Some EDA

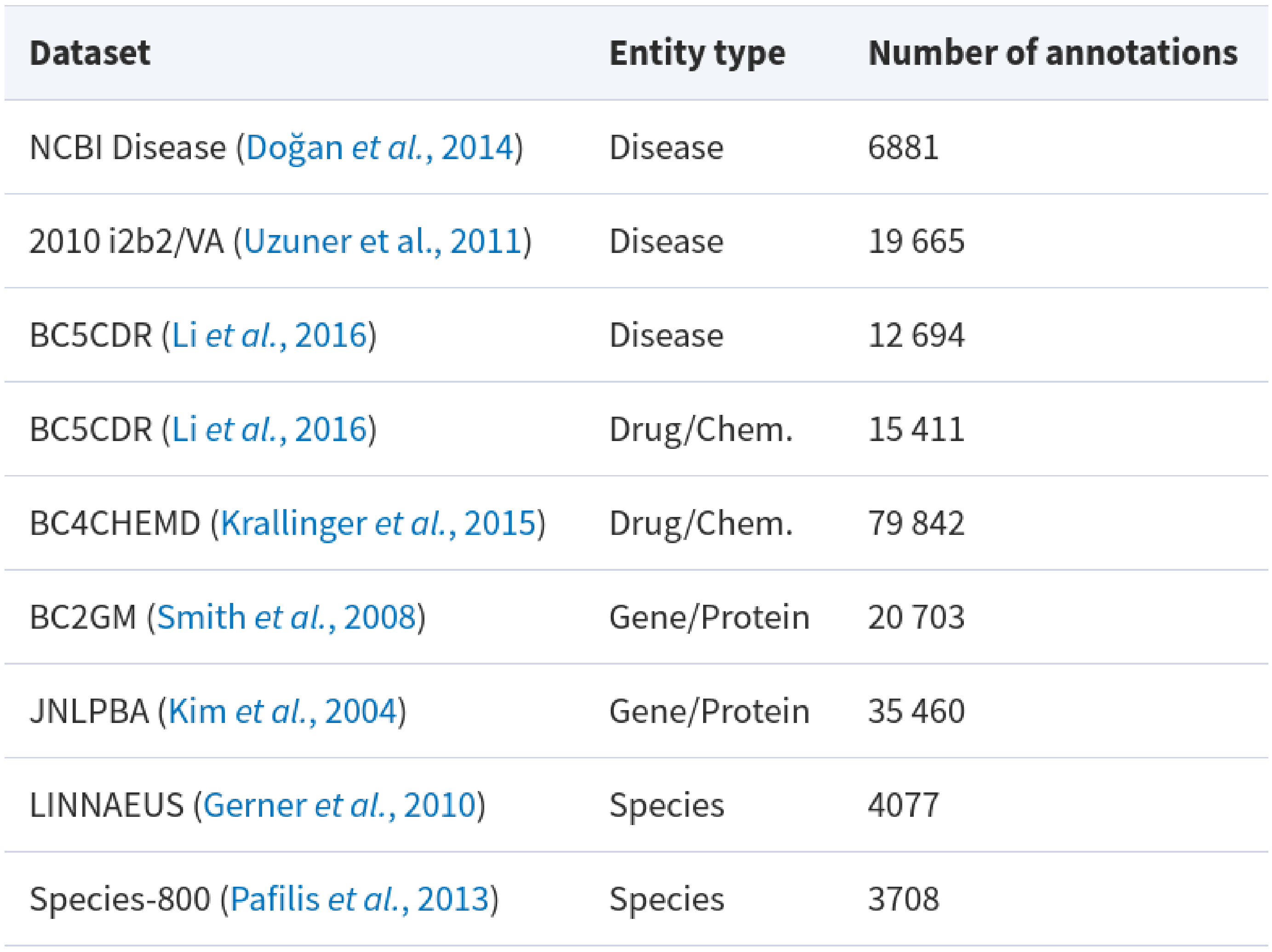
In [1]:
```
import os
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
from wordcloud import WordCloud
from utils import *
```

In [2]:
```
!ls ../data/
```

```
BC2GM        BC5CDR-disease  linnaeus      s800
BC4CHEMD     devel_all.tsv   NCBI-disease  test_all.tsv
BC5CDR-chem  JNLPBA          NERdata.zip   train_all.tsv
```

Table 3.

Statistics of the biomedical named entity recognition datasets



Dataset	Entity type	Number of annotations
NCBI Disease (Doğan *et al.*, 2014)	Disease	6881
2010 i2b2/VA (Uzuner et al., 2011)	Disease	19 665
BC5CDR (Li *et al.*, 2016)	Disease	12 694
BC5CDR (Li *et al.*, 2016)	Drug/Chem.	15 411
BC4CHEMD (Krallinger *et al.*, 2015)	Drug/Chem.	79 842
BC2GM (Smith *et al.*, 2008)	Gene/Protein	20 703
JNLPBA (Kim *et al.*, 2004)	Gene/Protein	35 460
LINNAEUS (Gerner *et al.*, 2010)	Species	4077
Species-800 (Pafilis *et al.*, 2013)	Species	3708

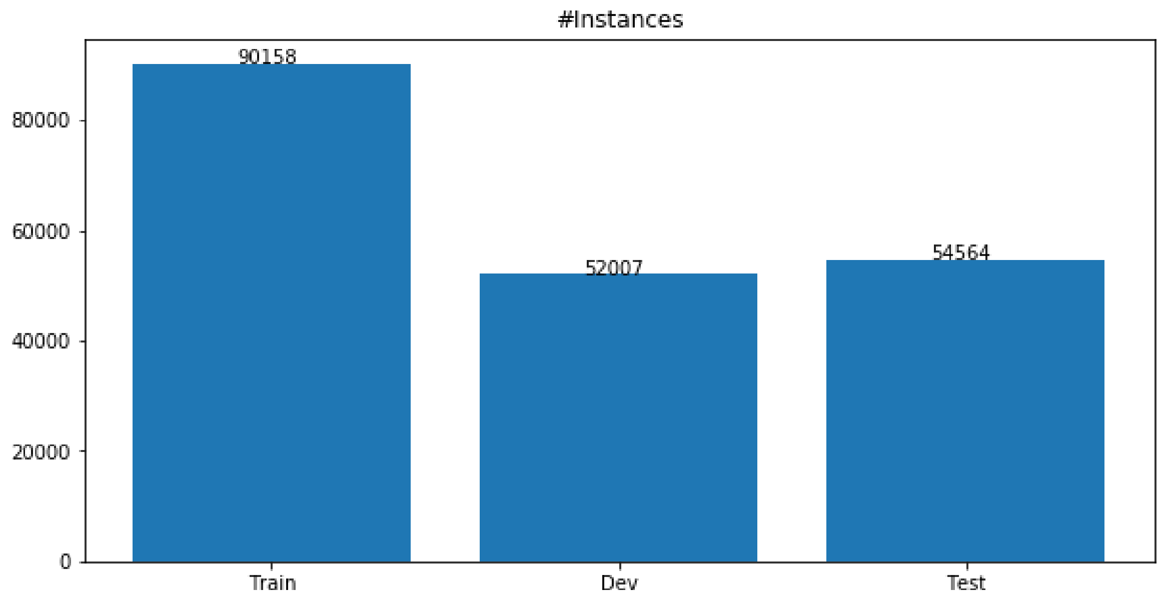
Load Data

In [3]:
```
#Data tags: IOB - Inside, Outside, Beginning. See [1, 2]
#[1]: https://github.com/dmis-lab/biobert/issues/56
#[2]: https://en.wikipedia.org/wiki/Inside%E2%80%93outside%E2%80%93be
ginning_(tagging)

DATA_DIR = "../data"
TRAIN = "train_all.tsv"
DEV = "devel_all.tsv"
TEST = "test_all.tsv"

train_data = read_data(path(DATA_DIR, TRAIN))
dev_data = read_data(path(DATA_DIR, DEV))
test_data = read_data(path(DATA_DIR, TEST))

print(f"Len train_data: {len(train_data)}")
print(f"Len dev_data: {len(dev_data)}")
print(f"Len test_data: {len(test_data)}")
```

```
Len train_data: 90158
Len dev_data: 52007
Len test_data: 54564
```

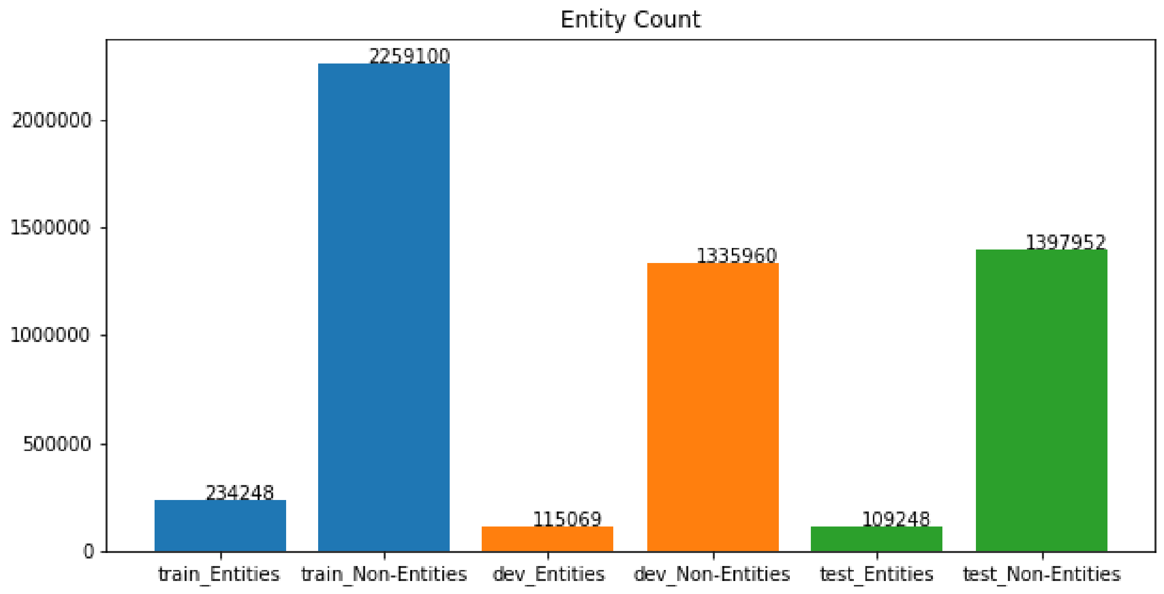
#Instances

In [4]:
```
plt.figure(figsize=(10, 5))
plt.title("#Instances")
plt.bar(["Train", "Dev", "Test"],
        [len(train_data),
         len(dev_data),
         len(test_data)]
       )

hfix = -.1
plt.annotate(f"{len(train_data)}", (0+hfix, len(train_data)))
plt.annotate(f"{len(dev_data)}", (1+hfix, len(dev_data)))
plt.annotate(f"{len(test_data)}", (2+hfix, len(test_data)))

plt.show()
```



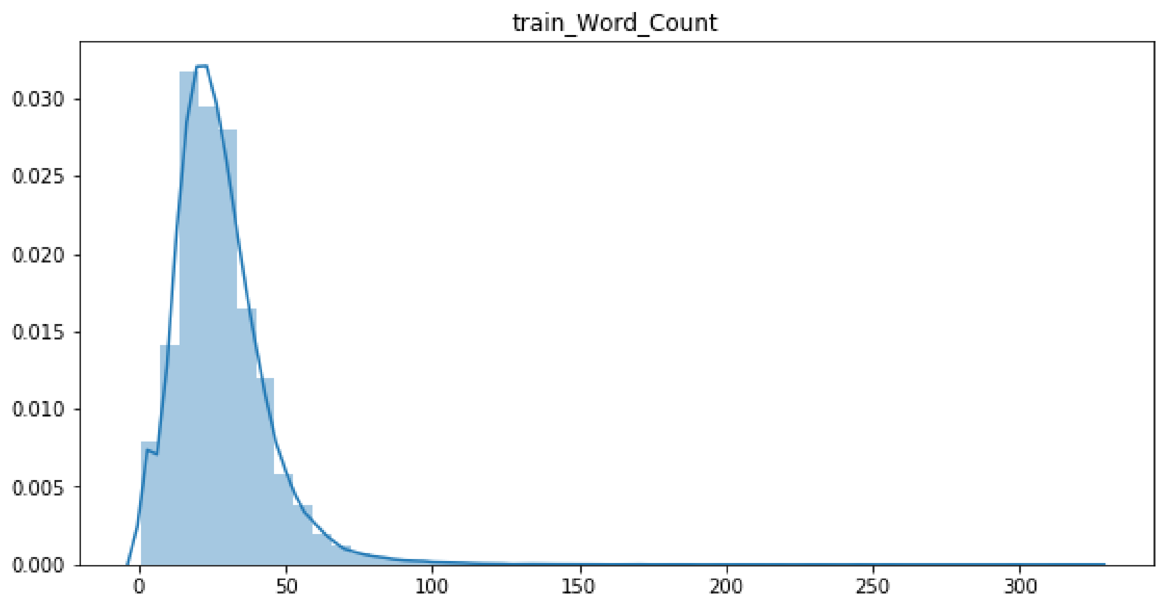
#Entities

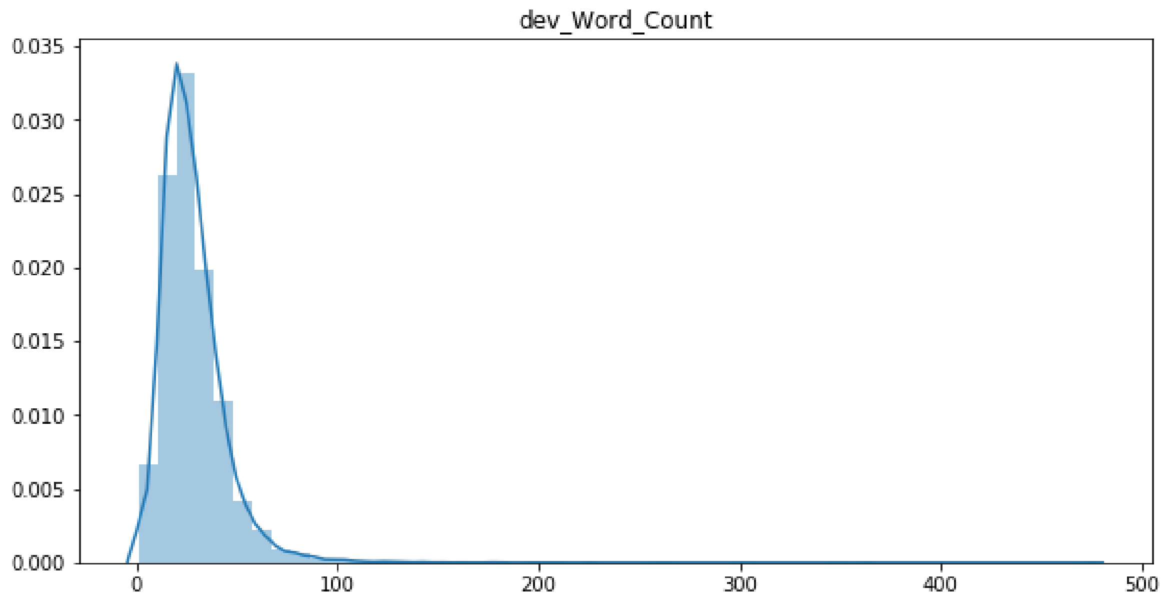
In [6]:
```python
plt.figure(figsize=(10, 5))
plt.title("Entity Count")
for i, (data, data_name) in enumerate(zip(
        [train_data, dev_data, test_data],
        ["train", "dev", "test"])):

    data_labels = " ".join([x[0] for x in data])
    data_label_arr = np.array(data_labels.split())
    counts = np.unique(data_label_arr, return_counts=True)[1]
    label_count = counts[0] + counts[1]
    normal_count = counts[2]

    plt.bar([f"{data_name}_Entities", f"{data_name}_Non-Entities"],
            [label_count,
             normal_count,]
           )

    hfix = 2*i - .1
    plt.annotate(f"{label_count}", (0+hfix, label_count))
    plt.annotate(f"{normal_count}", (1+hfix, normal_count))

plt.show()
```

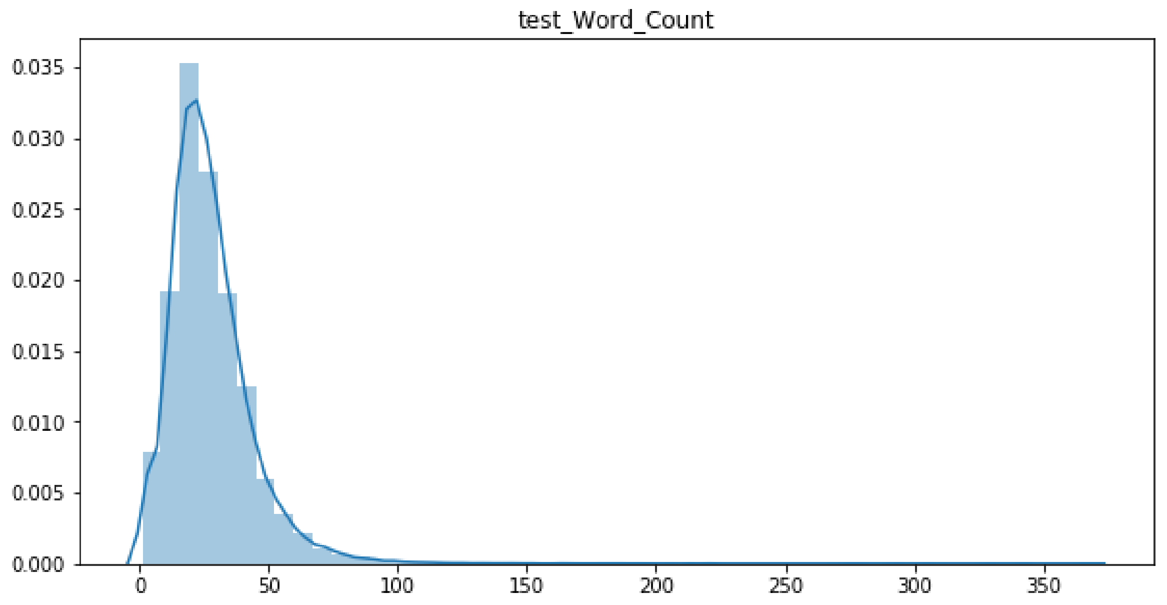


WordCount

In [7]:
```
for i, (data, data_name) in enumerate(zip(
        [train_data, dev_data, test_data],
        ["train", "dev", "test"])):

    word_counts = [len(x[1].split()) for x in data]
    plt.figure(figsize=(10, 5))
    sns.distplot(word_counts)
    plt.title(f"{data_name}_Word_Count")
    plt.show()
```

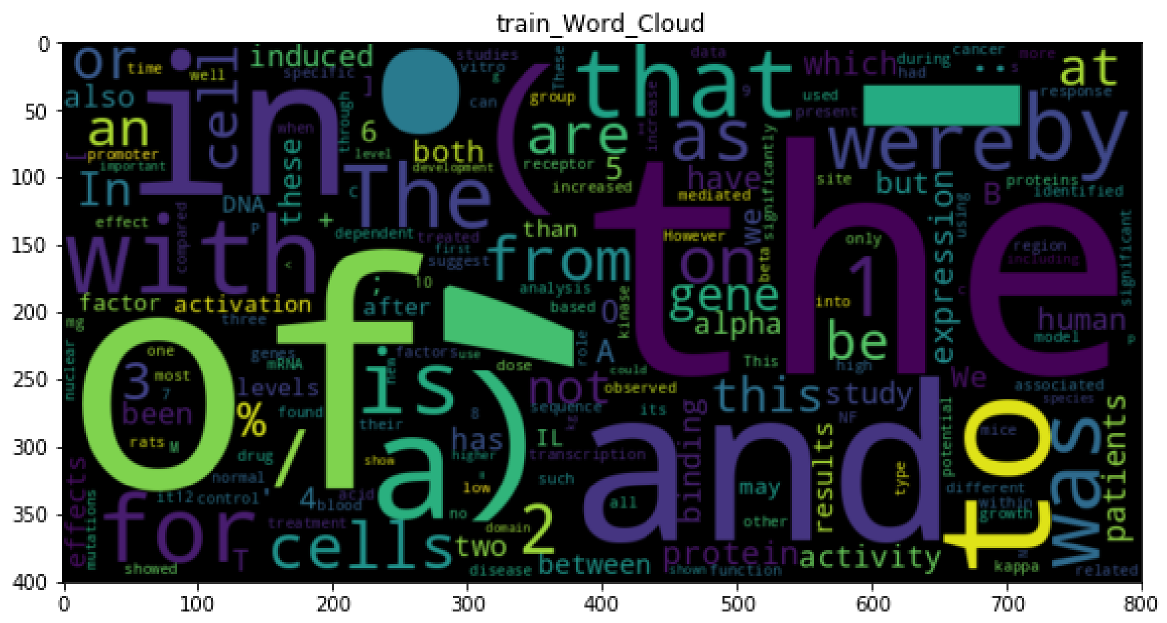

train_Word_Count
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0
50
100
150
200
250
300

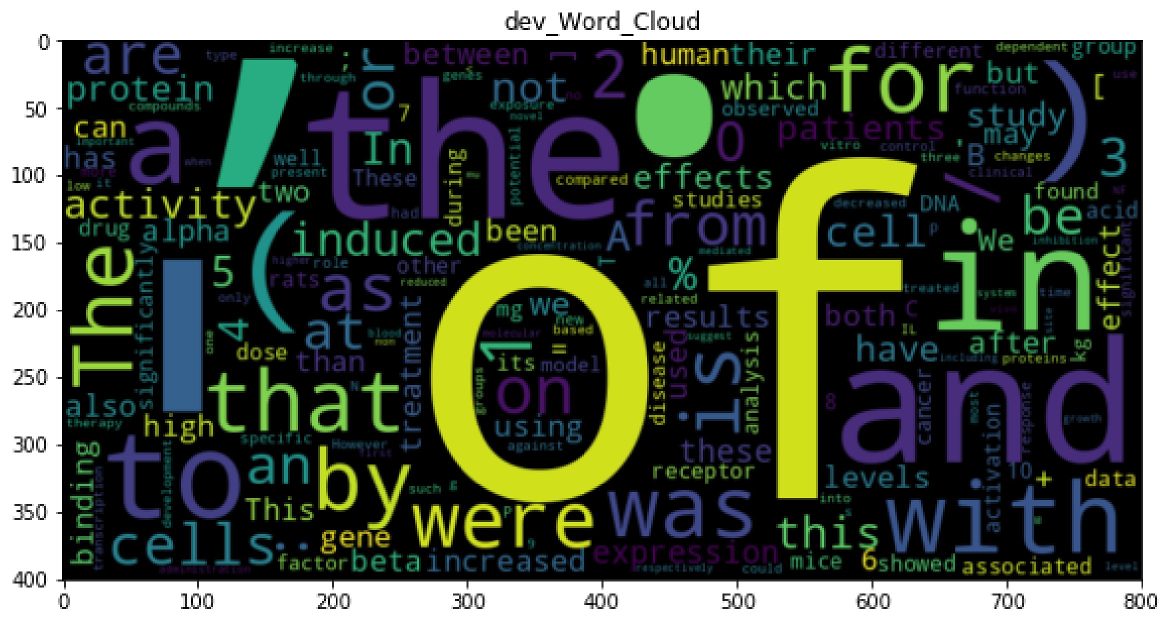

dev_Word_Count
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0
100
200
300
400
500

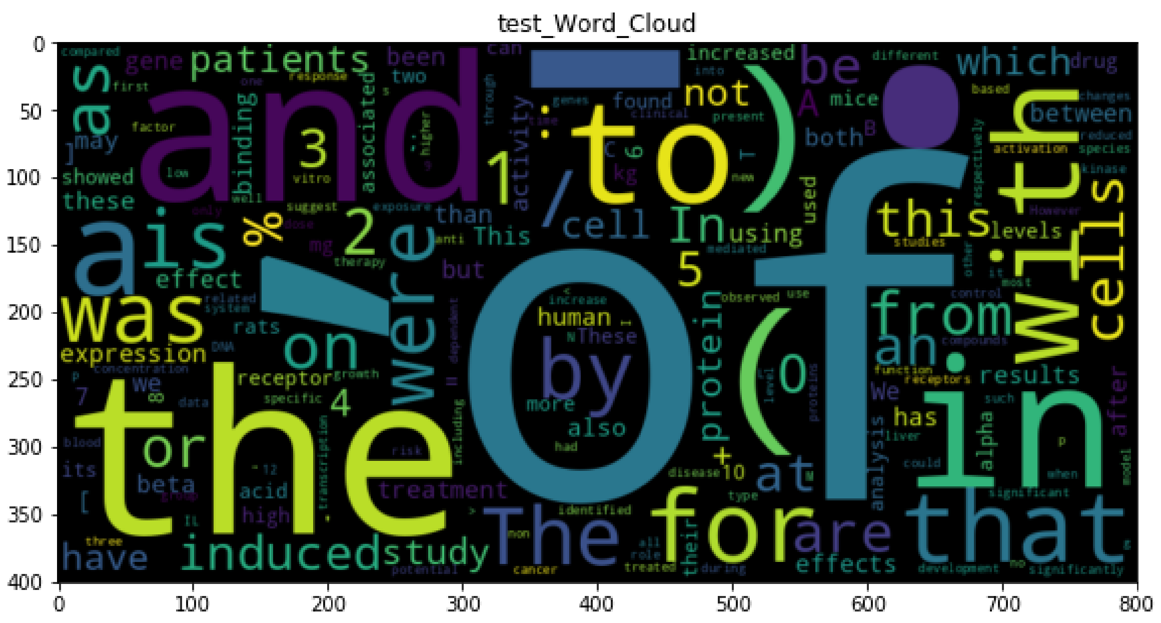

test_Word_Count
0.035
0.030
0.025
0.020
0.015
0.010
0.005
0.000
0
50
100
150
200
250
300
350

WordCloud for all the text

In [8]:
```python
for i, (data, data_name) in enumerate(zip(
        [train_data, dev_data, test_data],
        ["train", "dev", "test"])):

    text = " ".join([x[1] for x in data])
    freq_dict = np.unique(
            np.array(text.split()),
            return_counts=True
            )
    freq_dict = dict(zip(freq_dict[0], freq_dict[1]))

    plt.figure(figsize=(10, 5))
    wordcloud = WordCloud(width=800,
                height=400).generate_from_frequencies(freq_dict)
    plt.imshow(wordcloud, interpolation="bilinear")
    plt.title(f"{data_name}_Word_Cloud")
    plt.show()
```


train_Word_Cloud
the
of
in
and
that
to
with
were
by
was
for
is
a
The
as
are
cells
from
on
gene
this
study
expression
patients
protein
activity
binding
results
activation
factor
induced
human
alpha
cell
0
100
200
300
400
500
600
700
800
50
150
250
350


dev_Word_Cloud
of
the
and
in
for
with
was
by
were
that
to
is
a
The
cells
from
induced
activity
protein
patients
study
expression
effects
which
human
on
an
this
treatment
increased
0
100
200
300
400
500
600
700
800
50
150
250
350

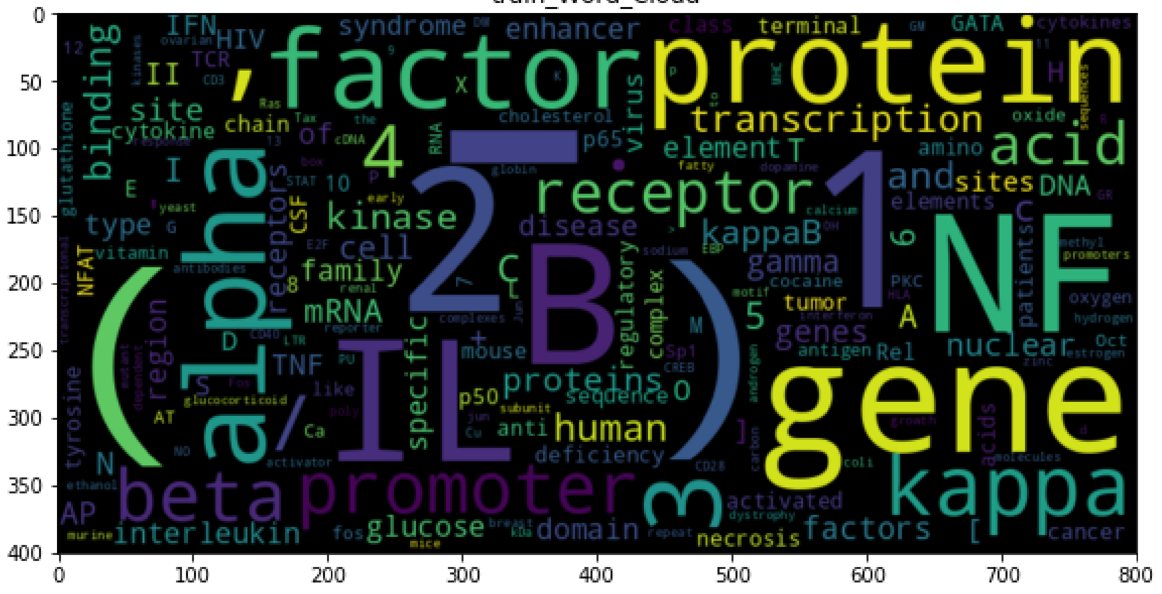


WordCloud only for named entities

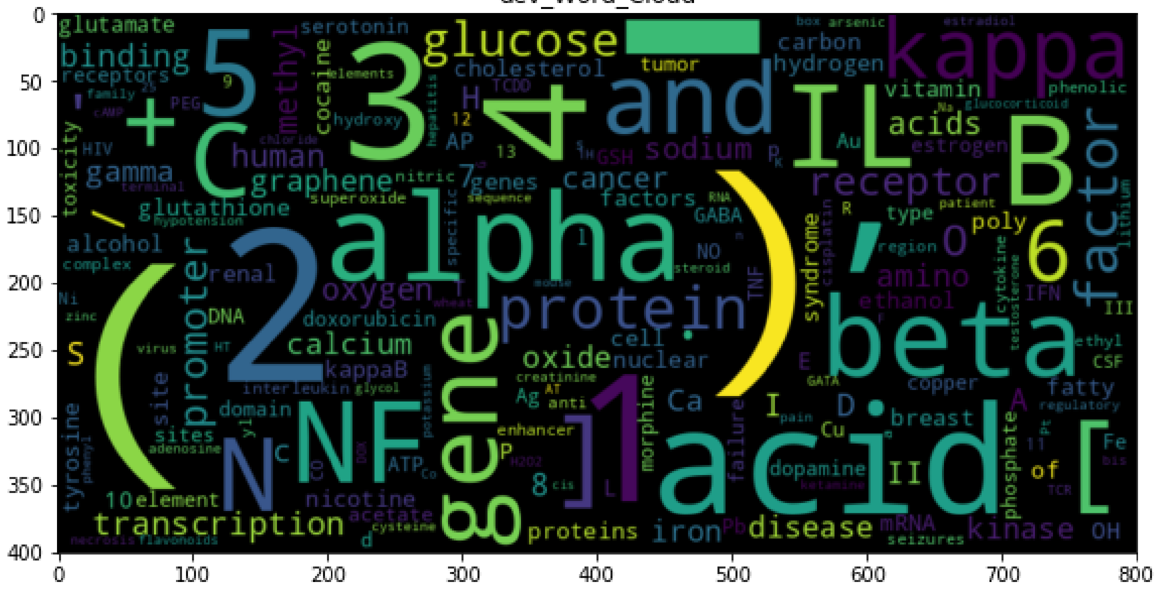
```
In [9]: def get_nes_only(data):
            nes = []
            for instance in data:
                labels, text = instance
                labels, text = labels.split(), text.split()
                for i in range(len(labels)):
                    if labels[i] != "O":
                        nes.append(text[i])
            return nes
```

In [10]:
```
for i, (data, data_name) in enumerate(zip(
        [train_data, dev_data, test_data],
        ["train", "dev", "test"])):

    text = get_nes_only(data)
    freq_dict = np.unique(
            np.array(text),
            return_counts=True
            )
    freq_dict = dict(zip(freq_dict[0], freq_dict[1]))

    plt.figure(figsize=(10, 5))
    wordcloud = WordCloud(width=800,
                height=400).generate_from_frequencies(freq_dict)
    plt.imshow(wordcloud, interpolation="bilinear")
    plt.title(f"{data_name}_Word_Cloud")
    plt.show()
```

train_Word_Cloud



dev_Word_Cloud



test_Word_Cloud