

Table S1. The B cell epitope candidates in the SARS-CoV-2 spike protein using BepiPred-2.0 algorithm

Peptide n°	Amino acid sequence	Position	Length
1	SQCVNLTTRTQLPPAYTNSFTRGVY	13-37	25
2	FSNVTWFHAIHVSGTNGTKRFDN	59-81	23
3	DPFLGVYYHKNNKSWME	138-154	17
4	MDLEGKQGNFKNL	177-189	13
5	KHTPINLVRDLPQGFS	206-221	16
6	TPGDSSSGWTA	250-260	11
7	KSFTVEKGIYQTSNFRVQP	304-322	19
8	FPNITNLCPFGEVFNATRFASVYAWNKRKISNCVA	329-363	35
9	YNSASFSTFKCYGVSPTKLNDLCFT	369-393	25
10	GDEVROIAPGQTGKIADYNYKLP	404-426	23
11	NLDSKVGNYLYRLEFRKSNLKPFRDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTN	440-501	62
12	ELLHAPATVCGPKKSTNLVKN	516-536	21
13	NCTEVPVAIHADQLTPT	616-632	17
14	RVYSTGSNVFQ	634-644	11
15	VNNSYECDIPI	656-666	11
16	ASYQTQTNSPPARRSVASQ	672-690	19
17	YTMSLGAENSVAYSNN	695-710	16
18	KQIYKTPPIKDFGGF	786-800	15
19	PDPSKPSK	807-814	8
20	LADAGFIKQYGDCLG	828-842	15
21	RNFYEPQIITTD	1107-1118	12
22	VNNTVYDPLQPELDSFKEELDKYFKNHTSPDVLGDISGI	1133-1172	40
23	SCCKFDEDDSEPVKLG	1252-1267	16

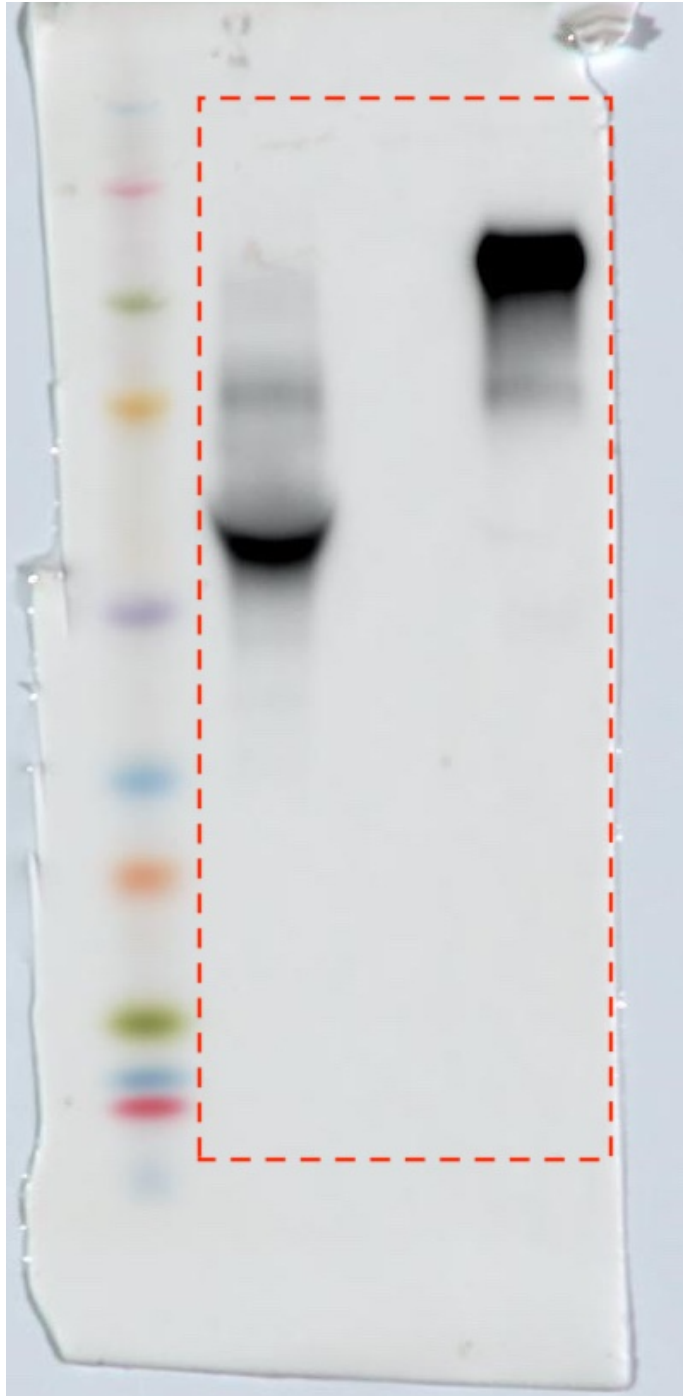


Figure S1. **Original and unprocessed immunoblot used in the Figure 2A.** The hatched red line depicts the portion of immunoblot gel shown in Fig. 2A.

Table S2. COVID-19 immune subject characteristics

donor n°	age ¹	gender	origin	date of specimen collection	IgM ²	IgG ²
1	13	F	France	11.20	+++	++
2	18	F	France	12.20	+	+++
3	23	M	France	11.20	++++	+++
4	23	M	France	11.20	++++	++
5	38	F	France	11.20	++++	+++
6	42	F	France	11.20	++++	+
7	45	F	France	12.20	++++	++
8	45	F	France	11.20	+	+++
9	46	F	France	11.20	+	+++
10	51	F	France	11.20	++	++
11	51	F	France	12.20	++	++
12	53	F	France	11.20	++++	++
13	59	M	France	11.20	+	+++
14	59	F	France	12.20	+++	+++
15	61	M	France	11.20	+++	+++
16	63	F	France	11.20	++	++++
17	64	F	France	11.20	+++	++
18	70	F	France	12.20	+	++++
19	71	F	France	12.20	++	++++
20	73	M	France	11.20	+	++++
21	77	F	France	11.20	+	++
22	79	F	France	12.20	+	++
23	80	F	France	12.20	++	+++
24	81	F	France	11.20	+	+++
25	85	F	France	11.20	++	++
26	85	F	France	11.20	++	++
27	87	F	France	11.20	+	+++
28	91	M	France	11.20	++	+++
29	91	F	France	11.20	++++	+++
30	97	F	France	11.20	+	++

¹years.

²anti-SARS-CoV-2 antibodies fold increase of normal range as a score: + (1.5-2.0), ++ (2.0-4.0), +++ (4.0-6.0), ++++ (> 6.0).

Table S3. Infection-naïve individual characteristics

donor n°	age ¹	gender	origin	date of specimen collection
1	17	F	France	09.19
2	23	F	France	09.19
3	27	M	France	09.19
4	36	F	France	09.19
5	41	F	France	09.19
6	45	M	France	09.19
7	54	M	France	09.19
8	56	M	France	09.19
9	64	M	France	09.19
10	74	F	France	09.19

¹years.

Table S4. COMIRNATY vaccine recipient characteristics.

donor n°	age ¹	gender	origin	date of vaccination	date of specimen collection
1	32	F	France ²	03.21	03.21
2	33	M	France	02.21	03.21
3	39	M	France	01.21	02.21
4	44	F	France	02.21	02.21
5	50	F	France	02.21	03.21
6	55	M	France	02.21	03.21
7	56	F	France	02.21	03.21
8	58	M	France	02.21	02.21
9	62	M	France	02.21	03.21

¹. years

². La Reunion island (France)

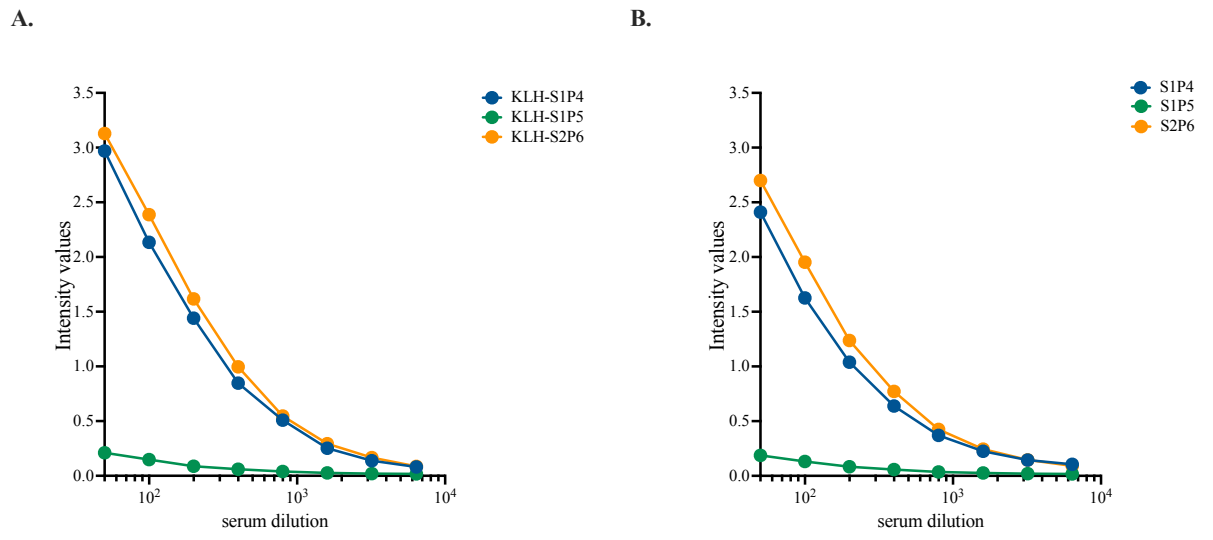


Figure S2. Antigenic reactivity of protein-peptide conjugates. Serum sample from a COVID-19 recovered patient who had been immunized with a single dose of COMIRNATY vaccine was collected 0.5 month after vaccine administration and serum dilutions were assayed on KLH-peptide conjugates through indirect ELISA (A) or synthetic peptides through peptide-based ELISA (B). The synthetic KLH-S1P5 conjugate and synthetic S1P5 peptide served as negative controls. The intensity values of serum samples were measured at O.D. 450 nm.

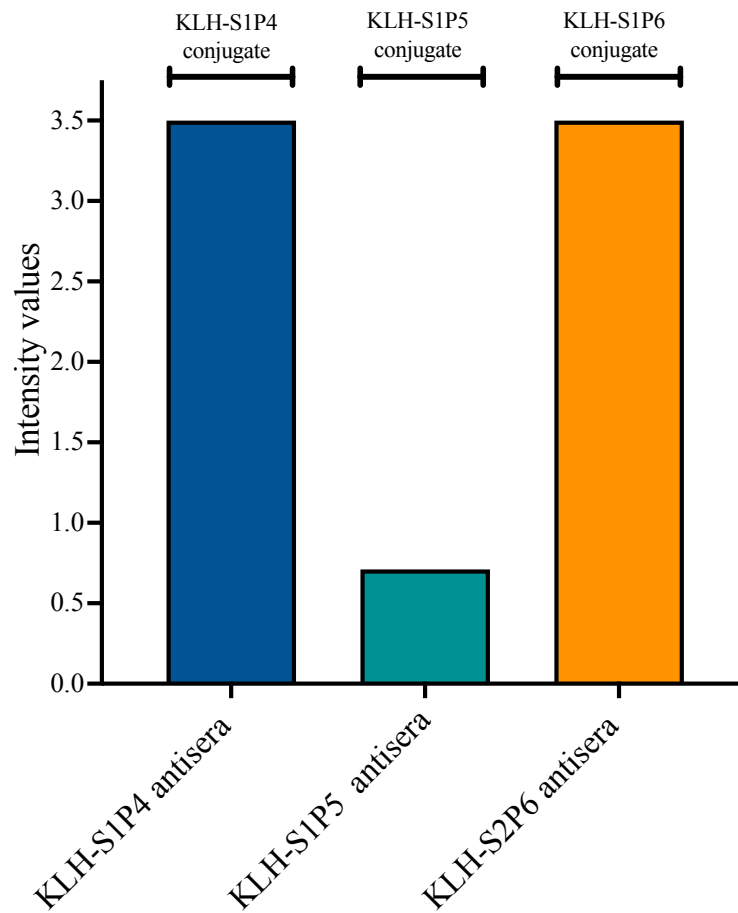


Fig. S3. Immune reactivity of mouse antisera raised against protein-peptide conjugates. Pools of serum samples from five mice that received KLH-peptide S1P4 (KLH-peptide S1P4 antisera), KLH-peptide S1P5 (KLH-peptide S1P5 antisera), or KLH-peptide S2P6 (KLH-peptide S2P6 antisera) in a prime-boost regimen were tested at serum dilution 1:100 for their immune reactivity in relation with protein-peptide conjugate (100 ng) by indirect ELISA. Intensity values or O.D. values at 450 nm.

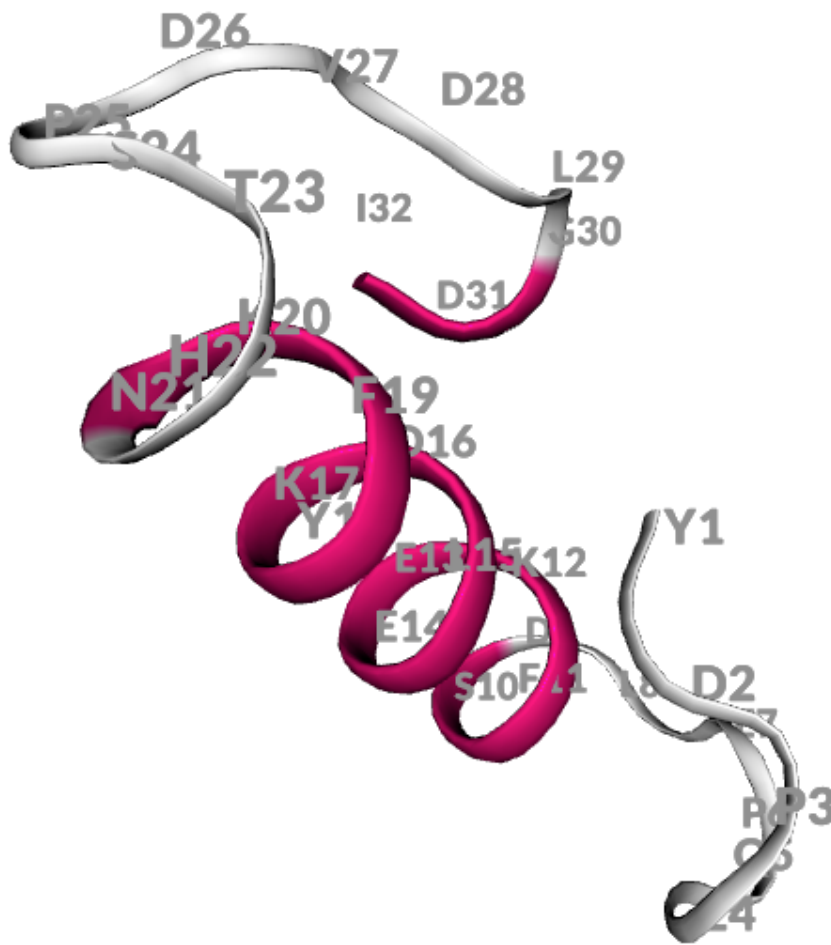


Fig.S4. Tridimensional structure prediction of S2P6 peptide. A 3D structure prediction of the B-cell epitope peptide S2P6 (residues Y1 to I32) was performed using PEP-FOLD3 protein recognition server (<https://mobylye.rpbs.univ-paris-diderot.fr/cgi-bin/portal.py#forms::PEP-FOLD3>) (34). The S2P6.2.0 peptide contains amino-acids S10 to D28.