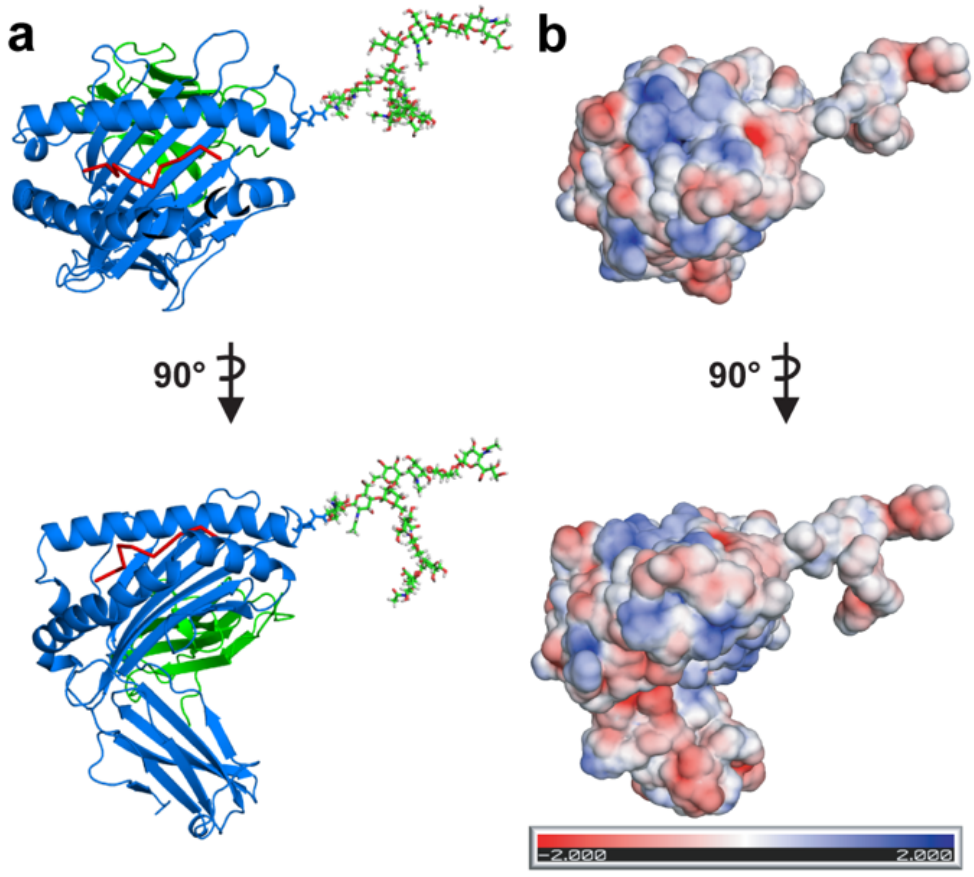
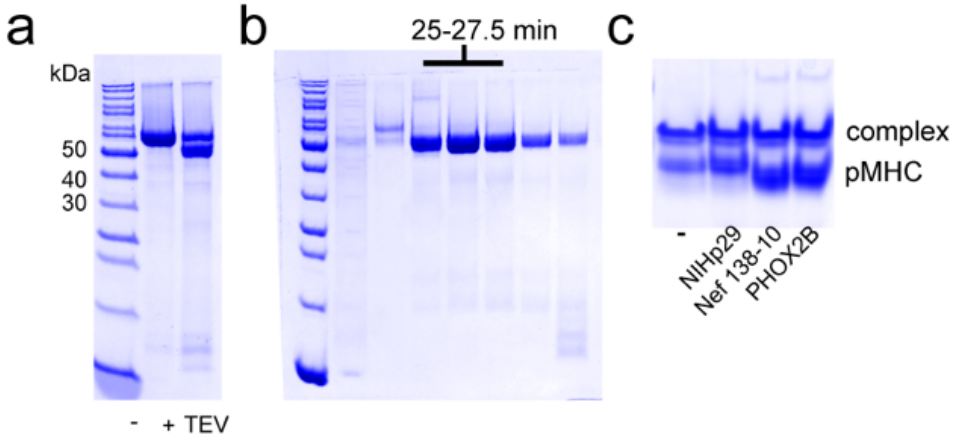
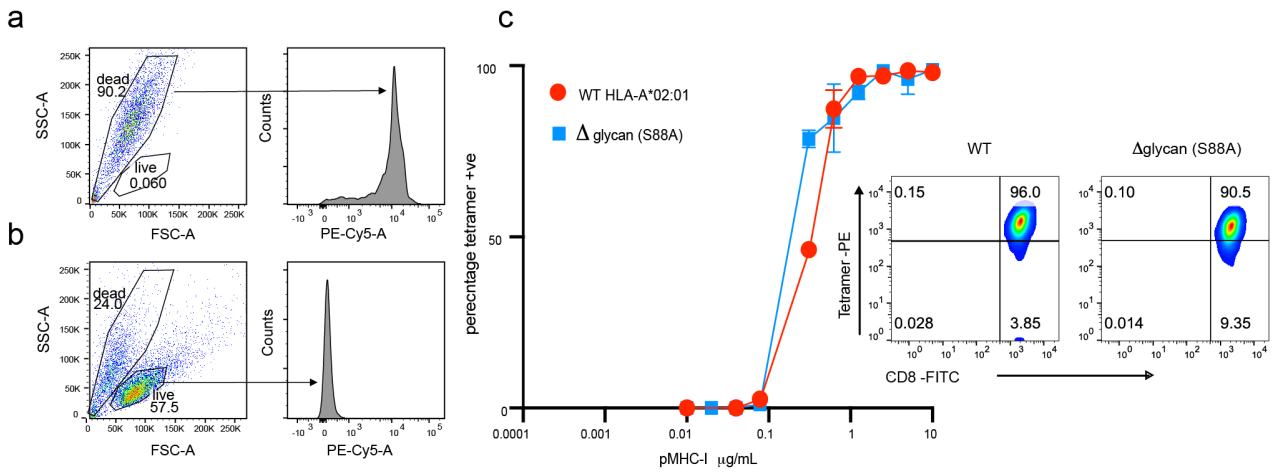
**Supplementary Figures**




**Supplementary Figure S1. Structure modeling of the glycan moiety on the conserved Asn 86 residue.** **(a)** HLA-A*02:01 in complex with the heteroclitic MART-1 peptide (PDB ID: 1JF1) modelled to show a biantennary di-sialated glycan at position N86. The heavy chain is colored blue, β2m green, MART-1 peptide, red. **(b)** Electrostatic surface representation of the MHC-I molecule and glycan from the top view and side view**.** Solvent-accessible surface representation with electrostatic potential in the indicated ranges ( −2 kcal/(mol·*e*) in red to +2kcal/(mol·*e*) in blue) were calculated using CHARMM-GUI. All calculations were performed at 150 mM ionic strength, 298 Kelvin, pH 7.2, protein dielectric 2.0, and solvent dielectric 78.54. Electrostatic potentials are given in units of kT/e. A 1.4 Å solvent (probe) radius and 10.0 points/Å$^2$ density was used to calculate molecular surfaces.




**Supplementary Figure S2. Analysis of HLA-A*24:02/TAPBPR leucine-zippered complex**. **(a)** Streptactin-purified complex was TEV digested and electrophoresed on a 12% SDS PAGE gel prior to size exclusion chromatography (SEC) **(b**) Gel electrophoresis of complex eluted from an SEC S200 16/300 increase column (50mM Tris, 100mM, NaCl, running at a rate of 0.5mL/min). The complex peak (25-27.5min) was collected. **(c)** Native gel electrophoresis of HLA-A*24:02/TAPBPR complex dissociation in the presence of relevant high affinity peptides (Nef 138_10 and PHOX2B) and irrelevant peptide (NIHp29).




**Supplementary Figure S3. Flow cytometry analysis.** (**a)** DMF5 cells are a HLA-A*02:01 restricted human lymphocyte line that express both the MART-1 specific TCR and CD8 co-receptor. For flow cytometry, dead-cells (PE-Cy5-A channel) were identified by treatment with ethanol followed by propidium iodide staining (**b)** Live singletons were selected by forward and side light scattering properties. The percentage of total population within each gate is indicated. **(c)** Titration of PE- HLA-A*02:01 MART-1 (WT) -and Δglycan (S88A) tetramers on DMF5 by flow cytometry with inset, 1.25 μg/mL tetramer, 1μg/mL anti-human CD8-FITC (BD San Jose).

**Table S1. Previously described epitopic peptides used in this study**

| Peptide | Sequence | Length | predicted IC50 (nM) HLA-A*02:01 | predicted IC50 (nM) HLA-A*68:02 | predicted IC50(nM) HLA-A*24:02 |
|---|---|---|---|---|---|
| TAX9 | LLFGVPVYV | 9 | 3.4 | 64 | - |
| NY-ESO-1 | SLLMWITQA | 9 | 23 | 7297 | - |
| GM1 | GLLGIGILTV | 10 | 15.9 | 12160.2 | - |
| GM2 | ETAGVPADV | 9 | 14820.3 | 5.3 | - |
| GM3 | ETAGIGILTV | 10 | 4436.9 | 4.4 | - |
| GM4 | GLLGVPLYV | 9 | 5.4 | 4662.9 | - |
| NIH p29 | YPNVNIHNF | 9 | 22457.6 | 13418.9 | - |
| P18_I10 | RGPGRAFVFI | 10 | 17132.2 | 12829.9 | - |
| MART-1 | EAAGIGILTV | 10 | 5322.6 | - | |
| PHOX2B | VYGFVRACL | 9 | - | - | 466.54 |
| Nef138-10 | RYPLTFGWCF | 10 | - | - | 6.57 |

* All predictions of IC50 values were made using NetMHCpan 4.0; Jurtz,V., Paul,S., Andreatta,M., Marcatili,P., Peters,B. and Nielsen,M. (2017) *J. Immunol. Baltim. Md 1950*, **199**, 3360–3368.

**Table S2. SARS-CoV-2 epitopic peptides used in this study**

| Swiss-Model Repository Reference | Sequence | Length | predicted IC50 (nM) HLA:A*02:01* | Structure-Based Model** | charge |
|---|---|---|---|---|---|
| YP_009724390.1 | ALNTLVKQL | 9 | 1633.23 | Weak binder | +1 |
| YP_009724390.1 | VLNDILSRL | 9 | 33.57 | Strong binder | 0 |
| YP_009724390.1 | RLNEVAKNL | 9 | 940.92 | Strong binder | +1 |
| YP_009724390.1 | NLNESLIDL | 9 | 177.32 | Strong binder | -2 |
| YP_009724390.1 | FIAGLIAIV | 9 | 10.29 | Strong binder | 0 |
| YP_009724392.1 | GLMWLSYFI | 9 | 3.87 | Strong binder | 0 |
| YP_009724392.1 | LLLDRLNQL | 9 | 14.81 | Strong binder | 0 |
| YP_009724389.1 | GMSRIGMEV | 9 | 50.61 | Strong binder | 0 |
| YP_009724389.1 | WLMWLIINL | 9 | 6.60 | Weak binder | 0 |
| YP_009724389.1 | ILLLDQALV | 9 | 27.11 | Strong binder | 0 |
| YP_009724389.1 | SLPGVFCGV | 9 | 24.07 | Strong binder | -1 |
| YP_009724393.1 | TLACFVLAAV | 10 | 20.28 | Strong binder | 0 |
| YP_009724390.1 | KLPDDFTGCV | 10 | 77.11 | Strong binder | -1 |

* Using NetMHCpan 4.0; Jurtz,V., Paul,S., Andreatta,M., Marcatili,P., Peters,B. and Nielsen,M. (2017) *J. Immunol. Baltim. Md 1950*, **199**, 3360–3368.

**Classified according to *Rosetta* binding energies, as outlined in; Nerli,S. and Sgourakis,N.G. (2020) *bioRxiv*, 2020.03.23.004176.