Electronic Supplementary Material (ESI) for Chemical Science.

Supporting information

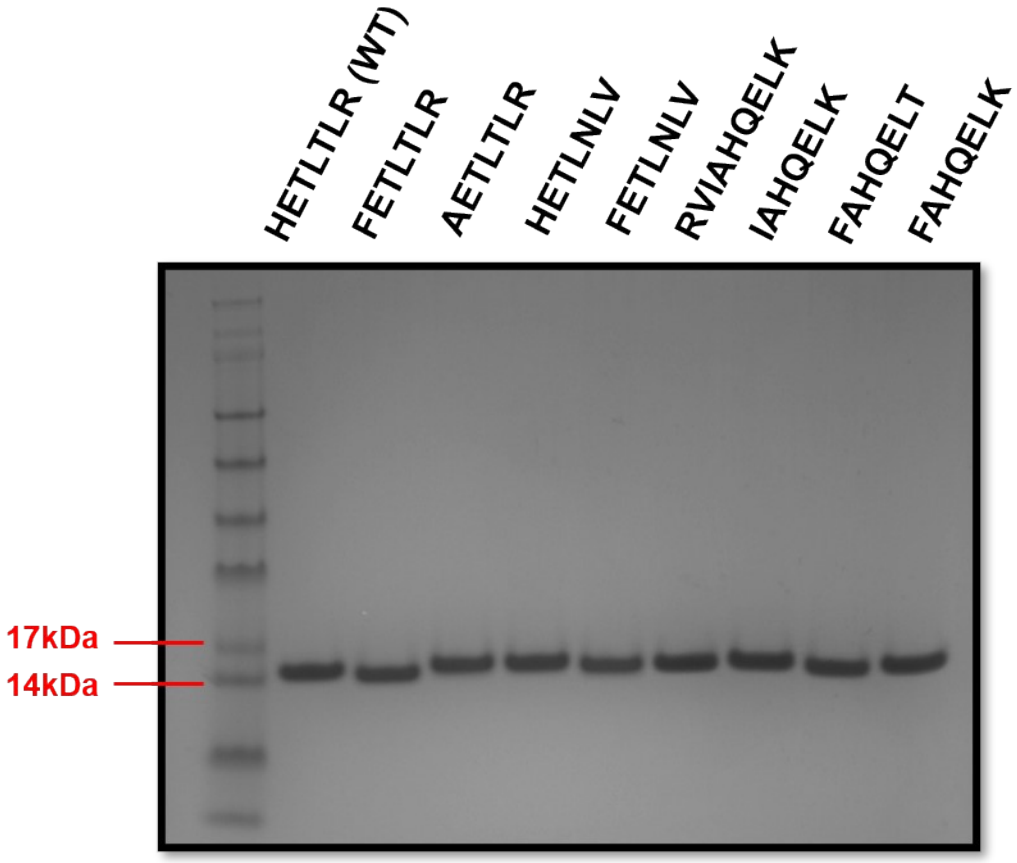

Figure S1. Purified DesAbs used in this study. SDS-PAGE analysis of the protein fractions obtained from an exemplary purification of the different DesAbs. All the DesAb samples were measured at the concentration of 10 μM.

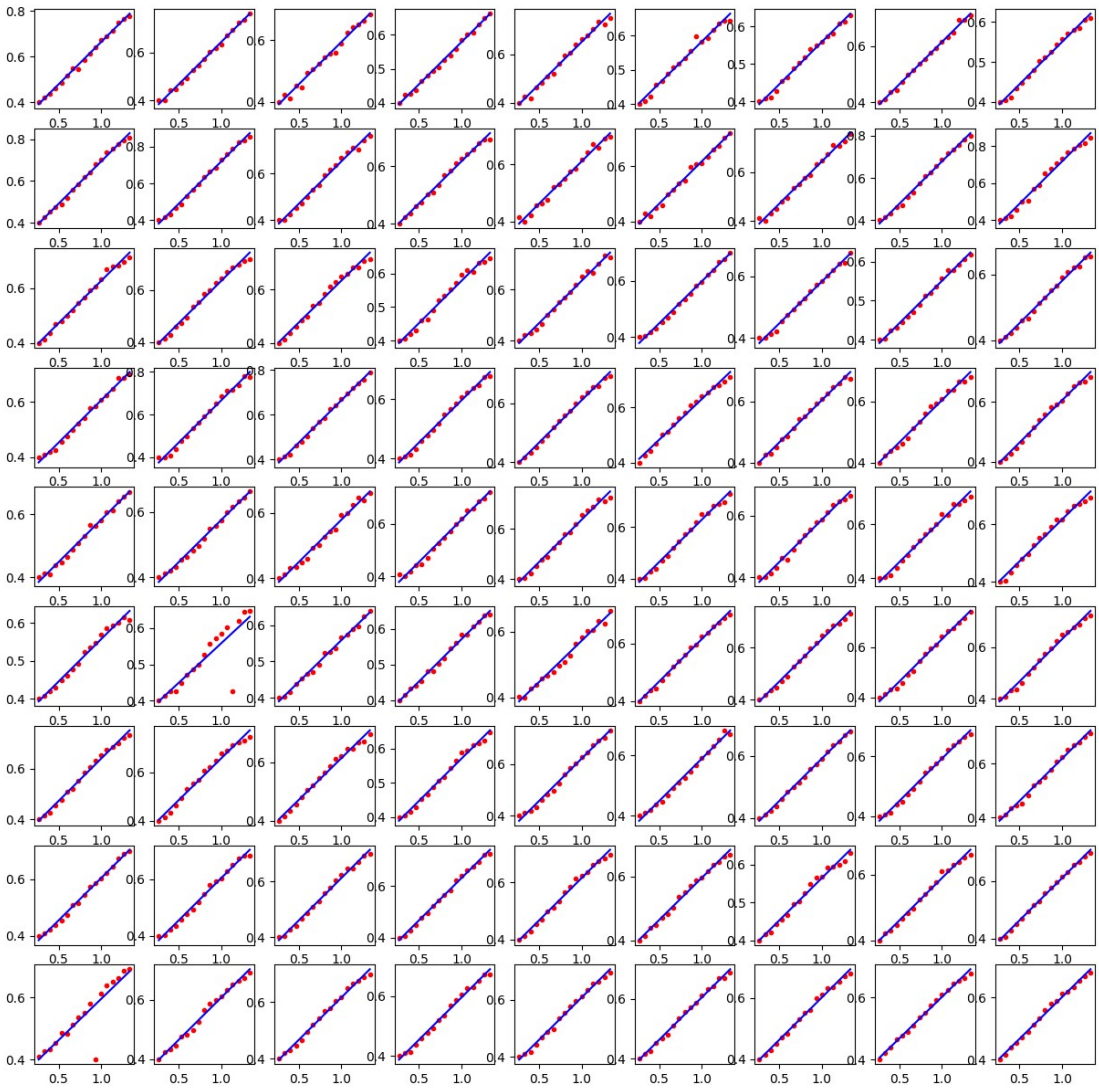

Figure S2. Fitting procedure to obtain k_+. We fitted the seeded aggregation data by using the equation $r = 2k_+P_0m$ from Ref.[16]. Red dots represent the original data and blue lines represent the fitting results. From top to bottom, each row represents one antibody: DesAb-HETLTLR, DesAb-FETLTLR, DesAb-AETLTLR, DesAb-HETLNLV, DesAb-FETLNLV, DesAb-RVIAHQELK, DesAb-IAHQELK, DesAb-FAHQELT and DesAb-FAHQELK. In each row, from left to right: DesAb:Aβ42 ratios 1:2(triplicate), DesAb:Aβ42 ratios 1:4(triplicate) and DesAb:Aβ42 ratios 1:8(triplicate).

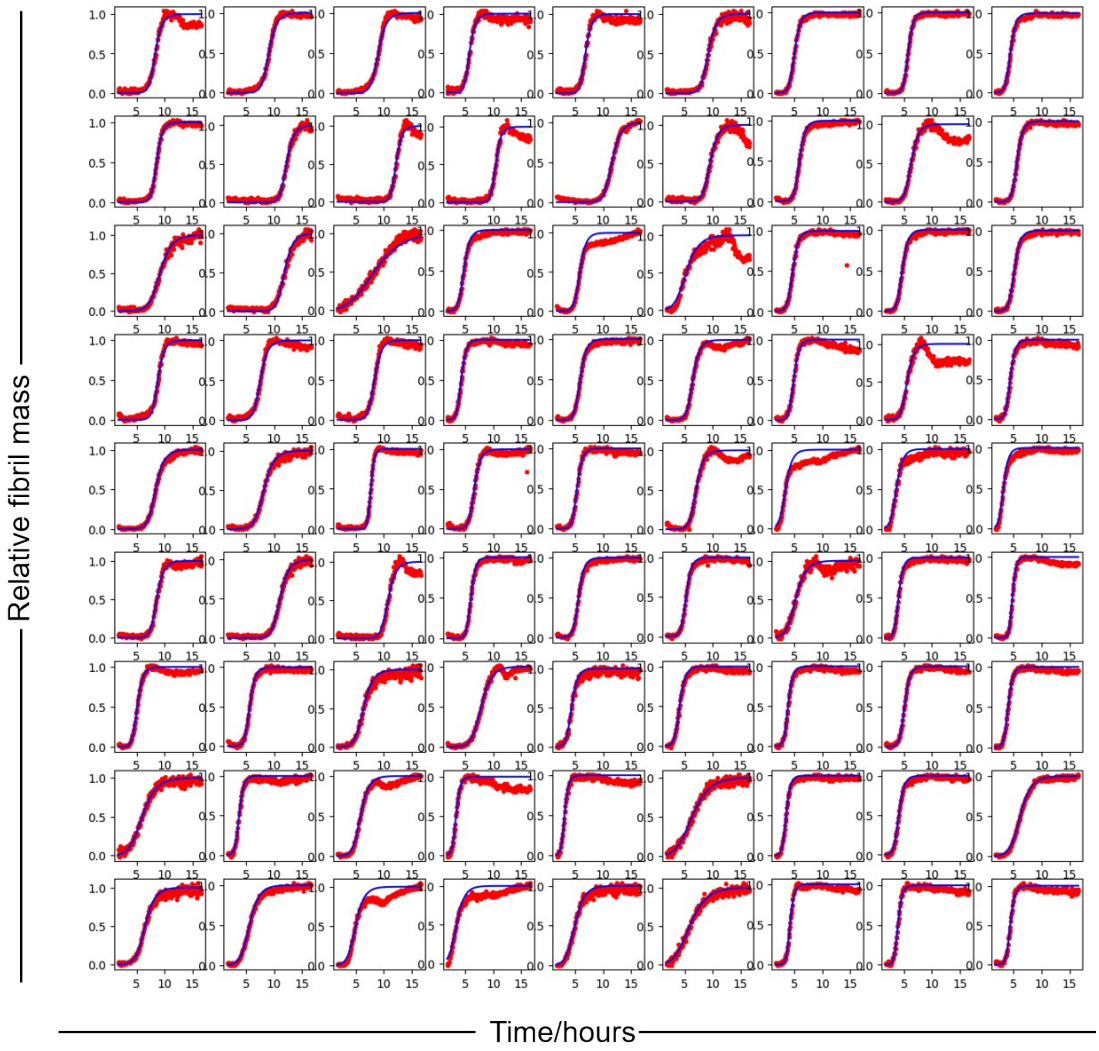

Figure S3. Fitting procedure to obtain k_n and k_2. We fitted the unseeded aggregation data, only using the experimental data points from 0.15 to 0.72 in the normalised relative fibril mass (y-axis). The k_+ values were obtained from the seeded kinetics aggregation assays (Figure S1). Red dots represent the experimental data for each replicate and blue lines represent the fitting results. From top to bottom, each row represents one antibody: DesAb-HETLTLR, DesAb-FETLTLR, DesAb-AETLTLR, DesAb-HETLNLV, DesAb-FETLNLV, DesAb-RVIAHQELK, DesAb-IAHQELK, DesAb-FAHQELT and DesAb-FAHQELK. In each row, from left to right: DesAb:Aβ42 ratios 1:2(triplicate), DesAb:Aβ42 ratios 1:4(triplicate) and DesAb:Aβ42 ratios 1:8(triplicate).

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M E V Q L V E S G G G L V Q P G G S L R L S C A A S G F N I              30
K D T Y I G W V R R A P G K G E E W V A S I Y P T N G Y T R              60
Y A D S V K G R F T I S A D T S K N T A Y L Q M N S L R A E              90
D T A V Y Y C A A G S Designed CDR3 E E E A A A W G Q G T L             120
V T V S S G S H H H H H H H
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Figure S4. Amino acid sequence of the DesAb scaffold used in this work. The sequences of the various designed CDR3 employed are in Fig. 1.

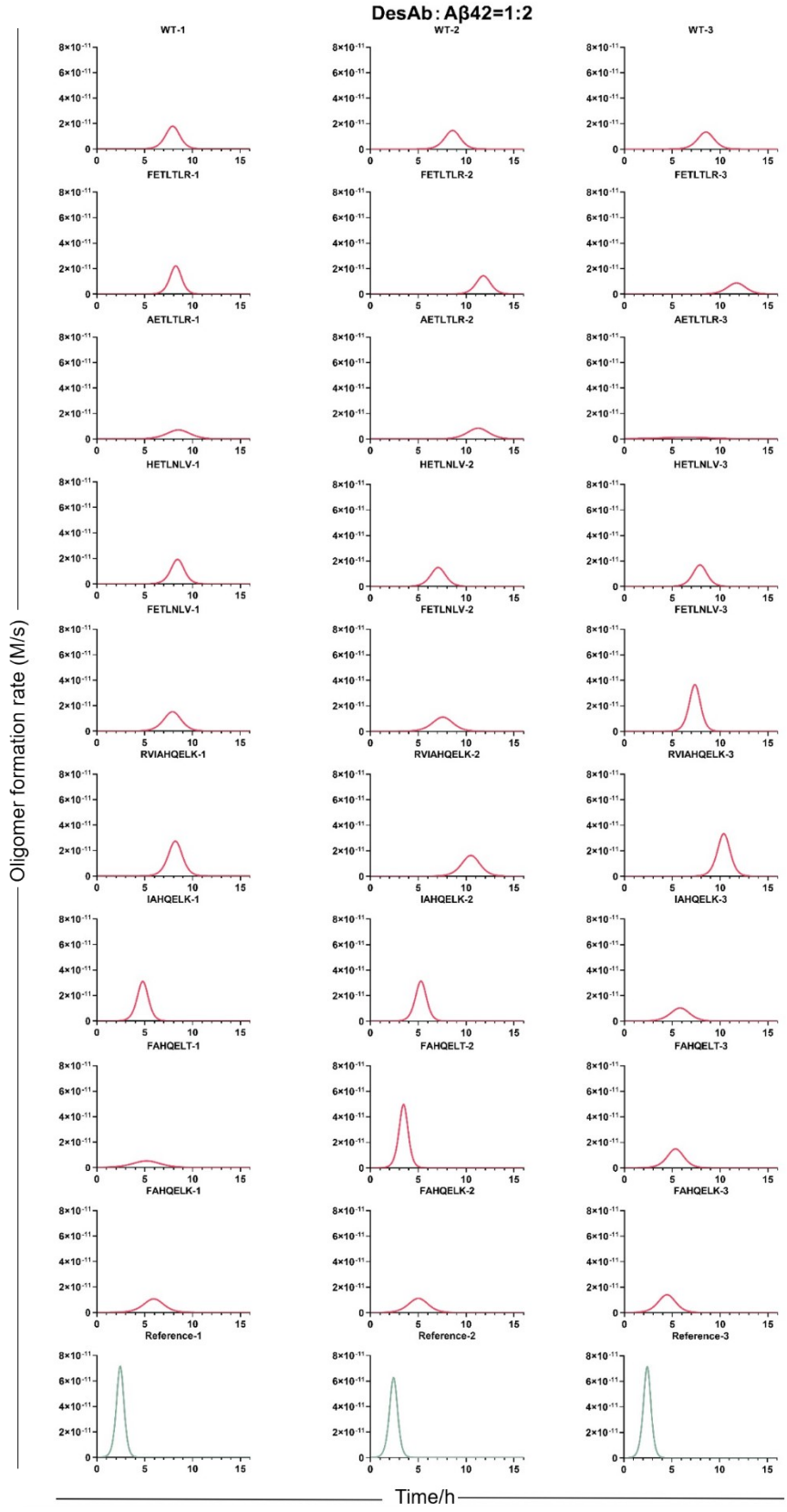

Figure S5. Time dependence of the reactive flux toward oligomers at 1:2 DesAb:Aβ42 ratio. A 1 μM Aβ42 solution in the presence of either buffer (green) alone or with 0.5 μM (red) of DesAb; results are averaged over three replicas.

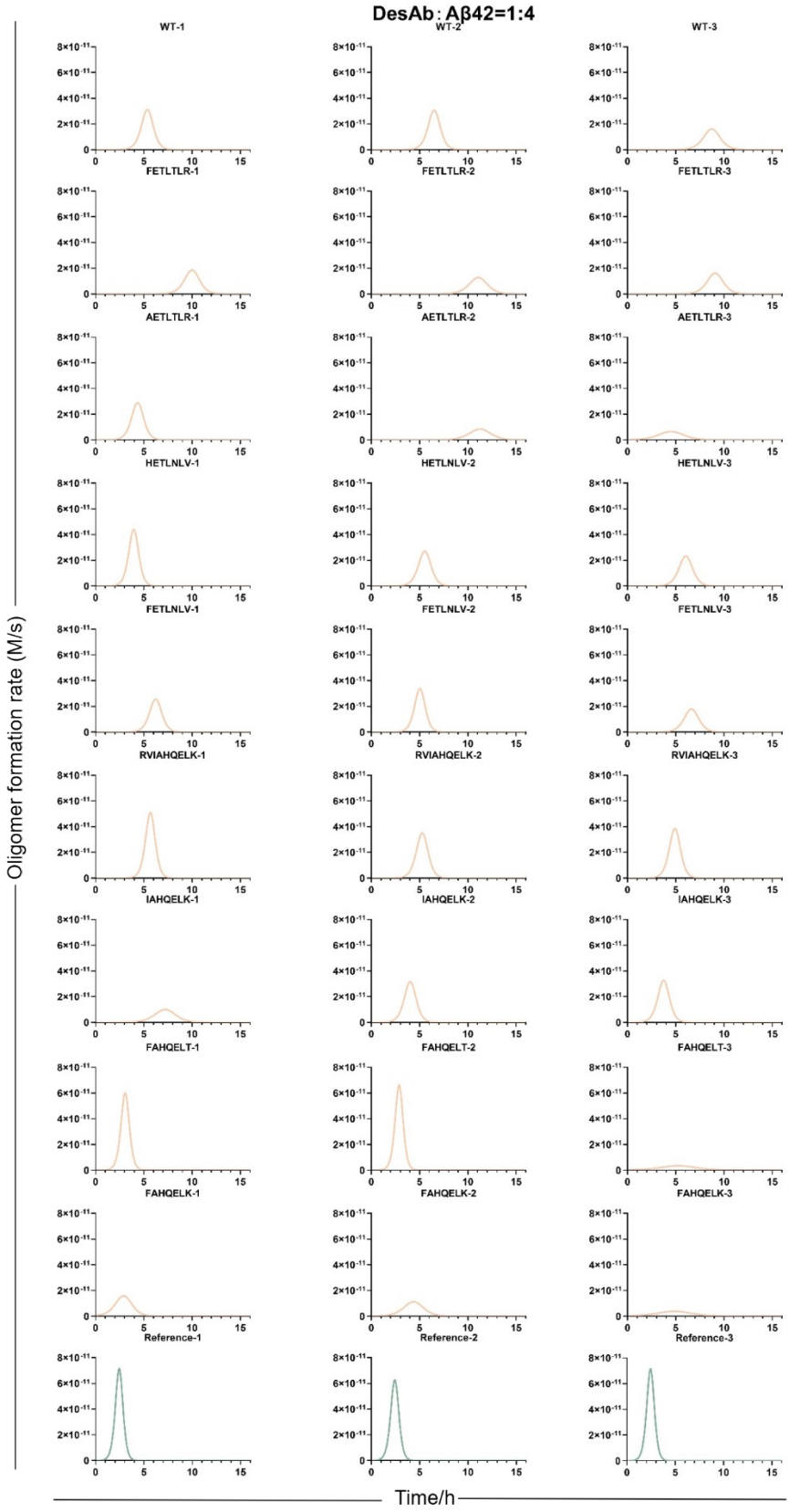

Figure S6. Time dependence of the reactive flux toward oligomers at 1:4 DesAb:Aβ42 ratio. A 1 μM Aβ42 solution in the presence of either buffer (green) alone or with 0.25 μM (red) of DesAb; results are averaged over three replicas.

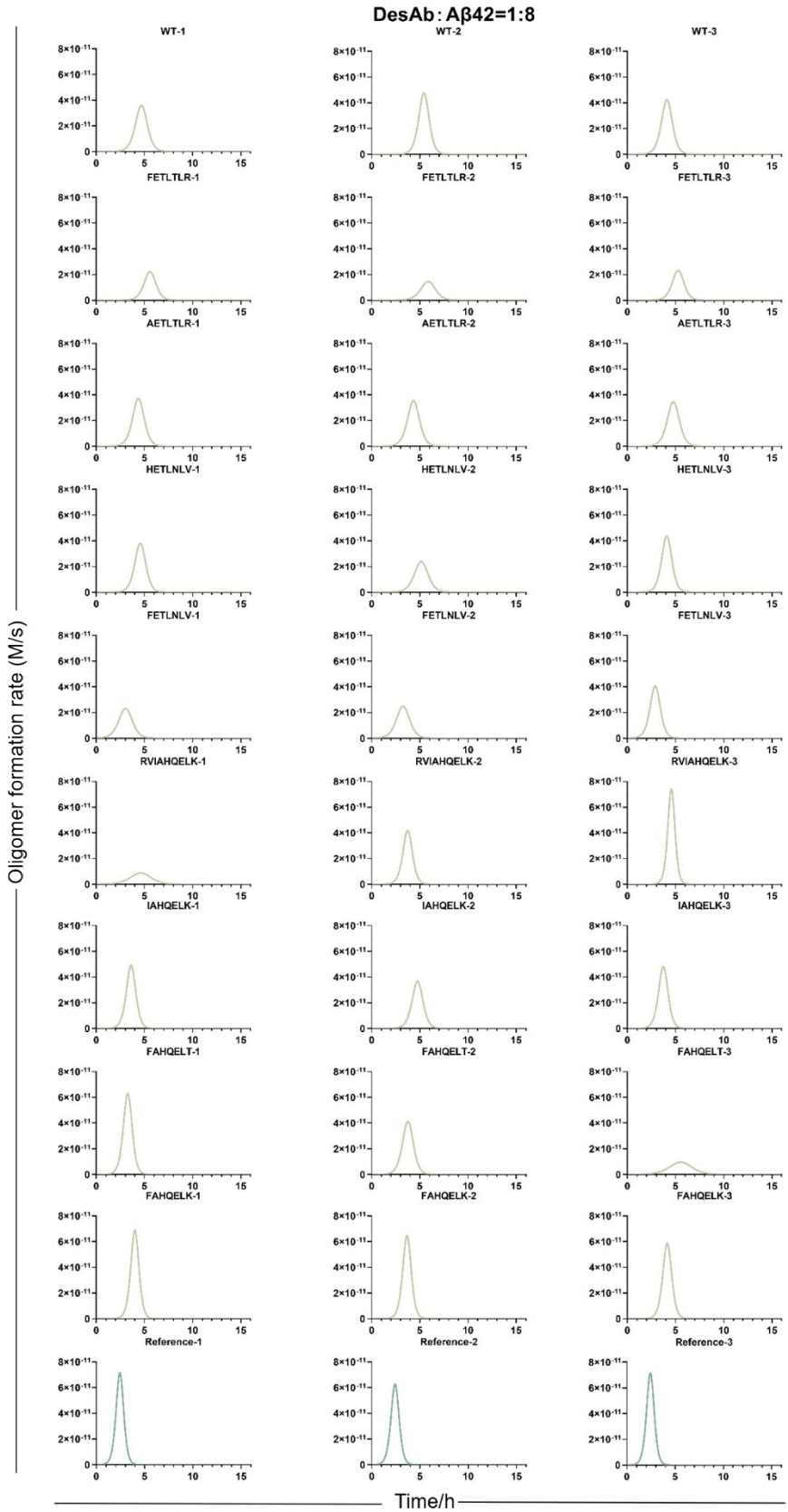

Figure S7. Time dependence of the reactive flux toward oligomers at 1:8 DesAb:Aβ42 ratio. A 1 μM Aβ42 solution in the presence of either buffer (green) alone or with 0.125 μM (red) of DesAb; results are averaged over three replicas.

Table S1. Oligonucleotide primer sequences of the DesAbs used in this work. These sequences of primers are based on the scaffold of DesAb-HETLTLR from Ref.[16].

DesAb-HETLNLV Fwd GAAACCCTGaacTTAgtgGAAGAGGAAGCGGCAGC Rev atgCGATCCTGCTGCGGAAACCCTGaacTTAg
DesAb-FETLTLR Fwd AGGATCGtttGAAACCCTGACCTTACGCGAAGA Rev GTTTCaaaCGATCCTGCTGCGCAATAGTACACC
DesAb-AETLTLR Fwd AGGATCGgcgGAAACCCTGACCTTACGCG Rev GCTGCGCAATAGTACACCAGGATCGgcgG
DesAb-FETLNLV Fwd AGCAGGATCGtttGAAACCCTGaacTTAgtgGAAGAGGAAGCGGCAGC Rev CaaaCGATCCTGCTGCGCAATAGTACACCGC
DesAb-RVIAHQELK Fwd ATCGcgcgtgattgcgcatcaggaactgaaaGAAGAGGAAGCGGCAGC Rev tcacgcgCGATCCTGCTGCGCAATAGTAC
DesAb-IAHQELK Fwd GGATCGattgcgcatcaggaactgaaaGAAGAGGAAGCGGCAGC Rev gcgcaatCGATCCTGCTGCGCAATAGTACACC
DesAb-FAHQELT Fwd TCGTTTgcgcatcaggaactgaccGAAGAGGAAGCGGCAGC Rev gatgcgcAAACGATCCTGCTGCGCAATAGTAC
DesAb-FAHQELK Fwd GGATCGTTTgcgcatcaggaactgaaaGAAGAGGAAGCGGCAGC Rev gcgcAAACGATCCTGCTGCGCAATAGTACACC