

```
#####  
#  
#  
# Aligned_sequences: 2  
# 1: SEQ_4  
# 2: '319_24A-C  
# Matrix: EBLOSUM62  
# Gap_penalty: 10.0  
# Extend_penalty: 0.5  
#  
# Length: 458  
# Identity:      458/458 (100.0%)  
# Similarity:    458/458 (100.0%)  
# Gaps:          0/458 ( 0.0%)  
# Score: 2437.0  
#  
#  
#####
```

Celltrion Exhibit - 1027

2/20/23, 8:39 PMhttps://www.ebi.ac.uk/Tools/services/rest/emboss\_needle/result/emboss\_needle-I20230221-013921-0301-73240000-p2m/aln

|            |     |                                                    |     |
|------------|-----|----------------------------------------------------|-----|
| '319_24A-C | 301 | KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA | 350 |
| SEQ_4      | 351 | KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN | 400 |
|            |     |                                                    |     |
| '319_24A-C | 351 | KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN | 400 |
| SEQ_4      | 401 | NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK | 450 |
|            |     |                                                    |     |
| '319_24A-C | 401 | NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK | 450 |
| SEQ_4      | 451 | SLSLSPGK                                           | 458 |
|            |     |                                                    |     |
| '319_24A-C | 451 | SLSLSPGK                                           | 458 |

#-----  
#-----