**Supplementary Material**

**Supplementary Methods**

**Antigen binding by biolayer interferometry**

SdAb constructs at 400 nM were immobilized to a nickel-coated BLI biosensor (ForteBio) and dipped into either heat inactivated *S. enterica* serovar Hadar, FliC of *S. enterica* (Sigma-Aldrich), or flagella of *C. jejuni* (purified according to (Newell, McBride, and Pearson 1984)). After loading for 10’, the biosensors were base lined in 1 x Kinetics PBS buffer (ForteBio) for 5’ then dipped into antigen solution. For KD determination, FliC was assayed at the following concentrations: 500, 250, 125, 62.5, 31.3, and 15.7 nM and flagella assayed at: 2400, 1200, 600, 300, 150, and 75 nM. For assessing bacteria binding, BSA was used in the mobile phase as a negative control. BLI signal (nm) was recorded with the Octet RED96 BLI (ForteBio).

**Thermostability assays by differential scanning fluorimetry**

Differential scanning fluorimetry was performed as previously described (Huynh and Partch 2015). Briefly, Sypro orange (5000 x, ThermoFisher) was added to proteins at a concentration of 6 xand scanned using 7500 Fast Dx RT-PCR instrument (Applied Biosystems). ROX (6-carboxy-X-rhodamine) was chosen as the fluorescence reporter and none for quencher. Method was set for 1 ⁰C increase per minute from 25 ⁰C to 95 ⁰C. Proteins at 0.9 mg/mL were scanned with five replicates for each construct.

**Molecular docking**

The structure of Abi-Se07 was modeled using SWISS-MODEL. Domains D2-D3 of FliC (Yonekura, Maki-Yonekura, and Namba 2003) was used for docking of Abi-Se07 using SnugDock (Sircar and Gray 2010). Docking was conducted with 100 iterations and the lowest energy solutions (Supplementary Table1) were analyzed and visualized as part of the filament molecule.

The homology model was generated by Swiss-Model with quality score in good range relative to all structures in Protein Data Bank. The quality score is an estimate of C-beta angle energies, all atom energies, solvation, and torsion compared to experimentally determined protein crystal structures. Quality of the model is higher in the framework than the CDR regions, which is not surprising as these regions are expected to be flexible and structurally different than CDRs of structurally available antibodies.

**A**

ERH38463.1 MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTSNIKG 60

AAT81621.1 MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTSNIKG 60

OLP51747.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

APH26739.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

KNU33033.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

RAT91061.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

OSY33027.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

KWV07712.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

AHA06007.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

AAT81640.1 MAQVINTNSLSLLTQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAIANRFTANIKG 60

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OLP51747.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

APH26739.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

KNU33033.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

RAT91061.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

OSY33027.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

KWV07712.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

AHA06007.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

AAT81640.1 LTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRL 120

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APH26739.1 NEIDRVSGQTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVQKAYD 180

KNU33033.1 NEIDRVSGQTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVQKAYD 180

RAT91061.1 NEIDRVSGQTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVQKKYD 180

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AAT81621.1 ATVGDLKSS--F-KNVTGYDTYAAGADKYRVDINSGAVVTDDAAPDKVYVNAANGQL--- 234

OLP51747.1 VKDTAVTTK-AYADNGTTLDASGLDDAAIKAA-IGGTTGTAAVTGGTVKFDADNNKYFVT 238

APH26739.1 VSATAAMDPKSFTDGTKNL--TAPDATAIKAA-LGNPAATGDSLSATL--SFKDGKYYAT 235

KNU33033.1 VSATAAMDPKSFTNGTKNL--TAPDATAIKAA-LGNPATTGDSLSATL--SFKDGKYYAT 235

RAT91061.1 VDSTGVTQS-LDL-KTAGIT-----GATLKAGITGTTTETGSVKDGKVYYDADSKNYYVE 233

OSY33027.1 VSDTAATVT-GYTDSATAID-----KSTFAASATTL-GGTP-AITGDLKFDDTTGKYYAD 232

KWV07712.1 VSDTAATVT-GYADTTIALD-----NSTFKASATGL-GGTDQKIDGDLKFDDTTGKYYAK 233

AHA06007.1 VSDTAATVT-GYADTTIALD-----NSTFKASATGL-GGTDQKIDGDLKFDDTTGKYYAK 233

AAT81640.1 VSDTAATVT-GYADTTIALD-----NSTFKASATGL-GGTDQKIDGDLKFDDTTGKYYAK 233

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OLP51747.1 IGGFTG-ADAAKNG---DYEVNVATDG--KVTLATGATKTTMPAG-----AATK-TEVQE 286

APH26739.1 VAGYTNAADTSKNG---KYEVNVDSAT-GAVTFNAAPTKATVT-G-----DTTV---TKV 282

KNU33033.1 VAGYTNAADTSKNG---KYEVNVDSAT-GAVTFNAAPTKATVT-G-----DTTV---TKV 282

RAT91061.1 VDFTDTTDKAAHAG---FYKADVD-AD-GNVSLATGATKEAK--------PTNAVEVEKT 280

OSY33027.1 V--SGTTA---KDG---VYEVTVA-AD-GKVTLTGTPTGPITAGF-----PSTATKDVKQ 277

KWV07712.1 VTVTGETG---KNG---YYEVSVNKTN-GEVTLAGGATSPLTGGL-----PATATEDVKN 281

AHA06007.1 VTVTGGTG---KDG---YYEVSVDKTN-GKVTLAGGATSPLTGGL-----PATATEDVKN 281

AAT81640.1 VTVTGGTG---KDG---YYEVSVDKTN-GKVTLAGGTTSPLTGGL-----PATATEDVKN 281

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OLP51747.1 LKDTPAVVSADA---KNAL----IAGGVDTADANGAELVKMSYTDKNGKTIEGGYALKAG 339

APH26739.1 QVNAPVAVSTDV---KKAL----EDGGVSNADATAAKLVKMSYTDKNGKSIDGGYALEAG 335

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RAT91061.1 IDEKPLKASSSV---QDAL----KASGIADAVAEAATVVKMSYTDKNGKTIDGGYGIKVG 333

OSY33027.1 TQQEN-ADLTEA---KAAL----TAAGV--AAAGTASVVKMSYTDNNGKTIDGGLAVKVG 327

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AAT81640.1 VQVAN-ADLTEA---KAAL----TAAGV----TGTASVVKMSYTDNNGKTIDGGLAVKVG 329

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ERH38463.1 TKNESAKLSDLEANNAVKGESKITVNGAEYTAN---------------ATGDKITLAGKT 390

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KNU33033.1 GKYYAA--------TYDEGTGKITANVTTYTDSTGATKTAANQLGGVDGKTEVVTIDGKT 387

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OSY33027.1 DDYYSA--------TQN-KDGSISINTTKYTADDGTSKTALNKLGGADGKTEVVSIGGKT 378

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AAT81640.1 DDYYSA--------TQN-KDGSISINTTKYTADDGTSKTALNKLGGADGKTEVVSIGGKT 380

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ERH38463.1 MFIDKTASGVSTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL 450

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AAT81640.1 YAASKAEGHNFKAQPDLAEAAATTTENPLQKIDAALAQVDTLRSDLGAVQNRFNSAITNL 440

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AAT81621.1 GNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR 505

OLP51747.1 GNTVNNLSEARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR 506

APH26739.1 GNTVNNLSEARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR 502

KNU33033.1 GNTVNNLSEARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR 502

RAT91061.1 GNTVNNLSSARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR 499

OSY33027.1 GNTVNNLTSARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR 493

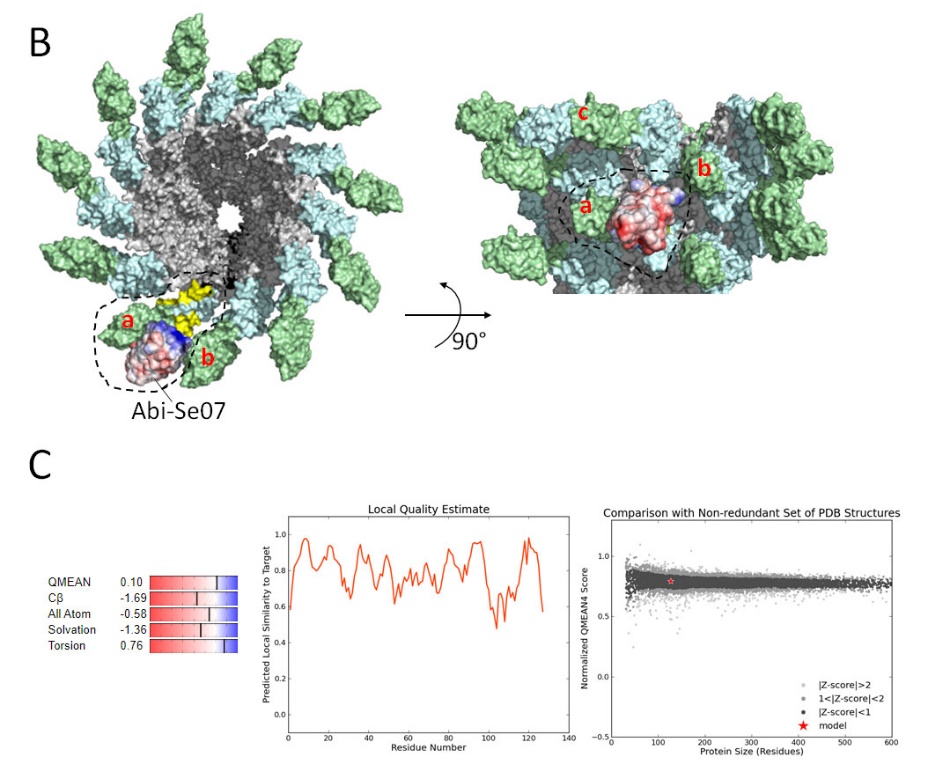
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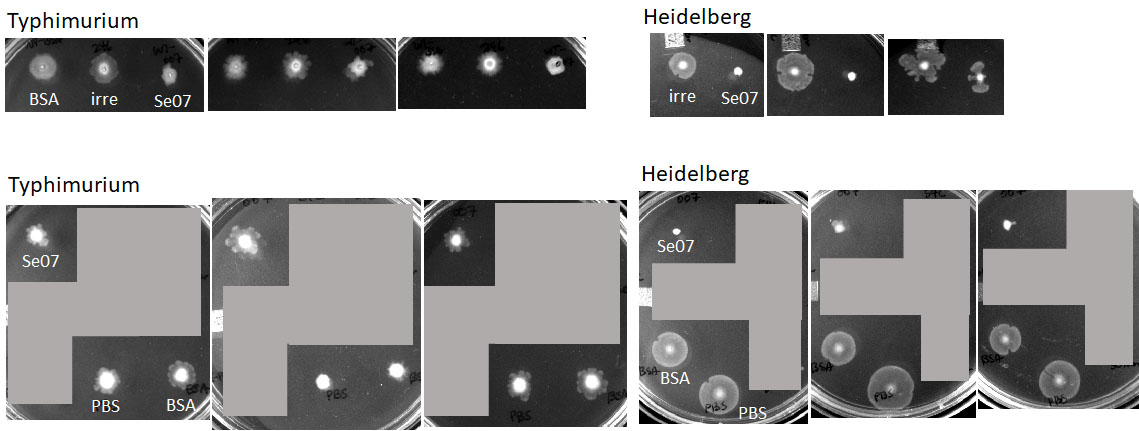
AAT81640.1 GNTVNNLTSARSRIEDSDYATEVSNMSRAQILQQAGTSVLAQANQVPQNVLSLLR 495

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**B**

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**Supplementary Figure S1. A.** Alignment of *S. enterica* serovar Hadar (RAT91061.1), Typhimurium (AHA06007.1), Heidelberg (AAT81640.1), Enteritidis (ERH38463.1), Newport (APH26739.1), Javiana (OLP51747.1), Senftenberg (ABR18492.1). Kentucky (KWV07712.1), Infantis (OSY33027.1), and Saint-Paul (KNU33033.1). Domains D0, D1, D2, and D3 are colored black, grey, cyan, and green, respectively. Underlined region corresponds to residues within 4 Å of Abi-Se07 CDRs in the simulated docking solution. **B.** Visualization of docking of Abi-Se07 to FliC. This docking is inaccurate due to low quality modeling of CDRs (see C) and is provided merely as a to-scale visualization. **C.** SWISS-MODEL QMEAN quality score relative to all non-redundant structures in the protein data bank (left and right panels). Local quality estimate along the length of the sdAb polypeptide (middle panel). Quality estimate declines around residue 100 to 120, corresponding to CDR3.



**Supplementary Figure S2.** Motility of *S. enterica* was assessed for serovars Typhimurium and Heidelberg. Three replicates were conducted for each set of experiments. In the presence of BSA, PBS or irrelevant sdAb, Typhimurium exhibited inconsistent motilities while Heidelberg exhibited consistent and reproducible motilities with the control treatment.