

Table S4. Gene Ontology analysis of source proteins which generated no treatment-exclusive HLA-I peptides.

Ontology domain	GO term ID	Term	Count	P-value
MF	GO:0045296	cadherin binding	14	1.84x10 ⁻⁵
MF	GO:0000030	mannosyltransferase activity	5	2.14x10 ⁻⁴
MF	GO:0003746	translation elongation factor activity	5	3.28x10 ⁻⁴
MF	GO:0098973	structural constituent of postsynaptic actin cytoskeleton	3	5.64x10 ⁻⁴
MF	GO:0038132	neuregulin binding	3	1.40x10 ⁻³
MF	GO:0044877	protein-containing complex binding	23	5.37x10 ⁻³
MF	GO:0140142	nucleocytoplasmic carrier activity	4	2.14x10 ⁻²
MF	GO:0097718	disordered domain specific binding	4	3.15x10 ⁻²
MF	GO:0043022	ribosome binding	6	3.85x10 ⁻²
BP	GO:1901566	organonitrogen compound biosynthetic process	35	2.42x10 ⁻⁷
BP	GO:0045901	positive regulation of translational elongation	3	1.39x10 ⁻³
BP	GO:0045905	positive regulation of translational termination	3	1.39x10 ⁻³
BP	GO:0097502	mannosylation	5	3.26x10 ⁻³
BP	GO:1901137	carbohydrate derivative biosynthetic process	16	3.29x10 ⁻³
BP	GO:0051128	regulation of cellular component organization	33	7.61x10 ⁻³
BP	GO:0051131	chaperone-mediated protein complex assembly	4	1.64x10 ⁻²
CC	GO:0070062	extracellular exosome	44	4.67x10 ⁻¹²
CC	GO:0005829	cytosol	70	1.54x10 ⁻¹⁰
CC	GO:1904813	ficolin-1-rich granule lumen	9	1.42x10 ⁻⁵
CC	GO:0032991	protein-containing complex	74	1.79x10 ⁻⁴
CC	GO:0005925	focal adhesion	12	2.24x10 ⁻³
CC	GO:0012505	endomembrane system	48	1.08x10 ⁻²
CC	GO:0015629	actin cytoskeleton	12	1.35x10 ⁻²
CC	GO:0030132	clathrin coat of coated pit	3	3.07x10 ⁻²

MF, Molecular Function; BP, Biological Process; Cellular Component, CC