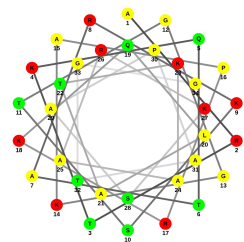


H3DP1 (MW 3451.94, pI 12.99, Net charge +10)

Sequence: ARTKQTARKSTGGKAPRKQLATKAARKSAPATGG

Secondary structure: CBBBBBBBCCCCCAAAAAAAAAAAAAAACCCCC

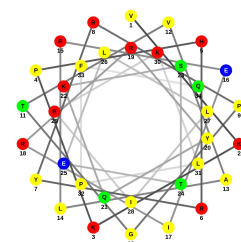


hydrophobic:	15 (44.1%)
neutral:	9 (26.5%)
hydrophilic:	10 (29.4%)

H3DP2 (MW 4178.93, pI 11.89, Net charge +8)

Sequence: VKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQ

Secondary structure: AAAAAACCCCB BBBBCBBBAAAAAAAAAAAAA

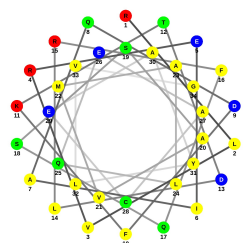


hydrophobic :	14 (41.2%)
neutral:	5 (14.7%)
hydrophilic:	15 (44.1%)

H3DP3 (MW 3859.41, pI 4.77, Net charge -1)

Sequence: RLVREIAQDFKTDLR FQSSAVMALQEACEAYLVG

Secondary structure: AAAAAAAAAABBBBBBAAAAAAAAAAAAAAC

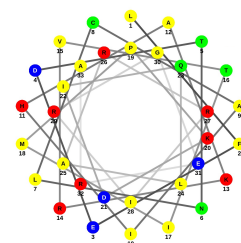


hydrophobic:	18 (52.9%)
neutral:	5 (14.7%)
hydrophilic:	11 (32.4%)

H3DP4 (MW 3836.52, pI 10.56, Net charge +4)

Sequence: LFEDTNLC AIHAKRVTIMPKDIQLARRIRGERA

Secondary structure: CCCBBBBBBBCCBBBBBAAAAAAAAAACCCCC



hydrophobic:	16 (48.5%)
neutral:	5 (15.1%)
hydrophilic:	12 (36.4%)

Figure S1. Amino acid sequences and compositions, molecular weight, isoelectric points, net charges, and predicted secondary structures and helical wheel projections of the histone H3-derived peptides, H3DP1–4. In the secondary structure, A, B, and C indicate α -helix, β -turn, and random coil, respectively. In the helical wheel projections, polar/basic, polar/acidic, polar/uncharged, and nonpolar amino acids are marked in red, blue, green, and yellow, respectively.