

**Table S5. Gene Ontology analysis of source proteins which generated gemcitabine-exclusive HLA-I peptides.**

<i>Ontology domain</i>	<i>GO term ID</i>	<i>Term</i>	<i>Count</i>	<i>P-value</i>
MF	GO:0005515	protein binding	377	1.44x10 <sup>-18</sup>
MF	GO:0017111	ribonucleoside triphosphate phosphatase activity	51	2.05x10 <sup>-12</sup>
MF	GO:0003723	RNA binding	107	7.39x10 <sup>-6</sup>
MF	GO:0008554	P-type sodium transporter activity	5	4.07x10 <sup>-5</sup>
MF	GO:0003697	single-stranded DNA binding	14	1.53x10 <sup>-4</sup>
MF	GO:0140640	catalytic activity, acting on a nucleic acid	33	2.75x10 <sup>-4</sup>
MF	GO:0045182	translation regulator activity	15	4.57x10 <sup>-4</sup>
MF	GO:0004711	ribosomal protein S6 kinase activity	4	3.32x10 <sup>-3</sup>
MF	GO:0004748	ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as acceptor	3	4.95x10 <sup>-3</sup>
MF	GO:0005220	inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity	3	4.95x10 <sup>-3</sup>
MF	GO:0000287	magnesium ion binding	16	1.04x10 <sup>-2</sup>
MF	GO:0004634	phosphopyruvate hydratase activity	3	1.95x10 <sup>-2</sup>
MF	GO:0097718	disordered domain specific binding	6	2.80x10 <sup>-2</sup>
MF	GO:0008199	ferric iron binding	4	2.94x10 <sup>-2</sup>
MF	GO:0005200	structural constituent of cytoskeleton	10	4.53x10 <sup>-2</sup>
MF	GO:0004749	ribose phosphate diphosphokinase activity	3	4.80x10 <sup>-2</sup>
MF	GO:0097100	supercoiled DNA binding	3	4.80x10 <sup>-2</sup>
BP	GO:0006996	organelle organization	144	2.72x10 <sup>-17</sup>
BP	GO:0006518	peptide metabolic process	59	7.36x10 <sup>-14</sup>
BP	GO:0051641	cellular localization	121	7.32x10 <sup>-8</sup>
BP	GO:0035556	intracellular signal transduction	86	5.63x10 <sup>-4</sup>
BP	GO:0010248	establishment or maintenance of transmembrane electrochemical gradient	5	1.99x10 <sup>-3</sup>
BP	GO:0006015	5-phosphoribose 1-diphosphate biosynthetic process	4	3.70x10 <sup>-3</sup>
BP	GO:0031396	regulation of protein ubiquitination	16	5.70x10 <sup>-3</sup>
BP	GO:0051301	cell division	31	6.46x10 <sup>-3</sup>
BP	GO:0032502	developmental process	164	7.70x10 <sup>-3</sup>
BP	GO:0009056	catabolic process	80	1.01x10 <sup>-2</sup>
BP	GO:0030007	intracellular potassium ion homeostasis	5	1.21x10 <sup>-2</sup>
BP	GO:0006901	vesicle coating	7	1.48x10 <sup>-2</sup>
BP	GO:0036376	sodium ion export across plasma membrane	5	1.74x10 <sup>-2</sup>
BP	GO:0034660	ncRNA metabolic process	29	2.11x10 <sup>-2</sup>
BP	GO:0010033	response to organic substance	83	2.95x10 <sup>-2</sup>
CC	GO:0005737	cytoplasm	338	1.70x10 <sup>-28</sup>

CC	GO:0045171	intercellular bridge	15	$4.58 \times 10^{-8}$
CC	GO:0030054	cell junction	84	$5.35 \times 10^{-8}$
CC	GO:0098687	chromosomal region	24	$1.38 \times 10^{-4}$
CC	GO:0000793	condensed chromosome	19	$3.63 \times 10^{-4}$
CC	GO:0030867	rough endoplasmic reticulum membrane	6	$2.68 \times 10^{-3}$
CC	GO:0090533	cation-transporting ATPase complex	5	$6.47 \times 10^{-3}$
CC	GO:0002189	ribose phosphate diphosphokinase complex	3	$1.99 \times 10^{-2}$
CC	GO:0005784	Sec61 translocon complex	3	$3.93 \times 10^{-2}$

---

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