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DBCLS
Database Center
for Life Science

GGGenome & CRISPRdirect

塩基配列検索およびゲノム編集のための ウェブツール

2019年10月5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



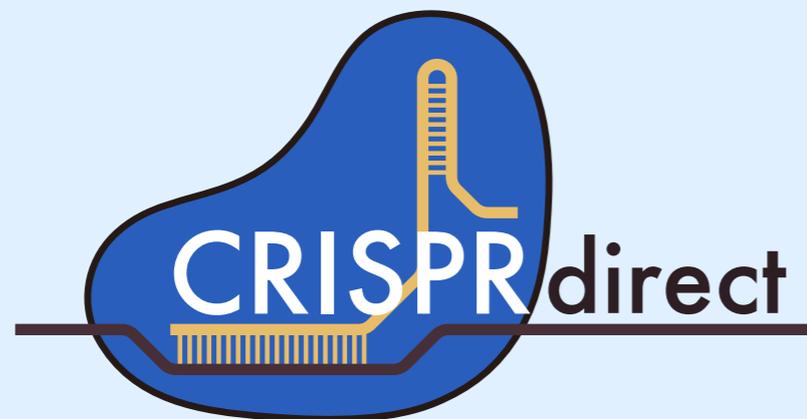
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GGGenome

塩基配列をさがす

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

- ゲノムを高速に検索可能
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

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

超絶高速ゲノム配列検索

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

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

GGGenome

TTCACTGACAACATTGAGTA

検索

Human genome, GRCh37/hg19 (Feb, 2009)

許容するミスマッチ/ギャップの数: (検索する塩基配列の長さの25%まで)

双方向を検索 +方向のみ検索 -方向のみ検索

2017-06-28 06:20:32, 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

GCCCCAGCCACTTATATGTATTTTTTAAATTCAC**TGACAACATTGAGTA**GAAAAGATAATTTTTTTTTTTTTTTGAGACAG

◀◀ ◀ | 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 [Help](#) | [English](#)

GGGenome

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:

- [TTCAGTACAACATT \(10\)](#)
- [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](#)
TTTTACATGCACTACCTTGCTGTCC**TTCAGTACAACATT**TCAGGGTCTCGCAAGGCATGGAATACAATG

[chr1:197463616-197463630](#) ▼[197463616](#)
AATGATCTTACTGTTAACTGCACTTTA**TTCAGTACAACATT**ACTTAAAGAAAGAGATTATGATTGGATAAA

[chr2:30898313-30898327](#) ▼[30898313](#)
GCCCCAGCCACTTATATGTATTTTTTAA**TTCAGTACAACATT**GAGTAGAAAAGATAATTTTTTTTTTTTGA

[chr2:163535086-163535100](#) ▼[163535086](#)
TGAGAAAGAGGACACCCTAAGAATTATGGC**TTCAGTACAACATT**AGAGAACATATCAAACCTCAAACGAATATTC

[chr3:117135824-117135838](#) ▼[117135824](#)
TCCCCTAGCAAATCAATTCACTTCTGTTA**TTCAGTACAACATT**GTTTTTCTACTGGCTGCAGCTTTTCACAA

[chr4:138011007-138011021](#)

ゲゲゲ GGGenome による塩基配列検索

超絶高速ゲノム配列検索 [Help](#) | [English](#)

GGGenome

TTCACTGACA

検索

Human genome, GRCh37/hg19 (Feb, 2009)

許容するミスマッチ/ギャップの数: (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](#)
ATACTAGAATTTTAAAAGCAAATGCTTTA **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

[chr1:6720005-6720004](#)

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: (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](#)

AGCAGTACTCAAGATCACCTTTTTTAAAGTTCACTG-CAACATTGAGTAGATGAAAAATGTGTAGCTGTAATTCATTGA

[chr1:106947513-106947532](#)

▼ [106947513](#)

TAGAAAACATACCACATAAAGAAGCAATCTTCACTGCACAA-ATTGAGTATAAATTTAACCCTTTGAAAGGGTCATTA

[chr2:30898313-30898332](#)

▼ [30898313](#)

GCCCCAGCCACTTATATGTATTTTTTAAATTCCTGACAACATTGAGTAGAAAAGATAATTTTTTTTTTTTTGAGACAG

[chr2:141517099-141517116](#)

▼ [141517099](#)

TTATTTTCTTTAACACAGCCTTTGATAAATTCCTGAC-ACATTGAGT-TAGCCATAGTGTGTAATGGGAGACTGCCCA

[chr2:163535086-163535103](#)

▼ [163535086](#)

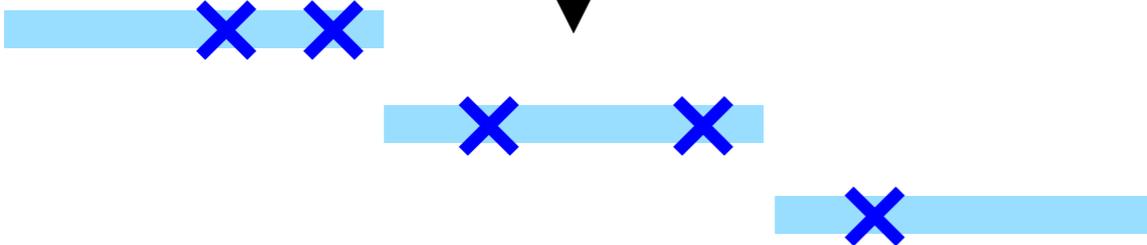
TGAGAAAGAGGACACCCTAAGAATTATGGCTTCCTGACAACATT-AG-A GAACATATCAAACCTCAAACGAATATTCTGG

[chr2:186201205-186201224](#)

● **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]://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。

ゲゲゲ GGGenome を他のツールとつないで使う

← → ↻ ⓘ 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
# name strand start end snippet snippet_pos snippet align edit match mis del ins
chr1 + 77930953 77930971
TCATGAAATGGAAGTGCTGCCACTTCAGGGTCTGTAAAGAGATAATGCTGATGCCAGGCCA
TACCTTTTTTTAAAGTTCACTGCAACATTGAGTAGATGAAAAATGTGTAGCTGTAATTCATTGAAGGC
AGTCTGTTCTTGAGTTACCATGGCAACTGCTCAATTAAGTGAAAAAAATGAAAAATA
77930855 77931071 TTCACTGACAACATTGAGTA TTCACTG-CAACATTGAGTA | | | | | |
| | | | | | I | | | | | X | | | | | 18 1 0 1
chr1 + 106947513 106947532
TCATCTGGTCTATATGTCCCATGTTTCATAAAGTTGATAACATCAAAACACGGAAAGTATAGGAAATAACATAGAAAACATACCACATAAAGAAGCAATCTTTCACTGCACAAATTGAGTATAAAATTTAACCCGTTTGAAAGGGTCATTATAT
ATGAGGAGCAGAAAGACAAGTGGAGTATAAAGAAAATGGGCTTTAAAGTCAAACCTTGCCCT
106947413 106947632 TTCACTG-ACAACATTGAGTA TTCACTGCACAA-ATTGAGTA | | | | | |
| | | | | | | | | | | | D | | | | | I | | | | | 19 0 1 1
chr2 + 30898315 30898352
TTGATCTCCTGACCTCGTGATCCACCTGCCTCGCCCTCCCAAAGTGGTGGGATTACAGGCGTGAGCCACCGCCCCAGCCACTTATATGTATTTTTTAAATTCAGTACAAACATTGAGTAGAAAAGATAATTTTTTTTTTTTGGAGACAGAGT
TGTTGCCAGGGGACTGCAGTGGCACAATCTTGCTCACTGCAACCTCCACCTCCCGTG
30898213 30898432 TTCACTGACAACATTGAGTA TTCACTGACAACATTGAGTA
| | | | | | | | | | | | | | | | | | | | | | 20 0 0 0
chr2 + 141517099 141517118
AATTTTCAGTAAAATTAATAATAAATAAAGGAA
GTATC
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | I | | | | | 14
chr2 + 163535086 163535105
CTCATGGTGAAGTCCACACATATTGGACAGAAGGG
GGTCT
TGTGGATTTTGTCTTAGAGTCCATGAGAGTAAGA
| | | | | | | | | | | | D | | | | | X | | | | | 19
chr2 + 186291305 186291324
CCCATCATCACAATATCATTATCTCATCTTCCA
TATCT
TTTTTTTGAGCAGGCTCTATAATAACAAAATGAA
| | | | | | | | | | | | D | | | | | 18
chr2 + 206339508 206339527
ATGAATCAAAGGCTTGAAACATATTGCCAACAAT
AATTT
GAAAAATAGTACTGTATCATTTTACATTGAACTT
| | | | | | | | | | | | I | | | | | X | | | | | 18
chr2 + 235498941 235498960
CTTGAAGGGGCCAGGTGGGCAGACAGATAGTTCA
GAGGC
GGACCTATTATAGAGCCTGGGCTCATGTTAGGTAATGCAGGGAAGGGGTCAAAGAACCGG
235498841 235499060 TTCACTGACAACATTG-AGTA TTCACTGAC-ACATTGAGTA | | | | | |
| | | | | | I | | | | | D | | | | | 19 0 1 1
chr3 + 7763221 7763239
CAGAGATGTGCATGGATAGCTTTGGTTGTAGTCTTTTGACAGCATCAGCTTGGTAGTTCTCCAGTCTTCACTTGATCAGTGCAGACATAGATCAATTCCTCACTGCAAAATTGAGTAGTGAATAAATAAACTTACTTCAGCTAACCTAACT
TTCTAGCACTAATCAGTAGATATCCAATTTATTAACCAAATGAATAAAATATATAAA
7763121 7763339 TTCACTGACAACATTGAGTA TTCACTG-CAAAATTGAGTA | | | | | | | | | | | |
| | | | | | I | | | | | X | | | | | 18 1 0 1
chr3 + 107912698 107912716
```

'txt'

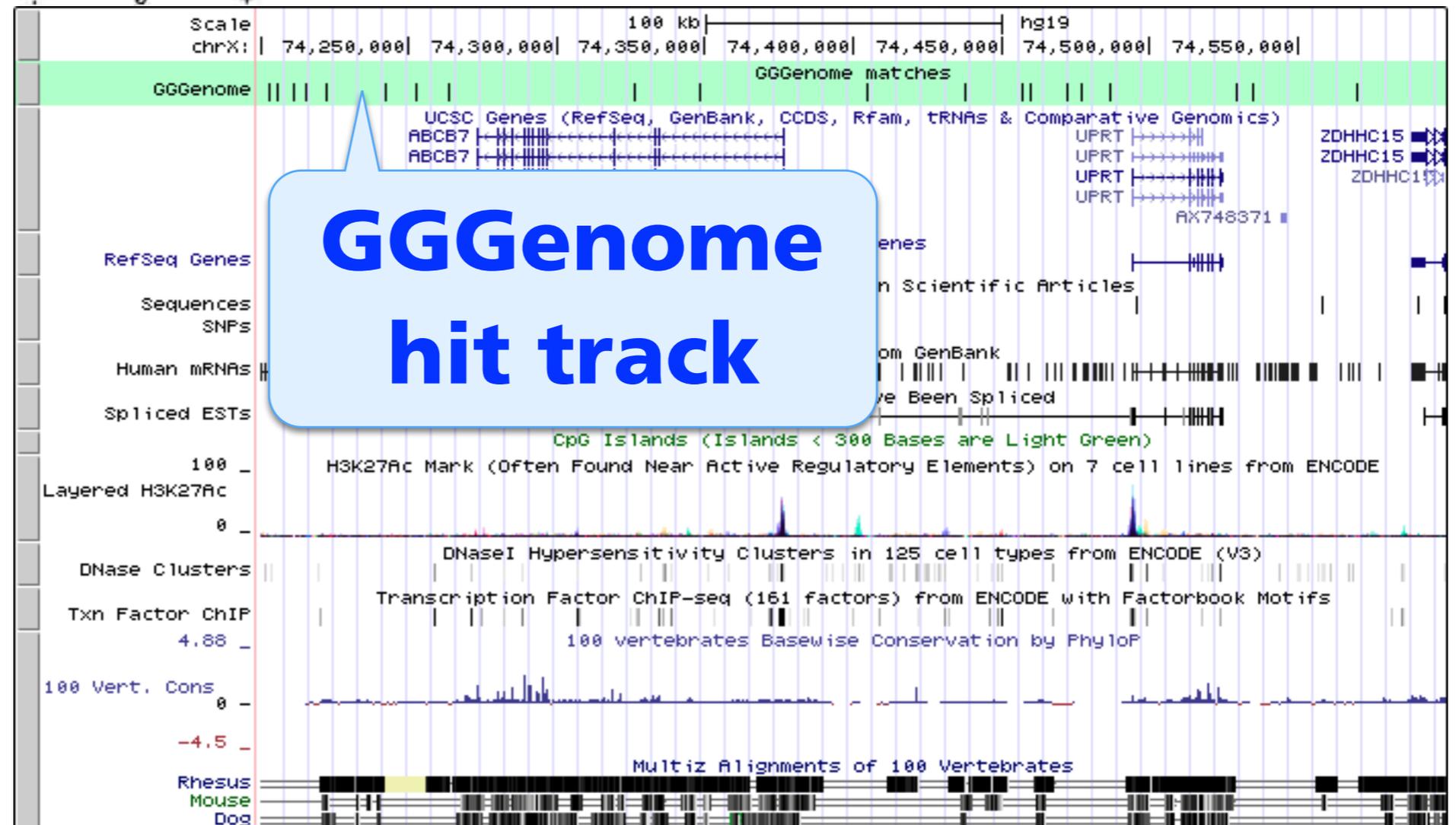
TTCA-ACAG	"query"	7	"match"
	"align"	1	"mis"
TTCACACGG	"sbjct"	1	"del"
====D==X=	"edit"	0	"ins"

ゲゲゲ GGGenome を他のツールとつないで使う

← → ↻ ⓘ gggenome.dbcls.jp/2/TTCACTGACAACATTGAGTA.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

ゲゲゲ GGGenome を他のツールとつないで使う

← → ↻ ⓘ 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'

TogoGenome を塩基配列から検索



Safari ファイル 編集 表示 履歴 ブックマーク ウィンドウ ヘルプ

togogenome.org

TOGO GENOME

Faceted search | Comparative genome | **Sequence search** | Text search | Hide

TGGAATTGTGAGCGGATAACAATT

Search Clear

Search genomic sequences by an arbitrary sub-string of any DNA sequence fragments (e.g., "TGGAATTGTGAGCGGATAACAATT" for *lac* operator reported by Gilbert W and Maxam A, 1973)

TogoGenome を塩基配列から検索



Sequence		Organism		Related Genes			Position begin	Position end
Sequence name	Locus tag	Product	Sequence ontology	Previous	Over Lap	Next		
Caenorhabditis briggsae chromosome IV, complete sequence.			• STS	• CBG01747		• CBG01748	10,301,046	10,301,069
Caenorhabditis briggsae chromosome V, complete sequence.			• STS	• CBG03537		• CBG12892	14,947,373	14,947,396
Caenorhabditis briggsae chromosome III, complete sequence.				• CBG22951		• CBG22952	12,649,919	12,649,942
Brassica napus cultivar ZS11 chromosome A1, Brassica napus v2.0		• uncharacterized protein LOC106437402	• protein_coding • gene • CDS • transcript	• LOC106425375	• LOC106437402	• LOC106437431	13,601,088	13,601,111

検索した配列を持つゲノムがリストになり、
マッチした領域の前後の遺伝子が表示されます。

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
chr2 218571531
chr12 55980766
chr12 116320454
chr15 91363640
chrX 151249981
chrX 151250002
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 -
```

**curl コマンド:
webから情報を取得**

**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 ^{ゲゲゲ}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) 100% 123 Arial 10 B I A

=ImportData(D2)

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

= ImportData(D2)

PCRプライマー配列

● **ゲノムを高速に検索可能**

<http://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少ない検索

● **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

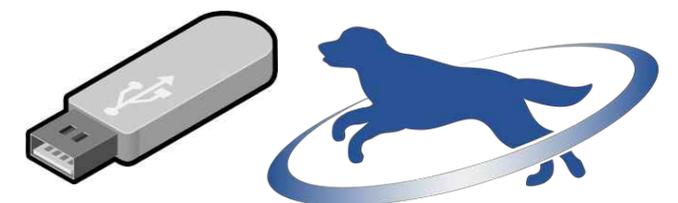
R、Ruby、Galaxy、ゲノムブラウザ・・・

● **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予定 →**

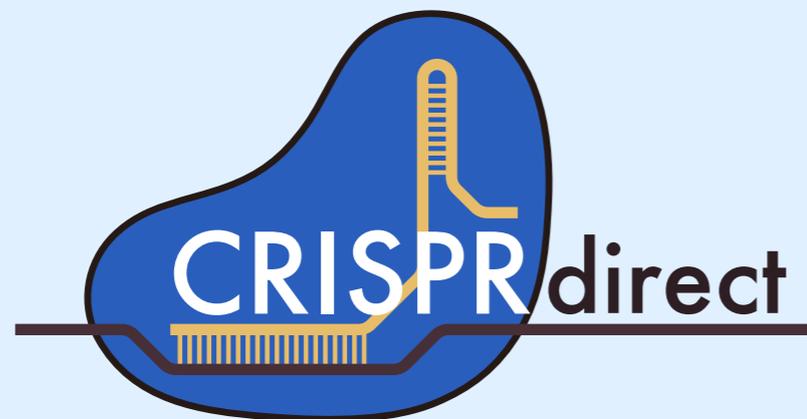


GGGenome

塩基配列をさがす

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

- **ゲノムを高速に検索可能**
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

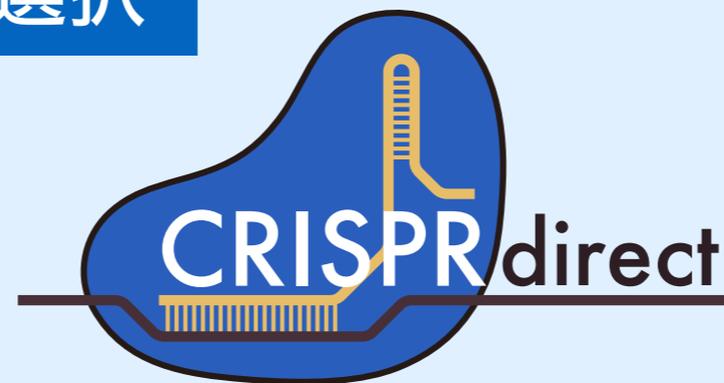
<https://crispr.dbcls.jp/>

- **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

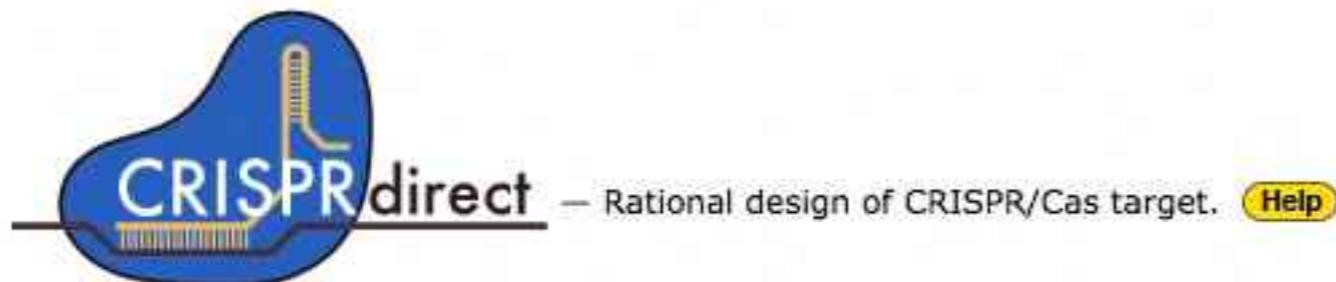
高速で正確な塩基配列検索ツール

```
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



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

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

Accession番号

or Paste a nucleotide sequence: ?

```
agtgcacctcccgttcgctcgctcgcgagctcgcgttactttacaccgcccgcgagctctccagactccggaggaggagcg  
atcgttacacgtacgcctcgtcaagcagaagcagaacatctgaagaatggctgacgaggatattcaacctattgtgtgcgacaatg  
gcactggaatggtaaggcaggttttgctggtgatgatgcaccaagggccgtcttccttagcattgtagggagaccacgtcacacc  
ggtgtcatggttgggatgggccaagaggatgcctatgtggatgatgaagctcaggcaaaaaggggtatcctgactctaaagtacc  
aattgaacatggaattgtcaataactgggatgacatggagaaaatattggcaccacaccttctacaatgagcttcgtgttgacctg  
aagatcacctgtattactaactgaagccctctcaatcccaagccaacagagagaagatgacacagatdatggttgagacctt  
aattgccagcaatgatgtcgcaatccaggctgttctatcctgt
```

**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

CRISPRdirect によるガイド RNA 設計

retrieve sequence

or Paste a nucleotide sequence: ?

```
agtgacactcccgttcgctcgcgagctcgcgttactttacaccgccgccgagctctccagactccggaggaggaagcg
atcgttacacgtacgcctcgtcaagcagaagcagaacatctgaagaatggctgacgaggatattcaacctattgtgtgcgacaatg
gcactggaatggtaaggcaggttttgctggtgatgatgcaccaagggccgtcttccttagcattgtagggagaccacgtcacacc
ggtgtcatggttgggatgggcccagaaggatgcctatgtgggtgatgaagctcaggcaaaaaggggtatcctgactctaagtacc
aattgaacatggaattgtcaataactgggatgacatggagaaaatattggcaccacaccttctacaatgagcttcgtgttgacctg
aagatcacctgtattactaactgaagcccccttcaatcccaagccaacagagagaagatgacacagatcatgittgagacctt
aattgccagcaatgtatgtcgcaatccaggctgttctatccttgt
```

or upload

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

Specificity check: rice

design

Whats' new:

- 2017-06-19
- 2017-06-09
- 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
- 2016-09-09 Australian wild rice (*Oryza meridionalis*) genome, *Oryza_meridionalis_v1.3* (Oct, 2014)
- 2016-08-30 Indian wild rice (*Oryza nivara*) genome, AWH000000000 (Aug, 2013)
- 2016-06-14 Red rice (*Oryza punctata*) genome, AVCL000000000 (Aug, 2013)
- 2015-10-09 Brownbeard rice (*Oryza rufipogon*) genome, PRJEB4137 (Aug, 2013)
- 2015-01-13
- 2014-11-21 Rice (*Oryza sativa ssp. indica*) genome, ASM465v1 (Jan, 2005)

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)

数文字ほど入力すると
生物種を検索 できる

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

- 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 cccgttcgcctcgctcgcgga [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 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]	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 gaggaggaagcgatcgttac [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 start - end	+	target sequence 20mer+PAM (total 23mer)	sequence information				number of target sites ?		
			GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	12mer +PAM	8mer +PAM
7 - 29	-	cctcccgttcgctcgctcgcgga [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cccggttcgctcgctcgcgagct [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccggttcgctcgctcgcgagctc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	4 [detail]	911 [detail]
18 - 40	-	cctcgctcgcgagctcgcgttac [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 69	-	ccgccgcccagactcaccaga [gRNA]	75.00 %	80.41 °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	-	ccggaggaggagcgaatcggtac [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]

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 start - end	+	target sequence 20mer+PAM (total 23mer)	sequence information				number of target sites ?		
			GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	12mer +PAM	8mer +PAM
7 - 29	-	cctcccgttcgctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10 - 32	-	cccggttcgctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccggttcgctcgctcgcgagctc [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]		
47 - 69	-	ccgccgcccagactcaccaga [gRNA]	75.00 %	84.25 °C	-	SacI			
50 - 72	-	ccgcccagactcaccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]		
53 - 75	+	ccgcccagactcaccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]		
53 - 75	-	ccgcccagactcaccagactc [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]		
56 - 78	+	ccgagctcaccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	-	ccgagctcaccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	+	agctcaccagactccggaggagg [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	-	ccggaggaggagcgaatcggtac [gRNA]	55.00 %	73.00 °C	-	BspEI 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]

配列に関する情報
制限酵素サイトも

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

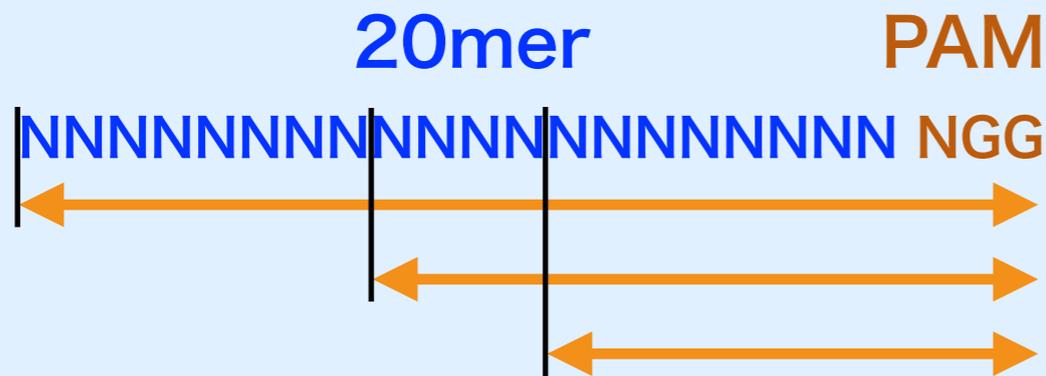
- Target sequences with TTTTs are also shown in gray. Avoid TTTTs in gRNA vectors with pol III promoter.

show highly specific target only

Show 20 entries

position start - end	target sequence 20mer+PAM (total 23mer)	sequence information				number of target sites ?		
		GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	12mer +PAM	8mer +PAM
7 - 29	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 - 31	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	NruI SacI	1 [detail]	4 [detail]	911 [detail]
18 - 41	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47 - 61	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 71	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 71	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 71	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 71	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 71	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	2 [detail]	608 [detail]
65 - 87	cctcccgttcgcctcgctcgcca [gRNA]	75.00 %	83.48 °C	-	BspEI	1 [detail]	6 [detail]	375 [detail]
72 - 94	ccggaggaggaagcgatcgttac [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？



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

show highly specific target only

緑：おすすめ

オフターゲット
サイトが少ない

Start	End	gRNA	sequence information			sites			
			GC% of 20mer	Tm of 20mer	TTTT in 20mer	sites	+PAM	+PAM	8mer +PAM
7	29	cctcccgttcgctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	5 [detail]	370 [detail]
10	32	cccgttcgctcgctcgcgagct [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]
18	40	cctcgctcgcgagctcgcgttac [gRNA]	70.00 %	80.24 °C	-	NruI SacI	1 [detail]	4 [detail]	1072 [detail]
47	69	ccgccgcccagactcaccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50	72	ccgcccagactcaccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53	75	ccgcccagactcaccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53	75	ccgcccagactcaccagactc [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	[detail]	2679 [detail]
56	78	ccgagctcaccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI			
56	78	ccgagctcaccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI			
59	81	agctcaccagactccggaggagg [gRNA]	65.00 %	79.68 °C	-	BspEI			
65	87	ccagactccggaggaggagcga [gRNA]	65.00 %	78.93 °C	-	BspEI			
72	94	ccggaggaggagcgaatcggtac [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

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 start - end	+	target sequence 20mer+PAM (total 23mer)	sequence information				number of target sites ?		
			GC% of 20mer	Tm of 20mer	TTTT in 20mer	restriction sites	20mer +PAM	2mer +PAM	8mer +PAM
7 - 29	-	cctcccgttcgctcgctcgcgca [gRNA]	75.00 %	83.48 °C	-	NruI	1 [detail]	[detail]	370 [detail]
10 - 32	-	cccggttcgctcgctcgcgagct [gRNA]	70.00 %	81.73 °C	-	NruI	1 [detail]	1 [detail]	276 [detail]
11 - 33	-	ccggttcgctcgctcgcgagctc [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	-	ccgccgcccagactcaccaga [gRNA]	75.00 %	84.25 °C	-	SacI	1 [detail]	305 [detail]	79033 [detail]
50 - 72	-	ccgcccagactcaccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	37 [detail]	3555 [detail]
53 - 75	+	ccgcccagactcaccagactc [gRNA]	70.00 %	80.41 °C	-	SacI	1 [detail]	3 [detail]	175 [detail]
53 - 75	-	ccgcccagactcaccagactc [gRNA]	70.00 %	80.27 °C	-	SacI	1 [detail]	15 [detail]	2679 [detail]
56 - 78	+	ccgagctcaccagactccggagg [gRNA]	70.00 %	80.27 °C	-	BspEI SacI	1 [detail]	4 [detail]	793 [detail]
56 - 78	-	ccgagctcaccagactccggagg [gRNA]	65.00 %	79.68 °C	-	BspEI SacI	1 [detail]	1 [detail]	1295 [detail]
59 - 81	+	agctcaccagactccggaggagg [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	-	ccggaggaggagcgaatcggtac [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

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:

- [CCNcccattcgcctcactcgcga \(1\)](#)
- [tcgcgagcggcgggtgtaaagtaacgcgagc \(4\)](#)
- **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
CCAACGAGGCCAGGTGAGCTCTCCCCCTCCCGGATTCGCCTCGCTTCGCGACCGAGTTCAGTTCGAGCTGGGTTGCACTGAC

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

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

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

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

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 - cctcccgttcgctcagctcgcga 75.00 83.48 0 NruI 1 5
370
10 32 - cccgttcgctcagctcgcgagct 70.00 81.73 0 NruI 1 1
276
11 33 - ccattcgcctcagctcgcgagctc 70.00 81.09 0 NruI,SacI 1
4 911
18 40 - cctcgtcgcgagctcagcttac 70.00 80.24 0 NruI,SacI 1
4 1072
47 69 - ccgcccgcgagctctccaga 75.00 84.25 0 SacI 1 305
79033
50 72 - ccgcccgcgagctctccagactc 70.00 80.41 0 SacI 1 37
3555
53 75 + ccaccgagctctccagactccga 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 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	-	cctcccgttcgctcgctcgcca	75	83.48	0	Nrul	1	5	370				
8	10	32	-	cccgttcgctcgctcgcgagct	70	81.73	0	Nrul	1	1	276				
9	11	33	-	ccgttcgctcgctcgcgagctc	70	81.09	0	Nrul,Sacl	1	4	911				
10	18	40	-	cctcgctcgcgagctcgcgttac	70	80.24	0	Nrul,Sacl	1	4	1072				
11	47	69	-	ccgccgccgagctctccaga	75	84.25	0	Sacl	1	305	79033				
12	50	72	-	ccgccgccgagctctccagactc	70	80.41	0	Sacl	1	37	3555				
13	53	75	+	ccgccgagctctccagactccgg	70	80.41	0	Sacl	1	3	175				
14	53	75	-	ccgccgagctctccagactccgg	70	80.27	0	Sacl	1	15	2679				
15	56	78	+	ccgagctctccagactccggagg	70	80.27	0	BspEI,Sacl	1	4	793				
16	56	78	-	ccgagctctccagactccggagg	65	79.68	0	BspEI,Sacl	1	1	1295				
17	59	81	+	agctctccagactccggaggagg	65	79.68	0	BspEI	1	2	608				
18	65	87	-	ccagactccggaggaggaagcga	65	78.93	0	BspEI	1	6	375				
19	72	94	-	ccggaggaggaagcgatcgttac	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	+	caacctattgtgtgacgaatgg	45	69.15	0		1	3	303				
24	154	176	-	cctattgtgtgacgaatggcac	50	72.27	0		1	1	667				
25	157	179	+	attgtgtgacgaatggcactgg	50	72.27	0		1	2	499				
26	162	184	+	gtgacgaatggcactggaatgg	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	+	atggtcaaggcaggtttgctgg	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	-	ccaagggccgtcttccctagcat	60	80.62	0		1	1	121				
33	220	242	+	gccgtctccctagcattgtagg	55	76.01	0		1	2	796				
34	221	243	+	ccgtctccctagcattgtaggg	50	72.87	0		1	3	538				
35	221	243	-	ccgtctccctagcattgtaggg	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>Arabis 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

ご清聴ありがとうございました

