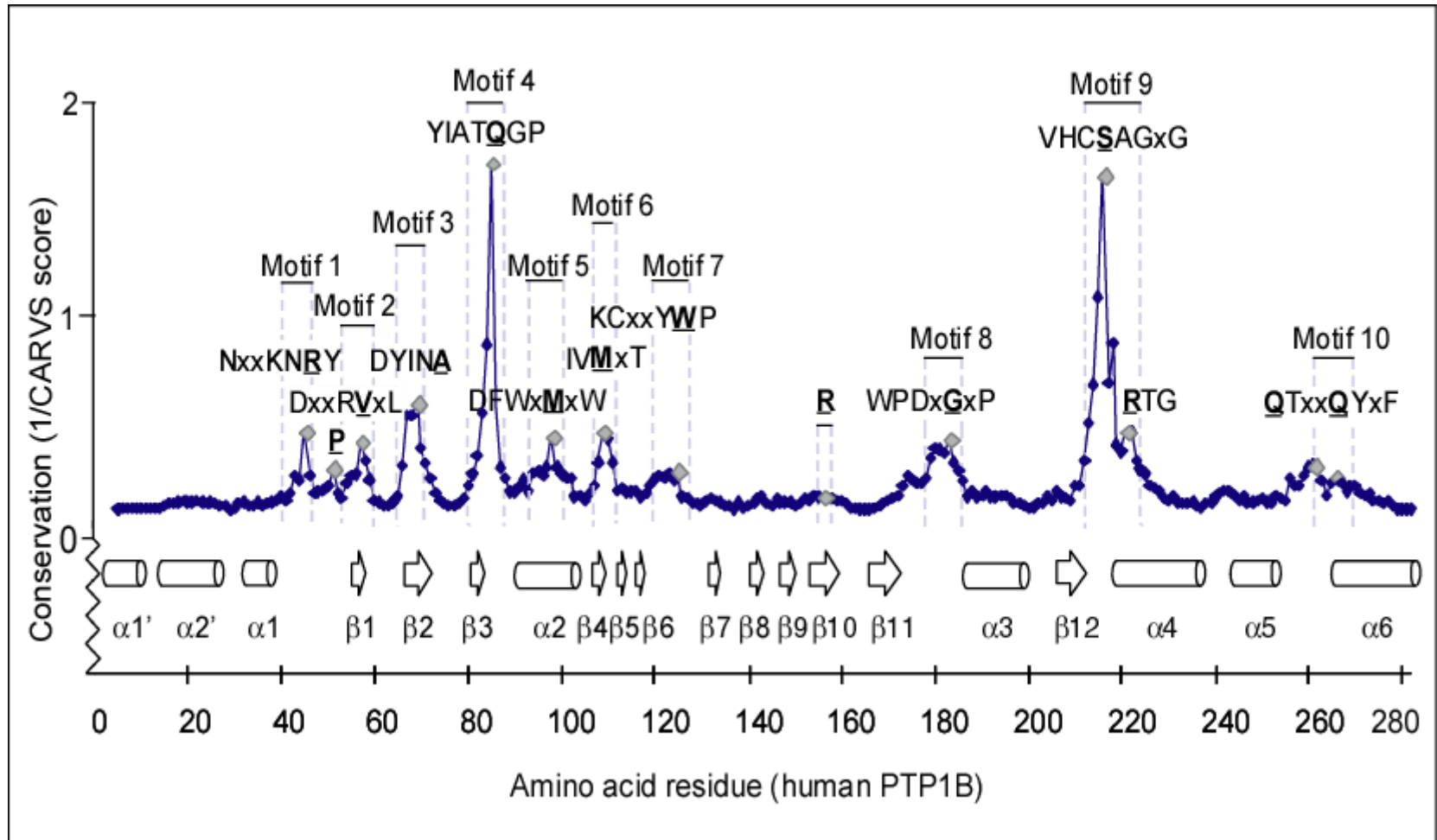


The HCSAGxGR and IAxQGP motifs reside within the most highly conserved microenvironment of the PTP structure



Residues located within a highly conserved three-dimensional space of the PTP structure are identified by peaks. The α -region variation score was calculated based on 37 aligned human PTP catalytic domains and using the tertiary structure of PTP1B as template. (See review for details).