

**< insert ACGT 40>  
print**

expected output:

**SequencIDs:  
ACGT  
Free Block List: none**

File: <sequence for ACGT (10 bytes)>

**< insert AAAA 40>  
print**

expected output:

**SequencIDs:  
AAAA  
ACGT  
Free Block List: none**

File: <sequence for ACGT(10 bytes)> <sequence for AAAA (10 bytes)>

**<insert AA 4>  
print**

expected output:

**SequencIDs:  
AAAA  
AA  
ACGT  
Free Block List: none**

File: <seq. for ACGT (10 bytes) > <seq. for AAAA (10 bytes) > <seq. for AA (1 byte) >

**<remove AA >  
print**

expected output:

**SequnceIDs:  
AAAA  
ACGT  
Free Block List:  
[Block 1] Starting Byte Location: 20, Size 1 byte**

File: <seq. for ACGT (10 bytes) > <seq. for AAAA (10 bytes) > **<free space (1 byte)>**

**<insert A 80>  
print**

expected output:

**SequnceIDs:  
AAAA  
ACGT  
A  
Free Block List: none**

File: <seq. for ACGT (10 bytes) > <seq. for AAAA (10 bytes) > <seq. for A (20 bytes) >

**<insert TATA 40>  
print**

expected output:

**SequnceIDs:  
AAAA  
ACGT  
A  
TATA  
Free Block List: none**

File: <seq. for ACGT (10 bytes) > <seq. for AAAA (10 bytes) > <seq. for A (20 bytes) >  
<seq. for TATA (10 bytes) >

**<remove ACGT>**  
**print**

expected output:

**SequnceIDs:**  
**AAAA**  
**A**  
**TATA**  
**Free Block List:**  
**[Block 1] Starting Byte Location: 0, Size 10 bytes**

File: **<free space (10 bytes)>** <seq. for AAAA (10 bytes) > <seq. for A (20 bytes) >  
<seq. for TATA (10 bytes) >

**<insert CCCC 40>**  
**print**

expected output:

**SequnceIDs:**  
**AAAA**  
**A**  
**CCCC**  
**TATA**  
**Free Block List: none**

File: <seq. for CCCC (10 bytes) > <seq. for AAAA (10 bytes) > <seq. for A (20 bytes) >  
<seq. for TATA (10 bytes) >

**<remove CCCC >  
print**

expected output:

**SequnceIDs:**

**AAAA**

**A**

**TATA**

**Free Block List:**

**[Block 1] Starting Byte Location: 0, Size 10 bytes**

File: **<free space (10 bytes)>** <seq. for AAAA (10 bytes) > <seq. for A (20 bytes) >  
<seq. for TATA (10 bytes) >

**<remove AAAA >  
print**

expected output:

**SequnceIDs:**

**A**

**TATA**

**Free Block List:**

**[Block 1] Starting Byte Location: 0, Size 20 bytes**

File: **<free space (20 bytes)>** <seq. for A (20 bytes) > <seq. for TATA (10 bytes) >

**<insert GGGG 51 >**  
**print**

expected output:

**SequnceIDs:**

**A**

**GGGG**

**TATA**

**Free Block List:**

**[Block 1] Starting Byte Location: 13, Size 7 bytes**

File: <seq. for GGGG (13 bytes)> **<free space (7 bytes)>** <seq. for A (20 bytes) > <seq. for TATA (10 bytes) >

**<remove TATA >**  
**print**

expected output:

**SequnceIDs:**

**A**

**GGGG**

**Free Block List:**

**[Block 1] Starting Byte Location: 13, Size 7 bytes**

**[Block 2] Starting Byte Location: 40, Size 10 bytes**

File: <seq. for GGGG (13 bytes)> **<free space (7 bytes)>** <seq. for A (20 bytes) > **<free space (10 bytes)>**

**<search A\$>**

expected output:

**# of nodes visited: 2**

**key: A**

**sequence:**

**AAAATTTTCCCCGGGGAAAACCCCGGGGTTTTAAAATTTTAAAATTTTCCCCGGGG  
AAAACCCCGGGGTTTTAAAATTTT**

**<search GGGG>**

expected output:

**# of nodes visited: 2**

**key: GGGG**

**sequence:**

**AAAATTTTCCCCGGGGAAAACCCCGGGGTTTTAAAATTTTGGGGTTTTAAA**