Available online at www.scholarsresearchlibrary.com



Scholars Research Library

Annals of Biological Research, 2013, 4 (1):29-38 (http://scholarsresearchlibrary.com/archive.html)



Resistance of rhizobia against different pesticides and detection of nitrogen fixing protien sequences

Sabeen Hashmi and Tarranum Sultana.

Department of Biotechnology. Maulana Azad College, Dr.Rafiq Zakaria Campus, Harsul Road, Aurangabad (MS) India.

ABSTRACT

Pesticides are used for the increase yield of the crops, Rhizobia are bacteria which fixes the nitrogen by the formation of legumes. In this paper we had checked whether the pesticide affects the Rhizobium or not i.e. the whether the rhizobium is resistant to the particular pesticide (e.g. Monochrotophos). Chick pea i.e. Cicer arietinum is one example rhizobium leguminosarum had showed the result, i:e it is resistant to the pesticide monocrotophos in additionally we had taken the sequence of the chick pea compare with the sequence of the other sequence of the rhizobium we had codended that other sequence matched with the cicer arietinum i.e. Fixes the nitrogen taken the 2d & 3D structure.

Keywords: Rhizobia, monocrotophos, MIC, alignment, 2D structure prediction, 3D structure prediction.

INTRODUCTION

RHIZOBIA-

This module introduces the general role of microorganisms in the soil, and specifically the rhizobia. Rhizobia are special bacteria that can live in the soil or in nodules formed on the Roots of legumes. In root nodules, they form a symbiotic association with the legume, obtaining nutrients from the plant and producing nitrogen in a process called biological nitrogen fixation, or BNF. The rhizobia are broadly classified as fast- or slow-growing based on their growth on laboratory media. Rhizobia are further classified according to their compatibility with particular legume species. Farmers can stimulate BNF by applying the correct rhizobia to their legume crops, a process called inoculation. The module describes the diversity of rhizobia and the selection of superior strains, as well as plant and environmental factors that affect rhizobia in the soil.

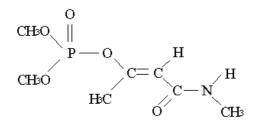
Soil microorganisms play many important roles. Rhizobia are special soil microorganisms that can form a symbiotic relationship with legumes resulting in biological nitrogen fixation, or BNF.Rhizobia are classified according to the legume species that they nodulate — a Concept known as "cross-inoculation" groups.

To achieve effective BNF, legumes must be inoculated with the correct rhizobia. Superior strains of rhizobia can be selected as inoculants. Plant and environmental factors affect native and introduced rhizobia in the soil.

MONOCROTOPHOS

Common Name-Monocrotophos CAS-No.6923-22-4 Use- Insecticide, acaricide with systemic and contact action Formulation Types - Water miscible, soluble concentrate; Ultra Low Volume Spray

1. Formula: C7H14N05P



2- Chemical Name : Dimethyl (E)-1-methyl-2-(methylcarbamoyl)vinyl phosphate (IUPAC)

3- Chemical Type : Organophosphate

4- Solubility : 1 kg/I (20°C, water) ; LogPow -0.22-0.5 (calculated)

- 5- *Vapour Pressure* : 0.29 mPa (20°C)
- 6- Melting Point : 54-55 °C

7- *Reactivity* - Decomposes above 38°C; unstable in short chain alcohols; half-life in aqueous solutions range from 96 days (pH 5) to 17 days (pH 9); monocrotophos is corrosive to black iron, drum steel and stainless steel. Further information in Tomlin, 1994 and IPCS, 1993

8- General

Mode of action : Monocrotophos affects the nervous system by inhibiting acetyl cholinesterase, an enzyme essential for normal nerve impulse transmission.

Uptake : Monocrotophos can be absorbed following ingestion, inhalation and skin contact.

Metabolism : In mammals, the primary conversion products of monocrotophos are dimethyl phosphate, O-desmethyl monocrotophos and N-desmethyl monocrotophos. N-desmethyl monocrotophos is more toxic than monocrotophos.

Concentration µg/ml	Growth of bacteria
100	+
200	+
300	+
400	+
500	+
600	+
700	-
800	-
900	-
1000	-
Blank	-

'+'indicates growth of bacteria (resistant to monocrotophos), '-'indicates inhibition of growth of bacteria (sensitive to monocrotophos).

Determination of MIC by agar plate dilution method. YEMA Agar plate dilution test was used to determine the Minimum Inhibitory Concentration (MIC) of an antimicrobial agent.

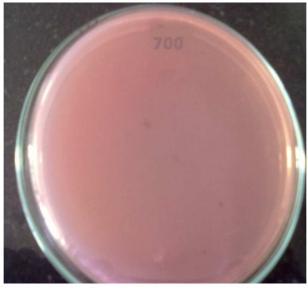
Scholars Research Library

Interpretation of results -

The MIC represents the concentration of antimicrobial at which there is complete inhibition of growth. In reading the end points, a barely visible haze of growth or a single colony is disregarded.

RESULTS AND DISCUSSION

Plates that have concentration 700 μ g/ml showed no growth hence that concentration is MIC for Rhizobia



Sequence use for alignment (GOR an chau fasman 2D and spdv for 3D)

Accession no. from Protein Data Bank

>gi|240856680|gb|ACS54347.1| Scaffold protein Nfu/NifU [Rhizobium leguminosarum bv. trifolii WSM1325] MFIQTEATPNPATQKFLPGKVVMENGTAEFRSTEEAQASPLAARLFEISGVTGVYFGYDFISVSKDNADW QHLKPAILGSIMEHFMSGKPVMGDASILSEDADAGDEFFDEGDESIVLTIKELLETRVRPAVAQDGGDIT FRGFKDGKVYLNMKGSCAGCPSSTATLKHGVQNLLRHFVPEVQEVIAA

E-value-1e.79

	<u>s:</u> ⊙ GenPept	Send to: 🖸	Change region shown
•	fixing NifU-like protein [Roseovarius sp. 1	[M1035]	Customize view
	e Sequence: ZP_01879943.1		
FASTA Graph	<u>cs</u>		
<u>Go to:</u> 🕑			Analyze this sequence Run BLAST
LOCUS	ZP_01879943 187 aa linear	BCT 09-NOV-	Identify Conserved Domains
2010 DEFINITION	niture dining Width Libe and in The second second	71 1 00 51	Highlight Sequence Features
ACCESSION	nitrogen-fixing NifU-like protein [Roseovarius sp. 2P 01879943	IM1035].	Find in this Sequence
VERSION	ZP_01879943.1 GI:149202972		
DESOURCE	REFSEQ: accession <u>NZ ABCL01000005.1</u>		
KEYWORDS SOURCE	Roseovarius sp. TM1035		Identical proteins for ZP_01879943.1
	Roseovarius sp. TH1035		nitrogen-fixing NifU-like protein [Ros [EDM3
	Bacteria; Proteobacteria; Alphaproteobacteria; Rhod	dobacterales;	Se
COMMENT	Rhodobacteraceae; Roseovarius. PREDICTED REFSEQ: This record has not been reviewed	l and the	
CONTRACT	function is unknown. The reference sequence was der		Related information
	<u>EDM31554</u> . Method: conceptual translation.		BLink
FEATURES	Location/Qualifiers		Related Sequences
source	1187		Identical Proteins
	/organism="Roseovarius sp. TM1035" /strain="TM1035"		
	/db xref="taxon:391613"		BioProject
Protein			CDD Search Results
	/product="nitrogen-fixing NifU-like protei	n"	Conserved Domains (Concise)
Region	/calculated_mol_wt=19872 389		Conserved Domains (Full)
Region	/region name="Nfu N"		Domain Relatives
	/note="Scaffold protein Nfu/NifU N termins	al: c107364"	Genome
	/db xref="CDD:208680"		Ochunic

>gi|209533392|gb|ACI53327.1| Scaffold protein Nfu/NifU [Rhizobium leguminosarum bv. trifolii WSM2304] MFIQTEATPNPATQKFLPGKVVMENGTAEFRSAEEAEASPLAARLFEIPGVTGVYFGYDFISVSKDDAEW QHLKPAILGSIMEHFMSGKPVMGDASILSEDVDAGDEFFDEGDESIVLTIKELLETRVRPAVAQDGGDIT FRGFKDGKVYLNMKGSCAGCPSSTATLKHGVQNLLRHFVPEVQEVIAA

Display Settings: 🕑	GenPept	Send to: 🕑	Change region shown	٠
nifU domain p	protein [Rhodobacterales bacterium HTCC2150]			
NCBI Reference Sec	guence: ZP 01740872.1		Customize view	*
FASTA Graphics				
			Analyze this sequence	
Go to: 🖂			Run BLAST	
LOCUS ZP 0174	10872 187 aa linear BCT 09-NOV-2010		Identify Conserved Domains	
DEFINITION nifU do	main protein [Rhodobacteraceae bacterium HTCC2150].		Highlight Sequence Features	
ACCESSION ZP_0174			Find in this Sequence	
	0872.1 GI:126725029 : accession NZ AAXZ01000001.1		Find in this dequence	
KEYWORDS .				
	cteraceae bacterium HTCC2150		Identical proteins for ZP_01740872	2.1 🖻
	acteraceae bacterium HTCC2150 a: Proteobacteria: Alphaproteobacteria: Rhodobacterales;		nifU domain protein [Rhodobacter [E	BA05283]
	icteraceae.			See all
COMMENT PREDICT	TED REFSEQ: This record has not been reviewed and the			Jee all
	on is unknown. The reference sequence was derived from			
EBA0528	3. conceptual translation.		Related information	
FEATURES	Location/Qualifiers		BLink	
source	1187		Related Sequences	
	/organism="Rhodobacteraceae bacterium HTCC2150" /strain="HTCC2150"		Identical Proteins	
	/db xref="taxon:388401"		BioProject	
Protein	1187		CDD Search Results	
	/product="nifU domain protein"			
Region	/calculated_mol_wt=19943 389		Conserved Domains (Concise)	
Negron	/region name="Nfu N"		Conserved Domains (Full)	
	/note="Scaffold protein Nfu/NifU N terminal; cl07364"		Domain Relatives	
	/db_xref="CDD: <u>208680</u> " 108185		Genome	
Region	108.185 /region name="NifU"		Nucleotide	
	/note="NifU-like domain; cl00484"		Related Structures (List)	
	/db_xref="CDD:153799"		Related Structures (Summary)	
CDS	1187 /coded by="NZ AAXZ01000001.1:775325775888"			
	/note="COG0694 Thioredoxin-like proteins and domains"		Taxonomy	
	/transl_table=11		WGS Project	
ORIGIN	n patlkflpgg tvletgtadf psaetadgsp latrifgigg iagvffgndf			
	e wdhikpailg aimehfgagg pylagentap ahaeaaneed keivggikel		Recent activity	
	a qdggditfhg fdrgivylhm qgacagcpss tltlkmgien llrhyipevv		· · · · · · · · · · · · · · · · · · ·	Off Clear
181 evrpvaa			nifU domain protein (Rhodobacte	
11			bacterium HTCC2150]	Protein
			Q gi[209533392]gb[ACI53327.1] Sc protein	affold BLAST
				See more

Alignment Result:-

Query sequence	Subject
Sequence no.1 >gi 240858659 gb ACS56326.1 nitrogen-fixing NifU domain protein [Rhizobium leguminosarum bv. trifolii WSM1325]	LOCUS CBI80951 145aa Linear BCT 25May2011 DEFINATION Conserved Hypothetical Protein [Bartonella sp. 1-1c] E-value 1e.40
Sequence no.2 >gi 209535198 gb ACI55133.1 nitrogen-fixing NifU domain protein [Rhizobium leguminosarum bv. trifolii WSM2304]	LOCUS CBI179370 145aa Linear BCT 25May2011 DEFINATION Conserved Hypothetical Protein [Bartonella sp.AR 15-3] E-value 1e.40
Sequence no.3 >gi 240856680 gb ACS54347.1 Scaffold protein Nfu/NifU [Rhizobium leguminosarum bv. trifolii WSM1325]	LOCUS ZP_01879943 187aa Linear BCT 09 Nov 2010 DEFINATION nitrogen fixing NifU-like protein [Roseovarius sp. TM1035] E-value 1e.79
Sequence no.4 >gi 209533392 gb ACI53327.1 Scaffold protein Nfu/NifU [Rhizobium leguminosarum bv. trifolii WSM2304]	LOCUS ZP_0174087 187 aa linear BCT 09-NOV-2010 DEFINITION nifU domain protein [Rhodobacteraceae bacterium HTCC2150]. E-value 1e.79

2D structure prediction method (GOR and chau fasman)

Sequence 3

		bv. trifolii									
quence co	onsis	ts of 188 a	mino a	acids.							
irget Sec	luei	ce:									
LXPAILGS	IME	KFLPGK VV GMSGKP VM GSCAGC PS:	DASIL:	SE DAI	AGDEFT	D EGDESIN	ALTI KELL				
	фш				n la lina	1			1 <mark>0 mi</mark>		- He1 - She - Tur - Co1
econdary	∕ Sta	ucture:									
li×1 ·	91F103 < EEEEE :		* EFLPGX EFFEEEE T	ovanenic >	* TAEFRS: < T	1		* GVTGVYFGYI > EEREEREER	< 60	1	
ery 61 lix 61 eet 61 l urns 61	 EE	* EDRADOQHLNI EEEEEI TTT		IMEHFN > EEEEE	* 13 GKPUM TT	* GDASILSEI < T	ADAGDEFT	EEE	- 12	0 0	
ery 121) lix 121) eet 121) mrs 121		* TEVEPAVAQ EEEE T T T	* DGGDITI EEE F T	≺	* OGKVYLN EEEE T	>	SSTATLKH < EEEEEE T T		- 18	0	
ery 181)	EVQE	71AA 188									
lix 181 eet 181 1		188									
INS 181		188									
tal Resi	due s	H: 139	E: 10	0 T:	25						
tal Resi Per	due <i>s</i> cent	H: 139 H: 73.9	E: 10 E: 53	0 T: .2 T:	25 13.3						
tal Resi Per	dues cent	H: 139 H: 73.9	E: 10 E: 53	0 T: .2 T:	25 13.3						
tal Resi Per	due <i>s</i> cent	H: 139 H: 73.9	E: 10 E: 53	0 T: .2 T:	25 13.3						
Per	cent	H: 139 H: 73.9	E: 53	.2 T:	13.3	60R meth	od and We	ural Netwo	rk m	ethod	
Per	of o	H: 73.9	E: 53	.2 T:	13.3 method,			ural Netwo	rk m	ethod	
Per	of o y: ম	H: 73.9 comparing C 없 단 뒤	E: 53 hov-Fa	.2 T: sman 1	13.3 method,	115	140	168 172 178	188	— alpha hi	
Per	of o y: ম	H: 73.9	E: 53 hov-Fa	.2 T: sman m	13.3 method,				188		
Per Result Summar	of of a	H: 73.9 :omparing C 의 용 뒤	E: 53 hov-Fa	.2 T: sman 1	13.3 method,	115	140	168 172 178	188	— alpha hi	
Per Result Summar	of e y: ন হ:	H: 72.9 comparing C 의 유 리 용 유	E: 53	. 2 T:	13.3 method,	115 115 115	142 142 152	- 170 168 172 178	188	— alpha hi	
Per Result Summar	of e y: ন হ:	H: 73.9	E: 53	.ž T: sman s ž 8 ž 8	13.3 eethod,	EEAQASPLAA	RLFEISGVTG	ACT	188	— alpha hi	
Result Summar Detail AAseq. CF GOR	of e y: ন হ:	H: 73.9	E: 53	.ž T: sman s ž ž ž š	12.3 eethod, E S GTAEFRST THAHAAH	НИНСКИИНИ	RLFEISGVTG HHHCEEEEEE	ACT ACT ACT ACT ACT ACT ACT ACT ACT ACT	188	— alpha hi	
Peri Result Summar Detail AAseq. CF	of e y: ন হ:	H: 73.9	E: 53	. ž T: sman	13.3 sethod, s S g GTAEFRST HIHHCHH	Н 9 Н 9 ННЮССИНИНИИ ИНИНАСНИИИ СССИНИНИИИ	RLFEISGVTCH HHHCEEEEEE HHEEETTEEEI	YFGYDF EEEEEE EEEEEE	188	— alpha hi	
Result Summar Detail AAseg. CF GOR NN	of a y: N SS: 1	METOCOCCCC	E: 53	SBAN I SBAN I SBAN I S KVVMEN SEEECOCC CEEEET CEEEECOCC	L3.3 Bethod, B S GTAEFRST HINHCCHT		RLFEISGYTGA HHHCEEEEEEI HHERETEEEI HHHCCCCEEEI	ALL CONTRACTOR OF CONTRACTOR O	188	— alpha hi	
Result Summar Detail AAseq. CF AAseq. CF	of a y: N SS: 1	N: 73.3	E: 53	SBAR S SBAR S SBAR S SBAR S S S S S S S S S S S S S S S S S S S	L3.3 sethod, g g TAEFRST HINHCOM THINHIGH CCCCCCC CCCCCCCH MSCKPVMC CCCCEECC		RLFEISGYTG RLFEISGYTG HHCEEEEEE HHEFETEEEE HHHCCCCEEI AGDEFFDEGDI HHHMCCC	YYFGYDF CEEEEEE EEEEEEE EEEEEEE SSIVLTI EEEEEH	188	— alpha hi	
Result Summar	of a y: N SS: 1	N: 73.9	E: 53 hou-Fa 5 3 3 ATOKFLP(CHIECCT) COCCCCCCC CHIECCT) COCCCCCCC CHIECCT) COCCCCCCC	SBAN S SBAN S SBAN S SBAN S SSIMENT SCIENCES SSIMENT S	13.3 sethod, graefsst hinhicchi Thinhichi cccccccc ccccccchi msgkPvmg cccccccc https://		RLFEISCVTG HHHCEEEEEEH HHHCEEEEEEH HHHCCCEEEEI HHHCCCEEEEI HHHCCCEEEEI	VYEGYDF CEEEEEEE EEEEEEE EEEEEEE EEEEEEE EEEEEE	188	— alpha hi	
Result Summar Detail AAseq. CF GOR NN Joint AAseq. CF GOR	of a y: N SS: 1	H: 73.9	E: 53 hou-Fa 5 3 3 ATOKFLP(CHIECCT) COCCCCCCC CHIECCT) COCCCCCCC CHIECCT) COCCCCCCC	SBAN S SBAN S SBAN S SBAN S SSIMENT SCIENCES SSIMENT S	13.3 sethod, graefsst hinhicchi Thinhichi cccccccc ccccccchi msgkPvmg cccccccc https://		RLFEISCVTG HHHCEEEEEEH HHHCEEEEEEH HHHCCCEEEEI HHHCCCEEEEI HHHCCCEEEEI	VYEGYDF CEEEEEEE EEEEEEE EEEEEEE EEEEEEE EEEEEE	188	— alpha hi	
Result Summar Detail AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint AAseq.	of (y: ਨ * s= 1	H: 73.9	E: 53 hou-Fa b a s s s s s s s s s s s s s s s s s	SBAR SBAR SBAR SBAR SBAR SBAR SBAR SBAR	13.3 sethod, s S S GTAEFEST HHHCHH MSGKPVMG CCCCCCCH MSGKPVMG CCCCCCCC CCCCCCCCC CCCCCCCCC CCCCCC		RLFEISGVTG HHOEEEEEE HHEEEEEEE HHEECEEEEE HHEECEEEE HHEECEEEE	VYFGYDF CEEEEEE	188	— alpha hi	
Result Summar Detail AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint	of (y: ਨ * s= 1	H: 73.9	E: 59 hou-Fa b a a a a a a a a a a a a a a a a a a	SBAR I SBAR I SBAR I SKYVMEN RCEEFT CEEFCC CEEFCC SIMEHT CEEFCCC CEEFCC CEEFCC CEEFCCCC CEEFCCCC CEEFCCCC CEEFCCCC CEEFCCCCCC CEEFCCCCCCC CEEFCCCCCCCC	13.3 sethod, s		RLFFISGYTG* RLFFISGYTG* HHPEEEEEEEH HHPEEEEEEEH HHPECCCEEET HHPECCCEEET HHPECCCEEET HHPECCCEEET HHPERHOCCCC HHPHPHCCCC HHPHPHCCCC	YAFGYDF SECENCE SECENCE SECENCE SSIVLTI SSIVLTI SSIVLT	188	— alpha hi	
Result Summar Detail AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint	of (y: ਨ * s= 1	N: 73.3	E: 59 hou-Fa bou-Fa bou	SBORN	L3.3 Hethod, CTAEFEST HETHORN GTAEFEST HETHORN HESKPARG CCCCCCCCH CCCCCCCCC CCCCCCCCC CCCCCCCC		RLFEISCVTG HHVCEREEEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE H	VYEGYDF CEEEEEE EEEEEEE EEEEEEE EEEEEEE SIVLTI EEEEEHH HILLBHFYP HILEDOOC HILEEOOC HILEEOOC	188	— alpha hi	
Result Summar Detail AAseq. CP GOR NN Joint AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint	of (y= ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	H: 73.3	E: 59 hou-Fa bou-Fa bou	SBORN	L3.3 Hethod, CTAEFEST HETHORN GTAEFEST HETHORN HESKPARG CCCCCCCCH CCCCCCCCC CCCCCCCCC CCCCCCCC		RLFEISCVTG HHVCEREEEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE H	VYEGYDF CEEEEEE EEEEEEE EEEEEEE EEEEEEE SIVLTI EEEEEHH HILLBHFYP HILEDOOC HILEEOOC HILEEOOC	188	— alpha hi	
Result Summar Detail AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint AAseq. CF	of (y= ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	H: 73.3	E: 59 hou-Fa bou-Fa bou	SBORN	L3.3 Hethod, CTAEFEST HETHORN GTAEFEST HETHORN HESKPARG CCCCCCCCH CCCCCCCCC CCCCCCCCC CCCCCCCC		RLFEISCVTG HHVCEREEEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE H	VYEGYDF CEEEEEE EEEEEEE EEEEEEE EEEEEEE SIVLTI EEEEEHH HILLBHFYP HILEDOOC HILEEOOC HILEEOOC	188	— alpha hi	
Result Summar Detail AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint AAseq. CF GOR NN Joint	of (y= ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	H: 73.3 Comparing C Pl P F R P R P R P R P R P R P R P R P	E: 59 hou-Fa bou-Fa bou	SBORN	L3.3 Hethod, CTAEFEST HETHORN GTAEFEST HETHORN HESKPARG CCCCCCCCH CCCCCCCCC CCCCCCCCC CCCCCCCC		RLFEISCVTG HHVCEREEEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE HHVHCCCCEE H	VYEGYDF CEEEEEE EEEEEEE EEEEEEE EEEEEEE SIVLTI EEEEEHH HILLBHFYP HILEDOOC HILEEOOC HILEEOOC	188	— alpha hi	

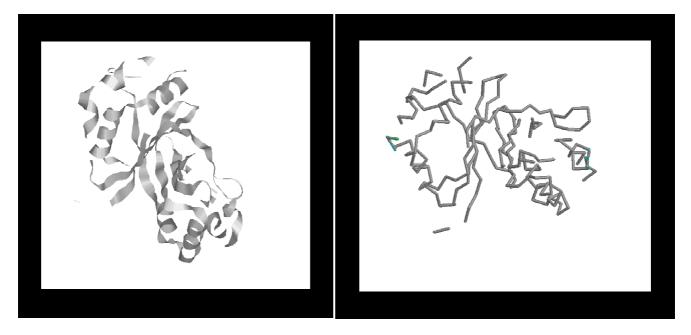
Sequence 4

Semier	nce consists of 188 amino acids.
-	
	t Sequence:
QHLKP	EATEN PATQATLPEK VAMERATAET ESTEERAGASP LAARLPEISE VTEVVPEVNEF ISVSKUNADO ALLES IMERANSEKP VMEDARILSE DADAGDEFTD EGEBSIVLTI KELLETKVEP AVAQDGEDIT DEKVY LINNESIGAET PSSTATLEG VQMLLENEVP EVQEVIAA
Secor	ndary Structure:
Query	* * * * * * 1 MFI (TEATPAPAT (KFLP6KVAMENGTAEFRSTEEA QASPLAARLFEI SGVTGVYFGYDF 60
Helix	$1 \langle \cdots \rangle \langle \cdots \rangle \langle \ \delta 0 \\$
Sheet Turns	1 EFFERE EFFEREE 60 1 T T T T 60
	* * * * *
Query	61 I SVSNIMATMORENDA I LES IMPERIMS ENDIMEDAS I LS EDADA EDPEDECTES I M.T. 1/20
Helix	61 120
Turns	
	* * * * *
Querv	121 KELLETKORPAVAQD56D1TFR6FKD6KVYLMMK63CA5CP3STATLKH6VQMLLRHFVP 180
Helix	121 180
Sheet Turns	THE PROPERTY TO A PROPERTY TO A PROPERTY TO A
Querv	181 EVQEVIAA 188
Helix	181> 188
Sheet Turns	181 EEEE 188 181 188
	Residues: H: 129 E: 100 T: 25 Percent: H: 73.9 E: 53.2 T: 13.3 comparing Chou-Fasman method, 60R method and Meural Network method
ult of mary:	Percent: H: 73.9 E: 53.2 T: 13.3 comparing Chou-Fasman method, 60R method and Meural Network method
ult of	Percent: H: 73.9 E: 53.2 T: 13.3
ult of mary: ਨ	Percence: H: 79.9 E: 59.2 T: 19.9 comparing Chov-Fasman method, GOR method and Neural Network method
ult of mary: ম	Percence: H: 79.9 E: 59.8 T: 19.9
ult of mary: ਨ	Percence: H: 79.9 E: 59.8 T: 19.9
ult of mary: 치 ails:	Percence: H: 79.9 E: 59.2 T: 19.9
ult of mary: ম	Percence: H: 72.9 E: 53.2 T: 12.9
ult of mary: 치 ails:	Percence: H: 72.9 E: 53.2 T: 12.9 comparing Chou-Fasman method, 60R method and Neural Network method A B B B B B B B B B B B B B B B B B B
ult of mary: 치 ails:	Percence: H: 72.9 E: 53.2 T: 12.9
ult of mary: 치 ails:	Percence: H: 79.9 E: 59.2 T: 19.9
ult of mary: না ails: বু.	Percence: H: 72.9 E: 53.2 T: 12.9 comparing Chov-Fasman method, 60R method and Neural Network method Method
ult of mary: ন ails: q.	Percence: H: 72.9 E: 53.2 T: 12.9 comparing Chov-Fasman method, 60R method and Neural Network method Method
ult of mary: ন ails: q.	Percence: H: 73.9 E: 53.2 T: 13.9
ult of mary: ন ails: q.	Percence: H: 73.9 E: 53.2 T: 13.3
ult of mary: ह ails: q. t t	Percence: H: 173.9 E: 53.2 T: 13.3
ult of mary: ন ails: q.	Percence: H: 73.9 E: 53.2 T: 13.3
ult of mary: रा बोls: प् t t	Percence: H: Y2.9 E: 53.2 T: 12.9
ult of mary: रा बोls: प् t t	Percence: H: 73.9 E: 53.2 T: 13.9
ult of mary: रा बोls: प् t t	Percence: H: Y2.9 E: 53.2 T: 12.9
ult of mary: रा बोls: प् t t	Percence: H: 73.9 E: 53.8 T: 13.9
ult of mary: रा बोls: प् t t	Percent: H: 19.9 E: 59.8 T: 19.9
u lt of ma ry : مils: q. t t t	Percence: H: 19.9 E: 59.8 T: 19.9 comparing Chou-Fasman method, 60B method and Meural Network method a B <
u lt of ma ry : مils: q. t t t t t	Percence: H: 19.9 E: 59.8 T: 19.9
u lt of ma ry : مils: q. t t t t t	Percent: B: 19.9 E: 59.8 T: 19.9 comparing Chou-Fasman method, 608 method and Meural Metwork method a
u lt of ma ry : مils: q. t t t t t	Percence: H: 19.9 E: 59.8 T: 19.9

3D structure prediction by using rasmol.

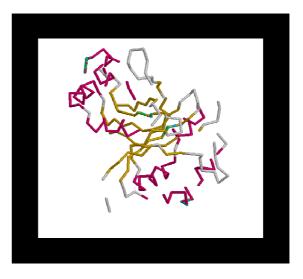
Pdb 2 ribbon

2QLW Crystal structure of rhamnose mutarotase RhaU of Rhizobium leguminosarum



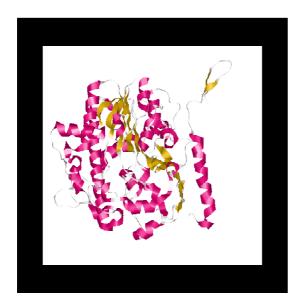
Pdb 3 ribbon 2QLX Crystal structure of rhamnose mutarotase RhaU of Rhizobium leguminosarum in complex with L-Rhamnose

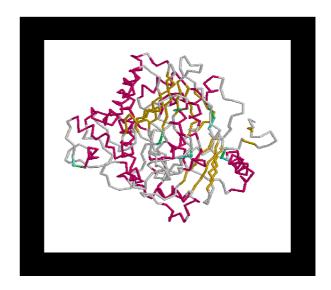




Pdb 4 ribbon

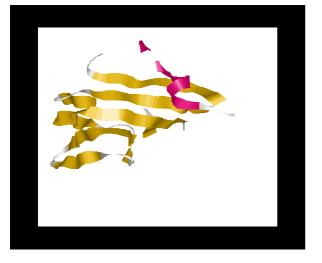
2VQR CRYSTAL STRUCTURE OF A PHOSPHONATE MONOESTER HYDROLASE FROM RHIZOBIUM LEGUMINOSARUM A NEW MEMBER OF THE ALKALINE PHOSPHATASE SUPERFAMILY

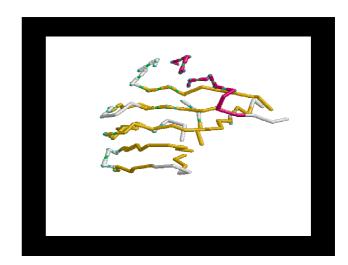




Pdb 5 ribbon

3LWC Crystal structure of Structural Genomics, unknown function (YP_766765.1) from Rhizobium leguminosarum BV. Viciae 3841 at 1.40 A resolution





CONCLUSION

On the basis of MIC & MBC the Nitrogen Fixing Rhizobia (Cicer arietinum) were Resistance to Pesticide (Monocrotophos), up to $600 \mu g/ml$ concentration, and Its growth is inhibited at concentration $700 \mu g/ml$.

After the NCBI searching we found four protein sequences that are similar to that of nitrogen fixing protein found in Rhizobia.

Scholars Research Library

From observation and results we can conclude that other than Rhizobia, there are four protein sequences that fix nitrogen, In future we plan to study these sequences for nitrogen fixation in other than leguminous plants.

REFERENCES

[1]- Andrews, J.M. Journal of Antimicrobial Chemotherapy 48 (Suppl. 1):5-16, (2001). PMID 11420333.

[2]- Turnidge JD, Ferraro MJ, Jorgensen JH (**2003**) Susceptibility Test Methods: General Considerations. In PR Murray, EJ Baron, JH Jorgensen, MA Pfaller, RH Yolken.Manual of Clinical Microbiology.8th Ed. Washington. American Society of Clinical Microbiology. p 1103

[3]- Medical microbiology, Mims and Playfair, Mosby Europe, 1993, 35.31.

[4]- French GL (December 2006). J.Antimicrob.Chemother. 58 (6): 1107–17.doi:10.1093/jac/dkl393. PMID 17040922.

[5]http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastp&BLAST_PROGRAMS=blastp&PAGE_TYPE=Blast Search&SHOW_DEFAULTS=on&LINK_LOC=blasthome

 $http://www.rcsb.org/pdb/results/results.do?outformat = \&qrid = DFB246C4\&tabtoshow = Current \\ \label{eq:constraint} between the the second s$

[6]-http://spdbv.vital-it.ch/

[7]- "Current taxonomy of rhizobia".Retrieved 2006-08-07.

[8]- "Taxonomy of legume nodule bacteria (rhizobia) and agrobacteria". Retrieved 2008-11-14.

[9]- "What is Rhizobia". Retrieved **2008**-07-01.

[10]-Giraud, Eric; et al., L; Vallenet, D; Barbe, V; Cytryn, E; Avarre, JC; Jaubert, M; Simon, D et al (**2007**). "Legumes symbioses: absence of nod genes in photosynthetic bradyrhizobia". *Science* 316 (5829): 1307–12. doi:10.1126/science.1139548.PMID17540897.

[11]- Denison, R. F. 2000. American Naturalist 156:567-576

[12]- Kiers ET, Rousseau RA, West SA, Denison RF 2003. Nature 425 : 79-81

[13]- Simms et al. **2006**. An empirical test of partner choice mechanisms in a wild legume-rhizobium interaction. *Proc. Roy. Soc.* B 273:77-81.

[14]- Heath, K. D., and P. Tiffin. 2009. Evolution 63:652-662

[15]- Marco, D. E., R. Perez-Arnedo, A. Hidalgo-Perea, J. Olivares, J. E. Ruiz-Sainz, and J. Sanjuan. 2009. Acta Oecologica-International Journal of Ecology 35:664-667