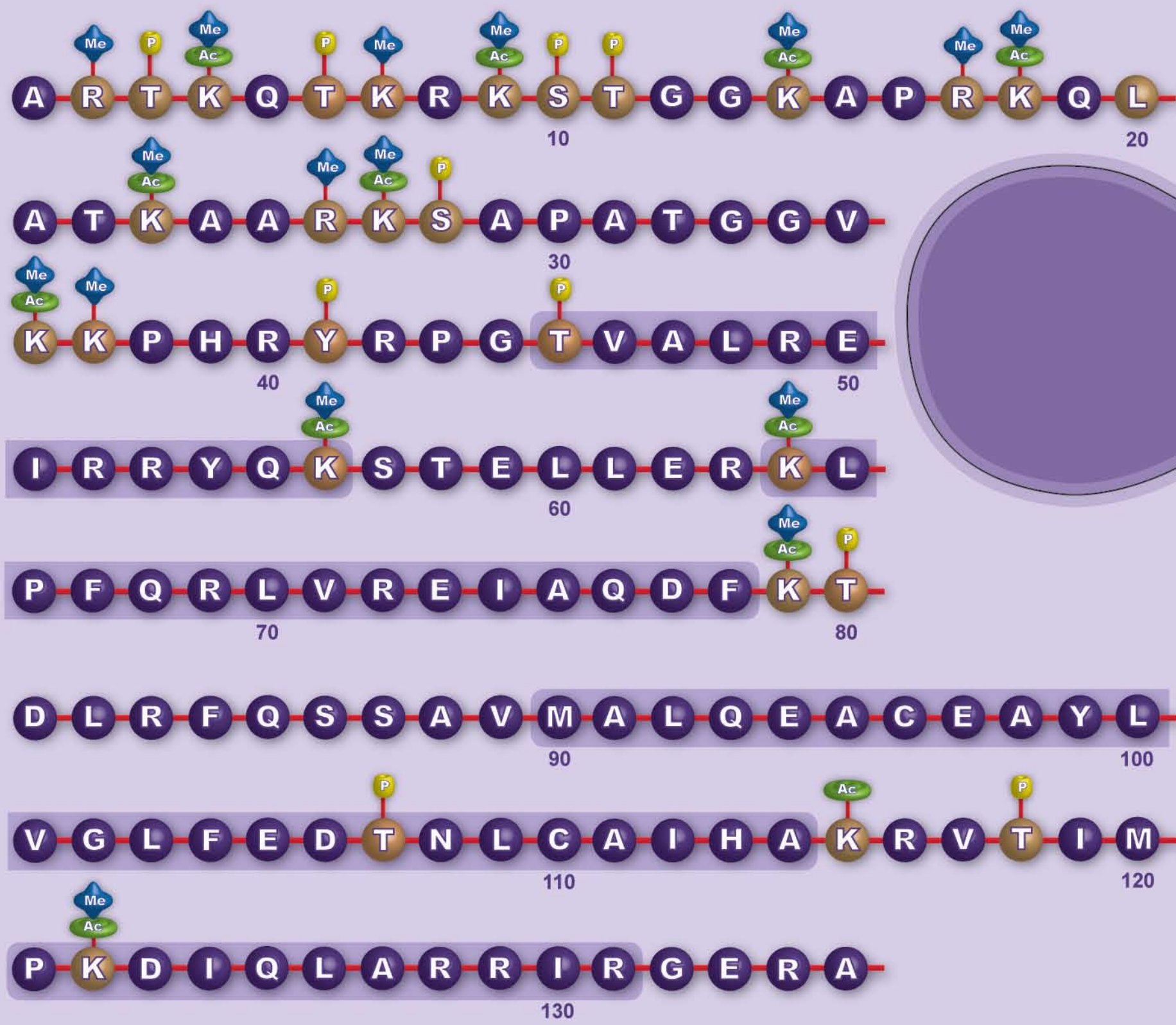
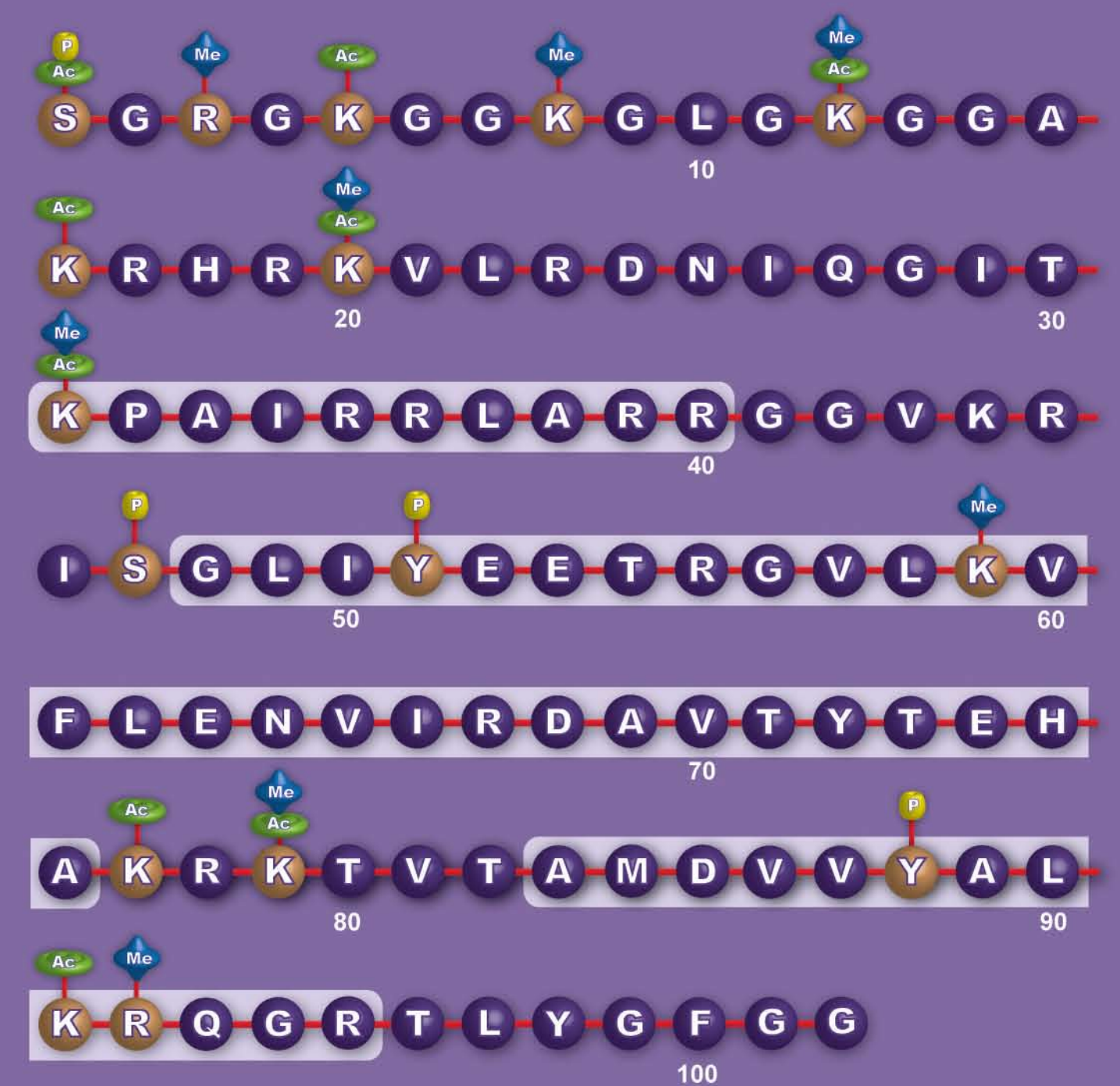


Histone Modifications

Histone H3



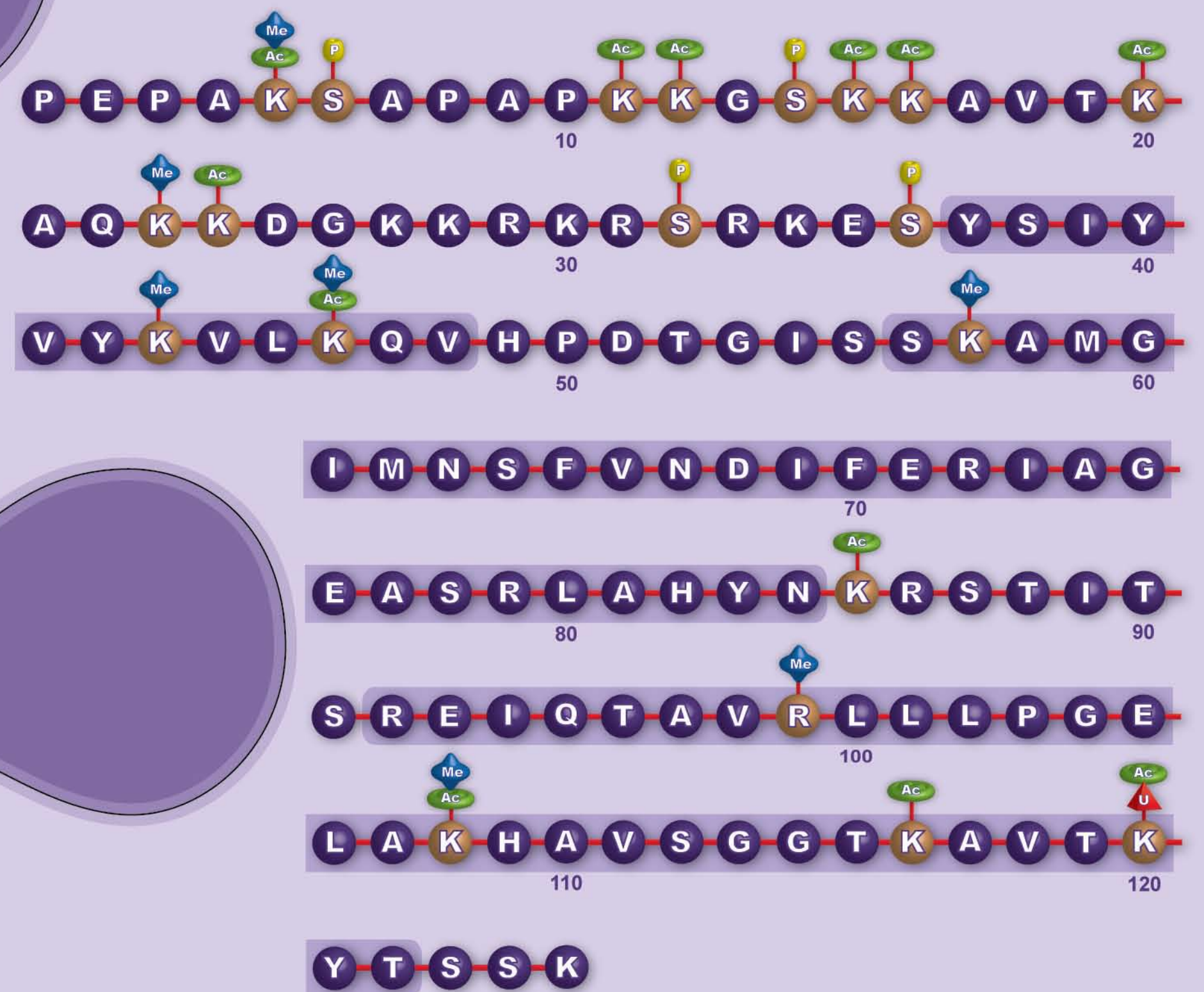
Histone H4



Histone H2A



Histone H2B



Ac Acetylation
 Me Methylation
 P Phosphorylation
 U Ubiquitylation
 Structured Domain

Histone Modifications and Associated Biological Function

Residue	Modification	Associated Function	Writer	Eraser	Reader
Histone H2A					
Ser 1	Phosphorylation	Mitosis	PKC		
Lys 5	Acetylation	Transcriptional activation	CBP, p300, HAT1		
Lys 119	Ubiquitylation	Spermatogenesis	RNF1		
Thr 120	Phosphorylation	Mitosis	NHK1		
Histone H2AX					
Ser 139	Phosphorylation	DNA Damage repair, apoptosis	ATM, ATR	PP4	MDC1
Tyr 142	Phosphorylation	Regulation of DNA damage foci formation	BAZ1B	EYA	APBB1
Histone H2B					
Lys 5	Acetylation	Transcriptional activation	p300		
Lys 12	Acetylation	Transcriptional activation	CBP, p300		
Ser 14	Phosphorylation	Apoptosis	MST1		
Lys 15	Acetylation	Transcriptional activation	CBP, p300		
Lys 20	Acetylation	Transcriptional activation	CBP, p300		
Lys 120	Ubiquitylation	Transcription (elongation ?)	RNF20		
Histone H3					
Arg 2	Methylation	Transcriptional activation	CARM1, PRMT6	JMJD6	
Thr 3	Phosphorylation	Mitosis	Hsp90, VIK1		Survivin
Lys 4	Acetylation	Transcriptional activation			
Lys 4	Methylation	Euchromatin, transcriptional activation	MLL, SET1, ASH1, SET7, SMYD2	LSD1/BHC10, JHDM1A / KDM2A, JHDM1B / KDM2B, JARID1A / KDM5A, JARID1B / KDM5B, JARID1C / KDM5C, JARID1D / KDM5D	CHD1, ING family, RAG2, TAF3, BPTF, BHC80, DNMT3L, PYGO1, JMJD2A, WDR5, JMJD2A, JMJD2C
Thr 6	Phosphorylation	Transcriptional activation	PKCβ		
Arg 8	Methylation	Transcriptional activation	PRMT5		
Lys 9	Acetylation	Histone deposition, Transcriptional activation	GCN5, PCAF, SRC1	SIRT6	BRD4, BAZ1B
Lys 9	Methylation	Transcriptional silencing, heterochromatin	SUV39H1/2, G9a, CLL1, SETDB1, EubMTL, Rtt1	JMJD1A / KDM3A, JMJD1B / KDM3B, JMJD1C / TRIP8, JMJD2A / KDM4A, JMJD2B / KDM4B, JMJD2C / KDM4C, JMJD2D / KDM4D	L3MBTL1/L2, HPI, MPP8, CDY family, TDRD7
Ser 10	Phosphorylation	Mitosis, immediate early gene activation	Aurora B, MSK1, IKKε	PP1	14-3-3
Thr 11	Phosphorylation	Mitosis, DNA damage induced transcription	DIK		
Lys 14	Acetylation	Transcriptional activation	GCN5, PCAF, CBP, p300, MOZ, MORF, TIP60, SRC1		BRD4
Arg 17	Methylation	Transcriptional activation	CARM1		
Lys 18	Acetylation	Transcriptional activation	GCN5, PCAF, CBP, p300		
Lys 23	Acetylation	Transcriptional activation	GCN5, PCAF, p300		
Arg 26	Methylation	Transcriptional activation	CARM1		
Lys 27	Methylation	Transcriptional silencing	EZH2, EZH1	JMJD1A / KDM3A, JMJD1B / KDM3B, KDM6A / UTX, JMJD3 / KDM6B	Pc, CDY family
Ser 28	Phosphorylation	Mitosis	Aurora B		
Lys 36	Acetylation	Transcriptional activation	GCN5, PCAF		
Lys 36	Methylation	Transcription elongation	NSD1, SET7, SMYD2, NSD2	JHDM1A / KDM3A, JHDM1B / KDM3B, JHDM3A / KDM4A, JHDM3B / KDM4B, JHDM3C / KDM4C, JHDM3D / KDM4D	MRG15
Thr 45	Phosphorylation	DNA replication, apoptosis	PKCδ		
Lys 56	Acetylation	DNA Damage repair, chromatin assembly	CBP, p300		
Lys 79	Methylation	Transcriptional activation	DOT1L		
Histone H4					
Ser 1	Phosphorylation	Transcriptional activation	CKII		
Arg 3	Methylation	Transcriptional activation	PRMT1, PRMT5	JMJD6	
Lys 5	Acetylation	Histone deposition, Transcriptional activation	ATF2, HAT1, CBP, p300, TIP60, HBO1		BRD4
Lys 8	Acetylation	Transcriptional activation	CBP, p300, TRPA4, HBO1		
Lys 12	Acetylation	Histone deposition, Transcriptional activation	HAT1, CBP, p300, TIP60, HBO1		BRD2, BRD4
Lys 16	Acetylation	Transcriptional activation	MOF, TIP60	SIRT1	
Lys 20	Methylation	Transcriptional silencing, heterochromatin	PR-SET7 (mono), SUV420H1 (di), SUV420H2 (tri)		L3MBTL1, JMJD2A, 53BP1, Pdp1, PHF20, JMJD2A
Lys 91	Acetylation	Histone deposition, DNA damage repair	HAT1		

HISTONE MODIFICATIONS, such as acetylation, phosphorylation, methylation, ubiquitylation, and ADP ribosylation of the highly conserved core histones, H2A, H2B, H3 and H4, are involved in the regulation of genome organization and function. The enormous regulatory potential of histone modifications is illustrated in the vast array of epigenetic markers found throughout the genome. More than the other types of histone modification, acetylation and methylation of specific lysine residues on N-terminal histone tails are fundamental to the formation of functional chromatin domains, such as active euchromatin or silent heterochromatin.

The poster above includes all known histone modifications, whereas the table to the left includes only modifications with known biological function. Also included in the table is information on the "Writers" (enzymes that deposit the modification), "Erasers" (enzymes that remove the modification) and "Readers" (proteins that specifically bind the modification).