

This is the RNA Dependent RNA Polymerase responsible for copying the Genome of the Virus

Vertical lines represent matching amino acids in the protein
Colons represent amino acids with compatible hydrophobic properties which are regularly substituted in nature based on the BLOSUM62 PAM matrix

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>orflab ; orflab polyprotein, pplab; expression of ORFlb-encoded region of pplab predicted to
involve ribosomal frameshifting into the -1 frame just upstream of the ORFla translation
termination codon, CodingLen:7218 ; Protein length = 7096 (QHO62106.1 Full gene position = Wuhan
seafood market pneumonia virus isolate 2019_nCoV WHU01 (2020_01_28):265-21554) (Wuhan seafood
market pneumonia...) (265)
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81 91 101 111 121 131 141 151
HGHHKVVVELVAEMDGIQYGRSGITLGVLPVPHVGETPIAYRNVLLRKNNGKAGGHSYGDIDLSYDLGDELGTDPIDYEQN
||| : ||||| : ||||| | ||||| | : || ||||| ||||| ||||| ||||| : ||||| ||||| ||||| : |||||
HGHHMVVELVAELEGIQYGRSGETLGVLPVPHVGEIPVAYRKVLLRKNNGKAGGHSYGADLKSFDLDELGTDPYDFQEN

161 171 181 191 201 211 221 231
WNTKKGSGALRELTRELNGGAVTRYVDN~~NNFC~~PGDPGYPLD~~CIKDF~~LARAGKSMCTLSEQLDYIESKRGVYCCRDHEHEIAW
||||| || ||| ||||||| |||||||||||||:|||||: |||||||:|::|||:|||||
WNTKHSSGV~~TREL~~MRELNGGAYTRYVDN~~NNFC~~PGDPGYPLE~~CIKDLL~~ARAGKASCTLSEQLDFIDTKRGVYCCREHEHEIAW

241 251 261 271 281 291 301 311
 FTERS~~DK~~SYEHQTPFEIKSAKKFDTFKGECPKFVFPLNSKV~~Q~~IPRVEKKKTEGFMGRIRSVYPVASPQECNNMHLSTL
 :|||:| | | | | | | | | | | | | | | | : | | | | | | : | | | | | | | | | | | | | | |
 YTERSEKSYELQTPFEIKLAKKFDTFNGECPNFVFPLNSIIKTIQPRVEKKKLDGFMGRIRSVYPVASPNECNQMCLSTL

321 331 341 351 361 371 381 391
MCKNCHDEVSWQTCDFLKATCEHCGTENLVIEGPTTCGYLPTNAVVKMPCPACQDPEIGPEHSVADYHNHNSNIETRLRKG
|||:| | |||| |::|||| ||||| | | |||||| |||||: ||| : |:|||||:|:|| | : :| ||||
MKCDHCGETSWSQTGDFVKA TCEFCGTENLTKEGATTCGYLPONAVVKIYCPACHNSEVGPPEHSLAEYHNESGLKTIILRKG

401 411 421 431 441 451 461 471
GRTRCFGGCVFAYVGCYNKRAYVWPRASADIGSGHTGITGDNVETLNEDLLEILSRERVNINIVGDFHLEEVAILASF
||| |||||:||||:| |||||:| |||: | ||::||| |:||||| |||:|||||
GRTIAFGGCVFSYVGCNHCAYVWPRASANIGCNHTGVVGEGSEGLNDNLLEILOKEKVNINIVGDFKLEEEIAIILASF

481 491 501 511 521 531 541 551
SASTSAFIDTIKSLDYKSFKTIVSCGNYKVTGKGPVKGAWNIGQORSVLTPLCGFPSQAAGVIRSIFARTLDAANHSIP
|||||:::|:| ||||:| | |||||:|||| | |||||:|:|:|:| | | :| | :|||:|:| | :|:
SASTSAFVETVKGGLDYAKFKOIVSCGNFKVTGKAKKGAWNIGEOKSILSPLYAFASEAARVRSIFSRTLETAQNSVR

561 571 581 591 601 611 621 631
DLQRAAVTILDGISEQSLRLVDAMVYTSDDLTSNSVIIMAYVTGGVLVQQTQSQWLSNLLGTTVEKLRPIFEWIEAKLSAGVE
||:|:|:|:|:|:|: |||:|:|:|:|:|: ||:::|:|:|:|:|: |||:|:|: || |:|:|: |:|:| | ||
VLQKAAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAYITGGVVQLTSQWLTNIFGTVYEKLPVLDWLEKFKEGVE

641 651 661 671 681 691 701 711
FLKDAWEILKFLITGVFDIVKGQIQVASDNKDCVKCFIDVVNKALEMCIDQVTIAGAKLRSLNLGEVFIAQSKGLYRQC
||:| |||:|:|:| | |:| || | : ||: |:| |:| |:| | |||:|:|:| |:| |||:|:|
FLRDGWEIVKFISTCACEIVGGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKC

721 731 741 751 761 771 781 791
IRGKEQLQLLMLPLKAPKEVTFLEGDSHDTVLTSEEVVVLKNGELEALETPVDSFTNGAIVGTPVCVNGMLMLEIKDKQCYC
:: |:| |||:|:|:|:|:|:|: |||:|: |:|:|:|:|:|:|: |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
VKSREETGLLMLPLKAPKEIIFLEGETLPTEVLTEEVVVLKTDGLQPLEQPTSEAVEAPLVGTPVCINGMLMLEIKDKTEKYC

801 811 821 831 841 851 861 871
ALSPGLLATNNVFRLLKGGAPIKGVTFGEDTVWEVQGYKKNVRITFELDERVDKVLNEKCSVYTVESGTEVTEFACVVAEAV
||:| :: ||| | ||| || | |||:|
ALAPNMMVTNNTFTLLKGGAPTK-VTFGDDTVIEVQGYKSVNITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVDADV

881 891 901 911 921 931 941 951
VKTLPQVSDLLTNMGIDLDEWSVATFYLFDDAGEENFSSRMYCSFYPPDEEEEDDAECEEEIDETCEHEYGTEDDYQGL
:|
IKTLQPVSELLTPLGIDLDEWSMATYYLFDESGEFKLASHMYCSFYPPDEDEE-EGDCEEEEFEPSTQYEYGTEDDYQGL

961 971 981 991 1001 1011 1021 1031
PLEFGASAEVTRVEEEEEEDWL-----D---D---TTEQS--EIEP--EPE--PTP-EEPVNQFTGYLKLTDNV
|||:|
PLEFGATSAALQPEEEQEEDWLDDDSQQTVGQQDGSSEDNQTTTIQTIVEVQPQLEMELTPVVQTIIEVNSFSGYLKLTDNV

1041 1051 1061 1071 1081 1091 1101 1111
AIKCVDIVKEAQSANPMVIINAANIHLKHGGGVAGALNKATNGAMQKESDDYIKLNGPLTVGGSCLLSGHNLAKKCLHVV
|| ||:|:|:|:| |:|
YIKNADIVEEAQKVKPTVVVNAANVYLKHGGGVAGALNKATNNAMQVESDDYIATNGPLKVGGSVCVLSGHNLAKHCLHVV

1121 1131 1141 1151 1161 1171 1181 1191
GPNLNAGEDIQLLKAAAYENFNSQDILLAPLLSAGIFGAKPLQSLQVCVQTVRTRQVYIAVNDKALYEQVVM DYLD-NLKPR
||:| | |||:|
GPNVNKGEDIQLLKSAYENFNQHEVLLAPLLSAGIFGADPIHSLRVCDTVRTRNVYLAVFDKNLYDKLVSSFLEMKSEKQ

1201 1211 1221 1231 1241 1251 1261 1271
VEAPKQEEPPNTEDSK-TEEKSVVQKPVVDVKPKIKACIDEVTTTLEETKFLTNKLLLFADINGKLYHDSQNLRGEDMSF
|| | | || | |:|
VEQKIAEIPKEEVKPFITESKPSVEQRKQDDKKIKACVEEVTTTLEETKFLTENLLLYIDINGNLHPDSATLVSDIDITF

1281 1291 1301 1311 1321 1331 1341 1351
LEKDAPYVMGDVITSGDITCVVIPSKKAGGTTEMLSRALKKVPVDEYITTPYQGQCAGYTLLEEAKTALKKCKSAFYVLPS
|:|:|:|:|:|:|:|:| |:| |||:|
LKKDAPYIVGDVVQEGVLTAVVIPTKKAGGTTEMLAKALRKVPDNYITTPYQGQLNGYTVVEEAKTVLKKCKSAFYILPS

1361 1371 1381 1391 1401 1411 1421 1431
EAPNAKEEILGTVSWNLREMLAHAEEETRKLMPICMDVRAIMATIQRKYKGIKIQEGIVDYGVRFFFTYSKEPVASIITKL
| |:|
IISNEKQEIILGTVSWNLREMLAHAEEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVDYGARFYFTSKTTVASLINT

1441 1451 1461 1471 1481 1491 1501 1511
NSLNEPLVTMPIGYVTHGFNLEEAARCMRSLKAPAVSVSSPDAVTTYNGYLTSSSKTSEEHFVETVSLAGSYRDWSYSG
| ||| |||||:||||| ||||| ||| ||| ||||| ||||| |||||:|:|||||:|||||
NDLNETLVTMPLGYVTHGLNLEEAARYMRSLKVPATVSVSSPDAVTAINGYLTSSSKTPEEHFIETISLAGSYKDWYSYG

1521 1531 1541 1551 1561 1571 1581 1591
QRTELGVFEFLKRGDKIVYHTLESFVEFHLDEVLSDLKLSLSLREVKTIKVFTTVDNTNLHTQLVDMSTYGOQFGPT
| |:|:||||||| ||:| :| |||||:| | |:|||||:||||||| ||||:|||||||
QSTQLGIEFLKRGDKSVYYT-SNPTTFHLDGEVITFDNLKTLSSLREVRTIKVFTTVDNINLHTQVVDMSTYGOQFGPT

1601 1611 1621 1631 1641 1651 1661 1671
YLDGADVTKIKPHVNHEGKTFVFLPSDDTLRSEAFEYHTLDESFLGRYMSALNHTKKWFPQVGGELTSIKWADNNCYLS
||||||| :|||||:|||:|||| ||||| | ||||| |||||:||| ||||| |||||:
YLDGADVTKIKPHNSHEGKTFYVLPNDTLRVEAFEYHTTDPNFLGRYMSALNHTKKWKYPQVNGLTSIKWADNNCYLA

1681 1691 1701 1711 1721 1731 1741 1751
SVLLALQQLEVKNAPALQEAYYRARAGDAANFCALILAYSNKTVGELGDVRETMTHLLQHANLESARKVNLNVCKKHCQ
: || |||:|:| |||:|||||:||||||| ||||| |||||:| ||||:| ||||| |||
TALLTLQQIELKNPPALQDAYYRARAGEAANFCALILAYCNKTVGELGDVRETMSTYLFQHANLDSCKRVNLNVCKTKCQ

1761 1771 1781 1791 1801 1811 1821 1831
KTTTLTGVEAVMYMGTLSDNLKTGVSIPCVGRDATQYLVQQESSFVMSAPPAEYKLQQTFLCANEYTGNYQCCHYT
: ||| ||||| |||||: | || ||| |: |:||||| |||||:|:| ||| |:|||||||
QQTTLKGVEAVMYMGTLSEYQFKKGVIPTCTCGKQATKYLQQESPFVMSAPPAQYELKHGFTTCASEYTGNYQCCHYK

1841 1851 1861 1871 1881 1891 1901 1911
HITAKETLYRIDGAHLTKMSEYKGPVTDVFYKETSyttTIKPVSYKLDGVTYTEIEPKLDGYKKDNAYYTEQPIDLVP
||:|||| ||| ||| |||||:||||| |||||:||||| ||:|||| |||||:|:|||||||
HITSKETLYCIDGALLTKSSEYKGPITDVFYKENSyttTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPN

1921 1931 1941 1951 1961 1971 1981 1991
QPLPNASFDNFKLTCSNTKFADDLNQMTGFTKSPASRELSVTFPPDLNGDVVAIDYRHSASFKKGAKLLHKPIVWHINQA
|| ||||| | | |||||:|:| ||||| ||||| |||||:|:| ||||| |||||:| |
QYPNASFDNFKFVCDNIKFADDLNLQLTGYKKPASRELKVTFFPDNLNGDVVAIDYKHYTPSFKKGAKLLHKPIVWHVNN

2001 2011 2021 2031 2041 2051 2061 2071
TTKTTFKPNTWCLRWSTKPVDTSNSEFVLAVEDTQGMNLAACESQQPTSEEVVENPTIQKEVIECDVKTTTEVGVNVL
| | |:|||||:|||||||:||||:| || ||||| :| ||||| |||||:|:|:|||||:|
TNKATYKPNWTCIRLWSTKPVETSNSEFVLKSEDAQGMNLALEDLKPVSEEVVENPTIQKDVLECNVKTTEVGVDIIL

2081 2091 2101 2111 2121 2131 2141 2151
KPSDEGVKVTQELGHEDLMAAYVENTSITIKPNELSLALGLKTIATHGIAAINSVPWSKILAYVKPFLGQAAITTSNCA
||:: :|:|:|:| |||||:|:| ||||| |||||:||||| |||||:|||||:| ||| : |||
KPANNSLKITEEVGHDTLMAAYVDNSSLTIKPNELSRVLGLKTLATHGLAAVNSVPWDTIANYAKPFLNKVVSTTTNIV

2161 2171 2181 2191 2201 2211 2221 2231
KRLAQRFVFNYPYVFTLLFQLCTFTKSTNSRIRASLPTTIKNSVKSVAKLCLDAGINYVKSFKLFTIAMWLLLLLS
| || |||| ||| |||||:|||||:|:|||||:|||| | |:| |:||| ||| | :| |||
TRCLNRVCTNYPYFFTLQLCTFTRSTNSRIKASMPPTTIKNTVKSVMKFCLEASFNYLKSFNFSKLNIIWFLLS

2241 2251 2261 2271 2281 2291 2301 2311
ICGLSLICVTAAGFVLLSNFGAPSYCNGVRELYLNSSNVTTMTDFCEGSFPCSICLSGLDSLDSYPALETIQVTISSYKLD
:||||| ||| |||:| | ||| | || |||:||| :| || |:|||||||:|:|||||:||||:| |
VCLGSLIYSTAALGVLMSNLGMPSYCTGYREGYLNSTNVTIATYCTGSIPCSVCLSGLDSLDTYPSLETIQITISSFKWD

[illegible]

[illegible]

4081 4091 4101 4111 4121 4131 4141 4151
GTYKNTCDGNTFTTYASALWEIQQVVDADSKIVQLSEINMDNSPNLAWPLIVTALRANSVAVKLQNNELSPVALRQMSCAAG
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
NTYKNTCDGTTFTTYASALWEIQQVVDADSKIVQLSEISMDNSPNLAWPLIVTALRANSVAVKLQNNELSPVALRQMSCAAG

4161 4171 4181 4191 4201 4211 4221 4231
TTQTACTDDNALAYYNNKSGGRFVLALLSDHQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGLNNL
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
TTQTACTDDNALAYYNTTKGGRFVLALLSDLQDLKWARFPKSDGTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGLNNL

4241 4251 4261 4271 4281 4291 4301 4311
NRGMVLGSLAATVRLQAGNATEVPANSTVLSFCAFAVDPAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMD
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
NRGMVLGSLAATVRLQAGNATEVPANSTVLSFCAFAVDAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMD

4321 4331 4341 4351 4361 4371 4381 4391
QESFGGASCCLYCRCHIDHPNPKGFCDLKGKVVQIPTTCANDPVGFTLRNTVCTVCGMWKGYGCSCDQLREPLMQSADAS
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
QESFGGASCCLYCRCHIDHPNPKGFCDLKGKVVQIPTTCANDPVGFTLRNTVCTVCGMWKGYGCSCDQLREPLMQSADAQ

4401 4411 4421 4431 4441 4451 4461 4471
TFLNRVCGVSAARLTPCGTGTSTDVVYRAFDIYNEKVAGFAKFLKTNCCRFQEKDEGNLLDSYFVVKRHTMSNYQHEET
:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
SFLNRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDEDDNIDSYFVVKRHTFSNYQHEET

4481 4491 4501 4511 4521 4531 4541 4551
IYNLVKDCPAVAVHDFKFRVDGDMVPHISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWYDF
|||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
IYNLLKDCPAVAKHDFKFRIDGDMVPHISRQRLTKYTMADLVYALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWYDF

4561 4571 4581 4591 4601 4611 4621 4631
VENPDILRVYANLGERVRQSLKTVQFCDAMRDAGIVGVLTLDNQDLNGNWDYDFGDFVQVAPGCGVPIVDSYYSLLMPIL
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
VENPDILRVYANLGERVRQALLKTVQFCDAMRNAGIVGVLTLDNQDLNGNWDYDFGDFIQTPGSGVPVDSYYSLLMPIL

4641 4651 4661 4671 4681 4691 4701 4711
TLTRALAAESHMDADLAKPLIKWDLKLYDFTEERLCLFDRYFKYWDQTYHPNCINCLDDRCILHCANFNVLFSTVFPPTS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
TLTRALTAESHVDTDLTKPYIKWDLKLYDFTEERLKLDFRYFKYWDQTYHPNCVNCCLDDRCILHCANFNVLFSTVFPPTS

4721 4731 4741 4751 4761 4771 4781 4791
FGPLVRKIFVDGVFPFVSTGYHFRELGVVHNQDVNLHSSRSLSFKELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNV
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
FGPLVRKIFVDGVFPFVSTGYHFRELGVVHNQDVNLHSSRSLSFKELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNV

4801 4811 4821 4831 4841 4851 4861 4871
AFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYRYNLPMTCDIRQLLFVVEVVDKYFDCYDG
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
AFQTVKPGNFNKDFYDFAVSKGFFKEGSSVELKHFFFAQDGNAAISDYDYRYNLPMTCDIRQLLFVVEVVDKYFDCYDG

4881 4891 4901 4911 4921 4931 4941 4951
GCINANQVIVNNLDKSAGFPFNKGWKARLYYDMSYEDQDALFAYTKRNVIPITITQMNLYAISAKNRARTVAGVSICST
|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
GCINANQVIVNNLDKSAGFPFNKGWKARLYYDMSYEDQDALFAYTKRNVIPITITQMNLYAISAKNRARTVAGVSICST

4961	4971	4981	4991	5001	5011	5021	5031
MTNRQHFQKLLKSIAATRGATVVIGTSKIFYGGWHNMLKTVYSDVETPHLMGWDYPKCDRAMPNMLRIMASVLARKHNTC 							
MTNRQHFQKLLKSIAATRGATVVIGTSKIFYGGWHNMLKTVYSDVENPHLMGWDYPKCDRAMPNMLRIMASVLARKHNTC 							
5041	5051	5061	5071	5081	5091	5101	5111
CNLSHRFYRLANECAQVLSEMMVCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGKNKIADKYVRNLQH :							
CSLSHRFYRLANECAQVLSEMMVCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGKNKIADKYVRNLQH :							
5121	5131	5141	5151	5161	5171	5181	5191
RLYECLYRNRDVDHEFVDEFYAYLRKHFSMMILSDDAVVCYNSNYAAQGLVASIKNFKAVLYYQNNVMSEAKCWTETDL :							
RLYECLYRNRDVTDFVNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVASIKNFKSVLYYQNNVMSEAKCWTETDL :							
5201	5211	5221	5231	5241	5251	5261	5271
TKGPHEFCSQHTMLVKQGDDYVYLPYPDPSPRILGAGCFVDDIVKTGDTLMIERFVSLAIDAYPLTKHPNQEYADVFLHYL :							
TKGPHEFCSQHTMLVKQGDDYVYLPYPDPSPRILGAGCFVDDIVKTGDTLMIERFVSLAIDAYPLTKHPNQEYADVFLHYL :							
5281	5291	5301	5311	5321	5331	5341	5351
QYIRKLHDELTDGHMLDMYSVMLTNDNTSRYWEPEFYEAMYPHTVLQAVGACVLCNSQTSLRGACIRRPFLCCKCCYDH :							
QYIRKLHDELTDGHMLDMYSVMLTNDNTSRYWEPEFYEAMYPHTVLQAVGACVLCNSQTSLRGACIRRPFLCCKCCYDH :							
5361	5371	5381	5391	5401	5411	5421	5431
VISTSHKLVLSVNPYVCNAPGCDVTDVDTQLYLGGMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVDNFNAIATCD :							
VISTSHKLVLSVNPYVCNAPGCDVTDVDTQLYLGGMSYYCKSHKPPISFPLCANGQVFGLYKNTCVGSDNVDNFNAIATCD :							
5441	5451	5461	5471	5481	5491	5501	5511
WTNAGDYILANTCTERLKLFAAETLKATEETFKLKSYGIATVREVLSRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKV :							
WTNAGDYILANTCTERLKLFAAETLKATEETFKLKSYGIATVREVLSRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKV :							
5521	5531	5541	5551	5561	5571	5581	5591
QIGEYTFEKGDYGDVAVYRGTTTYKLNVDYFVLTSHTVMPLSAPTLVQPEHYVRITGLYPTLNISDEFSSNVANYQKVG :							
QIGEYTFEKGDYGDVAVYRGTTTYKLNVDYFVLTSHTVMPLSAPTLVQPEHYVRITGLYPTLNISDEFSSNVANYQKVG :							
5601	5611	5621	5631	5641	5651	5661	5671
MQKYSTLQGPPGTGKSHFAIGLALYYPSARIVYTACSHAAVDALCEKALKYLPIDKCSRIIPARARVECFDKFKVNSTLE :							
MQKYSTLQGPPGTGKSHFAIGLALYYPSARIVYTACSHAAVDALCEKALKYLPIDKCSRIIPARARVECFDKFKVNSTLE :							
5681	5691	5701	5711	5721	5731	5741	5751
QYVFCTVNALPETTADIVVFEISMATNYDLSVNVNARLRAKHYYVIGDPAQLPAPRTLLTKGTLEPEYFNSVCRLMKTIG :							
QYVFCTVNALPETTADIVVFEISMATNYDLSVNVNARLRAKHYYVIGDPAQLPAPRTLLTKGTLEPEYFNSVCRLMKTIG :							
5761	5771	5781	5791	5801	5811	5821	5831
PDMFLGTCRRCPAEIVDTSALVYDNKLKAHKDKSAQCCKMFYKGVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFIS :							
PDMFLGTCRRCPAEIVDTSALVYDNKLKAHKDKSAQCCKMFYKGVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFIS :							

5841 5851 5861 5871 5881 5891 5901 5911
PYN SQNAVASKILGLPTQTV DSSQGSEYDYVIFTQT TETAHSCNVNRFNVAITRAKIGILCIMS DRDLYDKLQFTSLEIP
|||||:|||||
PYN SQNAVASKILGLPTQTV DSSQGSEYDYVIFTQT TETAHSCNVNRFNVAITRAKIGILCIMS DRDLYDKLQFTSLEIP

5921 5931 5941 5951 5961 5971 5981 5991
RRNVATLQAENV TGLFKDCSKIITGLHPTQAP THLSVDIKFKTEGLCVDIPGIPKDM TYRRLISMMGF KMNYQVNGYPNM
|||||:|||||
RRNVATLQAENV TGLFKDCSKVITGLHPTQAP THLSVDTKFKTEGLCVDIPGIPKDM TYRRLISMMGF KMNYQVNGYPNM

6001 6011 6021 6031 6041 6051 6061 6071
FITREEAIRHVRAWIGFDVEGCHATRDVGTNLPLQLGFSTGVNLVAVPTGYVDTENNT EFTRVNAKPPPGDQFKHLIPL
|||||:||||| |||:|:|:|
FITREEAIRHVRAWIGFDVEGCHATREAVGTNLPLQLGFSTGVNLVAVPTGYVDT PNNTDFSRVSAKPPPGDQFKHLIPL

6081 6091 6101 6111 6121 6131 6141 6151
MYKGLPWNVVRIKIVQMLS DTLKGLSDRVVFLWAHG FELTSMKYFVKIGIPERTCCLCDKRATCFSTSSD TYACWNH SVG
|||||:|||||:|||||:|:|
MYKGLPWNVVRIKIVQMLS DTLKNLSDRVVFLWAHG FELTSMKYFVKIGIPERTCCLCDRRATCFSTASD TYACWHHSIG

6161 6171 6181 6191 6201 6211 6221 6231
FDYVYNPF MIDVQQWGFTGNLQSNHDQHCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWSVEYPIIGDEL RVNSACRKV
|||||:|||||:|||||:|:|
FDYVYNPF MIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDAIMTRCLAVHECFVKRVDWTIEYPIIGDEL KINAACRKV

6241 6251 6261 6271 6281 6291 6301 6311
QHMVVKSALLADKFPVLHDIGNPKAIKCV PQAEVEWKFYDAQPCSDKAYKIEELFY SYATHHDKFTDGVCLFWNCNVDRY
|||||:|||||:|||||:|:|
QHMVVKALLADKFPVLHDIGNPKAIKCV PQADVEWKFYDAQPCSDKAYKIEELFY SYATHSDKFTDGVCLFWNCNVDRY

6321 6331 6341 6351 6361 6371 6381 6391
PANAIVCRFDTRVLSNLNLP GCGGSLYVNKHAFHTPAFDKSAFTNLKQLPFFYYS DSPCESHGKQVVS DIDIYVPLKSAT
|||:|||||:|||||:|:|
PANSIVCRFDTRVLSNLNLP GCGGSLYVNKHAFHTPAFDKSAFVNLKQLPFFYYS DSPCESHGKQVVS DIDIYVPLKSAT

6401 6411 6421 6431 6441 6451 6461 6471
CITRCNLGGAVCRHHANEYRQYLDAYNMMISAGFSLWIYKQFD TYNLWNTFTRLQSL ENVAYNVVNKGHFDGHAGEAPVS
|||||:|||||:|||||:|:|
CITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQFD TYNLWNTFTRLQSL ENVAFNVVNKGHFDGQGEVPVS

6481 6491 6501 6511 6521 6531 6541 6551
IINNAVYTKVDGIDVEIFENKTTLPVNVAFELWAKRNIKPVPEIKILNNLGVDIAANTVIWDYKREAPAHVSTIGVCTMT
|||:|||||:|||||:|:|
IINNTVYTKVDGVDVELFENKTTLPVNVAFELWAKRNIKPVPEVKILNNLGVDIAANTVIWDYKRDAPAHISTIGVCSMT

6561 6571 6581 6591 6601 6611 6621 6631
DIAKKPTESACSSLTVLFDGRVEGQVDLFRNARNGVLITEG SVKGLTPSKGPAQASVNGVT LIGESVKTQFN YFKKVDGI
|||||:|:| |||:||||| || |||:|||||:|||||:|:|
DIAKKPTETICAPLTVFFDGRVDGQVDLFRNARNGVLITEG SVKGLQPSVGPKQASLNGVT LIGEA VKTQFN YKKVDGV

6641 6651 6661 6671 6681 6691 6701 6711
IQQLPETYFTQSRDLEDFKPRSQMETDFLELAMDEFIQRYKLEGYAFEHIVYGDFSHGQLGGLHLMIGLAKRSQDSPLKL
:|||||:|:| |||:|||||:|||||:|:|
VQQLPETYFTQSRNLQEFKPRSQMEIDFLELAMDEFIERYKLEGYAFEHIVYGDFSHS QLGGHLHLIGLAKRFKESPFEL

241	251	261	271	281	291	301	311
NFRFA-I-L--TAFSPA-QDI-WGTSAAAYFVGYLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEDKGIYQTS							
:	:	:	:	:	:	:	:
RFQTLTALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTELLKYNENGITITDAVDCALDPLSETKCTLSFTVEKGIYQTS							
321	331	341	351	361	371	381	391
NFRVVPSPGDVVRFPNITNLCPFGEVFNATKFPSPVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNLDLCFNSVY							
:	:	:	:	:	:	:	:
NFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRRKRISNCVADYSVLYNASFSSTFKCYGVSPTKLNLDLCTFNVY							
401	411	421	431	441	451	461	471
ADSFVVKGDVDVRQIAPGQTVIADYNYKLPPDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPD							
:	:	:	:	:	:	:	:
ADSFVIRGDEVQRQIAPGQTKGIADYNYKLPPDFTGCVIAWNSNNLDSKVGGNVNYLYRLFRKSNLKPFERDISTEIIYQAG							
481	491	501	511	521	531	541	551
GKPCT-PPALNCYWLNDYGEYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNENGLTGTGVLTPSS							
:	:	:	:	:	:	:	:
STPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNENGLTGTGVLTESN							
561	571	581	591	601	611	621	631
KRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIY							
:	:	:	:	:	:	:	:
KKFLPFQQFGRDIADTTDAVRDPQTLIILDITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVY							
641	651	661	671	681	691	701	711
STGNNVFQTAGCLIGAHEVDTSYECDIPIGAGICASYHT-V-S--LLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPT							
:	:	:	:	:	:	:	:
STGSNVFQTRAGCLIGAHEVNNSYECDIPIGAGICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNNSIAIPT							
721	731	741	751	761	771	781	791
NFSISITTEVMPVSMAKTSVDCNMYYICGDSSTECANLLQYGSFCTQLNRALSGIAAEQDRNTRREVFAQVQKQMYKPTPLKY							
:	:	:	:	:	:	:	:
NFTISVTTEILPVSMTKTSVDCTMYICGDSSTECANLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVQKQIYKPTPIKD							
801	811	821	831	841	851	861	871
FGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFENGLTVLPPLLTDDMIAAYTAA							
:	:	:	:	:	:	:	:
FGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIARDLICAQKFENGLTVLPPLLTDEMAIQAQYTS							
881	891	901	911	921	931	941	951
LVSGTATAGWTFGAGAALQIPFAMQMAYRNGIGVTONVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNA							
:	:	:	:	:	:	:	:
LLAGTITSGWTFGAGAALQIPFAMQMAYRNGIGVTONVLYENQKLIANQFNKAISQIQESLTTTSTALGKLQDVVNQNA							
961	971	981	991	1001	1011	1021	1031
QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTVQQLIRAAEIRASANLAATKMSSECVLQ							
:	:	:	:	:	:	:	:
QALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTVQQLIRAAEIRASANLAATKMSSECVLQ							
1041	1051	1061	1071	1081	1091	1101	1111
SKRVDFCGKGYHLMSPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNGTWSWFTQRNFFSPQIIT							
:	:	:	:	:	:	:	:
SKRVDFCGKGYHLMSEFPOSAPHGVVFLHVTYVPAQEKNTTAPAICHGDKAHFPREGVVFVSNGTWHWFVTRNFFSPQIIT							

```

1121      1131      1141      1151      1161      1171      1181      1191
TDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
TDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNES

```

```

1201      1211      1221      1231      1241      1251      1261      1271
LIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCCLKGACSCGSCCKFDEDDSEPVKGVKLHYT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
LIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCCLKGCCSCGSCCKFDEDDSEPVKGVKLHYT

```

Similarity = 95.395 %

>E ; envelope protein E, structural protein, CodingLen:77 ; Protein length = 76 (AAQ94063.1 Full gene position = SARS coronavirus AS (2003_10_21):26101-26331) (SARS coronavirus AS (2003_10_2...) (26101)

>E ; envelope protein, structural protein, CodingLen:76 ; Protein length = 75 (QHO62108.1 Full gene position = Wuhan seafood market pneumonia virus isolate 2019_nCoV WHU01 (2020_01_28):26244-26471) (Wuhan seafood market pneumonia...) (26244)

```

1      11      21      31      41      51      61      71
MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVS�VKPTVYVYSRVKNLNSSEGVPDLLV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLAILTALRLCAYCCNIVNVS�VKPSFYVYSRVKNLNSR-VPDLLV

```

Similarity = 93.891 %

>M ; membrane protein M, structural protein, CodingLen:225 ; Protein length = 221 (AAQ94064.1 Full gene position = SARS coronavirus AS (2003_10_21):26382-27047) (SARS coronavirus AS (2003_10_2...) (26382)

>M ; matrix protein, structural protein, CodingLen:226 ; Protein length = 222 (QHO62109.1 Full gene position = Wuhan seafood market pneumonia virus isolate 2019_nCoV WHU01 (2020_01_28):26522-27190) (Wuhan seafood market pneumonia...) (26522)

```

1      11      21      31      41      51      61      71
MAD-NGTITVEELKQLEQWNLVIGFLFLAWIMLLQFAYSNNRNFYIIKLVFLWLLWPVTLACFVLAAYRINWVTGGI
||| |||||:|||||:||||| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
MADSNGTITVEELKKLLEQWNLVIGFLFTWICLLQFAYANRNFYIIKLVFLWLLWPVTLACFVLAAYRINWITGGI

```

```

81      91      101      111      121      131      141      151
AIAMACIVGLMWLSYFVASFRLFARTRSMWSFNPETNILLNVPLRGITVTRPLMESELVIGAVIIRGHLRMAGHSLGRCD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
AIAMACLVGLMWLSYFIASFRLFARTRSMWSFNPETNILLNVPLHGTILTRPLLESELVIGAVILRGHLRIAGHHLGRCD

```

```

161      171      181      191      201      211      221      231
IKDLPKEITVATSRTLSYYKLGASQVRGTDSGFAAYNRYRIGNYKLNTDHAGSNDNIALLVQ
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
IKDLPKEITVATSRTLSYYKLGASQVRAGDSGFAAYSRYRIGNYKLNTDHSSSDNIALLVQ

```

Similarity = 92.417 %

>N ; nucleocapsid protein N, structural protein, CodingLen:429 ; Protein length = 422 (AAQ94070.1
Full gene position = SARS coronavirus AS (2003_10_21):28104-29372) (SARS coronavirus AS
(2003_10_2...)(28104)

>N ; nucleocapsid protein, structural protein, CodingLen:426 ; Protein length = 419 (QHO62110.1
Full gene position = Wuhan seafood market pneumonia virus isolate 2019_nCoV WHU01
(2020_01_28):28273-29532) (Wuhan seafood market pneumonia...)(28273)

```

1      11      21      31      41      51      61      71
MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQGLPNNTASWFTALTQHGKEELRFPRGQGVPIINTNSG
||||| |||:|||||||:| | :||| |:| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
MSDNGPQ-NQRNAPRITFGGPSDSTGSNQNGERSGARSKQRRPQGLPNNTASWFTALTQHGKEDLKFFPRGQGVPIINTNSS

81      91      101     111     121     131     141     151
PDDQIGYYRRATRRVRGDKGKMKELSPRWYFYLLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
||||| |||||:|||||:||||| ||||| |||||:| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
PDDQIGYYRRATRRIRGGDKGKMDLSPRWYFYLLGTGPEAGLPYGANKDGIWVATEGALNTPKDHIGTRNPANNAIVL

161     171     181     191     201     211     221     231
QLPQGTTLPGKFYAEGSRGGSQASSRSSRSRGNSTPGSSRGNSPARMASGGGETALALLLLDRLNQLESKVSQKQ
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QLPQGTTLPGKFYAEGSRGGSQASSRSSRSRNSSTPGSSRGTSPTARMAGNGGDAALALLLLDRLNQLESKMSQKQ

241     251     261     271     281     291     301     311
QQQGQTVTKKSAAEASKKPRQKRTATKQYNVTQAFGRRGPEQTQGNFGDQDLIRQGTQDYKHWPQIAQFAPSASAFFGMSR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QQQGQTVTKKSAAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTQDYKHWPQIAQFAPSASAFFGMSR

321     331     341     351     361     371     381     391
IGMEVTPSGTWLTYHGAIKLDDKDPQFKDNVILLNKHIDAYKTFPPTEPKDKKKKTDEAQPLPQRQKKQPTVTLLPAAD
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
IGMEVTPSGTWLTYTGAIKLDDKDPNFKDQVILLNKHIDAYKTFPPTEPKDKKKKKADETQALPQRQKKQPTVTLLPAAD

401     411     421     431     441     451     461     471
MDDFSRQLQNSMSGASADSTQA
:||||:| | | | |||||
LDDFSKQLQQSMS--SADSTQA
```

LOCUS AY427439 29711 bp RNA linear VRL 21-OCT-2003
 DEFINITION SARS coronavirus AS, complete genome.
 ACCESSION AY427439
 VERSION AY427439.1
 KEYWORDS .
 SOURCE SARS coronavirus AS
 ORGANISM SARS coronavirus AS
 Viruses; Riboviria; Nidovirales; Coronidovirineae; Coronaviridae;
 Orthocoronavirinae; Betacoronavirus; Sarbecovirus.
 REFERENCE 1 (bases 1 to 29711)
 AUTHORS Balotta,C., Corvasce,S., Violin,M., Galli,M., Moroni,M.,
 Vigevani,G.M., Ruan,Y.J. and Salemi,M.
 TITLE Direct Submission
 JOURNAL Submitted (02-OCT-2003) Institute of Infectious and Tropical
 Diseases, 'L.Sacco' Hospital, University of Milan, Via G.B. Grassi,
 74, Milan 20157, Italy

 LOCUS MN988668 29881 bp RNA linear VRL 28-JAN-2020
 DEFINITION Wuhan seafood market pneumonia virus isolate 2019-nCoV WHU01,
 complete genome.
 ACCESSION MN988668
 VERSION MN988668.1
 KEYWORDS .
 SOURCE Wuhan seafood market pneumonia virus
 ORGANISM Wuhan seafood market pneumonia virus
 Viruses; Riboviria; Nidovirales; Coronidovirineae; Coronaviridae;
 Orthocoronavirinae; Betacoronavirus; unclassified Betacoronavirus.
 REFERENCE 1 (bases 1 to 29881)
 AUTHORS Chen,L., Liu,W., Zhang,Q., Xu,K., Ye,G., Wu,W., Sun,Z., Liu,F.,
 Wu,K., Mei,Y., Zhang,W., Chen,Y., Li,Y., Shi,M., Lan,K. and Liu,Y.
 TITLE RNA based mNGS approach identifies a novel human coronavirus from
 two individual pneumonia cases in 2019 Wuhan outbreak
 JOURNAL Emerg Microbes Infect (2019) In press
 REFERENCE 2 (bases 1 to 29881)
 AUTHORS Chen,L., Liu,W., Zhang,Q., Xu,K., Ye,G., Wu,W., Sun,Z., Liu,F.,
 Wu,K., Mei,Y., Zhang,W., Chen,Y., Li,Y., Shi,M., Lan,K. and Liu,Y.
 TITLE Direct Submission
 JOURNAL Submitted (23-JAN-2020) State Key Laboratory of Virology, Wuhan
 University, Bayi Road, Wuchang District, Wuhan, Hubei 430072, P.R.
 China

