

1 **Antigenic variation of SARS-CoV-2 in response to immune pressure**

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4 Diego Forni<sup>1,\*</sup>, Rachele Cagliani<sup>1</sup>, Chiara Pontremoli<sup>1</sup>, Alessandra Mozzi<sup>1</sup>, Uberto Pozzoli<sup>1</sup>, Mario

5 Clerici<sup>2,3</sup>, Manuela Sironi<sup>1</sup>

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8 <sup>1</sup> Scientific Institute IRCCS E. MEDEA, Bioinformatics, Bosisio Parini, Italy;

9 <sup>2</sup> Department of Physiopathology and Transplantation, University of Milan, Milan, Italy;

10 <sup>3</sup> Don C. Gnocchi Foundation ONLUS, IRCCS, Milan, Italy.

11 \* Correspondence: [diego.forni@lanostrafamiglia.it](mailto:diego.forni@lanostrafamiglia.it)

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16 **Summary**

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18 The ongoing evolution of SARS-CoV-2 is expected to be at least partially driven by the selective  
19 pressure imposed by the human immune system. We exploited the availability of a large number of  
20 high-quality SARS-CoV-2 genomes, as well as of validated epitope predictions, to show that B cell  
21 epitopes in the spike glycoprotein (S) and in the nucleocapsid protein (N) have higher diversity than  
22 non-epitope positions. Similar results were obtained for other human coronaviruses. Conversely, in the  
23 SARS-CoV-2 population, epitopes for CD4<sup>+</sup> and CD8<sup>+</sup> T cells were not more variable than non-epitope  
24 positions. A significant reduction in epitope variability was instead observed for some of the most  
25 immunogenic proteins (S, N, ORF8, and ORF3a). Analysis over longer evolutionary time-frames  
26 indicated that this effect is not due to differential constraints. These data indicate that SARS-CoV-2 is  
27 evolving to elude the host humoral immune response, whereas recognition by T cells might benefit the  
28 virus.

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33 **Keywords:** SARS-CoV-2; COVID-19; Human Coronavirus; Sarbecovirus; B cell epitope; T cell

34 epitope

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## 39 **Introduction**

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41 The COVID-19 pandemic is caused by a novel coronavirus named SARS-CoV-2 (Coronaviridae Study  
42 Group of the International Committee on Taxonomy, of Viruses, 2020). Most likely, SARS-CoV-2  
43 originated and evolved in bats, eventually spilling over to humans, either directly or through an  
44 intermediate host (Killerby et al., 2020; Lam et al., 2020; Liu et al., 2020; Sironi et al., 2020; Wong et  
45 al., 2020; Xiao et al., 2020; Zhou et al., 2020a). Sustained human-to-human transmission determined  
46 the global spread of the virus, which has now resulted in an unprecedented global sanitary crisis. In  
47 fact, whereas the majority of COVID-19 cases are relatively mild, a significant proportion of patients  
48 develop a serious, often fatal illness, characterized by acute respiratory distress syndrome (Wu and  
49 McGoogan, 2020). Both viral-induced lung pathology and overactive immune responses are thought to  
50 contribute to disease severity (St John and Rathore, 2020; Vabret et al., 2020).

51 Ample evidence suggests that coronaviruses can easily cross species barriers and have high zoonotic  
52 potential. Indeed, seven coronaviruses are known to infect humans and all of them originated in  
53 animals (Cui et al., 2019; Forni et al., 2017; Ye et al., 2020). Among these, HCoV-OC43, HCoV-  
54 HKU1, HCoV-NL63 and HCoV-229E have been circulating for decades in human populations and  
55 usually cause limited disease (Bucknall et al., 1972; Forni et al., 2017; Woo et al., 2005). They are thus  
56 referred to as “common cold” coronaviruses. Conversely, MERS-CoV and SARS-CoV, whose  
57 emergence in the 2000s preceded that of SARS-CoV-2, can cause serious illness and respiratory  
58 distress syndrome in a non-negligible proportion of infected individuals (Petrosillo et al., 2020). Like  
59 all coronaviruses, these human-infecting viruses have positive-sense, single stranded RNA genomes.  
60 Two thirds of the coronavirus genome are occupied by two large overlapping open reading frames  
61 (ORF1a and ORF1b), that are translated into polyproteins. These latter are processed to generate 16  
62 non-structural proteins (nsp1 to nsp16). The remaining portion of the genome includes ORFs for the

63 structural proteins (spike, envelope, membrane, and nucleocapsid) and a variable number of accessory  
64 proteins (Cui et al., 2019; Forni et al., 2017).

65 Analysis of the bat viruses most closely related to SARS-CoV-2 indicated that, in analogy to SARS-  
66 CoV, the virus most likely required limited adaptation to gain the ability to infect and spread in our  
67 species (Boni et al., 2020; Cagliani et al., 2020). Nonetheless, since its introduction in human  
68 populations SARS-CoV-2 must have been subject to the selective pressure imposed by the human  
69 immune system. In fact, as with most other viruses, data from COVID-19, SARS, and MERS patients  
70 indicate that both B and T lymphocytes play a role in controlling infection (Channappanavar et al.,  
71 2014; St John and Rathore, 2020; Vabret et al., 2020).

72 Recent efforts predicted B cell and T cell epitopes in SARS-CoV-2 proteins (Grifoni et al., 2020a) and  
73 validated such predictions using sera from convalescent COVID-19 patients (Grifoni et al., 2020b).

74 These works, as well as others (Farrera et al., 2020; Poh et al., 2020), revealed that the cell-mediated  
75 responses against SARS-CoV-2 are not restricted to the nucleocapsid (N) and spike (S) proteins, but  
76 rather target both structural and non-structural viral products. In parallel, analyses of B cell responses  
77 in SARS-CoV-2 infected patients showed that the S and N proteins are the major target of the antibody  
78 response and identified specific B cell epitopes in the S protein (Farrera et al., 2020; Jiang et al., 2020;  
79 Poh et al., 2020). We exploited this growing wealth of information to investigate whether, after a few  
80 months of sustained transmission, the selective pressure exerted by the human adaptive immune  
81 response is already detectable in the SARS-CoV-2 population and to investigate how the virus is  
82 evolving in response to such a pressure.

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## 84 **Results**

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### 86 **Antigenic variability of SARS-CoV-2 proteins**

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88 To analyze B cell epitope diversity in SARS-CoV-2, we randomly selected 10,000 high-quality viral  
89 genomes from those available in the GISAID database (as of June 5<sup>th</sup>, 2020) (Elbe and Buckland-  
90 Merrett, 2017). Potential epitopes were predicted using Immune Epitope Database (IEDB) tools, as  
91 previously described (Grifoni et al., 2020a). Specifically, because they are the major targets of the  
92 humoral immune response (Channappanavar et al., 2014; St John and Rathore, 2020; Vabret et al.,  
93 2020), we predicted both linear and conformational B epitopes for the S and N proteins, whereas only  
94 linear epitopes were predicted for the other viral proteins (Table S1). A good correspondence was  
95 observed between B cell epitope predictions for the S protein and epitopes identified in two works that  
96 systematically mapped antibody responses in the sera of convalescent COVID-19 patients (Farrera et  
97 al., 2020; Poh et al., 2020) (Figure 1).

98 Variability at each amino acid site of the proteins encoded by SARS-CoV-2 was quantified using  
99 Shannon's entropy (H). Specifically, only predicted proteins longer than 60 amino acids were analyzed.  
100 Because most positions in SARS-CoV-2 genomes are invariable across the sampled genomes, the  
101 distribution of H is zero-inflated, making the use of conventional statistical tests inappropriate  
102 (McElduff et al., 2010). We thus calculated statistical significance by permutations - i.e., by reshuffling  
103 epitope positions as amino acid stretches of the same size as the predicted epitopes. This approach also  
104 has the advantage of accounting for the possibility that, as a result of locally varying selective  
105 constraints, H is not independent among continuous protein positions.

106 Using this methodology, we found that, for the N and nsp16 proteins, positions mapping to predicted B  
107 cell linear epitopes are significantly more variable than those not mapping to these epitopes. Higher  
108 diversity of B cell epitopes was also observed for S, although it did not reach statistical significance  
109 (Figure 2). However, the H distribution for the spike protein includes a clear outlier represented by  
110 position 614 (Figure 1). Recent works indicated that the D614G variant, which is now prevalent

111 worldwide, enhances viral infectivity without affecting neutralization by convalescent patient plasma  
112 (Korber et al., 2020; Yurkovetskiy et al., 2020; Zhang et al., 2020b). Hence, the frequency increase of  
113 this variant is unlikely to be related to immune evasion. We thus repeated the analyses after excluding  
114 position 614 and we observed that predicted B cell linear epitopes in the spike protein are significantly  
115 more variable than non-epitope positions (Figure 2). The same analysis for B cell conformational  
116 epitopes in the N and S proteins indicated a similar trend, although statistical significance was not  
117 reached (not shown). This is most likely due to the small number of positions in these epitopes.  
118 Overall, these data fit very well with the observation that most humoral immune responses against  
119 SARS-CoV-2 and other human coronaviruses are directed against the S and N proteins (Farrera et al.,  
120 2020; Jiang et al., 2020; Poh et al., 2020). These results also support the notion that the selective  
121 pressure exerted by the human antibody response is already detectable in the SARS-CoV-2 population.  
122 We next assessed whether epitopes for cell-mediated immune responses are also more variable than  
123 non-epitope positions. We thus retrieved predicted CD4<sup>+</sup> and CD8<sup>+</sup> T cell epitopes from a previous  
124 work (Grifoni et al., 2020a). These epitope predictions were shown to be reliable, as they capture a  
125 significant proportion of T cell responses in the sera of convalescent COVID-19 patients (Grifoni et al.,  
126 2020b). Analysis of entropy values indicated that CD4<sup>+</sup> T cell epitopes are significantly less variable  
127 than non-epitope positions for the N and nsp16 proteins (Figure 2). A similar trend was observed for  
128 ORF8, E, and S, although significance was not reached. Reduction of variability was also observed for  
129 CD8<sup>+</sup> T cell epitopes for the N protein, as well as for ORF3a. Higher variability in epitope positions  
130 was observed for nsp8 and nsp14 for CD4<sup>+</sup> T cells alone (Figure 2). Because several epitopes for T  
131 cells co-map with B cell epitopes, which tend to show higher diversity, we compared positions within  
132 CD4<sup>+</sup> or CD8<sup>+</sup> T cell epitopes only (not overlapping with B cell epitopes) with positions not mapping  
133 to any of these epitopes. A significant reduction of variability was observed for S, N, ORF8, nsp15, and  
134 nsp16, whereas higher diversity was still evident for nsp8 (Figure 2).

135 Overall, these data indicate that T cell epitopes in the most immunogenic SARS-CoV-2 proteins (S, N,  
136 ORF3a, and ORF8) (Grifoni et al., 2020b; Peng et al., 2020b) tend to be more conserved than non-  
137 epitopes. However, this was not the case for other proteins targeted by T cell responses, namely M,  
138 ORF7a, nsp3, nsp4, and nsp6.

139 Clearly, protein sequence variability is strongly influenced by functional and structural constraints. We  
140 thus reasoned that if the observations reported above were secondary to the incidental co-localization of  
141 T cell epitopes with more constrained regions, a similar pattern should be observed for H values  
142 calculated on an alignment of proteins from other sarbecoviruses. In fact, all these viruses, with the  
143 exclusion of SARS-CoV, were sampled from bats. Thus, whereas structural/functional constraints are  
144 expected to be maintained across long evolutionary time frames, the pressure exerted by the human  
145 cell-mediated immune response is not, as, in different species, antigen processing within host cells  
146 results in the preferential presentation of diverse viral epitopes to T lymphocytes depending on the  
147 MHC gene repertoire and on distinct preferences of the antigen processing pathway (Abduriyim et al.,  
148 2019; Burgevin et al., 2008; Hammer et al., 2007; Lu, Dan AND Liu, Kefang AND Zhang, Di AND  
149 Yue, Can AND Lu, Qiong AND Cheng, Hao AND Wang, Liang AND Chai, Yan AND Qi, Jianxun  
150 AND Wang, Lin-Fa AND Gao, George F. AND Liu, William J., 2019; Wynne et al., 2016). Conversely,  
151 epitopes for antibodies tend to be conserved across species (Tse et al., 2017; Wiehe et al., 2014) and  
152 consequently the selective pressure acting on these positions is expected to be constant across time and  
153 hosts.

154 We thus aligned the SARS-CoV-2 reference sequences of proteins showing decreased or increased  
155 variability in T cell epitopes with those of 45 sarbecoviruses (Table S2). Calculation of H indicated a  
156 significant difference only for CD4<sup>+</sup> T cell epitopes in the N protein. Conversely, B cell epitopes were  
157 more variable than non-epitope positions for the S, N and nsp16 proteins (Figure 3). Overall, these  
158 results indicate that the variability within SARS-CoV-2 T cell epitopes is not primarily driven by

159 functional/structural constraints, but most likely results from the interaction with the human adaptive  
160 immune response.

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## 162 **Comparison with other human coronaviruses**

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164 Given the results above we set out to determine whether the other human coronaviruses show the same  
165 tendency of reduced and increased variability at T cell and B cell epitopes, respectively. For these  
166 viruses, analyses were restricted to the N and S proteins, as they are the most antigenic proteins and  
167 because the number of complete viral genomes is relatively limited (Table S3).

168 SARS-CoV, the human coronavirus most similar to SARS-CoV-2, caused the first human outbreak in  
169 2002/2003 after a spill-over from palm civets, followed by human-to-human transmission chains (Shi  
170 and Wang, 2017). A second zoonotic transmission occurred in December 2003 and caused a limited  
171 number of cases (Shi and Wang, 2017; Wang et al., 2005). Viral genomes sampled during the second

172 outbreak were not included in the analyses because their evolution occurred in the civet reservoir  
173 (Table S4). Four other human coronaviruses – HCoV-OC43, HCoV-HKU1 (members of the

174 *Embecovirus* subgenus), HCoV-229E (*Duvinavirus* subgenus), and HCoV-NL63 (*Setracovirus*  
175 subgenus) - have been transmitting within human populations for at least 70 years (Forni et al., 2017).

176 Thus, all available S and N sequences were included in the analyses (Table S4). Conversely, MERS-  
177 CoV displays limited ability of human-to-human transmission and outbreaks were caused by repeated  
178 spill-over events from the camel host (Cui et al., 2019). For this reason MERS-CoV was excluded from  
179 the analyses.

180 Quantification of sequence variability by H calculation indicated that B cell epitopes in the S protein  
181 are significantly more variable than non-epitopes for SARS-CoV, HCoV-OC43 and HCoV-HKU1  
182 (Figure 4). Analysis of CD4<sup>+</sup> and CD8<sup>+</sup> T cell epitopes in these viruses indicated no increased diversity

183 for epitope compared to non-epitope positions, with the exclusion of the S protein of SARS-CoV for  
184 CD4<sup>+</sup> T cells. However, when positions within B cell epitopes were excluded from the analysis, this  
185 difference disappeared and T cell epitopes were found to be significantly less variable than non-  
186 epitopes for the spike proteins of HCoV-HKU1 and HCoV-OC43, as well as for the N protein of  
187 HCoV-229E (figure 4). Thus, the lack of antigenic diversity at T cell epitopes is a common feature of  
188 human coronaviruses, which instead tend to maintain sequence conservation of such epitopes.

189

## 190 **Discussion**

191 The origin of SARS-CoV-2 is still uncertain and it is presently unknown whether the virus spilled over  
192 from a bat or another intermediate host. The hypothesis of a zoonotic origin is strongly supported by  
193 multiple lines of evidence, although it cannot be excluded that SARS-CoV-2 transmitted cryptically in  
194 humans before gaining the ability of spreading efficiently among people (Andersen et al., 2020; Sironi  
195 et al., 2020). Whatever the initial events associated with the early phases of the pandemic, it is clear  
196 that circulating SARS-CoV-2 viruses shared a common ancestor at the end of 2019 (Li et al., 2020; van  
197 Dorp et al., 2020). Due to its recent origin, the genetic diversity of the SARS-CoV-2 population is still  
198 limited. This is also the result of the relatively low mutation rate of coronaviruses (as compared to other  
199 RNA viruses), which encode enzymes with some proofreading ability (Denison et al., 2011; Forni et  
200 al., 2017). Nonetheless, the huge number of transmissions worldwide have allowed thousands of  
201 mutations to appear in the viral population and, thanks to enormous international sequencing efforts,  
202 more than 14,000 amino acid replacements have currently been reported (<http://cov-glue.cvr.gla.ac.uk>).  
203 Irrespective of the host, most variants are expected to be deleterious for viral fitness, or to have no  
204 consequences (Cagliani et al., 2020; Grubaugh et al., 2020; van Dorp et al., 2020). However, a portion  
205 of replacements may favor the virus and some of these may contribute to adaptation to the human host.  
206 In particular, the recent and ongoing evolution of SARS-CoV-2 is expected to be at least partially

207 driven by the selective pressure imposed by the human immune system. Indeed, antigenic drift or  
208 immune evasion mutations have been reported for other zoonotic viruses such as Lassa virus (Andersen  
209 et al., 2015) and Influenza A virus (Su et al., 2015). The emergence of immune evasion variants was  
210 also observed during an outbreak of MERS-CoV in South Korea, when mutations in the spike proteins  
211 were positively selected as they facilitated viral escape from neutralizing antibodies, even though the  
212 same variants decreased binding to the cellular receptor (Kim et al., 2019; Kim et al., 2019; Kleine-  
213 Weber et al., 2019; Rockx et al., 2010). This exemplifies a phenomenon often observed in other  
214 viruses, most notably HIV-1 (Liu et al., 2007; Martinez-Picado et al., 2006; Schneidewind et al., 2007;  
215 Schneidewind et al., 2008), whereby the virus trades off immune evasion with a fitness cost. As a  
216 consequence, immune evasion mutations may be only transiently maintained in viral populations. For  
217 this reason we decided to quantify epitope variability in terms of entropy, rather than relying on  
218 measures based on substitution rates (dN/dS), which were developed for application to variants that go  
219 to fixation in different lineages over time (Kryazhimskiy and Plotkin, 2008).

220 The MERS-CoV mutants responsible for the outbreak in South Korea also testify the relevance of the  
221 antibody response in coronavirus control and the selective pressure imposed by humoral immunity on  
222 the virus (Kim et al., 2019; Kleine-Weber et al., 2019; Rockx et al., 2010). This is most likely the case  
223 for SARS-CoV-2, as well, as recent report indicated that the sera of most COVID-19 convalescent  
224 patients have virus-neutralization activities and antibody titers negatively correlate with viral load  
225 (OKBA et al., 2020; Vabret et al., 2020; Wu et al., 2020; Zhou et al., 2020b). Nonetheless, studies on  
226 relatively large COVID-19 patient cohorts reported that patients with severe disease display stronger  
227 IgG responses than milder cases and a negative correlation between anti-S antibody titers and  
228 lymphocyte counts was reported (Jiang et al., 2020; Vabret et al., 2020; Wu et al., 2020; Zhang et al.,  
229 2020a; Zhao et al., 2020). Consistently, asymptomatic SARS-CoV-2 infected individuals were recently  
230 reported to have lower virus-specific IgG levels than COVID-19 patients (Long et al., 2020). These

231 observations raised concerns that humoral responses might not necessarily be protective, but rather  
232 pathogenic, either via antibody-dependent enhancement (ADE) or other mechanisms (Cao, 2020;  
233 Iwasaki and Yang, 2020; Wu et al., 2020).

234 Clearly, gaining insight into the dynamic interaction between SARS-CoV-2 and the human immune  
235 system is of fundamental importance not only to understand COVID-19 immunopathogenesis, but also  
236 to inform therapeutic and preventive viral control strategies. We thus exploited the availability of a  
237 large number of fully sequenced high-quality SARS-CoV-2 genomes, as well as validated predictions  
238 of B cell and T cell epitopes, to investigate whether the selective pressure exerted by the adaptive  
239 immune response is detectable in global SARS-CoV-2 population, and if the virus is evolving to evade  
240 it. Results indicated that B cell epitopes in the N and S proteins, which represent the major targets of  
241 the antibody response, have higher diversity than non-epitope positions. The same was observed for the  
242 spike proteins of HCoV-HKU1, HCoV-OC43 and SARS-CoV, although data on the latter virus should  
243 be taken with caution as they derive from a relatively small number of sequences sampled over a short  
244 time frame. Conversely, no evidence of antibody-mediated selective pressure was evident for HCoV-  
245 229E and HCoV-NL63. The reasons underlying these differences are unclear, but recent data on a  
246 relatively small population of patients with respiratory disease indicated that the titers of neutralizing  
247 antibodies against HCoV-OC43 tend to be higher compared to those against HCoV-229E and HCoV-  
248 NL63 (HCoV-HKU1 was not evaluated), suggesting the two latter viruses elicit mainly non-  
249 neutralizing responses (Gorse et al., 2020).

250 B cell epitopes within nsp16 were also found to be variable, although this protein was not reported to  
251 be immunogenic (Grifoni et al., 2020b). However, the antibody response to SARS-CoV-2 has presently  
252 been systematically analyzed in a relatively small number of patients and most studies focused on  
253 structural proteins. It is thus possible that, during infection, antibodies against nsp16 are raised but they  
254 have not been detected yet. An alternative possibility is that B cell epitopes in nsp16, which is highly

255 conserved in SARS-CoV-2 strains (Cagliani et al., 2020), coincide with regions of relatively weaker  
256 constraint. This hypothesis is partially supported by the observation that these same positions also  
257 display higher diversity when entropy is calculated on an alignment of sarbecovirus nsp16 proteins.  
258 More intriguingly, this result may indicate that nsp16, together with S and N, is a target of B cell  
259 responses in the bat reservoirs. In fact, as mentioned above, antibody binding sites tend to be conserved  
260 across species (Tse et al., 2017; Wiehe et al., 2014) and thus the selective pressure exerted on B cell  
261 epitopes is likely to be constant across hosts. Whereas the immunogenicity of nsp16 remains to be  
262 evaluated, these data suggest that SARS-CoV-2 is evolving to elude the host humoral immune  
263 response. We however note that this observation does not necessarily imply that antibodies against  
264 SARS-CoV-2 are protective and it does not rule out the possibility that humoral responses contribute to  
265 COVID-19 pathogenesis.

266 In COVID-19 patients, antibody titers were found to correlate with the strength of virus-specific T cell  
267 responses (Ni et al., 2020). Surprisingly, we found that, in the SARS-CoV-2 population, epitopes for  
268 CD4<sup>+</sup> and CD8<sup>+</sup> T cells are not more variable than non-epitope positions. Conversely, a significant  
269 reduction in epitope variability was observed for a subset of viral proteins, in particular for some of the  
270 most immunogenic ones (S, N, ORF8, and ORF3a) (Grifoni et al., 2020b; Peng et al., 2020a). To check  
271 that the result was not due to stronger structural/functional constraints acting on epitope positions, we  
272 again used H values calculated on an alignment of sarbecovirus genomes, all of which, with the  
273 exclusion of SARS-CoV, were sampled in bats. T cell responses are initiated by the presentation of  
274 antigenic epitopes by MHC (major histocompatibility complex) class I and class II molecules. Different  
275 mammals have diverse MHC gene repertoires and thus present distinct antigens. In particular, recent  
276 data from various bat species indicated that many MHC class I molecules have a 3- or 5-amino acid  
277 insertion in the peptide binding pocket, resulting in very different presented peptide repertoires  
278 compared to the MHC class I molecules of other mammals (Abduriyim et al., 2019; Lu, Dan AND Liu,

279 Kefang AND Zhang, Di AND Yue, Can AND Lu, Qiong AND Cheng, Hao AND Wang, Liang AND  
280 Chai, Yan AND Qi, Jianxun AND Wang, Lin-Fa AND Gao, George F. AND Liu, William J., 2019; Ng et  
281 al., 2016; Papenfuss et al., 2012; Wynne et al., 2016) . Thus, the selective pressure acting on T cell  
282 epitopes is most likely volatile and not conserved in humans and bats. Analysis of sarbecovirus proteins  
283 indicated that, apart from CD4<sup>+</sup> T cell epitopes in the N protein, the T cell epitopes predicted in SARS-  
284 CoV-2 proteins are not less diverse than non-epitope positions, suggesting that epitope conservation is  
285 not simply secondary to structural or functional constraints, but may result from interaction with human  
286 T cell responses. Of course, another possible explanation for this finding is that the prediction tools  
287 failed to identify real epitopes. However, we retrieved epitopes from a previous work and the authors  
288 validated their predictions using the sera of 20 patients who recovered from COVID-19 (Grifoni et al.,  
289 2020a; Grifoni et al., 2020b). Moreover, if a general artifact linked to epitope prediction was  
290 introduced, we would not expect to observe significant differences and not specifically in the proteins  
291 that represent the major targets of T cell responses.

292 Unexpected conservation of T cell epitopes was previously observed for HIV-1 and *Mycobacterium*  
293 *tuberculosis* (MTB), both of which cause chronic infections in humans (Comas et al., 2010; Coscolla et  
294 al., 2015; Lindestam Arlehamn et al., 2015; Sanjuán, Rafael AND Nebot, Miguel R. AND Peris, Joan  
295 B. AND Alcamí, José, 2013). In the case of HIV-1, immune activation most likely favors the virus by  
296 increasing the rate of CD4<sup>+</sup> T cell trans-infection (Sanjuán, Rafael AND Nebot, Miguel R. AND Peris,  
297 Joan B. AND Alcamí, José, 2013). Conversely, the mechanisms underlying MTB epitope conservation  
298 are not fully elucidated. A possible explanation is that conserved epitopes generate a decoy immune  
299 response and advantage the bacterium. An alternative possibility is that T cell activation results in lung  
300 tissue inflammation and damage (cavitary tuberculosis), which favors MTB transmission by aerosol  
301 (Coscolla et al., 2015; Lindestam Arlehamn et al., 2015). Although these mechanisms are unlikely to be  
302 at play in the case of SARS-CoV-2, a deregulated immune response has been associated with COVID-

303 19 pathogenesis (Hannan et al., 2020). Specifically, recent data indicated that patients recovering from  
304 severe COVID-19 have broader and stronger T cell responses compared to mild cases (Peng et al.,  
305 2020b). This was particularly evident for responses against the S, membrane (M), ORF3a, and ORF8  
306 proteins (Peng et al., 2020b). Although this observation might simply reflect higher viral loads in  
307 severe cases, the possibility that the T cell response itself is deleterious cannot be excluded. Moreover,  
308 the same authors reported that CD8<sup>+</sup> T cells targeting different virus proteins have distinct cytokine  
309 profiles, suggesting that the virus can modulate the host immune response to its benefit (Peng et al.,  
310 2020b). Additionally, a post-mortem study on six patients who died from COVID-19 indicated that  
311 infection of macrophages can lead to activation-induced T cell death, which may eventually be  
312 responsible for lymphocytopenia (chen et al., 2020). However, we also found a trend of lower diversity  
313 of T cell epitopes for common cold coronaviruses, indicating that epitope conservation *per se* is not  
314 directly linked to disease severity. Moreover, other SARS-CoV-2 immunogenic proteins such as M and  
315 ORF7 did not show differences in T cell epitope conservation, which was instead observed for nsp16  
316 and nsp15. These latter are not known to be T cell targets (Grifoni et al., 2020b). Clearly, further  
317 analyses will be required to clarify the significance of T cell epitope conservation in SARS-CoV-2. An  
318 interesting possibility is that both for SARS-CoV-2 and for common cold coronaviruses, conservation  
319 serves to maintain epitopes that elicit tolerizing T cell responses or induce T cells with regulatory  
320 activity. Indeed, we considered T cell epitopes as a whole, but differences exist in terms of variability  
321 and, most likely, antigenicity. This clearly represents a limitation of this study, but the modest amount  
322 of genetic diversity in the SARS-CoV-2 population does not presently allow analysis of single epitope  
323 regions. Moreover, more detailed and robust analyses will indubitably require the systematic,  
324 experimental definition of T and B cell epitopes in the SARS-CoV-2 proteome.

325

326

## 327 **Material and Methods**

### 328 **Epitope Prediction**

329 Epitope prediction was performed using different tools from The Immune Epitope Database (IEDB)  
330 (<https://www.iedb.org/>), as previously suggested (Grifoni et al., 2020a). Protein sequences from  
331 reference strains of human coronaviruses were used as input for all prediction analyses (SARS-CoV-2,  
332 NC\_045512; SARS-CoV, NC\_004718; Human coronavirus 229E, NC\_002645; Human coronavirus  
333 NL63, NC\_005831; Human coronavirus OC43, NC\_006213; Human coronavirus HKU1, NC\_006577).  
334 In particular, for linear B cell epitope prediction, we used the Bepipred Linear Epitope Prediction 2.0  
335 tool (Jespersen et al., 2017) with a cutoff of 0.550 and epitope length > 7. Conformational B epitopes  
336 for the S and N proteins of SARS-CoV-2 were calculated using Discotope 2.0 (Kringelum et al., 2012)  
337 with a threshold = -2.5 and published 3D protein structures (PDB IDs: 6VSB, spike; 6M3M (N-term)  
338 and 7C22 (C-term), nucleocapsid protein).

339 SARS-CoV-2 predicted T cell epitopes were retrieved from a previous work (Grifoni et al., 2020a). For  
340 all other coronaviruses, we applied the same methodology used by Grifoni et al. (Grifoni et al., 2020a).  
341 CD4<sup>+</sup> cell epitopes were predicted using TepiTool (Paul et al., 2016) with default parameters. CD8<sup>+</sup>  
342 epitopes were predicted by using MHC-I Binding Predictions v2.23 tool (<http://tools.iedb.org/mhci/>).  
343 The NetMHCpan EL 4.0 method (Jurtz et al., 2017) was applied and the 12 most frequent HLA class I  
344 alleles in human populations (HLA-A01:01, HLA-A02:01, HLA-A03:01, HLA-A11:01, HLA-A23:01,  
345 HLA-A24:02, HLA-B07:02, HLA-B08:01, HLA-B35:01, HLA-B40:01, HLA-B44:02, HLA-B44:03)  
346 were analyzed with a 8-14 kmer range. Only epitopes with a score rank  $\leq 0.1$  in one of the 12 HLA  
347 classes were selected.

### 348 **Sequences and alignments**

349

350 SARS-CoV-2 protein sequences were downloaded from the GISAID Initiative (<https://www.gisaid.org>)  
351 database (as of June, 5<sup>th</sup>). All protein sequences were retrieved and several filters were applied. Only  
352 complete genomes flagged as “high coverage only” and “human” were selected. Positions  
353 recommended to be masked by DeMaio and coworkers ([https://virological.org/t/masking-strategies-for-](https://virological.org/t/masking-strategies-for-sars-cov-2-alignments/480)  
354 [sars-cov-2-alignments/480](https://virological.org/t/masking-strategies-for-sars-cov-2-alignments/480), last accessed June, 5<sup>th</sup>, 2020) were also removed.

355 Finally, for each SARS-CoV-2 protein, we selected only strains that had the same length as the protein  
356 in the SARS-CoV-2 reference strain (NC\_045512), generating a set of at least 23625 sequences for  
357 each ORF. Proteins with less than 60 amino acids were excluded from the analyses.

358 The list of GISAID IDs along with the list of laboratories which generated the data is provided as Table  
359 S5.

360 For all the other human coronaviruses, as well as for a set of non-human infecting sarbecoviruses,  
361 sequences of either complete genome or single ORFs (i.e. nucleocapsid and spike protein) were  
362 retrieved from the National Center for Biotechnology Information database (NCBI,  
363 <http://www.ncbi.nlm.nih.gov/>). For all human coronaviruses, the only filter we applied was the host  
364 identification as “human”. SARS-CoV strains sampled during the second outbreak were excluded from  
365 the analyses. NCBI ID identifiers are listed as Table S2 and Table S4.

366 Alignments were generated using MAFFT (Kato and Standley, 2013).

367

### 368 **Protein variability and statistical analysis**

369 Variability at each amino acid position was estimated using the Shannon's entropy (H) index using the  
370 Shannon Entropy-One tool from the HIV database (<https://www.hiv.lanl.gov/content/index>), with  
371 ambiguous character (e.g. gaps) excluded from the analysis. For SARS-CoV-2 strains, H was calculated  
372 on alignments of 10000 randomly selected sequences for each protein. For each protein we evaluated  
373 the difference D between average H values at epitope and non-epitope positions.

374 Most positions of analyzed viruses are invariable along the alignments, so the distribution of H is zero-  
375 inflated. We thus calculated statistical significance by permutations. For each protein, the predicted  
376 epitope intervals were collapsed to a single position while non-epitope intervals were left unchanged.  
377 After randomly shuffling this collapsed sequence it was expanded back to full length and the difference  
378 between shuffled epitope and non-epitope H values was calculated. This procedure was repeated 1000  
379 times and the proportion of repetitions showing a difference more extreme than D was reported as p-  
380 value. An in house R script was written and is available as supplementary text S1.

381

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386

## 387 **Author Contributions**

388 Conceptualization, DF and MS; Formal Analysis, MS, UP, and DF; Investigation, DF, RC, CP, AM,  
389 and MS; Visualization, DF, RC; Writing –Original Draft, MS and DF Writing –Review & Editing, MS,  
390 MC, RC, UP; Funding Acquisition MS and DF; Supervision, MS and MC.

391

## 392 **Declaration of Interests**

393 The authors declare no competing interests.

394

395

396 **References**

397

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623

## 624 **Figure Legends**

625 **Figure 1. Amino acid variability of the SARS-CoV-2 spike protein.** Shannon's entropy (H) values  
626 for each amino acid position calculated using 10000 SARS-CoV-2 spike proteins are shown. B cell  
627 predicted epitopes and T cell predicted epitopes are also reported in blue and green, respectively. B cell  
628 epitopes identified in the sera of COVID-19 patients (Farrera et al., 2020; Poh et al., 2020) are also  
629 reported in red.

630

## 631 **Figure 2. Variability of epitope and non-epitope positions among SARS-CoV-2 proteins.**

632 Shannon's entropy (H) mean values along with standard errors are shown for all SARS-CoV-2 proteins  
633 longer than 60 residues. Epitope positions are shown in dark gray, non-epitopes in light gray.  
634 Significant comparisons, calculated by a permutation approach, are indicated with asterisks (\*,  $P <$   
635 0.05; \*\*,  $P <$  0.01; \*\*\*,  $P <$  0.001). Immunogenic proteins are shown in blue and the length of each  
636 protein is reported in the bottom panel.

637

638 **Figure 3. Variability of epitope and non-epitope positions among sarbecoviruses.** Shannon's  
639 entropy (H) mean values along with standard errors are shown for a set of sarbecovirus ORFs. SARS-  
640 CoV-2 epitope positions are shown in dark gray, non-epitopes in light gray. Significant comparisons,  
641 calculated by a permutation approach, are indicated with asterisks (\*,  $P <$  0.05; \*\*,  $P <$  0.01; \*\*\*,  $P <$   
642 0.001).

643

644

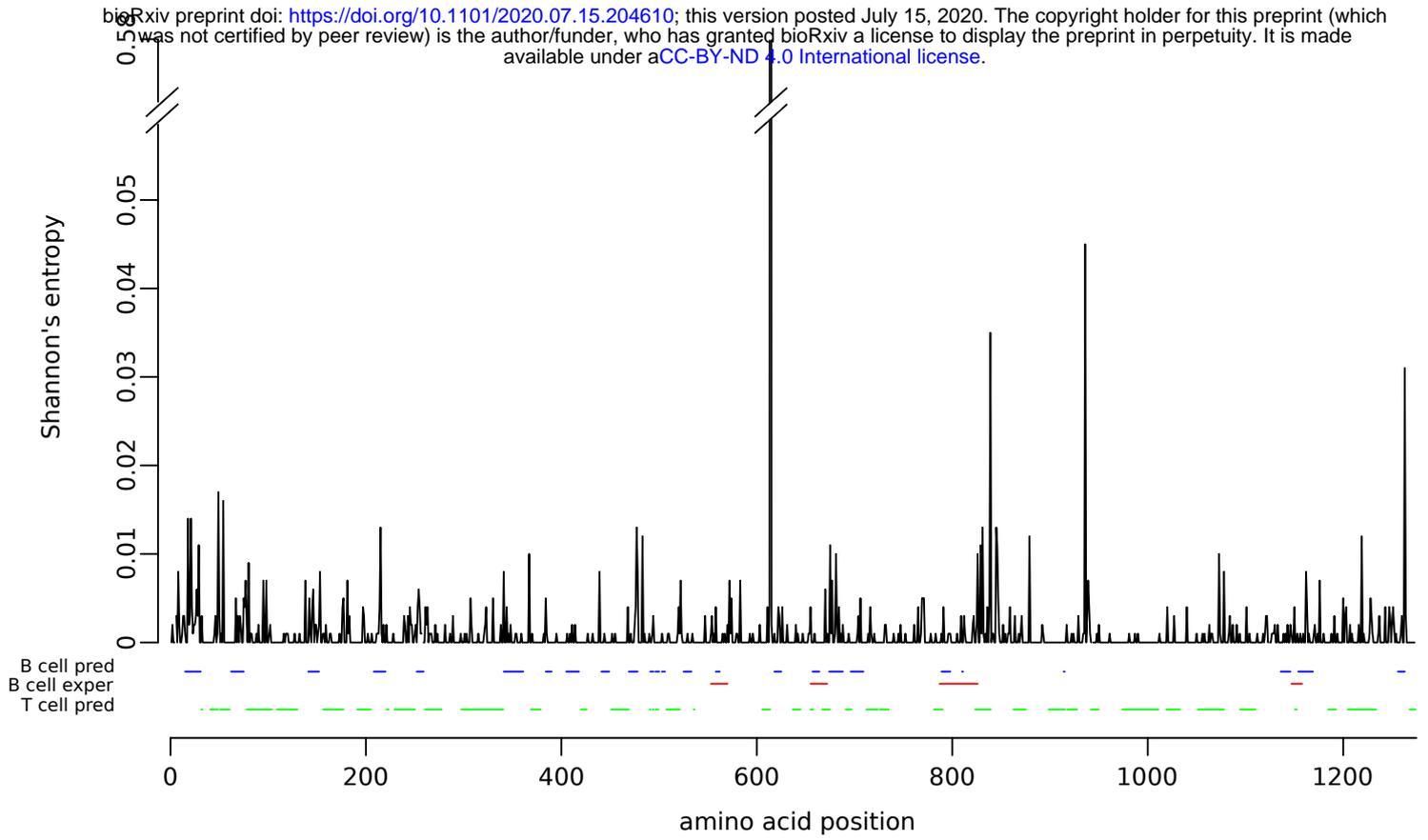
645 **Figure 4. Variability of epitope and non-epitope positions among human coronaviruses.** Shannon's  
646 entropy (H) mean values along with standard errors are shown for human coronavirus spike and

647 nucleocapsid proteins. Epitope positions are shown in dark gray, non-epitopes in light gray. Significant  
648 comparisons, calculated by a permutation approach, are indicated with asterisks (\*,  $P < 0.05$ ; \*\*,  $P <$   
649  $0.01$ ; \*\*\*,  $P < 0.001$ ).

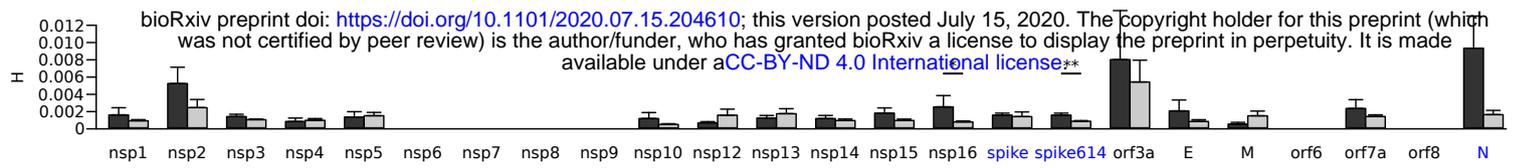
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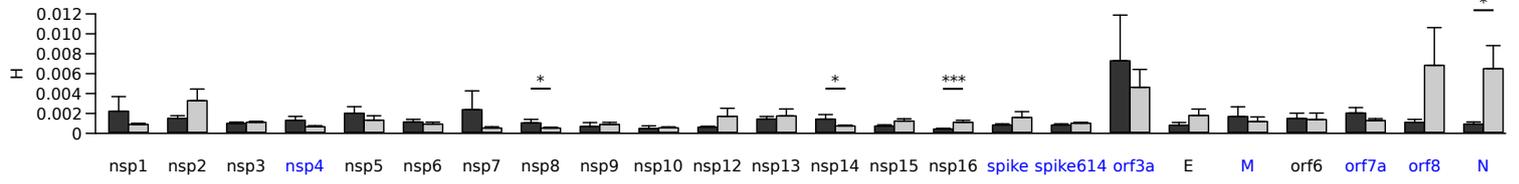
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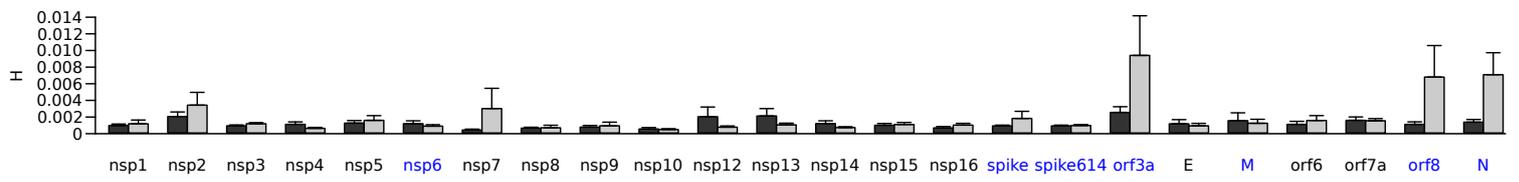
### linear B cell epitope



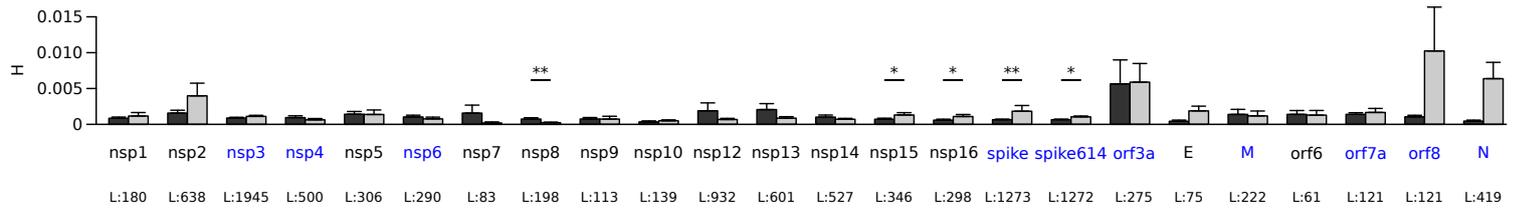
### CD4<sup>+</sup> T cell epitopes



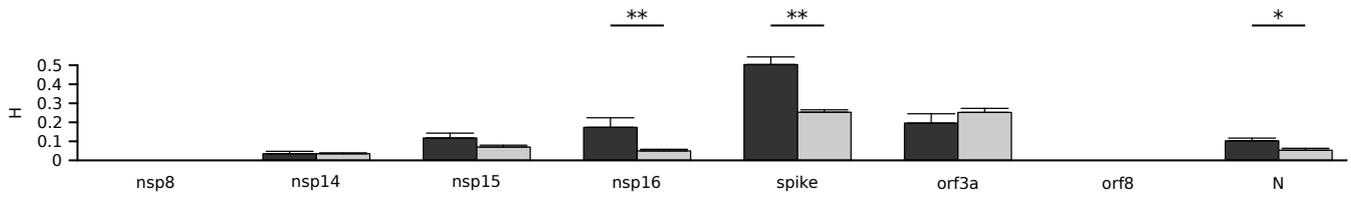
### CD8<sup>+</sup> T cell epitopes



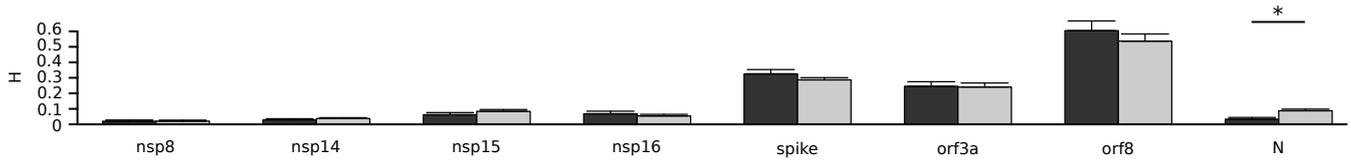
### T cell epitopes



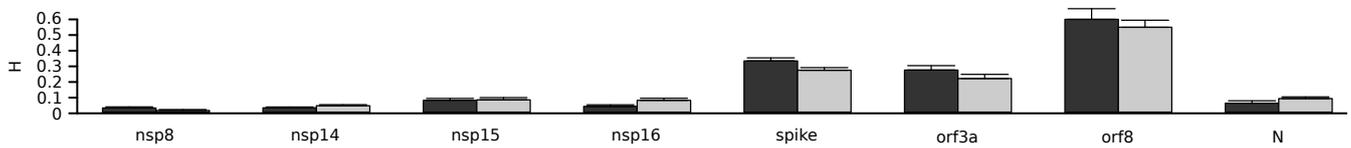
### linear B cell epitope



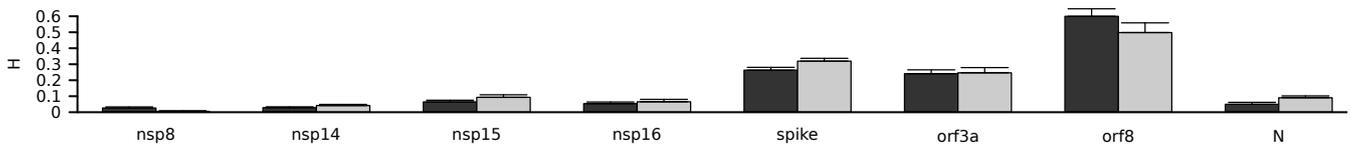
### CD4<sup>+</sup> T cell epitopes



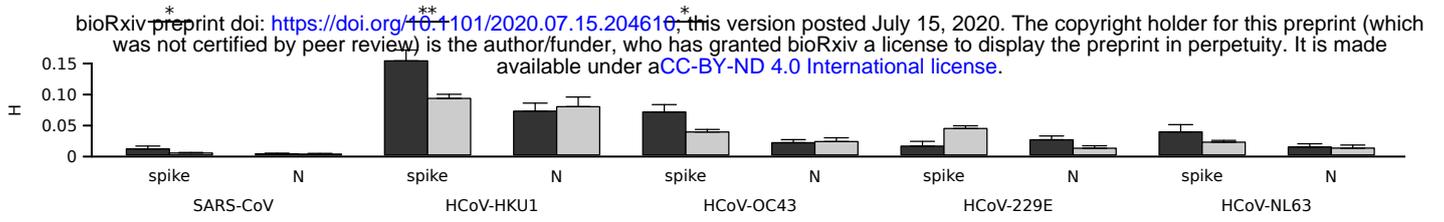
### CD8<sup>+</sup> T cell epitopes



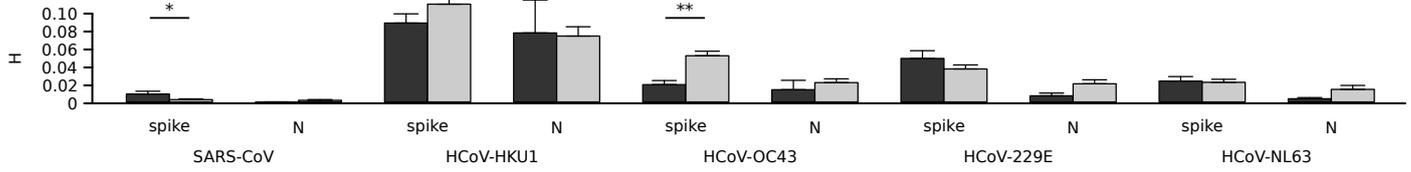
### T cell epitopes



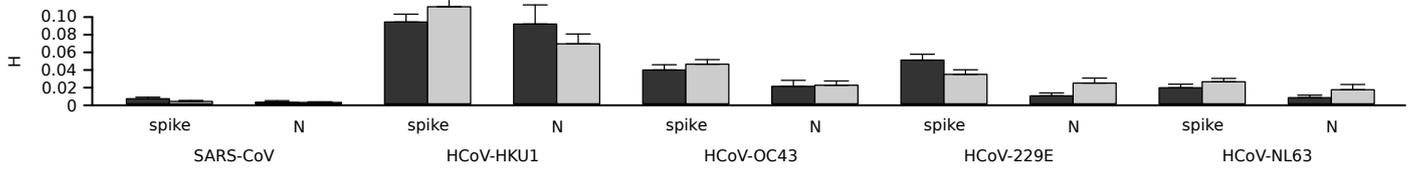
## linear B cell epitope



## CD4<sup>+</sup> T cell epitopes



## CD8<sup>+</sup> T cell epitopes



## T cell epitopes

