Figure S1

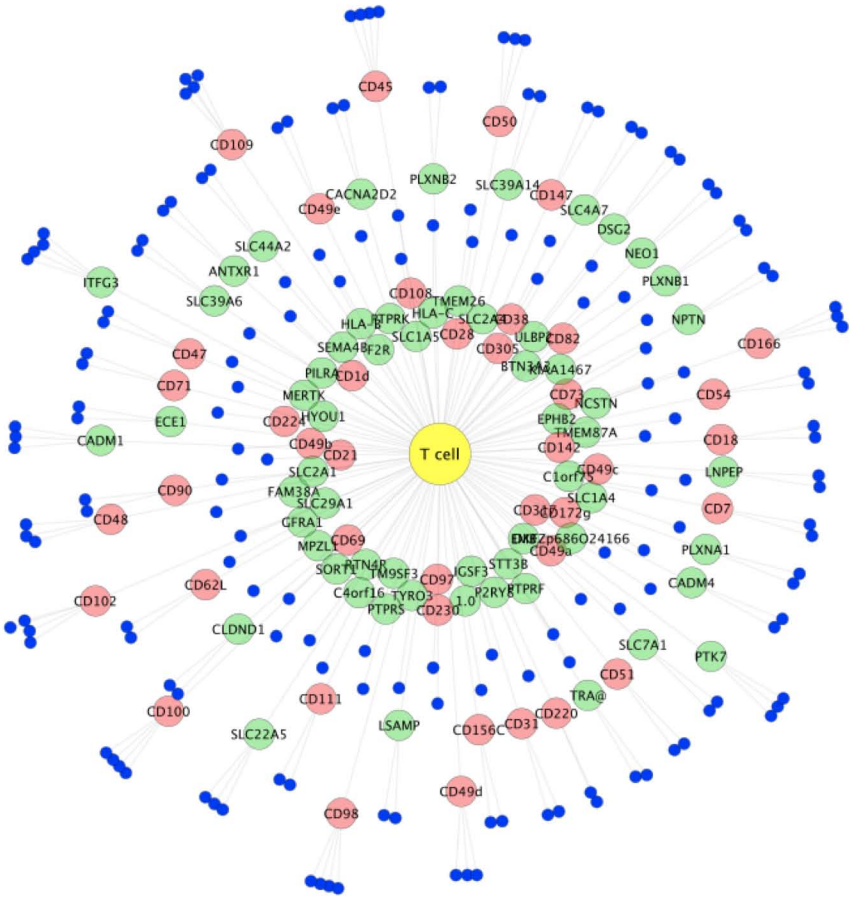


Figure S1: Jurkat T lymphocyte surface glycoproteome. CSC identified glycoproteins and their glycosites from Jurkat T lymphocytes [white middle circle: Jurkat cell; red circles: CD proteins (label:CD number); green circles: non CD annotated proteins (label: ENTREZ gene id); blue circles: glycopeptides containg glycosylation motif]. Glycoproteins towards the outside of the spring embedded Cytoscape view have more unique CSC identified glycopeptides containing an NXS/T motif.

Figure S2

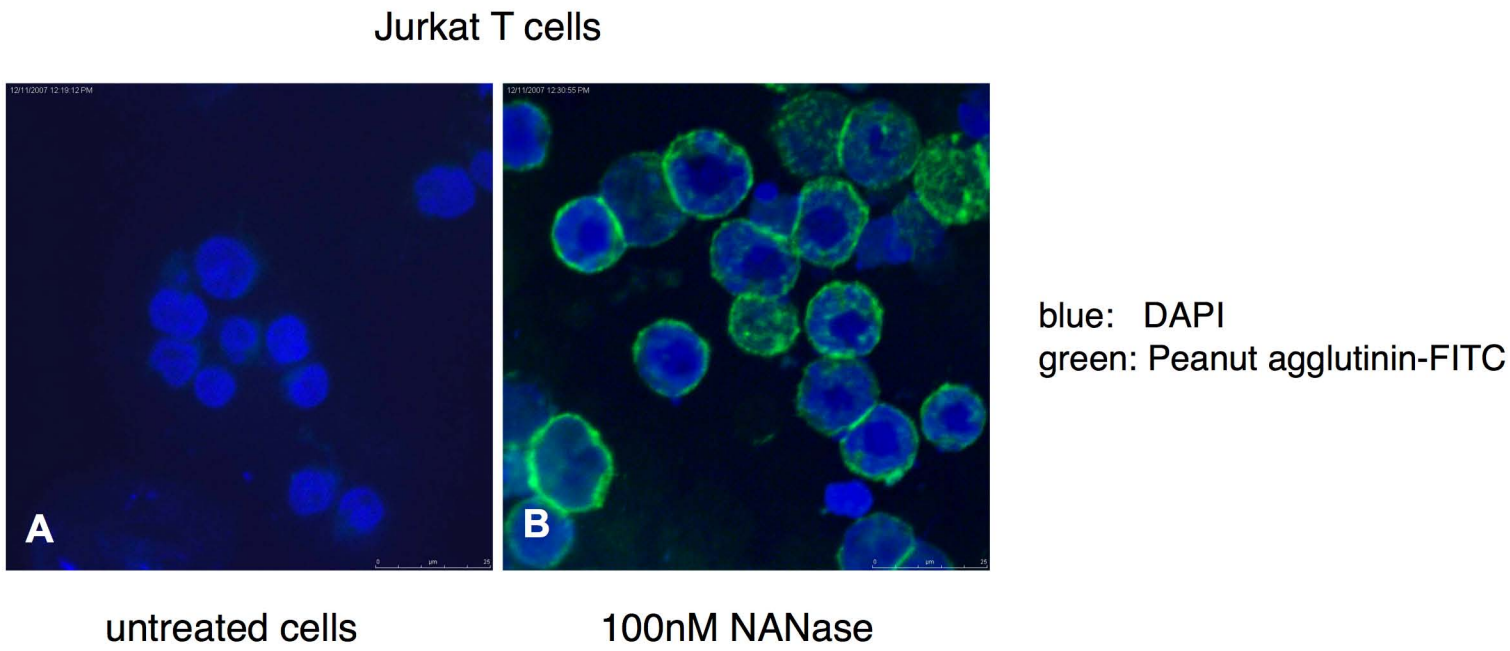


Figure S2: Neuramidase treatment removes terminal sialic acid residues and enables peanut agglutinin binding. Jurkat T cells were left untreated (A) or treated with 100mU Neuraminidase (B), fixed and stained with DAPI (blue) and peanut agglutinin (green).

Figure S3A

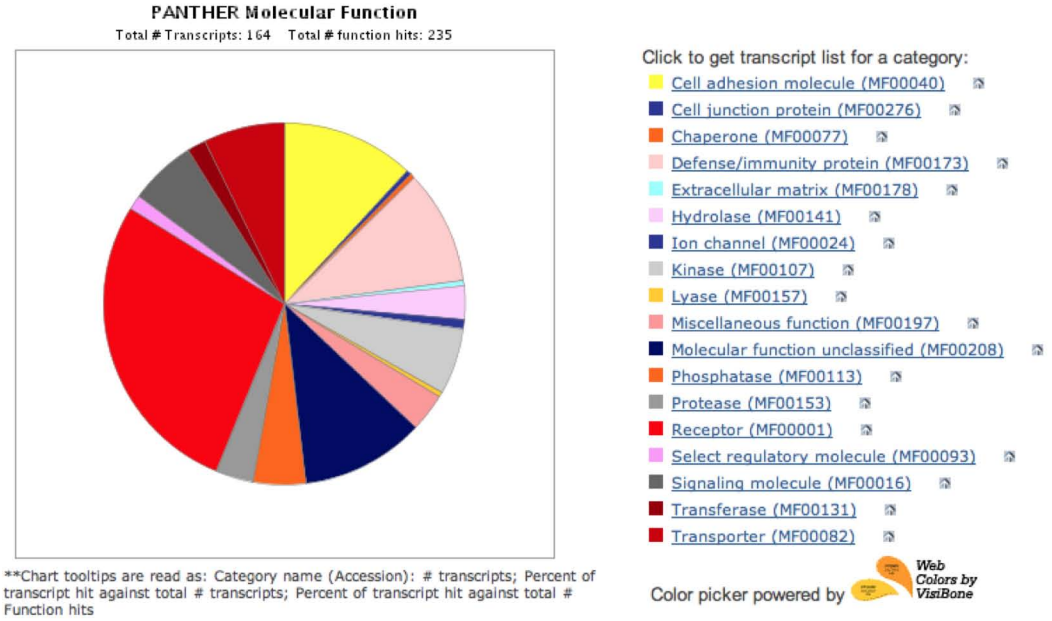


Figure S3: PANTHER classifications (Molecular Function (**A**), Pathways (**B**), Biological Process (**C**)) of identified CSC Jurkat T lymphocyte proteins. 115 ENTREZ gene identifiers from CSC identified cell surface proteins matched to 178 PANTHER transcripts and were classified.

Figure S3B

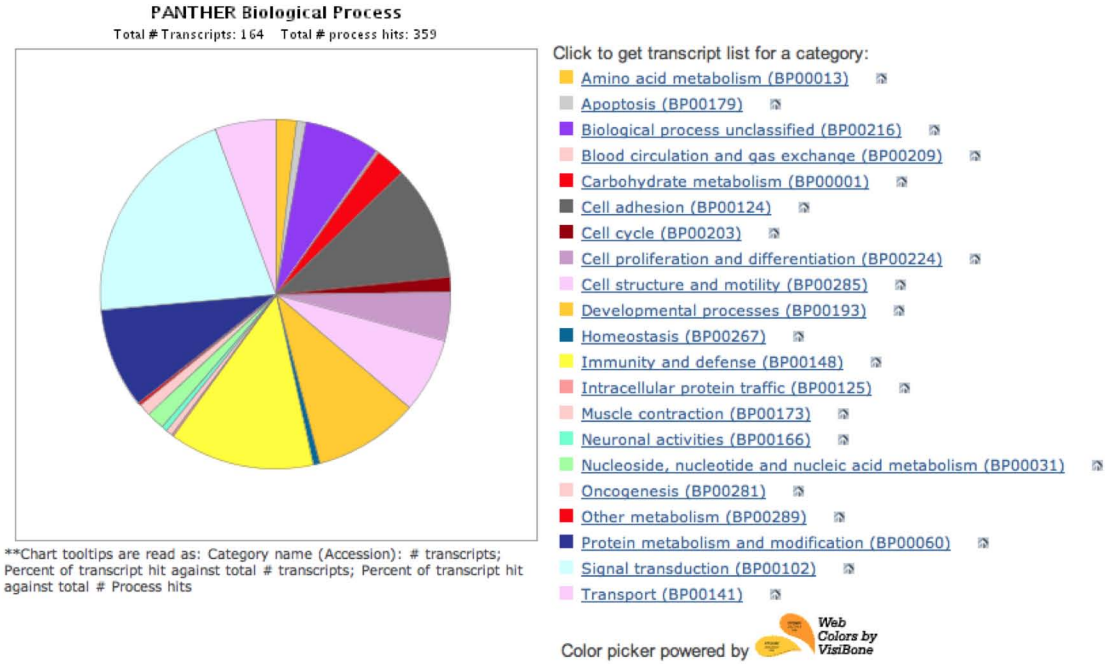


Figure S3: PANTHER classifications (Molecular Function (**A**), Pathways (**B**), Biological Process (**C**)) of identified CSC Jurkat T lymphocyte proteins. 115 ENTREZ gene identifiers from CSC identified cell surface proteins matched to 178 PANTHER transcripts and were classified.

Figure S3C

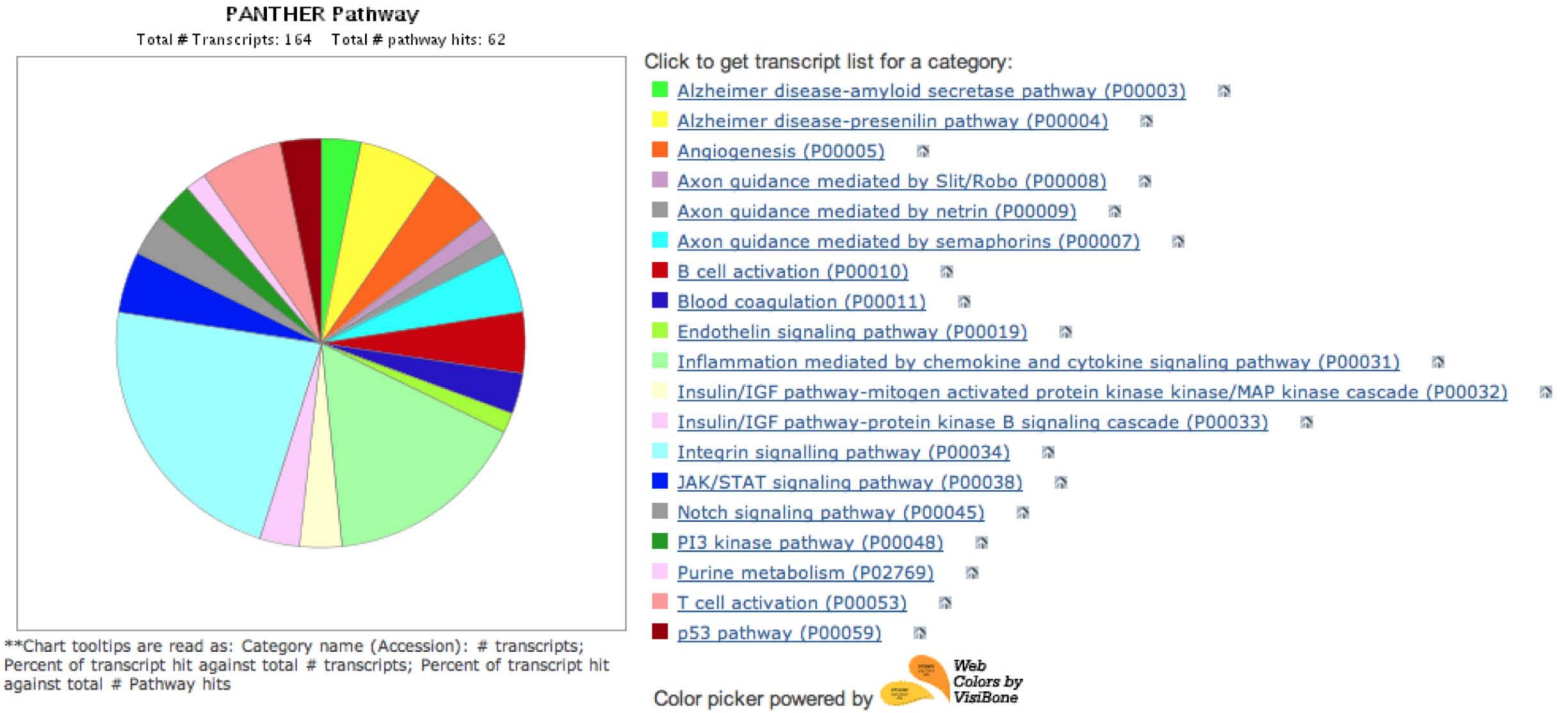
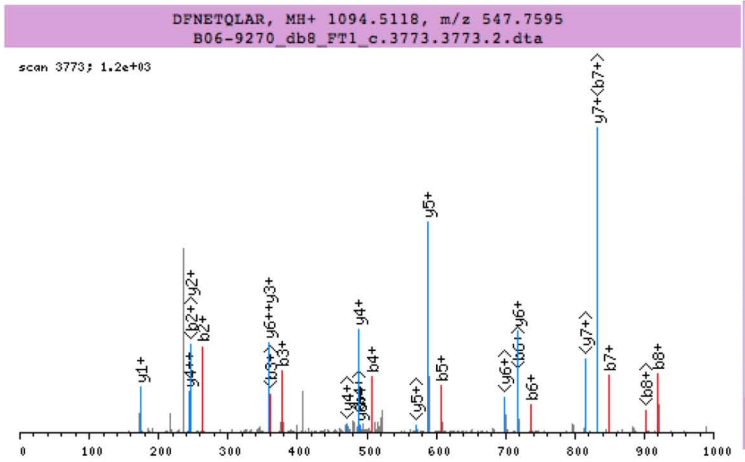


Figure S3: PANTHER classifications (Molecular Function (**A**), Pathways (**B**), Biological Process (**C**)) of identified CSC Jurkat T lymphocyte proteins. 115 ENTREZ gene identifiers from CSC identified cell surface proteins matched to 178 PANTHER transcripts and were classified.

Figure S4



b^+	#	AA	#	y^+	y^{2+}
116.0348	1	D	9		
263.1032	2	F	8	979.4849	490.2464
378.1301	3	N	7	832.4165	416.7121
507.1727	4	E	6	717.3895	359.1987
608.2204	5	T	5	588.3469	294.6774
736.2790	6	Q	4	487.2993	244.1535
849.3630	7	L	3	359.2407	180.1243
920.4001	8	A	2	246.1566	123.5822
	9	R	1	175.1195	88.0637

N(3):+115.03

Figure S4: Specific MS-based identification of cell surface glycoprotein N-glycosylation sites. Shown is the N-glycosite identification of the CSC peptide DFNETQLAR derived from the Anthrax toxin receptor detected on Jurkat T lymphocytes. Peptide MS CID spectrum is depicted on the left side. SEQUEST matched fragmentation ions are depicted on the right side. The experimentally identified cell surface N-glycosite is highlighted in yellow.