



The conservation scale:



- e - An exposed residue according to the neural-network algorithm.
- b - A buried residue according to the neural-network algorithm.
- f - A predicted functional residue (highly conserved and exposed).
- X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

Figure S4. ZFMP1/FOG1 ConSurf conservation analysis. The figure illustrates the conservation results for protein interval L420 – P480 using the color-coding bar; the highly variable and conserved residues are shown in turquoise and maroon, respectively. Yellow colored residues denote regions with low confidence of conservation level due to insufficient data and hence excluded from the analysis. [The ConSurf web server (<http://consurf.tau.ac.il>)]