High-resolution mapping of glycoprotein structure–activity relationships by shotgun scanning glycomutagenesis

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Abstract

N-linked glycosylation serves to diversify the proteome and is crucial for the folding and activity of numerous cellular proteins. Consequently, there is great interest in uncovering the rules that govern how glycosylation modulates protein properties so that the effects of site-specific glycosylation might eventually be predicted. Towards this goal, we describe a combinatorial strategy termed shotgun scanning glycomutagenesis (SSGM) that enables systematic investigation of the structural and functional consequences of glycan installation along a protein backbone. The utility of this approach was demonstrated with three different acceptor proteins, namely bacterial immunity protein Im7, bovine pancreatic ribonuclease A, and a human anti-HER2 single-chain Fv antibody, all of which were found to tolerate *N*-glycan attachment at a large number of positions and with relatively high efficiency. The stability and activity of many glycovariants was measurably altered by the *N*-linked glycan in a manner that critically depended on the precise location of the modification. Comparison of the results with calculations of simple geometrics and Rosetta energies reveals nuanced mechanisms whereby glycosylation can affect protein activity. By enabling high-resolution mapping of glycan-mediated effects on acceptor proteins, glycomutagenesis opens up possibilities for accessing unexplored regions of glycoprotein structural space and engineering protein variants with advantageous biophysical and biological properties.

Introduction

Glycosylation of asparagine residues is one of the most abundant and structurally complex protein post-translational modifications [1, 2] and occurs in all domains of life [3]. Owing to their relatively large size and hydrophilicity or simply their presence at definite locations, asparagine-linked (*N*-linked) glycans can significantly alter protein properties including biological activity, chemical solubility, folding and stability, immunogenicity, and serum half-life.[4, 5] Hence, glycosylation effectively increases the diversity of the proteome by enriching the repertoire of protein characteristics beyond that dictated by the twenty canonical amino acids. Glycan conjugation is also crucial in modern medicine, as many pharmaceutical products are glycoproteins that depend on glycosylation for efficacy [6-9]. Moreover, the profound effect of glycans on proteins has prompted widespread glycoengineering efforts to rationally manipulate key glycosylation parameters (*e.g.*, glycan size and structural composition, glycosite location and occupancy) as a means to optimize the therapeutic and immunologic properties of proteins [10-14]. Despite some notable successes, the routine use of glycosylation as a strategy for engineering proteins with advantageous properties is currently limited by our inability to generalize and predict how glycosylation affects protein structure and function.

Indeed, deciphering the "glycosylation code" that defines the interplay between a glycan and its underlying acceptor protein represents a grand challenge that requires access to large collections of chemically defined glycoproteins in sufficient quantities for characterization [15]. Such products are difficult to obtain because of the intrinsic variability with respect to the site of glycan attachment (macroheterogeneity) and glycan structure (microheterogeneity). This variability stems from the untemplated nature of glycosylation, which, unlike protein synthesis that involves a coding template, is defined by the relative activities of a number of glycosyltransferase enzymes. One way to circumvent this issue is through computational approaches that enable *in silico* exploration of glycosylation-induced effects on protein folding and stability [16, 17]; however, these involve a trade-off between molecular detail and glycoprotein size, with full-atomistic molecular dynamics simulations typically limited to only short glycopeptides (~10 residues) [16]. Another option is chemical synthesis, which can furnish defined glycopeptides for investigating the local effects of *N*-linked glycans on peptide conformation [18]. Although this approach is also not

amenable to full-length proteins, advances in expressed protein ligation (EPL) have opened the door to convergent assembly of chemically synthesized glycopeptides with recombinantly expressed protein domains to form larger glycoproteins bearing complex *N*-glycans installed at discrete sites [19]. Using this technology, Imperiali and colleagues created a panel of seven site-specifically glycosylated variants of the bacterial immunity protein Im7 modified with the chitobiose disaccharide (GlcNAc–GlcNAc) and assessed the kinetic and thermodynamic consequences of glycan installation at defined locations [20]. Unfortunately, EPL is a technically demanding procedure, requiring manual construction of each individual glycoprotein and thus limiting the number of testable glycosite designs to just a small handful. Hence, there remains an unmet need for more scalable techniques that can rapidly supply exhaustive collections of discretely glycosylated proteins for systematically interrogating the influence of *N*-glycans on the properties of conformationally complex proteins.

Herein, we describe shotgun scanning glycomutagenesis (SSGM), a general and high-throughput method for fine mapping of glycoprotein structure–activity relationships (glycoSARs) (**Fig. 1**). SSGM is inspired by protein engineering methods based on alanine-scanning mutagenesis that have proven particularly useful for probing the contributions of individual amino acid sidechains to the properties of proteins [21]. In conventional alanine-scanning, site-directed substitution with alanine eliminates the side chain beyond the β carbon, allowing the effects of individual alanine mutations to infer the roles of individual side chains [22]. In combinatorial variations of this method, rather than requiring many mutant proteins to be manually produced and separately characterized, combinatorial protein libraries are used in conjunction with high-throughput screens or selections thereby enabling a single library to simultaneously provide information about many different residues [23, 24]. Along conceptually similar lines, SSGM is a glycoprotein-focused method that involves design and construction of combinatorial acceptor protein libraries whereby: (i) each member of the library carries a single acceptor sequon "mutation" introduced at a defined position along the protein backbone; and (ii) the complete ensemble of sequon mutants in the library effectively covers every possible position in the acceptor protein. The resulting SSGM libraries are expressed using *N*-glycosylation-competent bacteria [25, 26] in the context of glycoSNAP (glycosylation of

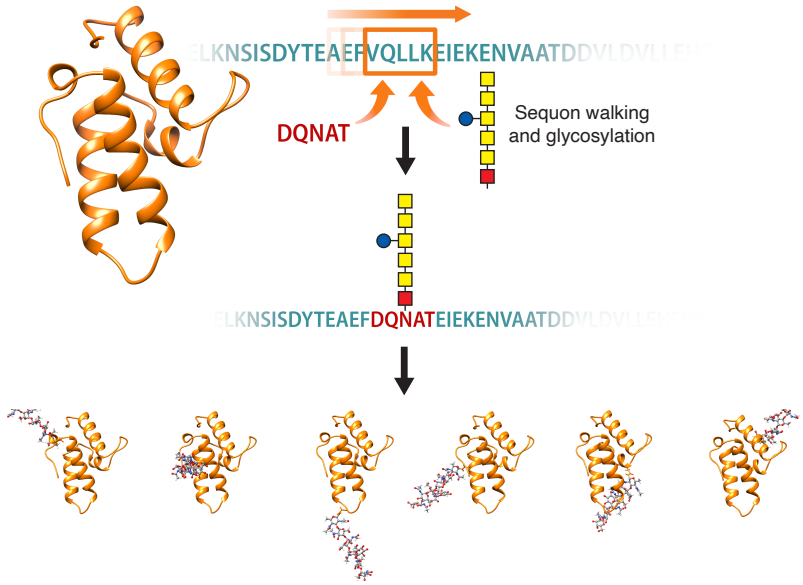

Figure 1. A new biosynthetic route to large-scale glycoprotein structure–activity relationships. Schematic of shotgun scanning glycomutagenesis (SSGM), a glycoprotein engineering method based on combinatorial protein libraries in which glycosylation "sequon walking" is used to introduce an acceptor site at every possible position along the protein backbone. Note that the multi-residue nature of a sequon (*e.g.*, N-X-S/T or D/E-X_1-N-X_2-S/T where X, X_1, $X_2 \neq$ P) necessitates insertion or replacement of up to four additional amino acid substitutions at each position. The resulting library is expressed in glycoengineered bacteria, providing an opportunity for each library member to be expressed and glycosylated in a manner that is compatible with high-throughput screening via glycoSNAP to interrogate the glycosylation phenotype of individual variants. By integrating bacterial SSGM libraries with multiplexable assays, the biochemical and biophysical properties of each glycovariant can be further interrogated, thereby opening the door to fine mapping of glycoSARs.

secreted *N*-linked acceptor proteins) [27], a versatile high-throughput screen based on glycosylation and extracellular secretion of the small (10 kDa in its mature form) *Escherichia coli* protein YebF [28].

Using this new glycoprotein engineering tool, we constructed and screened three different SSGM libraries corresponding to bacterial immunity protein Im7, bovine pancreatic ribonuclease A (RNase A), and a human single-chain Fv antibody specific for HER2 (scFv-HER2). Our results revealed that installation of *N*-glycans was tolerated at a large number of positions and within all types of secondary structure, and the observed *N*-glycosylation efficiency was quite high in the majority of cases. For many of these glycovariants, the presence of *N*-glycans was observed to significantly impact protein stability and/or activity in a manner that critically depended on the precise location of the modification. We computed simple geometric measures and Rosetta energetic estimates [29-32] to determine whether these factors correlate with the sequon insertion or

glycosylation effects on stability and activity. Taken together, these findings demonstrate the utility of SSGM for comprehensively and rapidly cataloging the biological and biophysical effects of *N*-glycan installation at single amino acid resolution and in a protein-agnostic manner, thereby providing access to largely unexplored regions of glycoprotein structural space and opening the door to novel protein variants endowed with advantageous properties.

Results

Reliable detection of acceptor protein glycosylation by glycoSNAP screening. To enable screening of SSGM libraries, we hypothesized that target proteins of interest could be fused to YebF and subsequently interrogated for *N*-glycosylation by glycoSNAP screening (**Fig. 2a**). Briefly, YebF modified with an artificial glycosite (*e.g.*, N-X-S/T or D/E-X_1-N-X_2-S/T where X, X_1, $X_2 \neq$ P) is expressed in the presence of heterologous *N*-glycosylation machinery in *E. coli* cells that are bound to a nitrocellulose filter membrane. Following secretion out of filter-bound colonies, putatively glycosylated YebF is captured on a second nitrocellulose membrane, which is probed with antibodies or lectins to detect *N*-linked glycans. In this way, glycoSNAP creates a convenient genotype–glycophenotype linkage for facile scoring (glycosylated versus aglycosylated) of YebF proteins secreted from individual bacterial colonies. We initially focused on *E. coli* Im7 for several reasons: (i) it is a small, globular 87-residue protein that lacks disulfide bonds and is well expressed in the periplasm where bacterial *N*-glycosylation occurs [33]; (ii) although not a native glycoprotein, Im7 modified at its C-terminus with a DQNAT glycosylation tag has been glycosylated by the *C. jejuni N*-glycosylation machinery in *E. coli* [33]; (iii) crystal structures are available for wild-type (wt) Im7 [34] and for Im7 in complex with its cognate toxin colicin E7 (ColE7) [35]; and (iv) a limited set of seven Im7 variants was previously generated to determine the effects of chitobiose attachment on folding and stability [20], providing some useful reference points for comparison.

To determine whether Im7 was compatible with the glycoSNAP procedure, *E. coli* strain CLM24 was co-transformed with a plasmid encoding YebF-Im7 that was modified at its C terminus with a DQNAT glycosylation tag [36] along with two additional plasmids,

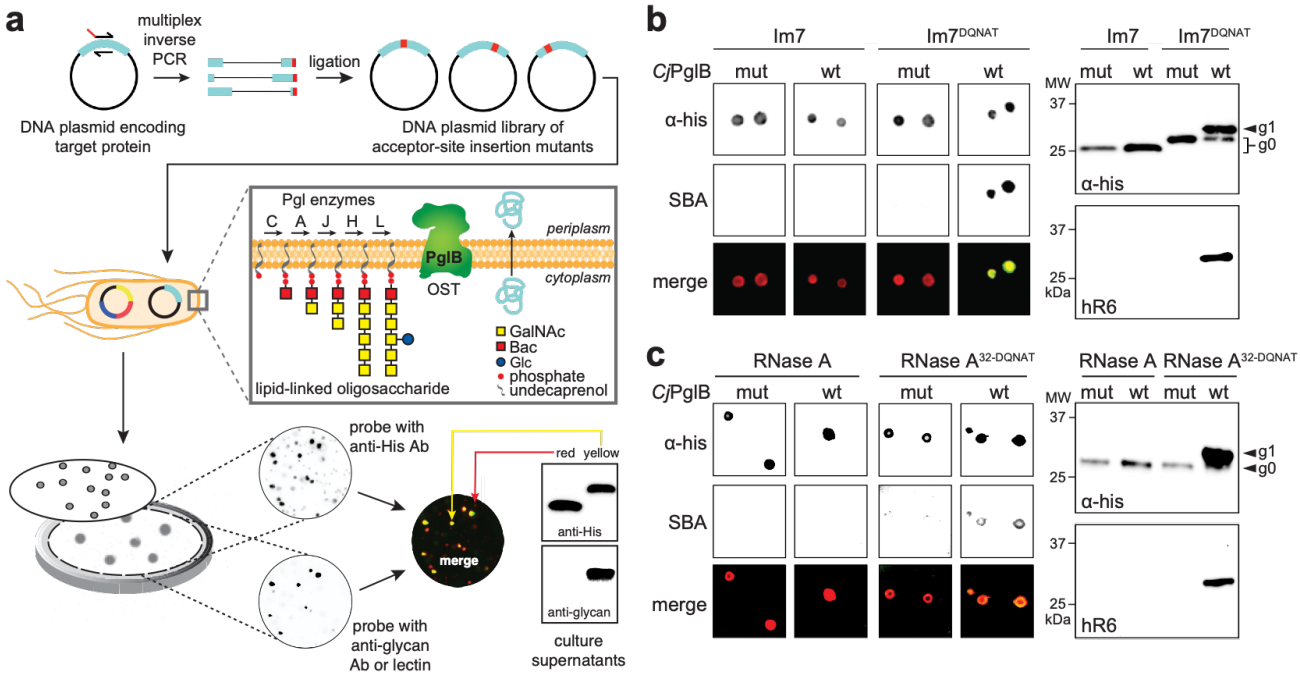

Figure 2. Construction and interrogation of SSGM libraries. (a) Schematic of SSGM library construction using multiplex inverse PCR approach. The resulting plasmid library, encoding acceptor protein variants with glycosite substitutions at every possible position, was used to co-transform *E. coli* strain CLM24 along with two additional plasmids encoding complete *N*-glycosylation machinery from *C. jejuni*. The resulting bacterial library was plated on solid agar, after which colonies and their secreted glycoproteins were replica plated on nitrocellulose membranes as described in the text. (b) Immunoblot analysis of acceptor proteins in colony secretions (left) and extracellular supernatant fractions (right) derived from *E. coli* CLM24 carrying plasmid encoding either YebF-Im7 or YebF-Im7^{DQNAT} along with plasmids encoding *N*-glycosylation machinery with either wild-type *Cj*PglB (wt) or an inactive mutant (mut). (c) Same as in (b) but with YebF-RNase A and YebF-RNase A$^{32\text{-}DQNAT}$ in colony secretions (left) and periplasmic fractions (right). Blots were probed with anti-polyhistidine antibody (α-His) to detect acceptor protein and SBA or hR6 serum to detect *C. jejuni* heptasaccharide glycan. Bottom color panels in (b) and (c) depicts overlay of α-His and SBA blots (merge). Arrows denote aglycosylated (g0) and singly glycosylated (g1) forms of YebF-Im7^{DQNAT} or YebF-RNase A$^{32\text{-}DQNAT}$. Molecular weight (MW) markers are indicated at left. Results are representative of at least three biological replicates.

one encoding the enzymes for biosynthesis of the *C. jejuni N*-glycan and the other encoding the oligosaccharyltransferase (OST) PglB from *C. jejuni* (*Cj*PglB) [26]. When plated on solid agar and subjected to the colony-blotting method, cells expressing YebF-Im7^{DQNAT}, or a control YebF-Im7 construct that lacked the glycosylation tag, were able to secrete the fusion into the extracellular medium as evidenced by cross-reaction of an anti-His antibody with the membranes (**Fig. 2b**). However, only the strain expressing YebF-Im7^{DQNAT} in the presence of wt *Cj*PglB, but not a *Cj*PglB variant rendered inactive by two active-site mutations (D54N and E316Q) [27, 37], gave rise to colonies that reacted with soybean agglutinin (SBA) (**Fig. 2b**), a lectin that binds terminal GalNAc residues in the

C. jejuni heptasaccharide glycan, $GalNAc_5(Glc)Bac$ [38]. The colony blotting results were corroborated by immunoblot analysis of culture supernatants, which revealed that both YebF-Im7 and YebF-Im7^{DQNAT} were secreted into the extracellular medium but only the latter was glycosylated as evidenced by the appearance of a higher molecular weight band in the blot probed with glycan-specific antiserum (**Fig. 2b**). As expected, no glycan-specific signal was detected in colony blots or immunoblots corresponding to cells carrying the mutant *Cj*PglB enzyme (**Fig. 2b**). Taken together, these results confirm the compatibility of bacterial Im7 with the glycoSNAP screening method.

Exhaustive identification of acceptor site permissiveness using SSGM. Next, the plasmid encoding YebF-Im7 was mutagenized to create a library of Im7 gene sequences, each carrying an individual sequon substitution and cumulatively covering all positions in the Im7 protein. Mutagenesis was performed using multiplex inverse PCR [39] with a set of divergent abutting primers that were designed to amplify the entire plasmid and introduce an acceptor asparagine residue at every position in the Im7 gene (with the two upstream and two downstream residues being changed to DQ and AT, respectively), thereby yielding a highly focused plasmid library enriched with in-frame clones each bearing a single DQNAT acceptor motif at a defined position (**Fig. 2a**). The resulting plasmid library was introduced into strain CLM24 carrying the complete *N*-glycosylation machinery, after which the library-transformed cells were plated on solid agar and subjected to glycoSNAP screening. From one membrane, we detected a total of ~200 glycosylation-positive colonies, of which 20 were randomly chosen for further analysis. Sequencing confirmed that a single in-frame DQNAT motif was present in each isolated hit, with the Im7^{N37} and Im7^{N58} variants (where the superscript denotes the location of the asparagine residue) occurring three and two times, respectively (**Fig. 3a**). The hits were fairly evenly distributed throughout the entire Im7 sequence and situated in every type of secondary structure including bends, turns, and α-helices, consistent with X-ray crystallographic data showing that occupied glycosylation sites can occur on all secondary structural elements [40]. Immunoblot analysis confirmed that each of the selected clones was efficiently glycosylated (**Fig. 3b**).

To exhaustively explore glycosylation sequence space, we manually constructed all possible individual Im7 sequon variants (80 in total) using the multiplex PCR primer

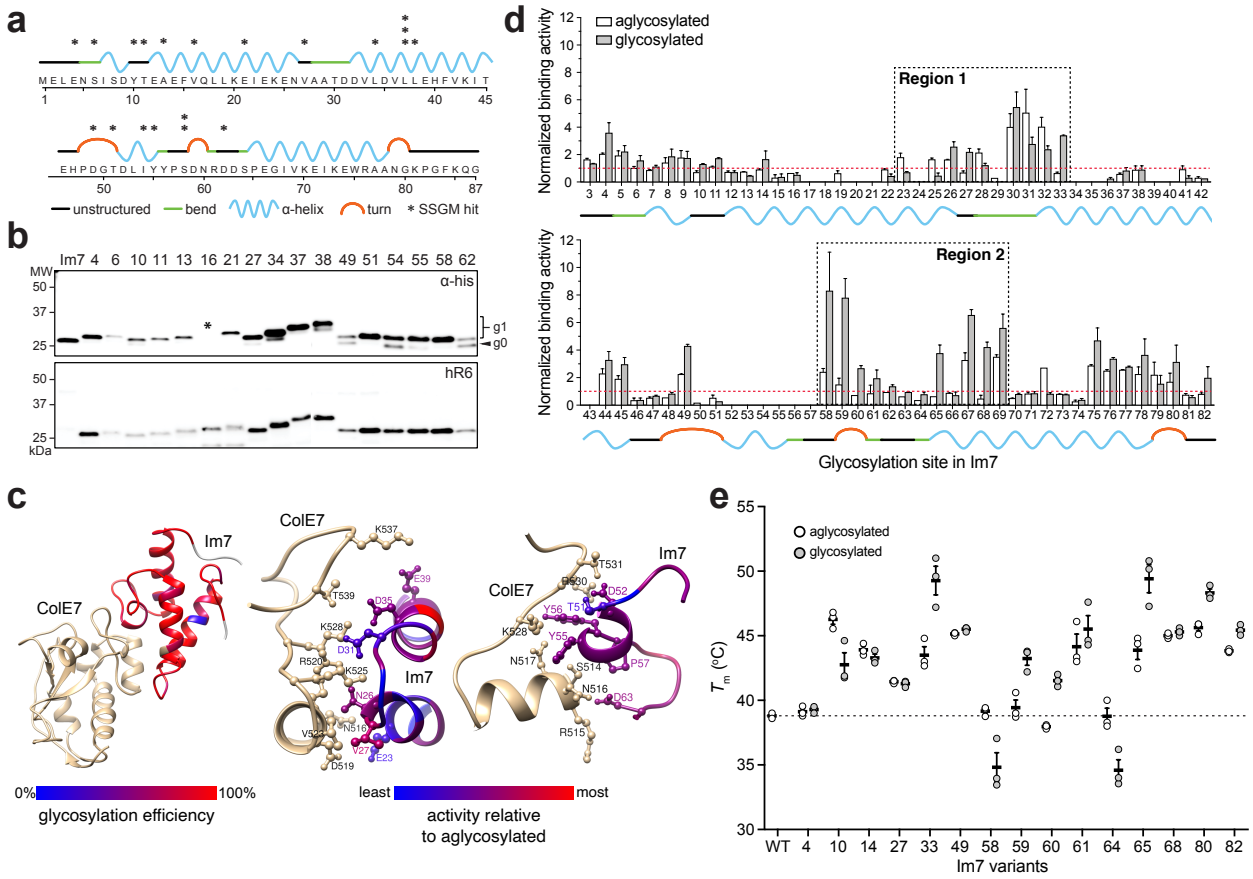

Figure 3. Exhaustive *N*-glycosylation of bacterial Im7 and its consequences. (a) Primary sequence and predicted secondary structure for *E. coli* Im7 immunity protein. Asterisks denote location and frequency of glycosite hits isolated using SSGM. Predicted structures adapted from PDB ID 1AYI. (b) Immunoblot analysis of supernatant fractions from CLM24 cells carrying plasmids encoding YebF-Im7 fusions with sequon mutations at indicated position and complete *N*-glycosylation machinery. Blots were probed with anti-polyhistidine antibody (α-His) to detect acceptor protein (top panel) and hR6 serum against *C. jejuni* glycan (bottom panel). Markers for aglycosylated (g0) and singly glycosylated (g1) forms of acceptor proteins are indicated at right. Molecular weight (MW) markers are indicated at left. Asterisk indicates construct with mutation that introduced stop codon just before 6xHis tag, preventing α-His detection. Results are representative of at least three biological replicates. (c) Mapping of *in vivo* glycosylation efficiency onto three-dimensional structure of Im7 in complex with ColE7 (left). Heatmap analysis of the glycosylation efficiency was determined based on densitometric quantification of the percent glycosylated (defined as g1/[g0+g1] ratio) for each acceptor protein in the anti-His immunoblot. Detailed interactions between ColE7 and Im7, highlighting sidechains of Im7 in the regions of α1*-loop12-α2* (residues 19-39; middle) and loop23-α3*-loop34 (residues 46-63; right). Heatmap analysis of change in binding activity was determined by normalizing activity measured for glycosylated sequon variant by aglycosylated counterpart. (d) Binding activity of glycosylated (gray bars) and aglycosylated (white bars) YebF-Im7 variants recovered from supernatants was measured by ELISA with ColE7 as immobilized antigen. All data were normalized to binding activity measured for aglycosylated YebF-Im7 lacking a sequon (wt), such that values greater than 1 (denoted by dashed red line) indicate enhanced binding activity relative to wt Im7. Dashed boxes correspond to two regions (Region 1: residues 23-33; Region 2: residues 58-69) that interact extensively with ColE7 according to crystal structure (Ko *et al.*, 1999). Data are average of three biological replicates and error bars represent standard deviation of the mean. (e) DSF analysis of 15 most active YebF-Im7 variants with and without glycosylation. T_m calculated as midpoint of thermal transition between native and unfolded states. Dashed line indicates T_m for wt YebF-Im7 (38.6 ± 1.0°C). Black bars are average of three independent replicates with error bars reported as standard error of the mean.

pairs to introduce DQNAT sequons at every position of the protein. A strikingly large number (79 out of 80) of these variants were found to be glycosylated when expressed in the presence of the complete *N*-glycosylation machinery, many with an efficiency that was at or near 100% as estimated from densitometry of the anti-His blot (**Fig. 3c** and **Supplementary Fig. 1a**). Because glycosylation by *Cj*PglB can occur both before and after protein folding is completed (**Supplementary Fig. 1b**) [25, 41], the secondary and tertiary structure around a glycosylation site is likely to have a direct effect on the extent to which a given site is occupied, if at all. Indeed, it has been observed that sequons located in structurally defined regions of folded acceptor proteins are poorly glycosylated and that partial unfolding is required to increase glycosylation efficiency at these sites [41, 42]. To determine if the structural context for any of the Im7 sequon variants was a determinant for the timing and efficiency of glycosylation, we performed *in vitro* glycosylation reactions in which already folded but yet-to-be glycosylated YebF-Im7 proteins derived from culture supernatants were incubated with purified *Cj*PglB and glycan donor. Remarkably, there was near perfect agreement between the *in vitro* and *in vivo* glycosylation results, with nearly all of the purified Im7 variants undergoing highly efficient glycosylation that was at or near 100% with few exceptions (**Supplementary Fig. 1c**). The observation that so many Im7 variants were efficiently glycosylated by the *Cj*PglB enzyme *in vitro* (*i.e.*, after folding had been completed) indicates that each sequon was located in either a structurally compliant position (*e.g.*, flexible and surface-exposed loops) within the folded protein or in a region of the protein that became partially unfolded during the *in vitro* glycosylation reaction. While broad accessibility is certainly plausible given the small size and simple topology of Im7, we cannot rule out the contribution of conformational destabilizing effects caused by replacement of five-residue stretches of native amino acids in the protein. Regardless of the exact reason, these results indicate that Im7 was extremely tolerant to the installation of *N*-glycans over its entire structure both *in vivo* and *in vitro*.

Structural and functional characterization of Im7 glycovariants. To systematically determine the effect of glycan attachment on acceptor protein properties, we first quantified binding activity of all 80 Im7 sequon variants with and without glycosylation by subjecting each to multiwell enzyme-linked immunosorbent assay (ELISA) using

purified ColE7 as immobilized antigen. Native Im7 interacts with colicin E7 (ColE7), a 60-kDa bacterial toxin that is cytotoxic in the absence of the cognate Im7 inhibitor [43]. With an eye towards multiplexibility, we chose to assay YebF-Im7 fusions directly because: (i) it obviated the need for molecular reformatting of the expression constructs; (ii) the fusions could be isolated as relatively pure species from cell-free supernatants, bypassing the need for extensive purification; and (iii) the introduction of the small YebF domain had no measurable effect on ColE7-binding activity (**Supplementary Fig. 2a**). Whereas nearly two thirds of the YebF-Im7 fusions were either unaffected by glycosylation or rendered inactive by introduction of the DQNAT motif alone, particularly in a contiguous stretch between residues 50-57 of Im7, the remaining one third exhibited significantly altered binding activity that was attributable to the presence of the *N*-glycan (**Fig. 3d**). These glycosylation-induced effects were clearly dependent on the precise location of the modification. Indeed, some of the most striking increases in binding activity for glycosylated variants over their aglycosylated counterparts were observed to occur at the transition between different types of secondary structure (*e.g.*, variants $Im7^{N33}$, $Im7^{N58}$ and $Im7^{N65}$). These results were particularly noteworthy in light of the elevated probability of finding naturally occurring sequons in locations where secondary structure changes [40].

Among the Im7 glycovariants whose activity was most significantly affected both positively and negatively by *N*-glycosylation, the majority were located in two distinct regions covering residues 23–33 and 58–69 (**Fig. 3d**). These regions coincided closely with the two arms of Im7 (one located in α1*–loop12–α2* from residue 19 to 39 and the other in loop23–α3*–loop34 from residue 46 to 63) that interact extensively with a continuous region in ColE7 in the crystal structure (**Fig. 3c**) [35]. The two interfaces are charge-complementary, and charge interactions are largely responsible for the tight and specific binding between the two proteins; hence, it was not surprising that binding activity was sensitive to *N*-glycan attachment in the vicinity of these interfaces. It should be pointed out that the presence of an *N*-glycan in these regions was uniquely modulatory, as substitution of DQNAT alone in these same locations generally had little effect on activity, as evidenced by the comparable ColE7 binding measured for aglycosylated Im7 variants versus wt Im7 (**Supplementary Fig. 2b**).

To determine whether any of the glycosylation-induced increases in binding activity were related to stabilization of the native fold, the most active Im7 glycovariants were subjected to differential scanning fluorimetry (DSF) with SYPRO Orange dye in a real-time PCR instrument [44]. Previous studies showed that melting temperature (T_m) values obtained by DSF correlated well with those determined by circular dichroism (CD) thermal denaturation [45]. Here too, we observed excellent agreement between these two methods, which both yielded T_m values for wt Im7 (~39 ^oC, **Supplementary Fig. 2c and d**) that agreed with a previously reported value [43]. Importantly, the presence of the small YebF domain did not significantly alter the T_m value for Im7 (**Supplementary Fig. 2d**), consistent with its lack of effect on ColE7-binding activity. We also confirmed that DSF results obtained using YebF-Im7 derived directly from cell-free supernatants were indistinguishable from those obtained with more extensively purified YebF-Im7 (**Supplementary Fig. 2d**). Using DSF, the average T_m values for glycosylated and aglycosylated versions of each Im7 variant were measured, and the change in unfolding temperature, ΔT_m, was calculated such that a positive ΔT_m signified an increase in structural order and a reduced conformational flexibility due to appending a glycan. Several of the variants exhibited positive ΔT_m values, with the largest increases corresponding to glycan installation at N33, N59, N60, N65 and N80 (**Fig. 3e**). Conversely, glycans at N10, N58, and N64 caused the largest decreases in T_m, indicative of glycan-induced protein structural changes that destabilized the protein.

To test whether protein-structure analyses could explain the observed effects of sequon insertion and glycosylation, we calculated simple geometric measures (secondary structure, burial, distance to the binding site) and Rosetta energy estimates (stability and interface score) (**Supplementary Figs. 3** and **4**; **Supplementary Results**). Surprisingly, none of these factors correlated with either stability or activity of the aglycosylated or glycosylated Im7 constructs. Only the attractive van der Waals energy had a weak correlation with stability (**Supplementary Fig. 5**), possibly because of Im7's marginal stability and the known flexibility of helix IV [46]. Additionally, we generated ensembles of glycan conformations for several glycovariants in the context of Im7 bound to E7 (**Supplementary Fig. 6**). In general, these results revealed that (i) the glycan and the bound protein must interact to change the binding activity positively or negatively and

(ii) enhanced binding appears to be mediated by multiple low-energy glycan conformations making favorable interactions with E7.

Extension of SSGM to a protein with more complex topology. We next turned our attention to bovine RNase A. Like Im7, RNase A has been intensely studied from a structure–function standpoint and has been pivotal to understanding many aspects of enzymology, biological chemistry, and protein folding and stability [47]. We chose RNase A because (i) it is a relatively small, basic protein, containing 124 residues but with a more complex topology than Im7, with all major types of secondary structure, namely α-helices, β-sheets, and turns, represented; (ii) the natively glycosylated form of RNase A, namely RNase B, contains a single *N*-linked oligosaccharide at N34, and crystal structures of both are available [48, 49]; (iii) glycosylation at N34 has no apparent effect on the secondary or tertiary structure [48, 50] and does not alter the folding kinetics or thermal stability [51]; and (iv) RNase A modified with an optimal bacterial sequon at the native N34 glycosylation site (RNase $A^{32\text{-}DQNAT}$) can undergo *Cj*PglB-dependent glycosylation *in vivo* and *in vitro* [25, 41]. For these reasons, RNase A represented an ideal target for SSGM.

Extracellular secretion of glycosylated YebF-RNase $A^{32\text{-}DQNAT}$ was observed in colony blots and immunoblots (**Fig. 1c**), confirming the compatibility of RNase A with glycoSNAP screening. An SSGM library was created by subjecting YebF-RNase A plasmid DNA to the multiplex inverse PCR method, after which glycoSNAP screening was performed using CLM24 cells carrying plasmids encoding the library and the *C. jejuni* glycosylation machinery. A total of ~100 glycosylation-positive colonies were randomly selected from two membranes and subjected to sequencing analysis. Of the 97 sequence-confirmed hits, only 50 were unique, as many of the sequences were isolated multiple times (*e.g.*, seven times each for RNase A^{N41} and RNase A^{N122}; **Fig. 4a**). The sequons of these hits were uniformly distributed throughout the primary sequence and found in every type of secondary structural element, akin to the results with Im7. Immunoblot analysis confirmed that all selected clones were glycosylated, and the efficiency for most was at or near 100% as estimated by densitometry analysis of the anti-His blots (**Fig. 4b** and **Supplementary Fig. 7**). To investigate whether the structural context of the sequon impacted the possible timing of PglB-mediated glycan installation, we performed *in vitro* glycosylation of folded RNase A variants. While some of the variants

were glycosylated as efficiently *in vitro* as they were *in vivo* (*e.g.*, RNase A^{N46} and RNase A^{N64}), an unexpectedly large number of variants showed significantly lower levels of glycosylation under *in vitro* conditions (**Fig. 4b** and **Supplementary Fig. 7**). Most notably among these were variants N34, N35, N36, N43, N51, N61, N69, N72, N80, N89, and

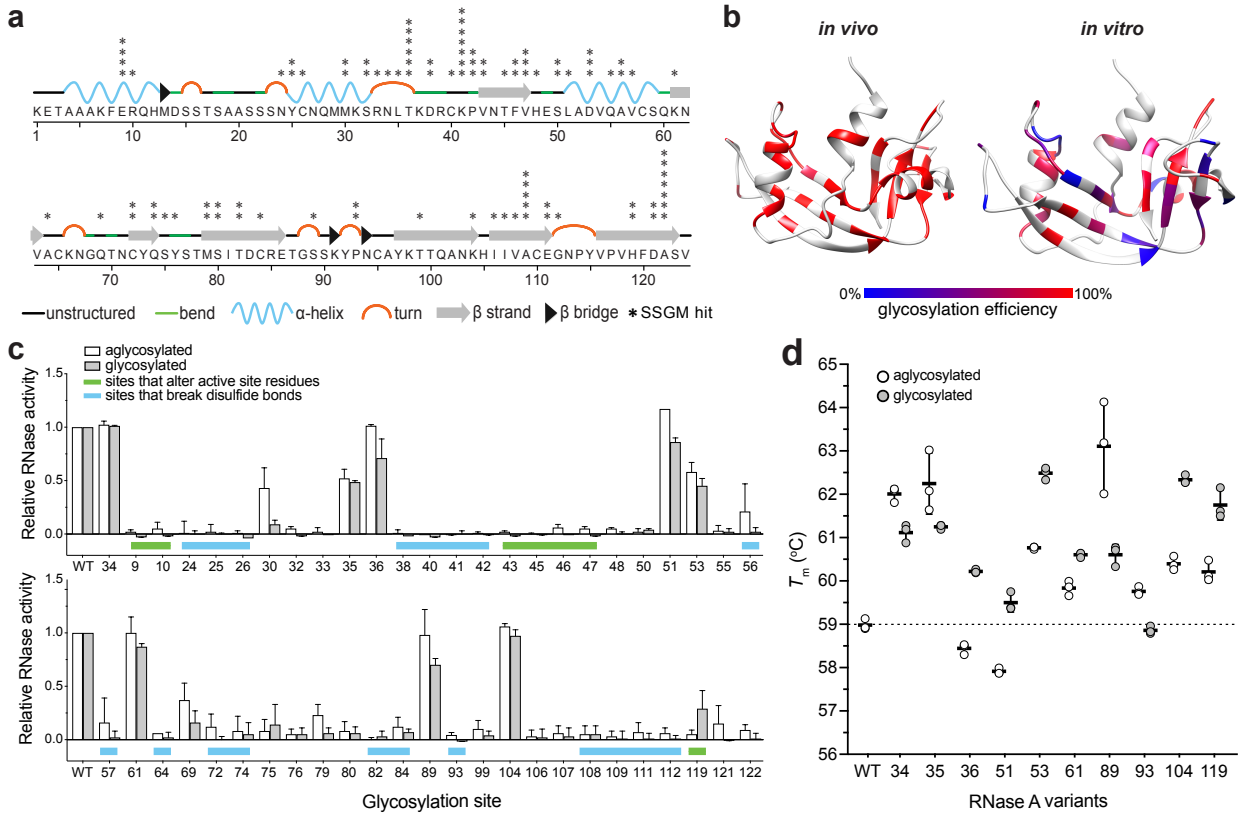

Figure 4. Glycomutagenesis of bovine pancreatic RNase A. (a) Primary sequence and predicted secondary structure for bovine pancreatic RNase A. Asterisks denote location and frequency of glycosite hits isolated using SSGM. Predicted structures adapted from PDB ID 1RBX. (b) Mapping of *in vivo* (left) and *in vitro* (right) glycosylation efficiency onto three-dimensional structure of RNase A. Heatmap analysis of glycosylation efficiency was determined based on densitometric quantification of percent glycosylated (defined as g1/[g0+g1] ratio) for each acceptor protein in anti-His immunoblot. (c) Enzymatic activity of glycosylated (gray bars) and aglycosylated (white bars) RNase A variants recovered from culture supernatants. All data were normalized to binding activity measured for aglycosylated YebF-RNase A lacking a sequon (wt). Data are average of three biological replicates and error bars represent standard deviation of the mean. (d) DSF analysis of YebF-RNase A variants with and without glycosylation. T_m was calculated as midpoint of thermal transition between native and unfolded states. Dashed line indicates T_m for wt YebF-RNase A (59.0 ± 0.1°C). Black bars are average of three independent replicates with error bars reported as standard error of the mean.

N104, which were all efficiently glycosylated *in vivo* but underwent little or no detectable glycosylation *in vitro*. These sequons occur at locations that were likely to be accessible to the OST during translation/translocation when the proteins are unfolded but became inaccessible after the protein completed folding. Indeed, the native *N*-glycosylation site at

N34 is located in a structured domain, suggesting that the poor *in vitro* glycosylation at this specific location (and perhaps also at the nearby N36 and N43 sites) was due to sequon inaccessibility in the folded state. Such folding-dependent recognition of this site has been observed previously [25, 41] and, together with the results presented here, supports a model whereby *in vivo* glycosylation of these particular sequons involves glycan installation prior to folding, either co- or post-translocationally (**Supplementary Fig. 1b**).

To determine the consequences of glycosylation at the 50 unique sites, the ability of glycosylated and aglycosylated versions of each sequon variant to catalyze the hydrolysis of the phosphodiester bonds in RNA was evaluated. While the addition of YebF had little to no effect on RNase activity (**Supplementary Fig. 8a**), more than half of the RNase A variants were inactivated by insertion of the DQNAT sequon (**Fig. 4c**). To determine if this might be due to the insertion of five residues in the target protein, a requirement for optimal recognition by *Cj*PglB [53], we mutated RNase A more conservatively. Specifically, we generated minimal sequons (D-X-N-X-T/S or X-X-N-X-T/S, where X represents the native amino acid), which in most cases required only 1 or 2 amino acid changes. Each of these mutants was completely inactive except for RNase $A^{53\text{-}DVNAT}$, which showed some activity but was still significantly less active than the wt enzyme (**Supplementary Fig. 8b**). Hence, even relatively minor sequence perturbations at these positions, in addition to the less subtle substitution with DQNAT, were all capable of inactivating RNase A. More careful inspection revealed that the majority of variants with little to no activity corresponded to the insertion of sequons in locations that would be predicted to disrupt catalytically important residues or disulfide bonds (**Fig. 4c** and **Supplementary Results**).

Among the variants that retained function, only eight (sequons at N34, N35, N36, N51, N53, N61, N89, and N104) showed activity that was on par (>50%) with wt RNase A but none were more active than their aglycosylated counterpart (**Fig. 4c**). In the case of RNase A^{N119}, introduction of the DQNAT sequence completely abrogated catalytic activity, consistent with previous findings that the relative activity of an H119N mutant was reduced to less than 1% of wt RNase A, with k_{cat}/K_M values reduced by 100- to 1000-fold depending on the substrate used [54]. Despite the importance of this residue for catalysis,

glycosylation at this position partially restored enzymatic activity, indicating an *N*-glycan-dependent gain-of-function. It is also worth mentioning that the activity of glycosylated RNase A^{N34} was nearly identical to that of aglycosylated RNase A^{N34} and wt RNase A, indicating that the bacterial *N*-glycan was functionally tolerated at the native N34 glycosylation site. Given that attachment of oligomannose glycans at N34 reduced activity by more than threefold [50], it appears that distinct glycan structures (*i.e.,* $Man_{5–9}GlcNAc_2$ versus $GalNAc_5$(Glc)Bac) attached to the same site in RNase A have profoundly different effects.

To determine whether glycosylation impacted stability, we again used DSF to analyze the most active RNase A glycovariants along with RNase A^{N93}, which was randomly chosen as a representative inactive variant. The measured T_m values for wt YebF-RNase A and its unfused counterpart were both ~59 °C (**Supplementary Fig. 8c**), in close agreement with previous reports [51, 55], while the T_m values for all the YebF-RNase A variants spanned a range from 58–63 °C (**Fig. 4d**). Most exhibited positive ΔT_m values compared to their aglycosylated counterpart, including the RNase A^{N119} variant, suggesting that the restoration of activity caused by glycan attachment at N119 also served to stabilize the protein. In contrast, RNase A^{N89} and RNase A^{N93} exhibited large negative ΔT_m values that coincided with slightly weakened activity due to glycan attachment in the case of N89 and complete inactivation in the case of N93.

Next, we measured geometries and calculated Rosetta metrics to determine the effect of sequon insertion and glycosylation on RNase A activity. For the activity of aglycosylated RNase A variants in the context of all seven metrics, the only correlated metric was the total Rosetta energy score (R^2 = 0.32; **Supplementary Fig. 3f**). To dissect the primary factors, we calculated the correlation between activity and decomposed Rosetta score terms. Unlike Im7, attractive van der Waals energy was not important, whereas repulsive interactions and Dunbrack rotamer terms (side-chain strains) showed modest correlations (**Supplementary Fig. 5c** and **d**). These terms suggest that steric clashes arising from the sequon insertion reduces stability and activity. None of our metrics captured the effects of *N*-glycosylation on the RNase A variants, possibly because the presence of *N*-glycans affected enzymatic activity much less than the sequon insertion itself.

Investigation of IgG variable domain glycosylation using glycomutagenesis. We next investigated antibody variable domain glycosylation, a phenomenon that is observed for ~15–25% of serum IgGs and leads to glycan installation within the variable domains of Fab arms [56]. Although Fab glycosylation has been long known, the rules governing the selection of Fab domain *N*-glycosylation sites that emerge during somatic hypermutation and the functional consequences of the attached glycans remain poorly understood. To systematically investigate this phenomenon using SSGM, the two variable domains, V_H and V_L, from the human anti-HER2 monoclonal antibody [57] were joined by a flexible linker to form scFv-HER2 that was subsequently modified at its N-terminus with YebF and at its C-terminus with a DQNAT motif. Extracellular secretion of glycosylated YebF-scFv-HER2^{DQNAT} was observed in colony blots and immunoblots (**Fig. 5a**), confirming the compatibility of scFv-HER2 with glycoSNAP screening. Because earlier studies revealed that variable domain glycosylation is subject to selection mechanisms that depend on the nature of the antigen [58], we modified the SSGM strategy to enable dual screening of glycosylation and antigen-binding activity by labeling colonies with SBA lectin and the extracellular domain (residues 1-652) of human HER2 (HER2-ED), which was avidly bound by scFv-HER2^{DQNAT} fused to YebF (**Supplementary Fig. 9a**). In this way, two-color screening could be used to identify colonies that were positive both for glycosylation and for antigen binding, as demonstrated with the YebF-scFv-HER2^{DQNAT} construct (**Fig. 5a**). Next, we constructed and screened an SSGM library, after which two-color glycoSNAP screening was performed with CLM24 cells carrying plasmids encoding the library and the *C. jejuni* glycosylation machinery. A total of ~60 dual-positive hits were isolated from membranes, of which 21 were determined to be non-redundant (*e.g.*, N58 in V_L and N42 in V_H were each isolated 12 times) (**Fig. 5b**) and subsequently confirmed for glycosylation by immunoblot analysis (**Supplementary Fig. 9b**). The sequons of these hits were sparsely distributed throughout the primary sequence, with a large proportion clustering just after the second and third complementarity-determining regions (CDRs) of the V_L domain and also in the flexible linker, suggesting a strong selection bias for specific sites that both tolerated glycosylation and retained function. Interestingly, a few of the identified sequons occurred in CDR2 of the V_L domain and CDR1 and CDR2 of the V_H domain, consistent with naturally occurring IgG repertoires in which *N*-glycosylation sites

were located preferentially in the CDRs [58]. With respect to function, all glycovariants exhibited HER2-ED binding activity above background (**Fig. 5c**), which was expected given that the screening process was adapted to include antigen binding. Importantly, seven of these glycovariants (N58, N64, and N109 in V_L; N3, N4, N9, N10 in linker; N42 and N113 in V_H) exhibited increased binding compared to their aglycosylated counterpart,

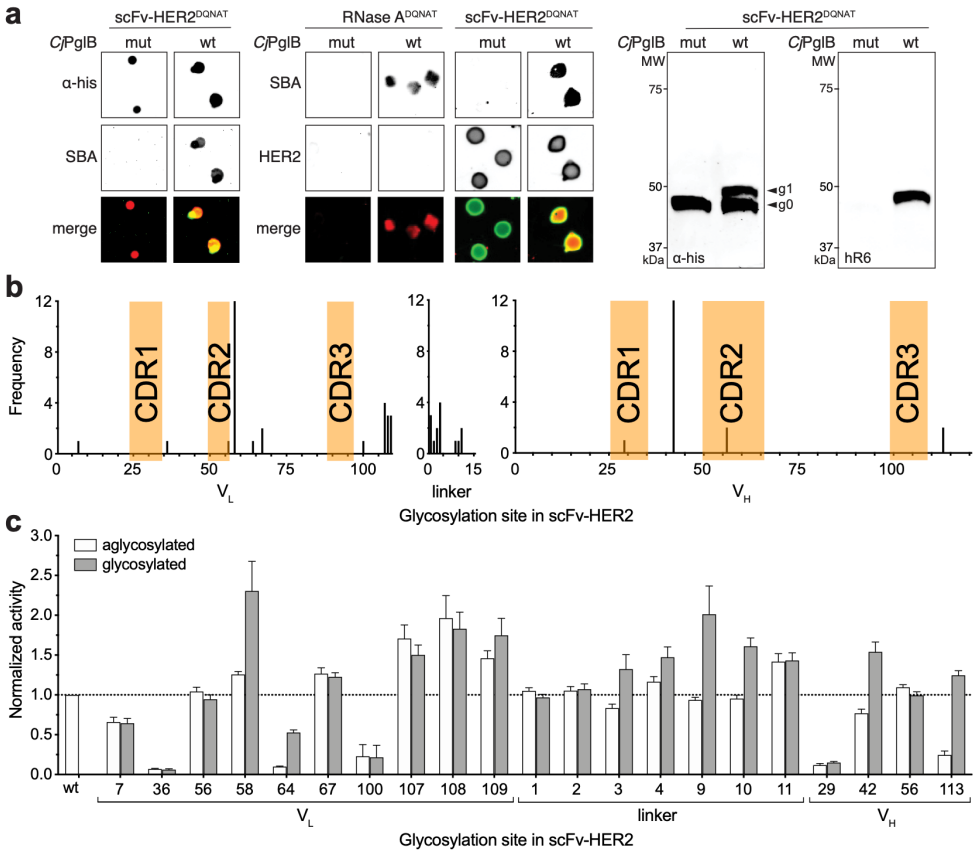

Figure 5. Probing scFv antibody glycosylation using glycomutagenesis. (a) Immunoblot analysis of acceptor proteins in colony secretions (left and middle) and periplasmic fractions (right) derived from *E. coli* CLM24 carrying plasmids encoding scFv-HER2^{DQNAT} and complete *N*-glycosylation machinery with either wild-type *Cj*PglB (wt) or an inactive mutant (mut). Blots were probed with anti-polyhistidine antibody (α-His) to detect acceptor protein, SBA or hR6 serum to detect *C. jejuni* heptasaccharide glycan, and HER2-ED to detect antibody binding. Bottom color panels depict overlay of α-His and SBA blots or SBA and HER2 blots (merge). Arrows denote aglycosylated (g0) and singly glycosylated (g1) forms of scFv-HER2^{DQNAT}. Molecular weight (MW) markers are indicated at left. Results are representative of at least three biological replicates. (b) Frequency and position of *N*-glycosylation sites in scFv-HER2^{DQNAT} glycovariants isolated using SSGM. (c) Binding activity of glycosylated (gray bars) and aglycosylated (white bars) scFv-HER2^{DQNAT} variants as measured by ELISA with HER2-ED as immobilized antigen. All data were normalized to binding activity measured for aglycosylated scFv-HER2 lacking a sequon (wt), such that values greater than 1 (denoted by dashed line) indicate enhanced binding activity relative to wt scFv-HER2. Data are average of three biological replicates and error bars represent standard deviation of the mean.

and most of these were also more active than the parental scFv-HER2. Overall, these results clearly establish that antibody variable domain glycosylation contributes directly

to binding of antigen in a manner that depends on the precise location of the glycan, consistent with several previous studies showing increased antigen-binding activity that was attributable to the presence of *N*-linked glycans in the variable domains [59-63].

Next, we compared the experimental binding activity for scFv-HER2 with multiple geometric and Rosetta metrics. Unlike Im7 or RNase A, scFv-HER2 activity correlated with three of our metrics. First, sequon burial reduces the binding affinity of scFv-HER2 for its antigen both in the aglycosylated (R^2 = 0.21) and glycosylated states (R^2 = 0.43) (**Fig. 6a** and **Supplementary Fig. 4b**). Similarly, the closer the sequon was to the paratope, the greater the likelihood of reduced activity (R^2 = 0.20 and 0.23 for the aglycosylated and glycosylated variants, respectively; **Fig. 6b** and **Supplementary Fig. 4c**). It is also noteworthy that the Rosetta score for the antibody–antigen complex correlated with experimental binding activity (R^2 = 0.27; **Fig. 6c**). We decomposed the Rosetta score (**Supplementary Fig. 5**) and identified the repulsive van der Waals energy and Dunbrack scoring terms as explainable factors, as was seen for RNase A.

We selected three variants for deeper analysis: two variants that had low binding activity and a poor Rosetta score (N36 V_L, N113 V_H: black circles in **Fig. 6c**) and one variant with high activity and a favorable Rosetta score (N108 V_L: red circle in **Fig. 6c**). Both N36 V_L and N113 V_H sites are situated on β-strands in compact regions of the anti-HER2 antibody on the side opposite the antigen-binding site (**Fig. 6d**, green sticks). The reduced stability arises from the steric clash of inserting a sequon inside (or near) a close-packed region of the protein (Rosetta terms for steric clashes and side-chain energies (rep+Dun) of 84.48 and 210.23 Rosetta Energy Units (REU) for the N36 V_L and N113 V_H, respectively). On the other hand, site N108 V_L is located at the C-terminal end of V_H (**Fig. 6d**, blue sticks). Sequon insertion had a small effect on the Dunbrack score (1.93 REU) and a greater effect on the van der Waals repulsion term (−47.56 REU), indicating that there is ample room to accommodate the new side chains, A similar outcome was reported following insertion mutation of a human monoclonal antibody [64]. To understand how *N*-glycosylation was able to improve binding activity, we selected mutant N58 V_L because the aglycosylated variant is 0.26 times more active than the wt scFv-HER2 and glycan addition improves the binding an additional 1.05-fold. Residue N58 V_L resides in the turn between strands 1 and 2 (**Fig. 6d**, blue stick). From Rosetta-generated potential

glycosylated structures, the low-energy states showed interfacial contact with surface residues of HER2 (**Fig. 6e**), which could underlie the binding activity improvement.

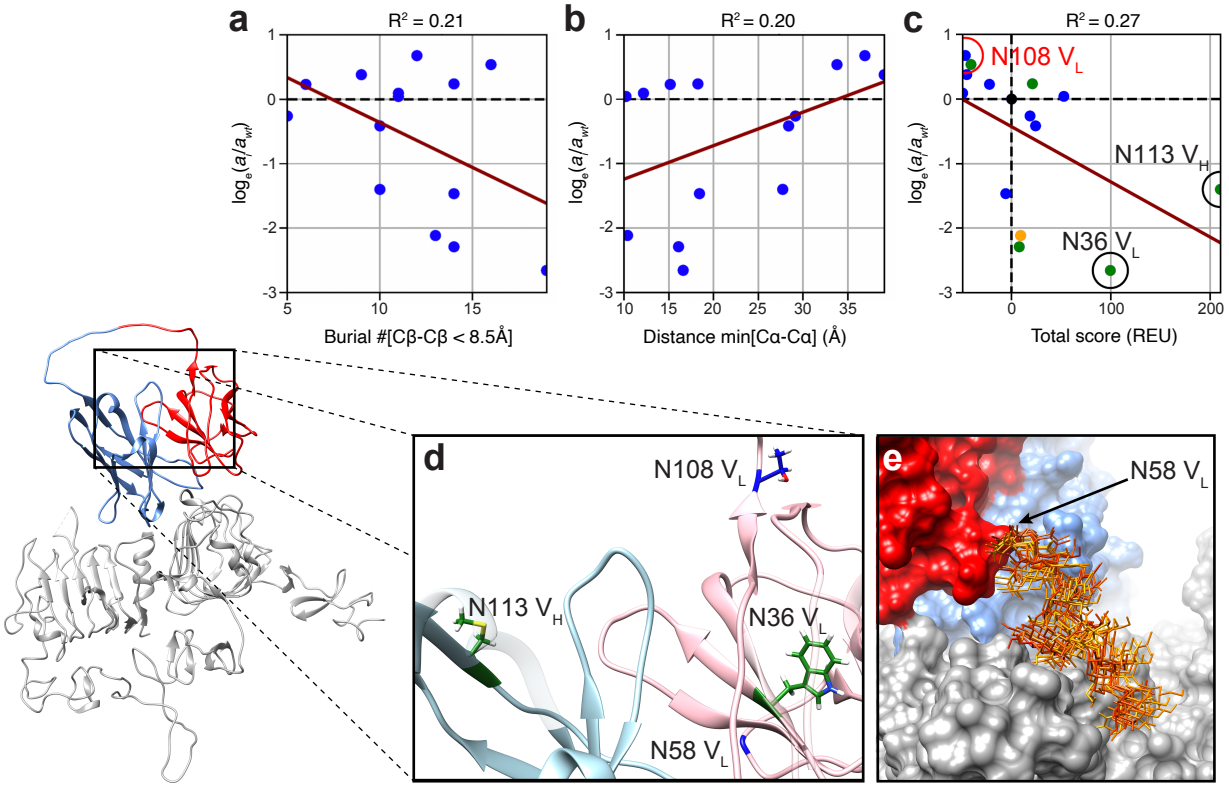

Figure 6: Quantitative analysis of scFv-HER2 variants. The structure of scFv-HER2 V_L (red) and V_H (blue) domains in complex with HER2 protein (gray) is shown at bottom left. Regression analyses of log activity ratio (aglycosylated / wild-type) versus (a) burial of sequon insertion site, (b) distance of closest HER2 residue from the sequon insertion site, and (c) total Rosetta score. In all three panels, the dark red lines are the respective regression lines. Colors of dots in (c) show the respective secondary structure of the sequon insertion site. Orange, green, and blue correspond to α-helix, β-strand, and loop regions, respectively. N108 V_L (red circle) and N36 V_L, N113 V_H (black circles) were selected for analyzing the effect of sequon insertion site on aglycosylated binding activity. (d) Wild-type representation of sites used for analysis of sequon insertion (36 V_L, 108 V_L, and 113 V_H) and glycosylation (58 V_L). Side-chain colors reflect their respective secondary structures. (e) Glycan arrangement (orange sticks) from eight low energy conformations of glycosylated N58 V_L variant of scFv-HER2, revealing possible glycan-HER2 interaction responsible for binding activity improvement.

Discussion

In this study, we developed a new protein engineering method called SSGM that enables comprehensive mapping of the structural and functional consequences of site-specific glycan installation for virtually any protein of interest. By combining synthetic glycosite libraries with a high-throughput screen for protein glycosylation [27], we showed that a single SSGM experiment allowed the effects of many different site-directed glycan

"mutations" to be probed for their contribution to the properties of a protein. In this way, SSGM is conceptually analogous to combinatorial alanine-scanning mutagenesis, which allows systematic determination of the importance of individual amino acids to protein structure and function [21-24]. Here, we demonstrated the utility and generality of the SSGM technique using three different acceptor proteins namely bacterial Im7, bovine RNase A, and human scFv-HER2. Consistent with the known modulatory effects of *N*-glycans [4, 5], many glycovariants of these proteins exhibited detectably altered stability and activity that resulted from covalent attachment of *N*-glycans at precise locations in the protein backbone. We show that high-resolution mapping of these effects is possible by systematic "sequon walking" experiments whereby a glycosylation site is introduced at every possible position of a protein, as we performed for Im7. In the future, we imagine that sequon walking on a large, even proteome-wide, scale could provide access to datasets that might eventually allow the effects of glycosylation to be generalized and predicted. Moreover, the fact that *N*-glycan attachment was able to significantly increase the binding activity of several Im7 and scFv-HER2 variants suggests that glycomutagenesis may become a useful tool for custom engineering of proteins with advantageous biophysical and biological properties.

A unique aspect of the SSGM method is the ability to generate combinatorial glycosite libraries and comprehensively assess which positions in a protein can tolerate glycan installation. The three proteins studied here were found to be efficiently *N*-glycosylated at an unexpectedly large number of positions and in all types of secondary structure although loops tended to be more receptive to glycosylation, consistent with the observation that naturally occurring *N*-glycans also exist on all forms of secondary structure [40]. Closer inspection of the data revealed some additional trends. For instance, installing *N*-glycans in the center of α-helices negatively affected activity (*e.g.*, positions 19, 42, 72 in Im7) whereas installing them at the transition between different types of secondary structure and at turns between motifs promoted enhanced activity and, in some cases, stability (*e.g.*, positions 33, 49, 58, 59, 60, 61, 65, 67, 68, 69, 78, 80 in Im7). These findings were in close agreement with the folding and stability effects contributed by chitobiose disaccharide attachment to discrete locations in Im7 [20] and also provide clues for why natural *N*-glycosylation sites occur with elevated frequency in turns and

bends and especially at points of change in secondary structure and with low frequency within ordered helices [40]. The studies performed here also provided insight on the possible timing and impact of glycosylation with respect to the folding process. For instance, Im7 tolerated a glycan at almost every position, even when the target asparagine side chain pointed inward and was considered buried (*e.g.*, positions N7, N68, and N76). Because these buried positions physically cannot be glycosylated by PglB when the target protein is in the folded state, they must either be glycosylated co-translationally or during a fluctuation to a partially unfolded state that provides access to that site. Then, after glycosylation, because Im7 presumably cannot fold back into the native structure, it must undergo some sort of backbone rearrangement to accommodate the newly added glycan, which would be feasible in light of the fact that Im7 is very flexible [46]. In the case of RNase A, several sites were identified (*e.g.*, N34, N36) that could be efficiently glycosylated *in vivo* but underwent little to no glycosylation *in vitro* (in the already folded state), providing clear evidence for glycan installation prior to folding and in a manner that may resemble the co-translocational process in mammalian cells [52]. The overall less efficient glycosylation seen for many RNase A variants is also consistent with the protein adopting a more stable folded structure compared to Im7 and providing less accessibility to buried sites.

Using the results of the SSGM studies, we also investigated explanatory factors that could be used to predict *a priori* the functional effect of glycosylation from the sequence. Here, we tested five simple structural metrics (secondary structure, distance to the active site, burial of the glycosylation site in the native fold, and change in buried surface area upon binding) and the change in energy of the protein alone and in complex with its substrate upon addition of the glycan (estimated with Rosetta). Whereas RNase A activity was more sensitive to sequon insertion than glycosylation, the effects of glycosylation on the function of Im7 and scFv-HER2 were quite interesting. Collectively, our results indicated that interactions between the glycan and the bound protein must occur for the binding activity to be altered (positively or negatively) and that enhanced binding likely arises from multiple low-energy glycan conformations making favorable interactions with the binding partner. In the case of scFv-HER2, mutant N58 V_L exhibited significantly higher binding activity compared to wt scFv-HER2. While part of the increase

was from the sequon substitution alone, perhaps from the additional contacts of the long Q57 side chain or from a stabilizing effect of the sequon on the CDR L2 loop (residues 51-57 in V_L), most of the effect was from the *N*-glycan itself. At residue N58 V_L, the heptameric glycan creates new contacts between scFv-HER2 and HER2-ED and buries more surface area upon binding. Glycans attached near (but not within) the binding site have previously been reported to increase antigen-binding affinity [65]. In fact, the Im7 variant that underwent the largest increase in binding activity upon glycosylation (at residue N58 in Im7) also acquired new contacts with its binding partner, E7, through the glycan, which strengthened binding activity by 3.5-fold. Thus, it is an intriguing possibility that binding affinity of a protein might be purposefully increased by rational introduction of *N*-glycans at predetermined locations, with SSGM serving as the discovery engine for precisely pinpointing the sites within a protein that lead to glycan-mediated affinity enhancement.

Materials and Methods

Strains and culture conditions. *E. coli* strain DH5α was used for all molecular biology, including plasmid construction, site-directed mutagenesis, and SSGM library construction. BL21(DE3) was used to purify ColE7 that was used to measure Im7 binding activity in ELISA format. All glycosylation studies were performed using *E. coli* strain CLM24 [66], which were initially grown at 37 °C in Luria–Bertani (LB) medium containing appropriate antibiotics at the following concentrations: 20 μg/mL chloramphenicol (Cm), 100 μg/mL trimethoprim (Tmp), and 50 μg/mL spectinomycin (Spec). When cells reached mid-log phase, protein expression was induced by adding 0.1 mM isopropyl-β-D-thiogalactoside (IPTG) and 0.2% (v/v) L-arabinose, after which cells were grown at 30 °C for 16–20 h.

Plasmid construction. For expression of glycosylation machinery, plasmid pMW07-pglΔB encoding the *C. jejuni* heptasaccharide glycan [27] and plasmid pMAF10 encoding *Cj*PglB [66] were used. A derivative of pMAF10 that encoded a catalytically inactive version of *Cj*PglB carrying two active-site mutations (D54N and E316Q) [27] was used as a negative control. The plasmids pTrc99S-YebF-Im7 and pTrc99S-YebF-Im7-DQNAT were constructed by inserting cloning cassettes YebF^{N24L}-XbaI-Im7-SalI-FLAG-6xHis and

YebF^{N24L}-XbaI-Im7-BamHI-DQNAT-SalI-FLAG-6xHis, respectively, into the SacI and HindIII sites of pTrc99S [67]. The genes encoding RNase A and scFv-HER2 were cloned into the cassette between XbaI and SalI sites in pTrc99S-YebF-Im7 or XbaI and BamHI sites in pTrc99S-YebF-Im7-DQNAT. The pTrc-spDsbA-POI plasmids (where POI corresponds to each of the proteins of interest, namely Im7, RNase A, and scFv-HER2) were cloned by one-step PCR integration of primers encoding the *E. coli* DsbA signal peptide (spDsbA) into each pTrc99S-YebF-POI plasmid as templates followed by Gibson assembly. PCR products were subjected to DpnI digestion to remove parental plasmid. The resulting PCR products were self-assembled by Gibson assembly and transformed into *E. coli* cells to obtain the desired plasmids. pET281-ColE7 (H569A) was constructed by inserting the DNA sequence of ColE7 H569A variant [68] bearing a C-terminal 6×His tag, which was synthesized by Integrated DNA Technologies, into the NcoI and SalI sites of pET28a. All plasmids were confirmed by DNA sequencing at the Biotechnology Resource Center of the Cornell Institute of Biotechnology.

SSGM library construction. SSGM mutagenesis libraries were constructed by multiplex inverse PCR [39] followed by T4 ligation. Each of the pTrc99S-YebF-POI plasmids was used as template for PCR amplification using primer sets specifically designed such that the DNA sequence 5′-GAT CAG AAT GCG ACC-3′ was included in the 5′ end of every forward primer to enable substitution of the adjacent five amino acids with DQNAT. Prior to PCR, the forward primers were phosphorylated using T4 polynucleotide kinase (New England Biolabs) to facilitate T4 ligation later. PCR reactions were performed using Phusion polymerase (New England Biolabs), and the PCR products were gel-purified from the product mixtures with a ratio of 1:1 to get rid of non-specific PCR products. The resulting PCR products were self-assembled using T4 ligase (New England Biolabs) to obtain the desired SSGM plasmid libraries, which were subsequently used to transform highly competent DH5α cells and then isolated using a QIAprep Spin Miniprep Kit (Qiagen) according to manufacturer's instructions.

GlycoSNAP assay. Screening of SSGM libraries was performed using glycoSNAP as described previously [27]. Briefly, *E. coli* strain CLM24 carrying pMW07-pglΔB and pMAF10 was transformed with corresponding SSGM library plasmids, and the resulting transformants were grown on 150-mm LB-agar plates containing 20 μg/mL Cm, 100

μg/mL Tmp, and 50 μg/mL Spec overnight at 37 °C. The second day, nitrocellulose transfer membranes were cut to fit 150-mm plates and pre-wet with sterile phosphate-buffered saline (PBS) before placement onto LB-agar plates containing 20 μg/mL Cm, 100 μg/mL Tmp, 50 μg/mL Spec, 0.1 mM IPTG, and 0.2% (w/v) L-arabinose. Library transformants were replicated onto 142-mm cellulose nitrate membrane filters (Whatman, 0.45 μm), which were then placed colony-side-up on transfer membranes and incubated at 30 °C for 16 h. The nitrocellulose transfer membranes were washed in Tris-buffered saline (TBS) for 10 min, blocked in 5% bovine serum albumin for 30 min and probed for 1 h with fluorescein-labeled SBA (Vector Laboratories, catalog # FL-1011) and Alexa Fluor 647® (AF647)-conjugated anti-His antibody (R&D Systems, catalog # IC0501R) or HER2-ED (R&D Systems, catalog # 10126-ER) that was conjugated with Alexa Fluor 647™ (AF647) (Thermo Fisher Scientific, catalog # A37573) following the manufacturer's instructions. All positive hits were re-streaked onto fresh LB-agar plates containing 20 μg/mL Cm, 100 μg/mL Tmp, 50 μg/mL Spec, and grown overnight at 37 °C. Individual colonies were grown in liquid culture and subjected to DNA sequencing to confirm the location of glycosites and to protein glycosylation analysis as described below.

Protein isolation. For Western blot analysis and protein activity assays, cell-free culture supernatants were generated by subjecting 1.5 mL of cells that had been induced for 16 h to centrifugation at 13,4000 × g at 4 °C for 2 min. Periplasmic fractions were generated by subjecting 3 mL of 16-h-induced cultures to centrifugation at 13,400 × g for 2 min. The resulting pellets were resuspended in 300 μL of 0.4 M arginine and incubated at 4 °C for 1 h with gentle shaking. After centrifugation at 13,400 × g for 2 min, the supernatant containing periplasmic extracts was collected. For stability assays, YebF-Im7 and YebF-RNase A variants were purified from supernatant fractions and soluble lysate fractions, respectively. To prepare the latter, cells expressing YebF-RNase A variants were harvested by centrifugation at 6000 × g at 4 °C for 20 min and the pellets were resuspended in PBS buffer supplemented with 10-mM imidazole followed by cell lysis using a Emulsiflex-C5 Homogenizer (Avestin) at 16,000–18,000 psi. The resulting lysate was clarified by centrifugation at 15,000 × g for 30 min at 4 °C to collect the soluble fraction. All soluble fractions, or supernatant fractions supplemented with 10-mM imidazole, were then applied twice to a gravity flow column loaded with Ni-NTA resin at

room temperature and washed with PBS containing 20-mM imidazole until the concentration was lower than 0.1 mg/mL. Proteins were eluted in 2.5 mL of PBS with 250 mM imidazole. The eluted proteins were desalted using PD10 Desalting Columns (GE Healthcare) and stored at 4 °C.

To produce ColE7 for ELISA experiments, an overnight culture BL21(DE3) cells carrying plasmid pET28a-ColE7 (H569A) was used to inoculate 1 L of LB supplemented with 50 µg/mL kanamycin. Cells were grown at 37 °C until mid-log phase and then were induced with 0.1 mM IPTG for 16 h at 16 °C before being harvested. Following centrifugation at 10,000× g, pellets were resuspended in PBS buffer supplemented with 10-mM imidazole and lysed at 16,000–18,000 psi using an Emulsiflex-C5 homogenizer (Avestin). The lysate was clarified by centrifugation at 15,000 × g for 30 min at 4 °C and the collected soluble fraction was mixed with Ni-NTA resin for 2 h at 4 °C. The mixture was then applied to a gravity flow column and washed with 5 column volumes of PBS containing 20 mM imidazole. Proteins were eluted in 4 column volumes of PBS with 250-mM imidazole. The eluted protein was desalted and concentrated to 5 mg/mL in PBS buffer using Ultra Centrifugal Filters with 10-kDa molecular weight cut-off (Amicon®) and stored at 4 °C.

Western blotting analysis. Supernatant or periplasmic fractions were diluted 3:1 in 4× Laemmli sample buffer (Bio-Rad) and were boiled at 100 °C for 10 min. The treated samples were subjected to SDS-polyacrylamide gel electrophoresis on 10% Mini-PROTEAN® TGX™ Precast Protein Gels (Bio-Rad). The separated protein samples were then transferred to nitrocellulose membranes. Following transfer, the membranes were blocked with 5% milk (w/v) in TBST (TBS, 0.1% Tween 20) and were probed with horseradish peroxidase (HRP) conjugated anti-His antibody (Abcam, catalog # ab1187) or the *C. jejuni* heptasaccharide glycan-specific antiserum hR6 for 1 h. For the later, goat anti-rabbit IgG (HRP) (Abcam, catalog # ab205718) was used as the secondary antibody to detect hR6 antiserum. After washing three times with TBST for 10 min, the membranes were visualized using a ChemiDoc™ MP Imaging System (Bio-Rad).

***In vitro* glycosylation.** Methods for purification of *C. jejuni* PglB and isolation of *C. jejuni* LLOs from *E. coli* were described previously [69]. *In vitro* glycosylation was carried out in 30-µL reactions containing either 20 µL of supernatant fraction containing aglycosylated

YebF-Im7 or 20 μL of periplasmic fraction containing YebF-RNase A, 2 μg of purified *Cj*PglB, and 5 μg extracted *Cj*LLOs in *in vitro* glycosylation buffer (10-mM HEPES, pH 7.5, 10-mM MnCl2, and 0.1% (w/v) *n*-dodecyl-β-D-maltoside (DDM)). Reaction mixtures were incubated at 30 °C for 16 h and stopped by adding 10 μL of 4× Laemmli sample buffer containing 5% β-mercaptoethanol followed by boiling at 100 °C for 15 min, after which they were subjected to Western blot analysis.

ELISA. Binding activity for Im7 and scFv-HER2 was determined by standard ELISA. Briefly, Costar 96-well ELISA plates (Corning) were coated overnight at 4 °C with 50 μL of 5 μg/mL purified ColE7 in 0.05-M sodium carbonate buffer (pH 9.6) for Im7 variants and 50 μL of 0.2 μg/mL HER2-ED (Sino Biological, catalog # 10004-HCCH) in PBS buffer for scFv-HER2 variants. After blocking with 5% (w/v) non-fat milk in PBS for 1 h at room temperature, the plates were washed three times with PBST (PBS, 0.05% (v/v) Tween-20) and incubated with serially diluted aglycosylated and glycosylated YebF-Im7 and YebF-scFv-HER2 glycovariants for 1 h at room temperature. After washing three times with PBST, 50 μL of 1:2,500-diluted HRP-conjugated anti-DDDK tag antibody (Abcam, catalog # ab49763) for Im7 variants or 50 μL of 1:5,000-diluted HRP-conjugated anti-6×His tag antibody (Abcam, catalog # ab1187) for scFv-HER2 variants, both in 1% PBST, was added to each well for 1 h. Plates were washed three times and then developed using 50 μL 1-Step Ultra TMB-ELISA substrate solution (ThermoFisher).

RNase A activity assay. The enzymatic activity of RNase A variants was assayed using RNaseAlert®-1 Kit (Integrated DNA Technologies) according to the manufacturer's protocol. Each of the 80-times-diluted supernatant samples were normalized to have an OD_{600} equivalent to the positive control strain expressing wt RNase A. Samples were then mixed with 20 pmol of RNase A substrate and 10 μL of 10× RNaseAlert Buffer and incubated in RNase-free black 96 well microplates (Fisher) at 37 °C for 30 min. Fluorescence values were measured at 490 nm/520 nm excitation/emission wavelengths.

Thermal stability analysis. Far-UV CD spectroscopy of purified Im7 (50-mM sodium phosphate, 400-mM sodium sulfate, pH 7.4) as a function of temperature was carried out in a 0.1-cm cuvette on a spectropolarimeter. Far-UV CD spectra were acquired between 200 nm and 260 nm with a step resolution of 1 nm. Melting temperatures of purified glycovariants was determined using high-throughput DSF as previously described [44].

Briefly, 5–10 μg of proteins were mixed with Protein Thermal Shift™ Buffer and Protein Thermal Shift™ Dye purchased as Protein Thermal Shift Dye Kit™ (Thermo Fischer Scientific) according to manufacturer's instructions. A melting curve was generated by monitoring fluorescence at 465 nm/610 nm excitation/emission wavelengths while increasing temperature from 10 °C to 90 °C at a rate of 0.06 °C/s on an Applied Biosystem ViiA 7 instrument (Life Technologies). To calculate T_m values, the collected data were analyzed by nonlinear regression analysis using the Boltzmann equation in Prism 8.3 (GraphPad).

Geometric and Rosetta calculations. Initial coordinates of structures used for analysis were obtained from the Protein Data Bank at RCSB.org as follows: the Im7–E7 complex (PDB: 2JBG), RNAse A bound to four-nucleotide-long DNA (PDB: 1RCN, DNA: ATAA) and the scFv-Her2–ErbB2 complex (PDB: 3WSQ). For RNase A, we modeled an eight-nucleotide-long RNA at the same binding site of the DNA. We used X3DNA [70] to identify nucleotide arrangement parameters from DNA, as a template, to model RNA. We replaced the thymine residue of bound DNA with its RNA counterpart uracil. Since an initial analysis showed that four-nucleotide-long RNA is small for an interface-interaction calculation, we added two extra nucleotides to both ends of the modeled RNA to make it eight nucleotides long. Finally, to remove any unwanted clashes coming from the base sugar (deoxyribose to ribose) and the nucleotide change (thymine to uracil), we used the Rosetta relax protocol with a restraint on protein backbone atoms to generate a pool of 100 RNA–protein structures ("decoys"). From this pool, we selected the decoy with the best score and maximum backbone similarity to the backbone of the templated DNA.

Geometric calculations. Secondary structure was identified using the DSSP protocol in PyRosetta [71]. Burial of a glycosylated residue was represented by a count of C_β atoms within 8.5 Å from the C_β atom of the selected amino acid residue (C_α for alanine). The distance of a glycosylated residue from its binding partner was estimated by the C_α–C_α distance from the glycosylated residue to the closest residue of the binding partner. For RNase A, the distance of glycosylated residue from the active site residue His-119 was used instead, as RNase A does not bind to a protein. This distance was used for both the "activity ratio" and the "activity improvement probability" analyses. Interface solvent-accessible surface area (SASA) was measured using the Rosetta interface analyzer [72].

Rosetta measures. The REF15 Rosetta score [29] was used to estimate the stability of a protein–protein complex. The interface score represented the binding energy of a complex and was calculated with the Rosetta Interface Analyzer [72] by subtracting the score of the separated monomers from the complex.

Rosetta protocols for sequon insertion and glycomutagenesis. We used the RosettaCarbohydrate framework [30] and the glycomutagenesis protocol for the computational study of the SSGM protocol. The glycomutagenesis protocol input a wt PDB file and generated all possible glycosylated variants for it, including mutation to the glycosylation sequon. Coordinate files after sequon substitution and side chain optimization steps were used as aglycosylated variants for analysis. Rosetta calculations were carried out in release version 2020.06 and using PyRosetta4 release 247 (www.rosettacommons.org). The command line for the glycomutagenesis calculation was:

```
glycomutagenesis.linuxgccrelease -in:file:s <PDB> -include_sugars
-nstruct <length of sequence selected for glycomutagenesis>
-n_cycles 100 -mute all
-out:path:pdb ./output
-out:path:score ./output
```

The command line for the relaxation runs was:

```
relax.linuxgccrelease -s <PDB> -nstruct 100
-relax:default_repeats 5
-relax:bb_move false
-out:path:pdb ./output_relax
-out:path:score ./output_relax
```

Rosetta's interface analysis requires definition of interface chains, so the command for analyzing aglycosylated structures was:

```
InterfaceAnalyzer.default.linuxgccrelease -s <PDB>
-interface A_B #(For chain A and B)
-mute all
-out:path:pdb ./output
-out:path:score ./output
```

and the command for glycosylated structures was:

```
InterfaceAnalyzer.default.linuxgccrelease -s <pdb file>
-interface AB_C #(For [protein A + Glycan B] and Protein C)
-fixedchains A B #(For Protein A + Glycan B)
-mute all
-out:path:pdb ./output
-out:path:score ./output
```

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Data availability. All data generated or analyzed during this study are included in this article (and its supplementary information) or are available from the corresponding authors on reasonable request.

Competing Interests. M.P.D. has a financial interest in Glycobia, Inc. and Versatope, Inc. M.P.D.'s interests are reviewed and managed by Cornell University in accordance

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