Table S20. Ramachandran plot of hub proteins

Proteins	Residues in most favored regions	Residues in additional allowed regions	Residues in generously allowed regions	Residues in disallowed regions
SELE	378/475 (79.6%)	73/475 (15.4%)	15/475 (3.2%)	9/475 (1.9%)
9930111J21RIK2	362/401 (90.3%)	31/401 (7.7%)	4/401 (1.0%)	4/401 (1.0%)
GZMB	167/184 (90.8%)	14/184 (7.6%)	3/184 (1.6%)	0/184 (0.0%)
LPAR3	287/317 (90.5%)	26/317 (8.2%)	4/317 (1.3%)	0/317 (0.0%)
CARD10	313/387 (80.9%)	62/387 (16.0%)	7/387 (1.8%)	5/387 (1.3%)
PLEKHH3	551/611 (90.2%%)	50/611 (8.2%)	4/611 (0.7%)	6/611 (1.0%)
HIGD1B	84/85 (98.8%)	1/85 (1.2%)	0/85 (0.0%)	0/85 (0.0%)
GM12689	70/89 (78.7%)	12/89 (13.5%)	4/89 (4.5%)	3/89 (3.4%)
PLXDC1	359/415 (86.5%)	50/415 (12.0%)	2/415 (0.5%)	4/415 (1.0%)
PKN3	428/555 (77.1%)	89/555 (16.0%)	24/555 (4.3%)	14/555 (2.5%)

Note: random coil parts of the N-terminal/C-terminal sequence of the hub proteins were deleted for molecular dynamics simulation.