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# 人IRF3(Interferon regulatory factor 3) 蛋白的生物信息学分析

G8: 巨艳 黄宁 李曾龙 管玉  
坤

2012-6-11



## The IRF family of transcription factors

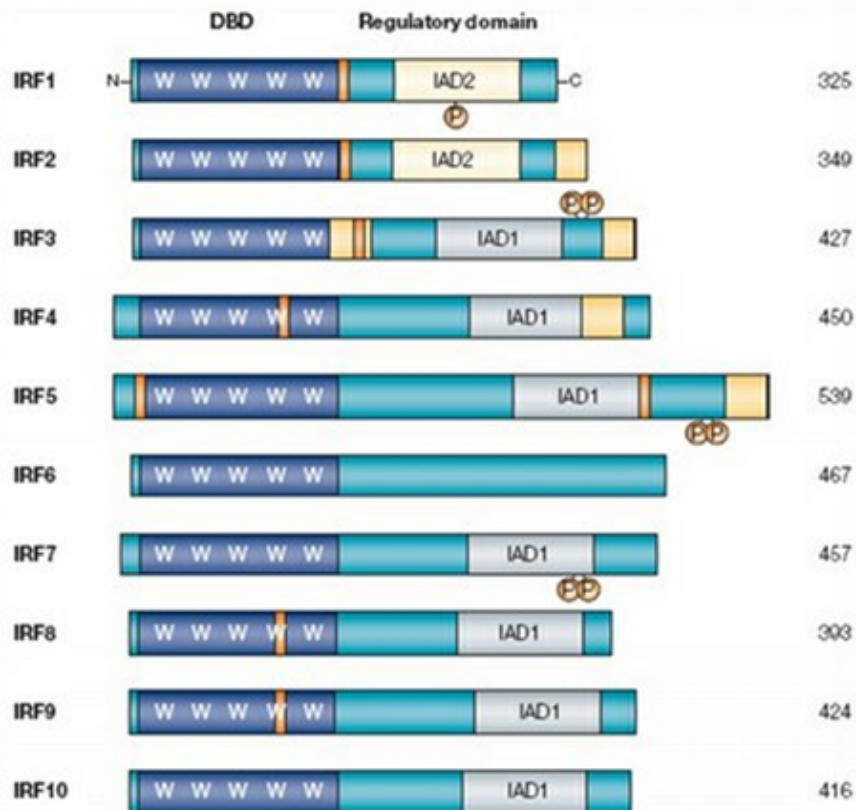
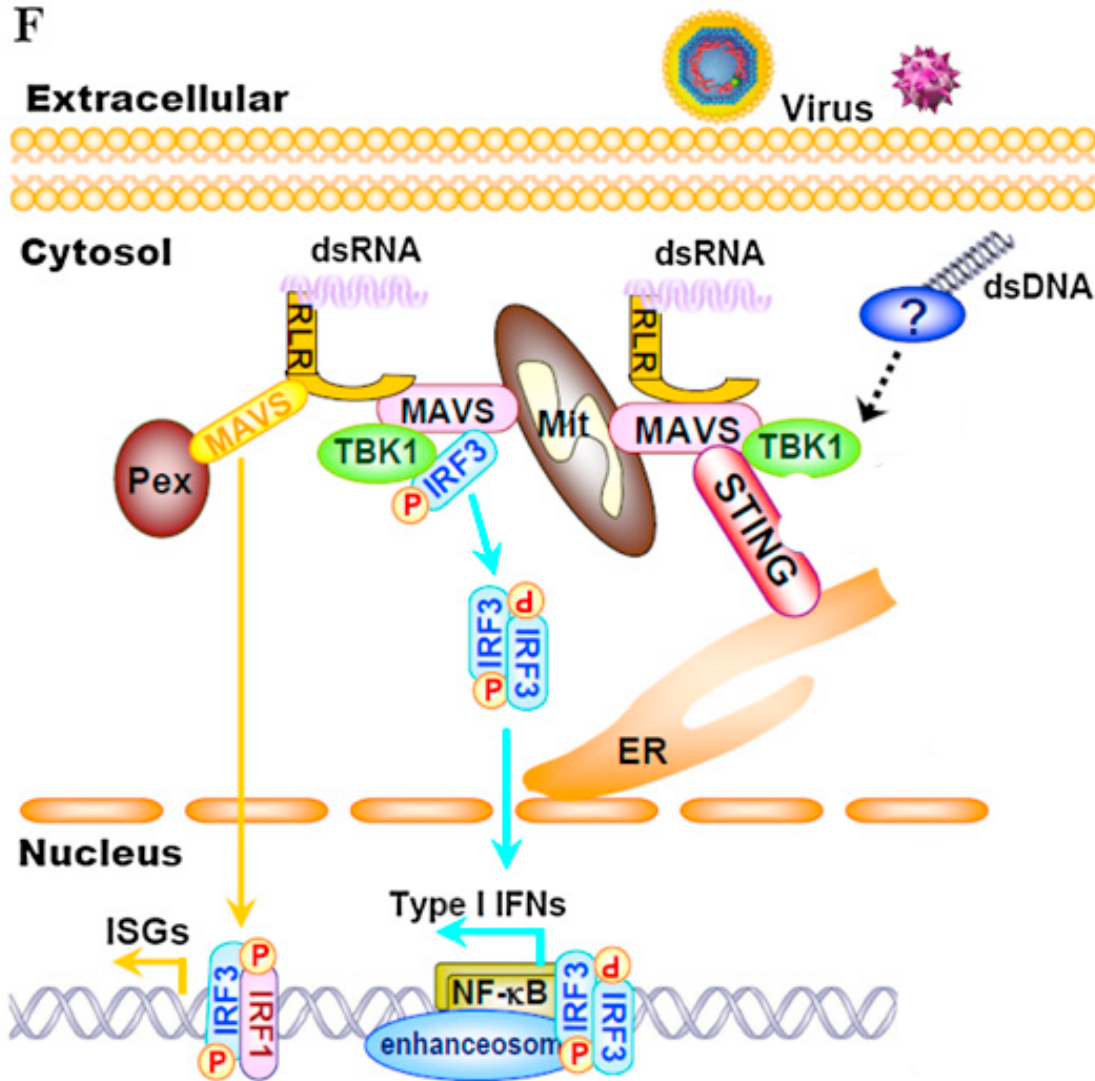


Figure 1 | Structure of interferon-regulatory factors. All interferon-regulatory factors (IRFs) are composed of a DNA-binding domain (DBD; blue) and a regulatory domain (green). For all IRFs, the DBD is defined by 5 tryptophan (W) residues that are each separated by 10–18 amino acids. Most IRFs also contain an IRF-association domain (IAD) of either type 1 (grey) or type 2 (pale yellow). Some IRFs contain a repression domain(s) (yellow) and a nuclear-import signal(s) (orange). [AU:IRF5 has 2 orange domains, correct?] For IRF1, -3, -5 and -7, activity depends on phosphorylation, as shown. The size of each IRF in number of amino acids is also indicated. C, carboxyl terminus; N, amino terminus.

modified from:  
Lohoff & Mak  
Nat. Immunol. 2005



# 背景介绍



- IRF3组成性表达在多种细胞中，主要存在于细胞浆中，病毒感染等因素可诱导IRF3磷酸化，使IRF3形成二聚体并移位至细胞核，并与其他转录因子如CBP/p300结合诱导具有ISRE启动子序列的基因表达，例如IFN  $\alpha / \beta$ ，在抗感染免疫中发挥重要作用。



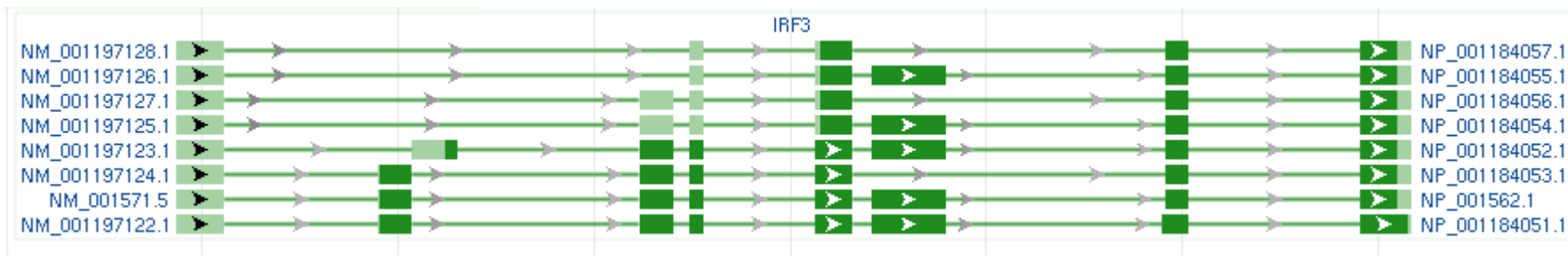
# NCBI IRF3

## IRF3 interferon regulatory factor 3 [ *Homo sapiens* ]

Gene ID: 3661, updated on 2-Jun-2012

**Location:** 19q13.3-q13.4

**Sequence:** Chromosome: 19; NC\_000019.9 (50162826..50169132, complement)





# Ensembl IRF3



Human (GRCh37) ▾

Location: 19:50,162,829-50,169,132

Gene: IRF3

- Gene-based displays
- Gene summary
  - Splice variants (4)
  - Supporting evidence
  - Sequence
  - External references
  - Regulation
  - Comparative Genomics
    - Genomic alignments
    - Gene Tree (image)
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    - Orthologues (44)
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    - Protein families (2)
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  - Genetic Variation
    - Variation Table
    - Variation Image
    - Structural Variation
  - External Data
    - Personal annotation
  - ID History
    - Gene history

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**Gene: IRF3** ENSG00000126456

**Description** interferon regulatory factor 3 [Source:HGNC Symbol;Acc:6118]  
**Location** [Chromosome 19: 50,162,829-50,169,132](#) reverse strand.  
**Transcripts** ☐ This gene has 4 transcripts

| Show/hide columns |                                 | Filter      |                                 |             |                |                           |
|-------------------|---------------------------------|-------------|---------------------------------|-------------|----------------|---------------------------|
| Name              | Transcript ID                   | Length (bp) | Protein ID                      | Length (aa) | Biotype        | CCDS                      |
| IRF3-201          | <a href="#">ENST00000309877</a> | 1690        | <a href="#">ENSP00000310127</a> | 427         | Protein coding | <a href="#">CCDS12775</a> |
| IRF3-202          | <a href="#">ENST00000377135</a> | 903         | <a href="#">ENSP00000366339</a> | 300         | Protein coding | <a href="#">CCDS56099</a> |
| IRF3-203          | <a href="#">ENST00000377139</a> | 1613        | <a href="#">ENSP00000366344</a> | 427         | Protein coding | <a href="#">CCDS12775</a> |
| IRF3-204          | <a href="#">ENST00000442265</a> | 315         | <a href="#">ENSP00000400378</a> | 104         | Protein coding | -                         |

**i Transcript and Gene level displays**

In Ensembl we provide displays at two levels:

- Transcript views which provide information specific to an individual transcript such as the cDNA and CDS se



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[Retrieve](#)
[ID Mapping \\*](#)

**Search in** Protein Knowledgebase (UniProtKB) ▾

**Q14653** (IRF3\_HUMAN) ★ Reviewed, UniProtKB/Swiss-Prot

Last modified May 16, 2012. Version 117. [History...](#)

Clusters with [100%](#), [90%](#), [50%](#) identity | 
 Documents (6) | 
 Third-party data

[Names](#) · [Attributes](#) · [General annotation](#) · [Ontologies](#) · [Interactions](#) · [Alt products](#)  
[Entry info](#) · [Documents](#) [Customize order](#)

## Names and origin

|                      |   |
|----------------------|---|
| Protein names        | <i>Recommended name:</i><br><b>Interferon regulatory factor 3</b><br>Short name=IRF-3                                       |
| Gene names           | Name: <b>IRF3</b>   |
| Organism             | <b>Homo sapiens (Human)</b>   |
| Taxonomic identifier | 9606 [NCBI]   |
| Taxonomic lineage    | Eukaryota › Metazoa › Chordata › Craniata › Vertebrata › Euteleostomi › Mammalia › Primates › Catarrhini › Hominidae › Homo |

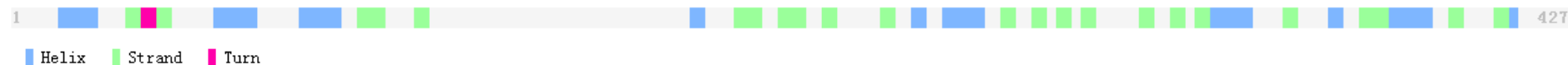
## Protein attributes

|                   |   |
|-------------------|---|
| Sequence length   | 427 AA.                                   |
| Sequence status   | Complete.                                 |
| Protein existence | <a href="#">Evidence at protein level</a> |



# IRF3 结构域

## Secondary structure



## Molecule processing

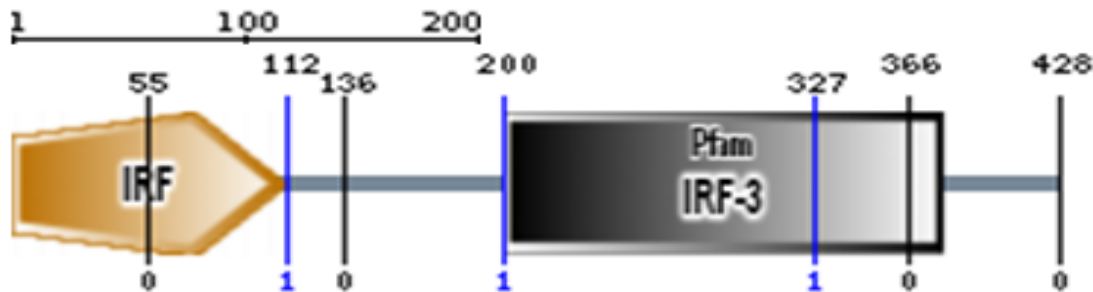
|                          |       |         |     |                                |  |
|--------------------------|-------|---------|-----|--------------------------------|--|
| <input type="checkbox"/> | Chain | 1 - 427 | 427 | Interferon regulatory factor 3 |  |
|--------------------------|-------|---------|-----|--------------------------------|--|

## Regions

|                          |                    |           |     |                              |  |
|--------------------------|--------------------|-----------|-----|------------------------------|--|
| <input type="checkbox"/> | DNA binding        | 5 - 111   | 107 | IRF tryptophan pentad repeat |  |
| <input type="checkbox"/> | Region             | 200 - 360 | 161 | Involved in HERC5 binding    |  |
| <input type="checkbox"/> | Motif              | 139 - 149 | 11  | Nuclear export signal        |  |
| <input type="checkbox"/> | Compositional bias | 151 - 191 | 41  | Pro-rich                     |  |



## Interferon regulatory factor 3

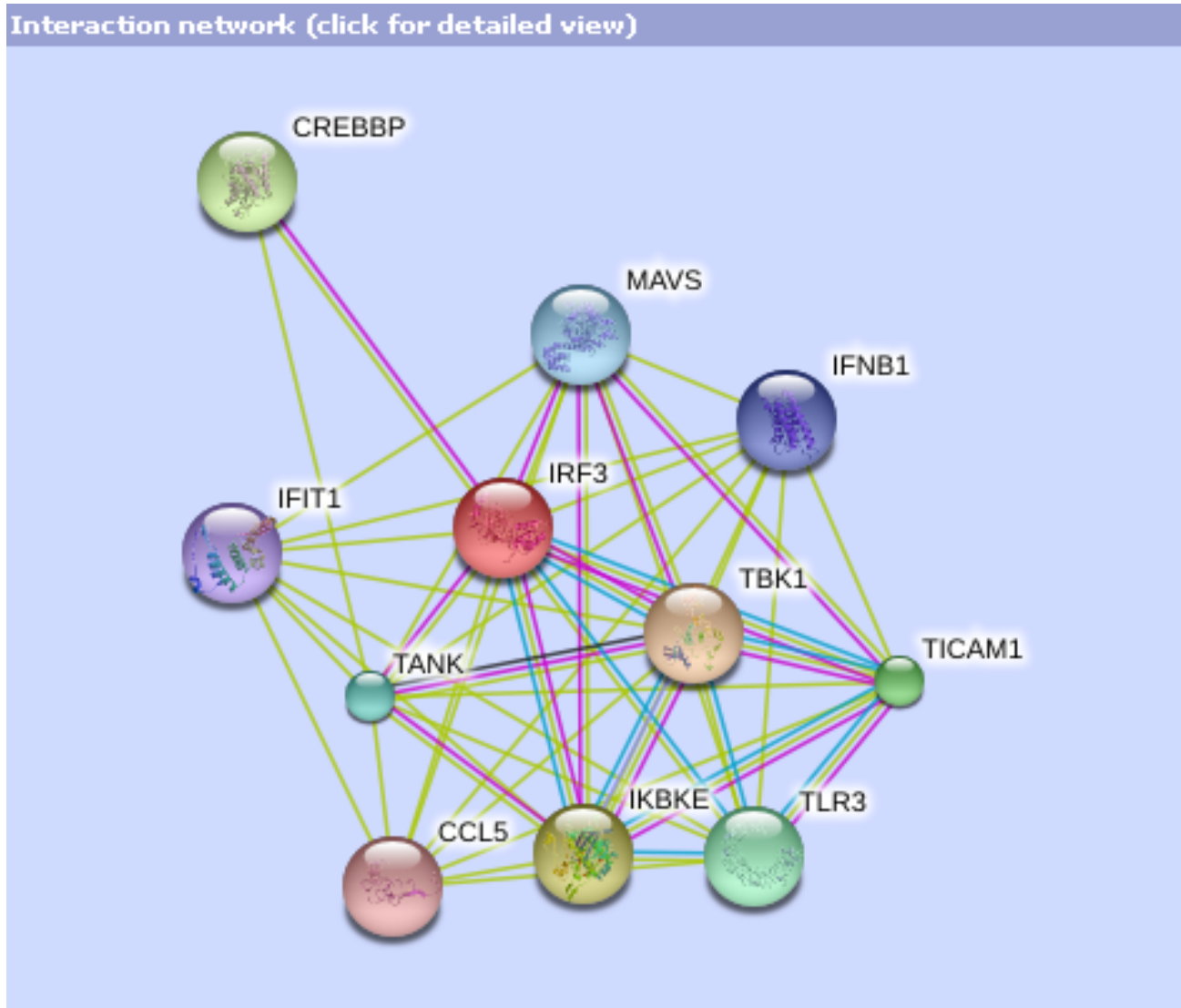


| Name       | Begin | End | E-value  |
|------------|-------|-----|----------|
| IRF        | 1     | 112 | 1.49e-54 |
| Pfam:IRF-3 | 201   | 380 | 7.60e-47 |





# IRF3 相互作用蛋白

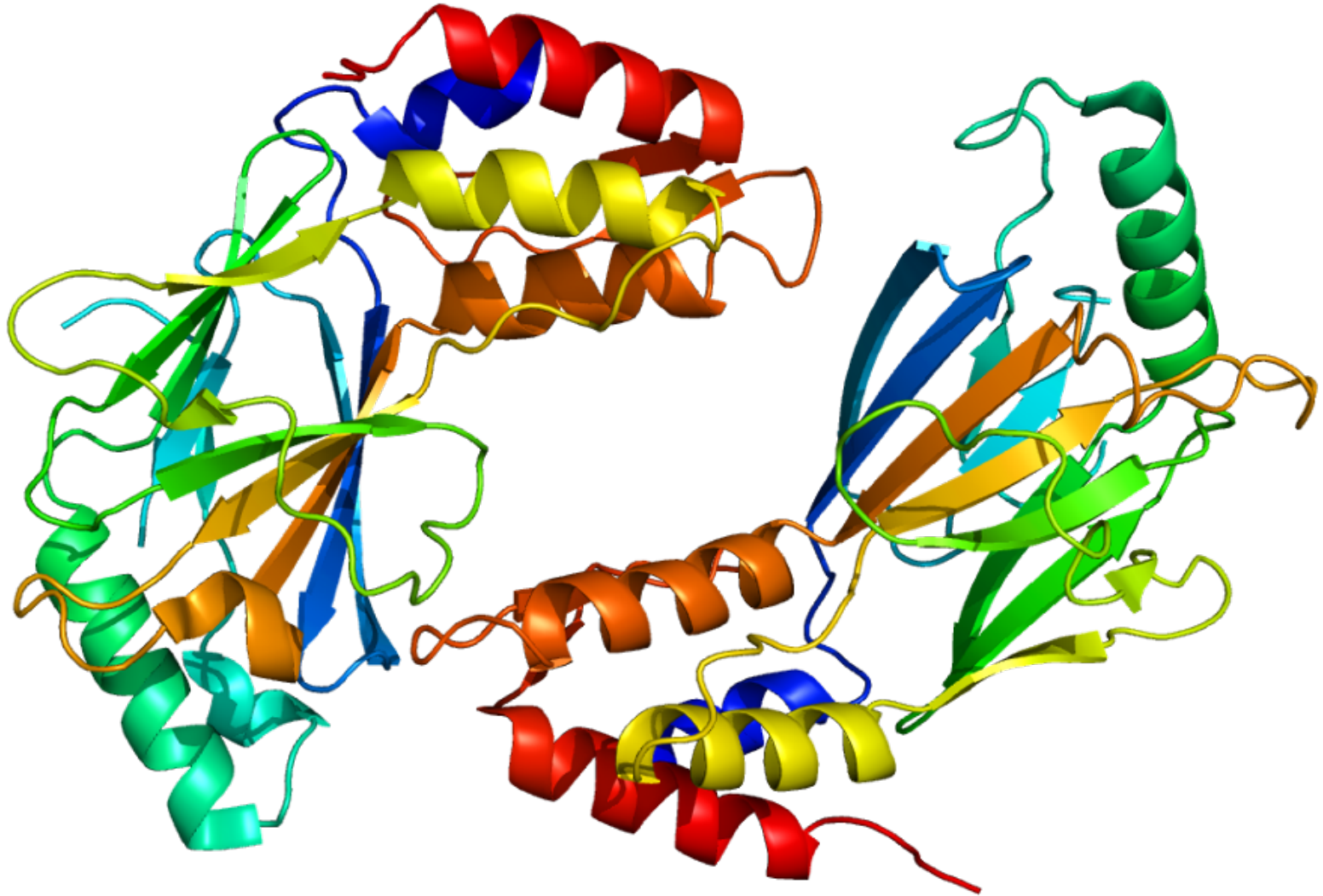






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# PDB IRF3 结构





## Alignment



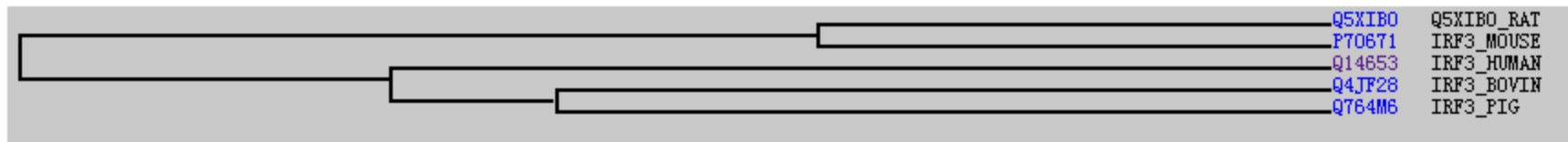
Learn how to print this alignment in color

```

1  MGTPKPRILPWLVSQLDLGGLEGVAWVNKSRTFRIPWKHGLRQDAQQEDFGIFQAWAEA  60  Q14653  IRF3_HUMAN
1  MGTQKPRILPWLISQLDRGELEGVAWLGESRTFRIPWKHGLRQDAQQEDFGIFQAWAVA  60  Q4JF28  IRF3_BOVIN
1  MGTPKPLILPWLVSQLDLGGLEGVAWLDESRTKFRIPWKHGLRQDAQMADFGIFQAWAEA  60  Q5XIBO  Q5XIBO_RAT
1  MGTQKPRILPWLISQLNQGGLEGVAWLDEGHTFRIPWKHGLRQDAQQEDFGIFQAWAEA  60  Q764M6  IRF3_PIG
1  METPKPRILPWLVSQLDLGGLEGVAWLDESRTFRIPWKHGLRQDAQMADFGIFQAWAEA  60  P70671  IRF3_MOUSE
* * * * *
81  TGAYVPGRDKFDLPTWKRNFERSALNRKEGLRLAEDRSKDPHDPHKIYEFVNSG-VGDFSQ  119  Q14653  IRF3_HUMAN
81  SGAYTPGKDKFDLPTWKRNFERSALNRKEVLRLAEDHSKDSQDPHKIYEFVNSG-VRDIPE  119  Q4JF28  IRF3_BOVIN
81  SGAYTPGKDKFDLSTWKRNFERSALNRKEVLRLAEDRSKDPFDPHKVYEFVTPGGARDFVH  120  Q5XIBO  Q5XIBO_RAT
81  SGAYTPGKDKFDLPTWKRNFERSALNRKEALRLAEDHSKDPHDPHKIYEFVTSG-VGDFPE  119  Q764M6  IRF3_PIG
81  SGAYTPGKDKFDVSTWKRNFERSALNRKEVLRLAADNSKDPYDPHKVYEFVTPG-ARDFVH  119  P70671  IRF3_MOUSE
:***:**:****: ***** ***** * ** * ** * ** * ** * ** *

```

## Guide tree





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# IRF3 酶切位点分析

```

161   GCGCAGCCTCGAGTTTGTAGAGCTACCCGGAGCTCCAAGACAGGGGTGGGTTCCAGCTGCCCCGACGCCCCGACCTTCCAT   240
161   CGCGTCGGAGCTCAAACCTCTCGATGGGCCTCGAGGTTCTGTCCCCACCCAAGGTCGACGGGCGTGCGGGGCTGGAAGGTA   240
      FspI   AvaI   BbvI           EcoICRI   BslI   NlaIV   Cac8I   FauI
              SmI   MnlI           BanII   XcmI           MspAII   Cac8I
              XhoI           BsiHKAI   BbvI           PvuII   Hin4I
                        Bsp1286I           Hin4I
                        SacI

241   CGTAGCCCGGACCATGGGAACCCCAAAGCCACGGATCCTGCCCTGGCTGGTGTGCGCAGCTGGACCTGGGGCAACTGGAGG   320
241   GCATCCGGCCTGGTACCCTTGGGGTTTTCGGTGCCTAGGACGGGACCACCACAGCGTCGACCTGGACCCCGTTGACCTCC   320
              BsaJI   NlaIV   AlwI   NlaIV   TspGWI   MspAII   BbvI   BsrI
              BtgI           BsaJI   AlwI   MwoI   PvuII           MnlI   TaqII
              NcoI           BtgI   BsaJI   HpyF10VI   BsaJI
              StyI           BamHI
              BslI           BstYI
              Hin4I
              Hin4I

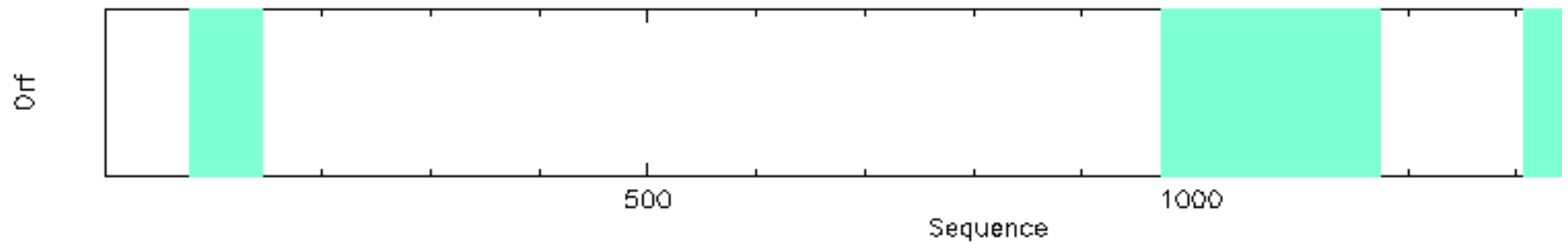
321   GCGTGGCCTGGGTGAACAAGAGCCGCACGCGTTCCGCATCCCTTGAAGCACGGCCTACGGCAGGATGCACAGCAGGAG   400
321   CGCACCGGACCCACTTGTCTCGGCGTGCGCGAAGGCGTAGGGAACCTTCGTGCCGGATGCCGTCCTACGTGTCGTCCCTC   400
              BsaJI   Hpy8I   HphI   HpyF10VI   BsaJI   SfaNI   BceAI   BceAI
              BpmI   FokI           BstF5I   SfaNI           EcoNI   BstF5I
              Eco57MI   Cac8I           StyI           BslI   MnlI   FokI
                        MwoI

```

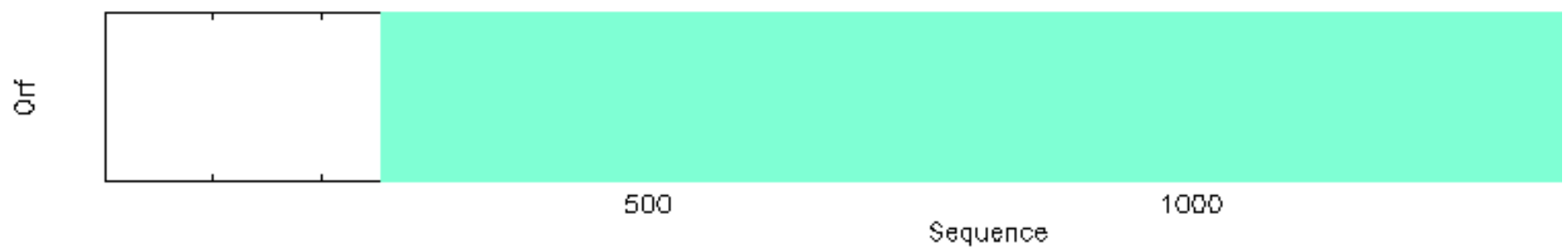


# IRF3 ORF分析

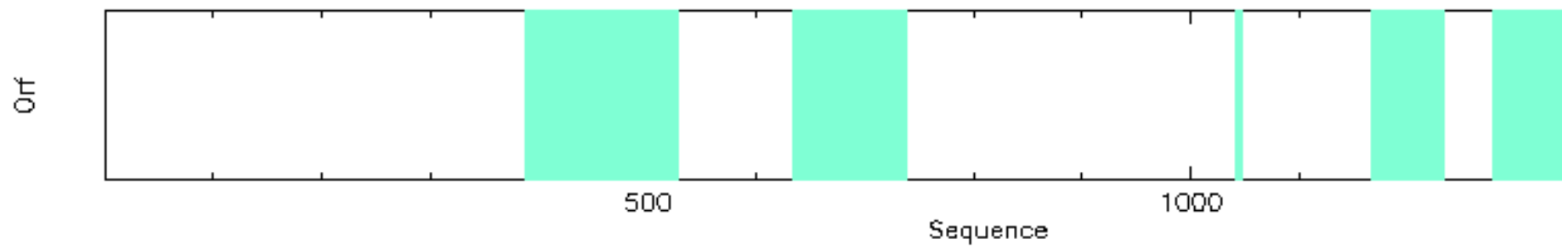
F1



F2

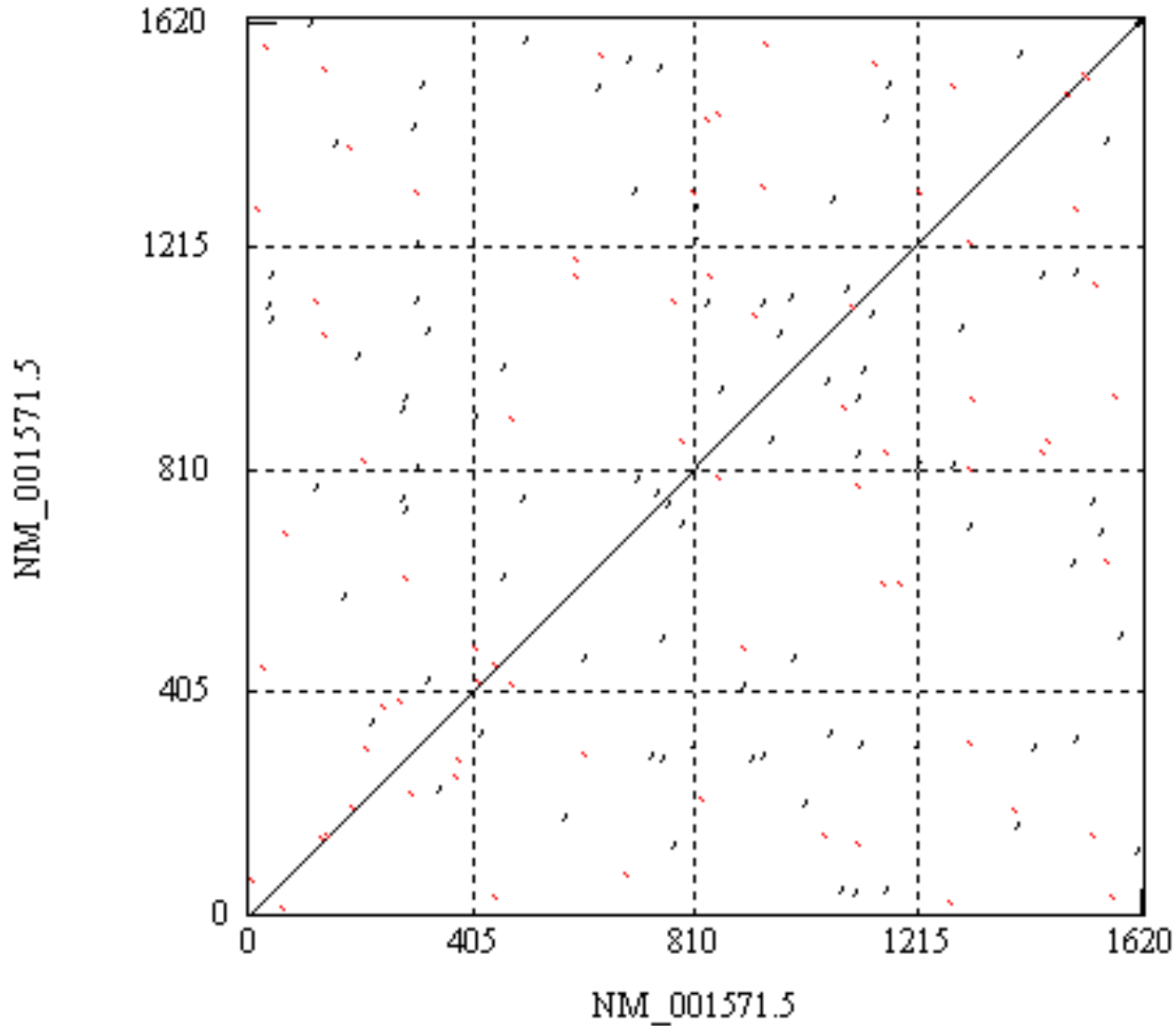


F3





# IRF3 mRNA点阵图分析





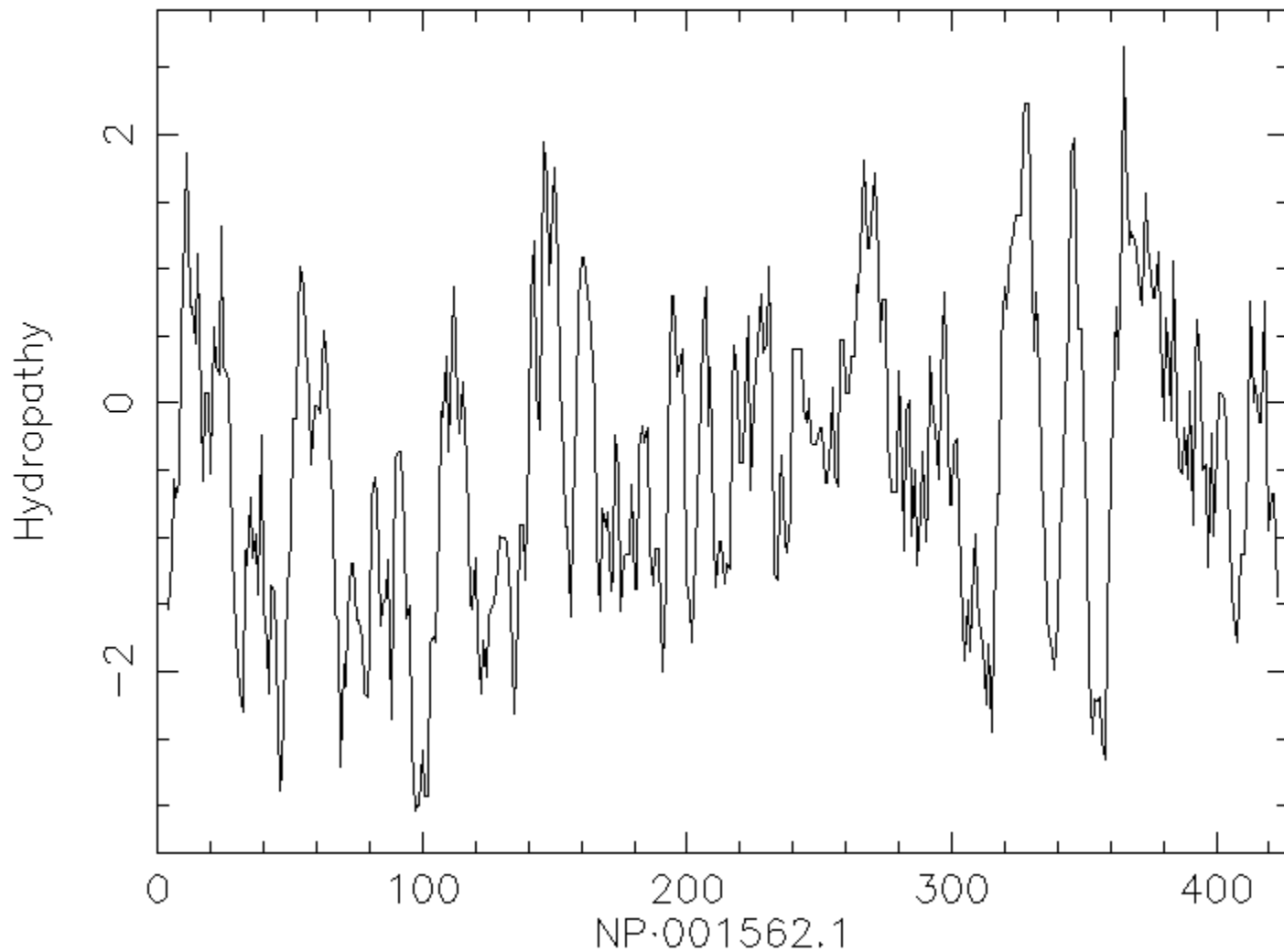
# IRF3 氨基酸组成分析

| Residue   | Number                  | Mole%  | DayhoffStat |        |
|-----------|-------------------------|--------|-------------|--------|
| A = Ala   | 21                      | 4.918  | 0.572       |        |
| B = Asx   | 0                       | 0.000  | 0.000       |        |
| C = Cys   | 6                       | 1.405  | 0.485       |        |
| D = Asp   | 28                      | 6.557  | 1.192       |        |
| E = Glu   | 26                      | 6.089  | 1.015       |        |
| F = Phe   | 15                      | 3.513  | 0.976       |        |
| G = Gly   | 43                      | 10.070 | 1.199       |        |
| H = His   | 9                       | 2.108  | 1.054       |        |
| I = Ile   | 9                       | 2.108  | 0.468       |        |
| J = ---   | 0                       | 0.000  | 0.000       |        |
| K = Lys   | 14                      | 3.279  | 0.497       |        |
| L = Leu   | 47                      | 11.007 | 1.487       |        |
| M = Met   | 7                       | 1.639  | 0.964       |        |
| N = Asn   | 12                      | 2.810  | 0.654       |        |
| O = ---   | 0                       | 0.000  | 0.000       |        |
| P = Pro   | 42                      | 9.836  | 1.892       |        |
| Q = Gln   | 19                      | 4.450  | 1.141       |        |
| R = Arg   | 26                      | 6.089  | 1.243       |        |
| S = Ser   | 30                      | 7.026  | 1.004       |        |
| T = Thr   | 21                      | 4.918  | 0.806       |        |
| U = ---   | 0                       | 0.000  | 0.000       |        |
| V = Val   | 30                      | 7.026  | 1.065       |        |
| W = Trp   | 14                      | 3.279  | 2.522       |        |
| X = Xaa   | 0                       | 0.000  | 0.000       |        |
| Y = Tyr   | 8                       | 1.874  | 0.551       |        |
| Z = Glx   | 0                       | 0.000  | 0.000       |        |
| Property  | Residues                | Number | Mole%       |        |
| Tiny      | (A+C+G+S+T)             | 121    |             | 28.337 |
| Small     | (A+B+C+D+G+N+P+S+T+V)   | 233    |             | 54.567 |
| Aliphatic | (A+I+L+V)               | 107    | 25.059      |        |
| Aromatic  | (F+H+W+Y)               | 46     | 10.773      |        |
| Non-polar | (A+C+F+G+I+L+M+P+V+W+Y) | 242    |             | 56.674 |
| Polar     | (D+E+H+K+N+Q+R+S+T+Z)   | 185    |             | 43.326 |
| Charged   | (B+D+E+H+K+R+Z)         | 103    |             | 24.122 |
| Basic     | (H+K+R)                 | 49     |             | 11.475 |



# IRF3 疏水性分析

Kyte-Doolittle Plot

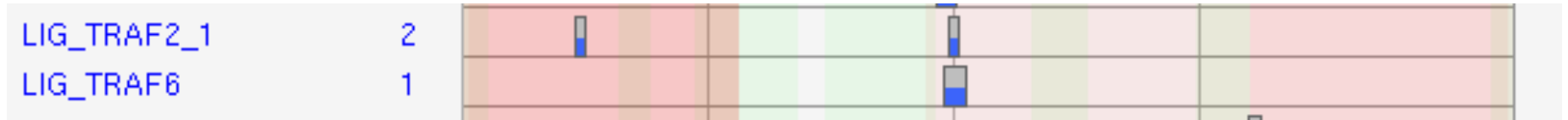








# TRAF结合位点



## LIG\_TRAF2\_1

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<< LIG\_TPR <<

Menu

>> LIG\_TRAF2\_2 >>

Functional Site Class: TRAF2 binding site

**Functional site description:** Endogenous TRAF2 is a cytosolic protein that is recruited to membrane associated receptors.

**ELMs:** [LIG\\_TRAF2\\_1](#) [LIG\\_TRAF2\\_2](#)

**Description:** Major TRAF2-binding consensus motif. Members of the tumor necrosis factor receptor (TNFR) superfamily initiate intracellular signaling by recruiting the C-domain of the TNFR-associated factors (TRAFs) through their cytoplasmic tails.

**Pattern:** [PSAT] . [QE] E

(Probability: 0.0042998)

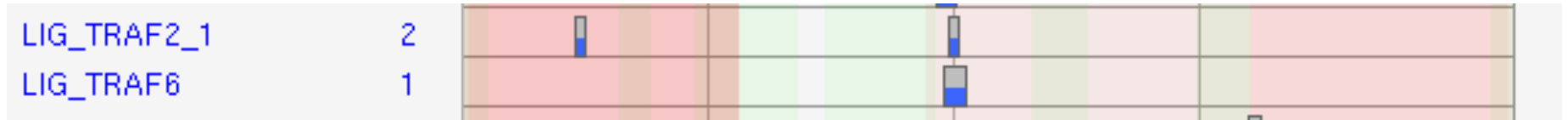
**Present in taxons:** [Eukaryota](#)

**Interaction Domain:** [MATH \(PF00917\)](#)  
MATH domain  
(Stoichiometry: 1 : 1)

■ [See 14 Instances for LIG\\_TRAF2\\_1](#)



# TRAF结合位点



## LIG\_TRAF6

133

<< LIG\_TRAF2\_2 <<

Menu

>> LIG\_TRFH\_1 >>

|                                     |  |
|-------------------------------------|--|
| <b>Functional Site Class:</b>       | TRAF6 binding site   |
| <b>Functional site description:</b> | TRAF6 protein acts as intracellular adaptor that is recruited to different receptors through its C-terminal TRAF domain.   |
| <b>ELMs:</b>                        | <a href="#">LIG_TRAF6</a>  |
| <b>Description:</b>                 | TRAF6 binding site. Members of the tumor necrosis factor receptor (TNFR) superfamily initiate intracellular signaling by recruiting the C-domain of the TNFR-associated factors (TRAFs) through their cytoplasmic tails. |
| <b>Pattern:</b>                     | ..P.E.. [FYWHDE] .<br><span style="float: right;">(Probability: 0.0017147)</span>  |
| <b>Present in taxons:</b>           | <a href="#">Vertebrata</a>   |
| <b>Interaction Domain:</b>          | <a href="#">MATH (PF00917)</a><br>MATH domain<br>(Stoichiometry: 1 : 1)  |

■ [See 20 Instances for LIG\\_TRAF6](#)



# 磷酸化位点预测

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Substrate: IRF3 (Transcription factor)  
 Seq-ID: Q14653 [*Homo sapiens*]  
 Interaction Network(s): [STRING](#) [NetworKIN](#)  
 External Source(s): [PhosphoSitePlus](#)  
 MINT Interaction(s): [\[show\]](#)  
 GO-Terms: [\[show\]](#)  
 Conservation:

[Click on table header](#)

| Res. ⚡ | Pos. ⚡ | Sequence ⚡                     | Kinase ⚡    | PMID ⚡   | Src ⚡ | Cons. ⚡ | ELM ⚡ | Binding Domain ⚡ | SMART/Pfam ⚡ | IUPRED score ⚡ | PDB ⚡ | P3D Acc. ⚡ |
|--------|--------|--------------------------------|-------------|----------|-------|---------|-------|------------------|--------------|----------------|-------|------------|
| S      | 385    | LVEMARVGGAS <b>S</b> LENTVDLHI | -           | 9463386  | LTP   | 1.00    |       | -                | -            | 0.32           | 1QWT  | 40.98%     |
| S      | 385    | LVEMARVGGAS <b>S</b> LENTVDLHI | -           | 14703513 | LTP   | 1.00    |       | -                | -            | 0.32           | 1QWT  | 40.98%     |
| S      | 385    | LVEMARVGGAS <b>S</b> LENTVDLHI | TBK1        | 17526488 | LTP   | 1.00    |       | -                | -            | 0.32           | 1QWT  | 40.98%     |
| S      | 386    | VEMARVGGAS <b>S</b> LENTVDLHIS | -           | 9463386  | LTP   | 0.99    |       | -                | -            | 0.35           | 1QWT  | 111.48%    |
| S      | 386    | VEMARVGGAS <b>S</b> LENTVDLHIS | IKK_epsilon | 14703513 | LTP   | 0.99    |       | -                | -            | 0.35           | 1QWT  | 111.48%    |
| S      | 386    | VEMARVGGAS <b>S</b> LENTVDLHIS | TBK1        | 14703513 | LTP   | 0.99    |       | -                | -            | 0.35           | 1QWT  | 111.48%    |
| S      | 386    | VEMARVGGAS <b>S</b> LENTVDLHIS | TBK1        | 17526488 | LTP   | 0.99    |       | -                | -            | 0.35           | 1QWT  | 111.48%    |
| S      | 396    | SENTVDLHIS <b>S</b> NSHPLSLTSD | -           | 12524442 | LTP   | 1.00    |       | -                | -            | 0.40           | 1QWT  | 23.77%     |
| S      | 396    | SENTVDLHIS <b>S</b> NSHPLSLTSD | -           | 17526488 | LTP   | 1.00    |       | -                | -            | 0.40           | 1QWT  | 23.77%     |
| S      | 398    | ENTVDLHIS <b>S</b> HPLSLTSDQY  | -           | 9566918  | LTP   | 0.31    |       | -                | -            | 0.36           | 1QWT  | 40.16%     |
| S      | 402    | DLHISNSHPL <b>S</b> LTSQYKAYL  | -           | 9566918  | LTP   | 0.20    |       | -                | -            | 0.26           | 1QWT  | 46.72%     |
| T      | 404    | HISNSHPLSL <b>T</b> SDQYKAYLQD | -           | 9566918  | LTP   | 0.16    |       | -                | -            | 0.25           | 1QWT  | 35.62%     |
| S      | 405    | ISNSHPLSL <b>T</b> SQYKAYLQDL  | -           | 9566918  | LTP   | 0.09    |       | -                | -            | 0.26           | 1QWT  | 33.61%     |
| S      | 405    | ISNSHPLSL <b>T</b> SQYKAYLQDL  | -           | 17526488 | LTP   | 0.09    |       | -                | -            | 0.26           | 1QWT  | 33.61%     |



# IRF 家族

Search Blast Align Retrieve ID Mapping \*

Search in: Protein Knowledgebase (UniProtKB) Query: organism:human AND family:irf AND reviewed:yes

12 results for organism:human AND family:irf AND reviewed:yes in UniProtKB sorted by score descending

Download

Browse by taxonomy, keyword, gene ontology, enzyme class or pathway |

Reduce sequence redundancy to 100%, 90% or 50%

Page 1 of 1

Results Customize

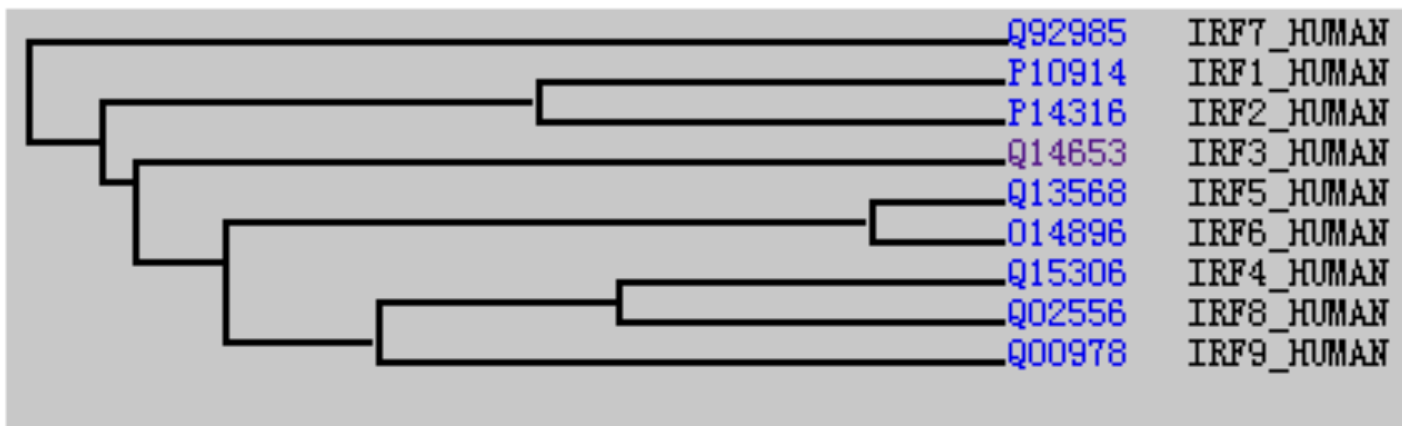
Add columns: Protein families

| Entry  | Entry name  | Status | Protein names                                    | Gene names                          | Organism             | Length |
|--------|-------------|--------|--|-------------------------------------|----------------------|--------|
| Q14653 | IRF3_HUMAN  | ★      | Interferon regulatory factor 3                   | IRF3                                | Homo sapiens (Human) | 427    |
| O14896 | IRF6_HUMAN  | ★      | Interferon regulatory factor 6                   | IRF6                                | Homo sapiens (Human) | 467    |
| Q92985 | IRF7_HUMAN  | ★      | Interferon regulatory factor 7                   | IRF7                                | Homo sapiens (Human) | 503    |
| P10914 | IRF1_HUMAN  | ★      | Interferon regulatory factor 1                   | IRF1                                | Homo sapiens (Human) | 325    |
| P14316 | IRF2_HUMAN  | ★      | Interferon regulatory factor 2                   | IRF2                                | Homo sapiens (Human) | 349    |
| Q15306 | IRF4_HUMAN  | ★      | Interferon regulatory factor 4                   | IRF4 MUM1                           | Homo sapiens (Human) | 451    |
| Q13568 | IRF5_HUMAN  | ★      | Interferon regulatory factor 5                   | IRF5                                | Homo sapiens (Human) | 498    |
| Q9H1B7 | I2BPL_HUMAN | ★      | Interferon regulatory factor 2-binding protei... | IRF2BPL C14orf4 EAP1 KIAA1865 My039 | Homo sapiens (Human) | 796    |
| Q02556 | IRF8_HUMAN  | ★      | Interferon regulatory factor 8                   | IRF8 ICSBP1                         | Homo sapiens (Human) | 426    |
| Q8IU81 | I2BP1_HUMAN | ★      | Interferon regulatory factor 2-binding protei... | IRF2BP1                             | Homo sapiens (Human) | 584    |
| Q7Z5L9 | I2BP2_HUMAN | ★      | Interferon regulatory factor 2-binding protei... | IRF2BP2                             | Homo sapiens (Human) | 587    |
| Q00978 | IRF9_HUMAN  | ★      | Interferon regulatory factor 9                   | IRF9 ISGF3G                         | Homo sapiens (Human) | 393    |



# IRF 家族

|    |  |     |        |            |
|----|--|-----|--------|------------|
| 1  | -----MALAPERAAPRVLFGEWLLGEISSGCYEGQLWLDEARTCFRVPWKHFARK      | 50  | Q92985 | IRF7_HUMAN |
| 1  | -----MNQSIPTVPTPPRRVRLKFWLVAQVNSCQYPGLQWVNGEKKLFCIPWRHATRH   | 53  | Q13568 | IRF5_HUMAN |
| 1  | MNLEGGGRGGEFGMSAVSCGNGLRQWLDIDQIDSGKYPGLWVNEEKSIFRIPWKHAGKQ  | 60  | Q15306 | IRF4_HUMAN |
| 1  | -----MCDRNGRRRLRQWLTIEQIDSSMYPGLWVNEEKSIFRIPWKHAGKQ          | 46  | Q02556 | IRF8_HUMAN |
| 1  | -----MASGRARCTRKLNRNWWVEQVESGQFPGVCWDDTAKTMFRIPWKHAGKQ       | 48  | Q00978 | IRF9_HUMAN |
| 1  | -----MALHPRRVRLKFWLVAQVDSGLYPGLIWLHRDSKRFQIPWKHATRH          | 46  | 014896 | IRF6_HUMAN |
| 1  | -----MPITRMRMRFPWLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKH           | 44  | P10914 | IRF1_HUMAN |
| 1  | -----MPVERMRMRFPWLEEQINSNTIPGLKWLNKEKKIFQIPWMMHAARH          | 44  | P14316 | IRF2_HUMAN |
| 1  | -----MGTPKPRILPWLVSQDLGLQLEGVAWVNKSRTFRIPWKHGLRQ             | 44  | Q14653 | IRF3_HUMAN |
|    | : * : : : * : * . * : * * : :                                |     |        |            |
|    |  |     |        |            |
| 51 | DLSE-ADARIFKAWAVARGRWPPSSRGGGPPPEAETAERAGWKTNFRCALRSTRRFVMLR | 109 | Q92985 | IRF7_HUMAN |
| 54 | GPSQDGDNTIFKAWAKETGKYTEGVD-----EADPAKWKANLRCALNKS RDFRLIY    | 104 | Q13568 | IRF5_HUMAN |
| 61 | DYNREEDAALFKAWALFKGKFRREGID-----KDPPTWKTRLRALNKSNDFEELV      | 111 | Q15306 | IRF4_HUMAN |
| 47 | DYNQEVDASIFKAWAVFKGKFKEG-D-----KAEPATWKTRLRALNKS P DFE EVT   | 96  | Q02556 | IRF8_HUMAN |
| 49 | DFREDQDAAFFKAWAIFKGKFKEG-D-----TGGPAVWKTRLRALNKSSEFKEVP      | 98  | Q00978 | IRF9_HUMAN |
| 47 | SPQEEENTIFKAWAVETGKYQEGVD-----DPDPKWKAKLRCALNKSREFNLMY       | 97  | 014896 | IRF6_HUMAN |
| 45 | GWDINKDACLFRSWAIHTGRYKAGEK-----EPDPKWKANFRFCAMNSLPDIEEVK     | 95  | P10914 | IRF1_HUMAN |
| 45 | GWDVEKDAPLFRNWAHTGKHQPGVD-----KDPKTKWKANFRFCAMNSLPDIEEVK     | 95  | P14316 | IRF2_HUMAN |
| 45 | DAQQ-EDFGIFQAWAEATGAYVPGRD-----KPDLPWKRNFRSALNRKEGLRLAE      | 94  | Q14653 | IRF3_HUMAN |
|    | : : * : * * * . * * : : * : * : :                            |     |        |            |





# 小结

- 利用实用生物信息学课上所学到数据库和软件对**IRF3**蛋白及其家族进行了初步分析，得到的结论和文献的结论是基本一致的。
- **IRF3**是非常保守的转录因子，在抗感染免疫中发挥重要作用。在小鼠、大鼠、猪、牛和人这五个物种中分析表明**IRF3**的氨基酸序列几乎一致，保守性很高。同时对其磷酸化位点进行了预测，和文献报道一致。
- **IRF**家族中，均含有非常保守的**DNA-binding**区域。





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PEKING UNIVERSITY

敬请各位老师同学批评指正

谢谢大家！