Table 3. Computational *in silico* studies on binding predictions of SARS-CoV-2 to the ACE2 receptor of the animal host cell.

Methods	Predicted Binding (at risk)	No Predicted Binding	Reference
Sequence and structural modelling of the five amino acids involved in the binding between SARS-CoV-2 RBD and ACE2 receptor.	Orangutan, monkey, chimpanzee, rhesus macaque, dog, cat, hamster, ferret, pig, baboon, marmoset, rabbit, stoat, civet, horseshoe and fruit bats, wild boar, fox, pangolin, horse, cattle, sheep, mole-rat, and squirrel.	Rat, mouse, raccoon, greater horseshoe bat, platypus, elephant, hedgehog, meerkat, guinea pig.	Luan et al.[1]
	Orangutan, monkey, cat, ferret, pig.	Rat and mouse.	Wan et al.[2]
Sequence and structural modelling of published 3D models of SARS-CoV-2 RBD and ACE2 receptor.	Macaque, hamster, dog, and ferret.	Guinea pigs, rabbit, mice and rats.	Brooke and Prischi [3]
Sequence and structural modelling of the 25 amino acids involved in the binding between SARS-CoV-2 RBD and ACE2 receptor.	Very high: Orangutan, monkey, chimpanzee, macaque, gorilla, gibbon, bonobo. High: Hamster, monkey (other species) lemur, whale, porpoise, mole-rat, deer, dolphin, anteater, muskrat. Medium: Other species of lemur, hamster, squirrel, whale, and monkey. Marmot, sheep, bison, wild yak, cattle, goat, buffalo, cat, giraffe, marmoset, bulbul, lynx, leopard, cheetah, cougar, hippopotamus, hare, gazelle, and rabbit.	Low: Other species of lemur and camel, rhinoceros, rat, mouse, tapir, bear, dog, wolf, donkey, horse, fox, porcupine, vole, horseshoe bat, pig, rodent, and manatee. Very low: other species of rodents, bats, and guinea pigs; skunk, pangolin, mink, stoat, seal, otter, ferret, fossa, armadillo, hyena, civet, panda, shrew, meerkat, hedgehog, platypus, and koala; and most reptiles, birds, amphibians, and fishes.	Damas et al.[4]
Sequence and structural modelling, plus binding energy calculations, of the 15-25 amino acid residues	Orangutan, monkey, chimpanzee, gorilla, rhesus macaque, bonobo, dog, cat, hamster, ferret, pig, mink, squirrel, rabbit, bushbaby, wild yak, cow,	Rat, mouse, hedgehog, shrew, and most birds, fishes, amphibians, and reptiles.	Lam et al. [5]

[1] Luan, J., Lu, Y., Jin, X., & Zhang, L. (2020). Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection. Biochemical and biophysical research communications, 526(1), 165–169. https://doi.org/10.1016/j.bbrc.2020.03.047

[2] Wan Y, Shang J, Graham R, Baric RS, Li F. 2020. Receptor recognition by the novel coronavirus from Wuhan: an analysis based on decade-long structural studies of SARS coronavirus. J Virol 94:e00127-20. https://doi.org/10.1128/JVI.00127-20.

[3] Brooke, G. N., & Prischi, F. (2020). Structural and functional modelling of SARS-CoV-2 entry in animal models. Scientific reports, 10(1), 15917. https://doi.org/10.1038/s41598-020-72528-z

[4] Damas, J., Hughes, G. M., Keough, K. C., Painter, C. A., Persky, N. S., et al. (2020). Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. Proceedings of the National Academy of Sciences of the United States of America, 117(36), 22311–22322. https://doi.org/10.1073/pnas.2010146117

[5] Lam, S.D., Bordin, N., Waman, V.P. et al. SARS-CoV-2 spike protein predicted to form complexes with host receptor protein orthologues from a broad range of mammals. Sci Rep 10, 16471 (2020). https://doi.org/10.1038/s41598-020-71936-5

involved in the direct contact between SARS-CoV-2 S-protein and ACE2 receptor.	sheep, goat, camel, dog, fox, bear, panda, leopard, bat, donkey, horse, elephant, koala, blue tit, carp, turbot, tilapia, turtle, crocodile.		
	Susceptible: Macaque, cat, lion, tiger, and hamster. Intermediate: pig, ferret, and dog.	Non-susceptible: Mouse, duck, and chicken. Unknown: horseshoe bat, horse, cow, pangolin, goat, sheep, and camel.	Alexander et al. [6]
	Orangutan, gibbon, gorilla, bonobo, pig, golden hamster, sheep, alpaca, horse, rabbit, and horseshoe bats.	Dog, tiger, dromedary, dingo, cat, and dwarf hamster.	Bouricha et al.[7]

Note: Other *in silico* studies that (1) make no predictions for possible binding between SARS-CoV-2 and ACE2 receptor or (2) compare only the sequence homology of ACE2 receptor between humans and other animals are not included.

[6] Alexander, M. R., Schoeder, C. T., Brown, J. A., Smart, C. D., Moth, C., et al. (2020). Predicting susceptibility to SARS-CoV-2 infection based on structural differences in ACE2 across species. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 10.1096/fj.202001808R. Advance online publication. https://doi.org/10.1096/fj.202001808R

[7] Bouricha, E. M., Hakmi, M., Akachar, J., Belyamani, L., & Ibrahimi, A. (2020). In silico analysis of ACE2 orthologues to predict animal host range with high susceptibility to SARS-CoV-2. 3 Biotech, 10(11), 483. https://doi.org/10.1007/s13205-020-02471-3