



鸭瘟强弱毒UL2蛋白差异比较

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小组成员：马丽 宫世玲 文晶亮



- 研究背景
- UL2蛋白核酸序列比对及系统发育进化树构建
- 强弱毒UL2蛋白氨基酸特性的差异比较
- 强弱毒UL2蛋白二级结构预测
- 强弱毒UL2蛋白三级结构预测及功能分析



研究背景



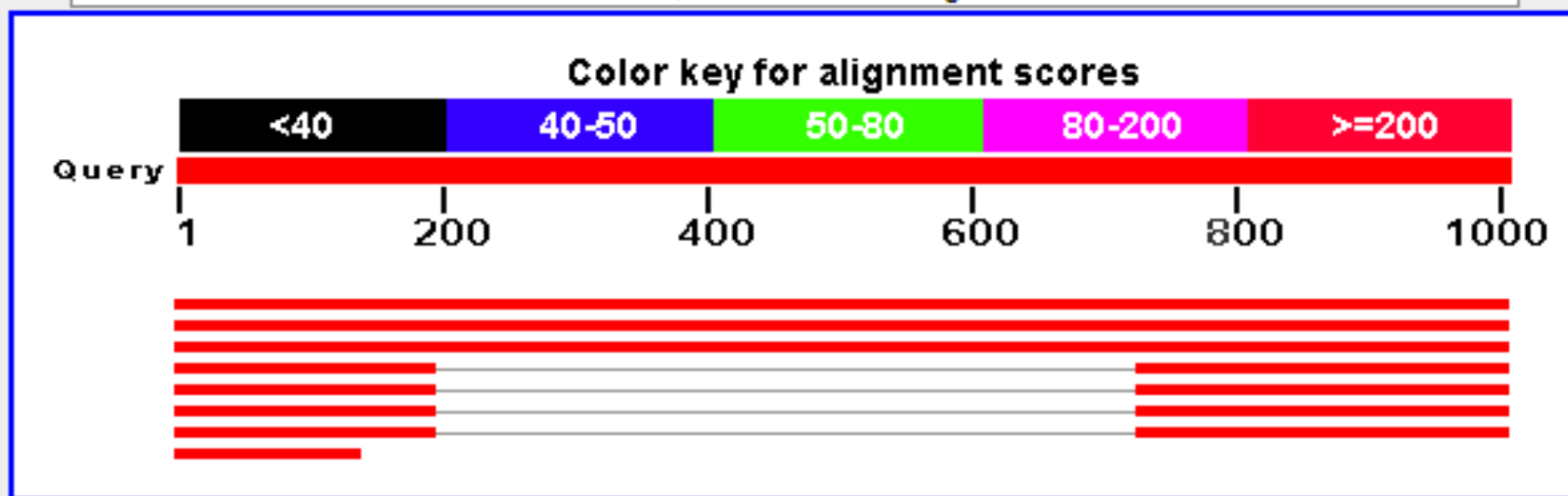
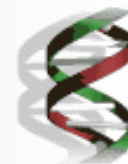
鸭瘟 (Duck Plague, DP) 又名鸭病毒性肠炎, 由鸭病毒性肠炎病毒 (duck enteritis virus, DEV) 引起, 是鸭、鹅及其他雁形目禽类一种急性、接触性、败血性传染病。

以血管损伤、消化道出血坏死、淋巴器官受损和实质性器官退形性变化为主要特征。





研究背景



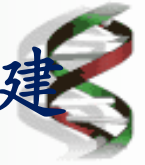
➤ 鸭瘟强弱毒UL2蛋白核苷酸差异:

- 1、强毒UL2蛋白核苷酸长度为1002bp，编码333个氨基酸（**B5LRM7**）
- 2、弱毒UL2蛋白核苷酸长度为474bp，编码157个氨基酸（**A3RMA6**）
- 3、弱毒与强毒相比，序列中间**连续缺失了528bp核苷酸**

推测：是否由于该片段的缺失导致两个蛋白之间的特性差异



UL2蛋白核酸序列比对及系统发育进化树构建



MEGA软件

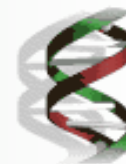
Species/Abbrv	* * *	*	*	*		*	* * *			* * *																																								
1. gi 384096355 gb JQ347518.1 Anatid herpesvirus 1 strain att	C	A	A	C	T	T	C	T	T	G	T	G	G	A	A	C	A	G	T	A	T	A	A	A	A																									
2. gi 384096353 gb JQ347517.1 Anatid herpesvirus 1 strain att	C	A	A	C	T	T	C	T	T	G	T	G	G	A	A	C	A	G	T	A	T	A	A	A	A																									
3. gi 380856102 gb JQ248597.1 Anatid herpesvirus 1 strain N3	G	A	A	A	T	A	T	T	A	C	A	T	G	G	A	C	G	A	G	G	T	A	C	T	G	T	G	C	T	C	C	A	T	C	G	G	A	T	G	T	A	A	A	A	G	T	C	A	T	C
4. gi 380856104 gb JQ248598.1 Anatid herpesvirus 1 strain LS	G	A	A	A	T	A	T	T	A	C	A	T	G	G	A	C	G	A	G	G	T	A	C	T	G	T	G	C	T	C	C	A	T	C	G	G	A	T	G	T	A	A	A	A	G	T	C	A	T	C
5. gi 380856100 gb JQ248596.1 Anatid herpesvirus 1 strain N2	G	A	A	A	T	A	T	T	A	C	A	T	G	G	A	C	G	A	G	G	T	A	C	T	G	T	G	C	T	C	C	A	T	C	G	G	A	T	G	T	A	A	A	A	G	T	C	A	T	C
6. gi 380468217 gb JQ043216.1 Anatid herpesvirus 1 strain N1	G	A	A	A	T	A	T	T	A	C	A	T	G	G	A	C	G	A	G	G	T	A	C	T	G	T	G	C	T	C	C	A	T	C	G	G	A	T	G	T	A	A	A	A	G	T	C	A	T	C
7. gi 197321001 gb EU885419.1 Duck enteritis virus strain CHV	G	A	A	A	T	A	T	T	A	C	A	T	G	G	A	C	G	A	G	G	T	A	C	T	G	T	G	C	T	C	C	A	T	C	G	G	A	T	G	T	A	A	A	A	G	T	C	A	T	C



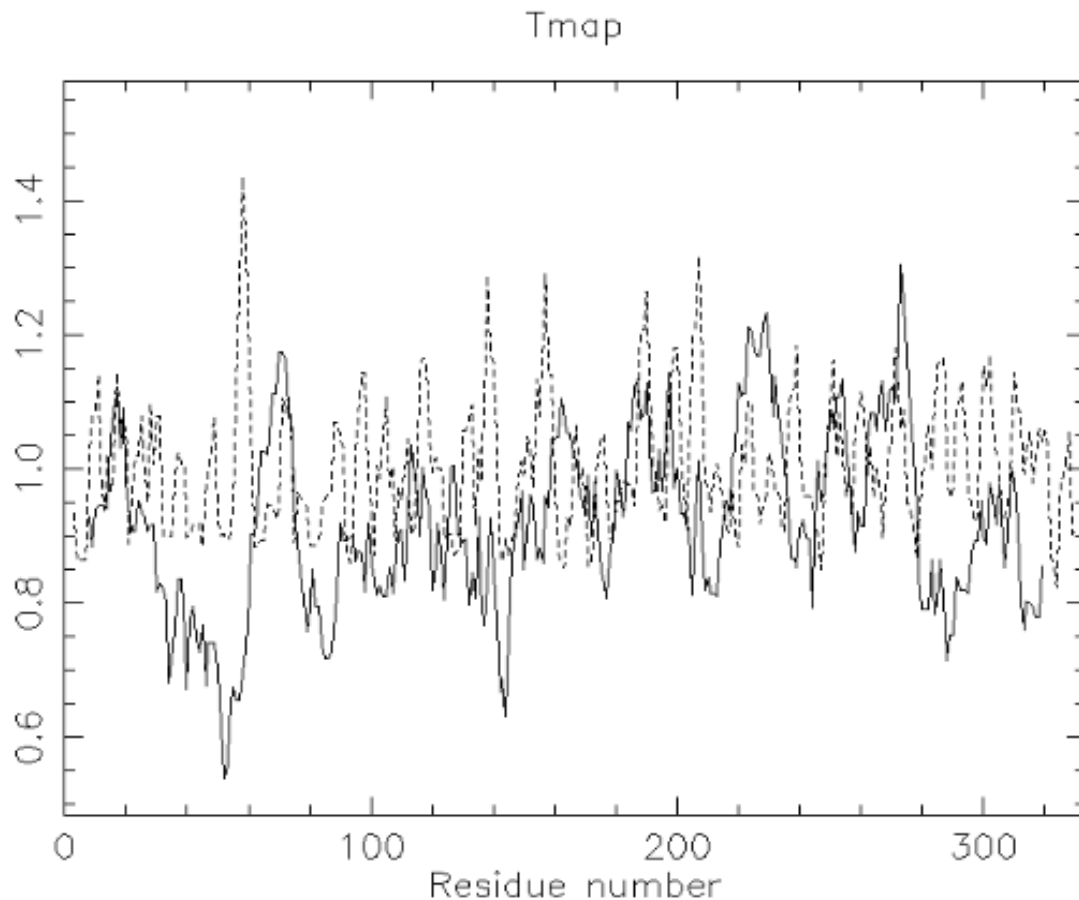
1



强弱毒UL2蛋白氨基酸特性的差异比较

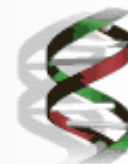


Tmap软件对强毒ul2蛋白进行跨膜螺旋预测

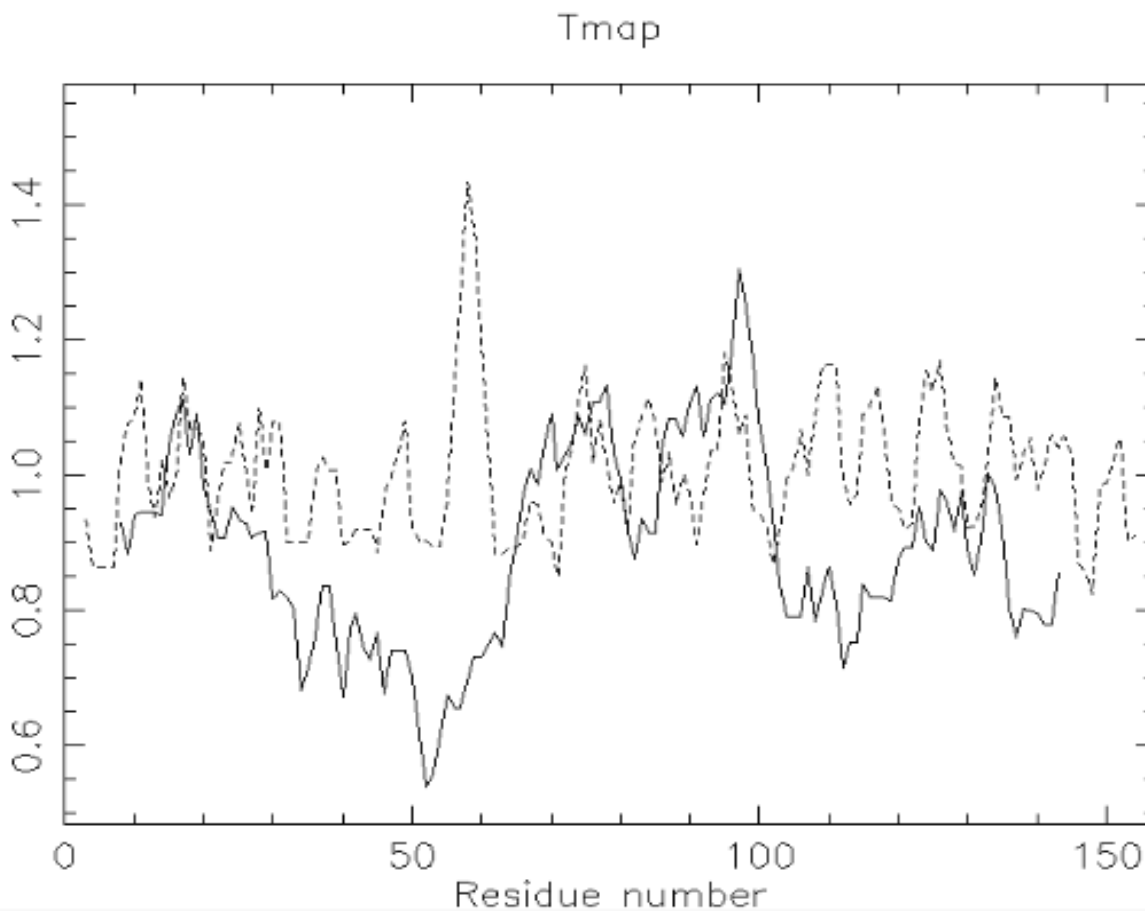




强弱毒UL2蛋白氨基酸特性的差异比较

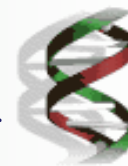


Tmap软件对弱毒ul2蛋白进行跨膜螺旋预测





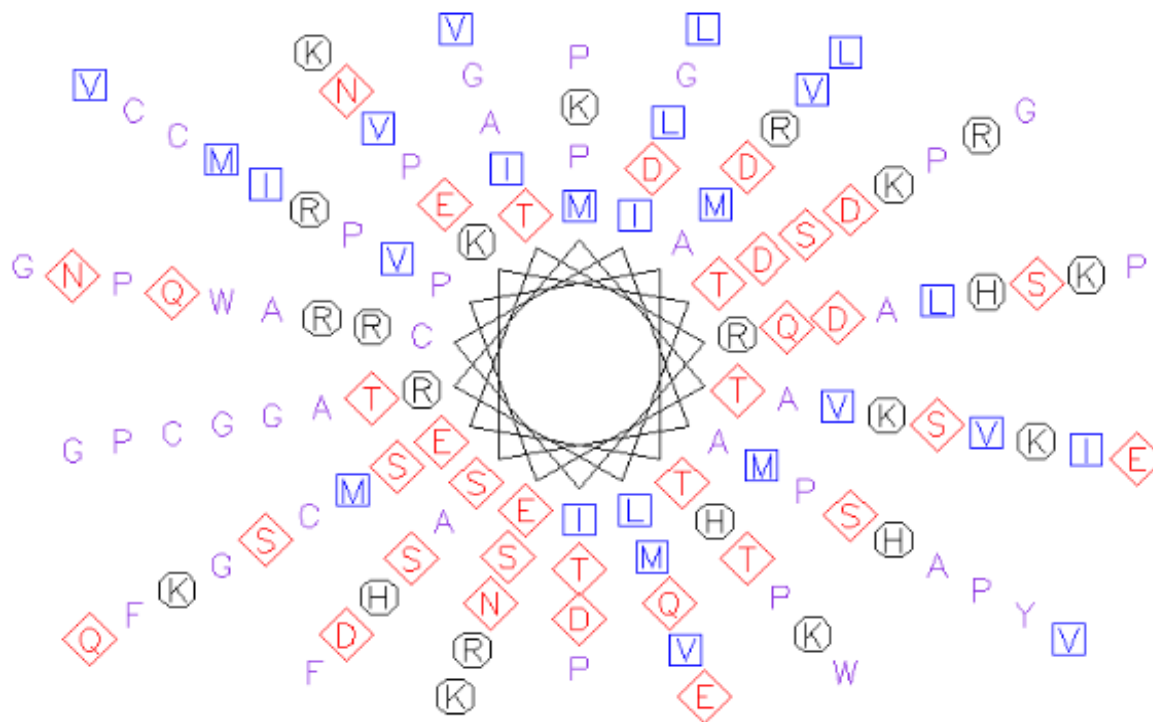
强弱毒UL2蛋白氨基酸特性的差异比较



WebLab中Pepwheel软件对强弱毒UL2蛋白差异氨基酸序列的螺旋轮分析

Helical wheel of fasta::586058:vacul2

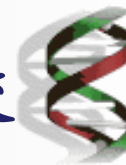
Wed 16 Jan 2013 21:39:20



方块为脂肪族氨基酸，菱形为亲水性，八边形为正极性



强弱毒UL2蛋白氨基酸特性的差异比较



ExPASy中TargetP软件分析强弱毒UL2蛋白亚细胞定位

```
### targetp v1.1 prediction results #####  
Number of query sequences: 1  
Cleavage site predictions not included.  
Using NON-PLANT networks.
```

Name	Len	mTP	SP	other	Loc	RC
cvul2	333	0.158	0.091	0.839	_	2
cutoff		0.000	0.000	0.000		

强
毒

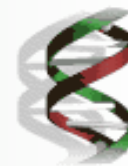
```
### targetp v1.1 prediction results #####  
Number of query sequences: 1  
Cleavage site predictions not included.  
Using NON-PLANT networks.
```

Name	Len	mTP	SP	other	Loc	RC
vacul2	157	0.152	0.065	0.868	_	2
cutoff		0.000	0.000	0.000		

弱
毒



强弱毒UL2蛋白氨基酸特性的差异比较

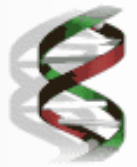


ExPASy中SOSUI软件分析强弱毒UL2蛋白亲水性

- ◆ 强毒ul2蛋白为可溶性蛋白，平均亲水性为-0.398809。
- ◆ 弱毒ul2蛋白为可溶性蛋白，平均亲水性为-0.416149。



强弱毒UL2蛋白二级结构预测



```
#####
#-----
#          10          20          30          40          50
# MTEPATETRICIASKTLRPASVMHSIQTRDMAEDMTKVNPDMTMADDRLPS
# helix  HHHHHHHHHH          HHHH          HHHHHHHHHHHH          H
# sheet
# turns      E          TT          EEE          T          EEE          T
# coil  CCC          CCC          CCC          CCC          CCCC
#          60          70          80          90          100
# PSQAPKRRRPPGAPAGFVACMREGGGIAQQPQTSNSSGRGEVAPSWFNSP
# helix      E          H          EEEEE          EEEE          EEE
# sheet
# turns  T  TTTT  TTT  T          TTTT          T          T          TT
# coil  C  CC          CC          CC          CCCCCC  C  C  CCCC
#          110          120          130          140          150
# TEWEKLSGDYICIGDAWREVLYQELQSEVGSRVLLLEVERRCDIEEVLPFKN
# helix  HH          HHHHHHHHHH          H          HHHHHHHHHH  H
# sheet
# turns  T  TTTTTT  T          TT          TT          T          T
# coil  C          CC          C  CC          CCCC          CCCC  C
#          160          170          180          190          200
# EIFTWTRYCAPSDVRKVIIVGQDPYHQPGQAHGLAFSVRRGIQIPPSLRNI
# helix  H          EE          EEEEE          EEEEE          EE          EE
# sheet
# turns  TTTTTT  TTT          T  TT          T          TTTT          T  T
# coil  C          CC          CCCC          C  CC          C  CC
#          210          220          230          240          250
# LSAVRRSYPETKIVDHGCLAWAKAGVLLNTTLTVRKGHGPGSHVDVQWS
# helix      EEEEE          EEE          EEEE          EEEEE          EEE
# sheet
# turns  T          TT          T          T          T          T          T
# coil  C          CCCC          CCCC          CCCC          CCCC
#          260          270          280          290          300
# KIVKSVLQWLHDNKEGLVFMLWGVHAQEAQKPNCRKHCVLKYSHPSPLSR
# helix  EEEEE          HHHH          HHHHHHHHHHHH  H          H
# sheet
# turns  T          TTT          T          TTTT          EEEEE          T          TTT
# coil  C          CCCC          CCCC          CCCC          CCCC
#          310          320          330
# KPFILCDHFKKANEYLEGRGVEPVVDWQLPCGTV
# helix  E  EE          HHHHHHHHHHHH          E          E
# sheet
# turns  #
# coil  #
#-----
# Residue totals: H:101  E: 75  T: 83  C: 74
# percent: H: 31.9 E: 23.7 T: 26.2 C: 23.3
#
```

Weblab 中

Garnier6.0

软件预测

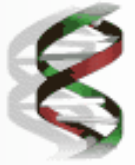
强弱毒ul2蛋

白质二级

结构



强弱毒UL2蛋白二级结构预测



```
..
#=====
      10      20      30      40      50
MTEPATETRICIASKTLRPASVMHSIQTRDMAEDMTKVNPDTMADDRLPS
helix  HHHHHHHHH      HHHH  HHHHHHHHHHH      H
sheet          E      EEE      EEE
turns          TT      T      T      T
coil  CCC      CCC      CCC      CCCC
      60      70      80      90      100
PSQAPKRRRPCGAPAGSHVDVGVWSKIVKSVLQWLHDNKEGLVFMWLVGVA
helix          E      H  HH      HHHH      HHHHHHHHHHH
sheet          E      EEEE      EEEEE
turns  T  TTTT  TT  T      T      TTT
coil  C  CC      CCC  C      C      CCC
      110      120      130      140      150
QEAFKPNCRKHCVLKYSHPSPLSRKPFILCDHFKKANEYLEGRGVEPVDW
helix  HHH  H      H      HHHHHHHHHHH
sheet          EEEEE      E  EE
turns  T  TTTT      T      TTT  T      TTTT  TTTT
coil          CCCCC      CC
      0
      QLPCGTV
helix
sheet  E      E
turns  TTTT
coil  C
#-----
..
#
# Residue totals: H: 60   E: 27   T: 38   C: 32
#                   percent: H: 42.6 E: 19.1 T: 27.0 C: 22.7
#
```

WebLab中

Garnier6.0

软件预测

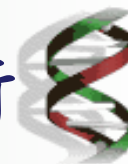
弱毒ul2蛋

白质二级

结构

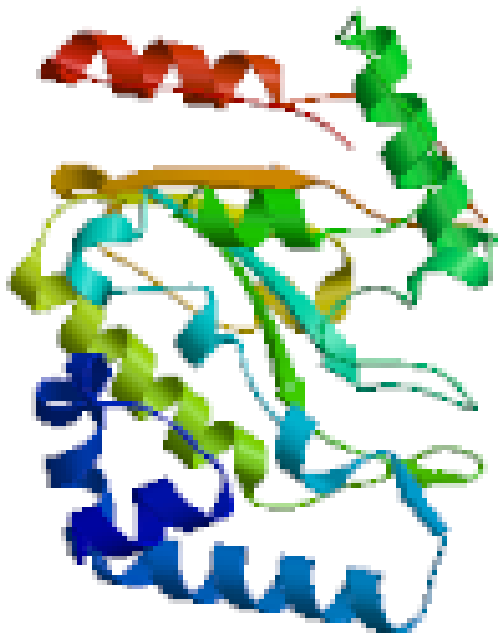


强弱毒UL2蛋白三级结构预测及功能分析

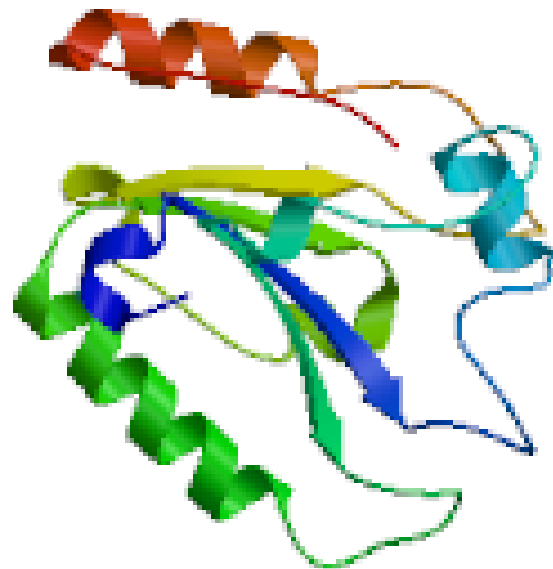


SWISS-MODEL Workspace 预测强弱毒UL2蛋白三级结构

强毒UL2蛋白

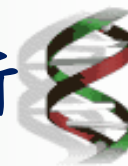


弱毒UL2蛋白

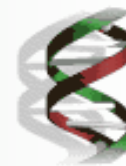




强弱毒UL2蛋白三级结构预测及功能分析



- UL2蛋白是一种**尿嘧啶DNA糖基化酶**，能水解单链DNA或者错配的双链DNA和多聚核苷酸，从而释放自由的尿嘧啶。该过程可能与鸭瘟病毒的**毒力**有关，UL2蛋白长片段的缺失可能导致该蛋白酶活性降低，从而引起毒力减弱。



谢谢

请大家批评指正！