

EXPERIMENT NO:2  
21BBT034

## BLAST

```
>tr|A4HSF7|A4HSF7_LEIIN Trypanothione reductase OS=Leishmania infantum OX=5671 GN=TRYR PE=1 SV=1
MSRAYDLVVLGAGSGGLEAGWNAAVTHKKKVAWVDVQATHGPPLFAALGGTCVNVGCVPK
KLMVTGAQYMDLIRESGGFGWEMDRESLCPNWKTLIAAKNKVVNSINESYKSMFADTEGL
SFHMGFGALQDAHTVVVRKSEDPHSDVLETLDTEYIL IATGSWPTRLGVPGDFCITSNE
AFYLEDAPKRMLCVGGGYIAVEFAGIFNGYKPCGGYVDLCYRGDLILRGFDTEVRKSLTK
QLGANGIRVRTNLNPTKITKNEDGSNHVHFNDGTEEDYDQVMLAIGRVPRSQALQLDKAG
VRTGKNGAVQVDAYSKTSVDNIYAIGDVTNRVMLTPVAINEGAAFVETVFGGKPRATDHT
KVACAVFSIPPIGTCGMTETEEAAKNYETVAVYASSFTPLMHNISGSKHKEFMIRIITNES
NGEVLGVHMLGDSAPEIIQSVGICMKMGAKISDFHSTIGVHPTSAEELCSMRTPAYFYES
GKRVEKLSSNL
```

**Figure 1.** Fasta sequence of the desired protein- *Trypanothione reductase* (PDB:2JK6)



**Figure 2.** 3D structure of the desired protein- *Trypanothione reductase*

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

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 10 sequences selected

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[Distance tree of results](#)
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[MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	RecName: Full=Trypanothione reductase; Short=TR; AltName: Full=N(1)-N(8)-bis(glutathionyl)spermidine reductase [...]	Leishmania dono...	967	967	100%	0.0	98.37%	491	P39050.1
<input checked="" type="checkbox"/>	RecName: Full=Trypanothione reductase; Short=TR; AltName: Full=N(1)-N(8)-bis(glutathionyl)spermidine reductase [...]	Crithidia fasciculata	802	802	100%	0.0	78.62%	491	P39040.1
<input checked="" type="checkbox"/>	RecName: Full=Trypanothione reductase; Short=TR; AltName: Full=N(1)-N(8)-bis(glutathionyl)spermidine reductase [...]	Trypanosoma co...	680	680	99%	0.0	67.97%	492	P13110.1
<input checked="" type="checkbox"/>	RecName: Full=Trypanothione reductase; Short=TR; AltName: Full=N(1)-N(8)-bis(glutathionyl)spermidine reductase [...]	Trypanosoma bru...	671	671	99%	0.0	66.74%	492	P39051.1
<input checked="" type="checkbox"/>	RecName: Full=Trypanothione reductase; Short=TR; AltName: Full=N(1)-N(8)-bis(glutathionyl)spermidine reductase [...]	Trypanosoma cruzi	667	667	99%	0.0	67.42%	492	P28593.1
<input checked="" type="checkbox"/>	RecName: Full=Glutathione reductase, cytosolic; Short=GR; Short=GRase [Oryza sativa Japonica Group]	Oryza sativa Jap...	354	354	95%	2e-116	42.55%	496	P48642.2
<input checked="" type="checkbox"/>	RecName: Full=Glutathione reductase, chloroplastic; Short=GR; Short=GRase; AltName: Full=Protein EMBRYO DEF...	Arabidopsis thalia...	350	350	95%	5e-114	42.77%	565	P42770.1
<input checked="" type="checkbox"/>	RecName: Full=Glutathione reductase, chloroplastic; Short=GR; Short=GRase; Flags: Precursor [Nicotiana tabacum]	Nicotiana tabacum	348	348	95%	4e-113	41.70%	557	P80461.1
<input checked="" type="checkbox"/>	RecName: Full=Glutathione reductase, chloroplastic/mitochondrial; Short=GR; Short=GRase; AltName: Full=GOR1...	Pisum sativum	347	347	95%	1e-112	40.64%	552	P27456.1
<input checked="" type="checkbox"/>	RecName: Full=Glutathione reductase, chloroplastic; Short=GR; Short=GRase; Flags: Precursor [Glycine max]	Glycine max	342	342	95%	3e-111	40.21%	544	P48640.1

Fig 3. Description summary of the BLAST results of the protein – CASE A

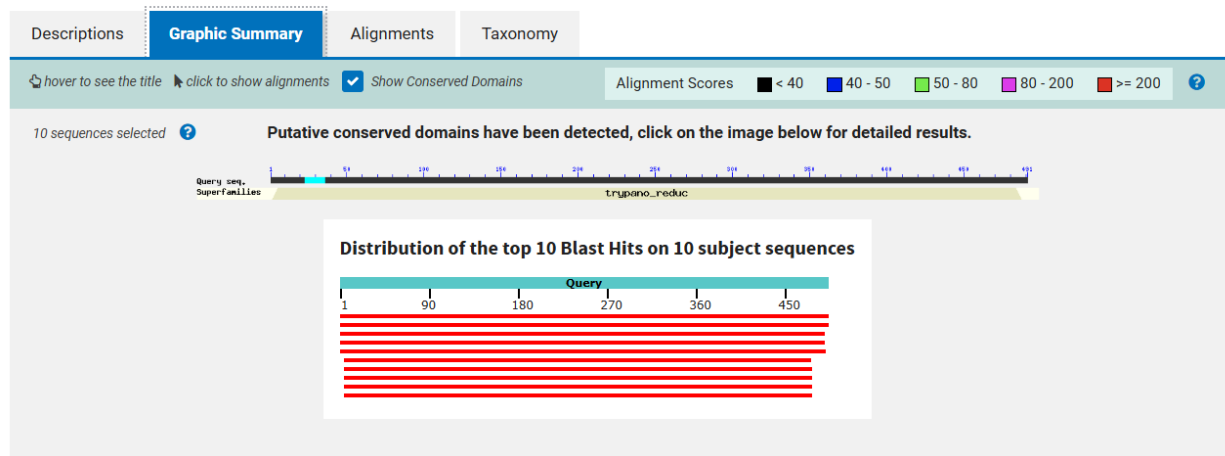
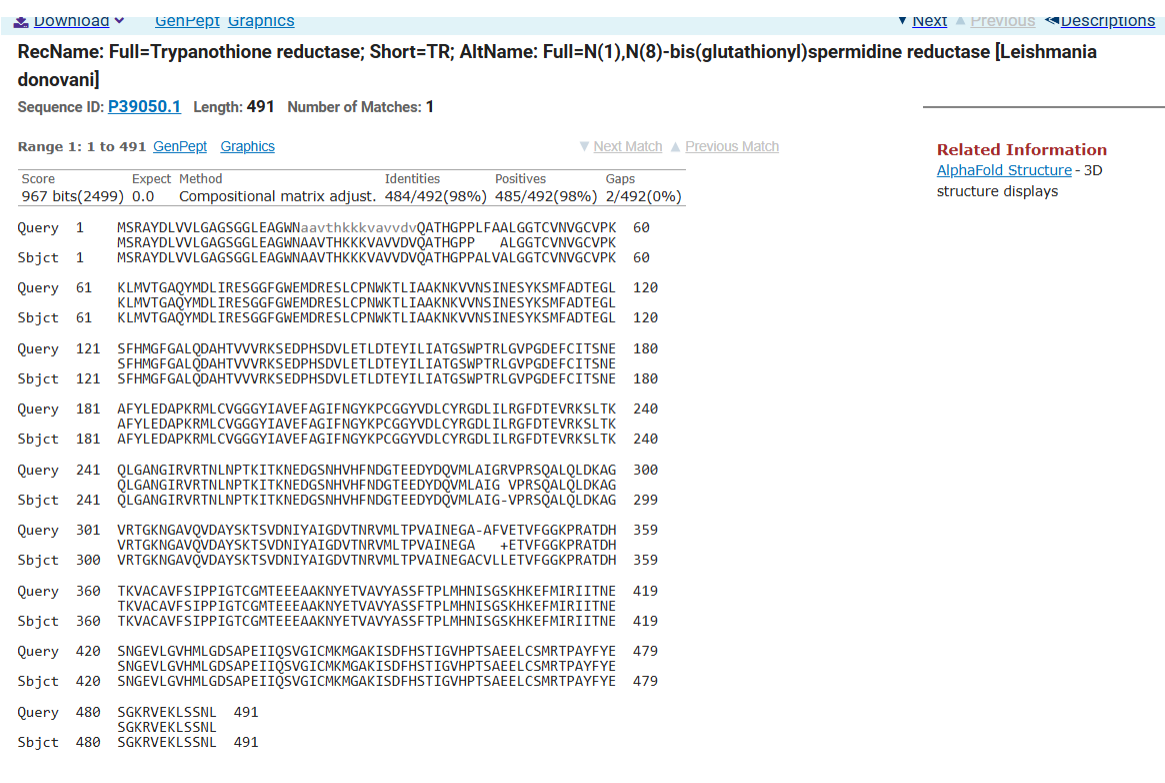


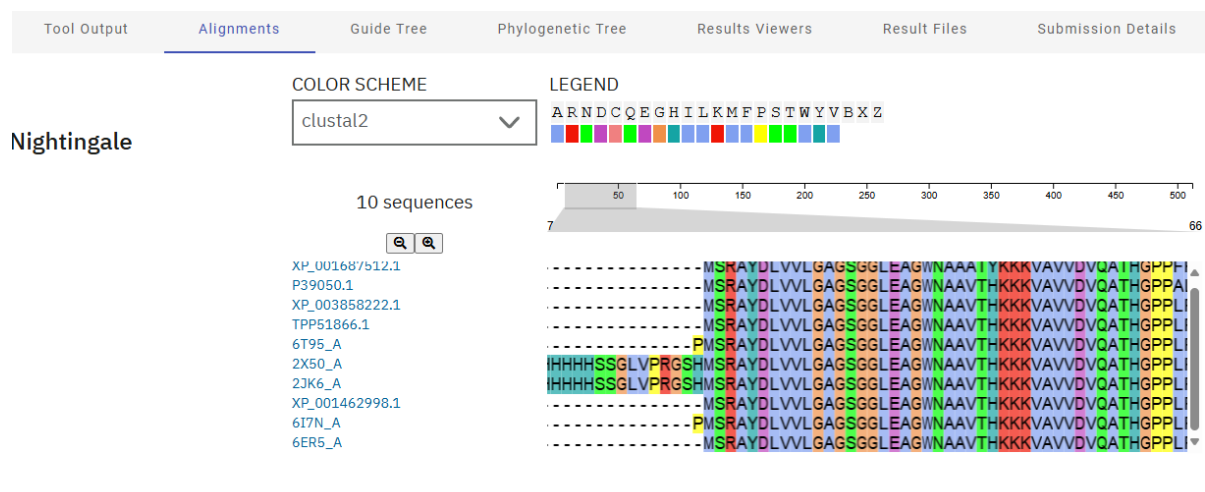
Fig 4. Graphical summary of the BLAST results of the protein

Phylogenetic Tree	Edit and Resubmit	Back to Blast Results	Download
Multiple Alignment Results - tr A4HSF7 A4HSF7_LEIIN Trypanothione reductase... - Cobalt RID 9KS8XRVH212 (10 seqs)			
Graphical Overview			
Find:	Tools	Columns	Rows
Sequence ID	Start	End	Organism
Query_7578845	1	491	Leishmania donovani
P39050.1	1	491	Crithidia fasciculata
P39040.1	1	491	Trypanosoma concolorense
P13110.1	1	492	Trypanosoma brucei
P39051.1	1	492	Trypanosoma cruzi
P28593.1	1	492	Oryza sativa Japonica Gr.
P48642.2	1	496	Arabidopsis thaliana
P42770.1	1	565	Nicotiana tabacum
P80461.1	1	557	Pisum sativum
P27456.1	1	552	
PROTEIN: 84 - 138 (55r shown)			
Rows shown: 10/10			
Descriptions <input checked="" type="checkbox"/> Select All <input type="radio"/> Re-align Alignment parameters			

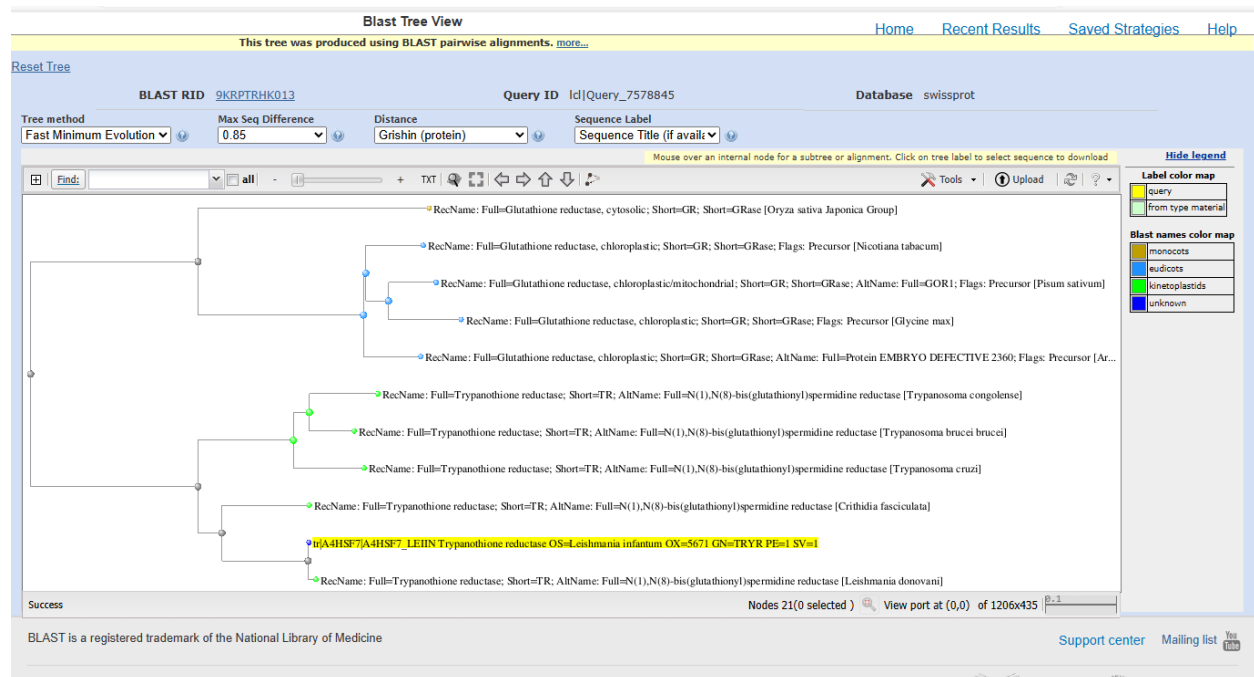
Fig 5. Multiple alignment summary of the BLAST results of the protein



**Fig 6.** Alignment summary of the BLAST results of the protein – The query seq and the subject seq is compared



**Fig 7.** The fasta seq is subjected to conservative domain search (Image from *CLUSTAL OMEGA*)



**Fig 8.** Distance tree alignment of the BLAST results of the protein

## CASE B

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GenPept

Graphics

Distance tree of results

Multiple alignment

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	trypanothione reductase [Leishmania infantum JPCM5]	Leishmania infa...	1037	1037	100%	0.0	100.00%	491	XP_001462998.1
<input checked="" type="checkbox"/>	Chain_A_Trypanothione reductase [Leishmania infantum]	Leishmania infa...	1036	1036	100%	0.0	100.00%	492	617N_A
<input checked="" type="checkbox"/>	Chain_A_TRYPANTHIONE REDUCTASE [Leishmania infantum]	Leishmania infa...	1036	1036	100%	0.0	100.00%	511	2JK6_A
<input checked="" type="checkbox"/>	trypanothione-disulfide reductase [Leishmania donovani]	Leishmania don...	1034	1034	100%	0.0	99.80%	491	TPP51866.1
<input checked="" type="checkbox"/>	Chain_A_TRYPANTHIONE REDUCTASE [Leishmania infantum]	Leishmania infa...	1034	1034	99%	0.0	100.00%	510	2X50_A
<input checked="" type="checkbox"/>	Chain_A_Trypanothione reductase [Leishmania infantum]	Leishmania infa...	1030	1030	99%	0.0	100.00%	488	6ER5_A
<input checked="" type="checkbox"/>	Chain_A_Trypanothione reductase [Leishmania infantum]	Leishmania infa...	1030	1030	99%	0.0	100.00%	489	6T95_A
<input checked="" type="checkbox"/>	trypanothione reductase [Leishmania donovani]	Leishmania don...	1029	1029	100%	0.0	99.59%	491	XP_003858222.1
<input checked="" type="checkbox"/>	RecName: Full=Trypanothione reductase; Short=TR; AltName: Full=N(1),N(8)-bis(glutathionyl)spermidine red...	Leishmania don...	1012	1012	100%	0.0	98.37%	491	P39050.1
<input checked="" type="checkbox"/>	trypanothione reductase [Leishmania major strain Friedlin]	Leishmania maj...	996	996	100%	0.0	95.72%	491	XP_001687512.1

**Fig 9.** The threshold and the matrices changed and the sequence is subjected to BLAST

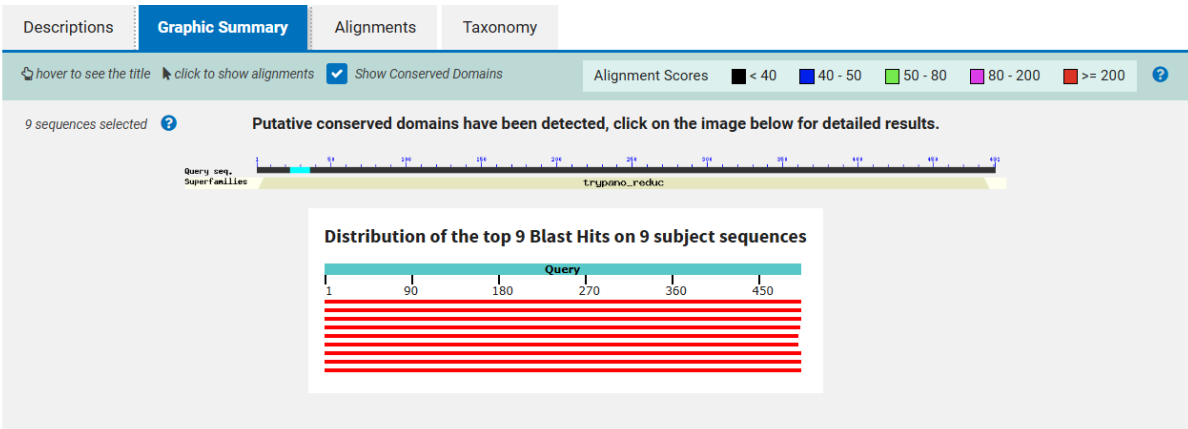


Fig 10. Graphical summary of the BLAST results of the protein

Sequence ID: **617N\_A** Length: 492 Number of Matches: 1  
[See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Range 1: 2 to 492 [GenPept](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Method	Identities	Positives	Gaps
1036 bits(3524)	0.0	Compositional matrix adjust.	491/491(100%)	491/491(100%)	0/491(0%)
Query 1	MSRAYDLVVLGAGSGGLEAGWNaavthkkkvavvdvQATHGPPLFAALGGTCVNVGCVPK				60
Sbjct 2	MSRAYDLVVLGAGSGGLEAGWNaavthkkkvavvdvQATHGPPLFAALGGTCVNVGCVPK				61
Query 61	KLMVTGAQYMDL IRESGGFGWEMDRESLCPNWKT LIAAKNKVVNS INESYKSMFADTEGL				120
Sbjct 62	KLMVTGAQYMDL IRESGGFGWEMDRESLCPNWKT LIAAKNKVVNS INESYKSMFADTEGL				121
Query 121	SFHMFGALQDAHTVVRKSEDPHSDVLETLDTEYILIATGSPWTRLGVPGDEFICITSNE				180
Sbjct 122	SFHMFGALQDAHTVVRKSEDPHSDVLETLDTEYILIATGSPWTRLGVPGDEFICITSNE				181
Query 181	AFYLEDAPKRMLCVGGGYIAVEFAGIFNGYKPCGGYVDLCYRGDILRGFDTEVRKSLTK				240
Sbjct 182	AFYLEDAPKRMLCVGGGYIAVEFAGIFNGYKPCGGYVDLCYRGDILRGFDTEVRKSLTK				241
Query 241	QLGANGIRVRTNLNPTKITKNEDGSNHVHFNDDTEEDYDQVMLAIGRVPRSQALQDKAG				300
Sbjct 242	QLGANGIRVRTNLNPTKITKNEDGSNHVHFNDDTEEDYDQVMLAIGRVPRSQALQDKAG				301
Query 301	VRTGKNGAVQVDAYSKTSDVNIYAIGDVTNRVMLTPVAINEGAAFVETVFGGKPRATDHT				360
Sbjct 302	VRTGKNGAVQVDAYSKTSDVNIYAIGDVTNRVMLTPVAINEGAAFVETVFGGKPRATDHT				361
Query 361	KVACAVFSIPPTGTCGMTEEEAAKNYETVAVYASSFTPLMHNISGSKHKEFMIRIITNES				420
Sbjct 362	KVACAVFSIPPTGTCGMTEEEAAKNYETVAVYASSFTPLMHNISGSKHKEFMIRIITNES				421
Query 421	NGEVLGVHMLGDSAPEIIQSVGICMKMGAKISDFHSTIGVHPTSAEELCSMRTPAYFYES				480
Sbjct 422	NGEVLGVHMLGDSAPEIIQSVGICMKMGAKISDFHSTIGVHPTSAEELCSMRTPAYFYES				481
Query 481	GKRVEKLSSNL 491				
Sbjct 482	GKRVEKLSSNL 492				

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Fig 3. Alignment summary of the BLAST results of the protein

## INFERENCE

A protein seq- Trypanothione reductase is obtained from the Uniprot and it's 3D- structure and it is subjected to BLAST. The Description, Graphical, Alignment summary were analysed.

The initial stage of CASE A was searched with default settings in BLAST (threshold, 10 seq, low complexity regions). The conservative domains were identified.

The CASE B had some changes in the threshold and matrices. This provided an insight on efficient search in BLAST.