

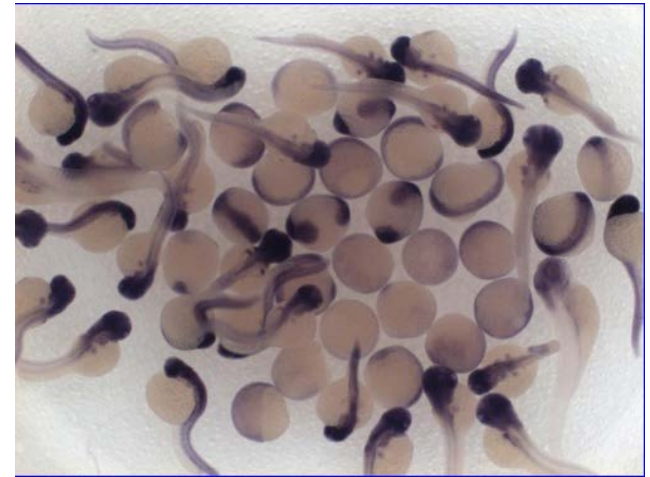
利用反向遗传学方法研究斑马鱼基因*gps1*

Analysis the Function of *gps1* in Zebrafish via Reverse Genetics

小组：**G10**

小组成员：陆小婵 王一琰 陈城 李齐恒

ZFIN 了解 *gps1* 具体信息



Gene Symbol: *gps1*

Previous Names: im:6909260, im:7145572, zgc:154082

Location: Chr: 3 [Details](#)

[Nomenclature History](#)

GENE EXPRESSION [i](#)

Directly Submitted Expression Data: 1 figure (1 image) from [Thisse *et al.*, 2004 \[IMAGE:6909260\]](#)

1 figure (1 image) from [Thisse *et al.*, 2004 \[IMAGE:7145572\]](#)

Wild-type Stages, Structures:

[Zygote:1-cell \(0.0h-0.75h\) to Hatching:Pec-fin \(60.0h-72.0h\)](#)

[unspecified](#)

Ontology [i](#)

GO Term

Biological Process

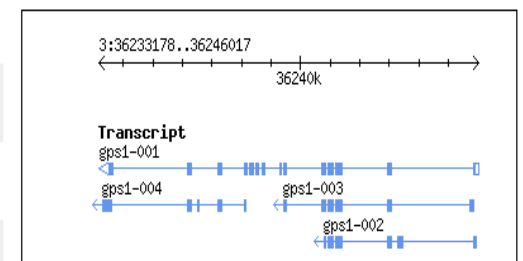
[cullin deneddylation](#) [\(more\)](#)

Cellular Component

[COP9 signalosome](#) [\(more\)](#)

TRANSCRIPTS

| Type i | Name | Length (bp) | Analysis i |
|------------------------|------------------------------|-------------|-----------------------------|
| mRNA | gps1-001 (1) | 1940 | Select Tool |
| ncRNA | gps1-002 (1) | 720 | Select Tool |
| | gps1-003 (1) | 785 | Select Tool |
| | gps1-004 (1) | 666 | Select Tool |





Uniprot初步了解研究现状




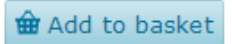

A0AUR9 - A0AUR9_DANRE

Protein Submitted name: **G protein pathway suppressor 1**

Gene **gps1**

Organism *Danio rerio (Zebrafish) (Brachydanio rerio)*

Status  Unreviewed -  - Experimental evidence at transcript level¹

 BLAST  Align  Format  Add to basket  History

Display

None

- FUNCTION
- NAMES & TAXONOMY
- SUBCELLULAR LOCATION
- PATHOLOGY & BIOTECH
- PTM / PROCESSING
- EXPRESSION
- INTERACTION
- STRUCTURE
- FAMILY & DOMAINS
- SEQUENCE
- CROSS-REFERENCES
- PUBLICATIONS
- ENTRY INFORMATION
- MISCELLANEOUS

Family and domain databases

| | |
|-----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| Gene3D ⁱ | 1.10.10.10. 1 hit. 1.25.40.10. 2 hits. |
| InterPro ⁱ | IPR019585. 26S_proteasome_reg_su-Rpn7. IPR000717. PCI_dom. IPR011990. TPR-like_helical_dom. IPR011991. WHTH_DNA-bd_dom. [Graphical view] |
| Pfam ⁱ | PF01399. PCI. 1 hit. PF10603. RPN7. 1 hit [Graphical view] |
| SMART ⁱ | SM00088. PINT. 1 hit. [Graphical view] |

Relative Literature



NIH Public Access
Author Manuscript

Circ Heart Fail. Author manuscript; available in PMC 2014 September 01.

Published in final edited form as:

Circ Heart Fail. 2013 September 1; 6(5): . doi:10.1161/CIRCHEARTFAILURE.113.000338.

The COP9 Signalosome Is Required for Autophagy, Proteasome-Mediated Proteolysis, and Cardiomyocyte Survival in Adult Mice

NIH-PA Author

OPEN ACCESS Freely available online



Hepatic Deficiency of COP9 Signalosome Subunit 8 Induces Ubiquitin-Proteasome System Impairment and Bim-Mediated Apoptosis in Murine Livers

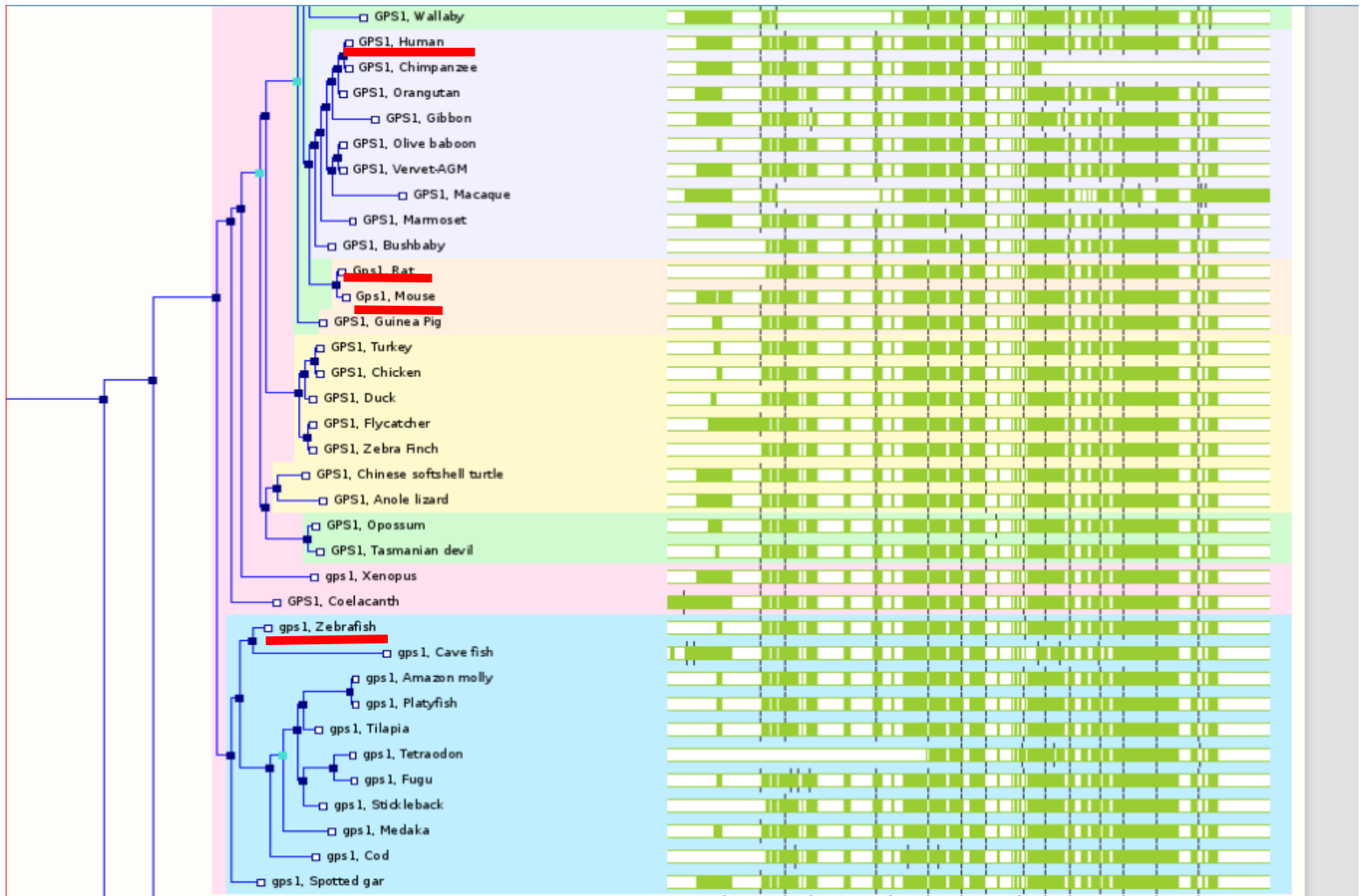
Daoxiong Lei^{1,2}, Faqian Li³, Huabo Su^{1,4}, Jinbao Liu^{1,5}, Ning Wei⁶, Xuejun Wang^{1*}



Dynamic Regulation of the COP9 Signalosome in Response to DNA Damage

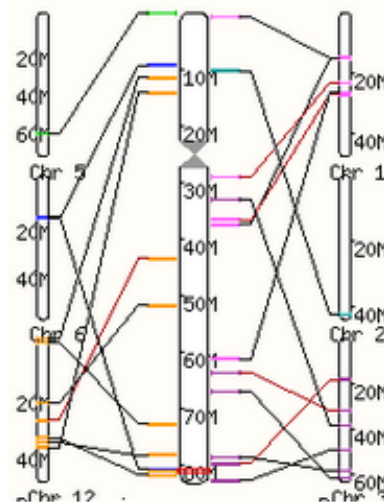
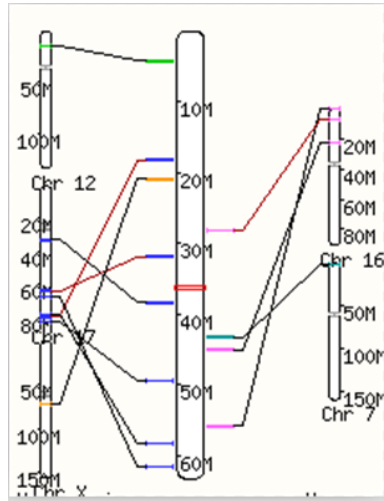
Maria G. Füzesi-Levi,^a Gili Ben-Nissan,^a Elisabetta Bianchi,^b Houjiang Zhou,^c Michael J. Deery,^c Kathryn S. Lilley,^c Yishai Levin,^d Michal Sharon^a

Gene Tree



(引自: Ensembl)

Synteny between zebrafish and human



| | | | | |
|----------------------------------------------------------|-------------------------------------|---|----------------------------------------------|--------------------------------------|
| scpep1 (ENSDARG00000040072) | 3:36126405-36134372 | → | SCPEP1 (ENSG00000121064) | 17:56978105-57006768 |
| engase (ENSDARG00000010035) | 3:36135648-36152092 | → | ENGASE (ENSG00000167280) | 17:79074939-79088599 |
| SLC16A3 (1 of 2) (ENSDARG00000028583) | 3:36160097-36166512 | → | SLC16A3 (ENSG00000141526) | 17:82228397-82261129 |
| csnk1da (ENSDARG00000008370) | 3:36172321-36209462 | → | CSNK1D (ENSG00000141551) | 17:82239023-82273731 |
| dus1l (ENSDARG00000089260) | 3:36221917-36231771 | → | DUS1L (ENSG00000169718) | 17:82057506-82065887 |
| gps1 (ENSDARG00000040650) | 3:36233178-36246017 | → | GPS1 (ENSG00000169727) | 17:82050691-82057470 |
| rac3a (ENSDARG00000090062) | 3:36247969-36259220 | → | RAC3 (ENSG00000169750) | 17:82031624-82034204 |
| prkar1aa (ENSDARG00000076128) | 3:36261711-36271831 | → | PRKAR1A (ENSG00000108946) | 17:68511780-68551319 |
| zgc:86896 (ENSDARG00000090369) | 3:36274834-36283400 | | No homologues | |

| | | | | |
|----------------------------------------------|--------------------------------------|---|-------------------------------------------------|--------------------------------------|
| LRR45 (ENSG00000169683) | 17:82023302-82031151 | | No homologues | |
| RAC3 (ENSG00000169750) | 17:82031624-82034204 | → | rac3b (ENSDARG00000020795) | 12:3614629-3633776 |
| DCXR (ENSG00000169738) | 17:82035136-82037732 | → | dcxr (ENSDARG00000079271) | 12:3635055-3645629 |
| RFNG (ENSG00000169733) | 17:82047902-82051831 | → | rfng (ENSDARG00000019746) | 12:3646187-3669142 |
| GPS1 (ENSG00000169727) | 17:82050691-82057470 | → | gps1 (ENSDARG00000040650) | 3:36233178-36246017 |
| DUS1L (ENSG00000169718) | 17:82057506-82065887 | → | dus1l (ENSDARG00000089260) | 3:36221917-36231771 |
| FASN (ENSG00000169710) | 17:82078338-82098332 | → | fasn (ENSDARG00000087657) | 12:34890656-34945420 |
| CCDC57 (ENSG00000176155) | 17:82101460-82212830 | → | CCDC57 (ENSDARG00000089863) | 12:34860158-34886418 |
| SLC16A3 (ENSG00000141526) | 17:82228397-82261129 | → | slc16a3 (ENSDARG00000045051) | 12:34845164-34854562 |
| CSNK1D (ENSG00000141551) | 17:82239023-82273731 | → | csnk1db (ENSDARG00000006125) | 12:34815412-34831695 |

(引自: Ensembl)

aa Alignment

zebrafish vs mouse

| LENGTH | SCORE | IDENTITY | SIMILARITY | GAPS |
|--------|--------|-----------------|-----------------|----------------|
| 490 | 2283.0 | 445/490 (90.8%) | 455/490 (92.9%) | 19/490 (3.9%) |

zebrafish vs human

| LENGTH | SCORE | IDENTITY | SIMILARITY | GAPS |
|--------|--------|-----------------|-----------------|---------------|
| 491 | 2339.0 | 453/491 (92.3%) | 470/491 (95.7%) | 1/491 (0.2%) |






mouse vs human

| LENGTH | SCORE | IDENTITY | SIMILARITY | GAPS |
|--------|--------|-----------------|-----------------|----------------|
| 491 | 2355.5 | 461/491 (93.9%) | 467/491 (95.1%) | 20/491 (4.1%) |

aa Alignment

 Columns  BLAST  **Align**  Download  Add to basket

◀ 1 to 25 of 128 ▶

| <input type="checkbox"/> | Entry | Entry name | | Protein names | Gene names | Organism |
|-----------------------------------------|--------|--------------|-------------------------------------------------------------------------------------|----------------------------------------------|-----------------------------------------|---------------------------------------------|
| 4 result(s) selected. (Clear selection) | | | | | | |
| <input checked="" type="checkbox"/> | Q13098 | CSN1_HUMAN |  | COP9 signalosome complex subunit 1 | GPS1 , COPS1, CSN1 | Homo sapiens (Human) |
| <input checked="" type="checkbox"/> | Q99LD4 | CSN1_MOUSE |  | COP9 signalosome complex subunit 1 | Gps1 , Cops1, Csn1 | Mus musculus (Mouse) |
| <input checked="" type="checkbox"/> | P97834 | CSN1_RAT |  | COP9 signalosome complex subunit 1 | Gps1 , Cops1, Csn1 | Rattus norvegicus (Rat) |
| <input type="checkbox"/> | Q5HZ00 | SPS3_ARATH |  | Solaneyl diphosphate synthase 3, c... | SPS3 , GPS1, At2g34630, T31E10.3 | Arabidopsis thaliana (Mouse-ear cress) |
| <input checked="" type="checkbox"/> | A0AUR9 | A0AUR9_DANRE |  | G protein pathway suppressor 1 | gps1 | Danio rerio (Zebrafish) (Brachydanio rerio) |

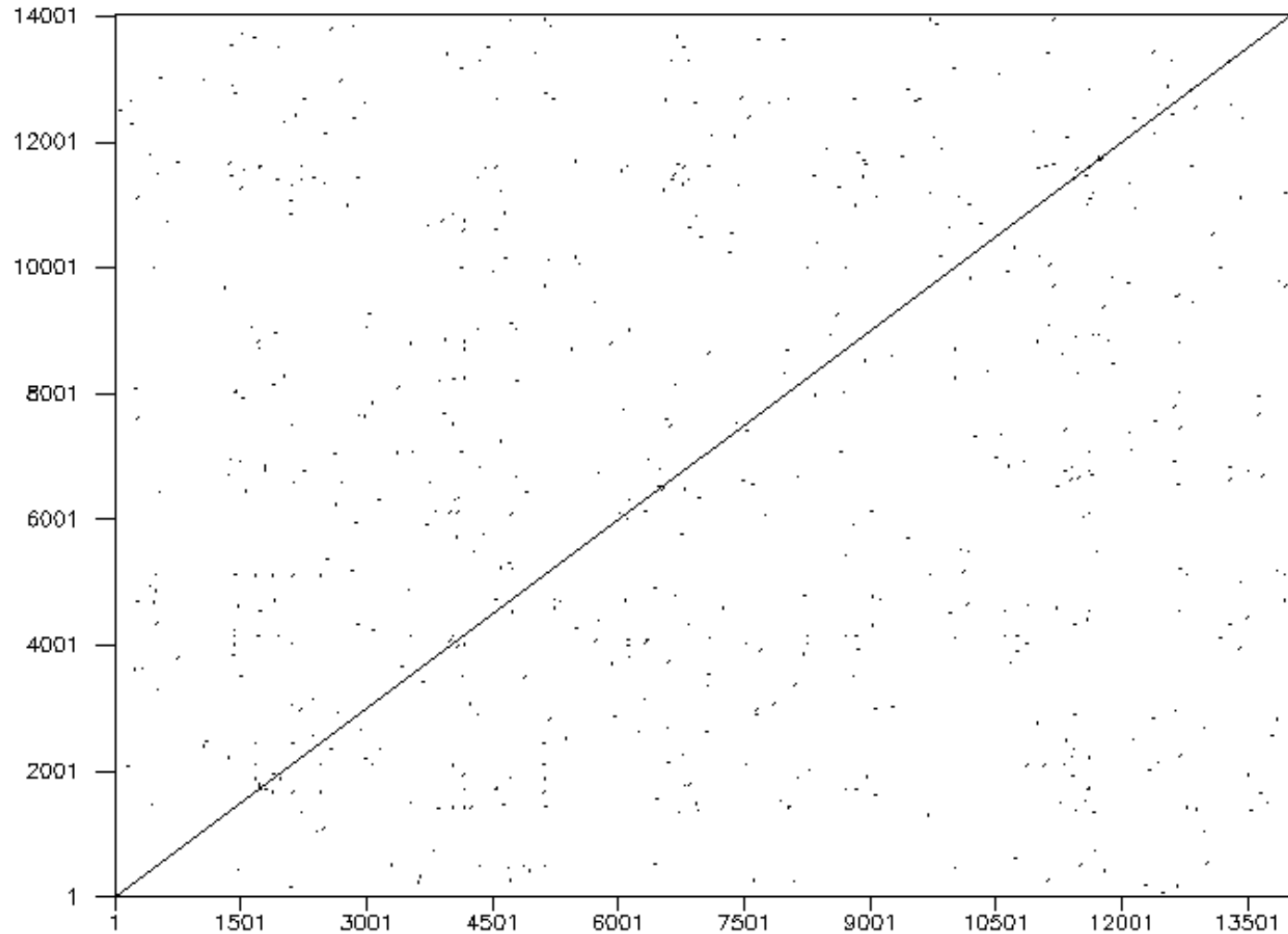
Conserved Domain

```
*_*_*:*****;**** ***:* *****;*****
FDRQELQRNVISSSSFKLFLELEPQVRDIIFKFYESKYASCLKMLDEMKNLLLDMYLAP
FDRQELQRNVISSSSFKLFLELEPQVRDIIFKFYESKYASCLKMLDEMKNLLLDMYLAP
FDRQELQRNVISSSSFKLFLELEPQVRDIIFKFYESKYASCLKMLDEMKNLLLDMYLAP
FDRQELQRNVISSSSFKLFLELEPQVRDIIFKFYESKYASCLKMLDEMKNLLLDMYLAP
*****
HVRTLYTQIRNRALIQYFSPYVSADMHEMAAAFNTTVAALEDELTLQILILEGLISARVDSH
HVRTLYTQIRNRALIQYFSPYVSADMHEMAAAFNTTVAALEDELTLQILILEGLINARIDSH
HVRTLYTQIRNRALIQYFSPYVSADMHEMAAAFNTTVAALEDELTLQVILEGLINARIDSH
HVRTLYTQIRNRALIQYFSPYVSADMNKMAVAFNTTVAALEDELTLQILILEGLINARIDSH
*****
SKILYARDVDQRSTTFEKSLLMGKEFQERRAKAMMLEAAVLENQIHVKSPPREGSQGELTP
SKILYARDVDQRSTTFEKSLLMGKEFQERRAKAMILEAAVLENQIHVKSPPREGSQGELTP
SKILYARDVDQRSTTFEKSLLMGKEFQERRAKAMILEAAVLENQIHVKSPPREGSQGELTP
SKILYARDVDQRSTTFEKSLLMGKEFQERRAKAMILEAAVLENQIHVKSPPREGSQGELTP
*****
```

No repeated sequence

Dottup: fasta::800001:1 vs fasta::800001:1

Sat 20 Dec 2014 05:21:39



(工具: Dottup)

Analysis the Function of *gps1* in Zebrafish via Reverse Genetics

1、 Knockdown

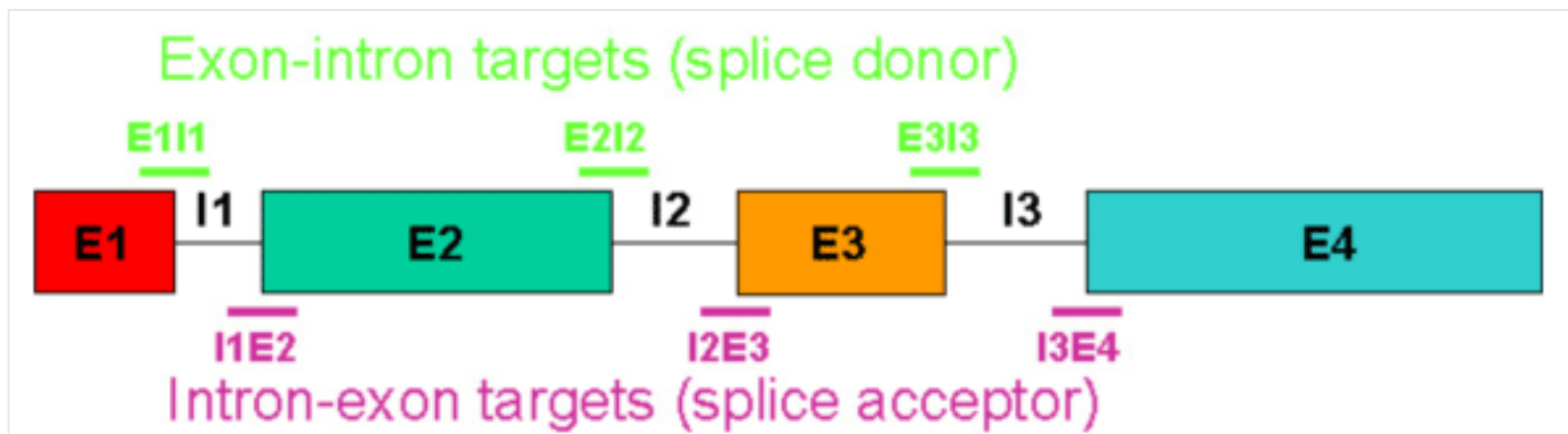
Morpholino、 siRNA...

2、 Knockout

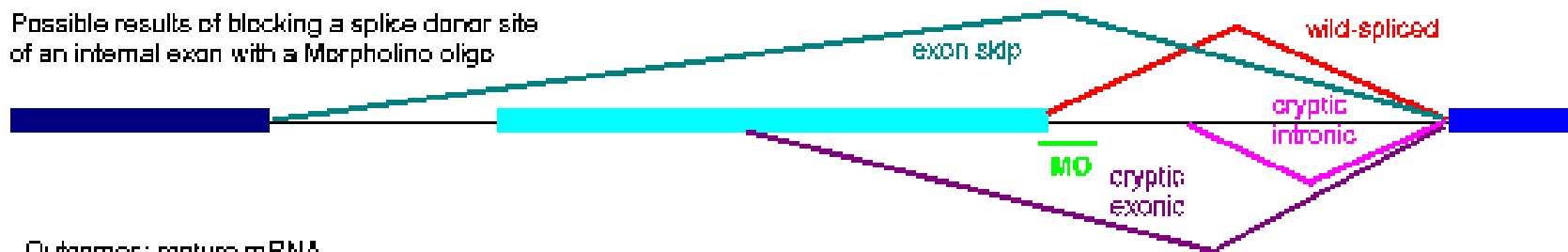
CRISPR/Cas9、 TALENs

3、 Overexpression

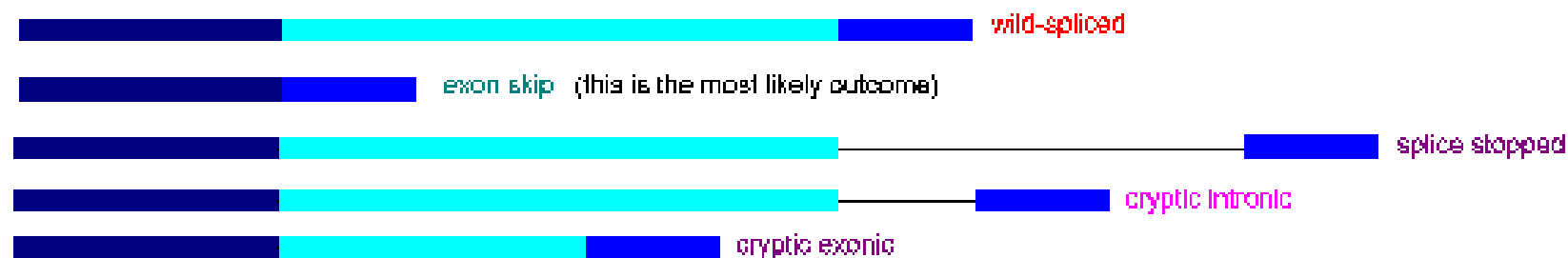
Morpholino



Possible results of blocking a splice donor site of an internal exon with a Morpholino oligo

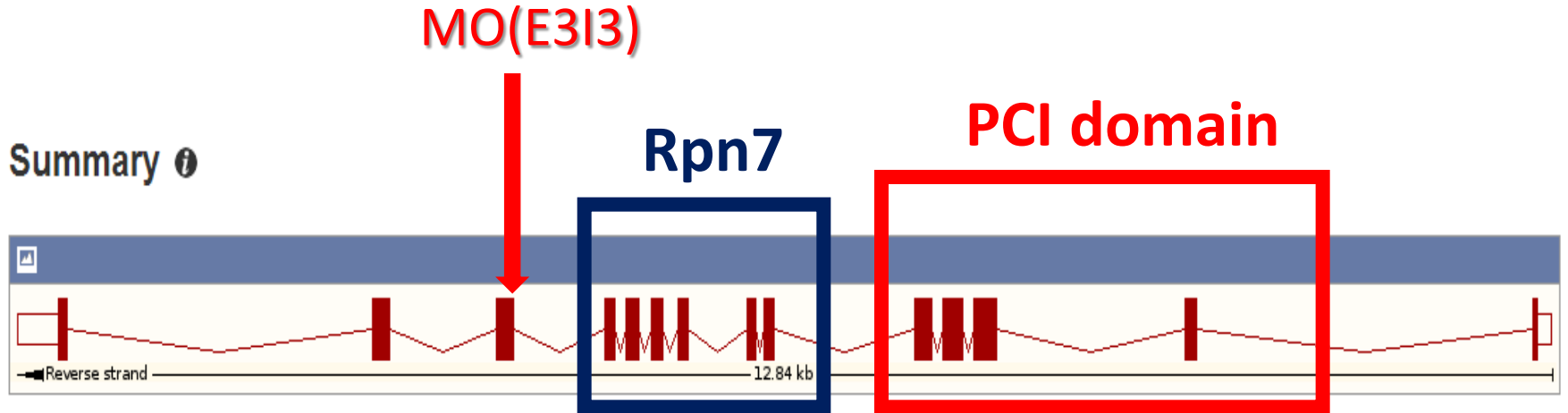


Outcomes: mature mRNA



(引自: Gene Tools)

Morpholino Target site



Summary ⓘ

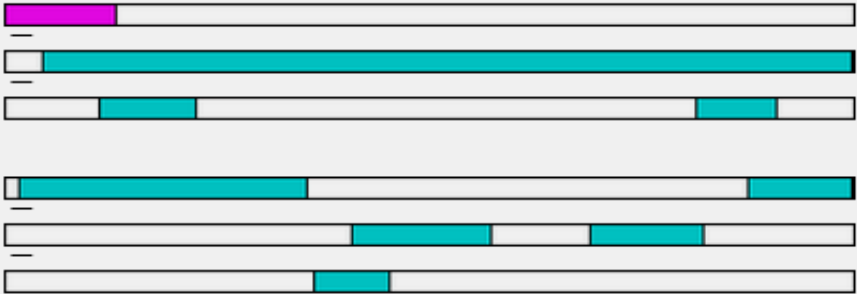
| | |
|-------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| Statistics | Exons: 14 Coding exons: 14 Transcript length: 1,940 bps Translation length: 490 residues |
| Ensembl version | ENSDART00000141106.1 |
| Type | Known protein coding |
| Prediction Method | Manual annotation (determined on a case-by-case basis) from the Havana project. |
| Alternative transcripts | This transcript corresponds to the following database identifiers: Havana transcript: OTTDART00000023686 |

effect prediction

gps1 skipexon3

Program Database with parameters

View



Length: 56 aa

| Frame | from | to | Length |
|-------|------|------|--------|
| +2 | 59 | 1281 | 1224 |
| -1 | 23 | 457 | 435 |
| -2 | 526 | 738 | 213 |
| -2 | 886 | 1056 | 171 |
| +1 | 1 | 171 | 171 |
| -1 | 1124 | 1281 | 159 |
| +3 | 147 | 290 | 144 |
| +3 | 1047 | 1166 | 120 |
| -3 | 471 | 584 | 114 |

```

1 atgccactaccogtgcagggtctttaactttcaggggtctgtagag
  M P L P V Q V F N F Q G S V E
46 cccatgcagatagatgotgaccctcaggaagaccagcagaatgcg
  P M Q I D A D P Q E D Q Q N A
91 cctgacaccaactatgttgtggaaaaccgacattgggaagtgca
  P D T N Y V V E N P T L G S A
136 aggagtcccagatgcggtaccagagggggcagttga 171
  R S P R C G T R G G S *
    
```

Exon3 skip

effect prediction

gps1-intron3

Program Database with parameters

View

| Frame | from | to | Length |
|-------|------|------|--------|
| +2 | 695 | 1569 | 876 |
| -1 | 293 | 745 | 453 |
| +1 | 1 | 342 | 342 |
| -2 | 814 | 1026 | 213 |
| -2 | 1174 | 1344 | 171 |
| -1 | 1412 | 1569 | 159 |
| +3 | 435 | 578 | 144 |
| -2 | 208 | 345 | 138 |
| +3 | 1335 | 1454 | 120 |
| -3 | 759 | 872 | 114 |
| -1 | 23 | 124 | 102 |

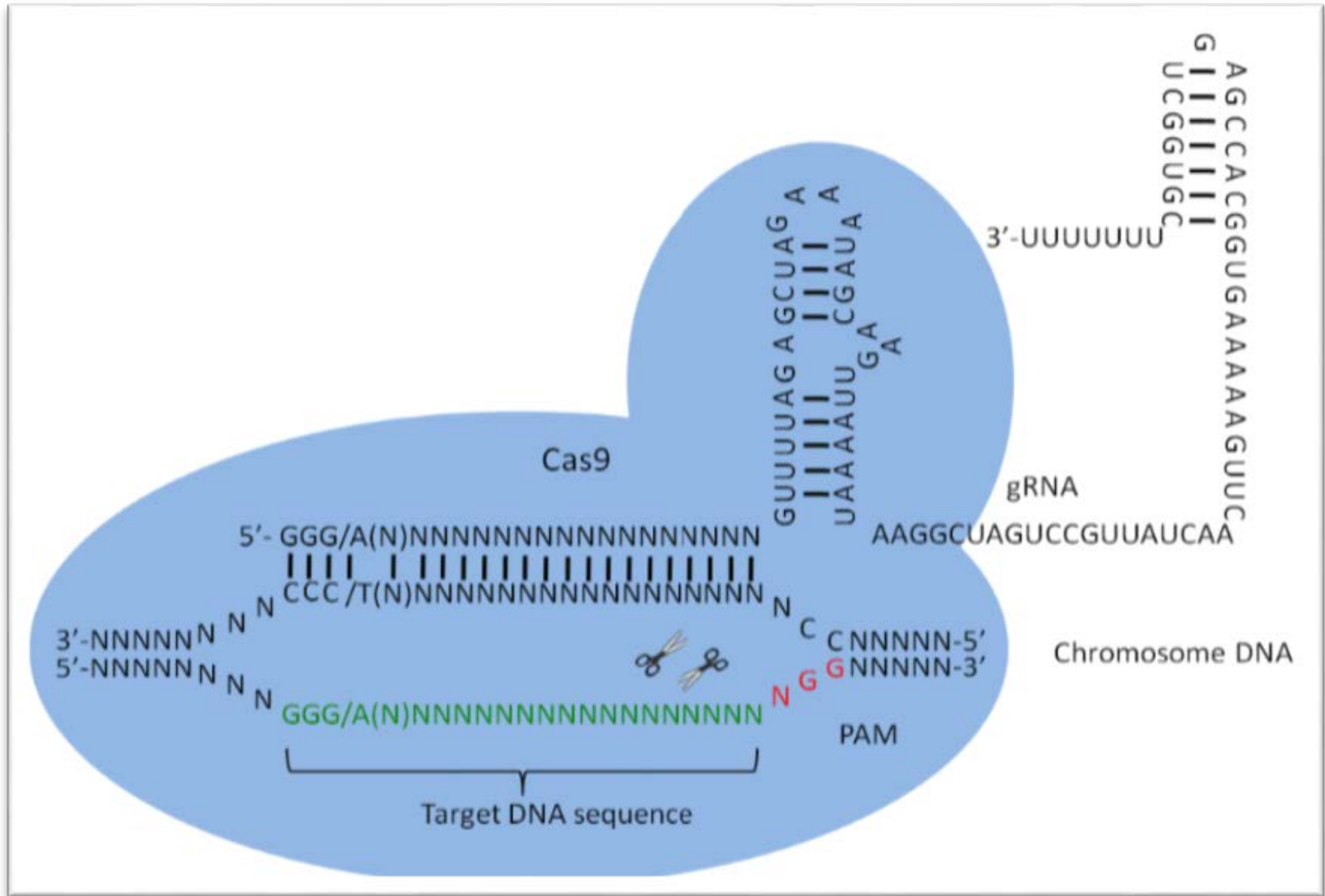
Length: **113 aa**

```

1 atgccactaccCGTgcaggTcttttaactttcaggggtctgtagag
M P L P V Q V F N F Q G S V E
46 cccatgCagatagatgctgaccctcaggaagaccagcagaatgCG
P M Q I D A D P Q E D Q Q N A
91 cctgacaccaactatgttTgtggaaaaccCGacattggatctagag
P D T N Y V V E N P T L D L E
136 cagtatgcgtccagctacagTggactgatgaggatcgagaggctg
Q Y A S S Y S G L M R I E R L
181 cagtttattTgcagaccactgcccctcagctacgagTggaagcactg
Q F I A D H C P Q L R V E A L
226 aagatgKccctgtcctttTgtccaagaacctttaatgttgatgtc
K M A L S F V Q R T F N V D V
271 tatgaagaaatccactgcGaaactcactGagccacaaggcaattc
Y E E I H R K L T E A T R Q F
316 ctgttttattttccctccatgcttaa 342
L F Y F P L H A *
  
```

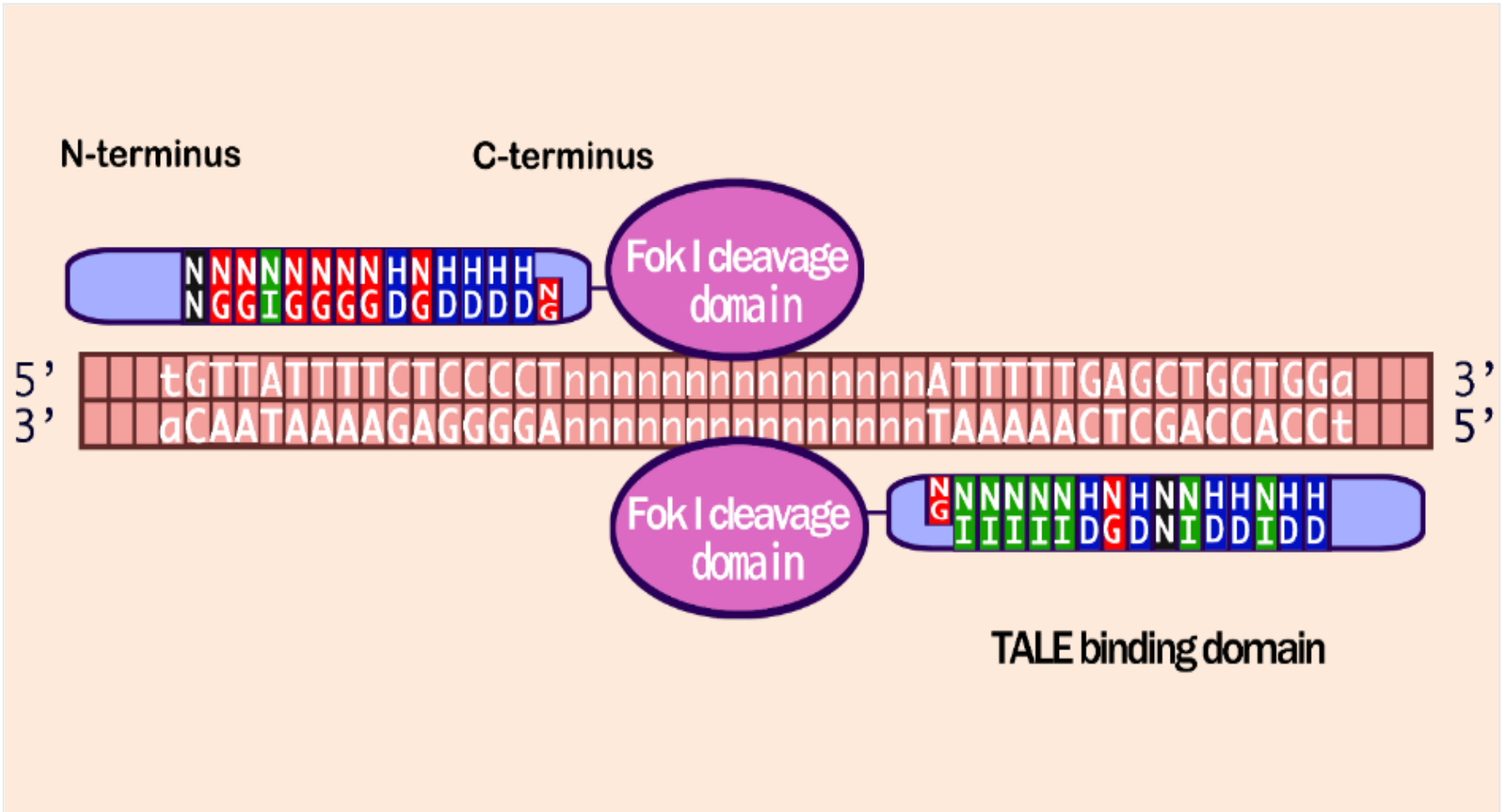
cryptic intronic

CRISPR/Cas9 System



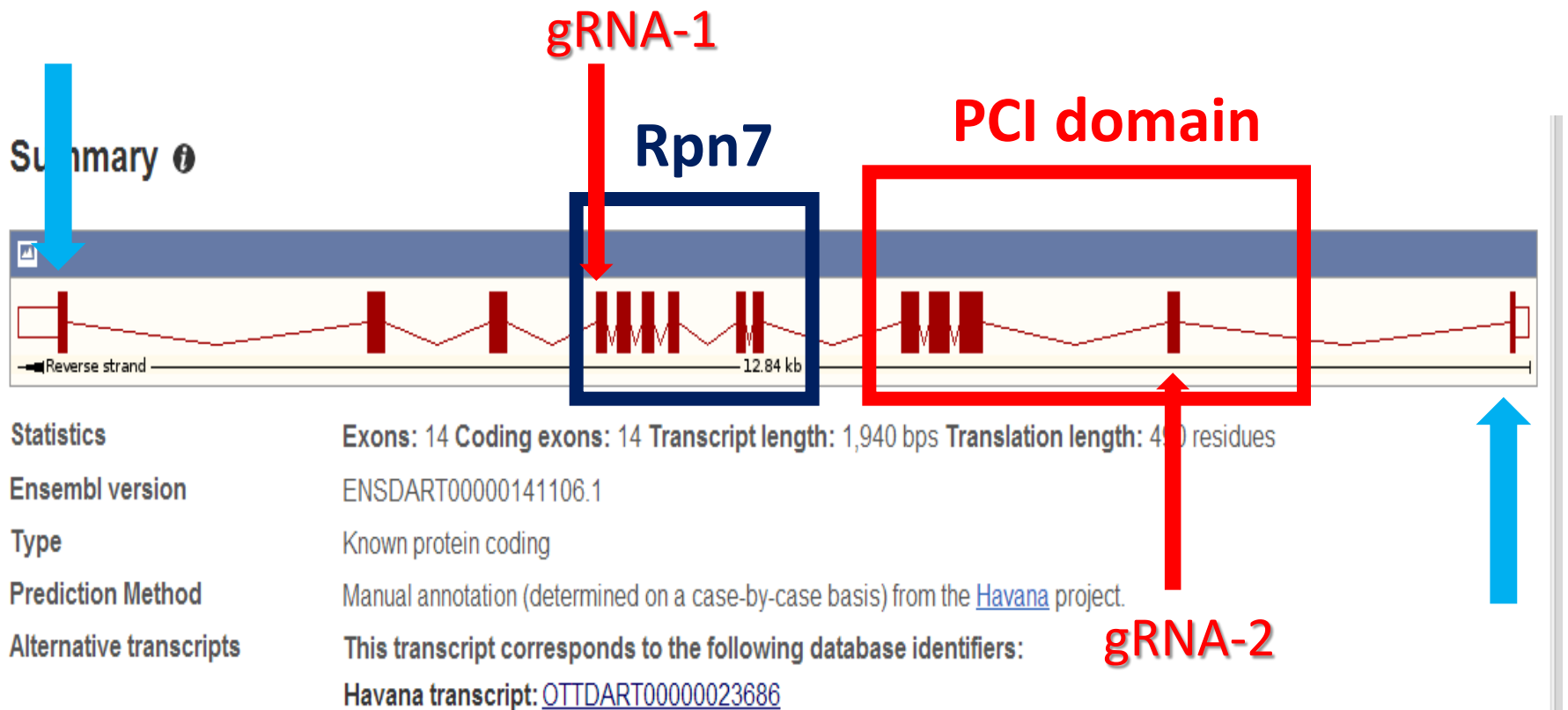
gRNA/Cas9系统工作原理 (引自Mali *et al.*, 2013)

TALEN System



TALEN系统工作原理（引自：Shen Y et al., 2013）

gRNA/Cas9 Target Site



Thanks~