

```
raw.reads username$ bash easydiver.sh -i ./ -o ./output -p GGCGGAAAGCACATCTGC -T 14  
-a -r
```

# EASYDIVER

```
+-----+  
| Thu Jan 30 13:06:22 PST 2020
```

```
| Welcome to the pipeline for Easy pre-processing and Dereplication of In Vitro  
| Evolution Reads  
+-----+
```

```
-----Input directory path: /Users/username/Desktop/raw.reads
```

```
-----Output directory path: /Users/username/Desktop/raw.reads/output
```

```
-----Forward Primer: GGCGGAAAGCACATCTGC
```

```
-----Individual lane outputs suppressed
```

```
-----# of threads = 14
```

```
-----Translation on
```

```
-----No additional PANDASeq flags
```

```
Input filecheck passed
```

```
Joining test1_S1_L001 reads & extracting primer...
```

```
Converting joined test1_S1_L001 FASTQ to FASTA...
```

```
Adding test1_S1_L001 reads to total test1_S1 reads...
```

```
Generating test1_S1_L001 nt length distribution for individual lanes...
```

```
Calculating unique & total reads for lane test1_S1_L001...
```

```
Collecting unique, total and sequences in file...
```

```
Joining test2_S2_L001 reads & extracting primer...
```

```
Converting joined test2_S2_L001 FASTQ to FASTA...
```

```
Adding test2_S2_L001 reads to total test2_S2 reads...
```

```
Generating test2_S2_L001 nt length distribution for individual lanes...
```

```
Calculating unique & total reads for lane test2_S2_L001...
```

```
Collecting unique, total and sequences in file...
```

```
Calculating unique & total reads for test1_S1...
```

```
Calculating unique & total reads for test2_S2...
```

```
Individual lane outputs will be retained
```

```
Generating test1_S1 DNA length distribution...
```

```
Translating test1_S1 DNA to peptides...
```

```
Generating test1_S1 aa length distribution...
```

```
Generating test2_S2 DNA length distribution...
```

```
Translating test2_S2 DNA to peptides...
```

```
Generating test2_S2 aa length distribution...
```

```
Run time: 79
```