Python Examples Accessing SGD API

http://bit.ly/apiexamples

```python
import requests

SGD_BASE_URL = 'https://www.yeastgenome.org/webservice'

def print_phenotype_loci():
    url = SGD_BASE_URL + '/phenotype/abnormal_mating_response/locus_details'
    response = requests.get(url=url).json()
    print('LOCI ANNOTATED TO abnormal_mating_response')
    for annotation in response:
        gene_name = annotation['locus']['display_name']
        reference_citation = annotation['reference']['display_name']
        print(gene_name + ', reference citation:' + reference_citation)

if __name__ == '__main__':
    print_phenotype_loci()
```

```python
import requests

SGD_BASE_URL = 'https://www.yeastgenome.org/webservice'

def print_chromosome_i_sequences():
    url = SGD_BASE_URL + '/contig/chromosome_i/sequence_details'
    response = requests.get(url=url).json()
    for locus in response['genomic_dna']:
        name = locus['locus']['display_name']
        sequence = locus['residues']
        print(name + ': ' + sequence)

if __name__ == '__main__':
    print_chromosome_i_sequences()
```

```python
import requests

SGD_BASE_URL = 'https://www.yeastgenome.org/webservice'

def print_act1_info():
    url = SGD_BASE_URL + '/locus/act1'
    response = requests.get(url=url).json()
    # print references
    print('ACT1 REFERENCES')
    for ref in response['references']:
        name = ref['display_name']
        pmid = str(ref['pubmed_id'])
        print(pmid + ': ' + name)
    # print large scale phenotypes
    print('ACT1 OVEREXPRESSION LARGE SCALE PHENOTYPES')
    for pheno in response['phenotype_overview']['large_scale_phenotypes']['overexpression']:
        name = pheno['display_name']
        print(name)

if __name__ == '__main__':
    print_act1_info()
```