

唐凯临 **2021.5**

REVIEW

local blast

• When meet few even no hits

- Check program
- Change parameters
- Accept it

MSA

• Dynamic programming - extension of pairwise sequence alignment

 Progressive sequence alignment - incorporates phylogeny information to guide the alignment process

• Iterative sequence alignment - correct for problems with progressive alignment by repeatedly realigning subgroups of sequence

MSA

• https://www.ebi.ac.uk/Tools/msa/

Multiple Sequence Alignment





Tools > Multiple Sequence Alignment

Multiple Sequence Alignment (MSA) is generally the alignment of three or more biological sequences (protein or nucleic acid) of similar length. From the output, homology can be inferred and the evolutionary relationships between the sequences studied.

By contrast, **Pairwise Sequence Alignment** tools are used to identify regions of similarity that may indicate functional, structural and/or evolutionary relationships between two biological sequences.

Clustal Omega

New MSA tool that uses seeded guide trees and HMM profile-profile techniques to generate alignments. Suitable for medium-large alignments.

▲Launch Clustal Omega

EMBOSS Cons

EMBOSS Cons creates a consensus sequence from a protein or nucleotide multiple alignment.

▲Launch EMBOSS Cons

Kalign

Very fast MSA tool that concentrates on local regions. Suitable for large alignments.

▲Launch Kalign

MAFFT

MSA tool that uses Fast Fourier Transforms. Suitable for medium-large alignments.

▲Launch MAFFT

MUSCLE

Accurate MSA tool, especially good with proteins. Suitable for medium alignments.

▲Launch MUSCLE

MView

Transform a Sequence Similarity Search result into a Multiple Sequence Alignment or reformat a Multiple Sequence Alignment using the MView program.

▲Launch MView

T-Coffee

Consistency-based MSA tool that attempts to mitigate the pitfalls of progressive alignment methods. Suitable for small alignments.

▲Launch T-Coffee

SELECTING AN APPROPRIATE MSA TOOL

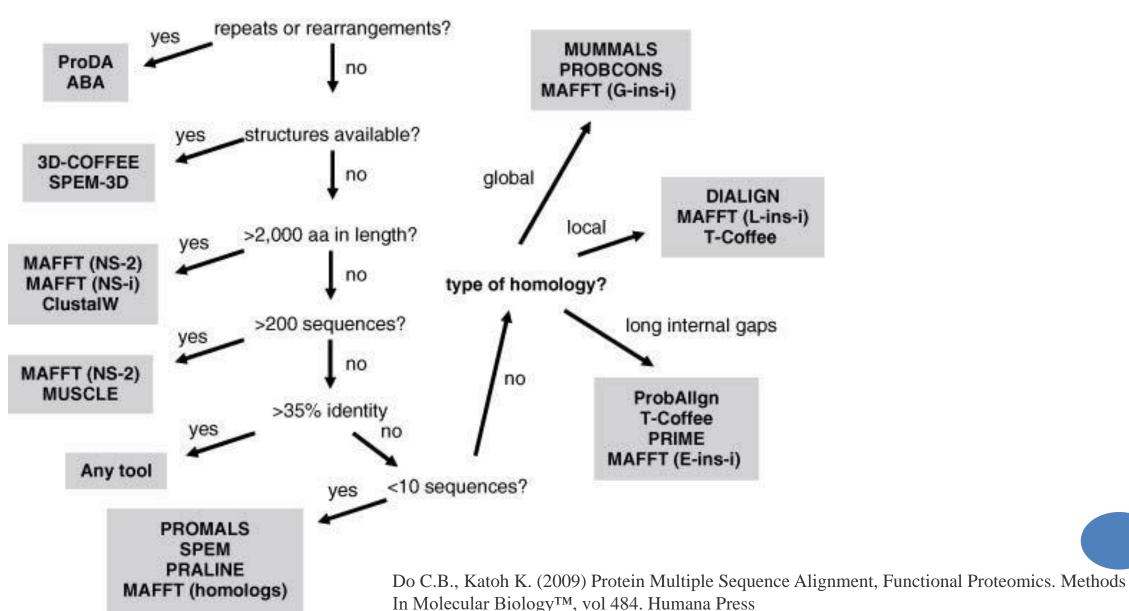
• Any tool:

- a small number (<20) of globally homologous sequences
- high percent identity (>40%)

Specific conditions

- repeated or rearranged protein domains
- large numbers (>200) of input sequences
- extremely long sequences (>2000 amino acids).

SELECTING AN APPROPRIATE MSA TOOL



MSA TOOLS

o 比对速度 Muscle, MAFFT, ClustalW, T-Coffee

o 比对准确性 MAFFT, Muscle, T-Coffee, ClustalW

o 比对数据量 Kalign, ClustalW, MAFFT, Muscle, T-Coffee

CLUSTAL



Clustal: Multiple Sequence Alignment

Multiple alignment of nucleic acid and protein sequences





Clustal Omega

- Latest version of Clustal fast and scalable (can align hundreds of thousands of sequences in hours), greater accuracy due to new HMM alignment engine
- · Command line/web server only (GUI public beta available soon)



ClustalW/ClustalX

- "Classic Clustal"
- . GUI (ClustalX), command line (ClustalW), web server versions available

Valid XHTML and Valid CSS | Viewable With Any Browser | Last modified on 08/31/2012 12:40:54

Clustal Omega

Input form

Web services

Help & Documentation

Bioinformatics Tools FAQ

Feedback

Tools > Multiple Sequence Alignment > Clustal Omega

Results for job clustalo-I20190301-024120-0727-33855618-p2m

Result Summary | Phylogenetic Tree | Submission Details Alignments Download Alignment File | Show Colors | View result with Jalview | Send to Simple Phylogeny Send to MView CLUSTAL 0(1.2.4) multiple sequence alignment sp | P69905 | HBA_HUMAN MVLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHG sp P01942 HBA_MOUSE MVLSGEDKSNIKAAWGKIGGHGAEYGAEALERMFASFPTTKTYFPHFDVSHGSAQVKGHG SD P13786 HBAZ CAPHI MSLTRTERTIILSLWSKISTQADVIGTETLERLFSCYPQAKTYFPHFDLHSGSAQLRAHG sp | P69905 | HBA_HUMAN KKVADALTNAVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTP sp P01942 HBA_MOUSE KKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTP sp P13786 HBAZ_CAPHI SKVVAAVGDAVKSIDNYTSALSKLSELHAYVLRVDPVNFKFLSHCLLVTLASHFPADFTA Sp P69905 HBA_HUMAN AVHASLDKFLASVSTVLTSKYR 142 sp P01942 HBA MOUSE AVHASLDKFLASVSTVLTSKYR 142 sp P13786 HBAZ CAPHI DAHAAWDKFLSIVSGVLTEKYR 142 , wokiji wokowiji woki woke, wokok

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Results for job clustalo-I20200422-161849-0013-13692949-p2m

Alignments

Result Summary | Guide Tree

Phylogenetic Tree Results Viewers Submission Details

120

Download Alignment File

Hide Colors

CLUSTAL O(1.2.4) multiple sequence alignment

```
sp P69905 HBA HUMAN
                           MVLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAOVKGHG
sp P01942 HBA MOUSE
                           MVLSGEDKSNIKAAWGKIGGHGAEYGAEALERMFASFPTTKTYFPHFDVSHGSAQVKGHG
sp P13786 HBAZ CAPHI
                           MSLTRTERTIILSLWSKISTOADVIGTETLERLFSCYPOAKTYFPHFDLHSGSAOLRAHG
                           i plant plant placolaria i planti. Il pola il i polaria placolaria planti i i i i placolaria i i i i i placolaria
sp P69905 HBA HUMAN
sp P01942 HBA MOUSE
                           KKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFTP
sp P13786 HBAZ_CAPHI
                           SKVVAAVGDAVKSIDNVTSALSKLSELHAYVLRVDPVNFKFLSHCLLVTLASHFPADFTA
                           sp P69905 HBA_HUMAN
                           AVHASLDKFLASVSTVLTSKYR
                                                           142
sp P01942 HBA MOUSE
                                                           142
                           AVHASLDKFLASVSTVLTSKYR
sp P13786 HBAZ_CAPHI
                           DAHAAWDKFLSIVSGVLTEKYR
                                                           142
                            Li ploble y il plobloblobe y il ploble il ploblobe il ploblobe
```

Red: 疏水

Blue: 酸性

Magenta: 碱性

Green: 羟基, 胺, 碱性

Gray: 其他

Results for job clustalo-I20210506-074909-0287-95464684-p1m

Alignments Result Summary Guide Tree Phylogenetic Tree Results Viewers Submission Details

Download Guide Tree Data

Phylogram

Branch length: Cladogram Real

sp|P69905|HBA_HUMAN 0.0704225 sp|P01942|HBA_MOUSE 0.0704225 sp|P13786|HBAZ_CAPHI 0.21831

Guide Tree

```
(
sp | P69905 | HBA_HUMAN: 0.0704225
,
sp | P01942 | HBA_MOUSE: 0.0704225
): 0.147887
,
sp | P13786 | HBAZ_CAPHI: 0.21831
)
```

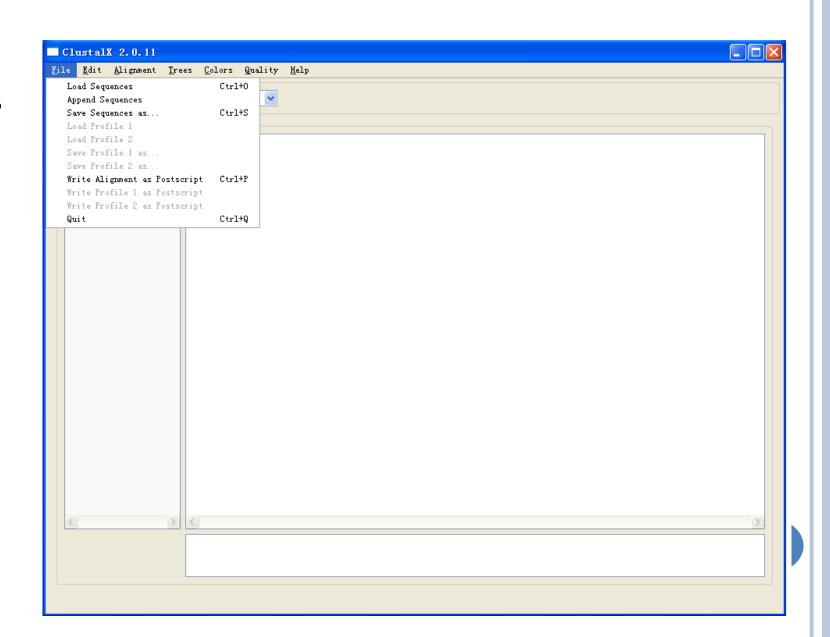
Result Summary Alignments Phylogenetic Tree Guide Tree Results Viewers Input Sequences clustalo-I20200426-140705-0035-68812116-p2m.input Tool Output clustalo-I20200426-140705-0035-68812116-p2m.output Alignment in CLUSTAL format with base/residue numbering clustalo-I20200426-140705-0035-68812116-p2m.clustal num Guide Tree clustalo-I20200426-140705-0035-68812116-p2m.dnd Phylogenetic Tree clustalo-I20200426-140705-0035-68812116-p2m.ph Percent Identity Matrix

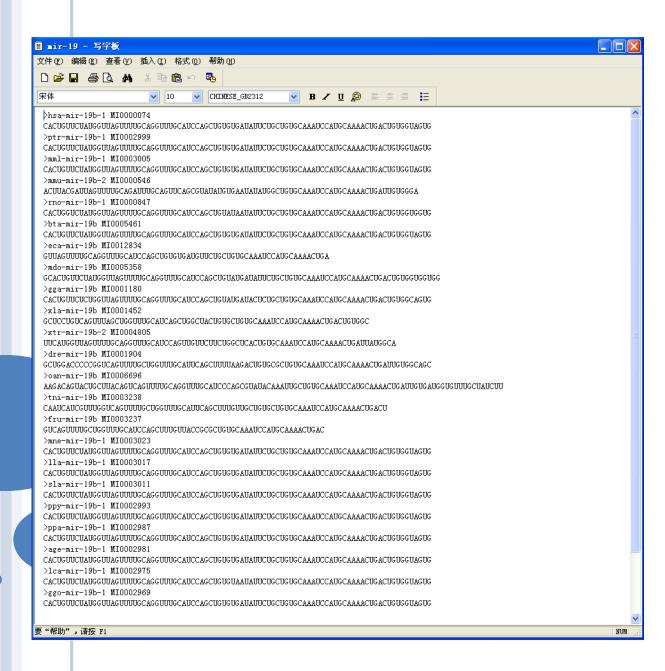
clustalo-I20200426-140705-0035-68812116-p2m.pim

Submission Details

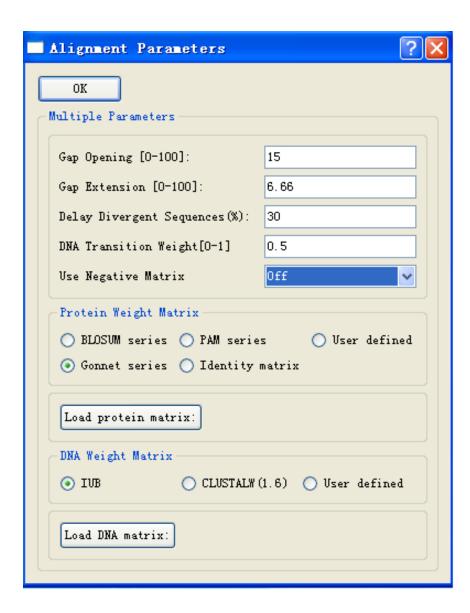
o 安装成功后的界面, Load Sequence用于 加载数据文件。

• 注意数据文件在 ClustalX目录里。

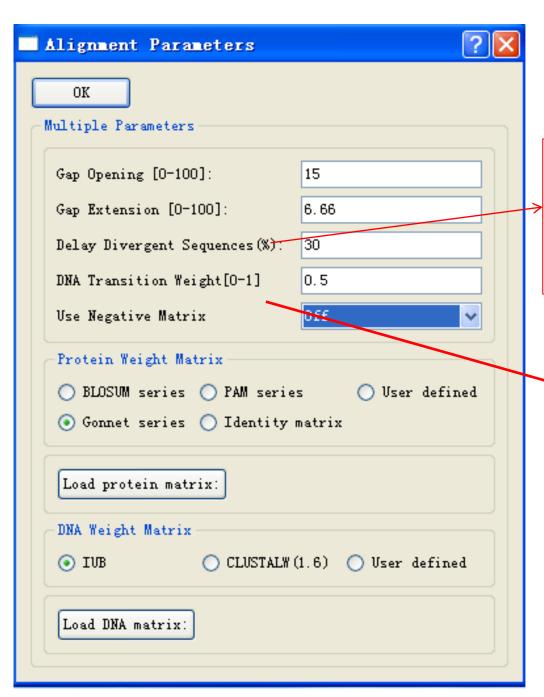




ClustalX使用FASTA格 式的数据文件。



由菜单 Alignment-> Alignment Parameters-> Multiple Alignment Parameters 进入参数设置 页面,这些参数包括Gap Opening、Gap Extension和各种替换计分矩阵。

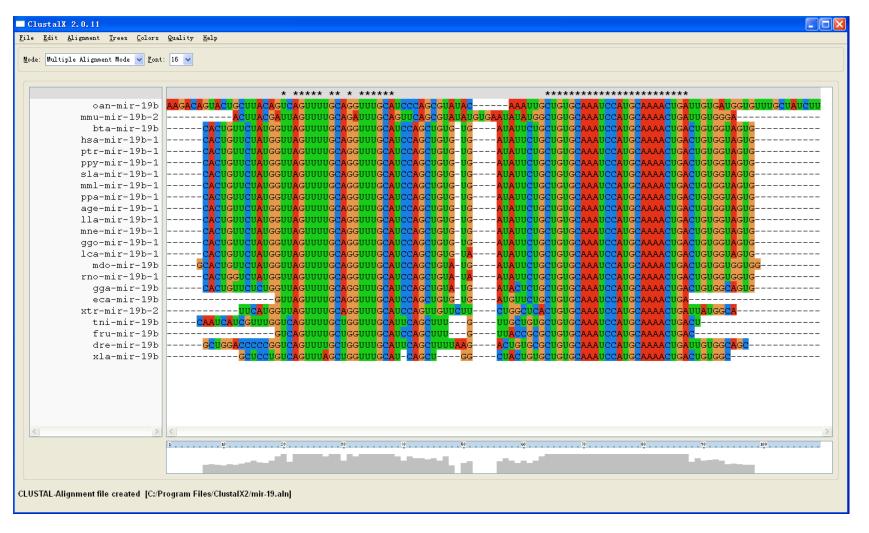


两条序列的差异大于某个值 (百分比),这两条序列的 比对将推迟进行,它们的比 对结果会在最后加入到最终 的多条序列比对结果

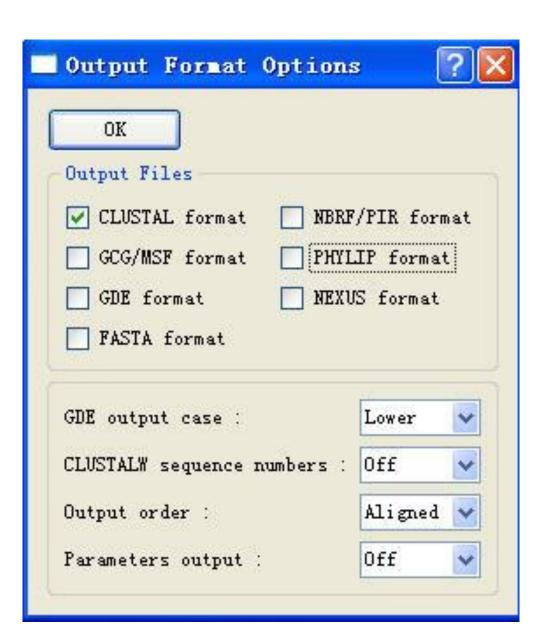
0: mismatch

1: transversion

当序列差异较大时,DNA transition Weight选择接近0; 序列差异较小时,DNA transition Weight可选择接近1



Alignment->Alignment Parameters->Pairwise Parameters, 选择Slow/Accurate Pairwise Parameters, 产生较高质量的结果。



CLUSTAL 2.0.10 multiple sequence alignment

HUMAN	GTTTGGGGCCAGAGTGGGCGAGGCG
COW	
MOUSE	
RAT	
ELEGANS	AZ DEL ENSTREDEL ENSTREDEL ENSTREDEL ENSTREDEL ENSTREDEL ENSTREDEL ENSTREDEL ENSTREDEL ENSTREDEL
FRUITFLY	
PIG	ATGCTGACGCTGCTCTGTGCTTACCTGCTCCTGGCGCCCCGGCGCCTCCGACGCCTTGACC
ARABIDOPSIS	ACATCTTAGTTCATGTTCGAGTTTCTCTGGTCTCTTACTCTTTCACCTAGAAATTTGTTT
HUMAN	*CGGAGGTCTGGCCTATAAAGTAGTCGCGGAGACGGGGTGCTGGTTTGCGTCGTAGTCTCC
COW	GTG-TGTTCTGCGGCGTCGTTTTC
MOUSE	GCCAGGGCCTCGTTTTTTTGCGCGGTCCTTTCCTGCGGCGCCTTC
RAT	GTTTTGCACCTTCGTTTCCTGCGGCGGCTTC
ELEGANS	TTTAGATCGGTGATGTT
FRUITFLY	GCATGTATTTCTAAGCTGCTCTGCTACGGTCACACC
PIG	CACGTGGACGTGGAGCGGCCAGGCTCCCACATGGAGGAGCAGATCCGGGACATGCAGGCC
ARABIDOPSIS	GGTCTCCCAACAACATAAACGCATGTATACATTTTCATGTGTCTTTGTAAGGATATTGAT
	*
HUMAN	TGCAGCGTCTGGGGTTTCCGTTGCAGTCCTCGGAACCAGGACCTCG
COW	TCTACTTGGTTGGGGCGTCTCTAGCGGTCCGGGCCGGAGA
MOUSE	CGTCCGTCGGCTTCTCGTCTTGCTCTCTGGTCCCTCCGGAGGAGGCCGCCGC
RAT	T-GTCGTCT-CCTTGCTTTTTGCTCTCCCAGGTTCCGAGGCCGCCGC
ELEGANS	T-ATGAATCTTCTCACTCAGGTCTCCAACGCGATTTTTCCGCAGG
FRUITFLY	ATAGAAGATACCTGGAAAGTTCTCAACTTTTTTCGTTTTGATAAATTG
PIG	AAAGTGACGGAGATCTGGCAGGAGTTGACGCAGCAGCGGGGGGGG
ARABIDOPSIS	TCATTTTTTTGGGCAAATAGATAATCAATTCAATGCTATGTTTTGTCTGAAATGTGC

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▼ 10 ▼ CHINESE_GB2312

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 eca-mir-19b:-0.02069,
 oan-mir-19b:0.12403.
 mmu-mir-19b-2:0.11407)
 :0.01514,
 tni-mir-19b:0.08437.
 fru-mir-19b:-0.02088)
 :0.02245,
 dre-mir-19b:0.09973.
 xla-mir-19b:0.02355)
 :0.04303)
 :0.03288)
 :0.02561,
 xtr-mir-19b-2:0.10695)
 :0.01695)
 :0.02672,
 gga-mir-19b:0.03422)
 :0.00174,
 mdo-mir-19b:0.00141,
 rno-mir-19b-1:0.02157)
 :0.01220)
 :0.00698,
 lca-mir-19b-1:0.00808)
 :0.00341.
 mne-mir-19b-1:0.00000,
 ggo-mir-19b-1:0.00000)
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 lla-mir-19b-1:0.00000,
 ppa-mir-19b-1:0.00000,
 age-mir-19b-1:0.00000)
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 sla-mir-19b-1:0.00000,
 mml-mir-19b-1:0.00000)
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 :0.00000,
 ptr-mir-19b-1:0.00000,
 ppy-mir-19b-1:0.00000)
 :0.00000)
 :0.00000,
 bta-mir-19b:0.00000,
 hsa-mir-19b-1:0.00000)
要"帮助",请按 F1
```

Alignment->
Alignment Parameters>
Pairwise Parameters,

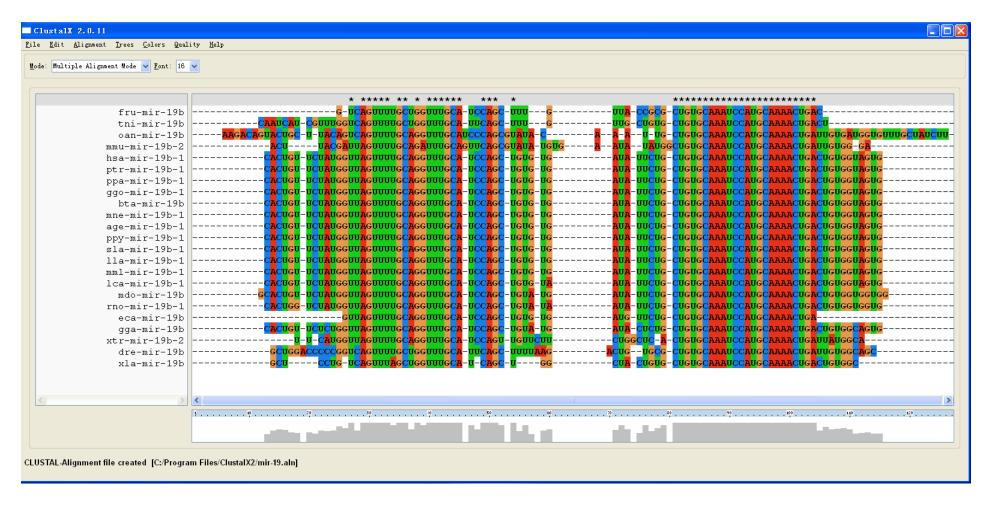
选择Slow/Accurate Pairwise Parameters, 产生输出的DND文件, 它是系统的种系树。



Alignment->Alignment Parameters->
Pairwise Parameters, Fast/Approx Pairwise Parameters

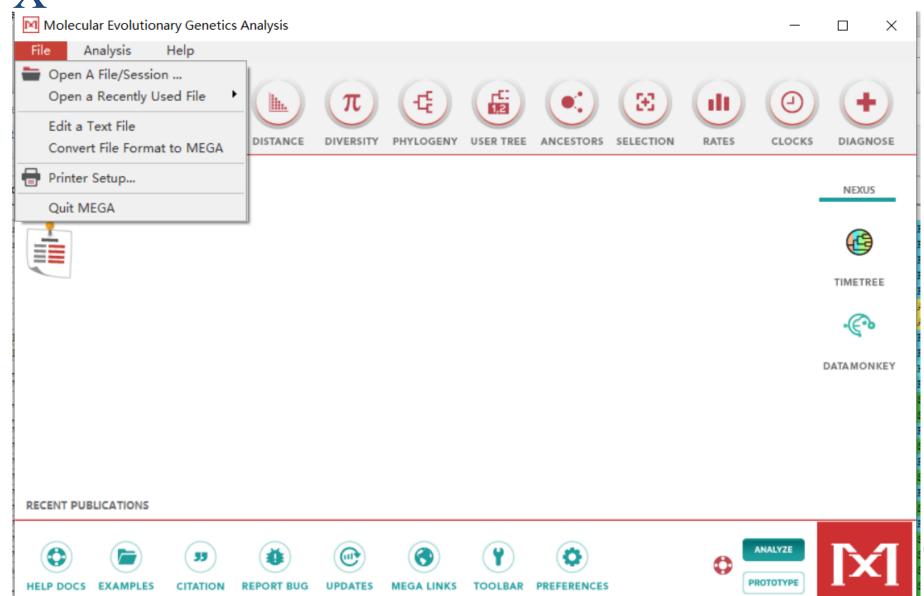


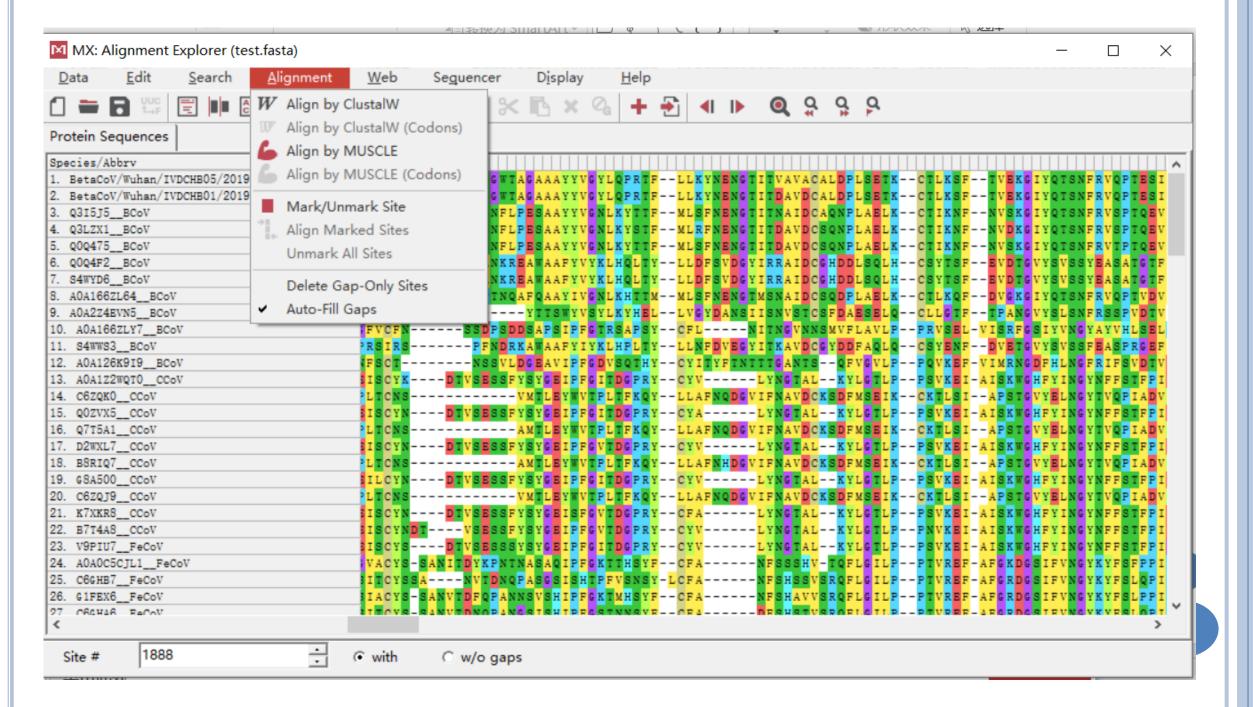
选择Fast/Approx Pairwise Parameters后,同时选择Alignment->Iteration->Iterate each alignment step,结果仍比选择Slow/Accurate Pairwise Parameters的差。



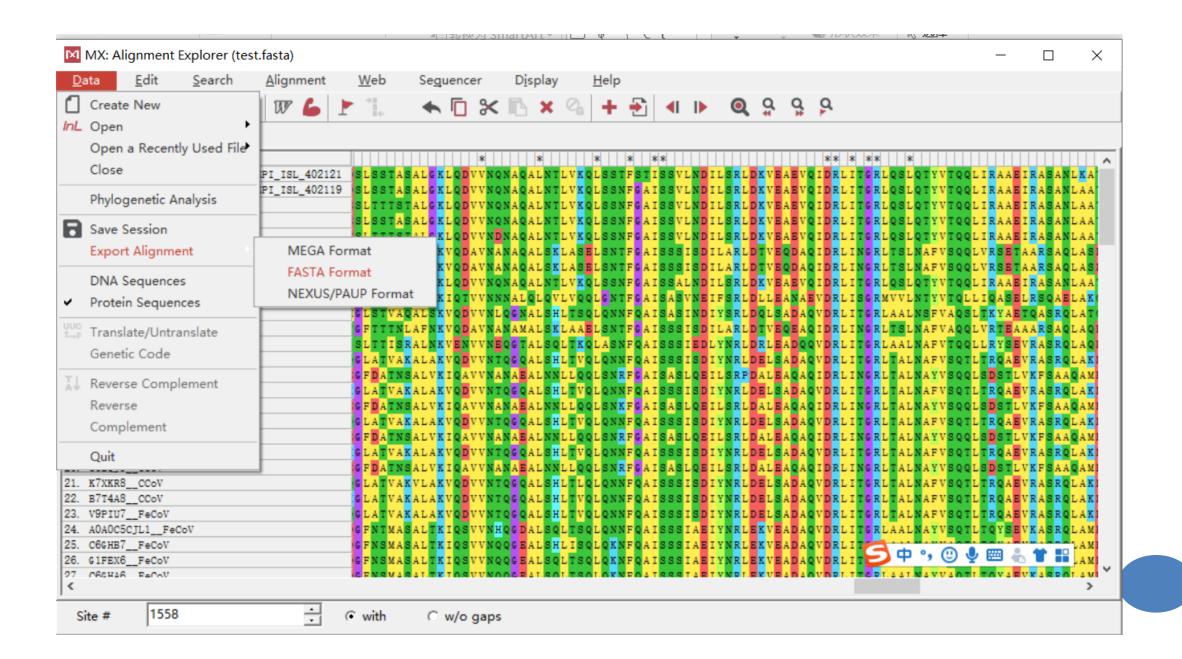
将Gap Opening和Gap Extension均改为3后,可以看到减轻空格罚分后更多的空格被引入比对中。

MEGA-X



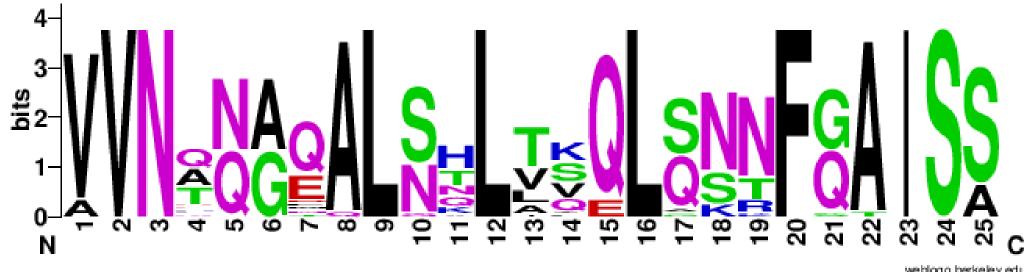


Species/Abbry 1. SetaCOV/Puhan/IVDCH805/2019 EPI_ISL_402121 2. SetaCOV/Puhan/IVDCH805/2019 EPI_ISL_402121 3. Q31575_BGOV 4. Q31271_BGOV 5. SETACOV/Puhan/IVDCH805/2019 EPI_ISL_402121 3. Q31575_BGOV 5. SETACOV/Puhan/IVDCH805/2019 EPI_ISL_402121 5. Q31575_BGOV 5. SETACOV/Puhan/IVDCH805/2019 EPI_ISL_402121 5. Q31575_BGOV 5. SETACOV/Puhan/IVDCH805/2019 EPI_ISL_402121 5. Q31575_BGOV 5. SETACOV SETACAL S																
1. BetgCOV/Whan/IVDCH805/2019 EPI_ISL_402121 SL STAS ALGK LGIVVNONA GALNILVKQ LSSTFSTISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ALKA 2. BetgCOV/Whan/IVDCH801/2019 EPI_ISL_402119 SL STAS ALGK LGIVVNONA GALNILVKQ LSSNFG AISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ALKA 4. GALZXI_BCOV SL STAS ALGK LGIVVNONA GALNILVKQ LSSNFG AISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ALKA 6. QOQ475 ECOV SL STAS ALGK LGIVVNONA GALNILVKQ LSSNFG AISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 6. QOQ475 ECOV SL STAS ALGK LGIVVNONA GALNILVKQ LSSNFG AISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 6. QOQ475 ECOV SL STAS ALGK LGIVVNONA GALNILVKQ LSSNFG AISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 6. QOQ475 ECOV SL STAS ALGK LGIVVNONA GALNILVKQ LSSNFG AISS VLNDILSRLDKVE AEV CIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 6. QOQ475 ECOV SETTSMLAFSK VCIAVNANA GALBELSNFFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 7. S4M106 ECOV SL STAS ALGK LGIVVNONA GALBELSNFFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 8. AOA16SILYT ECOV SL STAS ALGK LGIVVNONA GALBELS NFFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVVTQQL RAAE IRAS ANLAA 10. AOA16SILYT ECOV SL STAS ALGK VCIVVNONA GALBELD VXQ LSTAFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVVTYQQL RAAE IRAS ANLAA 11. AOA16SILYT ECOV SL STAS ALGK VCIVVNONA GALBELD VXQ LSTAFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVTYQQL RAAE IRAS ANLAA 12. AOA16SILYT ECOV SL STAS ALGK VCIVVNONA GALBELD VXQ LSTAFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVTYQQL RAAE IRAS ANLAA 13. AOA16SILYT ECOV SL STAS ALGK VCIVVNONA GALBELD VXQ LSTAFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVTYQQL RAAE IRAS ANLAA 14. CASLOON SL STAS ALGK VCIVVNONA GALBELD VXQ LSTAFG AISS SIDDLAR LDTVEQDA GIDRLITGR LGSLQTVTYQQL RAAE IRAS ANLAA 15. QOZVX5 CCOV SL STAS ALGK VCIVVNONA GALBELD VXQ LSTAFG AISS SIDDLAR LDTVEQDA GALBELT GRINDAL LTGR LTGR LTGR LGSLQTVTYTYQQL LTGR LGA ANA VCIVVNONA GALBELT GALBELT G	Protein Sequences															
2. BetaCov/Wuhan/IVDCH801/2019 EPT_ISL_402119 3. Q31575_BCOV 5. DISTA SALGKLOVVNONA ALNILVKQLSSNFG AISSVLNDILS RLDKVEAEVQIDRLITG RLQGLQTVVTQQLIR AAE TRABANLAA 4. Q31575_BCOV 5. SISTA SALGKLOVVNONA ALNILVKQLSSNFG AISSVLNDILS RLDKVEAEVQIDRLITG RLQGLQTVVTQQLIR AAE TRABANLAA 5. Q00475_BCOV 5. LITISTALGKLOGVVNDNA GALNILVKQLSSNFG AISSVLNDILS RLDKVEAEVQIDRLITG RLQGLQTVVTQQLIR AAE TRABANLAA 6. Q00475_BCOV 6. PITISNLAF SKVQLAVNANAQ ALNILVKQLSSNFG AISSSISDILAR LDTVEQDA QIDRLITG RLQGLQTVVTQQLIR AAE TRABANLAA 6. Q00475_BCOV 6. PITISNLAF SKVQLAVNANAQ ALSKLASELSNFG AISSSISDILAR LDTVEQDA QIDRLING RLTGLNAFVSQLVR SETAAR AQLAS 7. SAMYDG_BCOV 6. PITISNLAF SKVQLAVNANAQ ALSKLASELSNFG AISSSISDILAR LDTVEQDA QIDRLING RLTGLNAFVSQLVR SETAAR AQLAS 7. SAMYDG_BCOV 7. SAMYDG_BCOV 7. SAMYDG_BCOV 7. SAMYDG_BCOV 7. SAMYDG_BCOV 7. SAMYDG_BCOV 8. A01682187_BCOV 8. A01682187_BCOV 9. A0122887S_BCOV 9. FALNGALAN IN TOVANNA GALGAL SKVQLAVNANAQ ALSKLASELSNFG AISSSISDILAR LDTVEQDA QIDRLING RLTGLNAFVSQLVR SETAAR AQLAS 7. A01882187_BCOV 9. A01882187_BCOV 9. CATAGAR AND	Species/Abbrv		*	*	8 88				8 8 8	* *	*					^
3. Q31515_BCOV SLSTABALEKLQ IVNQNAQALNILVKQ LSSNFG AISSVLNDILBRLDKVBAEVQID RLITGRLQSLOTYVIQQLIRAABIRASANLAA 4. Q3LXXI_BCOV SLSTABALEKLQ IVNQNAQALNILVKQ LSSNFG AISSVLNDILBRLDKVBAEVQID RLITGRLQSLOTYVIQQLIRAABIRASANLAA 5. Q0Q475_BCOV SLTTISTALGKLQ VVNDNAQALNILVKQ LSSNFG AISSVLNDILBRLDKVBAEVQID RLITGRLQSLOTYVIQQLIRAABIRASANLAA 6. Q0Q492_BCOV GFITSNLAFSKVQ AVNANAQALSKLASELSNIFG AISSSISDILARLDIVEQDAQID RLINGRLTSLNAFVSQ LVRSETAARSAQ LAS 7. S4YDOG_BCOV GFITSNLAFSKVQ AVNANAQALSKLASELSNIFG AISSSISDILARLDIVEQDAQID RLINGRLTSLNAFVSQ LVRSETAARSAQ LAS 8. A0A1666LM_BCOV SLITIATALEKLQ VVNNNAQALNILVKQ LSSNFG AISSALNDILBRLDKVBAEVQ IDRLITGRIS NAFVSQ LVRSETAARSAQ LAS 9. A0A224EVNS_BCOV GFITSNLAFSKVQ VVNNNAQALNILVKQ LSSNFG AISSALNDILBRLDKVBAEVQ IDRLITGRIS NAFVSQ LVRSETAARSAQ LAS 10. A0A166LM_BCOV SLITIATALEKLQ VVNNNAL QLQ VLVQQ LGNTFG AISAS VNE IF BRLD LLEANAEVD RLIGGR MAVULNIYV QLQ LRABETRASANLAG 10. A0A166LM7_BCOV GFITSNLAFSKVQ VVNNAQALSKVQ VVNNAQALSKLASELSNIFG AISAS VNE IF BRLD LLEANAEVD RLIGGR MAVULNIYV QLQ LRABETRASANLAG 10. A0A166LM7_BCOV GFITSNLAFSKVQ VVNNAQALSKVQ VVNNAQALSKVQ VNNAQALSKVQ VVNTQA BARDON BRADEV	1. BetaCoV/Wuhan/IVDCHB05/2019 EPI_ISL_402121	SLSSTASALGKLQI	VVNQNAQA	LNTLVKQL	SSTFSTIS	SVLNDI	LSRLDK	VEAEVQ	IDRLII	GRLQS	LQTYV	TQQLI	RAA	EIRAS	ANLKA	
4. Q3LZXI_BCOV SLISTIAS ALCKLQIVVNQNAQALNILVXQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTVYTQQLIRAABIRAS ANLAA 5. Q0Q473_BCOV SLITITSIALCKLQIVVNQNAQALNILVXQLSSNFGAISSSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTVYTQQLIRAABIRAS ANLAA 6. Q0Q475_BCOV GFITSNLAFSKVQIAVNANAQALSKLASELSNIFGAISSSISDILARLDTVEQDAQIDRLINGRLISLNAFVSQQLIVSETAARS ANLAA 7. S4W706_BCOV GFITSNLAFSKVQIAVNANAQALSKLASELSNIFGAISSSISDILARLDTVEQDAQIDRLINGRLISLNAFVSQQLIVSETAARS ANLAA 8. A0A166ZL64_BCOV SLITITATALCKLQIVVNQNAQALNITLVXQLSSNFGAISSAINDILSRLDKVEAEVQIDRLITGRLQSLQTVVTQQLIRAABIRAS ANLAA 9. A0A224EVN5_BCOV GFITSNLAFSKVQIAVNANAQALSKLGIVVNQNAQALNITLVXQLSSNFGAISSAINDILSRLDKVEAEVQIDRLITGRLQSLQTVVTQQLIRAABIRAS ANLAA 11. S4WW33_BCOV GFITSNLAFSKVQIAVNANALSKLGIVVNNNALGUALSHLTSQLQNNFQAISSSISDILARLDTVEQEAQUBRLITGRLAALNSFVASSLKYAETGASAGLAX 12. A0A126M70_CCOV GFITSNLAFSKVQIAVNANAALSKLGAAELSNIFGAISSSISDILARLDTVEQEAQUBRLITGRLAALNSFVASSLKYAETGASAGLAX 13. A0A1227070_CCOV GFITSNLAFSKVQIAVNANAALSKLGAAELSHITVQLQNNFQAISSSISDILYNRLDRLAAGAGLARLNAFVTQQLVXTEAAARSAQLAX 14. C62080_CCOV GFITSNLAFVXQIAVNANAABALNNLQQLSNRFGAISSSISDILYNRLDELSABAQQDRLITGRLTALNAFVSQLLVTERAARSAQLAX 15. Q0ZVX5_CCOV GFITSNLAFVXQIVVNIQQQALSHLTVQLQNNFQAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLSTLRQABVXSTLKFSAAQAN 16. Q7T531_CCOV GFITSNLAFVXQIVVNIQQQALSHLTVQLQNNFQAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLSTLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLSTLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLITGRLTALNAFVSQLLTRQABVXSTLRYSSVANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLTTGRLTALNAFVSQLLTRQABVXSTLRYSQLXX 18. BSRTQT_CCOV GFITSNASALVKIQAVVNANABALNNLQQLSNRFGAISSSISDIYNRLDELSABAQQDRLTTGRLTALNAFVSQLLTRQABVXSTLRYSGLXX 22. C6CQJPQ-CCOV GFITSNASALVKIQAVVNANABALNNLQQLSNRFGAISSSISDIYNRLDE	2. BetaCoV/Wuhan/IVDCHB01/2019 EPI_ISL_402119	SLSSTASALGKLQI	V V N Q N A Q A	LNTLVKQL	SSNFGAIS	SVLNDI	LSRLDK	V B A B V Q	IDRLII	GRLQS	LQTYV	TQQLI	RAA	EIRAS	ANLAA	
S. QQQ475_BCOV CFITANA A QAL NILVX QLSSNFGAISSULNDILSRLDX VEAEVQIDRLITGRLOSL QIVTQQLIRAE IRASANLAA 6. QQQ475_BCOV CFITANA A QALSKLASELSNIFGAISSSISDILARLDIVE QAA IDELINGRISLA A LAYER QALSKLASELS A LAYER QUIDRLINGRISLA A LAYER QALSKLASELS A LAYER Q	3. Q3I5J5BCoV	SLTTTSTALGKLQI	V V N Q N A Q A	LNTLVKQL	SSNFGAIS	SVLNDI	LSRLDK	V B A B V Q	IDRLII	r <mark>g Rl</mark> QS	LQTYV	TQQLI	RAA	BIRAS	A N L A A	
6. QQQ4F2_BCOV 6 FITSNLAFSKVQIAVNANAQALSKLASELSNIFGAISSSISDILARLDIVEQDAQIDRLINGRLISLNAFVSQQLVRSETAARSAQLAS 7. SHWYD6_BCOV 6 FITSNLAFSKVQIAVNANAQALSKLASELSNIFGAISSSISDILARLDIVEQDAQIDRLINGRLISLNAFVSQQLVRSETAARSAQLAS 8. AOA166ZL64_BCOV 9. AOAZZENNS_BCOV 6 FAINQALNIQ VVNQNAQALNILVKQLSSNFGAISSSISDILARLDIVEQDAQIDRLINGRLISLNAFVSQQLVRSETAARSAQLAS 9. AOAZZENNS_BCOV 6 FAINQALNIQ VVNNNAQALNIQ VVNNNAQALNILVKQLSSNFGAISSSISDILARLDIVEQDAQIDRLINGRLISLNAFVSQQLVRSETAARSAQLAS 10. AOA166ZLYT_BCOV 6 LSTVAQALSKVQLVVNLQCNALSHLISQLQNNFGAISSSISDILYBRLDQLSADAQVDRLITGRLAALNSFVAQSLIKYABIQASRQLAY 11. SHWS3_BCOV 6 FITINLAFSKVQIAVNANAMALSKLASELSNIFGAISSSISDILARLDIVEQBAQUDRLITGRLAALNSFVAQSLIKYABIQASRQLAY 12. AOA126KSYB_BCOV 6 LATVAKALAKVQLVVNLQCQALSHLIVQLQNNFQAISSSISDILVRDDRLSADAQVDRLITGRLAALNSFVAQSLIKYBAARSAQLAQ 13. AOA12ZWQTO_CCOV 6 LATVAKALAKVQLVVNLQCQALSHLIVQLQNNFQAISSSISDIVNRLDELSADAQVDRLITGRLAALNAFVQQLLRYBEVRASRQLAX 14. C6ZQKO_CCOV 6 FDAINSALVKIQ VVNNAMABALNNLQQLSNNFGAISASLGEILSRPDALBAQQQUDRLITGRLTALNAFVSQQLLRYBEVRASRQLAX 15. QOZVXS_CCOV 6 FDAINSALVKIQ VVNNAMABALNNLQQLSNNFGAISASLGEILSRPDALBAQQQUDRLITGRLTALNAFVSQQLLSVSTLVKFSAAQAM 16. Q7TSA1_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLQNNFQAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQQLLSVSTLVKFSAAQAM 17. DZWKLT_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLQNNFQAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQQLLSVSTLVKFSAAQAM 18. BSRIQT_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLSNNFGAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQULTRQAEVRASRQLAX 19. QSXX5O_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLSNNFGAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQULTRQAEVRASRQLAX 20. C6ZQJB_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLSNNFGAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQULTRQAEVRASRQLAX 21. KYXKRB_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLSNNFGAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQULTRQAEVRASRQLAX 22. P5T4AS_CCOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLSNNFGAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQULTRQAEVRASRQLAX 23. V9PIUT_FECOV 6 CLAFVAKALAKVQIVVNTGGQALSHLIVQLSNNFGAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQULTRQAEVRASRQLAX 24. AOAC5CCIL_FECOV 6 CATVAKALAKVQIVVNTGGQALSHLIVQ	4. Q3LZX1_BCoV	SLSSTASALGKLQI	V V N Q N A Q A	LNTLVKQL	SSNFGAIS	SVLNDI	LSRLDK	V E A E V Q	IDRLII	GRLQS	LQTYV	TQQLI	RAA	EIRAS/	A <mark>N</mark> LAA	
7. 94WYD6_BCOV	5. Q0Q475_BCoV	SLTTTSTALGKLQI	V V N <mark>D</mark> N A Q A	LNTLVKQL	SSNFGAIS	SVLNDI	LSRLDK	VEAEVQ	IDRLII	GRLQS	LQTYV	TQQLI	RAA	EIRAS	A <mark>N</mark> LAA	
S. A0A166Z164_BCOV S. LITTATALGKLQIVVNQNAQALNILVKQLSSNFGAISSALNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAABIRASANLAA 9. A0A274EVNS_BCOV GFTAINQALNKIGTVVNNNALQIQVUQCLNTFGAISASVNETFSRLDLLBANABURLISGRUVULTYVIQLLIRASBLRSQABLAK 10. A0A166Z17_BCOV GFTTTNLAFNKVQIAVNANAALSKLAABISNTFGAISASINDIYSRLDQLBANABURLISGRUVULTYVIQLLIRASBLRSQABLAK 11. S4WWS3_BCOV GFTTTNLAFNKVQIAVNANAALSKLAABISNTFGAISSSISDILARLDTVEQBAQIDRLINGRLTSLNAFVAQQLVSTBAARRAQLAQ 12. A0A126K919_BCOV SLITISRALNKVEN VNNEQGTALSQLTKQLASNFQAISSSISDILARLDTVEQBAQIDRLINGRLTSLNAFVAQQLVSTBAARRAQLAQ 13. A0A122WQTO_CCOV GLATVAKALAKVQIVVNTQGQALSHLTVQLONNFQAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSVARSRQLAK 15. QOZVNS_CCOV GLATVAKALAKVQIVVNTQGQALSHLTVQLONNFQAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSVARSRQLAK 16. QOZVNS_CCOV GLATVAKALAKVQIVNTQGQALSHLTVQLONNFQAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSVARSRQLAK 16. QOZVNS_CCOV GFDAINSALVKIQ, VVNANABALNNLLQQLSNNFGAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSVARSRQLAK 17. DZWXLT_CCOV GFDAINSALVKIQ, VVNANABALNNLLQQLSNNFGAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSVARSRQLAK 18. BSRIQT_CCOV GFDAINSALVKIQ, VVNANABALNNLLQQLSNNFGAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSQABVRASRQLAK 19. G8A50O_CCOV GFDAINSALVKIQ, VVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSQABVRASRQLAK 20. CGZQP9_CCOV GFDAINSALVKIQ, VVNNABALNNLLQQLSNNFFGAISASLQEILSRLDALBAQQQIDRLINGRLTALNAFVSQLLSQABVRASRQLAK 21. K7XKRS_CCOV GFDAINSALVKIQ, VVNNABALNNLLQQLSNNFFGAISASLQEILSRLDALBAQQQIDRLINGRLTALNAFVSQLLSQABVRASRQLAK 22. B7TAAS_CCOV GLATVAKALAKVQIVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLSQABVRASRQLAK 23. V9PIUT_FECOV GLATVAKALAKVQIVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDELBADAQVDRLTIGRLTALNAFVSQLLTQABVRASRQLAK 24. A0ACCSCIL_FECOV GFNAMASALTKIQSVVNAQGBALSHLTVQLQNNFQAISSSIABIYNRLBEKVBADAQVDRLTIGRLTALNAFVSQTLTQABVRASRQLAK 25. CG6RBT_FECOV GFNSMASALTKIQSVVNAQGBALSHLTVQLQNNFQAISSSIABIYNRLBEKVBADAQVDRLTIGRLTALNAFVSQTLTQABVRASRQLAK 26. GFRBASALTKIQSVVNAQGBALSHLTVQLQNNFQAISSSIABIYNRLBKVBADAQVDRLTIGRLAALNAFVSQTLTQABVRASRQLA	6. Q0Q4F2_BCoV	G F T T S N L A F S K V Q I	AVNANAQA	LSKLASEL	SNTFGAIS	SSISDI	LARLDT	V E Q D A Q	IDRLIN	NGRLTS	LNAFV	SQQLV	RSE	TAARS	AQLAS	
9. AGAZZZEVNS_BCOV 10. AGAIGEZLYZ_BCOV 11. SAWWS3_BCOV 12. AGAIGEZLYZ_BCOV 13. AGAIGEZLYZ_BCOV 14. AGAIGEZLYZ_BCOV 15. CITTALAFNK VE VVNLQG MALSHLTSQ LONNFQ ALS SAINDIYS RLDQLS ADA QVDRLITCR LAALNSFY AQS LEKYAETQAS R CLAT 11. SAWWS3_BCOV 12. AGAIZEWS19_BCOV 13. AGAIZEWS10_CCOV 14. C6ZQKO_CCOV 15. AGAIZEWS10_CCOV 16. ATVAKALAKVOI VVNTQG QALSHLTVQ LONNFQ ALSSSISDIVNRLDELSAD AQVDRLITCR LTALNAFVSQ ILT R QAS VRAS R CLAY 15. QOZVS_CCOV 16. ATVAKALAKVOI VVNTQG QALSHLTVQ LONNFQ ALSSSISDIVNRLDELSAD AQVDRLITCR LTALNAFVSQ ILT R QAS VRAS R CLAY 16. QOZVS_CCOV 17. DZWXL_CCOV 18. ATVAKALAKVOI VVNTQG QALSHLTVQ LONNFQ ALSSSISDIVNRLDELSAD AQVDRLITCR LTALNAFVSQ ILT R QAS VRAS R CLAY 17. DZWXL_CCOV 18. ATVAKALAKVOI VVNTQG QALSHLTVQ LONNFQ ALSSSISDIVNRLDELSAD AQVDRLITCR LTALNAFVSQ ILT R QAS VRAS R QAM 18. QOZVS_CCOV 19. ATNS ALVKIQ. VVNANABALNNLLQ LSNKFG ALS SAS LQE ILS RLD ALEAQAQ ID RLING R LTALNAFVSQ ILT R QAS VRAS R QAM 17. DZWXL_CCOV 18. ATVAKALAKVOI VVNTQG QALSHLTVQ LONNFQ ALSSSISDIVNRLDELSAD AQVDRLITCR LTALNAFVSQ ILT R QAS VRAS R QAM 18. BSRIQT_CCOV 19. ATNS ALVKIQ. VVNANABALNNLLQ LSNKFG ALS SAS LQE ILS RLD ALEAQAQ ID RLING R LTALNAFVSQ ILT R QAS VRAS R QAM 19. G83500_CCOV 19. ATNS ALVKIQ. VVNANABALNNLLQ LSNKFG ALS SAS LQE ILS RLD ALEAQAQ ID RLING R LTALNAFVSQ ILT R QAS VRAS R QAM 19. G83500_CCOV 19. ATNS ALVKIQ. VVNANABALNNLLQ LSNKFG ALS SAS LQE ILS RLD ALEAQAQ ID RLING R LTALNAFVSQ ILT R QAS VRAS R QAM 19. G83500_CCOV 19. ATNS ALVKIQ. VVNANABALNNLLQ LSNKFG ALS SAS LQE ILS RLD ALEAQAQ ID RLING R LTALNAFVSQ ILT R QAS VRAS R QAM 20. C6ZQJ9_CCOV 21. KTXKRS_CCOV 22. BTT48S_CCOV 23. VPPIUT_FECOV 24. AQAOCSCILL_FECOV 25. C6GHST_FECOV 26. GAT VAKALAKVOI VVNTQG QALSHLTVQ LONNFQ ALSSSISDI VNRLDELS ADAQ VDRLITCR LTALNAFVSQ ILT R QAS VRAS R QAM 24. AQAOCSCILL_FECOV 25. C6GHST_FECOV 26. GFNS MAS ALTKICS VVNQQG BALS LTIS QLONNFQ ALSSSIAD INNR LDELS ADAQ VDRLITCR LAALNAFVSQ ILT R VAS VRAS R QAM 26. GFFNS MAS ALTKICS VVNQQG BALS LTIS QLONNFQ ALSSSIAD INNR LDELS ADAQ VDRLITCR LAALNAFVSQ ILT R VAS	7. S4WYD6_BCoV										_					
10. A0A166ZLYT_BCOV GFTTTNLAFNKVQIAVNANAMALSKLABLENTFGAISSSISDILARLDIVEGBAQIDRLINGRLISLMAFVAQSLIKYABTQASRQLAT 11. SAWNS3_BCOV GFTTTNLAFNKVQIAVNANAMALSKLABLENTFGAISSSISDILARLDIVEGBAQIDRLINGRLISLMAFVAQSLIKYBAARRAQLAQ 12. A0A126W919_BCOV SLITISRALMKVE, VVNQCQALSHLIVQLASNFQAISSSISDILARLDIVEGBAQIDRLINGRLISLMAFVAQSLIKYBAARRAQLAQ 13. AOA127W710_CCOV GLATVAKALAKVQIVVNIQQQALSHLIVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 14. C6ZQKO_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNRFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 15. QQZVK5_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 16. Q7T5A1_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 18. BSRIQT_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 19. GSASOO_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 19. GSASOO_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 20. C6ZQJ9_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 21. K7KKRS_CCOV GFDAINSALVKIQ, VVNANABALNNLLQUSNKFGAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 22. B7T4AS_CCOV GLATVAKALAKVQIVVNIQGQALSHLITQQLONNFQAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 23. VPPIUT_FECOV GLATVAKALAKVQIVVNIQGQALSHLITQQLONNFQAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 24. AOAOCSCIJLI_FECOV GFDAMASALTKIQSVVNQGCBALSHLITQQLONNFQAISSSISDIYNRLDELSADAQVDRLITGRLALMAFVSQTLITQABVRARQLAK 25. C6GHBT_FECOV GFNSMASALTKIQSVVNQGCBALSHLITQQLONNFQAISSSIABIYNRLEKVBADAQVDRLITGRLALMARAVAQTLITQABVKARQLAM 26. G1FEXO_FECOV	8. A0A166ZL64BCoV	SLTTTATALCKLQI	VVNQNAQA	LNTLVKQL	SSNFGAIS	SALNDI	LSRLDK	VEAEVQ	IDRLII	r <mark>g</mark> RLQS	LQTYV	TQQLI	RAA	EIRAS	ANLAA	
11. SAWWS3_BCOV SUTTIS RALMKYED VYNE QG TALSQUTK QLASH F QAISSSISDILAR LD TVE QB AQ ID R LING RLTSLNAFVA QQLY R TEAAARSA QLAQ A0A126K919_BCOV SUTTIS RALMKYED VYNE QG TALSQUTK QLASH F QAISSSISDILAR LD TVE QB AQ ID R LING R LTSLNAFVA QQLY R TEAAARSA QLAQ A0A122WQTD_CCOV	9. AOA2Z4EVN5BCoV															
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20. C6ZQJ9_CCoV GFDATNSALVKIQ; VVNANABALNNLLQQLSNRFGAISASLQBILSRLDALBAQAQIDRLINGRLTALNAYVSQQLSDSTLVKFSAAQAMI 21. K7XKRS_CCoV GLATVAKVLAKVQIVVNTQGQALSHLTLQLQNNFQAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQTLTRQABVRASRQLAKI 22. B714AS_CCoV GLATVAKALAKVQIVVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQTLTRQABVRASRQLAKI 23. V9PIU7_FeCoV GLATVAKALAKVQIVVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDBLSADAQVDRLITGRLTALNAFVSQTLTRQABVRASRQLAKI 24. A0A0C5CJL1_FeCoV GFNTMASALTKIQSVVNHQGDALSQLTSQLQNNFQAISSSIABIYNRLBKVBADAQVDRLITGRLAALNAYVSQTLTQYSBVKASRQLAMI 25. C6GHB7_FeCoV GFNSMASALTKIQSVVNQQGBALSHLISQLQKNFQAISSSIABIYNRLBKVBADAQVDRLITGRLAALNAYVAQTLTQYABVKASRQLAMI 26. G1FEX6_FeCOV GFNSMASALTKIQSVVNQQGBALSQLTSQLQKNFQAISSSIABIYNRLBKVBADAQVDRLITGRLAALNAYVSQTLTQYABVKASRQLAMI	18. B8RIQ7CCoV															
21. K7XKR8CCOV GLATVAKVLAKVQI VVNTQG QALSHLTLQLQNNFQAISSSISDIYNRLDELSADAQVDRLITG RLTALNAFVSQTLT RQAEVRASRQLAKI 22. B714ASCCOV GLATVAKALAKVQI VVNTQG QALSHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITG RLTALNAFVSQTLT RQAEVRASRQLAKI 23. V9PIU7FeCOV GLATVAKALAKVQI VVNTQG QALSHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITG RLTALNAFVSQTLT RQAEVRASRQLAKI 24. A0A0C5CJL1FeCOV GFNTMASALTKIQS VVNHQG DALSQLTSQLQNNFQAISSSIAEIYNRLEKVEADAQVDRLITG RLAALNAYVSQTLT QYSEVKASRQLAMI 25. C6GHB7FeCOV GFNSMASALTKIQS VVNQQG EALSHLISQLQKNFQAISSSIAEIYNRLEKVEADAQVDRLITG RLAALNAYVAQTLT QYSEVKASRQLAMI 26. G1FEX6FeCOV GFNSMASALTKIQS VVNQQG EALSQLTSQLQKNFQAISSSIAEIYNRLEKVEADAQVDRLITG RLAALNAYVSQTLT QYSEVKASRQLAMI	19. G8A500CCoV	G LATVAKALAKVQI	VVNTQGQA	LSHLTVQL	QNNFQAIS	SSSISDI	YNRLDE	LSADAQ	V D R L I 1	r g R L T A	LNAFV	SQTLT	RQA	EVRASI	RQLAK	1
22. B7T4A8CCoV GLATVAKALAKVQI VVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKI 23. V9PIU7FeCoV GLATVAKALAKVQI VVNTQGQALSHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITGRLTALNAFVSQTLTRQAEVRASRQLAKI 24. A0A0C5CJL1FeCoV GFNTMASALTKIQS VVNHQGDALSQLTSQLQNNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYSEVKASRQLAMI 25. C6GHB7FeCoV GFNSMASALTKIQS VVNQQGEALSHLISQLQKNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVAQTLTQYAEVKASRQLAMI 26. G1FEX6FeCoV GFNSMASALTKIQS VVNQQGEALSQLTSQLQKNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYAEVKASRQLAMI	20. C6ZQJ9CCoV	G FDATNSALVKIQA	V V <mark>N</mark> A N A E A	LNNLLQQL	SNRFGAIS	BASLQBI	LSRLDAI	LBAQAQ	IDRLIN	NGRLTA	LNAYV	SQQLS	DST	LVKFS	A A Q A M	
23. V9PIU7FeCoV GLATVAKALAKVQI VVNTQG QALSHLTVQLQNNFQAISSSISDIYNRLDELSADAQVDRLITG RLTALNAFVSQTLTRQAEVRASRQLAKI 24. A0A0C5CJL1FeCoV GFNSMASALTKIQS VVNHQG DALSQLTSQLQNNFQAISSSIAE IYNRLEKVEADAQVDRLITG RLAALNAYVSQTLTQYSEVKASRQLAMI 25. C6GHB7FeCoV GFNSMASALTKIQS VVNQQG EALSHLISQLQKNFQAISSSIAE IYNRLEKVEADAQVDRLITG RLAALNAYVAQTLTQYAEVKASRQLAMI 26. G1FEX6FeCoV GFNSMASALTKIQS VVNQQG EALSQLTSQLQKNFQAISSSIAE IYNRLEKVEADAQVDRLITG RLAALNAYVSQTLTQYAEVKASRQLAMI	21. K7XKR8CCoV	G LATVAKVLAKVQI	VVNTQGQA	LSHLTLQL	QNNFQAIS	SSSISDI	YNRLDE	LSADAQ	V D R L I 1	FG RLTA	LNAFV	SQTLT	RQA	EVRASI	RQLAK	
24. A0A0C5CJL1FeCoV GFNTMASALTKIQS VVNHQGDALSQLTSQLQNNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYSEVKASRQLAM. 25. C6GHB7FeCoV GFNSMASALTKIQS VVNQQGEALSHLISQLQKNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVAQTLTQYAEVKASRQLAM. 26. G1FEX6FeCoV GFNSMASALTKIQS VVNQQGEALSQLTSQLQKNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYAEVKASRQLAM.	22. B7T4A8CCoV	G LATVAKALAKVQI	VVNTQGQA	LSHLTVQL	QNNFQAIS	SSSISDI	YNRLDE	LSADAQ	V D R L I 1	F G R L T A	LNAFV	SQTLT	R Q A	EVRASI	RQLAK	
25. C6GHB7FeCoV GFNSMASALTKIQSVVNQQGEALSHLISQLQKNFQAISSSIAEIYNRLEKVEADAQVDRLITGRLAALNAYVAQTLTQYAEVKASRQLAMI 26. G1FEX6FeCoV GFNSMASALTKIQSVVNQQGEALSQLTSQLQKNFQAISSSIAEIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYAEVKASRQLAMI	23. V9PIU7FeCoV	G LATVAKALAKVQI	VVNTQGQA	LSHLTVQL	QNNFQAIS	SSSISDI	YNRLDE	LSADAQ	V D R L I 1	FGRLTA	LNAFV	SQTLT	RQA	EVRASI	RQLAK	
26. G1FEX6FeCoV GFNSMASALTKIQSVVNQQGEALSQLTSQLQKNFQAISSSIABIYNRLEKVEADAQVDRLITGRLAALNAYVSQTLTQYAEVKASRQLAM	24. A0A0C5CJL1_FeCoV	G FNTMASALTKIQS	VVNHQGDA	LSQLTSQL	QNNFQAIS	SSSIABI	YNRLEK	V E A D A Q	V D R L I 1	GRLAA	LNAYV	SQTLT	QYS	EVKASI	RQLAM	
	25. C6GHB7FeCoV	G F N S M A S A L T K I Q S	VVNQQGEA	LSHLISQL	QKNFQAIS	SSSIABI	YNRLEK	V E A D A Q	V D R L I I	GRLAA	LNAYV	AQTLT	QYA	EVKASI	RQLAM	1
27 CROHAR RACAU GENSMASALTKIAS UUNGGORALSGILTSGILKNEGAISSSIARIUNDIRKURANAUNDILTGOLAALNAUUATI.TOVARUKASPOLAMI Y	26. G1FEX6FeCoV	G F N S M A S A L T K I Q S	VVNQQGEA	LSQLTSQL	QKNFQAIS	SSIABI	YNRLEK	V B A D A Q	VDRLI1	GRLAA	LNAYV	SQTLT	QYA	EVKASI	RQLAM	1
	27 CROHAR RACAV	CENSUASALTE TOS	VVNOOGEA	LART TRAIL	OKNEGATS	SSSTART	VMRIEK	V R A D A O	V D R I. T	RT. A A	T. N A V V	AOTLT	NVΔ	EVKASI	RAT. AM	· ~



WEBLOGO

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- 保守区序列标识



ATTENTION

No objective functions

No way of quantifying whether or not the alignment is good

• No way of knowing if the alignment is 'correct'.

TIPS

- ○剔除太差的序列
- •对序列有一定的了解
- 使用多个算法、软件
- 尝试多种打分和参数
- 使用合适的打分和参数

SUMMARY

•对序列的特性(特别是非保守区的大小)要有大致的了解;

○使用不同参数进行多次比对,选取合理的结果。