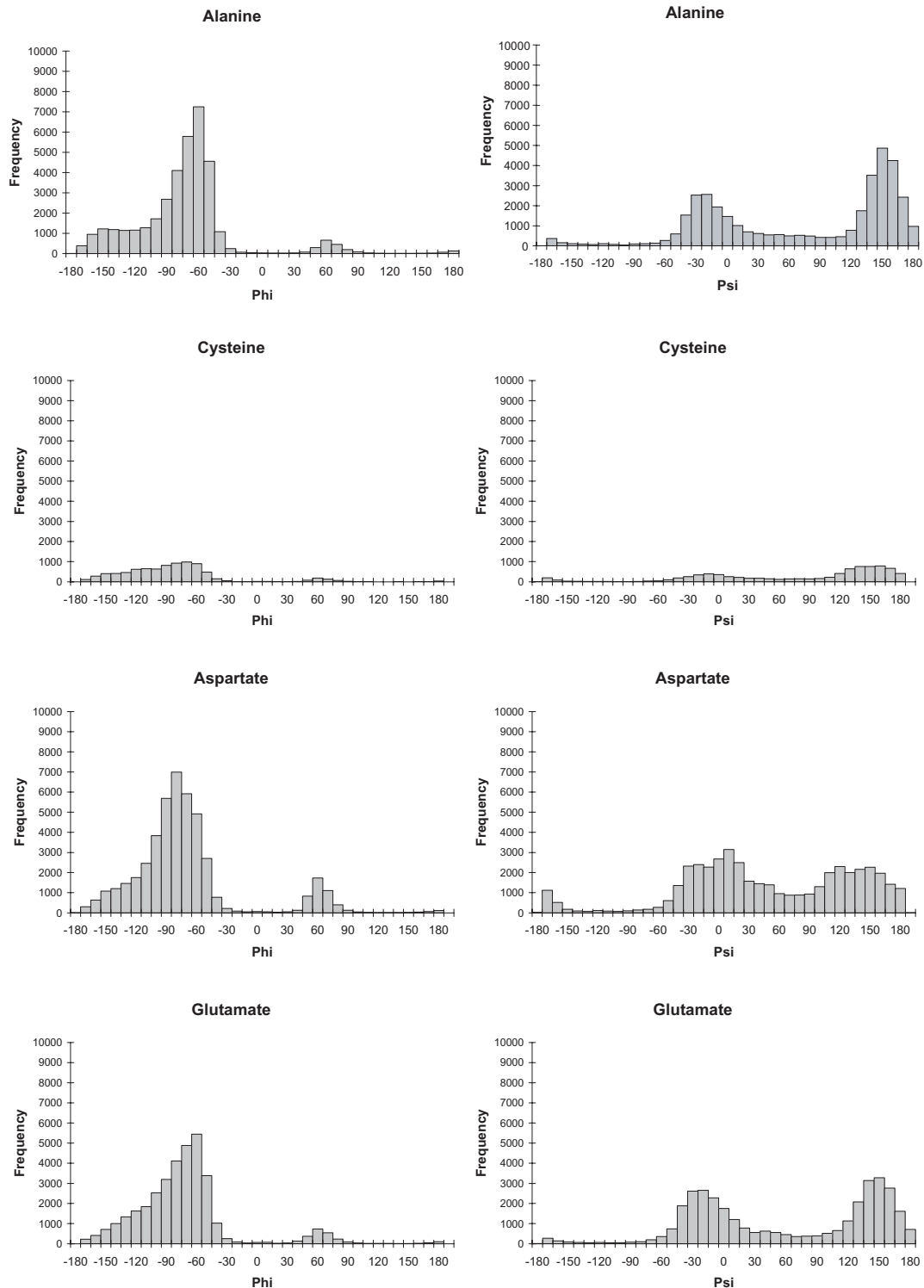


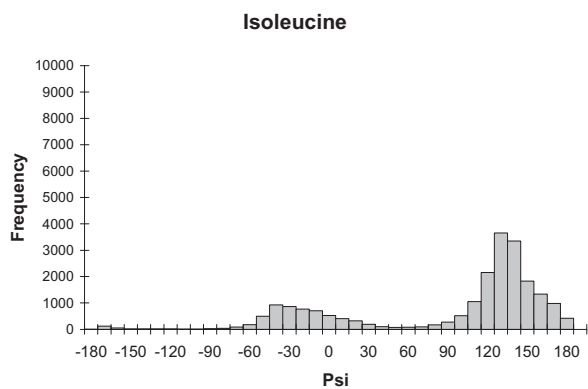
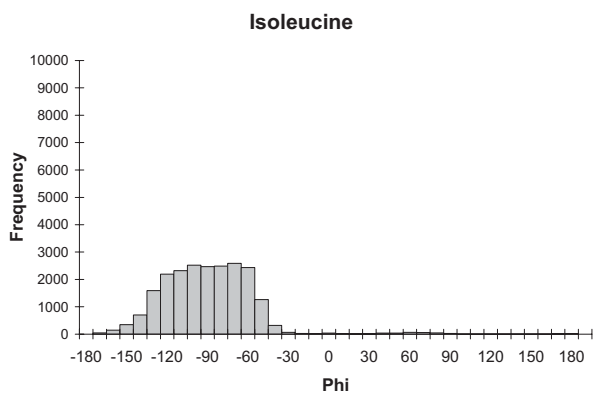
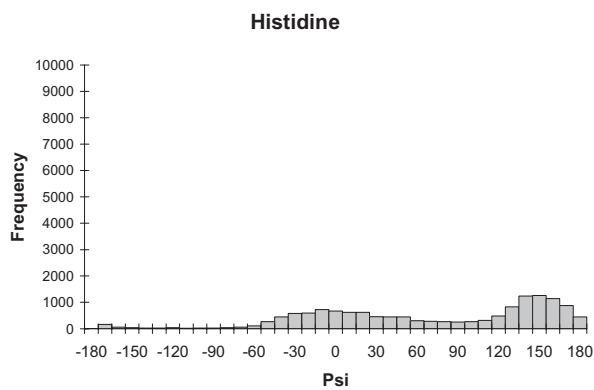
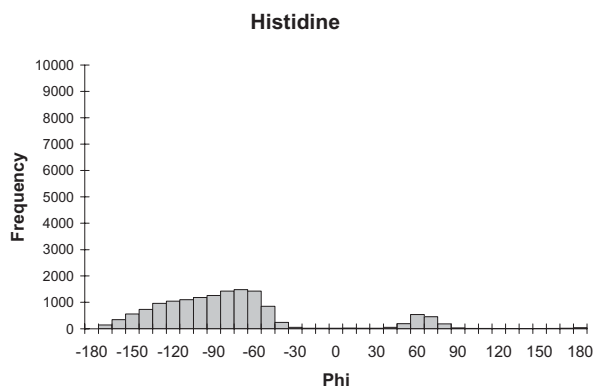
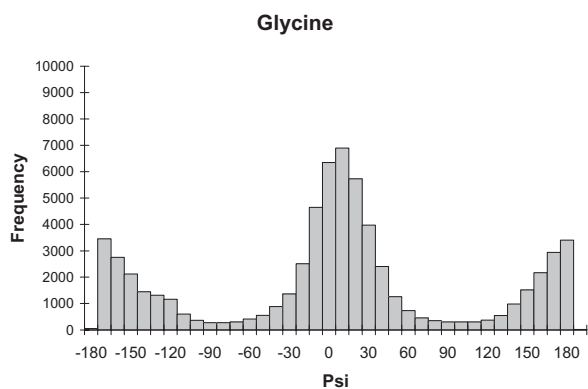
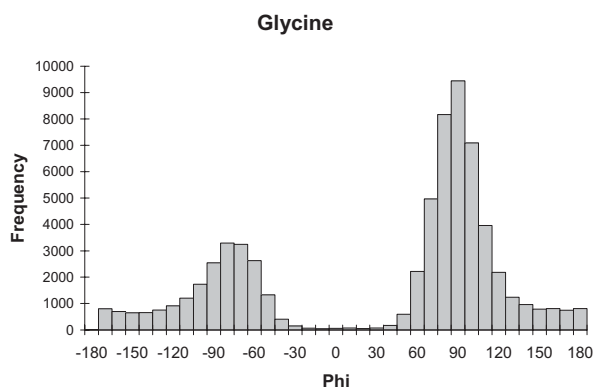
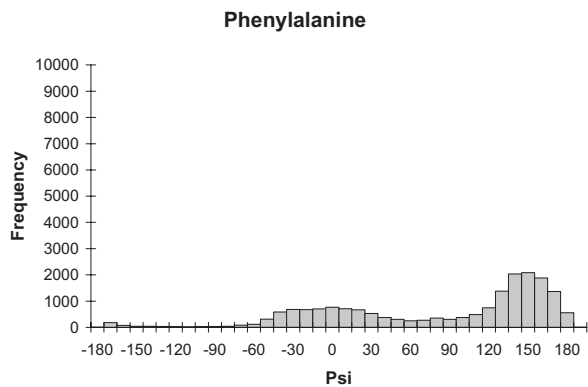
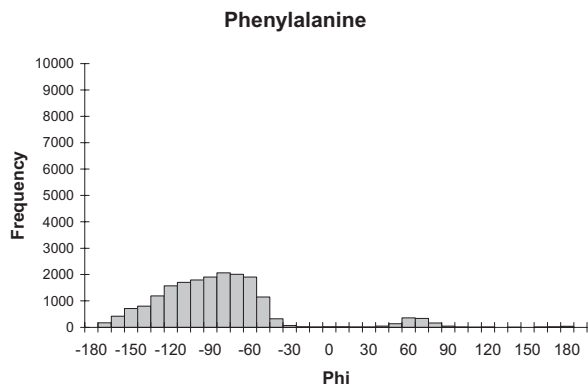
# ProRegIn: A regularity index for the selection of native-like tertiary structures of proteins

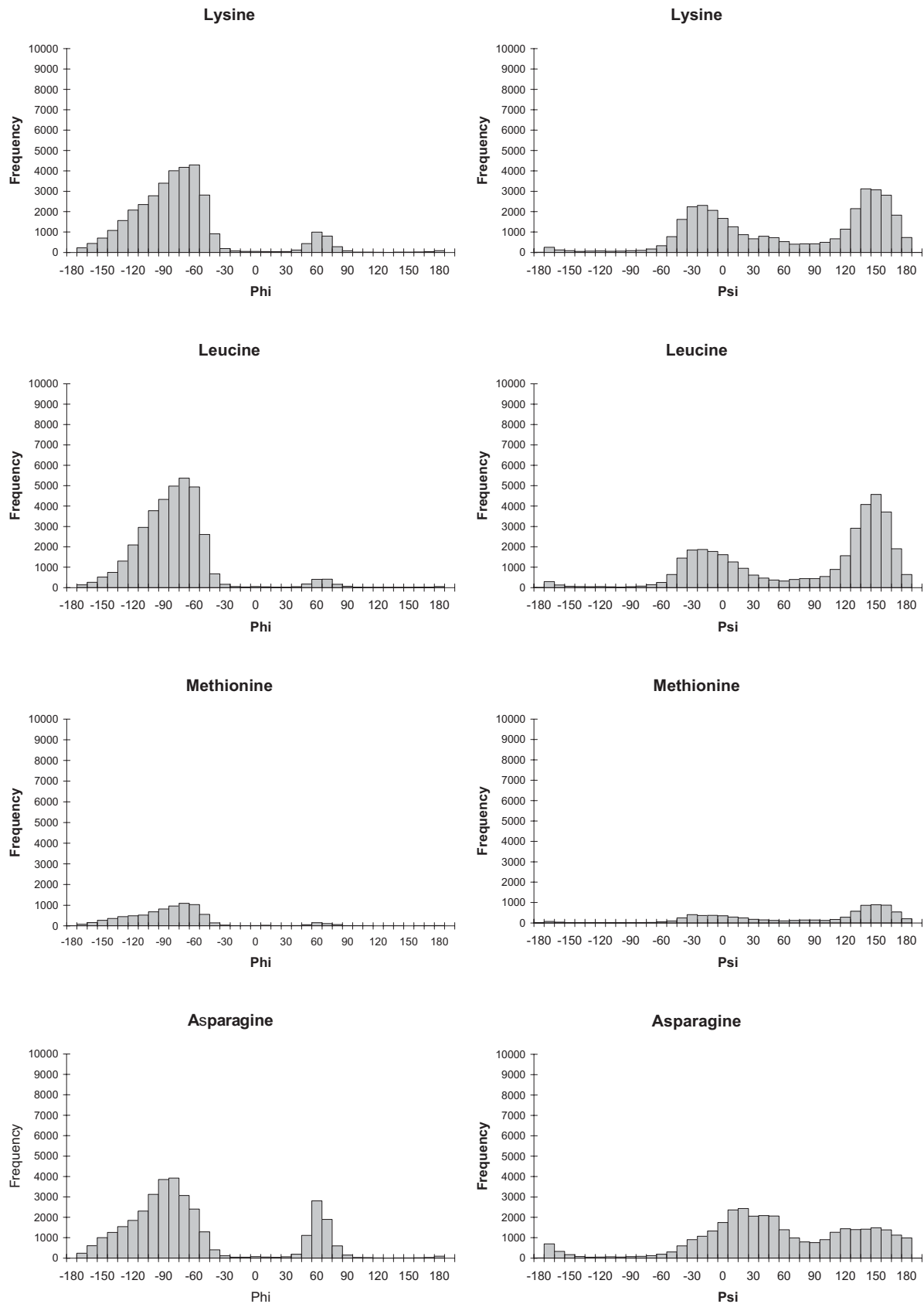
LIPI THUKRAL, SANDHYA R SHENOY, KUMKUM BHUSHAN and B JAYARAM  
*J. Biosci.* 32(1), January 2007, 71–81, © Indian Academy of Sciences

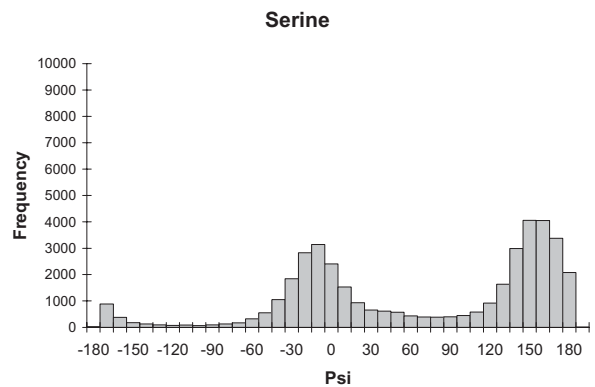
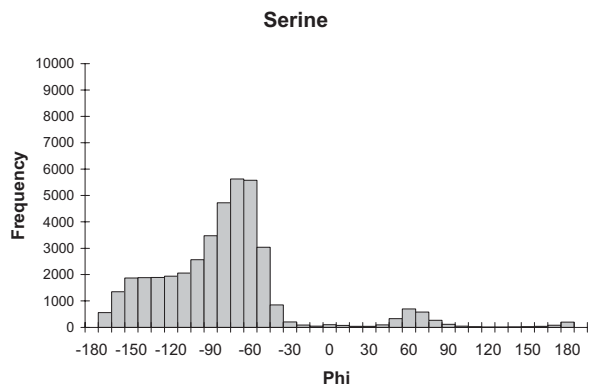
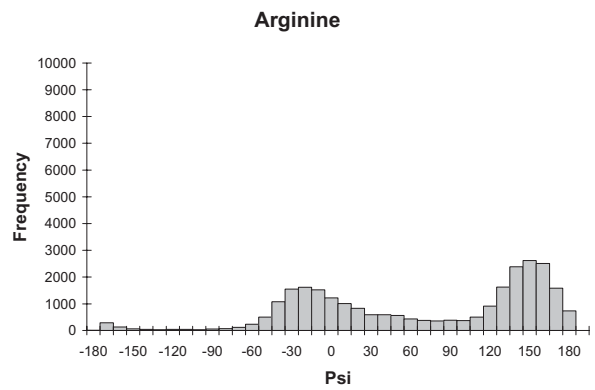
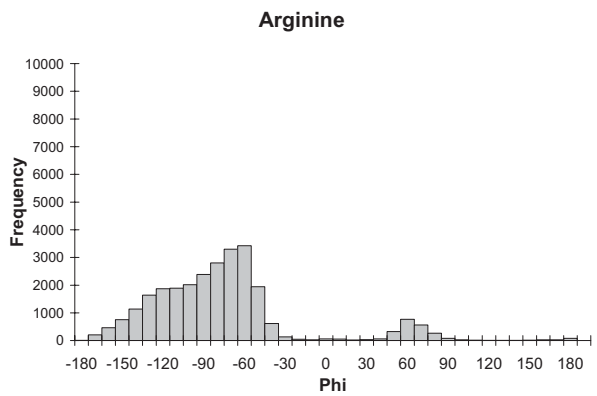
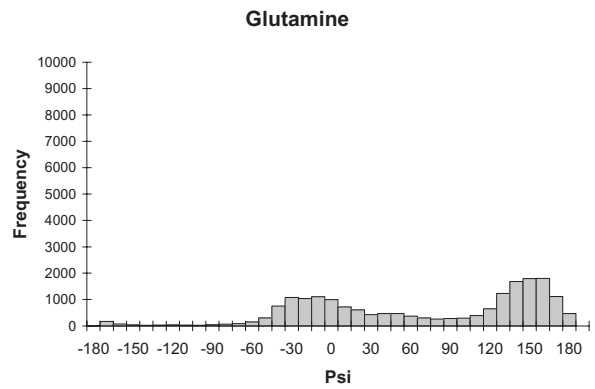
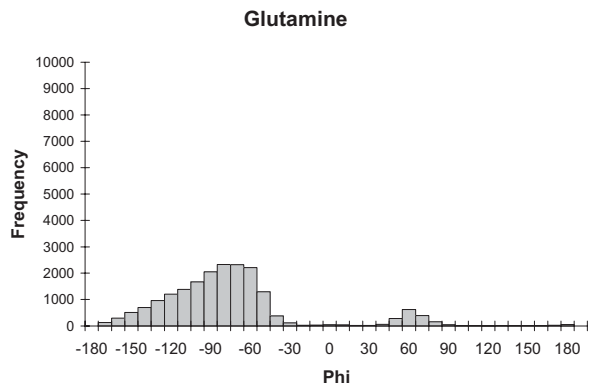
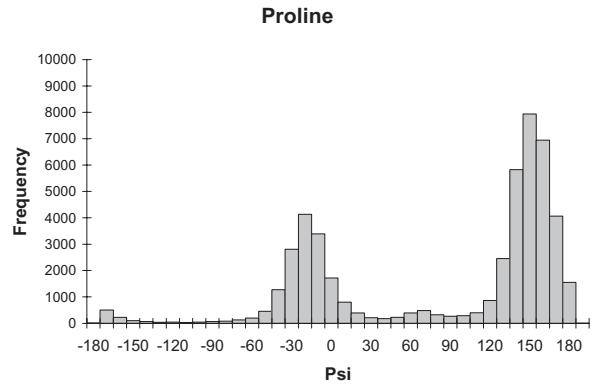
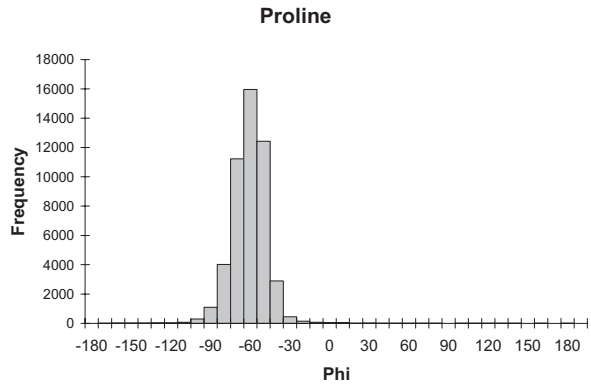
## Supplementary Data

Frequency plots of loop dihedrals of all the amino acids in the entire 7351 non-redundant protein dataset.

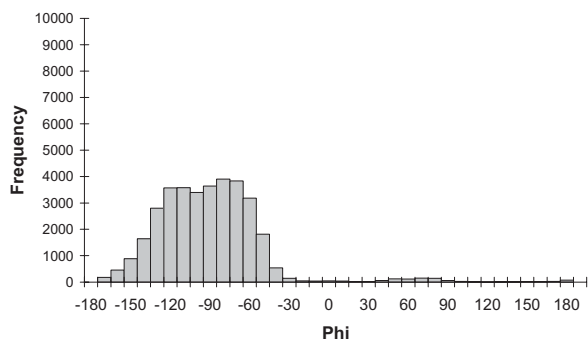




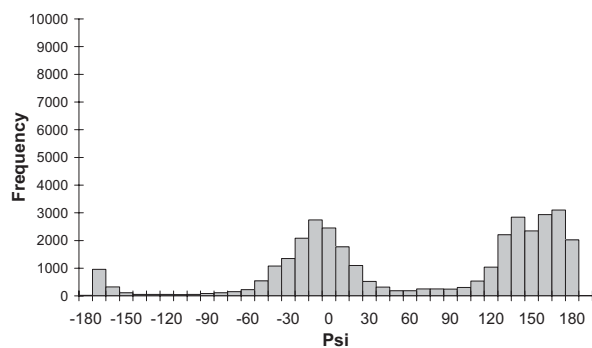




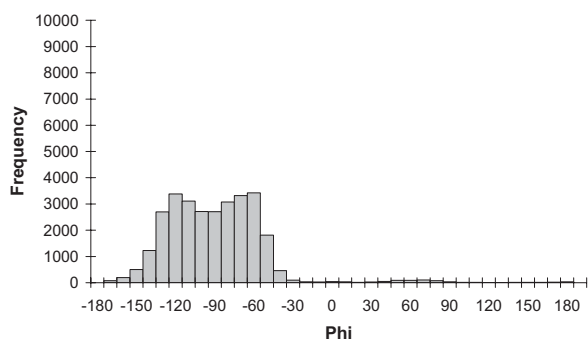
Threonine



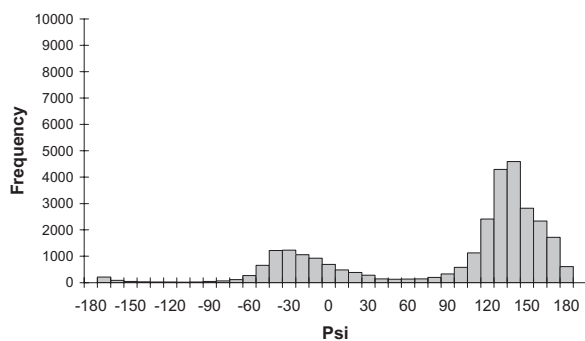
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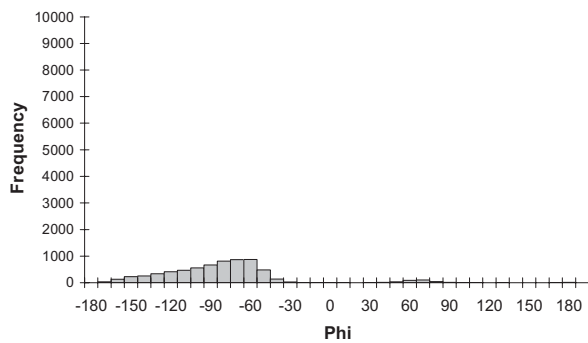
Valine



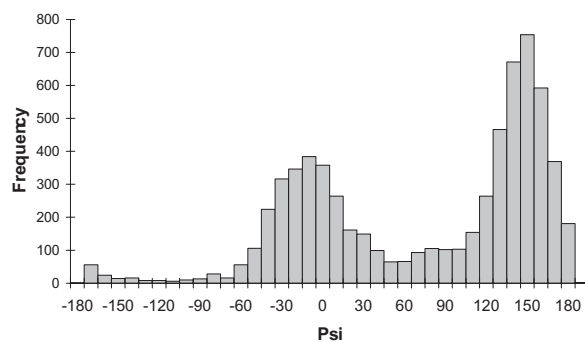
Valine



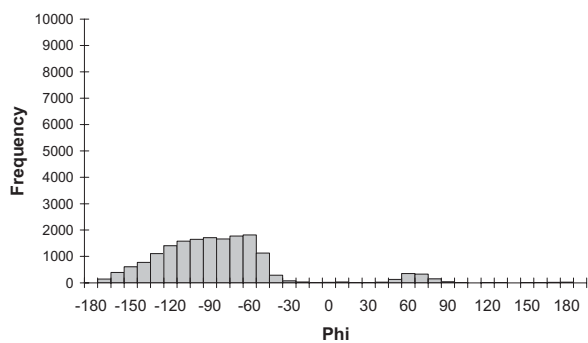
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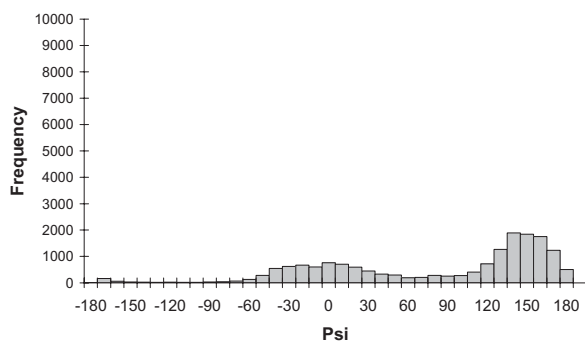
Tryptophan



Tyrosine



Tyrosine



Regularity Index for  $\Phi$  and  $\Psi$  for all twenty amino acids using STRIDE structural assignment method.

