

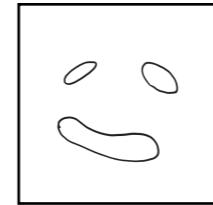
統合データベース講習会 in 広島大学

塩基配列解析およびゲノム編集を支援する
ためのデータベース・ウェブツール

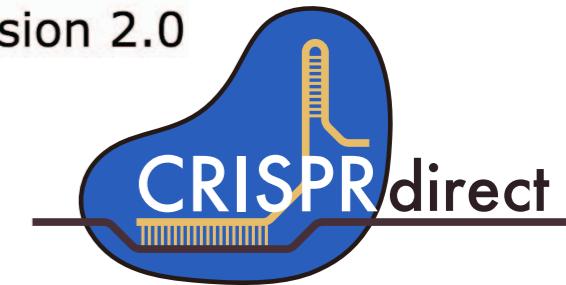
2018年 9月11日
ライフサイエンス統合データベースセンター (DBCLS)
内藤雄樹

- 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 =

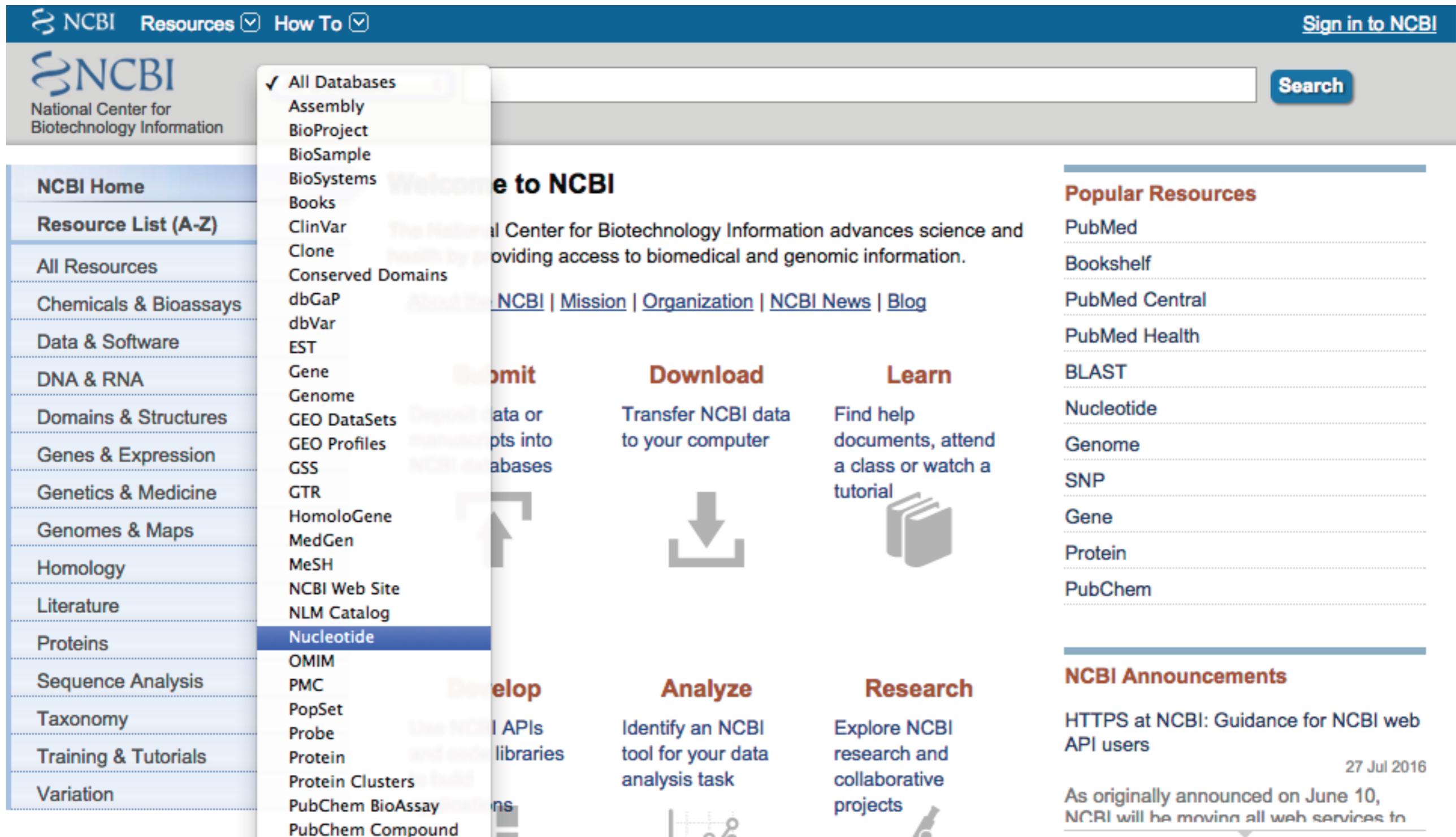


DBCLS
Database Center
for Life Science

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: 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.

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National Center for Biotechnology Information advances science and providing access to biomedical and genomic information.

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Popular Resources

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

NCBI Announcements

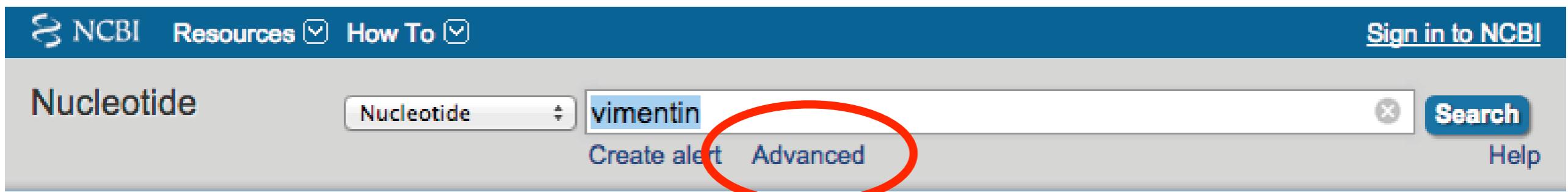
HTTPS at NCBI: Guidance for NCBI web API users

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

● 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)

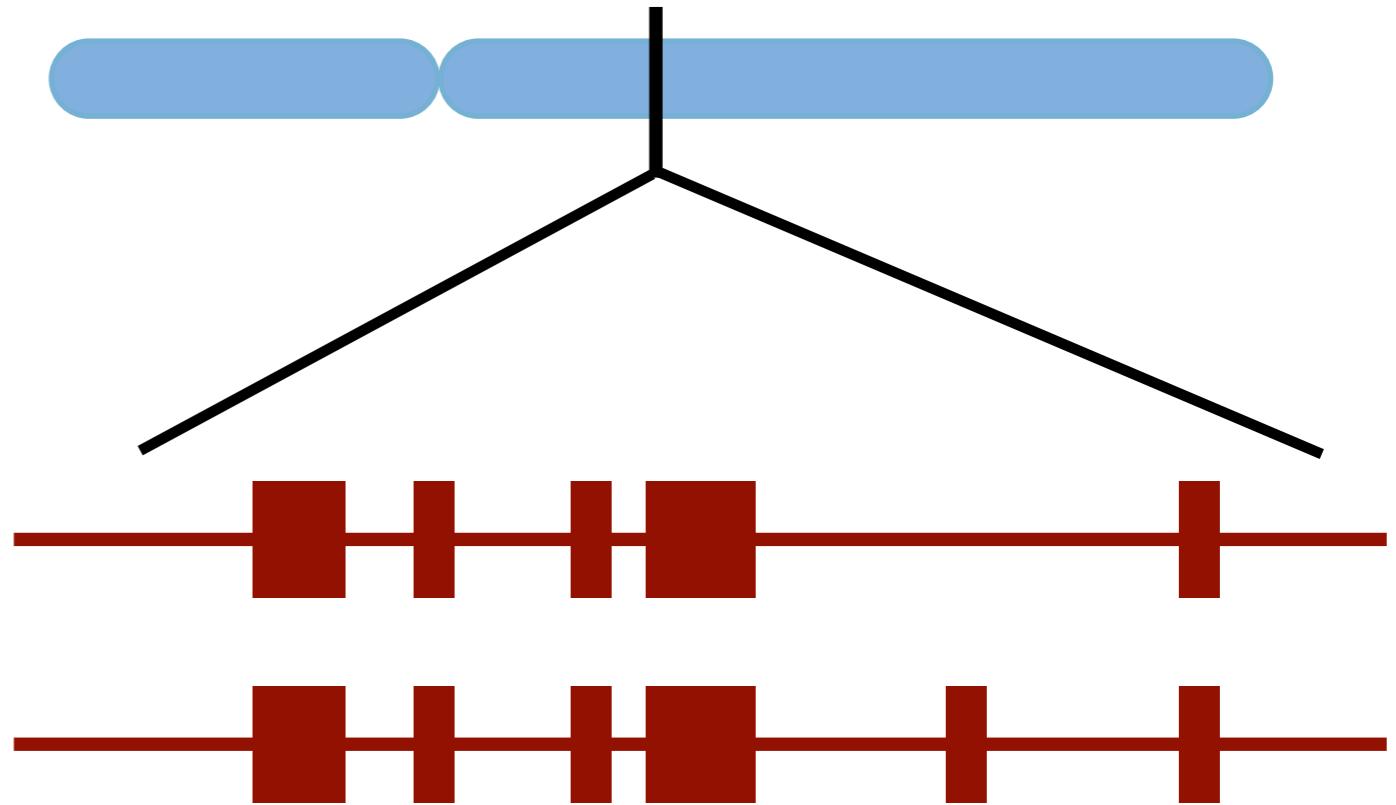
RefSeq ID:

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



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旧バージョン

nanog

検索

Homo sapiens (human)

4

2018-06-22 16:28:51, GGRNA : RefSeq release 88 (May, 2018)

Summary:

- nanog_(50)
 - INTERSECTION (50)

Results:

検索語に色がつきます。重なると色が濃く表示されます。

RefSeqの転写産物

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

Homo sapiens Nanog homeobox retrogene P8 (NANOGP8), mRNA. (1999 bp)

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

Synonym: NANOGP1; 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;

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



IMAGE GALLERY



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[旧バージョン](#)

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



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TODD



PICTURES



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TODD



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TODD

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</

塩基配列を検索

統合遺伝子検索

GGRNA

ver.2



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TODD



PICTURE



GALLERY



TODD



PICTURE



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TODD



PICTURE



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TODD



PICTURE



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TODD



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GALLERY



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PICTURE



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TODD

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塩基配列を検索

統合遺伝子検索

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GALLERY

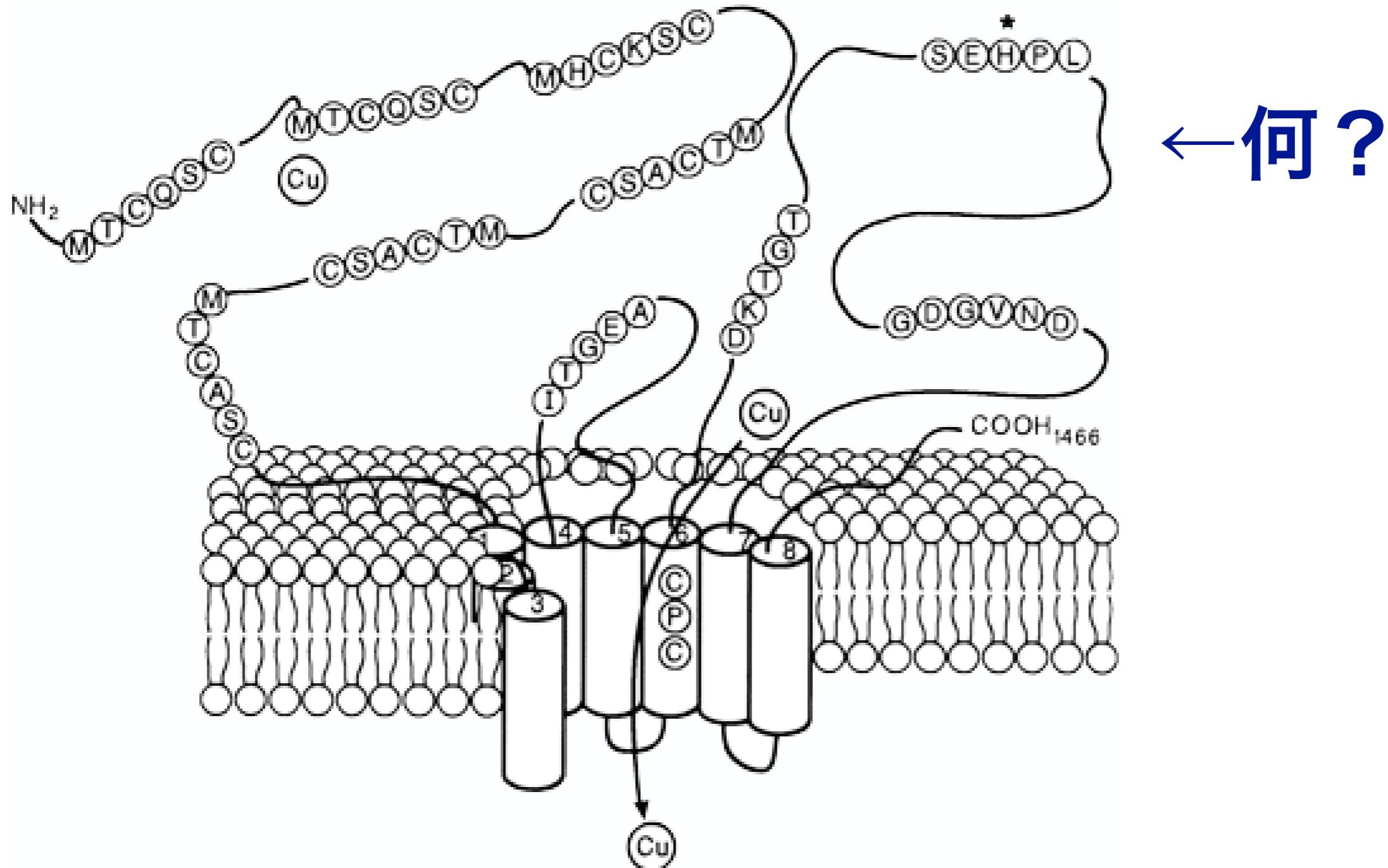
TODD

PICTURES

GALLERY

<p

アミノ酸配列を検索



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



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アミノ酸配列を検索

統合遺伝子検索

GGRNA
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[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・・・

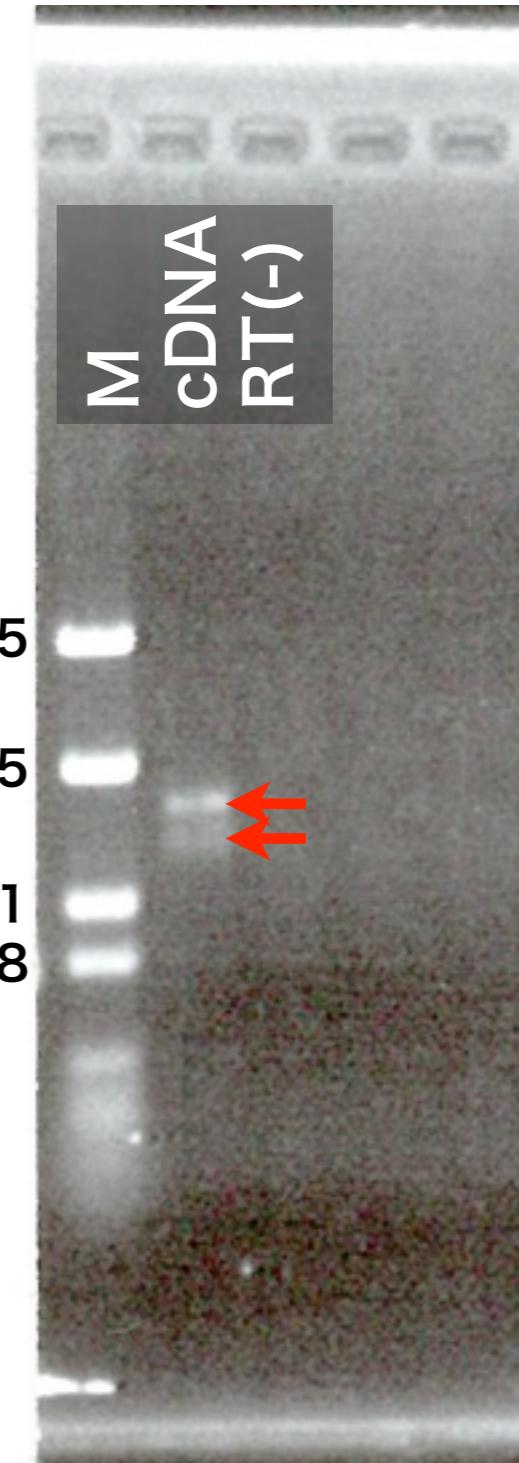
primer-F:

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？



※架空のデータです

PCRのプライマー

- seq: aqctcattactttatcaqtqca (2)
 - comp: tqacgtattcactttctqggtt (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)
tgaaaaaaattcaggacttggctgagcgccgcgaattcaatcgaaaatgaagcggaagcaggcgagtcgcagggccatcttgcaccaatcaga**agctcattactttatcagtgca**agatgcacccacaaag
aaagagttgttattaaccccaacggaaatccgaggctgcacccatcgcacgactatgcacgtgtcctcaaggccctgtataattttgaatgtgcccgactacactggaaatcctcatccctgactttgtta
aacagacctctgaagagaagccccaaagacagtgaagaactcgagtatttaaccacatcagcatcgaggactcgccggctacgagctgaccagcaaggctggctttgtccatatcagatcctccacgagtgccta
aaccagaagagtgaatacgtcatggcgtgtggcaagcacacagtgcgcgggtgggttaagaacaagagatggaaagc
agttagcctcacagaagatottcaactgtggccatg...
position 1892 2272 **2272 - 1892 = 380**
Synonym: C22orf12; DGCR8; Gy1; psnha
NM_001190326.1 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

Homo sapiens DGCR8 microprocessor complex subunit (DGCR8), transcript variant 1, mRNA. (4536 bp)
gaagcggaagcaggcgaggactccgagaggcccattttccagccaatcaga**agctcattactttatcgtgca**agatgcacccacaagaaagatgttattaaccccaacggaaatccgaggctgcatttcgca
cgagtacatgcagcgtgtctcaagggtccgcctgtctataattttttgaatgtgagaacccaagttagcgtttgggcctcggtgaccattgtatgggtgacttacggatctggaaactgcaagcagaaaaacttgcga
agaataaagctgcccgagctacactggaaatccatccctgactttttaaacagacacctctgaagagaagccaaagacagtgaagaactcgagtatttaaccacatcagcatcgaggactcgccggctacgagctg
ggcaagcacacagtgcgcgtgtgtataaaaaaaaacccatgggatgggtgacacgttatcaagttgaagtggttcctggaaa**aaccagaagagtgaatacgtcatggcggt**
position 1892 2371 **2371 - 1892 = 479**
Synonym: C22orf12; DGCR8; Gyr1; pasha
NM_022720.3 - Homo sapiens (human) - NCBI - UCSC - RefEx(expression)

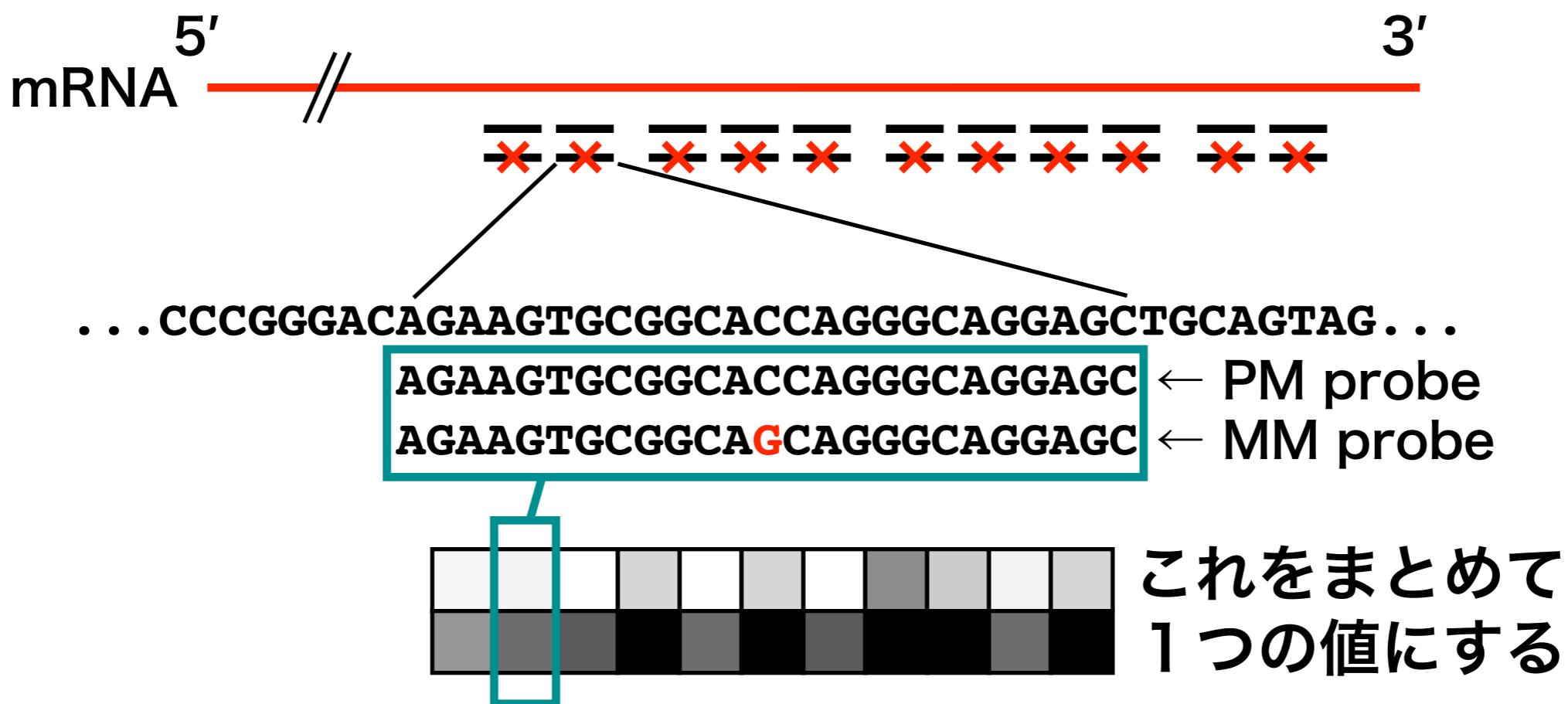
Data Export:

下記より最大10000件まで検索結果を取得できます。

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

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

GALLERY

IMAGE

<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。

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

超絶高速ゲノム配列検索 [Help](#) | [English](#)

GGGenome

検索窓 | [検索](#) Human genome, GRCh37/ng19 (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/](http://GGGenome.dbcls.jp/)  /k/[strand]/sequence[.format][.download]
 -  → 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  (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  で
 - 2 ミスマッチ/ギャップまで許容して

超絶高速ゲノム配列検索 [Help](#) | [English](#)

GGGenome

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

許容するミスマッチ/ギャップの数: 0 (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

2017-06-28 06:20:32, 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
GCCCGCCAGCCACTTATATGTATTTTAAATTCACTGACAACATTGAGTAGAAAAGATAATTTTTTTTGAGACAG

« ⏴ ページ 1 /1 ⏵ » C 1件中

Data Export:

下記のフォーマットで最大100000件まで検索結果を取得できます。

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

ゲ ゲ ゲ
GGGenome による塩基配列検索



超絶高速ゲノム配列検索

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

GGGenome

TTCACTGACAACATT

検索

Human genome, GRCh37/hg19 (Feb, 2009)



許容するミスマッチ/ギャップの数: 0 (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

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

Summary:

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

Results:

検索語に色がつきます (ミスマッチ・挿入欠失)。

[chr1:173400829-173400843](#) ▼173400829
TTTCACATGCACCTACCTGCCTGCTGCTTCAC TGACAACATT TCAGGGTCTCGCAAGGCATGGAATACAATG

[chr1:197463616-197463630](#) ▼197463616
AATGATCTTACTGTTAACACTGCACTTTATTCACTGACAACATT ACTTAAAGAAAAGAGATTATGATTGGATAAA

[chr2:30898313-30898327](#) ▼30898313
GCCCCCAGCCACTTATATGTATTTTAAATTCACTGACAACATT GAGTAGAAAAGATAATTTTTTTTTGA

[chr2:163535086-163535100](#) ▼163535086
TGAGAAAGAGGACACCCTAAGAATTATGGCTTCAC TGACAACATT AGAGAACATATCAAACGAAATATT

[chr3:117135824-117135838](#) ▼117135824
TCCCCTAGCAAATCAATTCAACTTCTGTTATTCACTGACAACATT GTTTTTCTACTGGCTGCAGCTTTCACAA

chr4:128011007-128011021

ゲ ゲ ゲ
GGGenome による塩基配列検索



超絶高速ゲノム配列検索 [Help](#) | [English](#)

GGGenome

TTCACTGACA 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
ATACTAGAATTTAAAAGCAAATGTCTTATTCACTGACAACATAATCATCTATAAAGAAAATCCTACAT

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

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

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

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

chr1:6720005-6720004

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: 2 (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

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

Summary:

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

Results:

検索語に色がつきます (ミスマッチ・挿入欠失)。

[chr1:77930953-77930971](#) ▼77930953
AGCAGTACTCAAGATCACCTTTTAAAGTTCACTG-CAACATT~~CAGTAGATGAAAAATGTGTAGCTGTAATT~~CATTGA

[chr1:106947513-106947532](#) ▼106947513
TAGAAAACATACCACATAAAGAACATCTTTCACTG~~CACAA-ATTGAGT~~A~~AAAATTTAACCC~~GTTGAAAGGGTCATTA

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

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

[chr2:163535086-163535103](#) ▼163535086
TGAGAAAGAGGACACCCTAAGAATTATGGCTTCACTGACAACATT-AG-AGAACATATCAAACGAATATTCTGG

chr2:186201205-186201224

Genomes Genome Browser Tools Mirrors Downloads My Data View Help About Us

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

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

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

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

Scale chr1: 5 bases hg19
 chr1: 77,930,955 77,930,960 77,930,965 77,930,970 77,930,971
 ---> T C A C T G C A A C A T C A G
 UCSC Genes (RefSeq, GenBank, CCDS, Rfam, tRNAs & Comparative Genomics)

AK5 AK5 RefSeq Genes

RefSeq Genes Publications: Sequences in Scientific Articles

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

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

100 0 DNase Clusters DNaseI Hypersensitivity Clusters in 125 cell types from ENCODE (V3)

Txn Factor ChIP 4.88 Transcription Factor ChIP-seq (161 factors) from ENCODE with Factorbook Motifs

100 Vert. Cons 0 100 vertebrates Basewise Conservation by PhyloP

-4.5 Gaps Multiz Alignments of 100 Vertebrates

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

Common SNPs(147) 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.dbcls.jp/2/TTCACTGACAACATTGAGTA.txt

TTCA-ACAG
||| | |
TTCACACGG
====D=X==

“query”
“align”
“sbjct”
“edit”

- 7 “match”
- 1 “mis”
- 1 “del”
- 0 “ins”

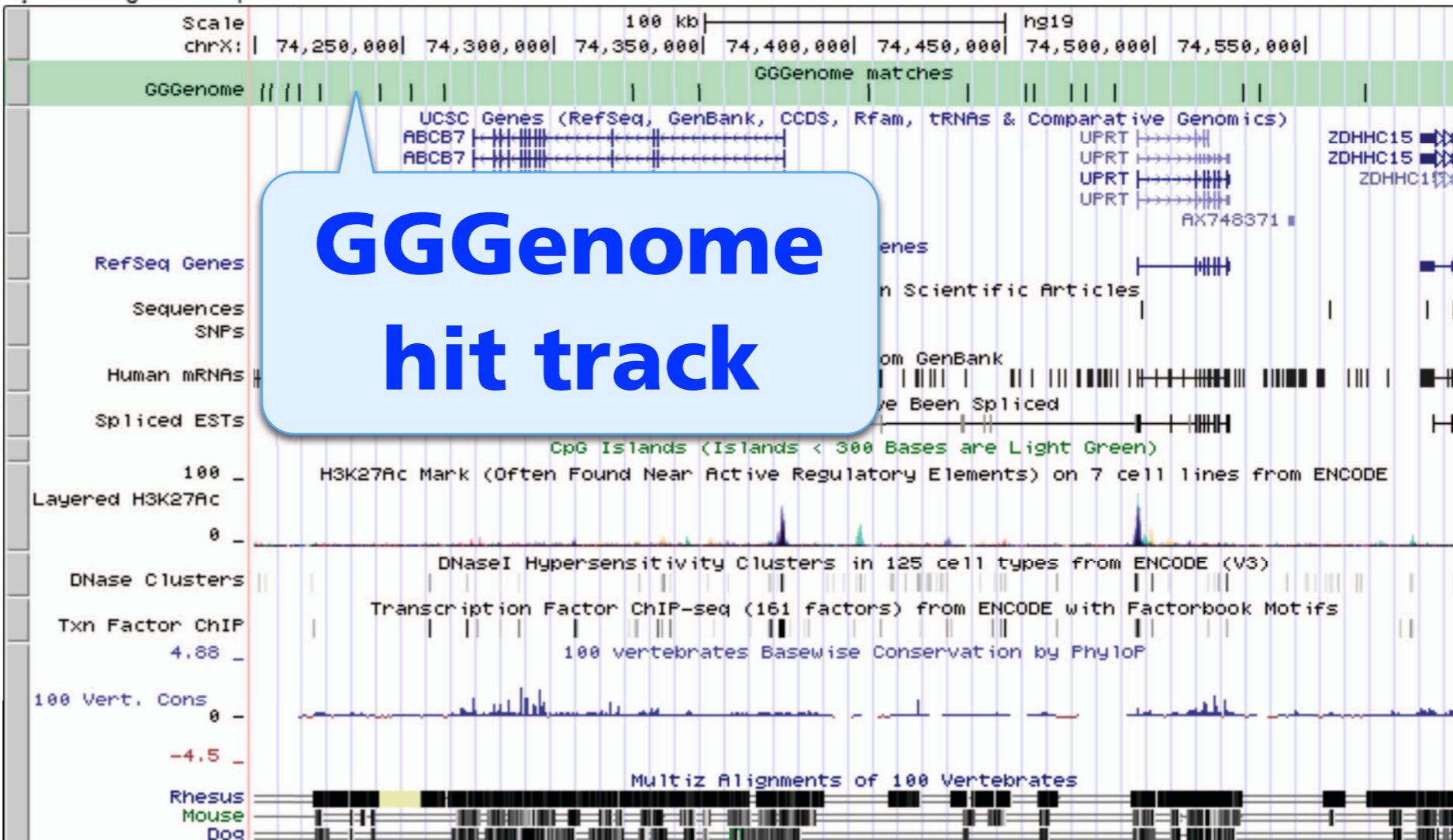
GGGenome を他のツールから呼び出す

← → ⌂ ⓘ gggenome.dbcls.jp/2/TTCACTGACAACATTGAGTA.bed

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

'bed'

GGGenome hit track



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: "+"  
      }  
    ]  
  }  
}  
}
```

A blue callout bubble with a white border and a light blue background contains the word 'json' in bold blue font. A blue arrow points from the top of the callout bubble towards the JSON data.

表計算ソフトから GGGenome 検索

GGGenome primer search ☆ meso cacase

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

A B C D E F G H I

=ImportData(D2)

	A	B	C	D	E	F	G	H	I
1	Primer name	(1) Sequence	(2) GGGenome URL	(3) ImportDATA function	name	strand	start	end	
2	YN001-F	caatcaccctcaccctttatatgc	http://GGGenome.dbcls.jp/rice/caatcaccctcaccctttatatgc.txt	=ImportData(D2)	chr01	+	27707	27	
3	YN001-R	ccgctgtgaac		chr01 - 28071 28092					
4	YN002-F	tgatccaata		ATATTGTTGGTACCGAGTA					
5	YN002-R	catgcaaggta		27971 28192					
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

CC BY-SA

表計算ソフトから GGGenome 検索

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

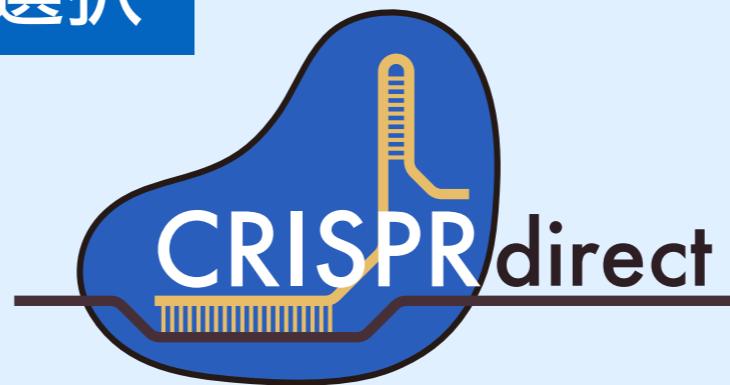
- **ゲノムを高速に検索可能**
350種の生物種（うち植物は80種）に対応
- **短い塩基配列の検索に強い**
ミスマッチや挿入欠失が多くても見落としのない検索
- **他のツールから呼び出すことができる（REST API）**
Googleスプレッドシートの ImportData() 関数
Excel 2013以降の WEBSERVICE() 関数
R、Ruby、Galaxy、ゲノムブラウザ・・・
- **無償で自由に利用可能**
商用利用であっても無償。
利用記録は当センターにおいて機密扱い。

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

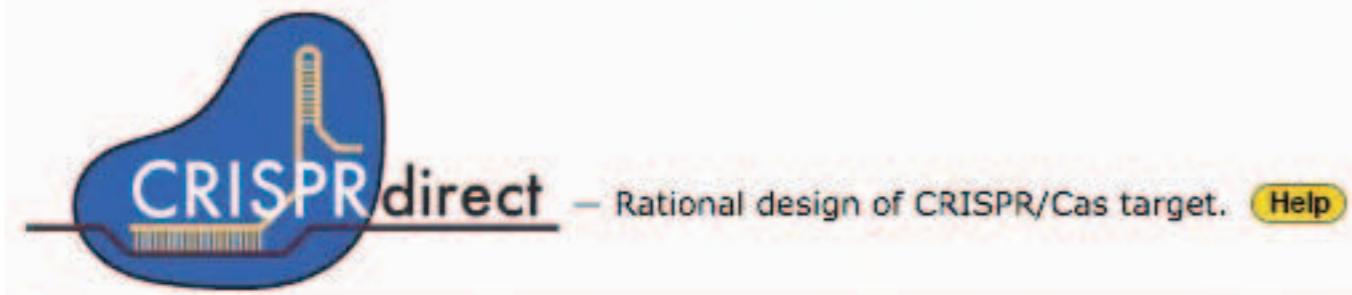


wordが完全一致せず
BLASTで検索できない



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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

or Paste a nucleotide sequence: ?

Accession番号

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

What's new:

- 2017-06-19 Added 8 species - List

オフターゲット検索のための
生物種 を選択

CRISPRdirect によるガイド RNA 設計

retrieve sequence

or Paste a nucleotide sequence: ?

```
agtgcaccccccgttcgcctcgctcgagctcgcttactttacaccggccggccgagctctccagactccggaggaggaaagcg  
atcggttacacgtacgcctcgtaaggcagaaggcagaacatctgaagaatggctgacgaggatattcaacctatttgtgtgcgacaatg  
gcactggaaatggtaaaggcagggttttgctggatgtatgcaccaaggccgtttcccttagcattgttagggagaccacgtcacacc  
ggtgtcatggttgggatggccaaaaggatgcctatgtgggtatgaagctcaggcaaaaagggtatcctgactctaaagtaccc  
aattgaacatgaaattgtcaataactgggatgacatggagaaaatatggcaccacaccttctacaatgagcttcgtttgcacctg  
aagatcacccgtattactaactgaagccccctctaattccaaagccaaacagagagaagatgacacagatcatgtttgagacccctc  
aattgcccagcaatgtatgtcgcaatccaggctgttctatccctgt
```

数文字ほど入力すると
生物種を検索 できる

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

Specificity check: rice

design

What's new:

- 2017-06-15 African wild rice (Oryza brachyantha) genome, Oryza_brachyantha.v1.4b (May, 2011)
- 2017-06-05 African wild rice (Oryza glaberrima) genome, AGI1.1 (May, 2011)
- 2017-02-17 Brazilian wild rice (Oryza glumaepatula) genome, ALNU02000000 (Aug, 2013)
- 2017-01-23 Longstamen rice (Oryza longistaminata) genome, v0117-2013Aug (Aug, 2013)
- 2016-12-14 Australian wild rice (Oryza meridionalis) genome, Oryza_meridionalis_v1.3 (Oct, 2014)
- 2016-09-05 Indian wild rice (Oryza nivara) genome, AWHD00000000 (Aug, 2013)
- 2016-08-30 Red rice (Oryza punctata) genome, AVCL00000000 (Aug, 2013)
- 2015-10-05 Brownbeard rice (Oryza rufipogon) genome, PRJEB4137 (Aug, 2013)
- 2015-01-13 Rice (Oryza sativa ssp. indica) genome, ASM465v1 (Jan, 2005)
- 2014-11-21 Rice (Oryza sativa ssp. japonica) genome, Os-Nipponbare-Reference-IRGSP-1.0 (Oct, 2011)

CRISPRdirect によるガイド RNA 設計

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

show **highly specific** target only

Show 20 entries

Search:

position		target sequence	sequence information				number of target sites		
start	- end	20mer+PAM (total 23mer)	GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	12mer +PAM	8mer +PAM
7 - 29	-	cct cccgttcgcctcgctcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	ccc gttcgccctcgctcgagct [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 cgctcgcgagctcgcttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccg ccggccggagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccg ccggccggagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccggagctctccagactc [cg] [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 gactccggaggaggaaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccg gaggaggaaagcgatcgttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cct cgtcaaggcagaaggcagaaca [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 attgtgtgcgacaaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaaatggcac [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:

CRISPRdirect によるガイド RNA 設計

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

show highly specific target only

Show 20 entries

Search:

position		target sequence	sequence information				number of target sites		
start	- end	20mer+PAM (total 23mer)	GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	12mer +PAM	8mer +PAM
7 - 29	-	cctcccggttcgcgcctcgctcgcg [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cccgtttcgccctcgctcgcgagct [gRNA]	70.00 %	83.41 °C	-	SacI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccgttccgcctcgctcgcgagctc [gRNA]	70.00 %	83.41 °C	-	SacI	4 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgcgagctcgcttac [gRNA]	70.00 %	83.41 °C	-	SacI	4 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccggccggccgagctctccaga [gRNA]	75.00 %	83.41 °C	-	SacI	305 [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	-	ccggagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 78	+	ccgagctctccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	-	ccggagctccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	+	agctctccagactccggaggagg [gRNA]	65.00 %	79.68 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	-	ccaaactccggaggaggaaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggaggaggaaagcgatcgttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cctcgtaaggcagaaggcagaaca [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	+	caaccttattgtgtgcgacaaatggc [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	cctattgtgtgcgacaaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaaatggcacatgg [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaaatggcactggaaatgg [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	677 [detail]

Showing 1 to 20 of 71 entries

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標的サイトの
位置と塩基配列

CRISPRdirect によるガイド RNA 設計

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

show **highly specific** target only

Show 20 entries

position		target sequence	sequence information				number of target sites		
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 cccgttcgcctcgctcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	ccc gttcgccctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccg ttgcgcctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cct cgctcgcgagctcgcttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [det]		
47 - 69	-	ccg ccgcccggcgagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI			
50 - 72	-	ccg ccgcccggagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [det]		
53 - 75	+	ccgcccggagctctccagactcgg [gRNA]	70.00 %	80.41 °C	-	SacI	1 [det]		
53 - 75	-	ccg ccgaggctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [det]		
56 - 78	+	ccgaggctctccagactccggagg [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	+	agctctccagactccggaggagg [gRNA]	65.00 %	79.68 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	-	cca gactccggaggaggaaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccg gagggaggaaagcgatcgttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cct cgtcangcagaaggcagoaca [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	+	caacctattgtgtgcgacaaatgg [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	303 [detail]
154 - 176	-	cct atttgtgtgcgacaaatggcac [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	+	gtacgcacaaatggcactggaaaatgg [gRNA]	55.00 %	74.69 °C	-		1 [detail]	5 [detail]	677 [detail]

配列に関する情報 制限酵素サイト も

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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

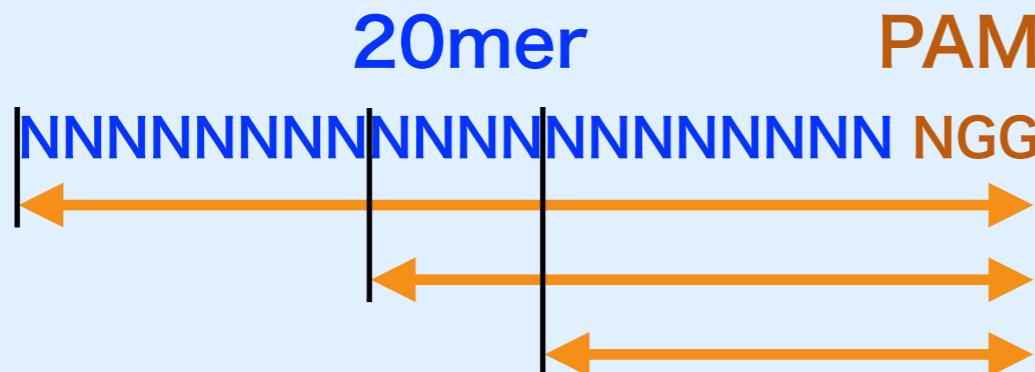
Show 20 entries

position start - end	target sequence 20mer+PAM (total 23mer)	sequence information				restriction sites	number of target sites ?		
		GC% of 20mer	Tm of 20mer	TTTT in 20mer	20mer +PAM		12mer +PAM	8mer +PAM	
7 - 29	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]	
10 - 32	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]	
11 - 33	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]	
18 - 40	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]	
47 - 69	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]	
50 - 72	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]	
53 - 75	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]	
53 - 75	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]	
56 - 78	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]	
56 - 78	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]	
59 - 81	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]	
65 - 87	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]	
72 - 94	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]	
102 - 124	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		0 [detail]	3 [detail]	588 [detail]	
114 - 136	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		0 [detail]	7 [detail]	1117 [detail]	
123 - 145	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		1 [detail]	2 [detail]	1388 [detail]	
151 - 173	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		1 [detail]	3 [detail]	303 [detail]	
154 - 176	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		1 [detail]	1 [detail]	667 [detail]	
157 - 179	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		1 [detail]	2 [detail]	499 [detail]	
162 - 184	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-		1 [detail]	6 [detail]	677 [detail]	

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ゲノムに何箇所あるか？



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

Show

緑：おすすめ

オフターゲット
サイトが少ない

Target sequence		sequence information				off-target sites			
		GC% of 20mer	Tm of 20mer	TTTT in 20mer	SITES	+PAM	+PAM	8mer +PAM	
-	-	cctcccggttcgcctcgctcgcgaa [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	
10 - 32	-	cccgttgcgcctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	
11 - 33	-	ccgtttcgcctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	
18 - 40	-	cctcgctcgcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	
47 - 69	-	ccggccggccgagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	
50 - 72	-	ccggccggagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	
53 - 75	+	ccggccggagctctccagactc [cg] [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	
53 - 75	-	ccggagctctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	1 [detail]	
56 - 78	+	ccggagctctccagactccgg [agg] [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	1 [detail]	
56 - 78	-	ccggagctctccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	
59 - 81	+	agctctccagactccggagg [agg] [gRNA]	65.00 %	79.68 °C	-	BspEI	1 [detail]	1 [detail]	
65 - 87	-	cccgactccggaggaggaaatcg [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	1 [detail]	
72 - 94	-	cccgaggaggaaatcgatcgttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	
102 - 124	-	cctcggtcaaggcagaaggcagaaca [gRNA]	50.00 %	71.33 °C	-		0 [detail]	3 [detail]	
114 - 136	+	gaatcgccggaaatctgtggaaatgg [gRNA]	40.00 %	65.99 °C	-		0 [detail]	7 [detail]	
123 - 145	+	catctgtggaaatggctgtgg [agg] [gRNA]	50.00 %	69.80 °C	-		1 [detail]	2 [detail]	
151 - 173	+	caacccatttgtgtggacaaatgg [agg] [gRNA]	45.00 %	69.15 °C	-		1 [detail]	3 [detail]	
154 - 176	-	cctatttgtgtggacaaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	
157 - 179	+	atttgtgtggacaaatggcac [tgg] [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	
162 - 184	+	gtggcacaatggcactggaaatgg [tgg] [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	

Showing 1 to 20 of 71 entries

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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

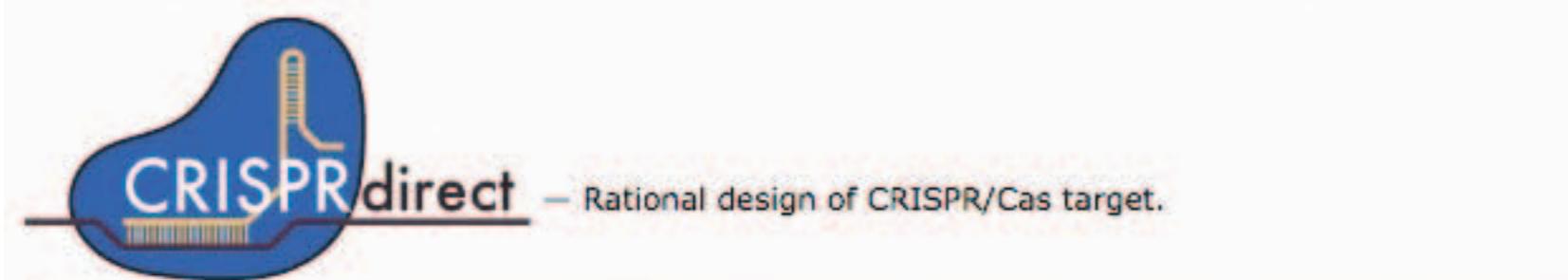
position		target sequence	sequence information				number of target sites		
start	- end		GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	2mer +PAM	8mer +PAM
7 - 29	-	cct cccgttcgcctcgctcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	[detail]	370 [detail]
10 - 32	-	ccc gttcgccctcgctcgcgagct [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 cgctcgcgagctcgcttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccg ccggccggagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccg ccggccggagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccggagctctccagactc 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 gactccggaggaggaaagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccg gaggaggaaagcgatcgttac [gRNA]	55.00 %	73.00 °C	-	BsiEI PvuI	1 [detail]	14 [detail]	3180 [detail]
102 - 124	-	cct cgtcaaggcagaaggcagaaca [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 attgtgtgcgacaaatggcac [gRNA]	50.00 %	72.27 °C	-		1 [detail]	1 [detail]	667 [detail]
157 - 179	+	attgtgtgcgacaaatggcac tgg [gRNA]	50.00 %	72.27 °C	-		1 [detail]	2 [detail]	499 [detail]
162 - 184	+	gtgcgacaaatggcactggaa tgg [gRNA]	55.00 %	74.69 °C	-		1 [detail]	6 [detail]	677 [detail]

Showing 1 to 20 of 71 entries

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Graphical View:

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:

- [CCNcccattcaccctcaactcgcaa \(1\)](#)
- [tcgcqaaqaaqaaqaaacgggNGG \(4\)](#)
- **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
CCAAACGAGGCCAGGTGAGCTCTCCCCCTCC**CC**CCC**G**ATT**C**GC**C**TC**G**CG**A**CC**G**AG**T**T**C**ACT**T**GAG**G**CT**GG**GT**T**GC**A**CT**G**

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGC**T**CG**C**GAG**C**GAG**G**CGA**A**C**GG****G****A****G****G**TGC**A**CT**G**CT**GG**GT**GG**AC**GG**AC**GA**AGA

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGC**T**CG**C**GAG**C**GAG**G**CGA**A**C**GG****G****A****G****G**TGC**A**CT**G**CT**GG**GT**GG**AC**GG**AC**GA**AGA

chr05:21504153-21504175 ▼21504153
TCGGCGGCCGGCGGTGTAAAGTAACCGCGAGC**T**CG**C**GAG**C**GAG**G**CGA**A**C**GG****G****A****G****G**TGC**A**CT**G**CT**GG**GT**GG**AC**GG**AC**GA**AGA

chr05:21504153-21504175 ▼21504153
T**CG**GGCGGCCGGCGGTGTAAAGTAACCGCGAGC**T**CG**C**GAG**C**GAG**G**CGA**A**C**GG****G****A****G****G**TGC**A**CT**G**CT**GG**GT**GG**AC**GG**AC**GA**AGA

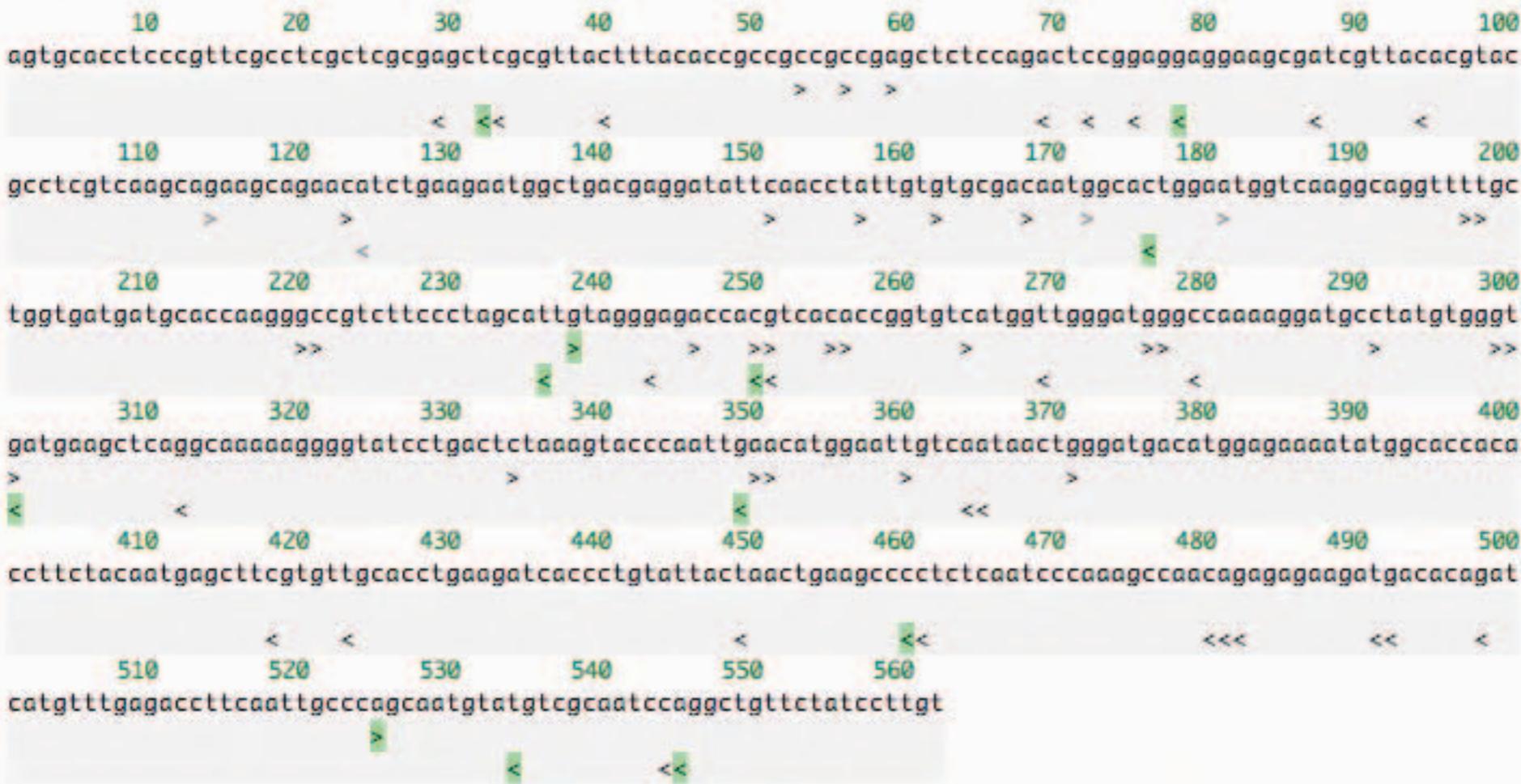
CRISPRdirect によるガイド RNA 設計

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

Showing 1 to 20 of 71 entries

First Previous 1 2 3 4 Next Last

Graphical View:



Data Export:

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

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

CRISPRdirect によるガイド RNA 設計

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

Data Export:

- Tab-delimited text: [Open in new window](#) | [Download](#)
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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	-	cctcccggttcgcctcgctcgcgaa	75	83.48	0	NruI	1	5	370				
8	10	32	-	cccggttcgcctcgctcgcgagct	70	81.73	0	NruI	1	1	276				
9	11	33	-	ccggttcgcctcgctcgcgagctc	70	81.09	0	NruI,SacI	1	4	911				
10	18	40	-	cctcgctcgcgagctcgcgttac	70	80.24	0	NruI,SacI	1	4	1072				
11	47	69	-	ccggccggccggagctctccaga	75	84.25	0	SacI	1	305	79033				
12	50	72	-	ccggccggccgagctctccagactc	70	80.41	0	SacI	1	37	3555				
13	53	75	+	ccggccgagctctccagactccgg	70	80.41	0	SacI	1	3	175				
14	53	75	-	ccggccgagctctccagactccgg	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	-	ccagactccggaggaggaaagcga	65	78.93	0	BspEI	1	6	375				
19	72	94	-	ccggaggaggaagcgatcgttac	55	73	0	BsiEI,PvuI	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	+	caatggcactggaaatggcaagg	50	72.31	0		5	8	545				
28	172	194	+	ggcactggaaatggcaaggcagg	60	77.26	0		0	2	447				
29	181	203	+	atggtcaaggcagggtttgtgg	50	73.64	1		0	1	1511				
30	197	219	+	ttgctggtgatgtatgcaccaagg	50	73.43	0		1	4	553				
31	198	220	+	tgctggtgatgtatgcaccaagg	50	73.43	0		1	9	616				
32	214	236	-	ccaaggggccgtttcccttagcat	60	80.62	0		1	1	121				
33	220	242	+	gccgtttcccttagcattgtagg	55	76.01	0		1	2	796				
34	221	243	+	ccgtttcccttagcattgtagg	50	72.87	0		1	3	538				
35	221	243	-	ccgtttcccttagcattgtagg	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	ASM34733v1 (Dec, 2013)
AMTR1.0	EnsemblPlants	Plant	A. trichopoda	アムボレラ・トリコポダ	Amborella trichopoda	AMTR1.0 (Jan, 2014)
Araly_v.1.0	EnsemblPlants	Plant	Lyre-leaved rock-cress	シロイヌナズナ属	Arabidopsis lyrata	v.1.0 (Dec, 2008)
TAIR10_en	EnsemblPlants	Plant	Thale cress	シロイヌナズナ	Arabidopsis thaliana	TAIR10 (Sep, 2010)
Bradi_v1.0	EnsemblPlants	Plant	Purple false brome	セイヨウヤマカモジ, ミナトカモジグサ	Brachypodium distachyon	v1.0 (Jan, 2009)
Braol_v2.1	EnsemblPlants	Plant	Wild cabbage	ヤセイカンラン, ワイルドキャベツ	Brassica oleracea	v2.1
IVFCAASv1	EnsemblPlants	Plant	Chinese cabbage	ハクサイ, サントウサイ	Brassica rapa ssp. pekinensis	IVFCAASv1 (Aug, 2009)
Chlre_v3.1	EnsemblPlants	Plant	Green algae	クラミドモナス	Chlamydomonas reinhardtii	v3.1 (Nov, 2007)
ASM9120v1	EnsemblPlants	Plant	Red alga	シアニディオシゾン	Cyanidioschyzon merolae	ASM9120v1 (Nov, 2008)
Soybn_V1.0	EnsemblPlants	Plant	Soybean	ダイズ	Glycine max	V1.0 (Jan, 2010)



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