

**Table S1. Predicted peptides and their binding to DLA-88\*001:04/β2m evaluated by *in vitro* refolding**

Derived protein <sup>a</sup>	name	Sequence	Stability <sup>b</sup>
Rabies-virus-glycoprotein	MTT9	MTTKSVSFR	++
	VSF9	VSFRRLSHL	++
H5N1-H	YNA9	YNAELLVLM	++
H7N9-NA	DGA9	DGAKIEYFL	--
H7N9-H	VAM9	VAMENQHTI	++
Canine-self	KLF9	KLFSGELTK	++
	CDV-H	VVL9	VVLPTQNFR
	ITN9	ITNHRGFLK	++
	TSV9	TSVGRFFPL	++
	RTI9	RTISYTYPF	++
	TSV9	TSVGRVFPL	++
	RVF9	RVFEIGFIK	--
CDV-N	FSA9	FSAGSYPLL	++
	YPA9	YPALGLHEF	++
	EAG9	EAGLASFIL	+-
CPV-VP1	PSN9	PSNIGMKI	+-
	TNP9	TNPSDAAAK	--
CPV-NS1	MSG9	MSGNQYTEE	--

<sup>a</sup>H5N1 and H7N9 are influenza virus subtypes; CDV, canine distemper virus; CPV, canine parvovirus; H, hemagglutinin; NA, neuraminidase; N, nucleocapsid; VP1 is a capsid protein; NS1, nonstructural protein 1

<sup>b</sup>++, peptide binds strongly and can tolerate anion-exchange chromatography.

+-, peptide binds DLA-88\*001:04 but cannot tolerate anion-exchange chromatography.

--, peptide does not bind DLA-88\*001:04.