



RVPSD: 一个全面且用户友好的RNA病毒蛋白质结构网络数据库

杨强震^{1,#}, 田忠帅^{2,#}, 胡弢^{3,4,#}, 娄江溶¹, 刘恒聪²,
Edward C. Holmes⁵, 师咏勇^{1,*}, 李娟^{3,4,6,*}, 史卫峰^{2,7,8,*}

¹ 上海交通大学Bio-X 研究院

² 上海交通大学医学院上海市病毒研究院

³ 山东第一医科大学第二附属医院

⁴ 山东第一医科大学 (山东省医学科学院) 山东省高等学校新发传染病重点实验室

⁵ 悉尼大学医学院

⁶ 山东第一医科大学 (山东省医学科学院) 临床与基础医学院

⁷ 上海交通大学医学院附属瑞金医院

⁸ 上海交通大学生命科学技术学院



Qiangzhen Yang, Zhongshuai Tian, Tao Hu, Jiangrong Lou, Hengcong Liu, Edward C. Holmes, Yongyong Shi, et al. 2026.

RVPSD: A comprehensive and user-friendly web database for RNA viral protein structures.

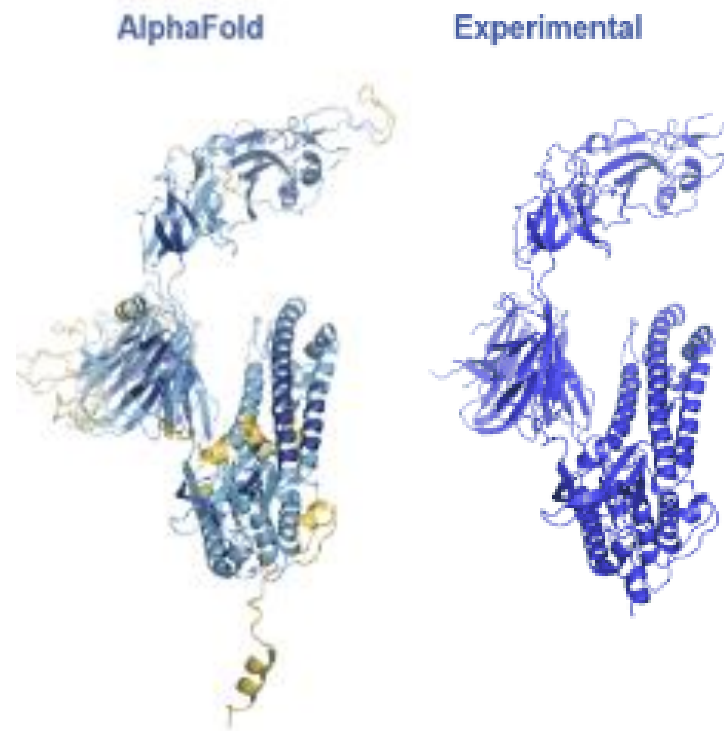
iMetaOmics 3: e70120. <https://doi.org/10.1002/imo2.70120>



研究背景

关键空白：缺乏覆盖不同谱系RNA病毒蛋白质结构的综合性数据库

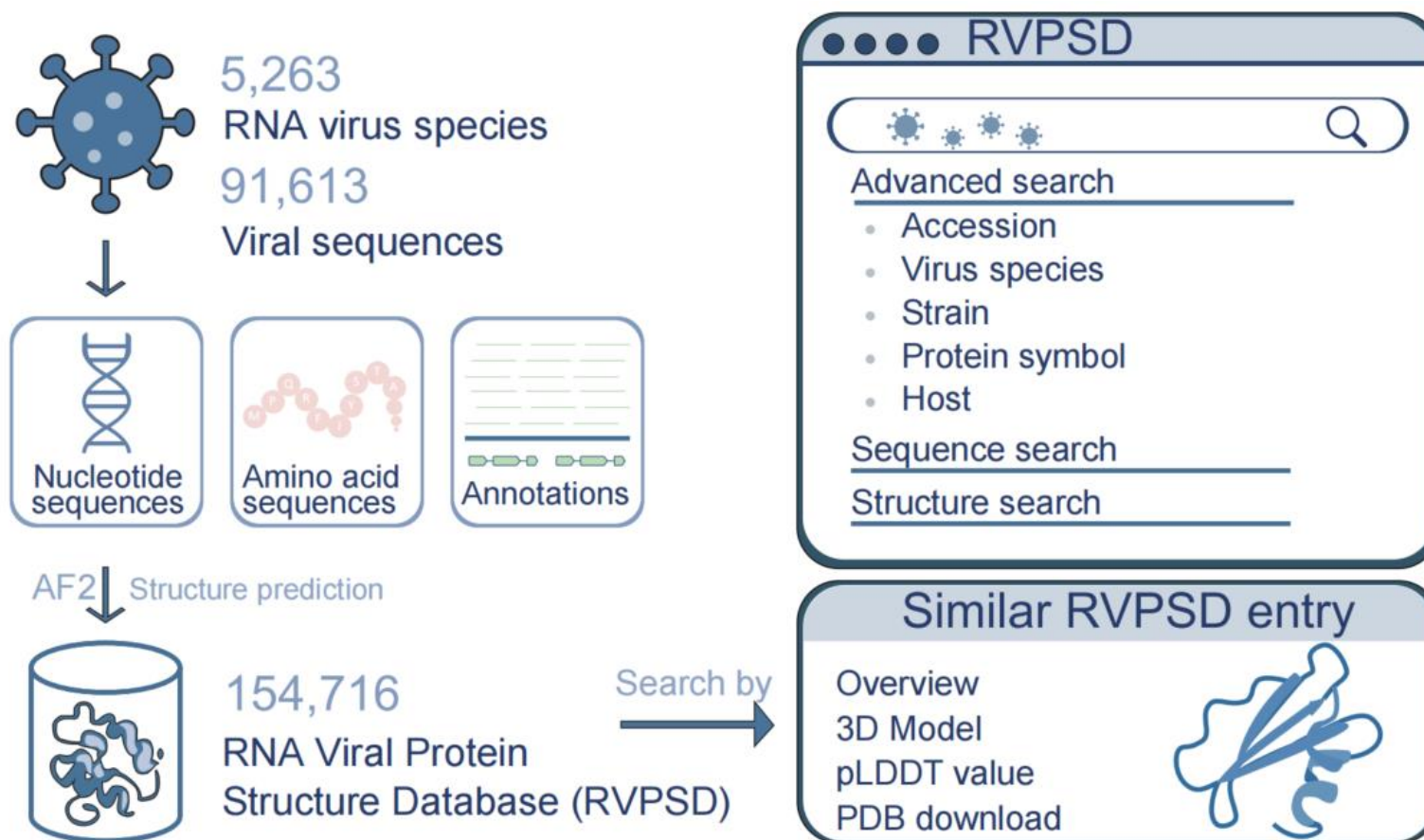
- RNA病毒具有高度多样性且进化迅速，对全球公共卫生构成重大威胁
- 蛋白质结构对于理解感染机制和指导治疗设计至关重要
- 受技术和生物安全限制，实验解析的结构数量仍然有限
- AI驱动方法（AlphaFold2）实现了大规模结构预测
- 现有资源较为分散或仅针对特定病毒科



RVPSD作为综合性资源填补了这一空白



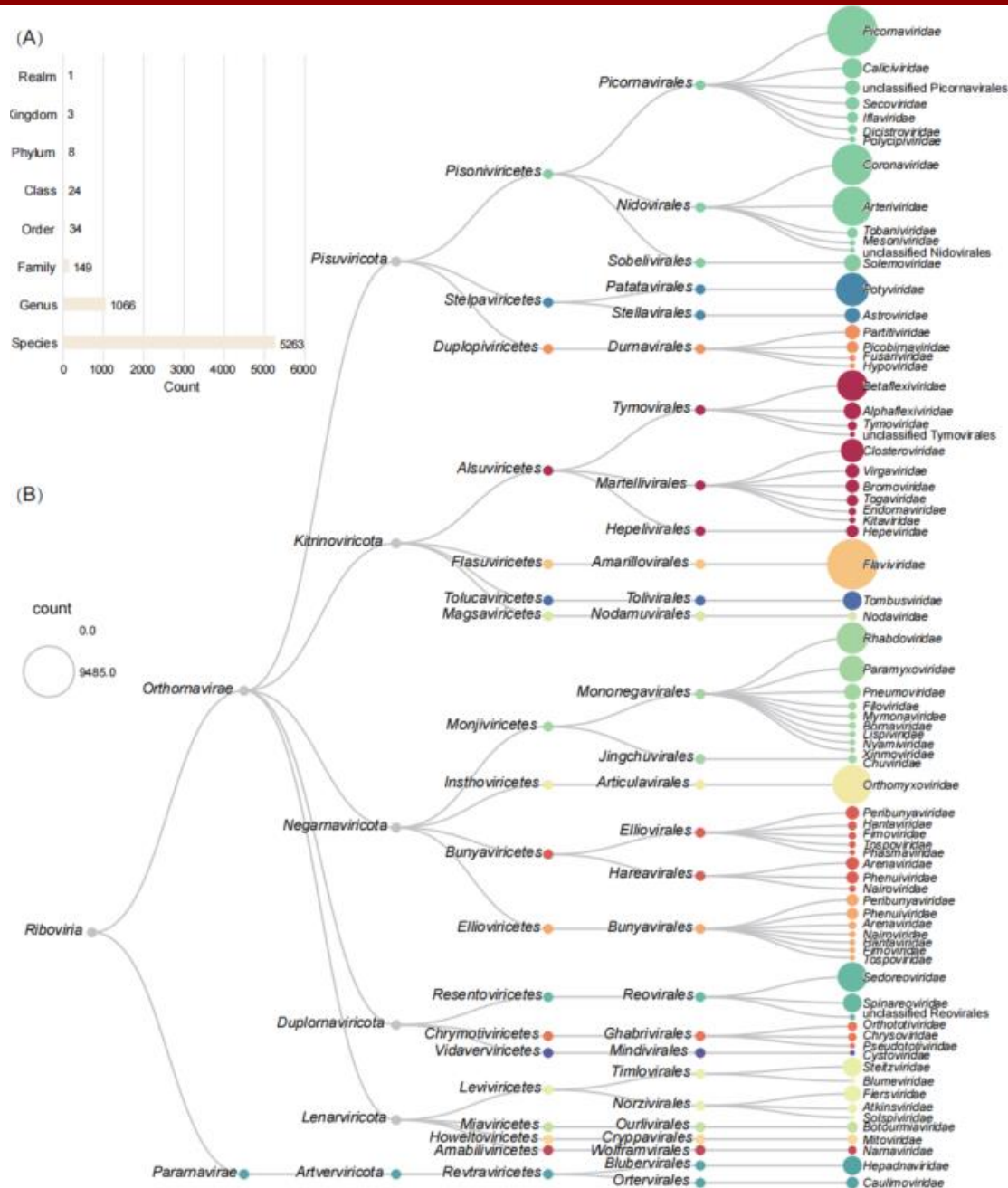
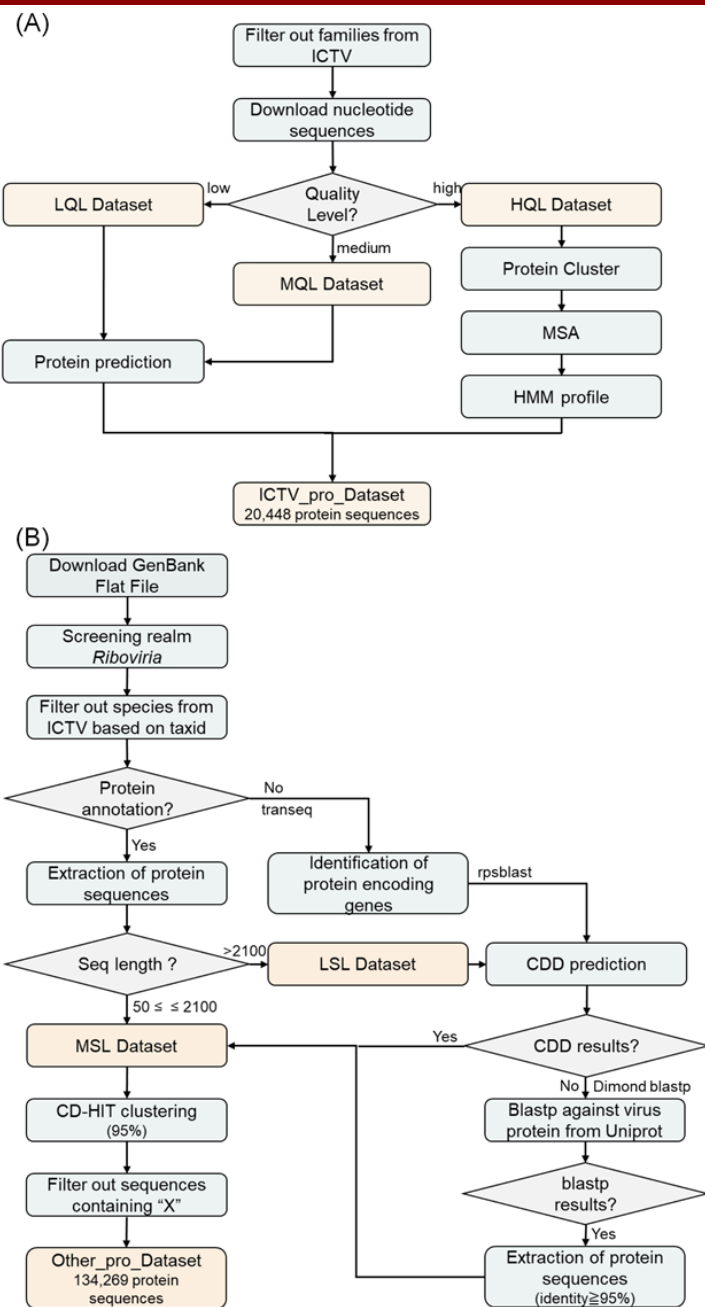
亮点



- RVPSD提供了超过5,200种RNA病毒的154,716个AlphaFold2预测蛋白质结构
- RVPSD将病毒蛋白质结构与丰富的元数据整合为综合性资源
- RVPSD支持基于序列与结构的RNA病毒暗物质发现分析



数据库概览与序列收集





预测建模与质量评估

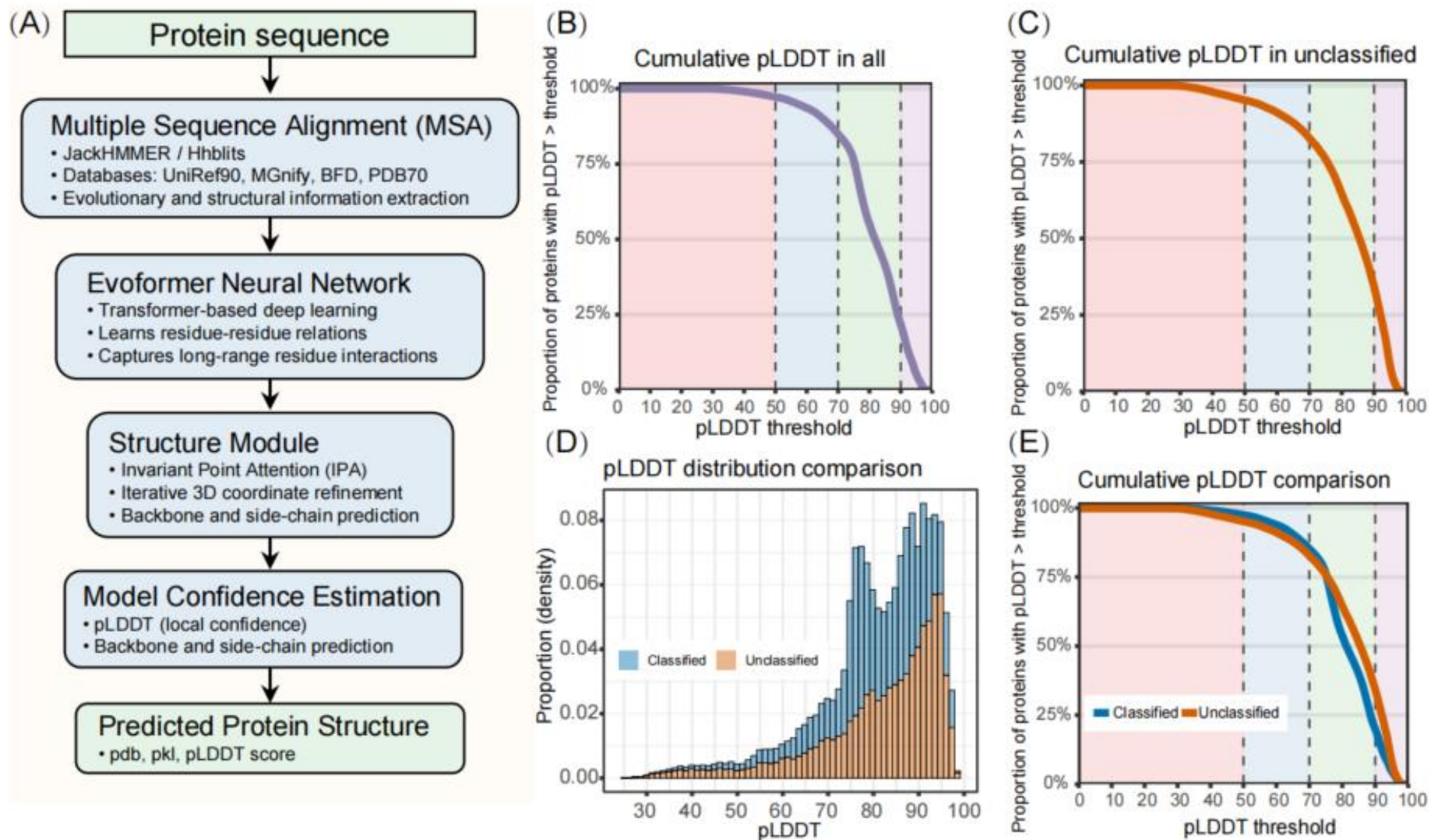


图2. 基于AlphaFold2的结构预测流程及预测局部距离差异检验 (pLDDT) 评分分布



数据库架构与功能实现

RNA Viral Protein Structure Database

Advanced Search

You can refine your queries using GenBank accession numbers for viral proteins or nucleotides, virus species names, strain names, protein symbols, taxonomy, viral hosts, collection site or date.

- GenBank Accession Numbers (Protein): Remove
- Virus Name: Remove
- Abbreviated Virus Name: Remove
- Protein Name: Remove
- GenBank Accession Numbers (Nucleotide): Remove
- Taxonomy: Remove
- Strain Name or Isolate Name: Remove
- Host: Remove
- Location: Remove
- Collection date: Remove

Cancel Search

Structure Alignment

* Job Title

Structure 1

- Upload a file [Download the test file](#)
- Or, input content

ATOM	1	N	MET	A	1	1.186	-5.674	-43.192	1.00	39.83	N
ATOM	2	CA	MET	A	1	2.145	-5.769	-42.073	1.00	39.83	C
ATOM	3	C	MET	A	1	1.364	-5.358	-40.945	1.00	39.83	C
ATOM	4	O	MET	A	1	1.296	-4.175	-40.542	1.00	39.83	O
ATOM	5	CB	MET	A	1	3.392	-4.884	-42.283	1.00	39.83	C

Structure 2

- Upload a file [Download the test file](#)
- Or, input content

ATOM	1	N	MET	A	1	1.186	-5.674	-43.192	1.00	39.83	N
ATOM	2	CA	MET	A	1	2.145	-5.769	-42.073	1.00	39.83	C
ATOM	3	C	MET	A	1	1.364	-5.358	-40.945	1.00	39.83	C
ATOM	4	O	MET	A	1	1.296	-4.175	-40.542	1.00	39.83	O
ATOM	5	CB	MET	A	1	3.392	-4.884	-42.283	1.00	39.83	C

* Email

Note: This result will be available for two weeks and please check them immediately.

Cancel Align

Sequence Search

Enter your job title and your protein sequence by uploading a .fasta, .fna, .fa, .fas, or .faa file, or by inserting a sequence in FASTA format.

* Job Title

Enter Query Sequence

- Please upload a file [Download the test file](#)
- Or, input content

```
>ABC123RD 1 viriplase RNA-binding protein NSP2 [Betavirus A]  
MALACPCYHLESDYDFIPNLADEKLTAKTRKSNKDFDI11G5APPQFRKSTNSDNGM  
SPETIMPTKXAMLCALNOLKVTQVSYNLSRYVSHREJLYIRKSPGDLPRKDLKASTLAI  
GQSKETTTITAGGGTYFGAFTWMLTLEKLMPLDGNFYEVYTLSEKPISSVYKELVABL  
RYVNFATITGGKGVETKTSSTANARVYATPEKNTKVSNSPFLDRI1QVNTAFTSEMGG  
TLVYCKLLFGWPKFCKPFGSLTRDNDEYGVGV
```

* Max Target Structures:

* Email

Note: This result will be available for two weeks and please check them immediately.

Cancel Search

Structure Search

Enter your job title and upload your protein structure file in .pdb format, or paste the content in PDB format.

* Job Title

Enter Query Sequence

- Please upload a file [Download the test file](#)
- Or, input content

ATOM	1	N	MET	A	1	1.186	-5.674	-43.192	1.00	39.83	N
ATOM	2	CA	MET <td>A</td> <td>1</td> <td>2.145</td> <th>-5.769</th> <th>-42.073</th> <th>1.00</th> <th>39.83</th> <th>C</th>	A	1	2.145	-5.769	-42.073	1.00	39.83	C
ATOM	3	C	MET <td>A</td> <td>1</td> <td>1.364</td> <th>-5.358</th> <th>-40.945</th> <th>1.00</th> <th>39.83</th> <th>C</th>	A	1	1.364	-5.358	-40.945	1.00	39.83	C
ATOM	4	O	MET <td>A</td> <td>1</td> <td>1.296</td> <th>-4.175</th> <th>-40.542</th> <th>1.00</th> <th>39.83</th> <th>O</th>	A	1	1.296	-4.175	-40.542	1.00	39.83	O
ATOM	5	CB	MET <td>A</td> <td>1</td> <td>3.392</td> <th>-4.884</th> <th>-42.283</th> <th>1.00</th> <th>39.83</th> <th>C</th>	A	1	3.392	-4.884	-42.283	1.00	39.83	C
ATOM	6	CG	MET <td>A</td> <td>1</td> <td>4.399</td> <th>-5.461</th> <th>-43.287</th> <th>1.00</th> <th>39.83</th> <th>C</th>	A	1	4.399	-5.461	-43.287	1.00	39.83	C
ATOM	7	SD	MET <td>A</td> <td>1</td> <td>5.321</td> <th>-6.896</th> <th>-42.675</th> <th>1.00</th> <th>39.83</th> <th>S</th>	A	1	5.321	-6.896	-42.675	1.00	39.83	S

* Max Target Structures:

* Email

Note: This result will be available for two weeks and please check them immediately.

Query History

Search Summary | This query matches 1 structures
1 to 10 of 1 Structures

Title	Type	Email	Upload time	Completion time	Status	Controls
blast	Sequence Search	809078811@qq.com	2026-05-11 12:53:38	2026-05-11 12:53:42	Processing is successful	view

Sequence of AXP33558.1 Chain 1

Structure Tools

- Structure
 - AXP33558.1
 - Type Model
 - Nothing Focused
- Quick Styles
 - Apply Representation
 - Default Cartoon Spacefill Surface
 - Apply Style
 - Default Illustrative
- Components
 - Preset + Add
- Measurements
 - + Add
- Export Animation
- Export Geometry

Information

GenBank Accession Numbers (Protein): AXP33558.1

Virus Name: Abras_virus

Abbreviated Virus Name: ABRV

Protein Name: RNA-dependent_RNA_polymerase

GenBank Accession Numbers (Nucleotide): MH017275.1

Taxonomy: [Riboviria](#) [Orthornavirae](#) [Negamaviricota](#) [Bunyaviricetes](#) [Eliovirales](#) [Peribunyaviridae](#) [Orthobunyavirus](#) [Orthobunyavirus abrasense](#)

Strain Name or Isolate Name: 75V1183

Host: Culex_paracrybda

Location: Ecuador

Predicted Local-Distance Difference Test: 90.39530959

Collection date: 1974-08-21

PDB download FASTA download

Search

Advanced Search

Search using virus metadata.

Sequence Search

Find structures using protein sequences via BLASTP.

Structure Search

Identify similar protein structures using Foldseek.

Structure Alignment

Perform protein structure alignment.

History

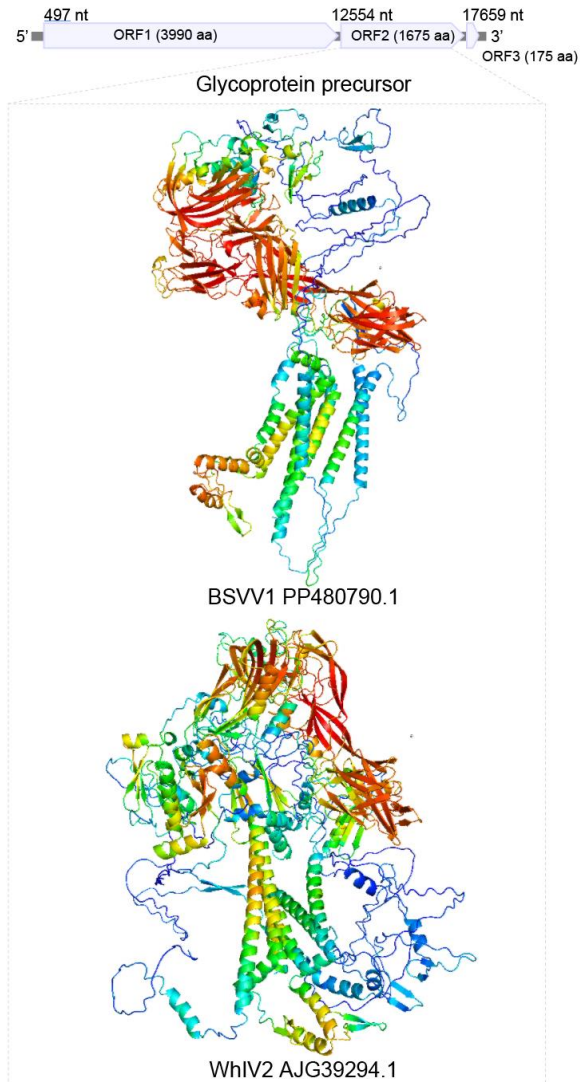
View your Sequence Search, Structure Search and structure alignment history.

Complete tasks

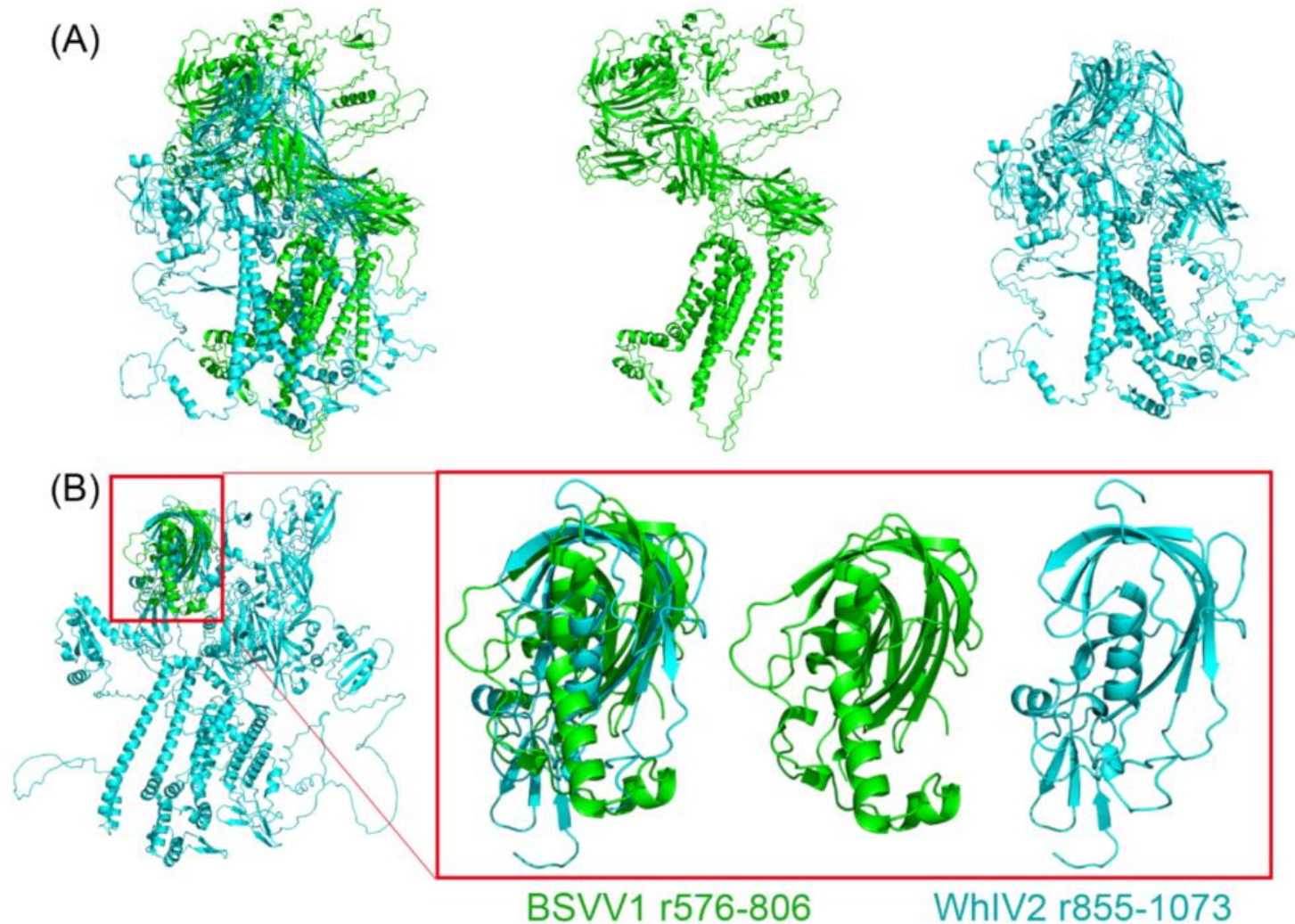


RVPD应用实例

案例I：“暗”病毒蛋白的功能推断



BSVV1与WhIV2糖蛋白结构的综合比较

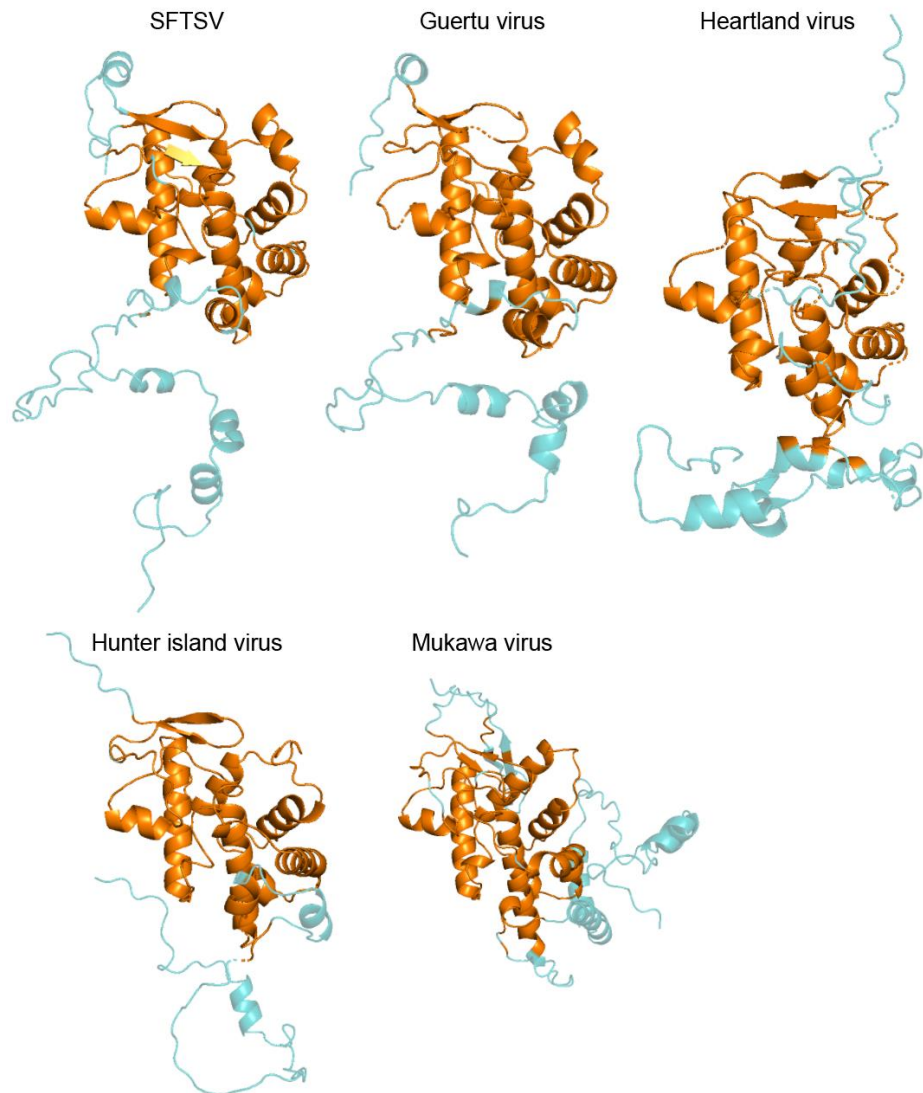


BSVV1 ORF2与WhIV2糖蛋白之间的保守区域



RVPSD应用实例

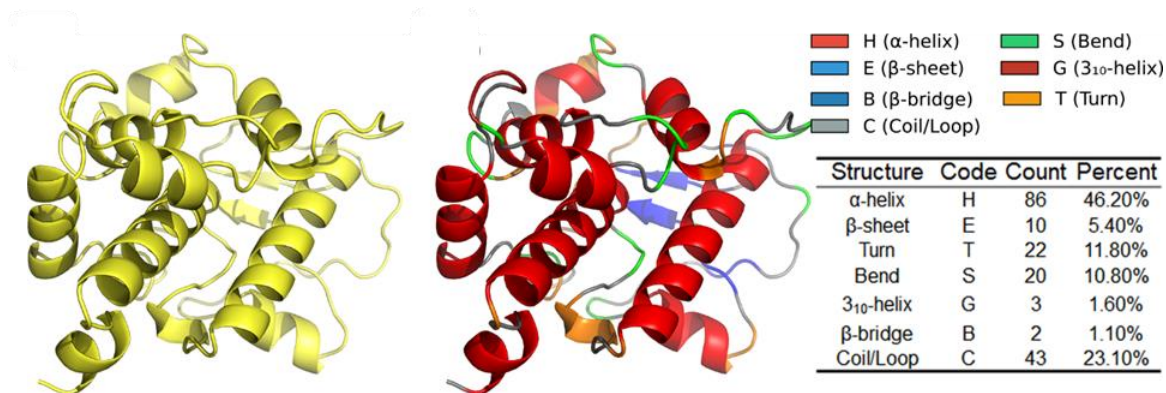
案例II：基于结构的布尼亚病毒NSs保守区域鉴定



多种布尼亚病毒NS蛋白的结构比较

SFTSV NSs AVV65325.1	MSLSKCSNVDLKSVAMNANTVRL-----PSLGEYPT-----LRR-----	35
Guertu virus NSs QBQ64951.1	MANSKHRDNLKSVALTNTVKLE-----PNLGEFPT-----VRR-----	35
Heartland virus NSs UDE22460.1	MSLSKAS-----QPSVKSAACVRL-----PIVVLEPNLAELSTSYV-----	35
Hunter Island virus NSs AHI10996.1	MACCL-----REQPTI VLM-----LSRK-----	25
Mukawa virus NSs BBE15817.1	MSSERV-----LYFSTLNRCAVRKKKNCKMGRSHI SAVHDASMSLCDADHFFMYNI YP	54
SFTSV NSs AVV65325.1	-----DLVECSCSVLTLTSMVKRMGKMTNTVWL-----FGNPKNPLHQLPEGLEQLL	81
Guertu virus NSs QBQ64951.1	-----GLVECSCSVLTVAMVKMGKMTNTVWL-----FGNPENPLHQLPAIEHLL	81
Heartland virus NSs UDE22460.1	-----GLVSCKCSVLTCMMRKAFNTNTVWL-----FGNPNNPLHALEPAVEQLL	81
Hunter Island virus NSs AHI10996.1	-----YSNQTTYNFKSWAEYKRRNLI PSEFWI-----LGDPKNEHLQTNHGLMSLF	71
Mukawa virus NSs BBE15817.1	NFGFSLKVEQRTVVGCE NTVYKFLDHGVMPARVCAWESSGSCVI PRRS WLDCGI SWQFCN	114
SFTSV NSs AVV65325.1	DMYYKDMRCYSQRELSALRWPSGKPSVWFLQAAHMFSSI KNSWAMETGRENWRGLFHRI T	141
Guertu virus NSs QBQ64951.1	EKYYIDLNCYSQREKSALRWPSGKPSVWFLQAAHMFSSVKNTWAMETGKENWRGLFHRI T	141
Heartland virus NSs UDE22460.1	DEYSGDLGSYSQQEKSALRWPSGKPSVHFLQAAHLFFSLKNTWAVETGQENWRGFFHRI T	141
Hunter Island virus NSs AHI10996.1	RRYHSSFNYSYCLEDDQAI MSWPSGFQDNFYLAQAATYFGEELTWEI NDGRVSPLGYLRKI A	131
Mukawa virus NSs BBE15817.1	WTI ENLMNGEVEVLRLALSWPTGRPTLQFI R- EFCRSKSFSTTSGFRSVRERVAKLI FKAA	173
SFTSV NSs AVV65325.1	KGRRYLFEGDMLDLSLEAIEKRRRLRGLPDLI LTGLSPI LDVALLQIESLARLRGMSLNH	201
Guertu virus NSs QBQ64951.1	RGCQYPFEGDMLDLDLDIEKRRRI RLGLPDSLITGLSPI LDVALLQIEALARLRGMSLNH	201
Heartland virus NSs UDE22460.1	PGKYYKFEGDMVIDSCYKIDERRRRMGLPDTFI TGLNPI MDVALLQIESLLRVRGLTLNY	201
Hunter Island virus NSs AHI10996.1	KHPKYSKAGDLII LACERI EAKRLERMPEPTEFI TGLSPI RDVALI QIEMMCRSRSQCLNV	191
Mukawa virus NSs BBE15817.1	KSEEGESLGEAITKCKWRKVRSEAMRLGVPEFDVPGVDLIRDI SLI QIERA-----YMRI	227
SFTSV NSs AVV65325.1	HLFTSSSLRKPLL-DCWDFFIPI RKKKTDGSYS-----VLDEDEDEPGVL-----	244
Guertu virus NSs QBQ64951.1	HMYTSSASLRKPLL-DCFNFFIPKRKKTSDSYS-----DDEHGEGD-FL-----	243
Heartland virus NSs UDE22460.1	HLFTSSFLDKPLL-DSL YFAIWRDKKKDDGYS-----QDKGARQDDPLNPLDELly-	252
Hunter Island virus NSs AHI10996.1	PLLSCCLATEEYLNSEPI LTLDSDEHYESP-----HPSLTTSRSS-----	234
Mukawa virus NSs BBE15817.1	NKCGSKWDNLPATGWDEPGCSMYEGVI PPFNLSQLSMKCAKVRNEPESRVWMRRKLKG	287
SFTSV NSs AVV65325.1	-----QGYPYLMAHYLNRC---PFHNLI RFDEELRTAALNTI WGRDWPAL GDPPKEV	296
Guertu virus NSs QBQ64951.1	-----KGYPLLMAHYLNKC---PFHNLI KYDEELREAALNTI WGKDWPKL-----	288
Heartland virus NSs UDE22460.1	-----LSDLPKPLAHYLNKC---PLHNIIMHDEEVREAYLNPI WGKDWPALSSSP---	302
Hunter Island virus NSs AHI10996.1	-----LPEPDY-----ESDLELREAMLNTAWGKDWP SLGEPsk--	270
Mukawa virus NSs BBE15817.1	KKVESKSQLIDLQEGITNI WMLDISDHFNMFPLINRVLDSFGKDWPALGAP---	343

布尼亚病毒NSs蛋白的序列比对



NS蛋白的保守核心结构域



总结

- ❑ 本研究介绍了RVPSD：一个综合性且用户友好的RNA病毒蛋白质结构网络数据库
- ❑ 目前，RVPSD提供了154,716个预测结构，覆盖度是现有资源的5至7倍
- ❑ 该平台集成了多种搜索和分析工具，案例研究展示了其在功能推断和保守特征鉴定方面的应用价值
- ❑ 网站：<https://virus.9itsg.net>

Qiangzhen Yang, Zhongshuai Tian, Tao Hu, Jiangrong Lou, Hengcong Liu, Edward C. Holmes, Yongyong Shi, et al. 2026.
RVPSD: A comprehensive and user-friendly web database for RNA viral protein structures.
iMetaOmics 3: e70120. <https://doi.org/10.1002/imo2.70120>

iMeta(宏): 生物和医学顶级成果发表平台

iMeta WILEY



iMeta(宏)期刊由宏科学创办，对标**Cell**的生物/医学综合期刊，**SCIE**、**PubMed**收录，影响因子(IF)44.4，位列全球第47，中国第4，**分区表生物学1区Top**，外审平均21天，投稿至发表中位数87天(比同水平期刊快3倍)，欢迎高影响力的研究、方法和综述投稿，CNS外审稿件可带意见和回复转投。

iMetaOmics (宏组学)，定位IF>15对标**NC/SA**的生物/医学综合期刊，已被**ESCI**、**PubMed**等收录。

iMetaMed (宏医学)定位IF>15的医学综合期刊，欢迎投稿！



主页: <http://www.imeta.science>

出版社: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

投稿: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



office@imeta.science

imetaomics@imeta.science



宣传片



iMeta



更新日期
2026/6/17