COBALT

Constraint-based Multiple Alignment Tool
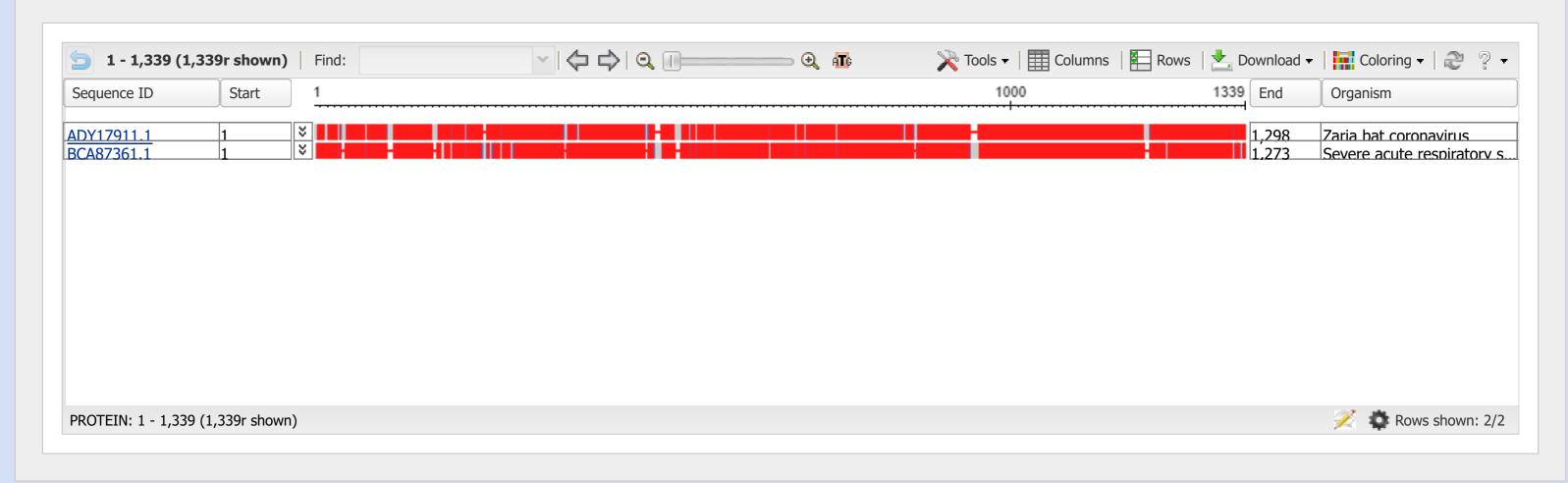
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Phylogenetic Tree   Edit and Resubmit   ▷ Download

- Cobalt RID PD4UPAKJ212 (2 seqs)

▼ **Graphical Overview**

| | 1 - 1,339 (1,339r shown) | Find: | | ◀ ▶ 🔍 ━━━ 🔍 🆎 | Tools ▾ | Columns | Rows | ⬇ Download ▾ | Coloring ▾ | 🔄 ? ▾ |

Sequence ID	Start	1	1000	1339	End	Organism
ADY17911.1	1				1,298	Zaria bat coronavirus
BCA87361.1	1				1,273	Severe acute respiratory s...

PROTEIN: 1 - 1,339 (1,339r shown)   Rows shown: 2/2

▼ **Descriptions**   ☑ Select All   [Re-align]   ▷ Alignment parameters

Accession	Description	Links
☑ ADY17911.1	putative spike glycoprotein [Zaria bat coronavirus]	
☑ BCA87361.1	surface glycoprotein [Severe acute respiratory syndrome coronavirus 2]	

▼ **Alignments**   ☑ Select All   [Re-align]   Mouse over the sequence identifer for sequence title

View Format: [Compact ▾]   Conservation Setting: [2 Bits ▾] ?

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☑ ADY17911.1  1     MSFIVAFTVLLPIVTAAPSFAGGCKTYSLSGAYTENNYTINGTVSYGLYYPDAIFRSNVSVLFTRPFLPLHAEAYQWYGA  80
☑ BCA87361.1  1     ---MFVFLVLLPLVSS--QCVNLTTRTQLPPAYT-NSFT------RGVYYPDKVFRSSVLHSTQDLFLPFFSNV-TWFHA  67

☑ ADY17911.1  81    YKDQGVSINYQYSYLPHPFKDGIAVKIFHRVREGYTKGFSTPAAYLFGSTFDSNSSTLLIGVNGTHRIIAVCQFVVCKSP  160
☑ BCA87361.1  68    IHVSGTNGTKRFDNPVLPFNDGVYF--------ASTEKSNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDP  139

☑ ADY17911.1  161   LVHLYPYNQTTPPDTFTKYYLEG---LFSAADNCSL-LIEQPLWLDNSTNSNRLVTAQTQYIFTYESGVFSVYHAHNPNG  236
☑ BCA87361.1  140   FLGVYYHKNN-------KSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLR-EFVFKNIDGYFKIYSKHTPIN  211

☑ ADY17911.1  237   SV-----GYATLA--FTIPVTIPITKFY-LPAVFDGLKASGDN--GVKRGNYHIEFAYLKRTTYMFTYDGNGYITSHVYC  306
☑ BCA87361.1  212   LVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDC  291

☑ ADY17911.1  307   AEGPLQELKCSQLSNNVPPGVYRTTNYRAEPQGHVVRYAADVADFQQSCGAERLLNASIDQIPDPAFWKRHVIRNCKFNF  386
☑ BCA87361.1  292   ALDPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFP----NITNLCPFGEVFNAT--RFASVYAWNRKRISNCVADY  365

☑ ADY17911.1  387   SHIMALSHVYDMQCYGIDASKLPSTCWNEVYADVFRLAQDDFYSFKPSASGDLATYNYKLPSDFLGCTLILTNPNLYCGN  466
☑ BCA87361.1  366   SVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNL---D  442

☑ ADY17911.1  467   STTCGIPGF----------NGVTGDLHYKVWRPGTTICPMKYVNPGEQNAMGYHCMSPTEHEKKLTPVSFRGGYYYMYGL  536
☑ BCA87361.1  443   SKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPC---------NGVEGFNCYFPLQ-SYGFQPTN-GVGYQPYRVV  511

☑ ADY17911.1  537   ALTLKPATVASTVCDVTAQQTNLTLDKCVSYTVYGYNGQGILVETNETFPSFQNVQLWPNGQLKAFKDPQSNQVIAVLPC  616
☑ BCA87361.1  512   VLSFELLHAPATVCG-PKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPC  590

☑ ADY17911.1  617   AEADVSVATAGNHT-NEVATLFTGAPCSGVQAKLLGVSTTSMWRRISENTTKGIDTPVGCLFGAVLSTSNSTECQFSLGL  695
☑ BCA87361.1  591   SFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNV-FQTRAGCLIGAE-HVNNSYECDIPIGA  668

☑ ADY17911.1  696   DTCLNITRGRVGSRSAGHLKESSTYNYFFQDMPKESEIPFSNFTVEIPDNFTIAIEYETLPIRMSKISVDCSRYVCGTDV  775
☑ BCA87361.1  669   GICASYQTQTNSPRRARSVASQSIIAYTMS-LGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDST  747

☑ ADY17911.1  776   VCANQLVQYGKFCDNINEALRGVSLQQDSNVAELLSDIKQLTRVSDLDLKDINGFNFSSLYNTDYLDATSSGRRSAIEDL  855
☑ BCA87361.1  748   ECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQIYKTPPI--KDFGGFNFSQILP----DPSKPSKRSFIEDL  821

☑ ADY17911.1  856   LFNKVVTADVGFMKKYEECTGGSVFKDLDCAQSFNGLKVLPPQMSDAHVGVYTTAAAMGSFFS-----------IPNTMQ  924
☑ BCA87361.1  822   LFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQ  901

☑ ADY17911.1  925   MAYRFNGIAVTQSVLVDNQKEIANKFNQALTSIQQGFTATNSAVQKLQDVVNANAAALNTLVTQLGNNFGAISSAINDIT  1004
☑ BCA87361.1  902   MAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDIL  981

☑ ADY17911.1  1005  QRLDKLEAAVQIDRLINGRLQVLQTFVTQQLIMASEIRASAQLAKQKMSECVLSQSKRQDFCGRGLHLMSFPQSAPQGMV  1084
☑ BCA87361.1  982   SRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVV  1061

☑ ADY17911.1  1085  FLHVLYRPTSYINVTSTPAICSENKAYFPTDGVFVLHDNQWMITKRNFYDPVNISLSNVRYAGSCDVITTYANHTIFEPD  1164
☑ BCA87361.1  1062  FLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVN-------  1134

☑ ADY17911.1  1165  NSTLQDFMHELEEIRKNLSMSAPN--SPNFTLPGLSDINASFVDLSKEMETLQNVVRQLNKSVIDLKELGTYEYYEKWPW  1242
☑ BCA87361.1  1135  NTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPW  1214

☑ ADY17911.1  1243  YIWLGFIAGLVAIALVLVLICCSTSCCSCFKGMCSCKKCCD-SYDDDEQIL--IKQHYP  1298
☑ BCA87361.1  1215  YIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKGVKLHYT  1273
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