



Figure S1. Graphic determination of optimal cut-off of OD for each peptide. Each cut-off has been chosen accordingly to the best balance between odds ratio of severity and its p-value. We proposed a graphical plot that illustrates the DO ability to classify the COVID-19 disease as severe according to the variations in the DO value distribution, giving a discrimination threshold = cut-off (on the same basis as ROC curves).

Table S1. Peptide sequences of putative immunodominant SARS-CoV-2 IgG linear B-cell epitopes.

Peptide ID	Position	Amino acid sequence
SK1	27-46	AYTNSFTRGVYYPDKVFRSS
SK2	59-78	FSNVTWFHAIHVSGTNGTKRF
SK3	75-94	GTKRFDNPVLPFNDGVYFAST
SK4	91-110	YFASTEKSNIRGWIFGTTLD
SK5	107-126	GTTLDSKTQSLIVNNATNVV
SK6	123-142	ATNVVIKVCEFQFCNDPFLGV
SK7	139-158	PFLGVYYHKNNKSWMESEFRV
SK8	155-174	SEFRVYSSANNCTFEYVSQPF
SK8'	150-180	KSWMESEFRVYSSANNCTFEYVSQPFMDLE
SK9	171-190	VSQPFMDLEGGKQGNFKNLRE
SK10	187-206	KNLREFVFKNIDGYFKIYSKH
SK11	203-222	IYSKHTPINLVRDLPQGFSAL
SK12	236-255	TRFQTLALHRSYLTGPDSSS
SK13	252-271	GDSSSGWTAGAAAYYVGYLQ
SK13'	247-276	SYLTGPDSSSGWTAGAAAYYVGYLQPRFTL
SK14	328-347	RFPNITNLCPFGEVFNATRFA
SK15	344-363	ATRFASVYAWNRKRISNCVAD
SK16	360-379	NCVADYSVLNYSASFSTFKC
SK16'	355-385	RKRISNCVADYSVLNYSASFSTFKCYGVSP
SK17	376-395	TFKCYGVSPTKLNDLCFTNVY
SK18	392-411	FTNVYADSFVIRGDEVQRQIAP
SK19	408-427	RQIAPGQTGKIADYNYKLPDD
SK18-19	391-428	CFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDD
SK20	424-443	KLPDDFTGCVIAWNSNNLDSK
SK22	456-475	FRKSNLKPFERDISTEIQAG
SK23	472-491	IYQAGSTPCNGVEGFNCYFPL
SK23'	467-497	DISTEIQAGSTPCNGVEGFNCYFPLQSYGF
SK24	488-507	YFPLQSYGFQPTNGVGYQPYR
SK25	504-523	GYQPYRVVLSFELLHAPATV
SK25'	499-529	PTNGVGYQPYRVVLSFELLHAPATVCGPKK
SK26	520-539	APATVCGPKKSTNLVKNKCVN
SK27	549-568	TGVLTESNKKFLPFQQFGRD
SK28	571-590	DTTDAVRDPQTLEILDITPCSF
SK28'	566-597	GRDIADTTDAVRDPQTLEILDITPCSFGGVSV
SK29	700-717	GAENSVAYSNNIAIPTNFT
SK30	782-801	FAQVKQIYKTPPIKDFGGFNF
SK31	798-817	GGFNFSQILPDPSKPSKRSF
SK32	877-896	LLAGTITSGWTFGAGAALQIP
SK33	893-912	ALQIPFAMQMAYRFNGIGVTQ
SK34	909-928	IGVTQNVLYENQKLIANQFN
SK34'	904-940	YRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSS
SK35	1067-1086	YVPAQEKNFTTAPAICHGDKA
SK35'	1062-1092	FLHVTYVPAQEKNFTTAPAICHGDKAHFPRE
SK36	1083-1102	HDGKAHFPRGVFVSNQTHWF
SK37	1099-1118	GTHWFVTQRNFPYEPQIITDN
SK39	1131-1150	GIVNNTVYDPLQPELDSFKE
NC1	22-42	DSTGSNQNGERSGARSKQRRP
NC2	87-108	YRRATRRIRGGDGKMKDLSPRW
NC2'	82-112	DQIGYYRRATRRIRGGDGKMKDLSPRWYFYY
NC3	153-172	NNAAIVLQLPQGTTLPKGFY
NC3'	148-177	TRNPANNAIVLQLPQGTTLPKGFYAEGSR
NC4	177-198	RGGSQASSRSSRSRNSRNST
NC5	371-390	DKKKKADETQALPQRQKKQQ
NC5'	366-395	TEPKKDKKKKADETQALPQRQKKQQTVTLL
NC6	1-23	MSDNGPQNQRNAPRITFGGPSDS
NC8	242-274	QGQTVTKKSAAEASKPRQKRTATKAYNVQAF
M1	1-19	MADSNGTITVEELKKLLEQ
NS1	24-44	SCTQHQPYYVDDPCPIHFYSK
NS2	38-59	PIHFYSKWYIRVGARKSAPLIE
NS3	61-82	CVDEAGSKSPIQYIDIGNYTVS
SKS-36	-	CESFATGVHFFHGDWRNPVGK

Table S2. Peptides of interest: selection. Peptides giving a mean optical density (OD) superior to 0.3 and at least 5 fold superior to the OD obtained with the negative control were selected for further analysis.

Peptide ID	OD (Mean \pm SD)	
	COVID – pool	COVID +
SK1	0.047 \pm 0.067	0.056 \pm 0.114
SK2	0.072 \pm 0.050	0.073 \pm 0.115
SK3	0.033 \pm 0.057	0.055 \pm 0.090
SK4	0.099 \pm 0.101	0.086 \pm 0.112
SK5	0.007 \pm 0.010	0.059 \pm 0.099
SK6	0.020 \pm 0.030	0.073 \pm 0.109
SK7	0.072 \pm 0.119	0.075 \pm 0.084
SK8	0.008 \pm 0.020	0.102 \pm 0.181
SK8'	0.005 \pm 0.010	0.050 \pm 0.085
SK9	0.056 \pm 0.046	0.101 \pm 0.151
SK10	0.087 \pm 0.128	0.126 \pm 0.140
SK11	0.031 \pm 0.059	0.086 \pm 0.184
SK12	0.066 \pm 0.063	0.082 \pm 0.084
SK13	0.023 \pm 0.027	0.099 \pm 0.124
SK13'	0.002 \pm 0.008	0.018 \pm 0.061
SK14	0.122 \pm 0.111	0.112 \pm 0.125
SK15	0.170 \pm 0.070	0.320 \pm 0.238
SK16	0.012 \pm 0.029	0.101 \pm 0.166
SK16'	0.019 \pm 0.051	0.020 \pm 0.047
SK17	0.034 \pm 0.05	0.152 \pm 0.186
SK18	0.084 \pm 0.094	0.075 \pm 0.097
SK19	0.022 \pm 0.021	0.117 \pm 0.170
SK18-19	0.016 \pm 0.014	0.042 \pm 0.095
SK20	0.062 \pm 0.088	0.078 \pm 0.129
SK22	0.047 \pm 0.060	0.129 \pm 0.263
SK23	0.009 \pm 0.014	0.128 \pm 0.223
SK23'	0.00043 \pm 0.002	0.062 \pm 0.161
SK24	0.077 \pm 0.101	0.123 \pm 0.232
SK25	0.027 \pm 0.057	0.018 \pm 0.038
SK25'	0.032 \pm 0.016	0.074 \pm 0.108
SK26	0.205 \pm 0.065	0.464 \pm 0.409
SK27	0.024 \pm 0.027	0.335 \pm 0.450
SK28	0.175 \pm 0.063	0.748 \pm 0.746
SK28'	0.034 \pm 0.076	0.349 \pm 0.425
SK29	0.084 \pm 0.103	0.085 \pm 0.110
SK30	0.063 \pm 0.051	0.328 \pm 0.556
SK31	0.134 \pm 0.223	0.112 \pm 0.158
SK32	0.136 \pm 0.178	0.086 \pm 0.134
SK33	0.017 \pm 0.042	0.058 \pm 0.144
SK34	0.056 \pm 0.095	0.036 \pm 0.084
SK34'	0.00018 \pm 0.001	0.055 \pm 0.224
SK35	0.164 \pm 0.167	0.123 \pm 0.198
SK35'	0.014 \pm 0.032	0.061 \pm 0.111
SK36	0.222 \pm 0.293	0.079 \pm 0.118
SK37	0.041 \pm 0.045	0.074 \pm 0.107
SK39	0.087 \pm 0.121	0.093 \pm 0.159
NC1	0.003 \pm 0.006	0.048 \pm 0.125
NC2	0.101 \pm 0.132	0.605 \pm 0.664
NC2'	0.009 \pm 0.034	0.212 \pm 0.304
NC3	0.002 \pm 0.007	0.454 \pm 0.700
NC3'	0.017 \pm 0.031	1.063 \pm 1.187
NC4	0.021 \pm 0.016	0.122 \pm 0.257
NC5	6.10 ⁻⁵ \pm 2.46.10 ⁻⁴	0.253 \pm 0.438
NC5'	0.082 \pm 0.038	1.103 \pm 0.856
NC6	0.005 \pm 0.019	0.088 \pm 0.284
NC8	0.202 \pm 0.058	0.237 \pm 0.286
M1	0.032 \pm 0.105	0.489 \pm 0.856
NS1	0.057 \pm 0.202	0.068 \pm 0.174
NS2	0.176 \pm 0.084	1.275 \pm 0.725
NS3	0.037 \pm 0.078	0.208 \pm 0.554