

斑马鱼*Tbx5* 及*Tbx*转录因子家族初步分析

第一组

2011年12月23日



斑马鱼 (*Danio Rerio*, 旧称*Brachydanio rerio*, 俗称Zebrafish) 原产于印度河流域的鲤科小型淡水热带鱼类。属于硬骨鱼类, 辐鳍纲

(*Actinopterygii*), 鲤形目 (*Cypriniformes*), 鲤科 (*Cyprinidae*), 鲇属 (*Danio*)。成鱼身长5厘米左右, 体形呈梭形, 从背部至腹部、臀鳍有多条蓝色横向条纹直达尾鳍, 满身条纹似斑马而得名。斑马鱼作为一种新兴的模式生物, 已经广泛运用于生命科学研究,

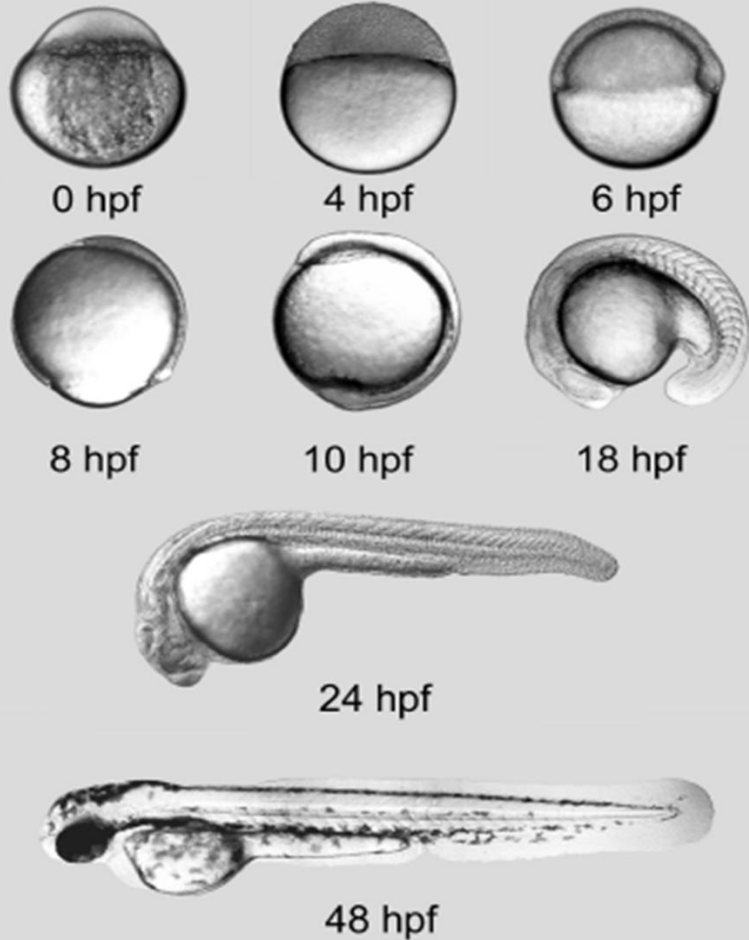
具有以下优势:

1、易于大规模饲养, 维持费用低。性成熟期短, 28℃条件下一般3个月左右可性成熟。

2、斑马鱼卵是体外受精和发育, 胚胎通体透明, 早期发育阶段在显微镜下可以观察到其整个发育状况, 显微注射等组织形态学实验。

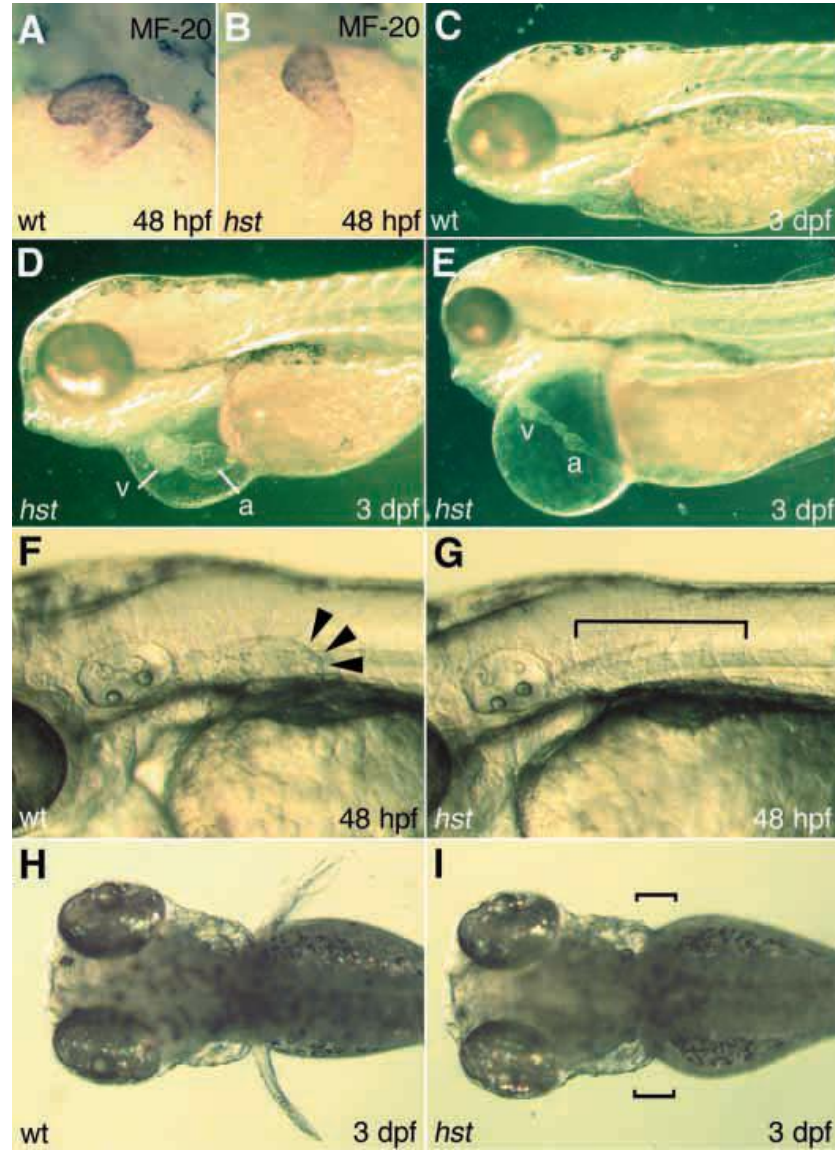
3、产卵量大, 雌鱼一次产卵可达几百枚, 产卵无季节性, 雌鱼可以每周产卵一次。

4、属于脊椎动物, 不仅具有与人类相似的消化、循环系统等结构。斑马鱼具有25对染色体, 基因组长度约19亿bp, 含有约20000个编码蛋白质的基因, 其全基因组测序工作已经接近完成。且基因与人类87%相似, 也具有许多无脊椎动物的特点。容易与其他模式生物及人进行跨物种比较研究。



斑马鱼Tbx5转录因子分析

Tbx5 转录因子功能



Mark C. Fishman etc. Development 129, 4635-4645 (2002)

斑马鱼Tbx5基因基本信息查询

Ensembl ^{AS1A} BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors Login · Register

Zebrafish (Zv9)

Ensembl ^{AS1A} BLAST/BLAT | BioMart | Tools | Downloads | Help & Documentation | Blog | Mirrors Login · Register

Zebrafish (Zv9)

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Zebrafish (Zv9)

Zebrafish (Zv9) Location: 5:75,451,438-75,476,894 Gene: **tbx5a**

- Gene-based displays**
- Gene summary
 - Splice variants (3)
 - Supporting evidence
 - Sequence
 - External references
 - Regulation
 - Comparative Genomics
 - Genomic alignments
 - Gene Tree (image)
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (53)**
 - Paralogues (22)
 - Protein families (1)
 - Phenotype
 - Genetic Variation
 - Variation Table
 - Variation Image
 - Structural Variation
 - External Data
 - Personal annotation
 - ID History
 - Gene history

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-
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Gene: tbx5a ENSDARG00000024894

Description T-box 5a [Source:ZFIN;Acc:ZDB-GENE-991124-7]
Location [Chromosome 5: 75,451,438-75,476,894](#) forward strand.
Transcripts This gene has 3 transcripts

Show/hide columns		Filter			
Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype
tbx5a-001	ENSDART00000037691	2059	ENSDARP00000033053	492	Protein coding
tbx5a-201	ENSDART00000037681	2054	ENSDARP00000033639	484	Protein coding
tbx5a-002	ENSDART00000114947	768	No protein product	-	Processed transcript

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 sequences and protein domain annotation.
- Gene views which provide displays for data associated at the gene level such as orthologues, paralogues, regulatory regions and splice variants.

This view is a gene level view. To access the transcript level displays select a Transcript ID in the table above and then navigate to the information you want using the menu at the left hand side of the page. To return to viewing gene level information click on the Gene tab in the menu bar at the top of the page.

Orthologues [help](#)

Summary of orthologues of this gene

Click on 'Show' to display the orthologues for one or more groups, or click on 'Configure this page' to choose a custom list of species

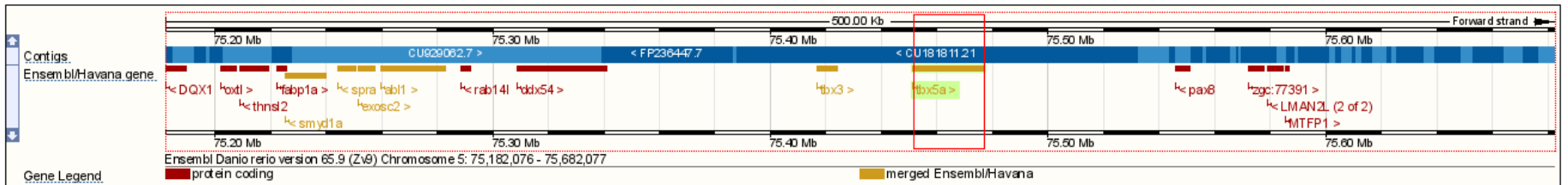
Species set	Show details	1:1	1:many	many:many	No orthologues
Primates Humans and other primates	<input type="checkbox"/>	10	0	0	0
Rodents Rodents, rabbits and related species	<input type="checkbox"/>	8	0	0	0
Laurasiatheria Carnivores, ungulates and insectivores	<input type="checkbox"/>	11	0	0	1
Placental Mammals All placental mammals	<input type="checkbox"/>	33	0	0	2
Sauropsida	<input type="checkbox"/>	4	0	0	0

Tbx5 基因结构

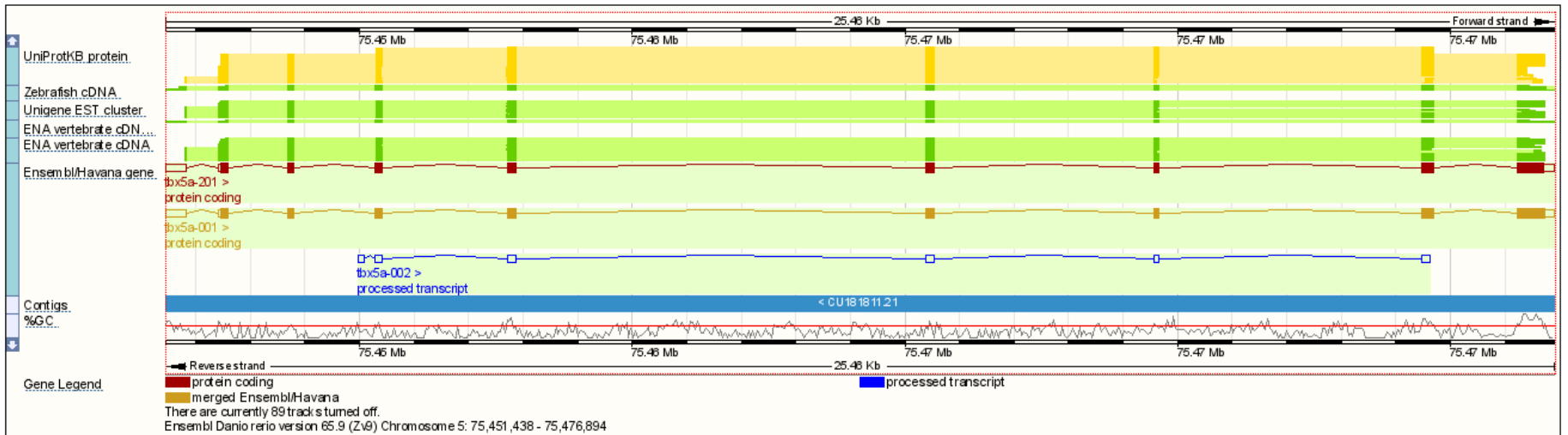
Chromosome 5: 75,451,438-75,476,894

chromosome 5 [Export Image](#)

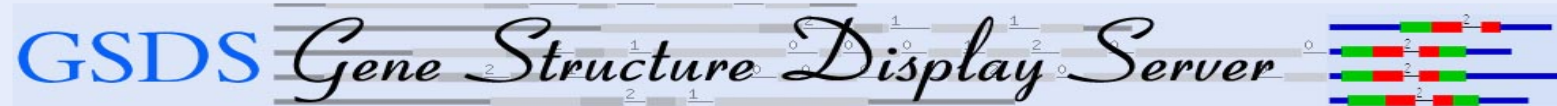
Region in detail [help](#)



Location: [Go](#) Gene: [Go](#)



利用GSDS显示Tbx5基因结构



Home By Sequence By GI By Site Help 中文

Gene Structure Display Server (GSDS) is a web server for drawing gene structure schematic diagram. GSDS can mark special regions (eg:domains) and intron phase in the displayed diagram. It can deal with batch genes once and the output graph is various including SVG format.

Users can choose to one of the following 3 data types:

- 1) CDS and genomic sequences
- 2) GenBank accession(s) or gi(s)
- 3) Exon Position and gene length

(required optional)

The CDS sequence and the genomic sequence of the same gene **must** use the **same sequence ID** in fasta file

CDS sequences (Fasta):

Genomic sequences (Fasta):

Load file: 未选择文件

Load file: 未选择文件

or paste data:

```
> T-box 5a (tbx5a), mRNA
TTCGCGCTTGGAAATATATTTATCAITCAAAGAGGGAAGTT
CGCTATCAACCCTAGTCTGGAAGTTGAT
ACGAGCITTTTAGGCTGTTTGTITGGTTGTTTAGGGATTC
GACCAGCGGGATCGGAAATTTAAGGCCTCAC
```

or paste data:

```
>chromosome:Zv9:5:75450838:75477494:1
ACTGAATAAGACTGAAATTTGGCCAGTCAAAAATCTAATAG
AGGTCTAGACATCAAAAACAG
ACGTTTGGCTAGAAATACTTAATGTGGGCAGTCGGTAAA
AATCTAATAGACCTCTAATA
```

Mark Special Region(s) (Format: ID start end)

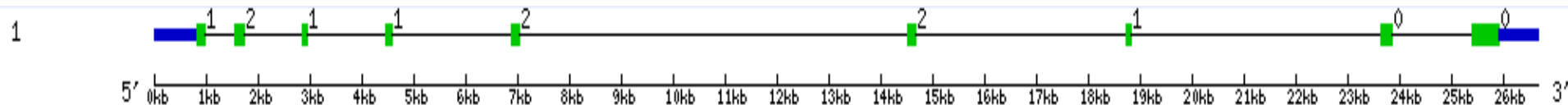
Output Order (sorted by IDs)

Image Format :

Image Color:

Intron Phase on Image:

Image Width: Pixels(500< Width <5000)



Legend:

exon marked region intron UTR intron phase

SMART数据库中Tbx5信息

SMART SETUP FAQ ABOUT GLOSSARY WHAT'S NEW FEEDBACK

Domains within *Danio rerio* protein B8JKS5_DANRE (B8JKS5)

T-box 5

TBOX domain ([go to full annotation](#))

Position: 52 to 242
E-value: 3.84e-128

Definition: Domain first found in the mice T locus (Brachyury) protein
Description: no definition

InterPro abstract (IPR001699):
Transcription factors of the T-box family are required both for early cell-fate decisions, such as those necessary for formation of the basic vertebrate body plan, and for differentiation and organogenesis [(PUBMED:12093383)]. The T-box is defined as the minimal region within the T-box protein that is both necessary and sufficient for sequence-specific DNA binding, all members of the family so far examined bind to the DNA consensus sequence TCACACCT. The T-box is a relatively large DNA-binding domain, generally comprising about a third of the entire protein (17-26 kDa).
These genes were uncovered on the basis of similarity to the DNA binding domain [(PUBMED:9504043)] of *Mus musculus* (Mouse) Brachyury (T) gene product, which similarity is the defining feature of the family. The Brachyury gene is named for its phenotype, which was identified 70 years ago as a mutant mouse strain with a short blunted tail. The gene, and its paralogues, have become a well-studied model for the family, and hence much of what is known about the T-box family is derived from the murine Brachyury gene.
Consistent with its nuclear location, Brachyury protein has a sequence-specific DNA-binding activity and can act as a transcriptional regulator [(PUBMED:9503012)]. Homozygous mutants for the gene undergo extensive developmental anomalies, thus rendering the mutation lethal [(PUBMED:9395282)]. The postulated role of Brachyury is as a transcription factor, regulating the specification and differentiation of posterior mesoderm during gastrulation in a dose-dependent manner [(PUBMED:9504043)].
T-box proteins tend to be expressed in specific organs or cell types, especially during development, and they are generally required for the development of those tissues, for example, Brachyury is expressed in posterior mesoderm and in the developing notochord, and it is required for the formation of these cells in mice [(PUBMED:9196325)].

Mouse over domain / undefined region for more info; click on it to go to detailed annotation; right-click to save whole protein as PNG image
Transmembrane segments as predicted by the *TMHMM2* program (■), coiled coil regions determined by the *Coils2* program (■), segments of low compositional complexity determined by the *SEG* program (■), Signal peptides determined by the *SignalP* program (■). Intron positions are indicated with vertical lines showing the intron phase and exact position in AA.

Protein information **Domain architecture analysis**
Display orthology and other data Display all proteins with similar domain ORGANISATION or COMPOSITION.
This domain architecture was probably invented with the emergence of Metazoa.

Interaction network

There are **996** TBOX domains in 984 proteins in SMART's nrdb database.

Click on the following links for more information.

- ▶ **Evolution** (species in which this domain is found)
- ▶ **Cellular role** (predicted cellular role)
- ▶ **Literature** (relevant references for this domain)
- ▶ **Disease** (disease genes where sequence variants are found in this domain)
- ▶ **Structure** (3D structures containing this domain)
- ▶ **Links** (links to other resources describing this domain)

蛋白质功能域识别网站SMART (<http://smart.embl-heidelberg.de/>)

OMIM疾病数据库中Tbx5的信息

Tbx5

Search

Sort by: Relevance Date updated

Advanced Search: [OMIM](#), [Clinical Synopses](#), [OMIM Gene Map](#) Display: [Toggle highlight](#)
Search History: [View](#), [Clear](#)

*601620

T-BOX 5; TBX5

HGNC Approved Gene Symbol: [TBX5](#)

Cytogenetic location: [12q24.21](#) Genomic coordinates (GRCh37): [12:114,791,734 - 114,846,246](#) (from NCBI)

Gene Phenotype Relationships

Location	Phenotype	Phenotype MIM number
12q24.21	Holt-Oram syndrome	142900

TEXT

Cloning

Holt-Oram syndrome (HOS; [142900](#)) is a developmental disorder affecting the heart and upper limbs. From linkage studies, the gene was known to be located on 12q21.3-q22. A translocation at 12q2 defined the interval containing the HOS locus ([Terrett et al., 1994](#)). Using exon trap analysis of genomic clones from this interval, [Li et al. \(1997\)](#) identified 2 developmentally expressed genes that are of the Brachyury (T) family. These genes share a common DNA-binding motif (T-box) and were designated TBX3 ([601621](#)) and [TBX5](#), in line with their mouse homologs.

[Basson et al. \(1997\)](#) refined the mapping of the HOS locus to 12q24.1 by fluorescence in situ hybridization using a cosmid containing D12S129, which was tightly linked to HOS. From the critical region they likewise isolated a gene with a high degree of homology to mouse [Tbx5](#) and identified several mutations in [TBX5](#) in affected members of HOS families.

Uniprot 蛋白数据库中Tbx5信息查询

UniProtKB > UniProtKB Downloads · Contact · Documentation/Help

Search Blast Align Retrieve ID Mapping *

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

7 results for **tbx5** AND **reviewed:yes** AND **gene:tbx5** in UniProtKB sorted by **score** descending

[Browse by taxonomy, keyword, gene ontology, enzyme class or pathway](#) | [Reduce sequence redundancy to 100%, 90% or 50%](#) [Download](#)

Page 1 of 1

Results [Customize](#)

> Restrict term "tbx5" to [gene name](#) (7), [protein name](#) (6)

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
<input checked="" type="checkbox"/> Q99593	TBX5_HUMAN	★	T-box transcription factor TBX5	TBX5	Homo sapiens (Human)	518
<input checked="" type="checkbox"/> P70326	TBX5_MOUSE	★	T-box transcription factor TBX5	Tbx5	Mus musculus (Mouse)	518
<input checked="" type="checkbox"/> Q9W7C2	TBX5_XENLA	★	T-box transcription factor TBX5	tbx5	Xenopus laevis (African clawed frog)	519
<input checked="" type="checkbox"/> Q9PWE8	TBX5_CHICK	★	T-box transcription factor TBX5	TBX5	Gallus gallus (Chicken)	521
<input checked="" type="checkbox"/> Q5I2P1	TBX5_RAT	★	T-box transcription factor TBX5	Tbx5	Rattus norvegicus (Rat)	517
<input checked="" type="checkbox"/> Q3SA47	TBX5_XENTR	★	T-box transcription factor TBX5	tbx5	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)	519
<input checked="" type="checkbox"/> Q9IAK8	TBX5A_DANRE	★	T-box transcription factor TBX5-A	tbx5a heartstrings hst tbx5 tbx5.1 si:ch211-245e21.2	Danio rerio (Zebrafish) (Brachydanio rerio)	492

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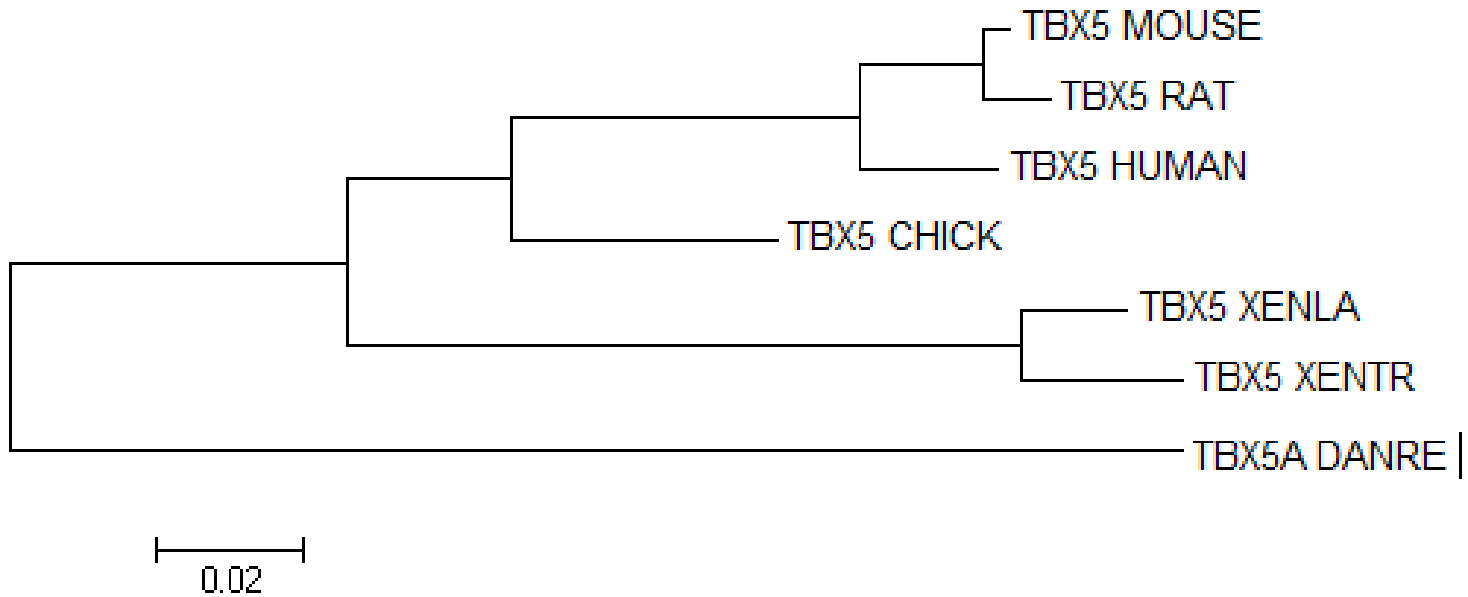
Sequence annotation (Features)

Feature key	Position(s)	Length	Description	Graphical view	Feature identifier
Molecule processing					
<input type="checkbox"/> Chain	1 - 492	492	T-box transcription factor TBX5-A		PRO_0000262468
Regions					
<input type="checkbox"/> DNA binding	62 - 237	176	T-box		
<input type="checkbox"/> Compositional bias	343 - 346	4	Poly-Ser		

7个物种Tbx5蛋白序列对比

1	MADTEEAYGMPDTPVEAEPKELQCEPKQDNQLGASSKTPTSPQAAFTQQGMEGIKVF LHE	60	Q9W7C2	TBX5_XENLA
1	MADTEEAYGMPDTPVEAEPKELQCEPKQDNQMGASSKTPTSPQAAFTQQGMEGIKVF LHE	60	Q3SA47	TBX5_XENTR
1	MADTDEEGFLARTPLEPDSKDRSCDKPESALGAPSKSPSSPQAAFTQQGMEGIKVF LHE	60	P70326	TBX5_MOUSE
1	MADADEEGFLARTPLEPDSKDRSCDKPESALGAPSKSPSSPQAAFTQQGMEGIKVF LHE	60	Q5I2P1	TBX5_RAT
1	MADADEEGFLARTPLEPDAKDLPCDSKPEALGAPSKSPSSPQAAFTQQGMEGIKVF LHE	60	Q99593	TBX5_HUMAN
1	MADTEEGFLPSTPVDSEAKELQAEAKQDPQLGTTSKAPTSPQAAFTQQGMEGIKVF LHE	60	Q9PW68	TBX5_CHICK
1	MADSEDTFRLQNSPDSSEPKDLQNEGSKDKQNAAVSKSPSS-QTTYIQQGMEGIKVF LHE	59	Q9IAK8	TBX5A_DANRE
	::: : : * : : : * : : : **:* * : : **:***			
61	RELWLKFEVGTETMIITKAGRRMFP SYKVKVTGLNPKTKYILLMDIVPADDHRYKFA DNK	120	Q9W7C2	TBX5_XENLA
61	RELWLKFEVGTETMIITKAGRRMFP SYKVKVTGLNPKTKYILLMDIVPADDHRYKFA DNK	120	Q3SA47	TBX5_XENTR
61	RELWLKFEVGTETMIITKAGRRMFP SYKVKVTGLNPKTKYILLMDIVPADDHRYKFA DNK	120	P70326	TBX5_MOUSE
61	RELWLKFEVGTETMIITKAGRRMFP SYKVKVTGLNPKTKYILLMDIVPADDHRYKFA DNK	120	Q5I2P1	TBX5_RAT
61	RELWLKFEVGTETMIITKAGRRMFP SYKVKVTGLNPKTKYILLMDIVPADDHRYKFA DNK	120	Q99593	TBX5_HUMAN
61	RELWLKFEVGTETMIITKAGRRMFP SYKVKVTGLNPKTKYILLMDIVPADDHRYKFA DNK	120	Q9PW68	TBX5_CHICK
60	RELWTKFEVGTETMIITKAGRRMFP SFKVKVTGLNPKTKYILLMDVVPADDHRYKFA DNK	119	Q9IAK8	TBX5A_DANRE
	**** *****:****:*****:*****:*****:*****			
121	WSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLV SFQKLKLTNNHLDPPFGHITLNSMHKYQ	180	Q9W7C2	TBX5_XENLA
121	WSVTGKAEPAMPGRLYVHPDSPATGTHWMRQLV SSQKLKLTNNHLDPPFGHITLNSMHKYQ	180	Q3SA47	TBX5_XENTR
121	WSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLV SFQKLKLTNNHLDPPFGHITLNSMHKYQ	180	P70326	TBX5_MOUSE
121	WSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLV SFQKLKLTNNHLDPPFGHITLNSMHKYQ	180	Q5I2P1	TBX5_RAT
121	WSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLV SFQKLKLTNNHLDPPFGHITLNSMHKYQ	180	Q99593	TBX5_HUMAN
121	WSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLV SFQKLKLTNNHLDPPFGHITLNSMHKYQ	180	Q9PW68	TBX5_CHICK
120	WSVTGKAEPAMPGRLYVHPDSPATGAHWMRQLV SFQKLKLTNNHLDPPFGHITLNSMHKYQ	179	Q9IAK8	TBX5A_DANRE
	*****:***** *****:*****:*****:*****:*****			
181	PRLHIVKADENNGFGSKNTAFCTHVFPSETDFIAVTSYQNHKITQLKIENNPFAKGFRGSD	240	Q9W7C2	TBX5_XENLA
181	PRLHIVKADENNGFGSKNTAFCTHVFPSETAFIAATS YQNHKITQLKIENNPFAKGFRGSD	240	Q3SA47	TBX5_XENTR
181	PRLHIVKADENNGFGSKNTAFCTHVFPETAFAIAVTSYQNHKITQLKIENNPFAKGFRGSD	240	P70326	TBX5_MOUSE
181	PRLHIVKADENNGFGSKNTAFCTHVFPETAFAIAVTSYQNHKITQLKIENNPFAKGFRGSD	240	Q5I2P1	TBX5_RAT
181	PRLHIVKADENNGFGSKNTAFCTHVFPETAFAIAVTSYQNHKITQLKIENNPFAKGFRGSD	240	Q99593	TBX5_HUMAN
181	PRLHIVKADENNGFGSKNTAFCTHVFPETAFAIAVTSYQNHKITQLKIENNPFAKGFRGSD	240	Q9PW68	TBX5_CHICK
180	PRHIVKADENNGFGSKNTAFCTHVFPETAFAIAVTSYQNHKITQLKIENNPFAKGFRGSD	239	Q9IAK8	TBX5A_DANRE
	:* ***:*** ***, *****:*****:*****			
241	DMELHRMSRMQS-KEYPVVPRSTVRQKVSSNHSPFSQETR NITGSSTLNSQYQCENGVSS	299	Q9W7C2	TBX5_XENLA
241	DMELHRMSRMQS-KEYPVVPRSTVRQKVSSNHSPFSQETR NITGSSTLNSQYQCENGVSS	299	Q3SA47	TBX5_XENTR
241	DLELHRMSRMQS-KEYPVVPRSTVRHKVTSNHSPFSSETRALSTSSNLGSQYQCENGVSG	299	P70326	TBX5_MOUSE
241	DLELHRMSRMQS-KEYPVVPRSTVRHKVAN-HSPFSSETRALSTSSNLGSQYQCENGVSG	298	Q5I2P1	TBX5_RAT
241	DMELHRMSRMQS-KEYPVVPRSTVRQKVASNHSPFSSETRALSTSSNLGSQYQCENGVSG	299	Q99593	TBX5_HUMAN
241	DMELHRMSRMQS-KEYPVVPRSTVRQKVSSNHSPFSQETR VLSTSSNLGSQYQCENGVSS	299	Q9PW68	TBX5_CHICK
240	DMELHRMSRMQSTKEYPVVPRSTVRQRVGSSQSPFSGDVQGLSASGAISSQYSCENGVSS	299	Q9IAK8	TBX5A_DANRE
	*:*****:* *****:*. . .*** : : : * . .***.*****			

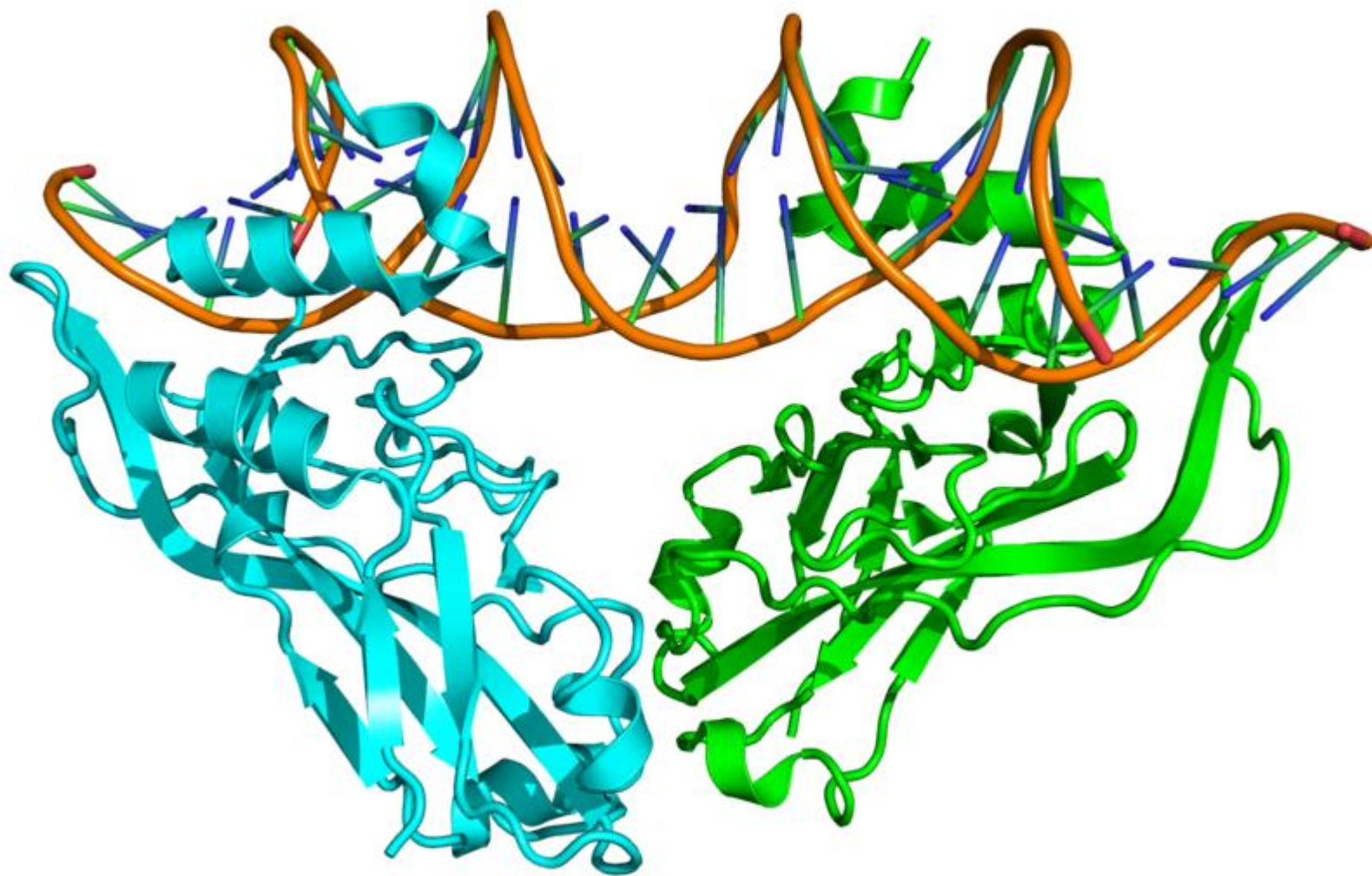
Tbx5 构建系统发育树



TBX5蛋白3D结构



TBX5蛋白结合DNA的3D结构



与Tbx5有相互作用的蛋白



斑马鱼**Tbx**基因家族分析

在斑马鱼数据库中检索Tbx家族



Site Search:

Home Genes / Markers / Clones BLAST GBrowse Expression Antibodies Mutants / Morphants / Tg Anatomy Publications Maps

Gene Search Results (17 records)

Your Input Welcome

Show genes with mutant(s)

Symbol - name	Expression	Phenotype	Map	Matching Text
<i>tbr1a</i> -T-box, brain, 1a	6 figures			Current name: T-box , brain, 1a
<i>tbr1b</i> -T-box, brain, 1b	12 figures		LG: 20 Details View Map: Merged Individual Panels	Current name: T-box , brain, 1b
<i>tbx1</i> -T-box 1	24 figures	26 figures MO	LG: 5 Details View Map: Merged Individual Panels	Current name: T-box 1
<i>tbx2a</i> -T-box gene 2a	7 figures	1 figure MO	LG: 5 Details	Current name: T-box gene 2a
<i>tbx2b</i> -T-box 2b	31 figures	10 figures MO	LG: 15 Details	Current name: T-box 2b
<i>tbx3</i> -T-box 3	2 figures	2 figures MO		Current name: T-box 3
<i>tbx4</i> -T-box 4	2 figures		LG: 15 Details View Map: Merged Individual Panels	Current name: T-box 4
<i>tbx5a</i> -T-box 5a	90 figures	17 figures MO	LG: 5 Details View Map: Merged Individual Panels	Current name: T-box 5a
<i>tbx5b</i> -T-box 5b	2 figures		LG: 5 Details	Current name: T-box 5b
<i>tbx6</i> -T-box gene 6	21 figures	15 figures MO	LG: 12 Details	Current name: T-box gene 6
<i>tbx6l</i> -T-box gene 6-like	43 figures		LG: 5, 7 Details View Map: Merged Individual Panels	Current name: T-box gene 6-like
<i>tbx15</i> -T-box 15	1 figure			Current name: T-box 15
<i>tbx16</i> -T-box gene 16	55 figures	14 figures MO	LG: 8 Details View Map: Merged Individual Panels	Current name: T-box gene 16
<i>tbx18</i> -T-box 18	12 figures		LG: 23 Details	Current name: T-box 18
<i>tbx20</i> -T-box 20	35 figures	4 figures MO	LG: 16 Details View Map: Merged Individual Panels	Current name: T-box 20
<i>tbx21</i> -T-box 21	2 figures		LG: 12 Details	Current name: T-box 21
<i>tbx22</i> -T-box 22	3 figures		LG: 14 Details	Current name: T-box 22

Modify your search.

斑马鱼数据库（www.zfin.org）中，输入Tbx查找得到17个条目，其中前两个不属于Tbx基因家族。

在斑马鱼Tbx家族信息

亚家族	基因名	RefSeq ID	mRNA	Gene	protein
Tbx1	Tbx1	NM_183339	2369	283397	460
	Tbx15	NM_153664	3023	151210	620
	Tbx18	NM_153665	2346	182686	554
	Tbx20	NM_131506	2134	144859	446
	Tbx22	NM_001164461	1969	203705	444
Tbx2	Tbx2b	NM_131051	2628	149122	687
	Tbx3	NM_001101670	3872	144158	689
	Tbx4	NM_130914	2236	149122	543
	Tbx5a	NM_130915	2590	144158	492
	Tbx5b	NM_001198771	1353	86752	422
Tbx6	Tbx6	NM_153666	3068	157568	874
	Tbx16	NM_131058	2561	101559	470

在Uniprot蛋白质数据库中检索Tbx家族

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Search Blast Align Retrieve ID Mapping *

Search in Protein Knowledgebase (UniProtKB) Query Tbx AND organism:zebrafish AND gene:tbx* Search Advanced Search » Clear

1 - 25 of 38 results for Tbx AND organism:zebrafish AND gene:tbx* in UniProtKB sorted by score descending

Browse by taxonomy, keyword, gene ontology, enzyme class or pathway | Reduce sequence redundancy to 100%, 90% or 50%

Page 1 of 2 | Next

Results Customize

- Show only reviewed (5) (UniProtKB/Swiss-Prot) or unreviewed (33) (UniProtKB/TrEMBL) entries
- Restrict term "tbx" to gene name (38), protein name (18)
- Show only entries from a Reference proteome set (16) or complete proteome set (16)

Entry	Entry name	Status	Protein names	Gene names	Organism	Length
<input type="checkbox"/> Q7ZTU9	TBX2_DANRE	★	T-box transcription factor TBX2b	tbx2b tbx-c	Danio rerio (Zebrafish) (Brachydanio rerio)	687
<input type="checkbox"/> Q8AXX2	TBX1_DANRE	★	T-box transcription factor TBX1	tbx1 zgc:136724	Danio rerio (Zebrafish) (Brachydanio rerio)	460
<input type="checkbox"/> Q9IAK8	TBX5A_DANRE	★	T-box transcription factor TBX5-A	tbx5a heartstrings hst tbx5 tbx5.1 si:ch211-245e21.2	Danio rerio (Zebrafish) (Brachydanio rerio)	492
<input type="checkbox"/> P79742	TBX6_DANRE	★	T-box transcription factor TBX6	tbx6	Danio rerio (Zebrafish) (Brachydanio rerio)	473
<input type="checkbox"/> Q9I9K7	TBX20_DANRE	★	T-box transcription factor TBX20	tbx20	Danio rerio (Zebrafish) (Brachydanio rerio)	446
<input type="checkbox"/> Q8JIS6	Q8JIS6_DANRE	★	Tbx24	tbx24	Danio rerio (Zebrafish) (Brachydanio rerio)	874
<input type="checkbox"/> A7MCH8	A7MCH8_DANRE	★	Tbx2a protein	tbx2a	Danio rerio (Zebrafish) (Brachydanio rerio)	287
<input type="checkbox"/> A2RUW2	A2RUW2_DANRE	★	Tbx3b protein	tbx3 tbx3b zgc:158110	Danio rerio (Zebrafish) (Brachydanio rerio)	689
<input type="checkbox"/> Q29R85	Q29R85_DANRE	★	Tbx3b protein	tbx3 tbx3b zgc:158110	Danio rerio (Zebrafish) (Brachydanio rerio)	279
<input type="checkbox"/> A8WGS2	A8WGS2_DANRE	★	Tbx18 protein	tbx18	Danio rerio (Zebrafish) (Brachydanio rerio)	494
<input type="checkbox"/> Q9PUS8	Q9PUS8_DANRE	★	T-box transcription factor Tbx4	tbx4	Danio rerio (Zebrafish) (Brachydanio rerio)	87
<input type="checkbox"/> A1A5U2	A1A5U2_DANRE	★	Tbx15 protein	tbx15	Danio rerio (Zebrafish) (Brachydanio rerio)	616
<input type="checkbox"/> Q7SYC5	Q7SYC5_DANRE	★	Tbx15 protein	tbx15	Danio rerio (Zebrafish) (Brachydanio rerio)	171
<input type="checkbox"/> Q8JIR5	Q8JIR5_DANRE	★	Tbx24 protein	tbx24 Dr. 83300	Danio rerio (Zebrafish) (Brachydanio rerio)	874

共找到38个条目，其中reviewed有5个。除去重复和序列不完整的。共有16个TBX蛋白的信息。

斑马鱼Tbx蛋白信息

Entry	Entry name	Protein names	Gene names	Length
Q8AXX2	TBX1_DANRE	T-box transcription factor TBX1 (T-box protein 1)	tbx1	460
Q9I9K7	TBX20_DANRE	T-box transcription factor TBX20 (T-box protein 20) (H15-related T-box transcription factor hrT)	tbx20	446
Q7ZTU9	TBX2_DANRE	T-box transcription factor TBX2b (T-box protein 2b)	tbx2b	687
Q9IAK8	TBX5A_DANRE	T-box transcription factor TBX5a (zftbx5a) (T-box protein 5) (zTbx5)	tbx5a	492
P79742	TBX6_DANRE	T-box transcription factor TBX6 (T-box protein 6)	tbx6	473
B3DJF0	B3DJF0_DANRE	T-box 18 (Uncharacterized protein)	tbx18	554
B8JL25	B8JL25_DANRE	T-box gene 16 (Uncharacterized protein)	tbx16	470
E3W6T6	E3W6T6_DANRE	T-box transcription factor 5b (Tbx5b transcription factor)	tbx5b	422
Q8JIR5	Q8JIR5_DANRE	Tbx24 protein (Uncharacterized protein)	tbx24	874
D1YT98	D1YT98_DANRE	T-box 21 like (Uncharacterized protein)	tbx21	609
Q8JFF9	Q8JFF9_DANRE	T-box containing transcription factor	tbx18	554
Q6NV02	Q6NV02_DANRE	T-box gene 2a	tbx2a	676
Q8JFF8	Q8JFF8_DANRE	T-box containing transcription factor	tbx15	620
A2RUW2	A2RUW2_DANRE	Tbx3b protein	tbx3	689
Q9IAK9	Q9IAK9_DANRE	T-box transcription factor tbx4	tbx4	543
C7FDJ3	C7FDJ3_DANRE	Transcription factor Tbx22-1	tbx22	444

Tbx1亚家族的成员序列比对结果

1	MEYTSSPKPQLSSRANAFSIAALMSSGKTK--DKESEENTIKPLEQFVEKS-SCHPNLGD	57	Q9I9K7	TBX20_DANRE
1	MAEKRRSPCTMSLKAHAFSVEALIGTEKKRKLSEEDSENCFEEINEVPRMTESPQPSTGR	60	Q8JFF9	Q8JFF9_DANRE
1	-MISAISSPWLTLQSHFCDVAFFTSSLSSLNTPGSYHLSPSPGDPYSHHESQFEPCPAA	59	Q8AXX2	TBX1_DANRE
	. . : : . : * : : . . . : . . . * .			
58	LPPLETHSDFSSGGGTGSG-----APLCTEPLIPTTPGVPSEEMAKISCSLETKE	110	Q9I9K7	TBX20_DANRE
61	TCPSTRSCEIDCTSDESPEPEDVLLDSPQPASQGAQVLVQSATSSGEEMRVDLQGSDLWK	120	Q8JFF9	Q8JFF9_DANRE
60	QHAYNYSGSNSAQAPAQGD SGTSNCS SSSSSSSTPNKTLVKK-NPKVANINVQLEMKAL	118	Q8AXX2	TBX1_DANRE
 : : . . . : : . * : . **.			
111	KFHELGTETMIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIVPVDNKRYRYAYHRSSWL	170	Q9I9K7	TBX20_DANRE
121	RFHEIGTETMIITKAGRRMFPPAMRVKIAGLDPHQYYIAMDIVPVDNKRYRYVYHSSKWMV	180	Q8JFF9	Q8JFF9_DANRE
119	EFNQLGTETMIVTKAGRRMFPTFQVKIFGMDPMADYMLLMDFLPVDDKRYRYAFHSSSWLV	178	Q8AXX2	TBX1_DANRE
	. * : : : * : : * : : * : : * : : * : : * : : * : : * : : * : : * : : *			
171	AGKADPPLPARLYVHPDSPFTGEQLLQMVSEFKVCLTNNELDQHGHIILNSMHKYQPRV	230	Q9I9K7	TBX20_DANRE
181	AGNADSPVPPRVYIHPDSPASGETWVRQVIFDKLKL TNNELDDQGHIILNSMHKYQPRV	240	Q8JFF9	Q8JFF9_DANRE
179	AGKADPATPGRVHYHPDSPA KGAQWMKQIVSFDK LKL TNLLDDNGHIILNSMHRYQPRF	238	Q8AXX2	TBX1_DANRE
	** : * . . * * : : * : : * . * : : : * : : * : : * : : * : : * : : * .			
231	HI IKKKD---HTASLLNLKSEEFRTFVFTETVFTA VTA VYQNQLITRLKIDSNPFAKGFRD	287	Q9I9K7	TBX20_DANRE
241	HVIRKECGEELSPVKAVPTGDGVKAFSFTETVFTT VTA VYQNQQITRLKIDRNPFAGFRD	300	Q8JFF9	Q8JFF9_DANRE
239	HVVYVDP---RKDSEKYAEENYKTFVFEETRFTA VTA VYQNHRTQLKIASNPFAKGFRD	294	Q8AXX2	TBX1_DANRE
	* : : . : : * * * * * : : * : : * : : * : : * : : * : : * : : * : : * : : *			

Tbx2亚家族的成员序列比对结果

1	MRDPVFTGTAMAYHPFHAHRPTDFPMSAFLAAAQPSFFPALTLPPGA-----LTKPIP	53	Q7ZTU9	TBX2_DANRE	← Tbx2b
1	-----MAYHPFHAHRPADFPMSAFLAAAQPSFFPALTLPPG-----LSKPLA	42	Q6NV02	Q6NV02_DANRE	← Tbx2a
1	MRDPVIQGSSMAYHPFLPHRGPEFAMSAMLG-HQPPFPALALPPNGSLSLPGALGKPIIM	59	A2RUW2	A2RUW2_DANRE	← Tbx3
1	-----MADSEDTFRLQNSPDSSE-----	18	Q9IAK8	TBX5A_DANRE	← Tbx5a
1	-----MLQEKASVVADEGMTVAQ-----	18	B3DGX3	B3DGX3_DANRE	← Tbx4
	: : .				
54	DHTLAGAAEAGLHPALSHHHQAAHLRSLKSLPEEEEEVEDDPKVITLEAKDLWDQFHKLGTE	113	Q7ZTU9	TBX2_DANRE	
43	DHALSGAAEAGLHAALGHHHQAHLRSFKGLEPEEDVEDDPKVITLEAKELWDQFHKIGTE	102	Q6NV02	Q6NV02_DANRE	
60	EQ-LMGAAETGLHFSS-LGHQAAHLRPLKTLPEEEEEVEDDPKVHLEAKELWELFHKRGTE	117	A2RUW2	A2RUW2_DANRE	
19	----PKDLQNEGKSDKQNAAVSKSPSS-QTTYIQQGMEG- IKVYLHERE LWTKFHEVGTE	72	Q9IAK8	TBX5A_DANRE	
19	----SGGRP-ELASDSSHLGLPTTPSNPQNNPEPQSIEN- IKVVLHRELWKKFHEAGTE	72	B3DGX3	B3DGX3_DANRE	
	. : : * . * . : * * * * * * * * * *				
114	MVITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYKFHNSRWMVAGKADPEMPK	173	Q7ZTU9	TBX2_DANRE	
103	MVITKSGRRMFPPFKVRVNGLDKKAKYILLMDIVAADDCRYKFHNSRWMVAGKADPEMPK	162	Q6NV02	Q6NV02_DANRE	
118	MVITKSGRRMFPPFKVRCTGLDKKAKYILLMDIVAADDCRYKFHNSRWMVAGKADPEMPK	177	A2RUW2	A2RUW2_DANRE	
73	MIITKAGRRMFPSFKVKVTGLNPKTKYILLMDVVPADHRYKFADNKWSVTGKAEPAMPG	132	Q9IAK8	TBX5A_DANRE	
73	MIITKAGRRMFPSYKVKVTGMNPKTKYILLTDIVPADHRYKFCDNKWMVAGKAEPAEPAMPG	132	B3DGX3	B3DGX3_DANRE	
	:				
174	RMYIHPDSPATGEQWMAKPVAFHKLKLTNNISDKHGFITLNSMHKYQPRFHIVRAN--DI	231	Q7ZTU9	TBX2_DANRE	
163	RMYIHPDSPATGEQWMAKPVAFHKLKLTNNISDKHGFITLNSMHKYQPRFHIVRAN--DI	220	Q6NV02	Q6NV02_DANRE	
178	RMYIHPDSPATGEQWMSKVVFHKLKLTNNISDKHGFITLNSMHKYQPRFHIVRAN--DI	235	A2RUW2	A2RUW2_DANRE	
133	RLYVHPDSPATGAHWMRQLVSPQKLLKLTNNHLDPFPGHILNSMHKYQPRIHIVKADENNG	192	Q9IAK8	TBX5A_DANRE	
133	RLYVHPDSPATGAHWMRQLVSPQKLLKLTNNHLDPFPGHILNSMHKYQPRLHIVKADENNA	192	B3DGX3	B3DGX3_DANRE	
	:				
232	LKLPYSTFRITYVFPETDFIAVTAYQNDKITQLKIDNPNFAKGFRTGNGRREKRKQLTLP	291	Q7ZTU9	TBX2_DANRE	
221	LKLPYSTFRITYVFPETDFIAVTAYQNDKITQLKIDNPNFAKGFRTGNGRREKRKQLAMP	280	Q6NV02	Q6NV02_DANRE	
236	LKLPYSTFRITYVFPETDFIAVTAYQNDKITQLKIDHNPFAKGFRTGNGRREKRKQLALQ	295	A2RUW2	A2RUW2_DANRE	
193	FGSKNTAFCTHVPETAFIAVTSYQNHKITQLKIENPNFAKGFRTGSDMELHRMSRMQST	252	Q9IAK8	TBX5A_DANRE	
193	FGSKNTAYCTHVPETAFISVTSYQNHKITQLKIENPNFAKGFRTGSDMELHRMSRMQST	250	B3DGX3	B3DGX3_DANRE	
	: : *:* *				

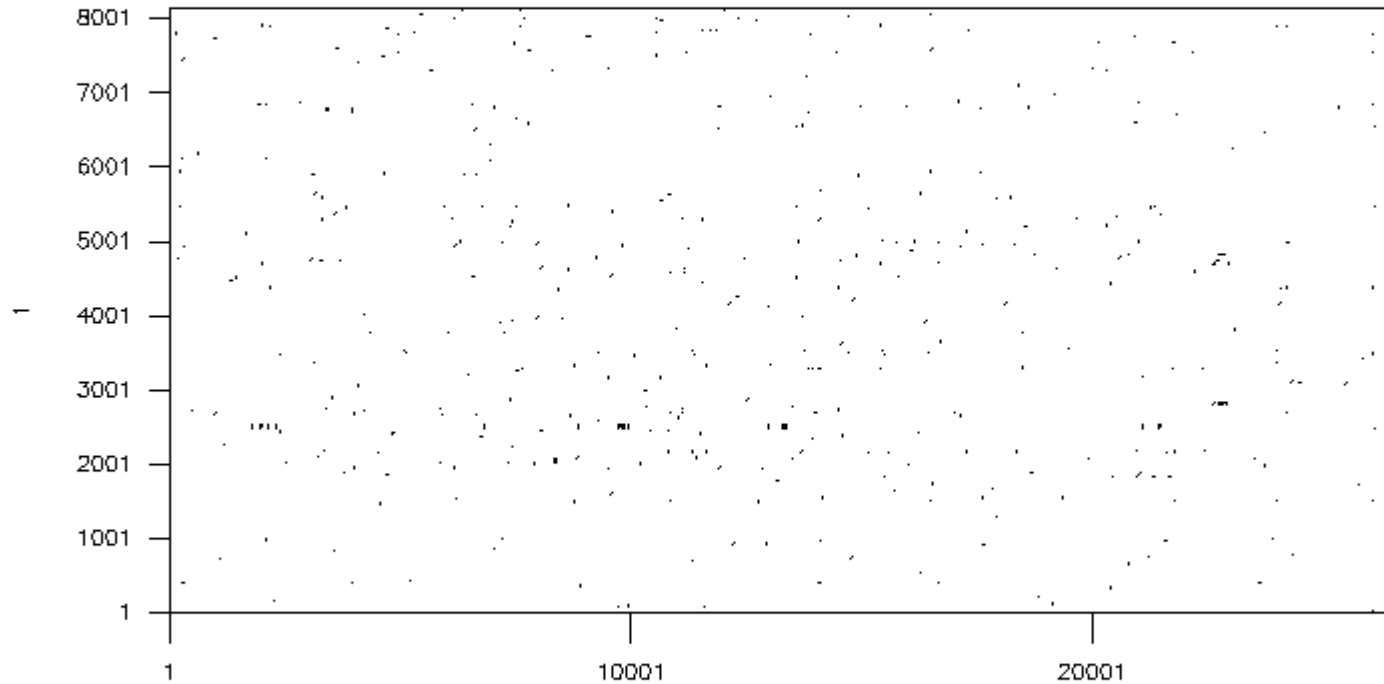
Tbx家族的成员序列比对结果

30	-----KQNAAVSKSPSSQTTYIQQMGEG- IKVYLHERE LW	63	Q9IAK8	TBX5A_DANRE
30	-----HHGRNKTGSPPLQTLQSQSMEG- IKVYLHEKDLW	63	E3W6T6	E3W6T6_DANRE
31	-----HLGLPTTPSNP-QNNEPDQSIEN- IKVVLHDRELW	63	Q9IAK9	Q9IAK9_DANRE
46	-GALTKP IPDHTLAGAAEAGLHPAL SHHHQAAHLRSLKSLPEEEVEEDDPKVTLLEAKD LW	104	Q7ZTU9	TBX2_DANRE
51	PGALGKP IMEQ-LMGAAETGLHFS- SLGHQAAHLRPLKLEPEEEVEEDDPKVHLEAKELW	108	A2RUW2	A2RUW2_DANRE
58	LPPLETHSDFSSGGGTGSG-----APLCTEPLIPTTPGWPSEEMAK- ICSLETKE LW	109	Q9I9K7	TBX20_DANRE
61	TCPSTRSCEIDCTSDESPEPEDVLLDSPQPASQGAQVLVQSATSSGEE-MRVDLQGSIDLW	119	Q8JFF9	Q8JFF9_DANRE
60	QHAYNYSGSNSAQAPAQGDSTNCSSSSSSSTPNKTLVKK-NPKVAN- INVQLEMKALW	117	Q8AXX2	TBX1_DANRE
10	-----YYPQDCRTQYSRMNSAEELTSLPVHVSLQDRELW	44	P79742	TBX6_DANRE
	* . **			
64	TKFHVEVGTETMIITKAGRRMFPSFKVKVTGLNPKTKYILLMDVVPADDHRYKFADN--KWS	121	Q9IAK8	TBX5A_DANRE
64	AKFHDVITETMIITKAGRRMFPSYKVKVTGLNPKAKYILLMDIISADEHRYKFADN--KWS	121	E3W6T6	E3W6T6_DANRE
64	KKLHEAGTETMIITKAGRRMFPSYKVKVTGMNPKTKYILLTDIVPADDHRYKFCDN--KWM	121	Q9IAK9	Q9IAK9_DANRE
105	DQFHKLCTEMVITKSGRRMFPPFKVRINGLDKKAKYILLMDIVAADDCRYKPHNS--RWM	162	Q7ZTU9	TBX2_DANRE
109	ELFHKRGTETMIITKSGRRMFPPFKVRCITGLDKKAKYILLMDIVAADDCRYKPHNS--RWM	166	A2RUW2	A2RUW2_DANRE
110	DKFHELCTEMLIITKSGRRMFPTIRVSFSGVDPDAKYIVLMDIVPVDNKKRYRYAYHRSSWL	169	Q9I9K7	TBX20_DANRE
120	KRFHEIGTETMIITKAGRRMFAMRVKIAGLDPHQYYIAMDIVPVDNKKRYRYVYHSSKWM	179	Q8JFF9	Q8JFF9_DANRE
118	DEFNQLCTEMIVTKAGRRMFPTQVKIFGMDPMADYMLLMDFLPVDNKKRYRYAFHSSSWL	177	Q8AXX2	TBX1_DANRE
45	DKFPSSIGTETMLITKSGRRMFPSCKVTVTGLNPKVKYVYVIMDMVFPDNNHKYKWNKD--CWE	102	P79742	TBX6_DANRE
	: . ***::*:***** :* *:: .* : *. : *::**			
122	VTGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKCLKLNNHLDPFPGHIIILNSMHKYQPR	181	Q9IAK8	TBX5A_DANRE
122	ISGKAEPaipGRLYVHPDSPASGAHWMRQLVSFQKCLKLNNHLDPFPGHIIILNSMHKYQPR	181	E3W6T6	E3W6T6_DANRE
122	VAGKAEPAMPGRLYVHPDSPATGAHWMRQLVSFQKCLKLNNHLDPFPGHIIILNSMHKYQPR	181	Q9IAK9	Q9IAK9_DANRE
163	VAGKADPEMPKRMYPHPDSPATGEBQWMAKPVAFHKLKLTNNISDKHGFTILNSMHKYQPR	222	Q7ZTU9	TBX2_DANRE
167	VAGKADPEMPKRMYPHPDSPATGEBQWMSKVVNFHKLKLTNNISDKHGFTILNSMHKYQPR	226	A2RUW2	A2RUW2_DANRE
170	VAGKADPPLPARLYVHPDSPFTGELLQKQMVSEFKVKLTNNELDQHGHIILNSMHKYQPR	229	Q9I9K7	TBX20_DANRE
180	VAGNADSPVPPRVYIHPDSPASGETWMRQVISFDKCLKLTNNELDQHGHIILNSMHKYQPR	239	Q8JFF9	Q8JFF9_DANRE
178	VAGKADPATPCRVHYHPDSPAAGAQWMMQIVSFDKCLKLTNNLLDDNGHIIILNSMHRVQPR	237	Q8AXX2	TBX1_DANRE
103	VNGSSDPHLNRRFFIHPDSPAPGQKQWQYPIFSHKLKLTNNLTNSNGLVVLHSMHYQPR	162	P79742	TBX6_DANRE
	: *::: * * . ***** * : : * * :***** : * :*:***:*****			
182	IHIVKADE----NNGFGSKNTAFCTHVPETAFIAVTSYQNHKITQLKIENPFARGFR	236	Q9IAK8	TBX5A_DANRE
182	LHIVKADE----RNSFGSSNTSFCTHSFAETTFIAVTSYQNHKITQLKIENPFARGFR	236	E3W6T6	E3W6T6_DANRE
182	LHIVKADE----NNAFGSKNTAYCTHVFHETAFISVTSYQNHKITQLKIENPFARGFR	236	Q9IAK9	Q9IAK9_DANRE
223	FHIVRAN-----DILKLPYSTIFRTYVFPETDFIAVTAYQNDKITQLKIDNPNFARGFR	275	Q7ZTU9	TBX2_DANRE
227	FHIVRAN-----DILKLPYSTIFRTYVFPETDFIAVTAYQNDKITQLKIDHNPARGFR	279	A2RUW2	A2RUW2_DANRE
230	VHI IKKD---HTASLLNLKSEEFRTFVFTEVFTAHTAYQNQLITRLKIDSNPFARGFR	286	Q9I9K7	TBX20_DANRE
240	VHVIRKECGEELSPYKAVPTGDGWKAFSFTETVFTVTAAYQNQLITRLKIDRNPARGFR	299	Q8JFF9	Q8JFF9_DANRE
238	FHVYVYVDP----RKDSEKYAEENYKTFVFEETRFTAHTAYQNHRITQLKIASNPFARGFR	293	Q8AXX2	TBX1_DANRE
163	LHIVQSPD-----PCTPHNPGAYLRFITFPEAAFIAVTAYQNQEITKLKIDNPNFARGFR	216	P79742	TBX6_DANRE
	.*:: . * * : * * :***** * * :***** *****			
237	GSDDM---ELHRMSRMQSTKEYPVVPRSTVRQRVGSQSPFSGDVQG--LSASGAISSQ-	290	Q9IAK8	TBX5A_DANRE

利用Dottup分析Tbx5a和Tbx2b序列

Dottup: fasta::493263:1 vs fasta::493392:1

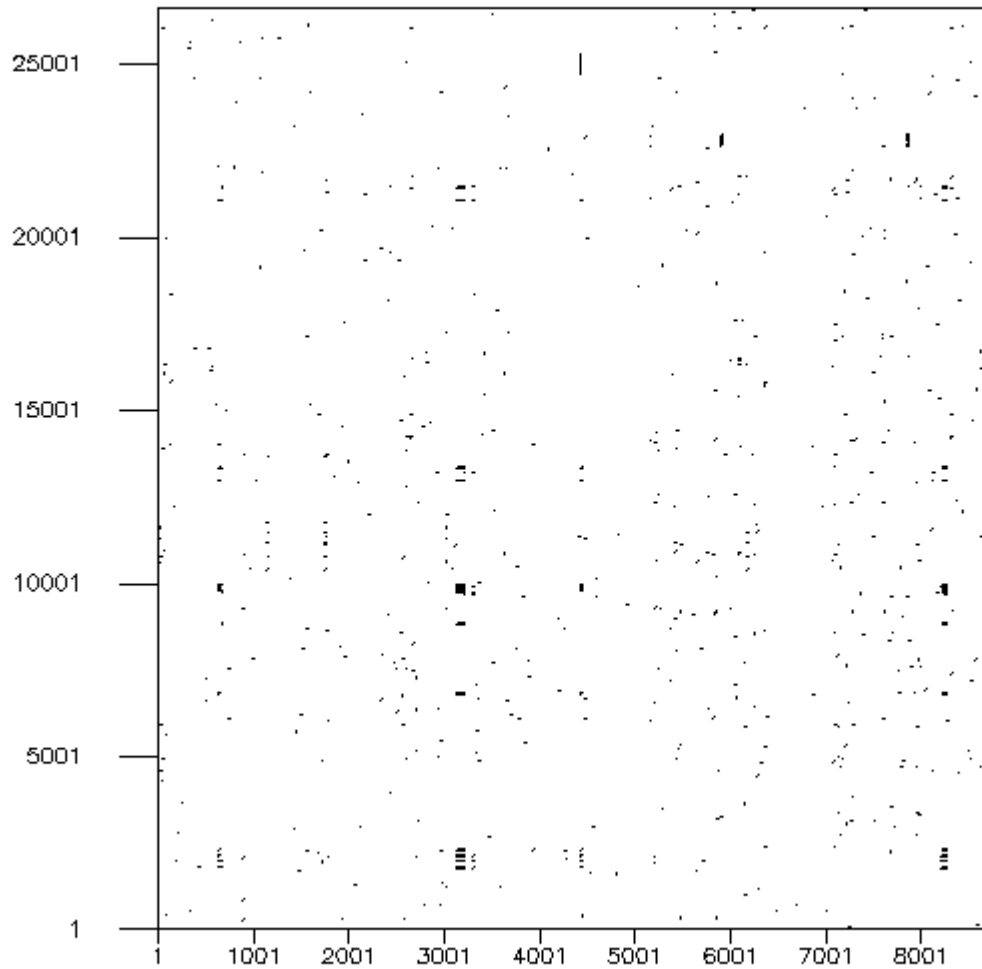
Fri 23 Dec 2011 17:00:49



利用Dottup分析Tbx5a和Tbx3序列

Dottup: fasta::493397:1 vs fasta::493263:1

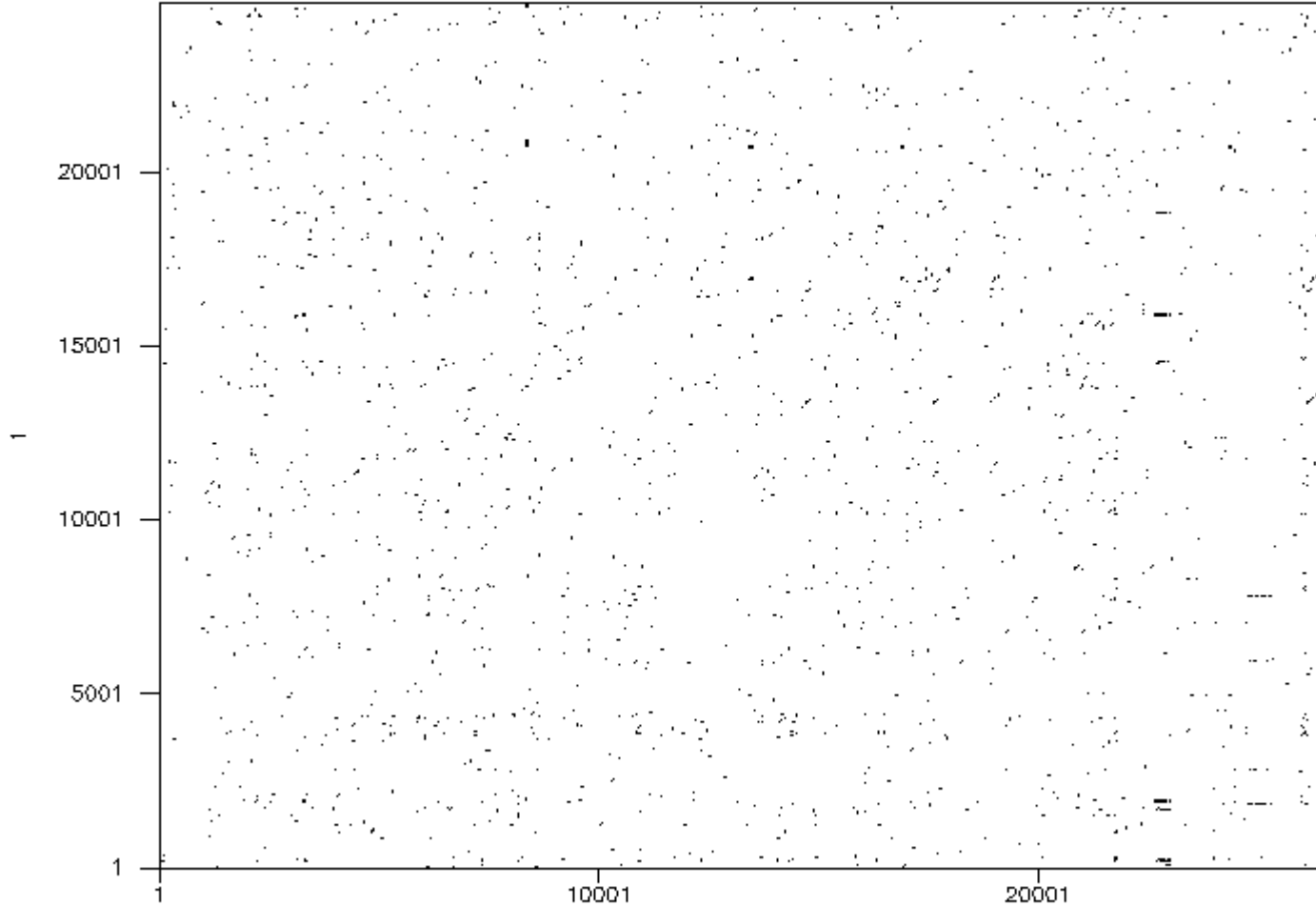
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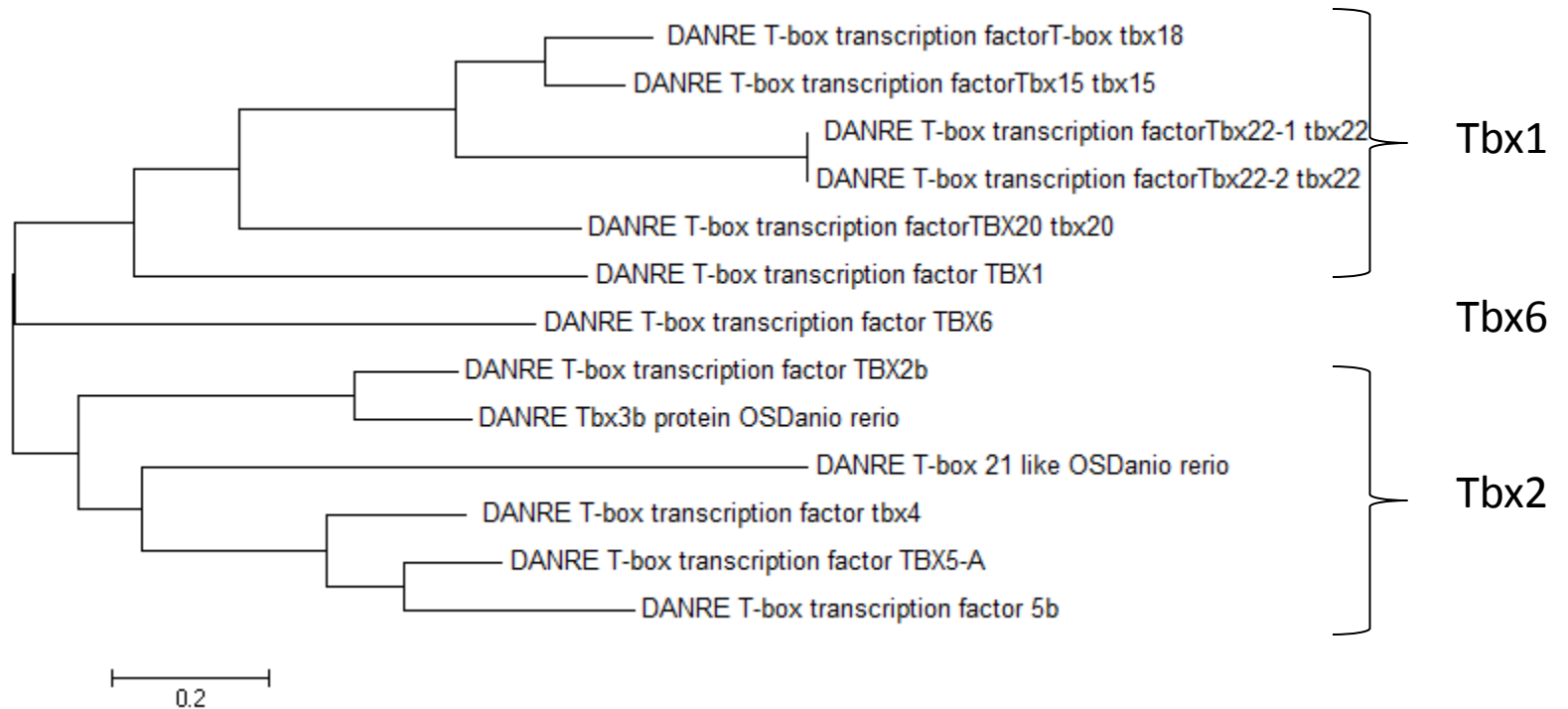
利用Dottup分析Tbx5a和Tbx4序列

Dottup: fasta::493263:1 vs fasta::493395:1

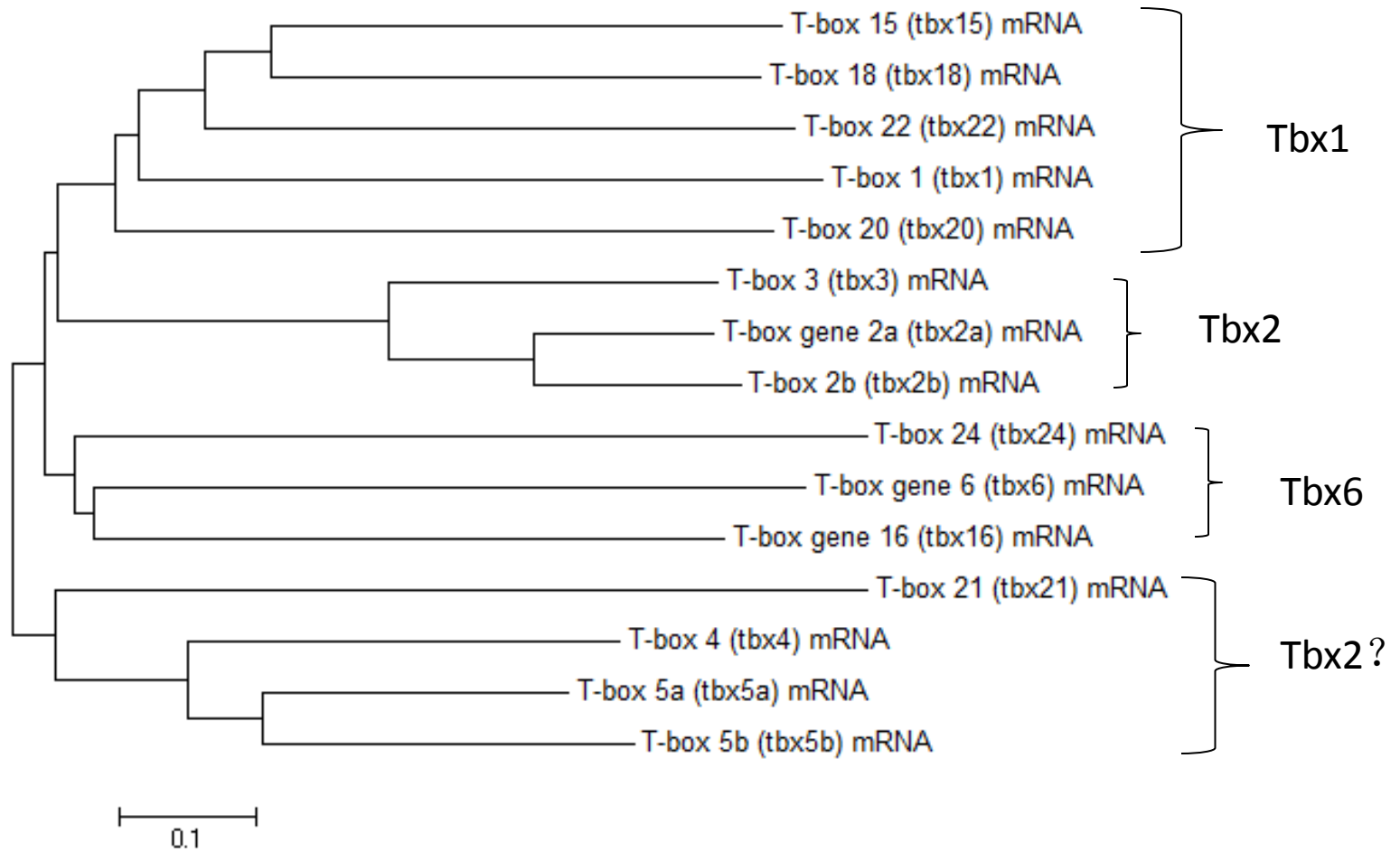
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利用MEGA对Tbx基因家族的分析



利用MEGA对Tbx基因家族的分析



小结：我们利用实用生物信息学课上所学到数据库和软件对斑马鱼Tbx5及Tbx基因家族进行了初步分析。所得到的结论和文献的结论是基本一致的。

1、Tbx5是非常保守转录因子，在脊椎动物心脏和前肢发育起到重要作用。所分析的7个不同物种Tbx5的DNA结合区域氨基酸序列是一样的，说明了Tbx5非常保守。

2、Tbx基因家族中，均含有非常保守的DNA-binding区域。根据氨基酸残基序列可将Tbx家族分为Tbx1，Tbx2和Tbx6三个亚家族。

Thank you!