

Supplementary Data 1:

Physiochemical properties of SARS-CoV-2 T-cell epitopes in comparison to common human coronaviruses

Nelde et al.

Information

- Physiochemical properties were calculated by the freely available software PepCalc (<https://pepcalc.com/>)
- y axis: Hopp-Woods hydrophilicity scale
 - top is hydrophylic
 - bottom is hydrophobic
- color code:
 - acidic
 - aromatic
 - basic
 - aliphatic
 - polar
 - cysteine

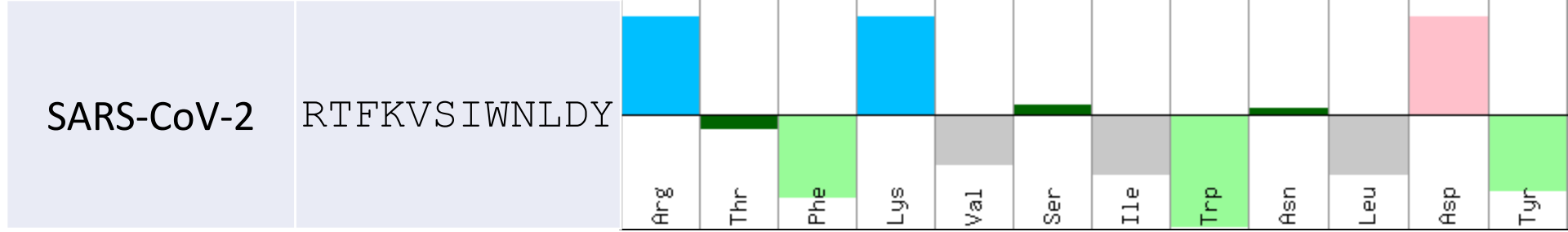
Cross-reactive T-cell epitopes

HLA class I

A01_P01

SARS-CoV-2	TTDPSFLGRY										
		Thr	Thr	Asp	Pro	Ser	Phe	Leu	Gly	Arg	Tyr
HCoV-OC43	NFDQKELLAY										
		Asn	Phe	Asp	Gln	Lys	Glu	Leu	Leu	Ala	Tyr
HCoV-229E	GFKDAVTFAT										
		Gly	Phe	Lys	Asp	Ala	Val	Thr	Phe	Ala	Thr
HCoV-NL63	GFEKAALFAS										
		Gly	Phe	Glu	Lys	Ala	Ala	Leu	Phe	Ala	Ser
HCoV-HKU1	GF'DQQQLLAY										
		Gly	Phe	Asp	Gln	Gln	Gln	Leu	Leu	Ala	Tyr

A01_P05



No alignments to common coronaviruses possible.

A03_P01

SARS-CoV-2	KLFAAETLK									
		Lys	Leu	Phe	Ala	Ala	Glu	Thr	Leu	Lys
HCoV-OC43	KLFAAETQK									
		Lys	Leu	Phe	Ala	Ala	Glu	Thr	Gln	Lys
HCoV-229E	RLFAAETVK									
		Arg	Leu	Phe	Ala	Ala	Glu	Thr	Val	Lys
HCoV-NL63	RLFAAETIK									
		Arg	Leu	Phe	Ala	Ala	Glu	Thr	Ile	Lys
HCoV-HKU1	KLFAAETQK									
		Lys	Leu	Phe	Ala	Ala	Glu	Thr	Gln	Lys

B08_P05

SARS-CoV-2	TPKYK FVRI	Thr	Pro	Lys	Tyr	Lys	Phe	Val	Arg	Ile
HCoV-OC43	TPKYT FGVV	Thr	Pro	Lys	Tyr	Thr	Phe	Gly	Val	Val
HCoV-229E	TPRHS FRTL	Thr	Pro	Arg	His	Ser	Phe	Arg	Thr	Leu
HCoV-NL63	TPKHV FKTL	Thr	Pro	Lys	His	Val	Phe	Lys	Thr	Leu
HCoV-HKU1	TPKYT FGNV	Thr	Pro	Lys	Tyr	Thr	Phe	Gly	Asn	Val

B08_P08

SARS-CoV-2	DLKGGKYVQI									
		Asp	Leu	Lys	Gly	Lys	Tyr	Val	Gln	Ile
HCoV-OC43	KLRGKGFVQV									
		Lys	Leu	Arg	Gly	Lys	Phe	Val	Gln	Val
HCoV-229E	QYKGGKWWQV									
		Gln	Tyr	Lys	Gly	Lys	Trp	Val	Gln	Val
HCoV-NL63	KFKGGKCVQV									
		Lys	Phe	Lys	Gly	Lys	Cys	Val	Gln	Val
HCoV-HKU1	KLRGKGFVQV									
		Lys	Leu	Arg	Gly	Lys	Phe	Val	Gln	Val

Cross-reactive T-cell epitopes

HLA-DR

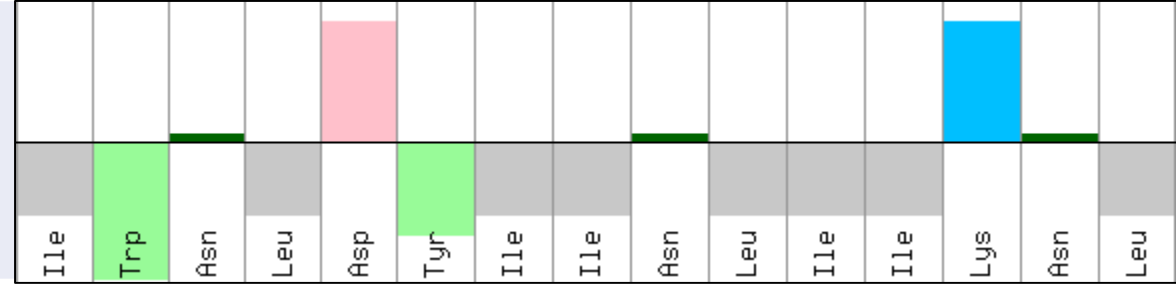
DR_P15

SARS-CoV-2	FYVYSRVK N LNS S SRV	Phe	Tyr	Val	Tyr	Ser	Arg	Val	Lys	Asn	Leu	Asn	Ser	Ser	Arg	Val
HCoV-OC43	IYVFNRGRQFYEFYN	Ile	Tyr	Val	Phe	Asn	Arg	Gly	Arg	Gln	Phe	Tyr	Glu	Phe	Tyr	Asn
HCoV-229E	KNVYHIYQSYM H IDP	Lys	Asn	Val	Tyr	His	Ile	Tyr	Gln	Ser	Tyr	Met	His	Ile	Asp	Pro
HCoV-NL63	YKIFL A YQDYMQIAP	Tyr	Lys	Ile	Phe	Leu	Ala	Tyr	Gln	Asp	Tyr	Met	Gln	Ile	Ala	Pro
HCoV-HKU1	AYVYK R GMQLYKSYS	Ala	Tyr	Val	Tyr	Lys	Arg	Gly	Met	Gln	Leu	Tyr	Lys	Ser	Tyr	Ser

DR_P17

SARS-CoV-2

IWNLDYIINLI IKNL

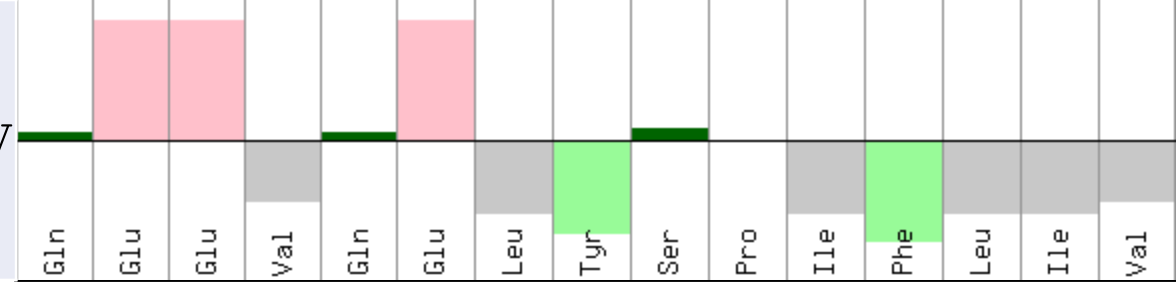


No alignments to common coronaviruses possible.

DR_P18

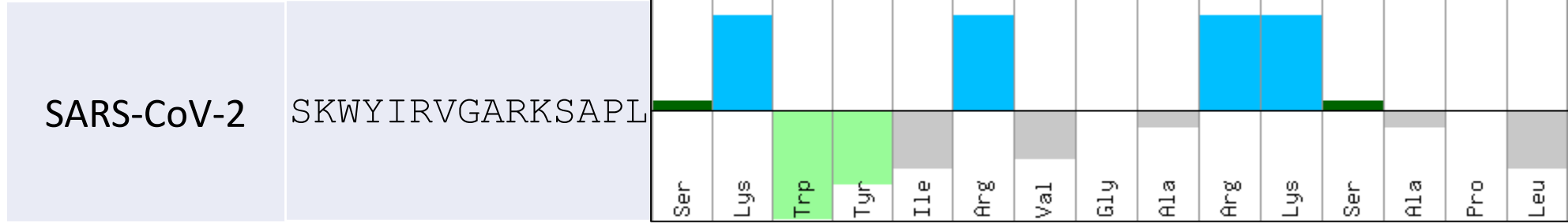
SARS-CoV-2

QEEVQELYSPIFLIV



No alignments to common coronaviruses possible.

DR_P19



No alignments to common coronaviruses possible.

DR_P07

SARS-CoV-2	LLLLDRLNQLESKMS	<p>Sequence alignment visualization for SARS-CoV-2. The sequence is LLLLLDRLNQLESKMS. The alignment shows conserved residues (Leu, Asp, Arg, Leu, Asn, Gln, Leu, Glu, Ser, Lys, Met, Ser) and highlighted residues (Asp, Arg, Glu, Lys) in red and blue. Green bars indicate gaps or specific modifications.</p>
HCoV-OC43	SLVLAKLGGKDATKPQ	<p>Sequence alignment visualization for HCoV-OC43. The sequence is SLVLAKLGGKDATKPQ. The alignment shows conserved residues (Ser, Leu, Val, Leu, Ala, Lys, Leu, Gly, Lys, Asp, Ala, Thr, Lys, Pro, Gln) and highlighted residues (Lys, Asp, Lys) in blue and red. Green bars indicate gaps or specific modifications.</p>
HCoV-229E	SLGF'DKPQEKDKKSA	<p>Sequence alignment visualization for HCoV-229E. The sequence is SLGF'DKPQEKDKKSA. The alignment shows conserved residues (Ser, Leu, Gly, Phe, Asp, Lys, Pro, Gln, Glu, Lys, Asp, Lys, Lys, Ser, Ala) and highlighted residues (Asp, Lys, Asp, Lys, Lys) in red and blue. Green bars indicate gaps or specific modifications.</p>
HCoV-NL63	NLGF'DNQSKSPSSSG	<p>Sequence alignment visualization for HCoV-NL63. The sequence is NLGF'DNQSKSPSSSG. The alignment shows conserved residues (Asn, Leu, Gly, Phe, Asp, Asn, Gln, Ser, Lys, Ser, Pro, Ser, Ser, Ser, Gly) and highlighted residues (Asp, Lys) in red and blue. Green bars indicate gaps or specific modifications.</p>
HCoV-HKU1	NLVLAKLGGKDSKPQQ	<p>Sequence alignment visualization for HCoV-HKU1. The sequence is NLVLAKLGGKDSKPQQ. The alignment shows conserved residues (Asn, Leu, Val, Leu, Ala, Lys, Leu, Gly, Lys, Asp, Ser, Lys, Pro, Gln, Gln) and highlighted residues (Lys, Asp, Lys) in blue and red. Green bars indicate gaps or specific modifications.</p>

DR_P04

SARS-CoV-2	ASWFTALTQHGKEDL	Ala	Ser	Trp	Phe	Thr	Ala	Leu	Thr	Gln	His	Gly	Lys	Glu	Asp	Leu
HCoV-OC43	YSWFSGITQFQKGKE	Tyr	Ser	Trp	Phe	Ser	Gly	Ile	Thr	Gln	Phe	Gln	Lys	Gly	Lys	Glu
HCoV-229E	YSLYSPLLVDSEQPW	Tyr	Ser	Leu	Tyr	Ser	Pro	Leu	Leu	Val	Asp	Ser	Glu	Gln	Pro	Trp
HCoV-NL63	PSFYMPLLVSSDKAP	Pro	Ser	Phe	Tyr	Met	Pro	Leu	Leu	Val	Ser	Ser	Asp	Lys	Ala	Pro
HCoV-HKU1	YSWFSGITQFQKGRD	Tyr	Ser	Trp	Phe	Ser	Gly	Ile	Thr	Gln	Phe	Gln	Lys	Gly	Arg	Asp

DR_P05

SARS-CoV-2	ASAFFGMSRIGMEVT																	
		Ala	Ser	Ala	Phe	Phe	Gly	Met	Ser	Arg	Ile	Gly	Met	Glu	Val	Thr		
HCoV-OC43	AGAFFFFGSRLELAKV																	
		Ala	Gly	Ala	Phe	Phe	Phe	Gly	Ser	Arg	Leu	Glu	Leu	Ala	Lys	Val		
HCoV-229E	TAAMLFD SHIVSKES																	
		Thr	Ala	Ala	Met	Leu	Phe	Asp	Ser	His	Ile	Val	Ser	Lys	Glu	Ser		
HCoV-NL63	QAALFFDSEVSTDEV																	
		Gln	Ala	Ala	Leu	Phe	Phe	Asp	Ser	Glu	Val	Ser	Thr	Asp	Glu	Val		
HCoV-HKU1	PGAFFFFGSKLDLVKR																	
		Pro	Gly	Ala	Phe	Phe	Phe	Gly	Ser	Lys	Leu	Asp	Leu	Val	Lys	Arg		