

水稻白叶枯病菌*PXO_03877*基因 表达蛋白质的结构域保守性分析

**Analysis of *PXO_03877* Putatively-Encoding c-di-GMP
Signaling Protein Domain Conservation**

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报告人：薛丁榕

小组成员：梁慧芳、黄凤霞、尚晓楠



汇报内容

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- 背景介绍
- 研究目的
- 路线设计
- 分析过程
- 结论



背景介绍



- 1、水稻白叶枯病是由水稻黄单胞水稻致病变种 (*Xanthomonas oryzae* pv. *oryzae*, 简称Xoo)引起的世界水稻生产上重要的细菌病害之一，是我国的一种检疫性病害。
- 2、环鸟苷二磷酸(c-di-GMP)是一种新发现的细菌的新型第二信使，并发现磷酸二脂酶(PDE) 控制其水解，EAL结构域是PDE的活性中心。
- 3、在Xoo中只有PXO_03877和PXO_04753两个基因的结构域蛋白单独存在EAL结构域。





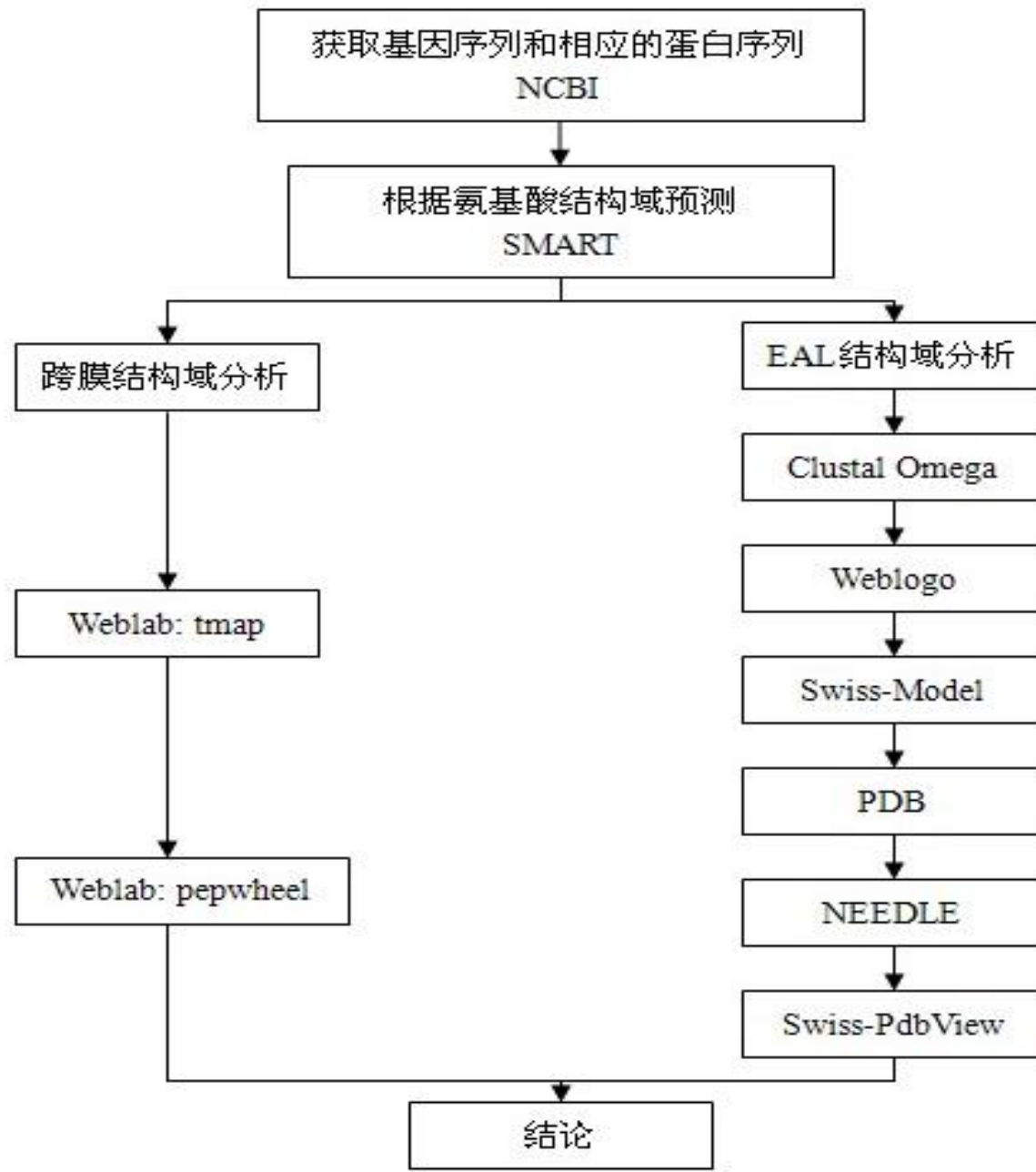
研究目的

明确水稻白叶枯病菌*PXO_03877*基因表达的蛋白质结构域是否保守，是否应该继续进行后续实验



路线设计

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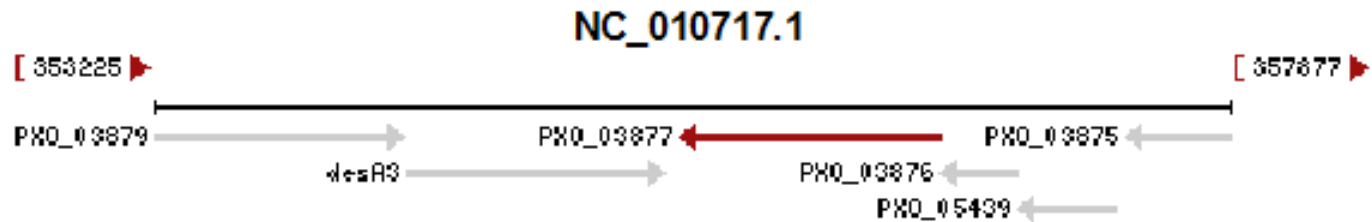
分析过程





■ NCBI Gene

NC_010717.1 (355498..356622, complement)



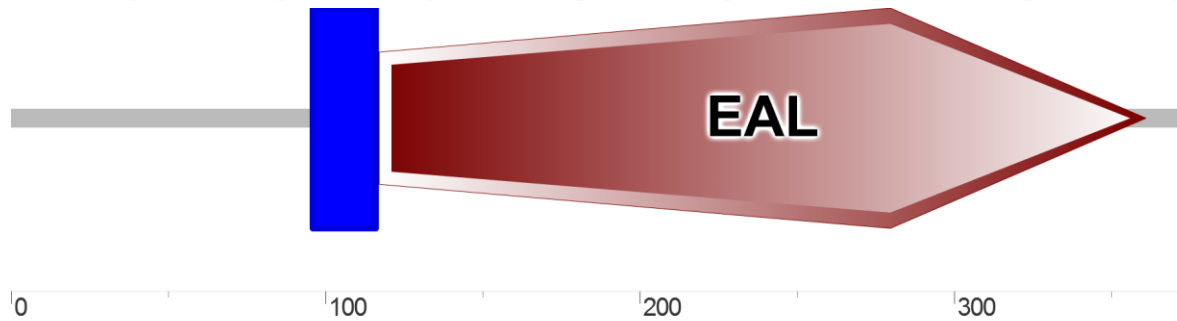
■ SMART



Length	374 aa
Source database	UniProt
Identifiers	B2SID8_XANOP, B2SID8



SMART



Confidently predicted domains, repeats, motifs and features:

Name	Start ▲	End	E-value
transmembrane region	96	115	N/A
EAL	117	361	5.18e-91

Transmembrane region

This is a transmembrane helix region, as detected by the [TMHMM v2.0](#) program. The region starts at position **96** and ends at position **115**.

Transmembrane region (20 aa):

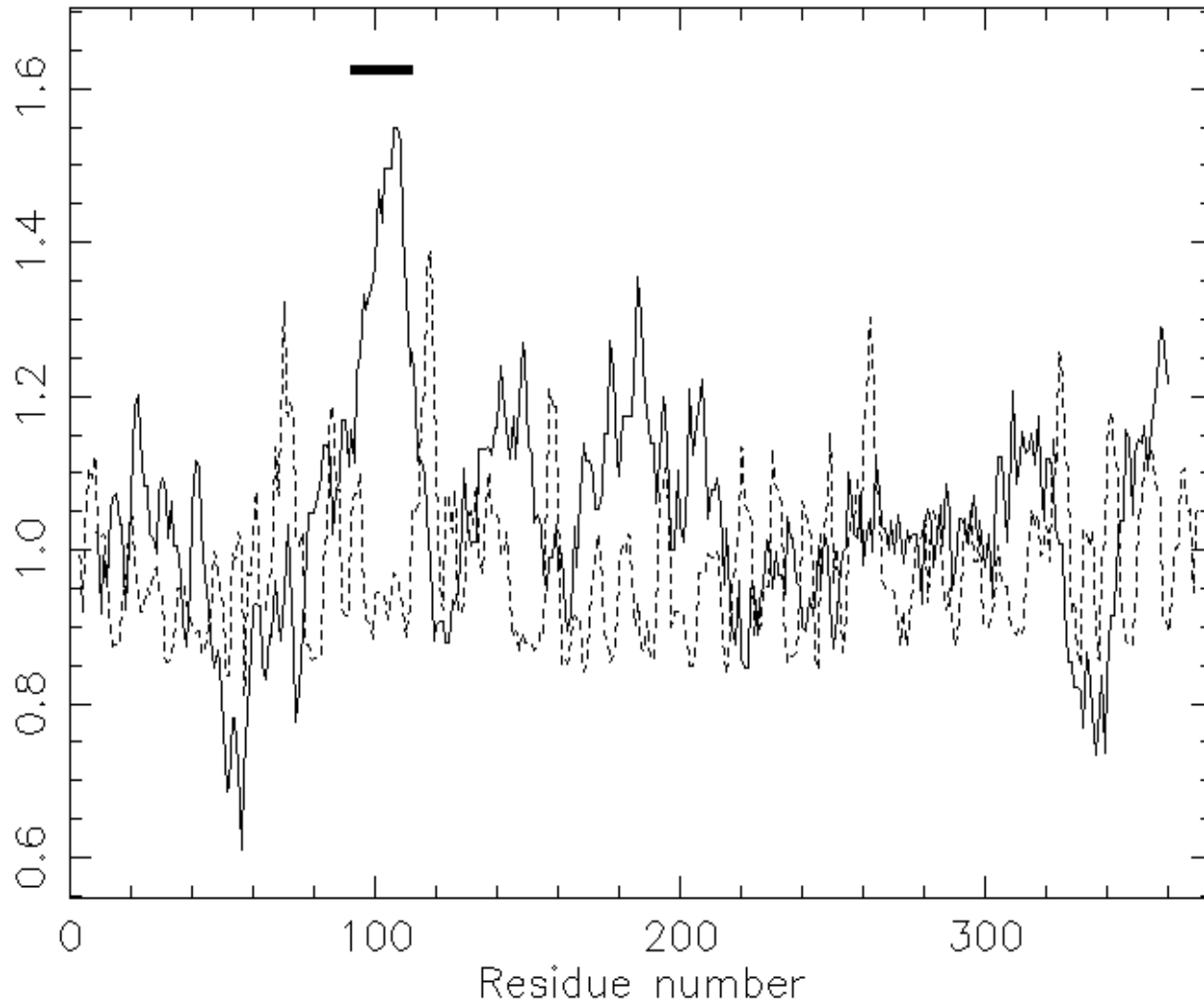
[Submit to BLAST](#)

[Copy to clipboard](#)

LVPVGI~~AVALLV~~GAVLWVS

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PLAAARLQLVPVGI A VALLV GAVLWVSR



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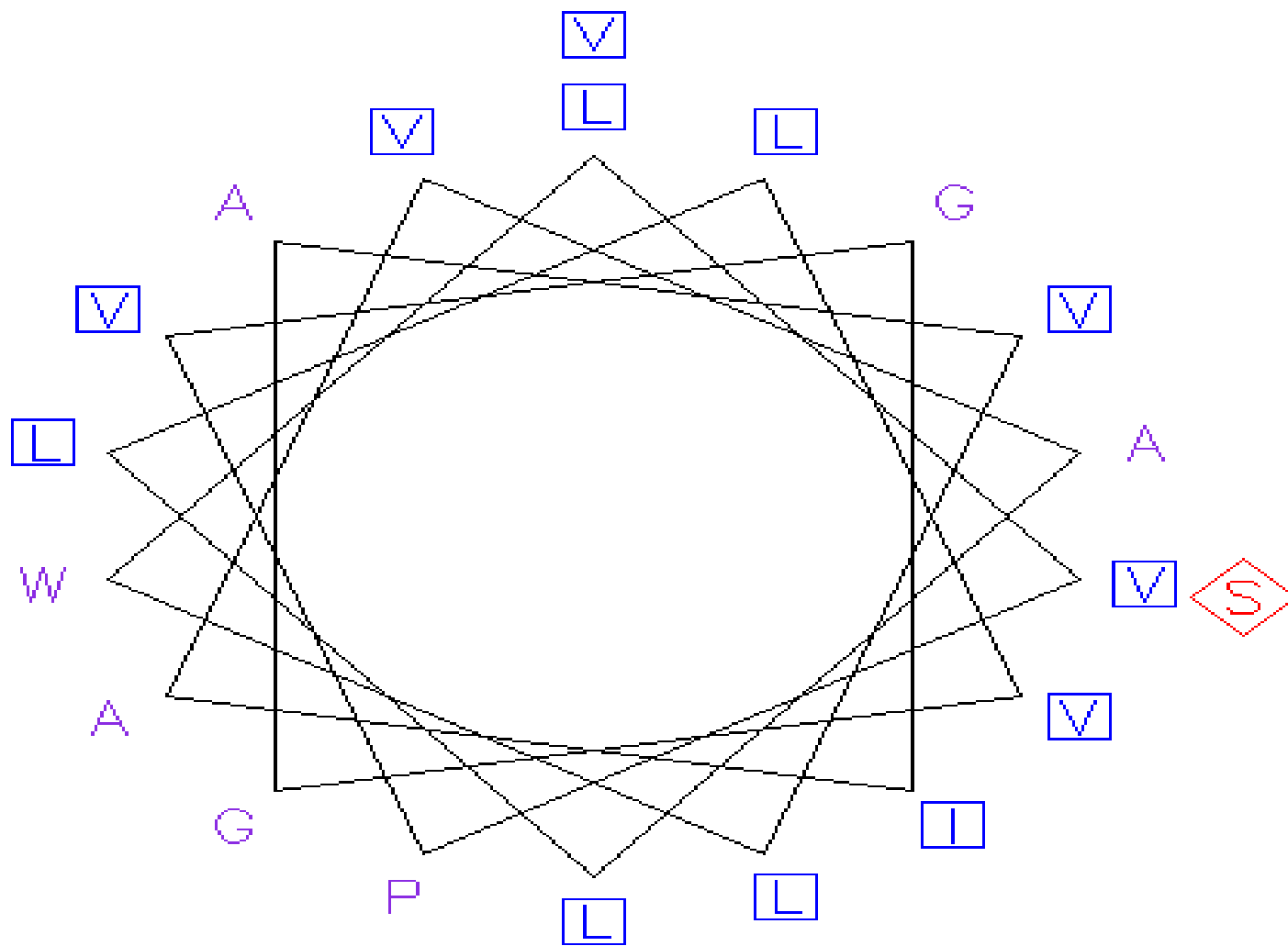
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EAL domain

This is a SMART **EAL** domain ([full annotation](#)).



Position: 117 to 361

E-value: 5.18390357802076e-91 ([HMMER2](#))

SMART ACC: [SM000052](#)

Definition: Putative diguanylate phosphodiesterase

Description: Putative diguanylate phosphodiesterase, present in a variety of bacteria.

**Interpro abstract
([IPR001633](#)):**

This domain is found in diverse bacterial signalling proteins. It is called EAL after its conserved residues. The EAL domain is a good candidate for a diguanylate phosphodiesterase function [([full abstract](#))]

EAL domain sequence (245 aa):

[Submit to BLAST](#)

[Align with the SMART alignment](#)

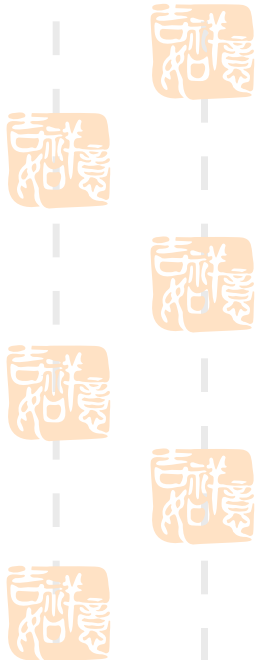
[Copy to clipboard](#)

```
RRLSPLARPEIAVQRGEFIVHYQPIIALDSGACVGAELVVRWQQPDGVLVPPDAFIPLAE  
ESGLILPITDLVVAEVIRELGPTLAADPALHVAINVSAEDIKSSRVQSVLEHALRGTGVD  
SGQLWVEATERSLMDIDAARTTIMRLRGAGHTVSIDDFGTGYSSLQYLQGLPLDALKIDK  
SFVDTIGTHSATSAVSAHIEMAKTLRLRTIAEGVERQEQLDYLRAGVDLAQGWLFSSRA  
LPATG
```

多序列比对: Clustal Omega



- * 表示该位点保守
- : 表示该位点次保守
- . 表示该位点较保守



CLUSTAL O(1.1.1) multiple sequence alignment

```

YkuT-Bs      -----DVLPHYQAIFSAEEQKVVGVEVLGRILADSEIQSLGPPFL-----
RocR-Pa      -----ADVVRGLDNGEFEAYYQPKVALDGGGLIGAEVLLARWNHPHLGVLPPSHFLYVME
VieA-Vc      -----EIEQAFLHDHIFNYYQPFDFRSGAMVGV EALVRYEHPHMGMLSPAVFLPLIE
PXO_03877    RRLSPLARPEIAVQRGEFIVHYQPIIALDMSGACVGA EALVRWQQPDGVLVPPDAFIPLAE
CC_3396-Cc   -----ADLRGAIGRGEITPYFQPIVRLSTGALSGFEALARWIHPRRGMLPPDEFPLPLIE
TBD1265      -----TRLRQALERNELVLHYQPIVELASGRIVGGEALVRWEDPERGLVMPSAFIPAAE

```

 .. :* * * * * :

```

YkuT-Bs      DAGIPEEYKLEVDNRIIRQALDRFLEAD---SDLLRFMNQDANLLMLDHGESFLELLKEY
RocR-Pa      TYNLVDKLFWQLFSQG---LATRRKLAQLGQPINLAFNVHPS--QLGSRALAENISALL
VieA-Vc      QCGLHEKLFLLTVLEKSVSA-LAS-----IGADLQLSVNISQR--NLQHSICDPI-LAIC
PXO_03877    ESSLILPITDLVVAEVIRE-LGPTLAAD---PALHVAINVSAE--DIKSSRVQSVLEHAL
CC_3396-Cc   EMGLMSELGAHMMHAAAQQ-LSTWRAAHPAMGNLTVSVNLSTG--EIDRPGLVADVAETL
TBD1265      DTGLIVALSDWVLEACCTQ-LRAWQQQGRAADDLTLSVNI STR--QFEGEHLTRAVDRAI

```

 : * : * :

```

YkuT-Bs      EAKGIELHRFVLEITEHNFEGDIEQLYHMLAYYRTYGIKIAVDNIGKESNLDRIALLSF
RocR-Pa      TEFHLPSSVMFEITETGLISAPASSLENLVRRLRIMGCCGLAMDDFGAGYSSLDRLCEFPF
VieA-Vc      ERYGFPAKLTLEMTHEVYNRTPISLANLARLRMYGVGLSIDDFTGTGYASLGQLAQLPF
PXO_03877    RGTGVDSGQLWVEATERSLMD-IDAARTIMRLRGAGHTVSIDDFTGTGYSSLQYLQGLPL
CC_3396-Cc   RVNRLPRGALKLEVTESDIMRDPERA AVILKTLRDAGAGLALDDFTGTGFSSLSYLTRLPF
TBD1265      ARSGLRPDCLELEITENVMLVMTDEVRTCLDALRARGVRLALDDFTGTGYSSLSYLSQLPF

```

 - * ** : * * :::*:* : * :

```

YkuT-Bs      DLLKIDLQALKVSPSPSYEHVLYSISLLARKIGAALLYEDIEANFQLQYAWRNG-----
RocR-Pa      SQIKLDRTFVQKMKIQRSCAVISSVVALAQALGISLVVEGVESDEQRVRLIELGCSIAQ
VieA-Vc      TELKIDRSFVHDLATNYKHQQLTNMCLLLAQSLGLHCVVVEGVENEETWQYLRQLGVDTCC
PXO_03877    DALKIDKSFVDTIGTHSATS AVSAHI IEMAKTLRLRTIAEGVERQEQLDYLRAGHVDLAQ
CC_3396-Cc   DTLKIDRYFVRTMGNNAGSAKIVRSVVKLGQDL DLEVVAEGVENAEMAHALQSLGCDYGG
TBD1265      HGLKIDQS FVRKIPAHPS ETQIVTTILALARGLGM EVVAEGIETAQQYAF LRDRGCEFGQ

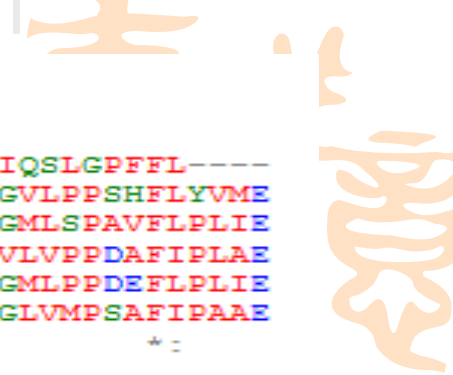
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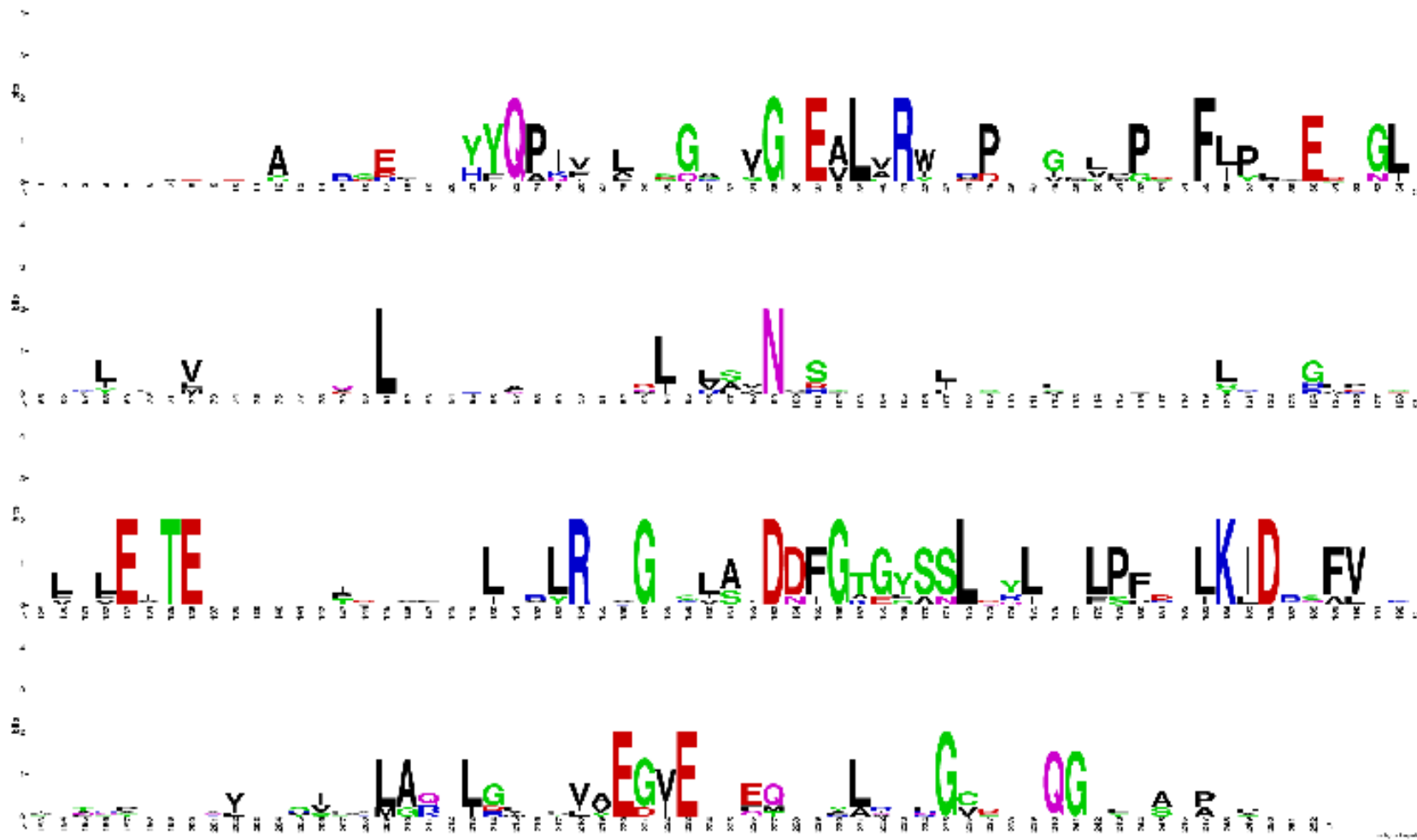
YkuT-Bs      -----
RocR-Pa      GYLFARPMPEQH
VieA-Vc      GYYAAKPMPIAQ
PXO_03877    GWLFSRALPATG
CC_3396-Cc   GFGYAPALSPQE
TBD1265      GNLMSTPQAADA

```



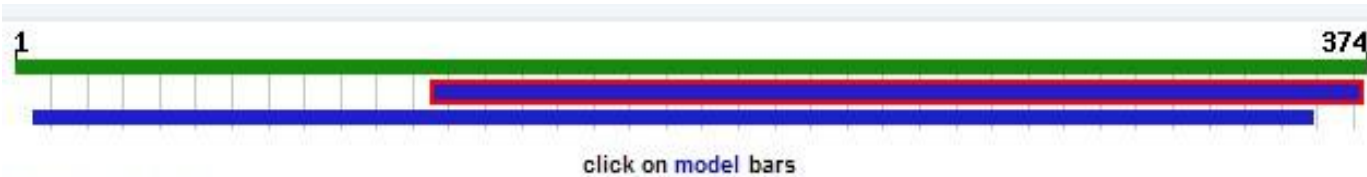
Weblogo

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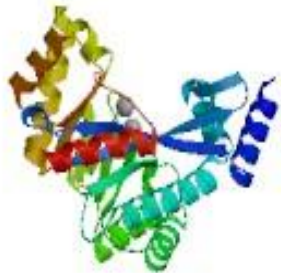
Swiss Model



Models: [1] [2]

Print/Save this page

Model Summary ?



Model information:

Modelled residue range: 117 to 372
Based on template: [3n3tB] (2.35 Å)
Sequence Identity [%]: 36.15
Evalue: 0.00e-1

Quality information: [details]▼

QMEAN Z-Score: -1.96



Quaternary structure information: [details]▼

Template (3n3t): DIMER
Model built: SINGLE CHAIN

Ligand information: [details]▼

Ligands in the template: C2E: 1, MG: 2.
Ligands in the model: MG: 2

logs: [Templates]▼ [Alignment]▼ [Modelling]▼

display model: as [pdb]▲ - as [DeepView project]▲ - in [AstexViewer]▼

download model: as [pdb]± - as [Deepview project]± - as [text]±



PDB 3n3t B链序列

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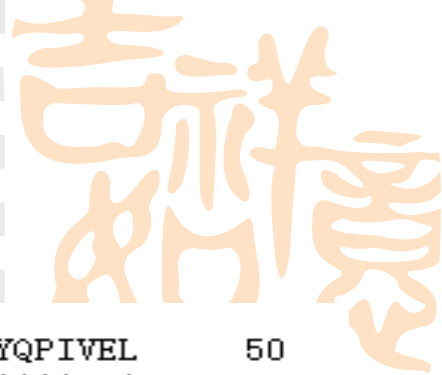
Site Record Legend

- BINDING SITE FOR RESIDUE MG B 802 (SOFTWARE)
- BINDING SITE FOR RESIDUE C2E B 801 (SOFTWARE)

DSSP Legend

- E: beta strand
- ↪ T: turn
- empty: no secondary structure assigned
- ~ G: 3/10-helix
- B: beta bridge
- S: bend
- ~ H: alpha helix

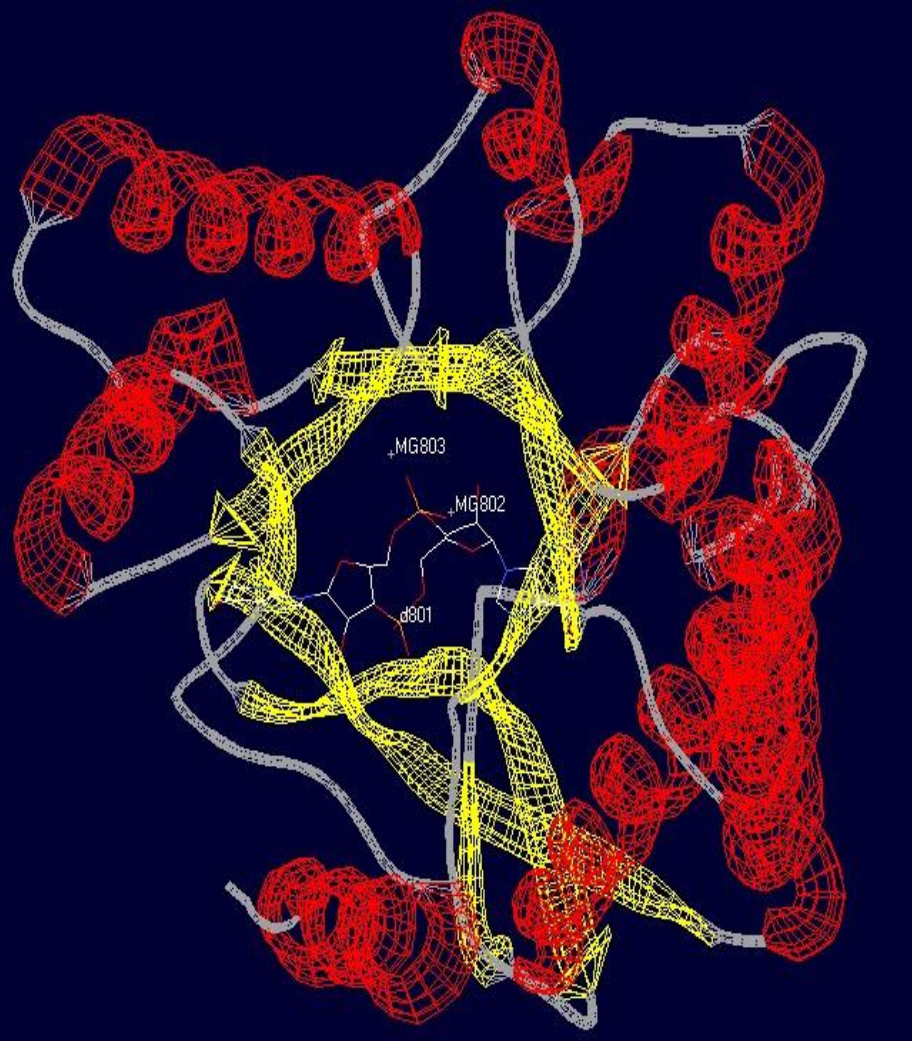
Jemboss NEEDLE



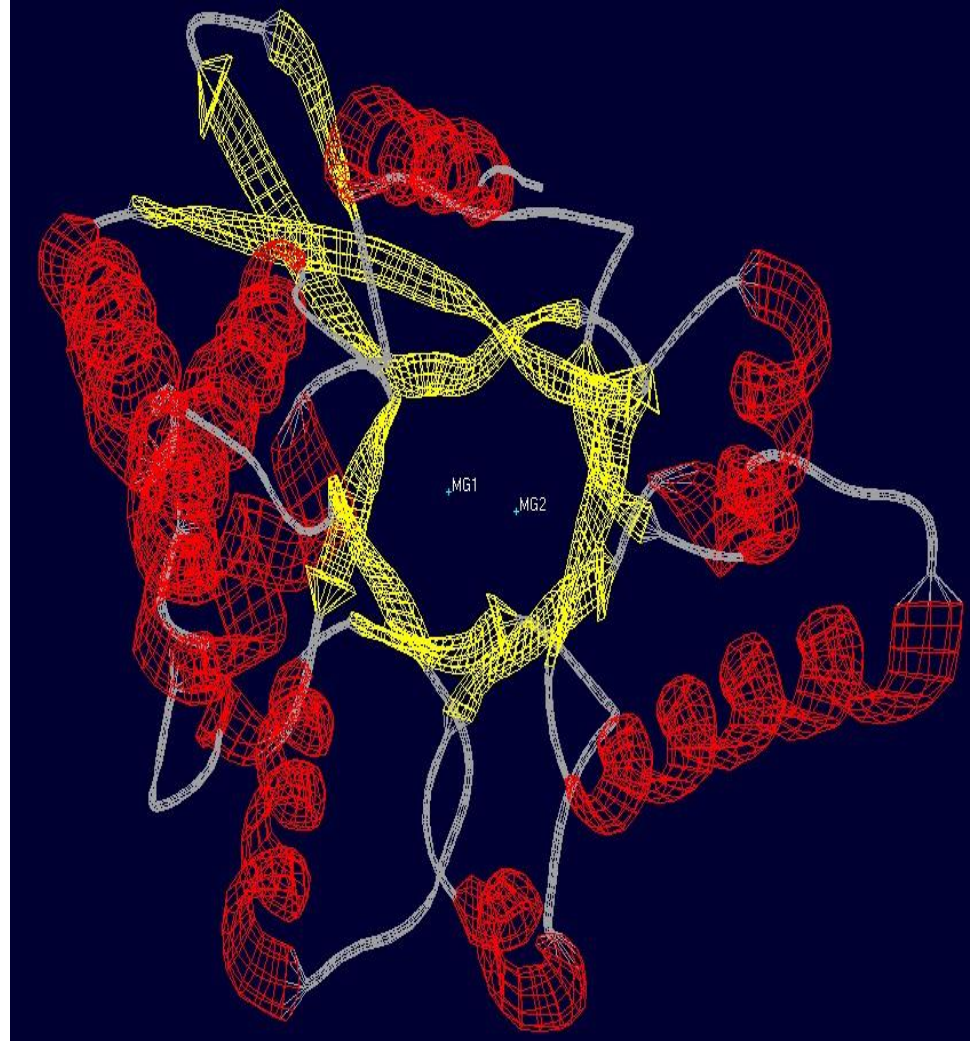
SEQUENCE	1	MGSSHHHHHSSGRENL YFQGERL TLD TRLRQALERNEL VLHYQP IVEL	50
		. : : . : : : .	
PXO_02877EAL	1	-----RRLSPLARPEIAVQRGEFIVHYQPIIAL	28
SEQUENCE	51	ASGRIVGG ^o EAL VRWEDPERGLVMP SAFIPAAEDTGLIVALSDWVLEACCT	100
		. . . : . : : : : : : . :	
PXO_02877EAL	29	DSGACVGA ^o EAL VRWQQPDGVLVPPDAFIPLAEE SGLILPITDLVVAEVIR	78
SEQUENCE	101	QI ^o RAWQQGRAADD-L T LSVNISTRQFEGEHL TRAVDRALARSGLRPDCL	149
		: : : : : : : : : : . : :	
PXO_02877EAL	79	EL ^o ----GPTLAADPALHVAINVSAEDIKSSRVQSVLEHALRG TGVD SGQL	124
SEQUENCE	150	ELEITENVMLVMTDEVRTCLDALRARGVRLALDDFG TGYSSLSYLSQLPF	199
		. : . . : : : : : . . .	
PXO_02877EAL	125	WWEATER-SLMDIDAARTTIMRLRGAGHTVSIDDFG TGYSSLQYLQGLPL	173
SEQUENCE	200	HGLKIDQSFVRKIPAHPS ^o ETQIVTTILALARGLGMEVVAEG IETAQQYAF	249
		. . : . . . : : : . . . : : : : : . : . . .	
PXO_02877EAL	174	DALKIDKSFVDTIGTHSATS AVSAHI IEMAKTLRLRTIAEG VERQEQLDY	223
SEQUENCE	250	LRDRGCEFGQGNLMSTPQAADAFASLLDRQKASGQRPVHG HETAP	294
		. . . :	
PXO_02877EAL	224	LRAHGVDLAQGWLFSRALPATG-----	245



Swiss-PDB Viewer

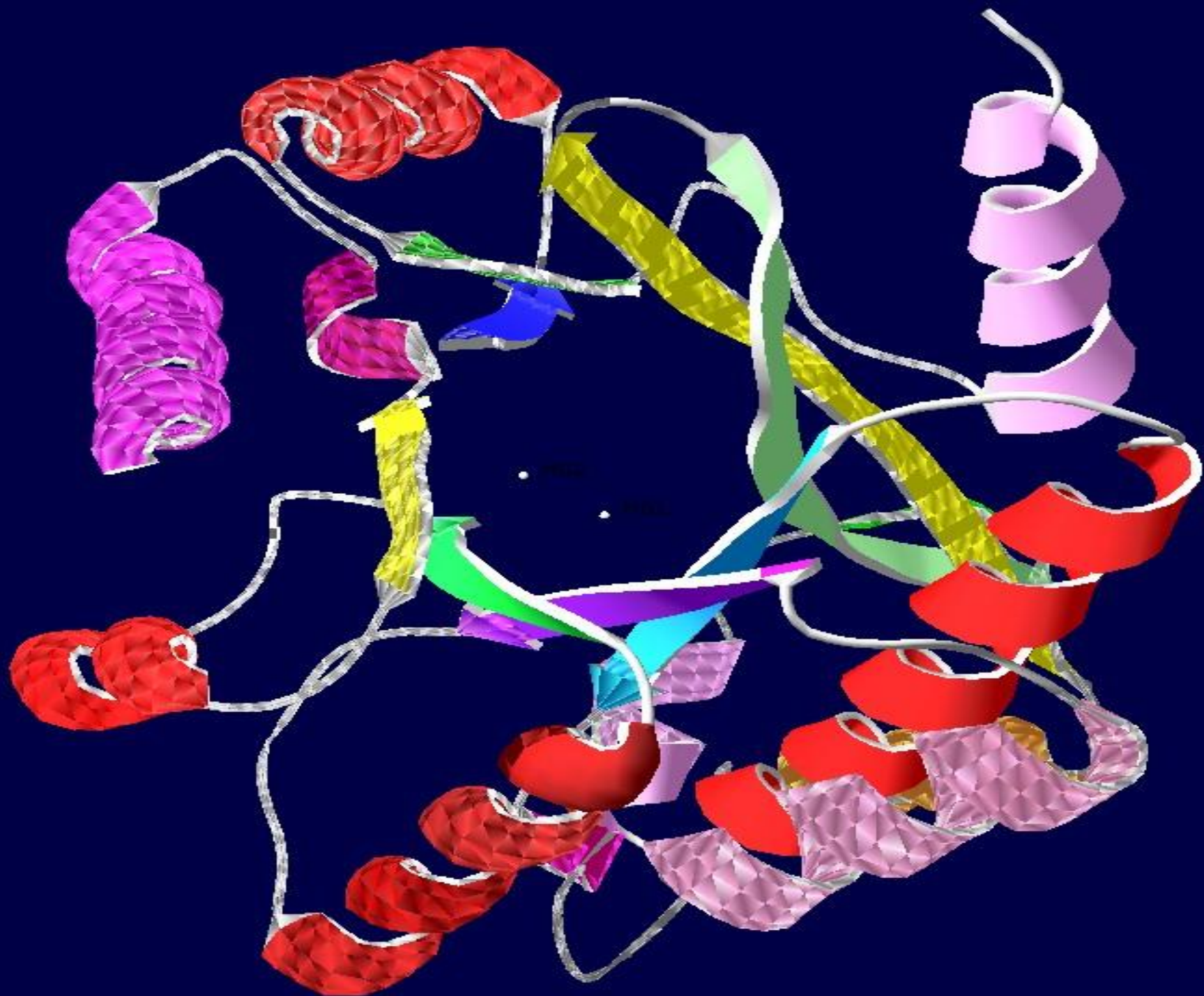


模板

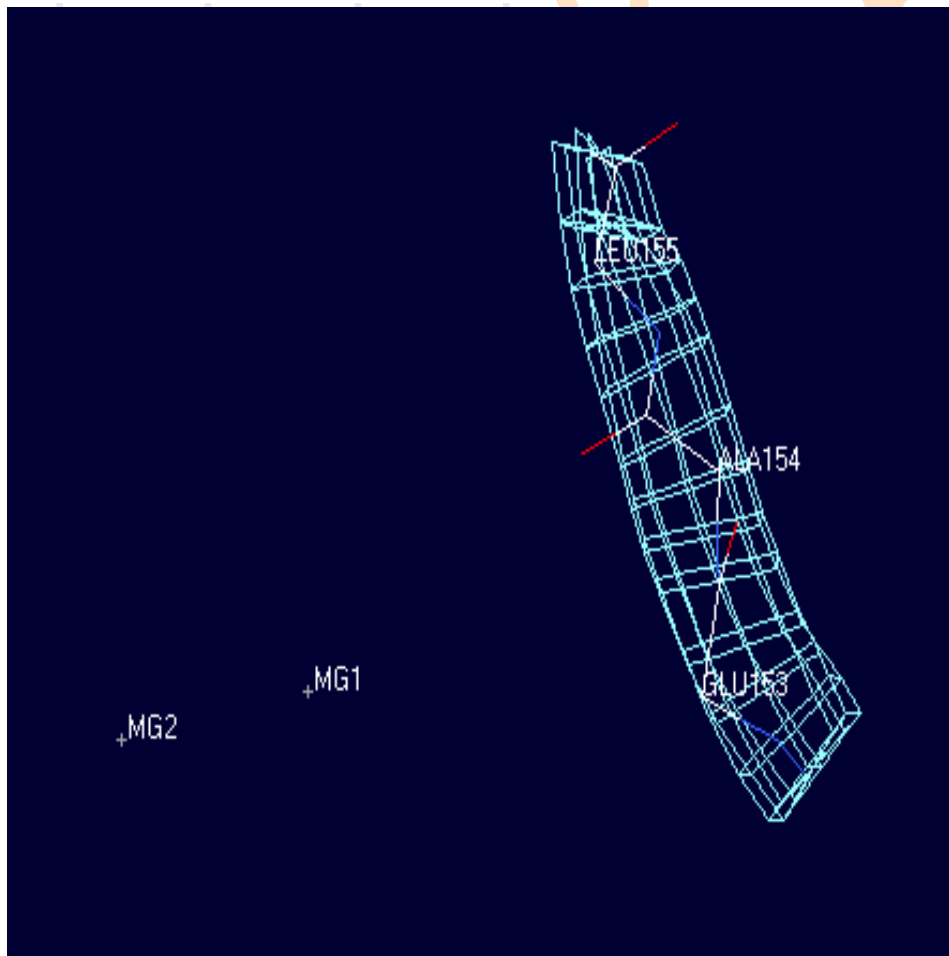
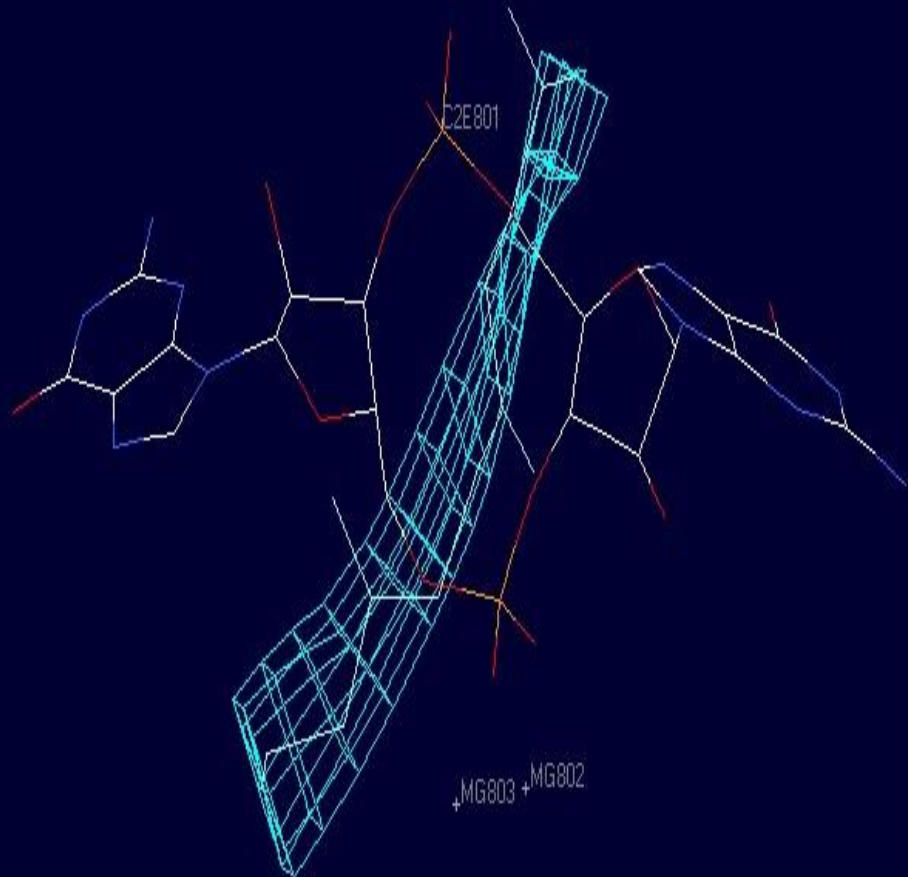


PXO_03877





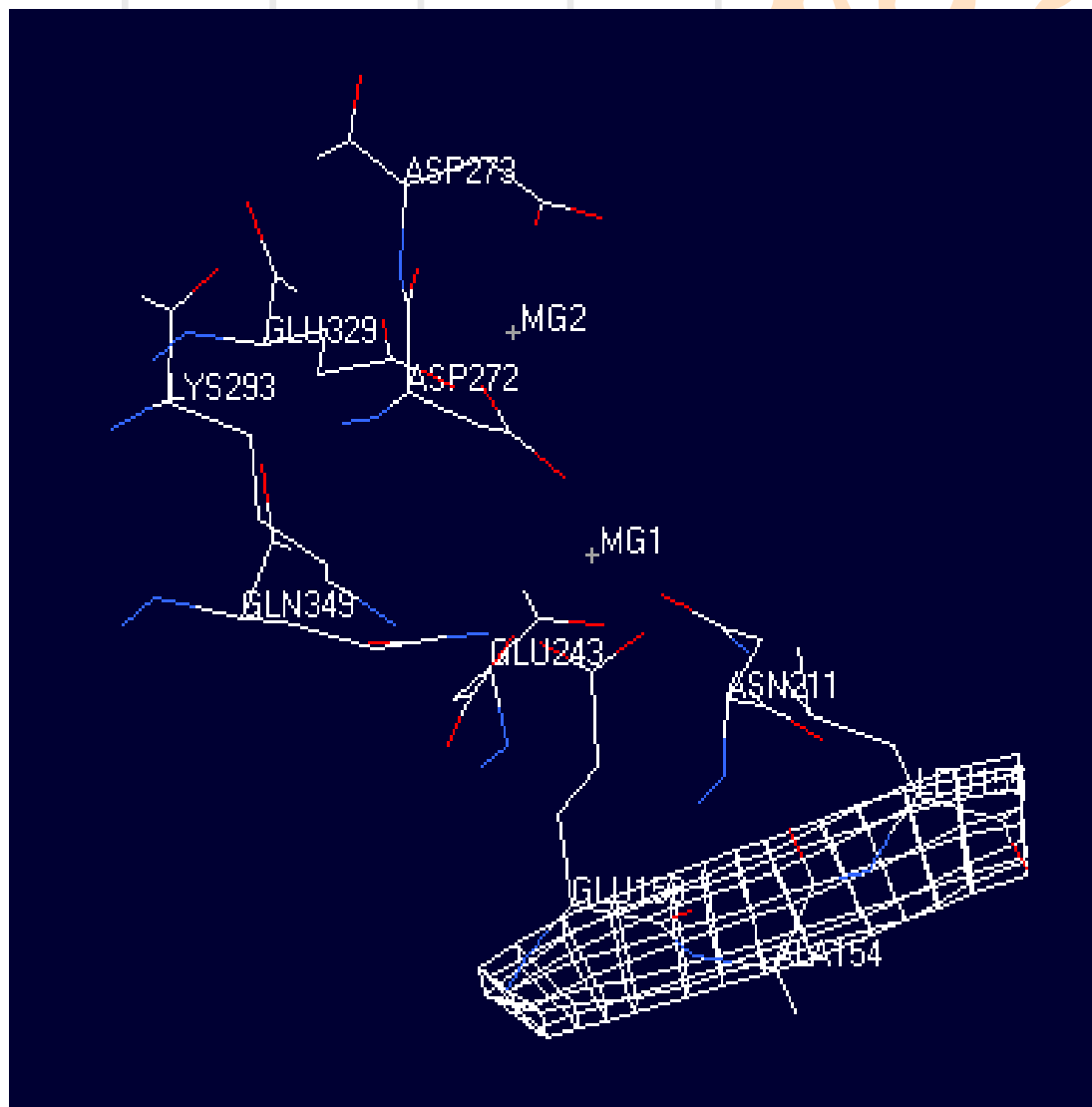
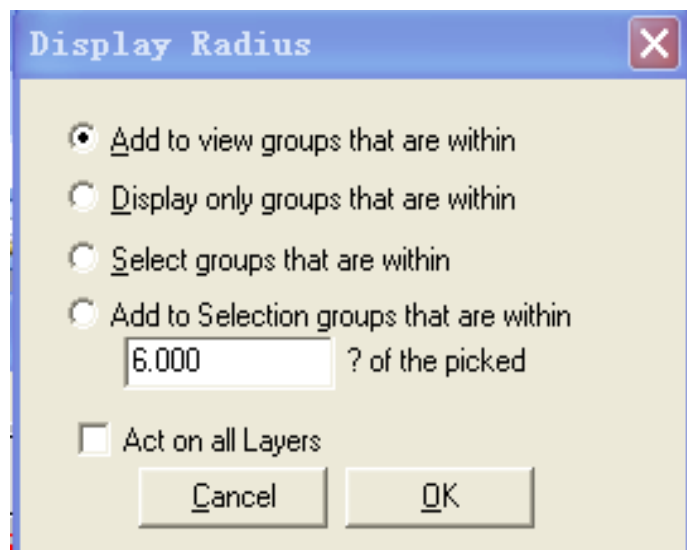
活性中心和EAL三个氨基酸位点



模 板

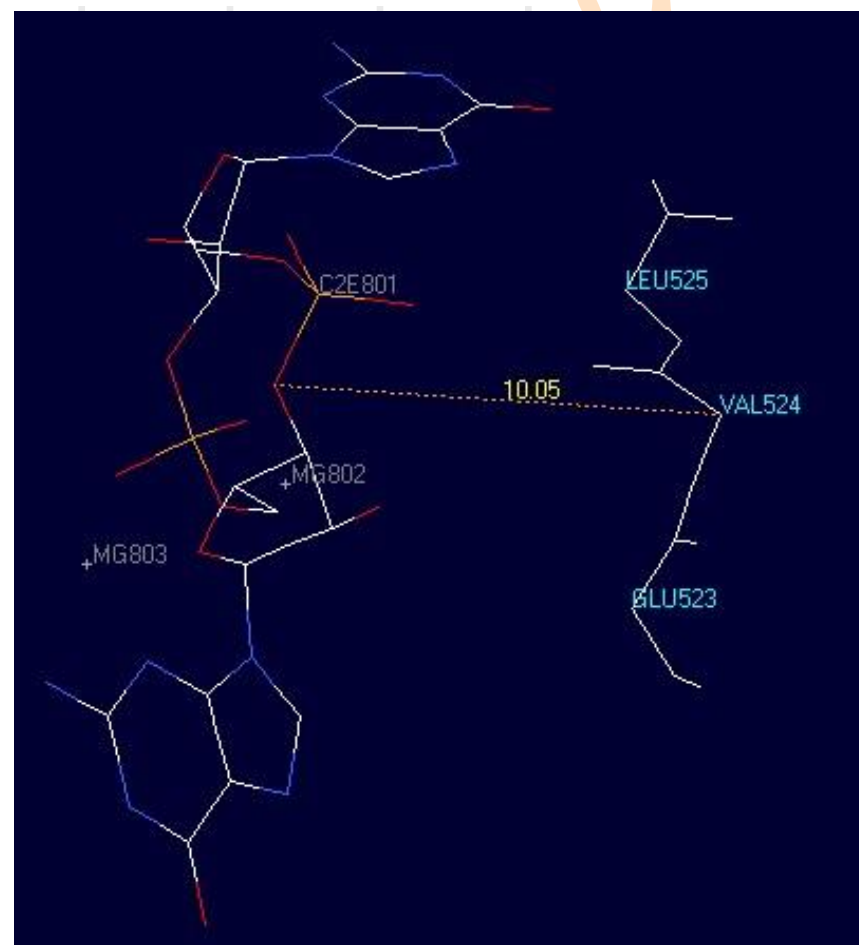
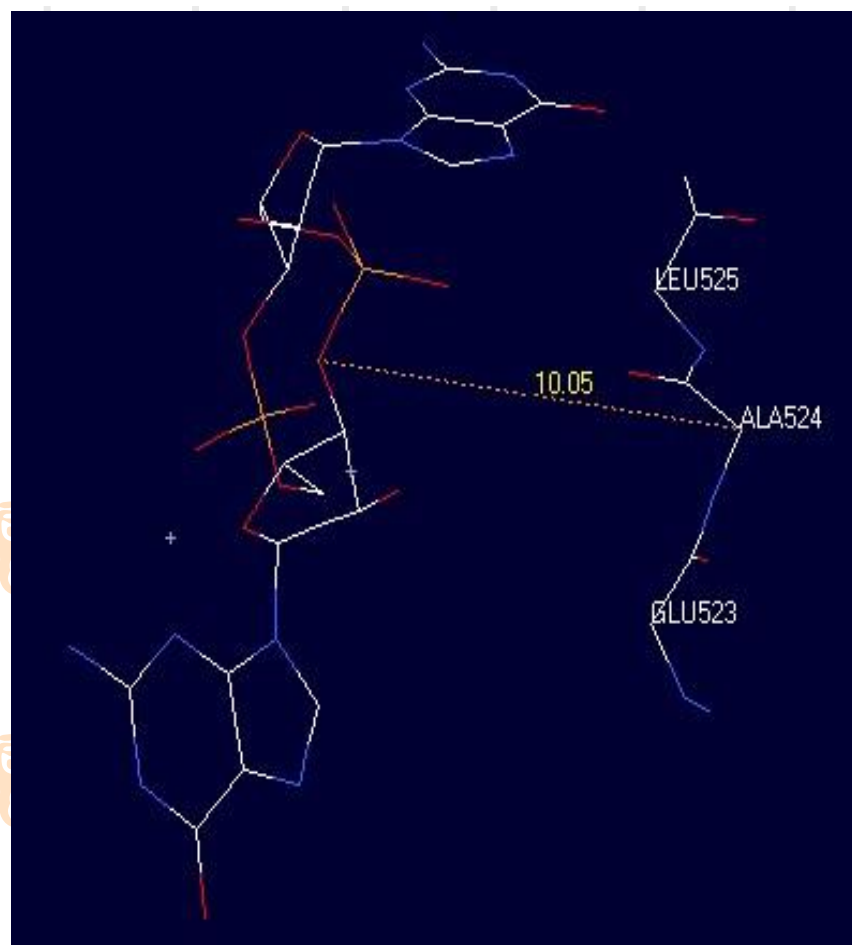
PXO_03877

距活性中心MG1为6个组时



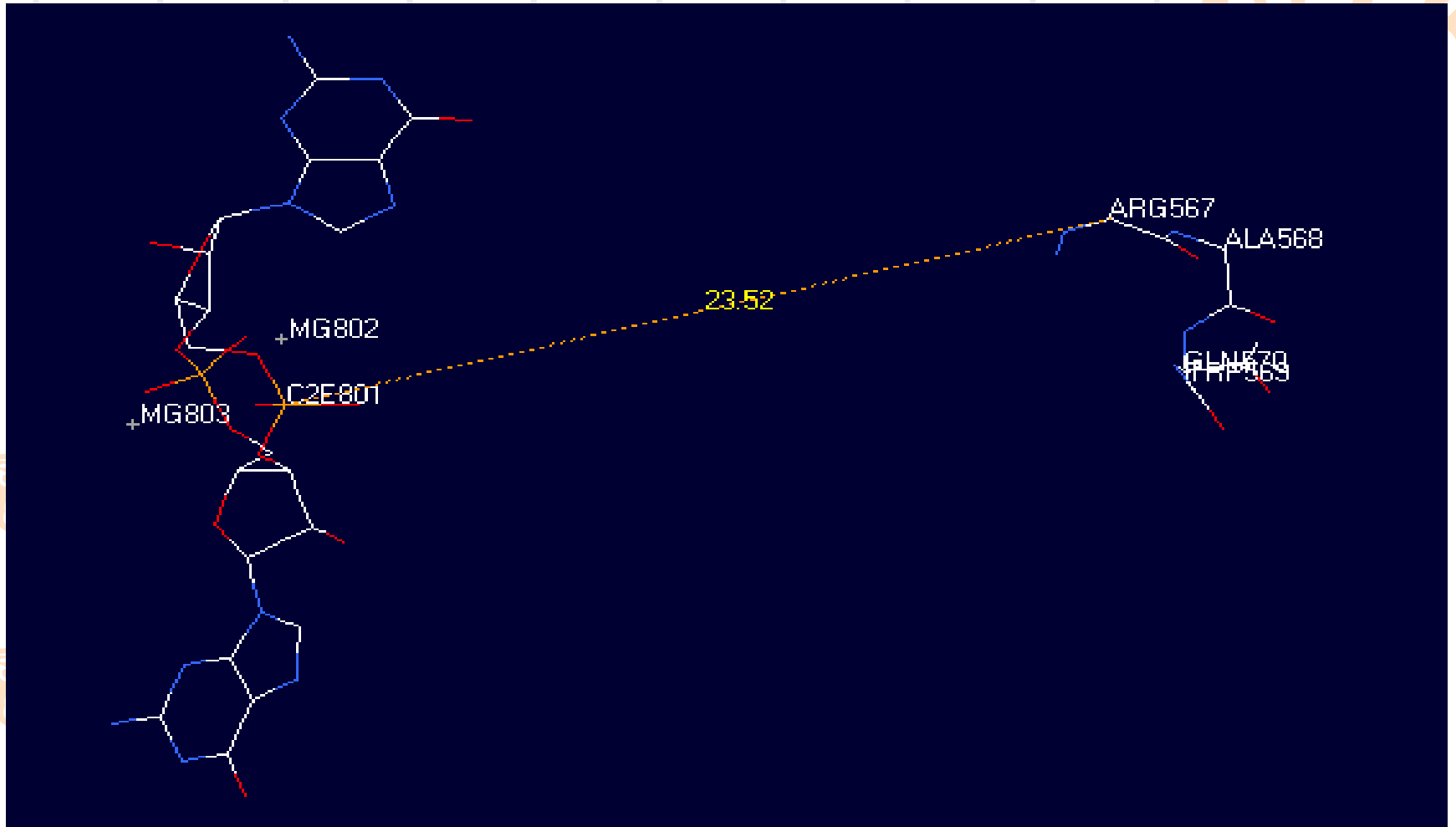
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活性中心和4个缺失氨基酸的距离



结论

虽然EAL3个氨基酸位点保守，4个氨基酸的缺失的影响也不是很明显，但由于其它序列的影响造成*PXO_03877*活性中心性质的改变。

根据分析认为*PXO_03877*表达的蛋白EAL结构域不保守

吉祥如意

致谢

- 非常感谢罗老师的悉心授课和耐心指导！
- 感谢G05小组各位成员的帮助！
- 感谢所有给予帮助的老师、师兄师姐和同学们！

