Brief summary of evidence of lab-made 2019 nCoV

From 2017-2019, a series academic papers about a novel zoonotic coronavirus isolated from bats in Zhoushan, Zhejiang (in short, ZS bat-CoV) were published in English (1) and Chinese

(1. post-graduate thesis: Preliminary study about bat-virus in South-east coastland http://le.cnki.net/kmobile/Master/detail/SYJT_PHAM/1017235765.nh)

(2. Molecular identification and analyse of bat-coronavirus in Zhoushan area

http://kns.cnki.net/kcms/detail/detail.aspx?filename=JSCY201901004&dbcode=CJFQ&dbname=CJFDTEMP&v=).

The main investigators were from Chinese military institution (The Third Military Medical University and Military medical institute of Nanjing Command) (*Pic. 1-3*).


Journal
Emerging Microbes & Infections ›
Volume 7, 2018 - Issue 1
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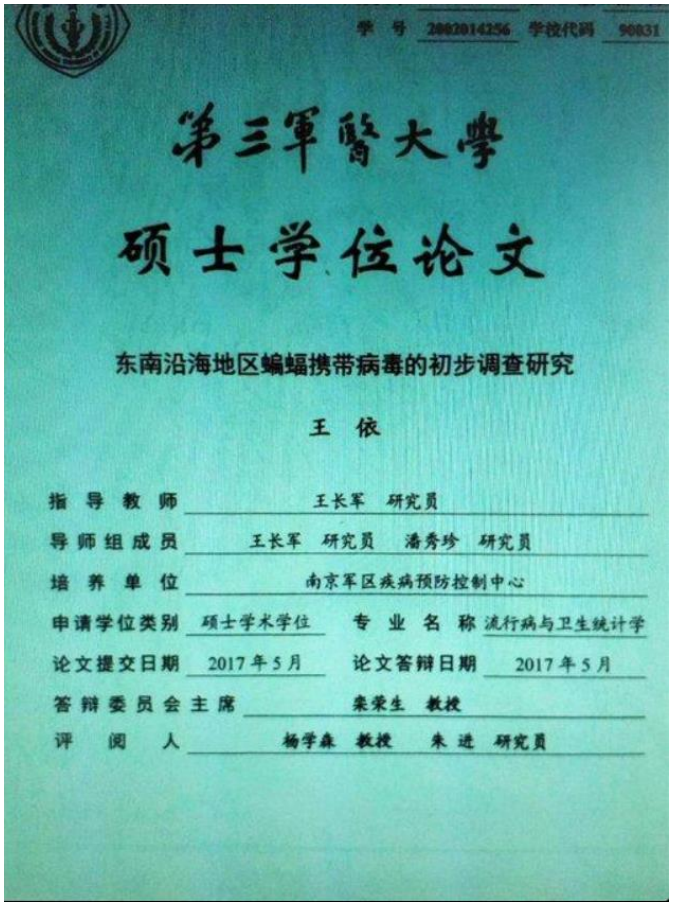
Original Articles
Genomic characterization and infectivity of a novel SARS-like coronavirus in Chinese bats
Dan Hu, Changqiang Zhu, Lele Ai, Ting He, Yi Wang, Fuqiang Ye, Lu Yang, Chenxi Ding, Xuhui Zhu, Ruicheng Lv, ong Tan & Changjun Wang
018, Published
Department of Epidemiology, College of Preventive MedicineThird Military Medical University 400038 Chongqing China; Department of EpidemiologyResearch Institute for Medicine of Nanjing Command 210002 Nanjing China

Pic. 1


学号 2002014256 学校代码 90831
第三軍醫大學
硕士学位论文
东南沿海地区蝙蝠携带病毒的初步调查研究
王依
指导教师 王长军 研究员
导师组成员 王长军 研究员 潘秀珍 研究员
培养单位 南京军区疾病预防控制中心
申请学位类别 硕士学术学位 专业名称 流行病与卫生统计学
论文提交日期 2017年5月 论文答辩日期 2017年5月
答辩委员会主席 栾荣生 教授
评阅人 杨学森 教授 朱进 研究员

Pic. 2

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舟山地区蝙蝠轮状病毒分子鉴定和分析

《寄生虫与医学昆虫学报》2019年 第1期 | 何婷 朱长强 艾乐乐 胡丹 吕瑞辰 谭伟龙 王长军 钱晖 江苏大学医学院 江苏镇江212000 东部战区疾病预防控制中心 江苏南京210000 中国人民解放军疾病预防控制中心 北京100071

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论文服务： 论文检测 论文选题

摘 要：为监测东南沿海舟山地区蝙蝠携带轮状病毒的流行情况,探索其流行机制,2015-2018年,在浙江省舟山地区采集蝙蝠,以蝙蝠肠组织为模板,设计针对轮状病毒VP3序列的特异引物进行RT-PCR检测。结果显示,2015年采集的65只蝙蝠,轮状病毒阳性率为6.15%(4/65),2016年采集的48只蝙蝠,阳性率为2.08%(1/48),2017年采集的70只蝙蝠,阳性率为2.86%(2/70),而2018年采集的101只蝙蝠,未检测到轮状病毒序列。针对2017年小菲菊头蝠Rhinolophus hipposideros体内发现的一株轮状病毒进行基因组扩增,获取部分基因组序列并进行生物信息学分析,发现VP7基因序列与蝙蝠源轮状病毒相似度最高,同源性为96%;VP3基因序列与人源轮状病毒同源性为90%;VP6基因序列与猫同源性为95%。根据上述结果,我们推测舟山蝙蝠来源轮状病毒是一株重组病毒株,具有潜在跨种传播给人类的可能性。本研究系首次在东南沿海舟山地区蝙蝠体内检测到轮状病毒,对该地区轮状病毒的监测和预警具有一定的公共卫生意义。

【分 类】 【生物科学】 > 动物学 > 动物分类学（系统动物学） > 哺乳纲 > 真兽亚纲 > 翼手目

【关键词】 蝙蝠 轮状病毒 进化分析

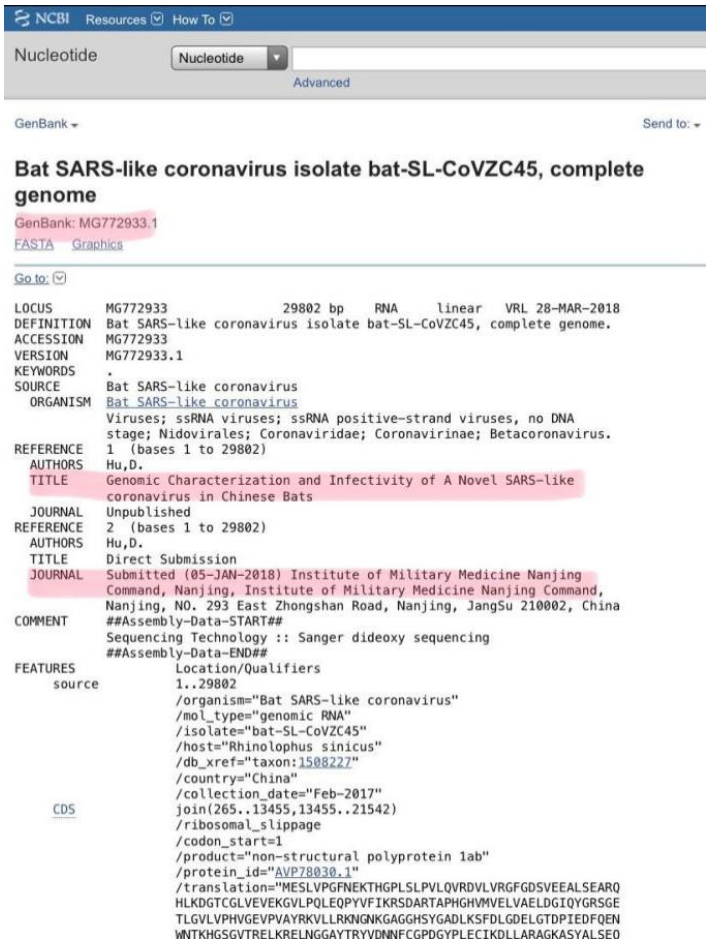
【出 处】 《寄生虫与医学昆虫学报》2019年 第1期 22-29页 共8页

【收 录】 中文科技期刊数据库

Pic. 3

It means the novel ZS bat-CoV was owned by Chinese military labs only. In the papers above, they have clarified that ZS bat-CoV has potential cross-species

transmission, including human, also emphasized that it is significant for public health. The full genome sequence of certain strains of ZS bat-CoV were released in Genbank of NIH (accession numbers MG772844 through MG772934), provided by Nanjing



NCBI Resources How To

Nucleotide Nucleotide Advanced

GenBank Send to:

Bat SARS-like coronavirus isolate bat-SL-CoVZC45, complete genome

GenBank: MG772933.1

FASTA Graphics

Go to:

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VERSION     MG772933.1
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  ORGANISM  Bat SARS-like coronavirus
            Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA
            stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE   1  (bases 1 to 29802)
  AUTHORS   Hu,D.
  TITLE     Genomic Characterization and Infectivity of A Novel SARS-like
            coronavirus in Chinese Bats
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 29802)
  AUTHORS   Hu,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2018) Institute of Military Medicine Nanjing
            Command, Nanjing, Institute of Military Medicine Nanjing Command,
            Nanjing, NO. 293 East Zhongshan Road, Nanjing, JangSu 210002, China
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            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
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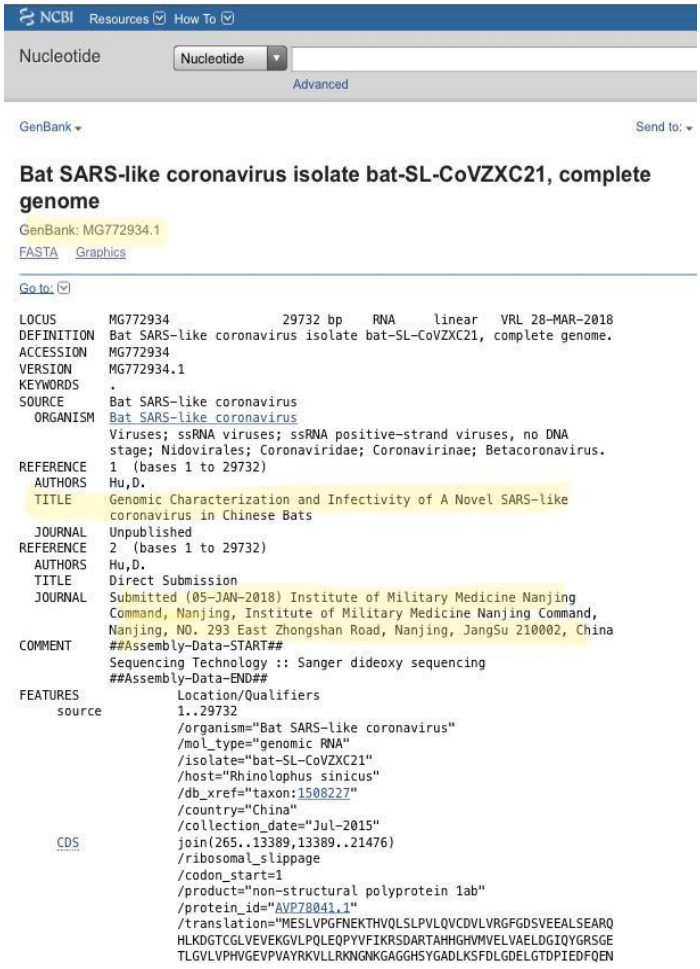
Pic. 4



NCBI Resources How To

Nucleotide Nucleotide Advanced

GenBank Send to:

Bat SARS-like coronavirus isolate bat-SL-CoVZXC21, complete genome

GenBank: MG772934.1

FASTA Graphics

Go to:

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ACCESSION   MG772934
VERSION     MG772934.1
KEYWORDS    .
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  ORGANISM  Bat SARS-like coronavirus
            Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA
            stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE   1  (bases 1 to 29732)
  AUTHORS   Hu,D.
  TITLE     Genomic Characterization and Infectivity of A Novel SARS-like
            coronavirus in Chinese Bats
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 29732)
  AUTHORS   Hu,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2018) Institute of Military Medicine Nanjing
            Command, Nanjing, Institute of Military Medicine Nanjing Command,
            Nanjing, NO. 293 East Zhongshan Road, Nanjing, JangSu 210002, China
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            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
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                     /db_xref="taxon:1508227"
                     /country="China"
                     /collection_date="Jul-2015"
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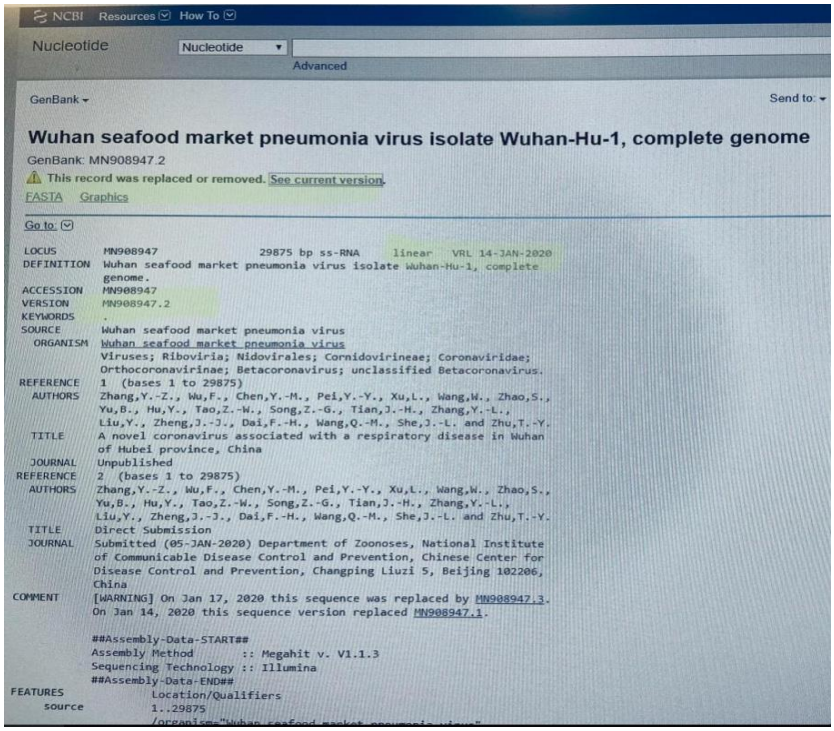
                     TLGVLVPHVGEVPVAYRKVLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPIEDFQEN
```

Pic. 5

command (*Pic. 4-5*).

11 Jan 2020, China CDC released the full genome sequence of 2019 nCoV, and it was upload to GenBank of NIH on 12 Jan (Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, accession number MN908947.1). 14 Jan, MN908947.1 was replaced by China CDC without announced (accession number MN908947.2). 17 Jan, MN908947.2 was replaced by them for unknown reasons (accession number MN908947.3) (*pic. 6-7*).



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GenBank Send to:

Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome

GenBank: MN908947.2

⚠ This record was replaced or removed. See current version.

FASTA Graphics

Go to:

```
LOCUS       MN908947              29875 bp ss-RNA     linear   VRL 14-JAN-2020
DEFINITION  Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete
            genome.
ACCESSION   MN908947
VERSION     MN908947.2
KEYWORDS    .
SOURCE      Wuhan seafood market pneumonia virus
  ORGANISM  Wuhan seafood market pneumonia virus
            Viruses; Riboviria; Nidovirales; Cornidovirineae; Coronaviridae;
            Orthocoronavirinae; Betacoronavirus; unclassified Betacoronavirus.
REFERENCE   1  (bases 1 to 29875)
  AUTHORS   Zhang,Y.-Z., Wu,F., Chen,Y.-M., Pei,Y.-Y., Xu,L., Wang,W., Zhao,S.,
            Yu,B., Hu,Y., Tao,Z.-W., Song,Z.-G., Tian,J.-H., Zhang,Y.-L.,
            Liu,Y., Zheng,J.-J., Dai,F.-H., Wang,Q.-M., She,J.-L. and Zhu,T.-Y.
  TITLE     A novel coronavirus associated with a respiratory disease in Wuhan
            of Hubei province, China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 29875)
  AUTHORS   Zhang,Y.-Z., Wu,F., Chen,Y.-M., Pei,Y.-Y., Xu,L., Wang,W., Zhao,S.,
            Yu,B., Hu,Y., Tao,Z.-W., Song,Z.-G., Tian,J.-H., Zhang,Y.-L.,
            Liu,Y., Zheng,J.-J., Dai,F.-H., Wang,Q.-M., She,J.-L. and Zhu,T.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2020) Department of Zoonoses, National Institute
            of Communicable Disease Control and Prevention, Chinese Center for
            Disease Control and Prevention, Changping Liuzi 5, Beijing 102206,
            China
COMMENT     [WARNING] On Jan 17, 2020 this sequence was replaced by MN908947.3.
            On Jan 14, 2020 this sequence version replaced MN908947.1.

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            Sequencing Technology :: Illumina
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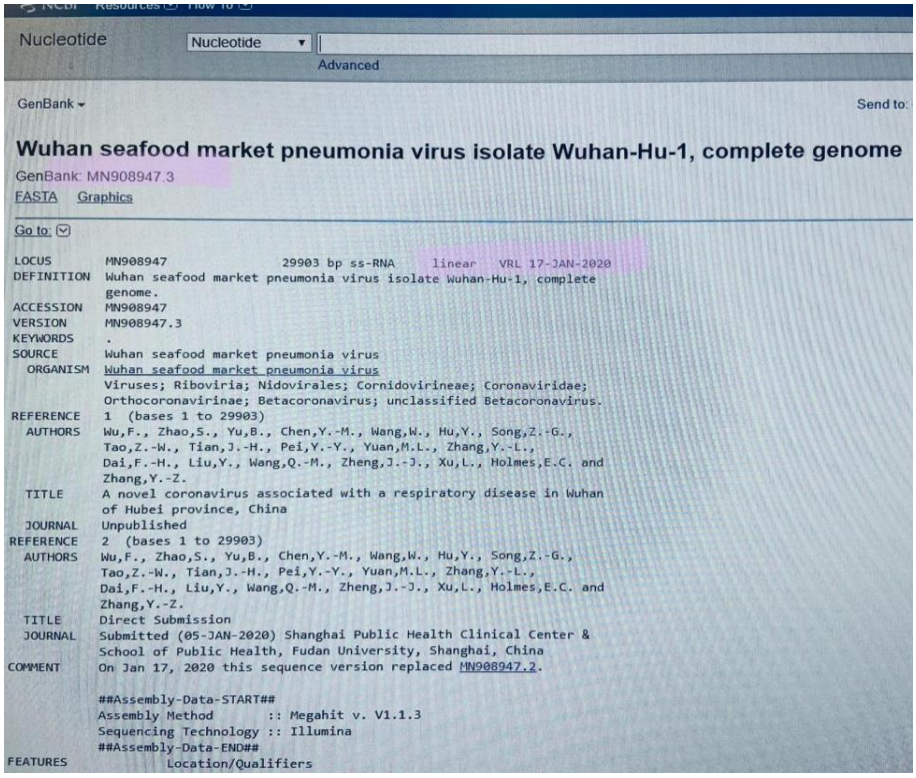
Pic. 6



Nucleotide Nucleotide Advanced

GenBank Send to:

Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete genome

GenBank: MN908947.3

FASTA Graphics

Go to:

```
LOCUS       MN908947              29903 bp ss-RNA     linear   VRL 17-JAN-2020
DEFINITION  Wuhan seafood market pneumonia virus isolate Wuhan-Hu-1, complete
            genome.
ACCESSION   MN908947
VERSION     MN908947.3
KEYWORDS    .
SOURCE      Wuhan seafood market pneumonia virus
  ORGANISM  Wuhan seafood market pneumonia virus
            Viruses; Riboviria; Nidovirales; Cornidovirineae; Coronaviridae;
            Orthocoronavirinae; Betacoronavirus; unclassified Betacoronavirus.
REFERENCE   1  (bases 1 to 29903)
  AUTHORS   Wu,F., Zhao,S., Yu,B., Chen,Y.-M., Wang,W., Hu,Y., Song,Z.-G.,
            Tao,Z.-W., Tian,J.-H., Pei,Y.-Y., Yuan,M.L., Zhang,Y.-L.,
            Dai,F.-H., Liu,Y., Wang,Q.-M., Zheng,J.-J., Xu,L., Holmes,E.C. and
            Zhang,Y.-Z.
  TITLE     A novel coronavirus associated with a respiratory disease in Wuhan
            of Hubei province, China
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 29903)
  AUTHORS   Wu,F., Zhao,S., Yu,B., Chen,Y.-M., Wang,W., Hu,Y., Song,Z.-G.,
            Tao,Z.-W., Tian,J.-H., Pei,Y.-Y., Yuan,M.L., Zhang,Y.-L.,
            Dai,F.-H., Liu,Y., Wang,Q.-M., Zheng,J.-J., Xu,L., Holmes,E.C. and
            Zhang,Y.-Z.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2020) Shanghai Public Health Clinical Center &
            School of Public Health, Fudan University, Shanghai, China
COMMENT     On Jan 17, 2020 this sequence version replaced MN908947.2.

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            Sequencing Technology :: Illumina
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FEATURES             Location/Qualifiers
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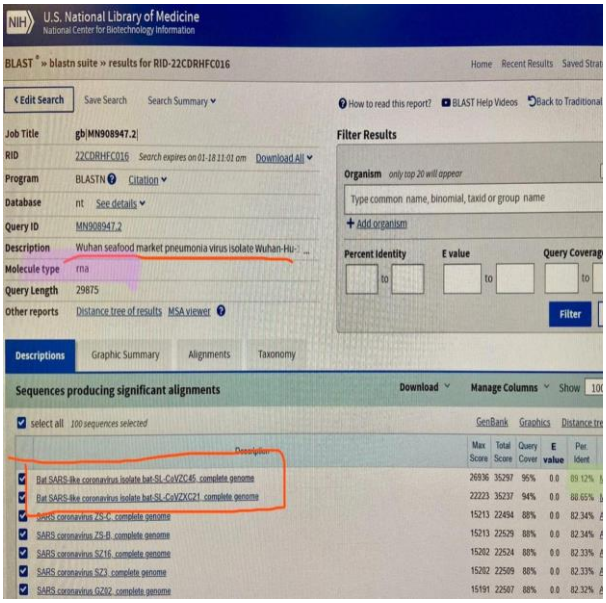
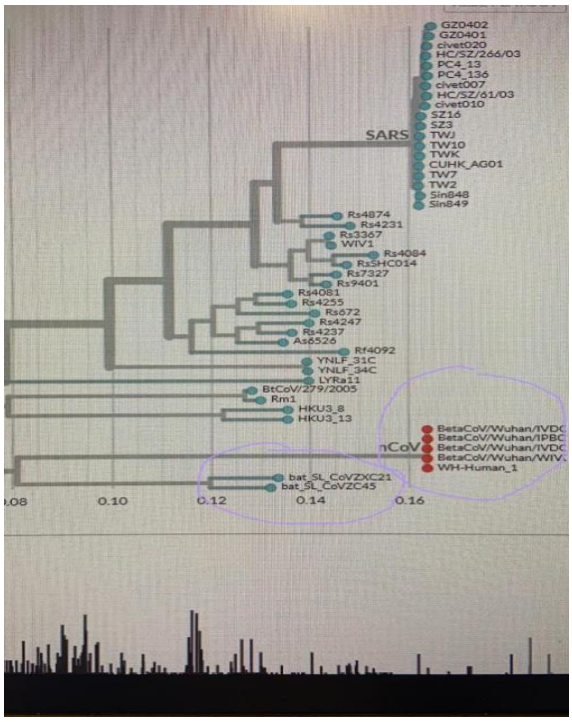
Pic. 7

The blast results based on full genome of MN908947.2 and MN908947.3 shown that ZS bat-CoV is the most closed known coronavirus to 2019 nCoV via online blast tool-NIH (per Identity is 88.65-89.12%, MG772933.1 and MG772934.1) (*pic. 8*). According to analysis of virus evolution tree, ZS bat-CoV is the most closed relative to 2019 nCoV (https://nextstrain.org/groups/blab/sars-like-cov) (*pic. 9*). To note, when blast MN908947.1 at that time, there were some error in the sequence which affected the results (no picture recorded).



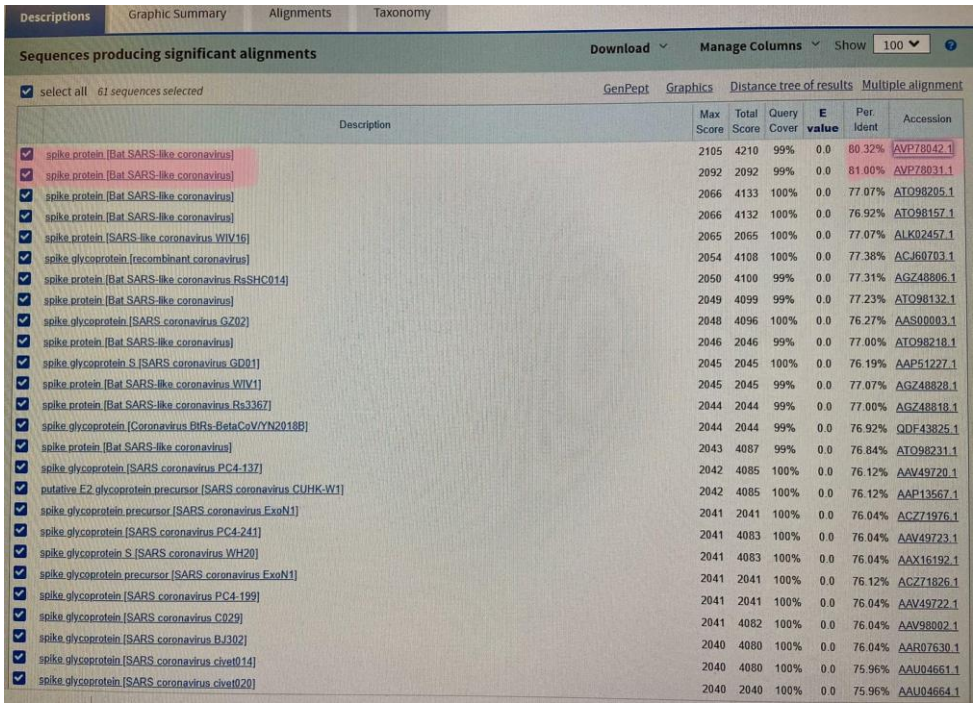
Pic. 8



Pic.9

Further blast results for the most critical proteins and segments between 2019 nCoV and all the other known coronavirus in Genbank, still show the most significant similarity to ZS bat-CoV, which is much higher than compared with any others. The similarity is Spike protein 80.32-81.00% (S protein) (*pic. 10-12*) and Nucleocapsid protein 94.03% (*pic. 13-15*) to two strains of ZS bat-CoV (MG772933.1 and MG772934.1), while Envelop protein **100%** (E protein) (*pic. 16-18*), ORF8 segment

94.21% (*pic. 19-20*), and Membrane glycoprotein 98.65% (*pic. 21-22*) to MG772933.1, as well as RdRp gene 95.75% (*pic. 23-24*) to MG772934.1.



Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments — Download | Manage Columns | Show 100

select all 61 sequences selected — GenPept | Graphics | Distance tree of results | Multiple alignment

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
spike protein [Bat SARS-like coronavirus]	2105	4210	99%	0.0	80.32%	AVP78042.1
spike protein [Bat SARS-like coronavirus]	2092	2092	99%	0.0	81.00%	AVP78031.1
spike protein [Bat SARS-like coronavirus]	2066	4133	100%	0.0	77.07%	ATO98205.1
spike protein [Bat SARS-like coronavirus]	2066	4132	100%	0.0	76.92%	ATO98157.1
spike protein [SARS-like coronavirus WIV16]	2065	2065	100%	0.0	77.07%	ALK02457.1
spike glycoprotein [recombinant coronavirus]	2054	4108	100%	0.0	77.38%	ACJ60703.1
spike protein [Bat SARS-like coronavirus RsSHC014]	2050	4100	99%	0.0	77.31%	AGZ48806.1
spike protein [Bat SARS-like coronavirus]	2049	4099	99%	0.0	77.23%	ATO98132.1
spike glycoprotein [SARS coronavirus GZ02]	2048	4096	100%	0.0	76.27%	AAS00003.1
spike protein [Bat SARS-like coronavirus]	2046	2046	99%	0.0	77.00%	ATO98218.1
spike glycoprotein S [SARS coronavirus GD01]	2045	2045	100%	0.0	76.19%	AAP51227.1
spike protein [Bat SARS-like coronavirus WIV1]	2045	2045	99%	0.0	77.07%	AGZ48828.1
spike protein [Bat SARS-like coronavirus Rs3367]	2044	2044	99%	0.0	77.00%	AGZ48818.1
spike glycoprotein [Coronavirus BtRs-BetaCoV/YN2018B]	2044	2044	99%	0.0	76.92%	QDF43825.1
spike protein [Bat SARS-like coronavirus]	2043	4087	99%	0.0	76.84%	ATO98231.1
spike glycoprotein [SARS coronavirus PC4-137]	2042	4085	100%	0.0	76.12%	AAV49720.1
putative E2 glycoprotein precursor [SARS coronavirus CUHK-W1]	2042	4085	100%	0.0	76.12%	AAP13567.1
spike glycoprotein precursor [SARS coronavirus ExoN1]	2041	2041	100%	0.0	76.04%	ACZ71976.1
spike glycoprotein [SARS coronavirus PC4-241]	2041	4083	100%	0.0	76.04%	AAV49723.1
spike glycoprotein S [SARS coronavirus WH20]	2041	4083	100%	0.0	76.04%	AAX16192.1
spike glycoprotein precursor [SARS coronavirus ExoN1]	2041	2041	100%	0.0	76.12%	ACZ71826.1
spike glycoprotein [SARS coronavirus PC4-199]	2041	2041	100%	0.0	76.04%	AAV49722.1
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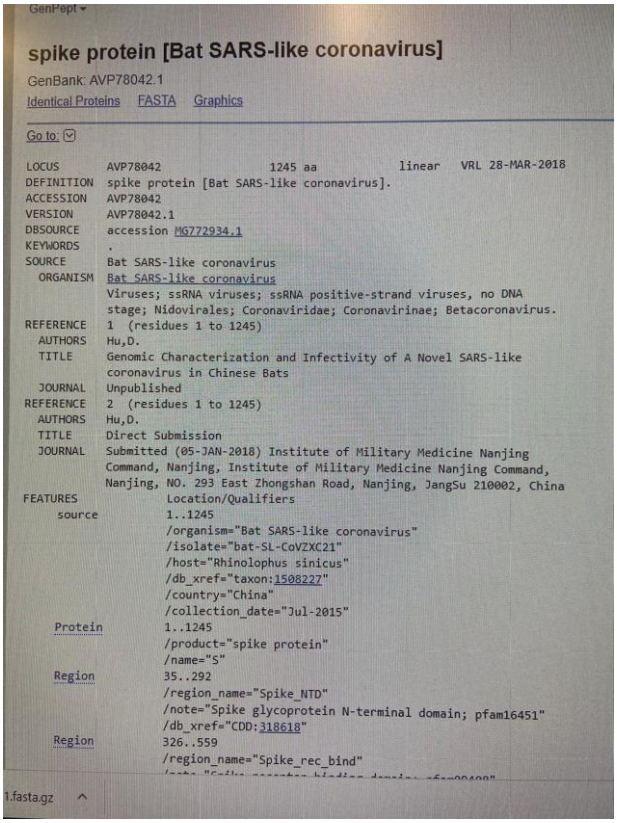
Pic. 10



GenPept

spike protein [Bat SARS-like coronavirus]

GenBank: AVP78042.1

Identical Proteins | FASTA | Graphics

Go to:

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ACCESSION   AVP78042
VERSION     AVP78042.1
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KEYWORDS    .
SOURCE      Bat SARS-like coronavirus
  ORGANISM  Bat SARS-like coronavirus
            Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA
            stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE   1  (residues 1 to 1245)
  AUTHORS   Hu,D.
  TITLE     Genomic Characterization and Infectivity of A Novel SARS-like
            coronavirus in Chinese Bats
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 1245)
  AUTHORS   Hu,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2018) Institute of Military Medicine Nanjing
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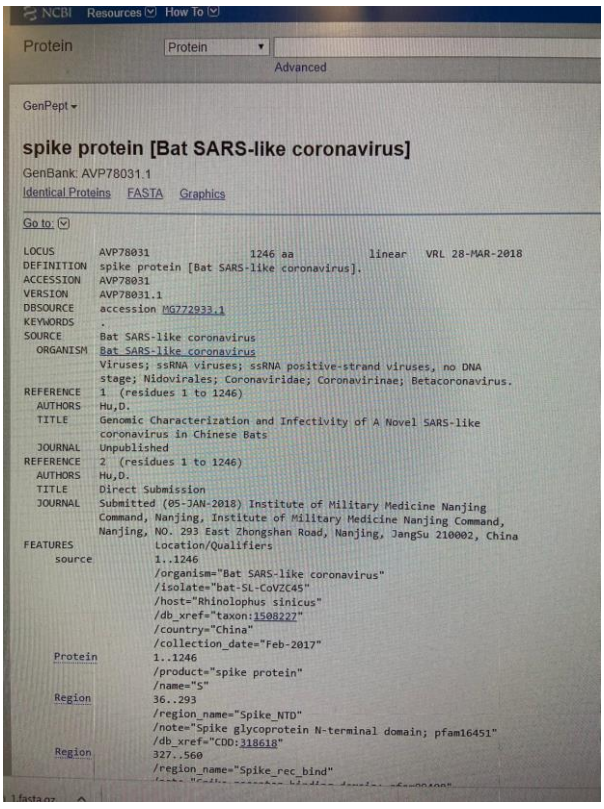
1.fasta.gz

Pic. 11



NCBI Resources How To

Protein — Protein — Advanced

GenPept

spike protein [Bat SARS-like coronavirus]

GenBank: AVP78031.1

Identical Proteins | FASTA | Graphics

Go to:

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ACCESSION   AVP78031
VERSION     AVP78031.1
DBSOURCE    accession MG772933.1
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  ORGANISM  Bat SARS-like coronavirus
            Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA
            stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE   1  (residues 1 to 1246)
  AUTHORS   Hu,D.
  TITLE     Genomic Characterization and Infectivity of A Novel SARS-like
            coronavirus in Chinese Bats
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 1246)
  AUTHORS   Hu,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2018) Institute of Military Medicine Nanjing
            Command, Nanjing, Institute of Military Medicine Nanjing Command,
            Nanjing, NO. 293 East Zhongshan Road, Nanjing, JangSu 210002, China
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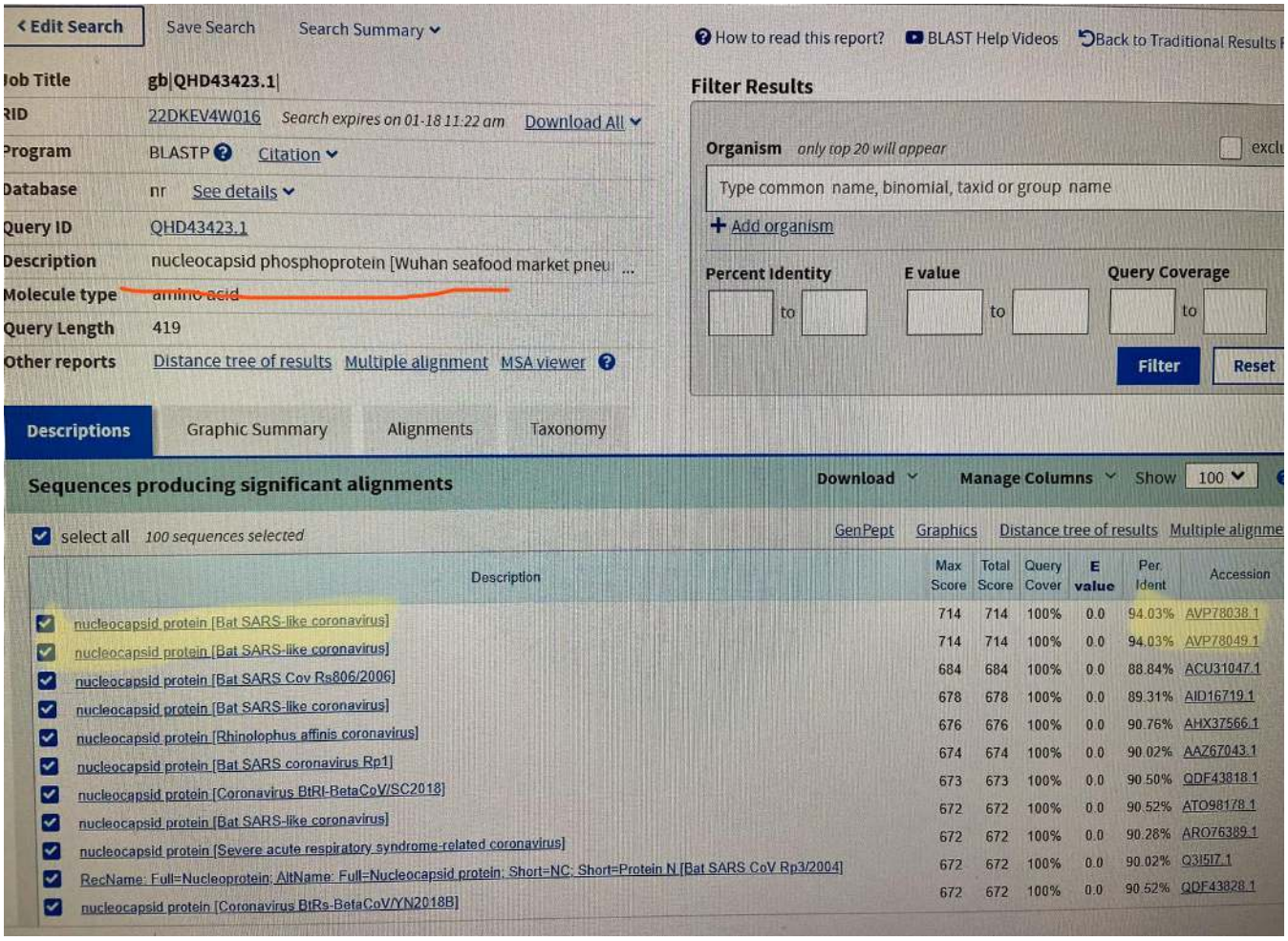
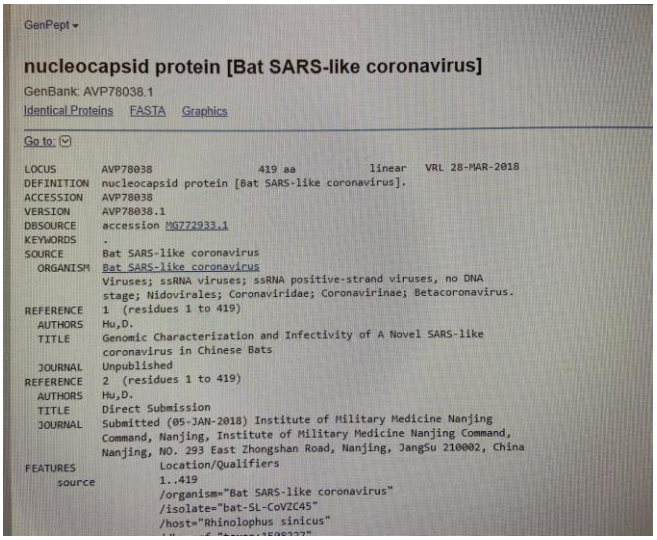
Pic. 12



Pic. 13



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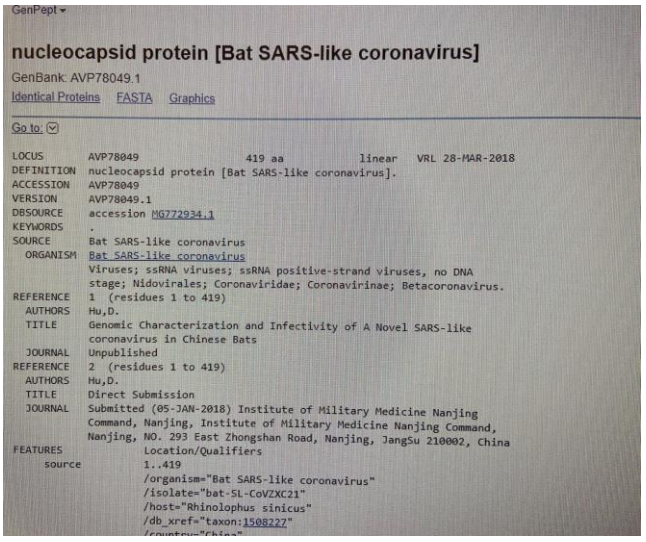

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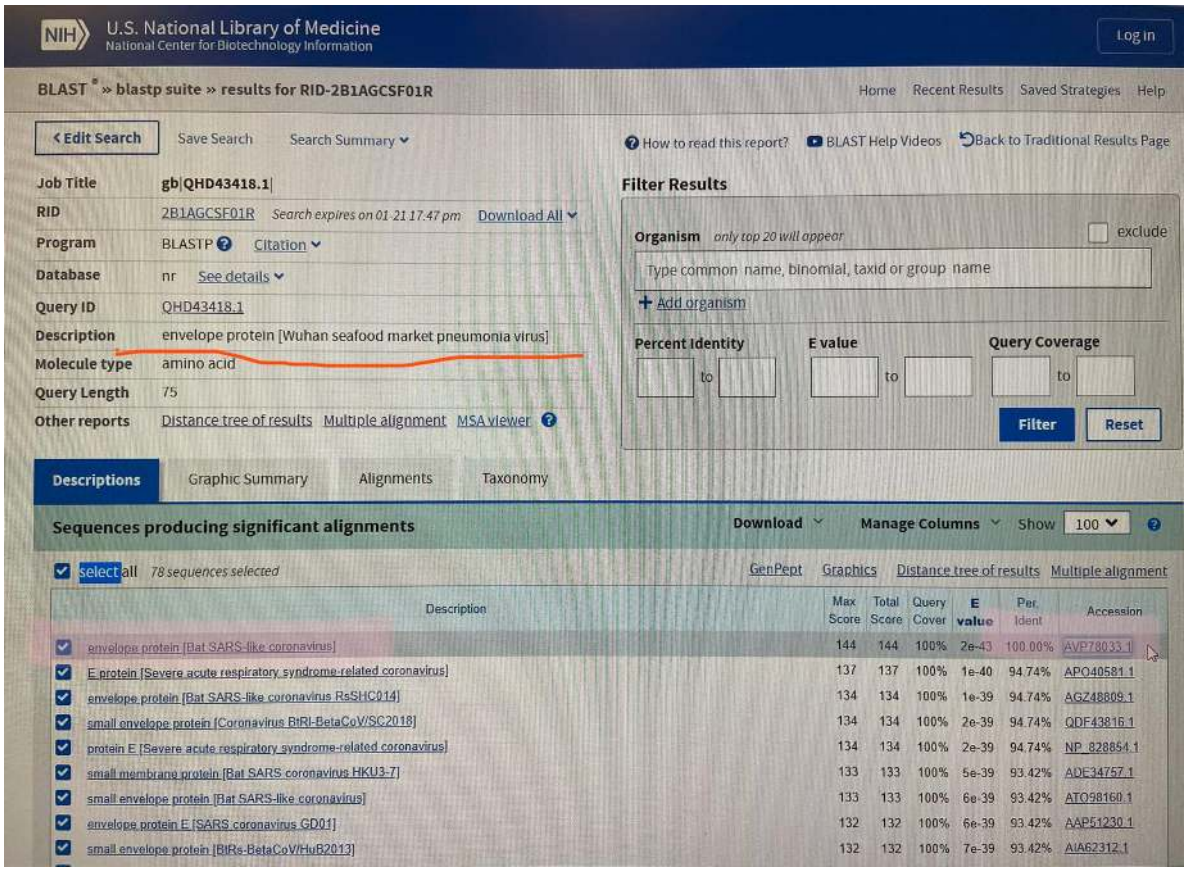
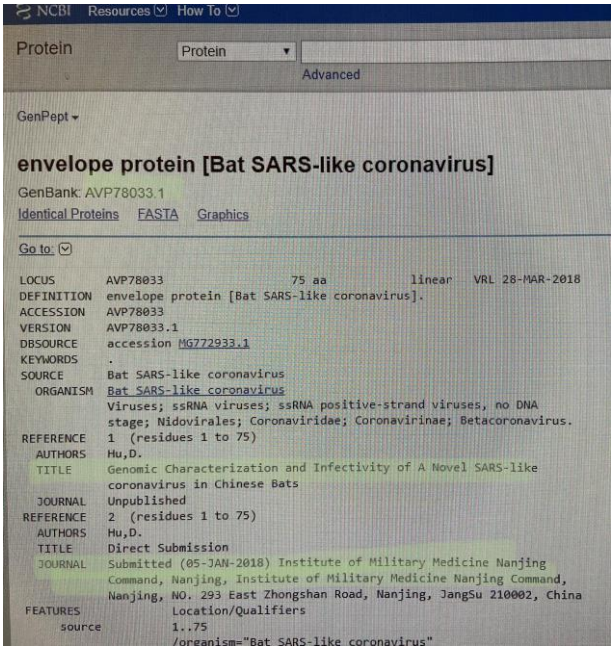


Pic. 16



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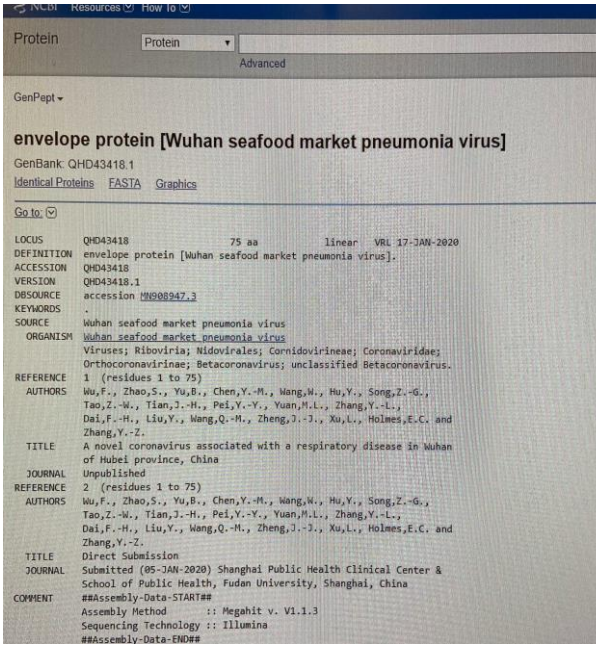

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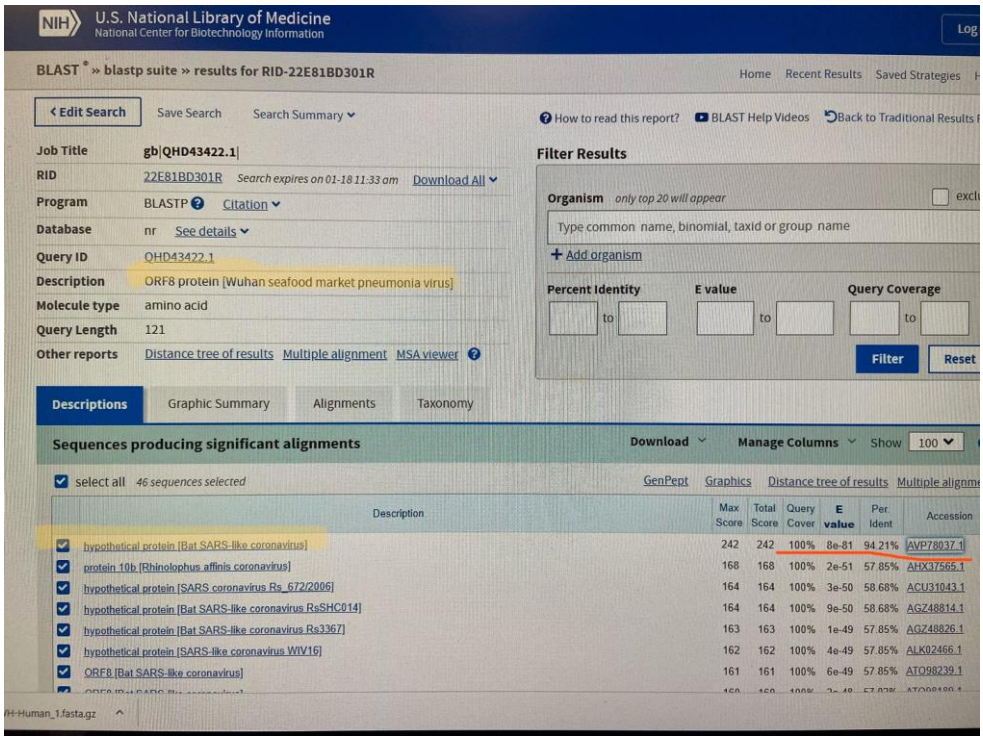
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RID 22E81BD301R Search expires on 01-18 11:33 am Download All
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Query ID QHD43422.1
Description ORF8 protein [Wuhan seafood market pneumonia virus]
Molecule type amino acid
Query Length 121
Other reports Distance tree of results Multiple alignment MSA viewer
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Type common name, binomial, taxid or group name
Add organism
Percent Identity
E value
Query Coverage
Filter
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Descriptions
Graphic Summary
Alignments
Taxonomy
Sequences producing significant alignments
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select all 46 sequences selected
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Graphics
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Description
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Accession
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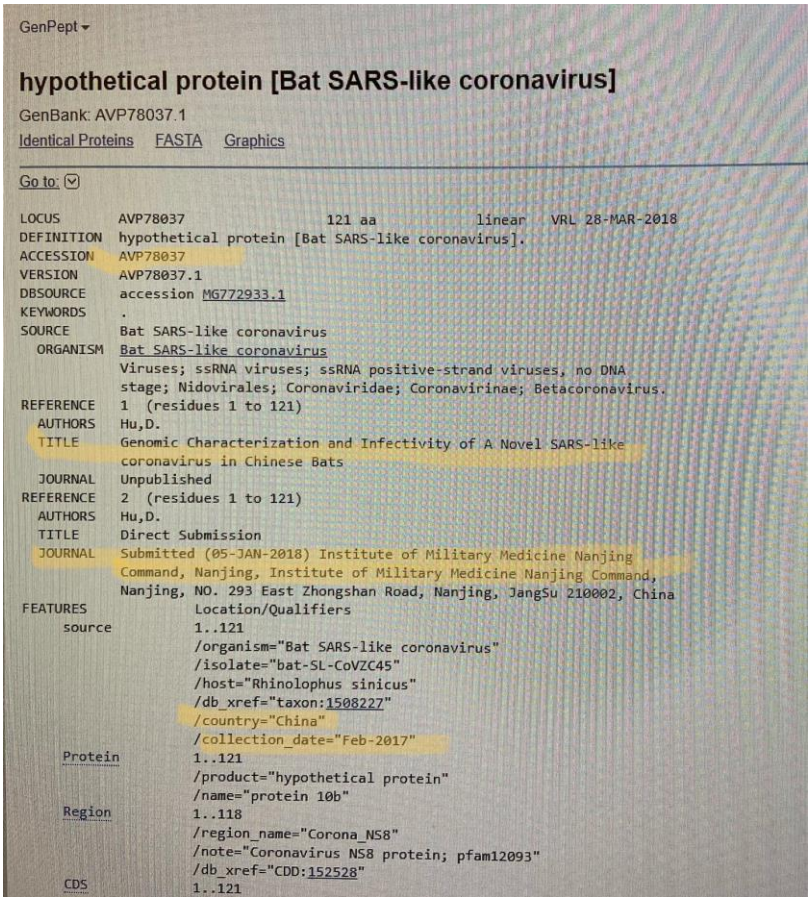
Pic. 19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VERSION AVP78037.1
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Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE 1 (residues 1 to 121)
AUTHORS Hu,D.
TITLE Genomic Characterization and Infectivity of A Novel SARS-like coronavirus in Chinese Bats
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 121)
AUTHORS Hu,D.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2018) Institute of Military Medicine Nanjing Command, Nanjing, Institute of Military Medicine Nanjing Command, Nanjing, NO. 293 East Zhongshan Road, Nanjing, JangSu 210002, China
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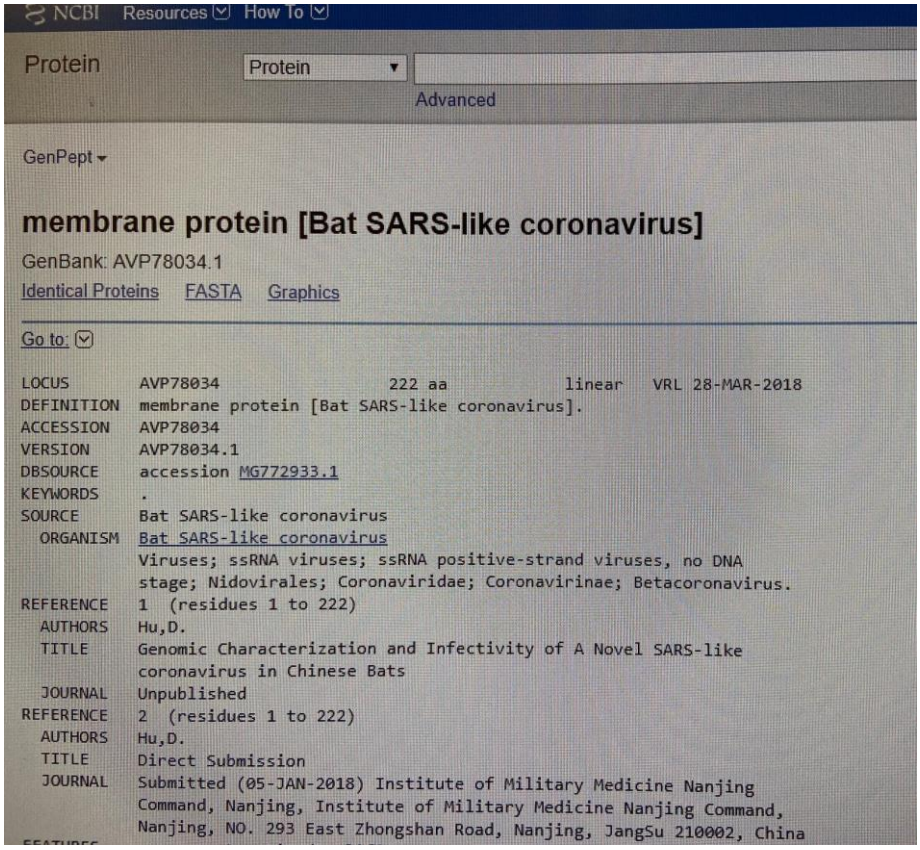
Pic. 20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Protein
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membrane protein [Bat SARS-like coronavirus]
GenBank: AVP78034.1
Identical Proteins FASTA Graphics
Go to:
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DEFINITION membrane protein [Bat SARS-like coronavirus].
ACCESSION AVP78034
VERSION AVP78034.1
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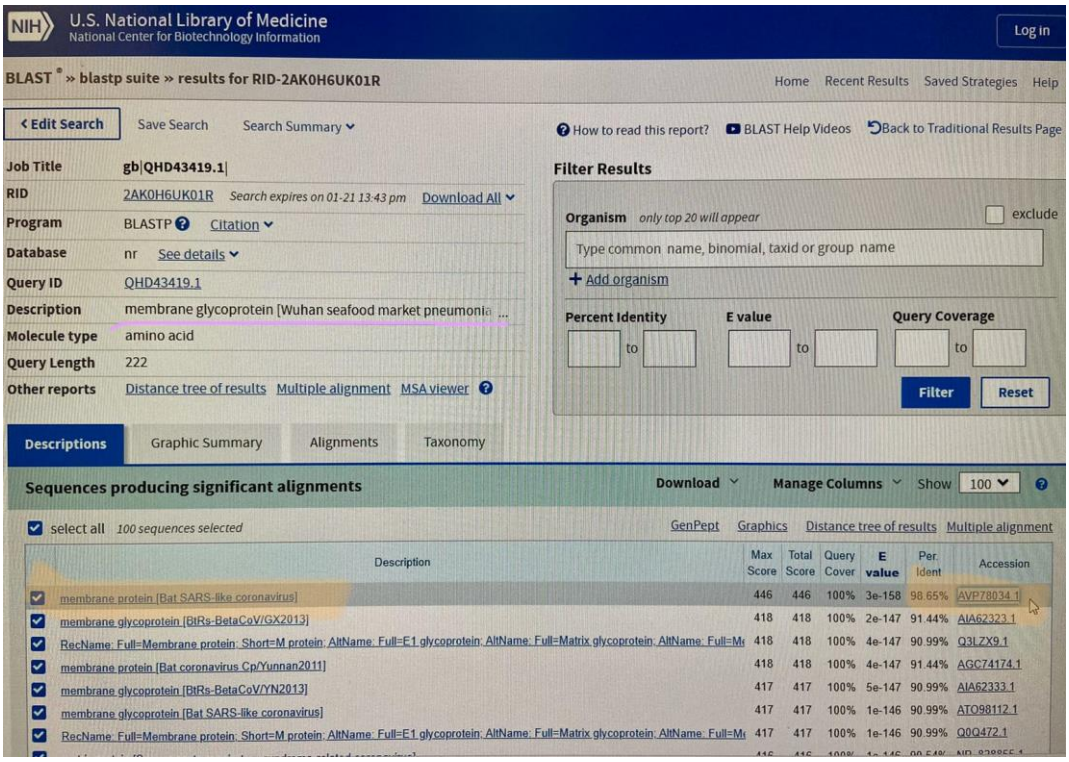
ORGANISM Bat SARS-like coronavirus
Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE 1 (residues 1 to 222)
AUTHORS Hu,D.
TITLE Genomic Characterization and Infectivity of A Novel SARS-like coronavirus in Chinese Bats
JOURNAL Unpublished
REFERENCE 2 (residues 1 to 222)
AUTHORS Hu,D.
TITLE Direct Submission
JOURNAL Submitted (05-JAN-2018) Institute of Military Medicine Nanjing Command, Nanjing, Institute of Military Medicine Nanjing Command, Nanjing, NO. 293 East Zhongshan Road, Nanjing, JangSu 210002, China

Pic. 21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Program BLASTP Citation
Database nr See details
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Description membrane glycoprotein [Wuhan seafood market pneumonia ...
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Query Length 222
Other reports Distance tree of results Multiple alignment MSA viewer
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Organism only top 20 will appear exclude
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select all 100 sequences selected
GenPept Graphics Distance tree of results Multiple alignment
Description Max Score Total Score Query Cover E value Per. Ident Accession
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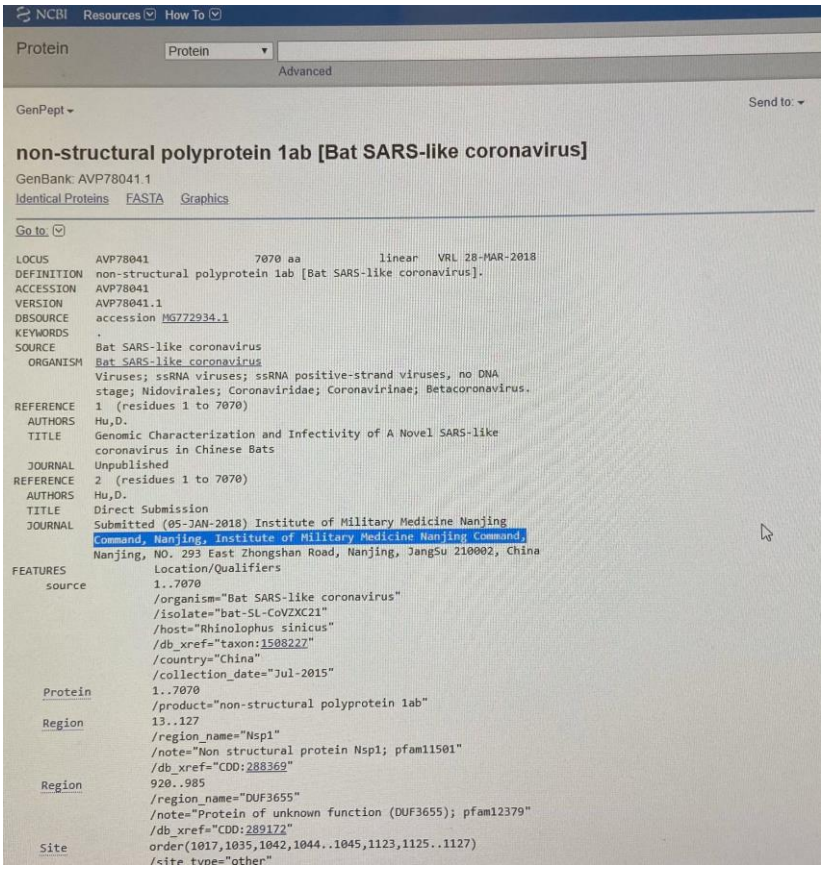
Pic. 22



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Protein Protein Advanced

GenPept Send to:

non-structural polyprotein 1ab [Bat SARS-like coronavirus]

GenBank: AVP78041.1

Identical Proteins FASTA Graphics

Go to:

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ACCESSION   AVP78041
VERSION     AVP78041.1
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            stage; Nidovirales; Coronaviridae; Coronavirinae; Betacoronavirus.
REFERENCE   1  (residues 1 to 7070)
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  TITLE     Genomic Characterization and Infectivity of A Novel SARS-like
            coronavirus in Chinese Bats
  JOURNAL   Unpublished
REFERENCE   2  (residues 1 to 7070)
  AUTHORS   Hu,D.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JAN-2018) Institute of Military Medicine Nanjing
            Command, Nanjing, Institute of Military Medicine Nanjing Command,
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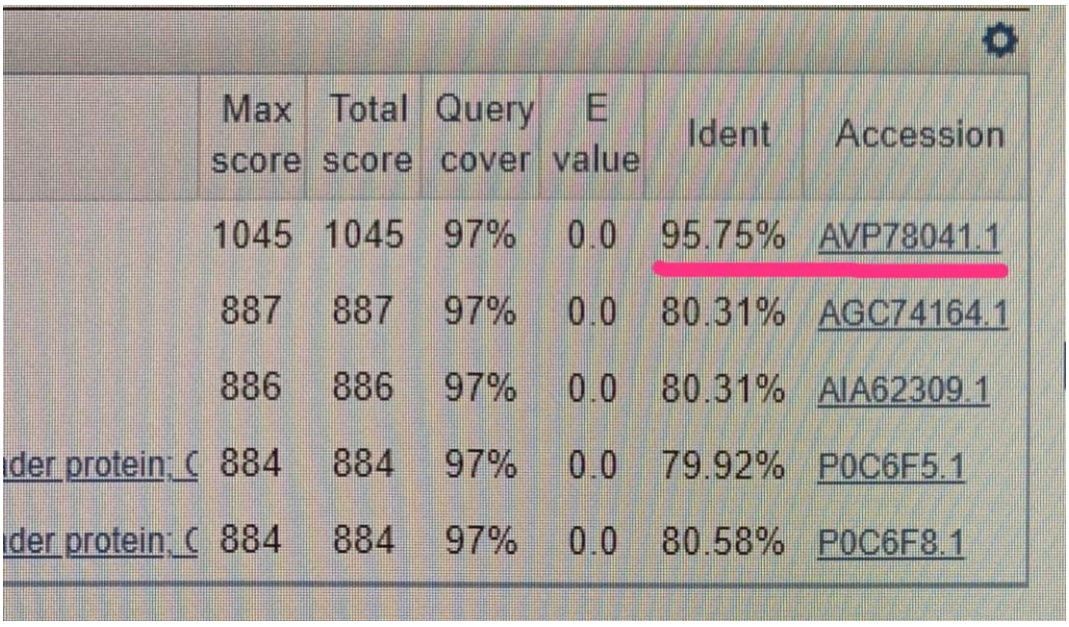
Pic. 23



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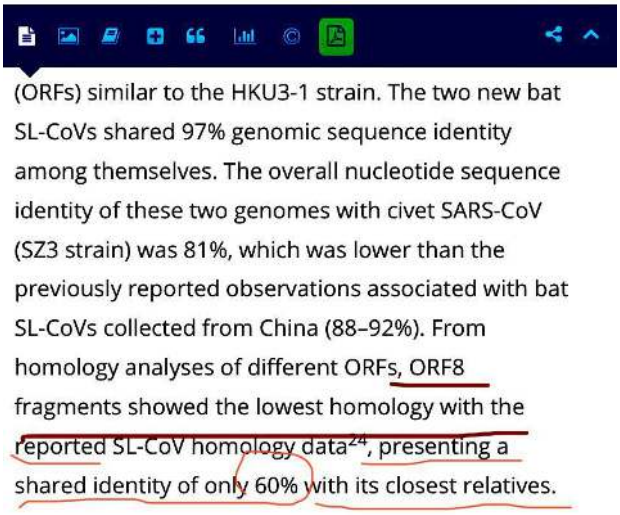
	887	887	97%	0.0	80.31%	AGC74164.1
	886	886	97%	0.0	80.31%	AIA62309.1
ıder protein; (	884	884	97%	0.0	79.92%	P0C6F5.1
ıder protein; (	884	884	97%	0.0	80.58%	P0C6F8.1

Pic. 24

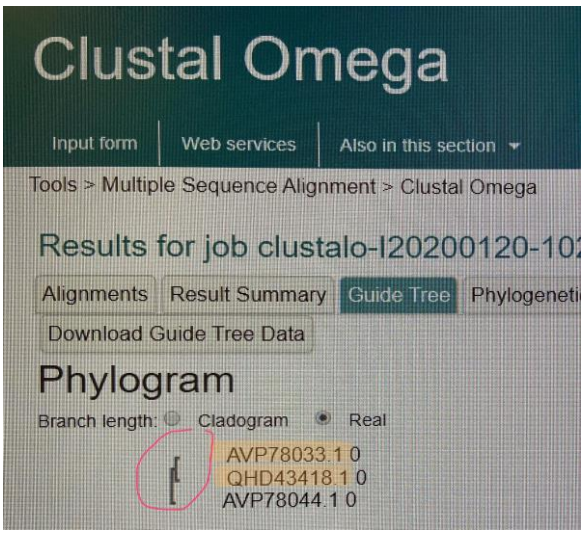
As mentioned in Nanjing military paper(1), from homology analyses of different

ORFs, ORF8 fragments in ZS bat-CoV showed the lowest homology, presenting only 60% identity with its closest relatives (**while 94.21% to 2019 nCoV**) (*pic. 25*). As well, analysis of the RNA-dependent RNA polymerase (RdRp) gene showed that the genomic sequences of bat CoV samples obtained from different parts of the world shared 80–90% identity among themselves and exhibited 87–92% identity with the SARS-CoVs extracted from human or civet sources (**while 95.75% to 2019 nCoV**).

Compared with high mutant S protein, E protein is more conserved (2). However, undergoing a natural evolution, the possibility of 100% identical E protein between the cross-species 2019 nCoV and ZS bat-CoV is almost impossible. It was simlply confirmed by using another online tool-Cluster Omega, which shows that the E protein of one strain of ZS bat-CoV (AVP78033.1, belong to MG772933.1) is more identical (100%) to 2019 nCoV, rather than another ZS bat-CoV (AVP78044.1,


(ORFs) similar to the HKU3-1 strain. The two new bat SL-CoVs shared 97% genomic sequence identity among themselves. The overall nucleotide sequence identity of these two genomes with civet SARS-CoV (SZ3 strain) was 81%, which was lower than the previously reported observations associated with bat SL-CoVs collected from China (88–92%). From homology analyses of different ORFs, ORF8 fragments showed the lowest homology with the reported SL-CoV homology data[24], presenting a shared identity of only 60% with its closest relatives.

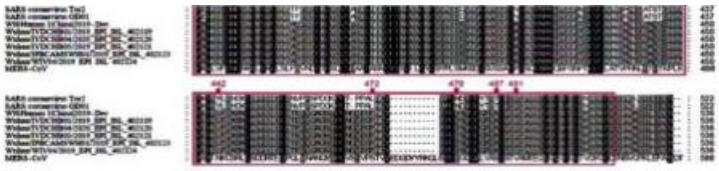
Pic. 25



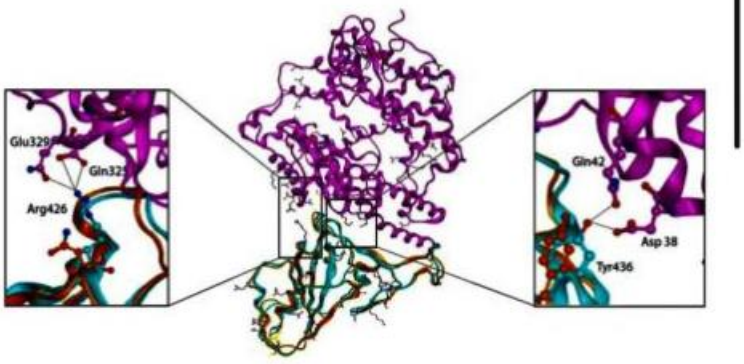
Pic. 26

belong to MG772934.1) (*pic. 26*).

21 Jan, the first paper studied 2019 nCoV is published in a journal under Chinese Academy of Sciences, from Beijing Institute of Pharmacology and Toxicology (belonging to military) and Chinese Academy of Sciences (3). In that paper, they mentioned that the natural host of 2019 nCoV may be certain bat (not directly mentioned ZS bat-CoV). In their official Chinese introduction for this paper, they stressed the key point of their finding as: **"To be surprised"**, compared with SARS CoV, 4 of 5 amino acid changed in the receptor binding domain (RBD) of S protein in 2019 nCoV, but still maintains the core structure to support strong interaction with human ACE2 molecules **"in a very perfect way".** It means 2019 nCoV could infect human respiratory epithelial cells in the same way as what SARS CoV did (*pic. 27*).



为了分析清楚这个问题，文章作者利用分子结构模拟的计算方法，对武汉冠状病毒S-蛋白和人ACE2蛋白进行了结构对接研究，获得了令人惊讶的结果。**虽然武汉冠状病毒S-蛋白中与ACE2蛋白结合的5个关键氨基酸有4个发生了变化，但变化后的氨基酸，却整体性上非常完美的维持了**SARS病毒S-蛋白与ACE2蛋白互作的原结构构象。尽管武汉新型冠状病毒的新结构与ACE2蛋白互作能力，由于丢失的少数氢键有所下降（相比SARS病毒S-蛋白与ACE2的作用有下降），但仍然达到很强的结合自由能（-50.6 kcal/mol）。**这一结果说明武汉冠状病毒是通过S-蛋白与人ACE2互作的分子机制，来感染人的呼吸道上皮细胞。研究成果预测了武汉冠状病毒有很强的对人感染能力**，为科学防控，制定防控策略和开发检测/干预技术手段奠定了科学理论基础。



pic.27

To noted, 23 Jan, another paper with similar content was upload to BioRxiv, which is from famous bat and SARS CoV investigator Zheng-li Shi's team (4).

There are also a lot of official news and poor-quality academic articles from end of last Dec show that no evidence about wild animals in Huanan seafood market as intermediate host for 2019 nCoV (which can be explained in a detail way later). Hence, one hypothesis of lab-made 2019 nCoV is recombined with SARS RBD of S

protein (to human ACE2 gene), based on ZS bat-CoV (esp. MG772933.1), going through in vitro and in vivo adaptation and amplification in a limited range in the lab, generated an ideal strain (2019 nCoV) with effective RBD, while the other comparable conserved sequence did not change much, or even without any change (E protein). Since stock virus kept in culture media at -80 ℃, slowly thaw it on ice could help the virus released in the environment better.

According to Mr. Miles Guo, thymosin is out of stock in commercial market in China. Thymosin is potential therapeutic in the treatment of severe SARS and MERS (5).

PS. More evidence from official media and government response along the time in 2019 nCoV crisis is not written in this brief report.

1. Hu D, Zhu C, Ai L, He T, Wang Y, Ye F, et al. Genomic characterization and infectivity of a novel SARS-like coronavirus in Chinese bats. Emerg Microbes Infect. 2018;7(1):154.
2. Schoeman D, Fielding BC. Coronavirus envelope protein: current knowledge. Virology journal. 2019;16(1):69.
3. Xu X, Chen, P., Wang, J., Feng, J., Zhou, H., Li, X., Zhong, W., and Hao, P. . Evolution of the novel coronavirus from the ongoing Wuhan outbreak and modeling of its spike protein for risk of human transmission. Sci China Life Sci. 2020.
4. Zhou P, Yang X-L, Wang X-G, Hu B, Zhang L, Zhang W, et al. Discovery of a novel coronavirus associated with the recent pneumonia outbreak in humans and its potential bat origin. bioRxiv. 2020:2020.01.22.914952.
5. Song Z, Xu Y, Bao L, Zhang L, Yu P, Qu Y, et al. From SARS to MERS, Thrusting Coronaviruses into the Spotlight. Viruses. 2019;11(1).