

```
CREATE_CONSENSUS_SEQ(alignment)
```

```
for i <- 1 to délka alignment.multiple_seq_alignment1,1
```

```
  for j <- 1 to délka alignment.multiple_seq_alignment
```

```
    temp_array <- alignment.multiple_seq_alignmentj
```

```
    nucleotides <- zřetěz nucleotides a temp_arrayi
```

```
  num_a <- suma kolik je v proměnné nucleotides znak A
```

```
  num_c <- suma kolik je v proměnné nucleotides znak C
```

```
  num_t <- suma kolik je v proměnné nucleotides znak T
```

```
  num_g <- suma kolik je v proměnné nucleotides znak G
```

```
  value_set <- vytvoř vector z proměnných num_a num_c num_g num_t
```

```
  value, position <- najdi hodnotu a pozici maxima vektoru value_set
```

```
  switch position
```

```
    case 1
```

```
      consensus_seq <- zřetěz consensus_seq a A
```

```
    case 2
```

```
      consensus_seq <- zřetěz consensus_seq a C
```

```
    case 3
```

```
      consensus_seq <- zřetěz consensus_seq a G
```

```
    case 4
```

```
      consensus_seq <- zřetěz consensus_seq a T
```

```
alignment.consensus_seq <- consensus_seq
```