Table S1: Propensity scores of amino acids at different positions on the peptide

Residue	Position 4	Position 5	Position 6	Position 7
A	0.01864	0.01592	0.00816	0.03534
C	0.01049	0.00233	0.00544	0
D	0.00777	0.00078	0.00466	0.02641
E	0.03650	0.03495	0.10330	0.10874
F	0.00155	0.03223	0.00350	0.12583
G	0.01126	0.00388	0.00311	0.02369
H	0.02913	0.26175	0.01786	0.08000
I	0.06252	0.11883	0.17243	0
K	0.04971	0.06369	0.01204	0.03689
L	0.13786	0.02524	0.12777	0.07223
M	0.04738	0.08816	0.18019	0
N	0.02447	0.0365	0.05864	0.03301
P	0	0.07184	0	0
Q	0.02718	0.01087	0.08155	0.04388
R	0.03417	0.08039	0.01087	0.03262
S	0.01709	0.00699	0.00350	0.02951
T	0.04272	0.02058	0.01476	0.02835
V	0.05204	0.05282	0.15107	0
W	0.00932	0.06990	0.03146	0
Y	0.38019	0.00233	0.00971	0.32350

Propensities were computed on a set of 2,575 heptapeptides that showed a binding affinity to Ydj1, which is comparable to that of wild-type peptide GWLYEIS. The sum of propensity values at each position is equal to 1.