In [5]:
```
%run Imports.ipynb
```

Introduction

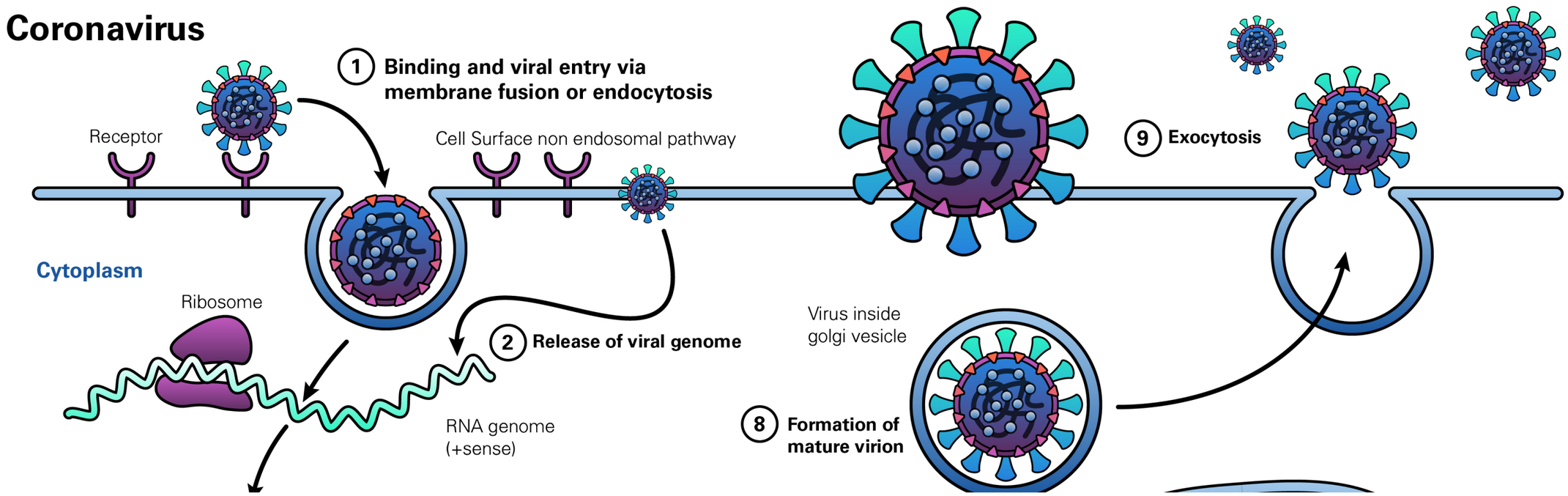
In this report, the biology of sars-cov-2 is discussed and the sars-cov-2 genome is analyzed. Machine learning will be used predict the translation transformations and deep learning will be used to predict the next nucleotide in the genome sequence.

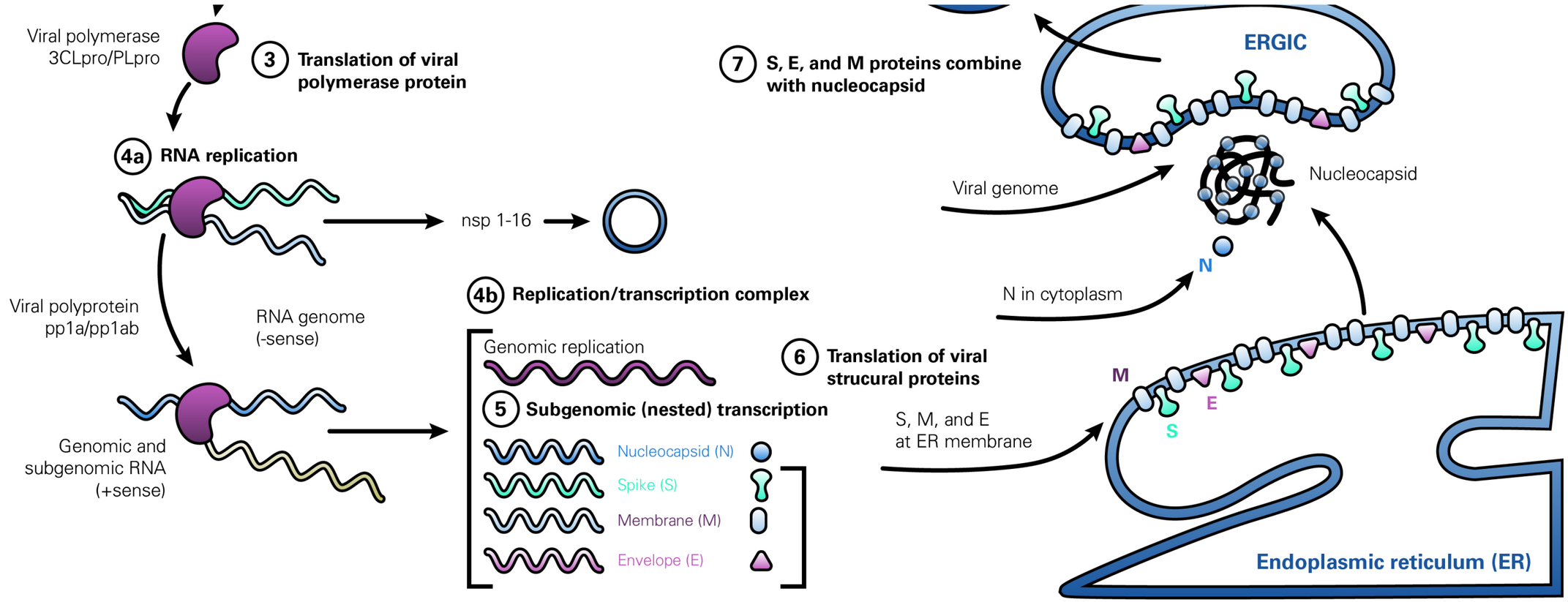
SARS-CoV-2 Biology

Coronaviruses are a sphere-like 20-sided polygon, icosahedron, shape and belong to the Nidovirales order. SARS-CoV-2 travels through the respitory tract and attaches itself to alveoli, air sacs, in the lungs. Coronaviruses are named after the dyed red spike glycoproteins (S) that cover them and attach these protiens by being activated by the host cell's proteases, ACE2 and TMPRSS2 ennzymes, at a sequential proteolytic cleavage S1 and S2 site to fuse with a host cell's enzymes to enter, endocytosis, the cell's plasma membrane to the cytosol. S1 is the end binding region of the S protein and S2 is the beam of the S protien. The spike glcoproteins can also attach to a cell's endosomes being activated by the host cell's CTSL enzyme. Inside of the icosahedron positive-sensed lipid bilayer envelope is a helical capsid that encloses an RNA genome (gRNA), which encodes the viral genetic information -- non-segmented-single-stranded RNA -- that is used during the lytic cycle to generate RNA polymerase, protease, and other proteins. The envelope is removed allowing genomic RNA to enter the cytoplasm where some of it is translated into pp1a and pp1ab proteins. Translation is when codons, groups of three nucleotides, move along a ribosome through tRNA that translates the codons to anticodons that generate an amino acid polypeptide chain of proteins. Both proteins are then cleaved by protease making 16 nonstructural proteins, NSPs. Some of the NSPs form a replication and transcription complex (RTC) in which gRNA is replicated and RNA-dependent RNA polymerase (RdRp) uses gRNA as a template to transcribe (-) subgenomic RNA (sgRNA) and then transcribe it back to (+) sgRNA, which is used as the genome of the new virus. sgRNA is translated into strutural proteins, wich are spike protein (S), envelope protein (E), membrane protein (M), and nucleocapsid protein (N). Nucleocapsid proteins assign the viral replication-transcription complexes (RTCs), where gRNA and sgRNAs are synthesized. Spike, envelope, and membrane proteins enter the endoplasmic reticulum, and the nucleocapsid protein encloses the sgRNA becoming a nucleoprotein complex. The proteins and nucleoprotein complex combine into a virus endoplasmic reticulum-Golgi apparatus, and then are excreted into a vesicle. The dyed yellow envelope proteins (E) and dyed orange membrane glycoproteins (M) assist in budding -- using the host cell's plasma membrane for envelope formation -- and then exiting, exocytosis, the host cell through lysis. The following is a diagram of the SARS-CoV-2 lifecycle,

In [4]:
```
Image(filename='Coronavirus_Life_Cycle.jpg')
```

Out[4]:

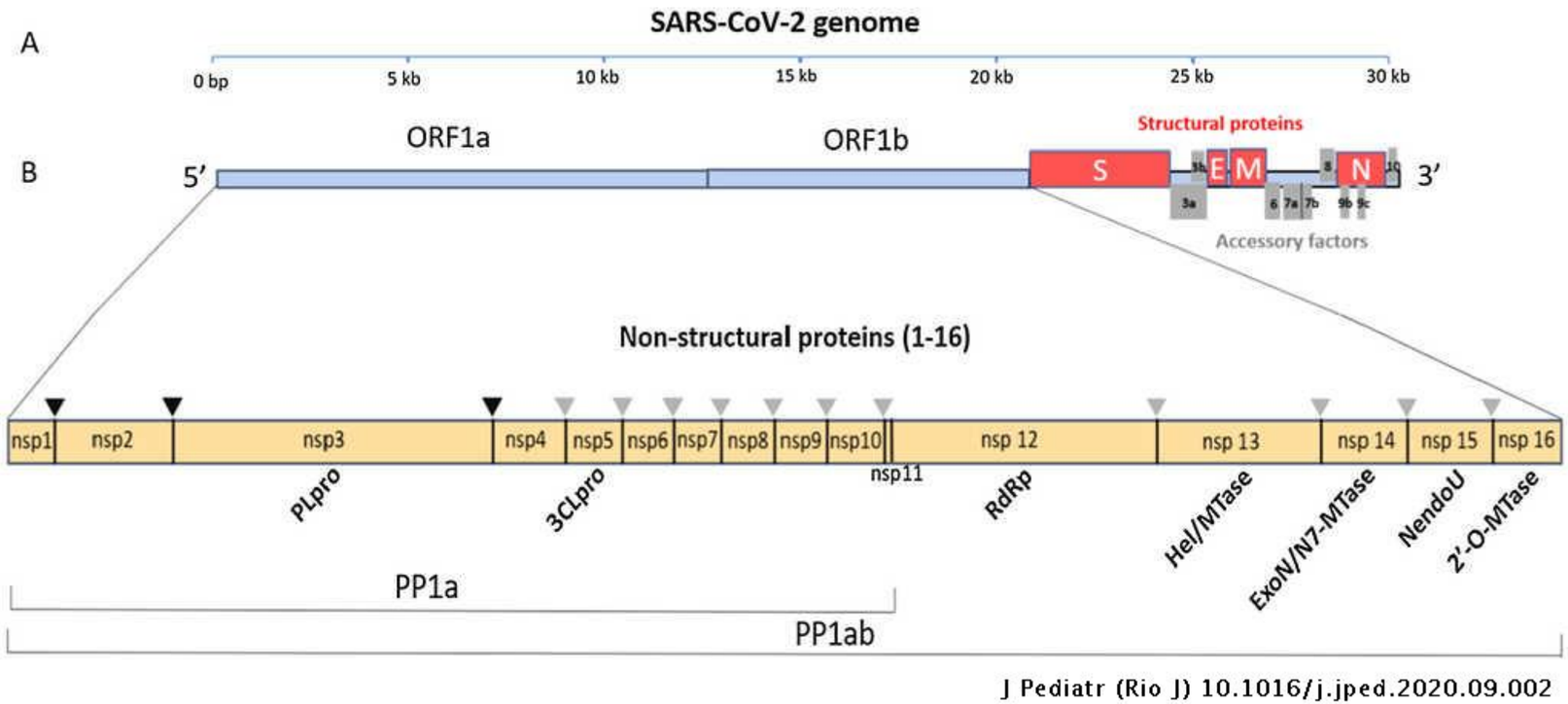




Sars-cov-2 has the largest RNA viral genome, which ranges from 26 to 32 kb. The genome of the virus starts with 5' carbon base, has an ORF1ab, S, E, M, N, and accesory region, and then end with 3' carbon base. ORF1ab are non-structural protiens. ORF1ab, open reading frames, comprises of 16 NSP regions. Nsp1 and nsp2 encode enzymes that bind to RNA and suppress gene expression. Nsp3 encodes enzymes that assist in the translation of viral mRNAs. Nsp4 encodes viroporin, which modify cellular membranes. Nsp5 encodes the organization of the viroplasm, where viral replication and assembly occur. Nsp6 generates autophagosomes, vesicles with cellular material that will be removed through autophagy. Nsp7 through 16 encode the generation of RNA synthesis and processing. Nsp7 through 11 encode the contribution to the nsp interactome, molecular interactions. Nsp12 encodes RNA polymerase. Nsp13 encodes helicase. Nsp14 through 16 encode mRNA capping, attaches the 5' cap to mRNA. The S region encodes the spike proteins, which bind to host cell receptors and fuse to the cell membrane. The M and E regions encode the membrane and envelope protiens, which assist in budding. The N region encodes the nucleocapsid protein, which assigns the viral replication-transcription complexes. The genome additionally contains an ORF coding for accessory proteins, which are not essential in virus replication but assist in pathogenesis, development of the virus.

In [13]:
```
Image(filename='SARS-COV-2_Genome.jpeg')
```

Out[13]:



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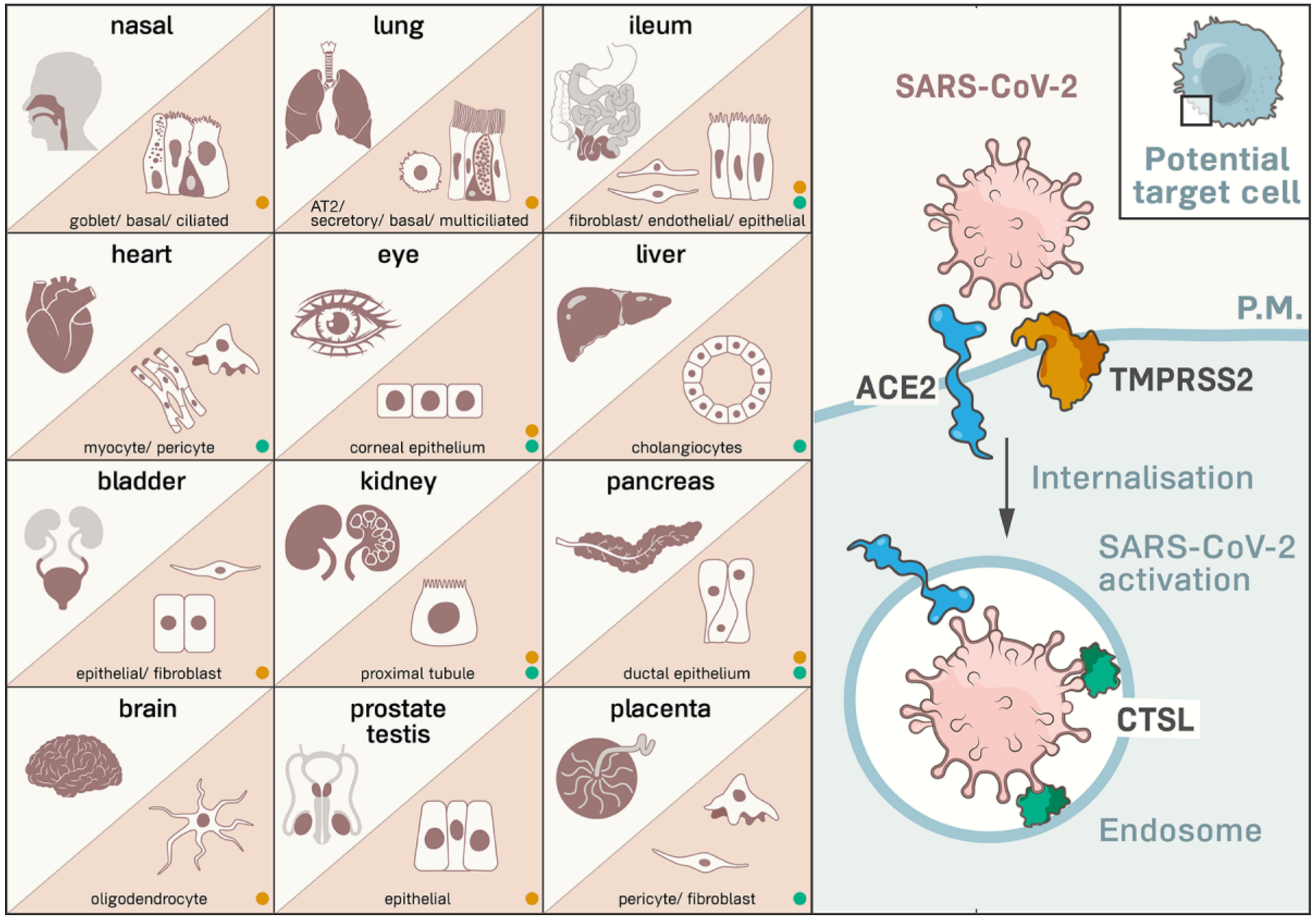
ACE2 modulates the activity of the angiotensin II protein, which increases blood pressure and inflammation. The SARS-CoV-2 virus binding to ACE2 inhibits ACE2 and can cause an increase in cell inflammation resulting in the death of cells in the alveoli units with hypoxic fluid flooding, an increase in blood preasure damaging blood vessels causing microvascular thrombosis, and the tranduction of the kidney podocytes resulting in acute kidney injury. The following is a diagram of the enzymes that get inhibited and the parts of the body that can get damaged.

In [5]:
```
Image(filename='ace2-thumb-l.png')
```

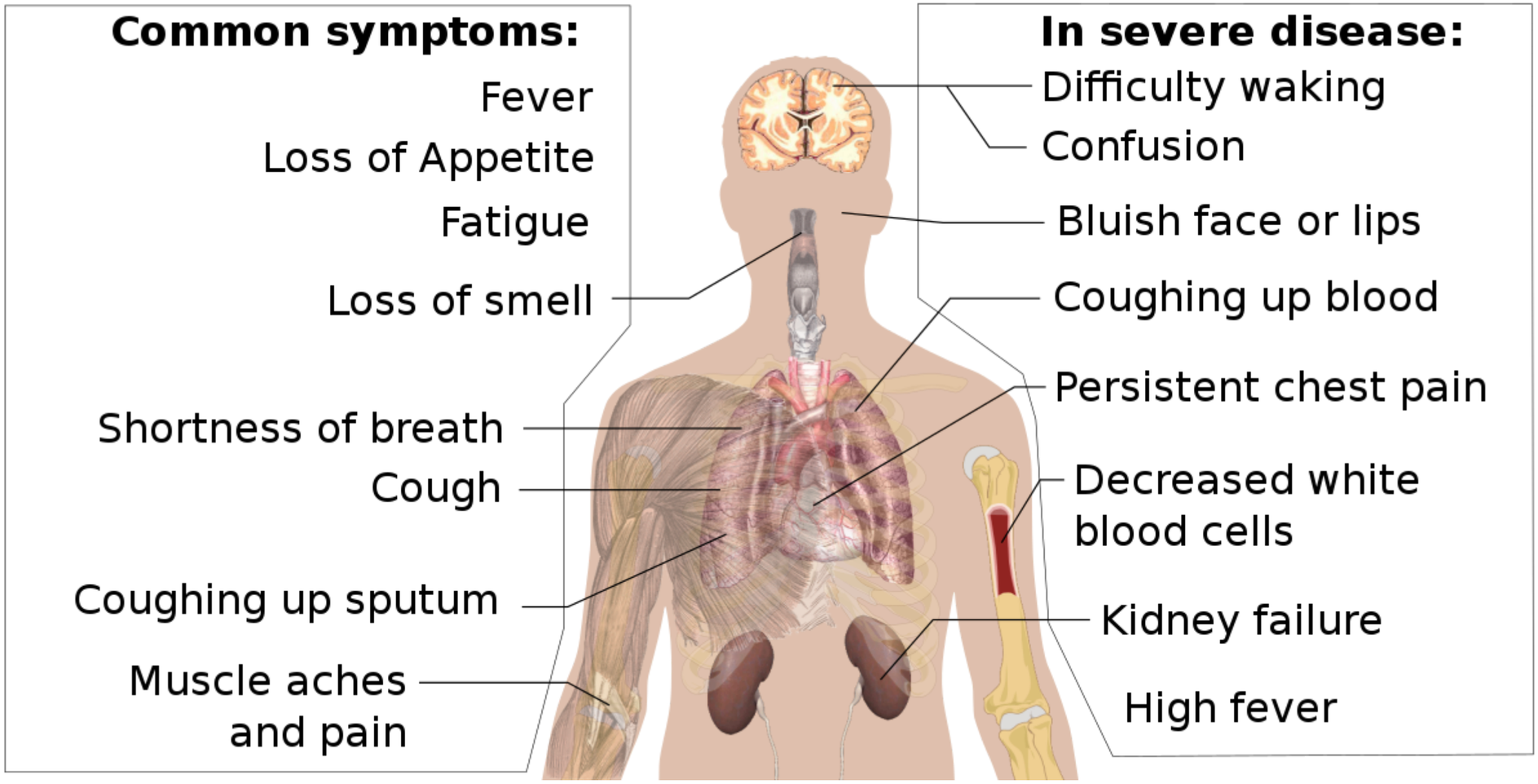
Out[5]:



SARS-CoV-2 is spread when an infected person coughs or sneezes droplets of saliva or mucus with the virus into the air. The respiratory droplets usually do not go further than a few feet, are airbourne for a few moments, and then land on a surface. SARS-CoV-2 has an incubation period of 2 to 14 days and the symptoms of the virus include cough, fever or chills, shortness of breath or difficulty breathing, muscle or body aches, sore throat, loss of taste or smell, diarrhea, headache, fatigue, nausea or vomiting, congestion or runny nose, and in rare cases the virus can lead to difficulty walking, confusion, bluish face or lips, coughing up blood, severe respiratory problems, kidney failure, high fever, or death. The following is a diagram of the symptoms.

In [4]:
```
Image(filename='Symptoms_of_coronavirus_disease_2019_4.0.svg.png')
```

Out[4]:

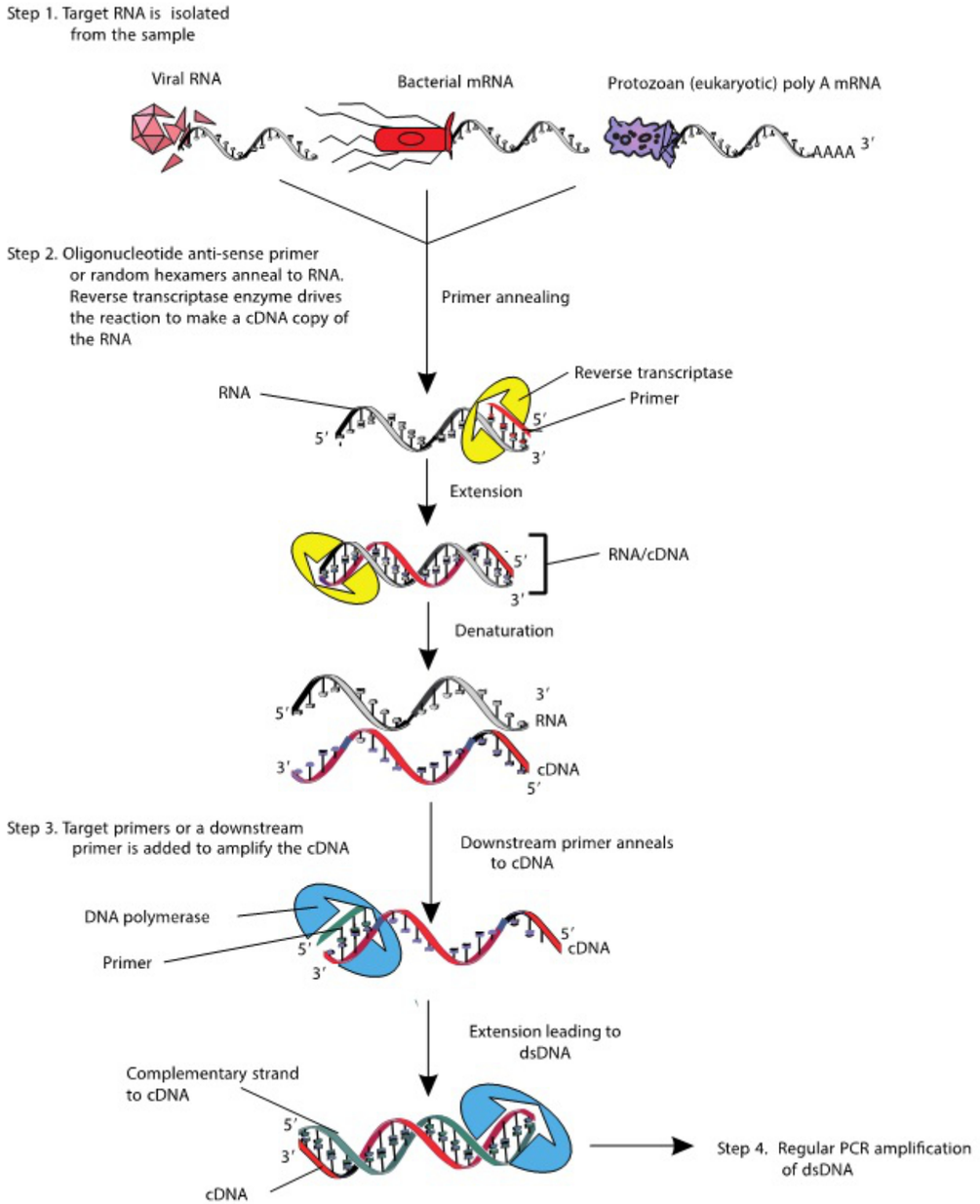


Testing for SARS-CoV-2

A patient can be tested for SARS-CoV-2 with the sequence-specific molecular nucleic acid assay, or the antigen-specific immunoassay. For a molecular-assay, a nasal or saliva sample is collected from upper respiratory fluid and then Real-time RT-PCR is conducted to quantify sequences within the RNA samples. Reverse transcriptase converts extracted RNA into cDNA that is used as a template for DNA polymerase to complete the strand of dsDNA and then RT-PCR amplifies the genetic regions and fluorescent probes bind to the regions for identification. For an immuno-assay, antibodies are put on a membrane and complexed with a potentialy virulent sample of which any antigen will be trapped that results in the membrane changing color. A SARS-CoV-2 recovered patient can be tested for whether the patient has developed anibodies against the virus by checking a blood sample for the antibodies. The following are diagrams of a molecular assay

In [6]:
```
Image(filename='10104fig1.jpg')
```

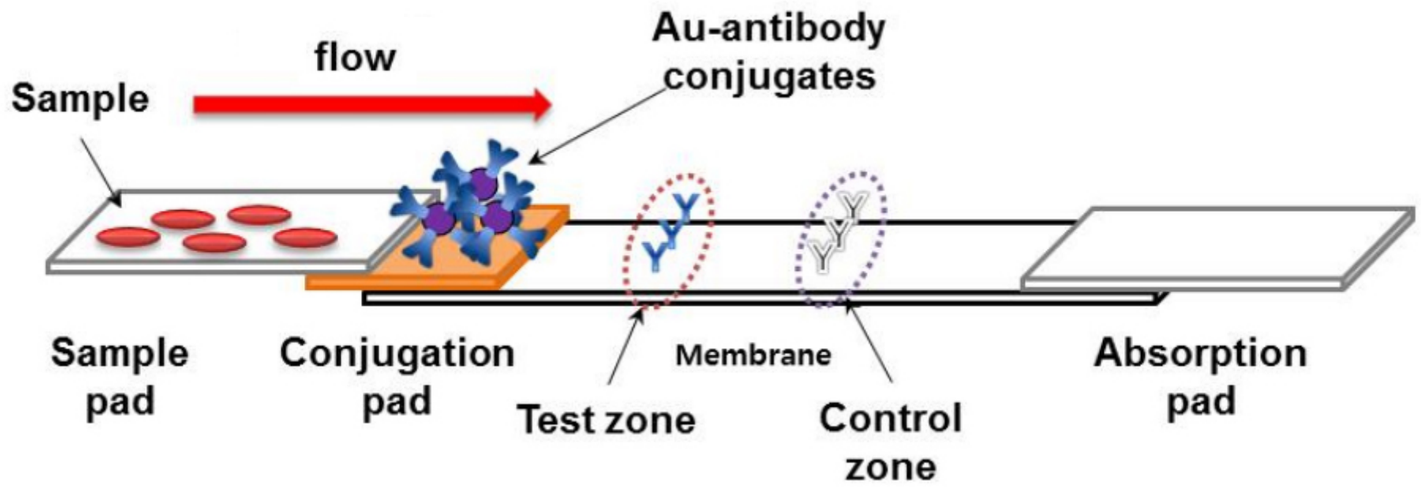
Out[6]:



and an immuno assay.

In [7]:
```
Image(filename='tag-lateral-flow-immunoassay-2.jpg')
```

Out[7]:



Vaccines for SARS-CoV-2

Vaccines have been developed to combat SARS-CoV-2. The Pfizer/BioNTech vaccine (BNT162b2) and The ModernaTX, Inc vaccine (mRNA-1273) are mRNA vaccines. mRNA vaccines deliver lab designed viral mRNA made by coding both the 5′-untranslated region (UTR) and the 3′-UTR into cells where it is translated into the encoded antigen to which an immune recognition by white blood cells, immunogenicity, results. The AstraZeneca in collaboration with the University of Oxford vaccine (AZD1222) is an adenovirus vaccine. Adenovirus vaccines are first gene sub-cloned into an intermediary vector, transfered to an adenovirus recombinant genome vector, transfected into packaging cells, amplified into a culture stock, and then titrated to determine the concentration of active adenoviruses in the stock. The adenoviruse is then delivered to cells where immunogenicity results. The following is a diagram of Virus vector DNA and mRNA vaccine immune response production.

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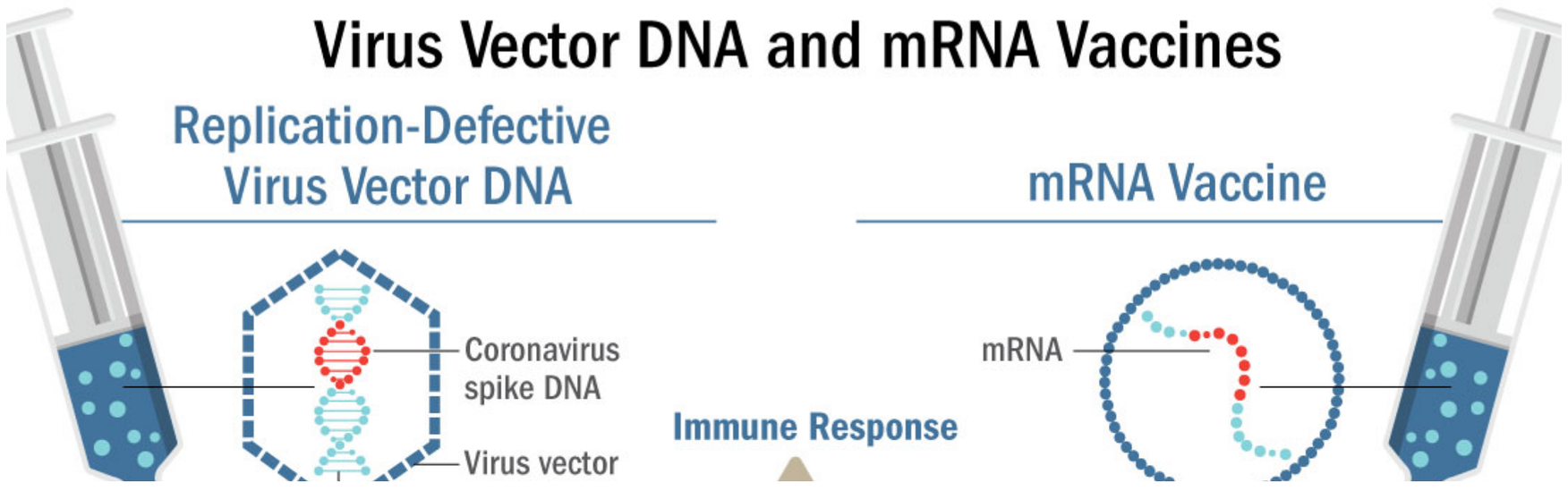
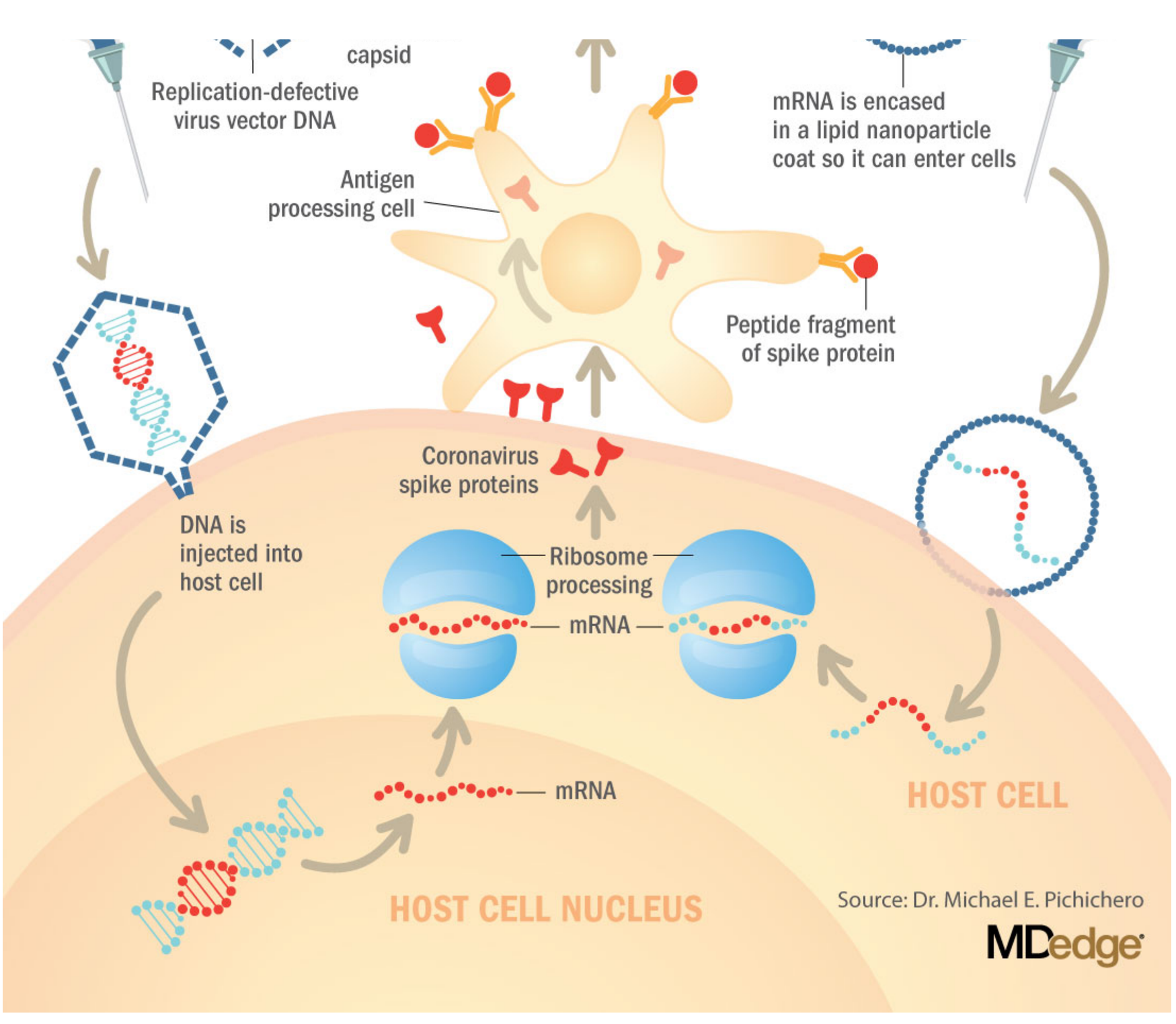
In [8]:
```
Image(filename='DNA_and_mrNA_Vaccines_web.jpeg')
```

Out[8]:





Import data of sars-cov-2 genome.

```
df=Json('sars-cov-2_genome')
```

In [6]:
```
df.file("genome.fna")
genome=json_storage['sars-cov-2_genome']
genome
```

Out[6]:
```
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GCUACUAGUAUAGUUGCAAAACAGGGUGCUGGUUUUAAACGUACUUAUAAUUUUCUGUGGUAUGUAUGUUUAUUUGUUGUUGCAUUGUUUAUGGUGUCUCAUUUAUUGAUUACACAACCACUGUAGAUUUUAAGUACAUUGAGAAUGGUCAGUUGAAGGUGUUUGA
AGCACCUUUACACUGUGUUCGUAAUGUUUUUGAUAAUUUUAAUCAAUGGCAUGAGGCUAAGUUUGGUGUUUACUACUAAUAGUGAUAAAUGUCCUAUAGUUGUUGGUGUUUCAGAGCGUAUUAAUGUUGUUCCUGGUGUUCCAACAAAUGUAUAUUUGGUAGGAAAGACUCUUGUUUUUUACAU
UACAGGCUGCUUUUGGAAACACAGGUGUUUGUUAUGACUUUGAUGGUGUUACCACUAGUGAUAAGUGUAUUUUUAAUUCUGCUUGUACUAGGUUGGAAGGUUUGGGUGGUGUGACAAUGUUUAUUGUUACAACACUGAUCUUAUUGAAGGUUCUAAACCUUAUAGUACUUUACAGCCCAAUGCUUAU
UAUAAGUAUGAUGUUAAAAAUUAUGUACGUUUUCCAGAAAUUUUAGCUAGAGGUUUUGGCUUACGUACUAUUAGAACUUUGGCUACACGUUAUUGUAGAGUUGGUGAAUGCCGUGACUCACAUAAAGGUGUUUGUUUUGGUUUUGAUAAAUGGUAUGUUAAUGAUGGACGUGUUGAUGAUGGUUA
CAUUUGUGGUGAUGGUCUUAUAGACCUUCUUGUUAAUGUACUCUCAAUCUUUAGUUCAUCUUUUAGCGUUGUGGCUAUGUCUGGACAUAUGUUGUUUAACUUUCUUUUUGCAGCAUUUAUUACAUUUUUGUGCUUUUUAGUUACUAAAUUUAAACGUGUUUUUGGUGAUCUUUCUUAUGGUGUUU
UUACUGUUGUUUGUGCAACUUUGAUUAAUAACAUUUCUUAUGUUGUUACUCAAAAUUUAUUUUUUAUGUUGCUUUAUGCUAUUUUGUAUUUUGUUUUUACUAGGACAGUGCGUUAUGCUUGGAUUUGGCAUAUUGCAUACAUUGUUGCAUACUUCUUGUUAAUACCAUGGUGGCUUCUCACAUGG
UUUAGUUUUGCUGCAUUUUUAGAGCUUUUACCUAAUGUUUUUAAGUUAAAAAUCUCUACUCAAUUGUUUGAAGGUGAUAAGUUUAUAGGUACUGCUGCAGGUACAUUUGUUCUUAUGAAAGGCUGAUAAAUACUAUUUCACCUGAGAAACUUAAGAAAUUA
UGCUGCAAGUUAUAAUAAAUAUAAAUAUUAUAGUGGUAGUGCUAGUGAGGCUGAUUAUCGUUGUGCUUGUUAUGCUCAUUUAGCCAAGGCUAUGUUAGAUUACGCAAAAGAUCAUAAUGACAUGUUAUAUUCUCCACCUACCAUUAGCUACAAUUCCACCUUACAAUCUGGUCCUUAAGAAGAUGG
CACAACCAUCUGGUUGUGUUGAGAGAUGUGUGGUUCGCGUCUGUUAUGGUAGUACUGUGCUUAAUGGAGUUUGGUUAGGUGACACUGUUACUUGUCCUAGACAUGUCAUAGCACCAUCAACCACUGUUCUUAUUGAUUAUGAUCAUGCAUAUAGUACUAUGCGUUUGCAUAAUUUUUCAGUGUCU
CAUAAUGGUGUCUUCUUGGGAGUUGUUGGUGUUACAAUGCAUGGUUCUGUGUUGCGUAUUAAGGUUUCACAAUCUAAUGUACAUACACCUAAACAUGUUUUUAAAACGUUGAAACCUGGUGAUUCUUUUAAUAUUUUAGCAUGUUAUGAAGGUAUUGCAUCUGGUGUUUUUGGUGUUAAUUUACG
UACAAACUUUACUAUUAAAGGUUCUUUUAUAAAUGGAGCUUGUGGUUCUCCUGGUUAUAAUGUUAGAAAUGAUGGUACUGUUGAGUUUUGUUAUUUACACCAAAUUGAGUUAGGUAGUGGUGCUCAUGUUGGUUCUGAUUUUACUGGUAGUGUUUAUGGUAAUUUUGAUGACCAACCUAGUUUGC
AAGUUGAGAGUGCCAACCUUAUGCUAUCAGAUAAUGUUGUUGCCUUUUUGUAUGCUGCUUUGUUGAAUGGUUGUAGGUGGUGGUUGCGUUCAACUAGAGUUAAUGUUGAUGGUUUUAAUGAAUGGGCUAUGGCUAAUGGUUAUACAAGUGUUUCUAGUGUUGAGUGCUAUUCUAUUUUGGCAGCA
AAAACUGGUGUUAGUGUUGAACAAUUGUUAGCUUCCAUUCAACAUCUUCAUGAAGGUUUUGGUGGUAAAAACAUACUUGGUUAUUCUAGUUUAUGUGAUGAGUUCACACUAGCUGAAGUUGUGAAGCAGAUGUAUGGUGUUAACUUGCAAAGUGGUAAGGUUAUUUUUGGUUUAAAAACAAUGUU
UUUAUUUAGCGUUUUCUUCACAAUGUUUUGGCAGAACUCUUUAUUAUACAAACACUAUAUGGAUAAACCCUGUGAUACUUACACCUAUAUUUUGUCUACUUUUGUUUUGUCUAUAGUUUUAACUAUGUUUCUUAAACAUAAGUUUUGUUUUUGCAAGUAUUUUUAUUACCUACUGUUAUUG
CAACUGCUUUAUAUAAUUGUGUUUUGGAUUAUUACAUAGUAAAAAUUUUUGGCUGACCAUUAUUGGAACUAUAAUGUUUCAGUAUUACAAAUGGAUGUUCUAUUUUUACACAACAUGGCGCUUUUCUAAAGAACGUUUUACACAUUGGUUUACA
UAUGUGUGUUCUCUUAUAGCAGUAGCUUACACUUAUUUUUAUAGUGGUGACUUUUUGAGUUUGCUUGUUAUGUUUUUAUGUGCUAUAUCUAGUGAUUGGUACAUUGGUGCCAUUGUUUUUAGGUUGUCACGUUUGAUUGUAAUUUUUUCACCUGAAAGUGUAUUUAGUGUUUUUGGUGAUGUGAA
ACUUACUUUAGUUGUUUAUUUAAUUUGUGGUUAUUUAGUUUGUACUUAUUGGGGCAUUUUGUAUUGGUUCAAUAGGUUUUUUAAAUGUACUAUGGGUGUUUAUGAUUUUAAGGUGAGUGCUGCUGAAUUUAAAUACAUGGUUGCUAAUGGACUUCAUGCACCACAUGGACCUUUUGAUGCACUUU
GGUUAUCAUUCAAACUACUUGGUAUUGGUGGUGACCGUUGUAUAAAAAUUUCAACUGUCCAAUCCAAACUGACUGAUUUGAAGUGUACUAAUGUUGUGUUAUUGGGUUGUUUGUCUAGUAUGAACAUUGCAGCUAAUUCUAGUGAAUGGGCUUAUUGUGUUGAUUUACACAAUAAGAUUAAUCUU
UGUGAUGACCCUGAAAAAGCUCAAGGUAUGUUGUUAGCACUCCUUGCGUUCUUUCUAAGUAAACAUAGUGAUUUUGGUCUUGAUGGCCUUAUUGAUUCUUAUUUUGAUAAUAGUAGCACCCUUCAGAGUGUUGCUUCAUCAUUUGUUAGUAUGCCAUCAUAUAUUGCUUAUGAAAAUGCUAGACA
AGCUUAUGAAGAUGCUAUUGCUAAUGGAUCUUCUUCUCAACUUAUUAAACAAUUGAAGCGUGCCAUGAAUAUCGCAAAGUCUGAAUUUGAUCAUGAGAUAUCUGUUCAGAAGAAAAUUAAUAGAAUGGCUGAACAAGCUGCUACACAGAUGUAUAAAGAAGCACGCUCUGUUAAUAGAAAAUCUA
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AAGUUAUUAGUGCUAUGCACUCUUUACUUUUUGGAAUGUUAAGACGUUUGGAUAUGUCUAGUGUUGAAACUGUUUUGAAUUUAGCACGUGAUGGUGUUGUGCCAUUGUCAGUUAUACCUGCAACUUCAGCUUCCAAACUAACUAUUGUUAGUCCAGAUCUUGAAUCUUAUUCUAAGAUUGUUUGU
GAUGGUUCUGUUCAUUAUGCUGGAGUUGUUUGGACACUUAAUGAUGUUAAAGACAAUGAUGGUAGACCUGUUCAUGUUAAAGAGAUUACAAAGGAAAAUGUUGAAACUUUGACAUGGCCUCUUAUCCUUAAUUGUGAACGUGUUGUUAAACUUCAAAAUAAUGAAAUUAUGCCUGGUAAACUUAA
GCAAAAACCUAUGAAAGCUGAGGGUGAUGGUGGUGUUUUAGGUGAUGGUAAUGCCUUGUAUAAUACUGAGGGUGGUAAAACUUUUAUGUACGCUUAUAUUUCUAAUAAAGCUGACCUUAAAUUUGUUAAGUGGGAGUAUGAGGGUGGUUGCAACACAAUCGAGUUAGACUCUCCUUGUCGAUUUA
UGGUCGAAACACCUAAUGGUCCUCAAGUGAAGUAUUUGUAUUUUGUUAAAAAUUUAAACACCUUACGUAGAGGUGCCGUUCUUGGUUUUAUAGGUGCCACAAUUCGUCUACAAGCUGGUAAACAAACUGAAUUGGCUGUUAAUUCUGGACUUUUAACUGCUUGUGCUUUUCUGUUGAUCCAGCA
ACUACUUACUUGGAAGCUGUUAAACAUGGUGCAAAACCUGUAAGUAAUUGUAUUAAGAUGUUAUCUAAUGGUGCUGGUAAUGGUCAAGCUAUAACAACUAGUGUAGAUGCUAACACCAAUCAAGAUUCUUAUGGUGGAGCGUCUAUUUGUUUGUAUUGUCGAGCUCACGUUCCUCACCCUAGUAU
GGAUGGUUACUGUAAGUUAAGGGUAAAUGUGUUCAGGUCCUAUUGGUUGUUUGGAUCCUAUUAGGUUUUGUUUAGAAAAUAAUGUGUGUAAUGUUUGUGGUUGCUGGUUGGGACAUGGAUGUGCUUGUGACCGUACAACUAUUCAAAGUGUUGACAUUUCUUAUUUAAACGAGCAAGGGGUUC
UAGUGCAGCUCGACUAGAACCCUGUAAUGGCACGGACAUCGAUAAGUGUGUUCGUGCUUUUGACAUUUAUAAUAAAAAUGUUUCAUUCUUGGGUAAGUGUUUGAAGAUGAACUGUGUUCGUUUUAAAAAUGCUGAUCUUAAGGAUGGUUAUUUUGUUAUAAAGAGGUGUACUAAGUCGGUUAUGG
AACACGAGCAAUCCAUGUAUAACCUACUUAACUUUUCUGGUGCUUUGGCUGAGCAUGACUUCUUUACUUGGAAAGAUGGCAGAGUCAUUUAUGGUAAUGUUAGUAGACAUAAUCUUACUAAAUAUACUAUGAUGGACUUGGUCUAUGCUAUGCGUAACUUUGAUGAACAAAAUUGUGAUGUUCUA
AAAGAAGUAUUAGUUUUAACUGGUUGUUGUGACAAUUCUUAUUUUGAUAGUAAGGGUUGGUAUGACCCAGUUGAAAAUGAAGAUAUACAUAGAGUUUAUGCAUCUCUUGGCAAAAUUGUAGCUAGAGCUAUGCUUAAAUGCGUUGCUCUAUGUGAUGCGAUGGUUGCUAAAGGUGUUGUUGGUGU
UUUAACAUUAGAUAACCAAGAUCUUAAUGGUAACUUUUAUGAUUUUGGUGAUUUUGUUGUUAGCUUACCUAAUAUGGGUGUUCCCUGUUGUACAUCAUAUUAUUCUUAUAUGAUGCCUAUUAUGGGUUUAACUAAUUGUUUAGCUAGUGAGUGUUUUGUCAAGAGUGAUAUUUUUGGUAGUGAUU
UUAAAACUUUUGAUUUGCUUAAGUAUGAUUUCACUGAACAUAAAGAAAAUUAUUCAAUAAGUACUUUAAGCAUUGGAGUUUUGAUUAUCAUCCUAAUUGUAGUGACUGUUAUGAUGAUAUGUGUGUUAUACAUUGUGCUAAUUUUAAUACACUAUUUGCCACAACUAUACCAGGUACUGCUUUU
GGUCCACUAUGUCGUAAAGUUUUUAUAGAUGGUGUUCCACUUGUUACAACUGCUGGUUAUCAUUUUAAGCAAUUAGGUUUGGUUUGGAAUAAAGAUGUUAACACACACUCAGUUAGGUUGACAAUUACUGAACUUUUGCAAUUUGUCACCGACCCUUCCUUGAUAAUAGCUUCUUCCCCAGCACU
CGUUGAUCAACGCACUAUUUGUUUUUCUGUUGCAGCAUUGAGUACUGGUUUGACAAAUCAAGUUGUUAAGCCAGGUCAUUUUAAUGAAGAGUUUUAUAACUUUCUUCGUUUAAGAGGUUUCUUUGAUGAAGGUUCUGAACUUACAUUAAAACAUUUCUUCUUCGCACAGAAUGGUGAUGCUGCUG
UUAAAGAUUUUGACUUUUACCGUUAUAAUAAGCCUACCAUUUUAGAUAUUUGUCAAGCUAGAGUCACAUAUAAGAUAGUCUCUCGUUAUUUUGACAUUUAUGAAGGUGGCUGUAUUAAGGCAUGUGAAGUUGUUGUAACAAAUCUUAAUAAGAGUGCUGGUUGGCCAUUAAAUAAGUUUGGUAAA
GCUAGUUUGUAUUAUGAAUCUAUAUCUUAUGAAGAACAGGAUGCUUUGUUUGCUUUGACAAAGCGUAAUGUCUUCCCUACUAUGACACAGCUGAAUCUUAAGUAUGCUAUUAGUGGUAAAGAACGUGCUAGAACUGUUGGUGGUGUUUCUCUGUUGUCCACAAUGACCACAAGACAAUACCAUCA
AAAACAUCUUAAAUCCAUUGUUAAUACACGCAAUGCCACUGUUGUUAUUGGUACUACCAAAUUUUAUGGUGGUUGGAAUAAUAUGUUGCGUACUUUAAUUGAUGGUGUUGAAAACCCUAUGCUCAUGGGUUGGGAUUAUCCCAAAUGUGAUAGAGCUUUGCCUAACAUGAUACGUAUGAUUUCAG
CCAUGGUGUUGGGCUCUAAGCAUGUUAAUUGUUGUACUGCAACAGAUAGGUUUUAUAGGCUUGGUAAUGAGUUGGCACAAGUUUUAACAGAAGUUGUUUAUUCUAAUGGUGGUUUUUAUUUUAAGCCAGGUGGUACGACUUCUGGUGACGCUAGUACAGCUUAUGCUAAUUCUAUUUUUAACAUU
UUUCAAGCCGUAAGCUCUAACAUUAACAGGUUGCUUAGUGUCCCAUCAGAUUCAUGUAAUAAUGUUAAUGUUAGGGAUCUACAACGACGUCUGUAUGAUAAUUGCUAUAGGUUAACUAGUGUUGAAGAGUCAUUCAUUGAUGAUUAUUAUGGUUAUCUUAGGAAACAUUUUUCAAUGAUGAUUCU
CUCUGAUGAUGGUGUUGUCUGUUAUAACAAGGAUUAUGCUGAGUUAGGUUAUAUAGCAGACAUUAGUGCUUUUAAAGCCACUUUGUAUUACCAGAAUAAUGUCUUUAUGAGUACUUCUAAAUGUUGGGUUGAAGAAGAUUUAACUAAGGGACCACAUGAGUUUUGUUCCCAGCAUACUAUGCAAA
UAGUUGACAAAGAUGGUACCUAUUAUUUGCCUUACCCAGAUCCUAGUAGGAUCUUGUCAGCUGGUGUUUUUGUUGAUGAUGUUGUUAAGACAGAGCUGUGUUUUGUUAGAACGUUAUGUGCUUUAGCUUAUUGAUGCAUACCCUCUUUCAAAACACCCUAAUUCUGAAUAUCGUAAGGUUUUU
UACGUAUUACUUGAUUGGGUUAAGCAUCUUAACAAAAAUUUGAAUGAGGGUGUUCUUGAAUCUUUUUCUGUUACACUUCUUGAUAAUCAAGAAGAUAAGUUUUGGUUGAGAAGAUUUUUAUGCUAGUAUGUAUGAAAAUUCUACGAUAUUGCAAGCUGCUGGUUUAUGUGUUGUUUGGUUCACA
AACUGUACUUCGUUGUGGUGAUUGUCUGCGUAAGCCUAUGUUGUGCACUAAAUGCGCAUAUGAUCAUGUAUUUGGUACCGACCACAAGUUUAUUUUGGCUAUAACACCGUAUGUAUGUAAUGCAUCAGGUUGUGGUGUUAGUGAUGUCAAAAAAUUGUAUCUUGGUGGUUUGAAUUACUAUUGUA
CAAAUCAUAAACCACAGUUGUCUUUUCCAUUAUGUUCAGCUGGUAAUAUAUUUGGUUUAUAUAAAAAUUCAGCAACUGGUUCCUUAGAUGUUGAAGUUUUUAAUAGGCUUGCAACGUCUGAUUGGACUGAUGUUAGGGACUAUAAACUUGCUAAUGAUGUUAAAGAUACACUUAGACUCUUUGCG
GCUGAAACUAUUAAAGCUAAAGAAGAGAGUGUUAAGUCUUCUUAUGCUUUUGCAACUCUUAAAGAGGUUGUUGGACCUAAAGAAUUGCUUCUUAGUUGGGAAAGUGGUAAAGUUAAACCACCUUUGAAUCGUAAUUCUGUUUUCACUUGUUUUCAAAUAAGUAAGGACUCAAAUUCCAAAUAGG
UGAGUUCAUCUUUGAGAAGGUUGAAUAUGGUUCUGAUACUGUUACGUAUAAGUCUACUGUAACUACUAAGUUAGUUCCUGGUAUGAUUUUUGUCUUAACAUCUCACAAUGUCCAACCUUUACGUGCACCAACUAUUGCUAACCAAGAGAAGUAUUCUAGCAUUUAUAAAUUGCACCCUGCUUUUA
AUGUCAGUGAUGCAUAUGCUAAUUUGGUUCCAUAUUACCAACUUAUUGGUAAACAAAAGAUAACUACAAUACAGGGUCCUCCUGGUAGUGGUAAGUCACAUUGUUCUAUUGGACUUGGAUUGUACUACCCAGGUGCGCGUAUUGUUUUUGUUGCUUGUGCCCAUGCUGCUGUUGAUUCCUUAUGU
GCAAAAGCUAUGACUGUUUAUAGCAUUGAUAAGUGUACUAGGAUUAUACCUGCAAGAGCUCGGGUUGAGUGUUAUAGUGGCUUUAAACCAAAUAACACUAGUGCACAAUACAUAUUUAGCACUGUUAACGCAUUACCUGAGUGUAAUGCUGAUAUCGUUGUUGUAGAUGAAGUUUCAAUGUGUAC
AAAUUAUGACCUUUCUGUUAUUAAUCAGCGUUUAUCAUAUAAACAUAUUGUUUAUGUUGGUGAUCCACAACAACUUCCUGCACCUAGAGUAAUGAUUACUAAAGGUGUUAUGGAGCCUGUUGAUUAUAACGUUGUUACUCAACGUAUGUGUGCUAUAGGCCCUGAUGUUUUUCUUCAUAAAUGUU
AUAGAUGUCCUGCUGAAAUAGUUAAUACAGUUUCUGAACUUGUUUAUGAGAACAAGUUUGUCCCUGUUAAACCUGCUAGUAAACAGUGUUUUAAAGUCUUUUUAAGGGUAAUGUACAGGUUGACAAUGGUUCUAGUAUUAACAGAAAGCAGCUGGAAAUAGUUAAGCUGUUUUUGUUAAAAAU
CCAAGUUGGAGUAAGGCUGUGUUUAUUUCUCCUUAUAAUAGUCAGAAUUAUGUUGCUAGUAGAUUUUUAGGACUUCAAAUUCAAACUGUUGAUUCUUCUCAAGGUAGUGAGUAUGAUUAUGUAAUCUAUGCACAAACUUCUGACACUGCACAUGCUUGCAAUGUAAACCGUUUUAAUGUUGCUAU
AACACGUGCUAAGAAGGGUAUAUUUUGUGUAAUGUGUGAUAAAACUUUGUUUGAUUCACUUAAGUUUUUUGAGAUUAAACAUGCAGAUUUACACUCUAGCCAGGUUUGUGGCUUGUUUAAAAAUUGUACACGCACUCCUCUUAAUUUACCACCAACUCAUGCACACUUUCUUGUCGUUGUCAG
AUCAGUUUAAGACUACAGGUGAUUUAGCUGUUCAAAUAGGUUCAAAUAACGUUUGUACUUAUGAACAUGUUAUAUCAUUUAUGGGUUUUAGGUUUGAUAUUAGUAUUCCUGGUAGUCAUAGUUUGUUUUGUACACGUGACUUUGCUAUUCGCAAUGUGCGUGGUUGGUUGGGUAUGGAUGUUGAA
AGUGCUCAUGUUUGUGGCGAUAACAUAGGUACUAAUGUUCCUUUACAGGUUGGUUUUUCAAAUGGUGUUAAUUUUGUUGUGCAAACUGAAGGUUGUGUGUCUACCAAUUUUGGUGAUGUUAUUAAACCUGUUUGUGCAAAAUCUCCACCAGGUGAACAAUUUAGACACCUUGUUCCUCUUUUACG
UAAAGGACAACCUUGGUUAAUUGUUCGUAGACGCAUUGUGCAAAUGAUAUCUGAUUAUUUGUCCAAUUUGUCUGACAUUCUUGUCUUUGUUUUGUGGGCAGGUAGUUUGGAAUUAACUACAAUGCGUUACUUUGUAAAAAUAGGGCCAAUUAAAUAUUGUUAUUGUGGUAAUUCUGCCACUUGU
AUAAUUCAGUUAGUAAUGAAUAUUGUUGUUUUAAACAUGCAUUGGGUUGUGAUUAUGUUUACAAUCCGUAUGCUUUUGAUAUACAACAGUGGGGUUAUGUUGGUUCCUUGAGCCAAAACCACCACACAUUCUGUAACAUUCAUAGAAACGAGCAUGAUGCCUCUGGUGAUGCUGUUAUGACACGU
UGUUUGGCAGUACAUGAUUGUUUUGUCAAAAAUGUUGAUUGGACUGUAACGUACCCCUUUAUUGCAAAUGAGAAAUUUAUCAAUGGCUGUGGGCGUAAUGUCCAGGGACAUGUUGUUCGUGCAGCCUUGAAAUUGUAUAAACCUAGUGUUAUUCAUGACAUUGGUAAUCCUAAAGGUGUACGUUG
UGCUGUUACUGAUGCCAAAUGGUACUGUUAUGACAAGCAACCUGUUAAUAGUAAUGUCAAGUUGUUGGAUUAUGAUUAUGCAACUCAUGGUCAACUUGAUGGUCUUUGUCUAUUCUGGAAUUGUAAUGUUGAUAUGUAUCCAGAAUUUUCAAUUGUGUGUCGUUUGACACACGUACUCGUUCUG
UUUUUAAUUUAGAAGGUGUUAAUGGUGUUCUCUUUAUGUUAACAAACAUGCGUUUCAUACACCAGCAUAUGAUAAACGUGCUUUUGUUAAAUUAAAACCUAUGCCCUUUUUUUACUUUGAUGACAGUGAUGUGAUUGUGAUGGCAAGAACAAGUAAUUAUGUACCCCUUCGCGCUAGUAGUUGA
GUUACCCGUUGUAAUAUAGGUGGUGCUGUUUGUUCAAAACAUGCAAAUUUGUAUCAAAAAUAUGUUGAGGCAUAUAAUACAUUUACACAGGCUGGUUUUAACAUUUGGGUACCACAUAGUUUUGAUGUUUAUAAUUUGUGGCAAAUUUUUAUUGAAACUAAUUUACAAAGUCUUGAAAAUAUAGC
AUUUAAUGUUGUAAAAAAAGGGUGUUUUACUGGUGUUGAUGGUGAGUUACCUGUUGCAGUUGUUAACGACAAAGUUUUUGUUCGCUAUGGCGAUGUUGACAACUUAGUUUUUACAAAUAAAACAACAUUGCCUACUAAUGUUGCUUUUGAAUUGUUUGCAAAACGAAAAAUGGGUUUAACACCAC
CAUUGUCUAUUCUCAAAAAUCUCGGUGUUGUUGCUACAUAUAAAUUUGUUUUAUGGGAUUAUGAAGCUGAAAGACCUUUUACCUCAUAUACUAAGAGUGUAUGUAAAUACACUGAUUUUAAUGAGGAUGUUUGUGUUUGUUUUGACAAUAGUAUCCAGGUUCGUAUGAGCGUUUUACGCUUACU
ACGAACGCUGUUUUAUUUUCUACUGUUGUCAUUAAAAAUUUAACACCUAUAAAGUUGAAUUUUGGUAUGUUGAAUGGUAUGCCAGUUUCUUCUAUUAAGGGUGAUAAAGGUGUUGAAAAAUUAGUUAAUUGGUACAUAUAUGUUCGUAAAAAUGGUCAAUUUCAAGAUCACUAUGAUGGUUUUUA
CACUCAAGGUAGGAAUUUAUCAGACUUUACACCAAGAAGUGAUAUGGAGUAUGAUUUUCUUAACAUGGAUAUGGUGUUGUUUUUAUUAAAUAAUGGUCUUGAGGAUUUUAAUUUUGAACAUGUGUAUAUGGUGAUGUUUCAAAAACUACAUUAGGAGGCUUCAUUUGUUGAUUCACAGUUUA
GGCUUAGUAAAAUGGGUGUUUUGAAAGCUGAUGAUUUUGUCAUUGCUUCUGACACAACUUUGAGGUGCUGCACUGUUACUUAUCUUAAUGAACUUAGUUCAAAAGUUGUUUGUACUUAUAUGGAUUUGUUGUUGGACGACUUUGUUACUAUACUAAAGAGUUUAGAUCUUGGUGUAAUAUCUAAA
GUUCAUGAAGUUAUUAUAGAUAAUAAACCUUAUAGGUGGAUGUUGUGGUGUAAAGAUAACCACUUGUCCACUUUUUAUCCACAGUUGCAGUCUGCUGAAUGGAAGUGUGGUUAUGCUAUGCCACAAAUUUAUAAGCUUCAACGUAUGUGUUUGGAACCUUGUAAUUUAUAUAAUUAUGGUGCUGG
UAUUAAGUUGCCUAGUGGUAUAAUGUUAAAUGUUGUUAAAUACACUCAGCUUUGUCAAUACCUAAAUAGCACUACAAUGUGCGUACCUCAUAAUAUGCGUGUUUUGCACUAUGGUGCUGGUUCUGACAAAGGUGUGGCACCUGGUACAACUGUUUUAAAACGUUGGCUACCACCUGAUGCAAUAA
UCAUUGAUAAUGACAUCAAUGAUUAUGUUAGUGAUGCAGAUUUUAGCAUUACAGGUGAUUGUGCUACUGUUUACCUUGAAGAUAAGUUUGACUUACUUAUUUCUGAUAUGUAUGAUGGUAGAAUUAAAUUUUUACUUAUCUUAAUGGUU
AUUAGAGAAAAAUUAGCUAUUGGUGGUAUGUGUUGCCAUUAAGAUUACAGAAUAUAGUUGGAAUAAGUAUCUUUAUGAAUUAAUACAGAGAUUUGCUUUUUGGACUUUGUUUUGCACGUCUGUUAAUACAUCCUCUUCAGAAGCUUUUCUUAUUGGUAUUAAUUAUUUAGGUGACUUUAUUCAAGG
UCCUUUUAUAGCUGGUAACACUGUUCAUGCUAAUUAUAUAUUUUGGCGUAAUUCUACUAUUAUGUCUUUGUCAUACAAUUCAGUUUUAGAUCUAAGUAAGUUUGAAUGUAAACAUAAGGCCACUGUUGUUGUUACACUUAAAGAUAGUGAUGUAAAUGAUAUGGUUUUGAGUUUGAUUAAGAGUG
GUAGGUUGUUGUUACGUAAUAGUGGCCGUUUUGGUGGUUUUAGUAAUCAUUUAGUCUCAACUAAAUGAAACUUUUCUUGAUUUUGCUUAUUUUGCCCCUGGUUUCUUGCUUUUCUACAUGUAACAGUAAUGCUAGUAUUUCUAUGUUACAAUUAGGUGUUCCUGAUAACUCUUCAACUAUUGUCA
CAGGUUUGUUGCCAGUCCAUUGGAUUUGUGCUAAUCAGAGCACAUCUAGUUACCCAGCCAAUGGCUUUUUCUAUAUUGAUGUCGGUAAACACCGUAGUGCUUUUGCACUCCAUAGUGGUUAUUAUGAUGCUAACCAGUAUUAUAUUUAUCUCACUAAUAAAAUACAUUUAAAUGCUCCUGUCACU
CUGAAGAUUUGUAAGUUUGGAAACACUUCUUUUGAUUUUUAAGUAAUGUUUCUACUUCUCAUCAUUGUAAUGUAAUUCGUCAUUCACAGAACAGUUAGGUGUGCCUUUGGGCAUAACUAUAUCGGGUGAAACUGUACGUUUGCAUUUAUAUAAUGCAACUCGCACCUUUUAUGUGCCUGCCGC
UUAUAAACUUACUAAACUUAGUGUUAAAUGUUACUUUAGUGAAUCCUGUGUUUUUAGUGUUGUCAAUGCUACCGUUACUGUUAAUGUCACCACACUUAAUGGCCGUAUAGUUAAUUACACUGUUUUGUGAUGAUUGUAAUGGUUACACUGAUAACAUAUUUUCUGUUCAACAGGAUGGCCGCAUUC
CUAAUGGUUUUUCUUUUAAUAAUUGGUUUUUGUUAACUAAUGGUUCUACACUAGUGGACGGUGUCUCUAGACUUUACCAACCACUUCGUUUAACUUGUUUUAUGGCCUGUACCUGGUCUUAAAUCUUCGACUGGUUUUUGUUUAUUUUAACGCCACUGGUUCUGAUGUUAAUUGUAAUGGUUAUCAA
CAUCAUUCUGUUGCUGAUGUUAUGCGUUACAAUCUUAACUUCAGUUCUAAUUCUGUGGAUAAUCUCAAGAGUGGUGUUAUAGUUUUUAAAACUCUACAGUACGAUGUUUUGUUUUACUGUAGUAAUUCUUCUUCGGGCGUUCUAGACACCACAAUACCUUUUGGCCCUUCCUCUCAACCUUAUUA
CUGUUUUAUAAAUAGUACCAUCAACACCACUCAUGUUAGCACUUUUGUGGGUGUCCUACCACCCAUUGUGCGUGAGAUUGUUGUGCUAGAACUGGUCAGUUUUAUAUUAAUGGUUUUAAGUAUUUUGAUUUGGGUUUUAUCGAAGCUGUUAAUUUUAAUGUCACGACAGCUAGUGCUACAGAUU
UUUGGACGGUUGCAUUUGCUACUUUUGUUGAUGUUUUGGUAAUGUUAGUGCAACUAACAUUCAAAACUUACUUAUUUGCGAUUCUCCAUUUGAAAAGUUGCAGUGUGAGCACUUGCAGUUUGGAUUGCAAGAUGGUUUUUAUUCUGCAAAUUUUCUUGAUGAUAAUGUUUUGCCGAUACUUAU
GUUGCACUUCCUAUUUAUUAUCAACAUACUGAUAUAAAUUUUACUGCGACUGCAUCUUUUGGUGGUUCUUGUUAUGUUUGCAAACCACAUCAGGUUAAUAUAUCUCUUAAUGGUAAUACUUCAGUGUGUGUUAGAACAUCUCAUUUUUCAAUUAGGUAUAUUUAUAACCGCGUUAAGAGUGGUUC
ACCAGGUGACUCUUCAUGGCACAUUUAUUUAAAGAGUGGCACUUGUCCAUUUUCUUUUUCUAAGUUAAAUAAUUUUCAAAAGUUUAAGACUAUUUGUUUCUCAACCGUCGUAGUGCCUGGUAGUUGUAAUUUUCCACUUGAAGCCACCUGGCAUUACACUUCUUAUACUAUUGUUGGUGCUUUGU
AUGUUACUUGGUCUGAAGGUAAUUCCAUUACUGGUGUACCUUAUCCUGUCUCUGGUAUUCGUGAGUUUAGUAAUUUAGUUUUAAAUAAUUGUACCAAAUAUAAUAUUUAUGAUUAUGUUGGUACUGGAAUUAUACGUUCUUCAAACCAGUCACUUGCUGGUGGUAUUACAUAUGUUUCUAACUCU
GGUAAUUUACUUGGUUUUAAAAUGUUUCCACUGGUAACAUUUUUAUGUGACACCAUGUAACCAACCAGACCAAGUAGCUGUUUAUCAACAAAGCAUUAUUGGUGCCAUGACUGCUGUUAAUGAGUCUAGAUAUGGCUUGCAAAACUUACUACAGUUACCUAACUUUUAUUAUGUUAGUAAUGG
UGGUAACAAUUGCACUACGGCCGUUAUGACUUAUUCUAAUUUUGGUAUUUGUGCUGAUGGUUCUUUAAUUCCUGUUCGUCCGCGUAAUUCUAGUGAUAAUGGUAUUUCAGCCAUAGUCACUGCUAAUUUAUCCAUUCCCUCUAACUGGACUACUUCAGUUCAAGUUGAGUACCUCCAAAUUACUA
GUACUCCAAUAGUUGUUGAUUGUGCUACUUAUGUGUGUAAUGGUAACCCUCGCUGUAAGAAUCUACUUAAGCAGUAUACUUCUGCUUGUAAAACUAUUGAAGAUGCCUUACGACUUAGUGCUCAUUUGGAAACUAAUGAUGUUAGUAGUAUGCUAACUUUUGAUAGCAAUGCUUUUAGUUUGGCU
AAUGUUACUAGUUUUGGAGAUUAUAACCUUUCUAGUGUUUUACCUCAGAGAAACAUUCAUUCAAGCCGUAUAGCAGGACGUAGUGCUUUGGAAGAUUUGUUGUUUAGCAAAGUUGUUACAUCUGGUUUGGGUACUGUUGAUGUUGACUAUAAGUCUUGUACUAAAGGUCUUUCUAUUGCUGACCU
UGCUUGUGCUCAGUACUACAAUGGCAUAAUGGUUUUGCCAGGUGUUGCUGAUGCUGAACGUAUGGCCAUGUACACAGGUUCUCUUAUAGGUGGCAUGGUGCUCGGAGGUCUUACAUCAGCAGCCGCCAUACCUUUUUCUUUGGCACUGCAAGCACGACUUAACUAUGUUGCUUUACAAACUGAUG

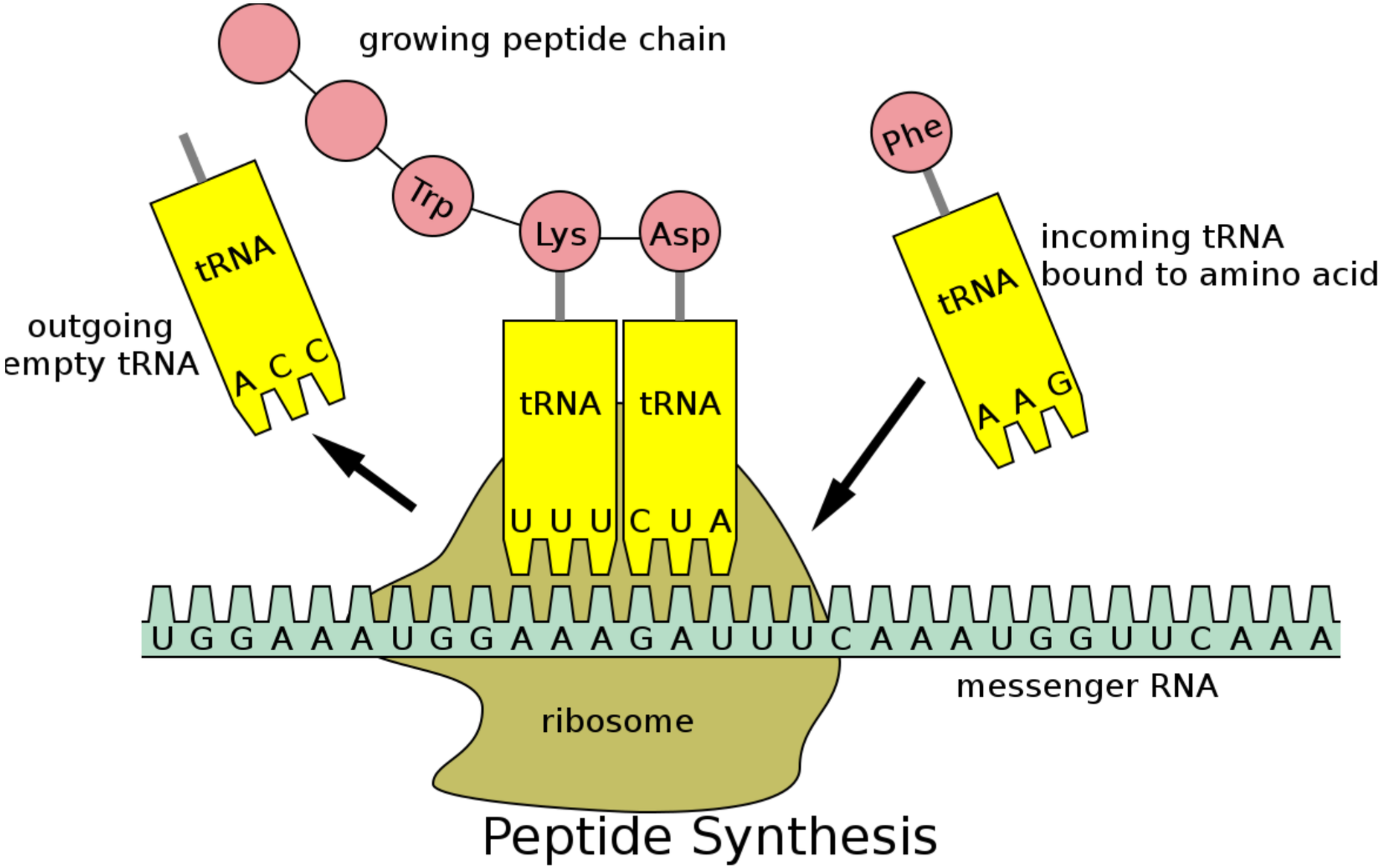
UGCUUCAAGAAAAUCAGAAAAUUUUGGCUGCAUCAUUUAAUAAGGCUAUUAAUAACAUUGUUGCUUCUUUUAGUAGCGUUAAUGAUGCUAUUACACAAACUGCAGAGGCUAUACAUACUGUUACUAUUGCACUUAAUAAGAUUCAGGAUGUUGUUAAUCAACAGGGUAGUGCUCUUAACCAUCUC
ACUUCACAAUUGAGACAUAAUUUUCAGGCCAUUUCUAAUUCAAUUCAAGCUAUUUAUGACCGGCUUGAUUCAAUUCAAGCCGAUCAACAAGUUGACAGAUUAAUUACUGGACGGCUUGCAGCUUUGAAUGCAUUUGUUUCCCAAGUUUUGAAUAAAUAUACUGAAGUUCGUAGUUCCAGACGCUU
AGCACAGCAGAAGAUUAAUGAAUGUGUCAAAUCACAAUCUAAUAGAUAUGGUUUUUGUGGCAAUGGCACCCAUAUCUUUUCAAUCGUCAACUCAGCUCCAGAUGGUUUGCUUUUUCUUCAUACUGUUUUGCUGCCAACCGACUACAAGAAUGUAAAGGCGUGGUCGGGUAUCUGUGUUGAUGGCA
UUUACGGCUAUGUUCUGCGUCAACCUAACUUGGUUCUUUAUUCUGAUAACGGUGUCUUUCGUGUAACUUCCAGGGUCAUGUUUCAACCUCGUUUACCUGUUUUGUCUGAUUUUGUGCAAAUAUAUAAUUGUAAUGUUACUUUUGUUAACAUAUCUCGUGUCGAGUUACAUACUGUCAUACCUGAC
UACGUUGAUGUUAAUAAAACAUUACAAGAGUUUGCACAAAACUUACCAAAGUAUGUUAAGCCUAAUUUUGACUUGACUCCUUUUAAUUUAACAUAUCUUAAUUUGAGUUCUGAGUUGAAGCAACUCGAAGCUAAAACUGCUAGUCUUUUCCAAACUACUGUUGAAUUACAAGGUCUUAUUGAUCA
GAUUAACAGUACAUAUGUUGAUUUGAAGUUGCUUAAUAGGUUUGAAAAUUAUAUUAAAUGGCCUUGGUGGGUUUGGCUCAUUAUUUCUGUUGUUUUUGUUGUAUUGUUGAGUCUUCUUGUGUUUUGUUGUCUUUCUACAGGUUGUUGUGGUUGUUGCAAUUGUUUAACUUCAUCAAUGCGAGGUU
GUUGUGAUUGUGGUUCAACUAAACUUCCUUAUUACGAAUUUGAAAAGGUCCACGUUCAAUAAUGCCUUUCGGUGGCCUAUUUCAACUUACUCUUGAAAGUACUAUUAAUAAGAGUGUGGCUAAUCUCAAAUUACCACCUCAUGAUGUUACUGUCUUGCGUGACAAUCUCAAACCUGUUACUACAC
UUAGUACUAUCACUGCUUAUUUGUUAGUUAGUUUGUUUGUCACUUAUUUUGCUUUAUUCAAACCUCUUACUGCUAGAGGUCGUGUUGCUUGUUUUGUUUUAAAACUAUUGACACUAUUUGUCUAUGUGCCUUUAUUGGUUCUUUUUGGUAUGUAUCUUGACAGUUUUAUAAUUUUUUCUACGCUG
UUGUUUCGAUUCAUACAUGUUGGCUAUUAUGCCUAUCUCUAUAAAAAUUUUUCAUUUGUUUUGUUCAAUGUUACUAAACUAUGCUUCGUUUCAGGCAAGUGUUGGUAUCUUGAACAAUCAUUUUAUGAAAAUCGUUUUGCUGCUAUUUAUGGUGGUGACCACUAUGUCGUUUUAGGUGGUGAAAC
UAUUACUUUUGUUUCUUUUGAUGACCUUUAUGUUGCUAUUAGAGGUUCUUGUGAAAAGAACCUACAACUUAUGCGUAAGGUUGACUUGUAUAAUGGUGCUGUCAUUUACAUUUUUGCCGAAGAGCCUGUUGUUGGUAUAGUCUACUCCUCUCAACUAUACGAAGAUGUUCCUUCGAUUAAUUGAU
GACAAUGGCAUUGUCCUCAAUUCCAUUUUAUGGCUCCUUGUUAUGAUAUUUUUCUUUGUGUUGGCAAUGACUUUUAUUAAACUGAUUCAAUUGUGUUUUACUUGUCAUUAUUUUUUUAGUAGGACAUUAUAUCAACCAGUUUAUAAAAUUUUUCUUGCUUACCAAGAUUAUAUGCAAAUAGCACC
UGUUCCAGCUGAAGUACUAAAUGUCUAAACUAAACGAUGUCUAAUAGUAGUGUGCCUCUUUCAGAGGUUUAUGUCCAUUUACGUAACUGGAACUUUAGUUGGAAUUUAAUUCUAACGCUUUUUAUAGUUGUGUUGCAGUAUGGGCAUUAUAAGUAUAGCAGACUUCUUUAUGGUUUAAAGAUGUC
UGUUUUAUGGUGUUUAUGGCCACUUGUUCUAGCUUUGUCUAUUUUUGACUGUUUUGUCAAUUUUAAUGUGGACUGGGUCUUUUUUGGUUUUAGUAUUCUUAUGUCUAUUAUUACACUUUGUUUGUGGGUUAUGUAUUUUGUUAAUAGUUUCAGACUUUGGCGCCGUGUUAAAACUUUUUGGGCUU
UUAAUCCUGAAACUAAUGCAAUCAUCUCUCUCCAGGUUUACGGACAUAAUUAUUACUUACCGGUGAUGGCUGCACCUACAGGUGUUACAUUAACACUUCUCAGUGGUGUACUUCUUGUUGAUGGCCAUAAGAUUGCUACUCGUGUUCAAGUGGGUCAGUUGCCUAAAUAUGUAAUAGUUGCUACA
CCUAGUACCACAAUUGUUUGUGACCGUGUUGGUCGCUCUGUUAAUGAAACAAGCCAGACUGGUUGGGCAUUCUACGUCCGUGCUAAACAUGGUGAUUUUUCUGGUGUUGCCUCUCAGGAGGGUGUUUUGUCAGAAAGAGAGAAGUUGCUUCAUUUAAUCUAAACUAAACAAAAUGGCUAGUGUAA
AUUGGGCCGAUGACAGAGCUGCUAGGAAGAAAUUUCCUCCUCCUUCAUUUUACAUGCCUCUUUUGGUUAGUUCUGAUAAGGCACCAUAUAGGGUCAUCCCCAGGAAUCUUGUCCCUAUUGGUAAGGGUAAUAAAGAUGAGCAGAUUGGUUAUUGGAAUGUUCAAGAGCGUUGGCGUAUGCGCAGG
GGGCAACGUGUUGAUUUGCCUCCUAAAGUUCAUUUUUAUUACCUAGGUACUGGACCUCAUAAGGACCUUAAAUUCAGACAACGUUCUGAUGGUGUUGUUUGGGUUGCUAAGGAAGGUGCUAAAACUGUUAAUACCAGUCUUGGUAAUCGCAAACGUAAUCAGAAACCUUUGGAACCAAAGUUCUC
UAUUGCUUUGCCUCCAGAGCUCUCUGUUGUUGAGUUUGAGGAUCGCUCUAAUAACUCAUCUCGUGCUAGCAGUCGUUCUUCAACUCGUAACAACUCACGAGACUCUUCUCGUAGCACUUCAAGACAACAGUCUCGCACUCGUUCUGAUUCUAACCAGUCUUCUUCAGACCUUGUUGCUGCUGUUA
CUUUGGCUUUAAAGAACUUAGGUUUUGAUAACCAGUCGAAGUCACCUAGUUCUUCUGGUACUUCCACUCCUAAGAAACCUAAUAAGCCUCUUUCUCAACCCAGGGCUGAUAAGCCUUCUCAGUUGAAGAAACCUCGUUGGAAGCGUGUUCCUACCAGAGAGGAAAAUGUUAUUCAGUGCUUUUGU
CCUCGUGAUUUUAAUCACAAUAUGGGGGAUUCAGAUCUUGUUCAGAAUGGUGUUGAUGCCAAAGGUUUUCCACAGCUUGCUGAAUUGAUUCCCAAUCAGGCUGCGUUAUUCUUUGAUAGUGAGGUUAGCACUGAUGAAGUGGGUGAUAAUGUUCAGAUUACCUAUACCUACAAAAUGCUUGUAGC
UAAGGAUAAUAAGAACCUUCCUAAGUUCAUUGAGCAGAUUAGUGCUUUUACUAAACCCAGUUCUAUCAAAGAAAUGCAGUCACAAUCAUCUCAUGCUGUUCAGAACACAGUACUUAAUGCUUCUAUUCCAGAAUCUAAACCAUUGGCUGAUGAUGAUUCAGCCAUUAUAGAAAUUGUCAACGAGG
UUUUGCAUUAAAUUGUUUUGUAAUUCCAGUUGAAUGUUUAUUAUUAUUAGUUGCAACCCCAUGCGUUUAGCGCAUGAUAAGGGUUUAGUCUUACACACAAUGGUAGGCCAGUGAUAGUAAAGUGUAAGUAAUUUGCUAUCAUAUUAACAUGUCUAGAGGAAAGUCAGAACUUUUUCUGUUUGUGU
UGUUGGAGUACUUAAAGAUCGCAUAGGCGCGCCAACAAUGGAAGAGCCAACAACAUAUCUAAAAAUGUUUUGUCUGGUACUUGUUAAUGAUA'

Translation has three steps: initiation, which is when a ribosome, mRNA (sgRNA is a type of mRNA), and tRNA connect; elongation, which is when tRNA brings amino acids to the ribosome to be linked; and termination, which is when the polypeptide chain is complete. In this report, machine learning is used in two steps to complete the elongation process. First, the alogorithm will bind the codons to anticodons and then it will transfer the anticodons to amino acids.

In [225…

```
Image(filename='translation.png')
```

Out[225…



Data Mining

The genome a '\n' character that is python for new line that will be removed.

In [192…
```
set(genome)
```

Out[192…
```
{'\n', 'A', 'C', 'G', 'U'}
```

Data Cleaning

Remove '\n' from genome and protein strings.

In [7]:

```
genome=genome.replace('\n','')
genome
```

Out[7]:

'ACUUUGUGUCUACUCCUCUCAACUAAACGAAAUUUUUCUAGUGCUGUCAUUUGUUAUGGCAGUCCUAGUGUAAUUGAAAUUUCGUCAAGUUUGUAAACUGGUUAGGCAAGUGUUGUAUUUUCUGUGUUUAAGCACUGGUGGUUCUGUCCACUAGUGCACACAUUGAUACUUAAGUGGUGUUCUG
UCACUGCUUAUUGUGGAAGCAACGUUCUGUCGUUGGAAACCAAUAACUGCUAACCAUGUUUUACAAUCAAGUGACACUUGCUGUUGCAAGUGAUUCGGAAAUUUCAGGUUUUGGUUUUGCCAUUCCUUCUGUAGCCGUUCGCGCUUAUAGCGAAGCCGCUGCACAAGGUUUUCAGGCAUGCCG
CUUUGUUGCUUUUGGCUUACAGGAUUGUGUAACCGGUAUUAAUGAUGACGAUUAUGUCAUUGCAUUGACUGGUACUAAUCAGCUUUGUGCCAAAAUUUUACUUUUUUCUGAUAGACCUCUUAAUUUGCGAGGUUGGCUCAUUUUUUCUAACAGCAAUUAUGUUCUUCAGGACUUUGAUGUUGUUU
UUGGCCAUGGUGCAGGAAGUGUGGUUUUUGUGGAUAAGUAUAUGUGUGGUUUUGAUGGUAAACCUGUGUUACCUAAAAACAUGUGGGAAUUUAGAGAUUACUUUAAUGAUAAUACUGAUAGUAUUGUUAUUGAUGGUGUCACUUAUCAAUUAGCAUGGGAUGUUAUACGUAAAGACCUUUCUUAU
GAACAGCAAAAUGUUUUAGCUAUUGAGAGCAUUCAUUAUCUUGGUACUACAGGUCAUACUUUGAAGUCUGGUUGCAAACUCAUUAAUGCCAAGCCGCCUAAAUAUUCUUCUAAGGUUGUUUUGAGUGGUGAAUGGAAUGCUGUGUAUAAGGCGUUUGGUUCACCAUUUAUUACAAAUGGUAUAUC
AUUGCUAGAUAUAAUUGUUAAACCAGUUUUCUUUAAUGCUUUUGUUAAAUGCAAUUGUGGUUCUGAGAAUUGGAGUGUUGGUGCAUGGGAUGGUUAUCUAUCUUCUUGUUGUGGCACACCUGCUAAGAAACUUUGUGUUGUUCCUGGUAAUGUUGUUCCUGGUGAUGUGAUCAUCACCUCAACUG
AUGCUGGUUGUGGUGUUAAAUACUAUGCUGGCUUAGUUGUUAAACAUAUUACUAACAUUACUGGUGUGUCUUUAUGGCGUGUUACAGCUGUUCAUUCUGAUGGAAUGUUUGUGGCAACAUCUUCUUAUGAUGCACUCUUGCAUAGAAAUUCAUUAGACCCUUUUUGCUUUGAUGUUAACACUUUA
CUUUCUAAUCAAUUACGUCUAGCUUUUCUUGGUGCUUCUGUUACAGAAGAUGUUAAAUUUGCUGCUAGCACUGGUGUUAUUGACAUUAGUGCUGGUAUGUUUGGUCUUUACGAUGACAUAUUGACAAACAAUAAACCUUGGUUUGUACGCAAAGCUUCUGGGCUUUUUGAUGCAAUCUGGGAUGC
UUUUGUUGCCGCUAUUAAGCUUGUGCCAACUACUACUGGUGGUUUGGUUAGGUUUGUUAAGUCUAUCGCUUCAACUGUUUUAACUGUUUCUAAUGGUGUUAUUAUUAUGUGUGCAGAUGUUCCAGAUGCUUUUCAACCAGUUUACCGUACAUUUACACAAGCCAUUUGUGCUGCAUUUGAUUUUU
CUUUAGAUGUAUUUAAAAUUGGUGAUGUUAAAUUUAAACGACUUGGUGAUUAUGUCUUACUGAAAAUGCUCUUGUUCGUUUGACUACUGAAGUUGUUCGUGGUGUUCGUGAUGCUCGCAUAAAGAAAGCCAUGUUUACUAAAGUAGUUGUAGGUCCUACAACUGAAGUUAAGUUUUCUGUUAUU
GAACUUGCCACUGUUAAUUUGCGUCUUGUUGAUUGUGCACCUGUAGUUUGCCCUAAAGGUAAAAUUGUUGUUAUUGCUGGACAAGCUUUUUUCUAUAGUGAUGGUUUUUAUCGUUUUAUGGUUGAUUCUACAACUGUAUUAAAUGACCCUGUUUUUACUGGUGAUUUAUUUUACACUAUUAAGUU
UAGUGGUUUUAAGCUUGAUGGUUUUAACCAUCAGUUUGUUAAUGCUAGUUCUGCUACAGAUGCCAUUAUUGCUGUUGAGCUGUGUUAUCGGAUUUUAAAACUGCAGUUUUUGUGUACACAUGUGUGGUUGAUGGUUGUAGUGUCAUUGUUAGACGUGAUGCUACAUUCGCCACACAUGUGUGUU
UUAAGGACUGUUAUAAUAUUUGGGAGCAAUUCUGCAUUGAUAAUUGUGGUGAGCCAUGGUUUUUGACUGAUUAUAAUGCUAUCUUGCAGAGUAAUAACCCUCAAUGUGCUAUUGUUCAAGCAUCGGAGUCUAAAGUUUUGCUUGAGAGGUUUUUACCUAAGUGUCCUGAAAUACUGUUGAGUAUU
GAUGAUGGCCAUUUAUGGAAUCUUUUUGUUGAAAAGUUUAAUUUUGUUACAGAUUGGUUAAAAACUCUUAAGCUUACACUUACUUCUAAUGGUCUUUUAGGUAAUUGUGCCAAACGUUUUAGACGUGUUUUGGUAAAAUUGCUUGAUGUCUAUAAUGGUUUUCUUGAAACUGUCUGUAGUGUCGU
ACACACUGCUGGUGUUUGCAUUAAAUAUUAUGCUGUUAAUGUUCCAUAUGUAGUUAUUAGUGGUUUUGUAAGUCGUGUAAUUCGUAGAGAAAGGUGUGACGUGACUUUUCCUUGUGUUAGUUGUGUCACUUUUUUCUAUGAAUUUUUAGACACGUGUUUAGUGUUAGUAAACCUAAUGCCAUUG
AUGUUGAACAUUUAGAGCUUAAAGAAACCGUUUUUGUUGAACCUAAGGAUGGUGGUCAAUUUUUUGUUUCUGAUGAUUAUCUUUGGUAUGUUGUAGAUGACAUUUAUUAUCCAGCUUCAUGUAAUGGUGUAUUGCCAGUUGCUUUUACAAAAUUGGCAGGUGGUAAAAUAUCUUUUUCUGAUGAU
GUUAUAGUCCAUGAUGUUGAACCUACCCAUAAAGUCAAGCUCAUAUUUGAGUUUGAAGAUGAUGUUGUUACCAGUCUUUGUAAGAAGAGUUUUGGUAAGUCUAUUAUUUAUACAGGUGAUUGGGAAGGUUUACAUGAAGUUCUUACAUCUGCAAUGAAUGUCAUUGGGCAACAUAUUAAGUUGCC
ACAAUUUUAUAUUUAUGAUGAAGAGGGUGGUUAUGAUGUUUCUAAACCAGUUAUGAUUUCACAAUGGCCUAUUAGUGAUGAUAGUGGUGAUUGUGUUGUUGAAGCGAGCACUGAUUUUCAUCAAUUAGAAUUUGUUAGAGAAGAGGUUGAUAUAAUUGAACAACCUUUUGGGGAAGUUGAACAUU
CGCUCCCAAUUAAACAACCUUUUUCUUUUUCUUUUAGAGAUGAAUUGGGUGUUCGUGUUUUAGAUCAAUCUGAUAAUAAUUGUUGGAUUAGUACCACACUUAUACAGUUGCAACUUACAAAGCUUUUGGAUGAUUCUAUUGAGAUGCAAUUGUUUAAAGUUGGUAAAGUUGAUUCAAUUGUUCAA
AAGUGUUAUGAGUUGUCUCAUUUAAUUAGUGGUUCACUUGGUGAUAGUGGUAAACUUCUUAGUGAACUUCUUAAAGAUAAAUAUACAUGUUCUAUAACUUUUGAGAUGUCUUGUGAUUGUGGUAAAAAGUUUGAUGAGCAAGUUGGUGUUUGUUUUGGAUUAUGCCUUACACAAACUUUUUCA
AAAAGGUGAGUGUUGUAUUUGUCAUAAAAUGCAGACUUAUAAGCUUGUUAGUAUGAAAGGUACUGGUGUGUUUGUACAGGAUCCAGCACCUAUUGACAUUGAUGCUUUCCCUGUGAGACCUAUAUGUUCAUCUGUAUAUUUAGGUGUUAAGGGUUCUGGUCAUUAUCAAACAAAUUUAUACAGUU
UUGACAAAGCUAUUGAUGGUUUUGGUGUCUUUGACAUUAAAAAUAGUAGUGUUAAUACUGUCUGUUUUGUUGAUGUUGAUUUUCAUAGUGUAGAAAUAGAAGCUGGUGAAGUUAAACCUUUUGCUGUAUAUAAAAAUGUUAAAUUUUAUUUAGGUGAUAUUUCACACCUUGUAAACUGUGUUUCU
UUUGACUUUGUUGUCAAUGCUGCUAAUGAAAAUCUCAUGCAUGGAGGCGGUGUUGCACGUGCUAUUGAUAUUUUGACUGAAGGUCAACUUCAGUCAUUAUCUAAAGAUUACAUUAGUAGUAAUGGUCCACUUAAGGUUGGAGCAGGUGUUAUGUUGGAGUGUGAAAAAUUCAAUGUAUUUAAUGU
UGUUGGUCCGCGAACUGGUAAACAUGAGCAUUCAUUACUUGUUGAAGCUUAUAAUUCUAUUUUAUUUGAAAAUGGUAUUCCACUUAUGCCUCUUCUUAGUUGUGGUAUUUUUGGUGUAAGGAUUGAAAAUUCUCUUAAAGCUUUGUUUAGUUGUGACAUUAAUAAACCGUUGCAAGUUUUUGUUU
AUUCUUCAAAUGAAGAACAAGCUGUUCUUAAGUUUUUAGAUGGUUUAGAUUUAACACCAGUCAUUGAUGAUGUUGAUGUUGUUAAACCUUUUAGAGUUGAAGGUAAUUUUUCAUUCUUUGAUUGUGGUGUCAAUGCCUUGGAUGGUGAUAUUUACUUAUUAUUUACUAACUCUAUUUUAAUGUUG
GAUAAACAAGGACAAUUAUUGGACACAAAACUUAAUGGUAUUUUGCAACAGGCAGCUCUUGAUUAUCUUGCUACAGUUAAAACUGUACCAGCUGGUAAUUUGGUUAAACUUGUUGUUGAGAGUUGUACCAUUUAUAUGUGUGUUGUACCAUCGAUAAAUGAUCUUUCUUUUGAUAAAAAUCUUGG
UCGUUGUGUGCGUAAACUUAAUAGAUUGAAAACUUGUGUUAUUGCCAAUGUUCCUGCUAUUGAUGUUUUGAAAAAGCUUCUUUCAAGUUUGACUUUAACUGUUAAAUUUGUUGUAGAGAGUAAUGUUAUGGAUGUUAACGACUGUUUUAAGAAUGAUAAUGUAGUUUUGAAAAUCACUGAAGAUG
GUAUUAAUGUUAAAGAUGUUGUUGUUGAGUCUUCUAAGUCACUUGGUAAACAAUUGGGUGUUGUGAGUGAUGGUGUUGACUCUUUUGAAGGUGUUUUACCUAUUAAUACUGAUACUGUCUUAUCUGUAGCUCCAGAAGUUGACUGGGUUGCUUUUUACGGUUUUGAAAAGGCAGCACUUUUUGCU
UCUUUGGAUGUAAAGCCAUAUGGUUACCCUAAUGAUUUUGUUGGUGGUUUUAGAGUUCUUGGGACCACCGACAAUAAUUGUUGGGUUAAUGCAACUUGUAUAAUUUUACAGUAUCUUAAGCCUACUUUUAAAUCUAAGGGUUUAAAUGUUCUUUGGAAUAAAUUUGUUACAGGUGAUGUUGGACC
UUUUGUUAGUUUUAUUUAUUUUAUAACUAUGUCUUCAAAGGGUCAAAAGGGUGAUGCUGAAGAGGCAUUAUCUAAAUUGUCAGAGUAUUUGAUUAGUGAUUCUAUUGUUACUCUUGAACAAUAUUCAACUUGUGACAUUUGUAAAAGUACUGUAGUUGAAGUUAAAAGUGCUAUUGUCUGUGCUA
GUGUGCUUAAAGAUGGUUGUGAUGUUGGUUUUUGUCCACACAGACAUAAAUUGCGUUCACGUGUUAAGUUUGUUAAUGGACGUGUUGUUAUUACCAAUGUUGGUGAACCUAUAAUUUCACAACCUUCUAAGUUGCUUAAUGGUAUUGCUUAUACAACAUUUUCAGGUUCUUUUGAUAACGGUCAC
UAUGUAGUUUAUGAUGCUGCUAAUAAUGCUGUCUAUGAUGGUGCUCGUUUAUUUGCUUCAGAUUUGUCUACUUUAGCUGUUACAGCUAUUGUUGUAGUAGGUGGUUGUGUAACAUCUAAUGUUCCAUCAAUUGUUAGUGAGAAAUUUCUGUUAUGGAUAAACUUGAUACUGGUGCACAAAAAUU
UUUCCAAUUUGGUGAUUUUGUUAUGAAUAACAUUGUUCUGUUUUUAACUUGGUUGCUUAGUAUGUUUAGUCUUUUACGUACUUCUAUUAUGAAGCAUGAUAUUAAAGUUAUUGCCAAGGCUCCUAAACGUACAGGUGUUAUUUUGACACGUAGUUUUAAGUAUAACAUUAGAUCUGCUUUGUUUG
UUAUAAAGCAGAAGUGGUGUGUUAUUGUUACUUUGUUUAAGUUCUUAUUGUUAUUAUAUGCUAUUUAUGCACUUGUUUUUAUGAUUGUGCAAUUUAGUCCUUUUAAUAGUCUUUUAUGUGGUGACAUUGUAAGUGGUUAUGAAAAAUCCACUUUUAAUAAGGAUAUUUAUUGUGGUAAUUCUAUG
GUUUGUAAGAUGUGUUUGUUCAGUUAUCAAGAGUUUAAUGAUUUGGAUCAUACUAGUCUUGUUUGGAAGCACAUUCGUGAUCCUAUAUUAAUCAGUUUACAACCAUUUGUUAUACUUGUUAUUUUGUUAAUUUUUGGUAAUAUGUAUUUGCGUUUUGGACUUUUAUAUUUUGUUGCACAAUUUAU
UAGUACUUUUGGUUCUUUCUUAGGCUUUCAUCAGAAACAGUGGUUUUUACAUUUUGUGCCGUUUGAUGUUUUAUGUAAUGAGUUUUUAGCUACAUUUAUUGUCUGCAAAAUUGUUUUAUUUGUUAGACAUAUUAUUGUUGGCUGUAAUAAUGCUGACUGUGUAGCUUGUUCUAAAAGUGCUAGAC
UUAAACGUGUACCACUUCAAACUAUUAUUAAUGGUAUGCAUAAAUCAUUCUAUGUUAAUGCUAAUGGUGGUACUUGUUUCUGUAAUAAACAUAACUUCUUUUGUGUUAAUUGUGAUUCUUUUGGGCCUGGUAACACUUUUAUUAAUGGUGAUAUUGCAAGAGAGCUUGGUAAUGUUGUUAAAACA
GCUGUUCAACCCACAGCUCCUGCAUAUAUUAUUAUUGAUAAGGUAGAUUUUGUUAAUGGAUUUUAUCGUCUUUAUAGUGGUGACACUUUUUGGCGGUAUGACUUUGACAUUACUGAAUCUAAGUAUAGUUGUAAAGAGGUUCUGAAGAAUUGUAAUGUUUUAGAAAAUUUUAUUGUUUACAAUAA
UAGUGGUAGUAACAUUACACAGAUUAAAAAUGCUUGUGUUUAUUUUUCUCAAUUGUUGUGUGAACCUAUAAAGUUGGUAAAUUCAGAGUUGUUGUCAACUUUAUCAGUUGAUUUUAAUGGUGUUUUGCAUAAGGCAUAUGUUGAUGUUUUGUGUAAUAGUUUUUUAAGGAGCUAACUGCUAACA
UGUCCAUGGCUGAAUGUAAAGCUACACUUGGUUUGACUGUUUCUGAUGAUGAUUUUGUUUCAGCUGUUGCCAAUGCACAUAGGUAUGACGUUUUGCUUUCAGAUUUGUCAUUUAAUAAUUUUUUUAUUUCUUAUGCUAAACCUGAAGAUAAGUUGUCCGUUUAUGAUAUUGCUUGUUGUAUGCGU
GCCGGUUCUAAGGUUGUUAACCAUAAUGUUUUAAUUAAAGAGUCAAUACCUAUUGUUUGGGGUGUCAAGGACUUUAAUACUCUUUCUCAAGAAGGUAAGAAGUACCUUGUUAAAACAACUAAAGCAAAGGGUUUGACUUUUUUAUUAACUUUUAAUGAUAACCAAGCAAUUACACAAGUCCUGC
UACUAGUAUAGUUGCAAAACAGGGUGCUGGUUUUAAACGUACUUAUAAUUUUCUGUGGUAUGUAUGUUUAUUUGUUGUUGCAUUGUUUAUUGGUGUCUCAUUUAUUGAUUACACAACCACUGUAACUAGCUUUCAUGGUUAUGAUUUUAAGUACAUUGAGAAUGGUCAGUUGAAGGUGUUUGAAG
CACCUUUACACUGUGUUCGUAAUGUUUUUGAUAAUUUUAAUCAAUGGCAUGAGGCUAAGUUUGGUGUUGUUACUACUAAUAGUGAUAAAUGUCCUAUAGUUGUUGGUGUUUCAGAGCGUAUUAAUGUUGUUCCUGGUGUUCCAACAAAUGUAUAUUUGGUAGGAAAGACUCUUGUUUUUACAUUA
CAGGCUGCUUUUGGAAACACAGGUGUUUGUUAUGACUUUGAUGGUGUUACCACUAGUGAUAAGUGUAUUUUUAAUUCUGCUUGUACUAGGUUGGAAGGUUUGGGUGGUGACAAUGUUUAUUGUUACAACACUGAUCUUAUUGAAGGUUCUAAACCUUAUAGUACUUUACAGCCCAAUGCUUAUUA
UAAGUAUGAUGUUAAAAAUUAUGUACGUUUUCCAGAAAUUUUAGCUAGAGGUUUUGGCUUACGUACUAUUAGAACUUUGGCUACACGUUAUUGUAGAGUUGGUGAAUGCCGUGACUCACAUAAAGGUGUUUGUUUUGGUUUUGAUAAAUGGUAUGUUAAUGAUGGACGUGUUGAUGAUGGUUACA
UUUGUGGUGAUGGUCUUAUAGACCUUCUUGUUAAUGUACUCUCAAUCUUUAGUUCAUCUUUUAGCGUUGUGGCUAUGUCUGGACAUAUGUUGUUUAACUUUCUUUUUGCAGCAUUUAUUACAUUUUUGUGCUUUUUAGUUACUAAAUUUAAACGUGUUUUUGGUGAUCUUUCUUAUGGUGUUUUU
ACUGUUGUUUGUGCAACUUUGAUUAAUAACAUUUCUUAUGUGUUACUCAAAAUUUAUUUUUAUGUUGCUUUAUGCUAUUUUGUAUUUUGUUUUUACUAGGACAGUGCGUUAUGCUUGGAUUUGGCAUAUUGCAUACAUUGUUGCAUACUUCUUGUUAAUACCAUGGUGGCUUCUCACAUGGUU
UAGUUUUGCUGCAUUUUUAGAGCUUUUACCUAAUGUUUUUAAGUUAAAAAUCUCUACUCAAUUGUUUGAAGGUGAUAAGUUUAUAGGUACUUUUGAGAGUGCUGCUGCAGGUACAUUUGUUCUUGACAUGCGUUCUUAUGAAAGGCUGAUAAAUACUAUUUCACCUGAGAAACUUAAGAAUUAUG
CUGCAAGUUAUAAUAAAUAUAAAUAUUAUAGUGGUAGUGCUAGUGAGGCUGAUUAUCGUUGUGCUUGUUAUGCUCAUUUAGCCAAGGCUAUGUUAGAUUACGCAAAAGAUCAUAAUGACAUGUUAUAUUCUCCACCUACCAUUAGCUACAAUUCCACCUUACAAUCUGGUCUUAAGAAGAUGGCA
CAACCAUCUGGUUGUGUUGAGAGAUGUGUGGUUCGCGUCUGUUAUGGUAGUACUGUGCUUAAUGGAGUUUGGUUAGGUGACACUGUUACUUGUCCUAGACAUGUCAUAGCACCAUCAACCACUGUUCUUAUUGAUUAUGAUCAUGCAUAUAGUACUAUGCGUUUGCAUAAUUUUUCAGUGUCUCA
UAAUGGUGUCUUCUUGGGAGUUGUUGGUGUUACAAUGCAUGGUUCUGUGUUGCGUAUUAAGGUUUCACAAUCUAAUGUACAUACACCUAAACAUGUUUUUAAAACGUUGAAACCUGGUGAUUCUUUUAAUAUUUUAGCAUGUUAUGAAGGUAUUGCAUCUGGUGUUUUUGGUGUUAAUUUACGUA
CAAACUUUACUAUUAAAGGUUCUUUUAUAAAUGGAGCUUGUGGUUCUCCUGGUUAUAAUGUUAGAAAUGAUGGUACUGUUGAGUUUUGUUAUUUACACCAAAUUGAGUUAGGUAGUGGUGCUCAUGUUGGUUCUGAUUUUACUGGUAGUGUUUAUGGUAAUUUUGAUGACCAACCUAGUUUGCAA
GUUGAGAGUGCCAACCUUAUGCUAUCAGAUAAUGUUGUUGCCUUUUUGUAUGCUGCUUUGUUGAAUGGUUGUAGGUGGUGGUUGCGUUCAACUAGAGUUAAUGUUGAUGGUUUUAAUGAAUGGGCUAUGGCUAAUGGUUAUACAAGUGUUUCUAGUGUUGAGUGCUAUUCUAUUUUGGCAGCAAA
AACUGGUGUUAGUGUUGAACAAUUGUUAGCUUCCAUUCAACAUCUUCAUGAAGGUUUUGGUGGUAAAAACAUACUUGGUUAUUCUAGUUUAUGUGAUGAGUUCACACUAGCUGAAGUUGUGAAGCAGAUGUAUGGUGUUAACUUGCAAAGUGGUAAGGUUAUUUUUGGUUUAAAACAAUGUUUU
UAUUUAGCGUUUUCUUCACAAUGUUUUGGGCAGAACUCUUUAUUUAUACAAACACUAUAUGGAUAAACCCUGUGAUACUUACACCUAUAUUUUGUCUACUUUUGUUUUUGUCAUUAGUUUUAACUAUGUUUCUUAAACAUAAGUUUUUGUUUUUGCAAGUAUUUUUAUUACCUACUGUUAUUGCA
ACUGCUUUAUAUAAUUGUGUUUUGGAUUAUUACAUAGUAAAAUUUUUGGCUGACCAUUUUAACUAUAAUGUUUCAGUAUUACAAAUGGAUGUUCAGGGUUUAGUUAAUGUUUUGGUUUGUUUAUUUGUUGUAUUUUUACACACAUGGCGCUUUUCUAAAGAACGUUUUACACAUUGGUUUACAUA
UGUGUGUUCUCUUAUAGCAGUAGCUUACACUUAUUUUUAUAGUGGUGACUUUUUGAGUUUGCUUGUUAUGUUUUUAUGUGCUAUAUCUAGUGAUUGGUACAUUGGUGCCAUUGUUUUUAGGUUGUCACGUUUGAUUGUAAUUUUUCACCUGAAAGUGUAUUUAGUGUUUUGGUGAUGUGAAAC
UUACUUUAGUUGUUUAUUUAAUUUGUGGUUAUUUAGUUUGUACUUAUUGGGGCAUUUUGUAUUGGUUCAAUAGGUUUUUUAAAUGUACUAUGGGUGUUUAUGAUUUUAAGGUGAGUGCUGCUGAAUUUAAAUACAUGGUUGCUAAUGGACUUCAUGCACCACAUGGACCUUUUGAUGCACUUUGG
UUAUCAUUCAAACUACUUGGUAUUGGUGGUGACCGUUGUAUAAAAAUUUCAACUGUCCAAUCCAAACUGACUGAUUUGAAGUGUACUAAUGUUGUGUUAUUGGGUUGUUUGUCUAGUAUGAACAUUGCAGCUAAUUCUAGUGAAUGGGCUUAUUGUGUUGAUUUACACAAUAAGAUUAAUCUUUG

UGAUGACCCUGAAAAAGCUCAAGGUAUGUUGUUAGCACUCCUUGCGUUCUUUCUAAGUAAACAUAGUGAUUUUGGUCUUGAUGGCCUUAUUGAUUCUUAUUUUGAUAAUAGUAGCACCCUUCAGAGUGUUGCUUCAUCAUUUGUUAGUAUGCCAUCAUAUAUUGCUUAUGAAAAUGCUAGACAAG
CUUAUGAAGAUGCUAUUGCUAAUGGAUCUUCUUCUCAACUUAUUAAACAAUUGAAGCGUGCCAUGAAUAUCGCAAAGUCUGAAUUUGAUCAUGAGAUAUCUGUUCAGAAGAAAAUUAAUAGAAUGGCUGAACAAGCUGCUACACAGAUGUAUAAAGAAGCACGCUCUGUUAAUAGAAAAUCUAAA
GUUAUUAGUGCUAUGCACUCUUUACUUUUUGGAAUGUUAAGACGUUUGGAUAUGUCUAGUGUUGAAACUGUUUUGAAUUUAGCACGUGAUGGUGUUGUGCCAUUGUCAGUUAUACCUGCAACUUCAGCUUCCAAACUAACUAUUGUUAUGCUGAAUCUUAUUCUAAGAUUGUUUGUGA
UGGUUCUGUUCAUUAUGCUGGAGUUGUUUGGACACUUAAUGAUGUUAAAGACAAUGAUGGUAGACCUGUUCAUGUUAAAGAGAUUACAAAGGAAAAUGUUGAAACUUUGACAUGGCCUCUUAUCCUUAAUUGUGAACGUGUUGUUAAACUUCAAAAUAAUGAAAUUAUGCCUGGUAAACUUAAGC
AAAAACCUAUGAAAGCUGAGGGUGAUGGUGGUGUUUUAGGUGAUGGUAAUGCCUUGUAUAAUACUGAGGGUGGUAAAACUUUUAUGUACGCUUAUAUUUCUAAUAAAGCUGACCUUAAAUUUGUUAAGUGGGAGUAUGAGGGUGGUUGCAACACAAUCGAGUUAGACUCUCCUUGUCGAUUUAUG
GUCGAAACACCUAAUGGUCCUCAAGUGAAGUAUUUGUAUUUUGUUAAAAAUUUAAACACCUUACGUAGAGGUGCCGUUCUUGGUUUUAUAGGUGCCACAAUUCGUCUACAAGCUGGUAAACAAACUGAAUUGGCUGUUAAUUCUGGACUUUUAACUGCUUGUGCUUUUUCUGUUGAUCCAGCAAC
UACUUACUUGGAAGCUGUUAAACAUGGUGCAAAACCUGUAAGUAAUUGUAUUAAGAUGUUAUCUAAUGGUGCUGGUAAUGGUCAAGCUAUAACAACUAGUGUAGAUGCUAACACCAAUCAAGAUUCUUAUGGUGGAGCGUCUAUUUGUUUGUAUUGUCGAGCUCACGUUCCUCACCCUAGUAUGG
AUGGUUACUGUAAGUUUAAGGGUAAAUGUGUUCAGGUUCCUAUUGGUUGUUUGGAUCCUAUUAGGUUUUGUUUAGAAAAUAAUGUGUGUAAUGUUUGUGGUUGCUGGUUGGGACAUGGAUGUGCUUGUGACCGUACAACUAUUCAAAGUGUUGACAUUUCUUAUUUAAACGAGCAAGGGGUUCUA
GUGCAGCUCGACUAGAACCCUGUAAUGGCACGGACAUCGAUAAGUGUGUUCGUGCUUUUGACAUUUAUAAUAAAAAUGUUUCAUUCUUGGGUAAGUGUUUGAAGAUGAACUGUGUUCGUUUUAAAAAUGCUGAUCUUAAGGAUGGUUAUUUUGUUAUAAAGAGGUGUACUAAGUCGGUUAUGGAA
CACGAGCAAUCCAUGUAUAACCUACUUAACUUUUCUGGUGCUUUGGCGAGCAUGACUUCUUUACUUCAUUGGAAAGAUGGCAGAGUCAUUUAUGGUAAUGUUAGUAGACAUAAUCUUACUAAAUAUACUAUGAUGGACUUGGUCUAUGCGUAACUUUGAUGAACAAAAUUGUGAUGUUCUAAA
AGAAGUAUUAGUUUUAACUGGUUGUUGUGACAAUUCUUAUUUUGAUAGUAAGGGUUGGUAUGACCCAGUUGAAAAUGAAGAUAUACAUAGAGUUUAUGCAUCUCUUGGCAAAAUUGUAGCUAGAGCUAUGCUUAAAUGCGUUGCUCUAUGUGAUGCGAUGGUUGCUAAAGGUGUUGUUGGUGUUU
UAACAUUAGAUAACCAAGAUCUUAAUGGUAACUUUUAUGAUUUUGGUGAUUUUGUUGUUAGCUUACCUAAUAUGGGUGUUCCCUGUUGUACAUCAUAUUAUUCUCUUAUAUGAUGCCUAUUAUGGGUUUAACUAAUUGUUUAGCUAGUGAGUGUUUUGUCAAGAGUGAUAUUUUUGGUAGUGAUUUU
AAAACUUUUGAUUUGCUUAAGUAUGAUUUCACUGAACAUAAAGAAAAUUUAUUCAAUAAGUACUUUAAGCAUUGGAGUUUUGAUUAUCAUCCUAAUUGUAGUGACUGUUAUGAUGAUAUGUGUGUUAUACAUUGUGCUAAUUUUAAUACACUAUUUGCCACAACUAUACCAGGUACUGCUUUUGG
UCCACUAUGUCGUAAAGUUUUUAUAGAUGGUGUUCCACUUGUUACAACUGCUGGUUAUCAUUUUAAGCAAUUAGGUUUGGUUUGGAAUAAAGAUGUUAACACACACUCAGUUAGGUUGACAAUUACUGAACUUUUGCAAUUUGUCACCGACCCUUCCUUGAUAAUAGCUUCUUCCCCAGCACUCG
UUGAUCAACGCACUAUUUGUUUUUCUGUUGCAGCAUUGAGUACUGGUUUGACAAAUCAAGUUGUUAAGCCAGGUCAUUUUAAUGAAGAGUUUUAUAACUUUCUUCGUUUAAGAGGUUUCUUUGAUGAAGGUUCUGAACUUACAUUAAAACAUUUCUUCUUCGCACAGAAUGGUGAUGCUGCUGUU
AAAGAUUUGACUUUUACCGUUAUAAUAAGCCUACCAUUUAGAUAUUUGUCAAGCUAGAGUCACAUAUAAGAUAGUCUCCUCGUUAUUUUGACAUUUAUGAAGGCAUGUGAAGUUGUUGUAACAAAUCUUAAUAAGAGUGCUGGUUGGCCAUUAAAUAAGUUUGGUAAAGC
UAGUUUGUAUUAUGAAUCUAUAUCUUAUGAAGAACAGGAUGCUUUGUUUGCUUUGACAAAGCGUAAUGUCUUCCCUACUAUGACACAGCUGAAUCUUAAGUAUGCUAUUAGUGGUAAAGAACGUGCUAGAACUGUUGGUGGUGUUUCUCUGUUGUCCACAAUGACCACAAGACAAUACCAUCAAA
AACAUCUUAAAUCCAUUGUUAAUACACGCAAUGCCACUGUUGUUAUUGGUACUACCAAAUUUUAUGGUGGUUGGAAUAAUAUGUUGCGUACUUUAAUUGAUGGUGUUGAAAACCCUAUGCUCAUGGGUUGGGAUUAUCCCAAAUGUGAUAGAGCUUUGCCUAACAUGAUACGUAUGAUUUCAGCC
AUGGUGUUGGGCUCUAAGCAUGUUAAUUGUUGUACUGCAACAGAUAGGUUUUAUAGGCUUGGUAAUGAGUUGGCACAAGUUUUAACAGAAGUUGUUUAUUCUAAUGGUGGUUUUUAUUUUAAGCCAGGUGGUACGACUUCUGGUGACGCUAGUACAGCUUAUGCUAAUUCUAUUUUUAACAUUUU
UCAAGCCGUAAGCUCUAACAUUAACAGGUUGCUUAGUGUCCCAUCAGAUUCAUGUAAUAAUGUUAAUGUUAGGGAUCUACAACGACGUCUGUAUGAUAAUUGCUAUAGGUUAACUAGUGUUGAAGAGUCAUUCAUUGAUGAUUAUUAUGGUUAUCUUAGGAAACAUUUUUCAAUGAUGAUUCUCU
CUGAUGAUGGUGUUGUCUGUUAUAACAAGGAUUAUGCUGAGUUAGGUUAUAUAGCAGACAUUAGUGCUUUUAAAGCCACUUUGUAUUACCAGAAUAAUGUCUUUAUGAGUACUUCUAAAUGUUGGGUUGAAGAAGAUUUAACUAAGGGACCACAUGAGUUUUGUUCCCAGCAUACUAUGCAAAUA
GUUGACAAAGAUGGUACCUAUUAUUUGCCUUACCCAGAUCCUAGUAGGAUCUUGUCAGCUGGUGUUUUUGUUGAUGAUGUUGUUAAGACAGAUGCUGUUGUUUUGUUAGAACGUUAUGUGUCUUUAGCUAUUGAUGCAUACCCUCUUUCAAAACACCCUAAUUCUGAAUAUCGUAAGGUUUUUUA
CGUAUUACUUGAUUGGUUAAGCAUCUUAACAAAAAUUUGAAUGAGGGUGUUCUUGAAUCUUUUUCUGUUACACUUCUUGAUAACGAAGAUAAGUUUUGGUGUGAAGAUUUUUAUGCUAGUAUGUAUGAAAAUUCUACGAUAUUGCAAGCUGCUGGUUUAUGUGGUUGUGGUUCGAACAA
CUGUACUUCGUUGUGGUGAUUGUCUGCGUAAGCCUAUGUUGUGCACUAAAUGCGCAUAUGAUCAUGUAUUUGGUACCGACCACAAGUUUAUUUUGGCUAUAACACCGUAUGUAUGUAAUGCAUCAGGUUGUGGUGUUAGUGAUGUCAAAAAAUUGUAUCUUGGUGGUUUGAAUUACUAUUGUACA
AAUCAUAAACCACAGUUGUCUUUUCCAUUAUGUUCAGCUGGUAAUAUAUUUGGUUUAUAUAAAAAUUCAGCAACUGGUUCCUUAGAUGUUGAAGUUUUUAAUAGGCUUGCAACGUCUGAUUGGACUGAUGUUAGGGACUAUAAACUUGCUAAUGAUGUUAAAGAUACACUUAGACUCUUUGCGGC
UGAAACUAUUAAAGCUAAAGAAGAGAGUGUUAAGUCUUCUUAUGCUUUUGCAACUCUUAAAGAGGUUGUUGGACCUAAAGAAUUGCUUCUUAGUUGGGAAAGUGGUAAAGUUAAACCACCUUUGAAUCGUAAUUCUGUUUUCACCUGUUUUCAAAUAAGUAAGGACUCAAAAUUCCAAAUAGGUG
AGUUCAUCUUUGAGAAGGUUGAAUAUGGUUCUGAUACUGUUACGUAUAAGUCUACUGUAACUACUAAGUUAGUUCCUGGUAUGAUUUUUGUCUUAACAUCUCACAAUGUCCAACCUUUACGUGCACCAACUAUUGCUAACCAAGAGAAGUAUUCUAGCAUUUAUAAAUUGCACCCUGCUUUUAAU
GUCAGUGAUGCAUAUGCUAAUUUGGUUCCAUAUUACCAACUUAUUGGUAAACAAAAGAUAACUACAAUACAGGGUCCUCCUGGUAGUGGUAAGUCACAUUGUUCUAUUGGACUUGGAUUGUACUACCCAGGUGCGCGUAUUGUUUUUGUUGCUUGUGCCCAUGCUGCUGUUGAUUCCUUAUGUGC
AAAAGCUAUGACUGUUUAUAGCAUUGAUAAGUGUACUAGGAUUAUACCUGCAAGAGCUCGGGUUGAGUGUUAUAGUGGCUUUAAACAAAUAACACUAGUGCACAAUACAUAUUUAGCACUGUUAACGCAUUACCUGAGUGUAAUGCUGAUAUCGUUGUUGUAGAUGAAGUUUCAAUGUGUACAA
AUUAUGACCCUUUCUGUUAUUAAUCAGCGUUUAUCAUAUAAACAUAUUGUUUAUGUUGGUGAUCCACAACAACUUCCUGCACCUAGAGUAAUGAUUACUAAAGGUGUUAUGGAGCCUGUUGAUUAUAACGUUGUUACUCAACGUAUGUUGUGCUAUAGGCCCUGAUGUUUUUCUUCAUAAAUGUGUACAA
AGAUGUCCUGCUGAAAUAGUUAAUACAGUUUCUGAACUUGUUUAUGAGAACAAGUUUGUCCCUGUUAAACCUGCUAGUAAACAGUGUUUUAAAGUCUUUUUUAAGGGUAAUGUACAGGUUGACAAUGGUUCUAGUAUUAACAGAAAGCAGCUUGAAAUAGUUAAGCUGUUUUUAGUUAAAAAUCC
AAGUUGGAGUAAGGCUGUGUUUAUUUCUCCUUAUAAUAGUCAGAAUUAUGUUGCUAGUAGAUUUUUAGGACUUCAAAUUCAAACUGUUGAUUCUUCUCAAGGUAGUGAGUAUGAUUAUGUAAUCUAUGCACAAACUUCUGACACUGCACAUGCUUGCAAUGUAAACCGUUUUAAUGUUGCUAUAA
CACGUGCUAAGAAGGGUAUAUUUUGUGUAAUGUGUGAUAAAACUUUGUUUGAUUCACUUAAGUUUUUUGAGAUUAAACAUGCAGAUUUACACUCUAGCCAGGUUUGUGGCUUGUUUAAAAAUUGUACACGCACUCCUCUUAAUUUACCACCAACUCAUGCACACACUUUCUUGUCGUUGUCAGAU
CAGUUUAAGACUACAGGUGAUUUAGCUGUUCAAAUAGGUUCAAAUAACGUUUGUACUUAUGAACAUGUUAUAUCAUUUAUGGGUUUUAGGUUUGAUAUUAGUAUUCCUGGUAGUCAUAGUUUGUUUUGUACACGUGACUUUGCUAUUCGCAAUGUGCGUGGUUGGUUGGGUAUGGAUGUUGAAAG
UGCUCAUGUUUGUGGCGAUAACAUAGGUACUAAUGUUCCUUUACAGGUUGGUUUUUCAAAUGGUGUUAAUUUUGUUGUGCAAACUGAAGGUUGUGUGUCUACCAAUUUUGGUGAUGUUAUUAAACCUGUUUGUGCAAAAUCUCCACCAGGUGAACAAUUUAGACACCUUGUUCCUCUUUUACGUA
AAGGACAACCUUGGUUAAUUGUUCGUAGACGCAUUGUGCAAAUGAUAUCUGAUUAUUUGUCCAAUUUGUCUGACAUUCUUGUCUUUGUUUUGUGGGCAGGUAGUUUGGAAUUAACUACAAUGCGUUACUUUGUAAAAAUAGGGCCAAUUAAAUAUUGUUAUUGUGGUAAUUCUGCCACAUUGUUAU
AAUUCAGUUAGUAAUGAAUAUUGUUGUUUUAAACAUGCAUUGGGUUGUGAUUAUGUUUACAAUCCGUAUGCUUUUGAUAUACAACAGUGGGGUUAUGUUGGUUCCUUGAGCCAAAACCACCACACAUUCUGUAACAUUCAUAGAAACGAGCAUGAUGCCUCUGGUGAUGCUGUUAUGACACGUUG
UUUGGCAGUACAUGAUUGUUUUGUCAAAAAUGUUGAUUGGACUGUAACGUACCCCUUUAUUGCAAAUGAGAAAUUUAUCAAUGGCUGUGGGCGUAAUGUCCAGGGACAUGUUGUUCGUGCAGCCUUGAAAUUGUAUAAACCUAGUGUUAUUCAUGACAUUGGUAAUCCUAAAGGUGUACGUUGUG
CUGUUACUGAUGCCAAAUGGUACUGUUAUGACAAGCAACCUGUUAAUAGUAAUGUCAAGUUGUUGGAUUAUGAUUAUGCAACUCAUGGUCAACUUGAUGGUCUUUGUCUAUUCUGGAAUUGUAAUGUUGAUAUGUAUCCAGAAUUUUCAAUUGUGUGUCGUUUUGACACACGUACUCGUUCUGUU
UUUAAUUUAGAAGGUGUUAAUGGUGGUUCUCUUUAUGUUAACAAACAUGCGUUUCAUACACCAGCAUAUGAUAAACGUGCUUUUGUUAAAUUAAAACCUAUGCCCUUUUUUUACUUUGAUGACAGUGAUUGUGAUGUUGUGCAAGAACAAGUUAAUUAUGUACCCCUUCGCGCUAGUAGUUGUGU
UACCCGUUGUAAUAUAGGUGGUGCUGUUUGUUCAAAACAUGCAAAUUUGUAUCAAAAAUAUGUUGAGGCAUAUAAUACAUUUACACAGGCUGGUUUUAACAUUUGGGUACCACAUAGUUUUGAUGUUUAUAAUUUGUGGCAAAUUUUUAUUGAAACUAAUUUACAAAGUCUUGAAAAUAUAGCAU
UUAAUGUUGUAAAAAAAGGGUGUUUUACUGGUGUUGAUGGUGAGUUACCUGUUGCAGUUGUUAACGACAAAGUUUUUGUUCGCUAUGGCGAUGUUGACAACUUAGUUUUUACAAAUAAAACAACAUUGCCUACUAAUGUUGCUUUUGAAUUGUUUGCAAAACGAAAAAUGGGUUUAACACCACCA
UUGUCUAUUCUCAAAAAUCUCGGUGUUGUUGCUACAUAUAAAUUUGUUUUAUGGGAUUAUGAAGCUGAAAGACCUUUUACCUCAUAUACUAAGAGUGUAUGUAAAUACACUGAUUUUAAUGAGGAUGUUUGUGUUUGUUUUGACAAUAGUAUUCAGGGUUCGUAUGAGCGUUUUACGCUUACUAC
GAACGCUGUUUUAUUUUCUACUGUUGUCAUUAAAAAUUUAACACCUAUAAAGUUGAAUUUGGUAUGUUGAAUGGUAUGCCAGUUUCUUCUAUAAGGGUGAUAAAGGUGUUGAAAAAUUAGUUAAUUGGUACAUUAUGUUGCUAAAAAUGGUCAAUUUCAAGAUCACUAUGAUGGUUUUUACA
CUCAAGGUAGGAAUUUAUCAGACUUUACACCAAGAAGUGAUAUGGAGUAUGAUUUUCUUAACAUGGAUAUGGGUGUUUUUAUUAAUAAAUAUGGUCUUGAGGAUUUUAAUUUUGAACAUGUUGUAUAUGGUGAUGUUUCAAAAACUACAUUAGGAGGUCUUCAUUUGUUGAUAUCACAGUUUAGG
CUUAGUAAAAUGGGUGUUUUGAAAGCUGAUGAUUUUGUCAUUGCUUCUGACACAACUUUGAGGUGCUGCACUGUUACUUAUCUUAAUGAACUUAGUUCAAAAGUUGUUUGUACUUAUAUGGAUUUGUUGUUGGACGACUUUGUUACUAUACUAAAGAGUUUAGAUCUUGGUGUAAUAUCUAAAGU
UCAUGAAGUUAUUAUAGAUAAUAAACCUUAUAGGUGGAUGUUGUGGUGUAAAGAUAACCACUUGUCCACUUUUUAUCCACAGUUGCAGUCUGCUGAAUGGAAGUGUGGUUAUGCUAUGCCACAAAUUUAUAAGCUUCAACGUAUGUGUUUGGAACCUUGUAAUUUAUAUAAUUAUGGUGCUGGUA
UUAAGUUGCCUAGUGGUAUAAUGUUAAAUGUUGUUAAAUACACUCAGCUUUGUCAAUACCUAAAUAGCACUACAAUGUGCGUACCUCAUAAUAUGCGUGUUUUGCACUAUGGUGCUGGUUCUGACAAAGGUGUGGCACCUGGUACAACUGUUUUAAAACGUUGGCUACCACCUGAUGCAAUAAUC
AUUGAUAAUGACAUCAAUGAUUAUGUUAGUGAUGCAGAUUUUAGCAUUACAGGUGAUUGUGCUACUGUUUACCUUGAAGAUAAGUUUGACUUACUUAUUUCUGAUAUGUAUGAUGGUAGAAUUAAAUUUUGUGAUGGUGAAAACGUCUCUAAAGAUGGUUUUUUUACUUAUCUUAAUGGUGUUAU
UAGAGAAAAAUUAGCUAUUGGUGGUAGUGUUGCCAUUAAGAUUACAGAAUAUAGUUGGAAUAAGUAUCUUUAUGAAUUAAUACAGAGAUUUGCUUUUUGGACUUUGUUUUGCACGUCUGUUAAUACAUCCUCUUCAGAAGCUUUUCUUAUUGGUAUUAAUUAUUUAGGUGACUUUAUUCAAGGUC
CUUUUAUAGCUGGUAACACUGUUCAUGCUAAUUAUAUAUUUUGGCGUAAUUCUACUAUUAUGUCUUUGUCAUACAAUUCAGUUUUAGAUCUAAGUAAGUUUGAAUGUAAACAUAAGGCCACUGUUGUUGUUACACUUAAAGAUAGUGAUGUAAAUGAUAUGGUUUUGAGUUUGAUUAAGAGUGGU
AGGUUGUUGUUACGUAAUAGUGGCCGUUUUGGUGGUUUUAGUAAUCAUUUAGUCUCAACUAAAUGAAACUUUUCUUGAUUUUGCUUAUUUUGCCCCUGGUUUCUUGCUUUUCUACAUGUAACAGUAAUGCUAGUAUUUCUAUGUUACAAUUAGGUGUUCCUGAUAACUCUUCAACUAUUGUCACA
GGUUUGUUGCCAGUCCAUUGGAUUUGUGCUAAUCAGAGCACAUCUAGUUACCCAGCCAAUGGCUUUUUCUAUAUUGAUGUCGGUAAACACCGUAGUGCUUUUGCACUCCAUAGUGGUUAUUAUGAUGCUAACCAGUAUUAUAUUUAUCUCACUAAUAAAAUACAUUUAAAUGCUCCUGUCACUCU
GAAGAUUUGUAAGUUUGGAAACACUUCUUUUGAUUUUUUAAGUAAUGUUUCUACUUCUCAUCAUUGUAUAGUUAAUUCGUCAUUCACAGAACAGUUAGGUGUGCCUUUGGGCAUAACUAUAUCGGGUGAAACUGUACGUUUGCAUUUAUAUAAUGCAACUCGCACCUUUUAUGUGCCUGCCGCUU
AUAAACUUACUAAACUUAGUGUUAAAUGUUACUUUAGUGAAUCCUGUGUUUUUAGUGUUGUCAAUGCUACCGUUACUGUUAAUGUCACCACACUUAAUGGCCGUAUAGUUAAUUACACUGUUUGUGAUGAUUGUAAUGGUUACACUGAUAACAUAUUUUCUGUUCAACAGGAUGGCCGCAUUCCU
AAUGGUUUUUCUUUUAAUAAUUGGUUUUUGUUACAUAGUGGACGUGUCUCUAGACUUUACCAACCACUUCGUUUAACUUGUUUAUGGCCUGUACCUGGUUUUGUUUAUUUUAACGCCACUGGUUUCUGAUGUUAAUUGUAAUGGUUACUCAA
UCAUUCUGUUGCUGAUGUUAUGCGUUACAAUCUUAACUUCAGUUCUAAUUCUGUGGAUAAUCUCAAGAGUGGUGUUAUAGUUUUUAAAACUCUACAGUACGAUGUUUUGUUUUACUGUAGUAAUUCUUCUUCGGGCGUUCUAGACACCACAAUACCUUUUGGCCCUUCCUCUCAACCUUAUUACU
GUUUUAUAAAUAGUACCAUCAACACCACUCAUGUUAGCACUUUUGUGGGUGUCCUACCACCCAUUGUGCGUGAGAUUGUUGUUGCUAGAACUGGUCAGUUUUAUAUUAAUGGUUUUAAGUAUUUUGAUUUGGGUUUUAUCGAAGCUGUUAAUUUUAAUGUCACGACAGCUAGUGCUACAGAUUUU
UGGACGGUUGCAUUUGCUACUUUUGUUGAUGUUUUGGUUAAUGUUAGUGCAACUAACAUUCAAAACUUACUUUAUUGCGAUUCUCCAUUUGAAAAGUUGCAGUGUGAGCACUUGCAGUUUGGAUUGCAAGAUGGUUUUUAUUCUGCAAAUUUUCUUGAUGAUAAUGUUUUGCCUGAUACUUAUGU
UGCACUUCCUAUUUAUUAUCAACAUACUGAUAUAAAUUUUACUGCGACUGCAUCUUUUGGUGGUUCCUUGUUAUGUUUGCAAACCACAUCAGGUUAAUAUAUCUCUUAAUGGUAAUACUUCAGUGUGUGUUAGAACAUCUCAUUUUUCAAUUAGGUAUAUUUAUAACCGCGUUAAGAGUGGUUCAC
CAGGUGACUCUUCAUGGCACAUUUAUUUAAAGAGUGGCACUUGUCCAUUUUCUUUUUCUAAGUUAAAUAAUUUUCAAAAGUUUAAGACUAUUUGUUUCUCAACCGUCGUAGUGCCUGGUAGUUGUAAUUUUCCACUUGAAGCCACCUGGCAUUACACUUCUUAUACUAUUGUUGGUGCUUUGUAU
GUUACUUGGUCUGAAGGUAAUUCCAUUACUGGUGUACCUUAUCCUGUCUCUGGUAUUCGUGAGUUUAGUAAUUUAGUUUAAAUAAUUGUACCAAAUAUAAUUAUGAUUAUGUUGGUACCUGGAAUUAUACGUUCUUCAAACCAGUCACUUGCUGGUGGUAUUACAUAUGUUCUAACCUGG
UAAUUUACUUGGUUUUAAAAAUGUUUCCACUGGUAACAUUUUUAUUGUGACACCAUGUAACCAACCAGACCAAGUAGCUGUUUAUCAACAAAGCAUUAUUGGUGCCAUGACUGCUGUUAAUGAGUCUAGAUAUGGCUUGCAAAACUUACUACAGUUACCUAACUUUUAUUAUGUUUACUAACUGG
GUAACAAUUGCACUACGGCCGUUAUGACUUAUUCUAAUUUUGGUAUUUGUGCUGAUGGUUCUUUAAUUCCUGUUCGUCCGCGUAAUUCUAGUGAUAAUGGUAUUUCAGCCAUAGUCACUGCUAAUUUAUCCAUUCCCUCUAACUGGACUACUUCAGUUCAAGUUGAGUACCUCCAAAUUACUAGU
ACUCCAAUAGUUGUUGAUUGUGCUACUUAUGUGUGUAAUGGUAACCCUCGCUGUAAGAAUCUACUUAAGCAGUAUACUUCUGCUUGUAAAACUAUUGAAGAUGCCUUACGACUUAGUGCUCAUUUGGAAACUAAUGAUGUUAGUAGUAUGCUAACUUUUGAUAGCAAUGCUUUUAGUUUGGCUAA

```
UGUUACUAGUUUUGGAGAUUAUAACCUUUCUAGUGUUUUACCUCAGAGAAACAUUCAUUCAAGCCGUAUAGCAGGACGUAGUGCUUUGGAAGAUUUGUUGUUUAGCAAAGUUGUUACAUCUGGUUUGGGUACUGUUGAUGUUGACUAUAAGUCUUGUACUAAAGGUCUUUCUAUUGCUGACCUUG
CUUGUGCUCAGUACUACAAUGGCAUAAUGGUUUUGCCAGGUGUUGCUGAUGCUGAACGUAUGGCCAUGUACACAGGUUCUCUUAUAGGUGGCAUGGUGCUCGGAGGUCUUACAUCAGCAGCCGCCAUACCUUUUUCUUUGGCACUGCAAGCACGACUUAACUAUGUUGCUUUACAAACUGAUGUG
CUUCAAGAAAAUCAGAAAAUUUUGGCUGCAUCAUUUAAUAAGGCUAUUAAUAACAUUGUUGCUUCUUUUAGUAGCGUUAAUGAUGCUAUUACACAAACUGCAGAGGCUAUACAUACUGUUACUAUUGCACUUAAUAAGAUUCAGGAUGUUGUUAAUCAACAGGGUAGUGCUCUUAACCAUCUCAC
UUCACAAUUGAGACAUAAUUUUCAGGCCAUUUCUAAUUCAAUUCAAGCUAUUUAUGACCGGCUUGAUUCAAUUCAAGCCGAUCAACAAGUUGACAGAUUAAUUACUGGACGGCUUGCAGCUUUGAAUGCAUUUGUUUCCCAAGUUUUGAAUAAAUAUACUGAAGUUCGUAGUUCCAGACGCUUAG
CACAGCAGAAGAUUAAUGAAUGUGUCAAAUCACAAUCUAAUAGAUAUGGUUUUUGUGGCAAUGGCACCCAUAUCUUUUCAAUCGUCAACUCAGCUCCAGAUGGUUUGCUUUUUCUUCAUACUGUUUUGCUGCCAACCGACUACAAGAAUGUAAAGGCGUGGUCGGGUAUCUGUGUUGAUGGCAUU
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CGUUGAUGUUAAUAAAACAUUACAAGAGUUUGCACAAAACUUACCAAAGUAUGUUAAGCCUAAUUUUGACUUGACUCCUUUUAAUUUAACAUAUCUUAAUUUGAGUUCUGAGUUGAAGCAACUCGAAGCUAAAACUGCUAGUCUUUUCCAAACUACUGUUGAAUUACAAGGUCUUAUUGAUCAGA
UUAACAGUACAUAUGUUGAUUUGAAGUUGCUUAAUAGGUUUGAAAAUUAUAUUAAAUGGCCUUGGUGGGUUUGGCUCAUUAUUUCUGUUGUUUUUGUUGUAUUGUUGAGUCUUCUUGUGUUUUGUUGUCUUUCUACAGGUUGUUGUGGUUGUUGCAAUUGUUUAACUUCAUCAAUGCGAGGUUGU
UGUGAUUGUGGUUCAACUAAACUUCCUUAUUACGAAUUUGAAAAGGUCCACGUUCAAUAAUGCCUUUCGGUGGCCUAUUUCAACUUACUCUUGAAAGUACUAUUAAUAAAGAGUGUGGCUAAUCUCAAAUUACCACCUCAUGAUGUUACUGUCUUGCGUGACAAUCUCAAACCUGUUACUACACUU
AGUACUAUCACUGCUUAUUUGUUAGUUAGUUUGUUUGUCACUUAUUUUGCUUUAUUCAAACCUCUUACUGCUAGAGGUCGUGUUGCUUGUUUUGUUUUAAAACUAUUGACACUAUUUGUCUAUGUGCCUUUUAUGGUAUGUAUCUUGACAGUUUUAUAAUUUUUUCUACGCUGUU
GUUUCGAUUCAUACAUGUUGGCUAUUAUGCCUAUCUCUAUAAAAAUUUUUCAUUUGUUUUGUUCAAUGUUACUAAACUAUGCUUCGUUUCAGGCAAGUGUUGGUAUCUUGAACAAUCAUUUUAUGAAAAUCGUUUUGCUGCUAUUUAUGGUGGUGACCACUAUGUCGUUUUAGGUGGUGAAACUA
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CAAUGGCAUUGUCCUCAAUUCCAUUUUAUGGCUCCUUGUUAUGAUAUUUUUCUUUGUGUUGGCAAUGACUUUUAUUAAACUGAUUCAAUUGUGUUUUACUUGUCAUUAUUUUUUUAGUAGGACAUUAUAUCAACCAGUUUAUAAAAUUUUUCUUGCUUACCAAGAUUAUAUGCAAAUAGCACCUG
UUCCAGCUGAAGUACUAAAUGUCUAAACUAAACGAUGUCUAAUAGUAGUGUGCCUCUUUCAGAGGUUUAUGUCCAUUUACGUAACUGGAACUUUAGUUGGAAUUUAAUUCUAACGCUUUUUAUAGUUGUGUUGCAGUAUGGGCAUUAUAAGUAUAGCAGACUUCUUUAUGGUUUAAAGAUGUCUG
UUUUAUGGUGUUUAUGGCCACUUGUUCUAGCUUUGUCUAUUUUUGACUGUUUUGUCAAUUUUAAUGUGGACUGGGUCUUUUUUGGUUUUAGUAUUCUUAUGUCUAUUAUUACACUUUGUUUGUGGGUUAUGUAUUUUGUUAAUAGUUUCAGACUUUGGCGCCGUGUUAAAACUUUUUGGGCUUUU
AAUCCUGAAACUAAUGCAAUCAUCUCUCCAGGUUUACGGACAUAAUUAUUACUUACCGGUGAUGGCUGCACCUACAGGUGUUACAUUAACACUUCUCAGUGGUGUAUCUUGUUUGAUGGCCAUAAGAUUGCUAACUCGUGUUCAAGUGGGUCAGUUGCCUAAAUAUGUAAUAGUUGCUACACC
UAGUACCACAAUUGUUUGUGACCGUGUUGGUCGCUCUGUUAAUGAAACAAGCCAGACUGGGUUGGGCAUUCUACGUCCGUGCUAAACAUGGUGAUUUUUCUGGUGUUGCCUCUCAGGAGGGUGUUUUGUCAGAAAGAGAGAAGUUGCUUCAUUUAAUCUAAACUAAACAAAAUGGCUAGUGUAAAU
UGGGCCGAUGACAGAGCUGCUAGGAAGAAAUUUCCUCCUCCUUCAUUUUACAUGCCUCUUUUGGUUAGUUCUGAUAAGGCACCAUAUAGGGUCAUCCCCAGGAAUCUUGUCCCUAUUGGUAAGGGUAAUAAAGAUGAGCAGAUUGGUUAUUGGAAUGUUCAAGAGCGUUGGCGUAUGCGCAGGGG
GCAACGUGUUGAUUUGCCUCCUAAAGUUCAUUUUUAUUACCUAGGUACUGGACCUCAUAAGGACCUUAAAUUCAGACAACGUUCUGAUGGUGUUGUUUUGGGUUGCUAAGGAAGGUGCUAAAACUGUUAAUACCAGUCUUGGUAAUCGCAAACGUAAUCAGAAACCUUUGGAACCAAAGUUCUCUA
UUGCUUUGCCUCCAGAGCUCUCUGUUGUUGAGUUUGAGGAUCGCUCUAAUAACUCAUCUCGUGCUAGCAGUCGUUCUUCAACUCGUAACAACUCACGAGACUCUUCUCGUAGCACUUCAAGACAACAGUCUCGCACUCGUUCUGAUUCUAACCAGUCUUCUUCAGACCUUGUUGCUGCUGUUACU
UUGGCUUUAAAGAACUUAGGUUUUGAUAACCAGUCGAAGUCACCUAGUUCUUCUGGUACUUCCACUCCUAAGAAACCUAAUAAGCCUCUUUCUCAACCCAGGGCUGAUAAGCCUUCUCAGUUGAAGAAACCUCGUUGGAAGCGUGUUCCUACCAGAGAGGAAAAUGUUAUUCAGUGCUUUUGUCC
UCGUGAUUUUAAUCACAAUAUGGGGGAUUCAGAUCUUGUUCAGAAUGGUGUUGAUGCCAAAGGUUUUCCACAGCUUGCUGAAUUGAUUCCCAAUCAGGCUGCGUUAUUCUUUGAUAGUGAGGUUAGCACUGAUGAAGUGGGUGAUAAUGUUCAGAUUACCUAUACCUACAAAAUGCUUGUAGCUA
AGGAUAAUAAGAACCUUCCUAAGUUCAUUGAGCAGAUUAGUGCUUUUACUAAACCCAGUUCUAUCAAAGAAAUGCAGUCACAAUCAACUCAUGCUGUUCAGAACACAGUACUUAAUGCUUCUAUUCCAGAACUCAUUAGCAUUAUAGAAAUUGUCAACGAGGUU
UUGCAUUAAAAUUGUUUUGUAAUUCCAGUUGAAUGUUUAUUAUUAUUAGUUGCAACCCCAUGCGUUUAGCGCAUGAUAAGGGUUUAGUCUUACACACAAUGGUAGGCCAGUGAUAGUAAAGUGUAAGUAAUUUGCUAUCAUAUUAACAUGUCUAGAGGAAAGUCAGAACUUUUUCUGUUUGUGUUG
UUGGAGUACUUAAAGAUCGCAUAGGCGCGCCAACAAUGGAAGAGCCAACAACAUAUCUAAAAAUGUUUUGUCUGGUACUUGUUAAUGAUA'
```

Makes a dataframe of sars-cov-2 mRNA nucleotides and mRNA antinucleotides.

In [8]:
```
translation_df1=pd.DataFrame(columns=['mRNA_Codons', 'mRNA_Codons_copy', 'Anticodons'])
for i in genome:
    translation_df1.loc[len(translation_df1.index)] = [i, i, i]
translation_df1
```

Out[8]:

	mRNA_Codons	mRNA_Codons_copy	Anticodons
0	A	A	A
1	C	C	C
2	U	U	U
3	U	U	U
4	U	U	U
...	...	...	...
27464	U	U	U
27465	G	G	G
27466	A	A	A
27467	U	U	U
27468	A	A	A

27469 rows × 3 columns

Translate codons into corresponding anticodons.

In [9]:
```
translation_df1['Anticodons']=translation_df1['Anticodons'].replace('A','1')
translation_df1['Anticodons']=translation_df1['Anticodons'].replace('U','A')
translation_df1['Anticodons']=translation_df1['Anticodons'].replace('1','U')
translation_df1['Anticodons']=translation_df1['Anticodons'].replace('C','2')
```

```
translation_df1['Anticodons']=translation_df1['Anticodons'].replace('G','C')
translation_df1['Anticodons']=translation_df1['Anticodons'].replace('2','G')
translation_df1
```

Out[9]:

	mRNA_Codons	mRNA_Codons_copy	Anticodons
0	A	A	U
1	C	C	G
2	U	U	A
3	U	U	A
4	U	U	A
...	...	...	...
27464	U	U	A
27465	G	G	C
27466	A	A	U
27467	U	U	A
27468	A	A	U

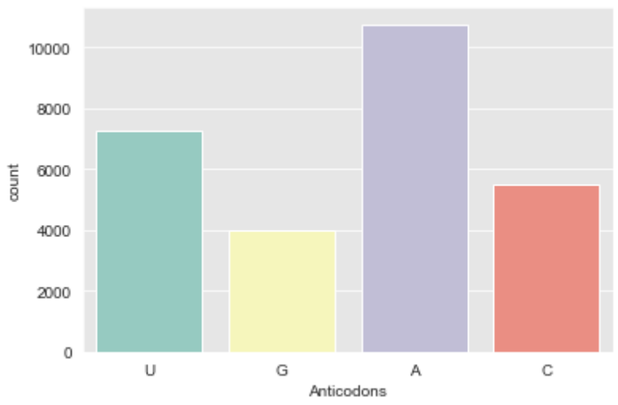
27469 rows × 3 columns

Data Exploration

Sars-cov-2 genome is made up of apoximatly 30% adenine, 18% guanine, 20% cytosine and 32% uracil.

In [199…
```
sns.countplot(translation_df1['Anticodons'], palette='Set3')
```

Out[199…
```
<AxesSubplot:xlabel='Anticodons', ylabel='count'>
```



Percentage of uricil in genome data.

In [200…
```
len(translation_df1['Anticodons'].loc[translation_df1['Anticodons']=='U'])/len(translation_df1['Anticodons'])*100
```

Out[200…
```
26.338781899595908
```

Percentage of guanine in genome data.

In [201…
```
len(translation_df1['Anticodons'].loc[translation_df1['Anticodons']=='G'])/len(translation_df1['Anticodons'])*100
```

Out[201…
```
14.49998179766282
```

Percentage of adonine in genome data.

In [202…
```
len(translation_df1['Anticodons'].loc[translation_df1['Anticodons']=='A'])/len(translation_df1['Anticodons'])*100
```

Out[202…
```
39.14594633950999
```

Percentage of cytosine in genome data.

In [203…
```
len(translation_df1['Anticodons'].loc[translation_df1['Anticodons']=='C'])/len(translation_df1['Anticodons'])*100
```

Out[203…
```
20.01528996323128
```

There is a class imbalance that will be resolved by oversampling.

Feature Engineering

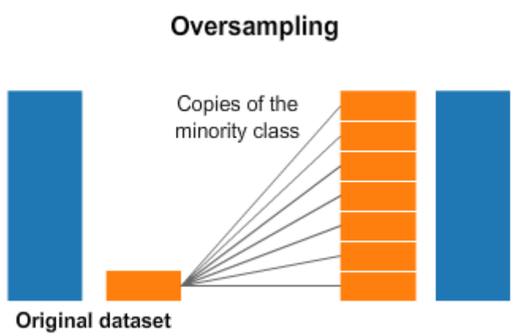
Represent nucleotides with numbers.

In [10]:
```
translation_df1['mRNA_Codons']=translation_df1['mRNA_Codons'].astype('category')
translation_df1['Anticodons']=translation_df1['Anticodons'].astype('category')
translation_df1['mRNA_Codons']=translation_df1['mRNA_Codons'].cat.codes
translation_df1['Anticodons']=translation_df1['Anticodons'].cat.codes
```

Oversampling selects data from minority class population to make up a larger share of the sample.

In [9]:
```
Image(filename='oversampling.png')
```

Out[9]:



In [11]:
```
oversample = RandomOverSampler(sampling_strategy='minority')
```

Reshape X and y so that they are 2d.

In [12]:
```
X1=translation_df1['mRNA_Codons'].values.reshape(-1, 1)
y1=translation_df1['Anticodons'].values.reshape(-1, 1)
```

Resample independent and dependent variable.

In [13]:
```
X1_resampled, y1_resampled = oversample.fit_resample(X1, y1)
```

Make a train test split of 80/20.

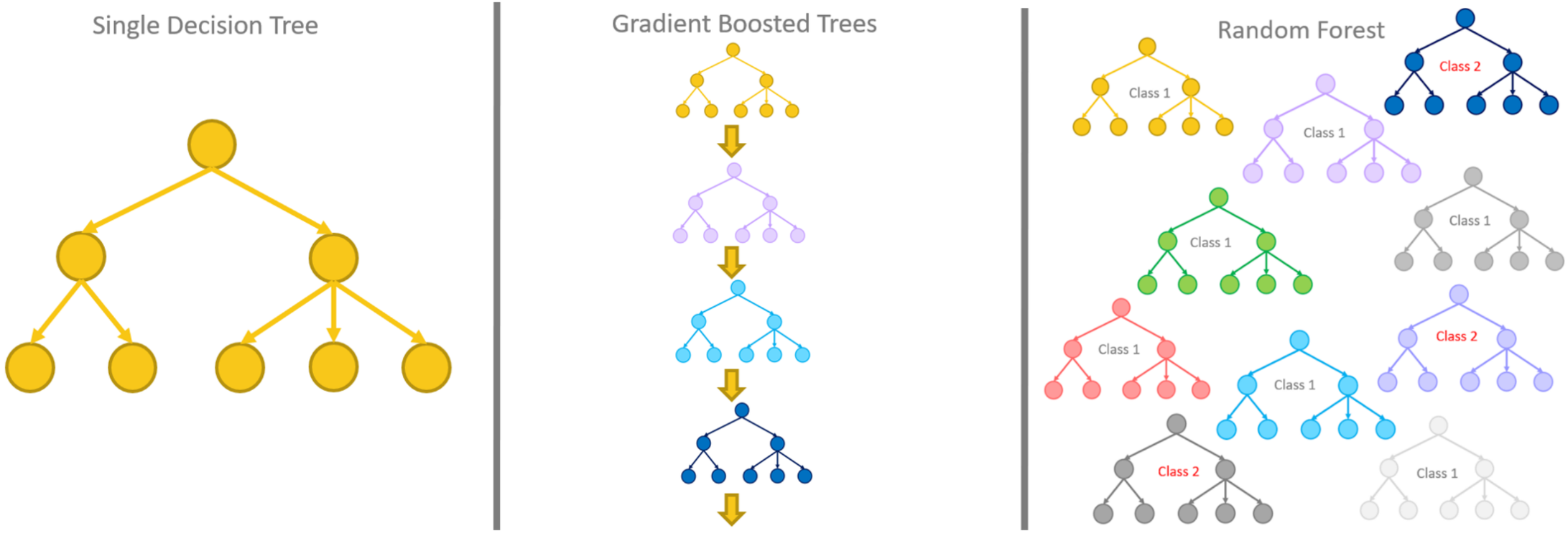
In [14]:
```
X1_train, X1_test, y1_train, y1_test = train_test_split(X1_resampled, y1_resampled, test_size=0.20, random_state=10)
```

Machine Learning Modeling

The following models will be used.

In [224…
```
Image(filename='trees.png')
```

Out[224…



Decision Trees split a node into two or more sub-nodes until node impurity is reduced and information gain is maximized.

Fit the model to the training data.

In [15]:
```
decision_tree = DecisionTreeClassifier()

decision_tree.fit(X1_train, y1_train)
```

Out[15]:
```
DecisionTreeClassifier()
```

Show hyperparameters.

In [143…
```
decision_tree.get_params()
```

Out[143…
```
{'ccp_alpha': 0.0,
 'class_weight': None,
 'criterion': 'gini',
 'max_depth': None,
 'max_features': None,
 'max_leaf_nodes': None,
 'min_impurity_decrease': 0.0,
 'min_impurity_split': None,
 'min_samples_leaf': 1,
 'min_samples_split': 2,
 'min_weight_fraction_leaf': 0.0,
 'presort': 'deprecated',
 'random_state': None,
 'splitter': 'best'}
```

The algorithm uses the gini index to reduce impurity during desicion splits. c is the number of classes and p is the probability of the class.

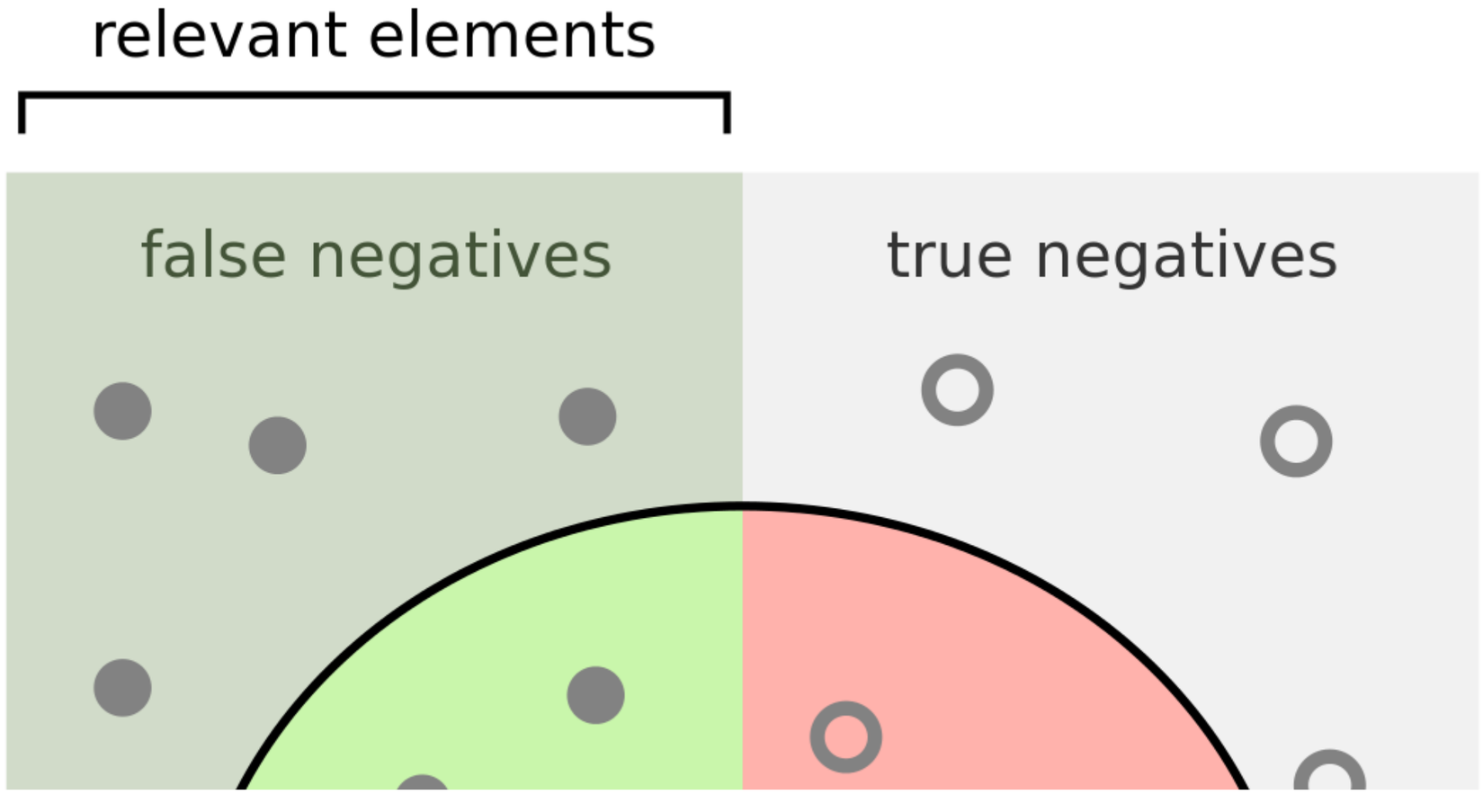
$$Gini = 1 - \sum_{i}^{c}(p_i)^2$$

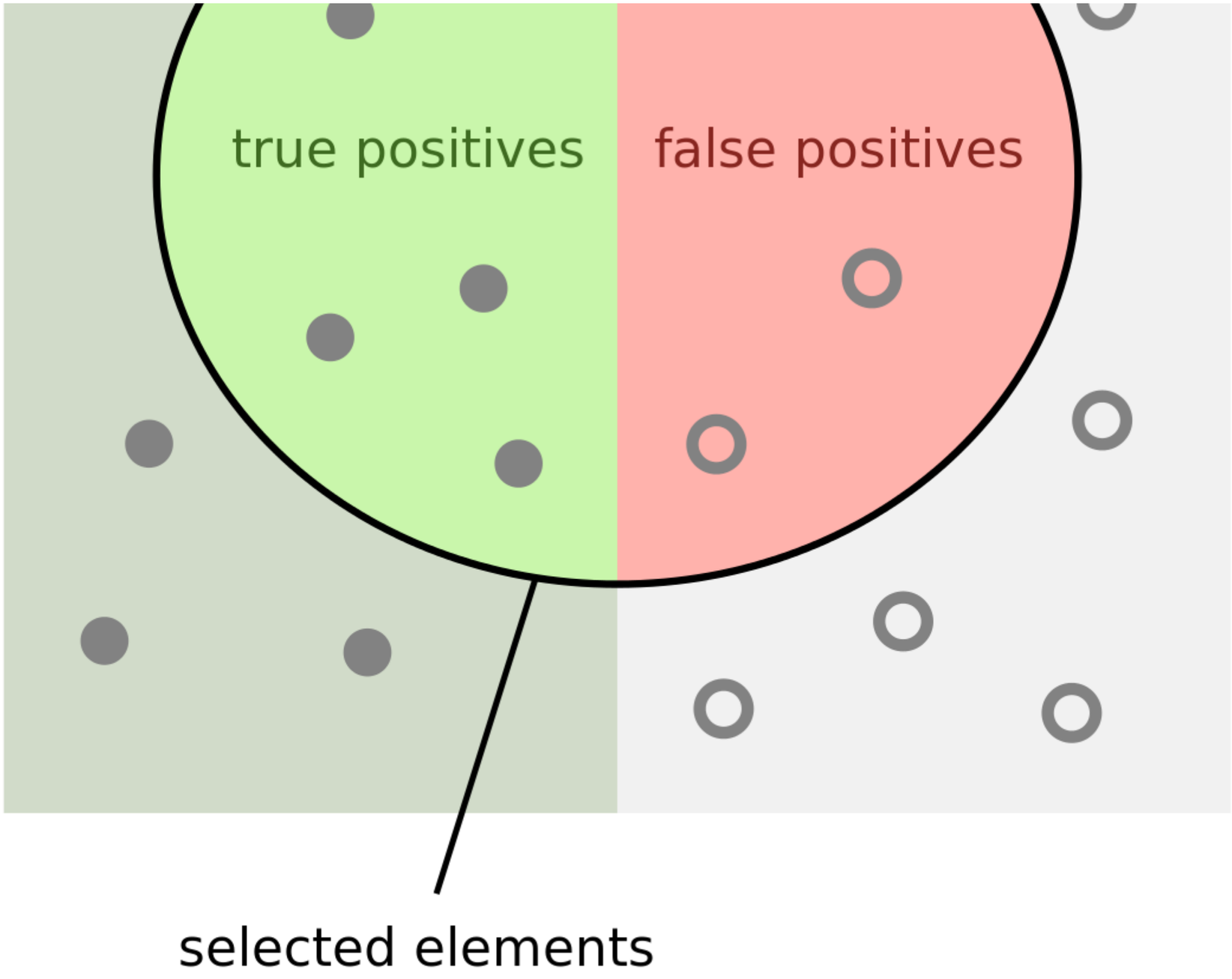
Make predictions.

In [16]:
```
y1_hat_train_dt = decision_tree.predict(X1_train)
```

In [325…
```
Image(filename='tptnfpfn.png')
```

Out[325…



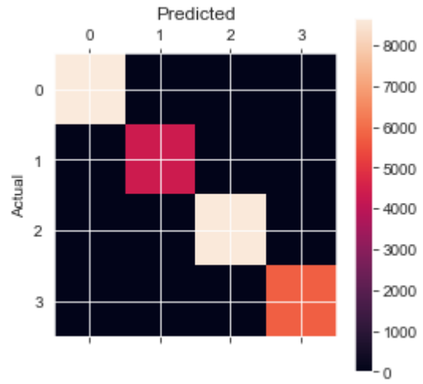


All predictions were classified correctly.

In [24]:
```
con_mat(y1_train,y1_hat_train_dt)
```

```
Confusion Matrix
----------------
       0      1      2      3
```

```
0  8653     0     0     0
1     0  4377     0     0
2     0     0  8588     0
3     0     0     0  5773
```



Seperate actual and predicted values into each class for metrics.

In [18]:
```
actual_class0=y1_train==0
actual_class1=y1_train==1
actual_class2=y1_train==2
actual_class3=y1_train==3
predictions_class0=y1_hat_train_dt==0
predictions_class1=y1_hat_train_dt==1
predictions_class2=y1_hat_train_dt==2
predictions_class3=y1_hat_train_dt==3
a=[actual_class0,actual_class1,actual_class2,actual_class3]
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3]
```

$$precision = \frac{TP}{TP + FP}$$

$$recall = \frac{TP}{TP + FN}$$

$$f1 = \frac{2 * precision * recall}{precision + recall}$$

$$accuracy = \frac{TP + TN}{TP + FN + TN + FP}$$

$$specificity = \frac{TN}{TN + FP}$$

$$TruePositiveRate = \frac{TP}{TP + FN}$$

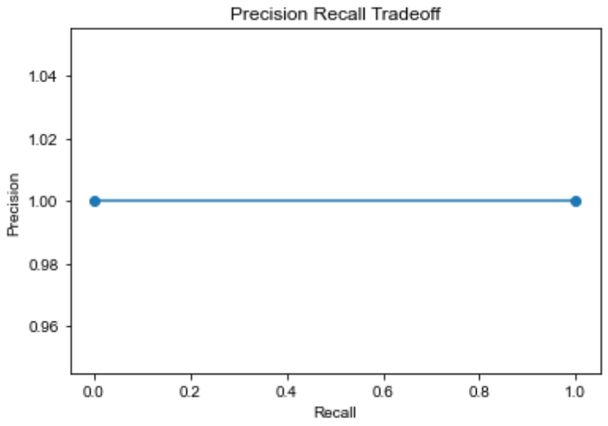
$$FalsePositiveRate = \frac{FP}{FP + TN}$$

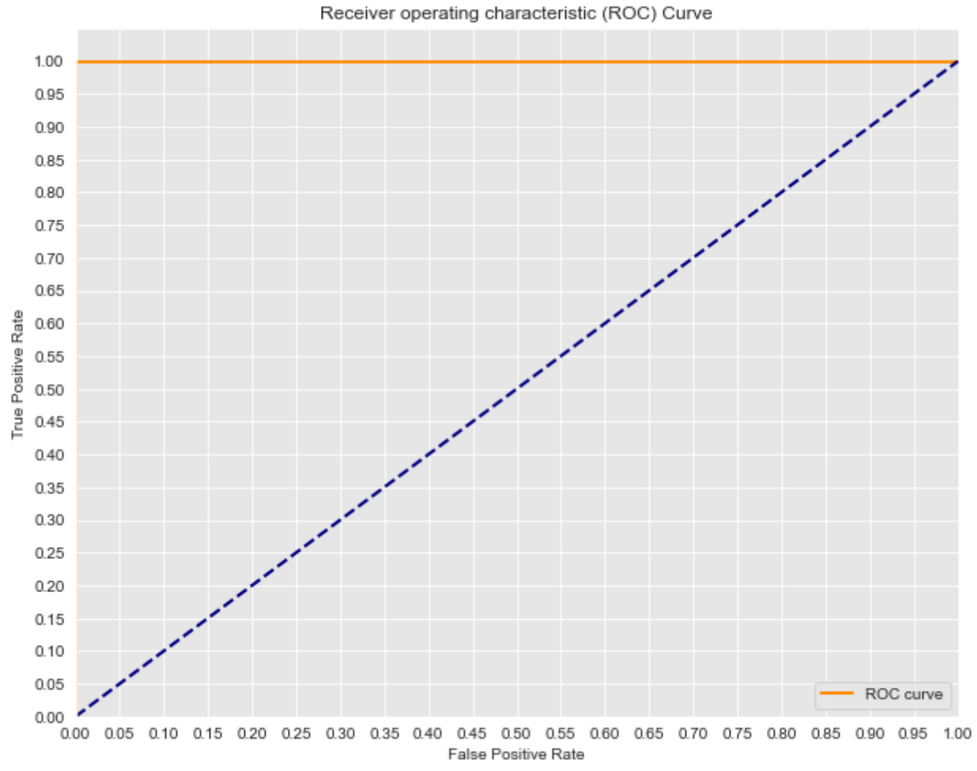
$$ReceiverOperatingCharacteristic = \frac{TPR}{FPR}$$

$$AreaUnderCurve = \int_a^b TPR(FPR^{-1}(x))dx$$

In [20]:
```
multiclass(decision_tree,X1_train,a,p,translation_df1['mRNA_Codons_copy'],'train')
```

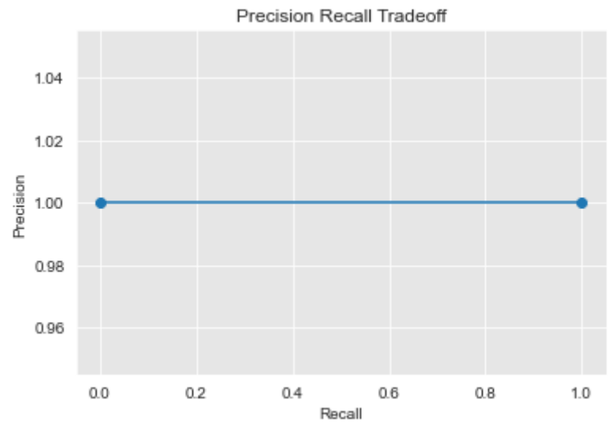
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

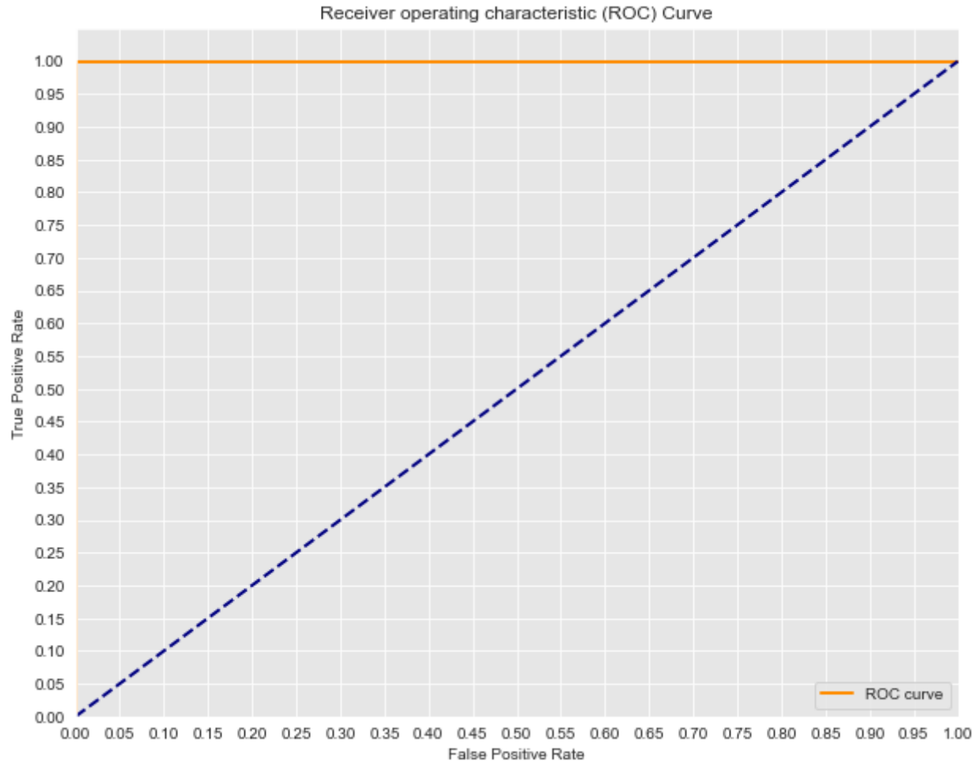





```
Cross Validated ROC AUC score: 1.0
```

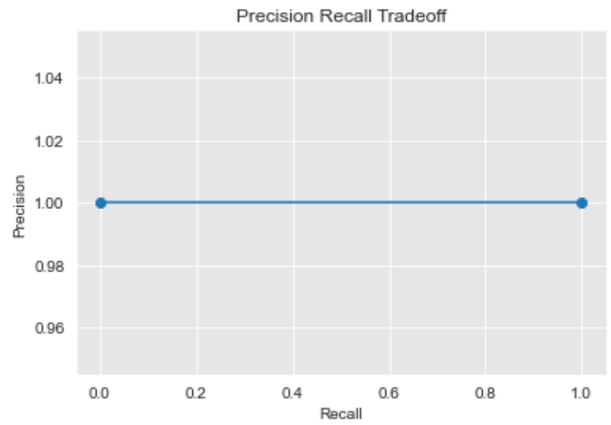
```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

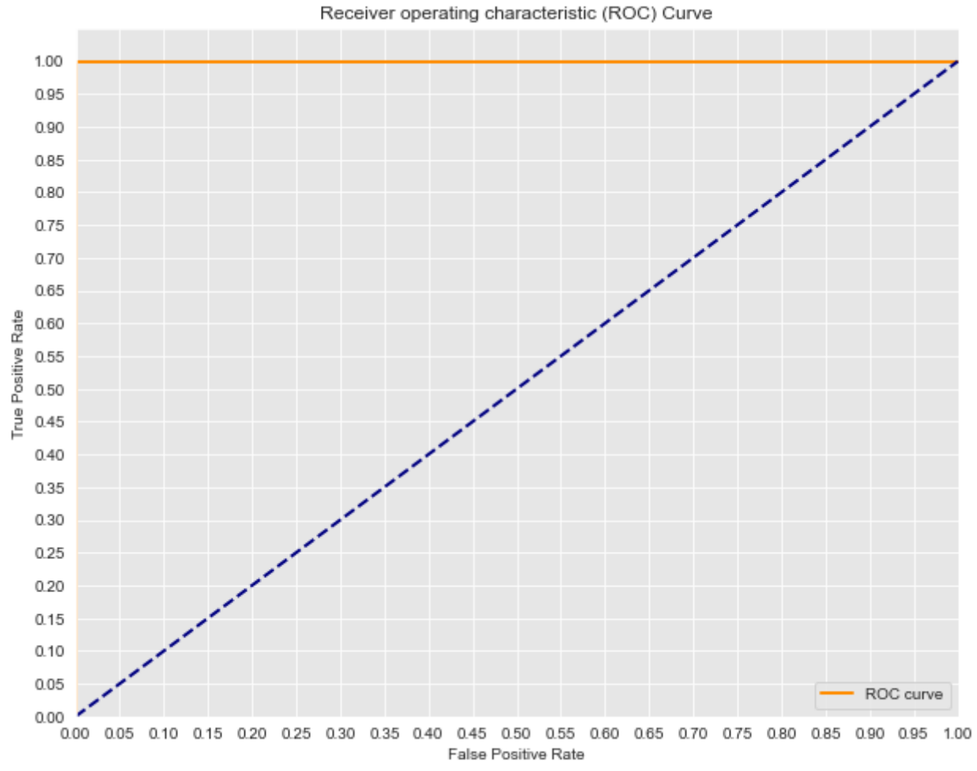





```
Cross Validated ROC AUC score: 1.0
```

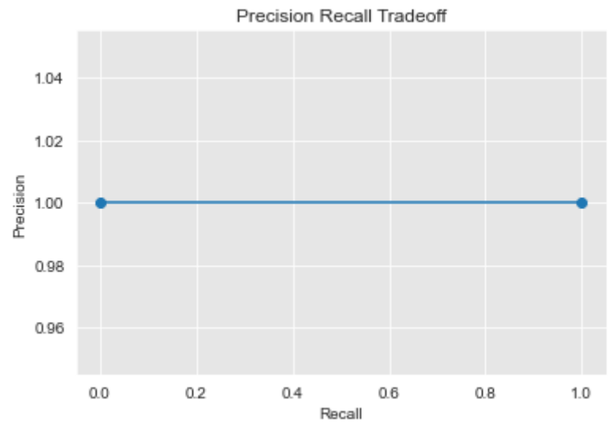
```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

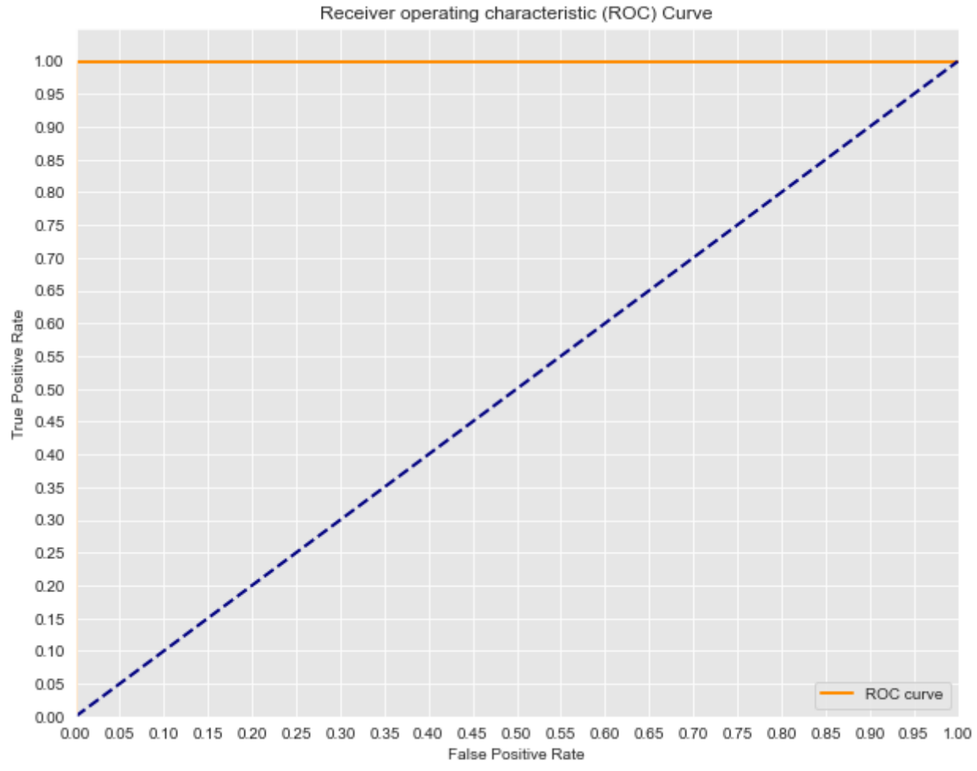





```
Cross Validated ROC AUC score: 1.0
```

```
Class:U
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Cross Validated ROC AUC score: 1.0
```

Random forests are an ensemble of decision trees that output the average prediction of the trees.

Fit the model to the training data.

In [21]:
```
random_forest = RandomForestClassifier()

random_forest.fit(X1_train, y1_train)
```

Out[21]:
```
RandomForestClassifier()
```

Show hyperparameters.

In [146…
```
random_forest.get_params()
```

Out[146…
```
{'bootstrap': True,
 'ccp_alpha': 0.0,
 'class_weight': None,
 'criterion': 'gini',
 'max_depth': None,
 'max_features': 'auto',
 'max_leaf_nodes': None,
 'max_samples': None,
 'min_impurity_decrease': 0.0,
 'min_impurity_split': None,
 'min_samples_leaf': 1,
 'min_samples_split': 2,
 'min_weight_fraction_leaf': 0.0,
 'n_estimators': 100,
```

```
 'n_jobs': None,
 'oob_score': False,
 'random_state': None,
 'verbose': 0,
 'warm_start': False}
```

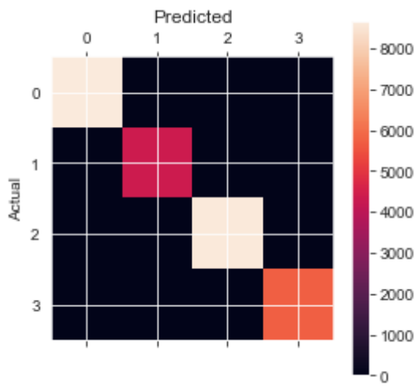
Make predictions.

In [22]:
```
y1_hat_train_rf = random_forest.predict(X1_train)
```

All predictions were classified correctly.

In [23]:
```
con_mat(y1_train,y1_hat_train_rf)
```

```
Confusion Matrix
----------------
      0     1     2     3
0  8653     0     0     0
1     0  4377     0     0
2     0     0  8588     0
3     0     0     0  5773
```

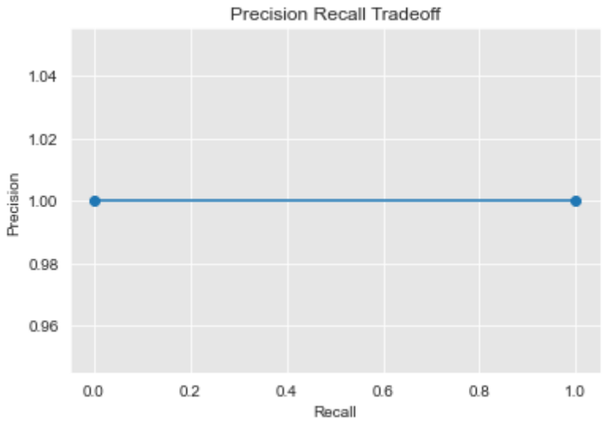


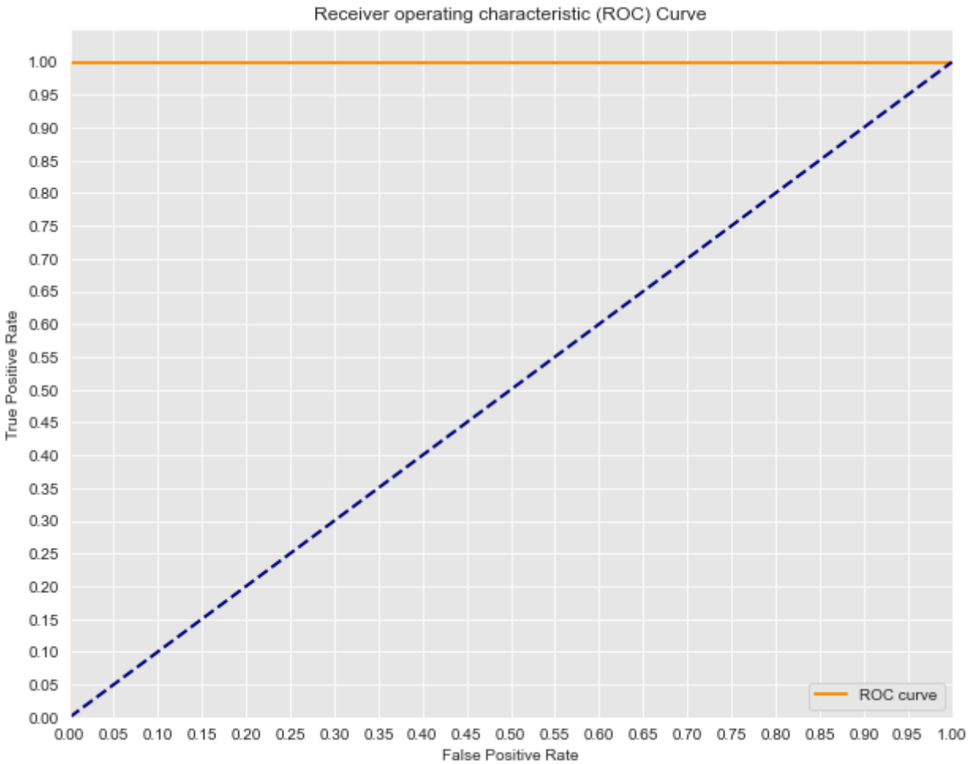
Seperate predicted values into each class for metrics.

In [25]:
```
predictions_class0=y1_hat_train_rf==0
predictions_class1=y1_hat_train_rf==1
predictions_class2=y1_hat_train_rf==2
predictions_class3=y1_hat_train_rf==3
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3]
```

In [27]:
```
multiclass(random_forest,X1_train,a,p,translation_df1['mRNA_Codons_copy'],'train')
```

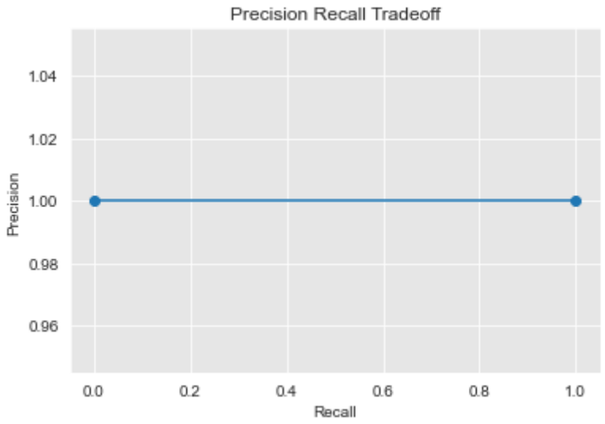
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

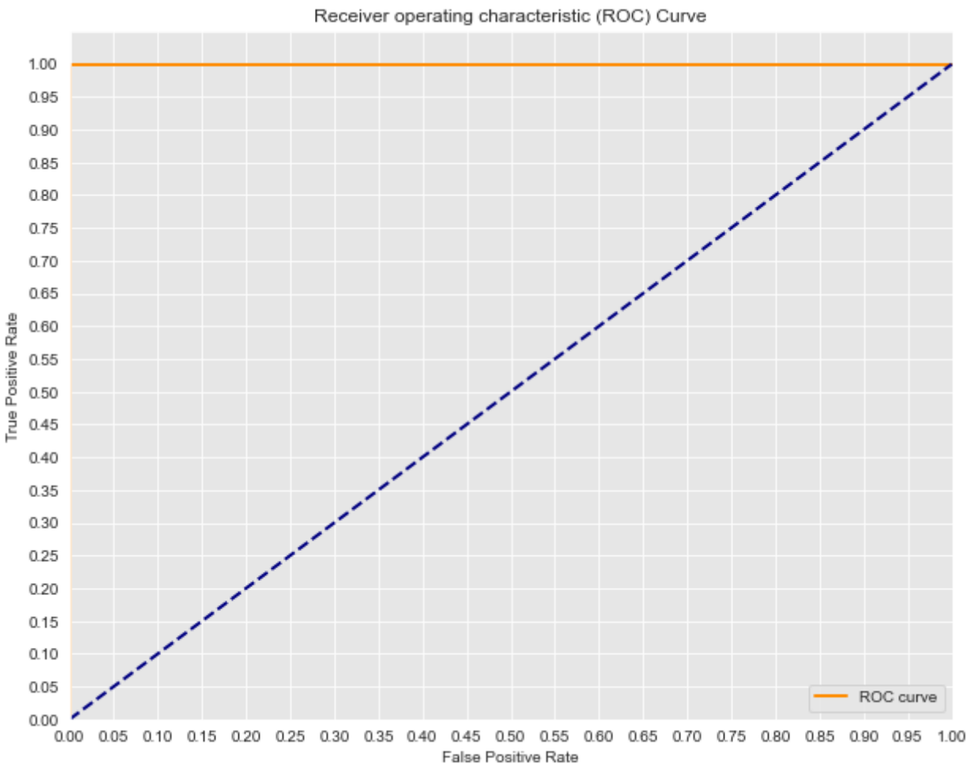





```
Cross Validated ROC AUC score: 1.0
```

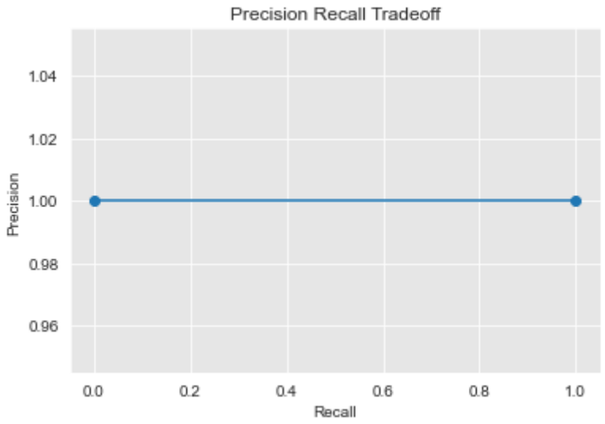
```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

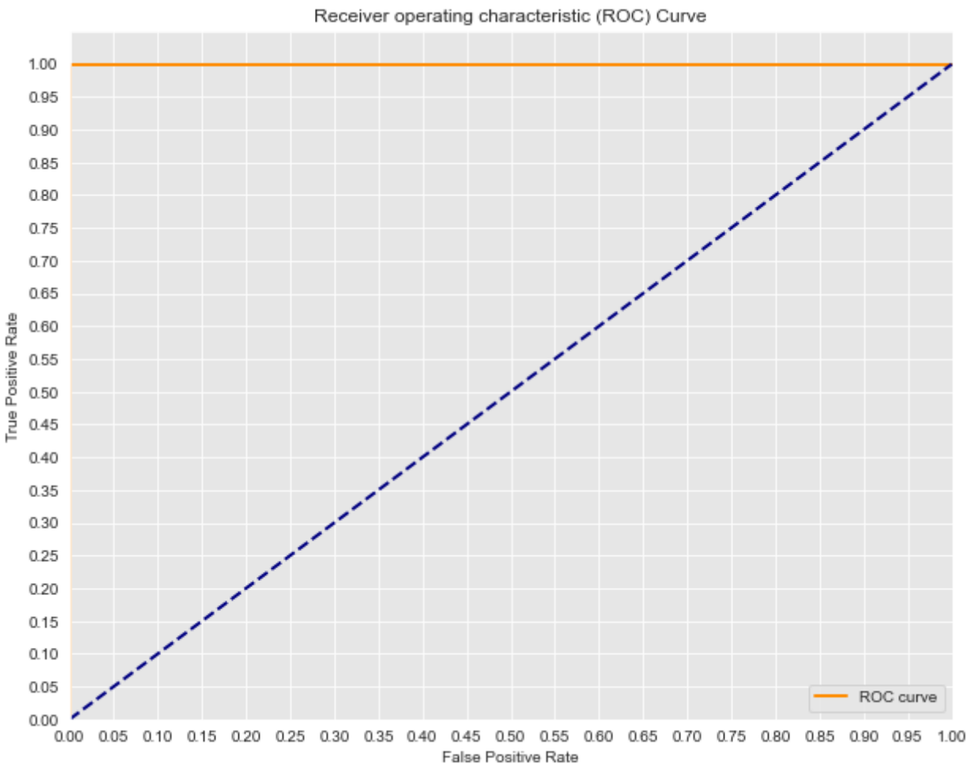





```
Cross Validated ROC AUC score: 1.0
```

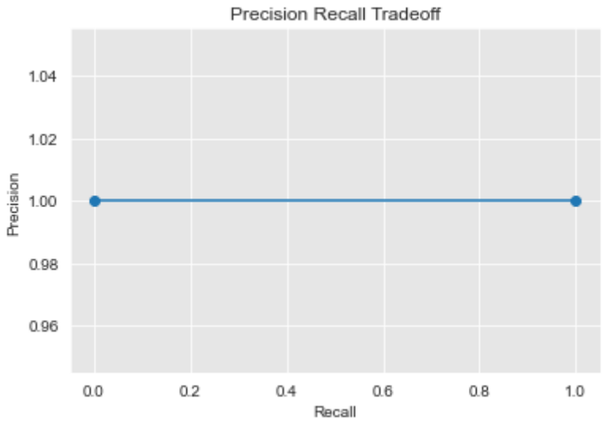
```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

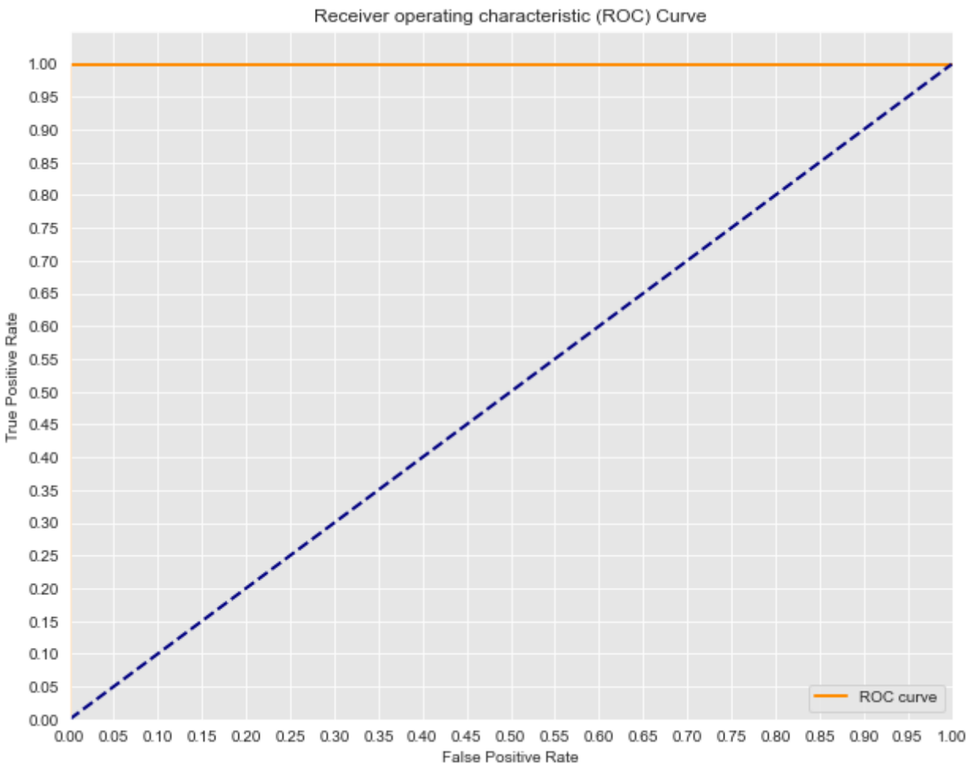





```
Cross Validated ROC AUC score: 1.0
```

```
Class:U
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Cross Validated ROC AUC score: 1.0
```

Gradient boosting is an ensemble of weak learning decision trees that iteratively combine into a single strong learner. Each tree is combined with the previous one in order to minimize the overall prediction error by optimizing a differentiable loss function. f0(x) is the initial tree, m is the iteration, $\phi m(x)$ is the current tree, and θm is the weight for iteration m.

$$f(x) = f_0(x) + \sum_m^M \theta_m \phi_m(x)$$

Fit the model to the training data.

In [28]:
```
gradient_boost = GradientBoostingClassifier()
```

```
gradient_boost.fit(X1_train, y1_train)
```

Out[28]:
```
GradientBoostingClassifier()
```

Show hyperparameters.

In [147…
```
gradient_boost.get_params()
```

Out[147…
```
{'ccp_alpha': 0.0,
 'criterion': 'friedman_mse',
 'init': None,
 'learning_rate': 0.1,
 'loss': 'deviance',
 'max_depth': 3,
 'max_features': None,
 'max_leaf_nodes': None,
 'min_impurity_decrease': 0.0,
 'min_impurity_split': None,
 'min_samples_leaf': 1,
 'min_samples_split': 2,
 'min_weight_fraction_leaf': 0.0,
 'n_estimators': 100,
 'n_iter_no_change': None,
 'presort': 'deprecated',
 'random_state': None,
 'subsample': 1.0,
 'tol': 0.0001,
 'validation_fraction': 0.1,
 'verbose': 0,
 'warm_start': False}
```

The direction of the steepest descent is given by the negative gradient, $-g(x)$, of the loss function, L. At each iteration, a tree is fitted to predict the negative gradient for the next tree, ϕm. The negative gradient determines the direction of the step and line search, proposed by Friedman, determines the step length of ρ with an η learning rate.

$$L_{MSE} = \frac{1}{N}\sum_{i}^{N}(y_i - \hat{y}_i)^2$$

$$-g_m(x) = -\nabla\frac{\partial L_{MSE}}{\partial f(x)}$$

$$\phi_m = argmin\sum_{i}^{N}[(-g_m(x_i)) - \phi_{m-1}(x_i)]^2$$

$$\rho_m = argmin\sum_{i}^{N}[((-g_m(x_i)) + \phi_m(x_i)) - y_i]^2$$

$$f(x) = f_0(x) + \sum_{m}^{M}\eta\rho_m\phi_m(x)$$

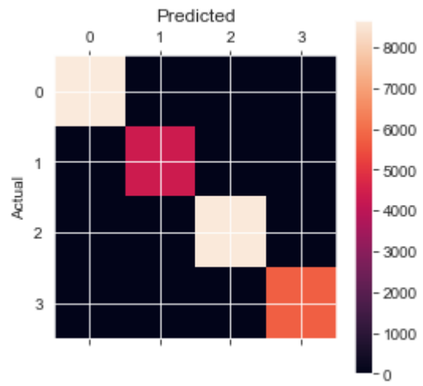
Make predictions.

In [29]:
```
y1_hat_train_gb = gradient_boost.predict(X1_train)
```

All predictions were classified correctly.

In [30]:
```
con_mat(y1_train,y1_hat_train_gb)
```

```
Confusion Matrix
----------------
      0     1     2     3
0  8653     0     0     0
1     0  4377     0     0
2     0     0  8588     0
3     0     0     0  5773
```

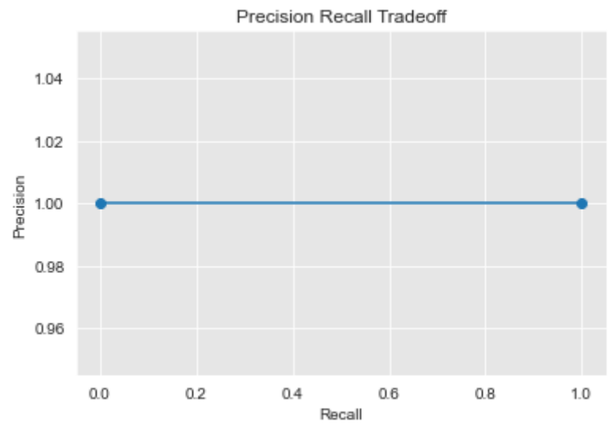


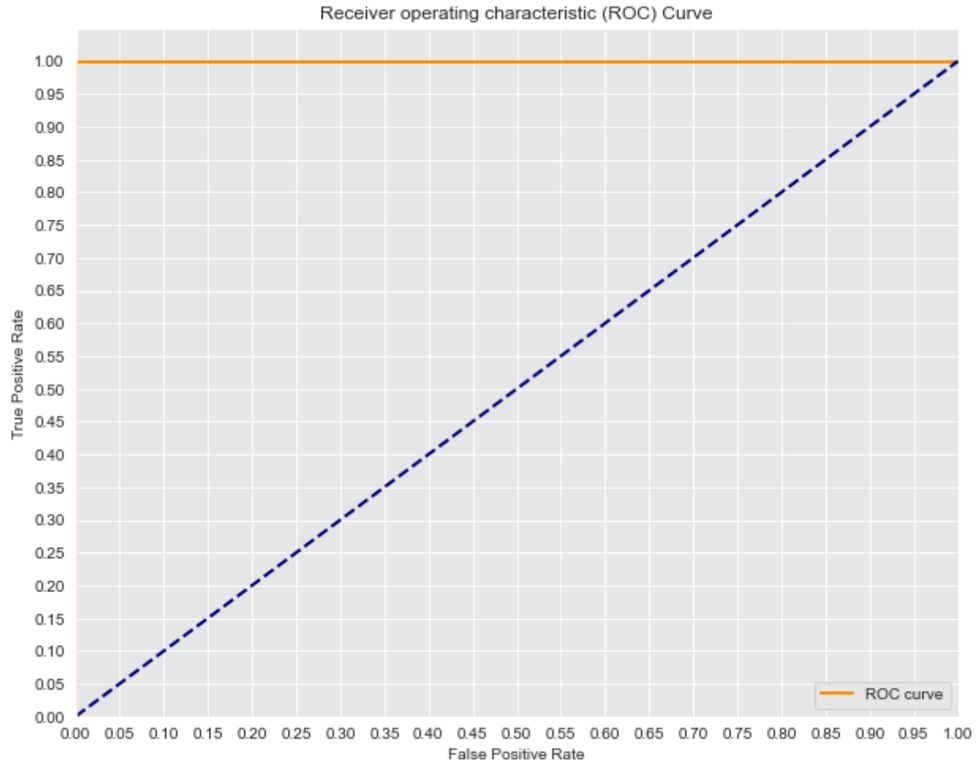
Seperate predicted values into each class for metrics.

In [31]:
```
predictions_class0=y1_hat_train_gb==0
predictions_class1=y1_hat_train_gb==1
predictions_class2=y1_hat_train_gb==2
predictions_class3=y1_hat_train_gb==3
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3]
```

In [32]:
```
multiclass(gradient_boost,X1_train,a,p,translation_df1['mRNA_Codons_copy'],'train')
```

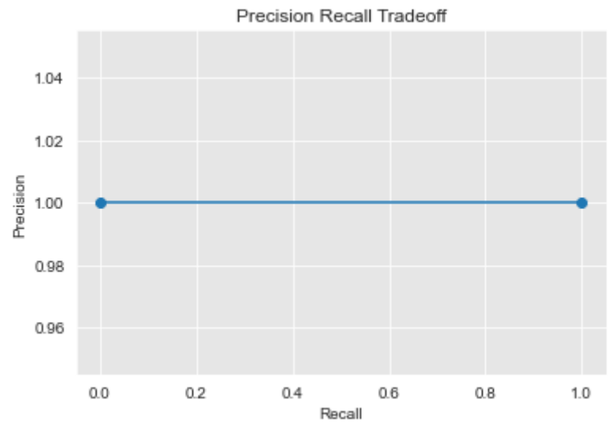
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

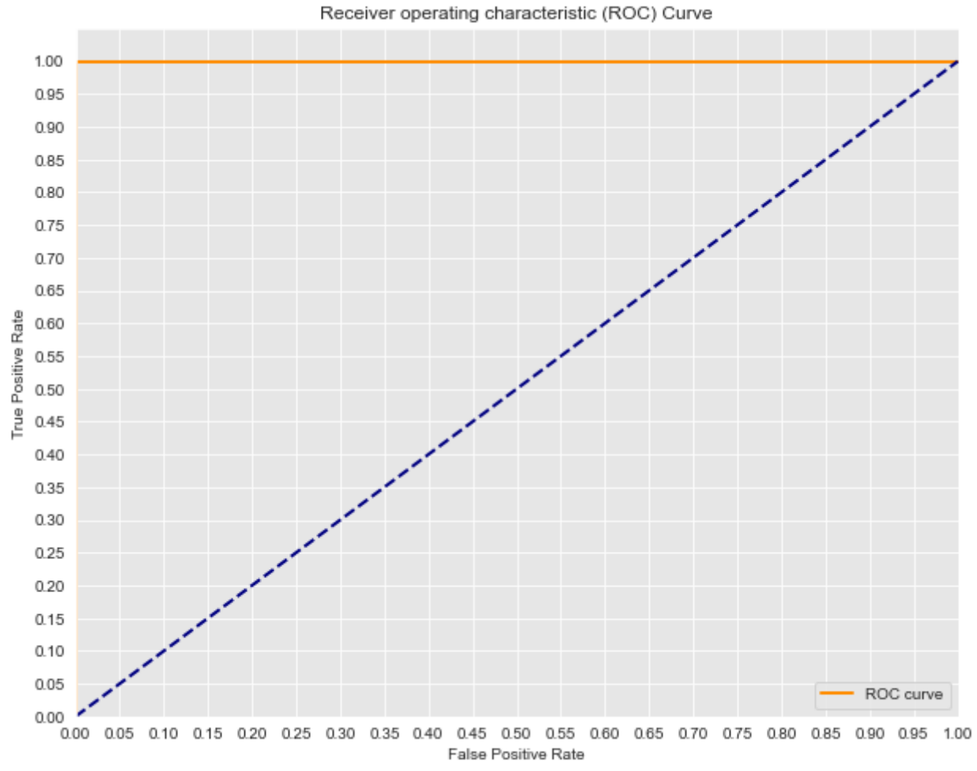





```
Cross Validated ROC AUC score: 1.0
```

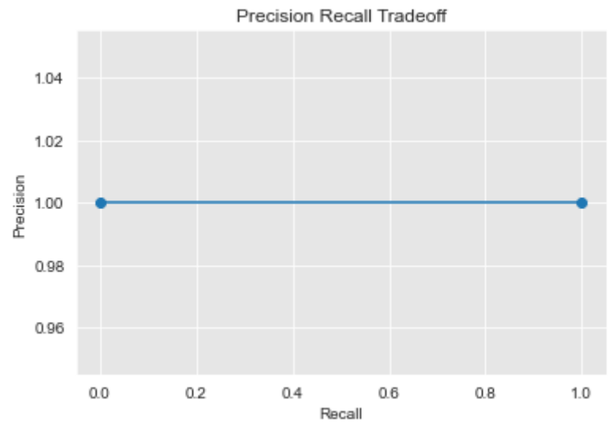
```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

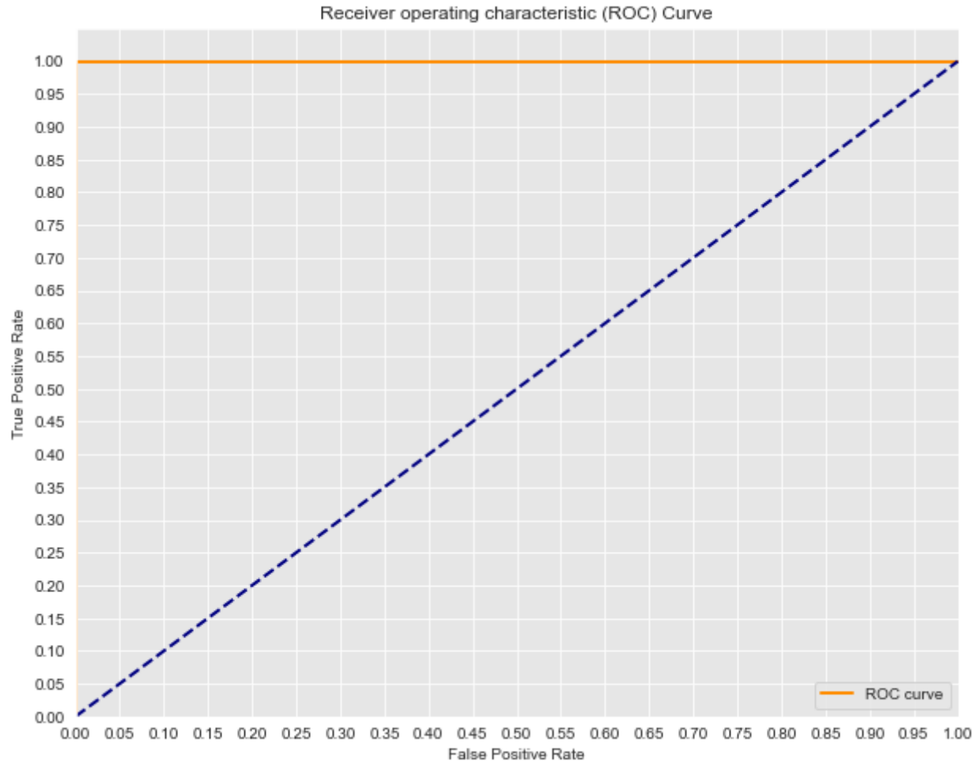





```
Cross Validated ROC AUC score: 1.0
```

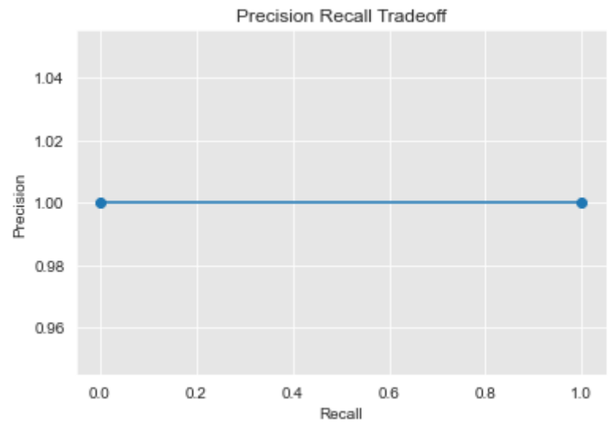
```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

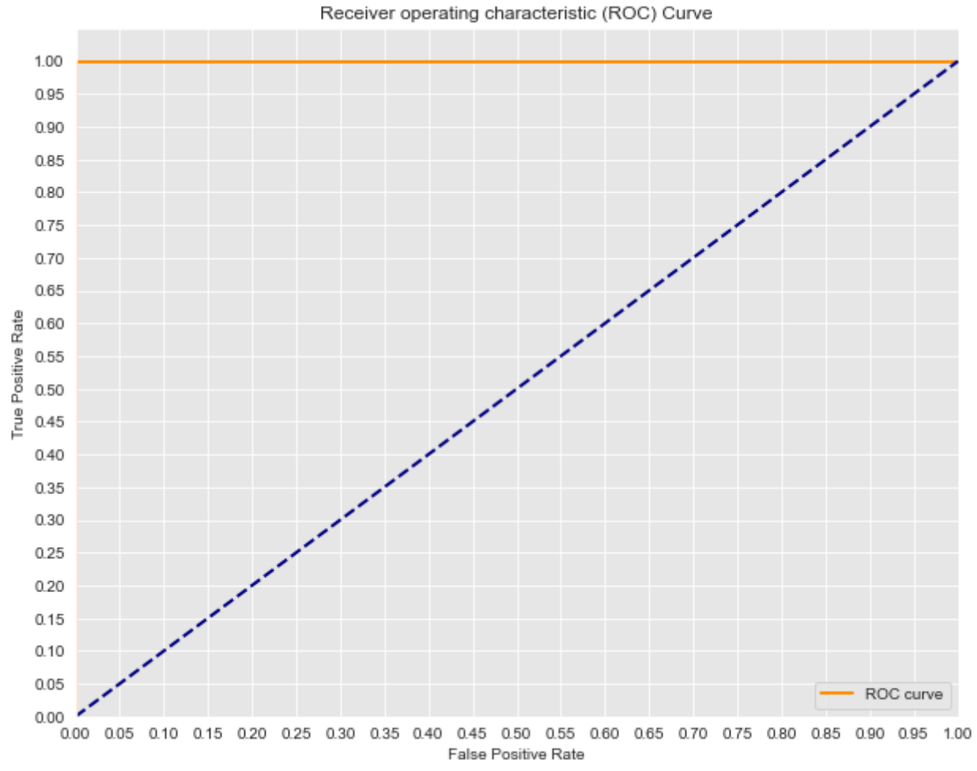





```
Cross Validated ROC AUC score: 1.0
```

```
Class:U
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Cross Validated ROC AUC score: 1.0
```

All models performed with a cross validated roc auc score of 1. Will test on gradient boost model.

Fit the model to the test data.

In [33]:
```
gradient_boost.fit(X1_test, y1_test)
```

Out[33]:
```
GradientBoostingClassifier()
```

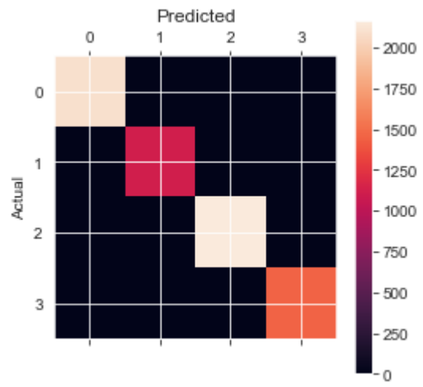
Make predictions.

In [34]:
```
y1_hat_test_gb = gradient_boost.predict(X1_test)
```

All predictions were classified correctly.

In [35]:
```
con_mat(y1_test,y1_hat_test_gb)
```

```
Confusion Matrix
----------------
      0     1     2     3
0  2100     0     0     0
1     0  1121     0     0
2     0     0  2165     0
3     0     0     0  1462
```

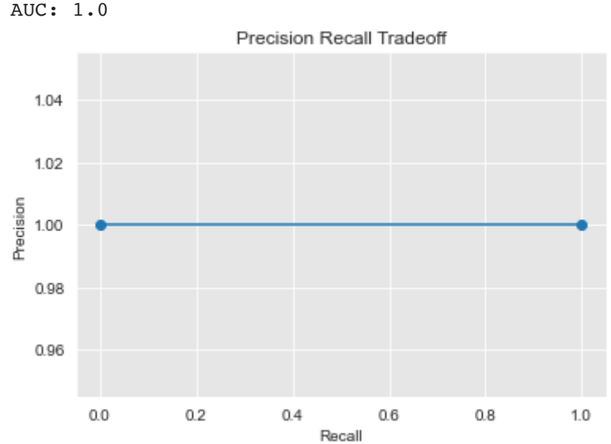


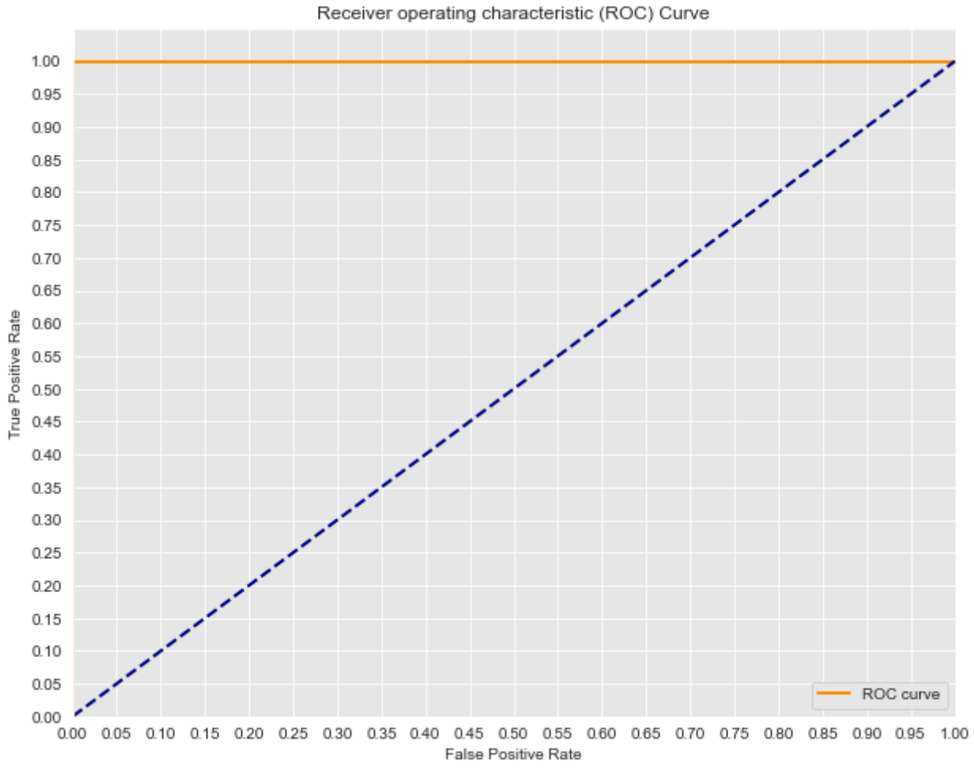
Seperate actual and predicted values into each class for metrics.

In [36]:
```
actual_class0=y1_test==0
actual_class1=y1_test==1
actual_class2=y1_test==2
actual_class3=y1_test==3
predictions_class0=y1_hat_test_gb==0
predictions_class1=y1_hat_test_gb==1
predictions_class2=y1_hat_test_gb==2
predictions_class3=y1_hat_test_gb==3
a=[actual_class0,actual_class1,actual_class2,actual_class3]
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3]
```

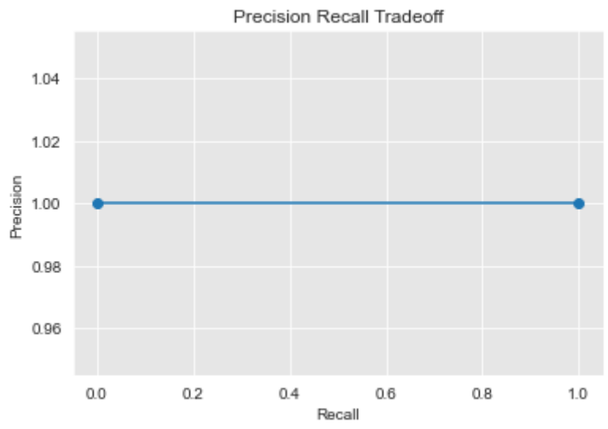
In [37]:
```
multiclass(gradient_boost,X1_test,a,p,translation_df1['mRNA_Codons_copy'],'test')
```

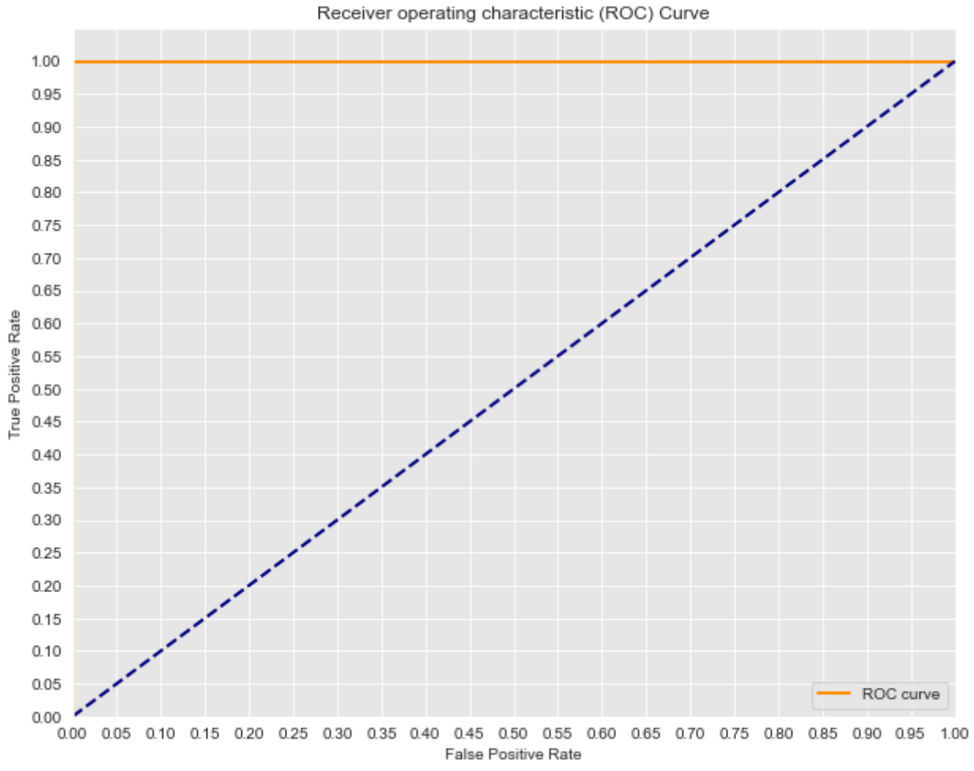
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



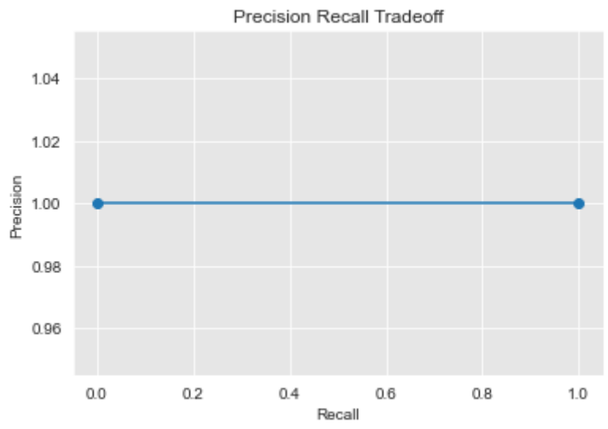


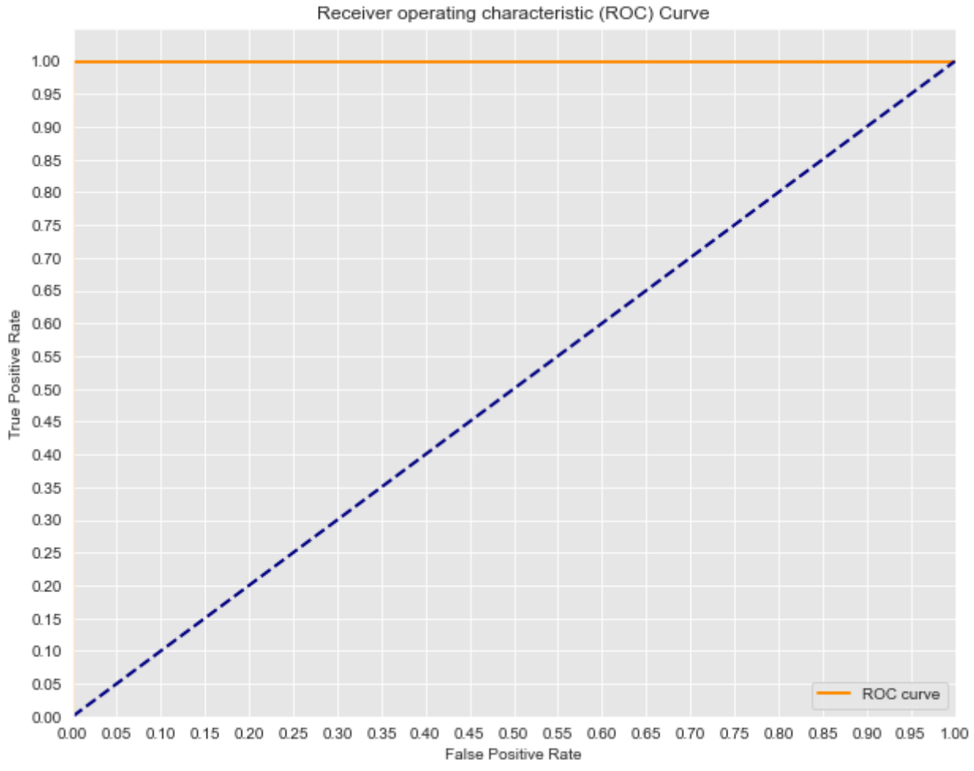

```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



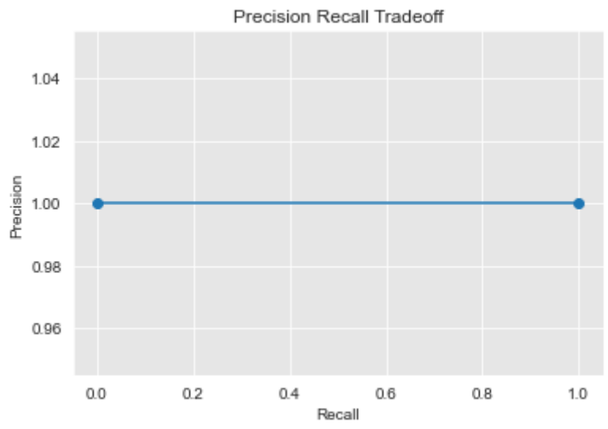


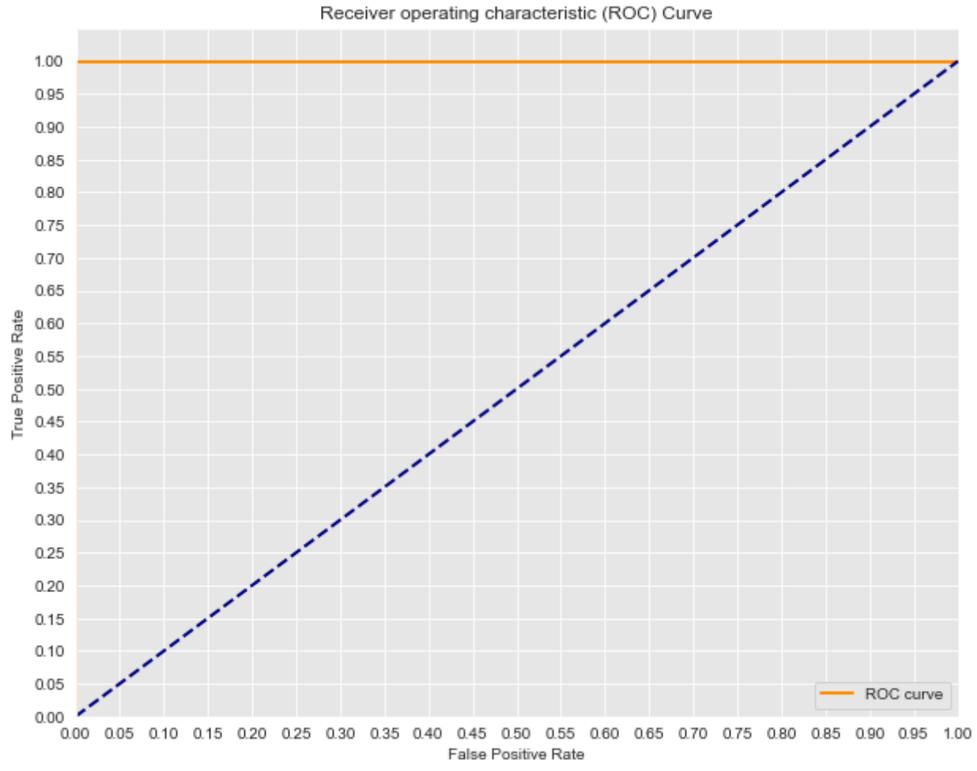

```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Class:U
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```





Next transfer anticodons to amino acids.

Data Cleaning

Take predictions from previous model and change them back to genome letters.

In [38]:
```
c=''
for i in y1_hat_train_gb:
    if i == 0:
        c+='A'
    elif i == 1:
        c+='C'
    elif i == 2:
        c+='G'
    elif i == 3:
        c+='U'
c
```

Out[38]:
```
'UACGACAGGAUAUACAUUAAUUUGUGGGGAAAAUCGGUGGGGGAUUCUAGGUAAUACACGUUUACGCGAAUUGAGGUUCGGCAUAGGUAGUCGGAUCAGCGAUGUCCUAAGAUAGAAGUGAAUAACAGAGAAGGUCAAUGUGGGACGCAAAUUUCAUCCCCCGACAAUCAUAUCGGCGAAGGCG
AUGCAAGGGUAUAGGGGAAAUAGUGCCGCAACGAAGAAGCGAAGUGUCGGCUCUUAGCGUUGAGAAACGGUUAGCAAAGCACGAGUAAGACCACAAGUGAAAAUGGCAUGGCAGAGUUUAACGUUGGAGCAGUCGGCAAAUGCACAAAGGGCACCUAACAGCUACUAAAAGGAACAAUGAGCAAA
GCAUAACAAGACAUAUGUGUCUCGAUUGAACGAUAAGUAGUUCUAGCUACUCACGAAGUGUCAGGCAGCCUAGAAUCAUGAACCUUGGCUGUUAAGCUAGGUAGCAGUGGACCGAAGGCACCGCUAGUACGUGGGUCGGAGUAAAGGAAGCUCGGGAUUCCCGUGCUUCCGGUAAAAACUCUGGU
GAGAAAGGCGGACCUAGAUCUAGAGGGCAAGGACUGGUACCGCGGAGGGGACGUGUAGUACGUAUUGAGCGACGUAAAAUCGGGAGGCAUUUUGGUCAAAAUUAUGAUAUAACCAUUUGAAUCUCGGAAUAGUGCUGUGGCCAAUGGGAGGAGCGAAGGCCGGAUCCGAAUCGCGGAGUAGCUAU
GAAGAAUGGGCAUUCUCCACAGGAUAAGAUCUGGGAAAGUUACAACAGCGUUUGUGGAGCUGGCAUAGGUAGAGCAACGCUAGGCAAAAUCAUGGGAGAAUCCGAUACAAACUUGAUGGAGGGCCGGUUUCGCUACGUCAGACGAAGCUUACCGGUGUAGGGGAGACCAAGUUAAAGAAGAACGC
AUAGAAAAAGUAAGUACAGAUGCACGAAAGAUAAUAGUUUAGGAUGAACGUCCUGAGACAGGGGGUGCCCAAUGACUGAGGAUUCGAAGUCGCUGAAAGCAAGUGGGCAUGCAUAGUACUGAAGGUGUCAAAUUGGCAACCACUUGUGGAAGAAUAAAUGAGAAUUGCUCGAGAAUAACAUGUCG
UAGAACUAACGAUUUACGGACGCAUGGCGAGAGGGCUGGUGAUAGCGACGAUGGAUUAAACCGAUUUAAUAGGGGAACUUAAGAUUCGGAAGGAGGAAGGAGGGACAGCAGAACUCUAAUGAGGUACGGUAAAAACCUAAAGGUCAGCCUAAGUGAAUGGGUGGGAGGCUCAGUGCCCAACGAGA
GAAGUAGCAUAGCUCAAACGAGAGAAACGUUAGGGUGACUAUAGGAGCGAAGGGAAUGUACUCAAGGACGACGGAGUUAAAACGAUGGGAAAAUGAGACCCAGGGACGCCCCGGGAAAGGGGAGAGAUUUGCACAAAUGGAAUAAGAUAUAGAGAGAGAUAAUCGCAUAGAAUGGAUUCAGUGAU
AGCGCGAGUAAAGUGAGAAGCCUUGGAGGUAGCCUGACACCAAUUCACUGAAUGAGUGGAGUGGAUGGGAAGUUGGUAUUAAGUACUAUGCAAAGGUCCGCCAUGCAAAAUAAGCACCGUUUGCCAGCUUAGACCAGAUGGUAUGGCUAUCGAAGCACUCAAAAUCGGGGCUAACCACGGCGUGA
GGGCAGCUACCAUGAGGAAGCACCCUGAGGUAUGGAUCGAGUCAGAGUCACGGGCGUCGUUGCAGAAAUUUAUACGUCUAGAUUUUGAGAAUGCGAAGGGGGGGGAAGAAUCUCAUGGAGACACAAAUGAGAUAGCAAGUGCUGCCAAGUCUUGAAGGUGGAGGUUAAGAUGGGAUACUAGUGAG
```

UAGGGACAGGCGGCGUGAACAAGCUGUAGGGCUGGUAGUACAGGUCGGGAGAAGGGCUGACCUAUUGUGGCGAGGGGUCUUUGCUAAGGAAUGGCUGCAGAGAGGACGGCCCGCGACACGGAGGGAUUAGUACCGGUCUAGAUUCAGAGAGAGUAUAUUGGGGAAGUGUAGGGACGACGGCGCAG
UGAAAAGAAGUAAGGUAACGCACUGGGAAUACAGAGAGCGUAUAGGUUUAGGUGAAAGGAAGUGUAUCUGACUGUUUGUUAGAGUUUAUGAGAAAUGUAUAGUUGUGGUAGCUUUAAACCAACGAUGGCAUUAUCUACCGGUGAACGGGCGCCAGGGCCUAGUAGUGCUACAUCCAUUACAUCUG
UUGCAGGUUACGUAAAGGUAAGUCUGAAAUGUGUCAAGUUAAAACACCGGCGAUCGCGGGUAGGAGGCCUACCAGAAUGUGGGGGAAUAGUCGUGGACUAGGGAAUCCACAAGAUGGAGAGAACGAGAUAAGCUGAACGGUCUUGCGAGUAGGAAUAGAGAGGCGCGAAAACGGAAUGCAGCAGG
CGAUGAUCUAGUAGAGGGCAGAACGCUCGGGAGGAAGGGUGCGCCGAUAACAGCGGUAGAAGUAUAGAGUAGAUGGUAAACGCAAAGUAAGUCAGGAGUUGAUCGUCAGGUUUAAUCGCUGGAUGAAACCUGCUCGAGGGGUGGGUUGUCUAGAACCGAUUCAGUGACUAGCGAAUCAGAAGUCC
AACGGGUGAAAAGCUCAAGACAUCAUCAUCGAGGCCCUGUGCUUAAAAGUUUGGAAAGCUUUUUAGGCGAGAAUAGAAGAUAGCAUGGUAAUACACUAGAGGGCGAGGGAGUUCAGGCAGUACAAAUAGUAAGAGAGUCCAAAUCAAAGGGUAACAAGAGGAUAUUAAAAGUUAGGUUAGAUUUG
GAAGGGGUGGUCGCGUGCAGGGUCUAUGCGCGACGAAAAGAUAUGGGGGAGCAAGCCUAGACGCUUUACUGGAUAAGGAUUGGGCUUAUUAUCAUGGCAAGUUAAGCAGUGGUAAGCAUUACAAUUUCGUUAGCACGGAUAGAGUGUCCGAGCGGCACGGGAAAGUUUAUGGUGUUUUAAAUAUG
AUUUCUGGAAGGAGUACAAAUGAGGGAACGUCGUUUGAUGUGGAAUGCGAGAGCUGGAGGUCCUUGAAGAGGGAUAGAAGUAUUCGCAAAGAUAGGGGUAUAACGUUAUUACAGAAAGAUUGAAUAGAGAACGGGAUAUUCAUUACUGGACUGUGAAGUUAUCCUGUGAGGAGAGAAUACGCACG
GGAAAUUGGUUCAUGCAGGUUAUUGAUGAUAGUUAGCUAGAAAAAGCGGAAUGUACCAGCAGCGACUUGGGAGGGAUGGGCAAUUAAGGGGGGACAUAAUUGGUUUGUAACCUAAUAGCGAAGUACUCAGAGCCUCAAGAGAUCGUAUAGGGUAGAGAAGGGAAGUGAGGAUAGGAUAGAGUGAC
CGGAAGUAACGAACUCAAACCUUCUGCAUAGACAAUGGUAAAAACGAUAUGAGAUGCAAAAGCGCGAAAGCGGAGUGUGUGAUUCAAGGCGUUAGAGCGGUCGACAAAGGCAGAUAACGAACAUUCCCUGCGGAACCUACAUUGGGAGUAGAUCGCAGUUGGAAUAAUAACACCCAGGGCCCAAG
CAUACAGUCAAGGGCAGAAGAAGCCCAAAAGAAGUGUAGGUCUGAGAGCUGGAAUUGAAAAAGAUUUGAGGAAAGUCUGAAAGUAGAUGGGCCAUAAGAUAAAGGAGACGUUAUGAAGUAUGUGUGGUUUGUUUCAAAAGUACGGCUUCGGAAGGUUUCCGAGGUCGAGGAAUAUAUCAACAA
AGCGGAGCGACAGGACACAAGACGUCGGGAGGACGUAAUGUCGGAGAUUGAAACGAUGAUUAAGCGGGAAGUAGUAAAAAAAAAGCGGAAACUGUAAGGCAAAAAUUAGGAGAUAAUUAGAAGAGCGUGAUGAAAUUGAGCUAAAGUAUUAUGAGGACUGCGGGUUGGUGGCAAUGGUAAAAACAU
AGGUGGAGUAUUCAAAAGCUGAGGGAAACUGCUUAAGGGAGUUGCCCCCCACGAUUAAAGUCAGUGAAACGACAAGGCAACGUGGUCAAGUCACUUCUGAAUACACAAAGUGAGGGUUUGGGGUACAAAGAAGAAAAUGGGCUCGGCCAGGUGAAGGGCUGCACAGCGAGGGAAGGUGAACGGGG
GAGUAAUAAAAGUCGGUUAUUUCAUGGUAGGGGGCAUAAUCCUGAAAAAUCGCAAGGGCUAGAAAGGUGAUGAAGAUAAGGGGCGGAAGGCUGGGGAUAGCGUGAGUUGAUAUGUGGCAUACAGUAGUCUGAUGGCCGACUGUUGUACGUAAUAGGCAUGUGGAAGGUUGGGGGCUAGGCGAGCA
GUUCAGGAGUUAUUGGAACACUAGACAUAAUUUCAAAUGCAUUCGGCCUAGCAUCUUCCACCGUAGAGAUUGUGCGGUCCGCUCCGGCAGUGGCGAUAGUUGCGAAUAGGAGUGCGAAAGCGUUUGGGCUUAGGGUAGUUGAUCCAGGCCCAUUAGUAAGGUGAAAUGCGCAGGAAAAGACCCUU
GCAGCAAAAAUUAGGAAAUGUCACUACUAAACAAGUAAUGGAGUAUAGAUGCCAUAUAUCCUGCUUGGCGUGAACGGGAGGAAGGAACCAAAGUGAGACAGAUAUGCCUCUGAAGCUCAGCGAAGGGCUAAAGAGCCCAAGAAAUAGAAAAGUACUGGAGGGUGAAGGCGACUAGAAAUGGAACU
GAGAAUGUUUAACUGUAAGGUUUCCCAAGGGAGUGGACGACAAAGAGUCAGUACUGGAGCGGAAAACUCCUUAUCGGCGUAGAAAAGGGCAAGUGCGGGAAUCAUGAGACGAAGGUGGACAUAAGCAAAAAUAAAAAGAGGAUAGUUCUGGGAGGUAGAACGGUAGGCAUGGCGUGUC
UGCUGAGGGGGAAGAAGAAGUAAGCAUUUGCGGGUCGGGGAACCAUGCCGUGCAAAGAUUAGCGGUAUAUAAUUGAAUAUGAUGAUGGUAUGUUGCGCACGGACUUAGGGUAUGUAGCACGUGAGGGUAAGAAGGAGAAUGAUGAAGAGCUUAACCACGGUGACCGGAGGGAUGCAUAAGGGGUG
GAGUGUCAAGUCAGUUUGGAGAUUAAACGAGGGGUGGGCUGGCGCGUCGAUACCUCUAAGAGGUGGUGACAGACAAAUGAACCAUGAUGAUGGAGAAUGGAUAUCUCGACAAUGAAUUUAAUAGUUGUGGGGCGACGGAUUGAGCACACGGAUGGUAGCAAAGAUGGUGAAUUGAUAGAAAAUAC
GAUAUCAAAAUUGCGAGUGAAGAAUACGGUUCAGGAACGAGAGUUGUUGUACACUUAACCUUGGCGAGGUAAAUCGUAAUGCCCUUCAACGAUAGUAGCGUUAAUUCAUUAACCUUAGAGAUUCUGGUGACACAGUAAUAAAGUUAGAACGUGUGCAAUCUUGGAUGACGUAGACACUGGGACUU
GGCGGUUAGGCGAUAUAUUCAGAAAGAAAGAGAACCGUCAAAAGGCGUCAGGUGUCGGGGCGCGAUCGUUAUAGUAGCGGCAUAUACCAGAAAUAGAAACCCUAUACACAACCUGUGUGAAAAUGGCUUAACGUAGCGCGGGUUACGUAAGAAACUUGCCAAGGGAGCAUAGGACAGACGGCGAC
GGGCCAUGUUUUAUCAGGGAGCGCGAUGGUCUAUCAUGUAAGAGUGUAAAAGAGGUAGUAGAGGGACGAUCGUGGUGACAAUUUCCCGAUGCAGAAGGAUGGGCACAGGAAUAAAUAGUGGUAGAUGCGGUAAGACUCCUCAGACCGGGCGACGCUUACACGCAAAAUGGAGAGAAUCUACAUCA
UGCGCAAUAUGCCGAAACCAAGGUAAAGAUCUUAAUGGCGUGUAAAGCUAUGGUGUCUAAAUACGGGGGGGCCGUCAUCGUGCCCGGAGUGGGUGGGUAGAAUGGGCUAACGAUCAAUUAGCACUUCGCUGUCAAGACUAACGAUUAAAAACGGUGCCAAUACGGCAGACUACUUGAUGGGACAGUU
AGUAUAGGUAAGUCCGUGGUGUGGUGGUUAGCCGCAGCGCGUUGGGUUACGACGUUUCCUUCGGAAGGACAGUGAGAGUAAGACGGAAUUACAAGGGUUAGGGGUUAACGAGGUUCAAGCAUUCGCCCCGCCAAUUUGGGUAGGAUGCGGGGAGUUUUGCAACUCAGAUCCCUAUGCAAAGUGAA
UCCACGAGGACCGAAUAGUAAAUGUCGGGUAUACAGUGCGAGCUAAGUAUGCGGAUGUGGUGCAAGAAGUGAAUGUGUAAAGAUAAAAGACGAGUUCGGAGAGGAAGAAGAUAGCUUUUGGAGCCAAGAUAGGGCAGAAAGGUAGCGUCAUGAAUAAAACAAGGCUGCAAGUUCUGUACAGCAAG
ACUUGAAGGAAUCUCAGGUGGGAUGGCGAUGUAAAUAACUUAUAAAGGGACUGGAAGUAGGAAGAAAAGAAAGCAUCUGGUGACUAGAAUCCGUCGAGGGCGCGAGCAAAUAGAAAUUCGAAGUAGUACUCUAUUGACCAAAUGGGUCUCAGAUGUGAUGGGUAUCUAUAUACUAAGAUCCCAGC
GACAGACGUGGUGGUAAGAGUUAUGCUGUUGGGAUUGAGUUACAAAGGAAAGAUGGAAUAAGCGAGUUGAUUUCAGUAGUGGGGGGGGGGCACAAGAAGUUACGUUGGCAUGUGACCAUGGGUUGAUACUUUUAGUACGGCAGAGAGGGUAUUCACAGCUGACCACGAUAUCAGUCCAGACAACC
AGGGGAUAUUGAGGAGGUUAAUCUUGAAACGCUUCAGGUAGUACGGUCUCCAAGUUGACGUAGGCGGAAACUCAGCUAGGCGAAUCGGAUUUACAAGGAUGCAAGGGCUUAUUAAUAGUCAGGAGAUCGAUCGGCUCUCUGCAUUAUUGACUGAUGAAAAAAAGAGAGGUUGGGCGCAUCGCGAG
AAGGUUCAUGCAAGUAACAUGGGUGUUCUUGCGAAAAAAUUAUUAGUUGUAACAGAAAGGGGACAGGAUAACAGGCUGUGAGGAGCAGGCGGUGAGUUACGAGAAGGUGUCAUAUAGGAUGCACAUGGACAUGAGAGCGGCAGUAAUAACGCAUGGGUGCUAGCCAAGCGGAGUUAACUAGGCGA
CCAAAUUAGAGAGGUAAUAUUCGGGACAUCCGGAACAAACCAACGAUGGUAGAACGUAGAAGAAAGAAGUUCCAAACAGUGGAUAGUUGGAGGAUAGUACGCGGUCGCGUAAGAGAUAUGACCAUGGGCGGAAACAUUGGGGACUGAGAGAGAGAGUGAGCAUACACGGUGGAAGUG
GCCGAGGAACCCACUCGCAUUAAGAAAGUUGUAGGGAAAGAAAGGAGUCCAUGGUAGCAGACCGGCUUAACAAUGUGGCAUGGGCAUGAUGUAACCAAUAUAGAGUACGGAAAGCAAUGUGGAUGUGGUCGAACGCAGACGUAGAAGACUCGCUGAGCAUGUCGGAAAACGGUCCUAUGGGGCG
GAACCACAGGAGACAUGGGGUUCGACGCUGCGGAGAAACGUUAAGGAUAUUGGUUGGCUAUUCAAGAGUGGGUCAUGUAUUCAACUUAGUGGGCGUGAGAUAGUGGGGAAUUCCGGCUAGUGGAAUACGGAUCUCCUACGGUAGGAACAAGAGAGAGAGUGGCCAGGAUACGGUUCAGGAUGUGU
GCGGGUAUAUGGUCGCGACGUGUGGACGCGUGGAGGGCUAAGGGGUAGCACCACUCCAGGAAAAAUUGUAUGGUGUAGAGUAUUUGAACAGACGAAGGAUUAAUGGAGCGGGUCAGGUGCAAGAAGAAUAAGACGAAGGAGUGACGGUUGCGACGGCUUGCCCAUCGGGUGGUCCAGCGAAGGAU
UAUGGAGACCAUGACAGACCUUUGAGUUGAGCGGCAGAGUCAUAAUUGCUGUGAAAGGAAGAUGAUGCACGGUCUUUCAUUGCAGAUUCUAUCGGGAUCAAAAGCAAUGUUGGCAGAGUACGGUCCGCAAGGGCGGUAACCAAAAAAACUGUUGAGGAUAUUAGUCUGCAACGUGGAAGACGAUG
AGCAAGCUAACUAAAAACCAAGGAGAAAUGUGGUACAUAUUGUAAAGGAUGAGCGUGACGGGAGGACAGAGAACUUUUUCGCAAGGGAAAGGUGAUAAUAAUGAUAGGUUAACAGAGGGCGGUGGAGCAAUAUCAUCAGAAGUACGGUCUACGUAAGAAUGUAACUGCCAAUAAAGGGAGGCGUC
UUGCUGGUACAAGGAAAAACAAAUAUUCCCCAGUUCAGUCUACGCCCGCGGGGGCGACGACAUAGAGUAGUGUCAGAGGAGUGGAUACGGGUGGAUAUGUUUAAUGUUGUGCAUGCCGCAGGUGAUCCAGGGACGACUAUGUCUACAGGGAGAGCUAGCGAUCGGCUUCACCCAUCGGAACUCUU
CCGGACGUUAAUAAUACUUAAAUUUGAGGAGCAAGGGGUUUCGGUCGUAACUAAGGGGUAUAGCGGGGUUUAUAACCCGGACAGGCAUGUUAACGUGCGUUAAAGAAACAAGAGGAACAGUAGUGAGAGAUUUAGAAUCGUACAUCAAGGGACGUUUGAGGGAAUGUACUCAGAUACAGACCCG
GGCCCCUCUCAAAAGGGAAUCAGAGGGGGGAGUGGAUGGAGAGUUAGUGUUCGGCCGAUGACGGAGUGAGAGCAUAAUAUGCGGUUACCUAGCGAAAUAUGGUGUCUAAGAGUUAUAAACGAUUAAAGUUAUGAUAGGUCACGGUAGGGUAGGUGCGCUAGGUUUUAACUACCUAGACGACCACC
UGGAUAGCAGACGGGUAAGAUCCACUGGGUUAACAACCCGGGCUCUGAGGACUGAUGAAGAGCUAAGGAGUGGAUCGUAUCUCACACUAAGGGGGAGCAGAAAUUGAAUGACGUUGAUUUUGGAGCGGAAUGAUGGGGGACAAUAUUUCGUCCUAAGCAGGAGCGAGAGAAGUUCUCACCAAUAU
UGGAUGUUGUGGGGGACUACCCGUGACAGUGUGUAUCCGCUUUAGGGAAGGCGACAUACAGUACCGACAUAGAAACGAACAAGAAGGGUAGUCUAUCGUUAGCGUUAAGUCCGUUCGCAGGACUGAGAGAAAUGUUUUUACAAAUUUCAAGAAGUUGGACGGGGGUAUAUCGGGACAUGUUCGGA
GAACAAAAUGUGAGAAGCAGGAAGAUCUAGGAUGGUUCAAGACGACCAAAUCUAUGAUCCUGAAGAGAGAAUCGAUGAGUUAUUGAGAUUAAAGAUUUGAUAUACGAGAAACCCAGGCGGUAGCUCGAACUGUGUCGAAAUAAAGAGUUGUAGACGAUUUUGAAACAGAAAGAAGUGUCCGUUAG
UCUAGAUUUUAACCAAUACAACAGGCCGUGGUGCUAAUCUCAUCAAAGCCAAUUAGCUUCGCAUAAGCGCUAGUUCAGGCUUUACCUUUACCCGUACGAGCAUACGAGGGGCUUAUCCAUGUGGAAACUCGGCGUGCGAAUUGUUUUCUGUAGAAGAUAGAAGUCGUAUGUGGAUGAAAAGUAAG
AUUGCUAAUAUCAGGGCACGAAUAAGCGAAAGGACUGUAUAUGGUAUGCAAAGACUUAAGUGUACCCGACUGAAUAAAAAGGGCUUUUAAGUGGUUUUAGAAGCGAGAGCACGGUCUCGACGAGAGGGAAAAGGACGUAAGAAUACUCGGUGUAAGGAAUGAGCUAAUAGAACGAAUUUAAUAUA
UGGUGCGAGGAGGAUGAUCGAGAGAAUGGGCGAGACGCAAGUCCUAUUGUGCGUAAUCUACGCGAAGACAUUGGAAUACAUAGACGCGUCACUGGCACGAAUUAUACGCGUUGGCGUUAGAGGAAGUGUACAUUCAAUGAGGAUGGUGAUAGUCAAUCGGAGUGAGGAAUGCGAAAUAUAAGAGA
GAUAGAAAAAAUGGUGACCGGGACUACCAGGCAAUCUGAGUGUAGUGGUGCAGAAAGAAGGUAGAGUGACGAGGAACAGUGAUUUAUGGGGGGUGUUCGGAAAAAAUGUAAGACAGGGAUAAAUUUAGGUAGAGGUAAUGAGAUUCGAAGGUACAGUGCUACAAGGUGUAGUGUAAUACCAAUUUC
GAUGCUGAUCAACGUACGUUGCGAGUAUAUCUACGUUUGCGCAGGCAAGGGCUUUUAGUGGGCGGAACAUGGGGAAGUUCUUUUAUCGUGCUAAACAUGAGAUAGAUUGGUACAGACGUAGGAUAAUGGAUACAGGGACGACGACAAUCUGGAAUACGUUGAUGCGCGAACAGUUAAGAGAGUAC
GGACGCAACUGUGUAUUAUAAGCCUCAAAGAUAAACUUCUAAAGAAAAGUAUGUCGGAACAACUGUCUGCACACUAAUAAAAGGGGCGGGCGGAUUAUACACAAAUUGUCGCGGACACGUCGGCCUAAAGGUCAUCCAGUAGAACGAAACAGUGUAUGCUGCCCCACGAGGGCUGGAAAUUGAAC
AAUGUGGGGCUGGCUUUACAGAUCAUAAUGUGGAACUCGAUGCGGGCACUGGCAACAAGUGAUAGGCGUGGCUGAUCCGACAGGGGUUGGAUUUAUACGUAGAUGAAGUUCGGGUGAGCAUCGGGAAAGAAAAGGUAUGUAAAUGGUAUUUGUCGUAAGGAGAACAAUAGGGGCUAUAUGCCCGA
GAAAUCUCCAAAAACGGCAACUCCUGGGGUCAGAGUGACUGGGACUCGAAAUCUGAAAAAAGGGCCUUCGAGAAGACGCAUGCGGGGAUGAGGACAGAAUCCGUAGACUAUUAGUCAAAGGCGGACGAUUGGACCGGGAGUUCGCGUUGUGGGGUAGCCAUAUAGGAUACUGUCGCGCUUGCUAG
AAAGUAGGAUGCAAAACGUUAGAAUUUACGUGGGUGAGAUGAGGUGUAGACCUGAGGCCCAGAUACAUGAUCGCAAAGAACUGGGUAGAGAGGGUGCAGUCCAGAAAUGCGGAGAAGGCAGCAUAAAGUGGAGAGACUACAUUAUAACCCGGAAAAUUGAAGAAAUGAGGGUAGUGUGAAAUG
UACAAAUCAGAUUGUGUGAAUGGAAAUCAAAAUGCAAAAUCUCGGCUAAUGACUACGAAAGGCGUAACAGGGGGAAACCUGAUACAUGCAACAAUGCCUCCUAGGAAGAGCGGAGAUGAGUGAAAGCGGACCUUCGAAGUGAACGGGUGGGGGGAGGUGUUGCCCGGGUUGUGAUAAGAGAACGGAC
UAGGUGGGGGGUACAACACUAAAUCGACUAACGAGUGCAAUAUAGAGAUCUCCGAACUGCUGGCUUAUUGCCGUACGGUGGAAUGAAGUGGACGGUUCAUCAGGGACCAGCUGACCGCUGAUCCGCAGAGACCAAGUCAAUAAAGGGUGCGUAGAUGGGAUCUAUUAGGCACGGCCGAGAGGAUG
AAGAAACUGCGCGUGCGGUUUUCCUAAAAGCCGUAAUGCCGUUUAGAAGACCGAAGUUGGAUGGUGAGGUGCAAGCGGAGCAAAAGGUGGGGACUGAUGUUGCAACGUCACAGUCCCGACGAGAACGGAUUUCAGGAGUCAAAACCAGGGGAGCGUUAGGAUGAUGACAAACUGGGAGAAGAGGCG
GCAUAUUAACACCUUCAGUUAGGGGGAAAAGUCAGAGGUAUCGUUCGUGAGCUGCGGAUAUAGAGUAAGAUUUACAAUUACUAUACACAGGCGGAGAAUGUAUCAAUGCAAACGUGUAUGGCCUCUAUAUAUGGCUUCAAUUAAACCUAAGUUCAAGGUGAAAAAGACGACGUAUGGAAGGGGCC
CCGGAUACCAAUGGCCGGAAGGUACGUUAAAGACUGUGUUGUAAUAUCAUGUUAAAUAAGCAACUAUACAUUGGAGGUCCGGUGCAAACCAGUAAGGAAAGAAGUAGAUUCUGAGUGAAAGUUGAUGGAGAAGCCGGGUAUGUGUAUGCUUGUUAAAUGAUGUUAGUUAAGCAGGGUCUUGGAUC
UGGAGUCUAAAGGCUUGCACUAAGGGACGACCCCGUACUACACAACGAUUCAAGUUGGGUGAGUUAGCAUACUAUUCCUUGAACCCAUAGAGCCGGCGACCAGGAGUGGGAAAAAGGUGGGUCAGUGCCGUGAGUGAGUUGAAAGAAAUAGAUAUAGACAGUAAGGUCGGGAGGUUGAGGGCACG
AAAGAAAUGGGAUAACGAUUAAGUGGGGUAGCGGGAAUUAACAGACUCACGGUUGCAUGAUUUGAAGCAUGAUUGAAGCAUUGUUAAGUGAAUGGACCAAUUGAGCACAUAAGAGAUCCAAGAGGAGCCUGUUAGCGAAGAGACGCUGUUGGGGAUAUAAAUUCGCGCU
GAGAUGGUGGUCUUUCCGGCAUUUUAUAGAGGCGACUUAAAAACUGCGAACGUCACGAAAACAGGGAGGCGAGGAUUGUGAGACAUUGAAGACAUCGAAAUAAUCUCGGGCCACAAGAAUCCGGCAGACGCACGAUGUCAAGAUACAGUUAGCCGGAGCGUAUGAAAAUAGAGCCUAAAGAACUG
UCUUCGUGUGGGUUGCGUAGUGUUGCUUAGGAUACAGCUGGACAGAUUUAACGCACAUAAGGGUUACAUUUCAUUUGGAAAGUGAAAUAGAGAUGGCUCUGGGACCGAAUAAGAAGUGCAGGAAUAAGUACGUAAGCGGUCAAAUGCAUAAUAAGAAUAGAGGCUAGAUCGCUCGACGGGCCACG
AUGCAGGAGGAGGGUUAUGUAGGCAGAGAUGAGACGUAAGUGGGGUAAGAUUCAGCAGGGGAUUUAGCAAGGAGAAAUUGAAAAGGAGAGCGCGGACUAGAUGAUAGUGGAAACAUCGAGUUCAAAGAAAUCUGAGUUAGGAUGCGUAGGAUGAGGAUGCUAGGUCCCAACGGGGUACGAGAUUA
GCGGCCGAUCACGAUAUAAUGAGGACAUCAGCUGAAGAAUAAUUGGCGAGGAUGACUGAGGUACAGCGGAUAUGAAGAUGGAGAGAAUUAGGCGGUACUAGUCUAACACGGAUAAAGGGCGUAGAACUAGGUGUGGGACGUAGGAGAUAUCUUAGCCUAGUAGAGCGUUUGUGAUAUACGAGAAG
AGCGGUCGUACUCGAUGUUGAAAGUGCCAGGAAGAUCGUGACACAUUAAUCUUGGGUAGGAAUCUAUUUGAGCACAGGAUGGAACAUAAUGCUCAAGUGAAGGAAUUACCUGGUCGCGAACGGAGGCGGAACCGGGCGAGACAGAAGGAAGAGAACGUAGCUUGUGGGUCGAAGGACAACAAGUCG
AACGGUUGCUAUACCCGGGAGAAUGAUUGCGUACCCUAGUUCUUGCCUAAACUCCUGCGGGGUACUAUCUCUAUGGACUAAAUUGCCUUGAAUUGGCCCGAAUGGAGAUAGGUAAGAGCAUUGAAGUCGCUGGAGCGCUCGCAGAUAAGUAGAGAUUUAAAUUGCAGUGUCGGUAAUUA
CUUAACUAUGGCAGCUCUGUUCGAUAGUCAUCCCAAAGGAGGCCAUGUUCAGAAAUACUUAAGUCGAGUGUAAUGAGACGAGUAUAUCACUGGGGAAUCCCGCACCAGAUAGUGGGGAUGGGCGAAAUAGUCGUUUGAUGAGCUGAAGCGGAAGCCCCUGAAGAGUGUUUCCUUACGAAUACAACG
GUAGUGUGAUAGUGGUAUCGUAAGGAAGACUUCAGUAUGGCCCUAGUGGCAAGAAGAGACGGCCGUGGUGCGCGGCGUAUAGAGCGGAUCGAGGUUAGUGAAGGAGAAAACCAUGUCUAAGAUUGAUUAUGGUCGUGAUGGAAGAGGGGAGAAAAAGCCAAAGGAAGACUGCCAGGGGGGAACCA
AGAGCCCAUCCAUGGGAGAACAACGAACGGAUAGGCAAUCGAAUGGAGCGUCACUUAGAAGUCUUCGACAAGGCGUGCGUGAAGUACUACUUCAGACAGACGUUUAAGUCAAGCGGUAGUUACCGCAUGUGGAGGCAGAUAGGCAGCGAGAGUACAUUCAAGGUGUAGCUAUCUAUUUAUGGGUU

AAAUCUAAAAGGGCAGACAGAAAGGUCGGUAGCAUGGCGGGAGGUCAAAGCGAUUCAUACAGGCUAAAAAGACCCCCAUGGGUAGAGGAGGUGUCCAAGGCUACGAUUCGGAACGGAAAGGGGCAGAGGAGUGGAGUUGAGAUAAAACGAGCACACCGUAGUUGGACACACCAGAAGAUCCGAAA
UAUAAUCACAAAAGCGUGAGAUGAAGGAAUCUGUGUCUACAAAUAAAAGAACCAUCAUGGCGGCUAAGAGAAAAUUUGGUGAUAAUUAGGAAGAAUAUGUUAGACGGCGACCAUAUGGAGGGUAUAACGGGGGUCACGGAAUACGAAGAACAGCGUUGUCAGUGUGAAAGUAGCUAGAUCGUAUU
UCUAAUUUAGGAUAAGAGGUAUCGGACGGCAAGACGAUGAAUAUUGAGGGAGACGACCAUACGGGGUAACCGGUACUUUAGUUAUGUAGCAAAGACGUGAGCGUACCUCUACAAACAAGCGCGGCUCCAGUACGCAAGCAGAAGAUGUAAGAGUAUAGAAUAGAAUGGCAUGCGUAAUGGGUAG
AGAGAUGGGUAACUUCCAUAAGGGGAGAUACAAGGGUACCAAAAAUGUACUUAAAGAGAAUGUGACUAAAGGACGGCAUCGAAGUAAACUCCCUUAAACGAAGGACAAGAUAUGCGCGAUGUAGAUUGGAGGUGAUAUCACAGAGACAGUUGAGUAAUAGUAAUGUUACCAACGUCGCUAGUUAA
GCCCAGUGGAACUACAACCGCGGAAGAGUUCGUAAAGAGGAGGAGAAGUAAGCAGCGGGAGUAGGAAGAUAGGAAGCAUAAAAAGGUGGAGGAUGCUGUUGGUCCCGAAGCGUUCAUAGUCGGCGCAUGAUAUCGCAUGCUGACAAUAAAUGUGUUAUGCGAACCCAUAAAGGUGAAAGUUUUGGU
AACCCAACCAAGAAGAGGGGCUACUUCGGGAAAGAGGAUGAGGAAUGCGGGCAGUCCUAGGGAAAUCACCUGUUCAGUAGGAGUUAAUCUGUAUAAUAUUGAAUAAAAAGACAGUAGUGCAAAGCAACAGGUGUAAGAGGAUGUGCACAAGUUUAUCAUGAAGGGUAAACAUUCAUCGGGAAACC
UAACGAUCGUUCUCACAAUCAGGGUGGGUAAUAAGUCCGGGCUUGAACCUGACUGUAAUAGCACCUCGUAUGAGGCGUAUAGAGUCAUUAGGGCAAGGAAACGAUCUUGUGUUGGGGAUGCGAUAGAUUUUAUCGUCGGACCGAUCUAGUGGACUCGAACUCUGGUUUCGCCGUAGGGGGAGACA
GGACGAAAGCUGUAUAGCAACGCAAAGGCACGAAGUUGGUAAAUACGAUGACGCCGGGAAGCAGAAGAAGAGAGGGGCGUUCAGCGUCAAGUAUGAAGUGAUCUAUACUGGAGGAUAAGGUGAGAGAUAGGCUUACAAGCAUGGUAGGCGCGAAAGAGAACUGAAUUAAGGAACAGGGCGCGGUG
GAGAGCCCUGUAUGUAUUUGUAAUUAGUGGUGCCGAGGUCUGAUUUGCCUUGGAUGAGCAGGUCGAAGCAUCCGCUGGCAGCUGUGCCCGAGGAAGCUACCUCAAACGGUUUUGGGAACGUGGUAGACAGACCUUUGAGAGCACGUGGGUGAACUAGGGAGUAAGGCAACGUGGGACGAUUACAG
AACAUGUACGCAAUUCAAGUAUUCAGACUGCGUGGAGAUCGAGAGGAUUCCUAAUAUCGUGUAACUCAUUGAACGACCCUGGUAUGUGGACUGAGUUUCAGUCGGCAGGGAGGUAGAGCACAACGCACUCAUGCAGGCUUGUGCAGGCAGGAGCAAGAAAAUAGCCUGUCCAAACCUUAAGUACA
AAUGGCCCAGGGGGAUAAUAAGACAGCGUAAGUGGCCACAGUAGAAGCAGAGUUAUUUGGAGCAUUAUAACGGUAGGUGCUAGAGUUAUGCCGGUGCCAGGGACGGUUAAAGCUGCUAAAGUCCACAUCGUGGGGCGAUAAUGGGAGAGGACUUUGUAUCCCAUUUUCUCGCUGUUAGGGAAAAA
CACUAAAUUAAGGACAUGACGAGGAAAGGAAAAUUUGGCUGUCCACGGGGUGGACUCUACGGCGCCCUGAGCAGAGCACUGUCUAGUGGUGAUACGCAAGGGGCGCAUAAGCUUGAAGAGGAAACCUUAUCCCAGAACUAAAACUAUGCAUAAAAAGGAGGCGUGGGGGAGUUGGACUUGACUGC
GACAAUAGAGCGCAGGGGACGGUUUGACAGCAUAAAAUCUUGUUGCGGGUGAUACAUAUAAAUGUCAGAAGUAGUGAGCGAUUGGUUAAAGCAGCAAGCUGUAUCGGAAGGGUCAACCUUCAGAGCCACGUGAGGAAAGAGUCUUCCGACAGACCAGUCUGUGUGGGGGGAGAUGAAUAGUAAUC
UGACAGGGUACAGGUCGUUAUCCGCAAGCAAAUAGUAUAGGCGUAGUGGUAAACCGACAAGGACUGGGGUGGACCAAAAUCGUAAGCGCGGUAAUAGUUGGACAUCGAAGAAUGUGGUUAUGAAGAUAGUUACAUUAGGGAGCUAGAUAUCUUCAAGAACGUGGAUUCUCUUGGGAUGUGACAGU
UUAAAGACAACAGUUCUAACAAAAGUGAGAAUACUACAAAAGAGUGGCAAUAAGAGUCAUGAACUGCGUAGUGUGUCUCCUGAUGCAAGAUAGGCUAAGAUAGUUUAUUCUGUCACGCGGGAGCUUAACCUUUGGAAGGAUAGAGGCGUGAAGUACUGACCCGGCGUCAAGUUACCGUUAAGGAU
UUAAUUGGACAUUCAAAAGAAGUGUUUAGUUAAGGCGUCACGGACGGUAUUUUAUAUAAGACCAGAGAAGAAAGCAGACAGCGUGAAGAGGCAACGGGGUUAAUGGGAUAUGUUAACUUAAUGAUCGUAGAGCCAGCUCAUUAGACGCCCAGAGUAGUACCGUUGUAGAAAUCUGUCAUGUGCAAAU
AAGCCUGAGAGUUAGCACCUGGUCGAUGGCAAGAAGGGAAGAGUGGUGUAAAAAGGAGACUGCGGUAAUGGUCAAACUAGUAGAUUAAUACCAAGGAUUGACAAUUAGUGAAACUUAGGUGCUGUAAUCUGCAACGGGGUGCCGGUAUGGCAUCUCUGGCGUGGCACGUAAUAACAUAGGGUUCA
CUGAAGCAGUAGAAAGAGAGAAACGCCGGCAUCAGCAAGUAUGAGGGGAGGAUAGAGCGGUGUUUACGGGAGGAUGUUAUCCGGAAGUUUCUUCGCAUGGAUAGAGAGUCCGGGGAGAUCCAGUGUGGAUUUGUAUGAUACUACAGGGUGGGCGAAUCUUGUCAGAGACCGUAGGGUGAAAUGUA
CAUCUACGGCGUGAGAGGAUGUUAAGAGCAUCGGAAGACAAUUGUCUUCAGGGGAGUAGGGCAGGCAGGAAUCGAACGCAACUUAAGAAUAAGAGUGGACAGACAUAAACGUGAAUAGGGUUUAAGUAACAAGGUGAAGCGUGUGCUGGAACUGUCGAGUCAAUCUGAACCCAGGAGAUUUGGAG
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AGGCCACAAGGC'
```

Break anticodons into threes.

In [39]:
```
anticodons = []
for i in range(0, len(c), 3):
    anticodons.append(c[i : i + 3])

anticodons
```

Out[39]:
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...]
```

Make a dataframe of anticodons and amino acids.

In [41]:
```
translation_df2=pd.DataFrame(columns=['Anticodons', 'Amino_Acids'])
for i in anticodons:
    translation_df2.loc[len(translation_df2.index)] = [i, i]
translation_df2
```

Out[41]:

	Anticodons	Amino_Acids
0	UAC	UAC
1	GAC	GAC
2	AGG	AGG
3	AUA	AUA
4	UAC	UAC
...	...	...

	Anticodons	Amino_Acids
9126	AAG	AAG
9127	GCC	GCC
9128	ACA	ACA
9129	AGG	AGG
9130	C	C

9131 rows × 2 columns

Remove extra nucleotide.

In [42]:
```
translation_df2=translation_df2.drop(9130)
translation_df2
```

Out[42]:

	Anticodons	Amino_Acids
0	UAC	UAC
1	GAC	GAC
2	AGG	AGG
3	AUA	AUA
4	UAC	UAC
...	...	...
9125	GGU	GGU
9126	AAG	AAG
9127	GCC	GCC
9128	ACA	ACA
9129	AGG	AGG

9130 rows × 2 columns

Anticodon conversion to amino acid chart.

- UUU Phe
- UCU Ser
- UAU Tyr
- UGU Cys
- UUC Phe
- UCC Ser
- UAC Tyr
- UGC Cys
- UUA Leu
- UCA Ser
- UAA Stop

- UGA Stop
- UUG Leu
- UCG Ser
- UAG Stop
- UGG Trp
- CUU Leu
- CCU Pro
- CAU His
- CGU Arg
- CUC Leu
- CCC Pro
- CAC His
- CGC Arg
- CUA Leu
- CCA Pro
- CAA Gln
- CGA Arg
- CUG Leu
- CCG Pro
- CAG Gln
- CGG Arg
- AUU Ile
- ACU Thr
- AAU Asn
- AGU Ser
- AUC Ile
- ACC Thr
- AAC Asn
- AGC Ser
- AUA Ile
- ACA Thr
- AAA Lys
- AGA Arg
- AUG Met
- ACG Thr
- AAG Lys
- AGG Arg
- GUU Val
- GCU Ala
- GAU Asp
- GGU Gly
- GUC Val
- GCC Ala
- GAC Asp

- GGC Gly
- GUA Val
- GCA Ala
- GAA Glu
- GGA Gly
- GUG Val
- GCG Ala
- GAG Glu
- GGG Gly

Amino acids chart.

- Ala A Alanine
- Arg R Arginine
- Asn N Asparagine
- Asp D Aspartic acid
- Cys C Cysteine
- Gln Q Glutamine
- Glu E Glutamic acid
- Gly G Glycine
- His H Histidine
- Ile I Isoleucine
- Leu L Leucine
- Lys K Lysine
- Met M Methionine
- Phe F Phenylalanine
- Pro P Proline
- Ser S Serine
- Thr T Threonine
- Trp W Tryptophan
- Tyr Y Tyrosine
- Val V Valine
- Asx B Asn or Asp
- Glx Z Gln or Glu
- Xle J Leu or Ile
- Sec U Selenocysteine
- Pyl O Pyrrolysine
- Unk X Unknown

Match anticodons with amino acids.

In [43]:
```
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UUU','F')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UUC','F')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UUA','L')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UUG','L')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CUU','L')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CUC','L')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CUA','L')
```

```
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CUG','L')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AUU','I')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AUC','I')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AUA','I')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AUG','M')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GUU','V')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GUC','V')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GUA','V')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GUG','V')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UCU','S')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UCC','S')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UCA','S')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UCG','S')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CCU','P')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CCC','P')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CCA','P')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CCG','P')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('ACU','T')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('ACC','T')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('ACA','T')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('ACG','T')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GCU','A')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GCC','A')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GCA','A')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GCG','A')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UAU','Y')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UAC','Y')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UAA','Stop')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UAG','Stop')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CAU','H')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CAC','H')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CAA','Q')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CAG','Q')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AAU','N')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AAC','N')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AAA','K')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AAG','K')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GAU','D')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GAC','D')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GAA','E')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GAG','E')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UGU','C')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UGC','C')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UGA','Stop')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('UGG','W')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CGU','R')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CGC','R')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CGA','R')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('CGG','R')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AGU','S')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AGC','S')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AGA','R')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('AGG','R')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GGU','G')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GGC','G')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GGA','G')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].replace('GGG','G')
translation_df2
```

Out[43]:

	Anticodons	Amino_Acids

	Anticodons	Amino_Acids
0	UAC	Y
1	GAC	D
2	AGG	R
3	AUA	I
4	UAC	Y
...	...	...
9125	GGU	G
9126	AAG	K
9127	GCC	A
9128	ACA	T
9129	AGG	R

9130 rows × 2 columns

In [44]:
```
translation_df2['Amino_Acids_copy']=translation_df2['Amino_Acids']
translation_df2
```

Out[44]:

	Anticodons	Amino_Acids	Amino_Acids_copy
0	UAC	Y	Y
1	GAC	D	D
2	AGG	R	R
3	AUA	I	I
4	UAC	Y	Y
...	...	...	...
9125	GGU	G	G
9126	AAG	K	K
9127	GCC	A	A
9128	ACA	T	T
9129	AGG	R	R

9130 rows × 3 columns

Data Exploration

In [288…
```
plt.figure(figsize=(15,8))
sns.countplot(translation_df2['Anticodons'], palette='Set3')
plt.xticks(rotation = 90)
```

Out[288…
```
(array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12, 13, 14, 15, 16,
        17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33,
```

```
       34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50,
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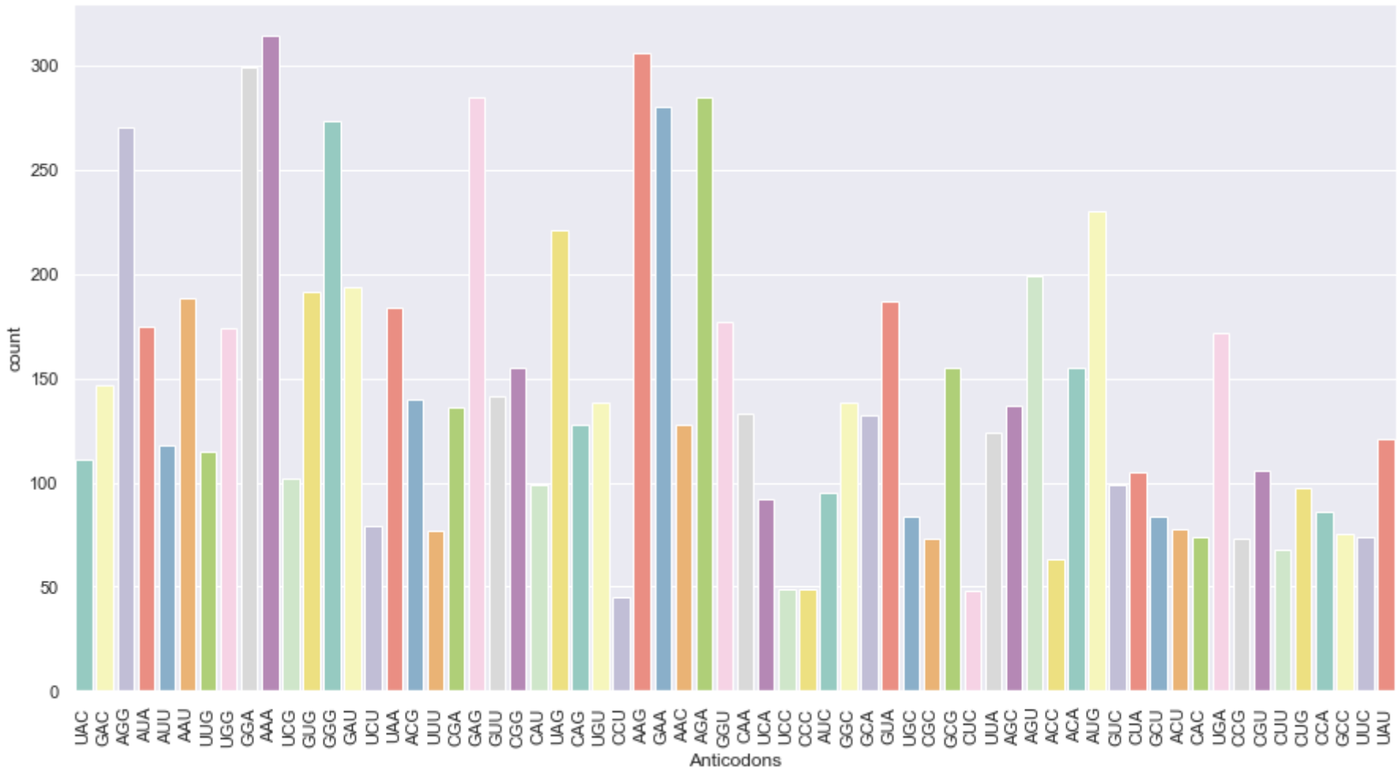
```
Text(62, 0, 'UUC'),
Text(63, 0, 'UAU')])
```

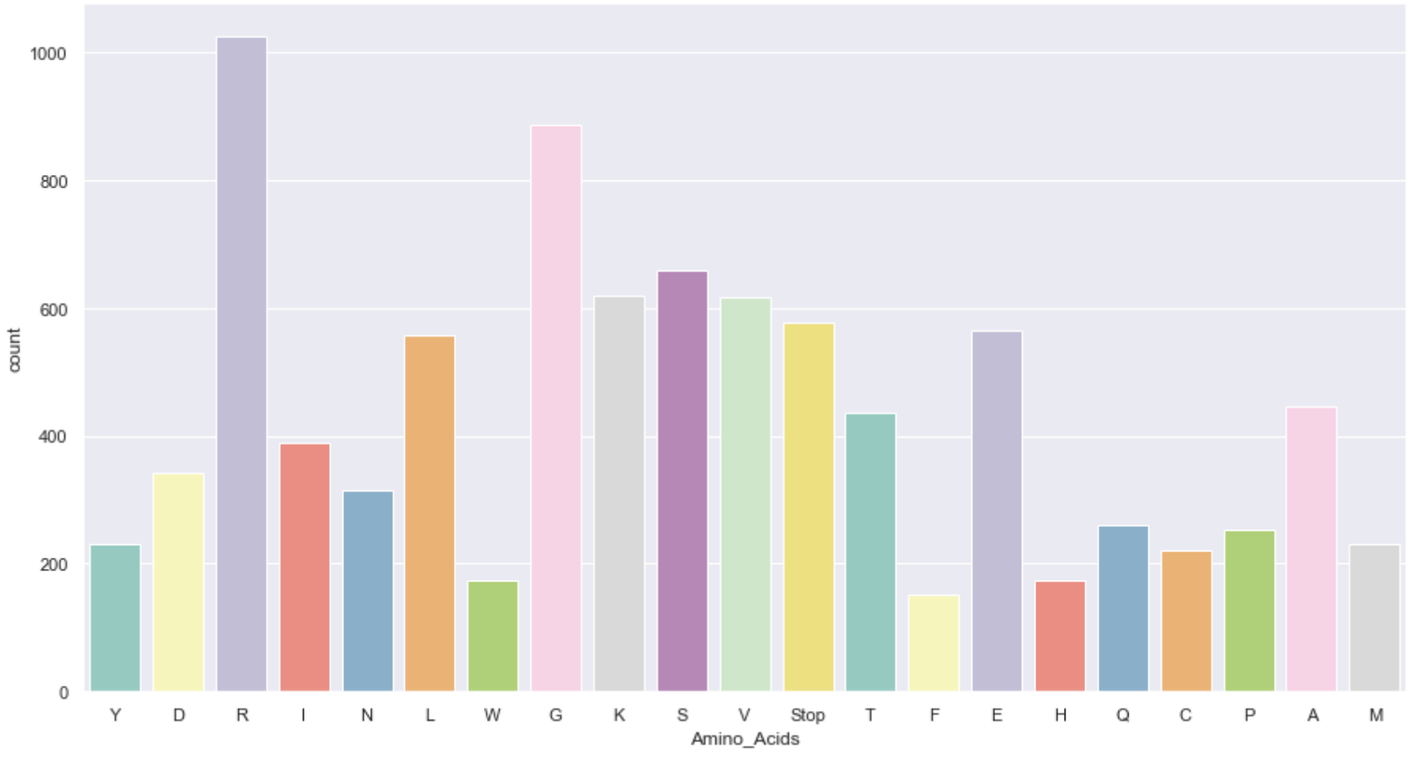


In [290…

```
plt.figure(figsize=(15,8))
sns.countplot(translation_df2['Amino_Acids'], palette='Set3')
```

Out[290…

```
<AxesSubplot:xlabel='Amino_Acids', ylabel='count'>
```



There is a class imbalance that will be resolved with oversampling.

Feature Engineering

Represent anticodons and amino acids with numbers.

In [45]:
```
translation_df2['Anticodons']=translation_df2['Anticodons'].astype('category')
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].astype('category')
translation_df2['Anticodons']=translation_df2['Anticodons'].cat.codes
translation_df2['Amino_Acids']=translation_df2['Amino_Acids'].cat.codes
```

Reshape X and y so that they are 2d.

In [46]:
```
X2=translation_df2['Anticodons'].values.reshape(-1, 1)
y2=translation_df2['Amino_Acids'].values.reshape(-1, 1)
```

Resample independent and dependent variable.

In [47]:
```
X2_resampled, y2_resampled = oversample.fit_resample(X2, y2)
```

Make a train test split of 80/20.

In [48]:
```
X2_train, X2_test, y2_train, y2_test = train_test_split(X2_resampled, y2_resampled, test_size=0.20, random_state=10)
```

Machine Learning Modeling

Fit the model to the training data.

In [49]:
```
decision_tree.fit(X2_train, y2_train)
```

Out[49]:
```
DecisionTreeClassifier()
```

Make predictions.

In [50]:
```
y2_hat_train_dt = decision_tree.predict(X2_train)
```

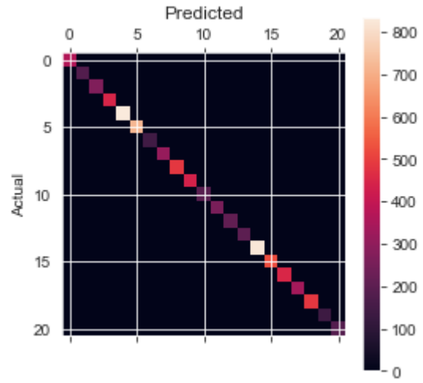
All predictions were classified correctly.

In [51]:
```
con_mat(y2_train,y2_hat_train_dt)
```

```
Confusion Matrix
----------------
      0    1    2    3    4    5    6    7    8    9   ...   11   12   13   14  \
0   370    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
1     0  182    0    0    0    0    0    0    0    0  ...    0    0    0    0
2     0    0  273    0    0    0    0    0    0    0  ...    0    0    0    0
3     0    0    0  447    0    0    0    0    0    0  ...    0    0    0    0
4     0    0    0    0  833    0    0    0    0    0  ...    0    0    0    0
5     0    0    0    0    0  720    0    0    0    0  ...    0    0    0    0
6     0    0    0    0    0    0  142    0    0    0  ...    0    0    0    0
7     0    0    0    0    0    0    0  315    0    0  ...    0    0    0    0
8     0    0    0    0    0    0    0    0  485    0  ...    0    0    0    0
9     0    0    0    0    0    0    0    0    0  437  ...    0    0    0    0
10    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
11    0    0    0    0    0    0    0    0    0    0  ...  259    0    0    0
12    0    0    0    0    0    0    0    0    0    0  ...    0  209    0    0
13    0    0    0    0    0    0    0    0    0    0  ...    0    0  200    0
14    0    0    0    0    0    0    0    0    0    0  ...    0    0    0  824
15    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
16    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
17    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
18    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
19    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
20    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0

     15   16   17   18   19   20
0     0    0    0    0    0    0
1     0    0    0    0    0    0
2     0    0    0    0    0    0
3     0    0    0    0    0    0
4     0    0    0    0    0    0
5     0    0    0    0    0    0
6     0    0    0    0    0    0
7     0    0    0    0    0    0
8     0    0    0    0    0    0
9     0    0    0    0    0    0
10    0    0    0    0    0    0
11    0    0    0    0    0    0
12    0    0    0    0    0    0
13    0    0    0    0    0    0
14    0    0    0    0    0    0
15  522    0    0    0    0    0
16    0  451    0    0    0    0
17    0    0  339    0    0    0
18    0    0    0  488    0    0
19    0    0    0    0  134    0
20    0    0    0    0    0  183

[21 rows x 21 columns]
```



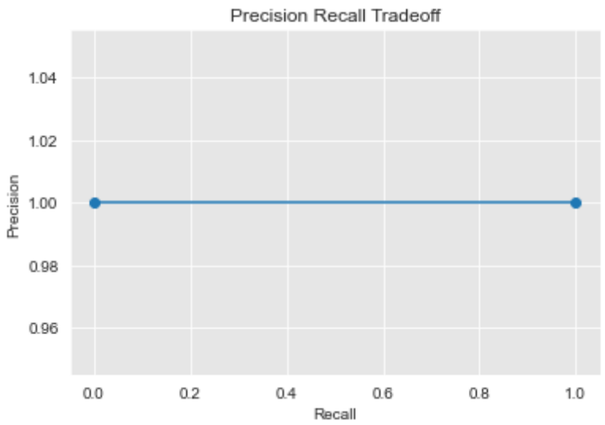
Seperate actual and predicted values into each class for metrics.

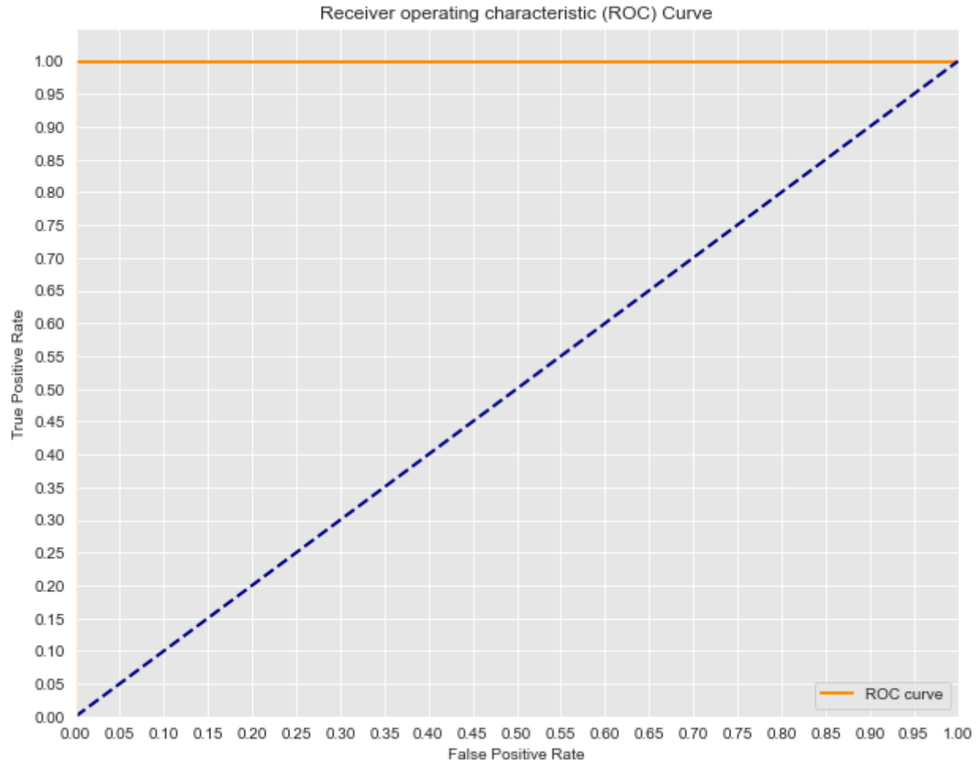
In [52]:
```
actual_class0=y2_train==0
actual_class1=y2_train==1
actual_class2=y2_train==2
actual_class3=y2_train==3
actual_class4=y2_train==4
actual_class5=y2_train==5
actual_class6=y2_train==6
actual_class7=y2_train==7
actual_class8=y2_train==8
actual_class9=y2_train==9
actual_class10=y2_train==10
actual_class11=y2_train==11
actual_class12=y2_train==12
actual_class13=y2_train==13
actual_class14=y2_train==14
actual_class15=y2_train==15
actual_class16=y2_train==16
actual_class17=y2_train==17
actual_class18=y2_train==18
actual_class19=y2_train==19
actual_class20=y2_train==20
predictions_class0=y2_hat_train_dt==0
predictions_class1=y2_hat_train_dt==1
predictions_class2=y2_hat_train_dt==2
predictions_class3=y2_hat_train_dt==3
predictions_class4=y2_hat_train_dt==4
predictions_class5=y2_hat_train_dt==5
predictions_class6=y2_hat_train_dt==6
predictions_class7=y2_hat_train_dt==7
predictions_class8=y2_hat_train_dt==8
predictions_class9=y2_hat_train_dt==9
predictions_class10=y2_hat_train_dt==10
predictions_class11=y2_hat_train_dt==11
predictions_class12=y2_hat_train_dt==12
predictions_class13=y2_hat_train_dt==13
predictions_class14=y2_hat_train_dt==14
predictions_class15=y2_hat_train_dt==15
predictions_class16=y2_hat_train_dt==16
predictions_class17=y2_hat_train_dt==17
predictions_class18=y2_hat_train_dt==18
predictions_class19=y2_hat_train_dt==19
predictions_class20=y2_hat_train_dt==20
```

```
a=[actual_class0,actual_class1,actual_class2,actual_class3,actual_class4,actual_class5,actual_class6,actual_class7,
   actual_class8,actual_class9,actual_class10,actual_class11,actual_class12,actual_class13,actual_class14,actual_class15
  ,actual_class16,actual_class17,actual_class18,actual_class19,actual_class20]
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3,predictions_class4,predictions_class5,predictions_class6
  ,predictions_class7,predictions_class8,predictions_class9,predictions_class10,predictions_class11,predictions_class12
  ,predictions_class13,predictions_class14,predictions_class15,predictions_class16,predictions_class17,predictions_class18
  ,predictions_class19,predictions_class20]
```

In [53]:
```
multiclass(decision_tree,X2_train,a,p,translation_df2['Amino_Acids_copy'],'train')
```

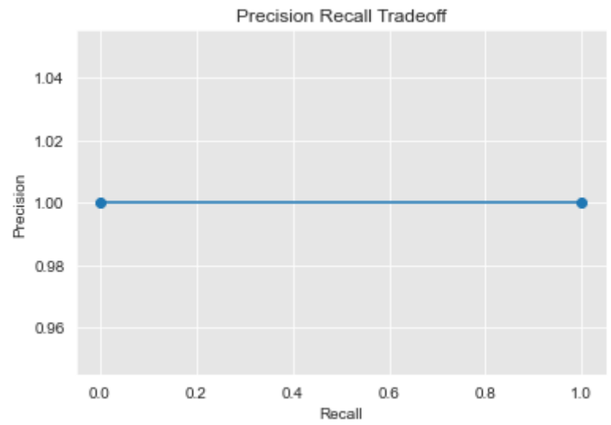
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

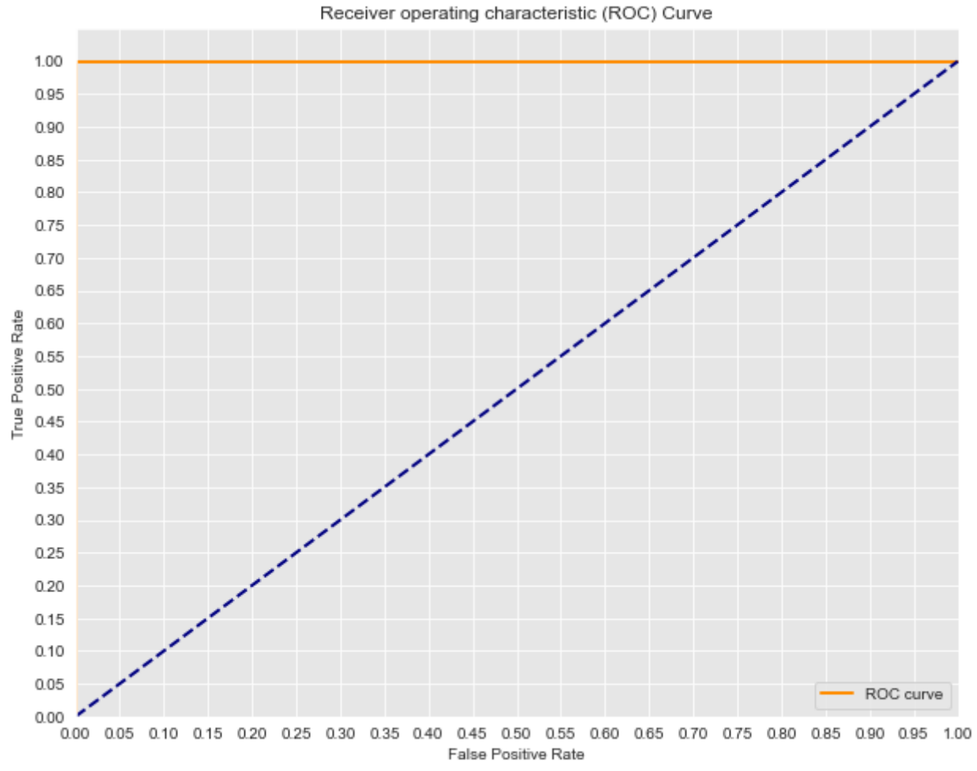





```
Cross Validated ROC AUC score: 1.0
```

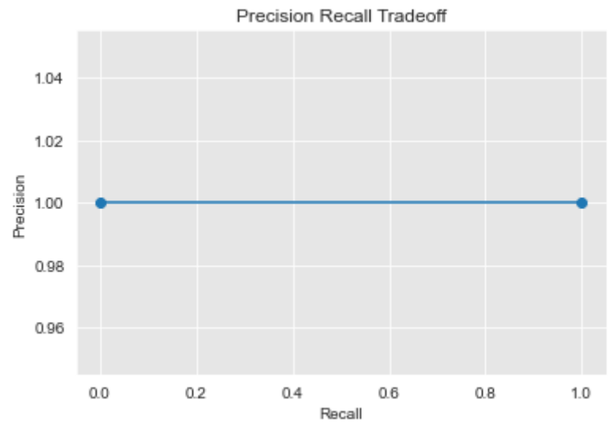
```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

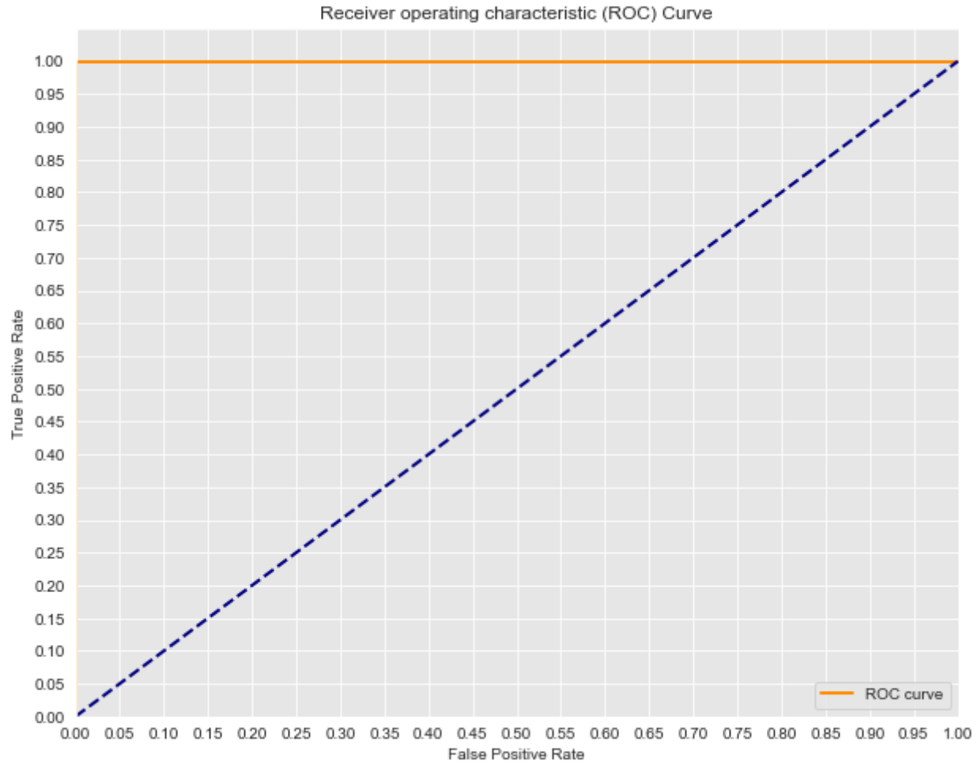





```
Cross Validated ROC AUC score: 1.0
```

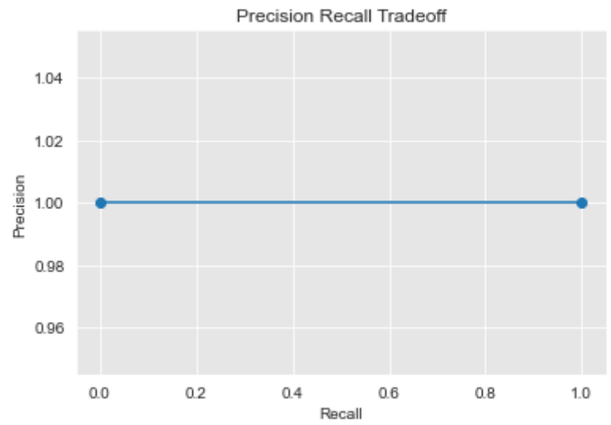
```
Class:D
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

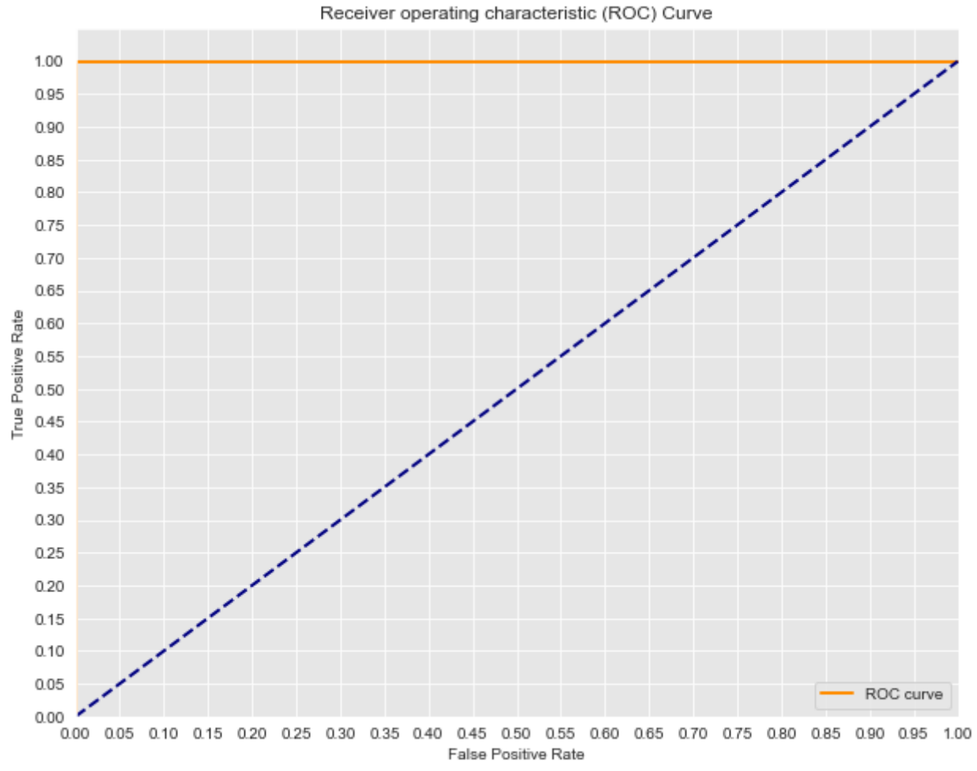





```
Cross Validated ROC AUC score: 1.0
```

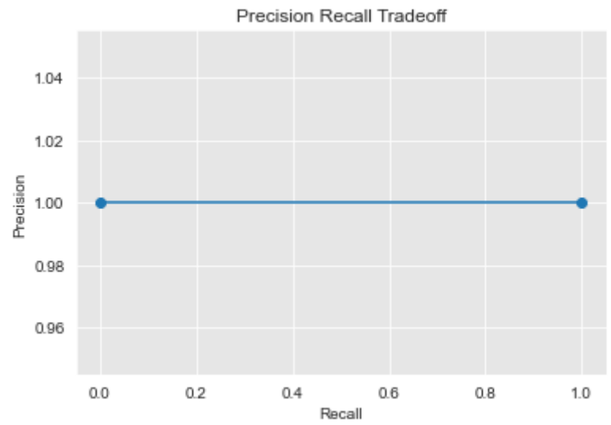
```
Class:E
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

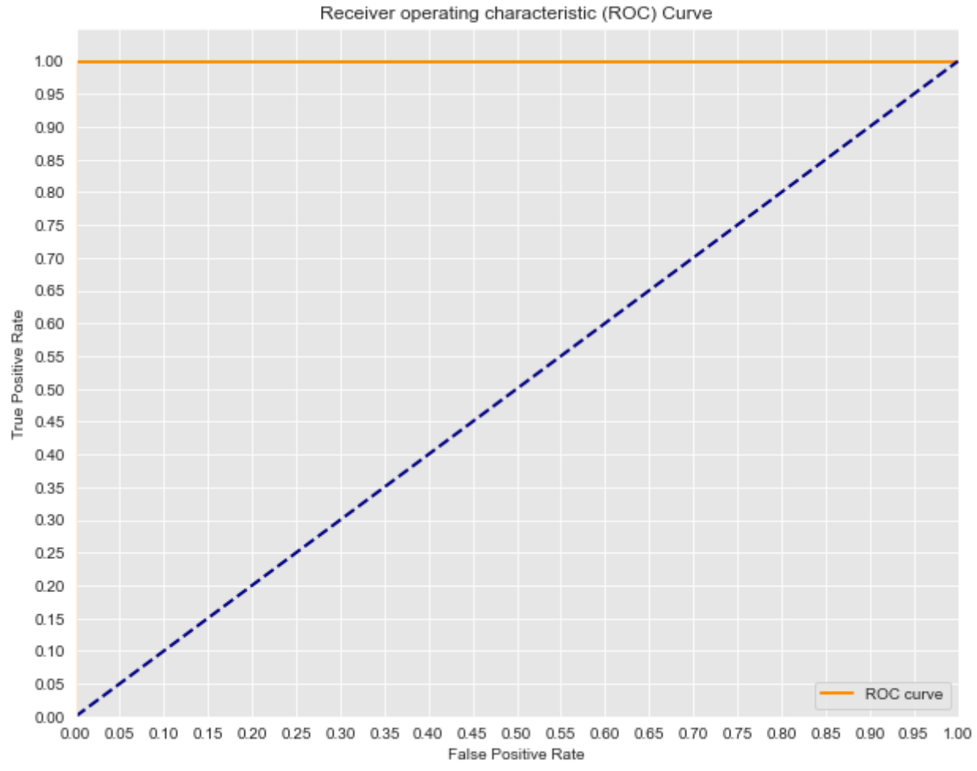





```
Cross Validated ROC AUC score: 1.0
```

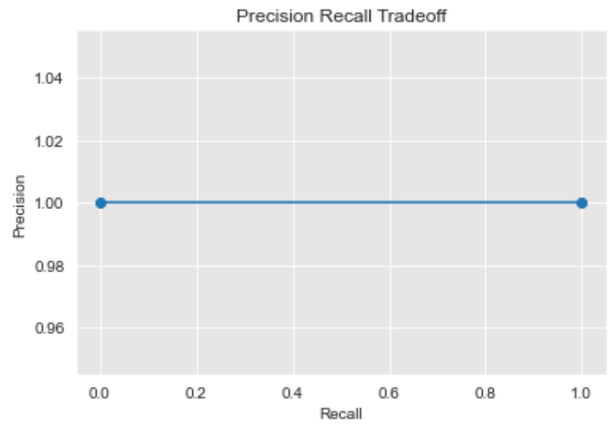
```
Class:F
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

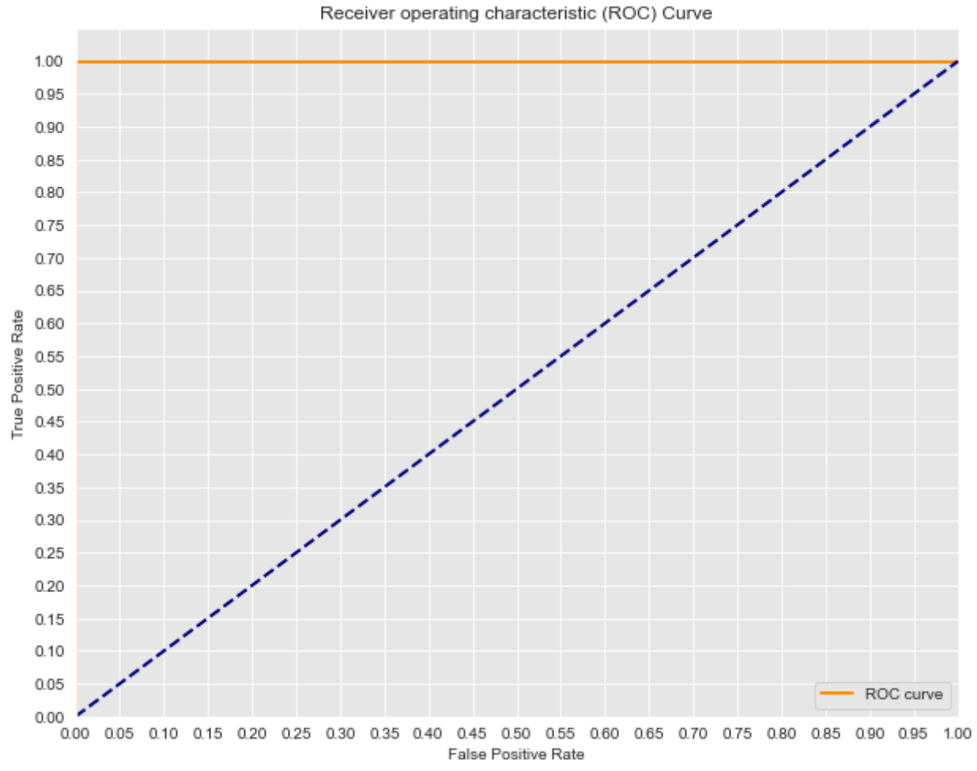





```
Cross Validated ROC AUC score: 1.0
```

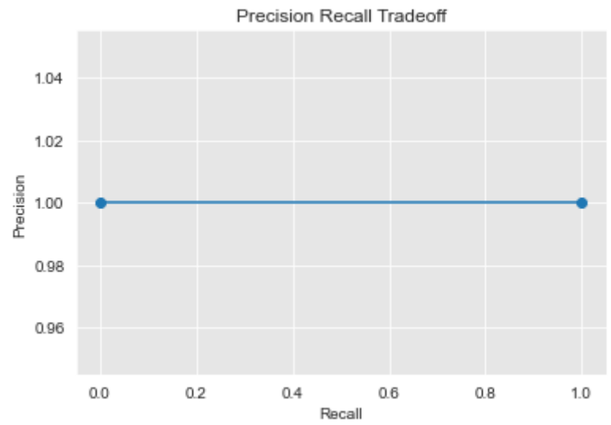
```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

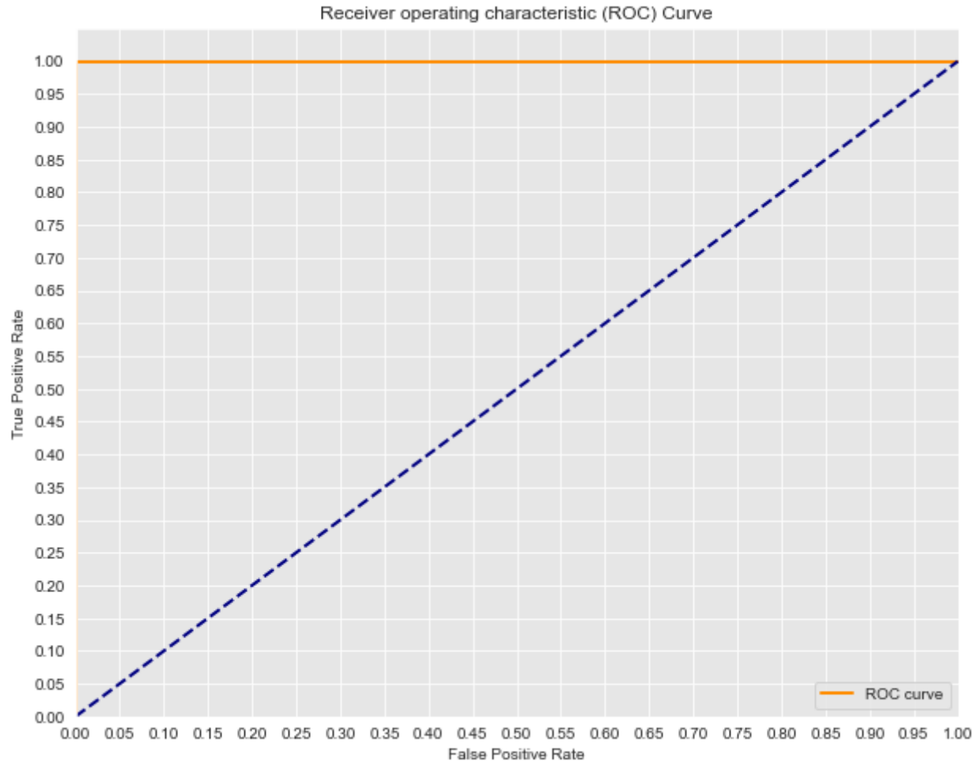





```
Cross Validated ROC AUC score: 1.0
```

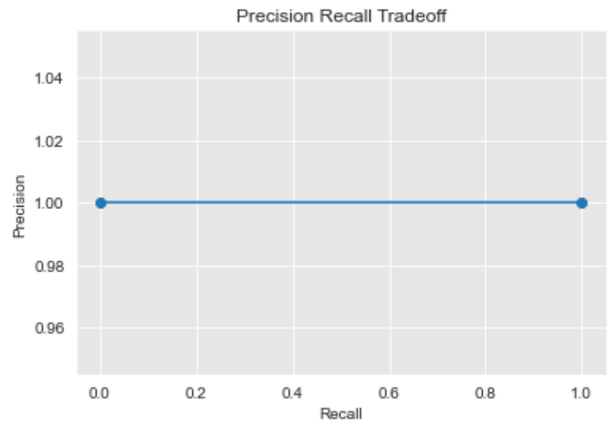
```
Class:H
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

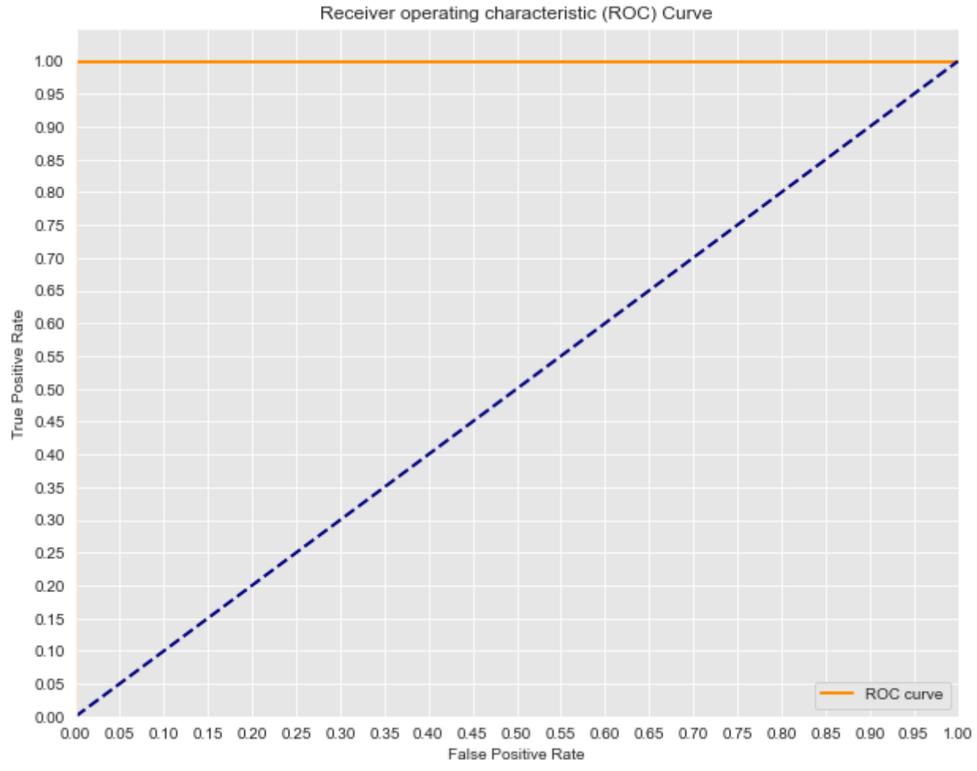





```
Cross Validated ROC AUC score: 1.0
```

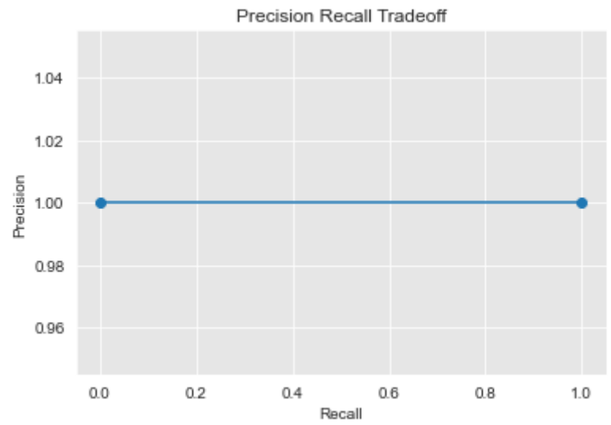
```
Class:I
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

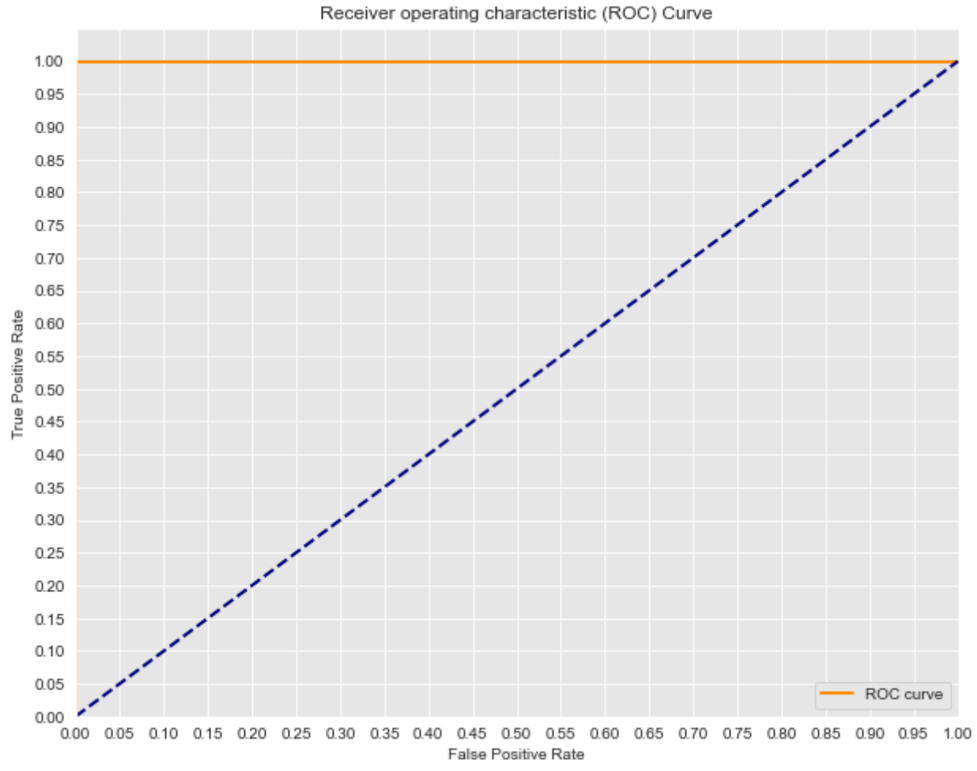





```
Cross Validated ROC AUC score: 1.0
```

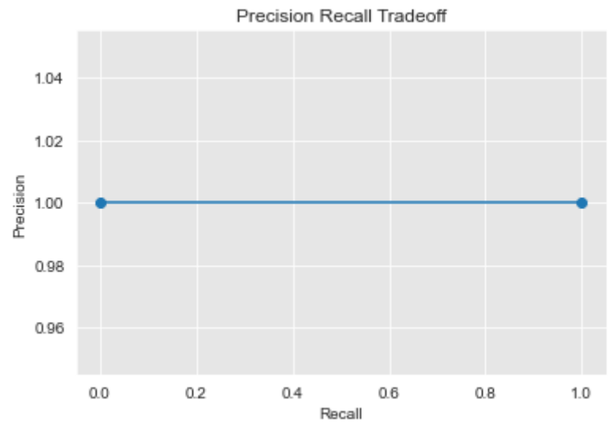
```
Class:K
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

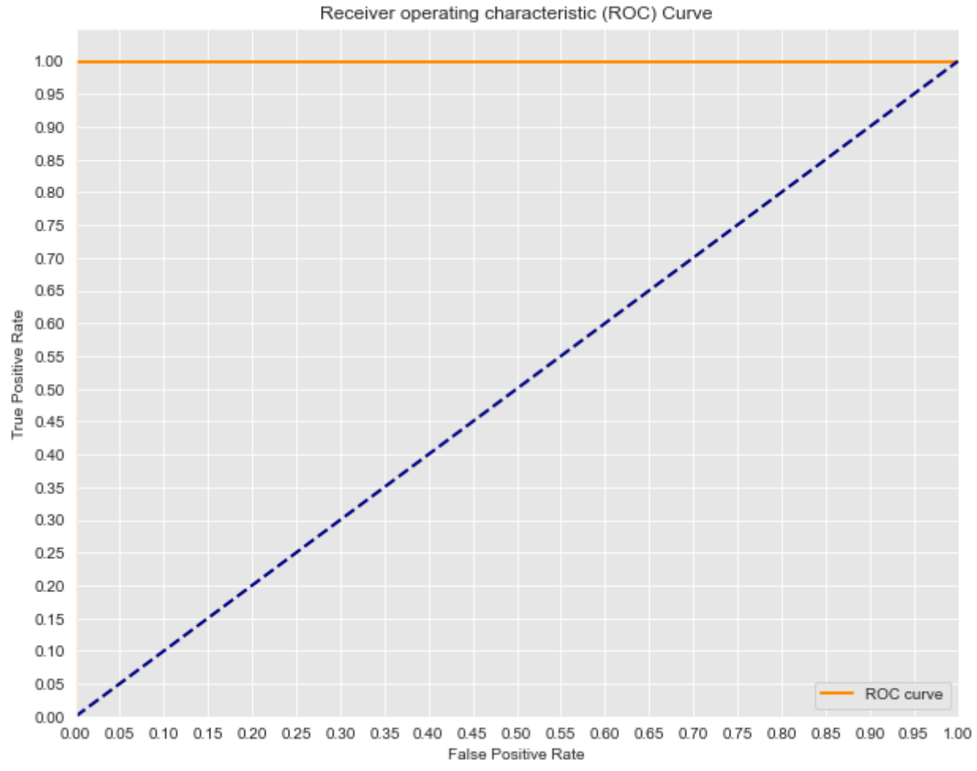





```
Cross Validated ROC AUC score: 1.0
```

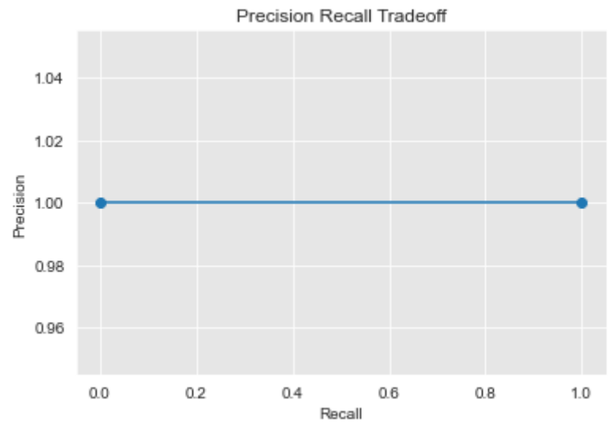
```
Class:L
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

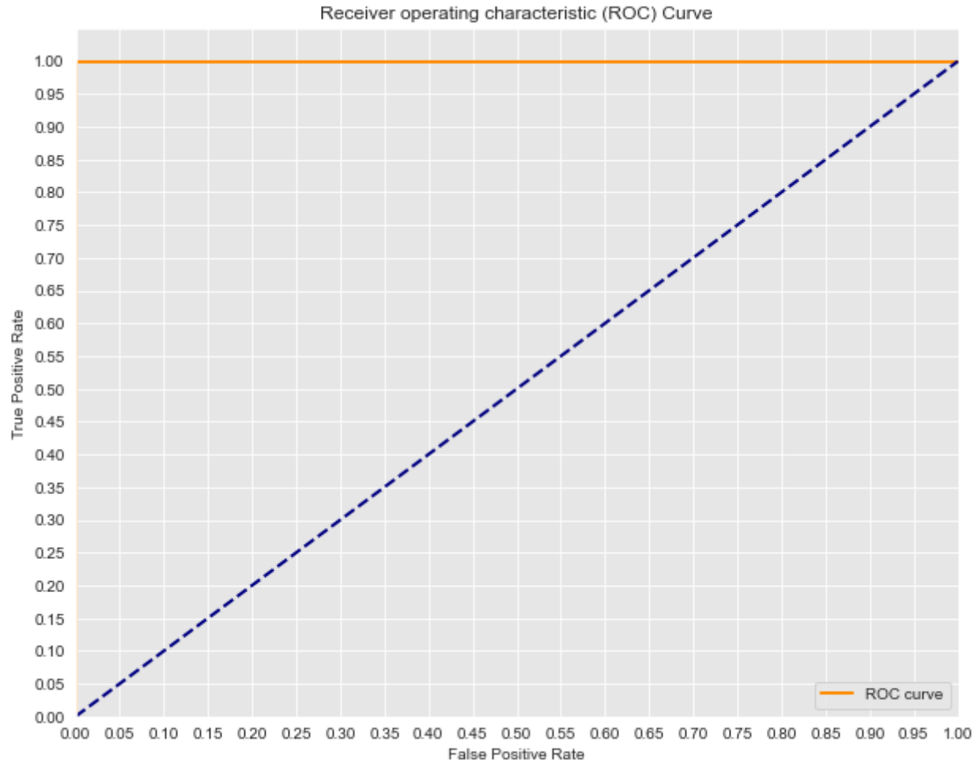





```
Cross Validated ROC AUC score: 1.0
```

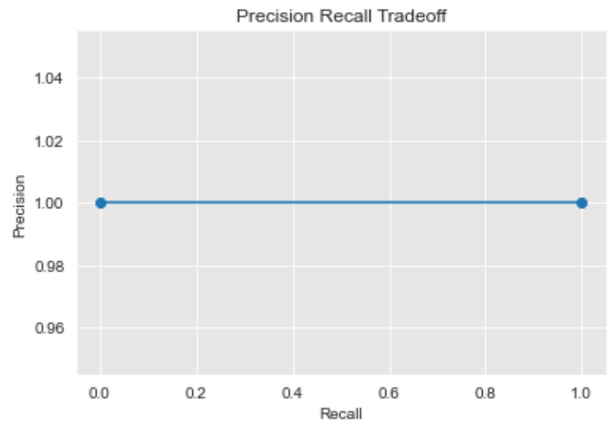
```
Class:M
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

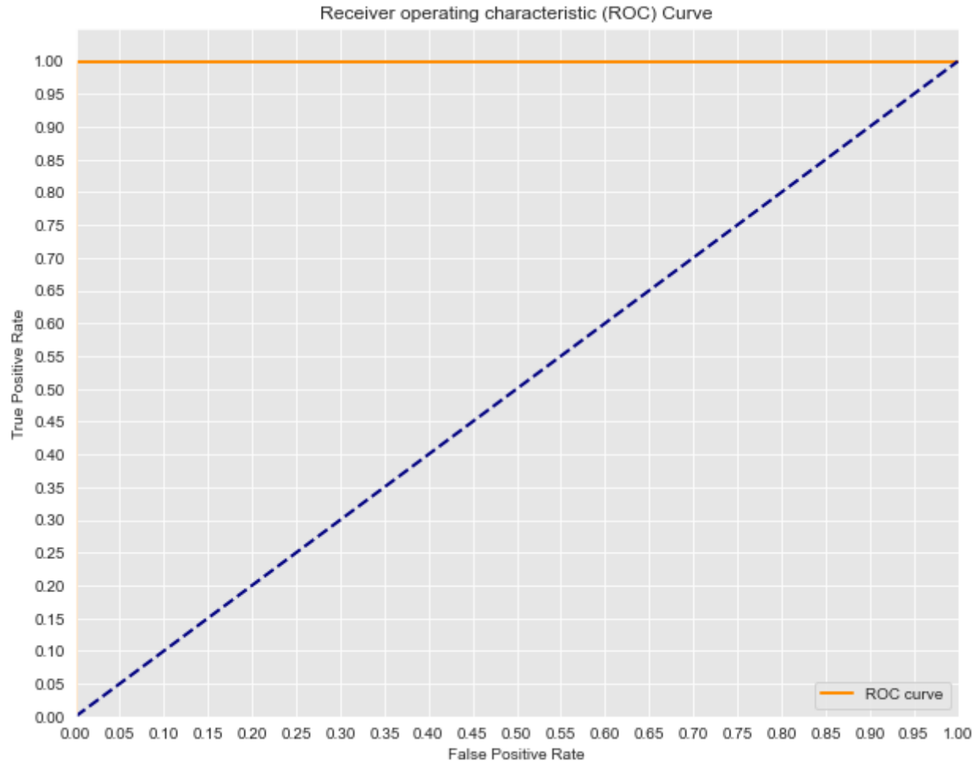





```
Cross Validated ROC AUC score: 1.0
```

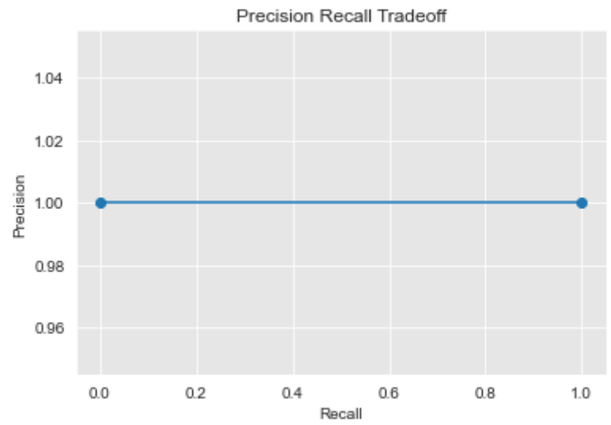
```
Class:N
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

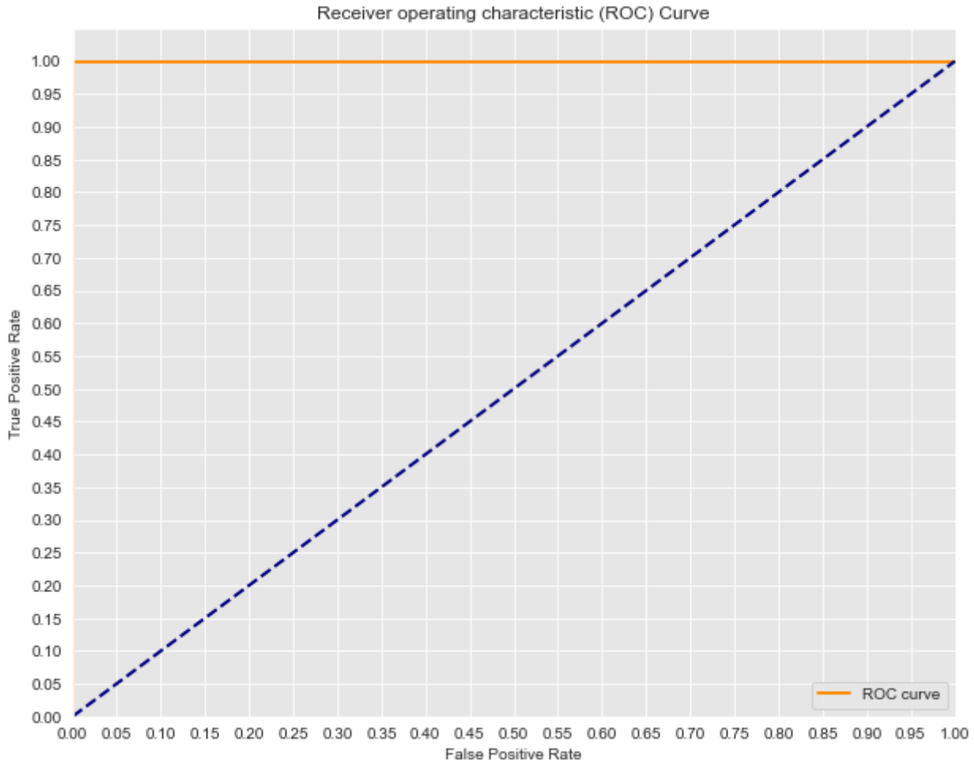





```
Cross Validated ROC AUC score: 1.0
```

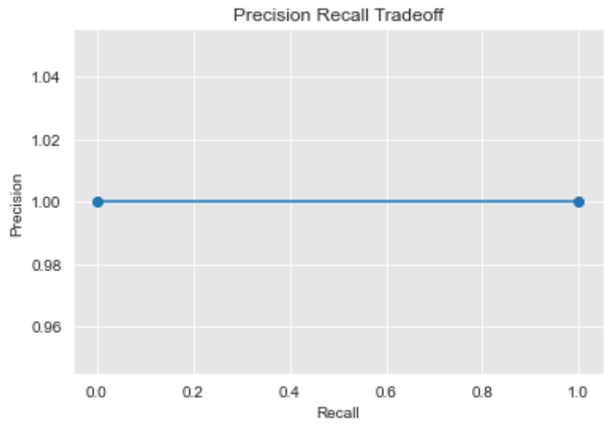
```
Class:P
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

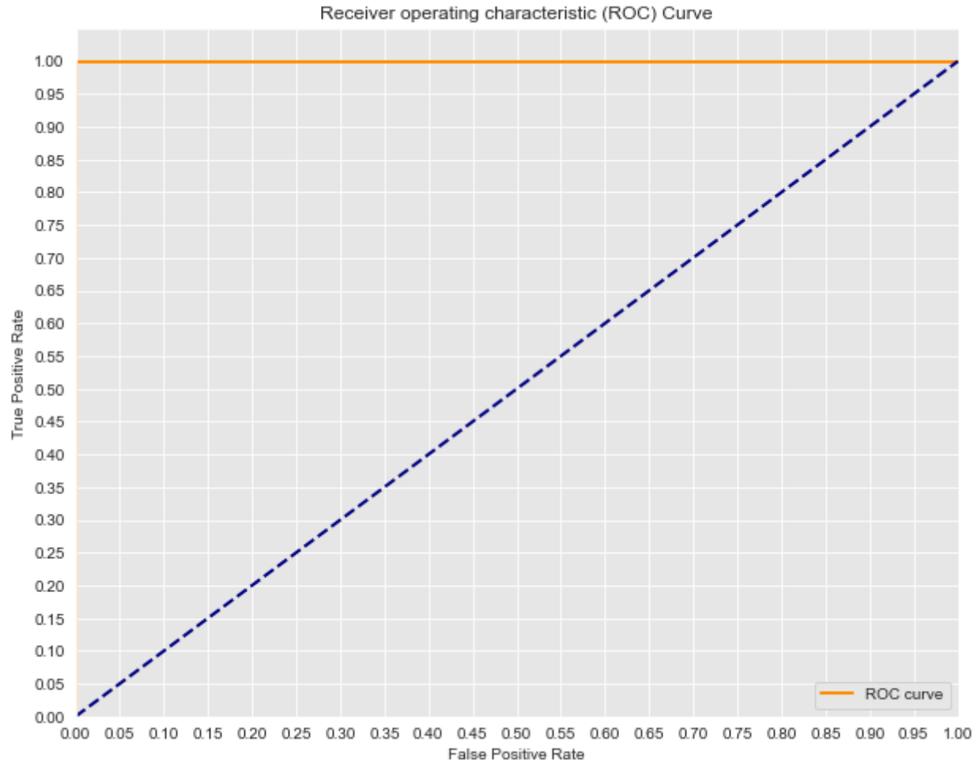





```
Cross Validated ROC AUC score: 1.0
```

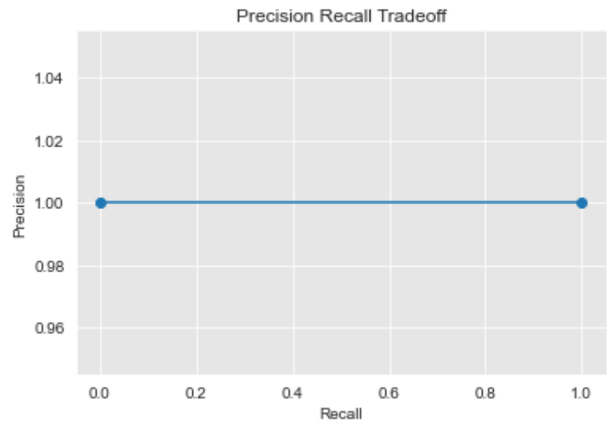
```
Class:Q
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

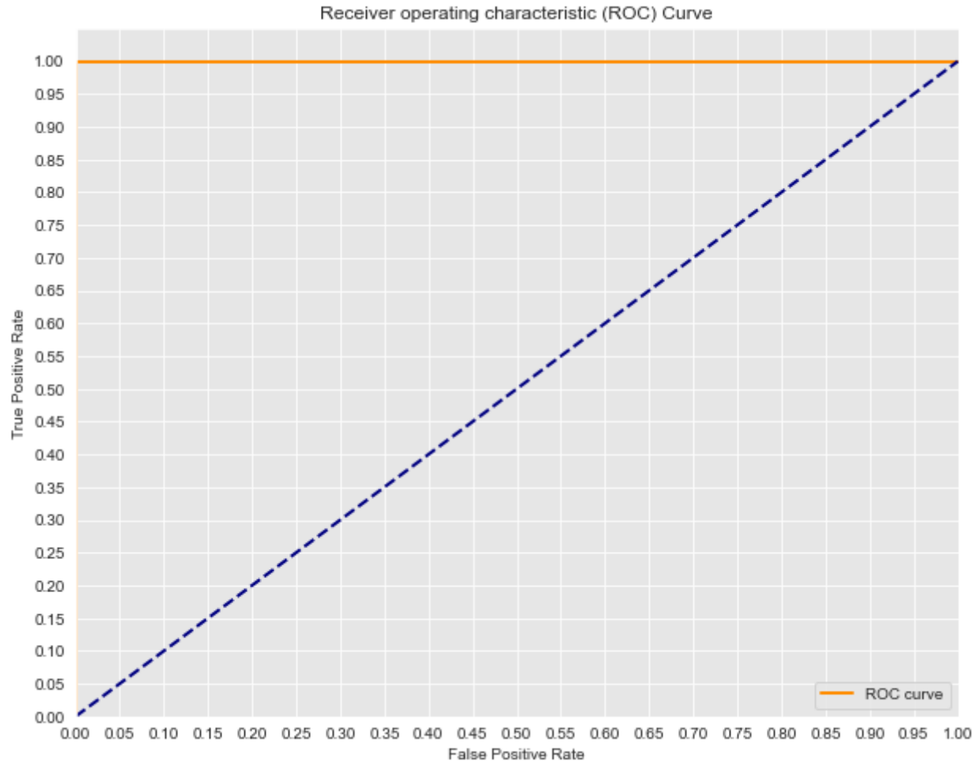





```
Cross Validated ROC AUC score: 1.0
```

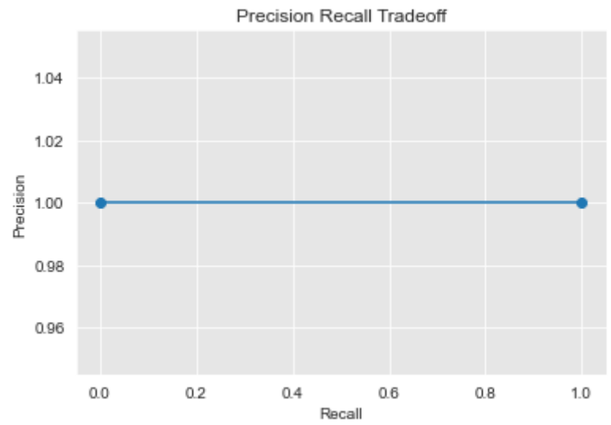
```
Class:R
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

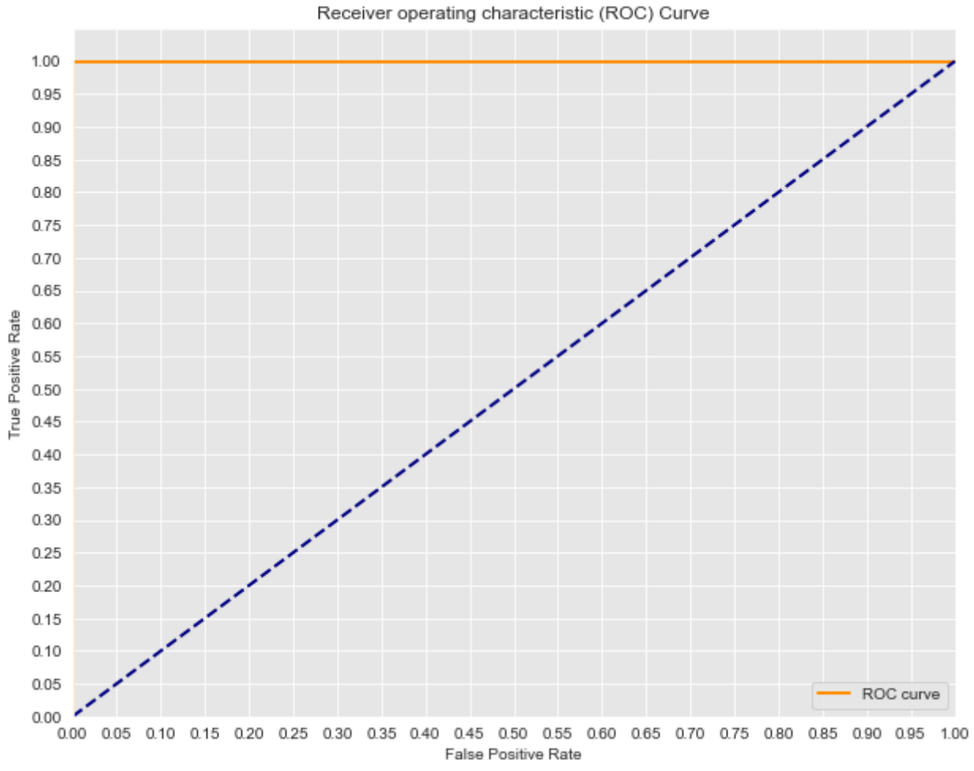





```
Cross Validated ROC AUC score: 1.0
```

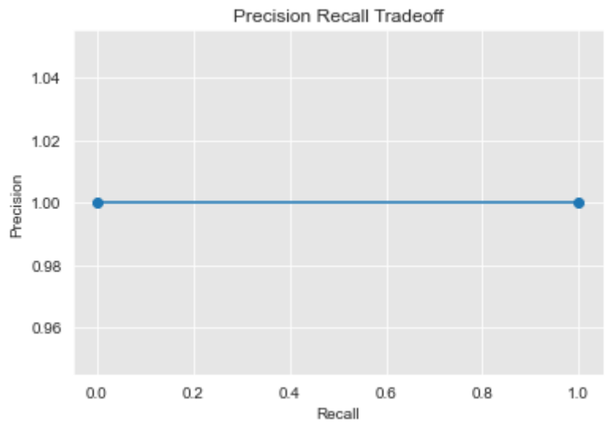
```
Class:S
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

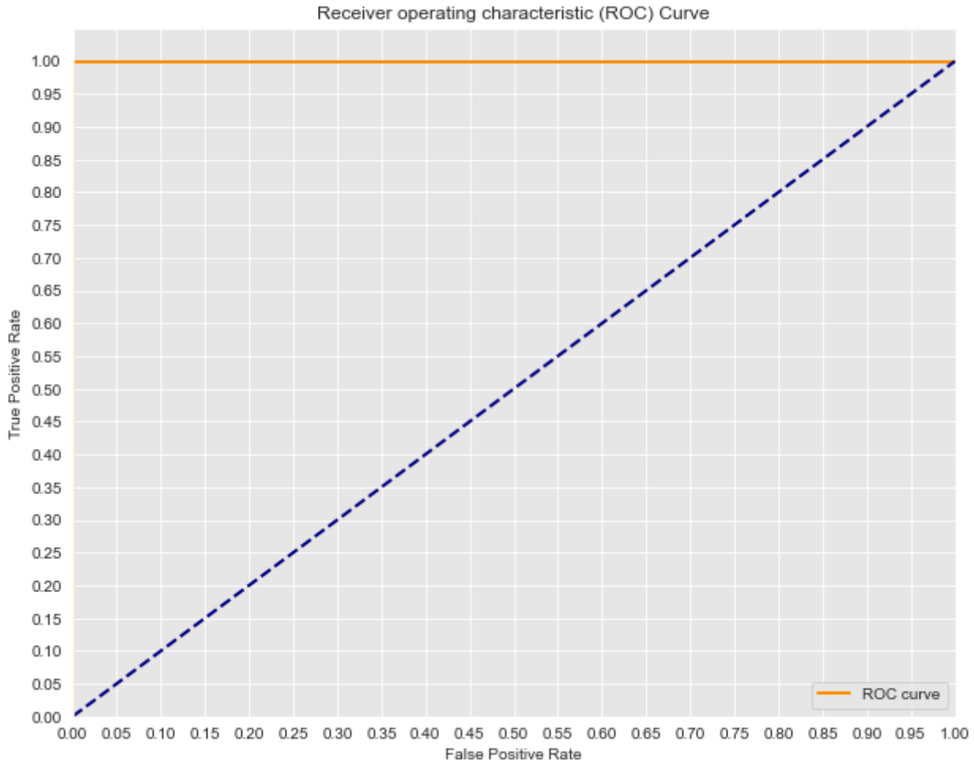





```
Cross Validated ROC AUC score: 1.0
```

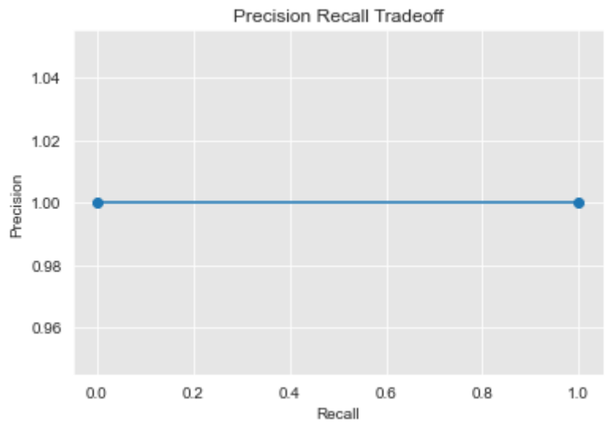
```
Class:Stop
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

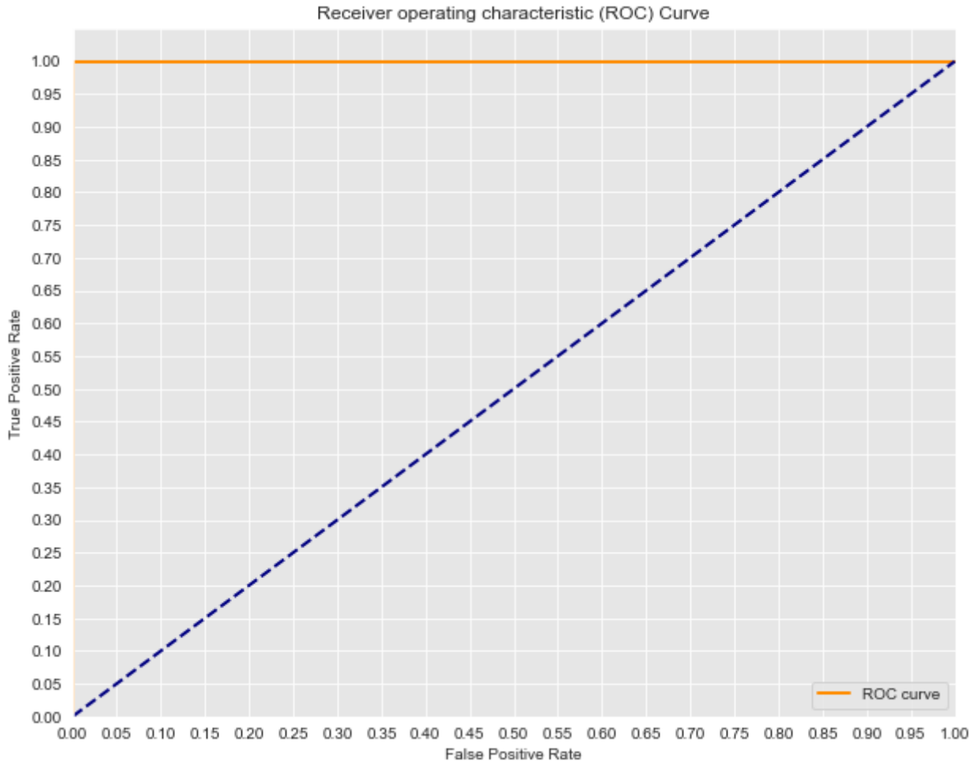





```
Cross Validated ROC AUC score: 1.0
```

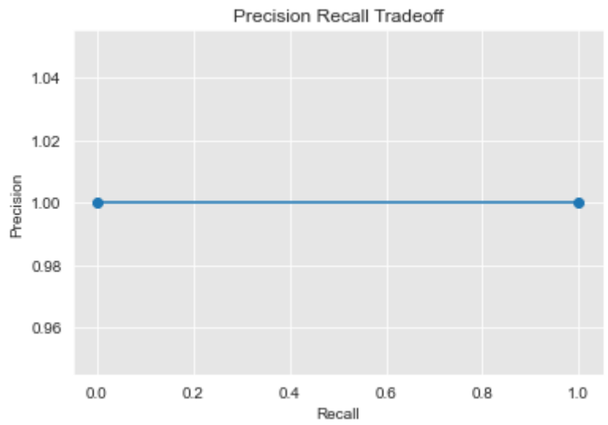
```
Class:T
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

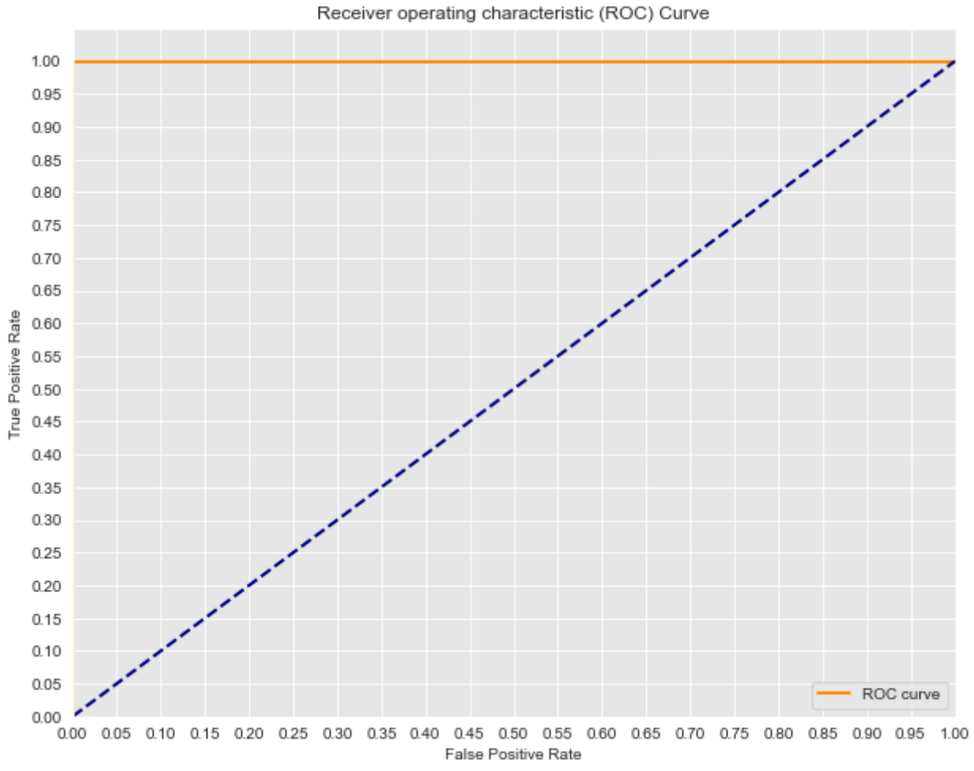





```
Cross Validated ROC AUC score: 1.0
```

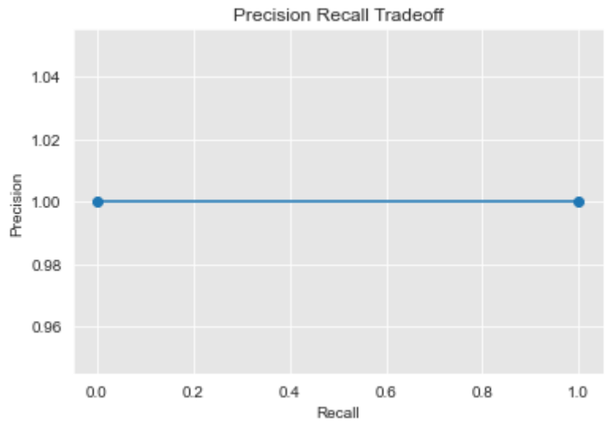
```
Class:V
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

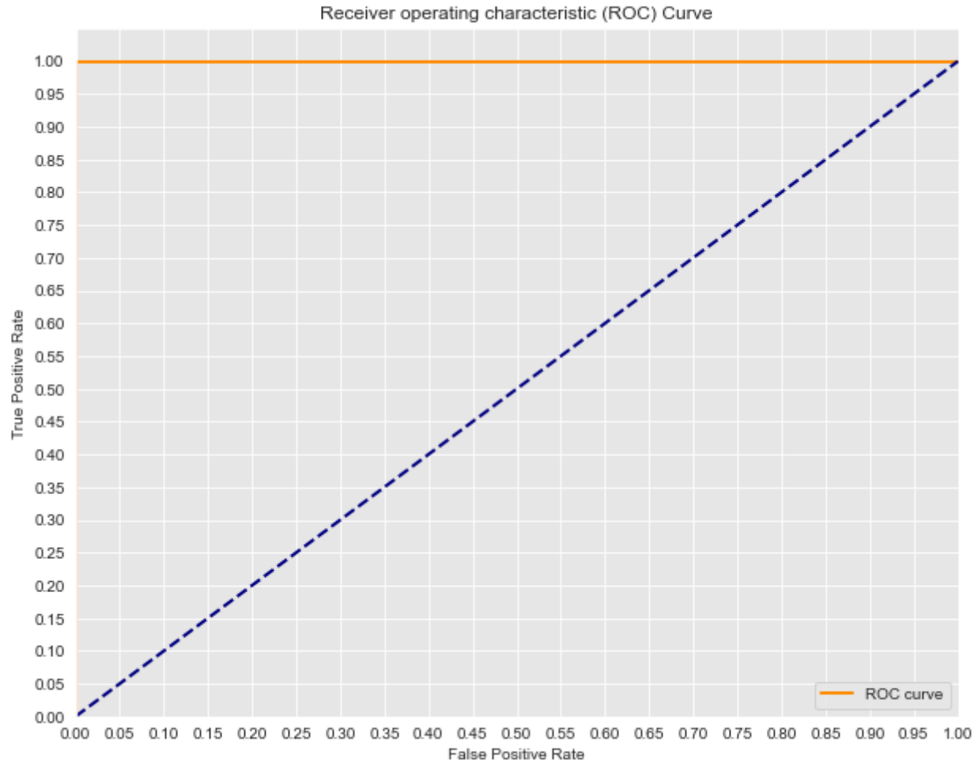





```
Cross Validated ROC AUC score: 1.0
```

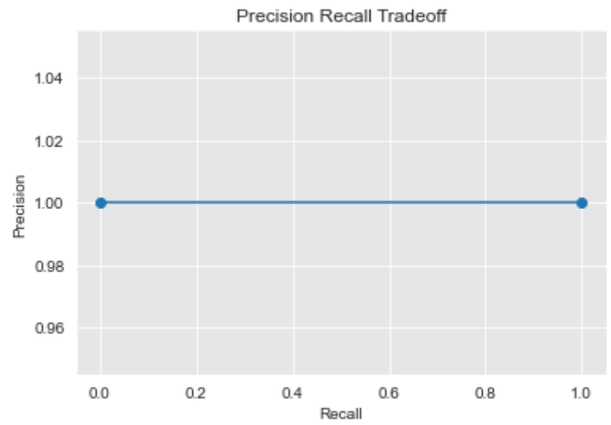
```
Class:W
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

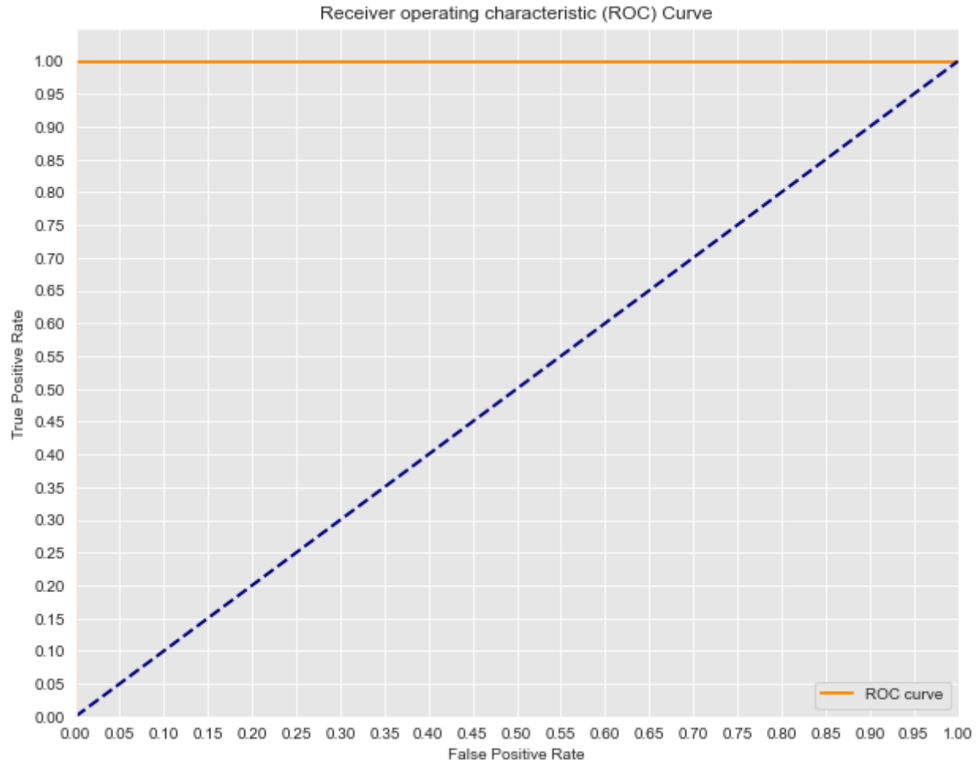





```
Cross Validated ROC AUC score: 1.0
```

```
Class:Y
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Cross Validated ROC AUC score: 1.0
```

Fit the model to the training data.

In [54]:
```
random_forest.fit(X2_train, y2_train)
```

Out[54]:
```
RandomForestClassifier()
```

Make predictions.

In [55]:
```
y2_hat_train_rf = random_forest.predict(X2_train)
```

All predictions were classified correctly.

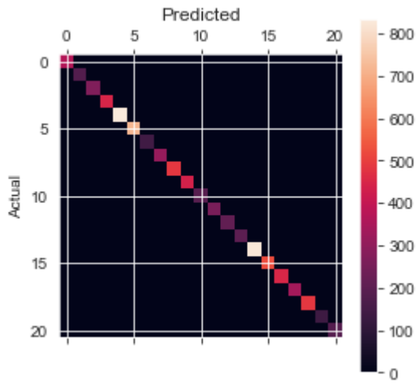
In [56]:
```
con_mat(y2_train,y2_hat_train_rf)
```

```
Confusion Matrix
----------------
      0    1    2    3    4    5    6    7    8    9   ...   11   12   13   14  \
0   370    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
1     0  182    0    0    0    0    0    0    0    0  ...    0    0    0    0
2     0    0  273    0    0    0    0    0    0    0  ...    0    0    0    0
3     0    0    0  447    0    0    0    0    0    0  ...    0    0    0    0
4     0    0    0    0  833    0    0    0    0    0  ...    0    0    0    0
5     0    0    0    0    0  720    0    0    0    0  ...    0    0    0    0
6     0    0    0    0    0    0  142    0    0    0  ...    0    0    0    0
7     0    0    0    0    0    0    0  315    0    0  ...    0    0    0    0
8     0    0    0    0    0    0    0    0  485    0  ...    0    0    0    0
9     0    0    0    0    0    0    0    0    0  437  ...    0    0    0    0
10    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
```

```
11    0    0    0    0    0    0    0    0    0    0  ...  259    0    0    0
12    0    0    0    0    0    0    0    0    0    0  ...    0  209    0    0
13    0    0    0    0    0    0    0    0    0    0  ...    0    0  200    0
14    0    0    0    0    0    0    0    0    0    0  ...    0    0    0  824
15    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
16    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
17    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
18    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
19    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
20    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0

     15   16   17   18   19   20
0     0    0    0    0    0    0
1     0    0    0    0    0    0
2     0    0    0    0    0    0
3     0    0    0    0    0    0
4     0    0    0    0    0    0
5     0    0    0    0    0    0
6     0    0    0    0    0    0
7     0    0    0    0    0    0
8     0    0    0    0    0    0
9     0    0    0    0    0    0
10    0    0    0    0    0    0
11    0    0    0    0    0    0
12    0    0    0    0    0    0
13    0    0    0    0    0    0
14    0    0    0    0    0    0
15  522    0    0    0    0    0
16    0  451    0    0    0    0
17    0    0  339    0    0    0
18    0    0    0  488    0    0
19    0    0    0    0  134    0
20    0    0    0    0    0  183

[21 rows x 21 columns]
```



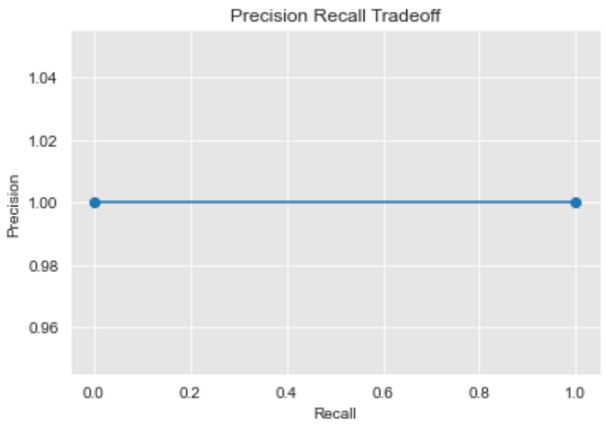
Seperate predicted values into each class for metrics.

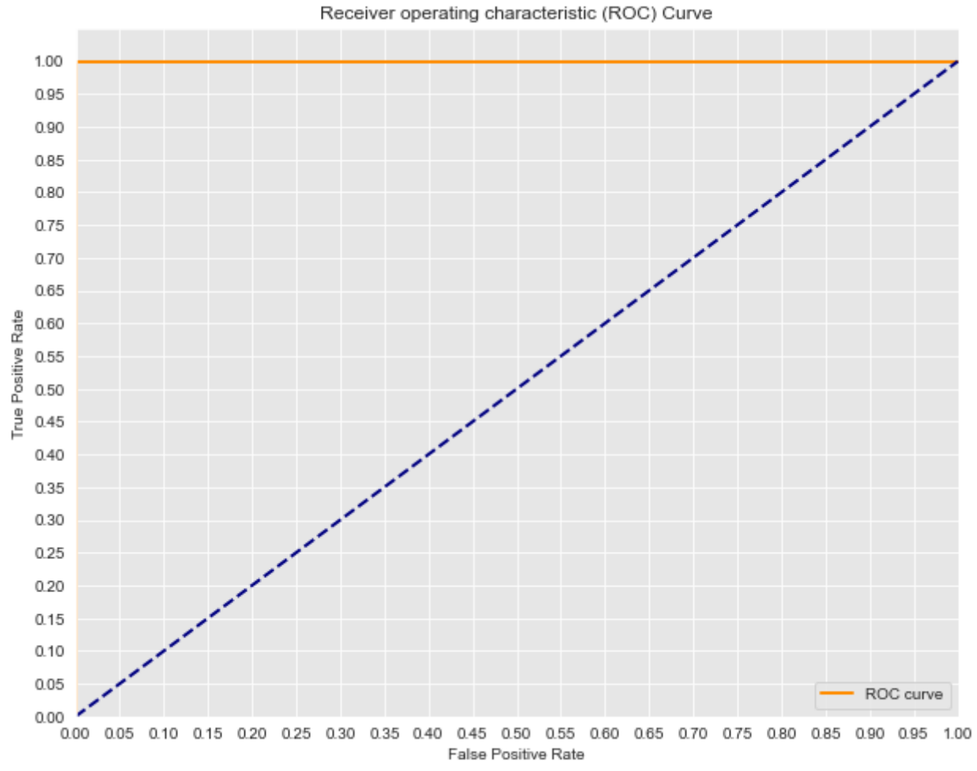
In [57]:
```
predictions_class0=y2_hat_train_rf==0
predictions_class1=y2_hat_train_rf==1
predictions_class2=y2_hat_train_rf==2
predictions_class3=y2_hat_train_rf==3
predictions_class4=y2_hat_train_rf==4
predictions_class5=y2_hat_train_rf==5
predictions_class6=y2_hat_train_rf==6
predictions_class7=y2_hat_train_rf==7
predictions_class8=y2_hat_train_rf==8
```

```
predictions_class9=y2_hat_train_rf==9
predictions_class10=y2_hat_train_rf==10
predictions_class11=y2_hat_train_rf==11
predictions_class12=y2_hat_train_rf==12
predictions_class13=y2_hat_train_rf==13
predictions_class14=y2_hat_train_rf==14
predictions_class15=y2_hat_train_rf==15
predictions_class16=y2_hat_train_rf==16
predictions_class17=y2_hat_train_rf==17
predictions_class18=y2_hat_train_rf==18
predictions_class19=y2_hat_train_rf==19
predictions_class20=y2_hat_train_rf==20
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3,predictions_class4,predictions_class5,predictions_class6
  ,predictions_class7,predictions_class8,predictions_class9,predictions_class10,predictions_class11,predictions_class12
  ,predictions_class13,predictions_class14,predictions_class15,predictions_class16,predictions_class17,predictions_class18
  ,predictions_class19,predictions_class20]
```

In [58]:
```
multiclass(random_forest,X2_train,a,p,translation_df2['Amino_Acids_copy'],'train')
```

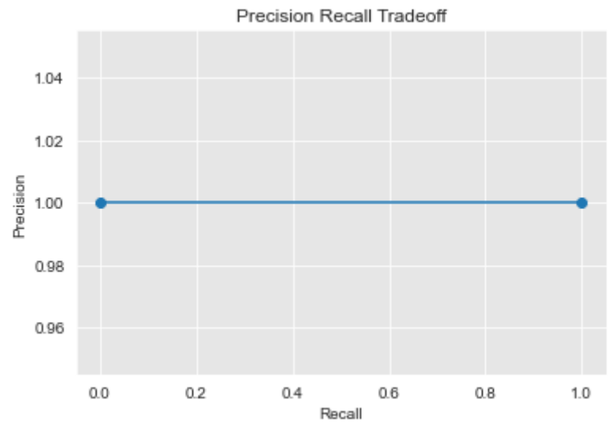
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

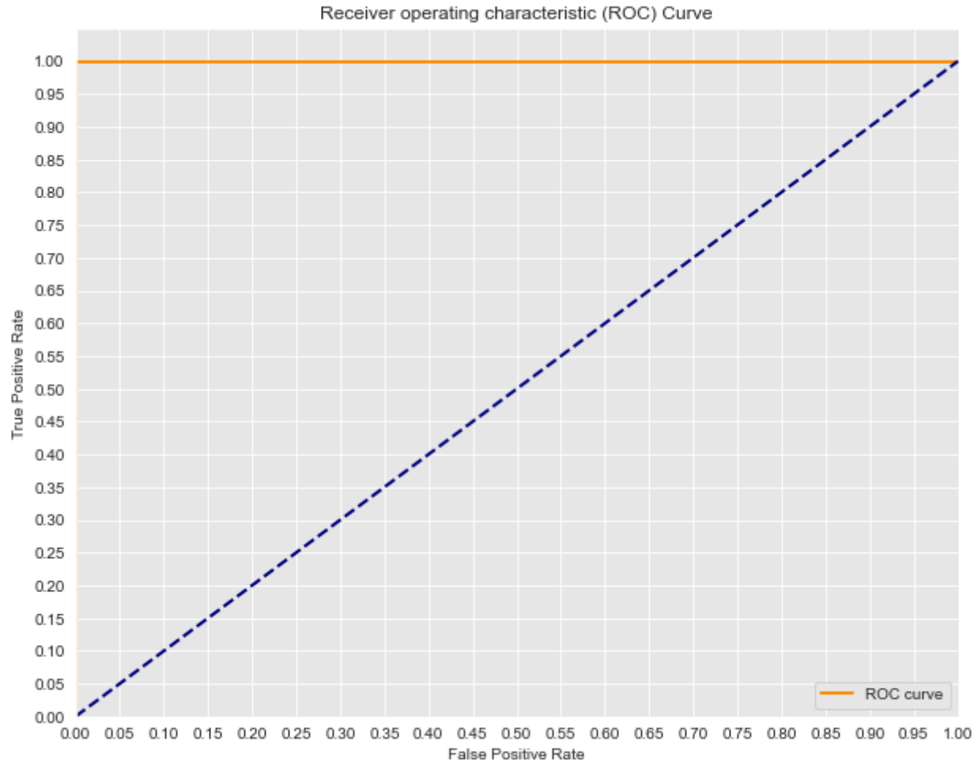





```
Cross Validated ROC AUC score: 1.0
```

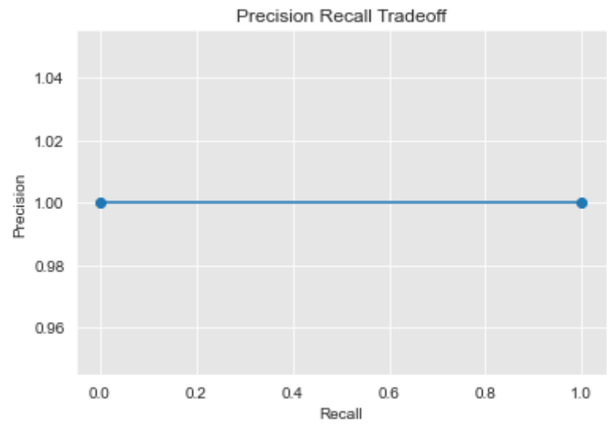
```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

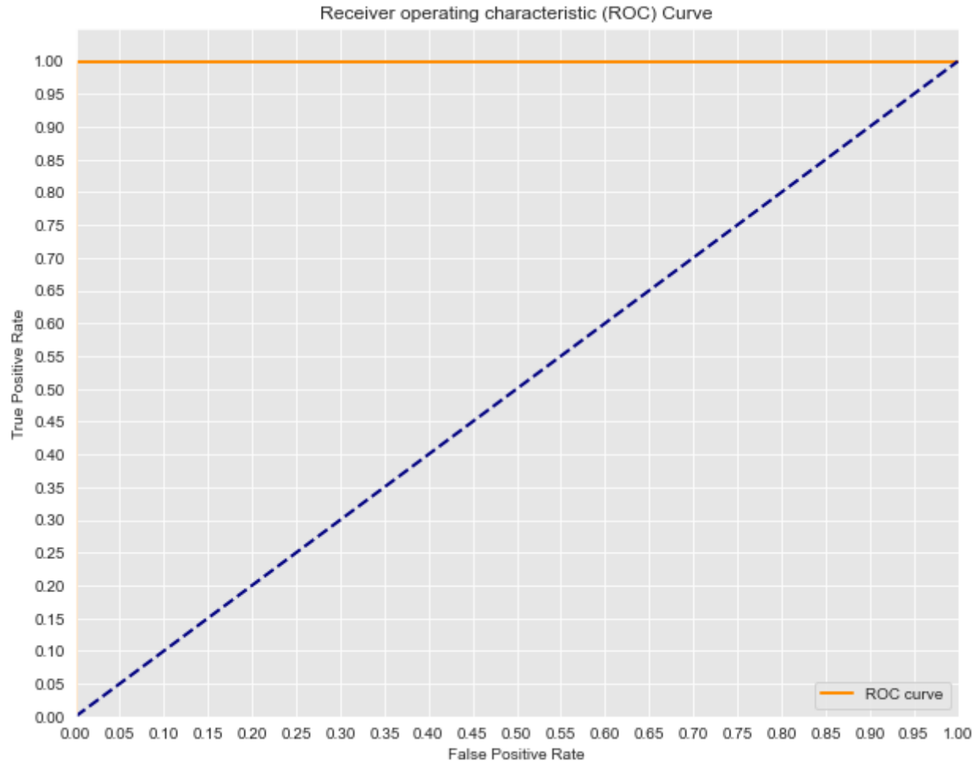





```
Cross Validated ROC AUC score: 1.0
```

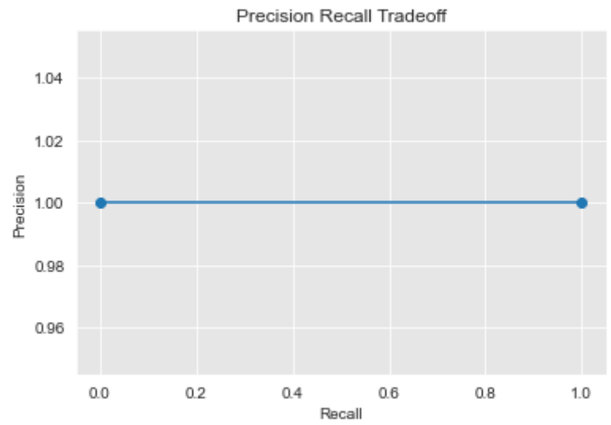
```
Class:D
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

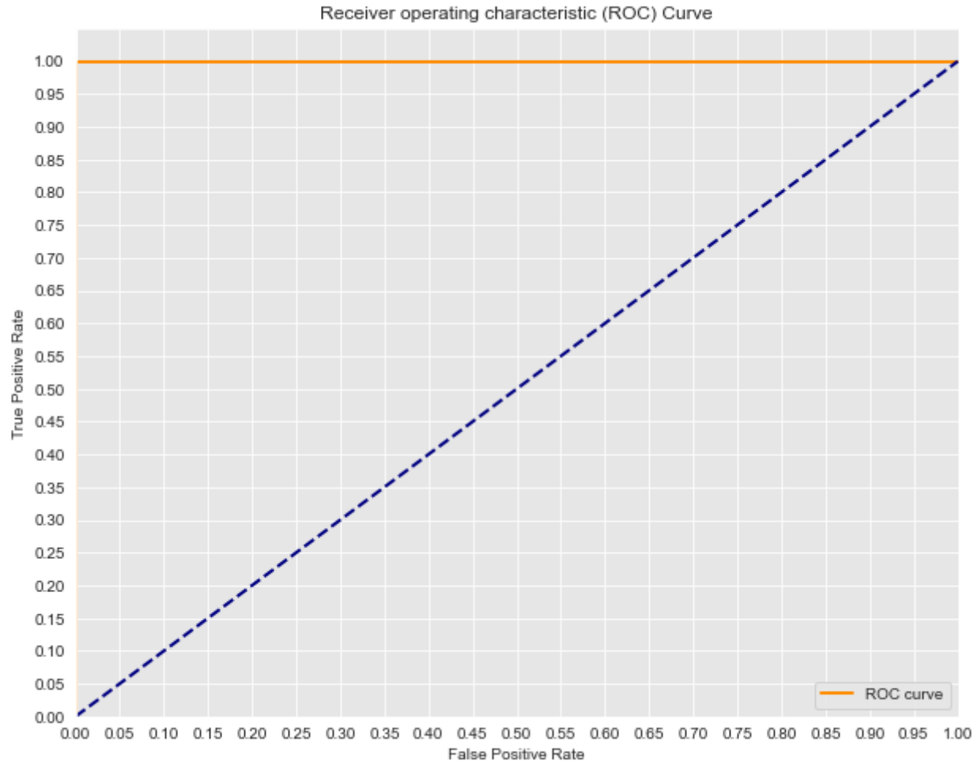





```
Cross Validated ROC AUC score: 1.0
```

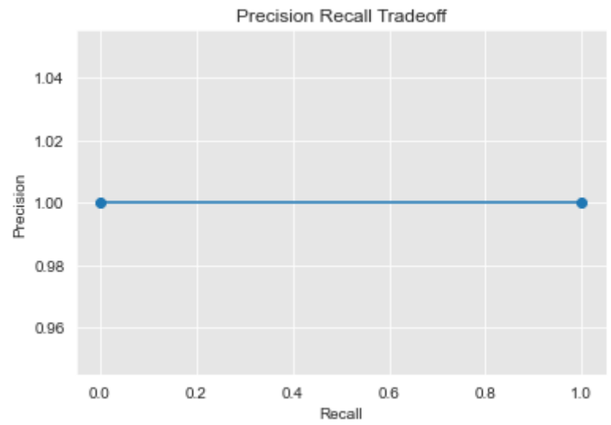
```
Class:E
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

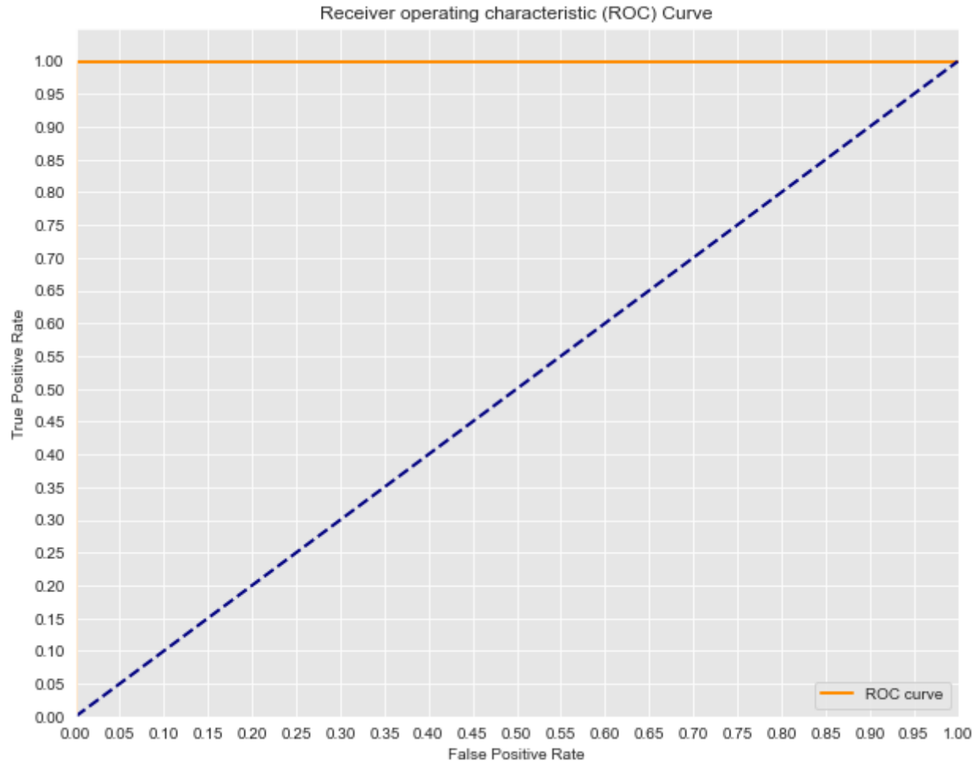





```
Cross Validated ROC AUC score: 1.0
```

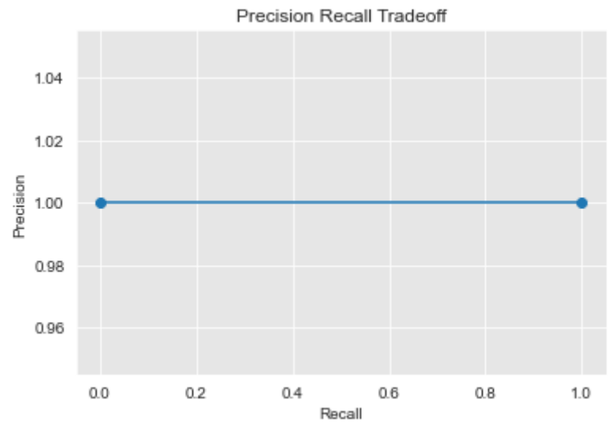
```
Class:F
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

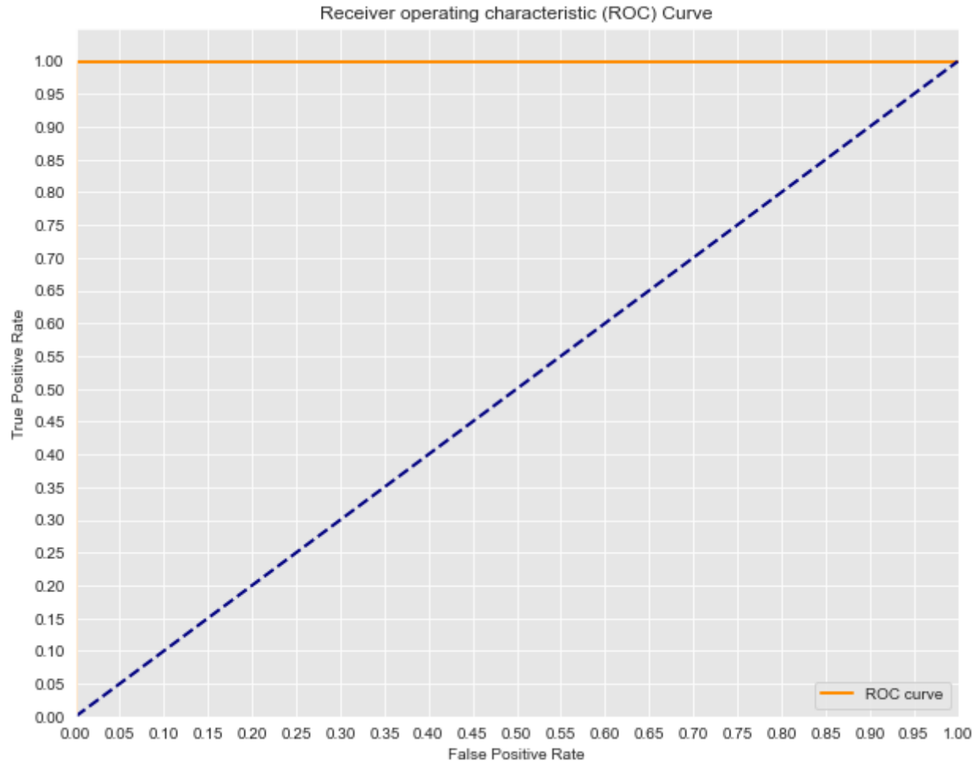





```
Cross Validated ROC AUC score: 1.0
```

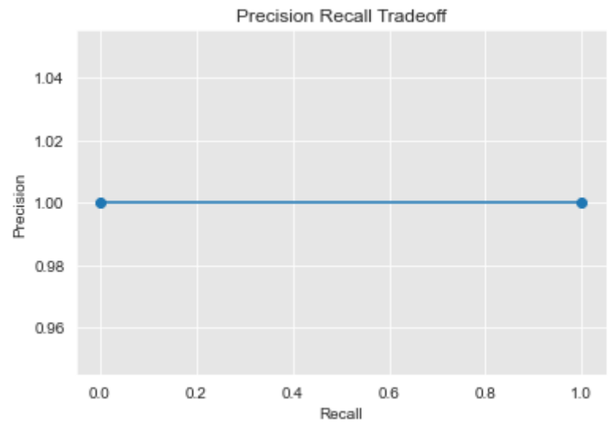
```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

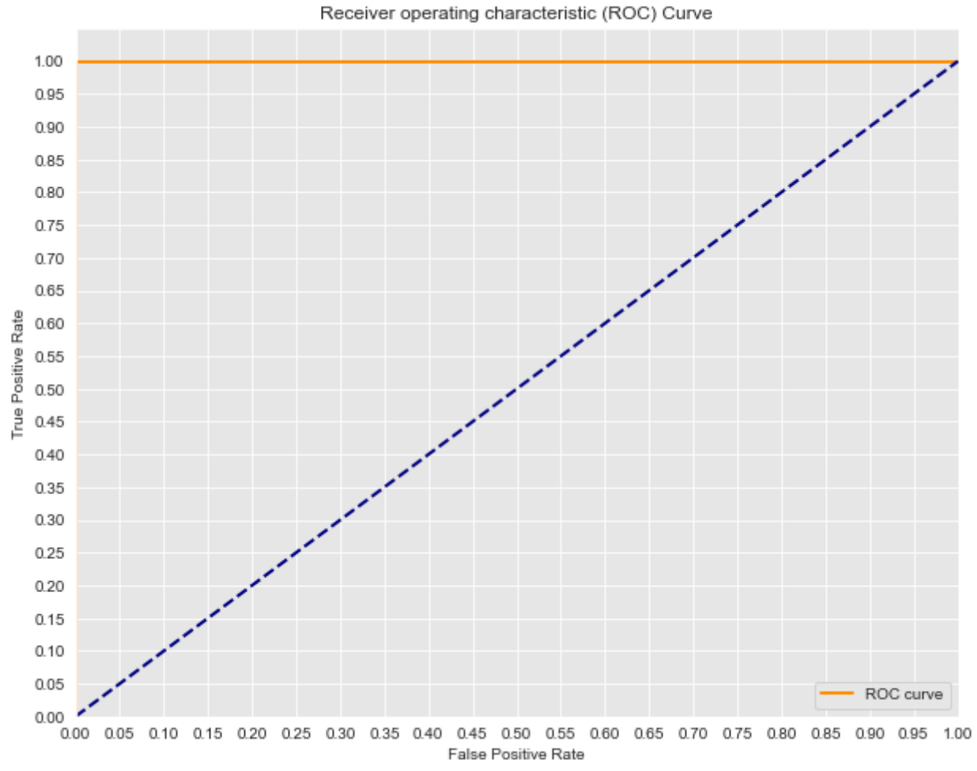





```
Cross Validated ROC AUC score: 1.0
```

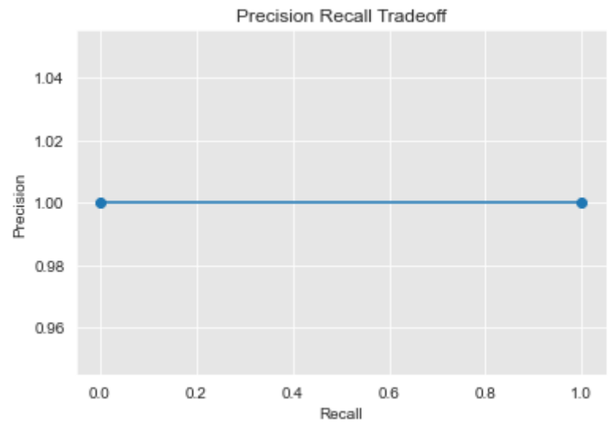
```
Class:H
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

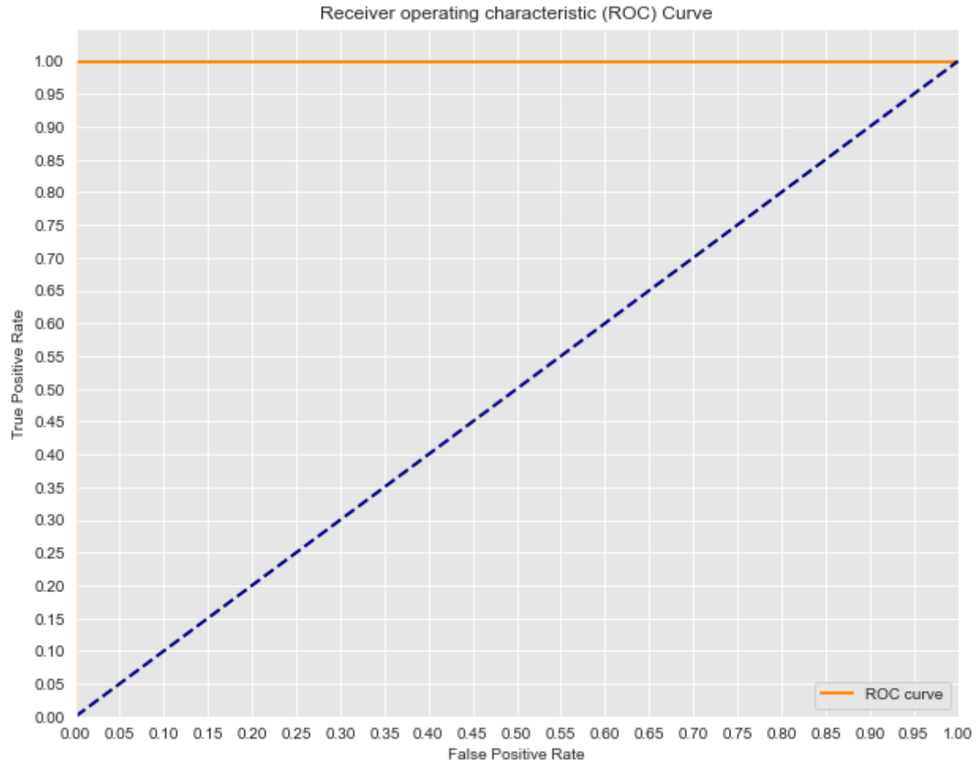





```
Cross Validated ROC AUC score: 1.0
```

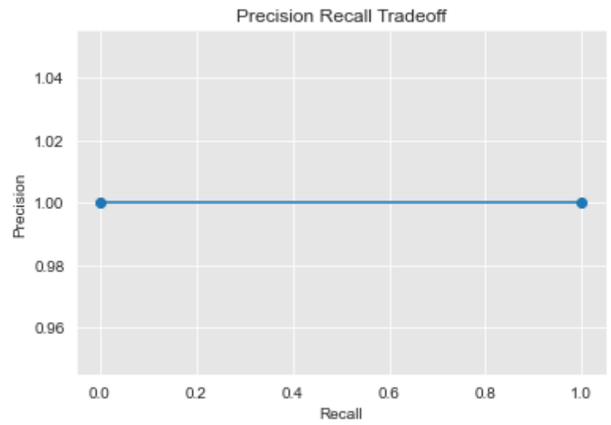
```
Class:I
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

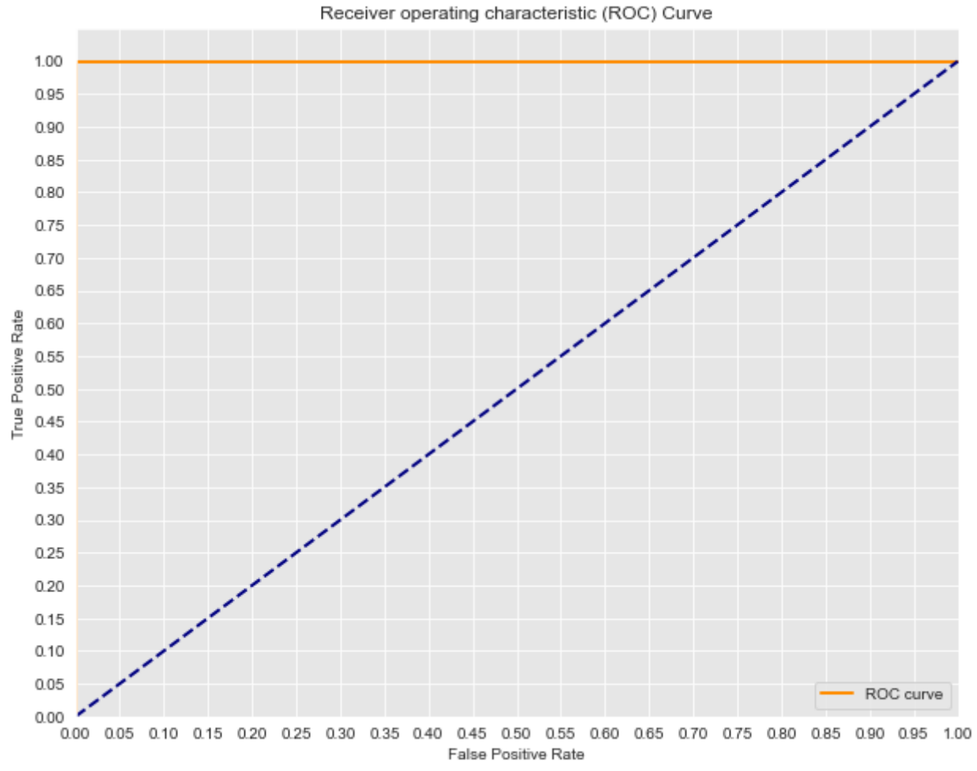





```
Cross Validated ROC AUC score: 1.0
```

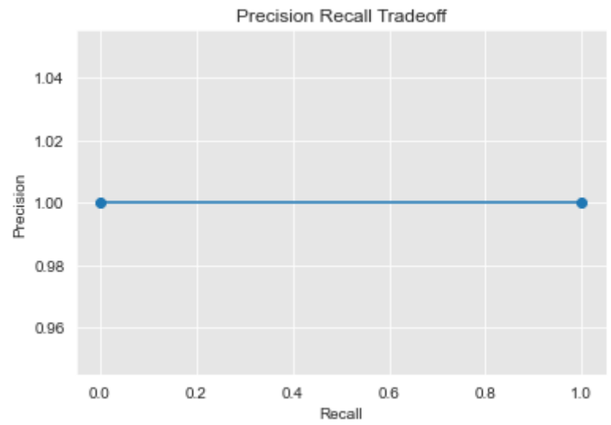
```
Class:K
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

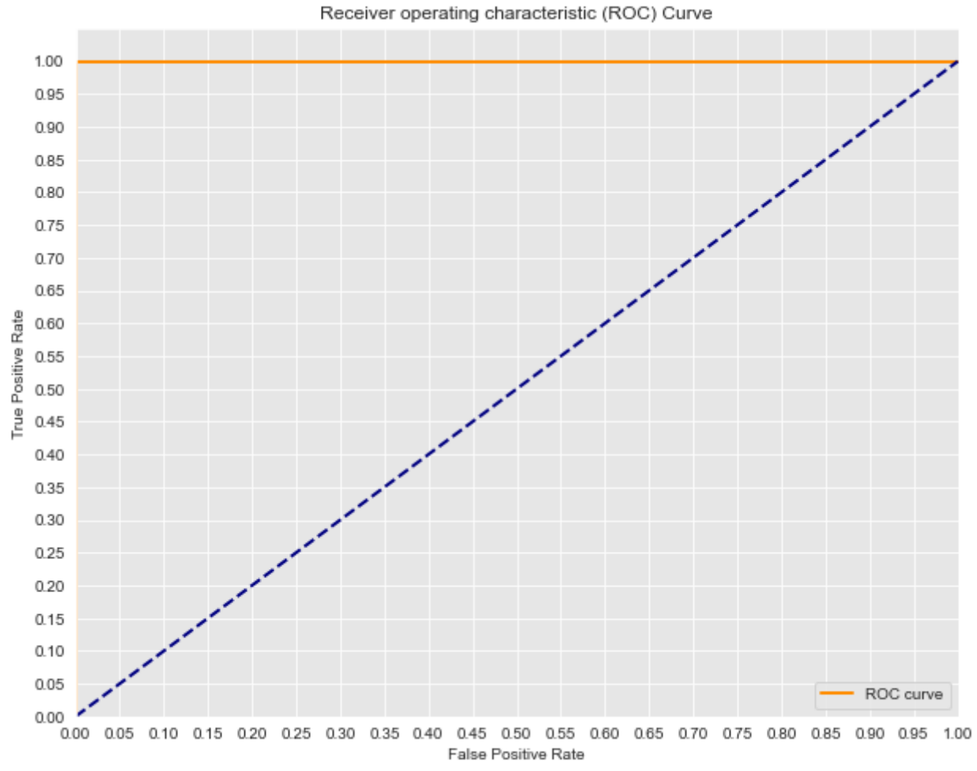





```
Cross Validated ROC AUC score: 1.0
```

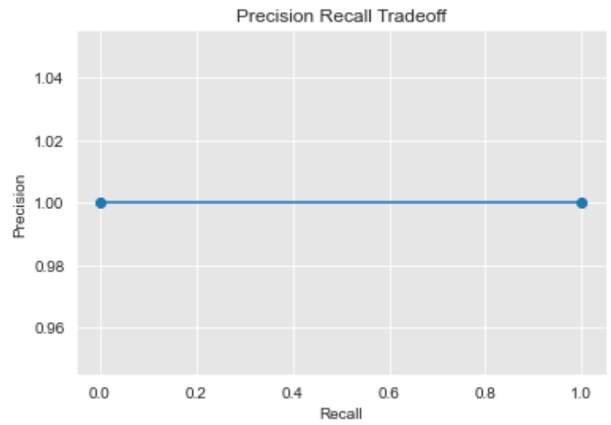
```
Class:L
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

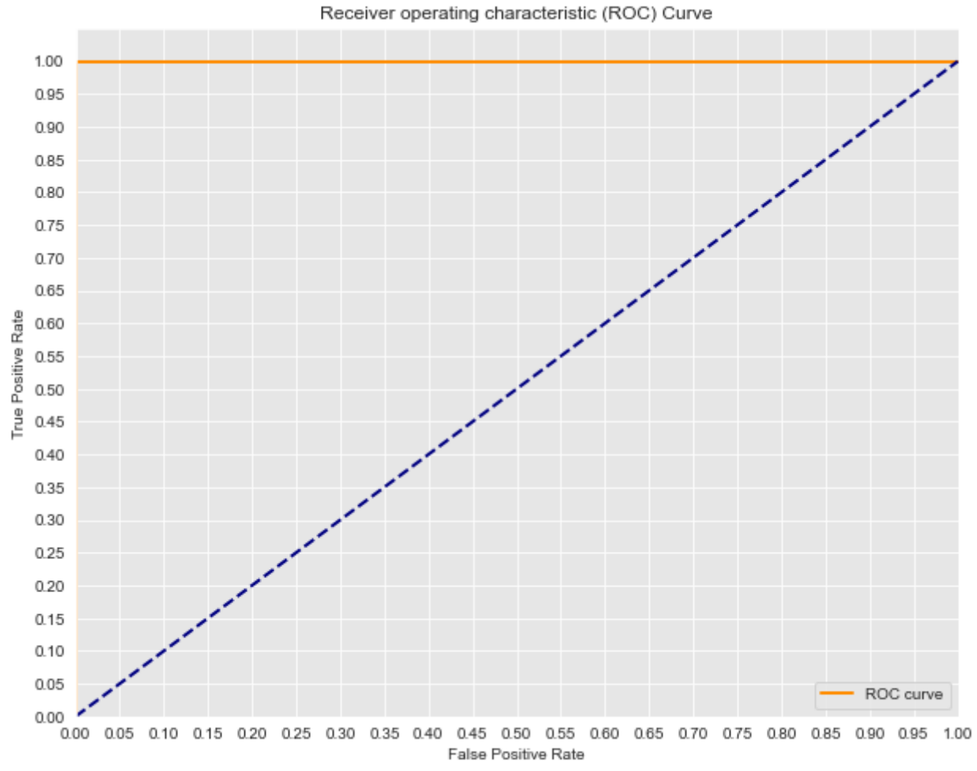





```
Cross Validated ROC AUC score: 1.0
```

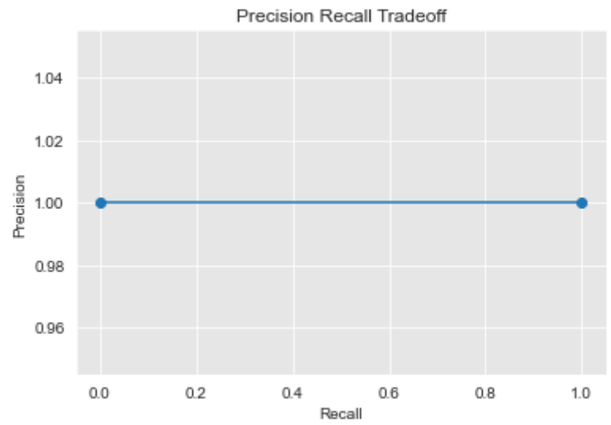
```
Class:M
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

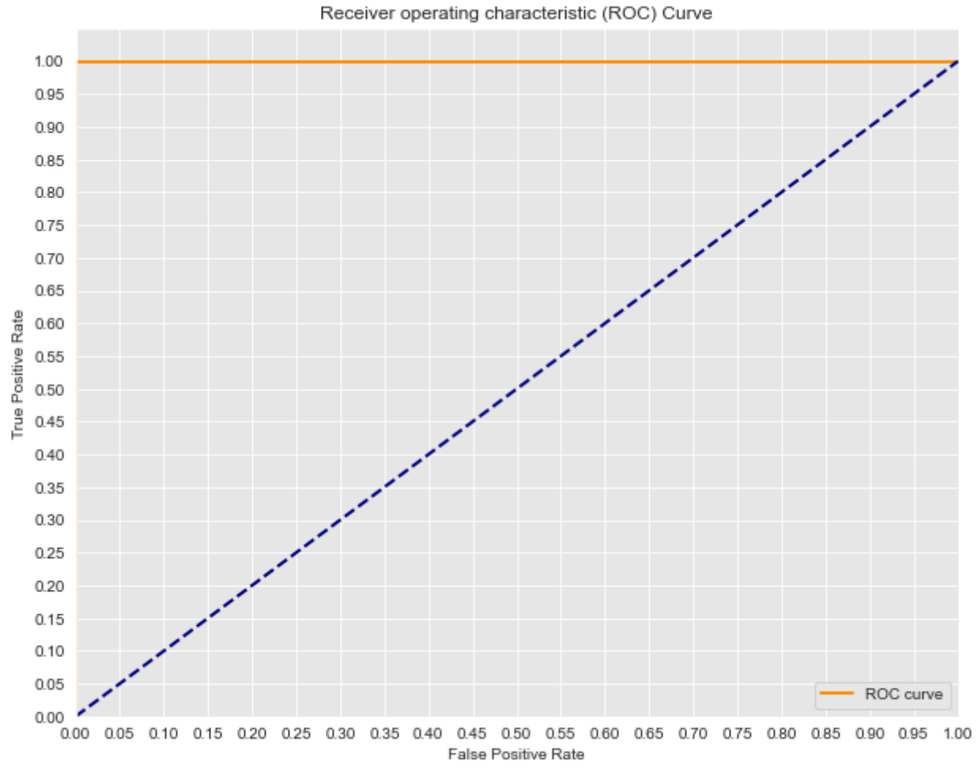





```
Cross Validated ROC AUC score: 1.0
```

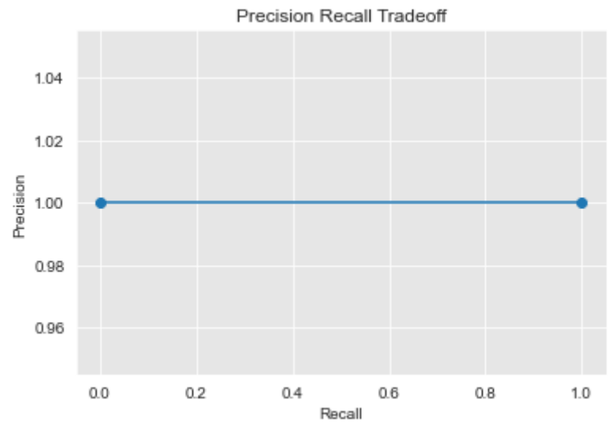
```
Class:N
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

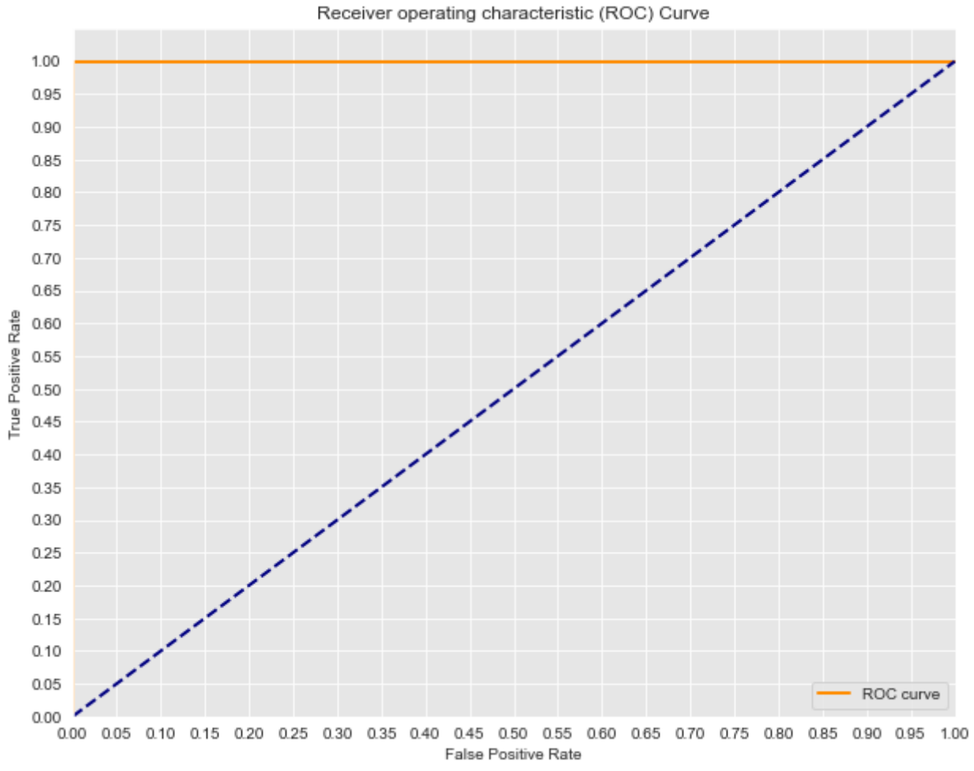





```
Cross Validated ROC AUC score: 1.0
```

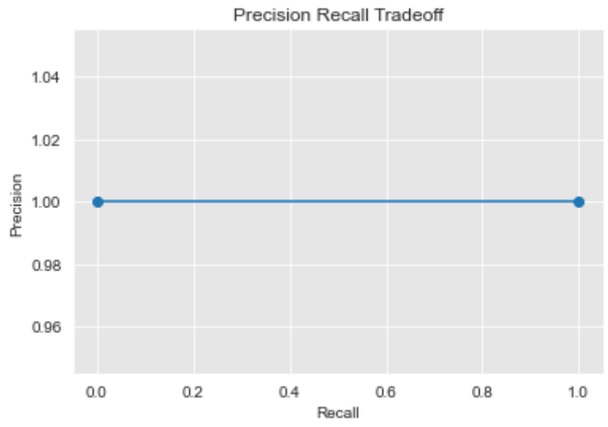
```
Class:P
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

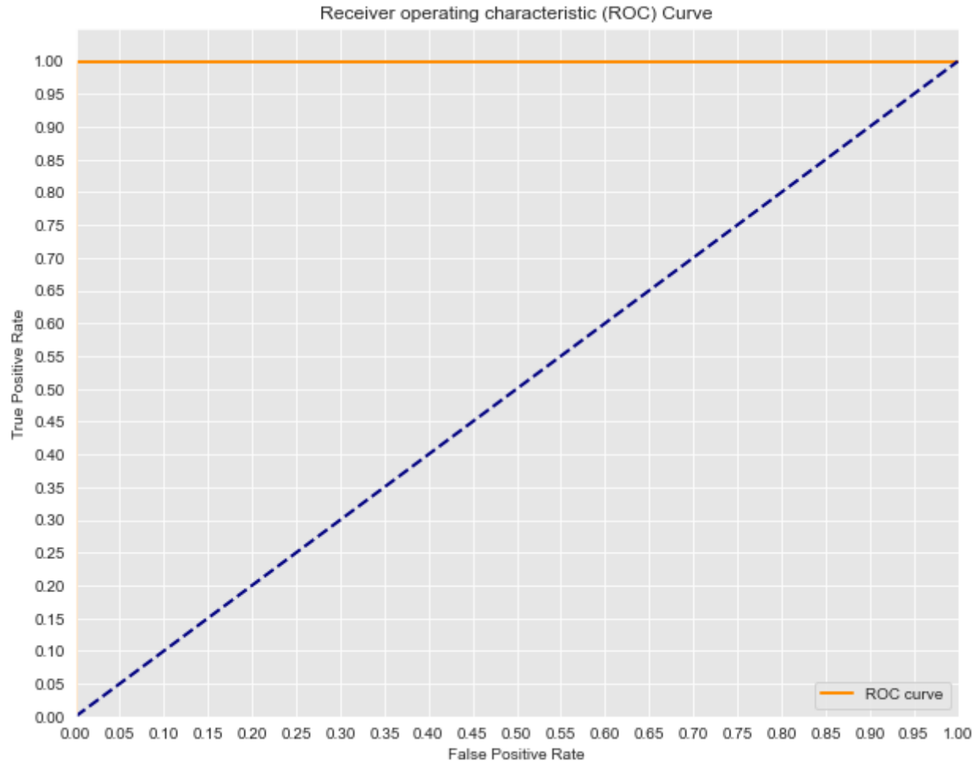





```
Cross Validated ROC AUC score: 1.0
```

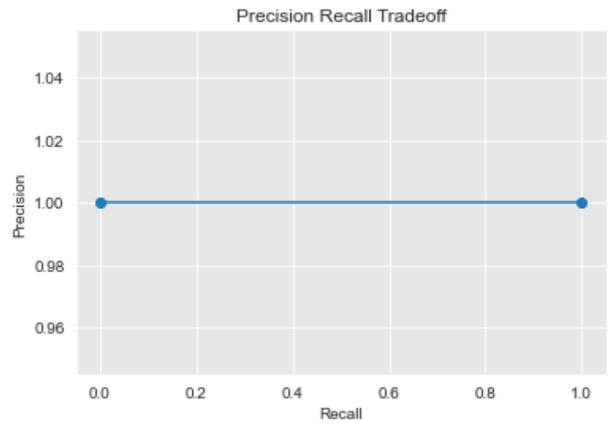
```
Class:Q
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

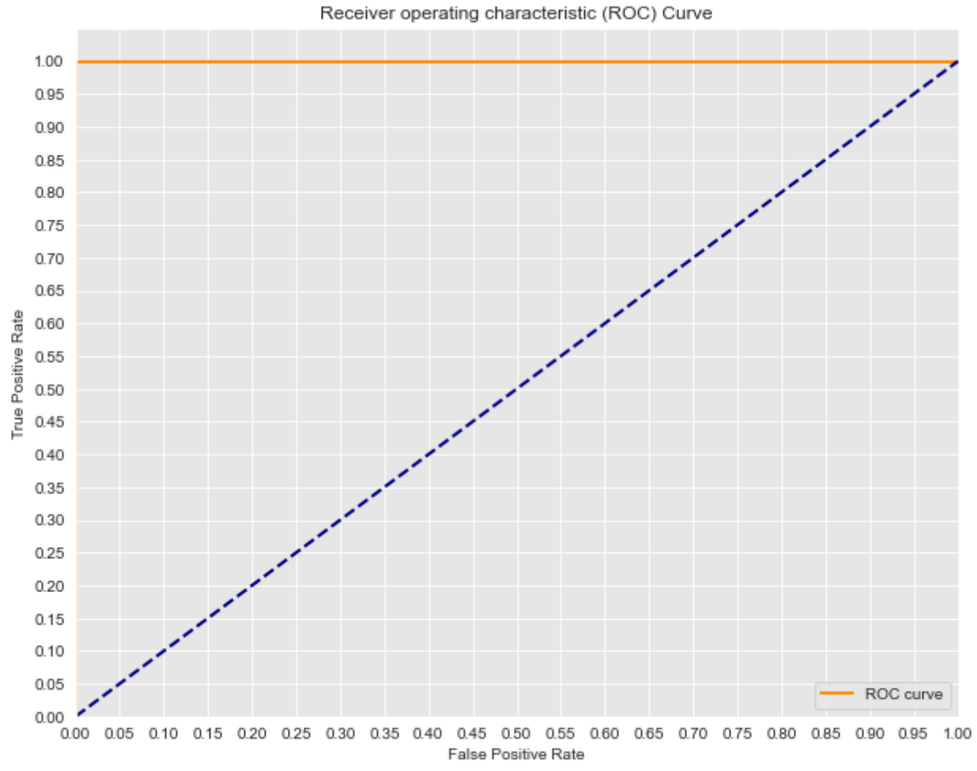





```
Cross Validated ROC AUC score: 1.0
```

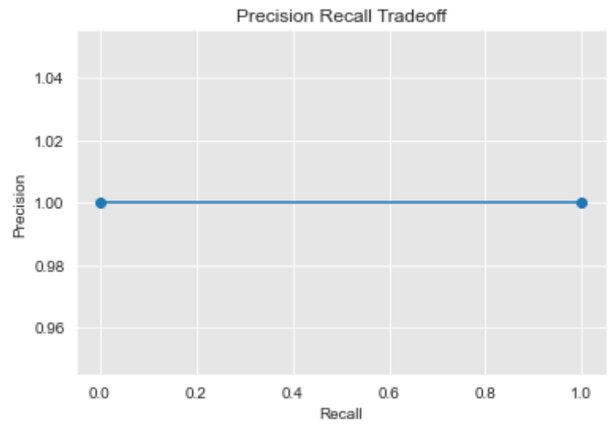
```
Class:R
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

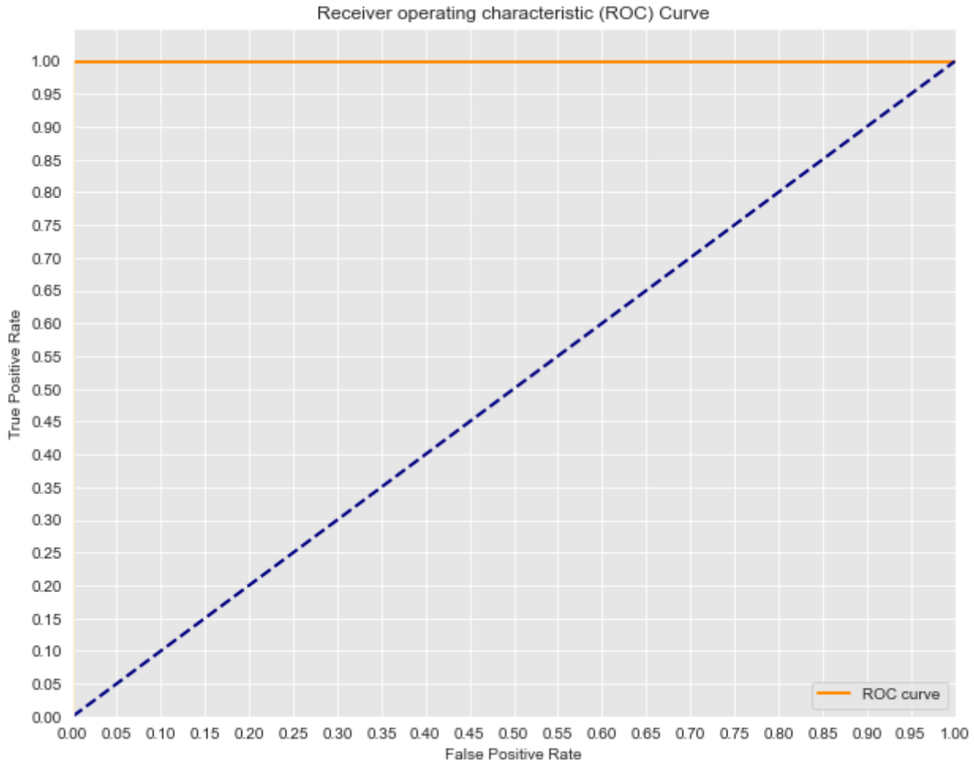





```
Cross Validated ROC AUC score: 1.0
```

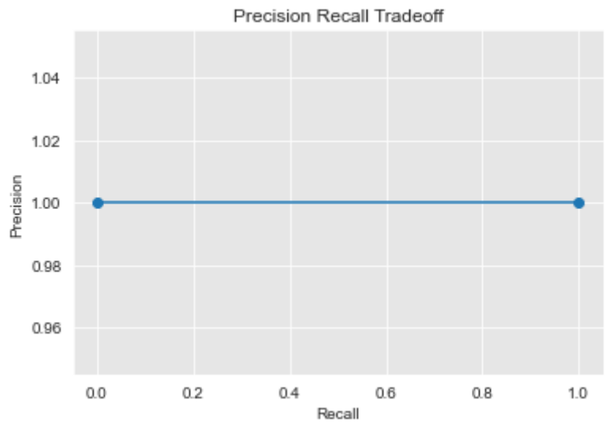
```
Class:S
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

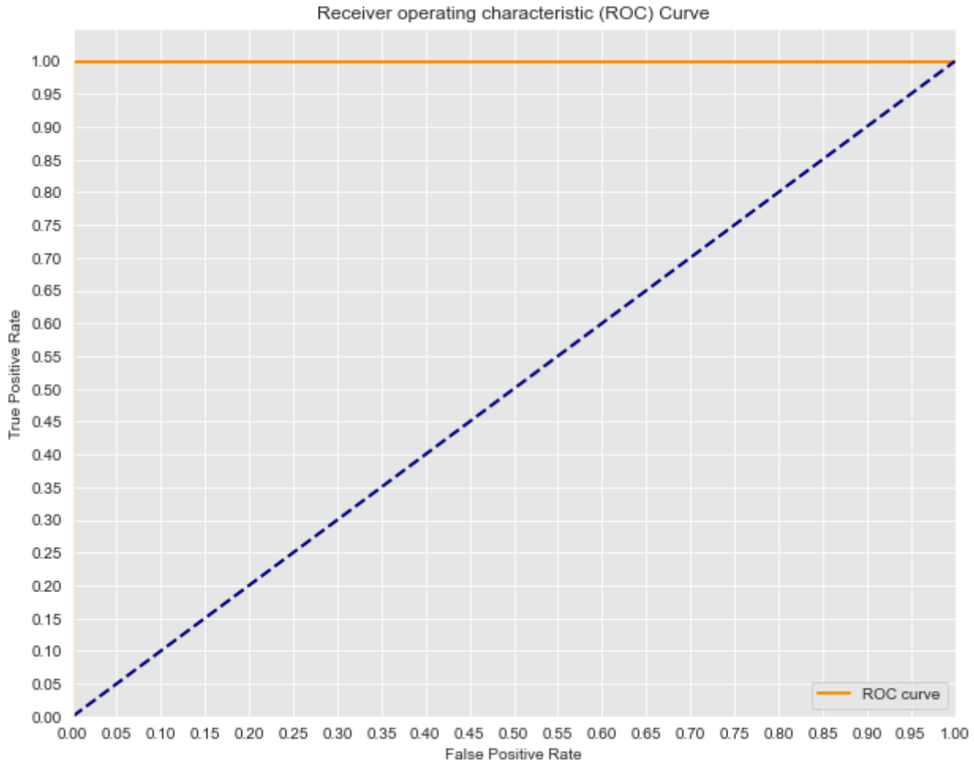





```
Cross Validated ROC AUC score: 1.0
```

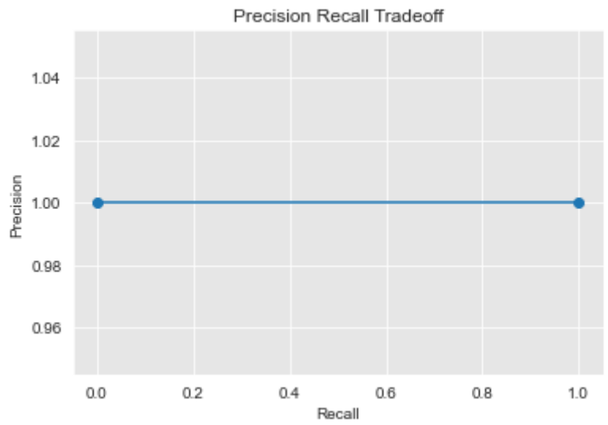
```
Class:Stop
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

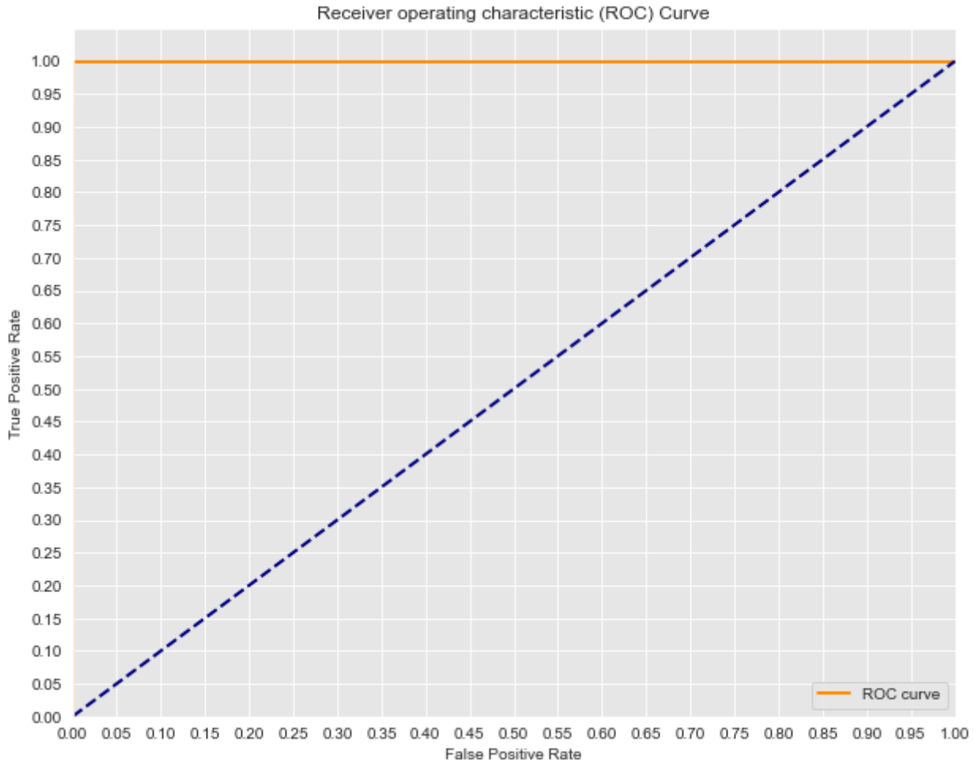





```
Cross Validated ROC AUC score: 1.0
```

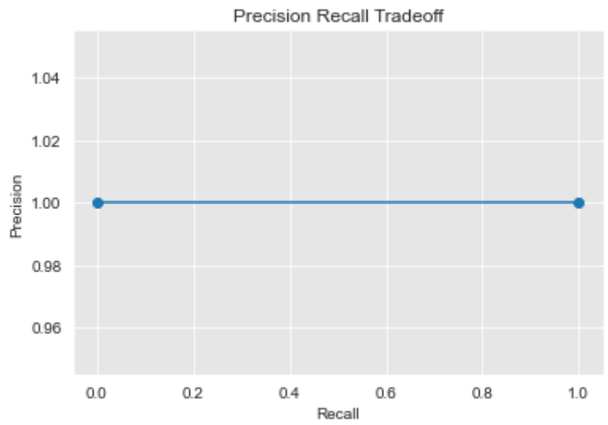
```
Class:T
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

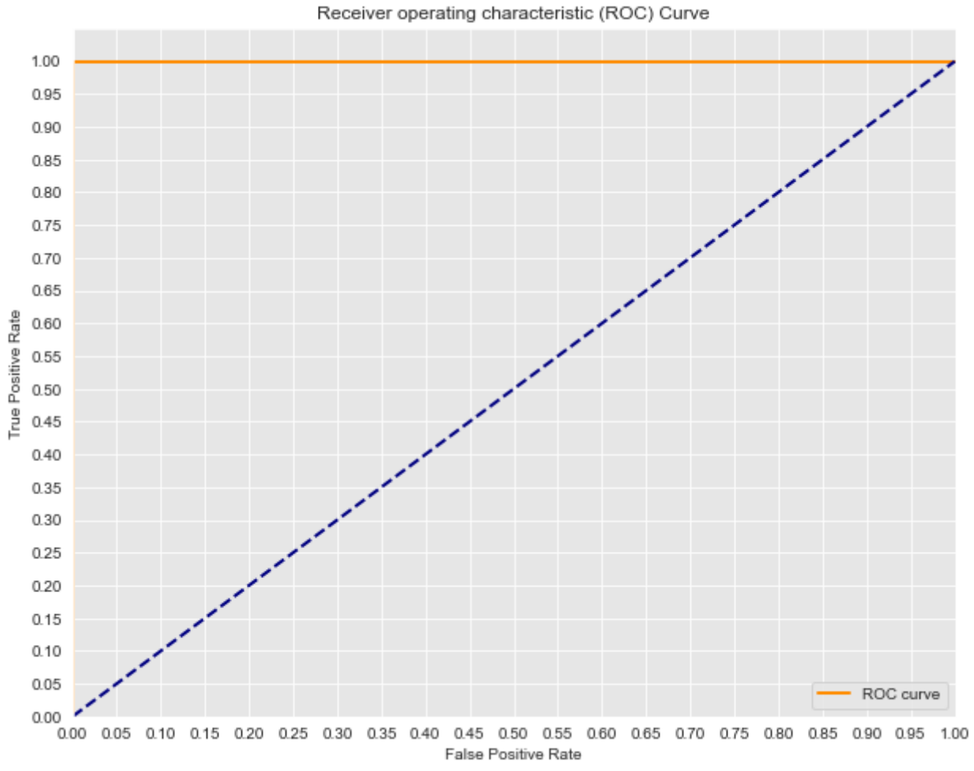





```
Cross Validated ROC AUC score: 1.0
```

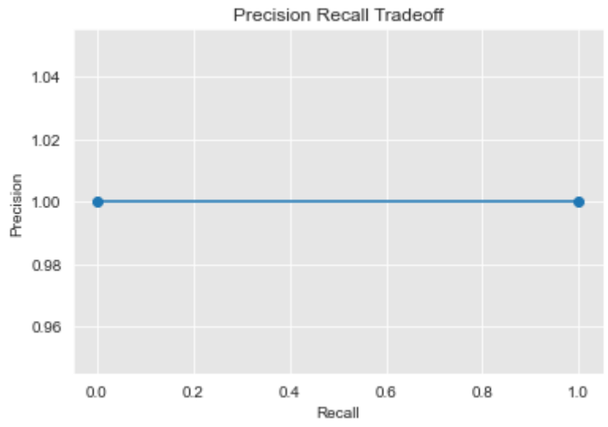
```
Class:V
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

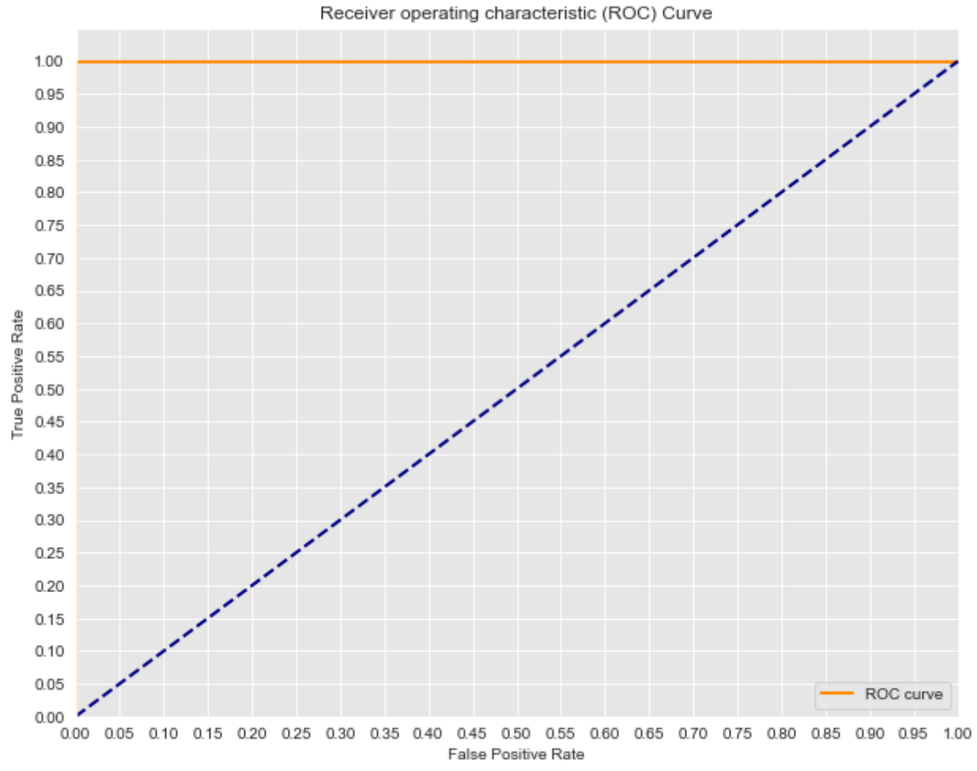





```
Cross Validated ROC AUC score: 1.0
```

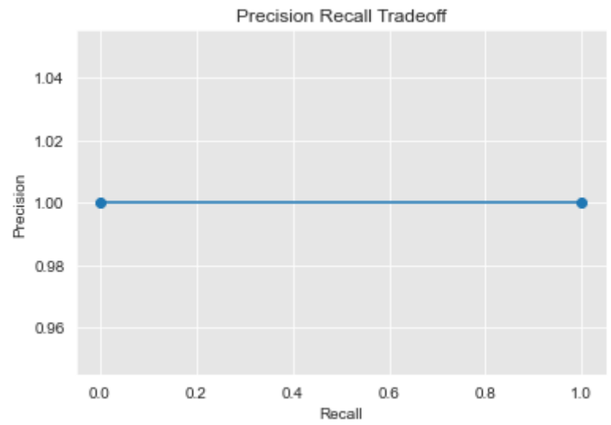
```
Class:W
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

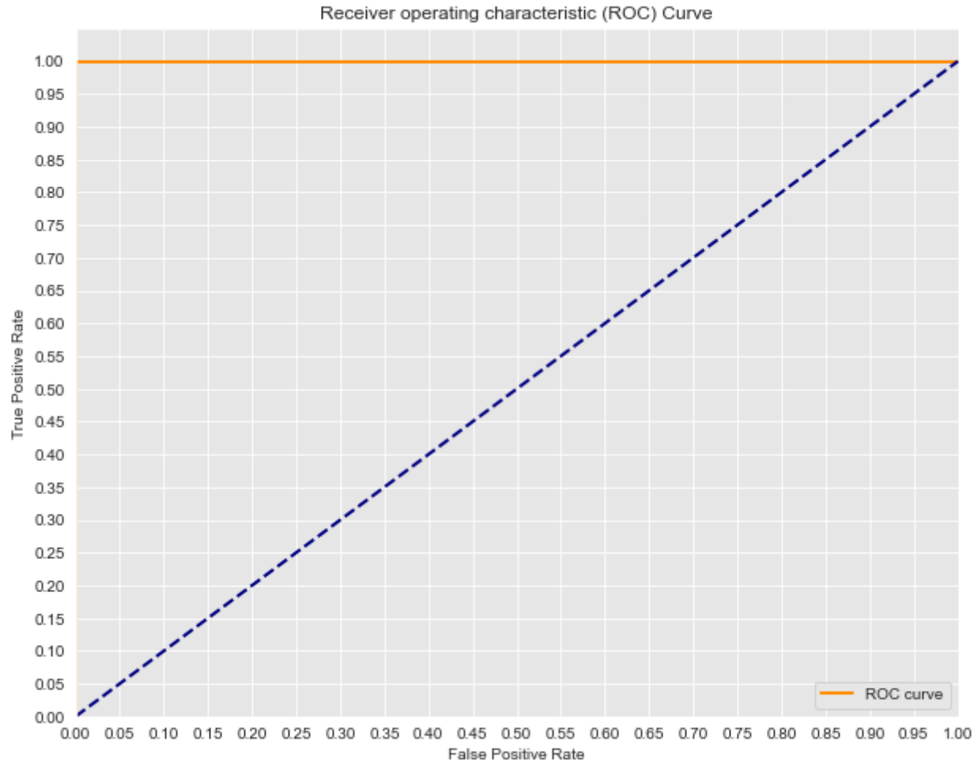





```
Cross Validated ROC AUC score: 1.0
```

```
Class:Y
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Cross Validated ROC AUC score: 1.0
```

Fit the model to the training data.

In [59]:
```
gradient_boost.fit(X2_train, y2_train)
```

Out[59]:
```
GradientBoostingClassifier()
```

Make predictions.

In [60]:
```
y2_hat_train_gb = gradient_boost.predict(X2_train)
```

All predictions were classified correctly.

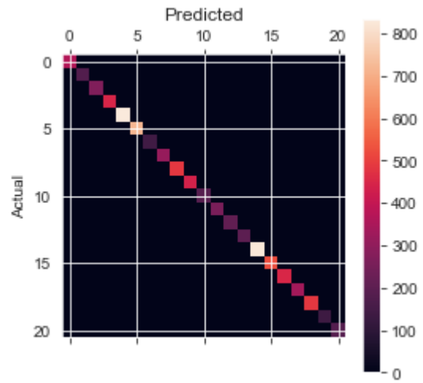
In [61]:
```
con_mat(y2_train,y2_hat_train_gb)
```

```
Confusion Matrix
----------------
      0    1    2    3    4    5    6    7    8    9   ...   11   12   13   14  \
0   370    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
1     0  182    0    0    0    0    0    0    0    0  ...    0    0    0    0
2     0    0  273    0    0    0    0    0    0    0  ...    0    0    0    0
3     0    0    0  447    0    0    0    0    0    0  ...    0    0    0    0
4     0    0    0    0  833    0    0    0    0    0  ...    0    0    0    0
5     0    0    0    0    0  720    0    0    0    0  ...    0    0    0    0
6     0    0    0    0    0    0  142    0    0    0  ...    0    0    0    0
7     0    0    0    0    0    0    0  315    0    0  ...    0    0    0    0
8     0    0    0    0    0    0    0    0  485    0  ...    0    0    0    0
9     0    0    0    0    0    0    0    0    0  437  ...    0    0    0    0
10    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
```

```
11    0    0    0    0    0    0    0    0    0    0  ...  259    0    0    0
12    0    0    0    0    0    0    0    0    0    0  ...    0  209    0    0
13    0    0    0    0    0    0    0    0    0    0  ...    0    0  200    0
14    0    0    0    0    0    0    0    0    0    0  ...    0    0    0  824
15    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
16    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
17    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
18    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
19    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0
20    0    0    0    0    0    0    0    0    0    0  ...    0    0    0    0

     15   16   17   18   19   20
0     0    0    0    0    0    0
1     0    0    0    0    0    0
2     0    0    0    0    0    0
3     0    0    0    0    0    0
4     0    0    0    0    0    0
5     0    0    0    0    0    0
6     0    0    0    0    0    0
7     0    0    0    0    0    0
8     0    0    0    0    0    0
9     0    0    0    0    0    0
10    0    0    0    0    0    0
11    0    0    0    0    0    0
12    0    0    0    0    0    0
13    0    0    0    0    0    0
14    0    0    0    0    0    0
15  522    0    0    0    0    0
16    0  451    0    0    0    0
17    0    0  339    0    0    0
18    0    0    0  488    0    0
19    0    0    0    0  134    0
20    0    0    0    0    0  183

[21 rows x 21 columns]
```



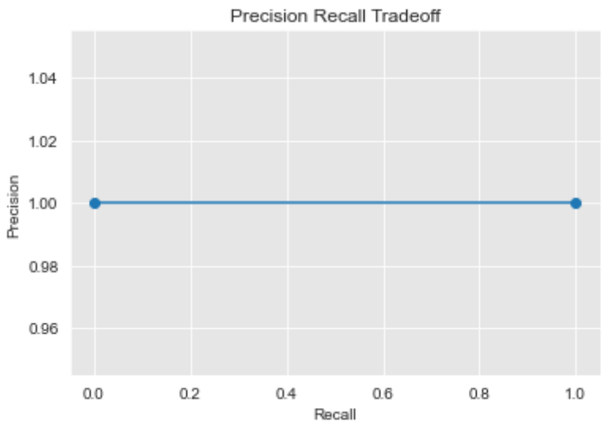
Seperate predicted values into each class for metrics.

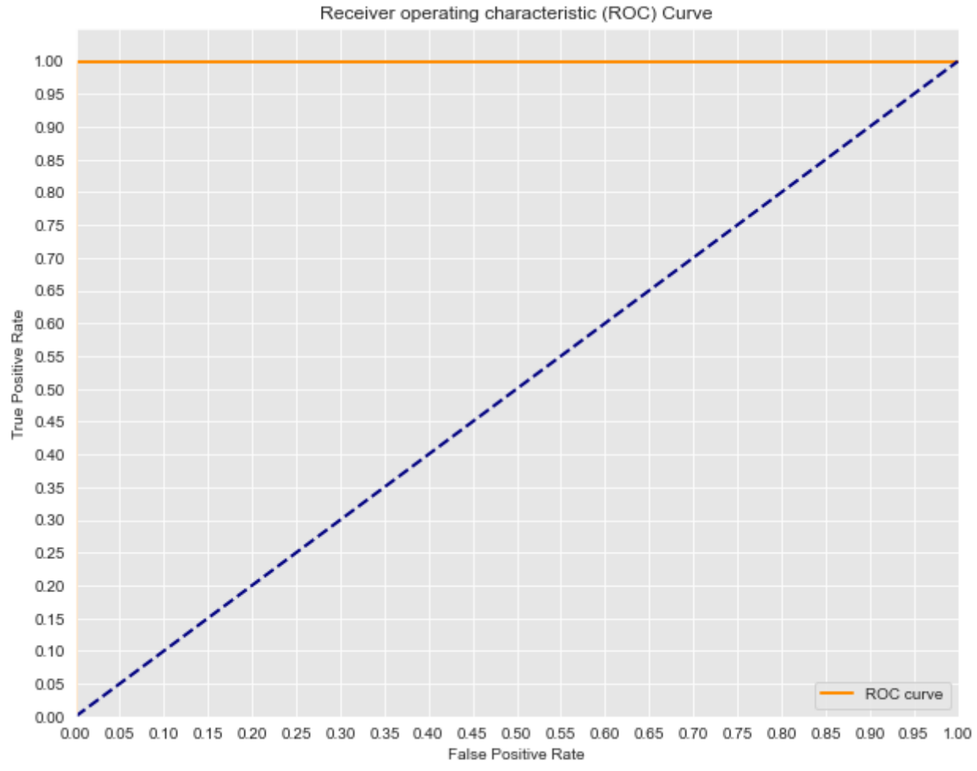
In [62]:
```
predictions_class0=y2_hat_train_gb==0
predictions_class1=y2_hat_train_gb==1
predictions_class2=y2_hat_train_gb==2
predictions_class3=y2_hat_train_gb==3
predictions_class4=y2_hat_train_gb==4
predictions_class5=y2_hat_train_gb==5
predictions_class6=y2_hat_train_gb==6
predictions_class7=y2_hat_train_gb==7
predictions_class8=y2_hat_train_gb==8
```

```
predictions_class9=y2_hat_train_gb==9
predictions_class10=y2_hat_train_gb==10
predictions_class11=y2_hat_train_gb==11
predictions_class12=y2_hat_train_gb==12
predictions_class13=y2_hat_train_gb==13
predictions_class14=y2_hat_train_gb==14
predictions_class15=y2_hat_train_gb==15
predictions_class16=y2_hat_train_gb==16
predictions_class17=y2_hat_train_gb==17
predictions_class18=y2_hat_train_gb==18
predictions_class19=y2_hat_train_gb==19
predictions_class20=y2_hat_train_gb==20
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3,predictions_class4,predictions_class5,predictions_class6
  ,predictions_class7,predictions_class8,predictions_class9,predictions_class10,predictions_class11,predictions_class12
  ,predictions_class13,predictions_class14,predictions_class15,predictions_class16,predictions_class17,predictions_class18
  ,predictions_class19,predictions_class20]
```

In [63]:
```
multiclass(gradient_boost,X2_train,a,p,translation_df2['Amino_Acids_copy'],'train')
```

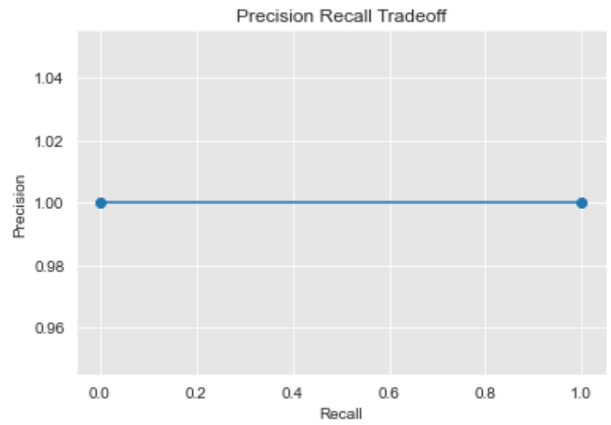
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

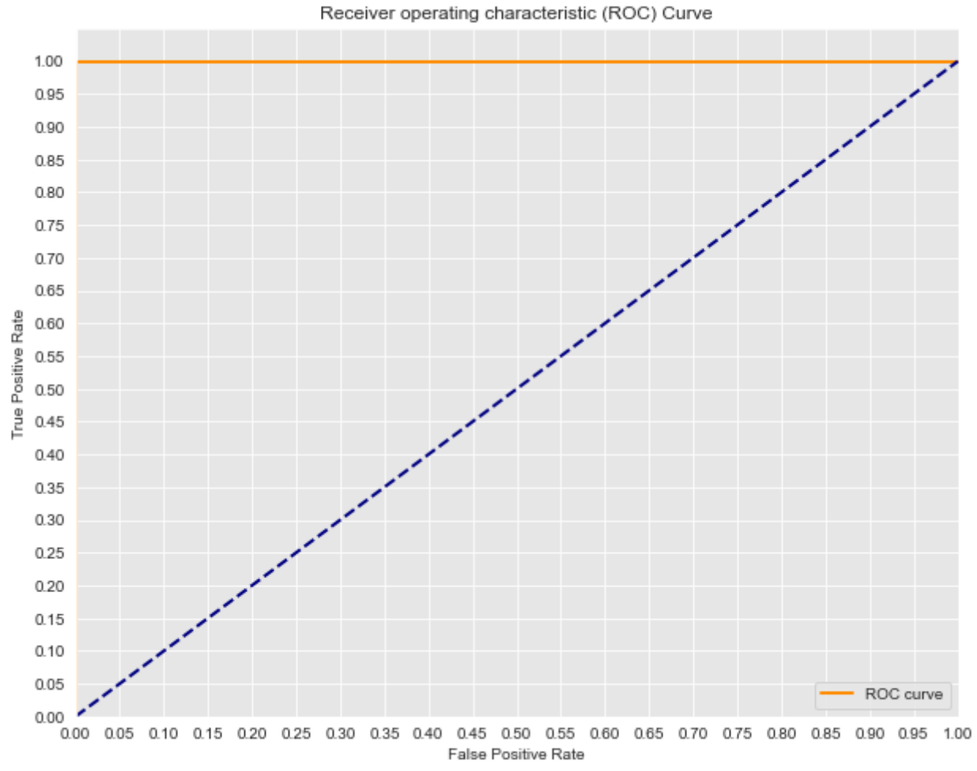





```
Cross Validated ROC AUC score: 1.0
```

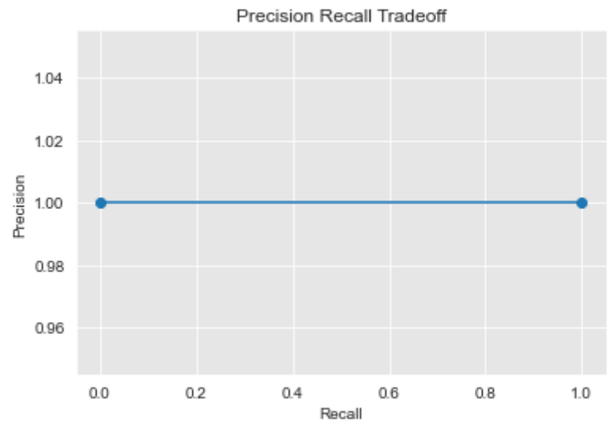
```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

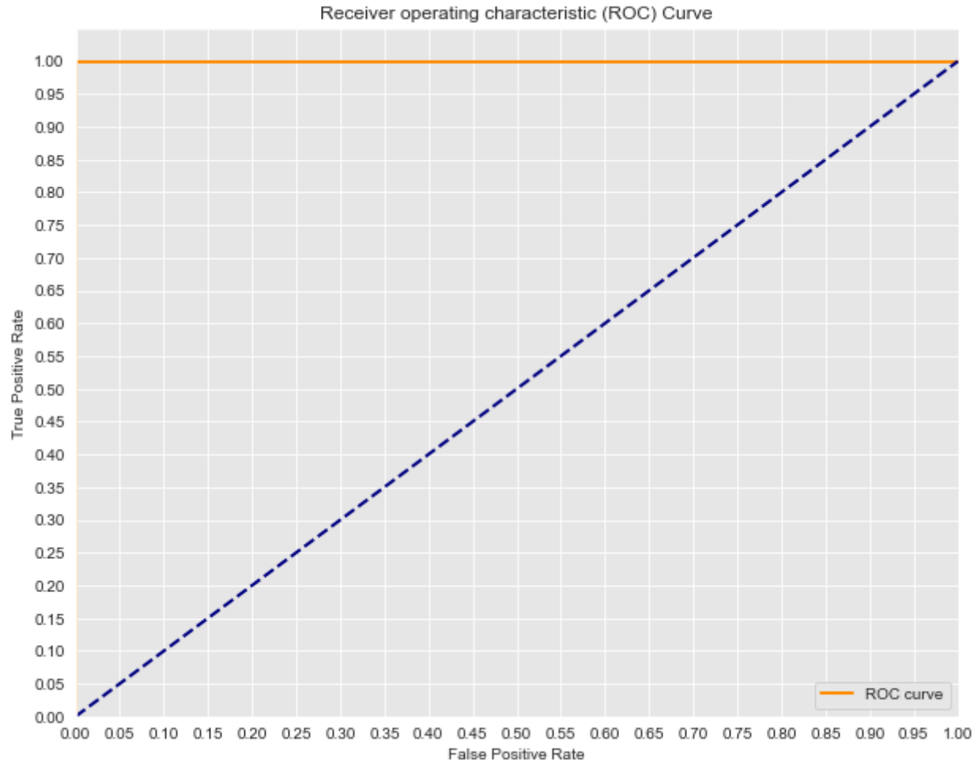





```
Cross Validated ROC AUC score: 1.0
```

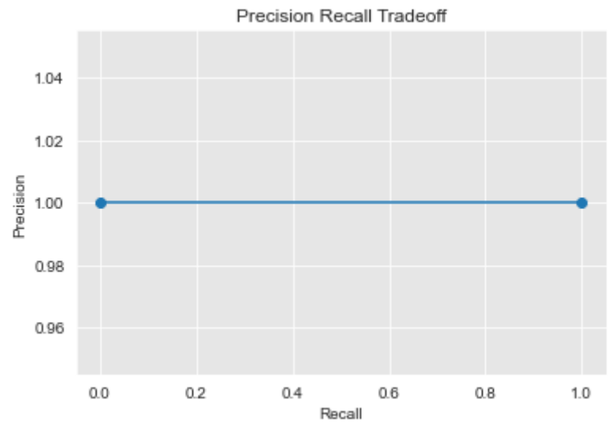
```
Class:D
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

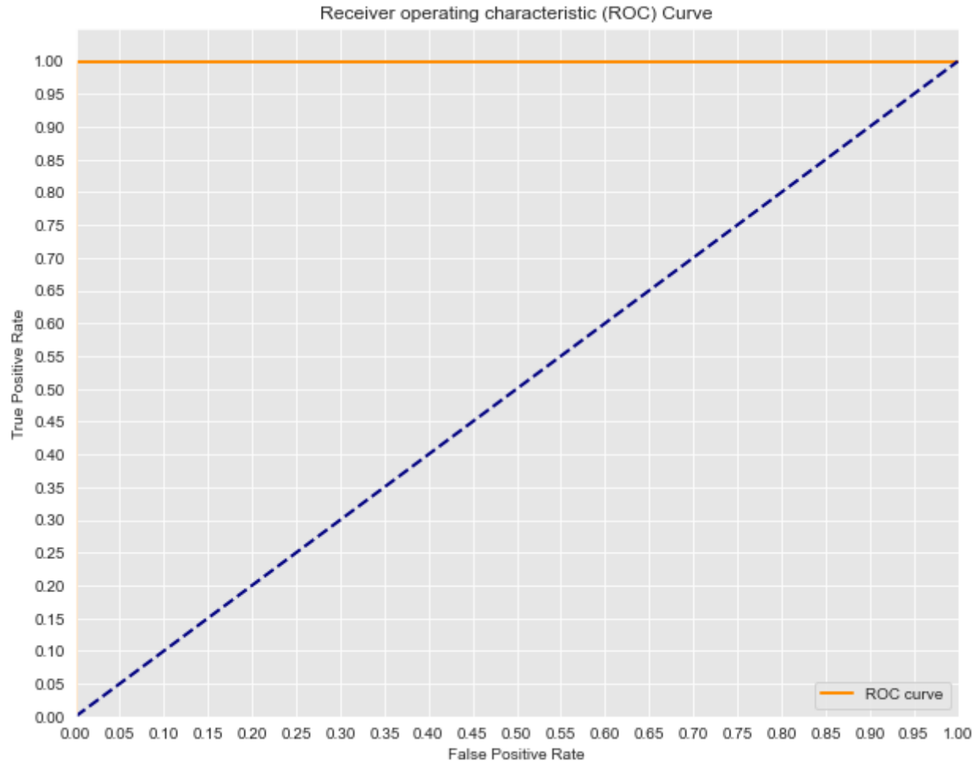





```
Cross Validated ROC AUC score: 1.0
```

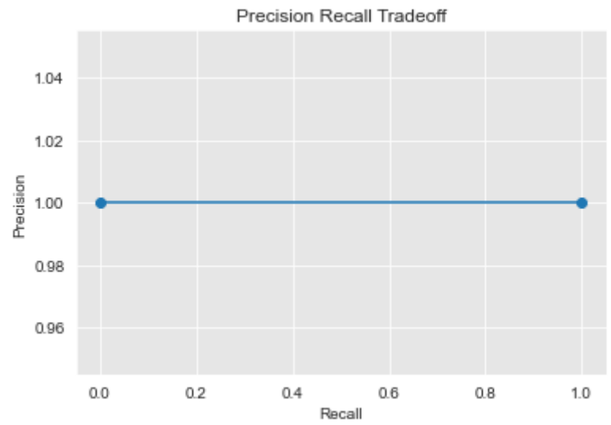
```
Class:E
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

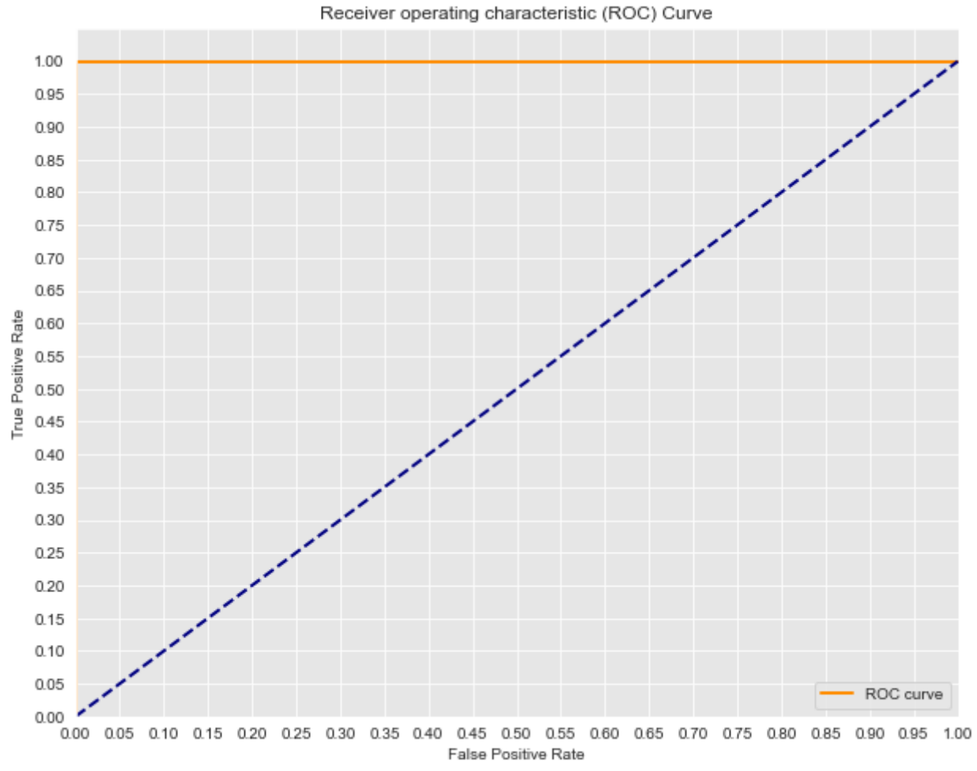





```
Cross Validated ROC AUC score: 1.0
```

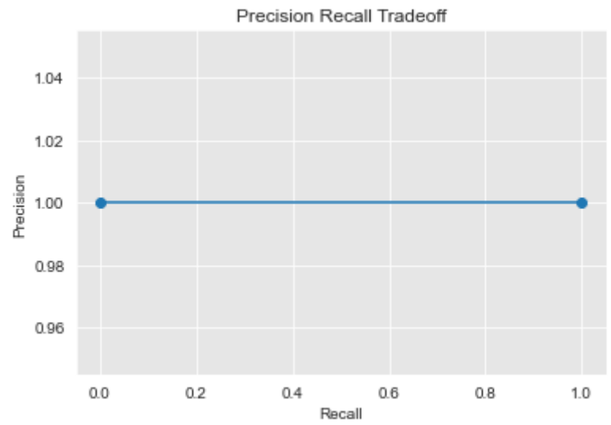
```
Class:F
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

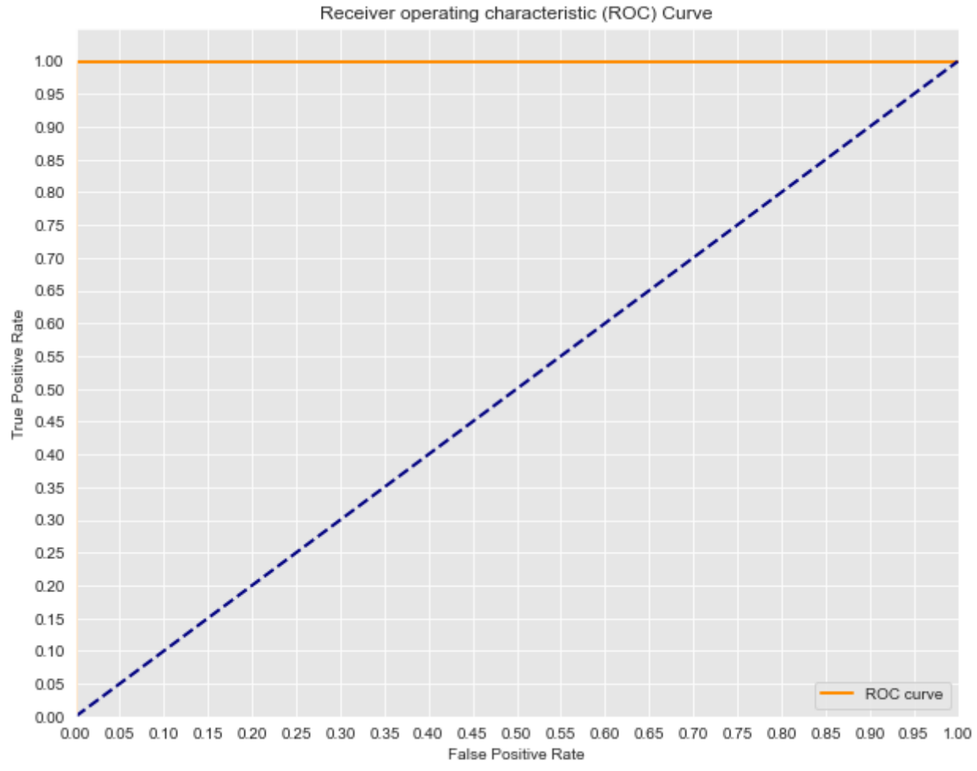





```
Cross Validated ROC AUC score: 1.0
```

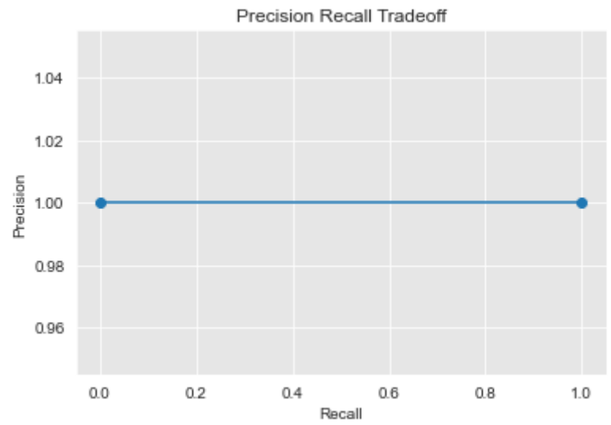
```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

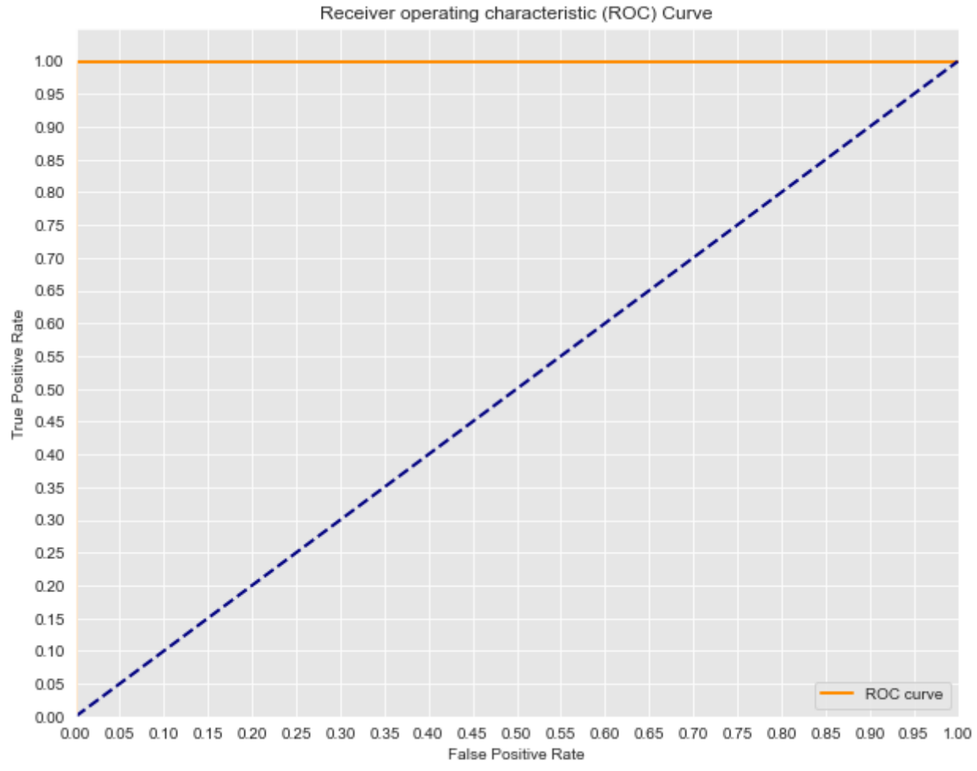





```
Cross Validated ROC AUC score: 1.0
```

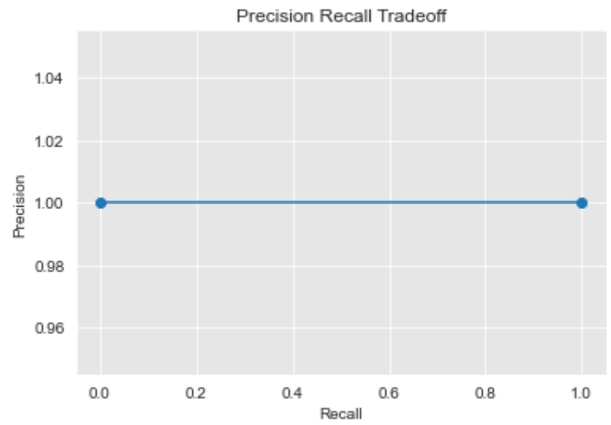
```
Class:H
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

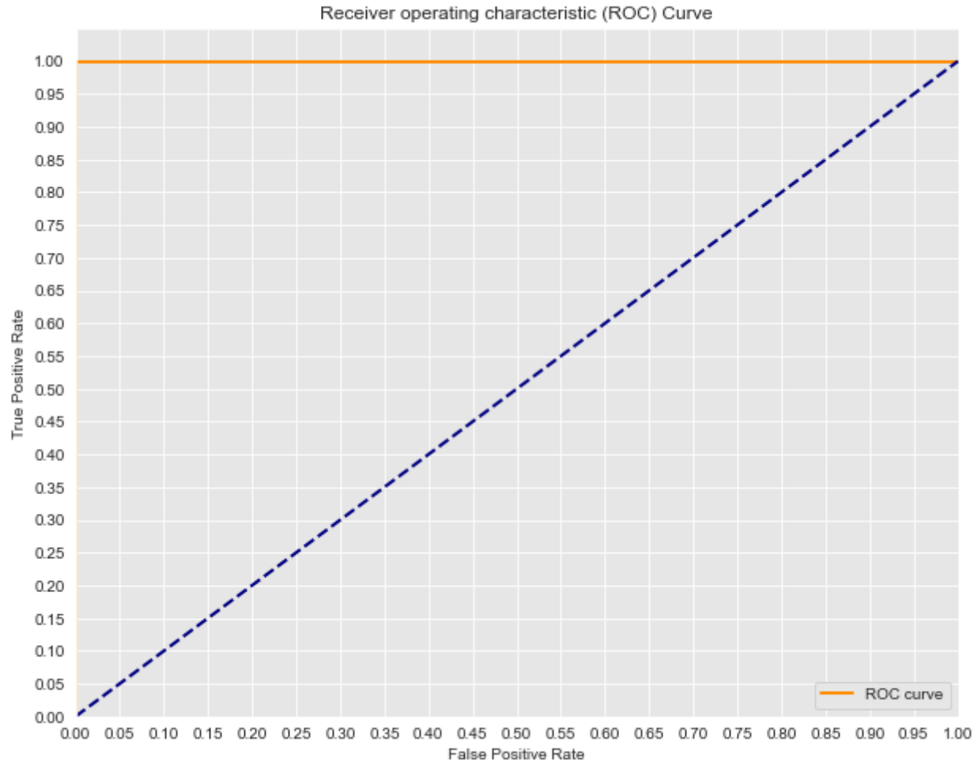





```
Cross Validated ROC AUC score: 1.0
```

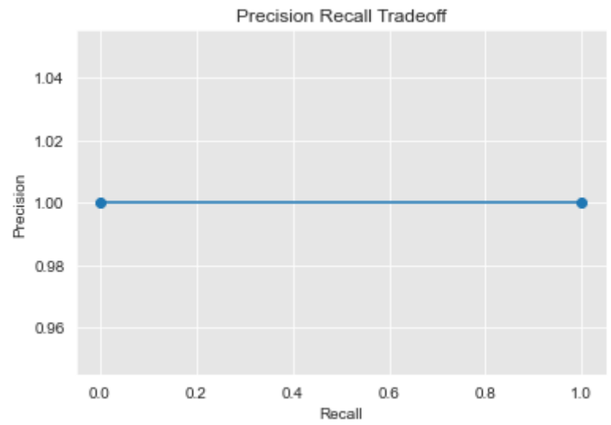
```
Class:I
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

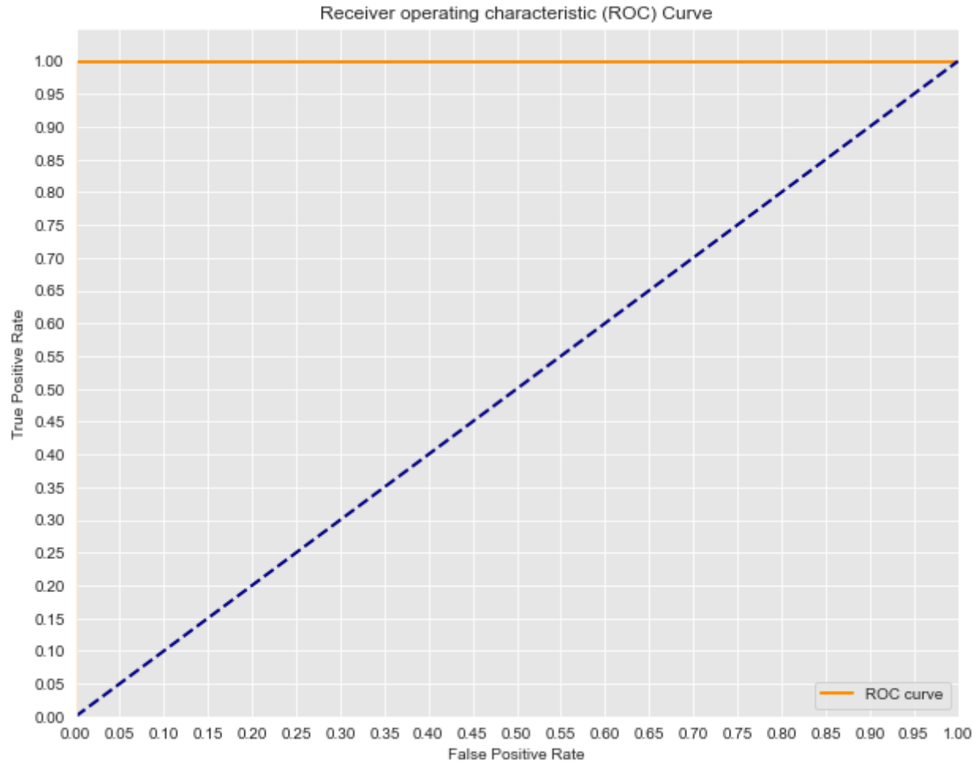





```
Cross Validated ROC AUC score: 1.0
```

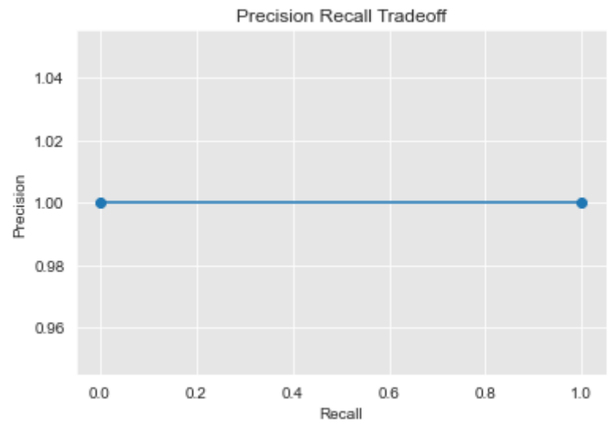
```
Class:K
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

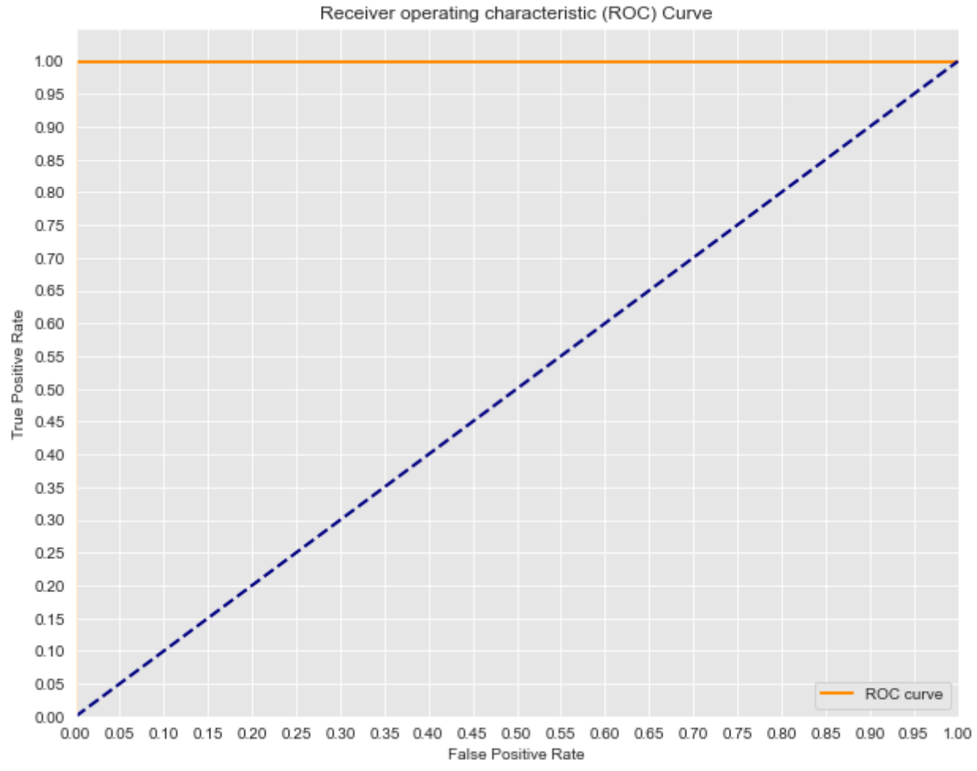





```
Cross Validated ROC AUC score: 1.0
```

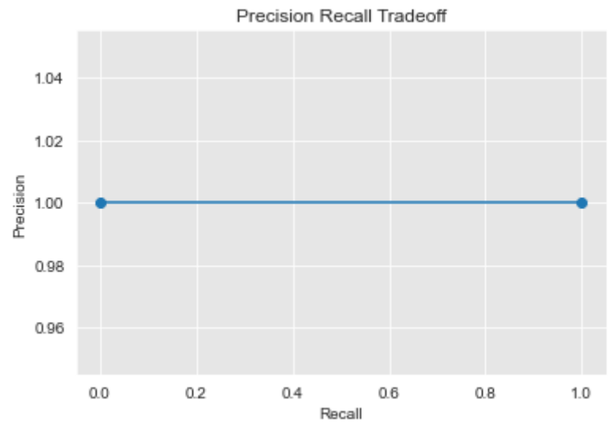
```
Class:L
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

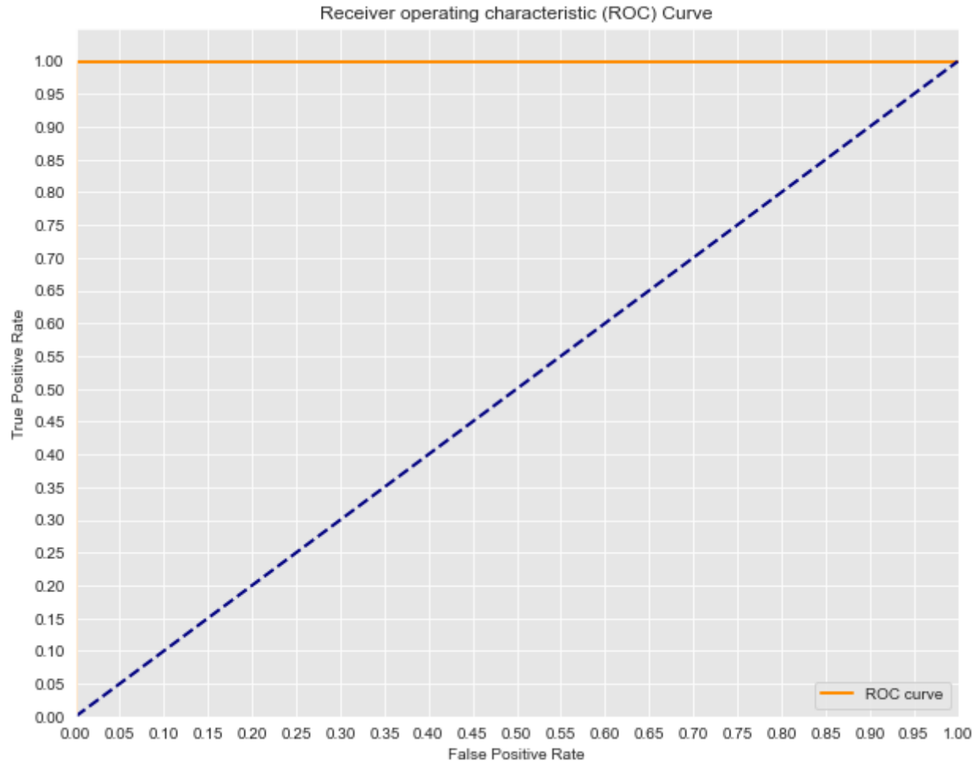





```
Cross Validated ROC AUC score: 1.0
```

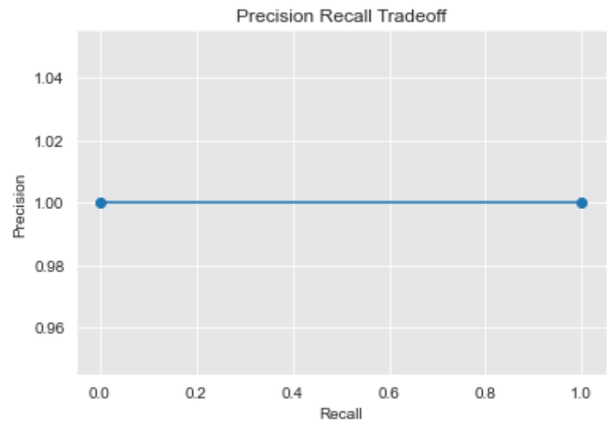
```
Class:M
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

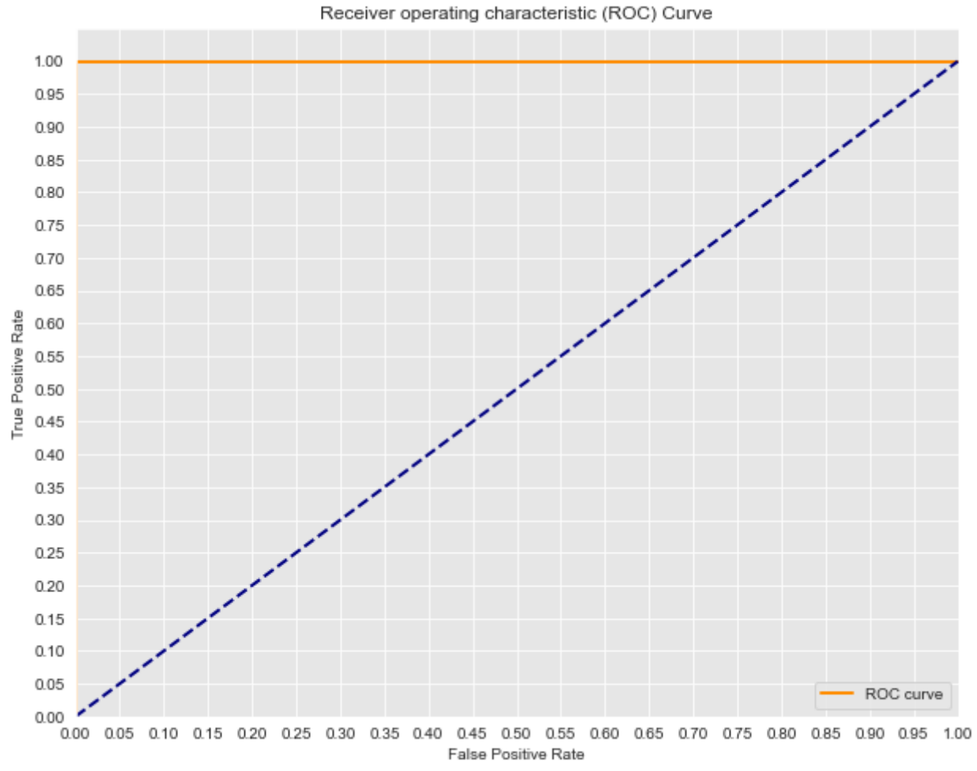





```
Cross Validated ROC AUC score: 1.0
```

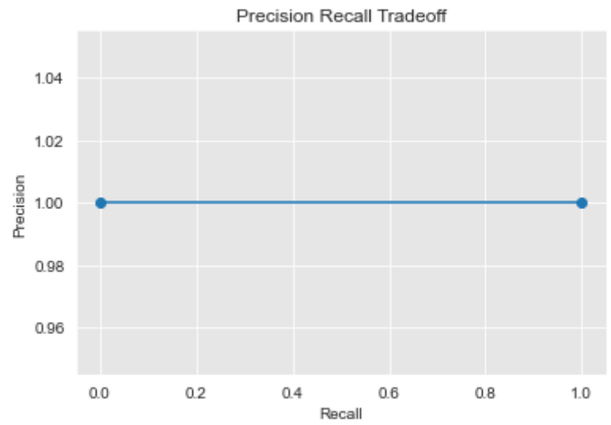
```
Class:N
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

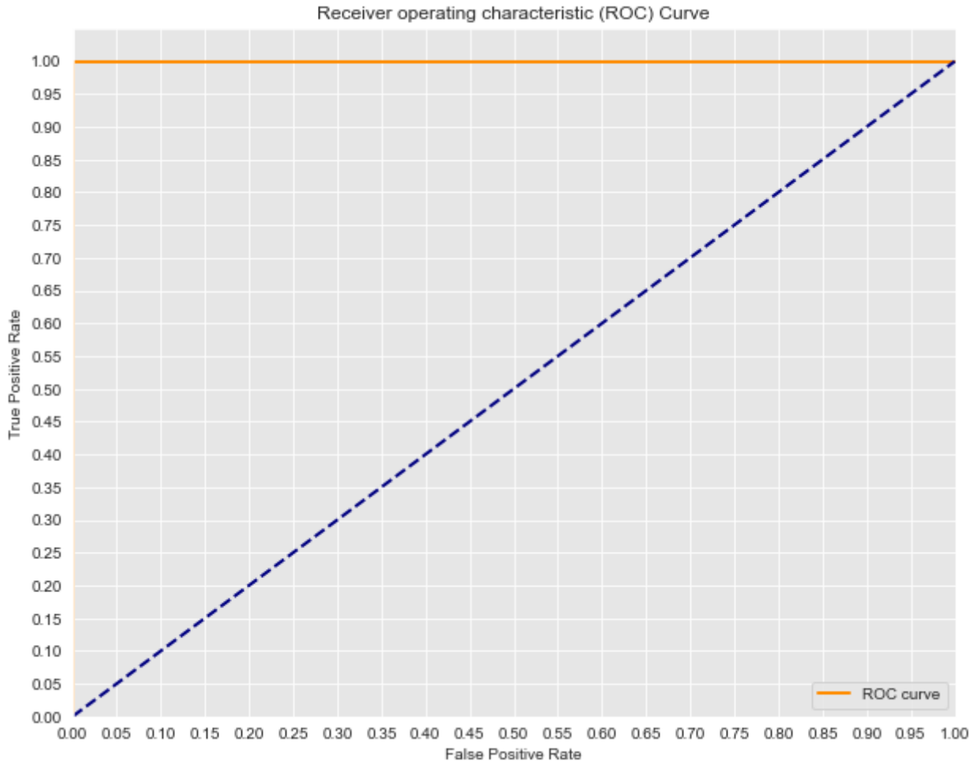





```
Cross Validated ROC AUC score: 1.0
```

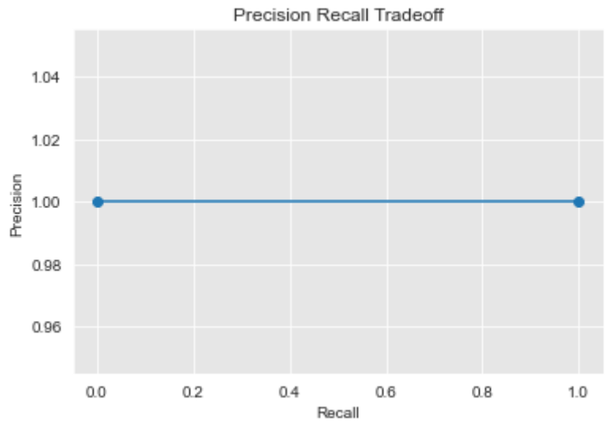
```
Class:P
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

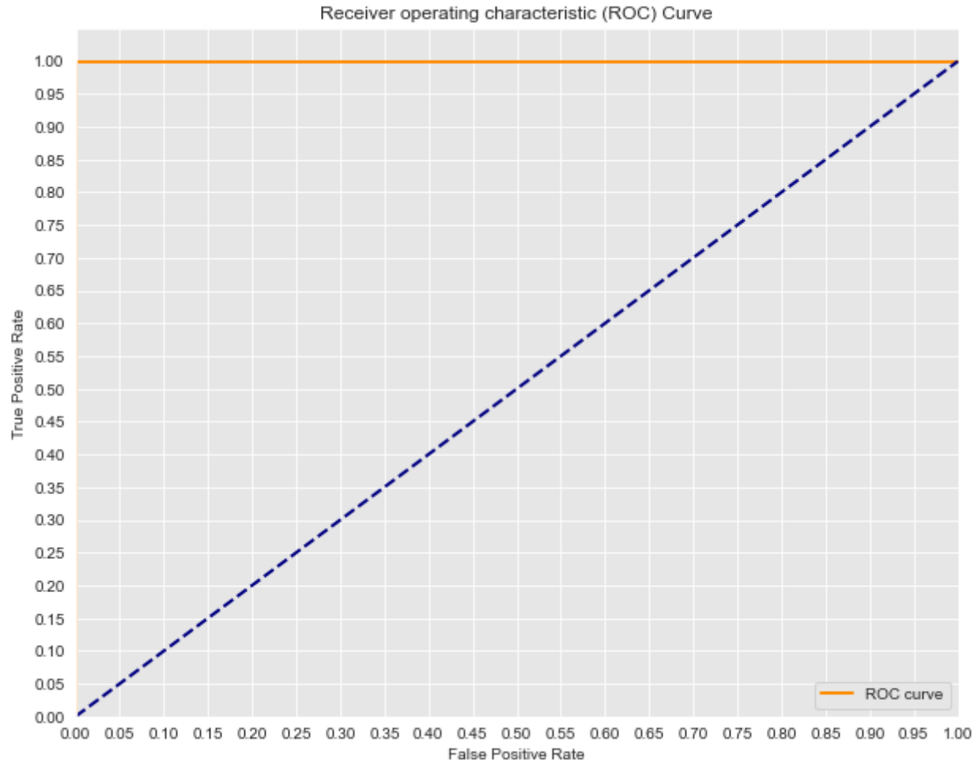





```
Cross Validated ROC AUC score: 1.0
```

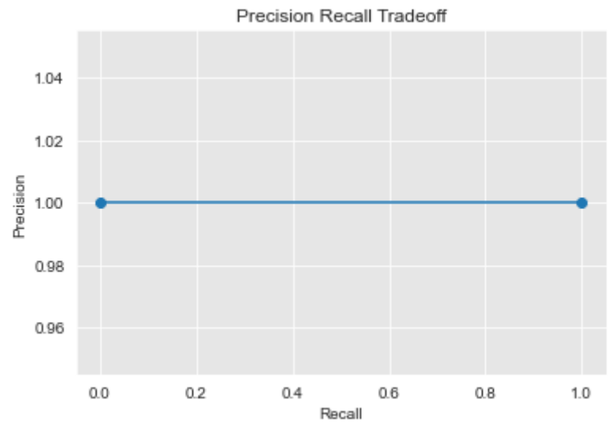
```
Class:Q
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

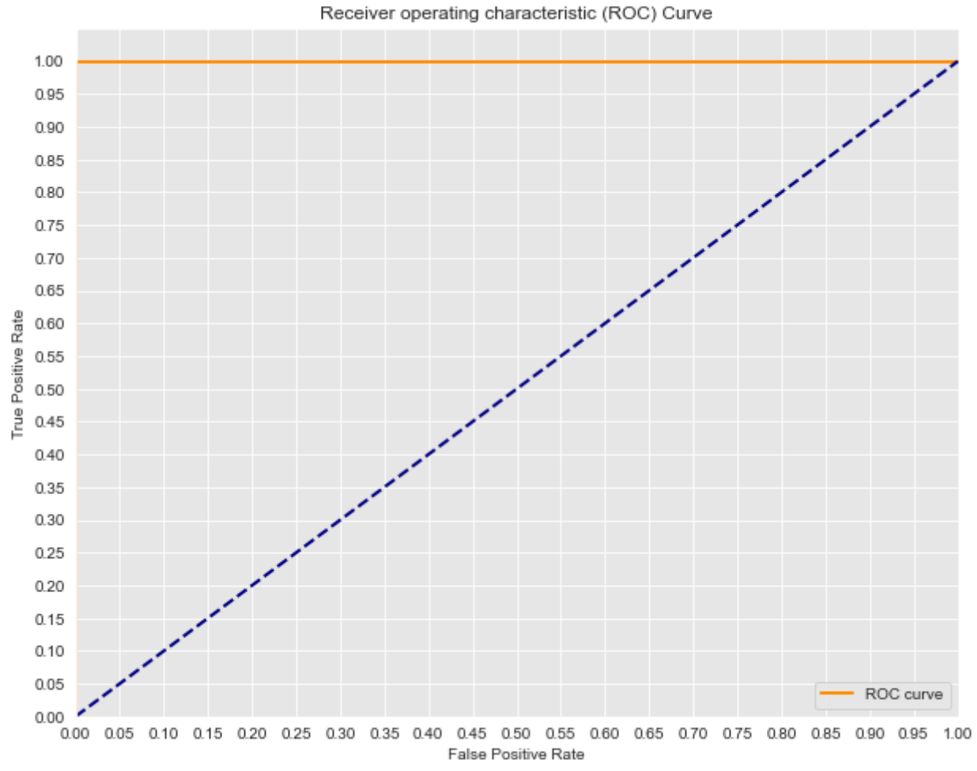





```
Cross Validated ROC AUC score: 1.0
```

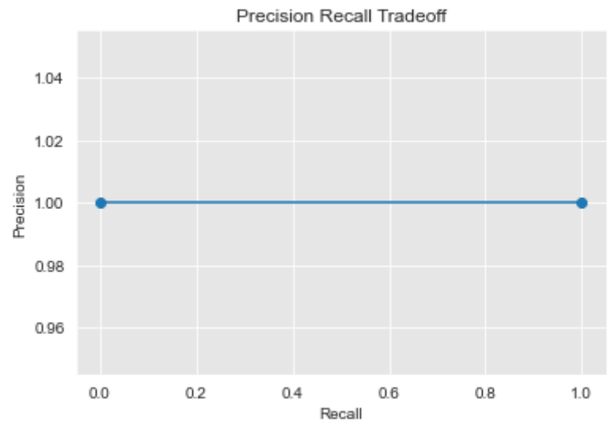
```
Class:R
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

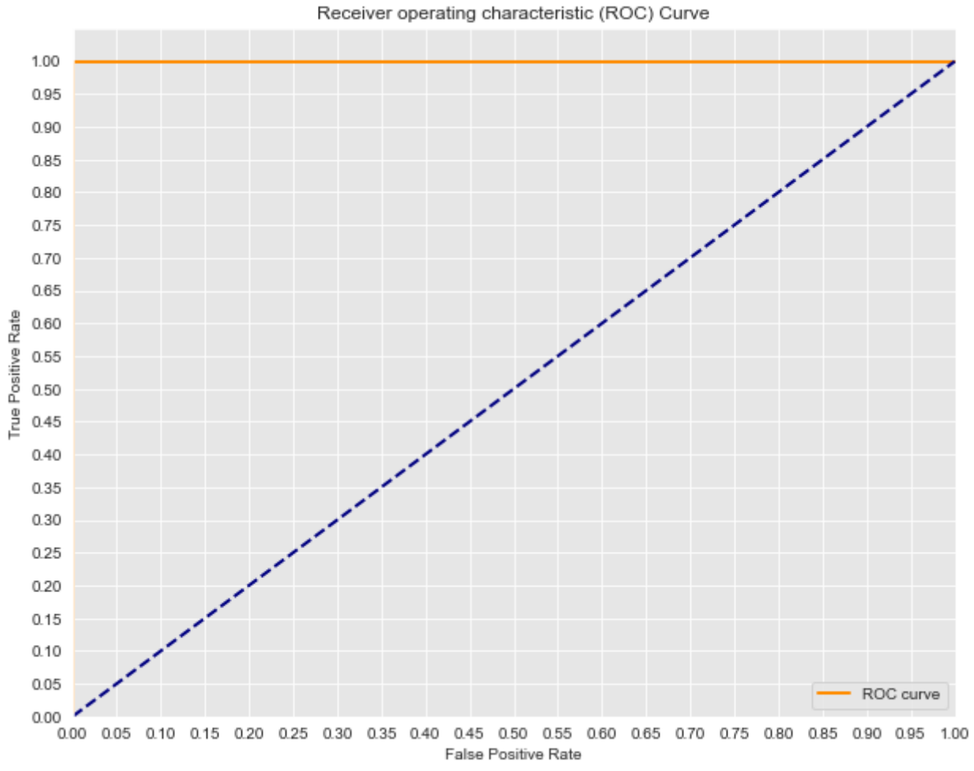





```
Cross Validated ROC AUC score: 1.0
```

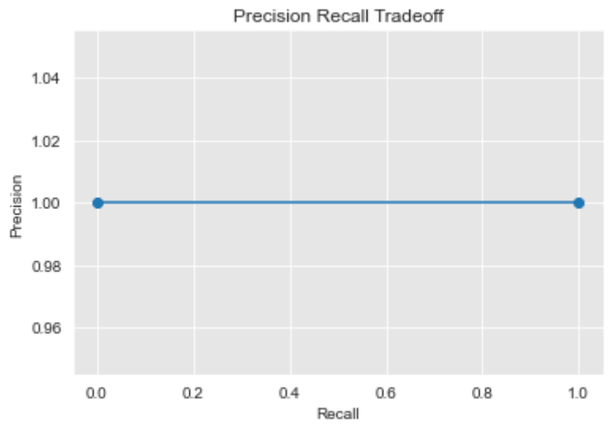
```
Class:S
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

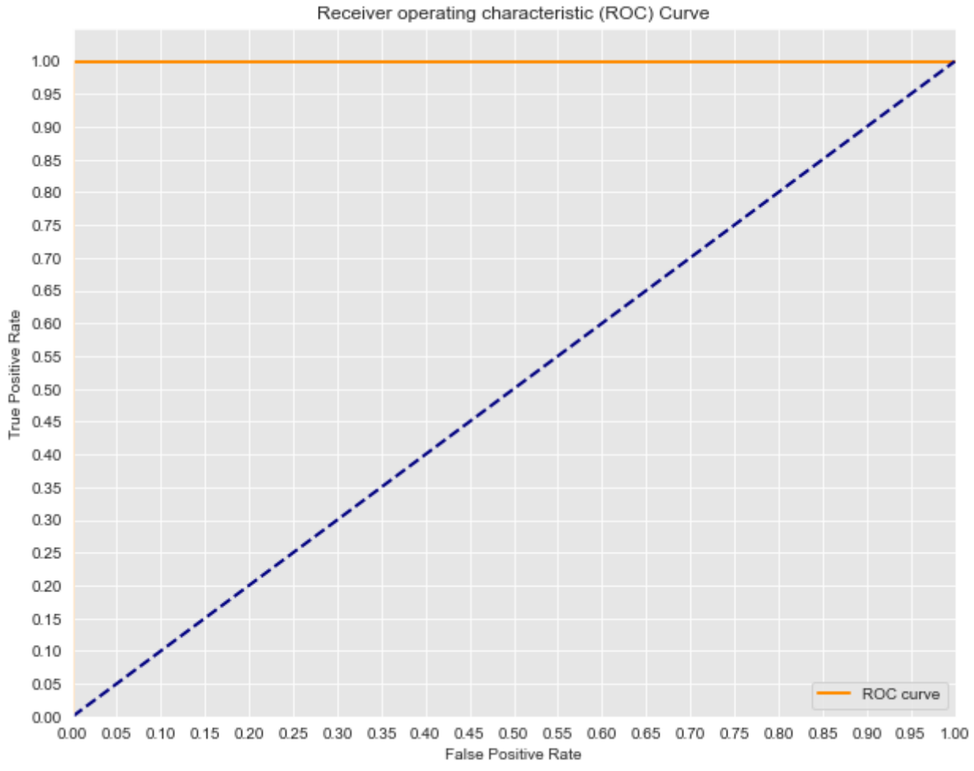





```
Cross Validated ROC AUC score: 1.0
```

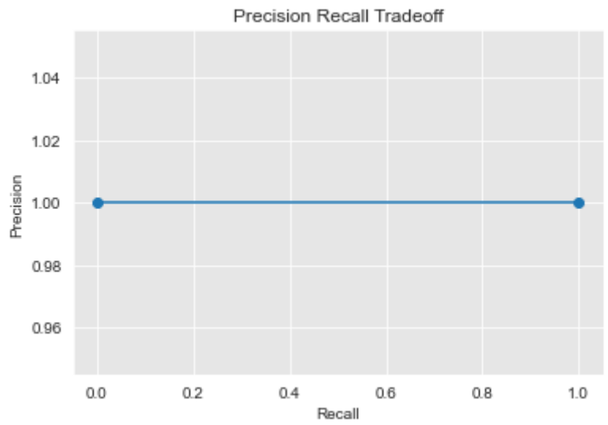
```
Class:Stop
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

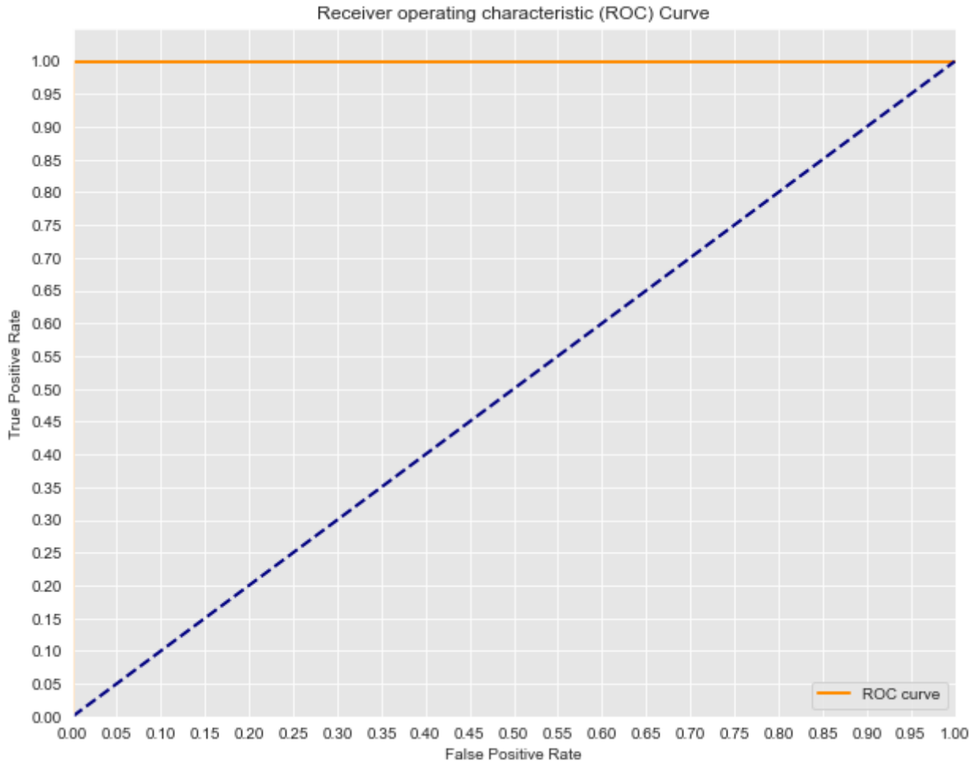





```
Cross Validated ROC AUC score: 1.0
```

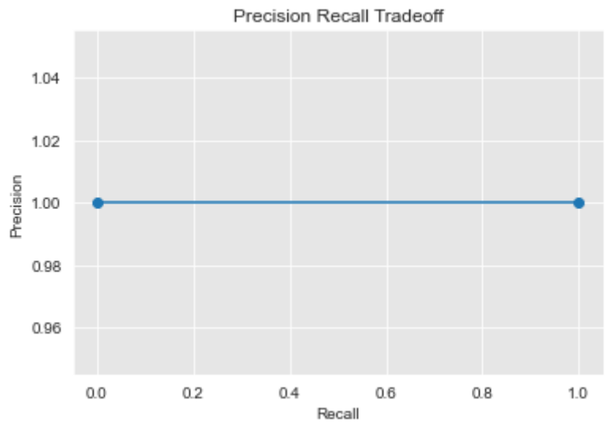
```
Class:T
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

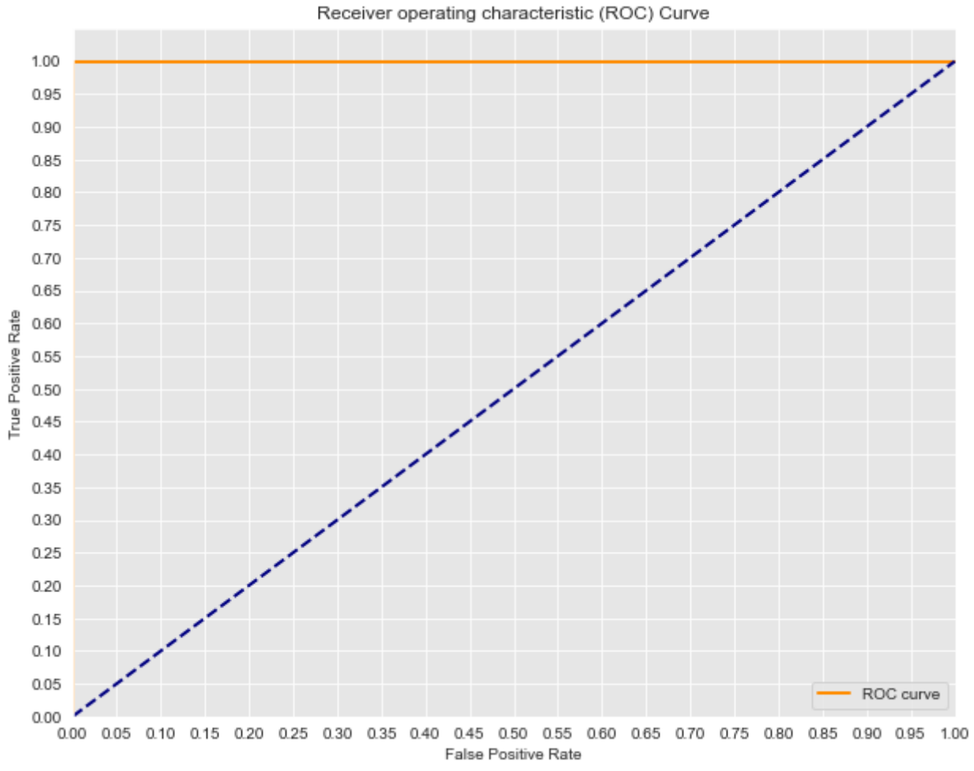





```
Cross Validated ROC AUC score: 1.0
```

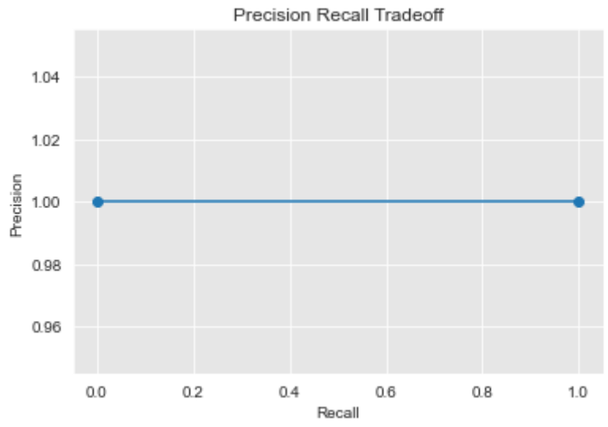
```
Class:V
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

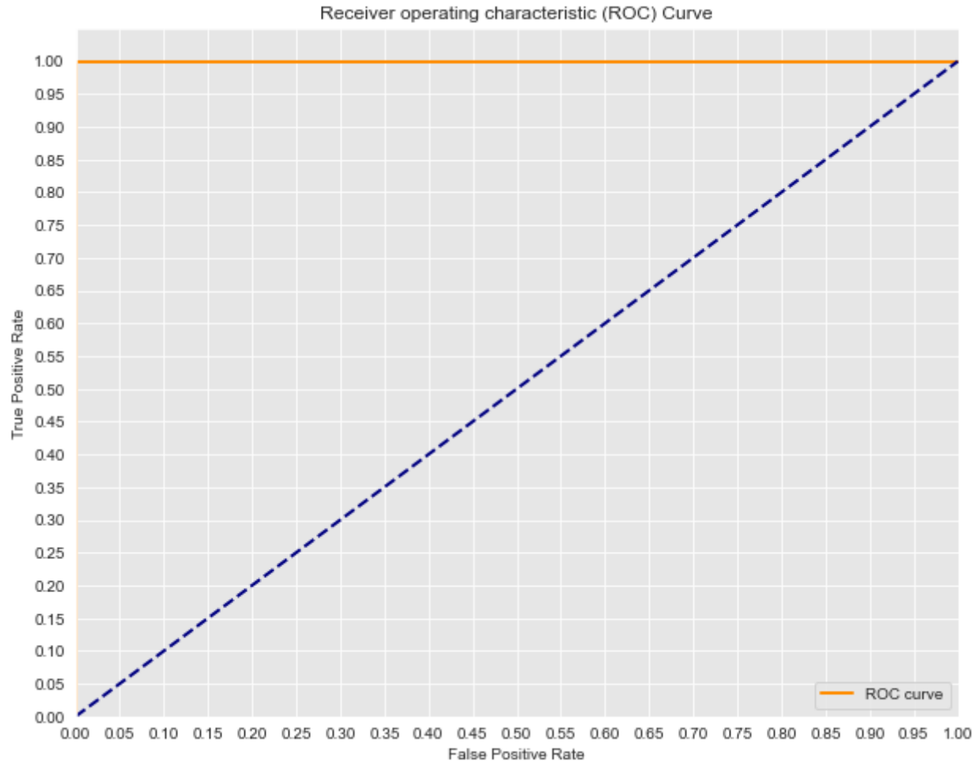





```
Cross Validated ROC AUC score: 1.0
```

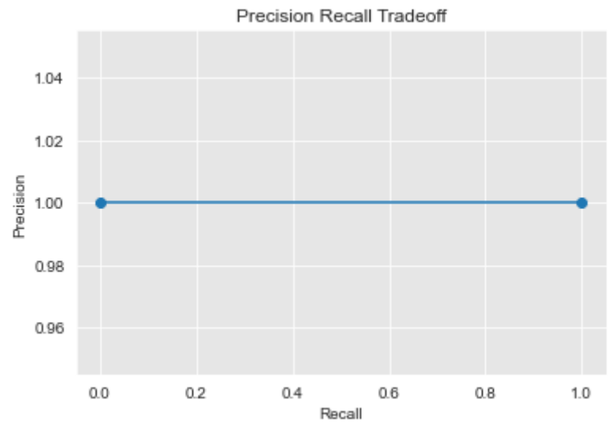
```
Class:W
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```

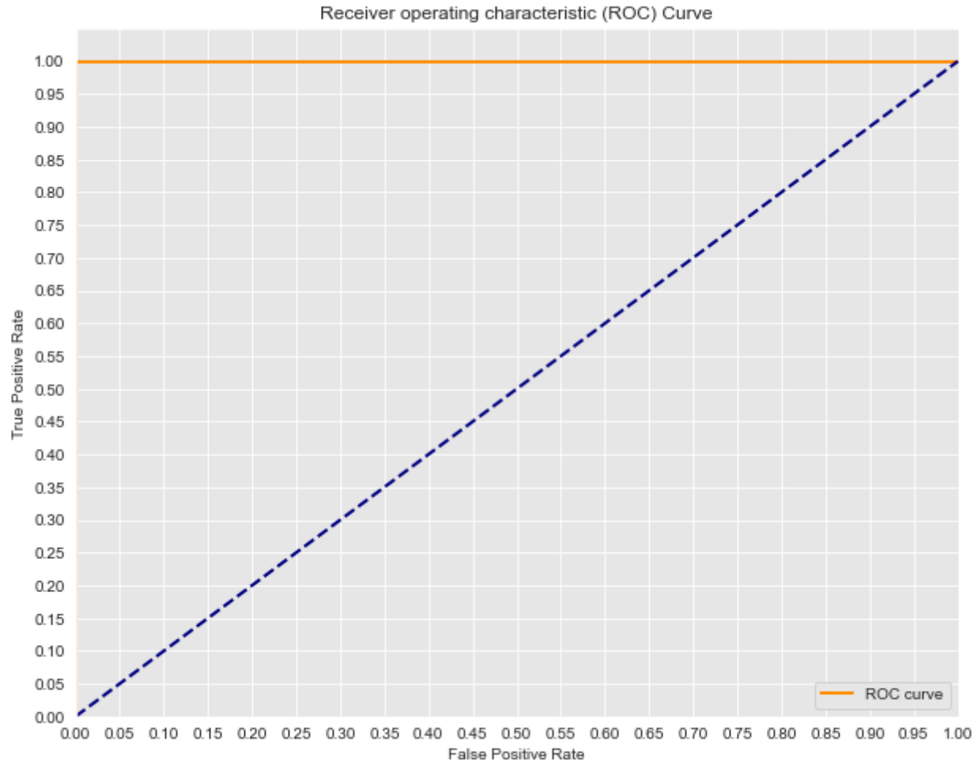





```
Cross Validated ROC AUC score: 1.0
```

```
Class:Y
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Cross Validated ROC AUC score: 1.0
```

All models performed with a cross validated roc auc score of 1. Will test on gradient boost model.

Fit model to test data.

In [64]:
```
gradient_boost.fit(X2_test, y2_test)
```

Out[64]:
```
GradientBoostingClassifier()
```

Make predictions.

In [65]:
```
y2_hat_test_gb = gradient_boost.predict(X2_test)
```

All predictions were classified correctly.

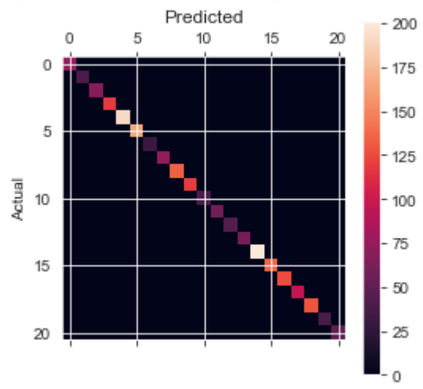
In [66]:
```
con_mat(y2_test,y2_hat_test_gb)
```

```
Confusion Matrix
----------------
     0   1   2    3    4    5   6   7    8    9   ...  11  12  13   14   15  \
0   76   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
1    0  40   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
2    0   0  68    0    0    0   0   0    0    0  ...   0   0   0    0    0
3    0   0   0  118    0    0   0   0    0    0  ...   0   0   0    0    0
4    0   0   0    0  192    0   0   0    0    0  ...   0   0   0    0    0
5    0   0   0    0    0  167   0   0    0    0  ...   0   0   0    0    0
6    0   0   0    0    0    0  31   0    0    0  ...   0   0   0    0    0
7    0   0   0    0    0    0   0  73    0    0  ...   0   0   0    0    0
8    0   0   0    0    0    0   0   0  135    0  ...   0   0   0    0    0
```

```
9    0   0   0    0    0    0   0   0    0  120  ...   0   0   0    0    0
10   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
11   0   0   0    0    0    0   0   0    0    0  ...  57   0   0    0    0
12   0   0   0    0    0    0   0   0    0    0  ...   0  44   0    0    0
13   0   0   0    0    0    0   0   0    0    0  ...   0   0  61    0    0
14   0   0   0    0    0    0   0   0    0    0  ...   0   0   0  201    0
15   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0  136
16   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
17   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
18   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
19   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0
20   0   0   0    0    0    0   0   0    0    0  ...   0   0   0    0    0

      16  17   18  19  20
0      0   0    0   0   0
1      0   0    0   0   0
2      0   0    0   0   0
3      0   0    0   0   0
4      0   0    0   0   0
5      0   0    0   0   0
6      0   0    0   0   0
7      0   0    0   0   0
8      0   0    0   0   0
9      0   0    0   0   0
10     0   0    0   0   0
11     0   0    0   0   0
12     0   0    0   0   0
13     0   0    0   0   0
14     0   0    0   0   0
15     0   0    0   0   0
16   126   0    0   0   0
17     0  97    0   0   0
18     0   0  130   0   0
19     0   0    0  40   0
20     0   0    0   0  49

[21 rows x 21 columns]
```



Seperate actual and predicted values into each class for metrics.

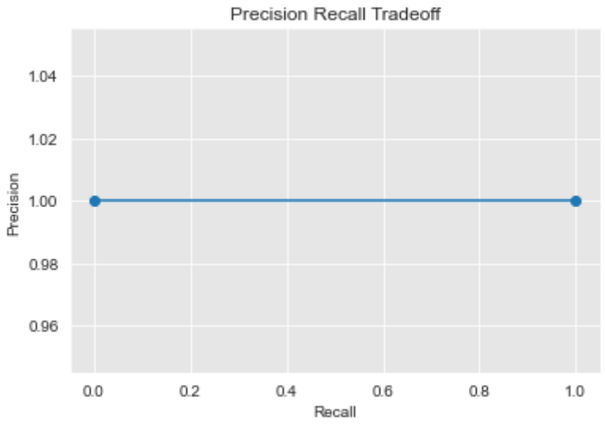
In [67]:
```
actual_class0=y2_test==0
actual_class1=y2_test==1
actual_class2=y2_test==2
actual_class3=y2_test==3
actual_class4=y2_test==4
actual_class5=y2_test==5
actual_class6=y2_test==6
```

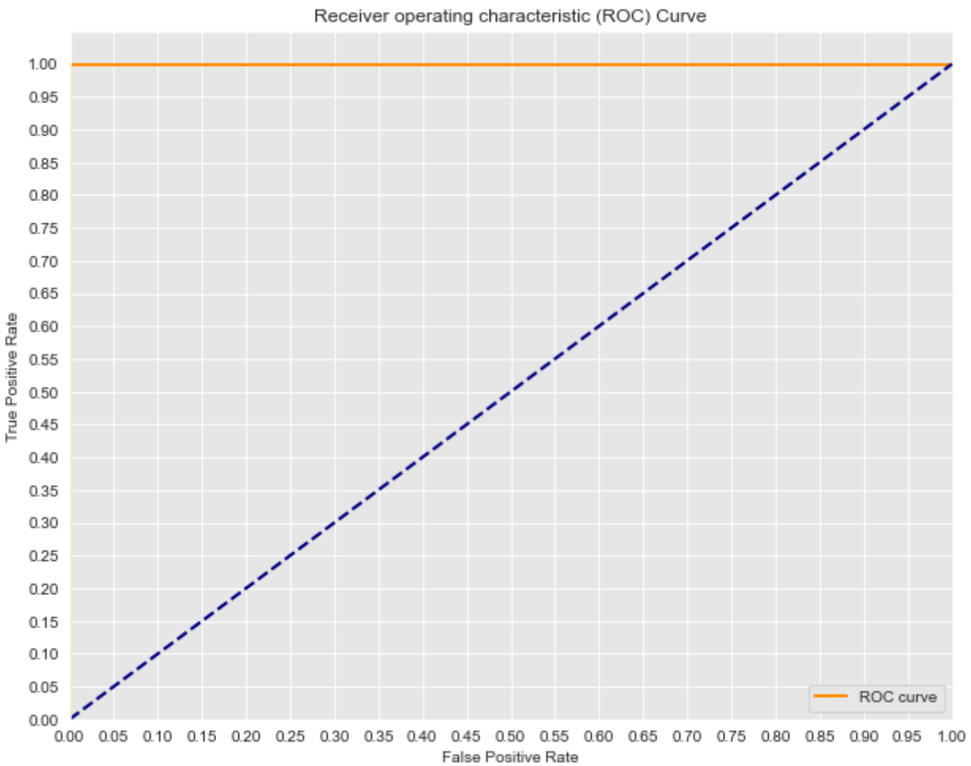
```
actual_class7=y2_test==7
actual_class8=y2_test==8
actual_class9=y2_test==9
actual_class10=y2_test==10
actual_class11=y2_test==11
actual_class12=y2_test==12
actual_class13=y2_test==13
actual_class14=y2_test==14
actual_class15=y2_test==15
actual_class16=y2_test==16
actual_class17=y2_test==17
actual_class18=y2_test==18
actual_class19=y2_test==19
actual_class20=y2_test==20
predictions_class0=y2_hat_test_gb==0
predictions_class1=y2_hat_test_gb==1
predictions_class2=y2_hat_test_gb==2
predictions_class3=y2_hat_test_gb==3
predictions_class4=y2_hat_test_gb==4
predictions_class5=y2_hat_test_gb==5
predictions_class6=y2_hat_test_gb==6
predictions_class7=y2_hat_test_gb==7
predictions_class8=y2_hat_test_gb==8
predictions_class9=y2_hat_test_gb==9
predictions_class10=y2_hat_test_gb==10
predictions_class11=y2_hat_test_gb==11
predictions_class12=y2_hat_test_gb==12
predictions_class13=y2_hat_test_gb==13
predictions_class14=y2_hat_test_gb==14
predictions_class15=y2_hat_test_gb==15
predictions_class16=y2_hat_test_gb==16
predictions_class17=y2_hat_test_gb==17
predictions_class18=y2_hat_test_gb==18
predictions_class19=y2_hat_test_gb==19
predictions_class20=y2_hat_test_gb==20
a=[actual_class0,actual_class1,actual_class2,actual_class3,actual_class4,actual_class5,actual_class6,actual_class7,
   actual_class8,actual_class9,actual_class10,actual_class11,actual_class12,actual_class13,actual_class14,actual_class15
  ,actual_class16,actual_class17,actual_class18,actual_class19,actual_class20]
p=[predictions_class0,predictions_class1,predictions_class2,predictions_class3,predictions_class4,predictions_class5,predictions_class6
  ,predictions_class7,predictions_class8,predictions_class9,predictions_class10,predictions_class11,predictions_class12
  ,predictions_class13,predictions_class14,predictions_class15,predictions_class16,predictions_class17,predictions_class18
  ,predictions_class19,predictions_class20]
```

In [68]:

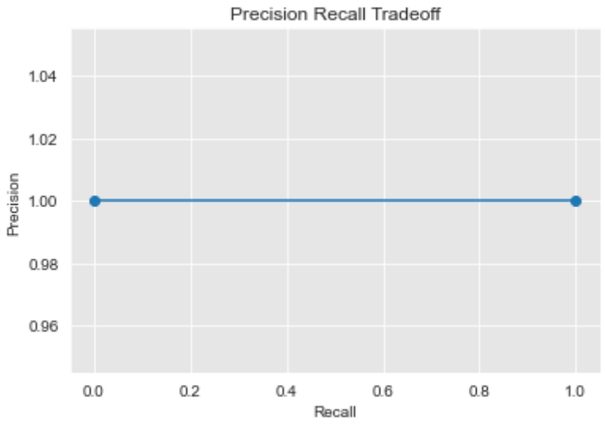
```
multiclass(gradient_boost,X2_test,a,p,translation_df2['Amino_Acids_copy'],'test')
```

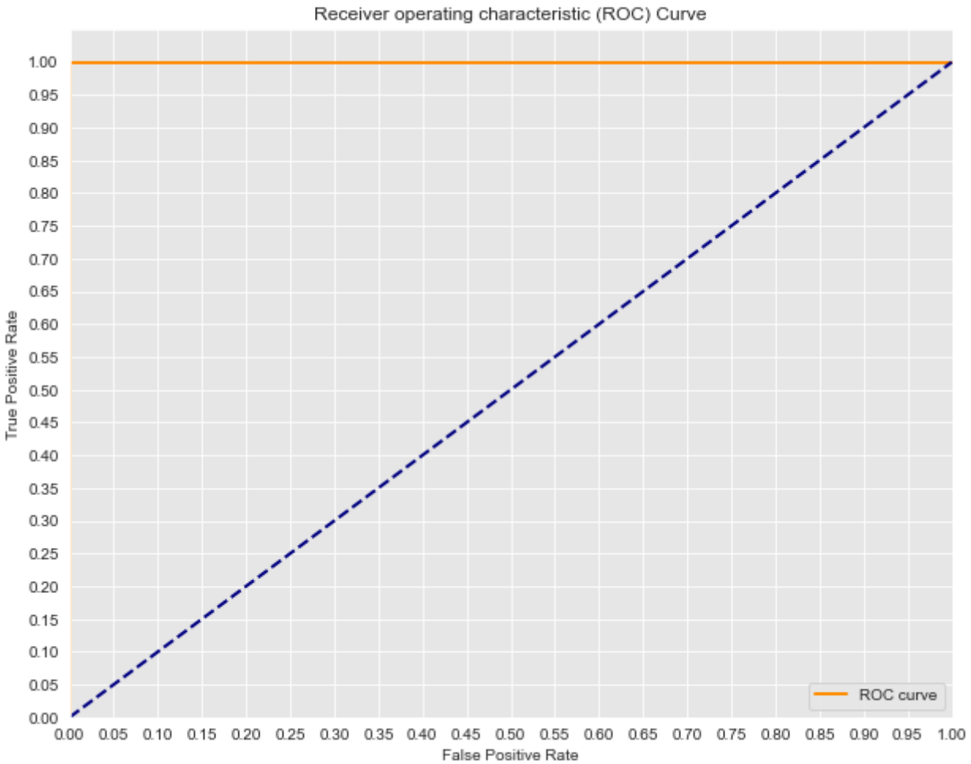
```
Class:A
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



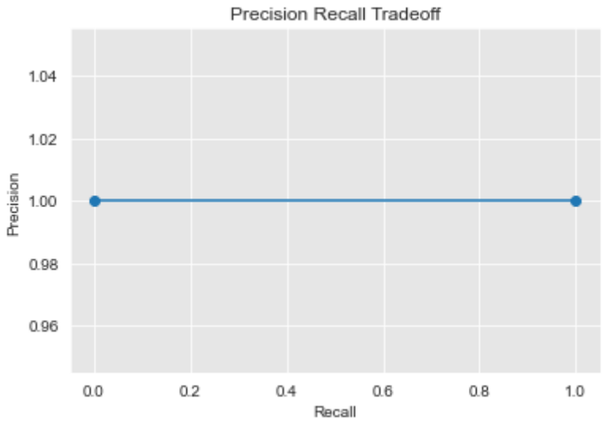


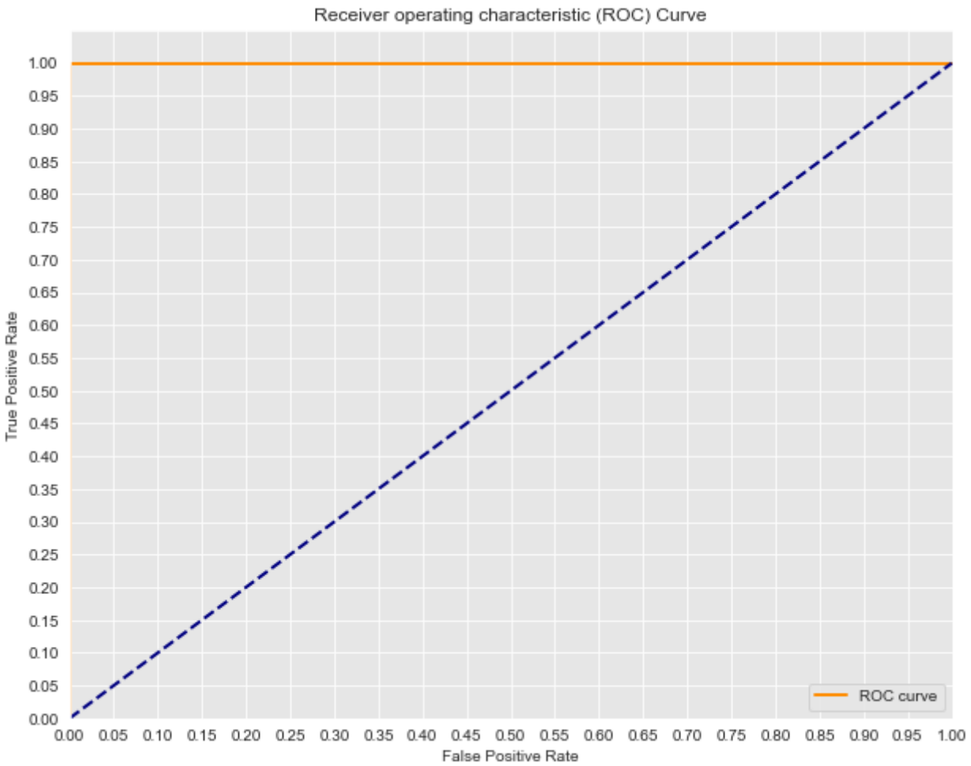

```
Class:C
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



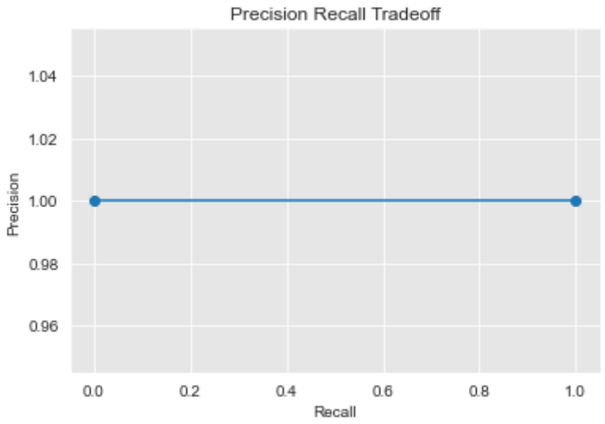


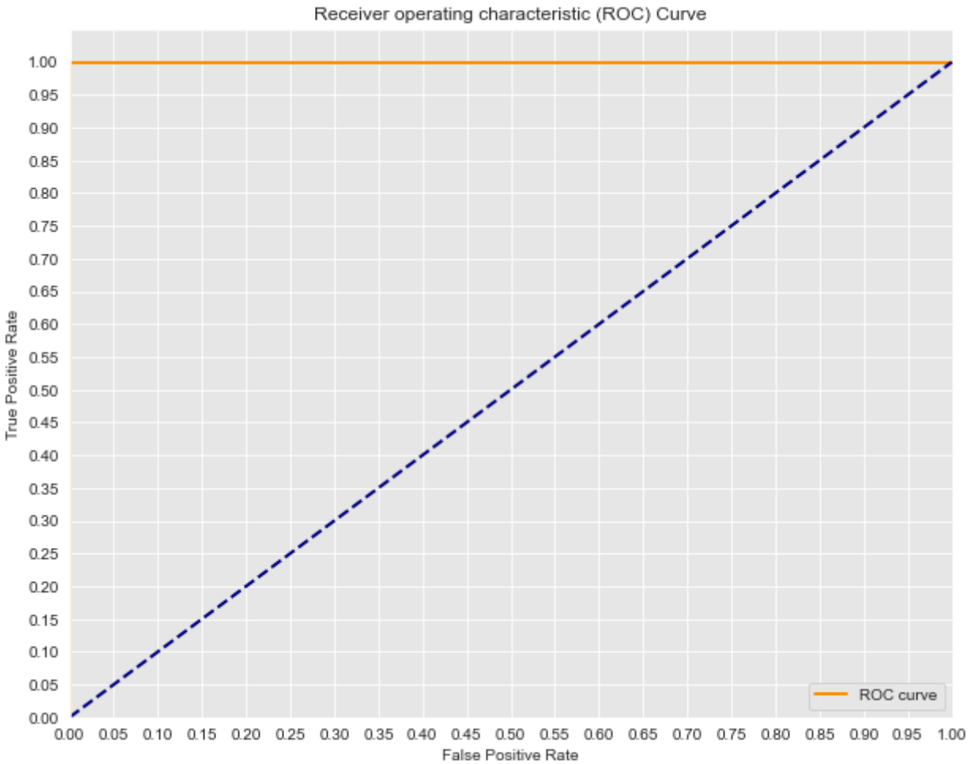

```
Class:D
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



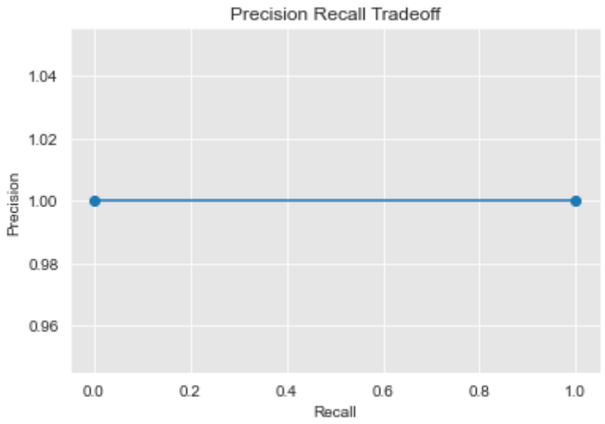


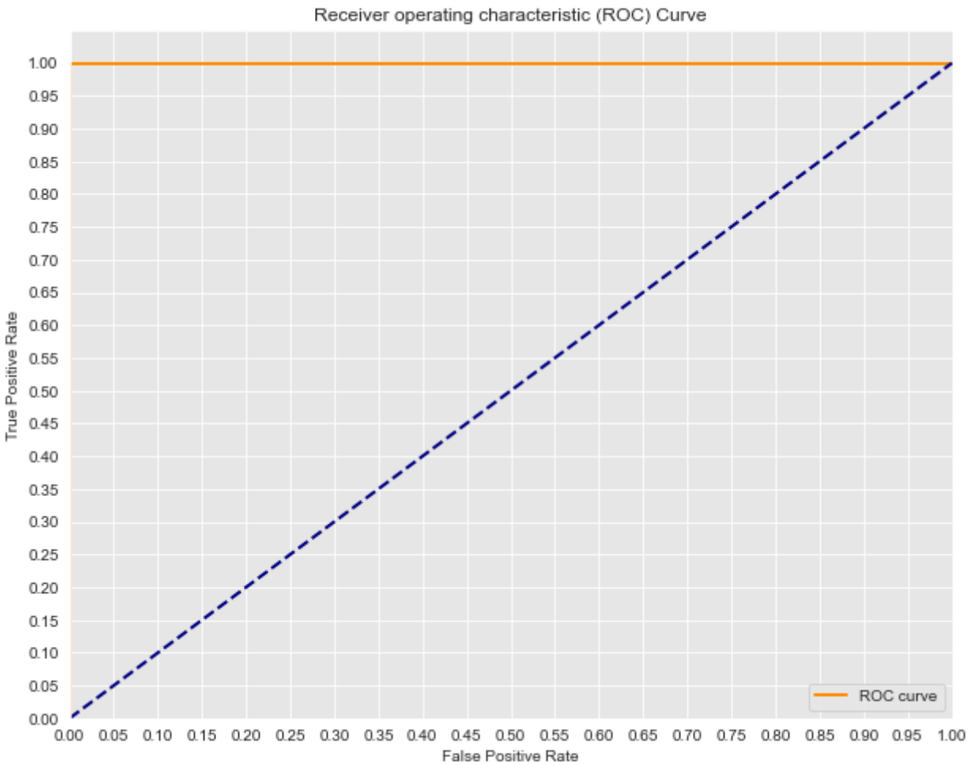

```
Class:E
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



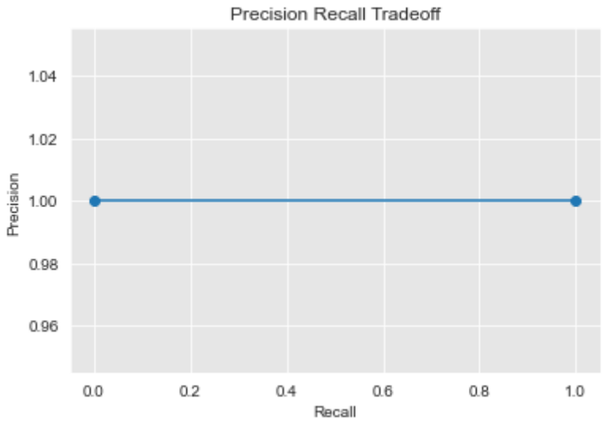


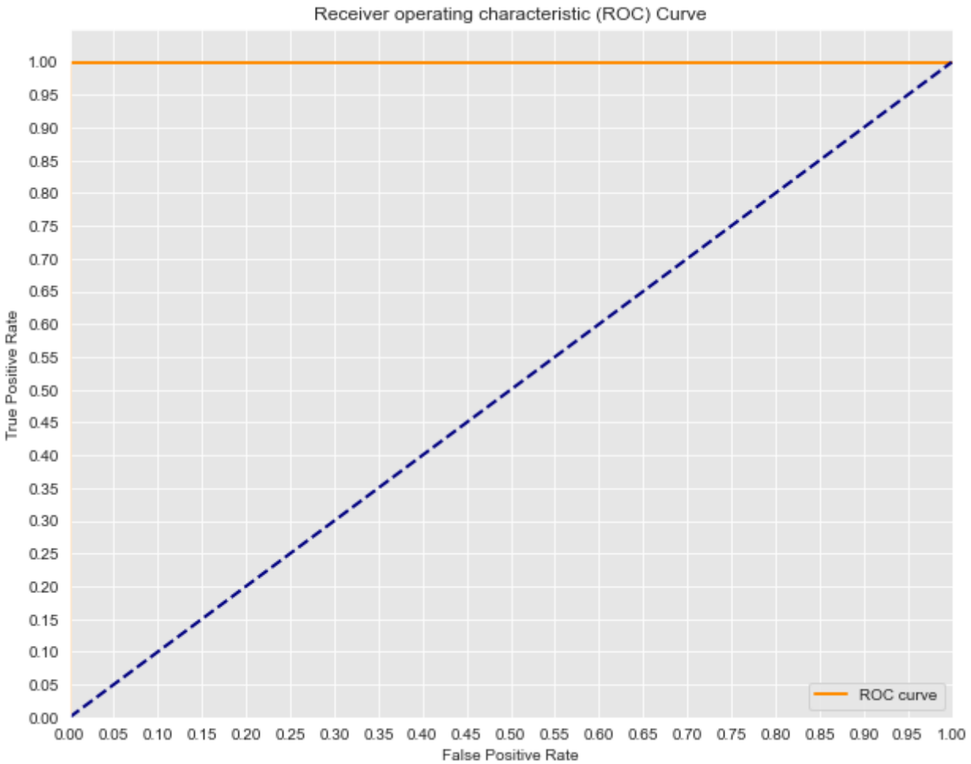

```
Class:F
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



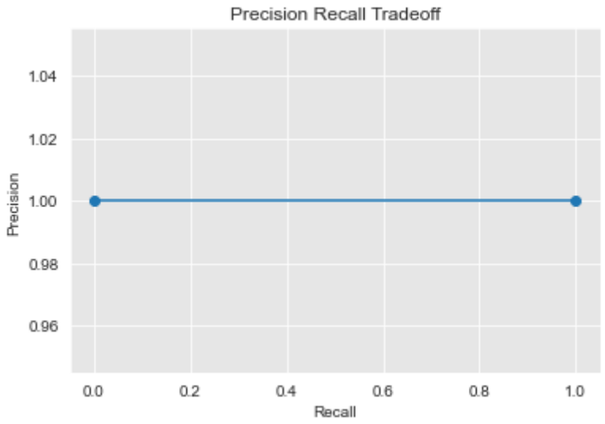


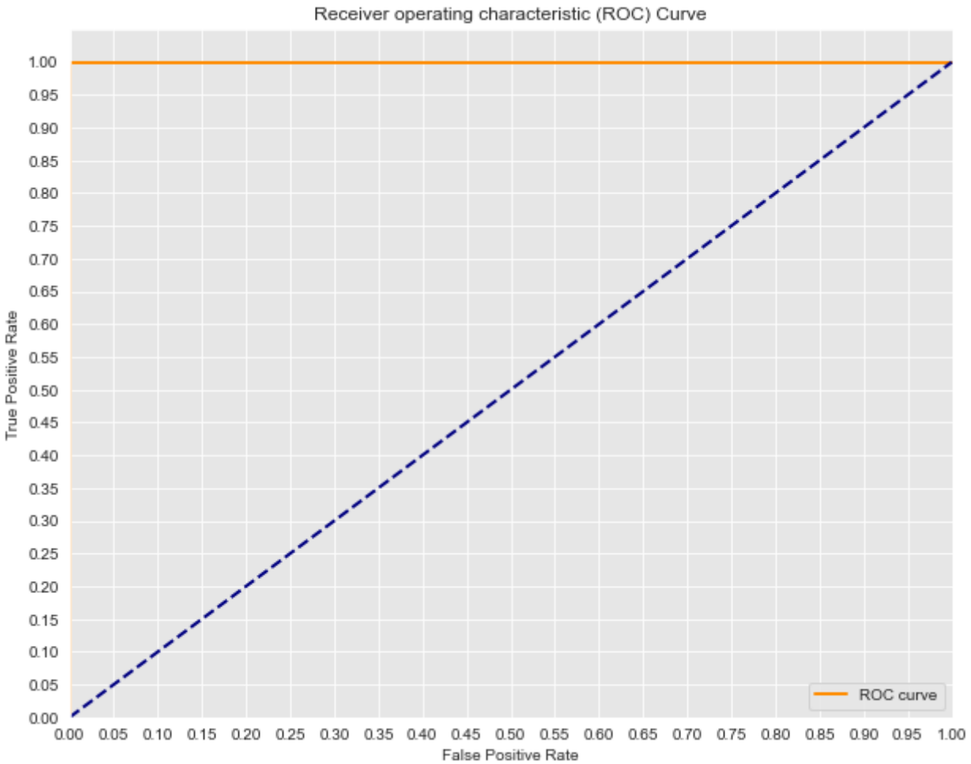

```
Class:G
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



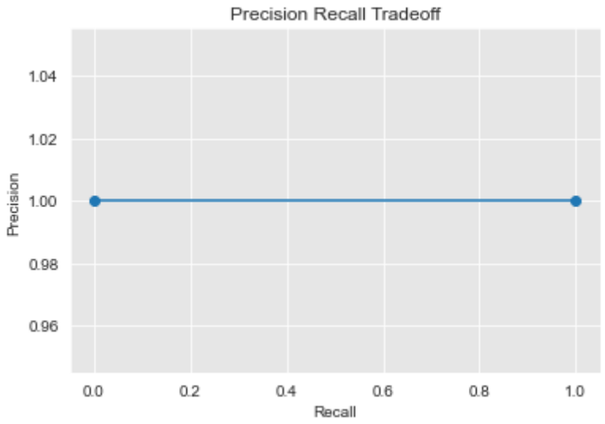


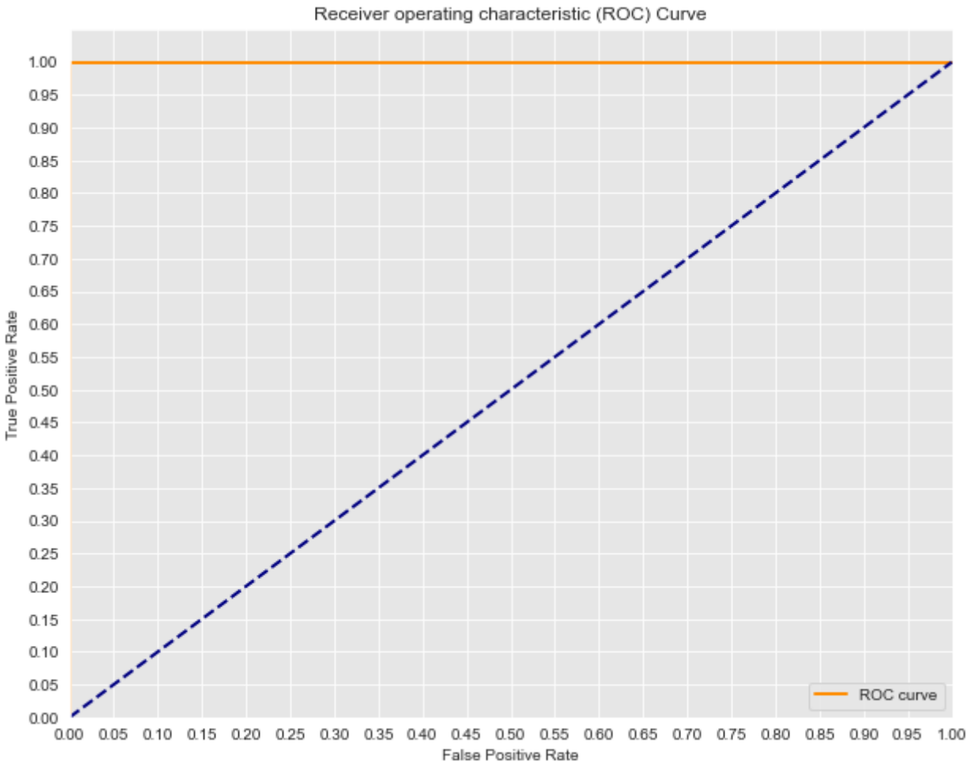

```
Class:H
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



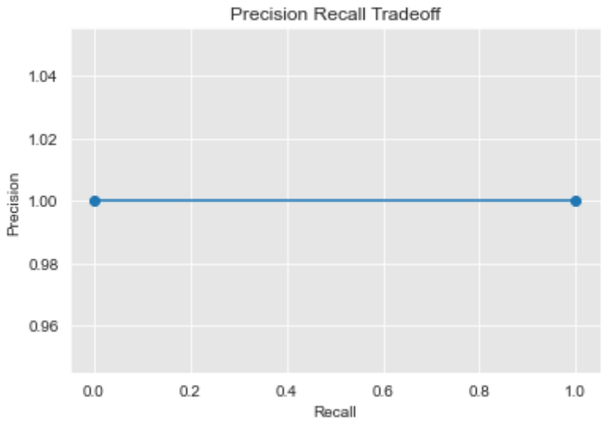


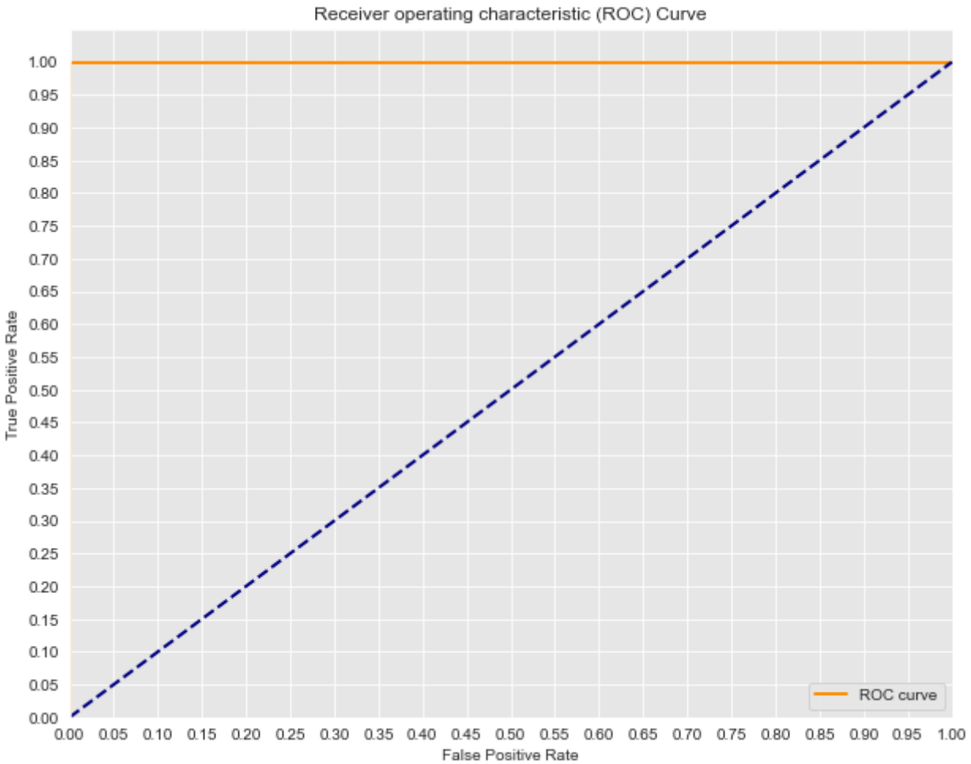

```
Class:I
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



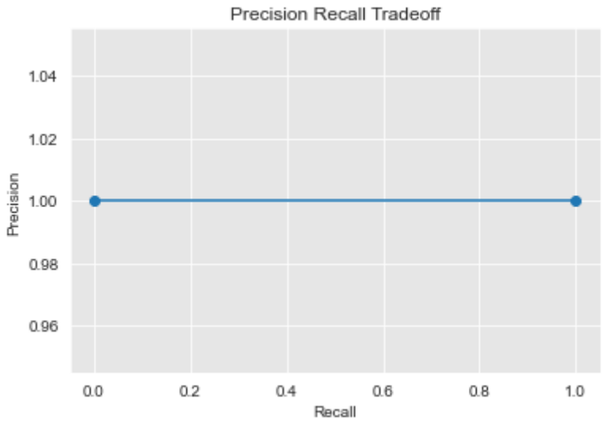


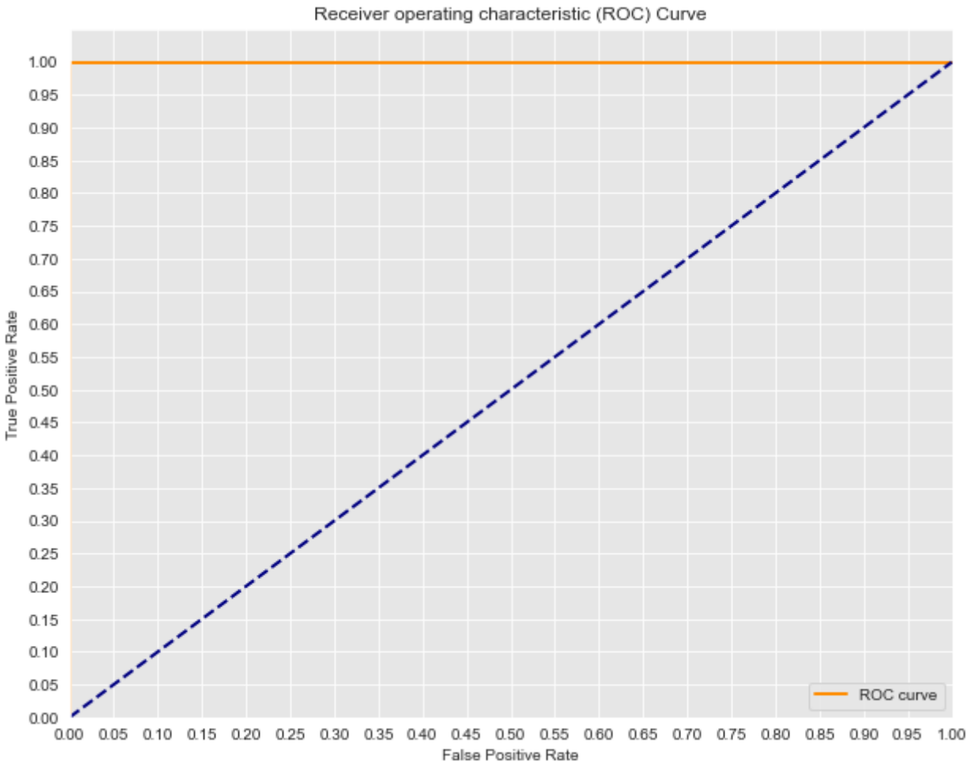

```
Class:K
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



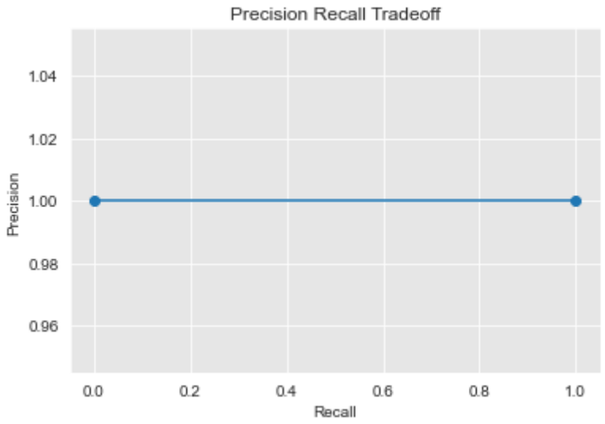


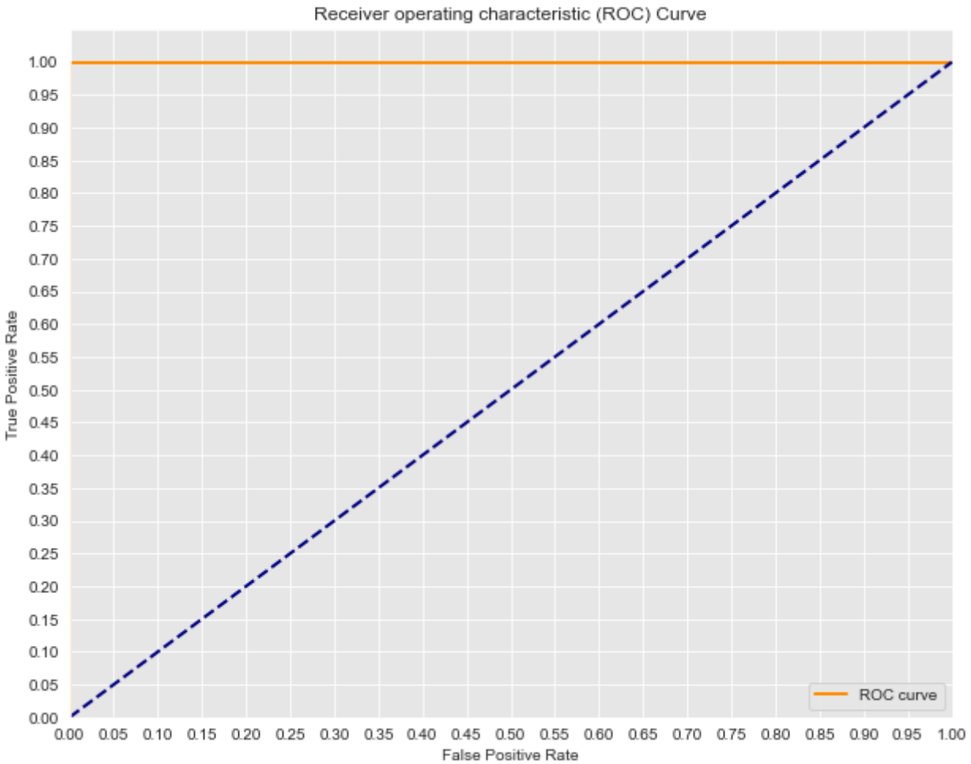

```
Class:L
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



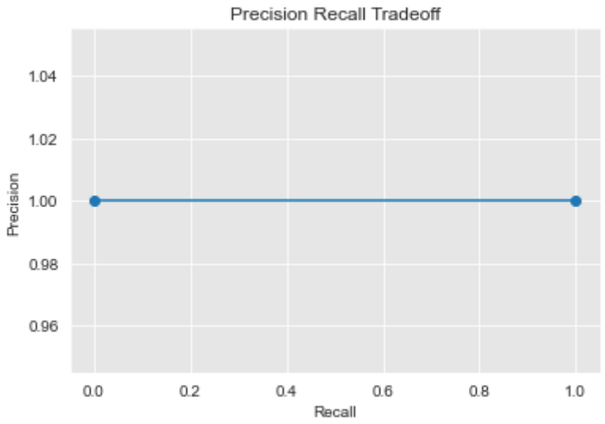


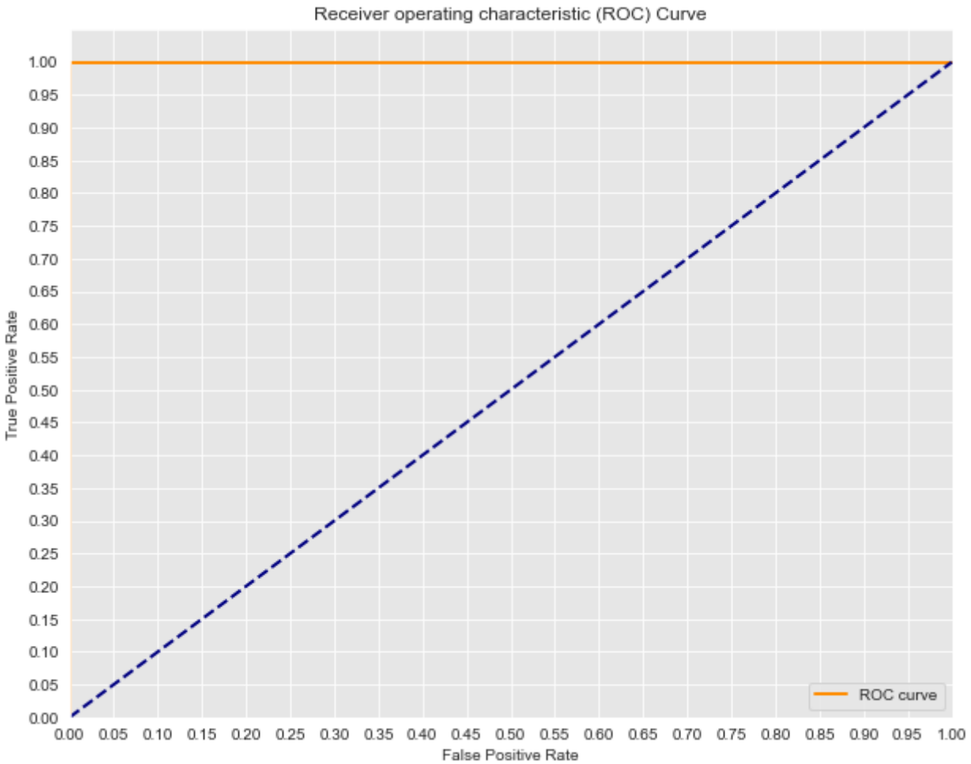

```
Class:M
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



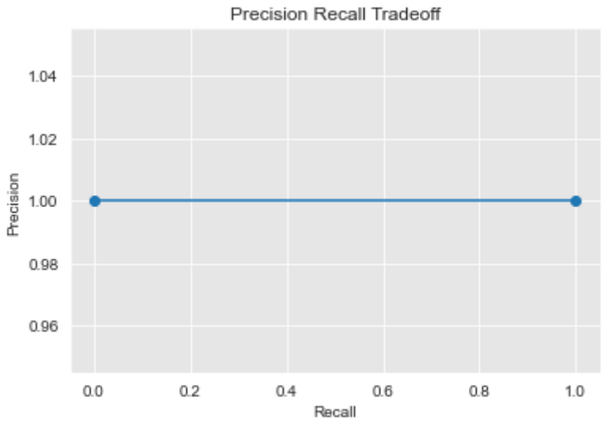


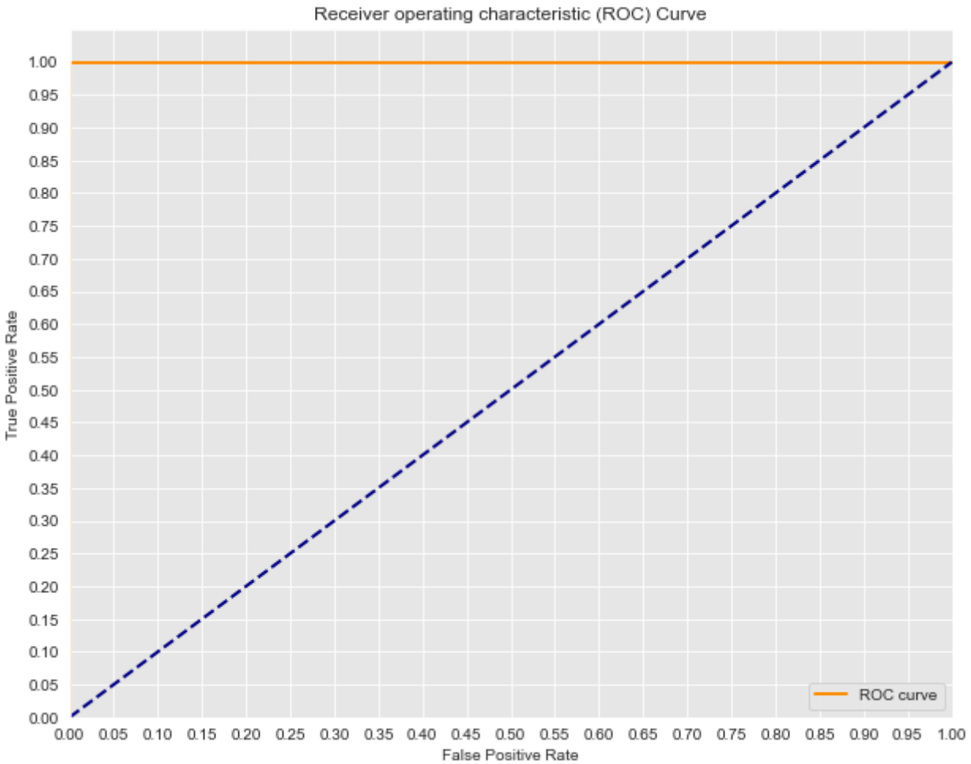

```
Class:N
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



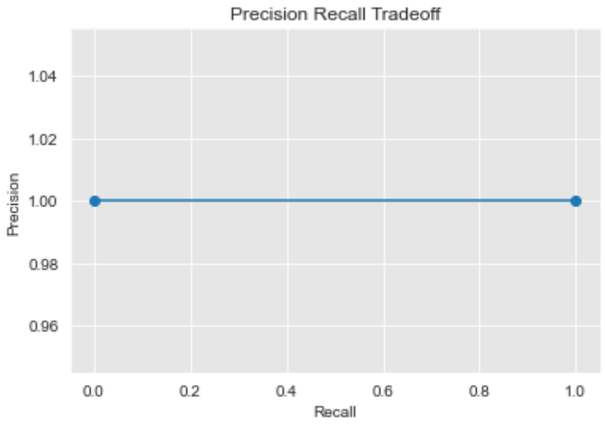


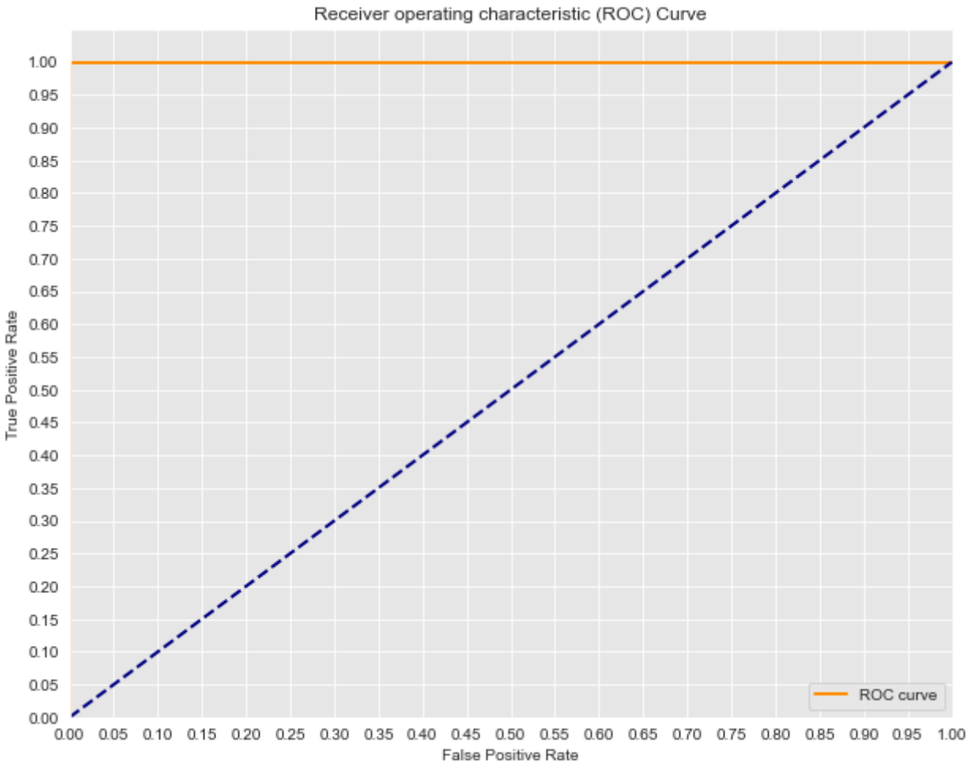

```
Class:P
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



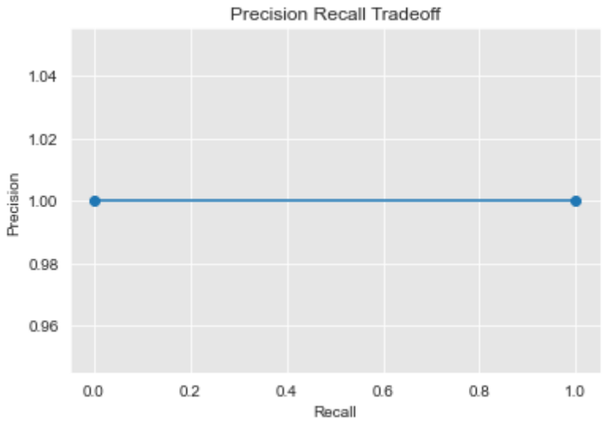


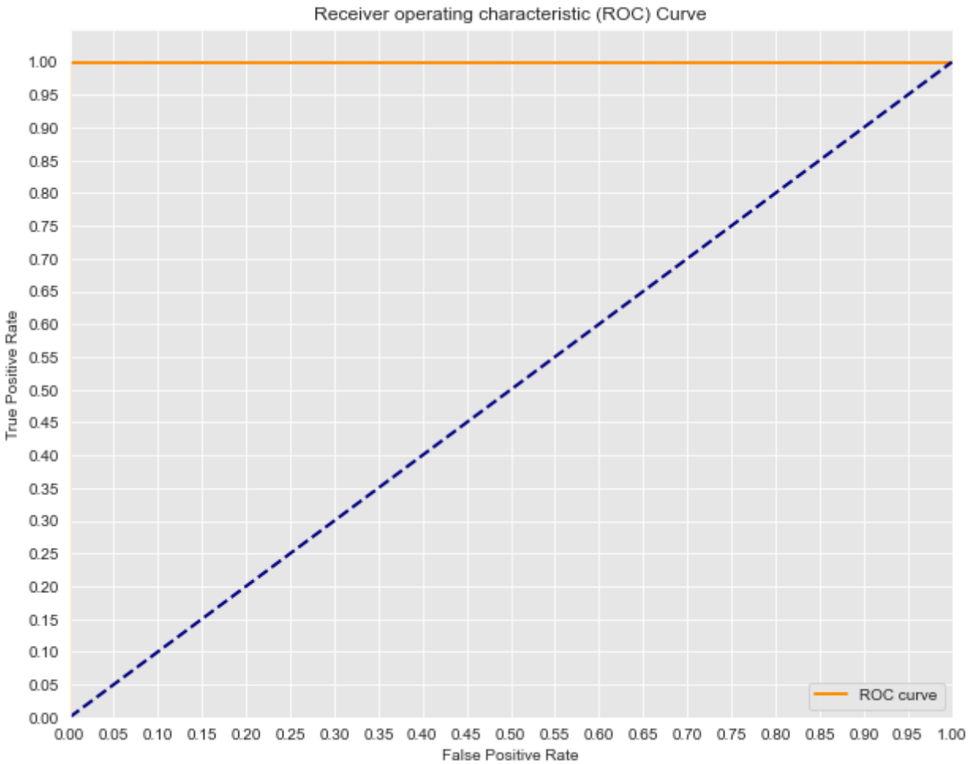

```
Class:Q
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



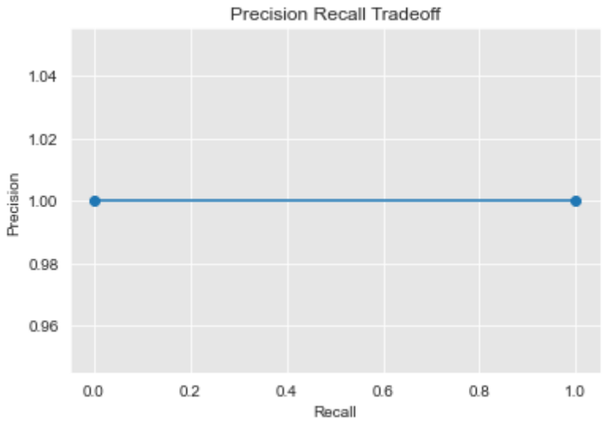


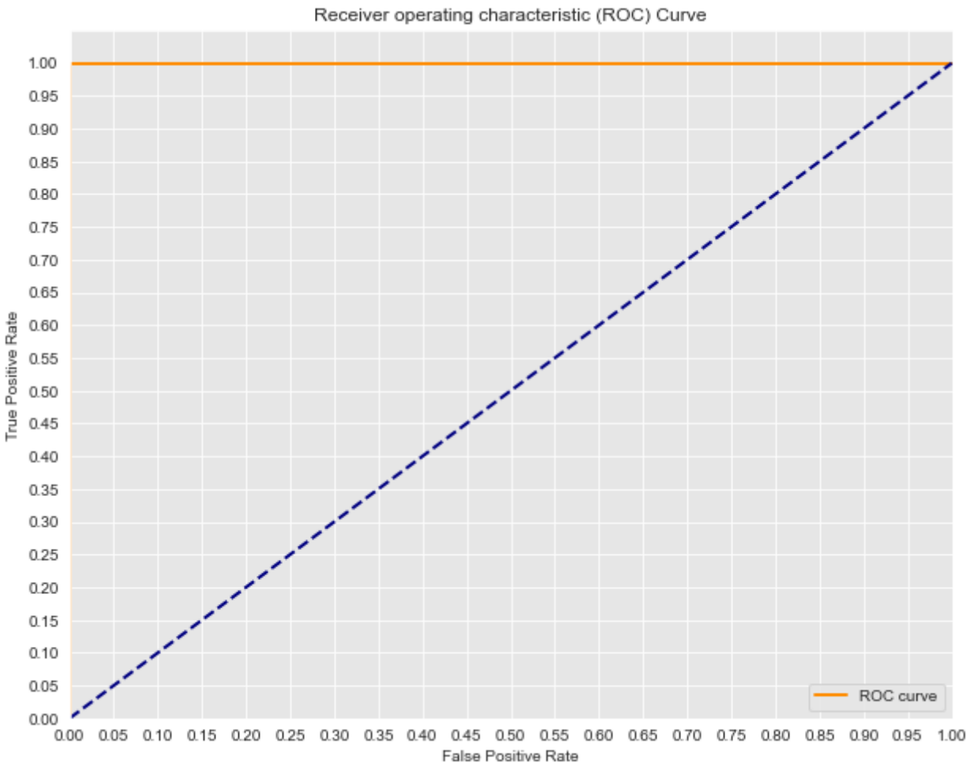

```
Class:R
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



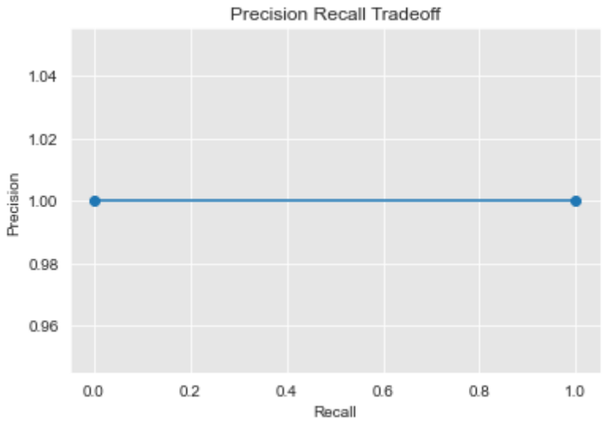


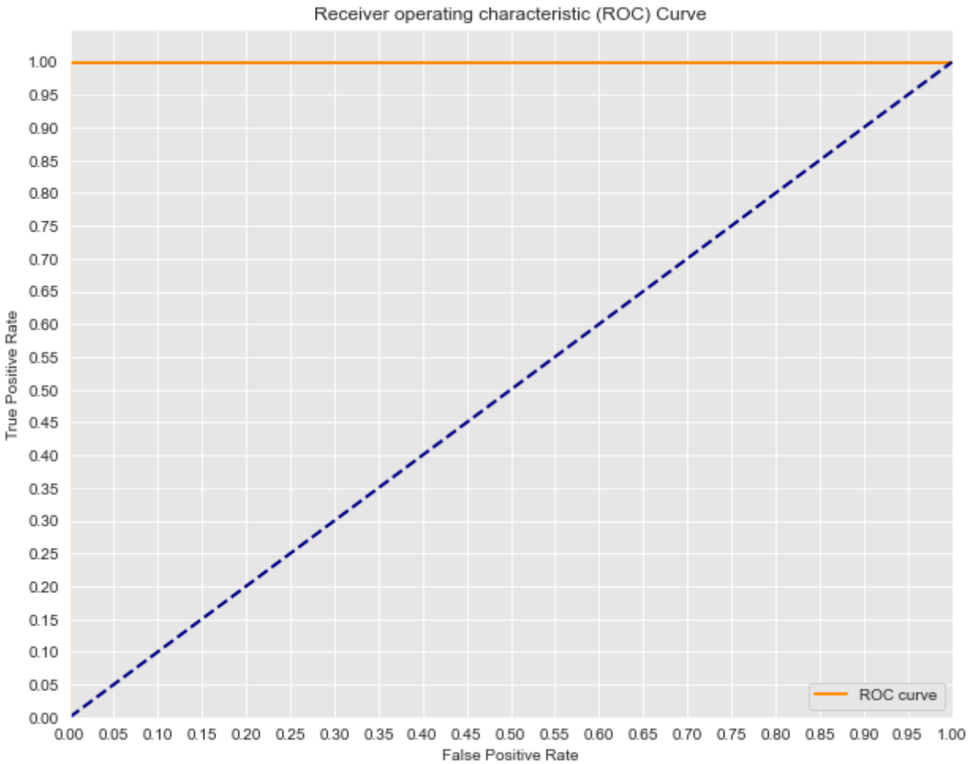

```
Class:S
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



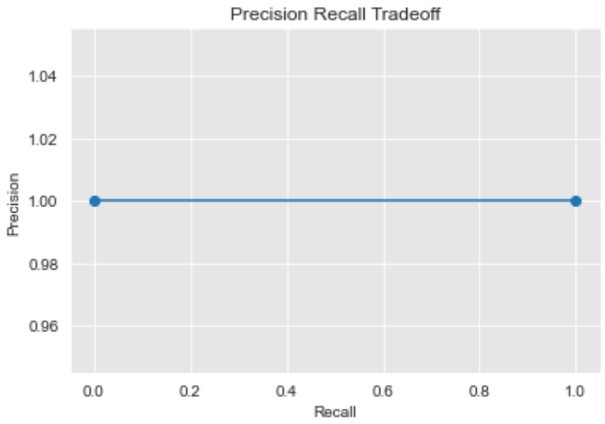


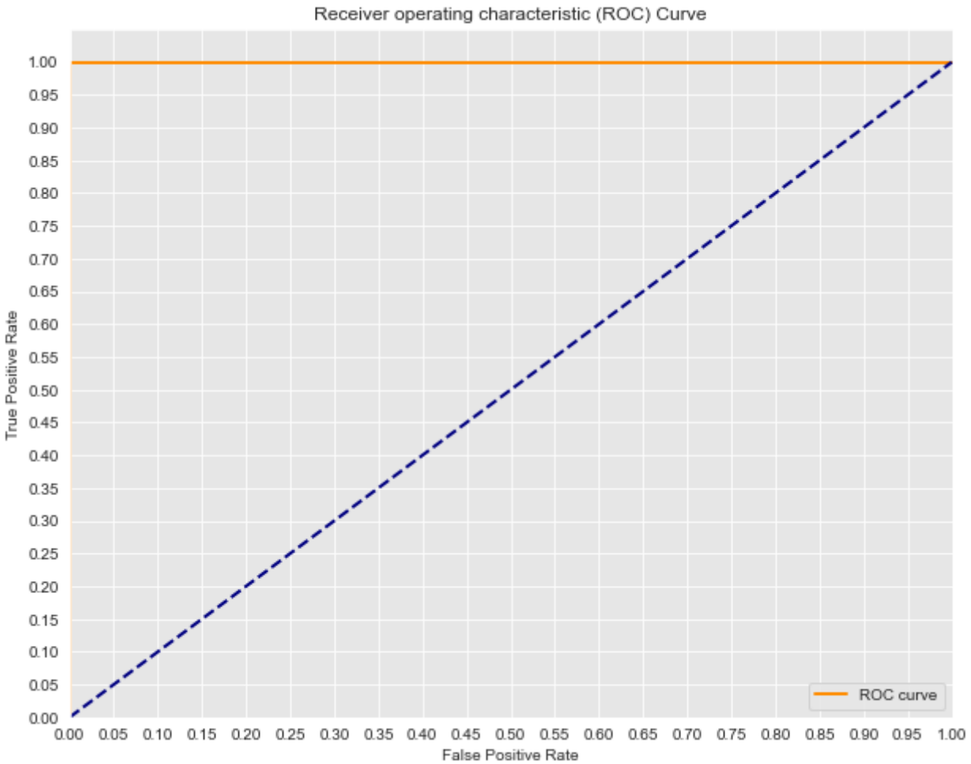

```
Class:Stop
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



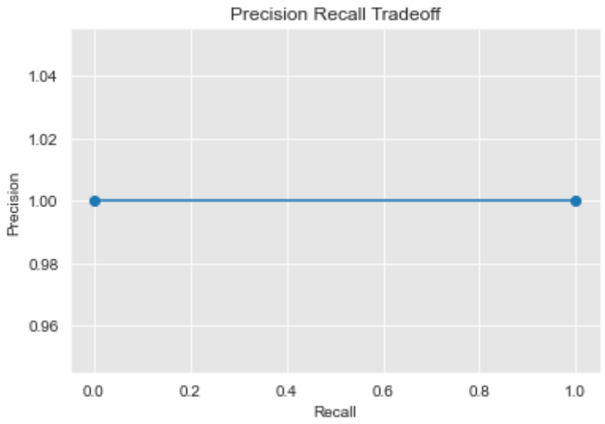


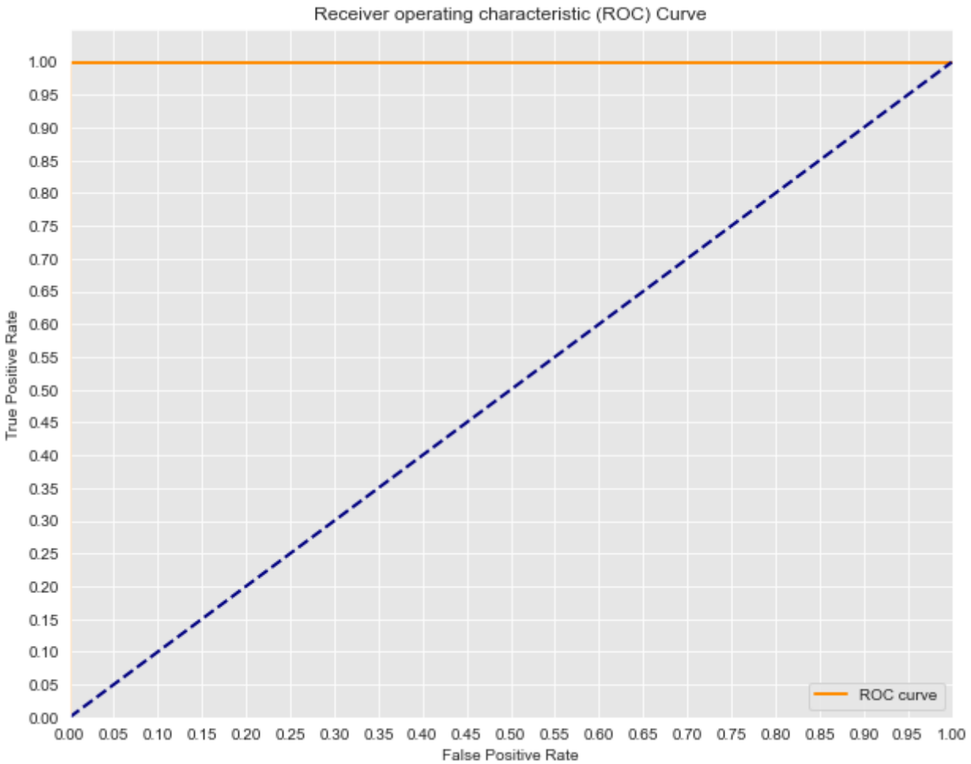

```
Class:T
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



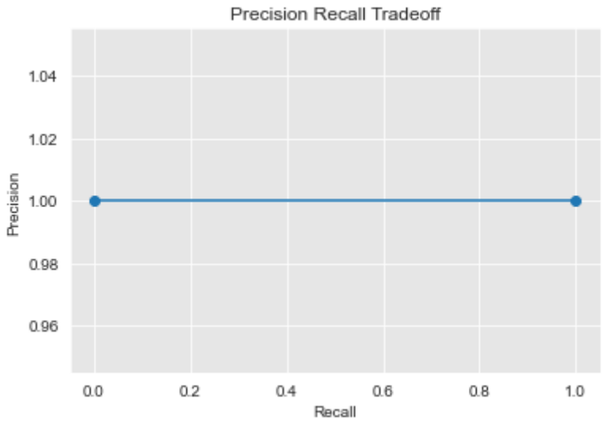


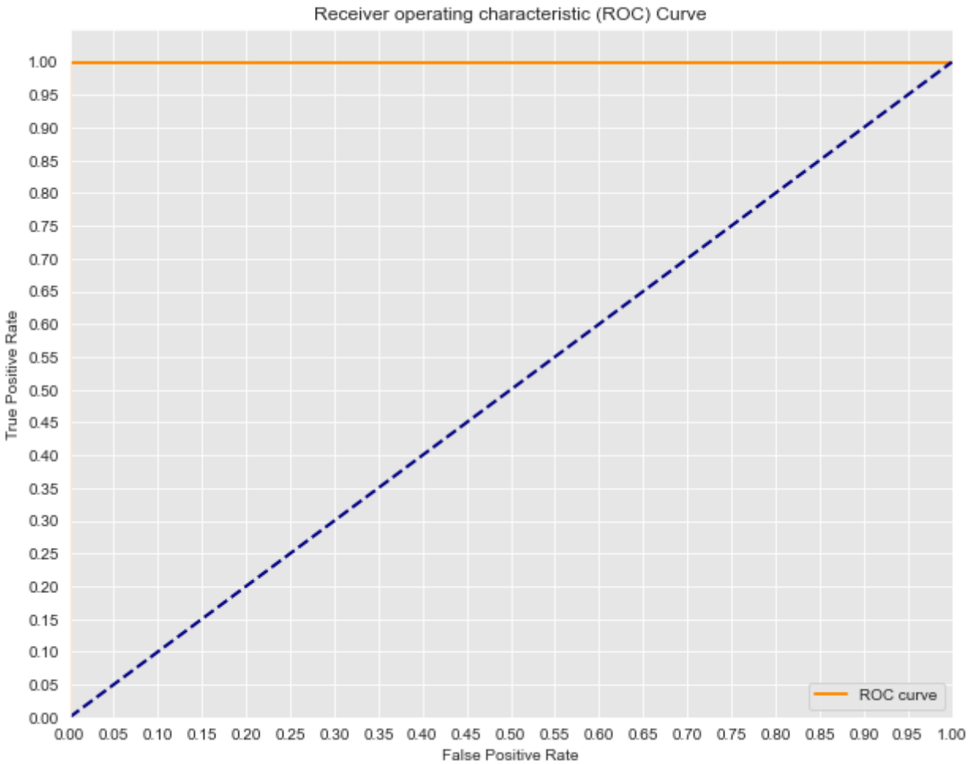

```
Class:V
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```



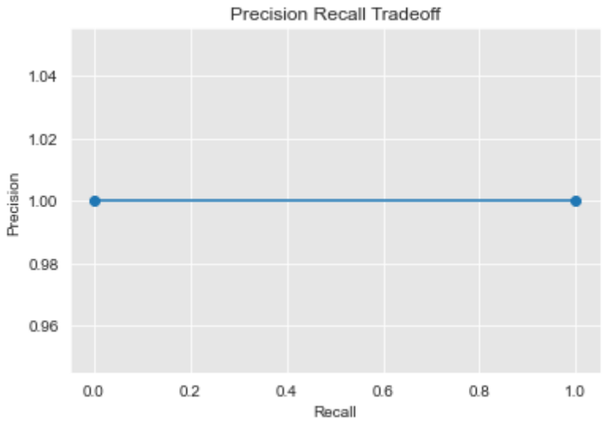


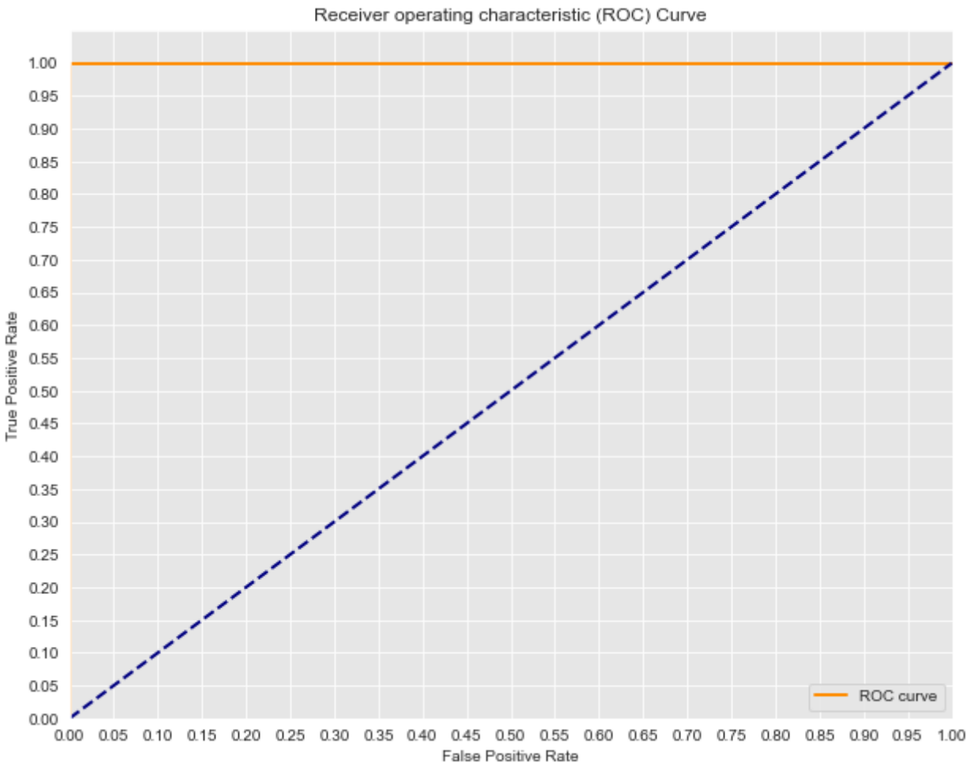

```
Class:W
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```






```
Class:Y
Precision Score: 1.0
Recall Score: 1.0
F1 Score: 1.0
Accuracy Score: 1.0
Specificity Score: 1.0
AUC: 1.0
```





The following is an rnn that is under development.

Data Cleaning

Adds a lagged RNA nucleotides column for nucleotide sequence prediction.

In [9]:
```
translation_df1['mRNA_Codons_lagged']=translation_df1['mRNA_Codons'].shift(-1)
translation_df1
```

Out[9]:

	mRNA_Codons	mRNA_Codons_copy	Anticodons	mRNA_Codons_lagged

	mRNA_Codons	mRNA_Codons_copy	Anticodons	mRNA_Codons_lagged
0	0	A	3	1.0
1	1	C	2	3.0
2	3	U	0	3.0
3	3	U	0	3.0
4	3	U	0	2.0
...	...	...	...	...
27464	3	U	0	2.0
27465	2	G	1	0.0
27466	0	A	3	3.0
27467	3	U	0	0.0
27468	0	A	3	NaN

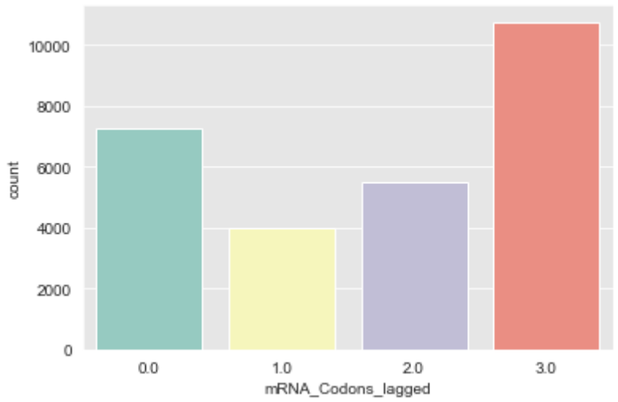
27469 rows × 4 columns

In [10]:
```
translation_df1['mRNA_Codons_lagged']=translation_df1['mRNA_Codons_lagged'].fillna(0)
```

Data Exploration

In [158…
```
sns.countplot(translation_df1['mRNA_Codons_lagged'], palette='Set3')
```

Out[158…
```
<AxesSubplot:xlabel='mRNA_Codons_lagged', ylabel='count'>
```



Feature Engineering

In [282…
```
X3=translation_df1['mRNA_Codons']
y3=translation_df1['mRNA_Codons_lagged']
```

In [239…
```
from sklearn.preprocessing import MinMaxScaler
# X3=X3.values.reshape(-1, 1)
```

```
# scaler = MinMaxScaler()
# data_set = scaler.fit_transform(X3)
```

In [283…
```
X3_train, X3_test, y3_train, y3_test = train_test_split(X3, y3, test_size=0.20, random_state=10)
```

In [284…
```
X3_train=X3_train.values.reshape(21975,1,1)
```

XOR

In [216…
```
X3_train=X3_train[:20000]
y3_train=y3_train[:20000]
```

In [217…
```
X3_train=X3_train.values.reshape(2000,10,1)
```

In [218…
```
y3_train=y3_train.values.reshape(2000,10,1)
```

In [285…
```
X3_train = np.asarray(X3_train).astype('float32')
y3_train = np.asarray(y3_train).astype('float32')
```

Deep learning Modeling

In [235…
```
from tensorflow.keras.models import Sequential

from tensorflow.keras.layers import Dense

from tensorflow.keras.layers import LSTM

from tensorflow.keras.layers import Dropout
```

In [204…
```
from keras.optimizers import Adam
adam=Adam(learning_rate=1e-05,
    beta_1=0.9,
    beta_2=0.999,
    epsilon=1e-07)
```

In [286…
```
rnn = Sequential()
rnn.add(LSTM(units = 50, activation='tanh', return_sequences = True, input_shape = (1,1)))
rnn.add(Dropout(0.2))
rnn.add(Dense(units = 1, activation='softmax'))
rnn.compile(optimizer = adam, loss='categorical_crossentropy', metrics=["accuracy"])
rnn.summary()
```

```
Model: "sequential_57"
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
lstm_60 (LSTM)               (None, 1, 50)             10400
_________________________________________________________________
dropout_59 (Dropout)         (None, 1, 50)             0
_________________________________________________________________
dense_53 (Dense)             (None, 1, 1)              51
=================================================================
Total params: 10,451
Trainable params: 10,451
```

```
Non-trainable params: 0
_________________________________________________________________
```

In [287…
```
rnn.fit(X3_train, y3_train, epochs = 5, batch_size = 20, verbose=1)
```

```
Epoch 1/5
1099/1099 [==============================] - 2s 2ms/step - loss: 2.0479e-07 - accuracy: 0.1445
Epoch 2/5
1099/1099 [==============================] - 2s 2ms/step - loss: 2.0479e-07 - accuracy: 0.1445
Epoch 3/5
1099/1099 [==============================] - 2s 2ms/step - loss: 2.0479e-07 - accuracy: 0.1445
Epoch 4/5
1099/1099 [==============================] - 2s 2ms/step - loss: 2.0479e-07 - accuracy: 0.1445
Epoch 5/5
1099/1099 [==============================] - 2s 2ms/step - loss: 2.0479e-07 - accuracy: 0.1445
```

Out[287…
```
<tensorflow.python.keras.callbacks.History at 0x7f9c5cd4e2b0>
```

In [288…
```
predictions=rnn.predict(X3_train, verbose=1)
predictions
```

```
687/687 [==============================] - 1s 793us/step
```

Out[288…
```
array([[[1.]],

       [[1.]],

       [[1.]],

       ...,

       [[1.]],

       [[1.]],

       [[1.]]], dtype=float32)
```

In [ ]:
```
scores = model.evaluate(X_test, y_test, batch_size=batch_size, verbose=0)
print("Model Accuracy: %.2f%%" % (scores[1]*100))
```