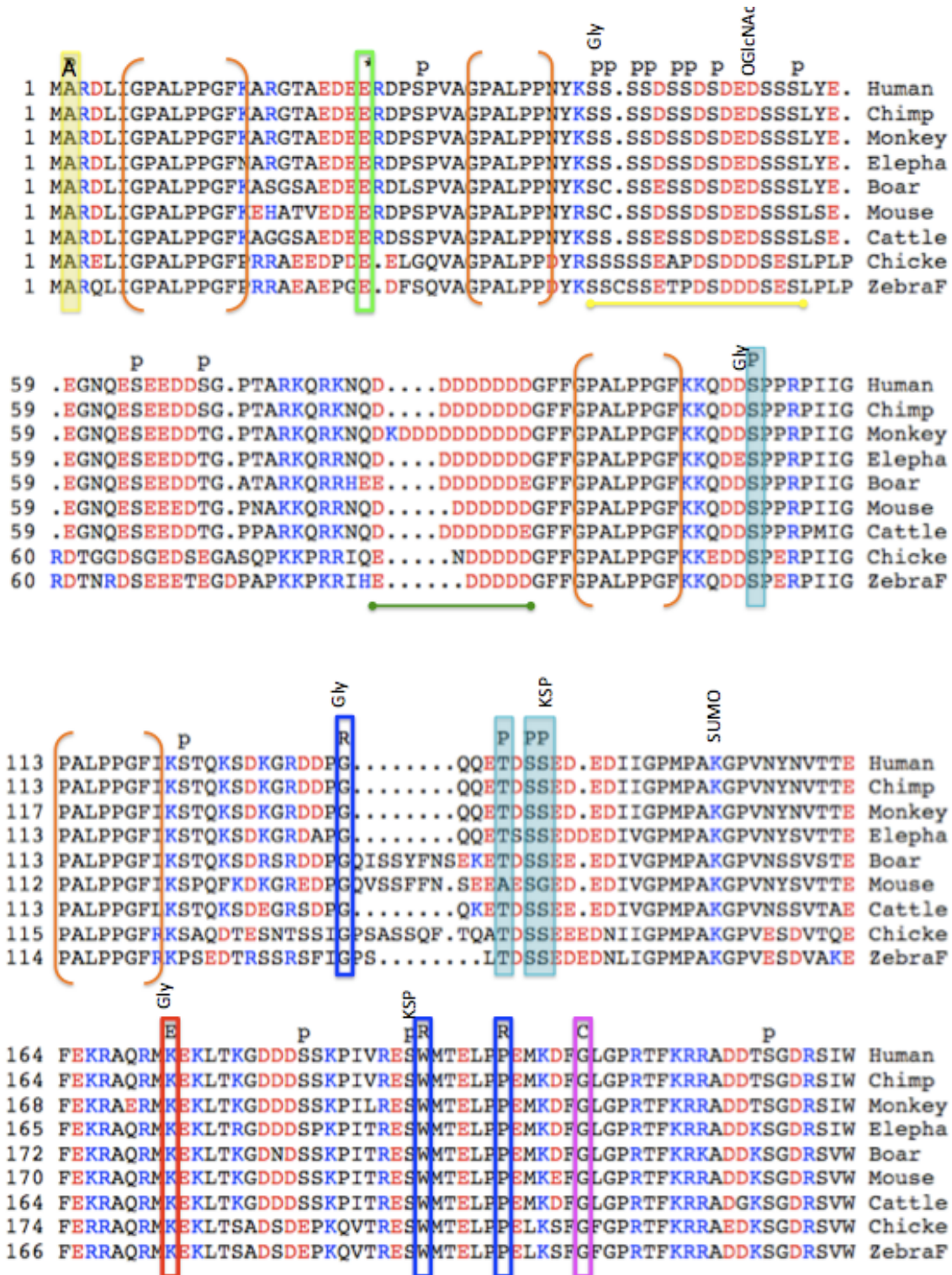


KIAA1704 Annotated Charge Multiple Sequence Alignment



KIAA1704 Annotated Charge Multiple Sequence Alignment

Charges

Acidic= Red font

Basic= Blue font

Neutral= Black font

Experimental Post-Translational Modification Sites

Acetylation

A2

Yellow Highlight

Phosphorylation

S105, T138, S140, S141

Teal Highlight

Conserved Predicted Post-Translational Modification Sites

Tool

Amino Acid Site

Sequence Label

Glycation

S41, D104, G134, K172, D306,
S332, N337, M338

Glyc

O-linked N-acetylglucosamine

D52

OGlcNAc

Kinase Specific Phosphorylation

S141 (CKII), S190 (PKA), S270
(PKC)

KSP

SUMO Protein Attachment

K153

SUMO

Serine Phosphorylation

28, 42, 43, 44, 46, 47, 49, 55, 64,
69, 105, 126, 140, 141, 182, 190,
217, 243, 244, 245, 254, 266, 275,
332

p above sequence

Threonine Phosphorylation

226

p above sequence

Conserved Single Nucleotide Polymorphisms (SNPs)

Normal Charge

Converted SNP Charge

Visual Representation

Acidic/ Neutral

Basic

Blue rectangle

Basic/ Neutral

Acidic

Red rectangle

Acidic/ Basic/ Neutral

Neutral

Purple rectangle

Basic

STOP

Lime green rectangle