Supporting Information

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a.

	a	b	c	d	e	f	g
134					E	K	E
137	L	E	E	K	K	E	A
144	L	E				L	A
148	I	D	Q	A	S	R	D
155	Y					H	R
158	A	T	A	L	E	K	E
165	L	E	E	K	K	K	A
172	L	E				L	A
176	I	D	Q	A	S	Q	D
183	Y					N	R
186	A	N	V	L	E	K	E

b. M1*^{1R}

	a	b	c	d	e	f	g
134	V	K	E	L	E	E	K
141	V	E	A	L	***E***	***L***	A
148	***I***	***D***	***Q***	***A***	***S***	R	***D***
155	***Y***	H	R	L	T	A	L
162	V	K	E	L	E	E	K
169	V	K	A	L	***E***	***L***	A
176	***I***	***D***	***Q***	***A***	***S***	Q	***D***
183	***Y***	N	R	L	N	V	L
190	V	K	E				

c. M1*^{2R}

	a	b	c	d	e	f	g
134					E	K	E
137	V	E	E	L	K	E	A
144	V	***E***	***L***	L	***I***	***D***	***Q***
151	***A***	***S***	R	***D***	***Y***	H	R
158	V	T	A	L	E	K	E
165	V	E	E	L	K	K	A
172	V	***E***	***L***	L	***I***	***D***	***Q***
179	***A***	***S***	Q	***D***	***Y***	N	R
186	V	N	V	L	E	K	E

Fig. S1. Idealization of the B repeats. (*A*) Heptad positions of residues in the B repeats as predicted by Coils (12). Residues that correspond to register 1 are in red, and those that correspond to register 2 are in blue. (*B*) Sequence of M1*^{1R}, with idealizing mutations in black and depicted in register 1. Residues that contact Fg in register 2 are bolded and italicized. (*C*) Sequence of M1*^{2R}, with idealizing mutations in black and depicted in register 2. Residues that contact Fg in register 2 are bolded and italicized.

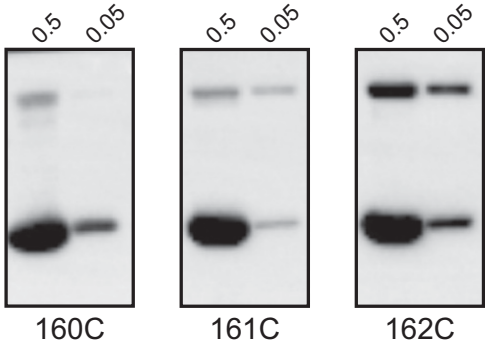

Fig. S2. Intradimer versus interdimer disulfide bond formation. Disulfide bond formation at 10-fold higher (0.5 mg/mL) or the same concentration (0.05 mg/mL) as in Fig. 4*A*, as assessed by nonreducing SDS/PAGE and visualized by Western blot using an anti-His antibody.

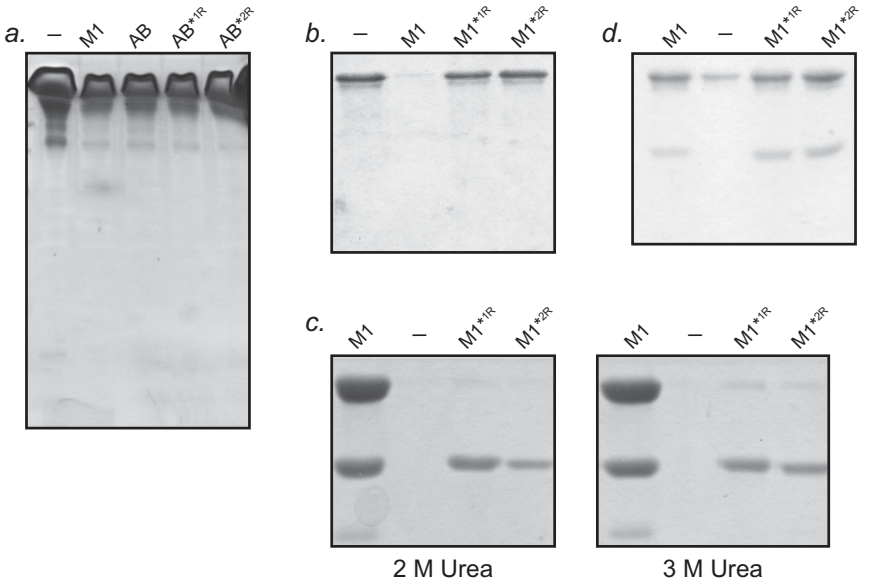

Fig. S3. Interaction with Fg. (*A*) Unbound proteins from Ni^{2+}-NTA coprecipitation assay for interaction of His-tagged AB proteins with FgD, as shown in Fig. 4*B*. (*B*) Unbound proteins from Ni^{2+}-NTA coprecipitation assay for interaction of His-tagged M1 proteins with FgD, as shown in Fig. 4*C*. (*C*) Ni^{2+}-NTA agarose coprecipitation assay for interaction of His-tagged M1 proteins with FgD at 37 °C carried out in the presence of 2 M (*Left*) or 3 M (*Right*) urea. Bound FgD was assessed through Coomassie-stained SDS/PAGE. (*D*) Unbound proteins from Ni^{2+}-NTA coprecipitation assay for interaction of His-tagged M1 proteins with FgD, as shown in Fig. 4*E*.

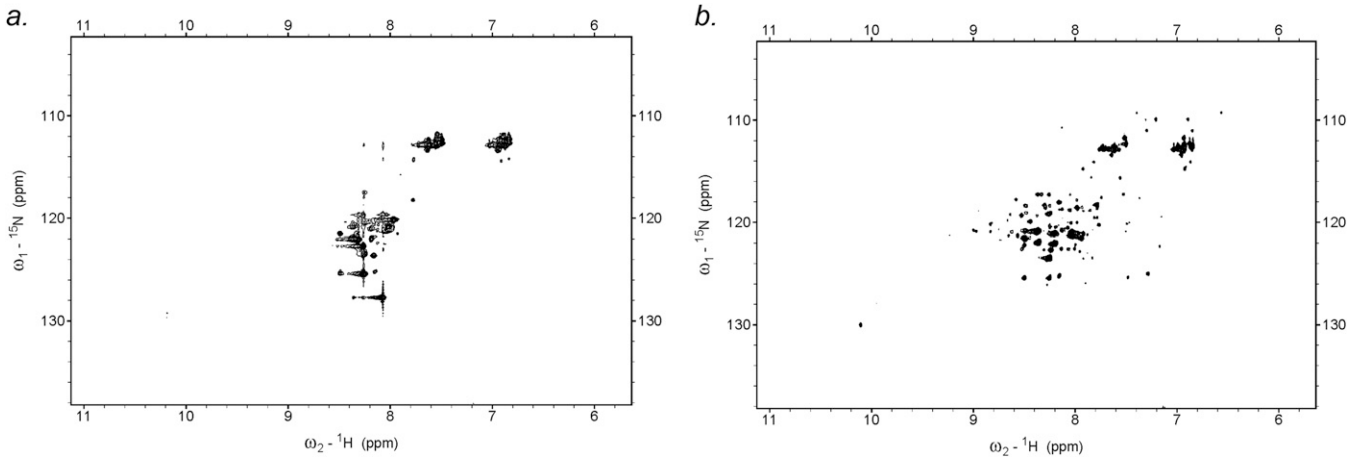

Fig. S4. AB*^{2R} is a structured protein. ^{1}H-^{15}N HSQC spectra of (*A*) AB (*B*) and AB*^{2R} collected at 26 °C.

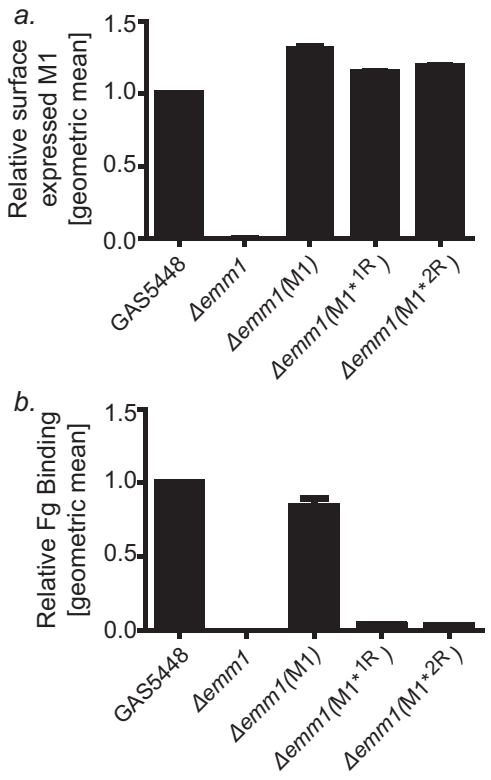

Fig. S5. Idealized M1 proteins on the GAS surface. (*A*) Surface expression of M1 protein by wild-type GAS 5448, GAS 5448 (*Δemm1*) carrying an empty plasmid or plasmids encoding wild-type M1, register 1-stabilized M1, or register 2-stabilized M1, as assayed by FACS, using a polyclonal anti-M1 protein antibody. The values are the means of three triplicates normalized to GAS 5448, with the SD shown. (*B*) Binding of FITC-labeled Fg to the same strains as in *A* as assayed by FACS. The values are normalized to the value for GAS 5448, with the SD shown.