

```
In [4]: # Load and process the protein sequences from the uploaded file
file_path = "K13_Protein_genes.txt"

# Read the file content
with open(file_path, "r") as file:
    data = file.readlines()
```

```
In [5]: # Prints the entire file as a single string to validate the protein sequence
print("Sequence List for Mutation Alayisis:")
print("".join(data))
print("\n" + "="*50 + "\n")
```

Sequence List for Mutation Alayisis:

>K13\_Target1

MEGEVKVTKANSISNFSMTYDRESGGNSNSDDKGSSSENDNSFMNLTSRKNEKTENNSSLNNSSYGNVKDSLLESIDM  
SVLDSNFDSKKDFLPSNLSTFNNMSKDIGNKYLNLKLLNKKDTITNENNINHNNNNNLTANNITNNLINNMNSPSI  
MNTNKKENFLDAANLINDDGLNNLKFSTVNNVNDTYEKKIETELSDASDFENMVGDLRITFINWLKKTQMNFIKEKDK  
LFKDKELEMERVRLYKELENRKNIIEQKLHDERKLDIDISNGYKQIKKEEEHRKRFDEERLRFQEQIDKIKLVLYLEK  
EKYYQEYKNFENDKKIVDANIATETMIDINVGAIFETSRHTLTQQKDSFIEKLLSGRHHVTRDKQGRIFLDRSELFR  
ILNFLRNPLTIPKDLSESEALLKEAEFYGIKFPLPVLFCIGGFDGVEYLNNSMELLDISQQCWRMCTPISTKKAYFGSA  
VLNNFLYVFGNNYDYKALFETEVYDRLRDWYVSSNLNIPRRNNCGVTSGRIYCIGGYDGSSIIPNVEAYDHRMKAWVE  
VAPLNTPRSSAMCVAFDNKIYVIGGTNGERLNSIEVYEEMNKWEQFPYALLEARSSGAAFNQIYVVGIDNEHNILD  
SVEQYQPFNKRQFLNGVPEKKMNGAATLSDSYIITGGENGEVLNSCHFFSPDTNEWQLGPSLLVPRFGHSVLIANI

>K13\_Target2

MEGEVKVTKANSISNFSMTYDRESGGNSNSDDKGSSSENDNSFMNLTSRKNEKTENNSSLNNSSYGNVKDSLLESIDM  
SVLDSNFDSKKDFLPSNLSTFNNMSKDIGNKYLNLKLLNKKDTITNENNINHNNNNNLTANNITNNLINNMNSPSI  
MNTNKKENFLDAANLINDDGLNNLKFSTVNNVNDTYEKKIETELSDASDFENMVGDLRITFINWLKKTQMNFIKEKDK  
LFKDKELEMERVRLYKELENRKNIIEQKLHDERKLDIDISNGYKQIKKEEEHRKRFDEERLRFQEQIDKIKLVLYLEK  
EKYYQEYKNFENDKKIVDANIATETMIDINVGAIFETSRHTLTQQKDSFIEKLLSGRHHVTRDKQGRIFLDRSELFR  
ILNFLRNPLTIPKDLSESEALLKEAEFYGIKFPLPVLFCIGGFDGVEYLNNSMELLDISQQCWRMCTPMSTKKAYFGSA  
VLNNFLYVFGNNYDYKALFETEVYDRLRDWYVSSNLNIPRRNNCGVTSGRIYCIGGYDGSSIIPNVEAYDHRMKAWVE  
VAPLNTPRSSAMCVAFDNKIYVIGGTNGERLNSIEVYEEMNKWEQFPYALLEARSSGAAFNQIYVVGIDNEHNILD  
SVEQYQPFNKRQFLNGVPEKKMNGAATLSDSYIITGGENGEVLNSCHFFSPDTNEWQLGPSLLVPRFGHSVLIANI

>K13\_Target3

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MNTNKKENFLDAANLINDDGLNNLKFSTVNNVNDTYEKKIETELSDASDFENMVGDLRITFINWLKKTQMNFIKEKDK  
LFKDKELEMERVRLYKELENRKNIIEQKLHDERKLDIDISNGYKQIKKEEEHRKRFDEERLRFQEQIDKIKLVLYLEK  
EKYYQEYKNFENDKKIVDANIATETMIDINVGAIFETSRHTLTQQKDSFIEKLLSGRHHVTRDKQGRIFLDRSELFR  
ILNFLRNPLTIPKDLSESEALLKEAEFYGIKFPLPVLFCIGGFDGVEYLNNSMELLDISQQCWRMCTPMSTKKAYFGSA  
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MNTNKKENFLDAANLINDDGLNNLKFSTVNNVNDTYEKKIETELSDASDFENMVGDLRITFINWLKKTQMNFIKEKDK  
LFKDKELEMERVRLYKELENRKNIIEQKLHDERKLDIDISNGYKQIKKEEEHRKRFDEERLRFQEQIDKIKLVLYLEK  
EKYYQEYKNFENDKKIVDANIATETMIDINVGAIFETSRHTLTQQKDSFIEKLLSGRHHVTRDKQGRIFLDRSELFR  
ILNFLRNPLTIPKDLSESEALLKEAEFYGIKFPLPVLFCIGGFDGVEYLNNSMELLDISQQCWRMCTPMSTKKAYFGSA  
VLNNFLYVFGNNYDYKALFETEVYDRLRDWYVSSNLNIPRRNNCGVTSGRIYCIGGYDGSSIIPNVEAYDHRMKAWVE  
VAPLNTPRSSAMCVAFDNKIYVIGGTNGERLNSIEVYEEMNKWEQFPYALLEARSSGAAFNQIYVVGIDNEHNILD  
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>K13\_Target5

MEGEVKVTKANSISNFSMTYDRESGGNSNSDDKGSSSENDNSFMNLTSRKNEKTENNSSLNNSSYGNVKDSLLESIDM  
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VLNNFLYVFGNNYDYKALFETEVYDRLRDWYVSSNLNIPRRNNCGVTSGRIYCIGGYDGSSIIPNVEAYDHRMKAWVE  
VAPLNTPRSSAMCVAFDNKIYVIGGTNGERLNSIEVYEEMNKWEQFPYALLEARSSGAAFNQIYVVGIDNEHNILD  
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>K13\_Target6

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MNTNKKENFLDAANLINDDGLNNLKFSTVNNVNDTYEKKIETELSDASDFENMVGDLRITFINWLKKTQMNFIKEKDK

LFKDKKELEMERVRLYKELENRKNIEEQLHDERKKLDIDISNGYKQIKKEEHRKRFDEERLRFQEI  
DNLQKLSVLEK  
EKYYQEYKNFENDKKIVDANIATETMIDINVGGAFETSRTLTQQKDSFIEKLLSGRHHVTRDKQGRIFLDRSEL  
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ILNFRNPLTIPPKDLSESEALLKEAEFYGIKFPLPVLFCIGGFDGVEYLN  
SMELLDISQCWRMCTPMSTKKAYFGSA  
VLNNFLYVFGNNYDYKALFETEVYDRLRDWYVSSNLNIPRRNNCGVTNSNGRIYCIGGYDGSSIIPNVEADH  
RMKAWE  
VAPLNTPRSSAMTVAFDNKIYVIGGTNGERLNSIEVYE  
EKMNKWEQFPYALLEARSSGA  
AFNYLNQIYV  
VGGIDNEHNILD  
SVEQYQPFNKRQFLNGVPEKKMF  
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>K13\_Target8

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>K13\_Target9

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>K13\_Target10

MEGEVKTKANSISNFSMTYDRESGGNSNSDDKGSSSENDNSFMNLTS  
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SFLLNNSSYGNVKDSLLESIDM  
SVLDNFDSKKDFPSNL  
SRTFNNMSKD  
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>K13\_Target11

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SFLLNNSSYGNVKDSLLESIDM  
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SVEQYQPENKRWQFLNGVPEKKMNFGAATLSDSYIITGGENGEVLNSCHFFSPDTNEWQLGPSLLVPRFGHSVLIANI

=====

```
In [6]: from tabulate import tabulate
# Parse the FASTA file format
sequences = {}
current_target = None

for line in data:
    line = line.strip()
    if line.startswith(">"): # New target identifier
        current_target = line[1:].strip()
        sequences[current_target] = ""
    else:
        sequences[current_target] += line # Append protein sequence

# Known resistance mutations and their reference amino acids
known_mutations = {
    580: "C", # C580Y (Cysteine → Tyrosine)
    539: "R", # R539T (Arginine → Threonine)
    493: "Y", # Y493H (Tyrosine → Histidine)
    675: "A", # A675V (Alanine → Valine)
    574: "P", # P574L (Proline → Leucine)
    476: "M", # M476I (Methionine → Isoleucine)
}

# Identify mutations in each target sequence
detected_mutations = []

for target, sequence in sequences.items():
    for pos, ref_aa in known_mutations.items():
        if pos <= len(sequence):
            observed_aa = sequence[pos - 1]
            if observed_aa != ref_aa:
                detected_mutations.append([target, pos, ref_aa, observed_aa])

# Print detected mutations in a table format
if detected_mutations:
    print(tabulate(detected_mutations, headers=["Target", "Position", "Reference"]
else:
    print("No mutations detected.")
```

Target	Position	Reference Amino-Acid	Observed Amino-Acid
K13_Target1	675	A	V
K13_Target1	476	M	I
K13_Target3	580	C	T
K13_Target3	539	R	T
K13_Target3	574	P	L
K13_Target6	580	C	T
K13_Target8	580	C	E
K13_Target8	539	R	V
K13_Target8	574	P	T
K13_Target8	476	M	I
K13_Target11	580	C	T
K13_Target11	493	Y	H