



Figure S1. DBD domain alignment of Hsf proteins from *L. japonicus*, *M. truncatula*, *C. arietinum*, *G. max*, *C. cajan*, *P. vulgaris* and three lower plants. The multiple alignment results clearly show the highly conserved DBD domains among Hsfs. The secondary structure of DBD domain is formed of a three-helical bundle and a four stranded antiparallel β -sheet.