

```
#!/usr/bin/python
__author__ = "morganlnance"
```

```
"""
```

HW2 Question 3 (Workshop #2 Exercise 2)

This program makes an alpha helix of a specified length out of alanines. Phi and psi values are idealized. This program dumps the resulting pose as 'helix.pdb'

Usage: ./make_helix.py <number of helix residues>

Example: ./make_helix.py 20

```
"""
```

```
#####
```

```
# IMPORTS #
```

```
#####
```

```
import sys
```

```
from pyrosetta import init, \
    pose_from_sequence, PyMOLMover
```

```
#####
```

```
# ARGUMENTS #
```

```
#####
```

```
try:
```

```
    n_helix_residues = int(sys.argv[1])
```

```
except:
```

```
    print "\nGive me an integer for the number of helix residues.\n"
```

```
    sys.exit()
```

```
#####
```

```
# MAIN #
```

```
#####
```

```
# initialize pyrosetta and load the pose
```

```
init()
```

```
pose = pose_from_sequence("A"*n_helix_residues, "fa_standard")
```

```
# PyMOLMover for visualization
```

```
pmm = PyMOLMover()
```

```
pmm.keep_history(True)
```

```
# ideal phi and psi values
```

```
phi = -60
```

```
psi = -45
```

```
# set phi and psi
```

```
pmm.apply(pose)
```

```
for ii in range(1, pose.size()+1):  
    pose.set_phi(ii, phi)  
    pose.set_psi(ii, psi)  
    pmm.apply(pose)  
pose.dump_pdb("helix.pdb")
```