

**Table 1 Histone post-translational modification and variant-specific turnover.<sup>1</sup>**

Peptide <sup>2-4,6</sup>	Turnover, per day <sup>5</sup>	Peptide <sup>2-4,6</sup>	Turnover, per day <sup>5</sup>
H3K65un	0.6230 ± 0.0001	H3K27unK36un	1.9213 ± 0.0001
H3K122un	0.6400 ± 0.0001	H3K27me1	1.1391 ± 0.0000
H3K4un	0.6638 ± 0.0001	H3K36me1	1.6913 ± 0.0000
H3K4me1	0.4863 ± 0.0000	H3K27me2	0.8207 ± 0.0000
H3K56un	0.6378 ± 0.0000	H3K36me2	1.0892 ± 0.0000
H3K56ac1	2.4335 ± 0.0014	H3K27me3	0.5148 ± 0.0000
H3K18K23un	0.6806 ± 0.0001	H3K27me1K36me2	0.7540 ± 0.0000
H3K18/K23ac1 <sup>4</sup>	0.8793 ± 0.0000	H3K27me2K36me1	0.6210 ± 0.0001
H3K18ac1K23ac1	1.1446 ± 0.0001	H3K27me2K36me2	0.4537 ± 0.0000
H3K79un	0.6785 ± 0.0001	H3K27me3K36me1	0.3681 ± 0.0000
H3K79me1	0.4526 ± 0.0000	H3K27me1K36me3	0.4547 ± 0.0000
H3K79me2	0.3841 ± 0.0000	H4K5K8K12K16un	0.6495 ± 0.0000
H3K9unK14un	1.1335 ± 0.0001	H4K5/K8/K12/ K16ac1 <sup>4</sup>	0.7773 ± 0.0000
H3K9me1	0.7967 ± 0.0001	H4K5/K8/K12/ K16ac2 <sup>4</sup>	0.9819 ± 0.0000
H3K9me2	0.6620 ± 0.0000	H4K5/K8/K12/ K16ac3 <sup>4</sup>	1.0423 ± 0.0000
H3K9me3	0.4652 ± 0.0000	H4K5K8K12K16ac4	1.0056 ± 0.0000
H3K9/K14ac1 <sup>4</sup>	1.3393 ± 0.0001	H4K20un	2.2672 ± 0.0005
H3K9me1K14ac1	0.9205 ± 0.0000	H4K20me1	1.3340 ± 0.0002
H3K9me2K14ac1	0.6454 ± 0.0000	H4K20me2	0.5177 ± 0.0000
H1.4K26un	0.7721 ± 0.0000	H4K20me3	0.3307 ± 0.0000
H4K31un	0.6182 ± 0.0001	H2A: ATIAGGGVIPHIHK	0.8016 ± 0.0001
H2A: GKQGGKAR	0.7222 ± 0.0000	H2A: NDEELNKLGR	0.7135 ± 0.0000
H2A: KGNYAER	0.6311 ± 0.0000	H2B: LAHYNKR	0.6448 ± 0.0000
H2A: KGNYSER	0.7215 ± 0.0001	H2B: PEPAK	0.6293 ± 0.0000

<sup>1</sup> Absolute turnover values (mean ± standard deviation per day) extrapolated from the relative distribution of the isotopically labeled bulk H3, H4 and H1.4 peptides with a particular post-translational modification.

<sup>2</sup>me = methyl

<sup>3</sup>ac = acetyl

<sup>4</sup>The H2A and H2B turnover values are averages of all histone variants containing the specific peptide sequence.

<sup>5</sup>The model was iterated 200 times for each individual peptide, where the average and standard deviation were taken for parameters within 105% of the determined optimum parameter.

<sup>6</sup>For H3K18/K23ac1, H3K9/K14ac1, and H4K5/K8/K12/K16ac1, ac2 and ac3, the localization of the acetyl(s) on the multiple lysines was not determined.