

Supplementary materials for the article:

Elssaig E.H. et al. Omicron SARS-CoV-2 Variants in an *in silico* Genomic Comparison Study with the Original Wuhan Strain and WHO-Recognized Variants of Concern.

Pol J Microbiol. 2022, Vol. 71, No 4, 577–587

ORF a/b gene:

Score	Expect	Method	Identities	Positives	Gaps	Frame
8672 bits(22502)	0.0	Compositional matrix adjust.	4391/4401(99%)	4394/4401(99%)	4/4401(0%)	+2
Query 1		MESLVPGFNEKTHVQLSLPVLQVRDVLVRGFGDSVVEEVLSEARQHLKDGTCGLVEVEKGV				60
Sbjct 212					391
Query 61		LPQLEQPYVFIKRSDARTAPHGHVMVELVAELEGIQYGRSGETLGVLVPHVGEIPVAYRK				120
Sbjct 392					571
Query 121		VLLRKNGNKGAGGHSYGADLKSFDLGDELGTDPYEDFQENWN TKHSSGVTRELMRELNGG				180
Sbjct 572					751
Query 181		AYTRYVDNNFCGPDGYPLECIKDLLARAGKASCTLSEQLDFIDTKRGVYCCREHEHEIAW				240
Sbjct 752					931
Query 241		YTERSEKSYELQTPFEIKLAKKFDTFN GECPNFVFP LNSIIKTIQPRVEKKKLDGFMGRI				300
Sbjct 932					1111
Query 301		RSVYPVASPNECNQMCLSTLMKCDHCGETSWQTGDFVKATCEFCGTENLTKEGATTCGYL				360
Sbjct 1112					1291
Query 361		PQNAVVKIYCPACHNSEVGP EHS LAEYHNESGLK TILRKGGRTIAFGGCVFSYVGCHNKC				420
Sbjct 1292					1471
Query 421		AYWVPRASANIGCNHTGVV GEGSEGLNDNLLEILQKEKVNINIVGDFKLN E EIAIILASF				480
Sbjct 1472					1651
Query 481		SASTSAFVETVKGLDYKAFKQIVESCGNFKVTKGKAKKGAWNIGE QKSILSPLYAFASEA				540
Sbjct 1652					1831

Query	541	ARVVRSIFSRTLETAQNSVRVLQKAAITILDGISQYSLRLIDAMMFTSDLATNNLVVMAY	600
Sbjct	1832	
2011			
Query	601	ITGGVVQLTSQWLTNIFGTVYEKLPVLDWLEEKFKEGVEFLRDGWEIVKFISTCACEIV	660
Sbjct	2012	
2191			
Query	661	GGQIVTCAKEIKESVQTFFKLVNKFLALCADSIIIGGAKLKALNLGETFVTHSKGLYRKC	720
Sbjct	2192	
2371			
Query	721	VKSREETGLLMPLKAPKEIIFlegetlpptevlteevlktGDLQPLEQPTSEAVEAPLVG	780
Sbjct	2372	
2551			
Query	781	TPVCINGLMLEIKDTEKYCALAPNMMVTNNTFTLKGKAPTKVTFGDDTVIEVQGYKSVN	840
Sbjct	2552	
2731			
Query	841	ITFELDERIDKVLNEKCSAYTVELGTEVNEFACVVADAVIKTLQPVSELLTPLGIDLDEW	900
Sbjct	2732 R	
2911			
Query	901	SMATYYLFDESGEFKLASHMYCSFYppdedeeegdcceeeefepSTQYEGTEDDYQGKPL	960
Sbjct	2912	
3091			
Query	961	EFGATSAALqpeeeqeedwldddsqqTVGQQDGSEDNqtttiqtiveVQPQLEMELTPVV	
1020			
Sbjct	3092	
3271			
Query	1021	QTIEVNSFSGYLKLTDNVYIKNADIVEEAKVKPTVVVNAANVYLKHGGGVAGALNKATN	
1080			
Sbjct	3272	
3451			
Query	1081	NAMQVESDDYIATNGPLKVGGSVLSGHNLAHCLHVVGPVNVKGEDIQLLKSAYENFNQ	
1140			

Sbjct 3452
3631

Query 1141 HEVLLAPLLSAGIFGADPIHSLRVCVDTVRTNVYLAVFDKNLYDKLVSSFLEMKSEKQVE
1200

Sbjct 3632
3811

Query 1201 QKIAEIPKEEVKPFITESKPSVEQRKQDDKKIKACVeevtttleetkfltenlllyIDIN
1260

Sbjct 3812
3991

Query 1261 GNLHPDSATLVSDIDITFLKKDAPYIVGDVVQEGVLTAVVIPTKKAGGTTEMLAKALRKV
1320

Sbjct 3992
4171

Query 1321 PTDNYITTYPGQGLNGYTVEEAKTVLKKCKSAFYILPSIISNEKQEILGTVSWNLREMLA
1380

Sbjct 4172
4351

Query 1381 HAEETRKLMPVCVETKAIVSTIQRKYKGIKIQEGVVDYGARFYFYTSKTTVASLINTLND
1440

Sbjct 4352
4531

Query 1441 LNETLVTMPLGYVTHGLNLEEAARYMRSCLKVPATVSVSSPDAVTAYNGYLTSSSKTPEEH
1500

Sbjct 4532
4711

Query 1501 FIETISLAGSYKDWSYSGQSTQLGIEFLKRGDKSVYYSNPPTTFHLDGEVITFDNLKTL
1560

Sbjct 4712
4891

Query 1561 SLREVRTIKVF'TTVDNINLHTQVVDMSMTYGQQFGPTYLDGADVTKIKPHNSHEGKTFYV
1620

Sbjct 4892
5071

Query	1621	LPNDDTLRVEAFEYHYHTDPSFLGRYMSALNHTKKWKYPQVNGLTSLIKWADNNCYLATAL
1680		
Sbjct	5072
5251		
Query	1681	LTLQQIELKFNPPALQDAYRARAGEAANFCALILAYCNKTVGELGDVRETMSYLFQHAN
1740		
Sbjct	5252
5431		
Query	1741	LDSCRVLNVVCKTCGQQQTTLKGVEAVMYMGTLSYEQFKKGVQIPCTCGKQATKYLVOQ
1800		
Sbjct	5432
5611		
Query	1801	ESPFVMSAPPAQYELKHGTFTCASEYTGNYQCGHYKHITSKETLYCIDGALLTKSSEYK
1860		
Sbjct	5612
5791		
Query	1861	GPITDVFYKENSYTTTTIKPVTYKLDGVVCTEIDPKLDNYYKKDNSYFTEQPIDLVPNQPY
1920		
Sbjct	5792
5971		
Query	1921	PNASFDNFKFVCDNIKFADDLNQLTGYKKPASRELKVTFPPDLNGDVVAIDYKHYTPSFK
1980		
Sbjct	5972
6151		
Query	1981	KGAKLLHKPIVWHVNNATNKATYKPNTWCIRCLWSTKPVETSNSFDVLKSEDAQGMDNLA
2040		
Sbjct	6152
6331		
Query	2041	CEDLKPVSEEVVENPTIQKDVLECNVKTTEVVGDIILKPANNSLKITEEVGHTDLMAAYV
2100		
Sbjct	6332 -I
6508		

Query 2101 DNSSLTIKKPNELSRVLGLKTLATHGLAAVNSVPWDTIANYAKPFLNKVVSTTTNIVTRC
2160

Sbjct 6509
6688

Query 2161 LNRVCTNYMPYfftl111qlctftRSTNSRIKASMPPTTIKNTVKSVMGKFCLEASFNYLKS
2220

Sbjct 6689
6868

Query 2221 PNFSKLINIIIWFLLLSVCLGSLIYSTAALGVLMNSNLGMPSTYCTGYREGYLNSTNVTIAT
2280

Sbjct 6869
7048

Query 2281 YCTGSIPCSVCLSGLDSDTYPSLETIQITISSFKWDLTAFGLVAEWFLAYILFTRFFYV
2340

Sbjct 7049
7228

Query 2341 LGLAAIMQLFFSYFAVHFISNSWLMWLIINLVQMAPISAMVRMYIFFASFYYVWKSYPVHV
2400

Sbjct 7229
7408

Query 2401 VDGCNSSTCMMCYKRNRRATRVECTTIVNGVRRSFYVYANGGKGFCKLHNWNCVNCDFCA
2460

Sbjct 7409
7588

Query 2461 GSTFISDEVARDLSLQFKRPINPTDQSSYIVDSVTVKNGSIHLYFDKAGQKTYERHSLSH
2520

Sbjct 7589
7768

Query 2521 FVNLDNLRANNTKGS L P I N V I V F D G k s k c e e s s a k s a s V Y Y S Q L M C Q P I L L L D Q A L V S D V
2580

Sbjct 7769
7948

Query 2581 GDSAEVAVKMF DAY V N T F S S T F N V P M E K L K T L V A T A E A E L A K N V S L D N V L S T F I S A A R Q G
2640

Sbjct 7949
8128

Query 2641 FVDSDVETKDVVECLKLSHQSDIEVTGDSCNNYMLTYNKVENMTPRDLGACIDCSARHIN
2700

Sbjct 8129
8308

Query 2701 AQVAKSHNIALIWNVKDFMSLSEQLRKQIRSAAKKNNLPFKLTCATTRQVVNVVTTKIAL
2760

Sbjct 8309 **T**
8488

Query 2761 KGGKIVNNWLKQLIKVTLVFLFVAAlFYLITPVHVMSKHTDFSSEIIGYKAIDGGVTRDI
2820

Sbjct 8489
8668

Query 2821 ASTDTCFANKHADFDTWFSQRGGSYTNDKACPLIAAVITREVGfVVPGLPGTILRTTNGD
2880

Sbjct 8669
8848

Query 2881 FLHFLPRVFSavgNICYTPSKLIEYTDfATSACVLAAECTIFKDASGKVPYCYDTNVLE
2940

Sbjct 8849
9028

Query 2941 GSVAYESLRPDTRYVLMdGSI IQfPNTYLEGSVRVVTTFDSEYCRHGTCERSEAGVCVST
3000

Sbjct 9029
9208

Query 3001 SGRWVLNNDYyRSLPGVFCGVDAVNLLTNMfTPLIQPIGALDisasivaggivaiVVtCL
3060

Sbjct 9209
9388

Query 3061 AYYfMRFRRAFGEYSHVVAfNTLLFLMSfTVLCLTPVYSfFLPGVYSVIYLYLTfYLTNDV
3120

Sbjct 9389
9568

Query 3121 SFLAHIQWMVMFTPLVPFWITIAIYIICISTKHFYWFFSNYLKRRVVFNGVSFSTFEEAAL
3180

Sbjct 9569
9748

Query 3181 CTFLLNKEMYLKLRSDVLLPLTQYNRYLALYNKYKYFSGAMDTTSYREAACCHLAKALND
3240

Sbjct 9749
9928

Query 3241 FSNSGSDVLYQPPQTSITSAVLQSGFRKMAFPSGKVEGCMVQVTCGTTTLNGLWLDDVVY
3300

Sbjct 9929 **I**
10108

Query 3301 CPRHVICTSEDMLNPNYEDLLIRKSNHNFLVQAGNVQLRVIGHSMQNCVLKLVDTANPK
3360

Sbjct 10109
10288

Query 3361 TPKYKFVRIQPGQTFSVLACYNGSPSGVYQCAMRPNFTIKGSFLNGSCGSVGFNIDYDCV
3420

Sbjct 10289 **H**
10468

Query 3421 SFCYMHMELPTGVHAGTDLEGNFYGPVDRQTAQAAGTDTTITVNVLAWLYAAVINGDR
3480

Sbjct 10469
10648

Query 3481 WFLNRFTTTLNDFNLVAMKYNYEPLTQDHVDILGPLSAQTGIAVLDMCASLKELLQNGMN
3540

Sbjct 10649
10828

Query 3541 GRTILGSALLEDEFTPFDDVVRQCSGVTFQSAVKRTIKGTHHWllltiltsllvlvqstqW
3600

Sbjct 10829
11008

Query 3601 SLFFFLYENAF L P F A M G I I A M S A F A M M F V K H K H A F L C L F L L P S L A T V A Y F N M V Y M P A S W V
3660

Sbjct 11009
11188

Query 3661 M R I M T W L D M V D T S L S G F K L K D C V M Y A S A V V L L I L M T A R T V Y D D G A R R V W T L M N V L T L V Y K
3720

Sbjct 11189 ---
11359

Query 3721 V Y Y G N A L D Q A I S M W A L I I S V T S N Y S G V V T T V M F L A R G I V F M C V E Y C P I F F I T G N T L Q C I M
3780

Sbjct 11360 **V**
11539

Query 3781 L V Y C F L G Y F C T C Y F G L F C L L N R Y F R L T L G V Y D Y L V S T Q E F R Y M N S Q G L L P P K N S I D A F K L
3840

Sbjct 11540
11719

Query 3841 N I K L L G V G G K P C I K V A T V Q S K M S D V K C T s v l l s v l q q l r v e s s s K L W A Q C V Q L H N D I L L
3900

Sbjct 11720
11899

Query 3901 A K D T T E A F E K M v s l l s v l l s M Q G A V D I N K L C E E M L D N R A T L Q A I A S E F S S L P S Y A A F A T A
3960

Sbjct 11900
12079

Query 3961 Q E A Y E Q A V A N G D s e v v l k k l k k s l n v a k s E F D R D A A M Q R K L E K M A D Q A M T Q M Y K Q A R S E D
4020

Sbjct 12080
12259

Query 4021 K R A K V T S A M Q T M L F T M L R K l d n d a l n n i i n n a R D G C V P L N I I P L T T A A K L M V V I P D Y N T Y
4080

Sbjct 12260
12439

Query 4081 K N T C D G T T F T Y A S A L W E I Q Q V V D A D S K I V Q L S E I S M D N S P N L A W P L I V T A L R A N S A V K L Q
4140

Sbjct 12440
12619

Query 4141 NNELSPVALRQMSCAAGTTQTACTDDNALAYYNTTKGGRFVLALLSDLQDLKWARFPKSD
4200

Sbjct 12620
12799

Query 4201 GTGTIYTELEPPCRFVTDTPKGPVKYLYFIKGLNNLNRMVLSLAATVRLQAGNATEV
4260

Sbjct 12800
12979

Query 4261 PANSTVLSFCAFAVDAAKAYKDYLASGGQPITNCVKMLCTHTGTGQAITVTPEANMDQES
4320

Sbjct 12980
13159

Query 4321 FGGASCCLYCRCHIDHPNPKGFCDLKGKYVQIPTTCANDPVGFLLKNTVCTVCGMWKGYG
4380

Sbjct 13160
13339

Query 4381 CSCDQLREPMLQSADAQSFLN 4401
Sbjct 13340 13402

Range 2: 13396 to 21486 [Graphics](#) [Next Match](#) [Previous Match](#) [First Match](#)

Alignment statistics for match #2

Score	Expect	Method	Identities	Positives	Gaps	Frame
5665 bits(14697)	0.0	Compositional matrix adjust.	2693/2697(99%)	2694/2697(99%)	0/2697(0%)	+1
Query 4400 LNRVCGVSAARLTPCGTGTSTDVVYRAFDIYNDKVAGFAKFLKTNCCRFQEKDEDDNLID 4459						
Sbjct 13396 FK 13575						
Query 4460 SYFVVKRHTFSNYQHEETIYNLLKDCPAVAKHDFFKFRIDGDMVPHISRQRLTKYTMADL 4519						

Sbjct 13576
13755

Query 4520 VYALRHFDEGNCDTLKEILVTYNCCDDDYFNKKDWYDFVENPDILRVYANLGERVRQALL
4579

Sbjct 13756
13935

Query 4580 KTVQFCDAMRNAGIVGVLTLDNQDLNGNWDYDFGDFIQTPGSGVPPVDSYYSLLMPILTL
4639

Sbjct 13936
14115

Query 4640 TRALTAESHVDTDLTKPYIKWDLKDYDFTEERLKLFDRYFKYWDQTYHPNCVNCLDDRCI
4699

Sbjct 14116
14295

Query 4700 LHCANFNVLFFSTVFPPTSFGPLVRKIFVDGVPFVSTGYHFRELGVVHNQDVNLHSSRLS
4759

Sbjct 14296**L**.....
14475

Query 4760 FKELLVYAADPAMHAASGNLLLDKRTTCFSVAALTNNVAFQTVKPGNFNKDFYDFAVSKG
4819

Sbjct 14476
14655

Query 4820 FFKEGSSVELKHFFFAQDGNAAISDYDYRYNLPTMCDIRQLLFVVEVVDKYFDCYDGGC
4879

Sbjct 14656
14835

Query 4880 INANQVIVNNLDKSAGFPFNKWKARLYYDSMSYEDQDALFAYTKRNVIPTITQMNLKYA
4939

Sbjct 14836
15015

Query 4940 ISAKNRARTVAGVSICSTMTNRQFHQKLLKSIAATRIGATVVIGTSKFYGGWHNMLKTVYS
4999

Sbjct 15016
15195

Query 5000 DVENPHLMGWDYPKCDRAMPNMLRIMASLVLARKHTTCCSLSHRFYRLANECAQVLSEMV
5059

Sbjct 15196
15375

Query 5060 MCGGSLYVKPGGTSSGDATTAYANSVFNICQAVTANVNALLSTDGNKIADKYVRNLQHRL
5119

Sbjct 15376
15555

Query 5120 YECLYRNRDVDTDFVNEFYAYLRKHFSMMILSDDAVVCFNSTYASQGLVASIKNFKSVLY
5179

Sbjct 15556
15735

Query 5180 YQNNVFMSEAKCWTEETDLTKGPHEFCSQHTMLVKQGDDYVYLPYPDPSRILGAGCFVDDI
5239

Sbjct 15736
15915

Query 5240 VKTDGTLMIERFVSLAIDAYPLTKHPNQEYADVFLYLQYIRKLHDELGHMLDMYSVML
5299

Sbjct 15916
16095

Query 5300 TNDNTRSRYWEPEFYEAMYTPHTVLQAVGACVLCNSQTSRLRCGACIRRPFLCCKCCYDHVI
5359

Sbjct 16096
16275

Query 5360 STSHKLVLSVNPYVCNAPGCDVTDVTQLYLGGMSYYCKSHKPPISFPLCANGQVFGLYKN
5419

Sbjct 16276
16455

Query 5420 TCVGSDNVTDFNAIATCDWTNAGDYILANTCTERLKLFAAETLKATEETFKLSYGIATVR
5479

Sbjct 16456
16635

Query 5480 EVLSDRELHLSWEVGKPRPPLNRNYVFTGYRVTKNSKVQIGEYTFEKGDYGDVAVYRGTT
5539

Sbjct 16636
16815

Query 5540 TYKLNVDYFVLTSHVTMPLSAPTLVPQEHYVRITGLYPTLNISDEFSSNVANYQKVGMO
5599

Sbjct 16816
16995

Query 5600 KYSTLQGPPGTGKSHFAIGLALYYP SARIVYTACSHA AVDALCEKALKYLPIDKCSRIIP
5659

Sbjct 16996
17175

Query 5660 ARARVECFDKFKVNSTLEQYVFCTVNALPETTADIVVFDEISMATNYDLSVVNARLRAKH
5719

Sbjct 17176
17355

Query 5720 YVYIGDPAQLPAPRTLLTKGTLEPEYFN SVCRLMKTIGPDMFLGTCRRCPAEIVDTVSAL
5779

Sbjct 17356
17535

Query 5780 VYDNKLKAHKDKSAQC FKM FYKGVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFISPY
5839

Sbjct 17536
17715

Query 5840 NSQNAVASKILGLPTQTVDSSQGSEYDYVIFTQTTE TAHS CNVNRFNVAITRAKVGILCI
5899

Sbjct 17716
17895

Query 5900 MSDRDLYDKLQFTSLEIPRRNVATLQAENV TGLFKDCSKVITGLHPTQAPTHLSVDTKFK
5959

Sbjct 17896
18075

Query 5960 TEGLCVDIPGIPKDMTYRRLISMMGFKMNYQVNGYPNMFITREEAIRHVRAWIGFDVEGC
6019

Sbjct 18076 **V**
18255

Query 6020 HATREAVGTNLPLQLGFSTGVNLVAVPTGYVDTPNNTDFSRVSAKPPPGDQFKHLIPLMY
6079

Sbjct 18256
18435

Query 6080 KGLPWNVVRIKIVQMLSDTLKNLSDRVVFLWAHGFELTSMKYFVKIGPERTCCLCDRRA
6139

Sbjct 18436
18615

Query 6140 TCFSTASDTYACWHHSIGFDYVYNPFMIDVQQWGFTGNLQSNHDLYCQVHGNAHVASCDA
6199

Sbjct 18616
18795

Query 6200 IMTRCLAVHECFVKRVDWTIEYPIIGDELKINAACRQVQHMVKAALLADKFPVLHDIGN
6259

Sbjct 18796
18975

Query 6260 PKAIKCVPOADVEWKFYDAQPCSDKAYKIEELFYASYATHSDKFTDGVCLFWNCNVDRYPA
6319

Sbjct 18976
19155

Query 6320 NSIVCRFDTRVLSNLNLPDGGSLYVKNHAFHTPAFDKSAFVNLKQLPFFYYSDSPCES
6379

Sbjct 19156
19335

Query 6380 HGKQVSDIDYVPLKSATCITRCNLGGAVCRHHANEYRLYLDAYNMMISAGFSLWVYKQF
6439

Sbjct 19336
19515

Query 6440 DTYNLWNTFTRLQSLNVAFNVVNKGHFDGQQGEVPSIINNTVYTKVDGVDVELFENKT
6499

Sbjct 19516
19695

Query 6500 TLPVNVAFELWAKRNIKPVPEVKILNNLGVDIAANTVIWDYKRDAPAHISTIGVCSMTDI
6559

Sbjct 19696
19875

Query 6560 AKKPTETICAPLTVFFDGRVDGQVDLFRNARNGVLI TEGSVKGLQPSVGPQASLNGVTL
6619

Sbjct 19876
20055

Query 6620 IGEAVKTQFNYYKKVDGVVQQLPETYFTQSRNLQEFKPRSQMEIDFLELAMDEFIERYKL
6679

Sbjct 20056
20235

Query 6680 EGYAFEHIVYGDFSHSQLGGLHLLIGLAKRFKESPFLEDFIPMDSTVKNYFITDAQTGS
6739

Sbjct 20236
20415

Query 6740 SKCVCSVIDLLLDFFVEI IKSQDLSVVSQVVKVTIDYTEISFMLWCKDGHVETFYPKLQS
6799

Sbjct 20416
20595

Query 6800 SQAWQPGVAMPNLYKMQRM LLEKCDLQNYGDSATLPKGIMMNVAKYTQLCQYLNTLTLAV
6859

Sbjct 20596
20775

Query 6860 PYNMRVIHFGAGSDKGVAPGTAVLRQWLPTG TLLVDSLNDVSDADSTLIGDCATVHTA
6919

Sbjct 20776
20955

Query 6920 NKWDLIIISDMYDPKTKNVTKENDSKEGFFTYICGFIQQKLALGGSVAIKITEHSWNADLY
6979

Sbjct 20956
21135

Query 6980 KLMGHFAWWTAFVTNVNASSSEAFLLIGCNLYLGKPREQIDGYVMHANYIFWRNTNPIQLSS 7039
 Sbjct 21136
 21315

Query 7040 YSLFDMSKFPLKLRGTAVMSLKEGQINDMILSLLSKGRLIIRENNRVVISDVLVNN 7096
 Sbjct 21316 21486

S gene:

Query 12 SSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVS 71
Sbjct 21530 **V.--** 21703

Query 72 GTNGTKRFDNPVLPFNDGVYFASTEKSNIIRGWIFGTTLDLSDKQSLIVNATNVVIKVC 131
Sbjct 21704 **I** 21883

Query 132 EFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLRE 191
Sbjct 21884 **D---** 22054

Query 192 FVFKNIDGYFKIYSKHTPINLVR---DLPQGFSALEPLVDLPIGINITRFQTLALHRSY 248
Sbjct 22055 **-I . EPE** 22231

Query 249 LTPGDSSSGWTAGAAAYVGYLQPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSFTV 308
 Sbjct 22232 22411

Query 309 EKGIIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNKRKRISNCVADYSVL 368
Sbjct 22412 **D** 22591

Query 369 YNSASFSTFKCYGVSPTKLNLDLCTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDD 428
Sbjct 22592 .. **L.P.F** **N** 22771

Query 429 FTGCVIAWNSNNLDSKVGGNYNLYRLFRKSNLKPFERDISTEIQAGSTPCNGVEGFNC 488
Sbjct 22772 **K . . S** **NK . . . A** 22951

Query 489 YFPLQSYGFQPTNGVGYQPYRVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNGLTG 548
Sbjct 22952 **R . S . R . Y . H** **K** 23131

Query 549 TGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLLEILDITPCSFGGVSVITPGTNTSNQV 608
 Sbjct 23132 23311

Query	609	AVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGA	668
Sbjct	23312 G Y	23491
Query	669	GICASYQTQTNSPRRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILP	728
Sbjct	23492 K.H	23671
Query	729	VSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQEVFAQVKQI	788
Sbjct	23672 K	23851
Query	789	YKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARD	848
Sbjct	23852 Y	24031
Query	849	LICAQKFNGLTVLPPLLTDEMIAQYTSALLAGTITSGWTFGAGAALQIPFAMQMAYRFNG	908
Sbjct	24032 K	24211
Query	909	IGVTQNVLYENQKLIANQFNNSAIGKIQDSLSTASALGKLQDVVNQNAQALNTLVKQLSS	968
Sbjct	24212 H	24391
Query	969	NFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATK	1028
Sbjct	24392	K F	24571
Query	1029	MSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTVYVPAQEKNFTTAPAICHGKAH	1088
Sbjct	24572	24751
Query	1089	FPREGVVFVSNNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSF	1148
Sbjct	24752	24931
Query	1149	KEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQ	1208
Sbjct	24932	25111
Query	1209	YIKWPWYIWLGFIAGLIAIVMVTImlccmtscscslkgccscgscckFDEDDSEPVLKGV	1268
Sbjct	25112	25291
Query	1269	KLHYT 1273	
Sbjct	25292 25306	

ORF3a:

Score	Expect	Method	Identities	Positives	Gaps	Frame
568 bits(1464)	0.0	Compositional matrix adjust.	275/275(100%)	275/275(100%)	0/275(0%)	+1
Query 1		MDLFMRIFTIGTVTLKQGEIKDATPSDFVRATATIPIQASLPFGWLIVGVALLAVFQSAS				60
Sbjct 25318 25497					
Query 61		KIITLKKRWQLALSkgVHFVCNLLLLFVTvySHLLLVAAGLEAPFLYLYALVYFLQSINF				120
Sbjct 25498 25677					
Query 121		VRIIMRLWLCWKCRSKNPLLYDANYFLCWHTNCYDYCIPYNSVTSSIVITSGDGTSPIS				180
Sbjct 25678 25857					
Query 181		EHDYQIGGYTEKWESGVKDCVVLHSYFTSDYYQLYSTQLSTDTGVEHVTFEYFNKIVDEP				240
Sbjct 25858 26037					
Query 241		EEHVQIHTIDGSSGVVNPVMEPIYDEPTTTTSVPL	275			
Sbjct 26038		26142			

E gene:

Score	Expect	Method	Identities	Positives	Gaps	Frame
97.4 bits(241)	1e-28	Compositional matrix adjust.	74/75(99%)	74/75(98%)	0/75(0%)	+1
Query 1		MYSFVSEETGTLIVNSvllflafvvflvtlailtalrlCAYCCNIVNVSLVKPSFYVYS				60
Sbjct 26170	 I				26349
Query 61		RVKNLNSSRVPDLLV	75			
Sbjct 26350		26394			

M gene:

Score	Expect	Method	Identities	Positives	Gaps	Frame
445 bits(1144)	2e-147	Compositional matrix adjust.	219/222(99%)	219/222(98%)	0/222(0%)	+3
Query 1	MADSNGTITVEELKKLLEQWNLVIGFLFLTWICLLQFAYANRNRFLYIIKLI FLWLLWPV				60	
Sbjct 26448	.. G X				26627	
Query 61	TLACFVLAAVYRINWITGGIAIAMACLVGLMWLSYFIASFRLFARTRSMWSEFNPETNILL				120	
Sbjct 26628	.. T				26807	
Query 121	NVPLHGTILTRP LLESELVIGAVILRGHLRIAGHHLGRCDIKDLPKEITVATSRTL SYYK				180	
Sbjct 26808				26987	
Query 181	LGASQRVAGDSGFAAYSRYRIGNYKLNTDHSSSSDNIALLVQ		222			
Sbjct 26988		27113			

ORF6:

Score	Expect	Method	Identities	Positives	Gaps	Frame
122 bits(306)	1e-37	Compositional matrix adjust.	61/61(100%)	61/61(100%)	0/61(0%)	+1
Query 1	MFHLVDFQVTIAEILLIIMRTFKVSIWNLDYIINLI IKNLSKSLTENKYSQLDEEQPMEI				60	
Sbjct 27127				27306	
Query 61	D 61					
Sbjct 27307	. 27309					

ORF7a:

Score	Expect	Method	Identities	Positives	Gaps	Frame
222 bits(565)	2e-71	Compositional matrix adjust.	121/121(100%)	121/121(100%)	0/121(0%)	+1
Query 1	MKiilflalitlatCELYHYQECVRGTTVLLKEPCSSGTYEGNSPFHPLADNKFALTCFS				60	

Sbjct 27319 27498

Query 61 TQFAFACPDGVKHHVYQLRARSVSPKLFIRQEEVQELYSPIFLIVAAIVFITLCFTLKRKT 120

Sbjct 27499 27678

Query 121 E 121

Sbjct 27679 . 27681

ORF7b:

Score	Expect	Method	Identities	Positives	Gaps	Fram
36.2 bits(82)	2e-07	Compositional matrix adjust.	43/43(100%)	43/43(100%)	0/43(0%)	+3
Query 1		MIELSLIDfylycflaflflvlmlifwfSLELQDHNETCHA		43		
Sbjct 27681			27809		

ORF8:

Score	Expect	Method	Identities	Positives	Gaps	Fram
251 bits(642)	8e-82	Compositional matrix adjust.	121/121(100%)	121/121(100%)	0/121(0%)	+3
Query 1		MKFLVFLGIITTVAAAFHQECSLQSQCTQHQPVVDDPCPIHFYSKWYIRVGARKSAPLIEL		60		
Sbjct 27819			27998		
Query 61		CVDEAGSKSPIQYIDIGNYTVSCLPFTINCQEPKLGSLVVRCSFYEDFLEYHDVRVVLDF		120		
Sbjct 27999			28178		
Query 121	I 121					
Sbjct 28179	. 28181					

N gene:

Score	Expect	Method	Identities	Positives	Gaps	Fram
640 bits(1650)	0.0	Compositional matrix adjust.	412/419(98%)	413/419(98%)	3/419(0%)	+2
Query 1		MSDNGPQNQRNAPRITFGGSPDSTGNSQNGERSGARSKQRRPQGLPNNTASWFTALTQHG		60		
Sbjct 28199	 L ---		28369		

Query	61	KEDLKFPRGQGVPIINTNSSPDDQIGYYRRATRRIRGGDGKMKDLSPRWYFYLLGTGPEAG	120
Sbjct	28370	28549
Query	121	LPYGANKDGIWVATEGALNTPKDHIGTRNPANNAAIVLQLPQGTTLPKGFYAEgstrggs	180
Sbjct	28550	28729
Query	181	qassrsssrsrnssrnstpgssrgtspaRMagnnggdaalalldrlnqlESKMSgkgqq	240
Sbjct	28730KR	28909
Query	241	qqgqvtvkSAAEASKKPRQKRTATKAYNVTQAFGRRGPEQTQGNFGDQELIRQGTDYKH	300
Sbjct	28910	29089
Query	301	WPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTYTAAIKLDDKDPNFKDQVILLNKHIDAY	360
Sbjct	29090 G	29269
Query	361	ktfpptepkkdkkkkadetQALPQRQKKQQTVTLLPAADLDDFSKQLQQSMSSADSTQA	419
Sbjct	29270	29446

ORF10:

Query	1	MGYINVFAFPFTIYSLLLCRMNSRNYIAQVDVVNFNLT	38
Sbjct	29474	29587

South Africa Omicron 5 nucleotide blast against Wuhan NC_045512:

Query	55	AGATCTGTTCTCTAAACGAACTTTAAAAATCTGTGTGGCTGTCACTCGGCTGCATGCTTAG	114
Sbjct	1	60
Query	115	TGCACTCACGCAGTATAATTAATAACTAATTACTGTCGTTGACAGGACACGAGTAACTCG	174
Sbjct	61	120
Query	175	TCTATCTTCTGCAGGCTGCTTACGGTTTCGTCCGTGTTGCAGCCGATCATCAGCACATCT	234
Sbjct	121	180
Query	235	AGGTTTCGTCCGGGTGTGACCGAAAGGTAAGATGGAGAGCCTTGTCCCTGGTTTCAACGA	294
Sbjct	181 T	240
Query	295	GAAAACACACGTCCAACCTCAGTTTGCCTGTTTTACAGGTTTCGCGACGTGCTCGTACGTGG	354
Sbjct	241	300
Query	355	CTTTGGGAGACTCCGTGGAGGAGGTCTTATCAGAGGCACGTCAACATCTTAAAGATGGCAC	414
Sbjct	301	360
Query	415	TTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAACTTGAACAGCCCTATGTGTT	474
Sbjct	361	420
Query	475	CATCAAACGTTCCGGATGCTCGAACTGCACCTCATGGTCATGTTATGGTTGAGCTGGTAGC	534
Sbjct	421	480
Query	535	AGAACTCGAAGGCATTCAGTACGGTCGTAGTGGTGAGACACTTGGTGTCCCTTGTCCCTCA	594
Sbjct	481	540
Query	595	TGTGGGCGAAAATACCAGTGGCTTACCGCAAGGTTCTTCTTCGTAAGAACGGTAATAAAGG	654
Sbjct	541	600
Query	655	AGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTTGACTTAGGCGACGAGCTTGG	714
Sbjct	601	660
Query	715	CACTGATCCTTATGAAGATTTTCAAGAAAACCTGGAACACTAAACATAGCAGTGGTGTAC	774
Sbjct	661	720
Query	775	CCGTGAACTCATGCGTGAGCTTAACGGAGGGGCATACACTCGCTATGTCGATAACAACCTT	834
Sbjct	721	780
Query	835	CTGTGGCCCTGATGGCTACCCTCTTGAGTGCATTAAGACCTTCTAGCACGTGCTGGTAA	894
Sbjct	781	840

Query	895	AGCTTCATGCACTTTGTCCGAACAACCTGGACTTTATTGACACTAAGAGGGGTGTATACTG	954
Sbjct	841	900
Query	955	CTGCCGTGAACATGAGCATGAAATTGCTTGGTACACGGAACGTTCTGAAAAGAGCTATGA	1014
Sbjct	901	960
Query	1015	ATTGCAGACACCTTTTGAAATTAAATTGGCAAAGAAATTTGACACCTTCAATGGGGAATG	1074
Sbjct	961	1020
Query	1075	TCCAAATTTTGTATTTCCCTTAAATTCCATAATCAAGACTATTCAACCAAGGGTTGAAAA	1134
Sbjct	1021	1080
Query	1135	GAAAAAGCTTGATGGCTTTATGGGTAGAATTCGATCTGTCTATCCAGTTGCGTCACCAAA	1194
Sbjct	1081	1140
Query	1195	TGAATGCAACCAAATGTGCCTTTCAACTCTCATGAAGTGTGATCATTGTGGTGAAACTTC	1254
Sbjct	1141	1200
Query	1255	ATGGCAGACGGGCGATTTTGTAAAGCCACTTGCGAATTTTGTGGCACTGAGAATTTGAC	1314
Sbjct	1201	1260
Query	1315	TAAAGAAGGTGCCACTACTTGTGGTTACTTACCCCAAATGCTGTTGTTAAAATTTATTG	1374
Sbjct	1261	1320
Query	1375	TCCAGCATGTCACAATTCAGAAGTAGGACCTGAGCATAGTCTTGCCGAATACCATAATGA	1434
Sbjct	1321	1380
Query	1435	ATCTGGCTTGAAAACCATTCTTCGTAAGGGTGGTCGCACTATTGCCTTTGGAGGCTGTGT	1494
Sbjct	1381	1440
Query	1495	GTTCTCTTATGTTGGTTGCCATAACAAGTGTGCCTATTGGGTTCCACGTGCTAGCGCTAA	1554
Sbjct	1441	1500
Query	1555	CATAGGTTGTAACCATACAGGTGTTGTTGGAGAAGGTTCCGAAGGTCTTAATGACAACCT	1614
Sbjct	1501	1560
Query	1615	TCTTGAAATACTCCAAAAAGAGAAAGTCAACATCAATATTGTTGGTACTTTAAACTTAA	1674
Sbjct	1561	1620
Query	1675	TGAAGAGATCGCCATTATTTTGGCATCTTTTTCTGCTTCCACAAGTGCTTTTGTGGAAAC	1734
Sbjct	1621	1680

Query	1735	TGTGAAAGGTTTGGATTATAAAGCATTCAAACAAATTGTTGAATCCTGTGGTAATTTTAA	1794
Sbjct	1681	1740
Query	1795	AGTTACAAAAGGAAAAGCTAAAAAAGGTGCCTGGAATATTGGTGAACAGAAATCAATACT	1854
Sbjct	1741	1800
Query	1855	GAGTCCTCTTTATGCATTTGCATCAGAGGCTGCTCGTGTGTACGATCAATTTTCTCCCG	1914
Sbjct	1801	1860
Query	1915	CACTCTTGAAACTGCTCAAAATTCTGTGCGTGTTTTACAGAAGGCCGCTATAACAATACT	1974
Sbjct	1861	1920
Query	1975	AGATGGAATTTACAGTATTCACTGAGACTCATTGATGCTATGATGTTACATCTGATTT	2034
Sbjct	1921	1980
Query	2035	GGCTACTAACAACTAGTTGTAATGGCCTACATTACAGGTGGTGTGTTTCAGTTGACTTC	2094
Sbjct	1981	2040
Query	2095	GCAGTGGCTAACTAACATCTTTGGCACTGTTTATGAAAACTCAAACCCGTCCTTGATTG	2154
Sbjct	2041	2100
Query	2155	GCTTGAAGAGAAGTTTAAGGAAGGTGTAGAGTTTCTTAGAGACGGTTGGGAAATTGTTAA	2214
Sbjct	2101	2160
Query	2215	ATTTATCTCAACCTGTGCTTGTGAAAATTGTCGGTGGACAAATTGTCACCTGTGCAAAGGA	2274
Sbjct	2161	2220
Query	2275	AATTAAGGAGAGTGTTTCAGACATTCTTTAAGCTTGTAATAAATTTTGGCTTTGTGTGC	2334
Sbjct	2221	2280
Query	2335	TGACTCTATCATTATTGGTGGAGCTAAACTTAAAGCCTTGAATTTAGGTGAAACATTTGT	2394
Sbjct	2281	2340
Query	2395	CACGCACTCAAAGGGATTGTACAGAAAGTGTGTTAAATCCAGAGAAGAACTGGCCTACT	2454
Sbjct	2341	2400
Query	2455	CATGCCTCTAAAAGCCCCAAAAGAAATATCTTCTTAGAGGGAGAAACACTTCCCACAGA	2514
Sbjct	2401	2460
Query	2515	AGTGTTAACAGAGGAAGTTGTCTTGAAAAGTGGTGAATTTACAACCATTAGAACAACCTAC	2574
Sbjct	2461	2520
Query	2575	TAGTGAAGCTGTTGAAGCTCCATTGGTTGGTACACCAGTTTGTATTAACGGGCTTATGTT	2634

Sbjct	2521	2580
Query	2635	GCTCGAAATCAAAGACACAGAAAAGTACTGTGCCCTTGCACCTAATATGATGGTAACAAA	2694
Sbjct	2581	2640
Query	2695	CAATACCTTCACACTCAAAGGCGGTGCACCAACAAAGGTTACTTTTGGTGATGACACTGT	2754
Sbjct	2641	2700
Query	2755	GATAGAAGTGCAAGGTTACAAGAGTGTGAATATCACTTTTGAACCTGATGAAAGGATTGA	2814
Sbjct	2701	2760
Query	2815	TAAAGTACTTAATGAGAAGTGCTCTGCCTATACAGTTGAACTCGGTACAGAAGTAAATGA	2874
Sbjct	2761 G	2820
Query	2875	GTTTCGCCTGTGTTGTGGCAGATGCTGTCATAAAAACTTTGCAACCAGTATCTGAATTACT	2934
Sbjct	2821	2880
Query	2935	TACACCACTGGGCATTGATTTAGATGAGTGGAGTATGGCTACATACTACTTATTTGATGA	2994
Sbjct	2881	2940
Query	2995	GTCTGGTGAGTTTAAATTGGCTTCACATATGTATTGTTCTTTCTACCCTCCAGATGAGGA	3054
Sbjct	2941 T	3000
Query	3055	TGAAGAAGAAGGTGATTGTGAAGAAGAAGAGTTTGAGCCATCAACTCAATATGAGTATGG	3114
Sbjct	3001	3060
Query	3115	TACTGAAGATGATTACCAAGGTAAACCTTTGGAATTTGGTGCCACTTCTGCTGCTCTTCA	3174
Sbjct	3061	3120
Query	3175	ACCTGAAGAAGAGCAAGAAGAAGATTGGTTAGATGATGATAGTCAACAACTGTTGGTCA	3234
Sbjct	3121	3180
Query	3235	ACAAGACGGCAGTGAGGACAATCAGACAACACTACTATTCAAACAATTGTTGAGGTTCAACC	3294
Sbjct	3181	3240
Query	3295	TCAATTAGAGATGGAACCTTACACCAGTTGTTTCAGACTATTGAAGTGAATAGTTTTAGTGG	3354
Sbjct	3241	3300
Query	3355	TTATTTAAAACTTACTGACAATGTATACATTAATAATGCAGACATTGTGGAAGAAGCTAA	3414
Sbjct	3301	3360
Query	3415	AAAGGTAAAACCAACAGTGGTTGTTAATGCAGCCAATGTTTACCTTAAACATGGAGGAGG	3474
Sbjct	3361	3420

Query	3475	TGTTGCAGGAGCCTTAAATAAGGCTACTAACAATGCCATGCAAGTTGAATCTGATGATTA	3534
Sbjct	3421	3480
Query	3535	CATAGCTACTAATGGACCACTTAAAGTGGGTGGTAGTTGTGTTTTAAGCGGACACAATCT	3594
Sbjct	3481	3540
Query	3595	TGCTAAACACTGTCTTCATGTTGTGCGGCCAAATGTTAACAAAGGTGAAGACATTCAACT	3654
Sbjct	3541	3600
Query	3655	TCTTAAGAGTGCTTATGAAAATTTAATCAGCACGAAGTTCTACTTGCACCATTATTATC	3714
Sbjct	3601	3660
Query	3715	AGCTGGTATTTTTGGTGCTGACCCTATACATTCTTTAAGAGTTTGTGTAGATACTGTTTCG	3774
Sbjct	3661	3720
Query	3775	CACAAATGTCTACTTAGCTGTCTTTGATAAAAATCTCTATGACAAACTTGTTTCAAGCTT	3834
Sbjct	3721	3780
Query	3835	TTTGAAAATGAAGAGTGAAAAGCAAGTTGAACAAAAGATCGCTGAGATTCCTAAAGAGGA	3894
Sbjct	3781	3840
Query	3895	AGTTAAGCCATTTATAACTGAAAGTAAACCTTCAGTTGAACAGAGAAAACAAGATGATAA	3954
Sbjct	3841	3900
Query	3955	GAAAATCAAAGCTTGTGTTGAAGAAGTTACAACAACCTCTGGAAGAACTAAGTTCCTCAC	4014
Sbjct	3901	3960
Query	4015	AGAAAACCTTGTTACTTTATATTGACATTAATGGCAATCTTCATCCAGATTCTGCCACTCT	4074
Sbjct	3961	4020
Query	4075	TGTTAGTGACATTGACATCACTTTCTTAAAGAAAGATGCTCCATATATAGTGGGTGATGT	4134
Sbjct	4021	4080
Query	4135	TGTTCAAGAGGGTGTTTTAACTGCTGTGGTTATACCTACTAAAAAGGCTGGTGGCACTAC	4194
Sbjct	4081	4140
Query	4195	TGAAATGCTAGCGAAAGCTTTGAGAAAAGTGCCAACAGACAATTATATAACCACTTACCC	4254
Sbjct	4141	4200
Query	4255	GGGTCAGGGTTTAAATGGTTACACTGTAGAGGAGGCAAAGACAGTGCTTAAAAAGTGTA	4314
Sbjct	4201	4260

Query	4315	AAGTGCCTTTTACATTCTACCATCTATTATCTCTAATGAGAAGCAAGAAATTCTTGGAAC	4374
Sbjct	4261	4320
Query	4375	TGTTTCTTGGAATTTGCGAGAAATGCTTGCACATGCAGAAGAAACACGCAAATTAATGCC	4434
Sbjct	4321	4380
Query	4435	TGTCTGTGTGGAAACTAAAGCCATAGTTTCAACTATACAGCGTAAATATAAGGGTATTAA	4494
Sbjct	4381	4440
Query	4495	AATACAAGAGGGTGTGGTTGATTATGGTGCTAGATTTTACTTTTACACCAGTAAAACAAC	4554
Sbjct	4441	4500
Query	4555	TGTAGCGTCACTTATCAACACACTTAACGATCTAAATGAAACTCTTGTTACAATGCCACT	4614
Sbjct	4501	4560
Query	4615	TGGCTATGTAACACATGGCTTAAATTTGGAAGAAGCTGCTCGGTATATGAGATCTCTCAA	4674
Sbjct	4561	4620
Query	4675	AGTGCCAGCTACAGTTTCTGTTTCTTCACCTGATGCTGTTACAGCGTATAATGGTTATCT	4734
Sbjct	4621	4680
Query	4735	TACTTCTTCTTCTAAAACACCTGAAGAACATTTTATTGAAACCATCTCACTTGCTGGTTC	4794
Sbjct	4681	4740
Query	4795	CTATAAAGATTGGTCCTATTCTGGACAATCTACACAACCTAGGTATAGAATTTCTTAAGAG	4854
Sbjct	4741	4800
Query	4855	AGGTGATAAAAAGTGTATATTACACTAGTAATCCTACCACATTCCACCTAGATGGTGAAGT	4914
Sbjct	4801	4860
Query	4915	TATCACCTTTGACAATCTTAAGACACTTCTTTCTTTGAGAGAAGTGAGGACTATTAAGGT	4974
Sbjct	4861	4920
Query	4975	GTTTACAACAGTAGACAACATTAACCTCCACACGCAAGTTGTGGACATGTCAATGACATA	5034
Sbjct	4921	4980
Query	5035	TGGACAACAGTTTGGTCCAACCTTATTTGGATGGAGCTGATGTTACTAAAATAAAACCTCA	5094
Sbjct	4981	5040
Query	5095	TAATTCACATGAAGGTAACAATTTTATGTTTTACCTAATGATGACACTCTACGTGTTGA	5154
Sbjct	5041	5100
Query	5155	GGCTTTTGAGTACTACCACACAACCTGATCCTAGTTTTCTGGGTAGGTACATGTCAGCATT	5214

Sbjct	5101	5160
Query	5215	AAATCACACTAAAAAGTGGAATACCCACAAGTTAATGGTTTAACTTCTATTAAATGGGC	5274
Sbjct	5161	5220
Query	5275	AGATAACAACCTGTTATCTTGCCACTGCATTGTTAACACTCCAACAAATAGAGTTGAAGTT	5334
Sbjct	5221	5280
Query	5335	TAATCCACCTGCTCTACAAGATGCTTATTACAGAGCAAGGGCTGGTGAAGCTGCTAACTT	5394
Sbjct	5281 G	5340
Query	5395	TTGTGCACTTATCTTAGCCTACTGTAATAAGACAGTAGGTGAGTTAGGTGATGTTAGAGA	5454
Sbjct	5341	5400
Query	5455	AACAATGAGTTACTTGTTC AACATGCCAATTTAGATTCTTGCAAAAGAGTCTTGAACGT	5514
Sbjct	5401	5460
Query	5515	GGTGTGTAAAACCTTGTGGACAACAGCAGACAACCCTTAAGGGTGTAGAAGCTGTTATGTA	5574
Sbjct	5461	5520
Query	5575	CATGGGCACACTTTCTTATGAACAATTTAAGAAAGGTGTTTCAGATACCTTGTACGTGTGG	5634
Sbjct	5521	5580
Query	5635	TAAACAAGCTACAAAATATCTAGTACAACAGGAGTCACCTTTTGTATGATGTCAGCACC	5694
Sbjct	5581	5640
Query	5695	ACCTGCTCAGTATGAACTTAAGCATGGTACATTTACTTGTGCTAGTGAGTACACTGGTAA	5754
Sbjct	5641	5700
Query	5755	TTACCAGTGTGGTCACTATAAACATATAACTTCTAAAGAACTTTGTATTGCATAGACGG	5814
Sbjct	5701	5760
Query	5815	TGCTTTACTTACAAAGTCCTCAGAATACAAAGGTCCTATTACGGATGTTTTCTACAAAGA	5874
Sbjct	5761	5820
Query	5875	AAACAGTTACACAACAACCATAAAAACCAGTTACTTATAAATTGGATGGTGTGTTTGTAC	5934
Sbjct	5821	5880
Query	5935	AGAAATTGACCCTAAGTTGGACAATTATTATAAGAAAGACAATCTTATTTACAGAGCA	5994
Sbjct	5881	5940
Query	5995	ACCAATTGATCTTGTACCAAACCAACCATATCCAAACGCAAGCTTCGATAATTTAAGTT	6054
Sbjct	5941	6000

Query	6055	TGTATGTGATAATATCAAATTTGCTGATGATTTAAACCAGTTAACTGGTTATAAGAAACC	6114
Sbjct	6001	6060
Query	6115	TGCTTCAAGAGAGCTTAAAGTTACATTTTCCCTGACTTAAATGGTGATGTGGTGGCTAT	6174
Sbjct	6061	6120
Query	6175	TGATTATAAACACTACACACCCTCTTTTAAGAAAGGAGCTAAATTGTTACATAAACCTAT	6234
Sbjct	6121	6180
Query	6235	TGTTTGGCATGTTAACAATGCAACTAATAAAGCCACGTATAAACCAAATACCTGGTGTAT	6294
Sbjct	6181	6240
Query	6295	ACGTTGTCTTTGGAGCACAAAACCAGTTGAAACATCAAATTCGTTTGATGTACTGAAGTC	6354
Sbjct	6241	6300
Query	6355	AGAGGACGCGCAGGGAATGGATAATCTTGCCTGCGAAGATCTAAAACCAGTCTCTGAAGA	6414
Sbjct	6301	6360
Query	6415	AGTAGTGAAAAATCCTACCATACAGAAAGACGTTCTTGAGTGTAATGTGAAAACCTACCGA	6474
Sbjct	6361	6420
Query	6475	AGTTGTAGGAGACATTATACTTAAACCAGCAAATAATAGTTTAAAAATTACAGAAGAGGT	6534
Sbjct	6421 ---	6477
Query	6535	TGGCCACACAGATCTAATGGCTGCTTATGTAGACAATTCTAGTCTTACTATTAAGAAACC	6594
Sbjct	6478	6537
Query	6595	TAATGAATTATCTAGAGTATTAGGTTTGAAAACCCTTGCTACTCATGGTTTAGCTGCTGT	6654
Sbjct	6538	6597
Query	6655	TAATAGTGTCCCTTGGGATACTATAGCTAATTATGCTAAGCCTTTTCTTAACAAAGTTGT	6714
Sbjct	6598	6657
Query	6715	TAGTACAACACTAACATAGTTACACGGTGTTTAAACCGTGTTTGTACTAATTATATGCC	6774
Sbjct	6658	6717
Query	6775	TTATTTCTTTACTTTATTGCTACAATTGTGTACTTTTACTAGAAGTACAAATTCTAGAAT	6834
Sbjct	6718	6777
Query	6835	TAAAGCATCTATGCCGACTACTATAGCAAAGAATACTGTAAAGAGTGTCGGTAAATTTTG	6894
Sbjct	6778	6837

Query	6895	TCTAGAGGCTTCATTTAATTATTTGAAGTCACCTAATTTTTCTAAACTGATAAATATTAT	6954
Sbjct	6838	6897
Query	6955	AATTTGGTTTTTACTATTAAGTGTTCCTAGGTTCTTTAATCTACTCAACCGCTGCTTT	7014
Sbjct	6898	6957
Query	7015	AGGTGTTTTAATGTCTAATTTAGGCATGCCTTCTTACTGTACTGGTTACAGAGAAGGCTA	7074
Sbjct	6958	7017
Query	7075	TTTGAACCTACTAATGTCACTATTGCAACCTACTGTACTGGTTCTATACCTTGTAGTGT	7134
Sbjct	7018	7077
Query	7135	TTGTCTTAGTGGTTTAGATTCTTTAGACACCTATCCTTCTTTAGAACTATACAAATTAC	7194
Sbjct	7078	7137
Query	7195	CATTTTCATCTTTTAAATGGGATTTAACTGCTTTTGGCTTAGTTGCAGAGTGGTTTTTGGC	7254
Sbjct	7138	7197
Query	7255	ATATATTCTTTTCACTAGGTTTTTCTATGTACTTGGATTGGCTGCAATCATGCAATTGTT	7314
Sbjct	7198	7257
Query	7315	TTTCAGCTATTTTGCAGTACATTTTATTAGTAATTCTTGGCTTATGTGGTTAATAATTAA	7374
Sbjct	7258	7317
Query	7375	TCTTGTACAAAATGGCCCCGATTTTCAGCTATGGTTAGAATGTACATCTTCTTTGCATCATT	7434
Sbjct	7318	7377
Query	7435	TTATTATGTATGGAAAAGTTATGTGCATGTTGTAGACGGTTGTAATTCATCAACTTGTAT	7494
Sbjct	7378	7437
Query	7495	GATGTGTTACAAACGTAATAGAGCAACAAGAGTCGAATGTACAACCTATTGTTAATGGTGT	7554
Sbjct	7438	7497
Query	7555	TAGAAGGTCCTTTTATGTCTATGCTAATGGAGGTAAAGGCTTTTGCAAACCTACACAATTG	7614
Sbjct	7498	7557
Query	7615	GAATTGTGTTAATTGTGATACATTCTGTGCTGGTAGTACATTTATTAGTGATGAAGTTGC	7674
Sbjct	7558	7617
Query	7675	GAGAGACTTGTCCTACTACAGTTTTAAAAGACCAATAAATCCTACTGACCAGTCTTCTTACAT	7734
Sbjct	7618	7677
Query	7735	CGTTGATAGTGTACAGTGAAGAATGGTTCCATCCATCTTTACTTTGATAAAGCTGGTCA	7794

Sbjct	7678	7737
Query	7795	AAAGACTTATGAAAGACATTCTCTCTCATTGTTAACTTAGACAACCTGAGAGCTAA	7854
Sbjct	7738	7797
Query	7855	TAACACTAAAGGTTTCATTGCCTATTAATGTTATAGTTTTTGGATGGTAAATCAAATGTGA	7914
Sbjct	7798	7857
Query	7915	AGAATCATCTGCAAAATCAGCGTCTGTTACTACAGTCAGCTTATGTGTCAACCTATACT	7974
Sbjct	7858	7917
Query	7975	GTTACTAGATCAGGCATTAGTGTCTGATGTTGGTGATAGTGC GGAAGTTGCAGTTAAAAT	8034
Sbjct	7918	7977
Query	8035	GTTTGATGCTTACGTTAATACGTTTTTCATCAACTTTTAACGTACCAATGGAAAACTCAA	8094
Sbjct	7978	8037
Query	8095	AACACTAGTTGCAACTGCAGAAGCTGAACTTGCAAAGAATGTGTCCTTAGACAATGTCTT	8154
Sbjct	8038	8097
Query	8155	ATCTACTTTTATTTTCAGCAGCTCGGCAAGGGTTTGTGATTTCAGATGTAGAACTAAAGA	8214
Sbjct	8098	8157
Query	8215	TGTTGTTGAATGTCTTAAATTGTCACATCAATCTGACATAGAAGTTACTGGCGATAGTTG	8274
Sbjct	8158	8217
Query	8275	TAATAACTATATGCTCACCTATAACAAAAGTTGAAAACATGACACCCCGTGACCTTGGTGC	8334
Sbjct	8218	8277
Query	8335	TTGTATTGACTGTAGTGCGGTCATATTAATGCGCAGGTAGCAAAAAGTCACAACATTGC	8394
Sbjct	8278 A.	8337
Query	8395	TTTGATATGGAACGTTAAAGATTTTCATGTCATTGTCTGAACAACCTACGAAAACAAATACG	8454
Sbjct	8338	8397
Query	8455	TAGTGCTGCTAAAAAGAATAACTTACCTTTTAAGTTGACATGTGCAACTACTAGACAAGT	8514
Sbjct	8398	8457
Query	8515	TGTTAATGTTGTAACAACAAAGATAGCACTTAAGGGTGGTAAAATTGTTAATAATTGGTT	8574
Sbjct	8458	8517
Query	8575	GAAGCAGTTAATTAAAGTTACACTTGTGTTCCTTTTTGGTTGCTGCTATTTTCTATTTAAT	8634
Sbjct	8518	8577

Query	24109	CATTTGTGCACAAAAGTTTAAACGGCCTTACTGTTTTGCCACCTTGTCTCACAGATGAAAT	24168
Sbjct	24034 A	24093
Query	24169	GATTGCTCAATACACTTCTGCACTGTTAGCGGGTACAATCACTTCTGGTTGGACCTTTGG	24228
Sbjct	24094	24153
Query	24229	TGCAGGTGCTGCATTACAAATACCATTTGCTATGCAAATGGCTTATAGGTTTAATGGTAT	24288
Sbjct	24154	24213
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Sbjct	24214	24273
Query	24349	TGCTATTGGCAA AATTC AAGACTCACTTCTTCCACAGCAAGTGCAC TTGGAAA CT TCA	24408
Sbjct	24274	24333
Query	24409	AGATGTGGTCAACCAA AATGCACAAGCTTTAAACACGCTTGTTAAACA ACTTAGCTCCAA	24468
Sbjct	24334 T	24393
Query	24469	TTTTGGTGCAATTTCAAGTGTTTTAAATGATATCCTTTCACGTCTTGACAAAGTTGAGGC	24528
Sbjct	24394	A T	24453
Query	24529	TGAAGTGCAA AATGATAGGTTGATCACAGGCAGACTTCAAAGTTTGCAGACATATGTGAC	24588
Sbjct	24454	24513
Query	24589	TCAACAATTAATTAGAGCTGCAGAAATCAGAGCTTCTGCTAATCTTGCTGCTACTAAAAT	24648
Sbjct	24514	24573
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Sbjct	24574	24633
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Sbjct	24634	24693
Query	24769	TGCACAAGAAAAGAACTTCACA ACTGCTCCTGCCATTTGTCATGATGGAAAAGCACACTT	24828
Sbjct	24694	24753
Query	24829	TCCTCGTGAAGGTGTCTTTGTTTCAAATGGCACACACTGGTTTGTAACACAAAGGAATTT	24888
Sbjct	24754	24813
Query	24889	TTATGAACCACAAATCATTACTACAGACAACACATTTGTGTCTGGTAACTGTGATGTTGT	24948
Sbjct	24814	24873

Query	24949	AATAGGAATTGTCAACAACACAGTTTATGATCCTTTGCAACCTGAATTAGACTCATTCAA	25008
Sbjct	24874 T	24933
Query	25009	GGAGGAGTTAGATAAATATTTTAAGAATCATAACATCACCAGATGTTGATTTAGGTGACAT	25068
Sbjct	24934	24993
Query	25069	CTCTGGCATTAAATGCTTCAGTTGTAAACATTCAAAAAGAAATTGACCGCCTCAATGAGGT	25128
Sbjct	24994	25053
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Sbjct	25054	25113
Query	25189	TATAAAATGGCCATGGTACATTTGGCTAGGTTTTATAGCTGGCTTGATTGCCATAGTAAT	25248
Sbjct	25114	25173
Query	25249	GGTGACAATTATGCTTTGCTGTATGACCAGTTGCTGTAGTTGTCTCAAGGGCTGTTGTTC	25308
Sbjct	25174	25233
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Sbjct	25234	25293
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Sbjct	25294	25353
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Sbjct	25474 T	25533
Query	25609	CTCTCCAAGGGTGTTCACTTTGTTTGCAACTTGCTGTTGTTGTTGTAAACAGTTTACTCA	25668
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Sbjct	26194	.T	26253
Query	26329	GTTACACTAGCCATCCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAAC	26388
Sbjct	26254	26313
Query	26389	GTGAGTCTTGTAACCTTCTTTTTACGTTTACTCTCGTGTTAAAAATCTGAATTCTTCT	26448
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Sbjct	26494 N	26553
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Query	26689	TGTTATGGCCAGTAACTTTAGCTTGTTTTGTGCTTGCTGCTGTTTACAGAATAAATTGGA	26748
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Sbjct	27154 C	27213
Query	27289	GATTACATCATAAACCTCATAATTAATAATTTATCTAAGTCACTAACTGAGAATAAATAT	27348
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Query	27409	TTCTTGGCACTGATAACACTCGCTACTTGTGAGCTTTATCACTACCAAGAGTGTGTTAGA	27468
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Query	28309	ACCCCGCATTACGTTTGGTGGACCCTCAGATTCAACTGGCAGTAACCAGAATGGAGAACG	28368
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Query	28369	CAGTGGGGCGCGATCAAACAACGTCGGCCCCAAGGTTTACCCAATAATACTGCGTCTTG	28428

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Sbjct	28765AAC	28824
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Sbjct	29065	29124
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Sbjct	29245	29304
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Sbjct	29305	29364
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Sbjct	29365	29424
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Sbjct	29425	29484
Query	29569	AAACGTTTTTCGCTTTTCCGTTTACGATATATAGTCTACTCTTGTGCAGAATGAATTCTCG	29628
Sbjct	29485	29544
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Sbjct	29545	29604
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Sbjct	29665	29724
Query	29809	TGTAATAATTAATTTTAGTAGTGCTATC	29835
Sbjct	29725	29751