

○内藤雄樹 ライフサイエンス統合データベースセンター (DBCLS)

【要 旨】

高速塩基配列検索ソフトウェア GGGenome (<https://GGGenome.dbcls.jp/>) および CRISPR-Cas9 によるゲノム編集のためのガイド RNA 設計ソフトウェア CRISPRdirect (<https://crispr.dbcls.jp/>) のアップデートを紹介する。GGGenome (ゲゲゲノム) は、ゲノムや転写産物などの塩基配列を高速に検索することができるツールである。十数塩基程度の短い配列の検索にも対応しており、ミスマッチや挿入・欠失を含む配列でも検索漏れがないため、核酸医薬品や CRISPR-Cas9 のガイド RNA の特異性を確認するためにも役立つ。CRISPRdirect は、GGGenome による配列検索を利用することにより、特異性の高いガイド RNA を簡便に設計できるツールである。従来の SpCas9 に加えて、PAM の異なる Cas9 のバリエーションにも対応している。GGGenome および CRISPRdirect は、多数の実験動植物や作物などのゲノムに対応しており、他のデータベースやソフトウェアとも容易に連携できるよう API を提供している。全ての機能は商用・非商用を問わず無償で自由に利用できる。



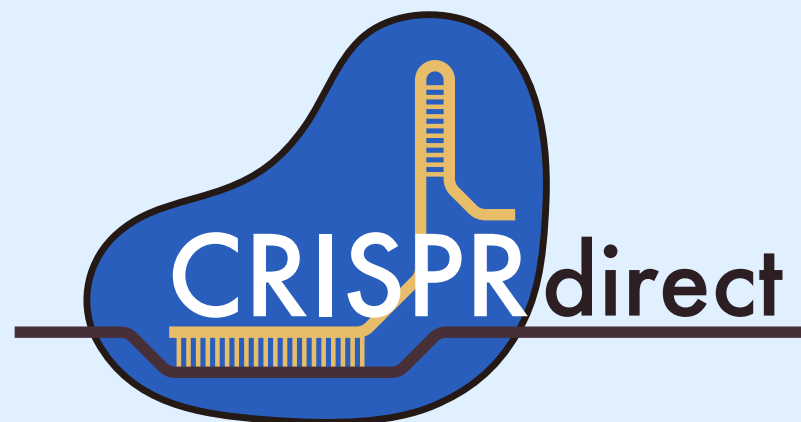
高速塩基配列検索

GGGenome

塩基配列をさがす

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

- 塩基配列を高速に検索
350種の生物種に対応
- ミスマッチや挿入欠失を含む短い配列の検索に強い



CRISPRガイドRNA設計

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

- CRISPRガイドRNA設計
PAMに隣接する20塩基の選択
- オフターゲット検索
powered by  **GGGenome**

ゲゲゲ GGGenome による塩基配列検索



高速塩基配列検索
GGGenome

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

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

データベース:

Human genome, GRCh38/hg38 (Dec, 2013)



- ☒ ミスマッチ/ギャップを許容 ☐ ミスマッチのみ許容 : 塩基まで (検索する配列長の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: <https://GGRNA.dbcls.jp/hs/nanog>

検索結果へのリンク:

- [http\[s\]://GGGenome.dbcls.jp/db/k/\[strand\]/\[nogap\]/sequence\[.format\]\[.download\]](http[s]://GGGenome.dbcls.jp/db/k/[strand]/[nogap]/sequence[.format][.download])
 - **db** → hg19, mm10, dm3, ce10, TAIR10, pombe, refseq, etc. 省略時は hg19
 - **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
 - **nogap** → ギャップを許容せず **k** 塩基以内のミスマッチのみ許容して検索する
 - **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: <https://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: <https://GGGenome.dbcls.jp/mm10/2/+/-/nogap/TTCATTGACAACATTGCGT.txt>



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ゲゲゲ GGGenome による塩基配列検索



高速塩基配列検索
GGGenome

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TTCACTGACAACATTGAGTA

検索

データベース:

Human genome, GRCh38/hg38 (Dec, 2013)

- ☒ ミスマッチ/ギャップを許容 ☐ ミスマッチのみ許容 : 塩基まで (検索する配列長の25%まで)
☒ 双方向を検索 ☐ +方向のみ検索 ☐ -方向のみ検索

2021-09-10 18:03:56, GGGenome : Human genome, GRCh38/hg38 (Dec, 2013)

Summary:

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

Results:

検索語に色がつきました (ミスマッチ・挿入欠失)。

[chr2:30675447-30675466](#)

▼30675447

GCCCCAGCCACTTATATGTATTTTTTAAATTCACCTGACAACATTGAGTAGAAAAGATAATTTTTTTTTTTTGGAGACAG

« ‹ | ページ 1 / 1 | › » | ↺

1 件中 1 - 1 を表示

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ーできます。
- CSV形式 → [表示](#) | [ダウンロード](#)



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ゲゲゲ GGGenome による塩基配列検索



高速塩基配列検索
GGGenome

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TTCAGTGAACATT

検索

データベース:

Human genome, GRCh38/hg38 (Dec, 2013)

- ☒ ミスマッチ/ギャップを許容 ☐ ミスマッチのみ許容 : 塩基まで (検索する配列長の25%まで)
☒ 双方向を検索 ☐ +方向のみ検索 ☐ -方向のみ検索

2021-09-10 18:04:09, GGGenome : Human genome, GRCh38/hg38 (Dec, 2013)

Summary:

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

Results:

検索語に色がつきます (ミスマッチ、挿入欠失)。

[chr1:173431690-173431704](#) ▼173431690
TTTTCACATGCACTACCTTGCTGCTGCTTTCAGTGAACATTTCAGGTCTCGCAAGGCATGGAATACAATG

[chr1:197494486-197494500](#) ▼197494486
AATGATCTTTACTGTAACTGCACTTTAATTCAGTGAACATTACTTAAAGAAAGAGATTATGATTGGATAAA

[chr2:30675447-30675461](#) ▼30675447
GCCCCAGCCACTTATATGTATTTTTTAAATTCAGTGAACATTGAGTAGAAAAGATAATTTTTTTTTTTTTTTGA

[chr2:162678576-162678590](#) ▼162678576
TGAGAAAGAGGACACCTAAGAATTATGGCTTCAGTGAACATTAGAGAACATATCAAACGAAATATTC

[chr3:117416977-117416991](#) ▼117416977
TCCCCTAGCAAATCAATTCACTTCTGTTATTCAGTGAACATTGTTTTTCTACTGGCTGCAGCTTTTCACAA



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ゲゲゲ GGGenome による塩基配列検索



高速塩基配列検索
GGGenome

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TTCAGTGACA

検索

データベース:

Human genome, GRCh38/hg38 (Dec, 2013)

- ☒ ミスマッチ/ギャップを許容 ☐ ミスマッチのみ許容 : 塩基まで (検索する配列長の25%まで)
☒ 双方向を検索 ☐ +方向のみ検索 ☐ -方向のみ検索

2021-09-10 18:04:23, GGGenome : Human genome, GRCh38/hg38 (Dec, 2013)

Summary:

- [TTCAGTGACA \(5186\)](#)
- [TGTCAGTGAA \(5240\)](#)
- **TOTAL (10426)**

Results:

検索語に色がつきます (ミスマッチ、挿入欠失)。

[chr1:450262-450271](#) ▼450262
ATACTAGAATTTTAAAGCAAATGTCTTTATTCAGTGACAACATAATCATCTATAAAGAAAATCCTACAT

[chr1:685238-685247](#) ▼685238
ATACTAGAATTTTAAAGCAAATGTCTTTATTCAGTGACAACATAATCATCTATAAAGAAAATCCTACAT

[chr1:792983-792992](#) ▼792983
CCCTCAGCCACACAGCTGACGCTGTAGAGATTCAGTGACATCCAGTCTGATGGACACTGTTTCTCCAGCC

[chr1:1400883-1400892](#) ▼1400883
CCGACGGGCTCTGCCACATCCCTGTCTTCCATTCAGTGACATGAAACGCAGAAAAGGCAGCTTTGCCACAA

[chr1:3358002-3358011](#) ▼3358002
AGAGGCCCACTCGTGAGCCTTGCTGTGCCATTCAGTGACATGCTCGCCCATGAGCTGAGTCTGCCTTGAC



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ゲゲゲ GGGenome による塩基配列検索



高速塩基配列検索
GGGenome

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TTCACTGACAACATTGAGTA

検索

データベース:

Human genome, GRCh38/hg38 (Dec, 2013)

- ☒ ミスマッチ/ギャップを許容 ☐ ミスマッチのみ許容 : 塩基まで (検索する配列長の25%まで)
☒ 双方向を検索 ☐ +方向のみ検索 ☐ -方向のみ検索

2021-09-10 18:04:39, GGGenome : Human genome, GRCh38/hg38 (Dec, 2013)

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)。

[chr1:77465268-77465286](#) ▼77465268
AGCAGTACTCAAGATCACCTTTTTTTTAAAGTTCACTG-CAACATTAGTATGATGAAAAATGTGTAGCTGTAATTCATTGA

[chr1:106404891-106404910](#) ▼106404891
TAGAAAACATACCACATAAAGAAGCAATCTTCACTGCACAA-ATTGAGTATATAATTTAACCCGTTTGAAAGGGTCATTA

[chr2:30675447-30675466](#) ▼30675447
GCCCCAGCCACTTATATGTATTTTTTAAATTCCTGACAACATTGAGTAGAAAAGATAATTTTTTTTTTTTGGAGACAG

[chr2:140759530-140759548](#) ▼140759530
TTTATTTTCTTTAACACAGCCTTTGATAAATTCCTGAC-ACATTGAGTTAGCCATAGTGTGTAATGGGAGACTGCCAG

[chr2:162678576-162678596](#) ▼162678576
TGAGAAAGAGGACACCCTAAGAATTATGGCTTCACTGACAACATTAGAGAAATATCAAACTCAAACGAATATTCTGGGGT



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ゲゲゲ GGGenome による塩基配列検索

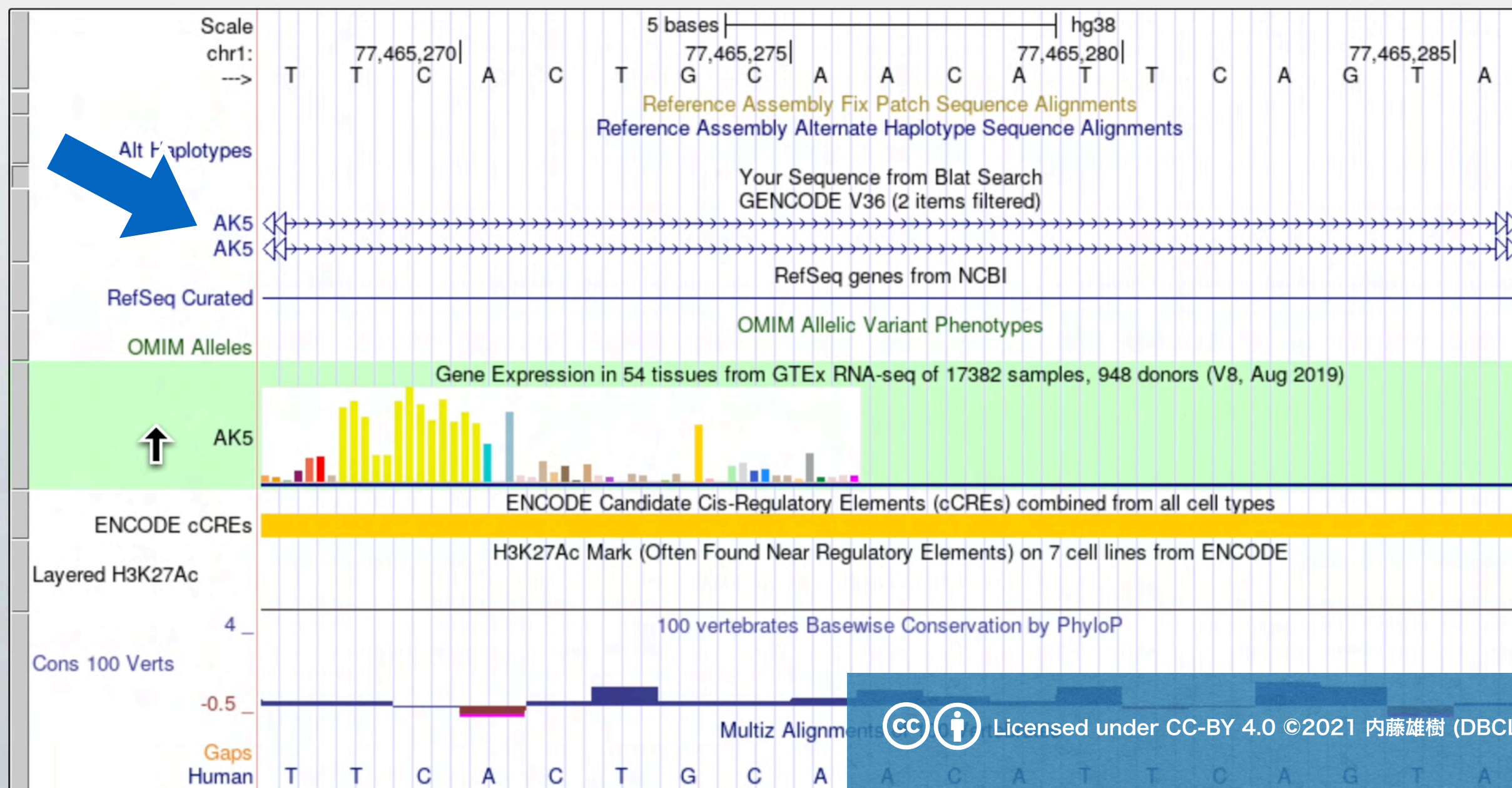
[Genomes](#)[Genome Browser](#)[Tools](#)[Mirrors](#)[Downloads](#)[My Data](#)[View](#)[Help](#)[About Us](#)

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly

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

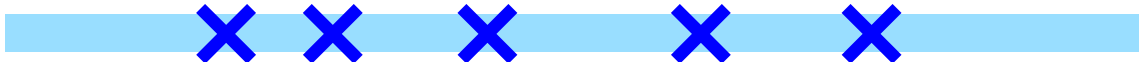
multi-region chr1:77,465,268-77,465,286 19 bp. enter position, gene symbol, HGVS or search terms go

chr1 (p31.1) 1p31.1 1q12 q41 43 44

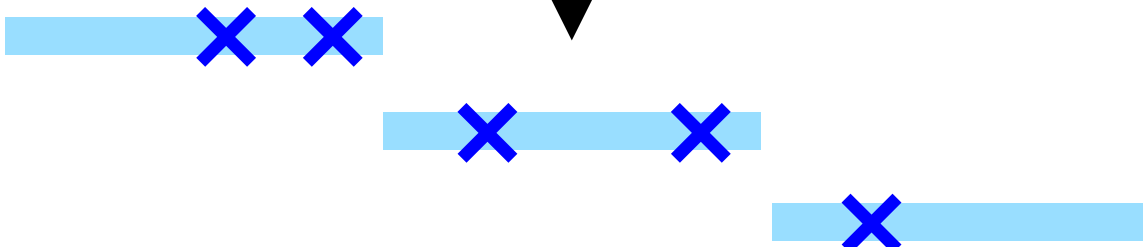


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● 分割統治法

 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

- 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\[s\]://GGenome.dbcls.jp/hg38/2/ATAGGACCATA.txt](http[s]://GGenome.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。

ゲゲゲ GGGenome を他のツールから呼び出す

← → ↺ ⓘ gggenome.dbcls.jp/2/TTCACTGACAACATTGAGTA.txt

```
# [ GGGenome | 2018-07-08 04:33:37 ]
# database: Human genome, GRCh37/hg19 (Feb, 2009)
# query: TTCACTGACAACATTGAGTA
# count: 36
# query: TACTCAATGTTGTCAGTGAA
# count: 33
```

'txt'

#	name	strand	start	end	snippet	snippet_pos	snippe	align	edit	match	mis	del	ins
chr1	+	77930953	77930971										
					TCTACCTTTTTTTAAAGTTCACTGCAACATTGAGTAGATGAAAAATGTGTAGCTGTAATTCATTGAAGGC								
					AGTCTGTTCTTGAGTTACCATGGCAACTGCTCAATTAAGTGAAAAAAATGAAAAATA	77930855	77931071			TTCACTGACAACATTGAGTA	TTCACTG-CAACATTGAGTA		
chr1	+	106947513	106947532										
					TCATCTGGTCTATATGTCCCATGTTTCATAAAGTTGATAACATCAAAACACGGAAAGTATAGGAAATAACATAGAAAACATACCACATAAAGAAGCAATCTTTCACTGCACAAATTGAGTATAAAATTTAACCCGTTTGAAAGGGTCATTATAT								
					ATGAGGAGCAGAAAGACAAGTGGAGTATAAAGAAAATGGGCTTTAAAGTCAAACCTTGCT	106947413	106947632			TTCACTG-ACAACATTGAGTA	TTCACTGCACAA-ATTGAGTA		
chr2	+	30898315	30898352										
					TTGATCTCCTGACCTCGTGATCCACCTGCCTCGCCCTCCCAAAGTGGTGGGATTACAGGCGTGAGCCACCGCCCCAGCCACTTATATGTATTTTTTAAATTCAGTACAAACATTGAGTAGAAAAAGATAATTTTTTTTTTTTGGAGACAGAGT								
					TGTTGCCAGGGGACTGCAGTGGCACAATCTTGCTCACTGCAACCTCCACCTCCCGTG	30898213	30898432			TTCACTGACAACATTGAGTA	TTCACTGACAACATTGAGTA		
						20	0	0	0				

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

```
chr2 + 141517099 14
AATTTTCAGTAAATTAATAATAATAAAGGAA
CTGATTTGTTTCATTGTTCTTGAGCACCATTGCA
|||||||
chr2 + 163535086 16
CTCATGGTGAATCCACACATATTGGACAGAAGGG
TGTGGATTTTGCTTTAGAGTCCATGAGAGTAAGA
|||I
chr2 + 186291305 18
CCCATCATCACAATATCATTATCTCATCTTCCA
TTTTTTTGAGCAGGCTCTATAATAACAAAACCTGA
|||||||I
chr2 + 206339508 20
ATGAATCAAAGGCTTGAAACATATTGCCAACAAT
GAAAAATAGTACTGTATCATTTTACATTGAACCTT
|||||||I
chr2 + 235498941 23
CTTGAAGGGGCCAGGTGGGCAGACAGATAGTTCA
GGACCTATTATAGAGCCTGGGCTCATGTTAGGTAATGCAGGGAAGGGGTCAAAGAACCGG
|||||
chr3 + 7763221 7763239
CAGAGATGTGCATGGATAGCTTTGGTTGTAGTCTTTTGACAGCATCAGCTTGGTAGTTCTCCAGTCTTCACTTGATCAGTGCAC
TTCTAGCACTAATCAGTAGATATCCAATTTATTAACCAAAATGAATAAAATATATAAA
=====I-X=====
chr3 + 107912698 107912716
```



ゲゲゲ GGenome を他のツールから呼び出す

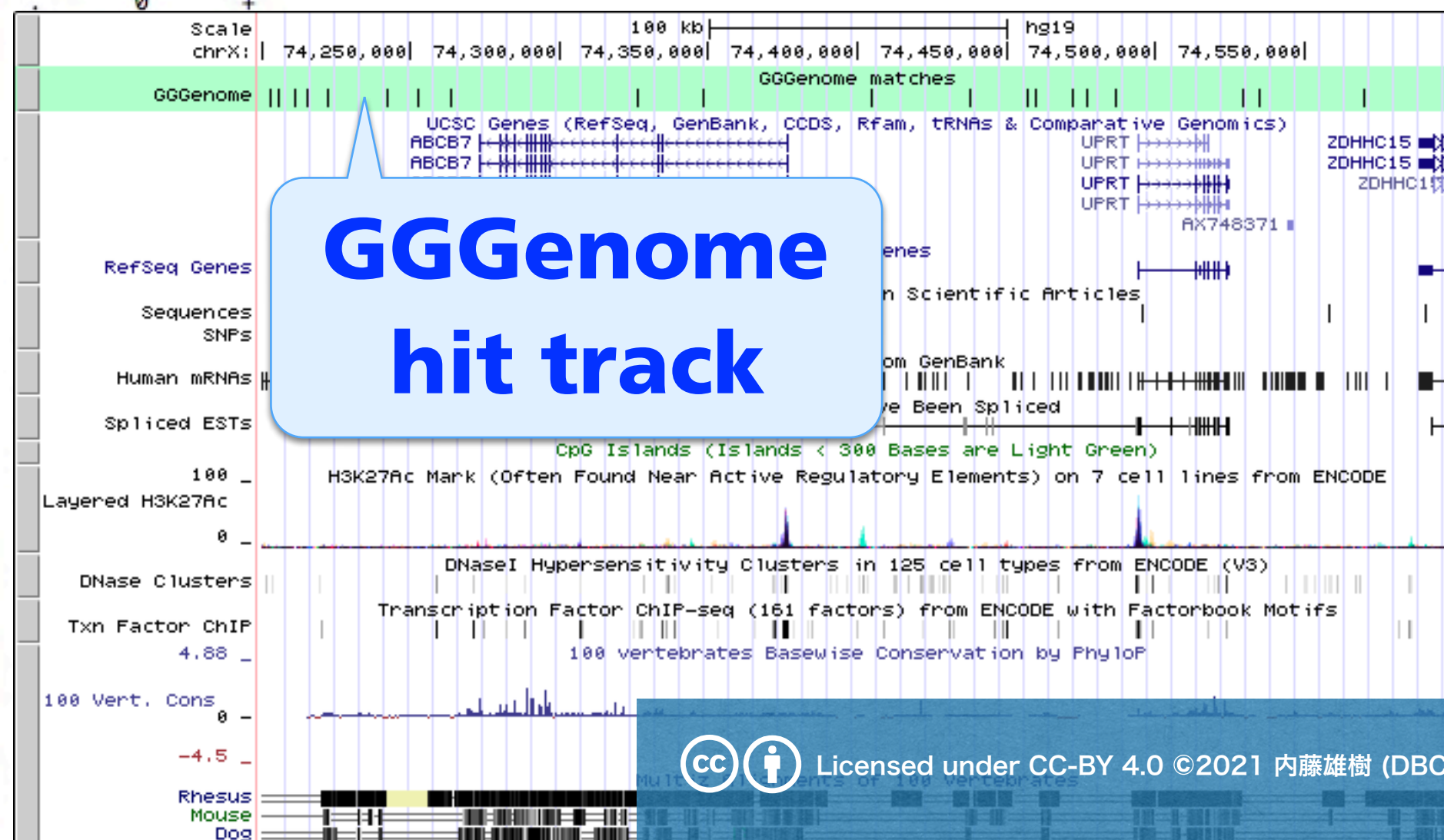
← → ↺ ⓘ gggenome.dbcls.jp/2/TTCACTGACAACATTGAGTA.bed

track name=GGenome description="GGenome 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'

GGenome
hit track



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ゲ ゲ ゲ 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'



19:46:08 meso@mesobook:% curl -s 'https://GGGenome.dbcls.jp/hg38/GTCGTATGCTAG.bed'

**curl コマンド:
webから情報を取得**

ターミナルから塩基配列検索


```
19:46:08 meso@mesobook:% curl -s 'https://GGGenome.dbcls.jp/hg38/GTCGTATGCTAG.bed'
```

```
track name=GGGenome description="GGGenome matches"
```

chr1	194830236	194830248	.	0	+
chr2	78670750	78670762	.	0	+
chr2	218571531	218571543	.	0	+
chr12	55980766	55980778	.	0	+
chr12	116320454	116320466	.	0	+
chr15	91363640	91363652	.	0	+
chrX	151249981	151249993	.	0	+
chrX	151250002	151250014	.	0	+
chr1	158411570	158411582	.	0	-
chr2	14459609	14459621	.	0	-
chr4	27155130	27155142	.	0	-
chr7	145345362	145345374	.	0	-
chr8	4213930	4213942	.	0	-
chr8	91253328	91253340	.	0	-
chr8	128369312	128369324	.	0	-
chr10	10395010	10395022	.	0	-
chr10	127341893	127341905	.	0	-
chr15	52581403	52581415	.	0	-

**wc コマンド:
行数をカウント**

```
19:46:25 meso@mesobook:% curl -s 'https://GGGenome.dbcls.jp/hg38/GTCGTATGCTAG.bed' | wc -l
```

```
19
```

```
19:46:31 meso@mesobook:% curl -s 'https://GGGenome.dbcls.jp/hg38/GTCGTATGCTAG.bed' | grep chr8
```

chr8	4213930	4213942	.	0	-
chr8	91253328	91253340	.	0	-
chr8	128369312	128369324	.	0	-

```
19:46:36 meso@mesobook:%
```

**grep コマンド:
キーワード抽出**



表計算ソフトから GGenome 検索

GGenome 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

¥ % 123 Arial 10 B I A

f_x | =ImportData(D2)

	A	B	C	D	E	F	G	H	I
1		Primer name	(1) Sequence	(2) GGenome URL	(3) ImportData function	name	strand	start	end
2		YN001-F	caatcacccctcacccctcttatatgc	http://GGenome.dbcls.jp/rice/caatcacccctcacccctcttatatgc.txt	=ImportData(D2)	chr01	+	27707	27
3		YN001-R	ccgctgtgaac		chr01 - 28071 28092 ATATTGTTTGGTACGAGTA				
4		YN002-F	tgatccaata		27971 28192	chr01	-	28071	28
5		YN002-R	catgcaaggta						
6		YN003-F	acgtactgtgg						
7		YN003-R	accacaccta						
8		YN004-F	atcagattccgccgcccgcg						
9		YN004-R	ggagagatctggttggggag						

= ImportData(D2)

PCRプライマー配列

数式が入っている



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表計算ソフトから GGenome 検索

GGGenome primer search ☆

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コメント

共有

fx | =concatenate("http://GGGenome.dbcls.jp/rice/",C4,".txt")

	E	F	G	H	I	J	M	N	O	P	Q
1	(3) ImpotDATA function	name	strand	start	end		(4) PCR product length				
2	chr01 + 27707 27731 CCCATCCAGGTCATCGTAG 27607 27831	chr01	+	27707	27731		385				
3	chr01 - 28071 28092 ATATTGTTTGGTACGAGTA 27971 28192	chr01	-	28071	28092						
4	chr03 + 9682634 9682653 TTTCCAAAGATGATAACCT 9682534 9682753	chr03	+	9682634	9682653		129				
5	chr03 - 9682744 9682763 AGTTGTTTATTTTGGACTC 9682644 9682863	chr03	-	9682744	9682763						
6	chr06 + 7494240 7494259 TAATTGTTGTAGGCATGAG 7494140 7494359	chr06	+	7494240	7494259		246				
7	chr06 - 7494467 7494486 GAAACATAGGACCGGATG 7494367 7494586	chr06	-	7494467	7494486						
8	chr01 + 27691273 27691292 CACCGGAACGAGACGACA 27691173 27691392	chr01	+	27691273	27691292		580				
9	chr01 - 27691834 27691853 GCCTCCCCCAGGCGTCGAC 27691734 27691953	chr01	-	27691834	27691853						
10											
11											
12											
13											
14											

配列を検索、
座標を表示、
PCR産物の
長さを計算



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- **ゲノムを高速に検索可能**

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

ゲノム、転写産物 (RefSeq, GENCODE)、pre-mRNA (理研D3G)

- **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

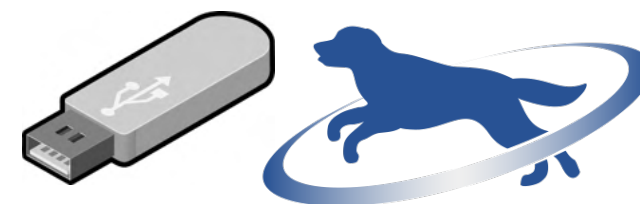
R、Ruby、Galaxy、ゲノムブラウザ・・・

- **ウェブ版は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。

- **Docker版をレトリバ社から販売開始 →**





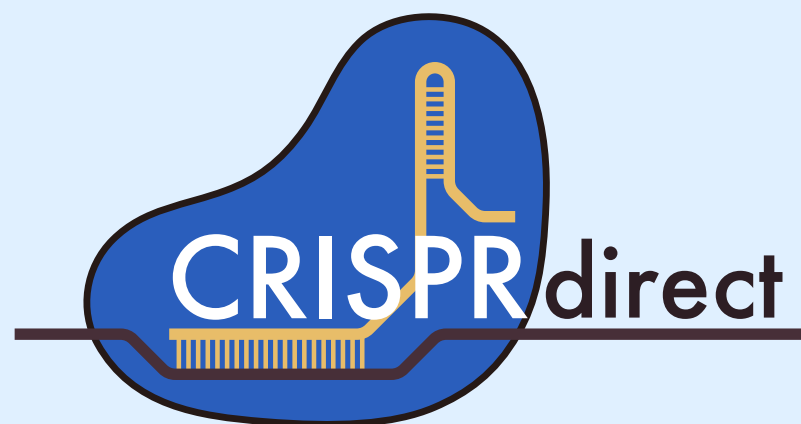
高速塩基配列検索

GGGenome

塩基配列をさがす

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

- 塩基配列を高速に検索
350種の生物種に対応
- ミスマッチや挿入欠失を含む短い配列の検索に強い



CRISPRガイドRNA設計

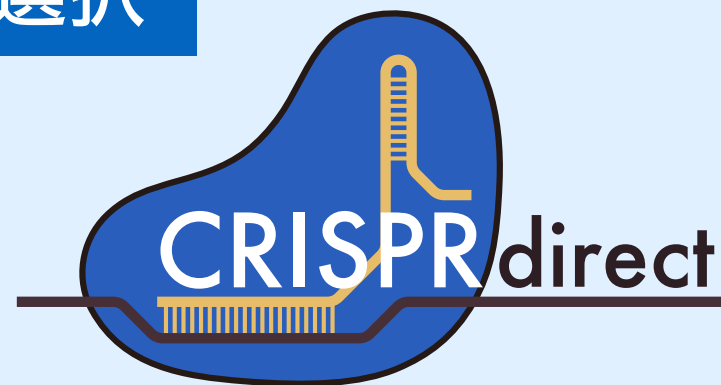
<https://crispr.dbcls.jp/>

- CRISPRガイドRNA設計
PAMに隣接する20塩基の選択
- オフターゲット検索
powered by  **GGGenome**

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

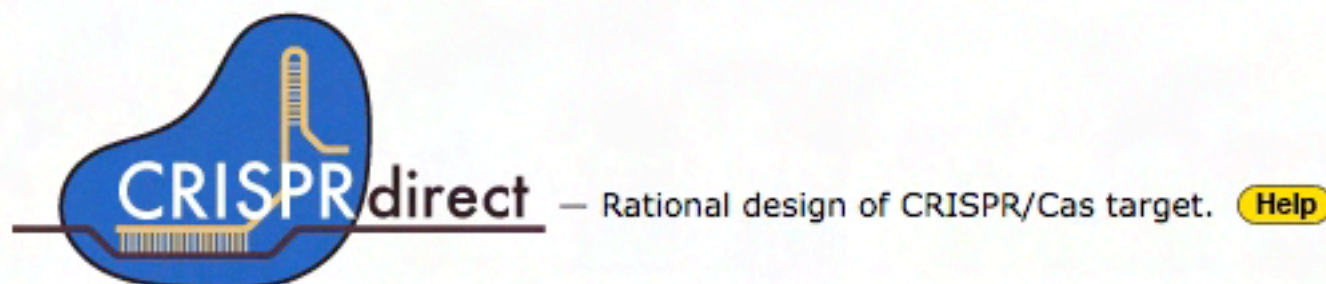
高速で正確な塩基配列検索ツール

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



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

Enter an accession number (e.g. NM_006299) or genome location (e.g. hg19:chr7:100000000-100000000)

Accession番号

or Paste a nucleotide sequence: ?

```
agtgcacctcccgttcgctcgctcgagctcggttactttacaccgcccgcgagctctccagactccggaggaggagcg  
atcgttacacgtacgctcgtaagcagaagcagaacatctgaagaatggctgacgaggatattcaacctattgtgtgcgacaatg  
gcactggaatggtaaggcagggttttgctggtgatgatgcaccaagggccgtcttccttagcatgttagggagaccacgtcacacc  
ggtgtcatggttggtggtggccaaaaggatgctatgtgggtgatgaagctcaggcaaaaaggggtatcctgactctaaagtacc  
aattgaacatggaattgtcaataactgggatgacatggagaaaatatggcaccacaccttctacaatgagcttcgtgttgacctg  
aagatcacctgtattactaactgaagccctctcaatcccaagccaacagagagaagatgacacagatgatgttgagaccttc  
aattgccagcaatgtatgtcgcaatccaggctgttctatccttgt
```

**または
塩基配列** を入力

or upload sequence file: ? 選択されていません

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

Specificity check: ?

Whats' new:

- 2017-06-19 Added 8 species - [List](#)



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CRISPRdirect によるガイド RNA 設計

or Paste a nucleotide sequence: ?

```
agtgcacctcccgttcgcctcgctcgcgagctcgcgttactttacaccgccgcccgcgagctctccagactccggaggaggaagcg  
atcgttacacgtacgcctcgtaagcagaagcagaacatctgaagaatggctgacgaggatattcaacctattgtgtgcgacaatg  
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 (*Cricetus 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)

数文字ほど入力すると
生物種を検索 できる



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 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccgttcgctcgctcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgagctcggttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccgcccgcgagctctccaga [gRNA]	75.00 %	84.25 °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	-	ccgcccgcgagctctccagactccg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 78	+	ccgagctctccagactccgagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	-	ccgagctctccagactccgagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	+	agctctccagactccgaggagg [gRNA]	65.00 %	79.68 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	-	ccagactccgaggaggagcga [gRNA]	65.00 %	78.93 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccggaggaggagcgcgttac [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:



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CRISPRdirect によるガイド RNA 設計

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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]
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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

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CRISPRdirect によるガイド RNA 設計

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18 - 40	-	cctcgctcgcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]		
47 - 69	-	ccgccgcccagactctccaga [gRNA]	75.00 %	84.25 °C	-	SacI			
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53 - 75	+	ccgcccagactctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]		
53 - 75	-	ccgcccagactctccagactccgg [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]		
56 - 78	+	ccgagctctccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
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114 - 136	+	gaagcagaacatctgaagaa [gRNA]	40.00 %	65.99 °C	-		0 [detail]	7 [detail]	1117 [detail]
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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

配列に関する情報
制限酵素サイト も

Graphical View:



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CRISPRdirect によるガイド RNA 設計

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59 - 81	-	cctcccgttcgctcgctcgca [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	-	cctcccgttcgctcgctcgca [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	-	ccgaggaggaagcgatcggtac [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]

ゲノムに何箇所あるか？

20mer

PAM

NNNNNNNNNNNNNNNNNNNNNNNN NGG

Showing 1 to 20 of 71 entries

First

Previous

1

2

3

4

Next

Last

Graphical View:



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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

緑：おすすめ

オフターゲット
サイトが少ない

緑：おすすめ

		sequence information			sites ?				
			GC% of 20mer	Tm of 20mer	TTTT in 20mer	sites	+PAM	+PAM	8mer +PAM
7 - 23	-	cct cccgttcgcctcgctcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cccgttcgcctcgctcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccgttcgcctcgctcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccg ccgccgagctctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccg ccgccgagctctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgccgagctctccagactc 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 gaggaggaagcgatcgttac [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]

サイトが少ない

オフターゲット
サイトが多い

Showing 1 to 20 of 71 entries

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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		
start - end	+ -	20mer+PAM (total 23mer)	GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	2mer +PAM	
7 - 29	-	cctcccgttcgctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]		
10 - 32	-	cccggttcgctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]		
11 - 33	-	ccgttcgctcgctcgcgagctc [gRNA]	70.00 %	81.09 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccgccgcccagactctccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccgcccagactctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccagactctccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 75	-	ccgcccagactctccagactc [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	-	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	+	catctgaagaatggctgacgagg [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

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オフターゲット
サイトのリスト

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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 \(1\)](#)
- [tcgcgagcgagcgacgagcggNGG \(4\)](#)
- **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
CCAACGAGGCCAGGTGAGCTCTCCCCCTCCCGGATTCGCCTCGCTTCGCGACCGAGTCACTTGAGCTGGGTGCACTGAC

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

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

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

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



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Showing 1 to 20 of 71 entries

Graphical View:

Data Export:

- 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
catgtttgagaccttcaattgcccagcaatgtatgtcgcaatccaggctgttctatccttgt
> < << <<< << <

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 + ccgcccgcgagctctccagactccga 70.00 80.41 0 SacI 1 3  
175  
53 75 - ccgcccgcgagctctccagactccga 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
```



CRISPRdirect によるガイド RNA 設計

	A	B	C	D	E	F	G	H	I	J	K	L	M
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	-	cctccggttcgca	75	83.48		0 Nrul	1	5	370		
8	10	32	-	cccggttcgctcg	70	81.73		0 Nrul	1	1	276		
9	11	33	-	ccggttcgctcg	70	81.09		0 Nrul,Sacl	1	4	911		
10	18	40	-	cctcgctcgcgag	70	80.24		0 Nrul,Sacl	1	4	1072		
11	47	69	-	ccgcccgcgcgcg	75	84.25		0 SacI	1	305	79033		
12	50	72	-	ccgcccgcgcgag	70	80.41		0 SacI	1	37	3555		
13	53	75	+	ccgcccgcgcctc	70	80.41		0 SacI	1	3	175		
14	53	75	-	ccgcccgcgcctc	70	80.27		0 SacI	1	15	2679		
15	56	78	+	ccgagctctccag	70	80.27		0 BspEI,SacI	1	4	793		
16	56	78	-	ccgagctctccag	65	79.68		0 BspEI,SacI	1	1	1295		
17	59	81	+	agctctccagact	65	79.68		0 BspEI	1	2	608		
18	65	87	-	ccagactccgga	65	78.93		0 BspEI	1	6	375		
19	72	94	-	ccggaggaggaa	55	73		0 BsiEI,PvuI	1	14	3180		
20	102	124	-	cctcgtcaagcag	50	71.33		0	0	3	588		
21	114	136	+	gaagcagaacat	40	65.99		0	0	7	1117		
22	123	145	+	catctgaagaatg	50	69.8		0	1	2	1388		
23	151	173	+	caacctattgtgt	45	69.15		0	1	3	303		
24	154	176	-	cctattgtgtgcg	50	72.27		0	1	1	667		
25	157	179	+	attgtgtgcgaca	50	72.27		0	1	2	499		
26	162	184	+	gtgcgacaatgg	55	74.69		0	1	6	677		
27	168	190	+	caatggcactgg	50	72.31		0	5	8	545		
28	172	194	+	ggcactggaatg	60	77.26		0	0	2	447		
29	181	203	+	atggtcaaggca	50	73.64		1	0	1	1511		
30	197	219	+	ttgctggtgatga	50	73.43		0	1	4	553		
31	198	220	+	tgctggtgatgat	50	73.43		0	1	9	616		
32	214	236	-	ccaagggccgctc	60	80.62		0	1	1	121		
33	220	242	+	gccgtcttccta	55	76.01		0	1	2	296		
34	221	243	+	ccgtcttccttag	50	72.87		0	1	3	538		
35	221	243	-	ccgtcttccttag	50	73.65		0	1	6	1777		



<https://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>Cyanobacteria</i>	



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