

1 *Classification:* BIOLOGICAL SCIENCES, Microbiology

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3 **Inhibitors of the *Neisseria meningitidis* PilF ATPase provoke**
4 **type IV pilus disassembly**

5

6 Short title: *Inhibitors of Neisseria adhesion*

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22 **Bacteria**

23 **Abstract**

24 Despite the availability of antibiotics and vaccines, *Neisseria meningitidis* remains a major cause
25 of meningitis and sepsis in humans. Due to its extracellular lifestyle, bacterial adhesion to host
26 cells constitutes an attractive therapeutic target. Here we present a high-throughput microscopy-
27 based approach that allowed the identification of compounds able to decrease type IV pilus-
28 mediated interaction of bacteria with endothelial cells in absence of bacterial or host cell toxicity.
29 Compounds specifically inhibit the PilF ATPase enzymatic activity that powers type IV pilus
30 extension but remain inefficient on the ATPase that promotes pilus retraction thus leading to rapid
31 pilus disappearance from the bacterial surface and loss of pili-mediated functions. Structure
32 activity relationship of the most active compound identifies specific moieties required for the
33 activity of this compound and highlights its specificity. This study therefore provides the first
34 compounds targeting pilus biogenesis, thereby inhibiting bacterial adhesion, and pave the way for
35 a novel therapeutic option for meningococcal infections.

36

37 **Significance Statement**

38 A number of multimeric protein nanomachines such as secretion systems and surface
39 appendages allow bacteria to adapt and survive in a variety of environments. Type IV pili are one
40 of the most common of such machineries. The human pathogen *Neisseria meningitidis* uses type
41 IV pili to colonize blood vessels and cause disease. Here, we identify compounds that trigger the
42 rapid retraction of type IV pili. Furthermore, we identify the target of these small molecules as an
43 ATPase known as PilF among the 20 proteins involved in pilus assembly and function. This study
44 paves the way for an innovative treatment strategy for different pathogens and provides new
45 information on the molecular mechanisms driving the assembly and dynamics of bacterial
46 machineries.

47 \body

48 **Introduction**

49 *Neisseria meningitidis* is a pathogenic bacterium responsible for sepsis and meningitis that remain
50 a major concern in emergency wards despite the availability of antibiotics (1). The human naso-
51 oropharynx is the only known natural reservoir for *N. meningitidis* and transmission to new hosts
52 occurs directly via droplets (2). This bacterium colonizes the naso-oropharynx of a substantial
53 proportion of the population, 3 to 30% depending on the study (3). Pathology is initiated when
54 bacteria reach the bloodstream where they survive and proliferate. When the bacteremia is not
55 cleared rapidly, two severe although fairly distinct disease manifestations can develop: sepsis or
56 meningitis if bacteria also crossed the blood-brain barrier (1). Fulminant meningococcal sepsis,
57 subsequent to septicemia, is the most devastating form of sepsis with a mortality rate varying from
58 20 to 30% despite antimicrobial treatment and medical care. It is characterized by a rapidly
59 evolving septic shock, disseminated intravascular coagulation (DIC) and skin haemorrhage
60 (*purpura fulminans*).

61 Because of the rapid evolution of the disease and the severity of the symptoms, industrial and
62 basic research efforts have focused on the design of vaccine strategies (4). Conjugated
63 polysaccharide vaccines have been very successful for specific serogroups, but these approaches
64 also show certain limits due to the diversity and variability of surface structures in *Neisseria*
65 *meningitidis* (5, 6). Serogroup B which represents the majority of cases in most other countries is
66 also a particular problem because its capsular polysaccharide is similar to one found in humans
67 (7). The reverse vaccinology approach addressed this issue by generating the Bexsero vaccine
68 (8) combining several surface structures but its efficiency is still under evaluation and it will always
69 be efficient on a subset of strains only (9). In addition to these efforts in the field of prevention,
70 new therapeutic approaches should thus also be considered.

71 To treat infections more efficiently, there is a need for a paradigm shift. It seems unlikely that a
72 super antibiotic with extended spectrum that can replace existing therapies without any of the side

73 effects generally associated with antibiotics will ever arise. New classes of anti-infectious
74 compounds need to be found to instigate this paradigm shift. To reach this goal, one must
75 investigate an avenue that remains largely unexplored in terms of medicinal chemistry: host-
76 bacteria interactions and virulence factors (10). By targeting these determinants of infection, these
77 new therapeutical approaches would greatly enhance classical antibacterial treatments and
78 improve therapy outcome and patient welfare.

79 Central virulent properties of *N. meningitidis* include adhesion to host cells (11), and this
80 constitutes an original and attractive target for treatments. Adhesion of *N. meningitidis* to human
81 cells is a key step in the life cycle of this organism by allowing nasopharynx colonization and
82 adhesion to endothelial cells, each of these events promoting blood and brain colonization by the
83 bacteria. Neisserial type IV pili (Tfp) have long been recognized as playing an essential role in the
84 pathogenesis of *N. meningitidis*, and primary cultures of clinical isolates of pathogenic *Neisseria*
85 are invariably piliated (12, 13). In a humanized animal model type IV pili were shown to be
86 responsible for adhesion along the endothelium and to trigger the vascular damages observed
87 during infection, including loss of vascular integrity, coagulation and congestion (13, 14). In
88 addition to type IV pili, *Neisseria meningitidis* expresses several other transmembrane adhesins,
89 the most studied being the Opa family of adhesins (15). These additional adhesins tune the
90 interaction with host cells by promoting host-pathogen intimate interactions, triggering intracellular
91 signalling events and favouring intracellular invasion. Adhesion is thus a key feature of *N.*
92 *meningitidis* pathogenesis that constitutes a promising therapeutic target.

93 In this study, we identified compounds that inhibit the adhesion of *N. meningitidis* to host cells by
94 screening a library of compounds and identified their mode of action down to the molecular and
95 chemical level.

96 **Results**

97 **Identification of compounds decreasing *Neisseria meningitidis* adhesion to human** 98 **endothelial cells**

99 Adhesion to the human endothelium can be recapitulated *in vitro* using cultured endothelial cells.
100 Bacteria rapidly adhere as individual diplococci to the host cell surface and subsequently divide,
101 forming tight roughly circular aggregates, termed microcolonies, which can reach 10-20 μm in
102 diameter within 2-4 hours. Thus, the size and number of these microcolonies as visualized by
103 fluorescence microscopy represent good markers for the ability of bacteria to adhere to endothelial
104 cells and proliferate on their surface. A microscopy-based high-throughput screening approach
105 was therefore selected and optimized to identify compounds that block *N. meningitidis* adhesion
106 onto endothelial cells. Monolayers of primary human umbilical vein endothelial cells (HUVEC) in
107 384-well plates were pre-treated with 1 μM of each compound for 30 minutes prior to be infected
108 with *N. meningitidis*. Non-adhering bacteria were washed-out following a 30-min incubation and
109 adhering bacteria were allowed to proliferate in the presence of the compounds for 4 hours (Fig.
110 1A). A library containing 2,239 compounds was used to block adhesion. This library contains a
111 combination of FDA approved drugs, inhibitors of Kegg pathways, kinase inhibitors and a selection
112 of Sanofi lead compounds (Fig. 1B). Microcolonies were visualized by labelling bacteria with an
113 antibody directed against capsular antigens, and host cells were detected with a DNA labelling
114 dye (Hoechst 33342). Images were then segmented and analysed, allowing extraction of several
115 parameters such as microcolony size and number but also cellular toxicity (number of nuclei per
116 field of view) (Fig. 1C). Compound activity was expressed as a percentage of adhesion inhibition
117 relative to positive (non-infected cells, 100 % inhibition) and negative (no compound, 0% inhibition)
118 controls in each plate of the two replicates. Among the tested compounds, 163 hits were selected
119 based on their effective inhibition of bacterial adhesion ($\geq 60\%$) and low cellular toxicity ($\leq 10\%$)
120 (Fig. 1D and SI Appendix Table S1). 72 compounds were confirmed in a validation assay and 59

121 of them (because of availability limitation) were further analysed using a dose response approach
122 ranging from 30 μ M to 1 nM. First, the potential of each compound to inhibit the formation of
123 bacterial colonies was used to calculate their half maximal inhibitory concentration (IC₅₀, SI
124 Appendix Table S2). Then, the cellular toxicity of each compound was evaluated on HepG2 cells
125 and their median toxic concentration (TC₅₀) was determined (SI Appendix Table S2). Correlation
126 analysis of IC₅₀ and TC₅₀ highlighted two main groups of compounds: one including compounds
127 showing intermediate cellular toxicity but very potent inhibition of bacterial adhesion (Fig. 2A, light
128 red) and a second group of compounds harbouring a lower cellular toxicity but also a lower
129 inhibitory efficiency (Fig. 2A, light grey). We therefore selected the best compounds of each group
130 that will be referred to as A, B and C, hereafter (Fig. 2A, red dots and SI Appendix Table S2) and
131 evaluated their cellular toxicity on both THP1 and HepG2 cells (SI Appendix Fig. S1). Their
132 chemical structures are indicated on figure 2B. Dose response curves confirmed that compound
133 A was the most active with an IC₅₀ of 7.20×10^{-9} M, followed by B with a value of 1.73×10^{-8} M, and
134 C was slightly less active with a value of 2.66×10^{-7} M (Fig. 2C and SI Appendix Table S2).
135 Despite the exclusion from the screening analysis of compounds with known bactericidal activity,
136 the effects of the three selected compounds could be indirectly due to an alteration of bacterial
137 viability. We therefore tested this potential effect by performing growth curves in the presence of
138 the compounds. None of the three compounds had any effect on bacterial growth at a
139 concentration of 1 μ M (Fig. 2D). This microscopy-based screening approach thus allowed us to
140 identify new compounds that can reduce the number of bacteria adhering to human endothelial
141 cells without affecting bacterial viability.

142

143 **Compounds affect type IV pili display on the bacterial surface**

144 To further validate the effects of the three compounds in conditions closer to a therapeutic
145 application, their ability to induce the detachment of adhering bacteria was then evaluated.
146 Bacteria were allowed to adhere at the surface of endothelial cells and then proliferate for 4 hours

147 before adding the compounds for 30 minutes, and bacterial adhesion was evaluated by counting
148 cell-associated colony forming units (CFU, Fig. 3A). In line with our screening data, this assay
149 confirmed the efficiency of the selected compounds and showed that they can act after bacterial
150 adhesion and proliferation. Compound B was the most potent in detaching previously adhering
151 bacteria with a five-fold decrease, whereas compounds A and C were slightly less efficient (Fig.
152 3B). The non-piliated strain *pilD* defective for adhesion to the host cells was used to determine a
153 base-line of bacterial adhesion and showed that the effect of the compounds is not complete (Fig.
154 3B). The compounds identified in the screen are thus efficient at detaching previously adhering
155 bacteria, pointing to an effect on adhesion itself.

156 Adhesion of *Neisseria meningitidis* to human endothelial cells is largely mediated by Tfp,
157 suggesting that the compounds identified in the screen could affect the function or assembly of
158 these structures. Since Tfp carry several other functions, including bacterial auto-aggregation, a
159 prediction is that bacterial aggregation would be affected by compounds that affect pilus assembly.
160 Bacterial aggregates in suspension (in the absence of endothelial cells) generated by GFP-
161 expressing *N. meningitidis* were treated with compound B and observed by video-microscopy (Fig.
162 3C). Addition of the compound led to a rapid disaggregation of the bacteria followed by their
163 progressive diffusion away from the aggregate centre. The effect was detectable as early as 30
164 seconds following compound B addition. Inhibition of bacterial aggregation was further quantified
165 using a 4x magnification lens and automated counting of aggregate number in wells of 96-well
166 plates. Using this approach, we first evaluated the effect of the three compounds on the ability of
167 individual bacteria to form aggregates (Fig. 3D). In these conditions, compounds A and B
168 completely blocked aggregate formation whereas compound C had only a partial effect (Fig. 3D).
169 We then evaluated the ability of a 30-minute treatment with the compounds to disaggregate
170 preformed aggregates (Fig. 3E). In absence of compounds, the number of bacteria engaged within
171 an aggregate increased over the 30-minute period (DMSO). In contrast, compounds A and B were
172 extremely efficient in disaggregating preformed bacterial aggregates while compound C only

173 showed a partial effect (Fig. 3E). Of note, compound B was also able to prevent the auto-
174 aggregation of *N. gonorrhoeae* and induced the disaggregation of preformed gonococcal
175 aggregates (Fig. 3D and E, left panels). These results show that the three compounds identified
176 in the screen affect the bacterial aggregation in addition to adhesion, most probably by altering
177 the function or biogenesis of type IV pili.

178 We therefore evaluated whether bacterial treatment with the compounds is associated with a
179 decrease in the amount of bacterial Tfp. The amount of Tfp displayed by the bacteria can be
180 assessed using an ELISA-based approach on whole bacteria immobilized in 96-well plates and
181 probed with an anti-Tfp antibody. This assay revealed that the three compounds affected bacterial
182 piliation at various levels (Fig. 3F), with compound B being again the most efficient with a five-fold
183 decrease in piliation. This effect was also visible when immunostaining Tfp (Fig. 3G). Although the
184 effect of compounds A and C on piliation might seem relatively mild, we have previously shown
185 that minor reductions in piliation levels strongly affect Tfp-mediated functions (16). Altogether, it
186 can be concluded from these results that the compounds identified in the screen exert their effect
187 by decreasing the surface expression levels of bacterial type IV pili.

188

189 **Structure activity relationship of compound B**

190 Since compound B was the most efficient, we decided to establish the structure activity
191 relationship (SAR) of this compound. To this end, we characterized the effect on bacterial
192 aggregation of a series of 49 compounds closely related to compound B. As described in figure
193 3D, individual bacteria were treated with 0.1 μM of each derivative and incubated 30 min to form
194 aggregates. Of note, at this concentration, treatment with compound B only led to the partial
195 inhibition of bacterial aggregation (Fig. 4A), giving the opportunity to highlight derivatives with an
196 increased (or decreased) activity. While most derivatives showed a reduced ability to inhibit
197 bacterial aggregation (Fig. 4B, light red), a few of them displayed a slightly higher effect (Fig. 4B,
198 light green) than compound B, allowing us to establish the SAR (SI Appendix Table S3). Therefore,

199 the relative importance of the three main groups forming compound B, the 2,4-dimethoxybenzene,
200 the piperidine and the naphthalene, could be deduced from this approach (Fig. 4C). Only minor
201 modifications on the 2,4-dimethoxybenzene, such as hydroxylation or O-ethylation, were tolerated
202 to maintain activity. Longer alkyl chain or different simple modifications led to a loss of activity.
203 Changes on the two piperidine moieties and the length of linker between these two also led to a
204 loss of activity. In contrast, the naphthalene moiety could be easily modified without any major loss
205 of activity. A benzene ring with variable groups, for instance, could be introduced. Halogen or alkyl
206 groups attached on this benzene even led to increase activity. The activity was in general
207 increased when lipophilic groups were introduced at this position. The introduction of basicity, as
208 with a pyridine moiety, was on the other hand not tolerated. These results point to the importance
209 of the 2,4-dimethoxybenzene and piperidine moieties for activity of this compound and highlight
210 its specificity. The possibility to modify the naphthalene group opens the way to further
211 optimization of compound B.

212

213 **Compounds specifically target the Tfp assembly ATPase PilF but not the disassembly**
214 **ATPase PilT**

215 Tfp are dynamic organelles that constantly undergo cycles of growth, reaching up to several
216 microns in length, and retraction at speeds up to one micron per second (17), and eventually
217 leading to their complete disappearance. This dynamic behaviour is due to the assembly of the
218 major pilin PilE, located into the bacterial inner membrane, into a helical fibre during growth and
219 disassembly of this homopolymer upon retraction. This whole process is made possible by a
220 complex machinery composed of over 15 proteins that spans the inner membrane, the periplasm
221 and the outer membrane. In search for the molecular mechanism responsible for the decrease in
222 piliation that we observed upon bacterial treatment with the compounds, we tested whether pilus
223 retraction was required to induce bacterial disaggregation upon compound treatment. We
224 evaluated the effects of the three compounds on the *pilT* mutant which is unable to retract its pili

225 and found that preformed *pilT* aggregates were not dissociated upon treatment with the
226 compounds A, B or C and only the formation of new aggregates during the incubation period was
227 inhibited (Fig. 5A, to be compared with Fig. 3E) showing that Tfp retraction is necessary to allow
228 the compounds to carry out their inhibitory effect.

229 Because these results pointed to an effect of the compounds on Tfp assembly, we turned our
230 attention to the PilF ATPase which generates the energy for the incorporation of pilin monomers
231 in the fibres. Molecular docking of compound B onto the crystal structure of a meningococcal PilF
232 homolog (PDB: 5TSG) indicated eight, sometimes overlapping, potential binding sites with binding
233 energy lower than -7.0 kcal/mol (SI Appendix Fig. S2A). Focusing on four of these sites, five point
234 mutations potentially altering compound B interaction were introduced in the bacteria (SI Appendix
235 Fig. S2B) and the generated strains tested for aggregation to quantify the functionality of their pili
236 (SI Appendix Fig. S2C). Two mutations led to an absence of aggregation likely reflecting a
237 perturbation of PilF enzymatic activity and the absence of pili at the surface of these mutant strains
238 (K371E and D207R; SI Appendix Fig. S2C). Interestingly, R457D and K371A mutations led to
239 normal basal aggregation but to an increase in resistance and sensitivity to compound B,
240 respectively (SI Appendix Fig. S2D). Changes of sensitivity of bacteria to compound B due to
241 single point mutations in PilF support the idea that this enzyme is the target of compound B.

242 We thus set out to characterize PilF recombinant proteins *in vitro* to evaluate the effect of the
243 compounds on its activity. The full-length *N. meningitidis* PilF recombinant protein was unstable
244 in solution and prone to precipitation at high concentration during purification steps. To circumvent
245 this problem, we produced a truncated form of PilF by deleting the first 165 amino acids
246 encompassing the first N-terminal domain (N1D) and a flexible inter-domain linker (Fig. 5B).
247 Indeed, the N1D-truncated PilF encompassing the second N-terminal domain to the C-terminal
248 end (N2D-CTD), referred to as PilF₁₆₆, remained stable during all purification steps and formed a
249 254 kDa hexamer as indicated by SEC-MALS (size exclusion chromatography coupled to multi-
250 angle light scattering) and AUC (analytical ultra-centrifugation) (Fig. 5C). Most importantly, the

251 purified enzyme was highly active in an ATPase activity assay ($K_m = 0.45 \pm 0.05$ mM ; $V_{max} =$
252 $25,074 \pm 2,482$ pmol/min/mg, Fig. 5D).

253 We next investigated whether the ATPase activity of PilF could be inhibited by compounds A-C.
254 At a ratio of 1: 200, the three compounds showed clear inhibitory effects on PilF₁₆₆, bringing its
255 activity down to $44.2 \pm 4.2\%$, $64.8 \pm 3.1\%$, and $29.7 \pm 3.6\%$, respectively (Fig. 5E). A dose
256 response curve indicated that compound B, which showed the most potent inhibitory effect on
257 meningococcal aggregation, has a relative IC₅₀ of 175.10 ± 13.08 μ M on PilF₁₆₆ (protein
258 concentration 1 μ M, Fig. 5F). This value is dependent on the conditions used in the solution-based
259 enzymatic assay and cannot not be easily compared with the IC₅₀ obtained for whole bacteria.

260 To test whether the same compounds have any effect on the type IV pilus disassembly ATPase
261 PilT, we purified the full-length enzyme and characterized its activity. PilT also readily forms a
262 stable hexamer in solution and exhibited a high ATPase activity (K_m of 0.10 ± 0.02 mM and a V_{max}
263 of $14,232 \pm 664$ pmol/min/mg). Consistently with the results from the aggregation assay, none of
264 the compounds showed any effect on PilT activity (Fig. 5G). The striking inhibitory effects of
265 compounds A, B and C on PilF but not PilT indicate that they target the Tfp assembly but not
266 disassembly process (SI Appendix Fig. S3).

267 **Discussion**

268 In this study, we used a high-throughput microscopy-based screening approach to identify novel
269 compounds preventing the formation of microcolonies on the surface of endothelial cells. We
270 choose this phenotypic approach because it has the potential to reveal active compounds while
271 remaining agnostic on the potential targets involved in bacterial adhesion. Converging with
272 previous studies identifying the role of meningococcal Tfp in the interaction with endothelial cells
273 (11, 13), we discovered compounds that inhibit type IV pili assembly. Because of the importance
274 of this virulence factor *in vivo* (13), these compounds represent attractive candidates for adjuvant
275 therapy in combination with existing antibiotics. Compounds targeting the biogenesis pathways
276 and/or actively blocking the function of large surface machineries involved in the virulence of
277 various bacterial human pathogens have been recently described (10, 18, 19). Various secretion
278 systems have been targeted as well as pilus structures. Certain compounds inhibit the biogenesis
279 of curli pili expressed by *E. coli*, thus reducing biofilm formation (20). Type I pilus biogenesis
280 inhibitors, termed pilicides, have been described to block enteropathogenic or uropathogenic *E.*
281 *coli* adhesion to host cells and biofilm formation (10). Interestingly, while an *in-silico* study has
282 considered the possibility to inhibit PilF to target type IV pili, no experimental follow up was
283 provided (21). Our study thus describes, for the first time, compounds that directly target type IV
284 pilus biogenesis. At the molecular level, these compounds have a high specificity for the PilF
285 ATPase that powers type IV pilus assembly as they do not affect the activity of the closely related
286 PilT ATPase. This is striking as PilF and PilT are structural homologs of the same AAA+ ATPase
287 family sharing a sequence identity of 30% and they likely act at the same site in the piliation
288 machinery. While compounds A and C are described to target human ATPases (a cyclin
289 dependent kinase and an Akt kinase, respectively), a potential cause of undesirable effects, the
290 structure of compound B, which is the most active, does not match to any known compounds
291 described as a human kinase inhibitor. Accordingly, at efficient concentrations this compound

292 shows little toxicity on host cells in culture or on the bacteria themselves. Although further studies
293 will need to be undertaken to demonstrate the absence of effects of compound B on cellular
294 proteins, limited side effects are expected. Furthermore, the structure activity relationship
295 performed in this study opens the way to the drug design of novel compounds optimized for *in*
296 *vivo* administration in terms of solubility and metabolic stability. Certain parts of the compound, in
297 particular the naphthalene group, can be modified without affecting its efficiency and this can be
298 used to make the molecule more soluble and stable. In a more general sense, the identification of
299 PilF as a drugable target also opens new perspectives to the identification of inhibitors affecting
300 not only bacterial adhesion but also pilus-associated virulence functions. Contrary to *in vitro* or *in*
301 *silico* identification of PilF enzymatic activity inhibitors, this study delivered compounds that are
302 already efficient on whole bacteria.

303
304 Beyond the identification of compounds of medical interest this study provides potent tools to
305 further investigate the basic functions of the type IV pilus machinery. Recent cryo-electron
306 microscopy images of Tfp machineries in *Myxococcus xanthus* revealed that the ATPases are
307 located at the base of the machinery on the cytoplasmic side of the inner membrane (22) and
308 further refined the molecular basis for cycles of pilus assembly and disassembly (SI Appendix Fig.
309 S3). PilF and PilT ATPases are thought to alternate at this site, determining the switch between
310 pilus assembly and disassembly. However, potential cues leading to this switch are unknown.
311 Results from our study indicate that the inhibition of PilF activity does not prevent PilT from exerting
312 its activity. Inactive PilF can thus detach from the machinery and be replaced by active PilT. A
313 particular characteristic of the compounds described here is that their effects on piliation rely on
314 the PilT-mediated disassembly of previously formed Tfp. By inhibiting pilus assembly, the
315 inhibitors trigger an unbalanced situation where the retraction of the existing pili leads to their
316 disappearance from the bacterial surface. In absence of PilT the inhibitors of PilF block the further
317 growth of pili but they do not retract, the situation is blocked at a standstill with steady state

318 amounts of pili. Those compounds will thus be efficient molecular tools to decipher the multiple
319 steps involved in the assembly and disassembly of type IV pili.

320
321 Tfp are multifunctional organelles that constitute a particularly appealing therapeutic target. Type
322 IV pili not only allow adhesion to human host cells but also support bacterial auto-aggregation,
323 twitching motility and natural transformation (23). Since the compounds decrease the amount of
324 Tfp, all the associated functions are likely to be affected. Accordingly, in this study we show that
325 bacterial auto-aggregation is affected in addition to adhesion. Further studies will be necessary to
326 test the effect on DNA transformation and twitching motility, two processes also linked to virulence
327 through genetic variation and dissemination on surfaces, respectively. Targeting the surface
328 expression of these organelles is thus a way to affect several virulence-associated properties with
329 the same compound. In addition, beyond *Neisseria meningitidis*, many bacterial species including
330 human pathogens express Tfp (24). The fact that *Neisseria gonorrhoeae* is also sensitive to
331 compound B suggests that such inhibitors could have a broad application. Considering the high
332 degree of conservation among the PilF orthologs, derivatives of those compounds could very well
333 affect additional piliation machineries with an even larger spectrum of effects, as other bacterial
334 systems have similar structures and function in a similar way (24). This is the case of type II
335 secretion systems which are also involved in pathogenesis via secretion of toxins for instance
336 (25). The results reported here have a broad range of applications by opening a way to affect
337 different virulence properties of a large number of pathogens.

338 This study thus provides, for the first time, compounds active in a *Neisseria meningitidis* adhesion
339 model, through the inhibition of pilus biogenesis. In addition, by identifying the PilF ATPase as a
340 new therapeutic drugable target, these results provide a framework that can be applied to further
341 optimize the obtained compounds and discover new ones. Pharmacokinetic and
342 pharmacodynamic studies will be required in particular to validate the efficiency of these

343 compounds *in vivo* and evaluate the therapeutic window of such pili inhibitors in the course of
344 human pathogenesis.

345 **Materials and Methods**

346 **Bacterial strains and growth conditions.** *N. meningitidis* 8013 clone 12 used in this
347 study is a serogroup C clinical isolate, expressing a class I SB pilin, Opa2, Opc2,
348 PilC1⁺/PilC2⁺ (26). *N. meningitidis* was grown over-night on GCB agar plates (Difco,
349 France) containing Kellogg's supplements (27) and antibiotics when required. For details,
350 see SI Materials and Methods.

351 **Cell culture.** Human umbilical vein endothelial cells (HUVECs; PromoCell) were used
352 between passages 1 and 8 and grown in endothelial serum-free medium (Endo-SFM;
353 Gibco) supplemented with 10% heat-inactivated fetal bovine serum (PAA Laboratories
354 GmbH) and 40 µg/ml of endothelial cell growth supplement (Sigma-Aldrich). For details,
355 see SI Materials and Methods.

356 **Screening method.** The SPAI (Signaling Pathways Activators and Inhibitors) library used
357 here is a Sanofi designed collection of 2,239 small compounds having a known target or
358 mechanism of action. HUVEC cells were seeded at a density of 5,000 cells per well in a
359 collagen-coated black 384-well plate with flat transparent bottom and infected at an MOI
360 of 100 bacteria per cell. 384-well plates were then imaged using an Arrayscan automated
361 microscope to visualize bacteria and cell nuclei. For details, see SI Materials and Methods.

362

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369

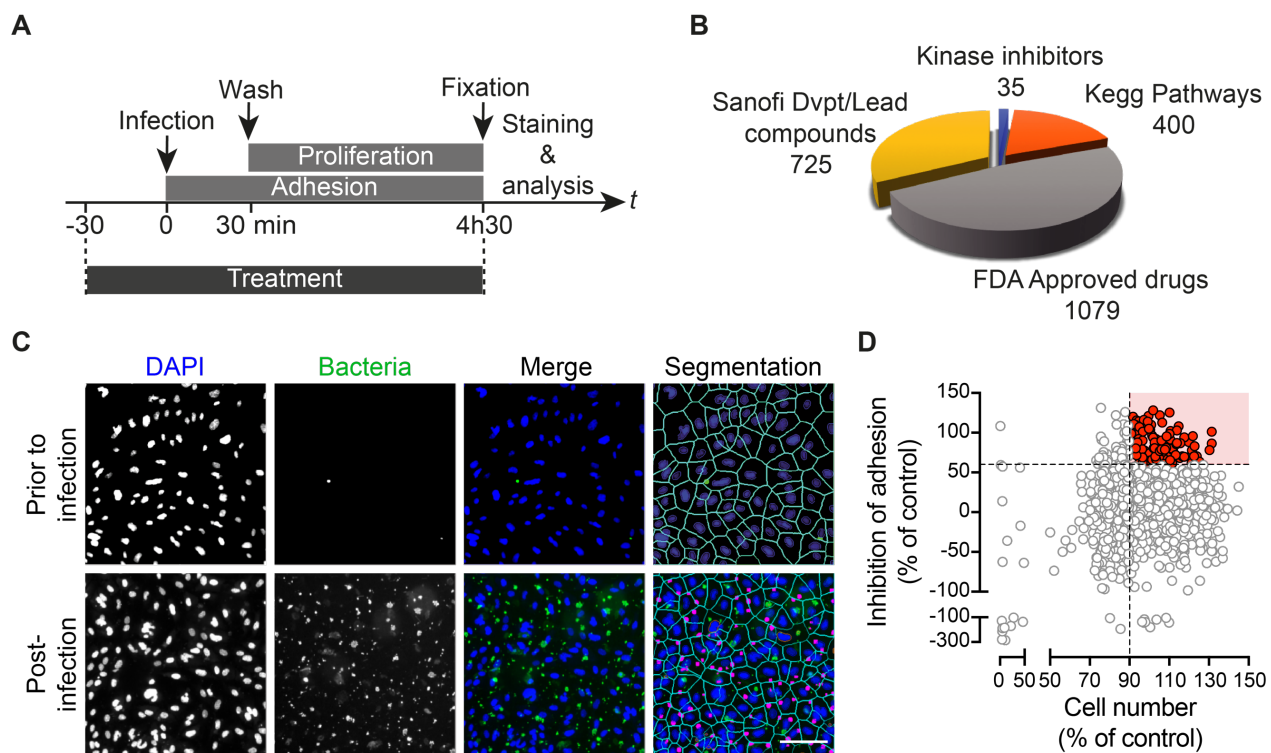
370 **Conflict of interests**

371 The authors declare no conflict of interests.

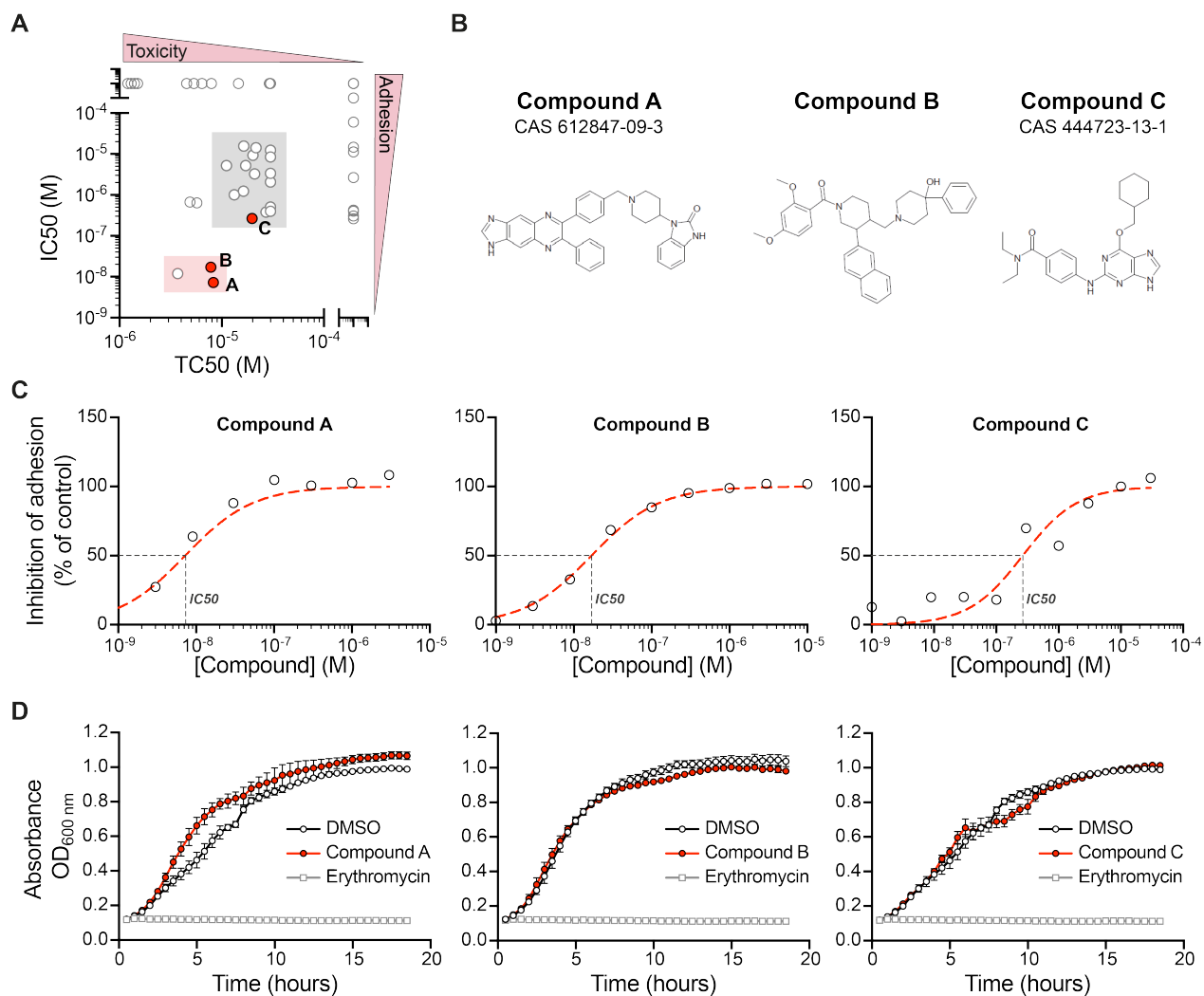
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439



440
 441 **Fig. 1: A high-throughput screening to discover new compounds inhibiting *N. meningitidis***
 442 **adhesion to human endothelial cells. (A)** Timeline of the infection and treatment protocol used
 443 in the screen. **(B)** Description of the library used in the screen. **(C)** Image analysis readout of the
 444 screen. Scale bar, 100 μ m. **(D)** XY plot showing the 163 compounds considered for further
 445 analysis (red dots) among the total of the 2,239 tested compounds. The horizontal and vertical
 446 dashed lines represent the thresholds used to select the hit compounds (inhibition of bacterial
 447 adhesion $\geq 60\%$ and cellular toxicity $\leq 10\%$, respectively). Data are representative of N=2
 448 independent experiments.
 449



450

451 **Fig. 2: Identification of hit compounds affecting bacterial adhesion but not bacterial**

452 **viability. (A)** XY plot showing the IC₅₀ of adhesion to HUVEC cells and TC₅₀ values of each of

453 the 59 tested compounds on HepG2 cells. Red dots highlight the 3 compounds chosen for further

454 characterization and referred to as A, B and C, hereafter. **(B)** Chemical structure of the selected

455 hits with their identification number. **(C)** Dose response curves of the efficiency of the 3 hit

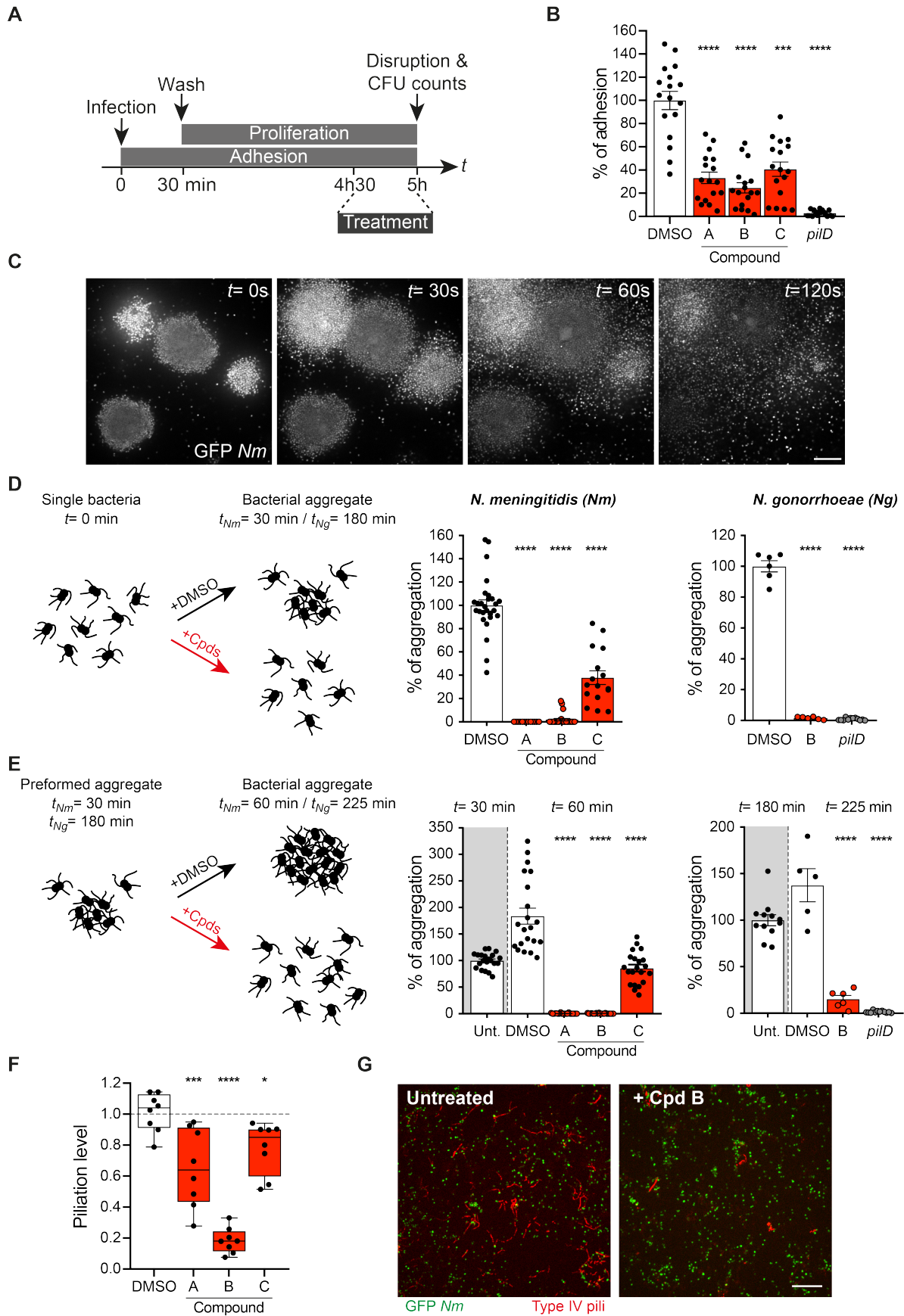
456 compounds in inhibiting bacterial adhesion. The red dashed lines show the non-linear fit used to

457 determine the IC₅₀. **(D)** Growth curves of *N. meningitidis* in the presence of either DMSO as

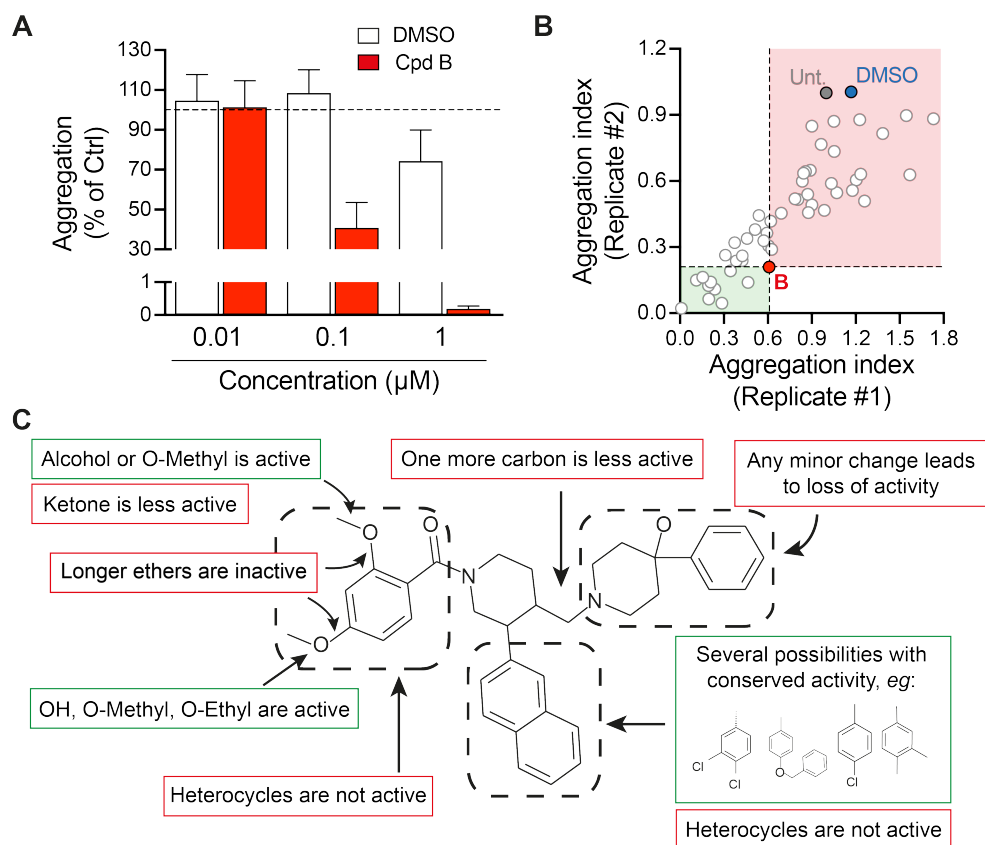
458 vehicle control, 1 μ M of the indicated hit compound or 3 μ g/ml of Erythromycin as negative growth

459 control. Data represent the mean \pm SEM of N=3 independent experiments, each performed in

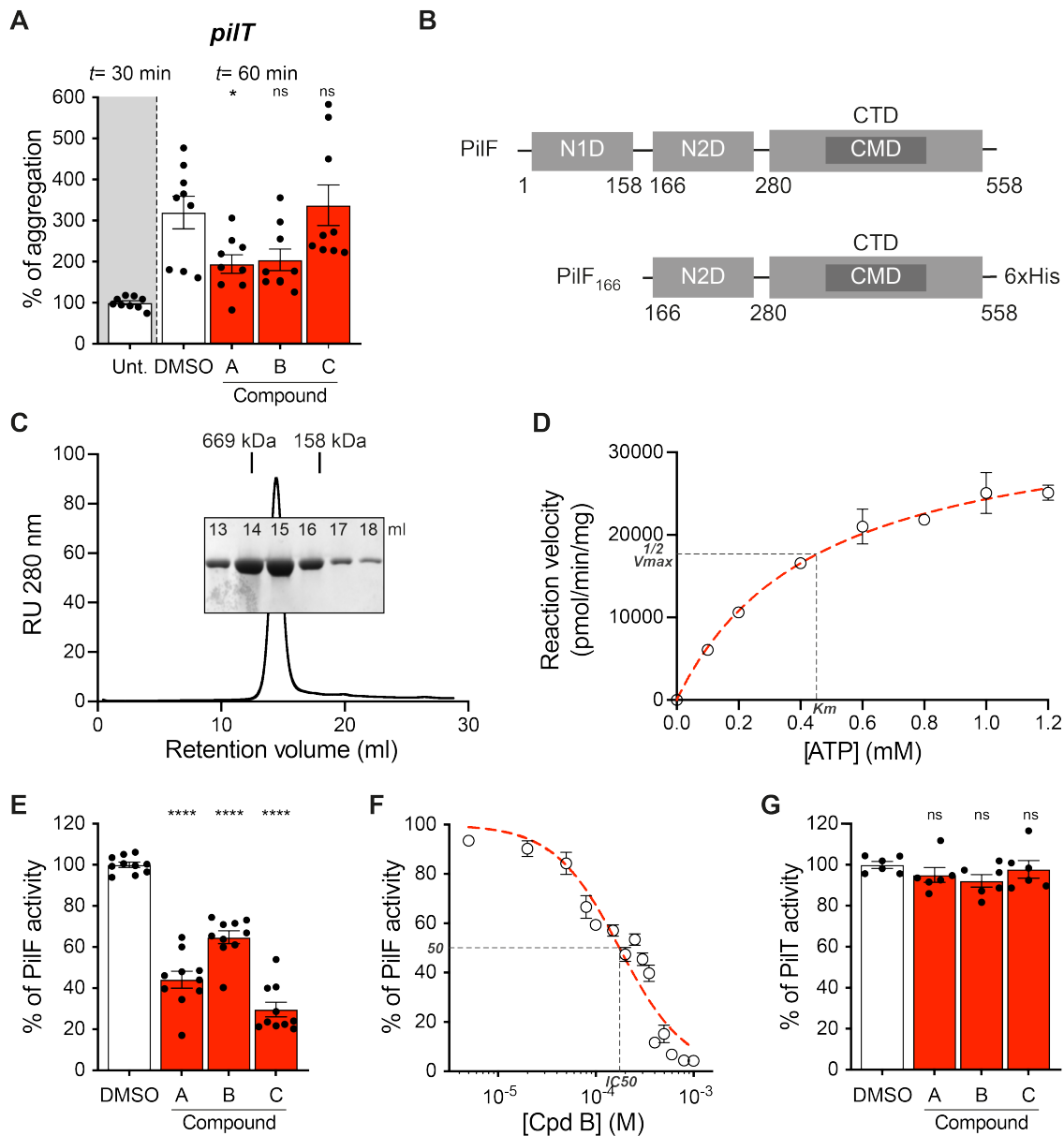
460 duplicate.



462 **Fig. 3: Compounds efficiently inhibit bacterial aggregation by decreasing their level of**
463 **piliation. (A)** Timeline of the infection and treatment protocol used to test the ability of the 3
464 compounds to detach previously adhering bacteria. **(B)** Quantification of the ability of the
465 compounds to detach adhering bacterial microcolonies as measured by colony forming units
466 (CFU) counts. DMSO, in which compounds are dissolved, is used as a control. The non-piliated
467 and thus non-adhesive *pilD* mutant is used as a negative control. Data were normalized with
468 respect to the mean value of the control condition per replicate. Data represent the mean \pm SEM
469 of N=6 independent experiments, each performed in triplicate. **(C)** Pre-formed aggregates of GFP-
470 expressing *N. meningitidis* were treated with 1 μ M of compound B while being observed by time-
471 lapse video fluorescence microscopy. Scale bar, 20 μ m. **(D-E)** Description and quantification of
472 the impact of treatment (1 μ M) on the ability **(D)** of the bacteria to form aggregates or **(E)** to induce
473 the disaggregation of preformed aggregates in both *N. meningitidis* (left) and *N. gonorrhoeae*
474 (right). Data represent the mean \pm SEM of N=6 and N=3 independent experiments for *N.*
475 *meningitidis* and *N. gonorrhoeae*, respectively, each performed in triplicate. **(F)** Effect of the hit
476 compounds on the surface expression of bacterial Tfp. Each dot represents an independent
477 experiment performed in triplicate. Data represent quartiles in box and whiskers format. **(G)**
478 Visualization by fluorescent microscopy of bacterial Tfp surface expression. GFP-expressing
479 bacteria appear as green dots while pili labelled with a monoclonal antibody appear as red
480 filaments. Scale bar, 20 μ m. Treatment with compound B (1 μ M) is compared to an untreated
481 sample. A one-way ANOVA test comparing with the DMSO condition was used to determine
482 statistical significance. * $P \leq 0.05$; ** $P \leq 0.01$; *** $P \leq 0.001$; **** $P \leq 0.0001$.
483



484
 485 **Fig. 4: Structure activity relationship of compound B.** (A) Quantification of the impact of
 486 indicated concentration of compound B on the ability of the bacteria to form aggregates. Data
 487 represent the mean \pm SEM of N=2 independent experiments, each performed in triplicate. (B)
 488 Quantification of the impact of the 49 derivatives of compound B on the ability of bacteria to form
 489 aggregates. Data were normalized with respect to the untreated condition in each replicate. The
 490 aggregation indexes of compound B in each of the two replicates were used as thresholds to
 491 determine derivative compounds with a better (light green) or a worst (light red) activity than
 492 compound B (red dot). (C) Molecular activity map of compound B.
 493



494

495 **Fig. 5: Compounds specifically target the Tfp assembly PilF ATPase. (A)** Effect of the hit

496 compounds on the disaggregation of pre-assembled bacterial aggregates formed by the *pilT*

497 mutant. Data represent the mean \pm SEM of N=3 independent experiments, each performed in

498 triplicate. Data were normalized with respect to the mean value of the untreated condition

499 (t=30min) per replicate. **(B)** Schematic illustration of *N. meningitidis* full-length and truncated PilF.

500 N1D, N-terminal domain 1; N2D, N-terminal domain 2; CTD, C-terminal domain; CMD,

501 coordinated metal domain. **(C)** Size exclusion profile of *N. meningitidis* PilF₁₆₆ on a Superose 6

502 column. SDS-PAGE followed by Coomassie staining shows the peak fraction of PilF₁₆₆ hexamer.
503 Elution volumes of aldolase (158 kDa) and thyroglobulin (669 kDa) are indicated. **(D)** Reaction
504 velocity of PilF in function of the ATP concentration in an ATPase activity assay. The Michaelis
505 constant K_m is determined as the concentration value corresponding to half of the maximum
506 velocity (V_{max}). **(E)** Effect of the hit compounds on the activity of PilF₁₆₆. 1 μ M of PilF₁₆₆ protein
507 was incubated with 200 μ M of indicated compound. Data represent mean \pm SEM of N=5
508 independent experiments, each performed in duplicate. Results were normalized with respect to
509 the mean value of the DMSO control condition per replicate. **(F)** Dose response curve of
510 compound B on the activity of PilF₁₆₆. 1 μ M of PilF₁₆₆ protein was incubated with various amounts
511 of compound B and ATPase activity was measured. Results are indicated as the percentage of
512 the untreated sample. **(G)** Effect of the hit compounds on the activity of the PilT ATPase. 1 μ M of
513 PilT protein was incubated with 200 μ M of indicated compound. Data represent mean \pm SEM of
514 N=3 independent experiments, each performed in duplicate. Results were normalized with
515 respect to the mean value of the DMSO control condition per replicate. A one-way ANOVA test
516 comparing with the DMSO condition was used to determine statistical significance. ns, non-
517 significant; * $P \leq 0.05$; **** $P \leq 0.0001$.

Supplementary Materials and Methods

Bacterial strains and growth conditions. *N. meningitidis* 8013 clone 12 used in this study is a serogroup C clinical isolate, expressing a class I SB pilin, Opa2, Opc2, PilC1⁺/PilC2⁺ (1). *N. meningitidis* was grown over-night on GCB agar plates (Difco, France) containing Kellogg's supplements (2) and antibiotics when required: 2 µg/ml erythromycin (*pilF*_{ind}), 50 µg/ml spectinomycin (Δ *pilF*) or chloramphenicol 5 µg/ml (GFP-expressing strains). For liquid cultures, bacteria were adjusted to an OD_{600nm} of 0.05 in GCB broth with Kellogg's supplement (3). *N. gonorrhoeae* MS11 was grown over-night on Chocolat + PolyVitex agar plates (bioMérieux) containing antibiotics when required: 2 µg/ml erythromycin (GFP-expressing strains) or 100 µg/ml kanamycin (Δ *pilD*). For liquid cultures, bacteria were adjusted to an OD_{600nm} of 0.1 in GCB broth with Kellogg's supplement (4). All cultures were incubated at 37°C under moist atmosphere containing 5% CO₂ (3, 4). *Escherichia coli* XL1-Blue, used to generate the *pilF* mutant strains of *N. meningitidis*, was grown at 37°C on liquid or solid Luria-Bertani medium (Difco) containing 50 µg/ml kanamycin.

Cell culture. Human umbilical vein endothelial cells (HUVECs; PromoCell) were used between passages 1 and 8 and grown in endothelial serum-free medium (Endo-SFM; Gibco) supplemented with 10% heat-inactivated fetal bovine serum (PAA Laboratories GmbH) and 40 µg/ml of endothelial cell growth supplement (Sigma-Aldrich) or in EBM-2 endothelium basal medium (Lonza) supplemented with EGM-2 endothelium medium kit (Lonza) and 10% decomplexed fetal calf serum.

Screening method. *Screening library.* The SPAI (Signaling Pathways Activators and Inhibitors) library is a Sanofi designed collection of 2,239 small compounds having a known target or mechanism of action and therefore serves as a pharmacological toolbox to probe phenotypes in disease relevant cellular models. This library includes: 1,079 small molecules that are FDA approved drugs (including 207 human targets and main classes of antibiotics), 400 compounds are known reference inhibitors of cellular and metabolic pathways, 725 compounds are Sanofi lead molecules discovered in previous screening projects, which are potent modulators of cellular pathways and 35 compounds are known kinase inhibitors. The detailed composition of this library is proprietary to Sanofi and screening hit structures and properties have been disclosed to the team after a clearance check-up where no conflict of interest has been identified with other internal projects.

Adhesion assay screening. *Neisseria meningitidis* were seeded a day before the screening on tryptic soy agar gelose from a stock conserved at -80°. On the screening day, a colony was picked for

dilution in 12 ml of culture medium and adjusted to an optical density at 600 nm (OD_{600nm}) of 0.16 for subsequent growth under agitation for 3 hours. The CFUs were evaluated by optical density and comparison to a reference growth curve and diluted in order to provide a MOI of 100 bacteria per cell, hence 500,000 CFUs per 5 μ l solution to be added to each well.

HUVEC cells were seeded at a density of 5,000 cells per well in a collagen-coated black 384-well plate with flat transparent bottom and incubated for 24 hours. Culture medium was replaced with culture medium supplemented with 20 μ g/ml Hoechst 33432, test compounds prepared in DMSO were added with a Bravo 384 wells Agilent dispenser (0.5 μ l per well for a final concentration of 10 μ M compound and 1% DMSO) and cells were incubated for 30 minutes. After 2 washes with a Tecan Hydrospeed washer, fresh culture medium containing the same compound concentrations was added at the lowest speed using a multidrop dispenser.

Bacteria in exponential phase from the 3-hour liquid culture were added in a 5 μ l volume using a multidrop dispenser. Columns 1 and 2 were not seeded with bacteria to serve as a reference for image analysis to evaluate a 100% adhesion inhibition. Columns 3 and 4 were not treated with compounds to serve as a reference for a 0% adhesion inhibition. After a 30-minutes incubation with bacteria, the supernatant was aspirated and replaced with fresh medium containing the same compound concentrations and plates incubated for an additional 4 hours. Culture medium was then aspirated and cells were fixed with formalin for 30 minutes at room temperature. After two washes with PBS, bacteria were stained using a Group C *Neisseria meningitidis* antiserum produced in rabbit (BD Bioscience) and an AlexaFluor488-conjugated goat anti-rabbit secondary antibody (Life Technologies) and host cells were detected with a DNA labelling dye (Hoechst 33342). Plates were then conserved at 4°C until ready to proceed to image acquisition.

Image acquisition and analysis. 384-well plates were imaged using an Arrayscan automated microscope equipped with a BGFR_386_23 filter (Hoechst 33342) and a BGFR_485_20 (AlexaFluor488) (Thermofischer). A minimum of 5 fields of view and 500 nuclei per well were quantified. For each condition, image analysis and segmentation allowed the determination of the mean number of spots (bacteria) per object (cells) (Spot Detector V3 Bioapplication, Thermofischer). The percentage of bacterial adhesion inhibition for each tested compound was then calculated with respect to columns 1-2 and 3-4 representing negative (no bacterium, 0% adhesion) and positive controls (no treatment, 100% adhesion), respectively.

Hit compound selection. The strategy of hit compound selection relied on both the ability of the tested compounds to efficiently inhibit bacterial adhesion but also to display a low cellular toxicity. Therefore, compounds inducing a decrease in the cell number superior at 90% of the control wells were discarded. Finally, were selected as hits, compounds leading to a percentage of adhesion

inhibition superior or equal to 60%.

Dose response assay. A dose response approach with compound concentrations ranging from 1 nM to 30 μ M was used to determine both the half maximal inhibitory concentration (IC₅₀) and the median toxic concentration (TC₅₀) of each selected compound. Briefly, for IC₅₀ calculation, 30 min post-infection of endothelial cells, compounds at the indicated concentrations were added to individual wells for 4 hours and the inhibition of bacterial adhesion was monitored as previously described. The cellular toxicity (TC₅₀) was evaluated on THP1 and HepG2 cells by monitoring their growth inhibition upon 40 hours' exposure to the indicated compound concentrations. Cell viability was assessed based on the quantitation of the ATP present in the culture using the CellTiter-Glo Luminescent Cell Viability Assay (Promega) according to manufacturer instructions.

***Neisseria meningitidis* growth curves.** Bacterial overnight cultures were diluted in Endo-SFM containing 10% fetal bovine serum to an OD_{600nm} of 0.05 and allowed to proliferate until an OD_{600nm} of 0.2. This pre-culture was then diluted to an OD_{600nm} of 0.05 and 150 μ l of the bacterial suspension was transferred into wells of a 96-well plate. Bacteria were then treated with either 1 μ M of the indicated compound, 3 μ g/ml of Erythromycin or DMSO as negative and positive growth controls, respectively, each performed in duplicate. Plates were then placed in a Cytation 5 multimode reader (Biotek) at 37°C with 5% CO₂ and continuous agitation and optical densities at 600 nm were recorded every 30 minutes for 18 hours.

Bacterial detachment assay. 10⁵ HUVECs were plated into wells of 24-well plates and incubated over-night. Monolayers were then infected with 10⁷ bacteria (MOI of 100). After 30 min, unbound bacteria were removed by three washes, and the infection was continued for 4 h. Compounds were then added at a final concentration of 1 μ M and incubated for additional 30 minutes. Finally, after 3 washes, adherent bacteria were recovered by trypsin treatment of the infected cells and bacteria counted by plating appropriate dilutions on GCB agar plates. Results were normalized according to the effective concentration of the bacterial inoculum, which was also determined by CFU counts.

Immunofluorescence on immobilized bacteria. A GFP-expressing bacterial suspension at OD_{600nm} of 0.1 in PBS was placed in a glass-bottom 96-well plate (Greiner), centrifuged for 10 min at 4,000 g. Medium was removed, the remaining film was dried for 10 minutes at 37°C and bacteria were fixed in PBS containing 4% paraformaldehyde for 15 min. After 3 washes, samples were blocked with PBS containing 0.2% gelatine (PBSG) for 20 min. Pili were detected using the 20D9 mouse monoclonal antibody diluted at 2.5 μ g/ml in PBSG followed by a AlexaFluor568-conjugated goat anti-mouse secondary antibody (Life technologies). Mowiol was then added to the wells prior to imaging.

Bacterial aggregation assay. *Neisseria meningitidis*: Bacteria grown over-night on GCB agar

plates were adjusted to an OD_{600nm} of 0.05 and incubated for 2 h at 37°C in RPMI medium supplemented with 10% FBS. The bacterial pre-culture was concentrated to an OD_{600nm} of 0.3 by a centrifugation at 15,000 g for 1 min followed by resuspension in medium containing DAPI (0.1 ng/ml) when required. Bacterial suspensions were briefly vortexed, transferred into wells of a 96-well μ -plate with square wells (Ibidi) and allowed to form aggregates for a period of 30 minutes either in the presence of or prior to the addition of the indicated compound at the indicated concentrations.

N. gonorrhoeae: GFP-expressing bacteria grown over-night on Chocolat + PolyVitek agar plates were adjusted to an OD_{600nm} of 0.1 in GCB broth with Kellogg's supplement, briefly vortexed and 100 μ l were transferred into wells of a 96-well μ -plate with square wells (Ibidi). Bacterial suspension was allowed to form aggregates for a period of 180 minutes, as previously described (5), either in the presence of or prior to the addition of compound B at a final concentration of 1 μ M or DMSO as control for 45 min.

Aggregation analysis: Aggregates/bacteria were then observed under the microscope and four fluorescence images per well were captured using a 4x objective. Size of aggregates and numbers of bacteria involved in aggregates relative to the total amount of bacteria were determined with a homemade script in the ImageJ software (6). Briefly, all the images were initially processed by converting to an 8-bit format. Background was subtracted, and the auto-threshold plug-in was used. Finally, aggregates were identified by particles analysis, their volume calculated and the number of bacteria involved determined allowing the calculation of the percentage of bacteria participating in aggregates relative to the total number of bacteria introduced in the well (7). Data shown were normalized with respect to the mean value of the control condition per replicate.

Statistics. All graphs and statistical analysis were performed with GraphPad Prism 7 (GraphPad Software). No statistical method was used to predetermine sample size. Kolmogorov–Smirnov test was used to assess normality of all data sets. Boxes in box plots extend from the 25th to 75th percentile, with a line at the median and whiskers extend from the 10th to the 90th percentile. Bar graphs show the mean \pm SEM.

Type IV pili quantification by ELISA. Bacteria were resuspended from fresh GCB plates in PBS at OD_{600nm} of 0.1. Serial two-fold dilutions were performed and dispensed within the wells of 96-well plates (Nunc). The plates were centrifuged for 10 min at 3,220 g, and the supernatant was carefully removed. Then, plates were incubated without cover at 37°C for 10 min to allow drying. Bacteria were fixed with a solution of PBS containing 4% paraformaldehyde for 15 min. Coated plates were washed 3 times with PBS and incubated in blocking solution (1X PBS, 1% BSA, 0.1% Tween-20) for 10 min. The 20D9 anti-PilE mouse monoclonal antibody, diluted at a concentration

of 0.25 µg/ml in blocking solution, was added to the plates and incubated for 1 h. After several washes, a peroxidase-conjugated anti-mouse IgG antibody, diluted at 1/10,000 in blocking solution, was added to the wells for 1 h. Finally, after three washes, the staining was revealed using TMB (tetramethylbenzidine) substrate and stop solution following the manufacturer's instructions (BD Bioscience). The absorbance was read at 450 nm using a microtiter plate reader (Flex station 3, Molecular Devices).

Autodocking. Docking was performed using AutoDock Vina (8) and AutoDock Tools 4.2 (9). A homology model of *Neisseria meningitidis* PilF was generated based on the crystal structure of *Geobacter metallireducens* PilB (PDB: 5TSG) using the HHpred server (10). The search was carried out using default parameters in a grid volume encompassing the entire PilF hexamer. The torsional degree of freedom for compound B (the ligand) is set manually based on its chemical properties. The flexibility of PilF (the receptor) is omitted.

Generation of *pilF* point mutations in *N. meningitidis*. Point mutations in the *pilF* gene of *N. meningitidis* were generated using a single-primer one-step mutagenesis process (11). Briefly, a mutagenic primer (listed in the table below where mutated nucleotides are shown in lower case and the corresponding codon in bold red) was used to amplify the pCR2.1*ΩpilF* plasmid (coding for the wild-type sequence of PilF) (7) by PCR using Phusion polymerase. The PCR product was digested using FastDigest DpnI at 37°C for 2 hours and then inactivated at 80°C for 5 minutes to degrade the pCR2.1*ΩpilF_{WT}* plasmid. The resulting product was transformed in XL1-Blue *E. coli*, which were then selected on kanamycin-containing LB plates. Plasmids from single colonies were isolated, sequenced and the mutated fragments were subcloned into the pGCC4 vector under the control of the Lac promoter (*pilF_{ind}*) (12) using PacI and PmeI restriction enzymes. The plasmids were used to transform GFP-expressing *N. meningitidis* (3) and transformants were selected on erythromycin plates. The wild type *pilF* gene was then inactivated as described (7).

Primer	Sequence
PilF-D207R	CGTTTCCGTGTGcgCGGGCAGCTCCGCGAG
PilF-K371E	TTTGCCGCTGCTTTGgAGTCTTTTCTGCGT
PilF-K371A	TTTGCCGCTGCTTTGgcGTCTTTTCTGCGT
PilF-E390K	GAGATTTCGTGATTTGaaAACTGCCGATATT
PilF-R457D	AAACAGGAAGTGGAAGAgaCCCGTCTGCCTCT

PilF and PilT purification. *Cloning.* Genomic DNA were extracted from the *N. meningitidis* 8013 strain using a commercial DNA extraction kit (Invitrogen). Various constructs containing different domain organizations of PilF and PilT conjugated to a 6xHis tag were cloned into the pET11a vector. Plasmids with the correct sequences were amplified in *E. Coli* DH5α cells and transformed into *E. Coli* BL21(DE3) competent cells for recombinant protein expression. Small scale

expression tests were performed to determine the best expression temperature, time and induction conditions prior to large scale protein production.

Production. A truncated form of *N. meningitidis* PilF containing the second N-terminal domain and the C-terminal domain (N2D-CTD, residues 166-568), PilF₁₆₆, was used in all *in vitro* assays in this study. PilF₁₆₆-expressing bacteria were inoculated and grown in 1 L of lysogenic broth (LB) Miller containing Ampicilin at 37°C under 180 rpm agitation. The PilF₁₆₆ culture was induced with 0.2 mM IPTG at an OD_{600nm} of 0.6. The cells were then cultured at 18°C under 180 rpm agitation for 18-20 hours. The same protocol was used to induce and express the full-length *N. meningitidis* PilT. Both PilF₁₆₆ and PilT cells were harvested by centrifugation at 4,700 rpm at 4°C for 45 min, washed briefly with PBS and pelleted again at 6,500 rpm, 4°C before being flash frozen with liquid nitrogen and stored at -80°C.

Purification. The deep-frozen pellets were thawed on ice for 30 min under 100 rpm agitation with added lysis buffer (20 mM Hepes pH 8.0, 500 mM NaCl, 10 mM MgCl₂, 5% glycerol, 1 mg/ml lysozyme and 5 units of benzonase). The resuspended cells were sonicated for 10 s with 30 s intervals and 30% amplitude for 15 rounds. The cell lysis was then centrifuged at 11,000 rpm for 1 hour. The supernatant was then loaded onto a 5 ml HP HisTrapTM IMAC column (GE Healthcare Life Sciences). A gradient wash procedure using 50 ml of wash buffer (20 mM Hepes pH 8.0, 500 mM NaCl, 10 mM MgCl₂, 5% glycerol, 0-10 mM imidazole) was performed. The His-tagged proteins were then eluted using elution buffer (20 mM Hepes pH 8.0, 500 mM NaCl, 10 mM MgCl₂, 5% glycerol, 350 mM imidazole). The eluted protein solution was concentrated to 1 mL using an Amicon Ultra-15 centrifugal filter (30 kDa cut-off) at 3,500 rpm, 4°C. The concentrated protein was injected into a Superose 6 10/30 column (GE Healthcare Life Sciences) for size exclusion chromatography (SEC). SEC was performed at 4°C in SEC buffer (20 mM Hepes pH 8.0, 150 mM NaCl, 10 mM MgCl₂). A SDS-page gel analysis was then performed to determine the protein purity of each peak fraction. Fractions containing PilF₁₆₆ or PilT (purity > 98%) were combined and concentrated to around 3 mg/ml. A fraction of the freshly purified proteins was used to perform SEC-MALS and AUC experiments while the remaining amount flash frozen with liquid nitrogen and stored at -80°C.

ATPase activity assay. Purified PilF₁₆₆ or PilT was thawed on ice and centrifuged at 130,000 rpm for 20 min at 4 °C to remove aggregated protein. In a 50 µL reaction volume, 1 µM PilF₁₆₆ or PilT was incubated with 0.1-1.2 mM freshly made ATP at 37 °C in activity buffer (20 mM Hepes pH 8.0, 150 mM NaCl, 5 mM MgCl₂). After an reaction time of 0 min, 20 min, 40 min and 60 min, a malachite green molybdate-based solution was added to measure the inorganic phosphate release, as described (13). The colorimetric reaction was stopped by adding 10 µL 34% citric acid. After

10-min incubation the absorbance at 630 nm was measured at room temperature and calibrated using a free phosphate standard. The activity of PilF₁₆₆ or PilT is represented by enzymatic velocity with unit pmol/min/μg. To extract the kinetic constants Km and Vmax, the reaction rate was plotted against ATP.

SDS–PAGE. Preparation of protein samples, SDS–PAGE separation, transfer to membranes, and immunoblotting were performed using standard biochemistry techniques (14). Proteins were separated by SDS–PAGE in Tris-glycine gels containing 12–15% acrylamide.

SEC-MALS. Freshly purified *N. meningitidis* PilF₁₆₆ and PilT was analysed in activity buffer at room temperature using a SEC-MALS (multi-angle light scattering) system in which an analytical Superose 6 10/30 column (GE Healthcare Life Sciences) was coupled to a static light-scattering (DAWN HELEOS II, Wyatt Technology) equipment. An Agilent 1200 UV (Agilent Technologies) detectors was used to capture the UV signal of each elution volume. Data analysis was done using the ASTRA software package (Wyatt Technology).

Analytical ultracentrifugation. AUC sedimentation velocity experiments were conducted in activity buffer at 20°C using a Beckman Optima XL-I analytical ultracentrifuge and an An-60 Ti rotor (Beckman) in absorbance mode (280 nm incident light) at 40,000 rpm rotor speed. A total number of 100 scans were collected with one scan every 6 min. Scans 6–100 were analysed with Sedfit (15) and a c(s)-based sedimentation profile analysis was performed. Expected sedimentation coefficients and molecular weight of the structural models were predicted using PROHYDROUS-SOMO (16).

Supplementary Figures

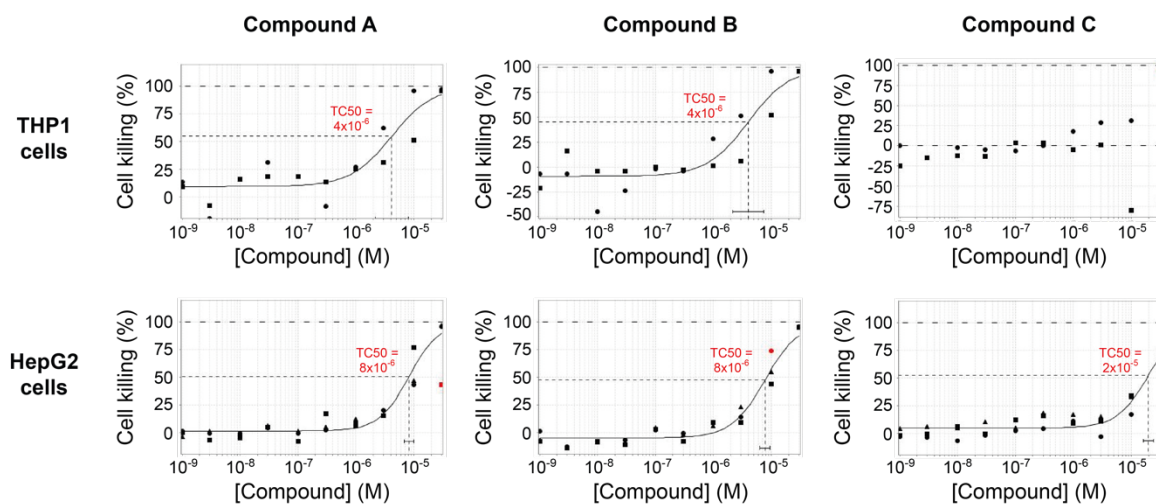


Fig. S1. Absence of cellular toxicity of the selected compounds. THP1 and HepG2 cells were cultured for 40 h at 37°C under moist atmosphere containing 5% CO₂ in presence of the indicated compound concentrations and cell viability was assessed based on the quantitation of the ATP present in the culture using the CellTiter-Glo Luminescent Cell Viability Assay (Promega) according to manufacturer instructions. Results were normalized with respect to the control condition per replicate and expressed as the percentage of cell killing. Dots, squares and triangles in graphs represent technical replicates (N=2 and N=3 independent experiments for THP1 and HepG2, respectively). Red symbols represent outliers excluded for curve fitting and TC50 calculation.

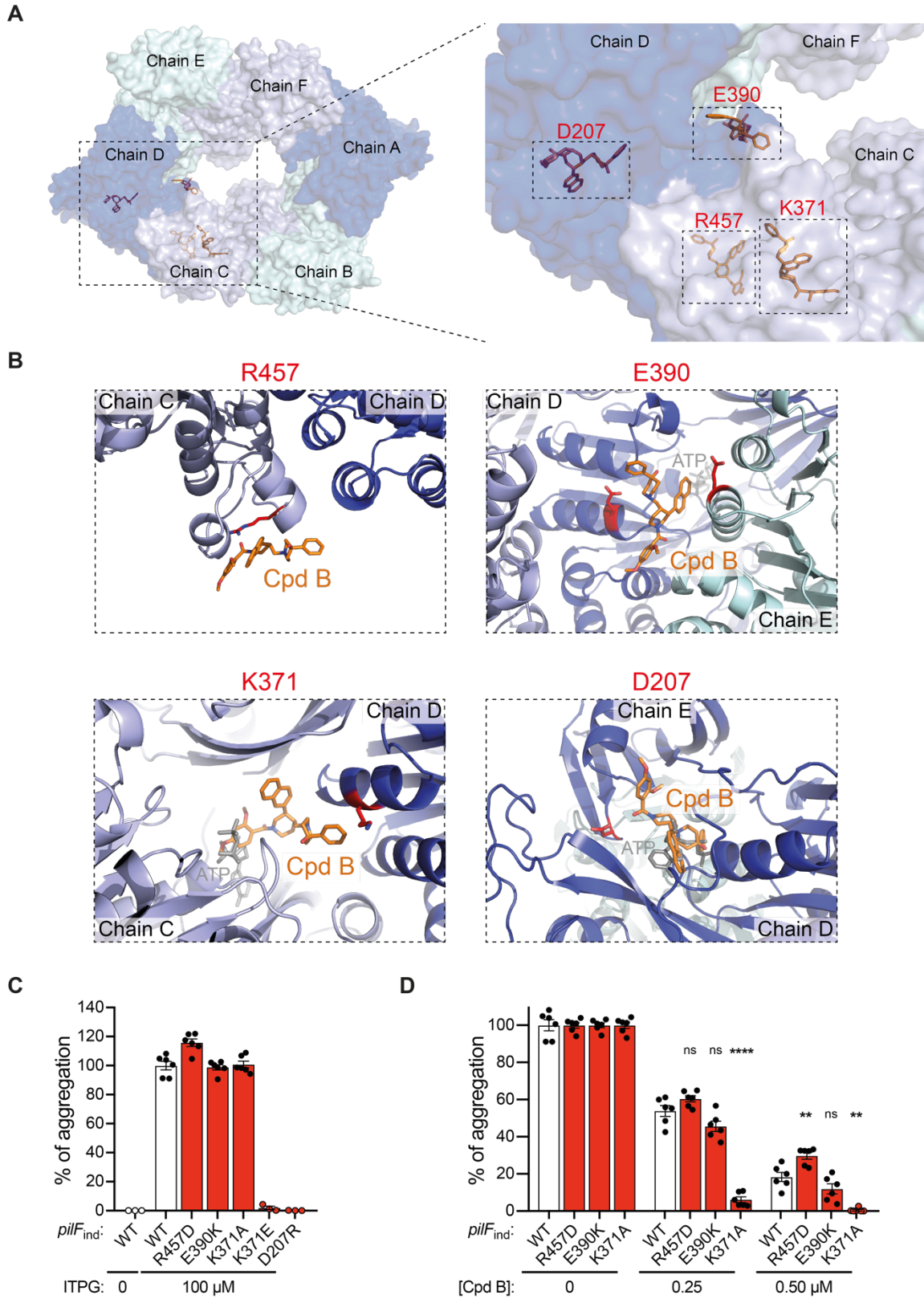


Fig. S2. Point mutations in *Neisseria meningitidis* PilF are sufficient to tune bacterial sensitivity to compound B. (A) *In silico* docking simulations between compound B and the

homology model of *Neisseria meningitidis* PilF. The represented top four docking solutions with a binding energy lower than -7.0 kcal/mol, which occupies four different predicted interaction sites are shown. The PilF hexamer, shown in surface representation (60% transparency), is colored in blue for chain A and D, in cyan for chain B and E, and in light blue for chain C and F, respectively. Compound B is colored in orange. A zoomed-in view is provided on the right. **(B)** Detailed view of the four putative binding sites. Compound B in stick representation is colored in orange. ATP molecule in the putative catalytic pocket is shown in grey. Amino-acids potentially involved in the compound B-PilF interaction and selected for mutagenesis are highlighted in red. **(C)** Aggregative properties of the different PilF mutant strains generated. Data were normalized with respect to the IPTG-induced (100 μ M, 2h) $\Delta pilF pilF_{ind}$ WT strain. **(D)** Effect of compound B on the aggregative property of the IPTG-induced (100 μ M, 2h) $\Delta pilF pilF_{ind}$ mutant stains generated. Data were normalized with respect to the DMSO control condition ([Cpd B]: 0 μ M) per bacterial strain and replicate to minimize the effects of inter-strain variation in absence of drug. **(C-D)** Data represent the mean \pm SEM of N=2 independent experiments, each performed in triplicate. A one-way ANOVA test comparing with the control condition was used to determine statistical significance. ns, non-significant; ** $P \leq 0.01$; **** $P \leq 0.0001$.

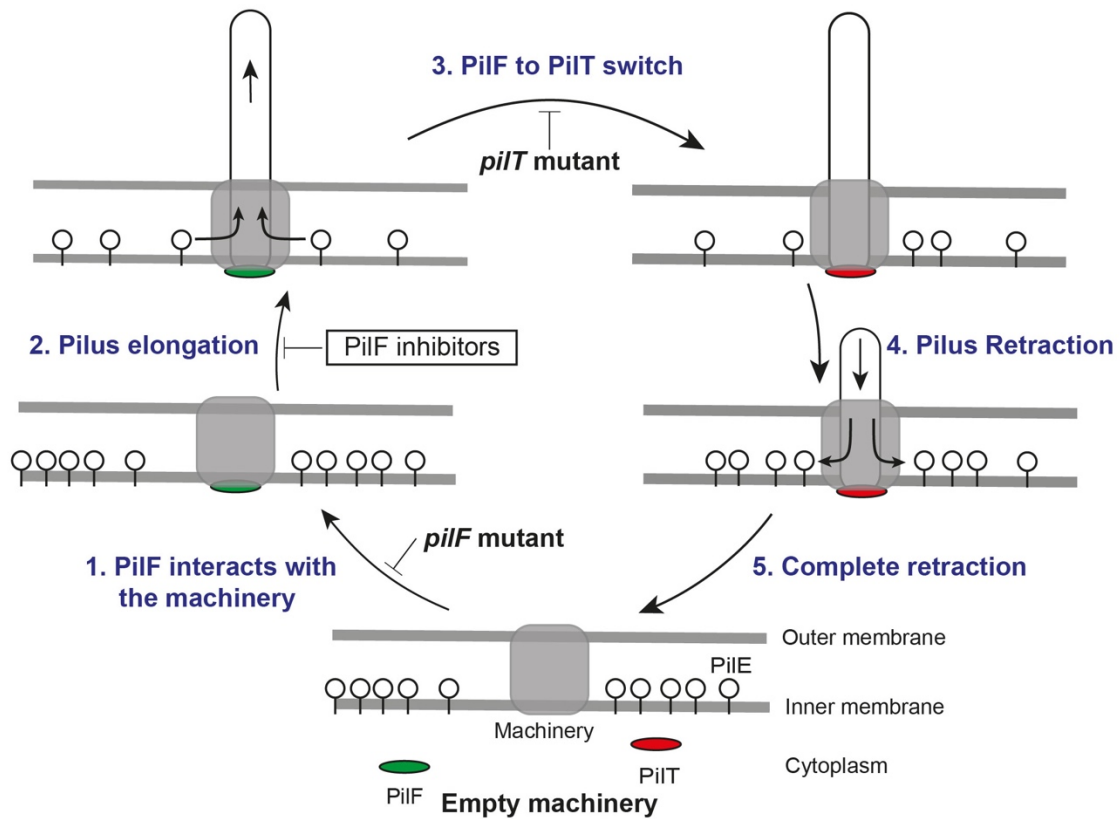


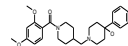

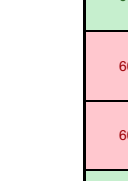


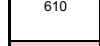

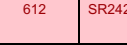
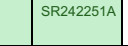
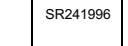
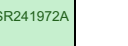
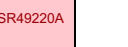



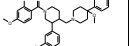
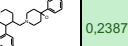
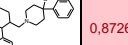
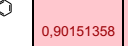
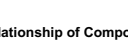



Fig. S3. Schematic representation of the pilus elongation/retraction cycle. Numerous empty piliation machineries can be found on the bacterial surfaces (17), suggesting a resting state where pilin monomers are in the inner membrane and the PilF/T ATPases in the cytoplasm. The piliation cycle is likely initiated with the interaction of PilF with a machinery (step 1). PilF activity then powers assembly of the monomers in a fibre (step 2), and can be inhibited by the hit compounds identified in this study. Then, PilF disengages and PilT comes into play (step 3). Pilus retraction can then take place (step 4), leading to complete retraction (step 5), and the cycle can start again.

Supplementary References

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Compound coordinate	Compound ID	Batch ID	IC50 (M)	TC50 (M)	Selected compound
004-E009	A000550256	LGK5282	1,19E-08	3,70E-06	
006-M017	A003703869	P-34898-092-1	7,20E-09	8,29E-06	A
007-L005	SR241866A	SR241866A-1	1,73E-08	7,83E-06	B
004-K018	SR57667B	SL40.0714-08-A	5,03E-07	>3.00E-05	
004-N023	SSR139812	SSR139812-1	5,21E-06	1,72E-05	
004-P022	RA03689183	SL34.0922-00-A	1,24E-05	>3.00E-05	
005-A022	SAR320933	CL21.003338-2	1,57E-05	1,64E-05	
005-K015	SR140174	SR140174-0	2,07E-06	>3.00E-05	
005-K023	SR300408A	SR300408A-2	3,25E-06	2,10E-05	
006-K016	SR240253A	SR240253A-1	8,45E-06	>3.00E-05	
006-L016	SAR128741	F-34666-001-1675	3,36E-06	>3.00E-05	
006-L023	A002243388	F-32966-126	5,21E-06	1,11E-05	
006-M023	A003572820B	T-1356JM-045-2	9,32E-06	2,02E-05	
007-D017	EX00046908A	FFT.REX1.030.017	1,42E-05	2,16E-05	
007-H018	A000124389	FFT.REX1.028.014	3,98E-07	>3.00E-05	
008-A009	EX00111885	FFT.REX1.133.053	2,66E-07	1,98E-05	C
001-M022	A000348503	W028455-E	4,02E-07	NoVal	
004-A016	SSR117249A	SSR117249A-1	1,01E-06	1,33E-05	
004-A021	EX00046846	FFT.REX1.029.007	6,37E-07	5,73E-06	
004-B015	A000160158	RU44675/2	NoVal	NoVal	
004-C022	A000384853	DRB1158-1	NoVal	NoVal	
004-D024	RA04244647	FFT.REX1.030.001	NoVal	NoVal	
004-I006	SSR133686	SSR133686-2	3,80E-07	2,71E-05	
004-J021	A000364254	SL82.0715-00-B	NoVal	1,46E-05	
004-K008	A001067195	CR11585	NoVal	<1.00E-09	
004-M022	SAR184370	SL92.0725-00-A	NoVal	NoVal	
004-N016	RA03683960A	SW9457-0	NoVal	NoVal	
004-O021	SAR144993	SAR144993-1	1,24E-06	1,63E-05	
005-B017	A000077521	CL21.004246-1	NoVal	6,40E-06	
005-C022	SR44144	CL21.001680-2	1,12E-05	NoVal	
005-C023	SSR107843	SSR107843-1	2,68E-06	NoVal	
005-E006	SR142742	SR142742-0	NoVal	7,93E-06	
005-G019	A003118102A	SL50.6538-10-A	6,02E-05	NoVal	
005-G022	SAR320770	CL21.003184-2	NoVal	NoVal	
005-K010	SAR409202	SW970-0	4,28E-07	NoVal	
005-K019	SSR340568	SSR340568-2	2,28E-03	NoVal	
005-L009	RA03717047A	CL21.003564A-1	3,07E-07	NoVal	
005-L017	RA03688136A	CL21.003146A-1	NoVal	4,63E-07	
005-L023	RA03685089	CL21.004350-1	NoVal	NoVal	
005-M012	SR80386	SR80386-0	NoVal	NoVal	
005-M018	A000074262	CL21.003560-2	NoVal	NoVal	
005-N022	CL21.004793	CL21.004793-1	NoVal	9,31E-07	
005-P021	SSR116575	SSR116575-1	NoVal	NoVal	
006-A021	A000325675D	T007185-1	NoVal	NoVal	
006-C010	A000436353A	T007373-1	NoVal	NoVal	
006-E019	SAR159550A	SAR159550A-1	2,63E-07	NoVal	
006-G012	A002647569A	T007549-1	NoVal	NoVal	
006-L015	A000334600	F-33589-084-SL415	1,47E-05	NoVal	
006-P018	A000163797	S861420-E	NoVal	NoVal	
007-A015	SL50.6260-17	SL50.6260-17-A	NoVal	>3.00E-05	
007-A021	SR149076A	SR149076A-0	6,75E-07	4,88E-06	
007-B011	A000366755	FFT.REX1.028.074	NoVal	2,93E-05	
007-K019	A003435970	P-34020-074-1	NoVal	4,54E-06	
007-L023	A000068880	FFT.REX1.028.059	NoVal	5,33E-06	
007-M022	SR150697	SR150697-1	NoVal	NoVal	
007-N016	A000388726A	FFT.REX1.028.008	NoVal	>3.00E-05	
007-P006	RA03683902A	CL21.003020A-1	NoVal	NoVal	
008-A005	RA06097987	CL21.002080-1	NoVal	7,54E-07	
008-M014	RA03681856	FFT.REX1.028.022	NoVal	NoVal	

Supplementary Table 2. Summary of compound IC50 and TC50.

Derivative #	Compound ID	Structure	Aggregation Index		Derivative #	Compound ID	Structure	Aggregation Index	
			Replicat #1	Replicat #2				Replicat #1	Replicat #2
Ctrl	-	-	1	1	624	SR126808A		0,89094713	0,648688
DMSO	-	-	1,16830336	1,00435496	625	SR126739		1,54600459	0,89671185
Compound B	SR241866A		0,609719962	0,209864961	626	SR126312A		1,22775082	0,87872452
601	SR126893A		0,42650228	0,238486	627	SR140306A		0,98612276	0,46759953
602	SR126546A		0,6053085	0,30650501	628	SR242124A		1,05299651	0,73469891
603	SR140314A		0,38375214	0,23748919	629	SR126115A		1,23409329	0,63098143
604	SR242079A		0,287558758	0,045618314	630	SR140485A		0,85645871	0,64356534
605	SAR151679		0,465438758	0,139783739	631	SR126892A		1,07113654	0,54691496
606	SR242462A		1,25962819	0,50913406	632	SR126361A		0,31061435	0,26296693
607	SR126178A		0,62000633	0,41835116	633	SR48388A		1,73185865	0,88282017
608	SR126695		0,197078267	0,064090347	634	SR242670A		0,54000576	0,44420974
609	SR242125A		0,6275706	0,28925333	635	SR126452A		1,38475325	0,81541015
610	SR126427A		0,42663094	0,26064471	636	SR126699A		0,195803394	0,126080336
611	SR126451A		0,90147473	0,4911623	637	SR126809A		0,59490547	0,36320443
612	SR242160A		0,80604821	0,51638437	638	SR126453A		0,57259999	0,3294846
613	SR242251A		0,010377469	0,022667427	639	SR126127A		0,3742833	0,32088924
614	SR241996		0,51236946	0,37941988	640	SR126441A		1,03341264	0,58891034
615	SR241972A		0,345815415	0,191877005	641	SR241865A		0,69140818	0,45331895
616	SR49220A		0,78577057	0,51905737	642	SAR151678		0,113274088	0,150259685
617	SR126442A		0,87757807	0,45620599	643	SR126362A		1,1768149	0,55701683
618	SR140712A		1,56908561	0,62796268	644	SR126837A		0,96325619	0,76704886
619	SR241781A		0,83481654	0,59867234	645	SR241956A		0,84378233	0,63609224
620	SR126650		1,20296372	0,60560303	646	SR126859A		0,45885153	0,33970585
621	SR241864A		0,238777312	0,109675625	647	SR242463A		1,05178961	0,87111127
622	SR241973A		0,87266368	0,53949866	648	SR126128A		0,209899286	0,141109329
623	SR126651A		0,90151358	0,84871816	649	SR241866A		0,156063497	0,163443338

Supplementary Table 3. Structure activity relationship of Compound B.

Highlighted in green or red are derivatives with a better or a worst inhibition activity than compound B, respectively.