

1 **Antibodies to Coagulase of *Staphylococcus aureus* crossreact to Efb and reveal**
2 **different binding of shared Fibrinogen binding repeats**

3 Federico Bertoglio^{a,b,c,#}, Ya-Ping Ko^d, Sheila Thomas^{d,§}, Liliana Giordano^a, Francesca Romana
4 Scommegna^{a,*}, Doris Meier^c, Saskia Helmsig Polten^c, Marlies Becker^c, Srishtee Arora^d, Michael
5 Hust^c, Magnus Höök^d, Livia Visai^{a,e}

6 ^aDepartment of Molecular Medicine (DMM), Center for Health Technologies (CHT), UdR
7 INSTM, University of Pavia, Pavia, Italy

8 ^b School of Advanced Studies IUSS Pavia, Pavia, Italy

9 ^cDepartment of Biotechnology , Institute for Biochemistry, Biotechnology and Bioinformatics,
10 Technische Universität Braunschweig, Braunschweig, Germany

11 ^dCenter for Infectious and Inflammatory Diseases, Institute of Biosciences and Technology, Texas
12 A&M University Health Science Center, Houston, TX, United States

13 ^eMedicina Clinica-Specialistica, UOR5 Laboratorio di Nanotecnologie, Istituti Clinici Scientifici
14 (ICS Maugeri), IRCCS, Pavia, Italy

15 [§] Present address: Department of Microbiology and Immunology, East Carolina University,
16 Greenville, North Carolina, USA

17 ^{*} Present address: Department of Oncology and Metabolism, Academic Unit of Molecular
18 Oncology, University of Sheffield, Sheffield, UK

19 **Running title: mAbs targeting Coa and Efb of *Staphylococcus aureus* (count 51)**

20 [#] Address correspondence to f.bertoglio@tu-bs.de

21 **Text word count: 4972**

22 **Abstract (count 220)**

23 *Staphylococcus aureus* pathology is caused by a plethora of virulence factors able to combat
24 multiple host defence mechanisms. Fibrinogen (Fg), a critical component in the host coagulation
25 cascade, plays an important role in the pathogenesis of this bacterium, as it is the target of multiple
26 staphylococcal virulence proteins. Amongst its secreted virulence factors, Coagulase (Coa) and
27 Extracellular fibrinogen-binding protein (Efb) share common Fg binding motives and have been
28 described to form a Fg shield around staphylococcal cells, thereby allowing efficient bacterial
29 spreading, phagocytosis escape and evasion of host immune system responses. Targeting these
30 proteins with monoclonal antibodies thus represents a new therapeutic option against *S. aureus*.
31 To this end, here we report the selection and characterization of fully human, sequence-defined,
32 monoclonal antibodies selected against the C-terminus of Coagulase. Given the functional
33 homology between Coa and Efb, we also investigated if the generated antibodies bound the two
34 virulence factors. Thirteen unique antibodies were isolated from naïve antibodies gene libraries by
35 antibody phage display. As anticipated, most of the selected antibodies showed cross-recognition
36 of these two proteins and among them, four were able to block the interaction between Coa/Efb
37 and Fg. Furthermore, our monoclonal antibodies could interact with the two main Fg binding
38 repeats present at the C-terminus of Coa and distinguish them, suggesting the presence of two
39 functionally different Fg-binding epitopes.

40 **Importance (count 110)**

41 The death toll related to methicillin-resistant *S. aureus* piled to almost 1 million people in only one
42 year (2019), ascribing *S. aureus* to the second leading cause of deaths associated with
43 antimicrobial resistance. Therefore, new therapeutic strategies must be investigated. Blocking the
44 adhesion step with the use of monoclonal antibodies is one promising alternative and Fg is a
45 central plasma protein involved in staphylococcal infection. We present here a panel of
46 monoclonal antibodies raised against Coa, cross-reacting to Efb and targeting the shared Fg

47 binding repeats of Coa. In addition, we describe new epitope determinants in the repeated region
48 of Coa, highlighted by differential binding of the newly selected antibodies.

49

50 **Keywords**

51 *Staphylococcus aureus*, monoclonal antibodies, phage display, fibrinogen-binding repeats,

52 Coagulase, Efb

53 **Introduction**

54 *Staphylococcus aureus* has a large set of finely-tuned virulence-associated genes that has endowed
55 this bacterium with highly adaptive and versatile strategies to survive in beneficial as well as in
56 hostile environments (1–6). Two major classes of virulence factors belong to Cell Wall-Anchored
57 (CWA) adhesins (2) and a group of secreted proteins called Secretable Expanded Repertoire
58 Adhesive Molecules (SERAMs) (7). The most represented activity in both groups of virulence
59 factors is their ability to bind fibrinogen (Fg), a host blood glycoprotein. For instance, SERAMs
60 Coagulase (Coa), von Willebrand factor binding protein (vWbp), Extracellular fibrinogen-binding
61 protein (Efb), Extracellular adhesive protein (Eap), Extracellular matrix binding protein (Emp) all
62 bind Fg (8). Amongst them, prothrombin-activating proteins Coa and vWbp engage Fg
63 independently from prothrombin (9–12). The Fg binding activity of SERAMs, especially well
64 studied for Coa, vWbp and Efb, is mainly located in unordered regions of these proteins (8, 9, 11).

65 Fg is a large, fibrous plasma glycoprotein with three pairs of polypeptide chains, designated A α , B β
66 and γ . During haemostasis and clot formation, it self-assembles into an insoluble fibrous gel upon
67 conversion to fibrin (13, 14). The role of Fg in bacterial infection has been mainly regarded as
68 protective “haemostatic containment”, owing to the ability of Fg/fibrin to entrap bacteria, reducing
69 their proliferation and dissemination, and fibrin-mediated recruitment of immune cells to clear
70 invading bacteria (15–17). As mentioned so far, *S. aureus* harnesses an impressive array of virulence
71 factors that can interact with Fg. Multiple recent evidence has demonstrated that the interaction with
72 Fg may drive different host responses based on the tissutal context (8). In peritonitis mouse
73 infection models, binding of Fg is fundamental to elicit an antibacterial response and contain
74 infection (18–21). However, the picture is completely reversed in bloodstream infections, where Fg
75 instead promotes spreading of *S. aureus* (22). Therefore, understanding the interactions between *S.*
76 *aureus* virulence factors and Fg is crucial to understand how new therapeutic opportunities should
77 be designed against the multiple antibiotic-resistant strains of this pathogen.

78 Efb and Coa are the best characterized SERAM proteins. Efb::Fg interaction is located in the N-
79 terminus half of Efb (23), whereas Coa can bind Fg all throughout its length, with the more potent
80 interactions located in the C-terminus domain (9, 11, 24). Furthermore, both Coa and Efb mediate
81 the formation of a Fg/fibrin shield around staphylococcal cells, thereby protecting bacteria from
82 host immune responses (23, 25–27). Coa also mediates allosteric activation of prothrombin through
83 its N-terminus D1D2 domains promoting fibrin formation (28–30). In respect to therapeutic
84 potential of Coa- and Efb-targeted antibodies, polyclonal rabbit sera raised against Coa (10, 25) or
85 Efb-specific antibodies derived from patients with *S. aureus* infection (31) were able to reduce Fg
86 binding *in vitro* and protect mice from lethal *S. aureus* sepsis.

87 **Figure 1A** shows the domain organization of Coa protein. The full length protein can be divided
88 into N-terminus and C-terminus halves. N-terminus half of the protein contains D1D2 domains. The
89 C-terminus part of Coa can be divided into two portions: the repeat region of Coa, located at the
90 most C-terminus of the protein, and a linker that connects the D1D2 domain and the repetitive
91 region of Coa. As mentioned earlier, both N-terminus and C-terminus halves can bind Fg but the
92 more potent binding region is located in the C-terminus half. Different recombinant constructs used
93 in the study are also indicated in **Figure 1A**. CoaF contains the linker region and harbours a first
94 slightly divergent and longer repeat, termed CoaR0 (**Figure 1A and C**). The remaining repeats are
95 covered in recombinant construct CoaR, which harbours relatively conserved tandem repeats I-V of
96 27-residue each. CoaR, together with CoaF, constitutes the C-terminal domain of Coa, expressed as
97 recombinant protein named CoaC. The number of repeats present in Coa protein varies from 1 to 9
98 copies depending on the *S. aureus* strain, 5 or more being the most common (32). These repeats are
99 shorter than CoaR0, which is the longest repeat able to bind Fg and is present in CoaF, spanning
100 residues from 474 to 505. Therefore, Coa can be divided into several functional domains that have
101 different affinities for Fg (9, 11).

102 As mentioned, *S. aureus* Efb also interacts with Fg and belongs to SERAMs (9, 23, 27, 33). It is
103 reported to inhibit complement activation by engaging C3b (34–37), block platelet aggregation (38)
104 and interact with immune cells blocking cellular-mediated immunity (23, 27, 39). Furthermore, Efb
105 can also bind to Complement Receptor 2 on B cells, further tackling adaptive responses of the host
106 (40). Fg-binding activity is located at the N-terminus of Efb and has been mapped to relatively long
107 amino acid stretches termed EfbO and EfbA (**Figure 1B**). The affinity of EfbO for Fg is 200 times
108 higher than that of EfbA, indicating that EfbO is the primary Fg binding site in Efb (23). Coa repeats
109 and Efb N-terminal share homology in their Fg binding mechanisms and likely target the same or
110 overlapping sites in Fg, given that EfbO, CoaR0 and CoaRI peptides are able to inhibit Fg binding
111 of both EfbN and CoaC (9).

112 The possibility to interfere with Fg binding is thus crucial to understand and block one *S. aureus*
113 pathogenic mechanism. Here, antibodies are not only a tool for blocking Coa and Efb interaction
114 with Fg for research but also potential therapeutic molecules. We used antibody phage display to
115 select several fully human, sequence-defined antibodies against CoaC and characterized them *in*
116 *vitro*. We found that the anti-CoaC antibodies showed crossreactivity with Efb and were able to
117 discriminate between CoaR0 and CoaRI peptides. In addition, we identified four antibodies that
118 were able to inhibit Coa and Efb Fg-binding.

119 **Results**

120 *Anti-Coa C antibody selection and production*

121 To select Coa-targeting antibodies, the naïve antibody gene libraries HAL9 (λ repertoire) and
122 HAL10 (κ repertoire) were used as sources for scFv selection by phage display (41). We reasoned
123 that because of the higher affinity of CoaC for Fg than CoaN (9, 11), CoaC would represent a
124 better target to inhibit Fg binding activity (**Figure 1A**). After three panning rounds, monoclonal
125 soluble scFv were expressed from a total of 95 colonies in order to identify specific binders
126 through a screening Enzyme-Linked ImmunoSorbent Assay (ELISA). All clones that gave an
127 Signal-to-Noise ratio > 11 were considered possible binders (**Supplementary Fig. 1**). This
128 selection yielded 45 positive specific hits, termed FBE5 antibodies. No signal was detected both
129 against Bovine Serum Albumin (BSA), used as a negative control, (**Supplementary Fig. 1**) and
130 GST (data not shown). After BstNI digestion, sequencing and analysis with VBASE2 Fab tool
131 (42), 11 unique antibodies were converted in scFv-Fc, an IgG-like divalent format, transiently
132 produced in HEK293.6E cells and Protein A-purified from the clarified supernatant (43). Pure
133 monoclonal Antibodies (mAbs) preparations were obtained, as indicated by SDS-PAGE (data not
134 shown).

135

136 *Anti-Coa C antibody dose-dependent binding to Coa and Efb*

137 The binding of the 11 scFv-Fcs raised against CoaC was further assessed with a titration ELISA,
138 to determine the EC_{50} . All FBE5 antibodies bound specifically to CoaC recombinant protein
139 (**Figure 2**) with half-maximum binding in the range between $1,35 \times 10^{-8}$ M (FBE5-C8) and
140 $5,13 \times 10^{-10}$ M (FBE5-F11) (**Table 1**).

141 Since Coa and Efb share Fg binding motifs, we reasoned that monoclonal antibodies raised against
142 CoaC may crossreact to Efb, specifically to the latter's N-terminal fragment, where the two

143 functional Fg binding sequences (EfbA and EfbO) are located. Furthermore, CoaC itself harbours
144 a linker region and different Fg binding repeats. Therefore, we wondered if the generated
145 antibodies were able to recognize distinct epitopes within different regions of CoaC and also if
146 any crossreactivity with Efb was detectable. To this end, a single-point ELISA was performed
147 against different recombinant fragments of Coa (namely CoaF, CoaR0, CoaR) (**Figure 1A**) and
148 Efb (EfbN, EfbA and EfbO) (**Figure 1B**). Strikingly, all mAbs bound CoaF and CoaR0 but not
149 CoaR, a construct containing CoaRI-homologous repeats, but not CoaR0 (**Figure 1C and Figure**
150 **3**). Similarly, all antibodies, except FBE5-C8 and FBE5-E5, bound to different extents to Efb
151 recombinant constructs tested (**Figure 3**).

152 To better investigate the binding of each antibody to the different Efb and Coa recombinant
153 proteins, each FBE5 antibody was titrated on CoaF, CoaR0, EfbN, EfbO and EfbA
154 (**Supplementary Figures 2 and 3**) and the respective apparent affinities were calculated (**Table**
155 **1**). The best antibody was FBE5-F11, which displayed EC₅₀ values in the sub-nanomolar range
156 towards each Coa and Efb construct. The antibodies that showed weak-to-absent binding to all Efb
157 and Coa fragments except CoaF were FBE5-C1, FBE5-C8 and FBE5-E5.

158

159 Generation and characterization of antibodies specific to Coa R

160 Given that during the previous round of selection none of the characterized antibodies recognized
161 CoaR, another panning was performed specifically to raise antibodies that are able to bind the Coa
162 RI-RV repeats contained in the CoaR fragment (**Figure 1A and 1C**). Isolation of antibodies with
163 this specificity proved particularly arduous in our setting. We screened 380 colonies and were able
164 to retrieve only 10 hits, which upon sequencing revealed to be only two unique antibodies, termed
165 LIG40-A11 and LIG40-D8. Similarly to FBE5 antibodies, the two anti-CoaR mAbs were
166 reformatted in the scFv-Fc divalent format and recombinantly expressed. Dose dependent binding
167 of LIG40 mAbs against Coa and Efb constructs was verified in titration ELISA (**Figure 4**). Both

168 mAbs showed specific high-apparent affinity binding to both CoaR and CoaC proteins, as
169 expected. In particular, LIG40-A11 was specific to CoaR, whereas LIG40-D8 showed binding
170 also to CoaF and to a low level to CoaR0, suggesting a cross-reactivity to CoaR0 repeat. Of note,
171 none of the two antibodies bound to Efb fragments. EC₅₀ values against the different Coa
172 constructs for both antibodies are reported in **Table 2** and are almost all in the sub-nanomolar
173 range.

174

175 *Inhibition of Coa and Efb fibrinogen binding by the selected mAbs*

176 Since we showed that FBE5 and LIG40 mAbs bind functional Fg-binding Coa fragments and
177 FBE5 mAbs also bind Efb fragments, we investigated if these mAbs can block the interaction
178 between Fg and their antigens. Binding of CoaF, CoaR0, EfbN, EfbA and EfbO to purified human
179 Fg, which was immobilized on an ELISA plate, was assessed in the presence of increasing
180 concentrations of FBE5 antibodies. CoaR was not tested since none of FBE5 mAbs did recognize
181 CoaR. FBE5-A12, FBE5-D10, FBE5-F9 and FBE5-F11 showed the best dose-dependent
182 inhibition of Fg binding in good accordance with binding data (**Figure 5**). Specifically, FBE5-F11
183 antibody was the most potent inhibitor of Fg binding to all Coa and Efb recombinant proteins
184 tested, reaching an almost complete inhibition of CoaF binding to Fg at 5 µg/ml. Similarly, below
185 20% of Coa R0 residual binding to Fg was detected at 5 µg/ml of FBE5-F11. The same antibody
186 inhibited EfbN, EfbA and EfbO binding to Fg less efficiently, resulting in more than 60%
187 inhibition only at the highest concentration tested. FBE5-A12, FBE5-D10 and FBE5-F9 inhibited
188 binding of Coa fragments to Fg more than binding of Efb. In particular, FBE5-A12 showed an
189 inhibition of CoaF comparable to FBE5-F11, but was less effective against CoaR0. FBE5-D10
190 and FBE5-F9 showed inhibition only at high concentration (50 µg/ml) of both CoaF (more than
191 70% and almost 100%, respectively) and CoaR0 (more than 70% for both mAbs). FBE5-A12,
192 FBE5-D10 and FBE5-F9 displayed a dose-dependent inhibition of only EfbA construct, with no

193 remarkable inhibition of EfbN and EfbO proteins. It is however to be highlighted that EfbA
194 harbours a less potent Fg binding sequence (23).

195 The remaining 7 antibodies showed limited-to-no inhibition of Coa fragments at high
196 concentration and essentially displayed no inhibition against Efb protein (**Supplementary Fig. 4**).
197 Similarly, both LIG40 antibodies were tested for inhibition of Fg binding to CoaC, CoaF, CoaR0
198 and CoaR but did not show any inhibiting activity (**Supplementary Fig. 5**).

199

200 *Binding of mAbs is affected differently by CoaR0 and CoaRI peptides*

201 In order to better understand if the generated monoclonal antibodies engage at their epitope the 2
202 Fg binding motives of Coa, peptides corresponding to CoaR0 and CoaRI repeats (**Figure 1C**) of *S.*
203 *aureus* strain Newman were synthetically manufactured and used to challenge binding of both
204 FBE5 and LIG40 mAbs to their respective antigens. To this end, a competition ELISA was
205 performed to evaluate the binding of a fixed concentration of antibody to immobilized Coa
206 constructs in the presence of increasing concentrations of either peptide CoaR0 or CoaRI. The
207 fixed quantity of antibody chosen allowed to detect sufficient binding of antibodies, yet to be able
208 to see any variation upon addition of the peptides.
209 Peptide CoaR0 inhibited FBE5 antibodies binding to CoaC in a dose-dependent manner (**Figure 6,**
210 **panels A and B**) whereas CoaRI had no effect (**Figure 6, panels C and D**). This result
211 corroborates the binding data that showed recognition of CoaF and CoaR0 fragments, but not of
212 CoaR (**Figure 3 and Supplementary Fig. 2 and 3**). CoaF and CoaR0 do indeed contain CoaR0
213 repeat, which is conversely absent in CoaR, where repeats similar to CoaRI peptide are located.
214 These data suggest that all FBE5 antibodies bind epitopes within CoaR0.

215 The effect of CoaR0 and CoaRI peptides was investigated also on CoaC and CoaR binding of both
216 LIG40 mAbs. Surprisingly, LIG40-A11 and LIG40-D8 behaved differently in the presence of the
217 two peptides (**Figure 7**). First and most importantly, LIG40-A11 was inhibited only by CoaRI

218 peptide, when tested against both CoaC and CoaR proteins (**Figure 7, panels A and C**). In a
219 symmetrical opposite way, LIG40-D8 was only impaired in its binding activity by CoaR0 peptide
220 (**Figure 7, panels B and D**). Secondly, to achieve appreciable inhibition, high concentration of
221 peptides needed to be used for both antibodies (above 10 μ M). These results show that LIG40-D8
222 targets an epitope similar to CoaR0 peptide, yet present in CoaR, which harbours only CoaRI-type
223 repeats. On the other hand, LIG40-A11 binds to an epitope specific of CoaR repeats.

224 Collectively, these data show that fully human, sequence-defined, monoclonal antibodies against
225 Coa C-terminal fragment were able to engage and block Fg-binding motives both in Coa and Efb.
226 Furthermore, we showed that it is possible to discriminate between CoaR0 and CoaRI repeats
227 through monoclonal antibodies.

228 **Discussion**

229 *S. aureus* has for a long time been a critical global healthcare threat owing to increase in spread
230 and virulence of antibiotic-resistant strains (44, 45). The discovery and introduction of radically
231 new antibiotic classes into the market has been lagging for two decades (46). Therefore, new
232 approaches to tackle *S. aureus* infections are of foremost interest. A first crucial aspect in *S.*
233 *aureus* pathogenesis is the attachment to host tissues. Among these interactions, Fg seems to play
234 a dominant role (8). Indeed, *S. aureus* has evolved a vast arsenal of proteins to interact with this
235 soluble plasma protein: first, Microbial Surface Components Recognizing Adhesive Matrix
236 Molecules (MSCRAMMs) are cell wall-bound proteins primarily involved in extracellular matrix
237 components binding to secure bacterial adhesion to host tissues (2). A second class is collectively
238 referred to as SERAMs proteins, which are secreted and still interact with several extracellular
239 matrix molecules displaying also an immune evasion and dissemination function (7). Among
240 MSCRAMMs, ClfA and ClfB, FnbpA and FnbpB and SdrE/Bbp bind different segments of Fg
241 molecule. Fg-binding activity is also prominent in SERAMs, where unordered regions of Coa,
242 vWbp, Efb, Eap and Emp present Fg binding as a common feature. The comprehensive picture of
243 these proteins seems not yet fully disclosed, as the recent initial characterization of vhp shows
244 (47).

245 Also the role of Fg is at the crossroad between its well described role in haemostasis and its
246 importance in mediating immune response (14, 48). Much preclinical evidence also showed that
247 mutated versions of Fg cannot efficiently clear infection mediated by *S. aureus* thus compromising
248 immune response towards the pathogen (19–21, 49). Furthermore, preclinical studies together with
249 vaccine candidates have shown that ClfA-mediated Fg interaction is a viable alternative for
250 possible therapeutic strategies (50–52). Therefore, all these presented interactions show how
251 intricate the interaction with *S. aureus* and Fg is and thus its extremely high potential as a
252 therapeutic target for alternative treatment strategies.

253 To this end, anti-Coa antibodies have been generated by antibody phage display, using human
254 naïve libraries (41), providing sequence-defined mAbs: 11 mAbs with unique sequences
255 recognized CoaF and CoaR0 fragments upon panning against CoaC (FBE5 mAbs) and 2 mAbs
256 directed against CoaR (LIG40 mAbs). Of note, to obtain the latter antibodies, 4 times our usual
257 number of clones had to be screened, to obtain only 10 hits and in the end 2 unique clones. In
258 comparison, selection of FBE 5 mAbs had a higher hit rate (45 positive hits/95 colonies screened).
259 This may be a consequence of the unstructured organization of CoaR (11, 30), even if selection
260 was performed on ELISA plates which should “immobilize” antigens in a fixed position. Further
261 support of the unordered nature of the Fg-binding portion of Coa and Efb is given by AlphFold
262 databases (Uniprot entries P07767 and P0C6P2) (53, 54). Interestingly, these structural predictions
263 show that the Fg-binding sequences appear to be more folded than the completely unordered
264 domain surrounding them, in apparent contradiction with prior experimental evidence (11, 30).
265 While AlphaFold predictions pave the way to new questions on how Fg is exactly bound by Coa
266 and Efb, experimental validation of *in silico* data is necessary to draw any solid conclusion.

267 Since Coa shares sequence and functional homology to Efb, cross-recognition of the generated
268 antibodies was investigated. All FBE5 antibodies showed binding to both Coa and Efb fragments
269 (**Figure 3** and **Supplementary Figures 2** and **3**). In particular, all FBE5 mAbs bound to different
270 extents CoaF, CoaR0, EfbN, EfbA and EfbO fragments, except FBE5-C8 and FBE5-E5 that
271 showed low-affinity binding to Coa and substantially no binding to Efb. Among them, FBE5-F11
272 had the highest affinity (**Table 1**) and showed the greatest inhibitory effect on Fg binding to CoaF,
273 CoaR0, EfbN, EfbA and EfbO constructs (**Figure 5**). FBE5-A12, FBE5-D10 and FBE5-F9 could
274 also efficiently inhibit all Efb and Coa fragments tested, although to a lower extent than FBE5-
275 F11 (**Figure 5**). This activity correlated with their apparent affinities determined in ELISA (**Table**
276 **1**). FBE5-A5, FBE5-A6, FBE5-B9, FBE5-C1 and FBE5-D9, instead, showed inhibition of CoaF,
277 CoaR0 and EfbA (**Supplementary Figure 4**). Essentially, these antibodies were able to inhibit

278 CoaR0-mediated Fg binding, since EfbA is unlikely to be the most functionally relevant Fg-
279 binding region in Efb, given its low affinity for Fg (1 μ M) (23). Finally, FBE5-C1, FBE5-C8 and
280 FBE5-E5 displayed only minor blocking activity on EfbA, matching the apparent affinity
281 measurement of these antibodies.

282 Concerning LIG40 antibodies raised against CoaR, they did not show any cross-reaction to Efb.
283 Surprisingly, both of them could not inhibit Fg-binding of both CoaC and CoaR (**Supplementary**
284 **Figure 5**), despite their high affinity binding to functional Fg-binding sequences CoaR0 and
285 CoaRI (**Figure 4** and **Table 2**). When binding of LIG40-A11 and LIG40-D8 to CoaC and CoaR
286 was challenged with synthetic CoaR0 and CoaRI peptides (**Figure 7**), high concentrations of
287 peptides were necessary for competition. This could indicate, on one side, that the epitope is not
288 properly represented in the peptide. On the other hand, it is very plausible that given the repetitive
289 nature of CoaR, multiple binding sites for these antibodies are available within the same construct,
290 thus higher concentration of peptide is needed in order to exert an competitive effect. It is also
291 highly unlikely that a single mAb's paratope could span the entire linear 27 amino acid-long Fg
292 binding repeat. These considerations hint that the inability of these antibodies to block Fg binding
293 might be due to the repetitive nature of CoaR.

294 Furthermore, CoaR0 peptide could inhibit all FBE5 and, surprisingly, LIG40-D8 mAbs binding to
295 CoaC, instead had no effect on LIG40-A11 binding to both CoaR and CoaC. Conversely, CoaRI
296 peptide did inhibit LIG40-A11 binding, leaving unaffected the binding of all FBE5 and LIG40-D8
297 mAbs. The latter antibody showed indeed binding, albeit weaker, to CoaF and CoaR0 constructs
298 (**Figure 4, Table 2**), even though its selection was performed on CoaR, which does not contain
299 CoaR0 repeat. These results together suggest that these antibodies are targeting different epitopes
300 in CoaR and that Fg binding repeats may assume similar conformations, however representing two
301 functionally distinct epitopes in Coa. It could be speculated that LIG40-D8 is targeting conserved
302 residues present both in CoaR0 and CoaRs repeats. Their role needs further clarification since it is

303 clear that the binding site of CoaR0 and CoaRI in the Fg molecule is similar or overlapping. Both
304 peptides are indeed able to inhibit Coa binding to Fg (9). Recent evidence has validated these
305 previous results, highlighting the role of the CoaR0 repeat in Fg binding, further confirming that
306 both CoaR0 and CoaRI are indeed the functional Fg binding repeats. It was also shown that
307 increasing the number of Fg binding repeats does not lead to a cooperative effect and the
308 stoichiometry remains 1:1 (number of repeats: Fg D molecule) (55). This is in further support of
309 the possibility that more than one antibody molecule is necessary to efficiently inhibit Fg binding
310 by all CoaRI-similar repeats, thereby giving a possible explanation why no efficient inhibition
311 could be seen by antibodies directed to CoaR.

312 Other antibodies that bind either Coa or Efb have been reported. Thomer and colleagues (24)
313 generated 13 mouse monoclonal antibodies by hybridoma technology targeting Coa and
314 investigated two of them (5D5 and 3B3) *in vivo* in a mouse model of *S. aureus* bacteraemia, with
315 no detailed biochemical characterization. 5D5 mAb was assessed to bind the D1 domain of Coa
316 and 3B3 bound the domain containing R repeats. No analysis of their crossreaction with Efb was
317 provided. The only information available about crossreactivity is that no binding to vWbp and
318 IsdA was detected. MAb 3B3 proved its clear efficacy in the bacteraemia mouse model, further
319 highlighting clinical relevance of the repeated region of Coa (24). A detailed biochemical analysis
320 of these antibodies would provide orthogonal confirmation to our results, also in respect to the
321 hypothesis of two classes of motives by CoaR0 and CoaRI repeats. It is also a possibility that the
322 efficacy of mAb 3B3 could be due to the parallel targeting of Coa and Efb. A clear obstacle for
323 5D5 and 3B3 clinical translation is their fully murine origin.

324 Shannon and colleagues found that antibodies against Efb from patient sera could be neutralizing
325 *in vitro* and also crossreacting to Coa (56). A further peculiar class of antibodies against Efb,
326 named catalytic antibodies, were isolated (57). This discovery led to the hypothesis that Efb could
327 also act as a B cell superantigen. Another group instead focused on the selection and

328 characterization of recombinant divalent (Fab)₂ mAbs from a synthetic phage display library
329 against Efb C-terminal domain (58). The latter work showed both the presence of antibodies
330 specific to Efb C-terminal in patient sera and also that blocking Efb interaction with C3b with the
331 selected divalent mAbs improved mice survival in an infection model.

332 This present work and research from other groups shows how pivotal may be blocking the
333 multiple activities of proteins engaging Fg, further strengthening a possible therapeutic strategy
334 involving Coa and Efb (59). To the best of our knowledge, this is the only report that investigates
335 these two proteins as potential targets for generation of monoclonal antibodies. None has provided
336 sequenced-defined human mAbs to the Fg-binding domain of Efb and Coa. The use of
337 combination(s) of antibodies directed against either N- or C-terminal of both these proteins most
338 presumably will result in additive effect in inhibiting *S. aureus* pathology. Selection of such
339 antibodies is already underway.

340 **Material and Methods**

341 *Recombinant proteins and Fg*

342 CoaC, CoaR, CoaF, CoaR0, EfbA and EfbO harbour an N-terminal GST tag, whereas EfbN has
343 been expressed with a 6 His N-terminal tag and the respective expression and purification
344 protocols were previously reported (9, 23). Human Fg was purchased from Enzyme Research and
345 further purified by size exclusion chromatography to eliminate contaminating fibronectin.

346 *Selection of scFv antibody fragments (panning).*

347 The selection was performed in ELISA plates (Costar), as described earlier (60). In short, 1µg/well
348 of CoaC or CoaR for each of the three panning rounds was immobilized. The immobilisation
349 conditions in this whole work were at 4°C overnight in 50 mM sodium carbonate, pH 9.6. After
350 blocking with 2%(w/v) Milk powder (M) dissolved in PBS 1x + 0.05% Tween20 (PBST), 5 x 10¹⁰
351 phage particles from each of both HAL9 and HAL10 hyperphage-packaged naïve antibody gene
352 libraries were used (41, 61). After incubation in the antigen-coated well, stringent washing with
353 PBST was performed by an ELISA washer (Tecan). Phages were eluted with trypsin (10µg/ml in
354 PBS).

355 *E. coli* TG1 (Lucigen) in 2xYT medium (yeast extract 1% w/v, tryptone 1.6% w/v, NaCl 0.5%
356 w/v) at OD₆₀₀ of 0.5 were infected with eluted phages for 30 min at 37°C and subsequent 30
357 minutes at 37°C, 500rpm. Cultures were pelleted, resuspended in 2xYT-GA (2xYT with 100mM
358 glucose and 100µg/ml ampicillin) and, upon OD₆₀₀ of 0.4-0.6, infected with M13K07 helper phage
359 (62). Phage particles were produced at 30°C and 500 rpm overnight in 2xYT with 100µg/ml
360 ampicillin and 70µg/ml kanamycin. After centrifugation, the phage-containing supernatant was
361 used for the next panning round. After the third panning round, instead, *E. coli* XL1Blue MRF'
362 (Stratagene) at OD₆₀₀ of 0.5 in 2xYT with 20 µg/ml tetracycline was infected with eluted phages,
363 plated on 2xYT-AG agar and cultivated overnight at 37°C.

364 *Production of soluble scFv in microtiter plates*

365 95 or more colonies per each panning were picked and the corresponding 96-well masterplate
366 inoculated in 2xYT-AG and grown overnight at 37°C and 250 rpm. A subculture in 2xYT-AG was
367 incubated at 37°C, 250 rpm for 90 minutes. Cells were pelleted and resuspended in 2xYT with
368 100µg/ml ampicillin and 50 µM IPTG and cultured at 30°C, 250 rpm overnight.

369 *Screening ELISA for monoclonal binder identification*

370 High-binding ELISA plates were coated with 2 µg/ml solution of CoaC or CoaR. As negative
371 controls, BSA and GST were tested. The coated plates were blocked with 2%MPBST and washed
372 with MilliQ + 0.05% Tween 20 in an ELISA washer (BioTek). Crude supernatant containing scFv
373 diluted 1:1 with 2%MPBST was transferred to the corresponding well of both the antigen-coated
374 and the control plates. As primary antibody, α-c Myc tag (9E10, in-house production) was diluted
375 1:1000. The primary antibody was detected with α-mouse IgG HRP (HorseRadish Peroxidase)-
376 conjugated antibody (A0168, Sigma), diluted 1:50000 in 2%MPBST. Development was
377 performed through the substrate Tetramethylbenzidine (TMB). The reaction was stopped adding
378 0.5M H₂SO₄. The plates were read in an ELISA reader (Tecan) at 450 nm and as a reference
379 wavelength 620 nm. The represented data (A450-A620) are the subtraction of the Absorbance (A)
380 at 450 nm (A450) minus those at 620 nm (A620).

381 *Colony PCR and BstNI digestion of the PCR product*

382 The scFv gene of positive hits was amplified with primers MHLacZ-Pro_f (5'-
383 GGCTCGTATGTTGTGTGG-3') and MHgIII_r (5'- CTAAAGTTTTGTCGTCTTTCC-3'). The
384 PCR products were analyzed through capillary gel electrophoresis with the QIAxel instrument
385 (Qiagen). The cPCR-amplified scFv gene was then digested with BstNI endonuclease to obtain
386 and compare the band patterning of each scFv amplified gene. Digestion products were analyzed
387 with the QIAxel (Qiagen). Unique binders were then confirmed by Sanger sequencing and
388 VBASE database analysis (42).

389 *Cloning of scFv gene into vector pCSE2.6-hIgG1-Fc-XP for scFv-Fc expression*

390 The scFv gene was digested from pHAL30 phagemid with NcoI-HFTM and NotI-HFTM (New
391 England BioLabs), separated by agarose gel electrophoresis and DNA was recovered with
392 QIAquick Gel Extraction Kit (Qiagen), according to supplier instructions. The scFv gene was then
393 ligated into pCSE2.6-hIgG1-Fc-XP vector (43) using T4 Ligase (Promega) and transformed into *E.*
394 *coli* XL1Blue MRF', according to standard procedures (63). Correct insertion was confirmed by
395 Sanger DNA sequencing, using softwares FinchTV (Geospiza, Inc.) and Multalin (64).

396 *Mammalian cell transfection, transient expression and purification of scFv-Fc fusions*

397 ScFv-Fcs were produced as described (43) with minor modifications. In particular, purification
398 was performed with a vacuum manifold (Macherey-Nagel) and a 24 deepwell filter plate loaded
399 with MabSelect SuReTM (rProtein A, GE Healthcare Life Sciences), according to manufacturer
400 instructions. Buffer exchange to PBS was performed with ZebaTM Spin Desalting columns
401 (Thermo Scientific). Protein purity was checked through SDS-PAGE, using standard protocols
402 (63).

403 *ELISA assays*

404 High-binding ELISA plates were coated with 200 ng/well of indicated recombinant proteins
405 (CoaF, CoaR0, CoaR, EfbN, EfbA and EfbO or BSA for negative controls). After blocking with
406 2%BSA in PBST and washing with PBST, scFv-Fc in 2%BSA-PBST were incubated on the
407 immobilized proteins. ScFv-Fc were revealed thanks to a polyclonal α -human IgG HRP-
408 conjugated Ab (P0214, Dako), diluted 1:10000. Final development was performed through
409 SigmaFAST-OPD tablets (P9187, Sigma), following producer instructions. Absorbance was
410 recorded in a microplate reader (Clariostar®, BMG-Labtech). Apparent Kd values were obtained
411 through analysis of half maximum binding using GraphPad Prism 6 software (non-linear
412 regression fit).

413 For inhibition ELISA, 0,25µg/well of Fg were immobilized. Indicated amounts of scFv-Fcs were
414 pre-incubated in a separate plate with a constant concentration of Coa or Efb fragments.
415 Specifically, CoaF, CoaR0, EfbN and EfbO were at a fixed final concentration of 10nM, whereas
416 EfbA was at 750µM. The pre-incubated mixture of Coa/Efb and anti-Coa scFv-Fc was transferred
417 onto the BSA-blocked Fg-coated plate. After incubation and washing, residual bound Coa and Efb
418 were detected with anti-tag HRP-conjugated antibodies diluted 1:10000 in 2%BSA-PBST: α-HIS-
419 tag antibody (A7058, Sigma) for EfbN; α-GST-tag antibody (600-103-200, Rockland) for all other
420 constructs. Development and acquisition were performed as indicated above. Binding of Coa and
421 Efb fragments to Fg (no mAb control) was set to 100% and residual binding to Fg of Coa and Efb
422 fragments in the presence of different concentrations of antibodies was calculated and represented.
423 For competition ELISAs with CoaR0 and CoaRI peptides, indicated constructs (200 ng/well) were
424 immobilized. Fixed concentration of mAbs (0,5 µg/ml) was added to the wells with indicated
425 amounts of CoaR0 and CoaRI peptides. Detection of residual mAbs bound was performed as
426 mentioned above.

427 *Peptides*

428 CoaR0 and CoaRI peptides were purchased from Shanghai Hanhong Scientific Co., Ltd. All the
429 peptides were purified using high-performance liquid chromatography and were >95% pure.

430

431 **Acknowledgments**

432 FB acknowledges a research travel grant from SIB (Società Italiana di Biochimica e Biologia
433 Molecolare -Italian Society of Biochemistry and Molecular Biology-) useful in the final stages of
434 this study. This research was supported by a grant of the Italian Ministry of Education, University
435 and Research (MIUR) to the Department of Molecular Medicine of the University of Pavia under

436 the initiative “Dipartimenti di Eccellenza (2018–2022)”. The funders had no role in study design,
437 data collection and interpretation, or the decision to submit the work for publication.

438

439 **Conflict of interests**

440 Findings of this manuscript are part of patent application US 2020/0283508 on which FB, YPK,
441 DM, SH, MHust, MHöök and LV are listed as inventors.

442

443 **References**

- 444 1. Foster TJ. 2005. Immune evasion by staphylococci. *Nat Rev Microbiol*.
- 445 2. Foster TJ, Geoghegan JA, Ganesh VK, Hook M. 2014. Adhesion, invasion and evasion: the
446 many functions of the surface proteins of *Staphylococcus aureus*. *Nat Rev Microbiol*.
- 447 3. Lowy FD. 1998. *Staphylococcus aureus* infections. *N Engl J Med*.
- 448 4. Lowy FD. 2011. How *Staphylococcus aureus* adapts to its host. *N Engl J Med*.
- 449 5. Otto M. 2014. *Staphylococcus aureus* toxins. *Curr Opin Microbiol*.
- 450 6. Spaan AN, van Strijp JAG, Torres VJ. 2017. Leukocidins: staphylococcal bi-component
451 pore-forming toxins find their receptors. *Nat Rev Microbiol*.
- 452 7. Chavakis T, Wiechmann K, Preissner KT, Herrmann M. 2005. *Staphylococcus aureus*
453 interactions with the endothelium: the role of bacterial “secretable expanded repertoire
454 adhesive molecules” (SERAM) in disturbing host defense systems. *Thromb Haemost*.
455 Germany.

- 456 8. Ko YP, Flick MJ. 2016. Fibrinogen Is at the Interface of Host Defense and Pathogen
457 Virulence in *Staphylococcus aureus* Infection. *Semin Thromb Hemost.*
- 458 9. Ko YP, Kang M, Ganesh VK, Ravirajan D, Li B, Höök M. 2016. Coagulase and Efb of
459 *Staphylococcus aureus* Have a Common Fibrinogen Binding Motif. *MBio.*
- 460 10. McAdow M, DeDent AC, Emolo C, Cheng AG, Kreiswirth BN, Missiakas DM, Schneewind
461 O. 2012. Coagulases as determinants of protective immune responses against *Staphylococcus*
462 *aureus*. *Infect Immun.*
- 463 11. Thomas S, Liu W, Arora S, Ganesh V, Ko Y-P, Höök M. 2019. The Complex Fibrinogen
464 Interactions of the *Staphylococcus aureus* Coagulases. *Front Cell Infect Microbiol.*
- 465 12. Thomer L, Schneewind O, Missiakas D. 2013. Multiple ligands of von Willebrand factor-
466 binding protein (vWbp) promote *Staphylococcus aureus* clot formation in human plasma. *J*
467 *Biol Chem.*
- 468 13. Mosesson MW, Siebenlist KR, Meh DA. 2001. The Structure and Biological Features of
469 Fibrinogen and Fibrin. *Ann N Y Acad Sci.*
- 470 14. Weisel JW. 2005. Fibrinogen and fibrin. *Adv Protein Chem.*
- 471 15. Alcock J, Brainard AH. 2008. Hemostatic containment - an evolutionary hypothesis of injury
472 by innate immune cells. *Med Hypotheses.*
- 473 16. Crosby HA, Kwiecinski J, Horswill AR. 2016. *Staphylococcus aureus* Aggregation and
474 Coagulation Mechanisms, and Their Function in Host-Pathogen Interactions. *Adv Appl*
475 *Microbiol.*

- 476 17. Fiusa MM, Carvalho-Filho MA, Annichino-Bizzacchi JM, De Paula EV. 2015. Causes and
477 consequences of coagulation activation in sepsis: an evolutionary medicine perspective.
478 BMC Med.
- 479 18. Dunn DL, Simmons RL. 1982. Fibrin in peritonitis. III. The mechanism of bacterial trapping
480 by polymerizing fibrin. Surgery.
- 481 19. Negrón O, Hur WS, Prasad J, Paul DS, Rowe SE, Degen JL, Abrahams SR, Antoniak S,
482 Conlon BP, Bergmeier W, Höök M, Flick MJ. 2022. Fibrin(ogen) engagement of *S. aureus*
483 promotes the host antimicrobial response and suppression of microbe dissemination
484 following peritoneal infection. PLoS Pathog.
- 485 20. Prasad JM, Negrón O, Du X, Mullins ES, Palumbo JS, Gilbertie JM, Höök M, Grover SP,
486 Pawlinski R, Mackman N, Degen JL, Flick MJ. 2021. Host fibrinogen drives antimicrobial
487 function in *Staphylococcus aureus* peritonitis through bacterial-mediated prothrombin
488 activation. Proc Natl Acad Sci U A.
- 489 21. Prasad JM, Gorkun OV, Raghu H, Thornton S, Mullins ES, Palumbo JS, Ko YP, Höök M,
490 David T, Coughlin SR, Degen JL, Flick MJ. 2015. Mice expressing a mutant form of
491 fibrinogen that cannot support fibrin formation exhibit compromised antimicrobial host
492 defense. Blood.
- 493 22. Flick MJ, Du X, Prasad JM, Raghu H, Palumbo JS, Smeds E, Höök M, Degen JL. 2013.
494 Genetic elimination of the binding motif on fibrinogen for the *S. aureus* virulence factor ClfA
495 improves host survival in septicemia. Blood.
- 496 23. Ko YP, Liang X, Smith CW, Degen JL, Höök M. 2011. Binding of Efb from *Staphylococcus*
497 *aureus* to fibrinogen blocks neutrophil adherence. J Biol Chem.

- 498 24. Thomer L, Emolo C, Thammavongsa V, Kim HK, McAdow ME, Yu W, Kieffer M,
499 Schneewind O, Missiakas D. 2016. Antibodies against a secreted product of *Staphylococcus*
500 *aureus* trigger phagocytic killing. *J Exp Med*.
- 501 25. Cheng AG, McAdow M, Kim HK, Bae T, Missiakas DM, Schneewind O. 2010. Contribution
502 of coagulases towards *Staphylococcus aureus* disease and protective immunity. *PLoS Pathog*.
- 503 26. Guggenberger C, Wolz C, Morrissey JA, Heesemann J. 2012. Two distinct coagulase-
504 dependent barriers protect *Staphylococcus aureus* from neutrophils in a three dimensional in
505 vitro infection model. *PLoS Pathog*.
- 506 27. Ko YP, Kuipers A, Freitag CM, Jongerius I, Medina E, van Rooijen WJ, Spaan AN, van
507 Kessel KP, Höök M, Rooijackers SH. 2013. Phagocytosis escape by a *Staphylococcus aureus*
508 protein that connects complement and coagulation proteins at the bacterial surface. *PLoS*
509 *Pathog*.
- 510 28. Bjerketorp J, Jacobsson K, Frykberg L. 2004. The von Willebrand factor-binding protein
511 (vWbp) of *Staphylococcus aureus* is a coagulase. *FEMS Microbiol Lett*.
- 512 29. Bjerketorp J, Nilsson M, Ljungh A, Flock JI, Jacobsson K, Frykberg L. 2002. A novel von
513 Willebrand factor binding protein expressed by *Staphylococcus aureus*. *Microbiology*.
- 514 30. Friedrich R, Panizzi P, Fuentes-Prior P, Richter K, Verhamme I, Anderson PJ, Kawabata S,
515 Huber R, Bode W, Bock PE. 2003. Staphylocoagulase is a prototype for the mechanism of
516 cofactor-induced zymogen activation. *Nature*.
- 517 31. Colque-Navarro P, Palma M, Söderquist B, Flock JI, Möllby R. 2000. Antibody responses in
518 patients with staphylococcal septicemia against two *Staphylococcus aureus* fibrinogen
519 binding proteins: clumping factor and an extracellular fibrinogen binding protein. *Clin Diagn*
520 *Lab Immunol*.

- 521 32. Watanabe S, Ito T, Sasaki T, Li S, Uchiyama I, Kishii K, Kikuchi K, Skov RL, Hiramatsu K.
522 2009. Genetic diversity of staphylocoagulase genes (coa): insight into the evolution of
523 variable chromosomal virulence factors in *Staphylococcus aureus*. PLoS One.
- 524 33. Palma M, Shannon O, Quezada HC, Berg A, Flock JI. 2001. Extracellular fibrinogen-binding
525 protein, Efb, from *Staphylococcus aureus* blocks platelet aggregation due to its binding to the
526 alpha-chain. J Biol Chem.
- 527 34. Garcia BL, Ramyar KX, Ricklin D, Lambris JD, Geisbrecht BV. 2012. Advances in
528 understanding the structure, function, and mechanism of the SCIN and Efb families of
529 Staphylococcal immune evasion proteins. Adv Exp Med Biol.
- 530 35. Hammel M, Nemecek D, Keightley JA, Thomas GJ, Geisbrecht BV. 2007. The
531 *Staphylococcus aureus* extracellular adherence protein (Eap) adopts an elongated but
532 structured conformation in solution. Protein Sci.
- 533 36. Lee LY, Höök M, Haviland D, Wetsel RA, Yonter EO, Syribeys P, Vernachio J, Brown EL.
534 2004. Inhibition of complement activation by a secreted *Staphylococcus aureus* protein. J
535 Infect Dis.
- 536 37. Lee LY, Liang X, Höök M, Brown EL. 2004. Identification and characterization of the C3
537 binding domain of the *Staphylococcus aureus* extracellular fibrinogen-binding protein (Efb).
538 J Biol Chem.
- 539 38. Shannon O, Flock JI. 2004. Extracellular fibrinogen binding protein, Efb, from
540 *Staphylococcus aureus* binds to platelets and inhibits platelet aggregation. Thromb Haemost.
- 541 39. Posner MG, Upadhyay A, Abubaker AA, Fortunato TM, Vara D, Canobbio I, Bagby S, Pula
542 G. 2016. Extracellular Fibrinogen-binding Protein (Efb) from *Staphylococcus aureus* Inhibits
543 the Formation of Platelet-Leukocyte Complexes. J Biol Chem.

- 544 40. Ricklin D, Ricklin-Lichtsteiner SK, Markiewski MM, Geisbrecht BV, Lambris JD. 2008.
545 Cutting edge: members of the Staphylococcus aureus extracellular fibrinogen-binding protein
546 family inhibit the interaction of C3d with complement receptor 2. *J Immunol*.
- 547 41. Kügler J, Wilke S, Meier D, Tomszak F, Frenzel A, Schirrmann T, Dübel S, Garritsen H,
548 Hock B, Toleikis L, Schütte M, Hust M. 2015. Generation and analysis of the improved
549 human HAL9/10 antibody phage display libraries. *BMC Biotechnol*.
- 550 42. Mollova S, Retter I, Hust M, Dübel S, Müller W. 2010. Analysis of single chain antibody
551 sequences using the VBASE2 Fab Analysis Tool. *Antib Eng*. Springer-Verlag, Berlin
552 Heidelberg.
- 553 43. Jäger V, Büssow K, Wagner A, Weber S, Hust M, Frenzel A, Schirrmann T. 2013. High
554 level transient production of recombinant antibodies and antibody fusion proteins in HEK293
555 cells. *BMC Biotechnol*.
- 556 44. Collaborators AR. 2022. Global burden of bacterial antimicrobial resistance in 2019: a
557 systematic analysis. *Lancet*.
- 558 45. Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, Pulcini C,
559 Kahlmeter G, Kluytmans J, Carmeli Y, Ouellette M, Outtersen K, Patel J, Cavaleri M, Cox
560 EM, Houchens CR, Grayson ML, Hansen P, Singh N, Theuretzbacher U, Magrini N, Group
561 WPPLW. 2018. Discovery, research, and development of new antibiotics: the WHO priority
562 list of antibiotic-resistant bacteria and tuberculosis. *Lancet Infect Dis*.
- 563 46. Hutchings MI, Truman AW, Wilkinson B. 2019. Antibiotics: past, present and future. *Curr*
564 *Opin Microbiol*.
- 565 47. Thomas S, Arora S, Liu W, Churion K, Wu Y, Höök M. 2021. vhp Is a Fibrinogen-Binding
566 Protein Related to vWbp in Staphylococcus aureus. *mBio*.

- 567 48. Rubel C, Gómez S, Fernández GC, Isturiz MA, Caamaño J, Palermo MS. 2003. Fibrinogen-
568 CD11b/CD18 interaction activates the NF-kappa B pathway and delays apoptosis in human
569 neutrophils. *Eur J Immunol*.
- 570 49. Flick MJ, Du X, Witte DP, Jirousková M, Soloviev DA, Busuttill SJ, Plow EF, Degen JL.
571 2004. Leukocyte engagement of fibrin(ogen) via the integrin receptor alphaMbeta2/Mac-1 is
572 critical for host inflammatory response in vivo. *J Clin Invest*.
- 573 50. Anderson AS, Scully IL, Buurman ET, Eiden J, Jansen KU. 2016. Staphylococcus aureus
574 Clumping Factor A Remains a Viable Vaccine Target for Prevention of S. aureus Infection.
575 *MBio*.
- 576 51. Dayan GH, Mohamed N, Scully IL, Cooper D, Begier E, Eiden J, Jansen KU, Gurtman A,
577 Anderson AS. 2016. Staphylococcus aureus: the current state of disease, pathophysiology
578 and strategies for prevention. *Expert Rev Vaccines*.
- 579 52. Scully IL, Timofeyeva Y, Keeney D, Matsuka YV, Severina E, McNeil LK, Nanra J, Hu G,
580 Liberator PA, Jansen KU, Anderson AS. 2015. Demonstration of the preclinical correlate of
581 protection for Staphylococcus aureus clumping factor A in a murine model of infection.
582 *Vaccine*.
- 583 53. Jumper J, Evans R, Pritzel A, Green T, Figurnov M, Ronneberger O, Tunyasuvunakool K,
584 Bates R, Židek A, Potapenko A, Bridgland A, Meyer C, Kohl SAA, Ballard AJ, Cowie A,
585 Romera-Paredes B, Nikolov S, Jain R, Adler J, Back T, Petersen S, Reiman D, Clancy E,
586 Zielinski M, Steinegger M, Pacholska M, Berghammer T, Bodenstein S, Silver D, Vinyals O,
587 Senior AW, Kavukcuoglu K, Kohli P, Hassabis D. 2021. Highly accurate protein structure
588 prediction with AlphaFold. *Nature*.

- 589 54. Varadi M, Anyango S, Deshpande M, Nair S, Natassia C, Yordanova G, Yuan D, Stroe O,
590 Wood G, Laydon A, Židek A, Green T, Tunyasuvunakool K, Petersen S, Jumper J, Clancy E,
591 Green R, Vora A, Lutfi M, Figurnov M, Cowie A, Hobbs N, Kohli P, Kleywegt G, Birney E,
592 Hassabis D, Velankar S. 2022. AlphaFold Protein Structure Database: massively expanding
593 the structural coverage of protein-sequence space with high-accuracy models. *Nucleic Acids*
594 *Res.*
- 595 55. Maddur AA, Voehler M, Panizzi P, Meiler J, Bock PE, Verhamme IM. 2022. Mapping of the
596 fibrinogen-binding site on the staphylocoagulase C-terminal repeat region. *J Biol Chem.*
- 597 56. Shannon O, Uekotter A, Flock JI. 2006. The neutralizing effects of hyperimmune antibodies
598 against extracellular fibrinogen-binding protein, Efb, from *Staphylococcus aureus*. *Scand J*
599 *Immunol.*
- 600 57. Brown EL, Nishiyama Y, Dunkle JW, Aggarwal S, Planque S, Watanabe K, Csencsits-Smith
601 K, Bowden MG, Kaplan SL, Paul S. 2012. Constitutive production of catalytic antibodies to
602 a *Staphylococcus aureus* virulence factor and effect of infection. *J Biol Chem.*
- 603 58. Georgoutsou-Spyridonos M, Ricklin D, Pratsinis H, Perivolioti E, Pirmettis I, Garcia BL,
604 Geisbrecht BV, Foukas PG, Lambris JD, Mastellos DC, Sfyroera G. 2015. Attenuation of
605 *Staphylococcus aureus*-Induced Bacteremia by Human Mini-Antibodies Targeting the
606 Complement Inhibitory Protein Efb. *J Immunol.*
- 607 59. Pozzi C, Bagnoli F, Rappuoli R. 2016. *Staphylococcus aureus* coagulase R domain, a new
608 evasion mechanism and vaccine target. *J Exp Med.*
- 609 60. Russo G, Meier D, Helmsing S, Wenzel E, Oberle F, Frenzel A, Hust M. 2018. Parallelized
610 Antibody Selection in Microtiter Plates. *Methods Mol Biol.*

- 611 61. Rondot S, Koch J, Breitling F, Dübel S. 2001. A helper phage to improve single-chain
612 antibody presentation in phage display. *Nat Biotechnol.*
- 613 62. Vieira J, Messing J. 1987. Production of single-stranded plasmid DNA. *Methods Enzym.*
- 614 63. Green MR, Sambrook J. 2012. *Molecular Cloning: A Laboratory Manual* Fourth Edition.
- 615 64. Corpet F. 1988. Multiple sequence alignment with hierarchical clustering. *Nucleic Acids*
616 *Res.*
- 617 65. Ren J, Wen L, Gao X, Jin C, Xue Y, Yao X. 2009. DOG 1.0: illustrator of protein domain
618 structures. *Cell Res.*
- 619

620 **Figure Legends**

621

622 **Figure 1 . Domain organization and recombinant constructs of Coagulase and Efb**

623 Domains and recombinant constructs of Coagulase (A) and Efb (B) derived from full length protein
624 of *S. aureus* Newman strain are shown. Residues, fibrinogen (Fg)- and prothrombin-binding regions
625 are indicated, Signal peptide (S) is necessary for extracellular release. Gluthation-S-Transferase
626 (GST) tag is in red (not to scale), 6 His tag in grey. Image were prepared with DOG2.0 (65). Panel C
627 shows an alignment, generated with Geneious, of CoaR0 and R repeats of Coa with a sequence logo
628 and identity to highlight the most conserved amino acids. Amino acids in the single repeats are
629 highlighted with Clustal colour scheme if they are present in more than 50% of the sequences.

630

631 **Figure 2. FBE5 antibodies dose-dependently bind CoaC fragment**

632 Titration ELISA to evaluate the binding of FBE5 scFv-Fcs to the antigen CoaC (200ng/well
633 immobilized protein). BSA binding curves were always below 0,1 and are not reported for clarity.
634 Isotype control is an unrelated scFv-Fc with human Fc moiety. Data±SEM are representative of
635 two independent experiments.

636

637 **Figure 3. Antibodies generated against CoaC bind CoaR0 repeat, but not CoaRI-RV
638 repeats, and cross react with EfbN**

639 Single point ELISA to evaluate the binding of FBE5 scFv-Fc to fragments of Coa and Efb
640 (200ng/well immobilized protein, [scFv-Fc] = 0,5µg/ml). Represented is the average ±SEM.

641

642

643

644

645

646 **Figure 4. Dose-dependent binding of anti-CoaR mAbs to Coa and Efb recombinant proteins**

647 Titration ELISA to investigate binding of LIG40-A11 (A) and LIG40-D8 (B) to CoaC, CoaR,
648 CoaR0, CoaF, EfbN, EfbA, EfbO recombinant fragments and determine EC₅₀. BSA and an
649 unrelated human scFv-Fc (both not represented for clarity) were used as negative and isotype
650 controls, respectively, and showed no binding.

651

652 **Figure 5. Anti-CoaC antibodies inhibit both Coa and Efb fibrinogen binding activity**

653 Antibodies FBE5-A12 (A), FBE5-D10 (B), FBE5-F9 (C) and FBE5-F11 (D) were pre-incubated
654 at the indicated amounts with Coa or Efb recombinant constructs (CoaF, CoaR0, EfbN and EfbO
655 at final concentration of 10nM, EfbA at 750µM) and then transferred to a Fg-coated ELISA plate.
656 The remaining Fg-bound antigens were detected through their tags (GST, except for EfbN which
657 harbours a 6xHis tag). Control wells with no antibody were set to 100% and the residual binding
658 of Coa and Efb constructs was determined by comparing control wells with the ones where
659 indicated amounts of mAbs were added. Average ± SEM of two independent experiments is
660 represented.

661

662 **Figure 6. Binding of FBE 5 mAbs to Coa C is inhibited by CoaR0 peptide but not by CoaRI**
663 **peptide**

664 CoaC was immobilized on an ELISA plate and a fixed quantity of each mAb was added
665 (0.5µg/ml) with different dilutions of either CoaR0 (A and B) or CoaRI (C and D) peptide.
666 Detection of mAb was performed through anti-human HRP (HorseRadish Peroxidase)-conjugated
667 secondary antibody. Data ± SEM are reported and are representative of two independent
668 experiments.

669

670 **Figure 7. Anti-CoaR antibodies are inhibited differently by CoaR0 and CoaRI peptides**

671 CoaC and CoaR were immobilized on an ELISA plate. 0.5ug/ml of LIG40-A11 (A and C) or
672 LIG40-D8 (B and D) were incubated with different dilutions of either CoaR0 (A and B) or CoaRI
673 (C and D) peptides. Detection of mAb was performed through anti-human HRP-conjugated
674 secondary antibody. Data \pm SEM are reported and are representative of two independent
675 experiments.

676

677 **Supplementary Figures Legends**

678 **Supplementary Fig. 1- Screening ELISA results after 3 panning rounds on CoaC**

679 Both signals (Optical Density 450-620nm) on CoaC and BSA for each of the 95 tested clones are
680 represented as sided bars.

681

682 **Supplementary Fig. 2- Dose-dependent binding of anti-CoaC mAbs to Coa recombinant**
683 **proteins**

684 Titration ELISA to investigate binding of FBE5 mAbs to CoaF (A) and CoaR0 (B) recombinant
685 constructs and determine EC50. BSA (not represented) and an unrelated human scFv-Fc were used
686 as negative and isotype controls, respectively.

687

688 **Supplementary Fig. 3 Dose-dependent binding of anti-CoaC mAbs to Efb recombinant**
689 **proteins**

690 Titration ELISA to investigate binding of FBE5 mAbs EfbN (A), EfbA (B), EfbO (C) recombinant
691 constructs and determine EC50. BSA (not represented) and an unrelated human scFv-Fc were used
692 as negative and isotype controls, respectively.

693

694 **Supplementary Fig. 4 - Anti-CoaC antibodies not inhibiting both Coa and Efb fibrinogen**
695 **binding activity**

696 Antibodies FBE5-A5 (A), FBE5-A6 (B), FBE5-B9 (C) and FBE5-C1 (D), FBE5-D9 (E), FBE5-C8
697 (F), FBE5-E5 (G) were pre-incubated at the indicated amounts with the fixed amounts of Coa or

698 Efb recombinant constructs (CoaF, CoaR0, EfbN and EfbO at final concentration of 10nM, EfbA at
699 750µM) and then transferred on a Fg-coated ELISA plate. The remaining Fg-bound antigens were
700 detected through their tags (GST, except for EfbN that harbours a 6xHis tag). Control wells in
701 which no antibody was added were set to 100% and the residual binding of Coa and Efb constructs
702 were determined by comparing control wells with the ones where indicated amounts of mAbs were
703 added. Average +- SEM of two independent experiments is represented.

704

705 **Supplementary Fig. 5 - Anti-CoaR antibodies do not inhibit Coa Fg binding**

706 Antibodies LIG40-A11 (left) and LIG40-D8 (right) were pre-incubated at the indicated amounts
707 with the fixed amounts of Coa recombinant constructs (CoaF, CoaR0, CoaR at final concentration
708 of 10nM, CoaC at 2nM) and then transferred on a Fg-coated ELISA plate. The remaining Fg-bound
709 antigens were detected through their GST tag. Control wells in which no antibody was added were
710 set to 100% and the residual binding of Coa constructs were determined by comparing control wells
711 with the ones where indicated amounts of mAbs were added. Average +- SEM of two independent
712 experiments is represented.

713

714

Table 1- Apparent K_d for FBE 5 antibodies expressed in M derived from half-maximum binding determined in ELISA. ND: not determinable. NSB: Non-Sigmoidal weak Binding

ANTIBODY	K_d app (M) for CoaC	K_d app (M) for CoaF	K_d app (M) for CoaR0	K_d app (M) for EfbN	K_d app (M) for EfbA	K_d app (M) for EfbO
FBE5-A5	$5,34 \times 10^{-9}$	$1,47 \times 10^{-9}$	$1,86 \times 10^{-9}$	$3,24 \times 10^{-9}$	$4,38 \times 10^{-9}$	$4,27 \times 10^{-9}$
FBE5-A6	$1,24 \times 10^{-9}$	$1,15 \times 10^{-9}$	$1,9 \times 10^{-9}$	$3,54 \times 10^{-9}$	$8,54 \times 10^{-9}$	$1,3 \times 10^{-8}$ (NSB)
FBE5-A12	$5,55 \times 10^{-10}$	$6,47 \times 10^{-10}$	$2,44 \times 10^{-9}$	$8,66 \times 10^{-9}$	$7,28 \times 10^{-8}$ (NSB)	$3,51 \times 10^{-8}$ (NSB)
FBE5-B9	$1,74 \times 10^{-9}$	$1,12 \times 10^{-9}$	$2,19 \times 10^{-9}$	$3,45 \times 10^{-9}$	$2,59 \times 10^{-8}$	$8,27 \times 10^{-9}$
FBE5-C1	$1,13 \times 10^{-9}$	$4,59 \times 10^{-9}$	$2,43 \times 10^{-8}$ (NSB)	$2,44 \times 10^{-8}$ (NSB)	$4,09 \times 10^{-8}$ (NSB)	ND
FBE5-C8	$1,35 \times 10^{-8}$	7×10^{-9}	$1,93 \times 10^{-7}$ (NSB)	$1,7 \times 10^{-7}$ (NSB)	ND	ND
FBE5-D9	$7,79 \times 10^{-10}$	$5,36 \times 10^{-10}$	$1,14 \times 10^{-9}$	$1,31 \times 10^{-9}$	$4,48 \times 10^{-9}$	$2,68 \times 10^{-9}$
FBE5-D10	$1,4 \times 10^{-9}$	$9,5 \times 10^{-10}$	$8,56 \times 10^{-10}$	$1,97 \times 10^{-9}$	$1,57 \times 10^{-9}$	$3,65 \times 10^{-9}$
FBE5-E5	$6,27 \times 10^{-9}$	$9,5 \times 10^{-9}$	$8,64 \times 10^{-7}$ (NSB)	ND	ND	ND
FBE5-F9	$2,85 \times 10^{-9}$	$1,63 \times 10^{-9}$	$3,16 \times 10^{-9}$	$6,01 \times 10^{-9}$	$2,15 \times 10^{-8}$	$7,97 \times 10^{-9}$
FBE5-F11	$5,13 \times 10^{-10}$	$2,44 \times 10^{-10}$	$2,13 \times 10^{-10}$	$2,19 \times 10^{-10}$	$4,83 \times 10^{-10}$	$3,96 \times 10^{-10}$

Table 2- Apparent K_d for LIG40 antibodies expressed in M derived from half-maximum binding determined in ELISA. ND: not determinable. NSB: Non-Sigmoidal weak Binding

ANTIBODY	K_d app (M) for CoaC	K_d app (M) for CoaF	K_d app (M) for CoaR0	K_d app (M) for CoaR
LIG40-A11	$1,33 \times 10^{-10}$	ND	ND	$7,05 \times 10^{-11}$
LIG40-D8	$9,39 \times 10^{-11}$	$1,12 \times 10^{-10}$	$2,52 \times 10^{-9}$ (NSB)	$8,62 \times 10^{-11}$

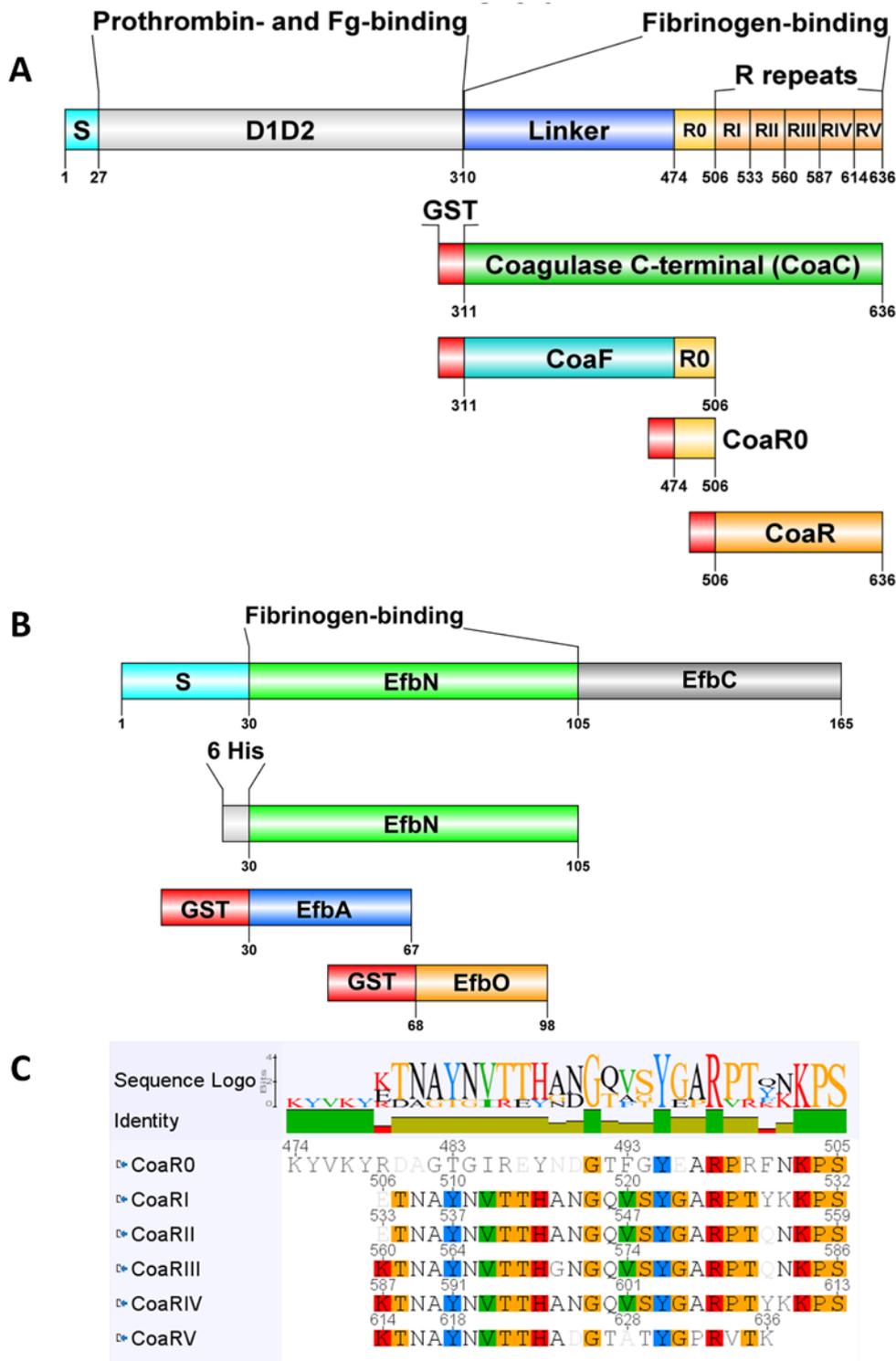


Figure 1 . Domain organization and recombinant constructs of Coagulase and Efb

Domains and recombinant constructs of Coagulase (A) and Efb (B) derived from full length protein of *S. aureus* Newman strain are shown. Residues, fibrinogen (Fg)- and prothrombin-binding regions are indicated, Signal peptide (S) is necessary for extracellular release. Gluthation-S-Transferase (GST) tag is in red (not to scale), 6 His tag in grey. Image were prepared with DOG2.0 (65). Panel C shows an alignment, generated with Geneious, of CoaR0 and R repeats of Coa with a sequence logo and identity to highlight the most conserved amino acids. Amino acids in the single repeats are highlighted with Clustal colour scheme if they are present in more than 50% of the sequences.

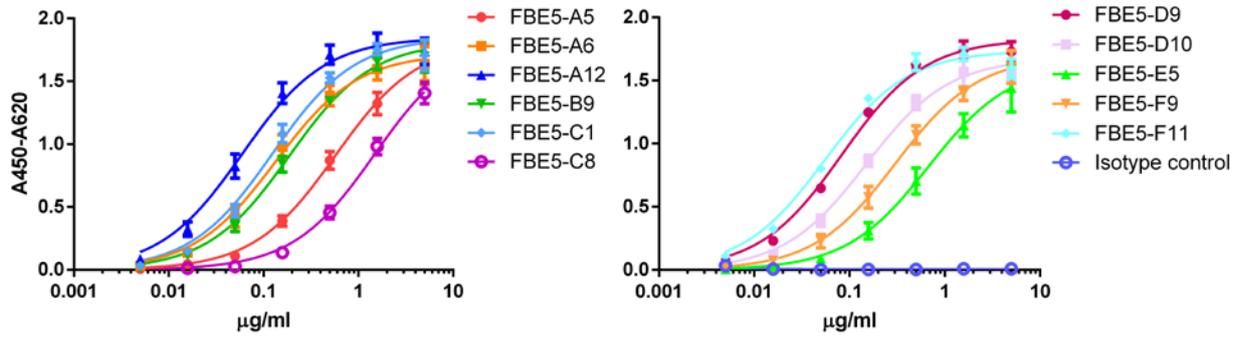


Figure 2. FBE5 antibodies dose-dependently bind CoaC fragment

Titration ELISA to evaluate the binding of FBE5 scFv-Fcs to the antigen CoaC (200ng/well immobilized protein). BSA binding curves were always below 0,1 and are not reported for clarity. Isotype control is an unrelated scFv-Fc with human Fc moiety. Data \pm SEM are representative of two independent experiments.

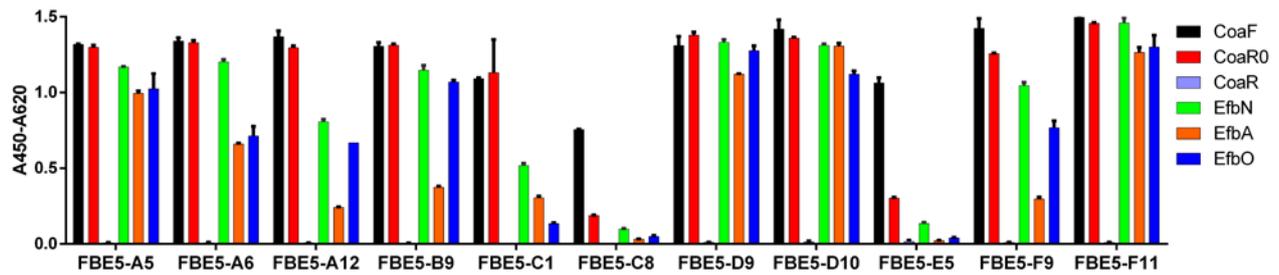


Figure 3. Antibodies generated against CoaC bind CoaR0 repeat, but not CoaRI-RV repeats, and cross react with EfbN

Single point ELISA to evaluate the binding of FBE5 scFv-Fc to fragments of Coa and Efb (200ng/well immobilized protein, [scFv-Fc] = 0,5 μ g/ml). Represented is the average \pm SEM.

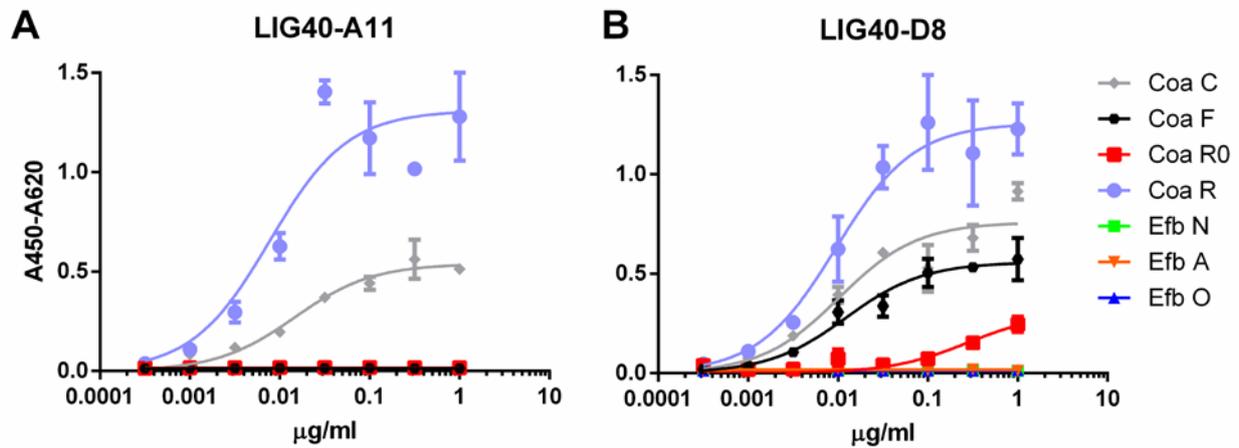


Figure 4. Dose-dependent binding of anti-CoaR mAbs to Coa and Efb recombinant proteins

Titration ELISA to investigate binding of LIG40-A11 (A) and LIG40-D8 (B) to CoaC, CoaR, CoaR0, CoaF, EfbN, EfbA, EfbO recombinant fragments and determine EC₅₀. BSA and an unrelated human scFv-Fc (both not represented for clarity) were used as negative and isotype controls, respectively, and showed no binding.

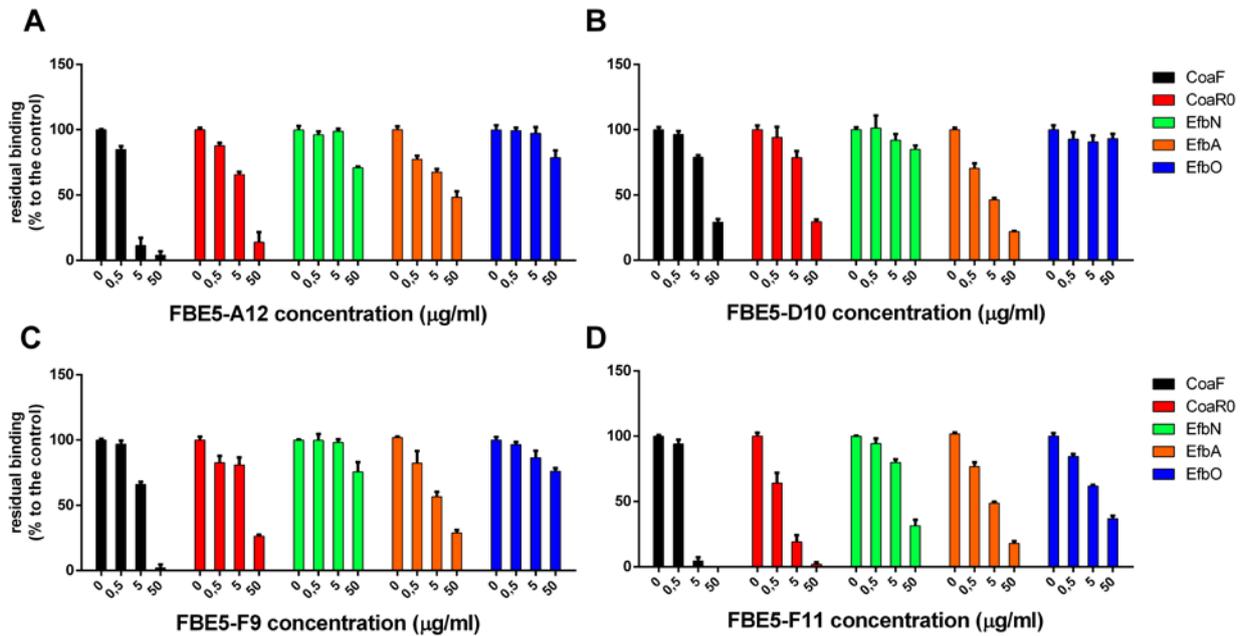


Figure 5. Anti-CoaC antibodies inhibit both Coa and Efb fibrinogen binding activity

Antibodies FBE5-A12 (A), FBE5-D10 (B), FBE5-F9 (C) and FBE5-F11 (D) were pre-incubated at the indicated amounts with Coa or Efb recombinant constructs (CoaF, CoaR0, EfbN and EfbO at final concentration of 10nM, EfbA at 750µM) and then transferred to a Fg-coated ELISA plate. The remaining Fg-bound antigens were detected through their tags (GST, except for EfbN which harbours a 6xHis tag). Control wells with no antibody were set to 100% and the residual binding of Coa and Efb constructs was determined by comparing control wells with the ones where indicated amounts of mAbs were added. Average \pm SEM of two independent experiments is represented.

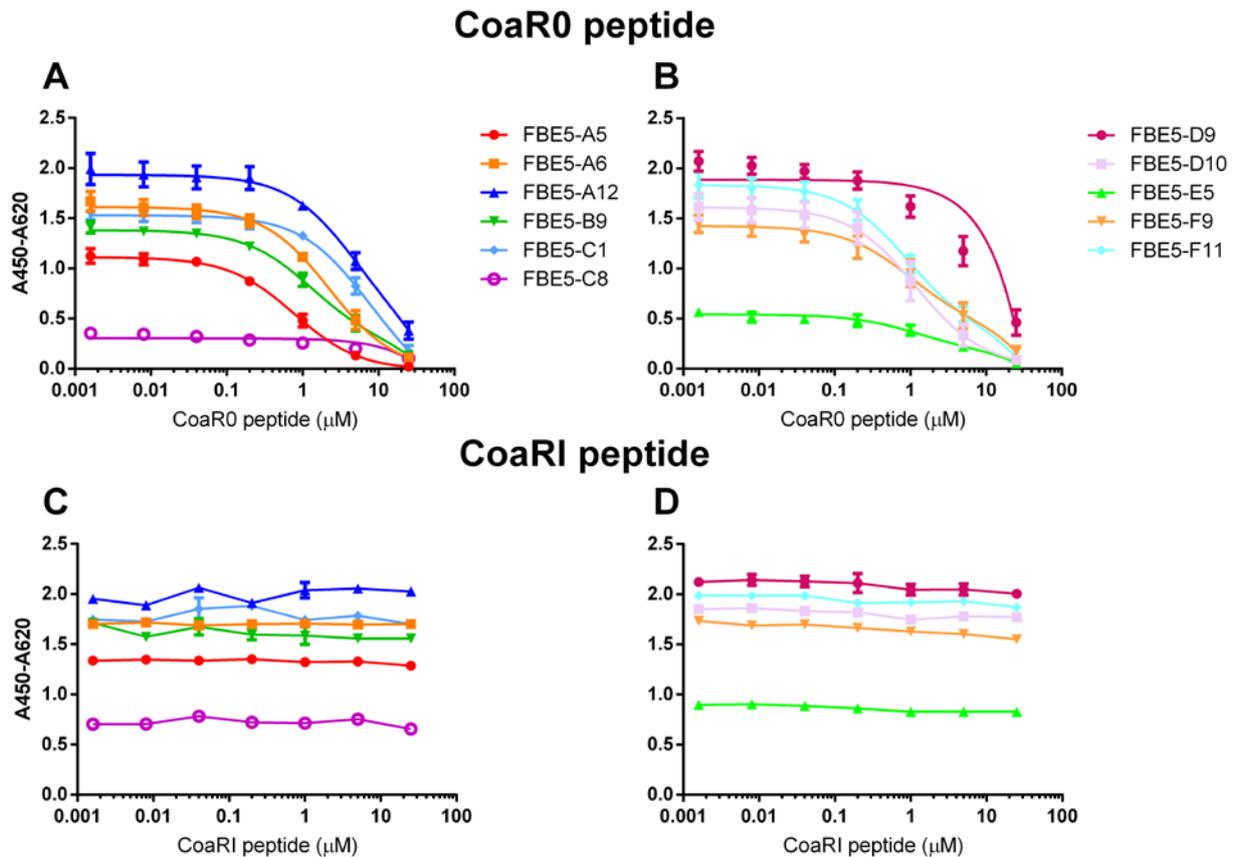


Figure 6. Binding of FBE 5 mAbs to Coa C is inhibited by CoaR0 peptide but not by CoaRI peptide

CoaC was immobilized on an ELISA plate and a fixed quantity of each mAb was added (0.5 $\mu\text{g}/\text{ml}$) with different dilutions of either CoaR0 (A and B) or CoaRI (C and D) peptide. Detection of mAb was performed through anti-human HRP (HorseRadish Peroxidase)-conjugated secondary antibody. Data \pm SEM are reported and are representative of two independent experiments.

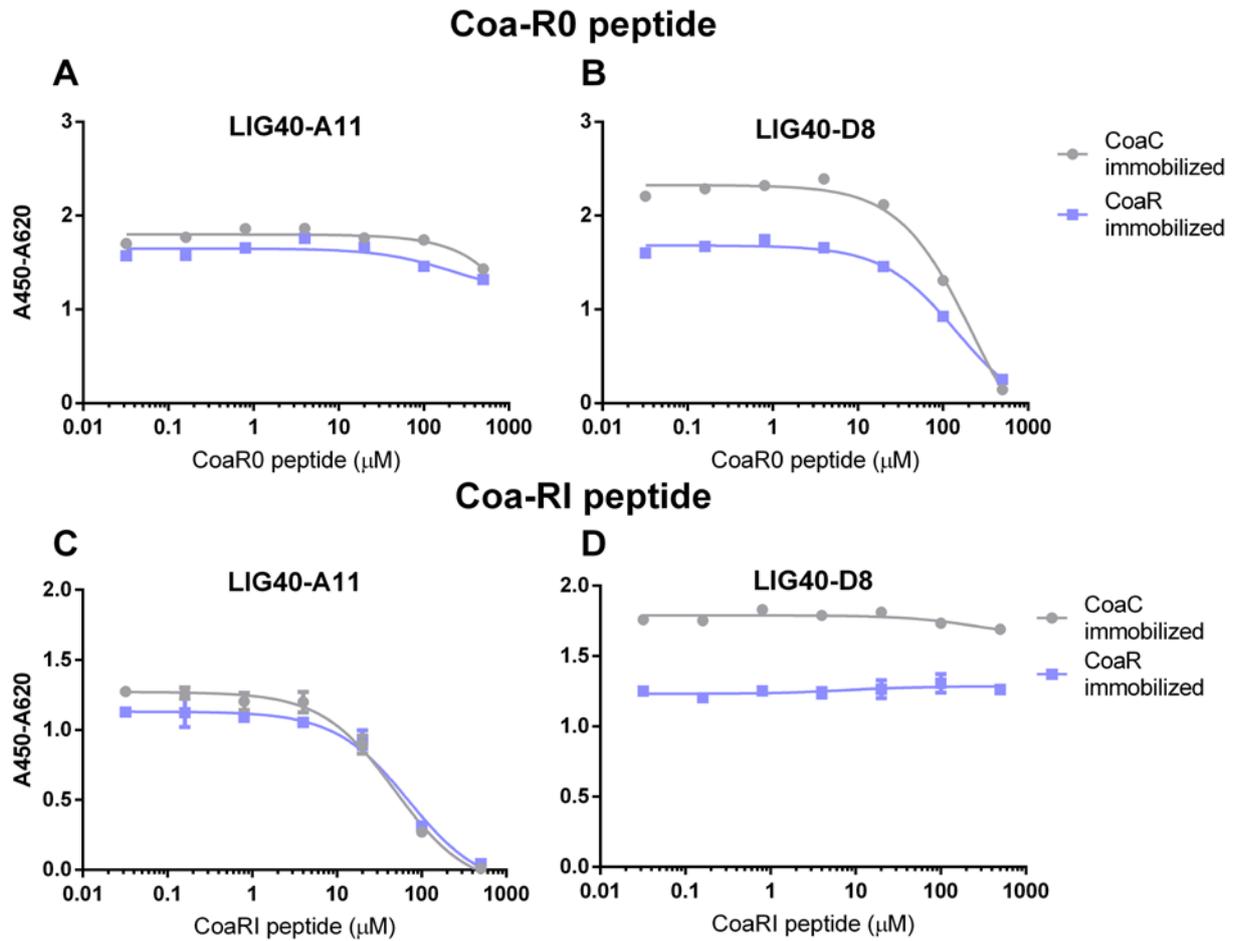


Figure 7. Anti-CoaR antibodies are inhibited differently by CoaR0 and CoaRI peptides

CoaC and CoaR were immobilized on an ELISA plate. 0.5ug/ml of LIG40-A11 (A and C) or LIG40-D8 (B and D) were incubated with different dilutions of either CoaR0 (A and B) or CoaRI (C and D) peptides. Detection of mAb was performed through anti-human HRP-conjugated secondary antibody. Data \pm SEM are reported and are representative of two independent experiments.