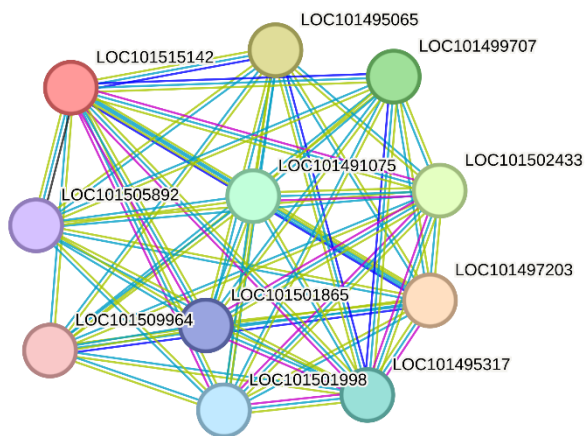


a

LOC101515142

Mediator of RNA polymerase II transcription subunit 16-like

**Edges:**

Edges represent protein-protein associations

associations are meant to be specific and meaningful, i.e. proteins jointly contribute to a shared function; this does not necessarily mean they are physically binding to each other.

Known Interactions

- from curated databases
- experimentally determined

Predicted Interactions

- gene neighborhood
- gene fusions
- gene co-occurrence

Others

- textmining
- co-expression
- protein homology

Your Input:

● LOC101515142 Mediator of RNA polymerase II transcription subunit 16-like isoform X1. (1247 aa)

Predicted Functional Partners:

	Neighborhood	Gene Fusion	Cooccurrence	Coexpression	Experiments	Databases	Textmining	Protein Homology	Score
● LOC101497203 Mediator of RNA polymerase II transcription subunit 32.			●		●	●	●		0.797
● LOC101495065 Mediator of RNA polymerase II transcription subunit 19a-like.			●			●	●		0.708
● LOC101502433 Mediator of RNA polymerase II transcription subunit 14; Component of the Mediator complex, a coactivator involved in ...				●	●	●	●		0.706
● LOC101499707 Probable mediator of RNA polymerase II transcription subunit 19b.			●		●	●	●		0.691
● LOC101491075 Mediator of RNA polymerase II transcription subunit 18 isoform X1.						●	●		0.670
● LOC101495317 Mediator of RNA polymerase II transcription subunit 27.				●	●	●	●		0.640
● LOC101501998 Mediator of RNA polymerase II transcription subunit 8-like isoform X1.					●	●	●		0.605
● LOC101501865 Mediator of RNA polymerase II transcription subunit 8-like isoform X1.					●	●	●		0.605
● LOC101505892 Mediator of RNA polymerase II transcription subunit 13; Component of the Mediator complex, a coactivator involved in ...				●	●	●	●		0.584
● LOC101509964 Mediator of RNA polymerase II transcription subunit 28.					●	●	●		0.568

Your Current Organism:

Cicer arietinum

NCBI taxonomy id: 3827

Other names: C. arietinum, Cicer arietinum L., chickpea, garbanzo

Network Stats

number of nodes: 11
number of edges: 52
average node degree: 9.45
avg. local clustering coefficient: 0.939

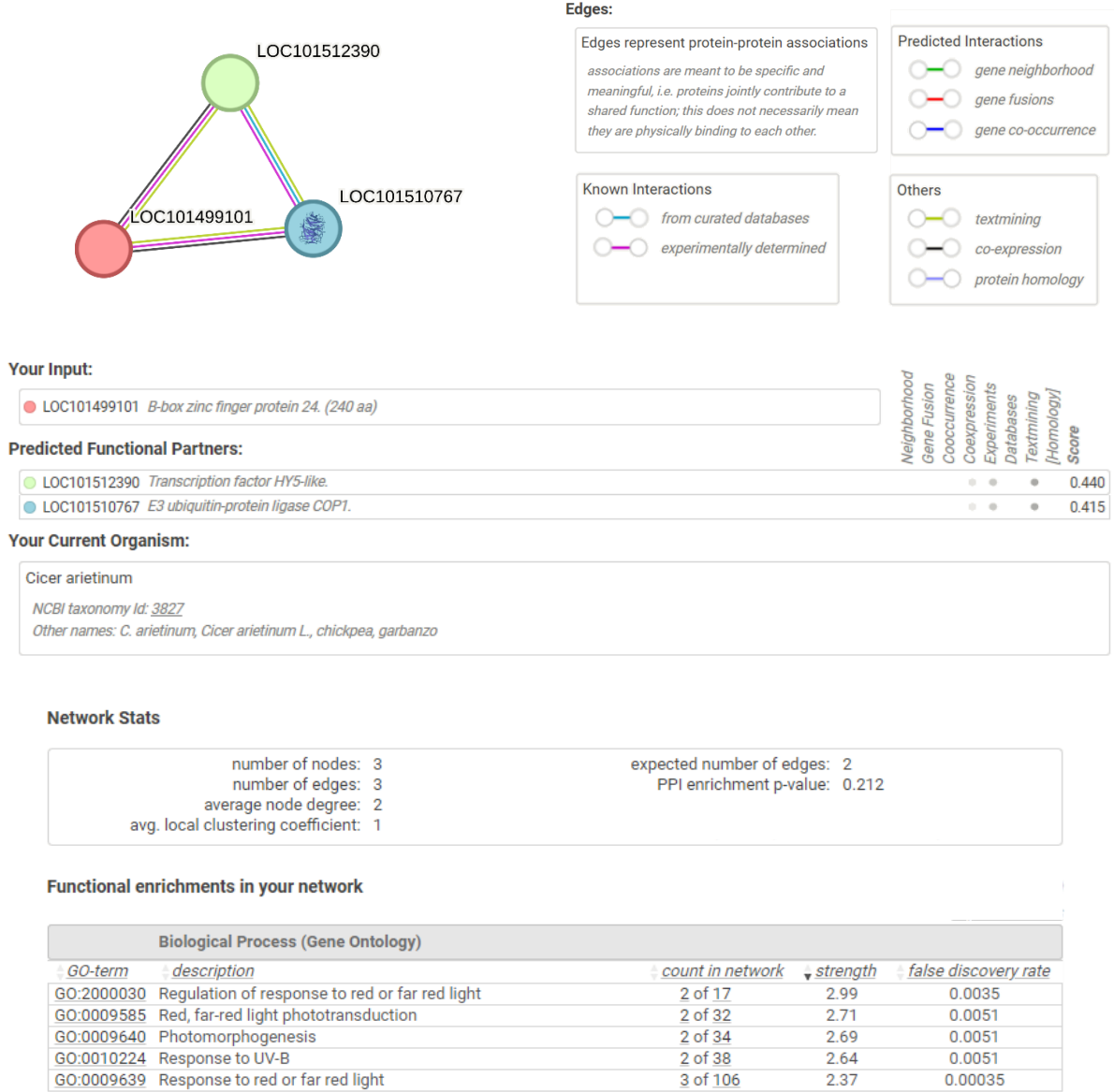
expected number of edges: 10
PPI enrichment p-value: < 1.0e-16

Functional enrichments in your network

GO-term	description	count in network	strength	false discovery rate
GO:0040034	Regulation of development, heterochronic	2 of 24	2.27	0.0056
GO:0009631	Cold acclimation	2 of 24	2.27	0.0056
GO:2000028	Regulation of photoperiodism, flowering	2 of 38	2.07	0.0128
GO:0009738	Abscisic acid-activated signaling pathway	4 of 106	1.93	2.52e-05
GO:0045944	Positive regulation of transcription by RNA polymerase II	5 of 207	1.74	1.76e-05
GO:0009909	Regulation of flower development	2 of 82	1.74	0.0473
GO:2000241	Regulation of reproductive process	4 of 200	1.65	0.00017
GO:0045893	Positive regulation of transcription, DNA-templated	6 of 402	1.53	1.76e-05
GO:0006357	Regulation of transcription by RNA polymerase II	8 of 557	1.51	4.60e-08
GO:0051239	Regulation of multicellular organismal process	3 of 253	1.43	0.0151
GO:0050793	Regulation of developmental process	5 of 438	1.41	9.44e-05
GO:0098542	Defense response to other organism	3 of 406	1.22	0.0497
GO:0006952	Defense response	4 of 812	1.04	0.0262
GO:0006355	Regulation of transcription, DNA-templated	9 of 2201	0.96	1.76e-05
GO:0006950	Response to stress	6 of 2436	0.74	0.0226
GO:0050789	Regulation of biological process	11 of 5261	0.67	1.76e-05

b

LOC101499101
B-box zinc finger protein 24



Additional file 11. Fig. S1 Protein-protein interaction network using STRING chickpea database for **(a)** LOC101515142 and **(b)** LOC101499101