Analysis

BLOSUM matrix values were given as logarithms of odds scores of the ratio of the observed frequency of amino acid substitutions divided by the frequency expected by chance (Mount, 2008). In other words, if the score of two amino acid sequences calculated by BLOSUM matrix is large, the probability of homology is high.

Therefore, the score of the comparison between ACE2\_human and ACE2\_cat is the largest among the three comparisons, so human and cat sequences are most closely related.

Additionally, the score of the three comparisons are all relatively large, so we can speculated that human, cat and mouse sequences are closely related to each other. There is a high probability that the ACE2 genes of the three species are homologous and have genetic similarity.

References

Mount D. W. (2008). Using BLOSUM in Sequence Alignments. *CSH protocols*, *2008*, pdb.top39.