In [1]:

```
# impoting necessary libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt # visualizing data
%matplotlib inline
import seaborn as sns
```

In [2]:

```
# importing the csv file
df = pd.read_csv(r'C:\Users\hp\Desktop\bio Project\1-Amylase.csv',encoding= 'unicode_escape')
```

In [3]:

```
# checking for Content loaded in Juypyter notebook
df.head()
```

Out[3]:

	Days	niger cells- CuS Che NPs	niger cells- CuS Bio NPs	niger cells-CuS Che NBs	niger cells- CuS Bio NBs
0	day 1	9.52	7.28	14.96	11.96
1	day 2	5.12	4.16	9.28	8.32
2	day 3	4.07	3.43	6.60	5.72
3	day 4	2.32	1.85	3.82	3.70
4	day 5	1.52	1.22	2.57	2.44

In [4]:

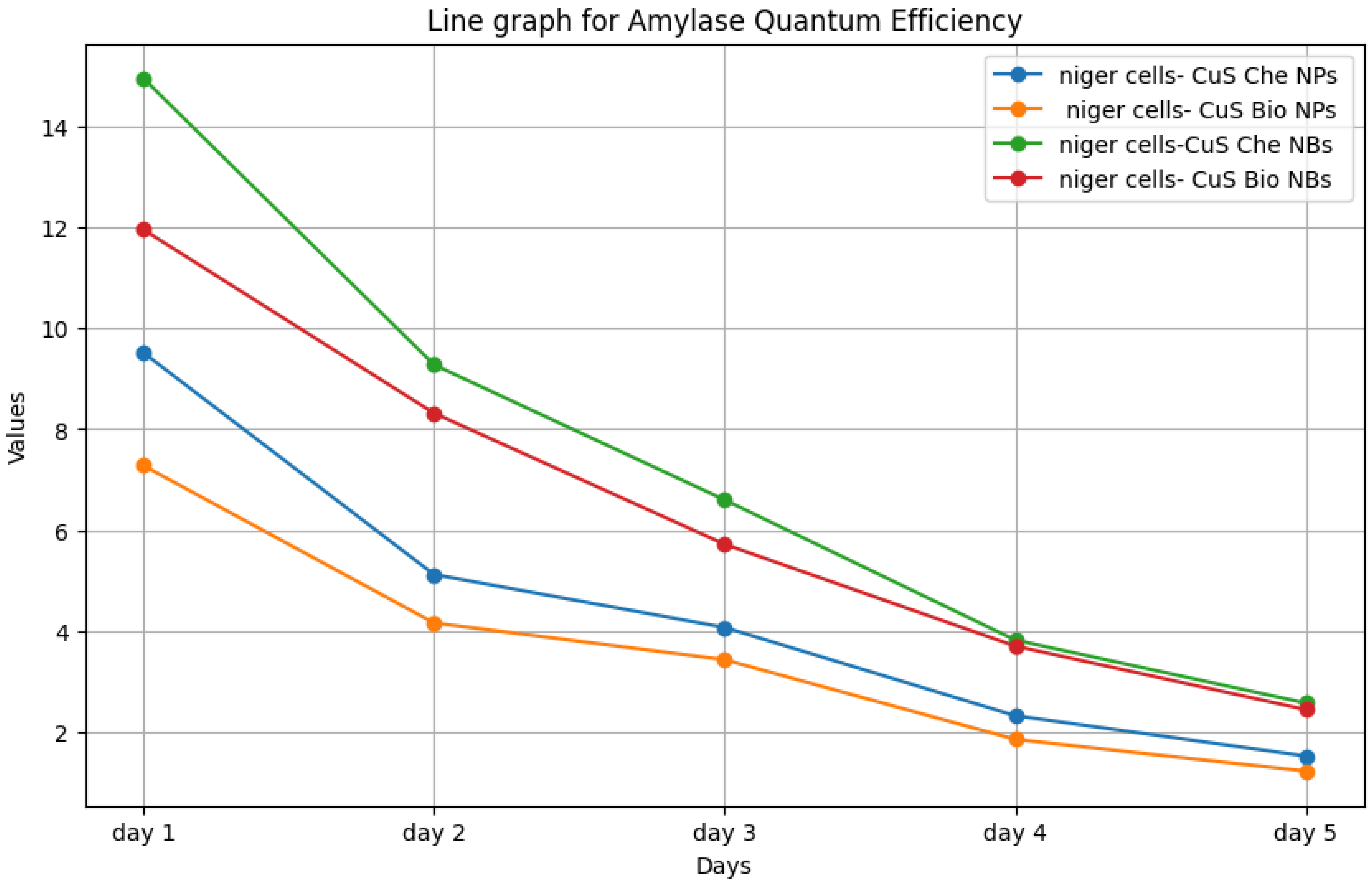
```
# Statistics of the loaded data
df.describe()
```

Out[4]:

	niger cells- CuS Che NPs	niger cells- CuS Bio NPs	niger cells-CuS Che NBs	niger cells- CuS Bio NBs
count	5.000000	5.000000	5.00000	5.000000
mean	4.510000	3.588000	7.44600	6.428000
std	3.138551	2.377555	4.93616	3.808874
min	1.520000	1.220000	2.57000	2.440000
25%	2.320000	1.850000	3.82000	3.700000
50%	4.070000	3.430000	6.60000	5.720000
75%	5.120000	4.160000	9.28000	8.320000
max	9.520000	7.280000	14.96000	11.960000

In [5]:

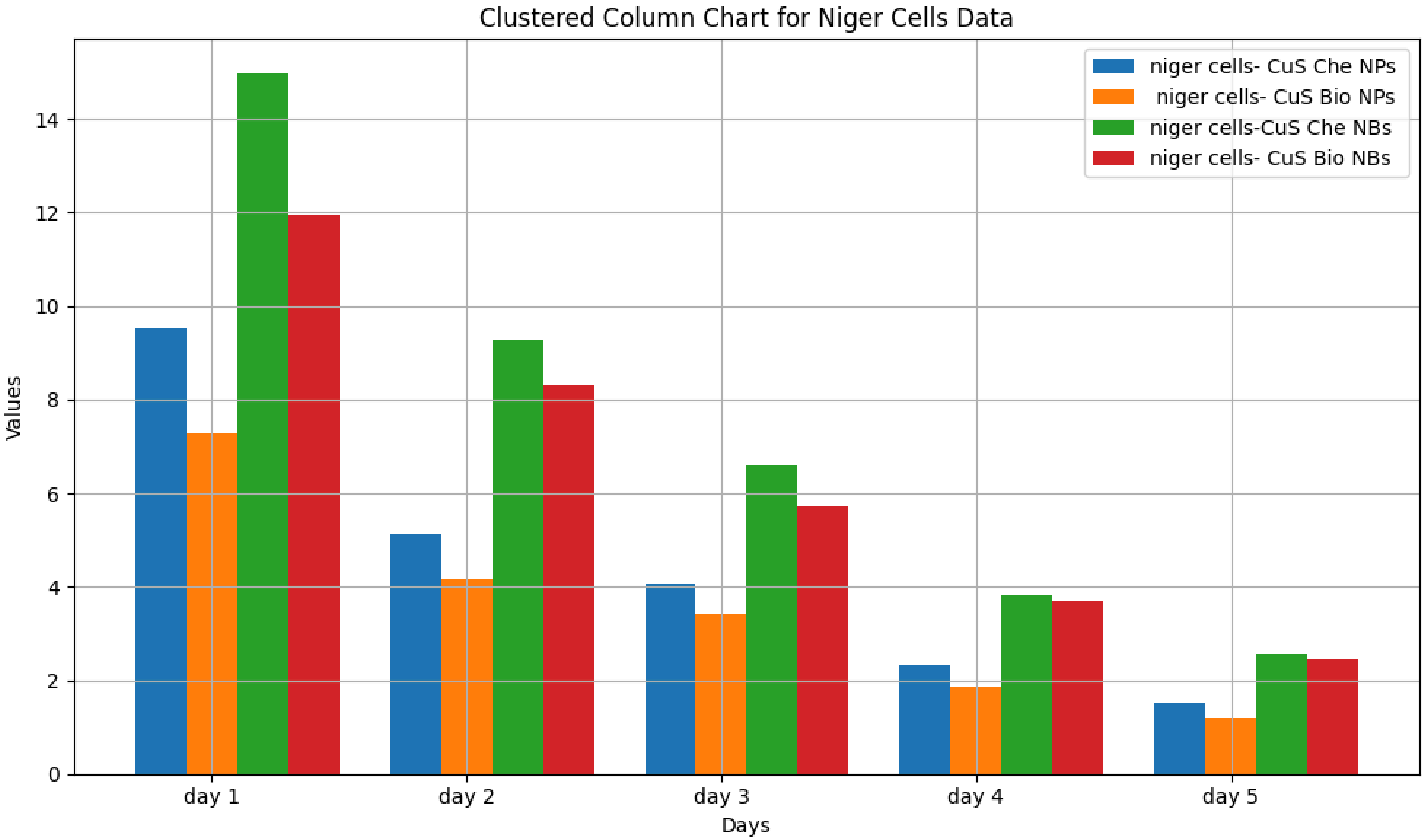
```
# Drawing Linegrpah
plt.figure(figsize=(10, 6))
for column in df.columns[1:]:
    plt.plot(df['Days'], df[column], marker='o', label=column)
    plt.xlabel('Days')
plt.ylabel('Values')
plt.title('Line graph for Amylase Quantum Efficiency')
plt.legend()
plt.grid(True)
plt.show()
```



In [6]:

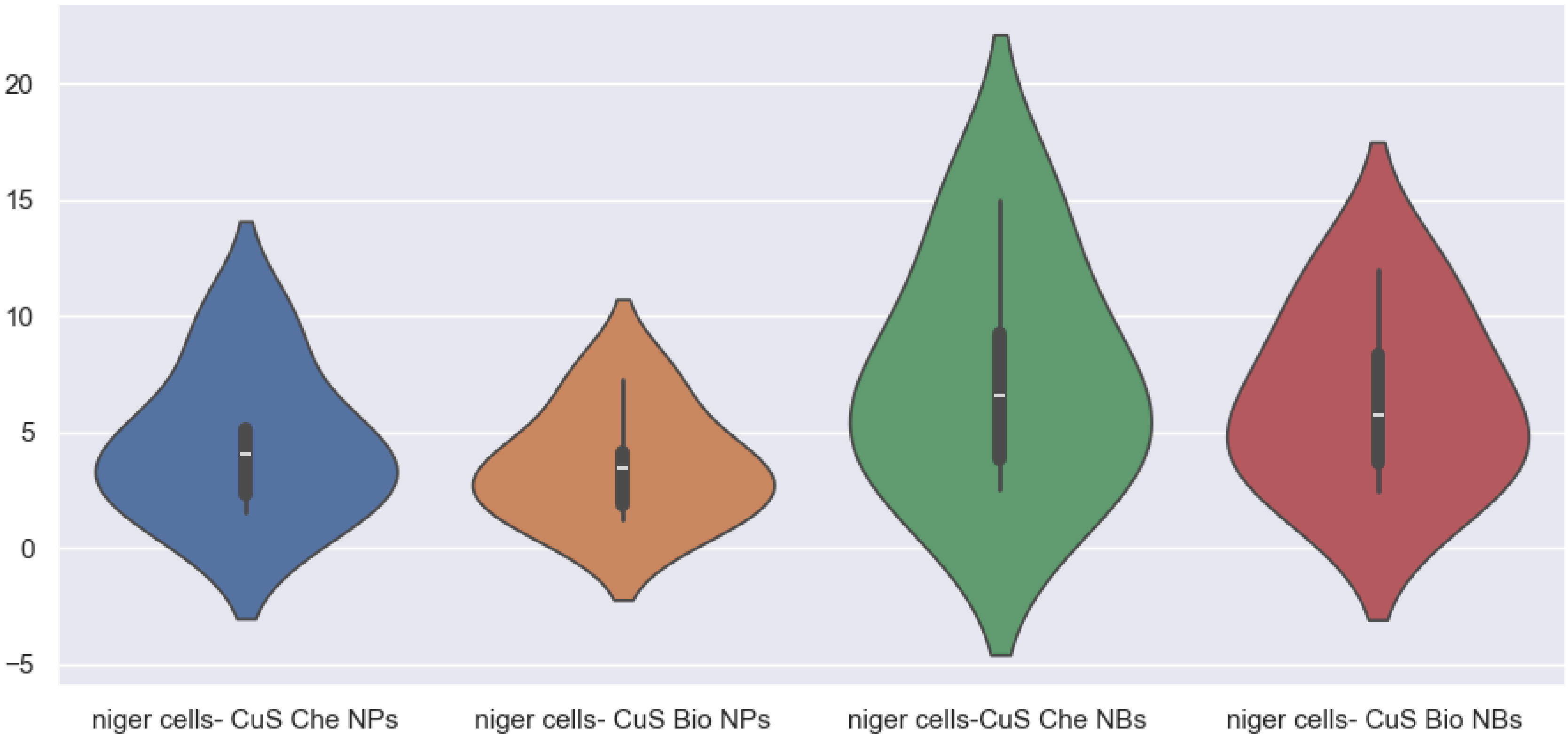
```
Drawing clustered column chart
plt.figure(figsize=(10, 6))
num_columns = len(df.columns[1:])
bar_width = 0.2
index = np.arange(len(df['Days']))

for i, column in enumerate(df.columns[1:], start=1):
    plt.bar(index + i * bar_width, df[column], bar_width, label=column)
    plt.xlabel('Days')
```

```python
plt.ylabel('Values')
plt.title('Clustered Column Chart for Niger Cells Data')
plt.xticks(index + (num_columns / 2) * bar_width, df['Days'])  # Aligning x-ticks with column groups
plt.legend()
plt.grid(True)
plt.tight_layout()  # Adjust layout to prevent clipping of labels
plt.show()
```



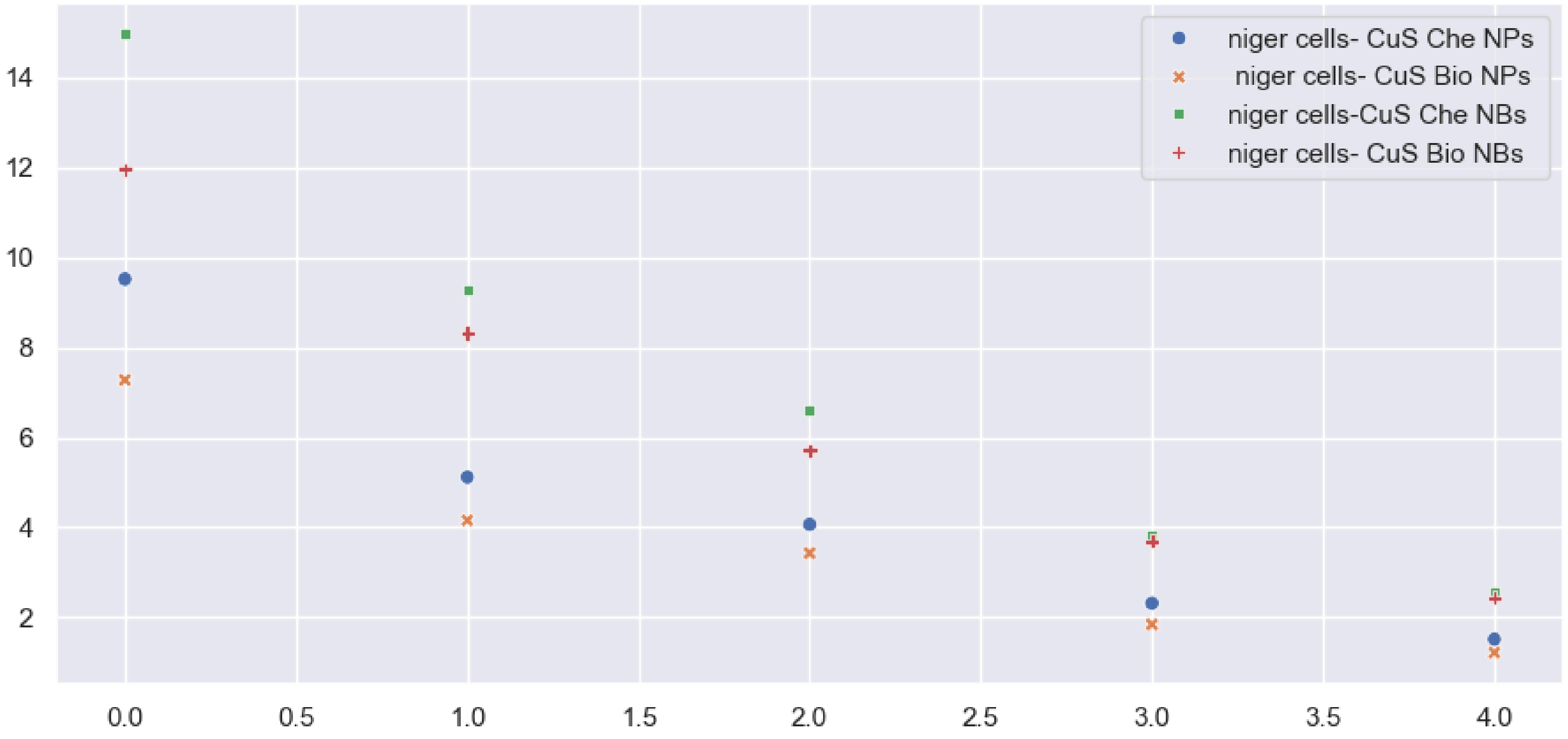
In [95]:

```python
# Drawing violingraph
sns.violinplot(data=df)
sns.set(rc={'figure.figsize':(11,5)})
```



In [96]:

```
Drawing scatteredgraph
sns.scatterplot(data=df)
sns.set(rc={'figure.figsize':(3,3)})
```


14
12
10
8
6
4
2
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
niger cells- CuS Che NPs
niger cells- CuS Bio NPs
niger cells-CuS Che NBs
niger cells- CuS Bio NBs

```
In [ ]:
```