**Table S2.** Predicted binding score of protein-protein interactions obtained from HPEPDOCK server

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **α** | **Hydrolysate peptides (Ligands)** | **Predicted Binding Score (no unit)** | | | | | | | | | | | | | | | | | |
| **A** | **B** | **C** | **D** | **E** | **F** | **G** | **H** | **I** | **J** | **K** | **L** | **M** | **N** | **O** | **P** | **Q** | **R** |
| 1 | GSIGAASM | -180.1 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | CPIAIM | -195.7 | -141.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | SAL | -103.6 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | GAK | -93.4 |  | -80.9 | -73.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 8 | VVR |  |  |  |  | -123.3 | -126.3 |  |  |  |  |  |  |  |  |  |  |  |  |
| 9 | PGF |  |  |  |  |  |  | -129.3 | -137.8 | -146.9 |  |  |  |  |  |  |  |  |  |
| 11 | SSL | -110.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 13 | QITK |  |  |  |  |  |  |  |  |  | -146.4 |  |  |  |  |  |  |  |  |
| 17 | PIL |  |  |  |  |  |  | -128.3 |  | -133.7 |  | -132.6 |  |  |  |  |  |  |  |
| 20 | GGL |  |  |  |  |  |  |  | -78.1 |  |  |  |  |  |  |  |  |  |  |
| 22 | QTAADQAR |  |  |  |  |  |  |  |  |  |  |  | -167.2 |  |  |  |  |  |  |
| 24 | GIIR |  |  |  |  |  | -130.1 |  |  |  |  |  |  |  |  |  |  |  |  |
| 26 | AIVF |  | -132.2 |  |  |  |  | -139.3 | -146.9 | -160.2 |  |  |  | -169.3 | -175.3 |  |  |  |  |
| 29 | PVQM |  | -126.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 30 | QIGL |  |  |  |  |  |  | -117.7 |  | -145.0 |  | -134.7 |  |  |  |  |  |  |  |
| 42 | GITDVF |  |  |  |  |  |  |  |  |  |  |  |  |  |  | -136.7 | -142.4 |  |  |
| 44 | SGISSAESL | -191.4 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 53 | AVL | -119.7 |  | -83.9 |  |  |  | -95.3 | -95.9 | -100.8 |  | -94.7 |  |  |  |  |  |  |  |
| 55 | VY |  |  | -110.9 |  |  |  |  |  |  | -114.0 |  |  |  |  |  |  | -102.1 |  |
| 60 | IL |  |  | -82.0 |  |  |  |  |  | -90.3 |  |  |  |  |  |  |  |  |  |
| 67 | YLG |  |  |  |  |  |  |  |  | -147.7 |  |  |  |  | -151.4 |  |  |  |  |
| 68 | LPF |  |  |  |  |  |  | -136.2 |  | -146.3 |  |  |  |  | -153.2 |  |  |  |  |
| 69 | QIGLF |  |  |  |  |  |  | -153.8 |  | -193.2 |  |  |  |  |  |  |  |  |  |
| 70 | VSP |  |  |  |  |  |  |  |  | -104.2 | -111.4 |  |  |  |  |  |  |  | -82.8 |
| 71 | LWE |  |  |  |  |  |  |  |  | -159.6 |  |  |  |  |  |  |  |  |  |

**A**: HLA class I histocompatibility antigen A-3 ([1AKJ](https://www.rcsb.org/structure/1AKJ)). **B**: Protein farnesyltransferase ([2H6I](https://www.rcsb.org/structure/2H6I)). **C**: Calpain 1 (AF-P07384-F1-model\_v2). **D**: Cathepsin (B and K) ([2PBH](https://www.rcsb.org/structure/2PBH)). **E**: Complement factor B ([2OK5](https://www.rcsb.org/structure/2OK5)). **F**: Furin ([6HLD](https://www.rcsb.org/structure/6HLD)). **G**: Inhibitor of apoptosis protein 3 (E3 ubiquitin-protein ligase XIAP) (AF-P98170-F1-model\_v2). **H**: Cyclooxygenase-2 ([5KIR](https://www.rcsb.org/structure/5KIR)). **I**: Angiotensin-converting enzyme ([4C2N](https://www.rcsb.org/structure/4C2N)). **J**: Lipoxin A4 receptor (human formyl peptide receptor 2) *(by homology)* ([6LW5](https://www.rcsb.org/structure/6LW5)). **K**: Dipeptidyl peptidase IV ([3Q8W](http://doi.org/10.2210/pdb3Q8W/pdb)). **L**: Integrin alpha-V/beta-3 and alpha-5/beta-1 ([4O02](https://www.rcsb.org/structure/4O02)). **M**: Neurokinin 1 receptor *(by homology)* ([6HLO](https://www.rcsb.org/structure/6HLO)). **N**: Mu/Delta opioid receptors *(by homology)* (AF-P35372-F1-model\_v2). **O**: Beta-secretase 1 ([2OHM](https://www.rcsb.org/structure/2OHM)). **P**: HMG-CoA reductase (AF-P04035-F1-model\_v2). **Q**: Tyrosyl-tRNA synthetase ([4QBT](https://www.rcsb.org/structure/4QBT)). **R**: Sodium/glucose cotransporter 1 (AF-P13866-F1-model\_v2). AF represent Alphafold monomer v2.0 prediction obtained from UniProt structure section for each of the selected proteins, while structure of other proteins was obtained from RCSB protein databank.