

ACE2 residue	<i>Homo sapiens</i>				<i>Felis catus</i>					<i>Canis lupus fam.</i>					<i>Oryctolagus cuniculus</i>				
	aa1	aa2	num	dist	aa1	aa2	num	dist	var	aa1	aa2	num	dist	var	aa1	aa2	num	dist	var
24	GLN	ALA	475	3.695	LEU	ALA	475	3.079	-	LEU	ALA	475	3.073	-	LEU	ALA	475	3.060	-
	GLN	GLY	476	4.121	LEU	GLY	476	3.465	-	LEU	GLY	476	3.546	-	LEU	GLY	476	3.453	-
	GLN	ASN	487	2.954	LEU	ASN	487	3.617	+	LEU	ASN	487	3.745	+	LEU	ASN	487	3.610	+
27	THR	PHE	456	3.553															
	THR	ALA	475	3.890															
	THR	TYR	489	3.637															
28	PHE	TYR	489	3.526															
	PHE	TYR	489	3.531															
30	ASP	LYS	417	2.547	GLU	LYS	417	2.614	+	GLU	LYS	417	3.035	+	GLU	LYS	417	2.574	+
					GLU	LEU	455	3.328	-						GLU	LEU	455	3.302	-
	ASP	PHE	456	3.886	GLU	PHE	456	3.574	-	GLU	PHE	456	3.357	-	GLU	PHE	456	3.567	-
31	LYS	TYR	489	3.993															
34	HIS	TYR	453	2.936						TYR	TYR	453	3.055	+	GLN	TYR	453	2.944	=
	HIS	LEU	455	3.336						TYR	LEU	455	3.284	-	GLN	LEU	455	3.908	+
	HIS	GLN	493	3.606						TYR	GLN	493	3.707	+	GLN	GLN	493	3.694	+
38	ASP	TYR	449	2.560	GLU	TYR	449	3.339	+	GLU	TYR	449	3.344	+					
	ASP	GLY	496	3.357	GLU	GLY	496	2.592	-	GLU	GLY	496	2.600	-					
41	TYR	GLN	498	3.937															
	TYR	THR	500	2.866															
	TYR	ASN	501	2.831															
42	GLN	GLY	446	3.361															
	GLN	TYR	449	2.882															
	GLN	GLN	498	3.212															
79																			
82	MET	PHE	486	3.545	THR	PHE	486	2.968	-	THR	PHE	486	2.970	-	THR	PHE	486	2.976	-
83	TYR	PHE	486	3.232															
	TYR	ASN	487	2.947															
353	LYS	GLY	496	2.899															
	LYS	ASN	501	3.762															
	LYS	GLY	502	2.847															
	LYS	TYR	505	3.339															
354	GLY																		
	GLY																		
	GLY																		
	GLY																		
355	ASP	THR	500	3.503															
357	ARG	THR	500	3.437															

#### Distances among residues involved in contacts between ACE2 and SARS-CoV-2 calculated by Chimera software.

Data are reported only for residues showing substitutions. The lowest distance is reported when an ACE2 residue shows more than one contact with the same SARS-CoV-2 residue.

**Legend:** aa1 is ACE2 aminoacid; aa2 is SARS-CoV-2 RBD aminoacid; num is the number of the aa2 position in the SARS-CoV-2 spike protein; dist is the predicted distance between aa1 and aa2 expressed in Angstrom; var is the variation of the distance in comparison with humans

(+) means a longer distance, (-) means a shorter distance, (=) means that no significant difference between distances was observed in comparison with contacts between human ACE2 and SARS-CoV-2

	<i>Homo sapiens</i>					<i>Ochotona princeps</i>					<i>Cricetulus griseus</i>					<i>Mesocricetus auratus</i>						
ACE2 residue	aa1	aa2	num	dist		aa1	aa2	num	dist	var		aa1	aa2	num	dist	var		aa1	aa2	num	dist	var
24	GLN	ALA	475	3.695		LEU	ALA	475	3.073	-												
	GLN	GLY	476	4.121		LEU	GLY	476	3.459	-												
	GLN	ASN	487	2.954		LEU	ASN	487	3.624	+												
27	THR	PHE	456	3.553																		
	THR	ALA	475	3.890																		
	THR	TYR	489	3.637																		
28	PHE	TYR	489	3.526																		
	PHE	TYR	489	3.531																		
30	ASP	LYS	417	2.547																		
	ASP	PHE	456	3.886																		
31	LYS	TYR	489	3.993																		
34	HIS	TYR	453	2.936		GLN	TYR	453	2.914	-		GLN	TYR	453	2.925	-		GLN	TYR	453	2.925	-
	HIS	LEU	455	3.336		GLN	LEU	455	3.921	-		GLN	LEU	455	3.919	+		GLN	LEU	455	3.919	+
	HIS	GLN	493	3.606		GLN	GLN	493	3.694	+		GLN	GLN	493	3.691	+		GLN	GLN	493	3.691	+
38	ASP	TYR	449	2.560																		
	ASP	GLY	496	3.357																		
41	TYR	GLN	498	3.937																		
	TYR	THR	500	2.866																		
	TYR	ASN	501	2.831																		
42	GLN	GLY	446	3.361																		
	GLN	TYR	449	2.882																		
	GLN	GLN	498	3.212																		
79																						
82	MET	PHE	486	3.545		THR	PHE	486	2.960	-		ASN	PHE	486	3.575	+		ASN	PHE	486	3.575	+
83	TYR	PHE	486	3.232																		
	TYR	ASN	487	2.947																		
353	LYS	GLY	496	2.899																		
	LYS	ASN	501	3.762																		
	LYS	GLY	502	2.847																		
	LYS	TYR	505	3.339																		
354	GLY																					
	GLY					ASP	GLY	502	3.757	-												
	GLY					ASP	VAL	503	3.417	-												
	GLY					ASP	TYR	505	3.696	-												
355	ASP	THR	500	3.503																		
357	ARG	THR	500	3.437																		

ACE2 residue	<i>Homo sapiens</i>				<i>Mus musculus</i>					<i>Rattus norvegicus</i>					<i>Mustela putorius furo</i>				
	aa1	aa2	num	dist	aa1	aa2	num	dist	var	aa1	aa2	num	dist	var	aa1	aa2	num	dist	var
24	GLN	ALA	475	3.695	ASN	ALA	475	2.928	-						LEU	ALA	475	3.054	-
	GLN	GLY	476	4.121						LYS	GLY	476	3.840	+	LEU	GLY	476	3.518	-
	GLN	ASN	487	2.954	ASN	ASN	487	3.692	+	LYS	ASN	487	3.348	+	LEU	ASN	487	3.695	+
27	THR	PHE	456	3.553															
	THR	ALA	475	3.890						SER	ALA	475	3.376	-					
	THR	TYR	489	3.637															
28	PHE	TYR	489	3.526															
	PHE	TYR	489	3.531															
30	ASP	LYS	417	2.547											GLU	LYS	417	3.154	+
	ASP	PHE	456	3.886	ASN	PHE	456	3.850	-	ASN	PHE	456	3.857	-					
31	LYS	TYR	489	3.993	LYS	TYR	489	4.012	+										
34	HIS	TYR	453	2.936	GLN	TYR	453	2.876	-	GLN	TYR	453	2.886	-	TYR	TYR	453	3.054	+
	HIS	LEU	455	3.336	GLN	LEU	455	3.920	+	GLN	LEU	455	3.920	+	TYR	LEU	455	3.266	-
	HIS	GLN	493	3.606	GLN	GLN	493	3.684	+	GLN	GLN	493	3.697	+	TYR	GLN	493	3.649	+
38	ASP	TYR	449	2.560											GLU	TYR	449	3.353	+
	ASP	GLY	496	3.357											GLU	GLY	496	2.617	-
41	TYR	GLN	498	3.937															
	TYR	THR	500	2.866															
	TYR	ASN	501	2.831															
42	GLN	GLY	446	3.361															
	GLN	TYR	449	2.882															
	GLN	GLN	498	3.212															
79					THR					ILE					HIS				
82	MET	PHE	486	3.545	SER	PHE	486	3.602	+	ASN	PHE	486	3.584	+	THR	PHE	486	2.944	-
83	TYR	PHE	486	3.232	PHE	PHE	486	3.446	+	PHE	PHE	486	3.453	+					
	TYR	ASN	487	2.947															
353	LYS	GLY	496	2.899															
	LYS	ASN	501	3.762	HIS	ASN	501	3.741	+	HIS	ASN	501	3.737	+					
	LYS	GLY	502	2.847	HIS	GLY	502	2.853	-	HIS	GLY	502	2.849	-					
	LYS	TYR	505	3.339	HIS	TYR	505	3.370	+	HIS	TYR	505	3.367	+					
354	GLY														ARG	ASP	405	2.858	-
	GLY														ARG	GLY	502	3.483	-
	GLY																		
	GLY														ARG	TYR	505	3.400	-
355	ASP	THR	500	3.503															
357	ARG	THR	500	3.437															