



STRING数据库 操作指南

欧易生物



STRING介绍

- 研究一个基因及其编码的蛋白质，一方面要了解它们的功能，另一方面需研究与此蛋白质相互作用的其他蛋白质的信息，以使研究人员能够更加深入地认清相关蛋白质的功能，更清楚地理解其调控机制。



- **STRING数据库**(<http://string-db.org/>)是一个搜寻已知蛋白质之间和预测蛋白质之间相互作用的系统。这种相互作用既包括蛋白质之间直接的物理的相互作用，也包括蛋白质之间间接的功能的相关性。



- 它除了包含有实验数据、从PubMed摘要中文本挖掘的结果和综合其他数据库数据外，还有利用生物信息学的方法预测的结果。所应用的生物信息学的方法有：染色体临近、基因融合、系统进化谱和基于芯片数据的基因共表达。
- 该系统利用一个打分机制对这些不同方法得来的结果给予一定的权重，最终给出一个综合的得分。

STRING网站首页

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STRING 9.0

STRING - Known and Predicted Protein-Protein Interactions

已更新至9.0版本

检索框

search by name

search by protein sequence

multiple names

multiple sequences

protein name: (examples: #1 #2 #3)

(STRING understands a variety of protein names and accessions; you can also try a [random entry](#))

organism:

interactors wanted:
☐ COGs ☒ Proteins

please enter your protein of interest...

What it does ...

STRING is a database of known and predicted protein interactions. The interactions include direct (physical) and indirect (functional) associations; they are derived from four sources:

Genomic
Context

High-throughput
Experiments

(Conserved)
Coexpression

Previous
Knowledge

STRING quantitatively integrates interaction data from these sources for a large number of organisms, and transfers information between these organisms where applicable. The database currently covers 5'214'234 proteins from 1133 organisms.

STRING9.0 覆盖1133个物种，包含5214234种蛋白质

More Info

Funding / Support

Acknowledgements

Use Scenarios

STRING (*Search Tool for the Retrieval of Interacting Genes/Proteins*) is being developed at [CPR](#), [EMBL](#), [SIB](#), [KU](#), [TUD](#) and [UZH](#).
STRING references: [Szklarczyk et al. 2011](#) / [2009](#) / [2007](#) / [2005](#) / [2003](#) / [Snel et al. 2000](#).
Miscellaneous: [Access Statistics](#), [Robot Access Guide](#), [STRING/STITCH Blog](#), [Supported Browsers](#).

What's New? This is version 9.0 of STRING - now covering more than 1100 organisms (and counting) !

Sister Projects: check out [STITCH](#) and [eggNOG](#) - two sister projects built on STRING data!

Previous Releases: Trying to reproduce an earlier finding? Confused? Refer to our [old releases](#).

检索与某个特定蛋白质（如trpA）相互作用的其他蛋白信息

按名称查找

按氨基酸序列查找

The screenshot shows a web-based search interface for protein interactions. At the top, there are four tabs: 'search by name', 'search by protein sequence', 'multiple names', and 'multiple sequences'. The 'search by name' tab is selected. Below the tabs, there is a 'protein name:' label followed by a text input field containing 'trpA'. To the right of the input field is a link '(examples: #1 #2 #3)'. Below the input field, there is a note: '(STRING understands a variety of protein names and accessions; you can also try a random entry)'. Below this, there is an 'organism:' label followed by a dropdown menu showing 'Escherichia coli K12_MG1655'. Below the dropdown menu, there is a section 'interactors wanted:' with two radio buttons: 'COGs' and 'Proteins'. The 'Proteins' radio button is selected. At the bottom right, there are two buttons: 'Reset' and 'GO!'. A blue circle with the text '开始检索!' (Start Search!) points to the 'GO!' button. A large, faint watermark '易' (Easy) is visible in the background of the interface.

点击此处可以查看示例

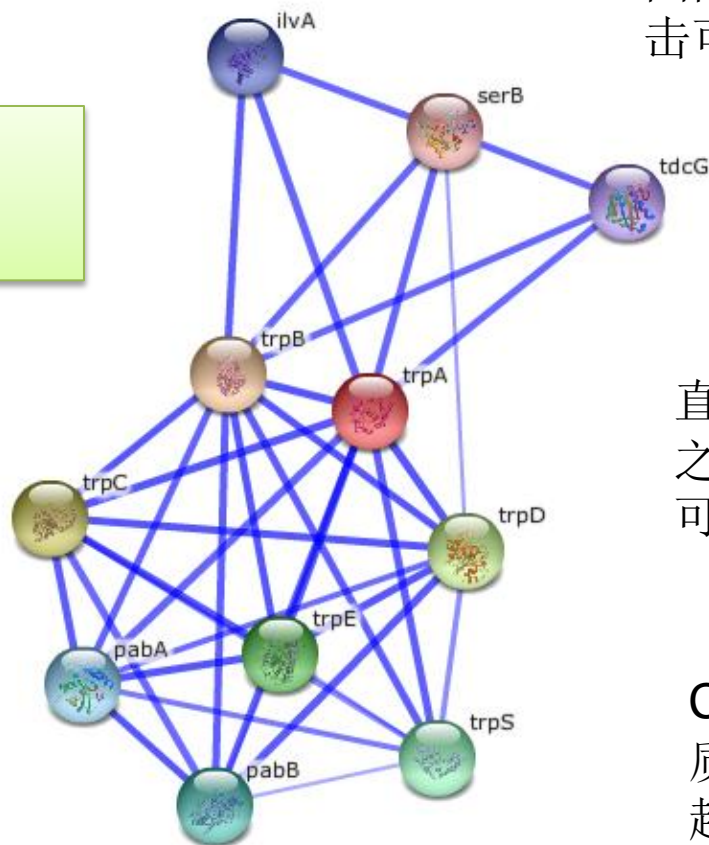
此处输入需要检索的蛋白质名称或者登录号

物种选择。如选择auto-detect, 则在查询的过程中, 如果相关的蛋白质名称出现在几个不同的物种中, 则数据库系统会将这些物种全部显示出来, 用户可自己选择感兴趣的蛋白质进行下一步的查询。

开始检索!

检索结果

Confidence
view

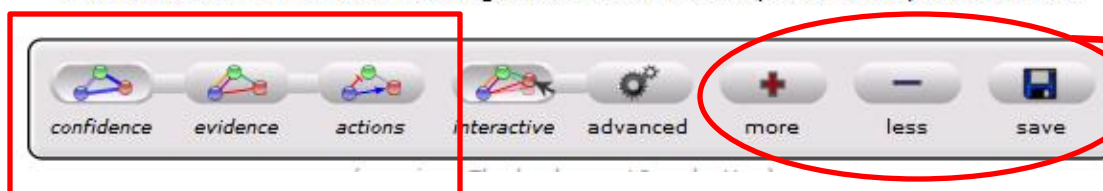


圆圈（**node**）表示蛋白质，点击可以查看该蛋白质相关信息。

直线（**edge**）表示蛋白质之间的相互作用关系。点击可以查看两蛋白互作信息。

Confidence view表示蛋白质之间相互作用关系，线越粗表示两者之间互作更强。

This is the **confidence view**. Stronger associations are represented by thicker lines.



点击此处可以查看其它类型视图

视图进行放大或缩小及保存，保存为png格式


tdcG Close

Actions

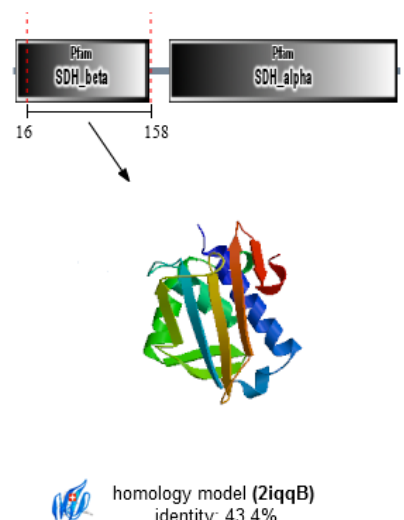
- [re-center network on this node](#)
- [add this node to input nodes](#)

Information

L-serine dehydratase 3

Identifier: b4471 

- [show protein sequence](#)
- [homologs among STRING organisms](#)




homology model (2iqqB)
identity: 43.4%

Node点击后出现的对话框
tdcG相关信息描述


易

Interaction Close

 trpA [b1260]

tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3- phosphate (By similarity)

↔

 tdcG [b4471]

L-serine dehydratase 3

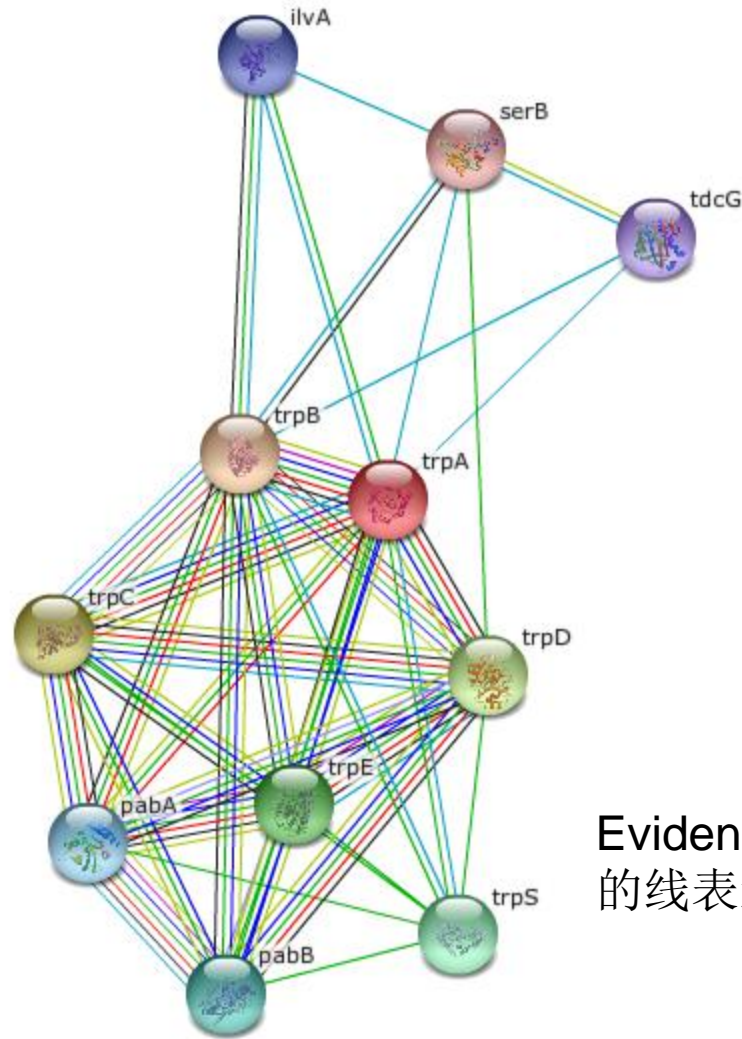
Evidence suggesting a functional link:

Neighborhood in the Genome:	none / insignificant.
Gene Fusions:	none / insignificant.
Cooccurrence Across Genomes:	none / insignificant.
Co-Expression:	none / insignificant.
Experimental/Biochemical Data:	none / insignificant.
Association in Curated Databases:	yes (score 0.900). Show
Co-Mentioned in PubMed Abstracts:	none / insignificant.

Combined Score: 0.899

edge点击后出现的对话框
trpA与tdcG间互作关系

Evidence view

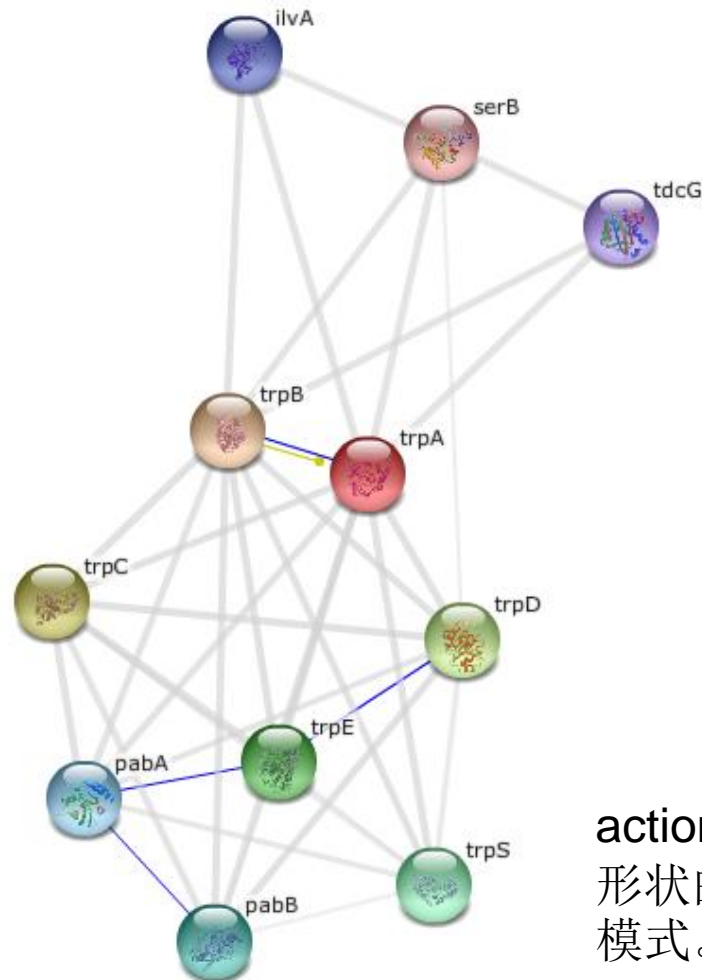


Evidence view: 不同颜色的线表示不同的证据。

This is the **evidence view**. Different line colors represent the types of evidence for the association.



actions view



actions view: 不同颜色和形状的线表示不同的作用模式。

This is the **actions view**. Modes of action are shown in different colors.



Your Input:

检索的蛋白质相关描述

- trpA tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3- phosphate (By similarity) (268 aa)
(*Escherichia coli* K12_MG1655)

Predicted Functional Partners:

与该蛋白相互作用的其他蛋白质信息

		Score
●	trpB tryptophan synthase, beta subunit; The beta subunit is responsible for the synthesis of L- tryp [...] (397 aa)	0.999
●	trpC fused indole-3-glycerolphosphate synthetase/N-(5-phosphoribosyl)anthranilate isomerase; Bifunct [...] (452 aa)	0.999
●	trpD fused glutamine amidotransferase (component II) of anthranilate synthase/anthranilate phosphori [...] (531 aa)	0.999
●	trpE component I of anthranilate synthase (520 aa)	0.999
●	trpS tryptophanyl-tRNA synthetase (334 aa)	0.945
●	pabB aminodeoxychorismate synthase, subunit I; Catalyzes the biosynthesis of 4-amino-4-deoxychorisma [...] (453 aa)	0.942
●	pabA aminodeoxychorismate synthase, subunit II; Catalyzes the biosynthesis of 4-amino-4-deoxychorism [...] (187 aa)	0.912
●	ilvA threonine deaminase; Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step [...] (514 aa)	0.910
●	tdcG L-serine dehydratase 3 (454 aa)	0.899
●	serB 3-phosphoserine phosphatase (322 aa)	0.899

与trpA互作蛋白质，按照打分排列，用不同的颜色标识

系统打分



参数设置

Info & Parameters ...

Network Display - Nodes are either colored (if they are directly linked to the input - as in the table) or white (nodes of a higher iteration/depth). Edges, i.e. predicted functional links, consist of up to eight lines: one color for each type of evidence. Hover or click to reveal more information about the node/edge.

Active Prediction Methods:

- ☒ Neighborhood ☒ Gene Fusion ☒ Co-occurrence
☒ Co-expression ☒ Experiments ☒ Databases ☒ Textmining

required confidence (score):

medium confidence (0.400) ▼

or custom value:

interactors shown:

no more than 10 interactors ▼

or custom limit:

additional (white) nodes

Update Parameters

检索某些蛋白质（如trpA、trpB、TRPC_ECOLI、b1263）相互作用关系

search by name search by protein sequence **multiple names** multiple sequences

list of names: (one per line; examples: #1 #2 #3)

trpA
trpB
TRPC_ECOLI
b1263

... or upload a file: 浏览...

organism:
Escherichia coli K12_MG1655 ▼

interactors wanted:
☐ COGs ☒ Proteins Reset **GO !**

点击此处
输入多个
蛋白质名
称或氨基
酸序列

please enter your protein of interest...



输入蛋白质名称描述

The following proteins in *Escherichia coli* K12_MG1655 appear to match your input.
Please review the list, then click 'Continue' to proceed to the association network.

<- Back

Continue ->

点击继续

'trpA':

- ☒ **trpA** - tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3- phosphate (By similarity)

'trpB':

- ☒ **trpB** - tryptophan synthase, beta subunit; The beta subunit is responsible for the synthesis of L- tryptophan from indole and L-serine (By similarity)

'TRPC_ECOLI':

- ☒ **trpC** - fused indole-3-glycerolphosphate synthetase/N-(5-phosphoribosyl)anthranilate isomerase; Bifunctional enzyme that catalyzes two sequential steps of tryptophan biosynthetic pathway. The first reaction is catalyzed by the isomerase, coded by the trpF domain; the second reaction is catalyzed by the synthase, coded by the trpC domain

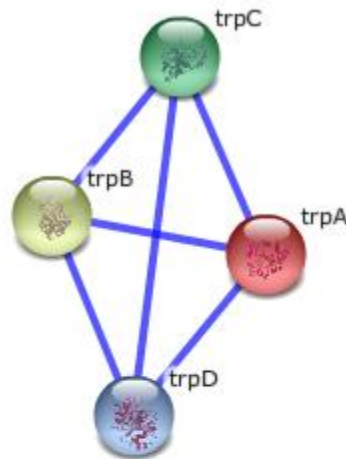
'b1263':

- ☒ **trpD** - fused glutamine amidotransferase (component II) of anthranilate synthase/anthranilate phosphoribosyl transferase

<- Back

Continue ->

检索结果



This is the **confidence view**. Stronger associations are represented by thicker lines.



(requires Flash player 10 or better)

Your Input:

- trpA tryptophan synthase, alpha subunit; The alpha subunit is responsible for the aldol cleavage of indoleglycerol phosphate to indole and glyceraldehyde 3- phosphate (By similarity) (268 aa)
- trpB tryptophan synthase, beta subunit; The beta subunit is responsible for the synthesis of L- tryptophan from indole and L-serine (By similarity) (397 aa)
- trpC fused indole-3-glycerolphosphate synthetase/N-(5-phosphoribosyl)anthranilate isomerase; Bifunctional enzyme that catalyzes two sequential steps of tryptophan biosynthetic pathway. The first reaction is catalyzed by the isomerase, coded by the trpF domain; the second reaction is catalyzed by the synthase, coded by the trpC domain (452 aa)
- trpD fused glutamine amidotransferase (component II) of anthranilate synthase/anthranilate phosphoribosyl transferase (531 aa)
(*Escherichia coli* K12_MG1655)



- 有任何疑问，请致电021-38760130，或将您的疑问发邮件至service@oebiotech.com，谢谢！

上海欧易