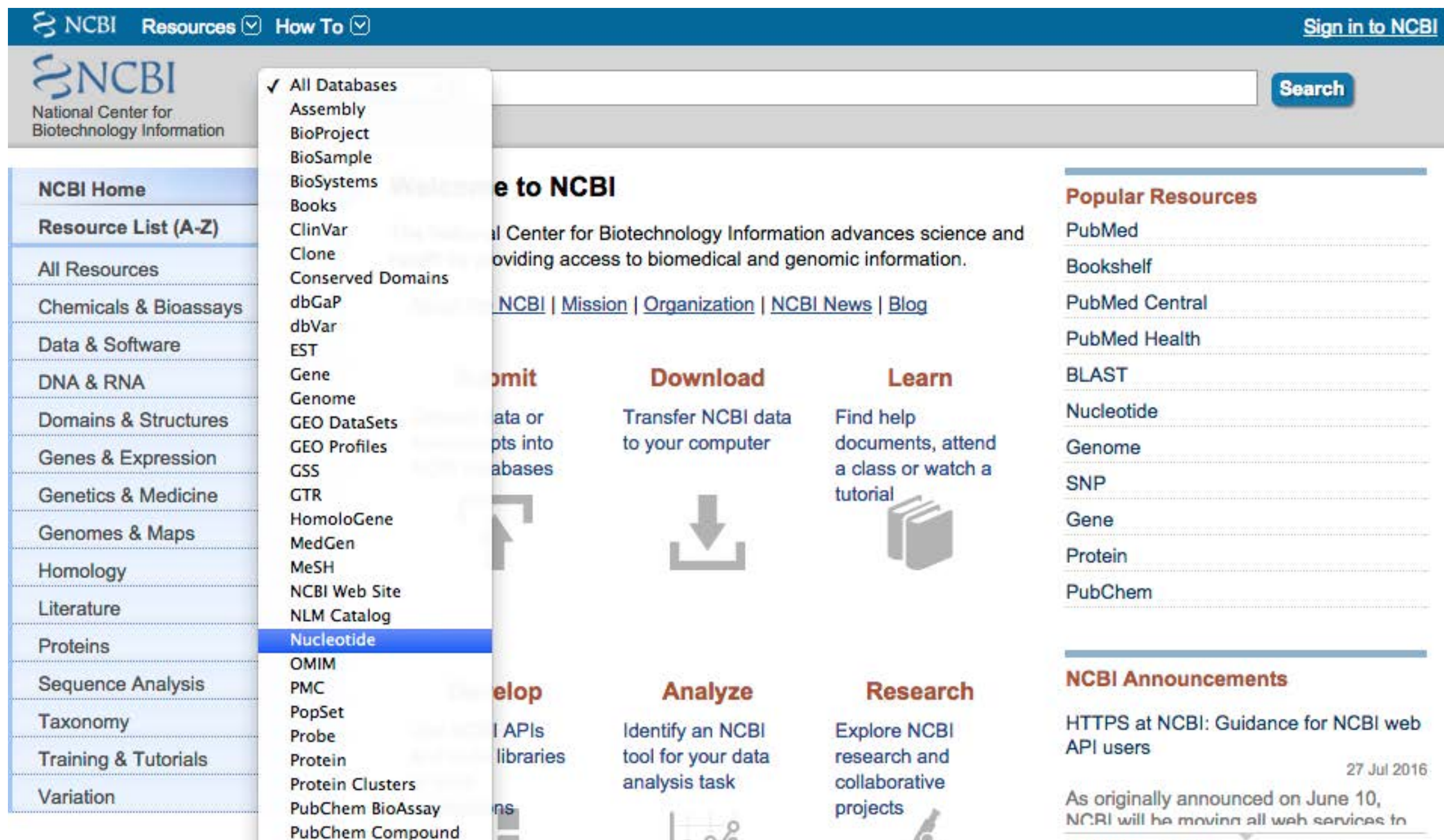


生命科学データベース研究開発のための機関
東大(柏)と三島の国立遺伝学研究所に間借り

- 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

遺伝子に関するデータベース

● NCBI トップページ



The screenshot shows the NCBI homepage with a blue header bar containing the NCBI logo, navigation links (Resources, How To), and a sign-in link. A search bar is located on the right. A left sidebar contains a 'Resource List (A-Z)' menu. A central dropdown menu is open, listing various databases. The main content area features a 'Welcome to NCBI' message, a list of links (NCBI, Mission, Organization, NCBI News, Blog), and three large sections: 'Submit', 'Download', and 'Learn'. A right sidebar lists 'Popular Resources' and 'NCBI Announcements'.

NCBI Resources How To Sign in to NCBI

NCBI
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Data & Software
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Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
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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
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MeSH
NCBI Web Site
NLM Catalog
Nucleotide
OMIM
PMC
PopSet
Probe
Protein
Protein Clusters
PubChem BioAssay
PubChem Compound

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APIs
libraries

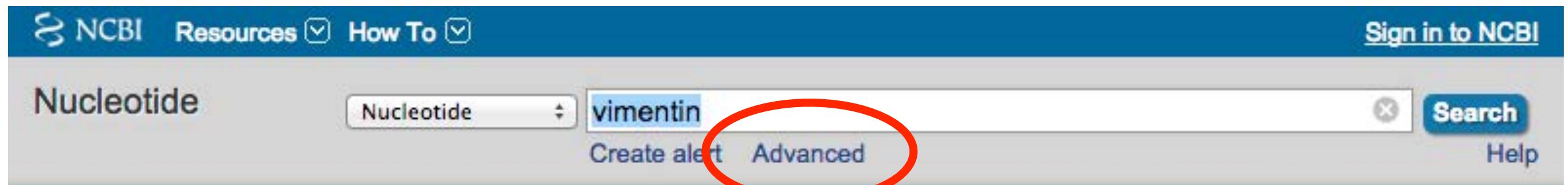
Analyze
Identify an NCBI
tool for your data
analysis task

Research
Explore NCBI
research and
collaborative
projects

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
27 Jul 2016
As originally announced on June 10,
NCBI will be moving all web services to

- 検索窓にキーワードを追加していく
 - ... **AND** “Bombyx mori” [Organism]
 - ... **AND** AGO1 [Gene Name]
 - ... **AND** patent [Title]
- または、Advanced searchに行く



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

- **GenBank/ENA/DDDBJ 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もあるが、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

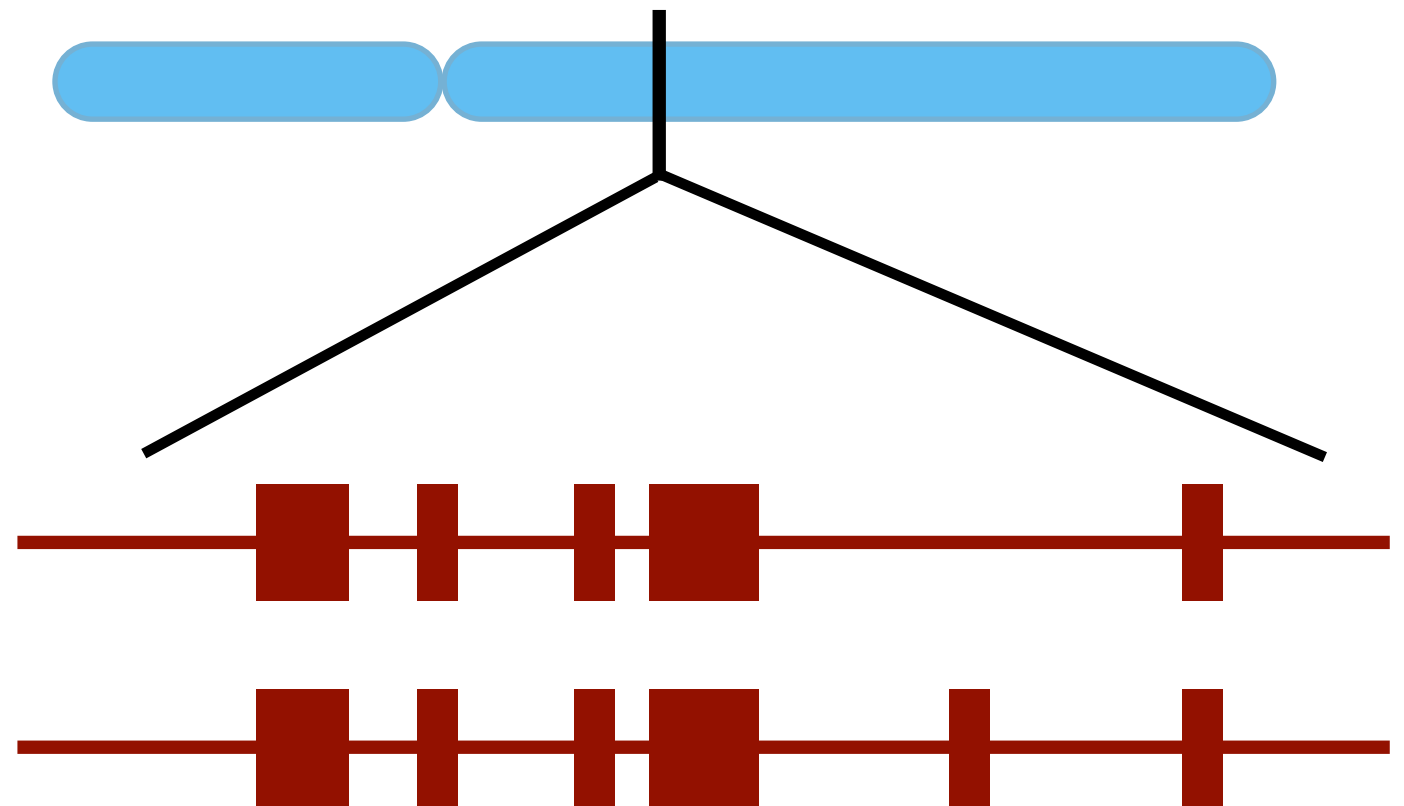
ヒト Chr22 (q11)

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

統合遺伝子検索 **GGRNA** (ぐぐるな)

統合遺伝子検索

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GGRNA ver.2

Zoo (All organisms in RefSeq) 

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

検索例：

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

新着情報：

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

遺伝子名を検索

統合遺伝子検索
GGRNA ver.2 

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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。

[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**; PN8

[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;

RefSeqの転写産物

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

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, Nimura 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

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旧バージョン

NM_003380

検索

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。重なり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 / 1 › » ↻

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](#)

塩基配列を検索

統合遺伝子検索

GGRNA ver.2



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English

旧バージョン

caagaagagattgc

検索

Homo sapiens (human)

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。重なりと色が濃く表示されます。

[PREDICTED: Homo sapiens vimentin \(VIM\), transcript variant X1, mRNA.](#) (1873 bp)

tctgctggccgagctcgagcagctcaaggccaaggcaagtcgcgcctgggggacctctacgaggaggagatgcgggagctgcgccggcagggtggaccagctaaccaacgacaaagcccgcgtcgaggtgga
gctgcgacaacctggccgaggacatcatgcgcctccgggagaaattgcaggaggagatgcttcagagagaggaagccgaaaacaccctgcaatcttcagacaggatgttgacaatgcgtctctggcacgtcttgac
cttgaacgcaaagtggaaatctttgcaagaagagattgccttttgaagaaactccacgaagaggaaatccaggagctgcaggctcagattcaggaacagcatgtccaaatcgatgtggatgtttccaagcctgacc
tcacggctgccctgcgtgacgtacgtcagcaatatgaaagtgtggctgccagaacctgcaggaggcagaagaatggtacaaatccaagtttgctgacctcttgaggctgccaaaccggaacaatgacgccctgcgc
caggcaaagcaggagtcactgagtaccggagacaggtgcagtcctcacctgtgaag...

position 832

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

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

tctgctggccgagctcgagcagctcaaggccaaggcaagtcgcgcctgggggacctctacgaggaggagatgcgggagctgcgccggcagggtggaccagctaaccaacgacaaagcccgcgtcgaggtgga
gctgcgacaacctggccgaggacatcatgcgcctccgggagaaattgcaggaggagatgcttcagagagaggaagccgaaaacaccctgcaatcttcagacaggatgttgacaatgcgtctctggcacgtcttgac
cttgaacgcaaagtggaaatctttgcaagaagagattgccttttgaagaaactccacgaagaggaaatccaggagctgcaggctcagattcaggaacagcatgtccaaatcgatgtggatgtttccaagcctgacc
tcacggctgccctgcgtgacgtacgtcagcaatatgaaagtgtggctgccagaacctgcaggaggcagaagaatggtacaaatccaagtttgctgacctcttgaggctgccaaaccggaacaatgacgccctgcgc
caggcaaagcaggagtcactgagtaccggagacaggtgcagtcctcacctgtgaag...

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)

aaggctcggaagtctggcatccctacttccgagcctggatcccagtaaggatcttgccctccctgcaacaccgagtgcttagacagctgctgctgagaactggcctccagccggtgtctcattccatggggctccctg
ctgactgcatttctgactgctggaatgattttaccagcccaaaaccagtcatttcttccaaaagcttcttcttgaatagaattttgagcccatgccacctccctccagtcacatggaattccagaatcagtcacagcctctg

塩基配列を検索

統合遺伝子検索

GGRNA ver.2



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caagaagagat

検索

Homo sapiens (human)

2018-06-26 04:46:20, GGRNA : RefSeq release 88 (May, 2018)

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

ttacgacgaatgacagagaaaaggagcgaagtccaagtccccagcagcagcagcgaagctccgacgcagacatttcccagaactcccaagagaaaatgcaggaagcctggaaggagccagcagaagattg
ttgttctgagggatcctaccatgccactgctgtccacaccac**caagaagagat**ctgtctgggcccctgtgtccacaggtccaccgctgtcaaaaacccgagatgagattactctgcccttcgggtcacaacgatt
cacctcaactgagcacctgtggaccaccaaaggacatggcagggacgttactgctccctgtccctgttctgaagagctcccaccagacccccactctcagtgccaggctgccagccaacaggcctgacatgtctc
ccatggtgctctccagcctgccatgcaggcgttgcctgggtcctggccttaaatcccaggcagaaatcaa...

[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)

caccagcaacgggtgtggtcagcagcccaagtccgctagcaggcccgcccttcagtcgaagtcctggcacagtgggaagccgagtagcacccaggccaggaagcggatcctgggcagcgcgaacccgaggagaa
gcaggagaaacccatcctcgataggtcttctctgacttcttcccttcaggccaaccaggatctcctaaccggaagacagcagacagcccaataatgtgatcagacagcctctgggtcctgatgggtcacacggctca
aacagcgcagataaatgcagg**caagaagagat**ggcgcgactgccgcgtcaacgcgtcctgggtcgtccgccaaggggtgactaccgtggcagacagctggacttgagcagcgggaacttgacttacttgcttg
tgatccccgttgctccgcccactgtgaccttgaatcccatgactgtgacctcccccttctcctcctccactgtgattggcactttgacaaggactgtccaagtcaatgaaagggaaggggtgaggggttaggag
aagggtggggggaacccaccaattactcagagtagagagtcagacagggc...

[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)

tgcagccccttgactcgcggagtcactacgcaaggtcgggctctgcaggcagcagcttctgggtctcaccgggcttgtgcgcacacctggggacatgtgggaaggtcgctcttgcggccactgagcggcctggcct
cagggaaacgaagcccccccccgggaagaaagctccttcccggaagccgaacgtattgggaacccgggaacccgaacccgcgctcaccgaagagccgctggggccttcgctgtgggaacccgggaag

塩基配列を検索

統合遺伝子検索

GGRNA ver.2



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caagaaga

検索

Homo sapiens (human)

2018-06-26 04:46:32, 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

tttaccttctgtataagcactgtgctaaaattgcagacactaggaccatgtcttgggcaataatgctagcagagtacaca**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 //

gggtgccaaatgggtgttttgggctcttctttcc**caagaaga**gactagcccattgtcaccaatgcagagctggaagctgaaattgttaaggcagaatgaaagggagaaaagcacgtcctgagcac**caagaaga**ag
ataactcgaagttaagaagacgtgatgggtactttggagaagaaagcaacacctgagtcacaaattgcactgagcaacgttcttgttgtgtgagatattgataaatctccagggtcttcaacaaggggagtcgagaatagg
aaactcatttcaaatcataatctcagggtgacaagaagggtaccatatttgaggcagcctgttgggtgc...

[position](#) 35

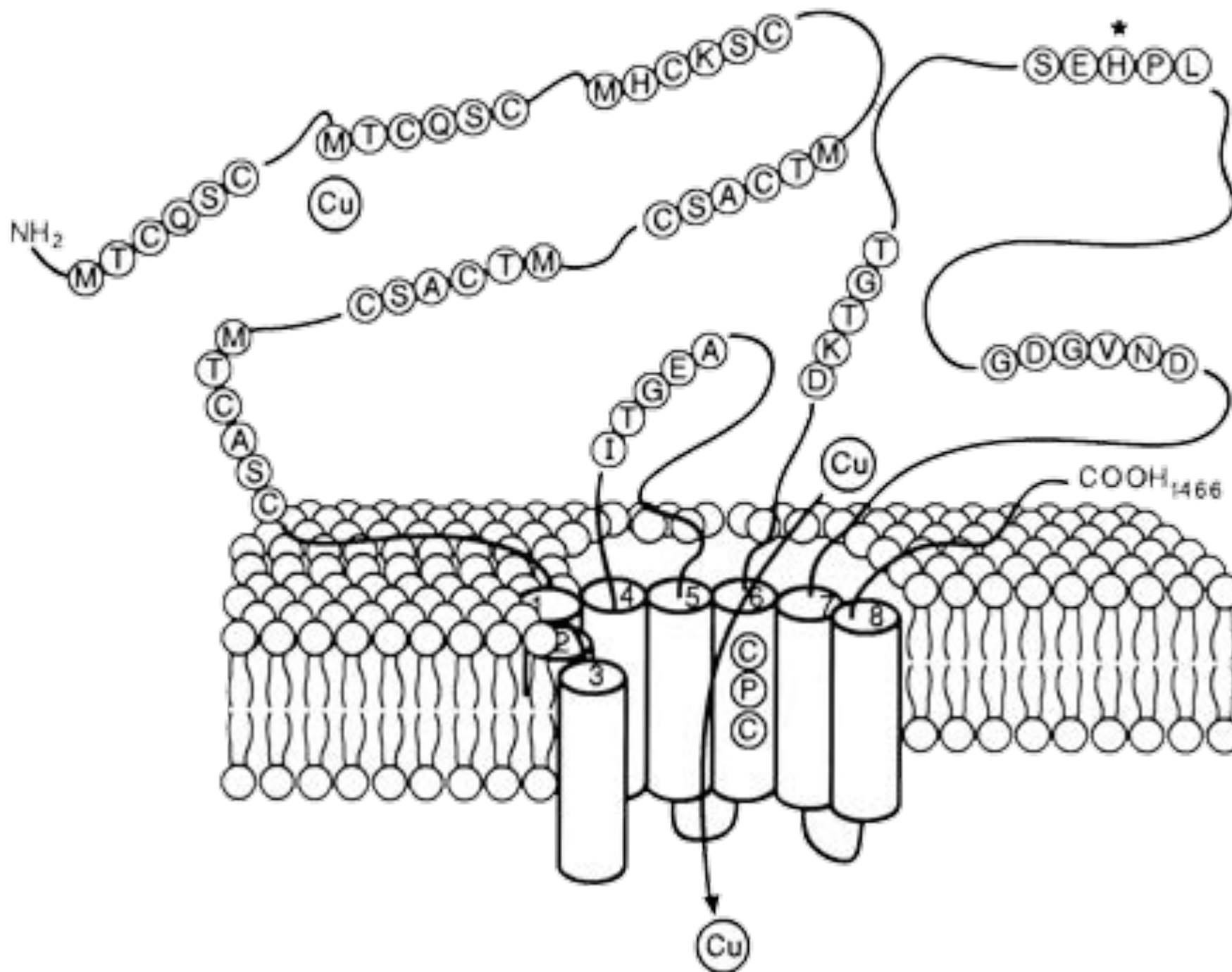
[NR_120624.1 - Homo sapiens \(human\) - NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

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

agagtcagggtgtattgtcatcacctcccccaagatctgtgcaaagggtgaaatcagctcatgaggacacagaacttcagcttgatgcagatgtgtgggaggtggggaacagctgttattcttctggggaatatgaag

ggttcagtcaggaaattggaatgataatcttccgaccactaacagcctcttccagtcactggaataatgcttacagccagtaagccaccatcatgtgacacaaagtggccatcatcctagtgtctaacatttaagctgtggtt

アミノ酸配列を検索



←何？

アミノ酸配列を検索

統合遺伝子検索

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[旧バージョン](#)

GGRNA ver.2

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**VKSIEDRISSLKGI VSMKVSLEQGSATVKYVPSVVS LQQVCHQIGDMGFEASIAEGKAAS
WPSRSLPAQEAVVKLRVEG**MTCQSC**VGSIEGKVRKLQGVVRVKVSLSNQEAVITYQPYLIQPEDLRDHVNDMGFEAAIKNKVAPLSLG...RFSGYFVPLIIMSTLTLVWIV
IGFIDFGVVQKYFPNPNKHISQTEVIIRFAFQTSITVLCIACPCSLGLATPTAVMVG TGVA A QNGILIKGGKPLEMAHKIKTVMFDKTGTITHGVPRVMRVLLLGDVATLPLRKV
LAVVGTA EAS**SEHPL**GVAVTKYCKEELGTETLG YCTDFQAVPGCGIGCKVSNVEGILAHSERPLSAPASHLNEAGNLPAEKDAAPQTFSVLIGNREWLRRNGLTISSDVSDA
MTDHEMKGQTAILVAIDGMLCGMIAIADAVKQEAALAVHTLQSMGVDDVVL...

[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**VKSIEDRISSLKGI VSMKVSLEQGSATVKYVPSVVS LQQVCHQIGDMGFEASIAEGKAAS
WPSRSLPAQEAVVKLRVEG**MTCQSC**VGSIEGKVRKLQGVVRVKVSLSNQEAVITYQPYLIQPEDLRDHVNDMGFEAAIKNKVAPLSLG...RFSGYFVPLIIMSTLTLVWIV
IGFIDFGVVQKYFPNPNKHISQTEVIIRFAFQTSITVLCIACPCSLGLATPTAVMVG TGVA A QNGILIKGGKPLEMAHKIKTVMFDKTGTITHGVPRVMRVLLLGDVATLPLRKV
LAVVGTA EAS**SEHPL**GVAVTKYCKEELGTETLG YCTDFQAVPGCGIGCKVSNVEGILAHSERPLSAPASHLNEAGNLPAEKDAAPQTFSVLIGNREWLRRNGLTISSDVSDA
MTDHEMKGQTAILVAIDGMLCGMIAIADAVKQEAALAVHTLQSMGVDDVVL...

[AA_position](#) 35 1035

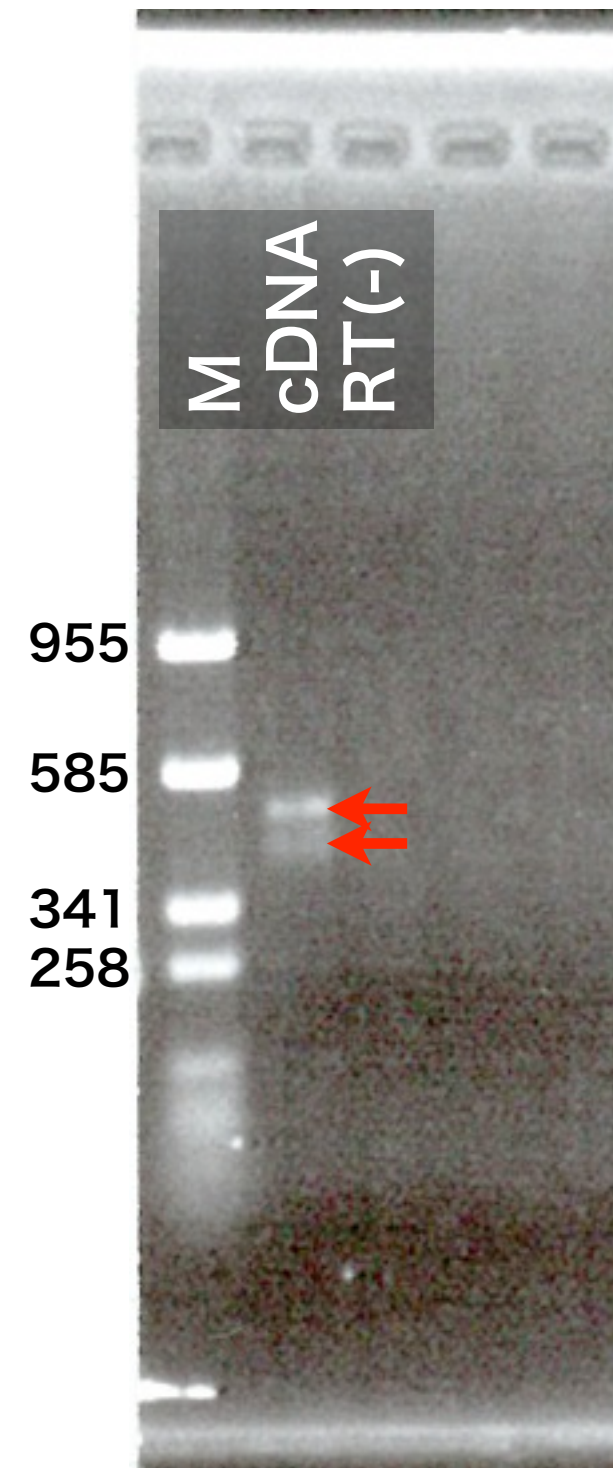
[XM_011756663.2](#) - Macaca nemestrina (pig-tailed macaque) - [NCBI](#)

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:
tgacgtattcactcttctgggtt

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:agctcattactttatcagtqca \(2\)](#)
- [comp:tgacgtattcactcttcttggtt \(2\)](#)
- **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. \(4437 bp\)](#)

tgaaaaaattcaggacttgggctgagcggcggcaattcaatcgggaaatgaagcgggaagcaggcggagtcgagaggcccatcttgccagccaatcagaagctcattactttatcagtqcaagatgcacccacaaag
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agttagcctcacagaagatcttcagctgtgacccacatg...

position 1892 2272

Synonym: C22orf12, DGCRK6, Gyl; pasha

NM_001190326.1 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

$$2272 - 1892 = 380$$

[Homo sapiens DGCR8 microprocessor complex subunit \(DGCR8\), transcript variant 1, mRNA. \(4536 bp\)](#)

gaagcgggaagcaggcggagtcgagaggcccatcttgccagccaatcagaagctcattactttatcagtqcaagatgcacccacaaagaaagagtttggtattaaccccaacgggaaatccgaggtctgcacctgca
cgagtacatgcagcgtgtcctcaaggctcgccctgtctataatttcttgaatgtgagaacccaagtgaagccttttggtgcctcggtgaccattgatggtgtgacttacggatctggaactgcaagcagcaaaaaacttgca
agaataaagctgcccgagctacactggaaatcctcatcctgactttgttaaacagacctctgaagagaagcccaaagacagtgaagaactcgagtatTTTaaaccacatcagcatcgaggactcgcggtgtctacgagctg
accagcaagctggcctgtgtctccatcatcagatcctccacgagtgccttaaaagaaaccatgggatgggtgacacgtctatcaagtttgaagtgggtcctgggaaa**aaccagaagagtgaatacgtcat**ggcgtgt
ggcaagcacacagtgcgcggtgtgtgtaagaacaagagagt...

position 1892 2371

Synonym: C22orf12, DGCRK6, Gyl; pasha

NM_022720.6 - Homo sapiens (human) - [NCBI](#) - [UCSC](#) - [RefEx\(expression\)](#)

$$2371 - 1892 = 479$$

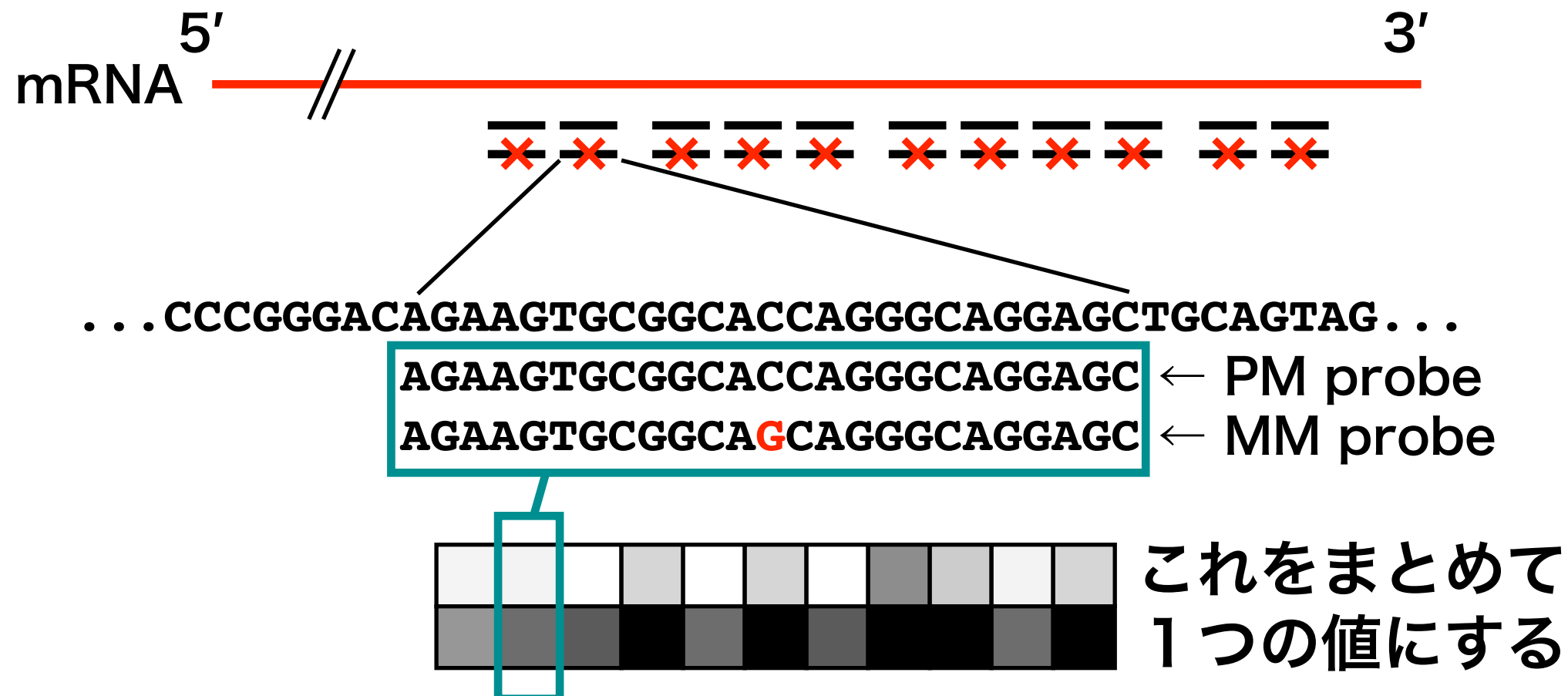
Data Export:

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



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1552311_a_at

検索

Homo sapiens (human)

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

Summary:

- [seq:TCTCCACAAACGTTTTTAAATGTG \(2\)](#)
- [seq:GGGACACGGCAGTAAGCACAAGAAA \(2\)](#)
- [seq:GGCAGGAGCTGCAGTAGCTACCCTC \(2\)](#)
- [seq:GCATGGGATGGGACAGTCTGGGCCA \(2\)](#)
- [seq:ATGTGCCGGGTGTACTGGTGACAC \(2\)](#)
- [seq:AGGTCACCCCATCTCTAGGCGGCAC \(2\)](#)
- [seq:AGATCACTCCCAGATCACCAGGTCA \(2\)](#)
- [seq:AGAAGTGCGGCACCAGGGCAGGAGC \(2\)](#)
- [seq:ACGGCAGTAAGCACAAGAAAGATT \(2\)](#)
- [seq:AATGTCACCGCACACCAGGCAGTGG \(2\)](#)
- [seq:AAAATGTGCCGGGTGTACTGGTGCA \(2\)](#)
- **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)

cagccgcacgcccagagctctgagcaaggaggctgtcgcggggcccagagaacccgctgggactggcaagcacggctggccagtgagcaggagggggccctgaggcatgggatgggacagctctgggccagcg
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atcccagtgcttgggaggctgaggtgggaggattgcttgagaccagcctgggtgacacagcaagaccccactccacaaacgttttaaaatgtgccgggtgtactgggtgcacacctgtcatcccagctaccaag
aagctgaggcaagaggatcacttgagcccagaaggtcgaggctgcagggagctgtgatcacactg...

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

```
variation      complement(1972)
                /gene="RAX2"
                /gene_synonym="ARMD6; CORD11; QRX; RAXL1"
                /replace="a"
                /replace="t"
                /db_xref="dbSNP:8103165"
variation      complement(1989)
                /gene="RAX2"
                /gene_synonym="ARMD6; CORD11; QRX; RAXL1"
                /replace="c"
                /replace="g"
                /db_xref="dbSNP:6510769"
polyA_signal    2131..2136
                /gene="RAX2"
                /gene_synonym="ARMD6; CORD11; QRX; RAXL1"
polyA_site      2155
                /gene="RAX2"
                /gene_synonym="ARMD6; CORD11; QRX; RAXL1"
```

ORIGIN

```
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aaatctaaaaacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

<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。

ゲゲゲ GGGenome による塩基配列検索

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

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GGGenome

Human genome, GRCh37/hg19 (Feb, 2009)

許容するミスマッチ/ギャップの数: (検索する塩基配列の長さの25%まで)

☒ 双方向を検索 ☐ +方向のみ検索 ☐ -方向のみ検索

検索例:

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

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

TTCAGTGAACATTGAGTA

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:

- [TTCAGTGAACATTGAGTA \(1\)](#)
- [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

GCCCCAGCCACTTATATGTATTTTTTAAATTCAGTGAACATTGAGTAGAAAAGATAATTTTTTTTTTTTGGAGACAG

« ‹ ページ / 1 › » ↺

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

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GGGenome

TTCAGTGACAACATT

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:

- [TTCAGTGACAACATT \(10\)](#)
- [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
TTTTCACATGCACTACCTTGCCTGCTGTCC**TTCAGTGACAACATT**TCAGGGTCTCGCAAGGCATGGAATACAATG

[chr1:197463616-197463630](#) ▼197463616
AATGATCTTTACTGTAACTGCACTTTA**TTCAGTGACAACATT**ACTTAAAGAAAGAGATTATGATTGGATAAA

[chr2:30898313-30898327](#) ▼30898313
GCCCCAGCCACTTATATGTATTTTTTAA**TTCAGTGACAACATT**GAGTAGAAAAGATAATTTTTTTTTTTTTTTGA

[chr2:163535086-163535100](#) ▼163535086
TGAGAAAGAGGACACCCTAAGAATTATGGC**TTCAGTGACAACATT**AGAGAACATATCAAACGAATATTC

[chr3:117135824-117135838](#) ▼117135824
TCCCCTAGCAAATCAATTCACTTCTGT**TTCAGTGACAACATT**GTTTTTCTACTGGCTGCAGCTTTTCACAA

[chr4:128011007-128011021](#) ▼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

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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: (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

ATACTAGAATTTTAAAAGCAAATGTCTTTA**TTCACTGACA**ACATAATCATCTATAAAGAAAATCCTACAT

[chr1:728363-728372](#)

▼728363

CCCTCAGCCACACAGCTGACGCTGTAGAGA**TTCACTGACA**TCCAGTCTGATGGACACTGTTTCTCCAGCC

[chr1:1336263-1336272](#)

▼1336263

CCGCAGGGCTCTGCCACATCCCTGTCTTCC**TTCACTGACA**TGAAACGCAGAAAAGGCAGCTTTGCCACAA

[chr1:3274566-3274575](#)

▼3274566

AGAGGCCCACTCGTGAGCCTTGCTGTGCC**TTCACTGACA**TGCTCGCCCATGAGCTGAGTCTGCCTTGAC

[chr1:3783925-3783934](#)

▼3783925

CTCCGCTGCGTGTAGATACCACACTGTCTA**TTCACTGACA**CTTGGGTTGCTTCCACCTTTTGGCCTGGCC

[chr1:6720005-6720014](#)

▼6720005

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

TTCAGTGACAACATTGAGTA

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:

- [TTCAGTGACAACATTGAGTA \(36\)](#)
- [TACTCAATGTTGTCAAGTGAA \(33\)](#)
- **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

AGCAGTACTCAAGATCACCTTTTTTTAAAGTTCAGTG-CAACATTGAGTAGATGAAAAATGTGTAGCTGTAATTCATTGA

[chr1:106947513-106947532](#)

▼ 106947513

TAGAAAACATACCACATAAAGAAGCAATCTTTCAGTGACAA-ATTGAGTAGTAAATTTAACCCGTTTGAAAGGGTCATTA

[chr2:30898313-30898332](#)

▼ 30898313

GCCCCAGCCACTTATATGTATTTTTTAAATTCAGTGACAACATTGAGTAGAAAAGATAATTTTTTTTTTTTGAGACAG

[chr2:141517099-141517116](#)

▼ 141517099

TTATTTTCTTTAACACAGCCTTTGATAAATTCAGTGAC-ACATTGAGT-TAGCCATAGTGTGTAATGGGAGACTGCCCA

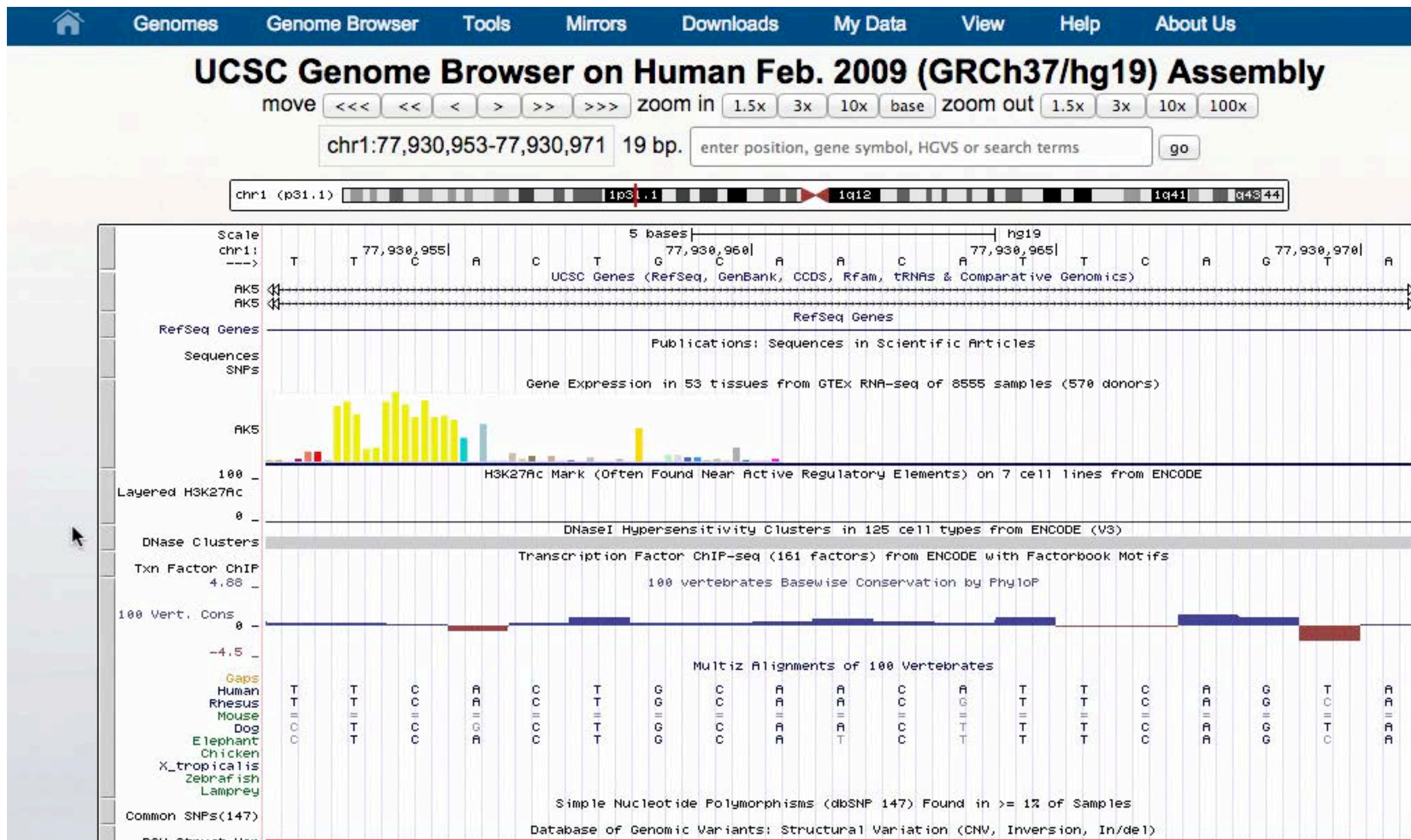
[chr2:163535086-163535103](#)

▼ 163535086

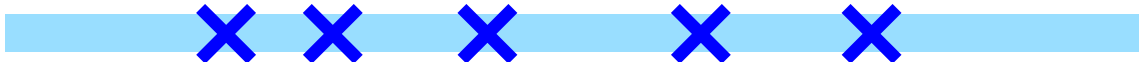
TGAGAAAGAGGACACCCTAAGAATTATGGCTTCAGTGACAACATT-AG-A GAACATATCAAACCAACGAATATTCTGG

[chr2:186201205-186201224](#)

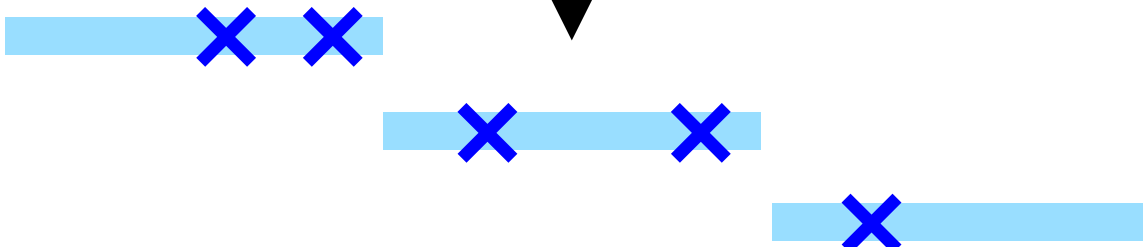
ゲゲゲ GGGenome による塩基配列検索



● 分割統治法

 30 mer / **5ミスマッチ**以内

↓

 分割すると、どれかは必ず
10 mer / **1ミスマッチ**以内

● 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

GGGenome を他のツールから呼び出す

- 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](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。


```

# [ GGenome | 2018-07-08 04:33:37 ]
# database: Human genome, GRCh37/hg19 (Feb, 2009)
# query: TTCACTGACAACATTGAGTA
# count: 36
# query: TACTCAATGTTGTCAGTGAA
# count: 33
# name strand start end snippet snippet_pos snippet align edit match mis del ins
chr1 + 77930953 77930971
TCATGAAATGGAAGTGCTGCCACTTCAGGGTCTGTAAAGAGATAATGCTGATGCCAGGCCA
AGTCTGTTCTTGAGTTACCATGGCAACTGCTCAATTAAGTGAAAAAATGAAAAATA
|||||-----I-----X----- 18 1 0 1
chr1 + 106947513 106947532
TCATCTGGTCTATATGTCCCATGTTTATAAAGTTGATAACATCAAAACACGGAAAGTATAGGAAATAACATAGAAAACATACCACATAAAGAAGCAATCTTTCACTGCACAAATTGAGTATAAAATTTAACCCGTTTGAAAGGGTCATTATAT
ATGAGGAGCAGAAAGACAAGTGGAGTATAAAGAAAATGGGCTTTAAAGTCAAACCTTGCTT 106947413 106947632 TTTCACTG-ACAACATTGAGTA TTTCACTGCACAA-ATTGAGTA |||||
|||||-----D-----I----- 19 0 1 1
chr2 + 30898313 30898332
TTGATCTCCTGACCTCGTGATCCACCTGCCTCGCCCTCCCAAAGTGGTGGGATTACAGGCGTGAGCCACCGCCCCAGCCACTTATATGTATTTTTTAAATTCAGTACAACATTGAGTAGAAAAAGATAATTTTTTTTTTTTGGAGACAGAGT
TGTTGCCAGGGGACTGCAGTGGCACAATCTTGCTCACTGCAACCTCCACCTCCCGTG 30898213 30898432 TTTCACTGACAACATTGAGTA TTTCACTGACAACATTGAGTA
|||||----- 20 0 0 0
chr2 + 141517099 141517118
AATTTTCAGTAAATTAATAAATAAATAAAGGAA
CTGATTTGTTTATTGTTCTTGAGCACCATTGCA
|||||-----I----- 15 1 0 1
chr2 + 163535086 163535105
CTCATGGTGACTCCACACATATTGGACAGAAGGG
TGTGGATTTGCTTTAGAGTCCATGAGAGTAAGA
|||I-----D-----X----- 19 1 0 1
chr2 + 186291305 186291324
CCCATCATCACCAATATCATTATCTCATCTTCCA
TTTTTTTGAGCAGGCTCTATAATAACAAAACCTGA
|||||-----D----- 18 0 0 0
chr2 + 206339508 206339527
ATGAATCAAAGGCTTGAAACATATTGCCAACAAT
GAAAAATAGTACTGTATCATTTTACATTGAACCTT
|||||-----I-----X----- 18 1 0 1
chr2 + 235498941 235498960
CTTGAAGGGGCCAGGTGGGCAGACAGATAGTTCA
GGACCTATTATAGAGCCTGGGCTCATGTTAGGTAATGCAGGGAAGGGGTCAAAGAACCGG 235498841 235499060 TTTCACTGACAACATTG-AGTA TTTCACTGAC-ACATTGCAGTA |||||
|||||-----I-----D----- 19 0 1 1
chr3 + 7763221 7763239
CAGAGATGTGCATGGATAGCTTTGGTTGTAGTCTTTTGACAGCATCAGCTTGGTAGTTCTCCAGTCTTCACTTGATCAGTGCAGACATAGATCAATTCTTCACTGCAAAATTGAGTAGTGAATAAATAAACTTACTTCAGCTAACCTAACT
TTCTAGCACTAATCAGTAGATATCCAATTTATTAACCAAAAATGAATAAAATATATAAA 7763121 7763339 TTTCACTGACAACATTGAGTA TTTCACTG-CAAAATTGAGTA |||||
-----I-----X----- 18 1 0 1
chr3 + 107912698 107912716

```


GGGenome を他のツールから呼び出す

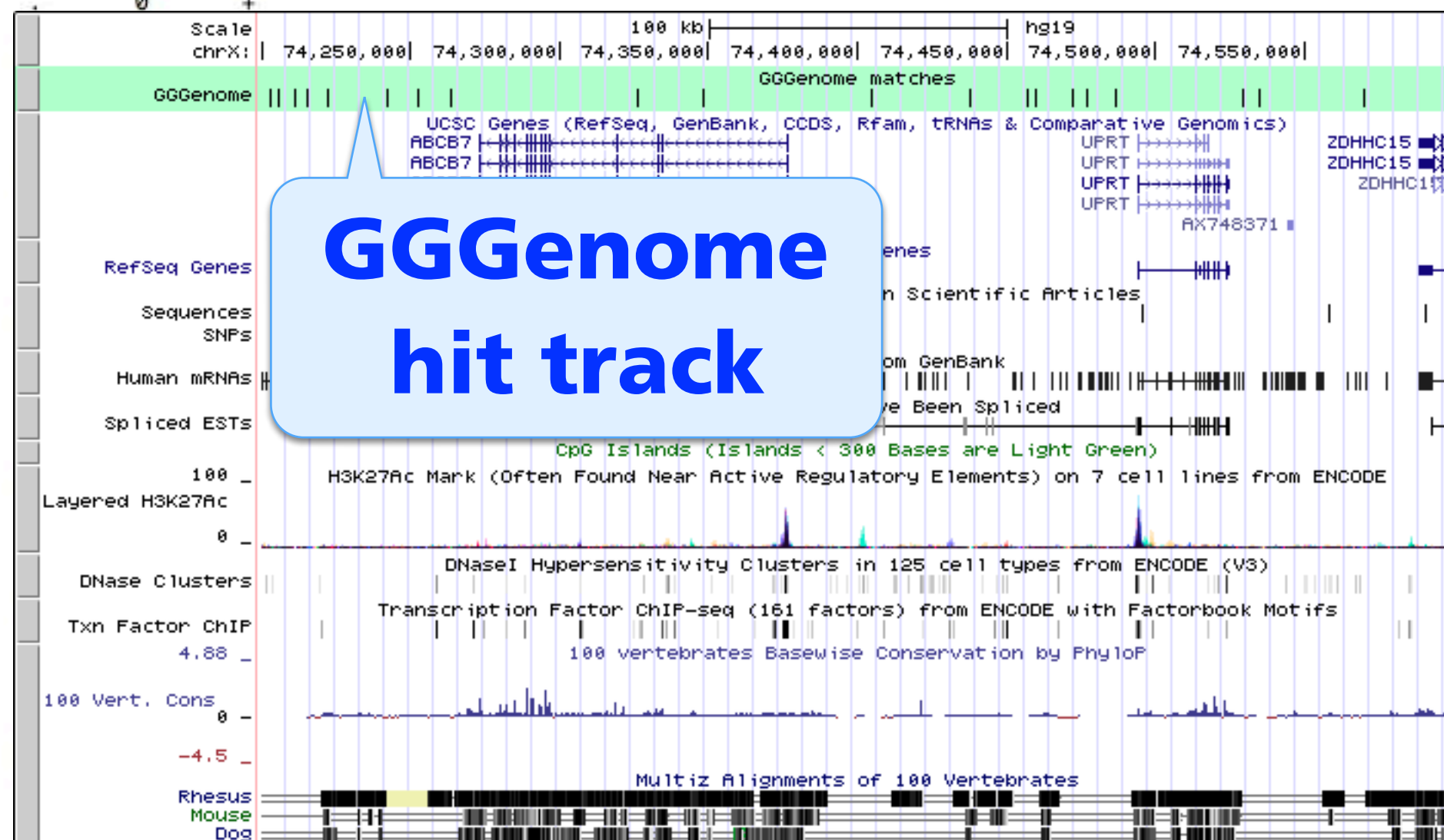
← → ↺ ⓘ gggenome.dbcls.jp/2/TTCAGTGACAACATTGAGTA.bed

track name=GGGenome description="GGGenome matches"

chr1	77930952	77930971	.	0	+
chr1	106947512	106947532	.	0	+
chr2	30898312	30898332	.	0	+
chr2	141517098	141517117	.	0	+
chr2	163535085	163535106	.	0	+
chr2	186291304	186291324	.	0	+
chr2	206339507	206339526	.	0	+
chr2	235498940	235498960	.	0	+
chr3	7763220	7763239	.	0	+
chr3	107912697	107912716	.	0	+
chr3	119451772	119451792	.	0	+
chr3	176282653	176282673	.	0	+
chr4	127134995	127135015	.	0	+
chr4	128011906	128011924	.	0	+
chr5	59044792	59044811	.	0	+
chr5	86132916	86132934	.	0	+
chr6	22543168	22543188	.	0	+
chr6	82260242	82260261	.	0	+
chr6	95214802	95214821	.	0	+
chr6	105109671	105109690	.	0	+
chr6	151088191	151088209	.	0	+
chr7	8118613	8118632	.	0	+
chr7	41689137	41689156	.	0	+
chr8	90913783	90913803	.	0	+
chr8	93876074	93876095	.	0	+
chr11	22831616	22831635	.	0	+
chr11	92192200	92192219	.	0	+
chr12	104489309	104489329	.	0	+
chr14	81126955	81126975	.	0	+
chr15	97446661	97446682	.	0	+
chr19	41567265	41567284	.	0	+
chrX	24337848	24337867	.	0	+
chrX	130867380	130867399	.	0	+
chrX	130886147	130886166	.	0	+
chrX	130892291	130892310	.	0	+
chrX	130920565	130920584	.	0	+
chr1	1930392	1930411	.	0	+
chr1	155825360	155825379	.	0	+
chr3	49831282	49831301	.	0	+
chr3	185466112	185466131	.	0	+
chr4	19225839	19225857	.	0	+
chr4	74112900	74112919	.	0	+
chr5	128909691	128909711	.	0	+

'bed'

GGGenome
hit track



GGGenome を他のツールから呼び出す

← → ↺ gggenome.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: "TCATGAAATGGAAGTGCTGCCACTTCAGGGTCTGTAAAGAGATAATGCTGATGCCAGGCCAGGGAAAAAAGCAGTACTCAAGATCACCTTTTTTTAAAGTTCACTGCAACA",
- 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",

'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

fx | =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	caatcaccctcaccctcttatatgc	http://GGGenome.dbcls.jp/rice/caatcaccctcaccctcttatatgc.txt	=ImportData(D2)	chr01	+	27707	27
3		YN001-R	ccgctgtgaac		chr01 - 28071 28092 ATATTGTTTGGTACGAGTA	chr01	-	28071	28
4		YN002-F	tgatccaata						
5		YN002-R	catgcaaggta						
6		YN003-F	acgtactgtgg						
7		YN003-R	acccaacctat						
8		YN004-F	atcagattccgcccggccg						
9		YN004-R	ggagagatctggtggggag						

= ImportData(D2)

PCRプライマー配列

DBCLS
Database Center
for Life Science

[illegible]

<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**

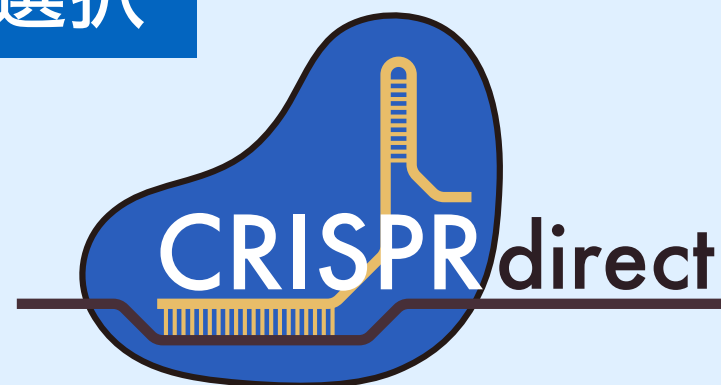
商用利用であっても無償。

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

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

PAM

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) ?

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

design

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

or Paste a nucleotide sequence: ?

```
agtgcacctcccgttcgctcgcgagctcgcgttactttacaccgcccgcgagctctccagactccggaggaggaagcg  
atcgttacacgtacgcctcgtcaagcagaagcagaacatctgaagaatggctgacgaggatattcaacctattgtgtgcgacaatg  
gcactggaatggtaaggcaggttttgctggtgatgatgcaccaagggccgtcttccttagcattgtagggagaccacgtcacacc  
ggtgtcatggttgggatgggccaagaggatgcctatgtgggtgatgaagctcaggcaaaaaggggtatcctgactctaagtagcc  
aattgaacatggaattgtcaataactgggatgacatggagaaaatatggcaccacaccttctacaatgagcttcgtgttgacctg  
aagatcacctgtattactaactgaagccctctcaatcccaagccaacagagagaagatgacacagatcatgtttgagaccttc  
aattgccagcaatgtatgtcgcaatccaggtgttctatccttgt
```

or upload

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

Specificity check: ?

Whats' new:

- 2017-06-19
- 2017-06-09
- 2017-02-17
- 2017-01-23
- 2016-12-14
- 2016-09-09
- 2016-08-30
- 2016-06-14
- 2015-10-05
- 2015-01-13
- 2014-11-21

Rice (*Oryza sativa* ssp. *japonica*) genome, Os-Nipponbare-Reference-IRGSP-1.0 (Oct, 2011)

Chinese hamster (*Cricetulus griseus*) genome, C_griseus_v1.0/crigr1 (Jul, 2013)

Golden hamster (*Mesocricetus auratus*) genome, MesAur1.0 (Mar, 2013)

African wild rice (*Oryza barthii*) genome, Obart_v1.0 (Apr, 2014)

African wild rice (*Oryza brachyantha*) genome, Oryza_brachyantha.v1.4b (May, 2011)

African wild rice (*Oryza glaberrima*) genome, AGI1.1 (May, 2011)

Brazilian wild rice (*Oryza glumaepatula*) genome, ALNU02000000 (Aug, 2013)

Longstamen rice (*Oryza longistaminata*) genome, v0117-2013Aug (Aug, 2013)

Australian wild rice (*Oryza meridionalis*) genome, Oryza_meridionalis_v1.3 (Oct, 2014)

Indian wild rice (*Oryza nivara*) genome, AWH000000000 (Aug, 2013)

Red rice (*Oryza punctata*) genome, AVCL000000000 (Aug, 2013)

Brownbeard rice (*Oryza rufipogon*) genome, PRJEB4137 (Aug, 2013)

Rice (*Oryza sativa* ssp. *indica*) genome, ASM465v1 (Jan, 2005)

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	-	cct cccgttcgcctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	ccc gttcgcctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccg ttcgcctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cct cgctcgcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccg ccgcccgcgagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccg ccgcccgcgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccgcgagctctccagactc ccg [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 75	-	ccg ccgagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 78	+	ccgagctctccagactccgg agg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	-	ccg agctctccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	+	agctctccagactccggagg agg [gRNA]	65.00 %	79.68 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	-	cca gactccggaggaggaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccg gaggaggaagcgatcggttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cct cgtaagcagaagcagaaca [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	-	cct attgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaatggcac tgg [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaatggcactggaa 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:

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	-	cctcccgttcgctcgctcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cccggttcgctcgctcgagct [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccgttcgctcgctcgagctc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgagctcgcttac [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccgcccgcgagctctccaga [gRNA]	75.00 %	80.41 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccgcccgcgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccgcgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 75	-	ccgcccgcgagctctccagactccgg [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	-	ccagactccggaggaggaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggaggaggaagcgatcggttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cctcgtcaagcagaagcagaaca [gRNA]	50.00 %	71.33 °C	-		0 [detail]	3 [detail]	588 [detail]
114 - 136	+	gaagcagaacatctgaagaa [gRNA]	40.00 %	65.99 °C	-		0 [detail]	7 [detail]	1117 [detail]
123 - 145	+	catctgaagaatggctgacg [gRNA]	50.00 %	69.80 °C	-		1 [detail]	2 [detail]	1388 [detail]
151 - 173	+	caacctattgtgtgcgacaa [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	cctattgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaatggcactggaa [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	677 [detail]

標的サイトの
位置と塩基配列

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

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	-	cct	cccgttcgcctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	ccc	gttcgcctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccg	ttcgctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cct	cgctcgcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]		
47 - 69	-	ccg	ccgcccgcgagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI			
50 - 72	-	ccg	ccgcccgcgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]		
53 - 75	+	ccg	ccgcccgcgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]		
53 - 75	-	ccg	ccgagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]		
56 - 78	+	ccg	agctctccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	-	ccg	agctctccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	+	agg	agctctccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	-	cca	gactccggaggaggaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccg	gaggaggaagcgatcggttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cct	cgtaagcagaagcagaaca [gRNA]	50.00 %	71.33 °C	-		0 [detail]	3 [detail]	588 [detail]
114 - 136	+	tgg	gaagcagaacatctgaagaa [gRNA]	40.00 %	65.99 °C	-		0 [detail]	7 [detail]	1117 [detail]
123 - 145	+	agg	catctgaagaatggctgacg [gRNA]	50.00 %	69.80 °C	-		1 [detail]	2 [detail]	1388 [detail]
151 - 173	+	tgg	caacctattgtgtgcgacaa [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	cct	attgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	tgg	attgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	tgg	gtgcgacaatggcactggaa [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	677 [detail]

Showing 1 to 20 of 71 entries

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配列に関する情報
制限酵素サイト も

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	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 60	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 73	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 76	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 76	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 79	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 79	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 82	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 88	-	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggaggaggaagcgatcggttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cctcgtcaagcagaagcagaaca [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	-	cctattgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaatggcac [tgg] [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaatggcactggaa [tgg] [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	677 [detail]

ゲノムに何箇所あるか？

20mer

PAM

NNNNNNNNNNNNNNNNNNNNNNNN NGG

Showing 1 to 20 of 71 entries

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Graphical View:

CRISPRdirect によるガイド RNA 設計

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☐ show highly specific target only

緑：おすすめ

オフターゲット
サイトが少ない

Sh	en	23mer)	sequence information			sites ?			
			GC% of 20mer	Tm of 20mer	TTTT in 20mer	sites	+PAM	+PAM	8mer +PAM
7 - 23	-	cct cccgttcgctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	ccc gttcgctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccg ttcgctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cct cgctcgcgagctcgcggttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccg ccgcccgcgagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccg ccgcccgcgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccgcgagctctccagactc cgg [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 75	-	ccg ccgagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	[detail]	2679 [detail]
56 - 78	+	ccgagctctccagactccgg agg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI			
56 - 78	-	ccg agctctccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI			
59 - 81	+	agctctccagactccggagg agg [gRNA]	65.00 %	79.68 °C	-	BspEI			
65 - 87	-	cca gactccggaggaggaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI			
72 - 94	-	ccg gaggaggaagcgatcggttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cct cgtcaagcagaagcagaaca [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	-	cct attgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaatggcac tgg [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaatggcactggaa tgg [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	677 [detail]

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First Previous 1 2 3 4 Next Last

Graphical View:

オフターゲット
サイトが多い

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10 - 32	-	cccggttcgctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccgttcgctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
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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	-	ccagactccggaggaggagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggaggaggagcgcgacgttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cctcgtcaagcagaagcagaaca [gRNA]	50.00 %	71.33 °C	-		0 [detail]	3 [detail]	588 [detail]
114 - 136	+	gaagcagaacatctgaagaa [gRNA]	40.00 %	65.99 °C	-		0 [detail]	7 [detail]	1117 [detail]
123 - 145	+	catctgaagaatggctgacg [gRNA]	50.00 %	69.80 °C	-		1 [detail]	2 [detail]	1388 [detail]
151 - 173	+	caacctattgtgtgcgacaa [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	cctattgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaatggcactggaa [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



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:

- [CCNcccgttcgcctcgctcgca \(1\)](#)
- [tcgcgaacgagacgaacgggNGG \(4\)](#)
- **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
CCAACGAGGCCAGGTGAGCTCTCCCCCTCCCGGATTCGCCTCGCTTCGCGACCGAGTTCAGTTGAGCTGGGTGCACTGAC

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

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

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

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

CRISPRdirect によるガイド RNA 設計

151 - 173	+	caacctattgtgtgacgacaa[tg g] [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	[cc t]attgtgtgacgacaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgacgacaatggcac[tg g] [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgacgacaatggcactggaa[tg g] [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
catgtttgagaccttcaattgccagcaatgtatgtcgcaatccaggctgttctatccttgt
> < <<

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 | 2017-06-28 07:12:12 ]
# sequence_name:
# pam_sequence: NGG
# specificity_check: Rice (Oryza sativa ssp. japonica) genome, Os-Nipponbare-Reference-IRGSP-1.0 (Oct, 2011)
# start end strand sequence GC Tm TTTT RE_sites hit_20mer
hit_12mer hit_8mer
#
7 29 - cctcccgttcgctcgtcgcga 75.00 83.48 0 NruI 1 5
370
10 32 - cccgttcgctcgtcgcgagct 70.00 81.73 0 NruI 1 1
276
11 33 - ccgttcgctcgtcgcgagctc 70.00 81.09 0 NruI,SacI 1
4 911
18 40 - cctcgtcgcgagctcgcgttac 70.00 80.24 0 NruI,SacI 1
4 1072
47 69 - ccgcccgcgcgagctctccaga 75.00 84.25 0 SacI 1 305
79033
50 72 - ccgcccgcgagctctccagactc 70.00 80.41 0 SacI 1 37
3555
53 75 + ccgcccgcgagctctccagactccg 70.00 80.41 0 SacI 1 3
175
53 75 - ccgcccgcgagctctccagactccg 70.00 80.27 0 SacI 1 15
2679
56 78 + ccgagctctccagactccggagg 70.00 80.27 0 BspEI,SacI 1
4 793
56 78 - ccgagctctccagactccggagg 65.00 79.68 0 BspEI,SacI 1
1 1295
59 81 + agctctccagactccggaggagg 65.00 79.68 0 BspEI 1 2
```


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	-	cctccggttcgctcgctcgca	75	83.48	0	Nrul	1	5	370				
8	10	32	-	cccgttcgctcgctcgagct	70	81.73	0	Nrul	1	1	276				
9	11	33	-	ccgttcgctcgctcgagctc	70	81.09	0	Nrul,SacI	1	4	911				
10	18	40	-	cctcgctcgagctcgcggtac	70	80.24	0	Nrul,SacI	1	4	1072				
11	47	69	-	ccgccgccgagctctccaga	75	84.25	0	SacI	1	305	79033				
12	50	72	-	ccgccgccgagctctccagactc	70	80.41	0	SacI	1	37	3555				
13	53	75	+	ccgccgagctctccagactccgg	70	80.41	0	SacI	1	3	175				
14	53	75	-	ccgccgagctctccagactccgg	70	80.27	0	SacI	1	15	2679				
15	56	78	+	ccgagctctccagactccggagg	70	80.27	0	BspEI,SacI	1	4	793				
16	56	78	-	ccgagctctccagactccggagg	65	79.68	0	BspEI,SacI	1	1	1295				
17	59	81	+	agctctccagactccggaggagg	65	79.68	0	BspEI	1	2	608				
18	65	87	-	ccagactccggaggaggaagcga	65	78.93	0	BspEI	1	6	375				
19	72	94	-	ccggaggaggaagcgatcggtac	55	73	0	BsiEI,PvuI	1	14	3180				
20	102	124	-	cctcgtcaagcagaagcagaaca	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	+	caacctattgtgtgcgacaatgg	45	69.15	0		1	3	303				
24	154	176	-	cctattgtgtgcgacaatggcac	50	72.27	0		1	1	667				
25	157	179	+	attgtgtgcgacaatggcactgg	50	72.27	0		1	2	499				
26	162	184	+	gtgcgacaatggcactggaatgg	55	74.69	0		1	6	677				
27	168	190	+	caatggcactggaatggtcaagg	50	72.31	0		5	8	545				
28	172	194	+	ggcactggaatggtcaaggcagg	60	77.26	0		0	2	447				
29	181	203	+	atggtcaaggcaggtttgtctgg	50	73.64	1		0	1	1511				
30	197	219	+	ttgctggtgatgatgcaccaagg	50	73.43	0		1	4	553				
31	198	220	+	tgctggtgatgatgcaccaaggg	50	73.43	0		1	9	616				
32	214	236	-	ccaagggccgtcttccttagcat	60	80.62	0		1	1	121				
33	220	242	+	gccgtcttccttagcattgtagg	55	76.01	0		1	2	796				
34	221	243	+	ccgtcttccttagcattgtaggg	50	72.87	0		1	3	538				
35	221	243	-	ccgtcttccttagcattgtaggg	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	<i>Aegilops tauschii</i>	ASM34733v1 (Dec, 2013)
AMTR1.0	EnsemblPlants	Plant	A. trichopoda	アムボレラ・トリコポダ	<i>Amborella trichopoda</i>	AMTR1.0 (Jan, 2014)
Araly v.1.0	EnsemblPlants	Plant	Lyre-leaved rock-cress	シロイヌナズナ属	<i>Arabidopsis lyrata</i>	v.1.0 (Dec, 2008)
TAIR10 en	EnsemblPlants	Plant	Thale cress	シロイヌナズナ	<i>Arabidopsis thaliana</i>	TAIR10 (Sep, 2010)
Bradi v1.0	EnsemblPlants	Plant	Purple false brome	セイヨウヤマカモジ, ミナトカモジグサ	<i>Brachypodium distachyon</i>	v1.0 (Jan, 2009)
Braol v2.1	EnsemblPlants	Plant	Wild cabbage	ヤセイカンラン, ワイルドキャベツ	<i>Brassica oleracea</i>	v2.1
IVFCAASv1	EnsemblPlants	Plant	Chinese cabbage	ハクサイ, サントウサイ	<i>Brassica rapa ssp. pekinensis</i>	IVFCAASv1 (Aug, 2009)
Chlre v3.1	EnsemblPlants	Plant	Green algae	クラミドモナス	<i>Chlamydomonas reinhardtii</i>	v3.1 (Nov, 2007)
ASM9120v1	EnsemblPlants	Plant	Red alga	シアニディオシゾン	<i>Cyanidioschyzon merolae</i>	ASM9120v1 (Nov, 2008)
Soybn V1.0	EnsemblPlants	Plant	Soybean	ダイズ	<i>Glycine max</i>	V1.0 (Jan, 2010)



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