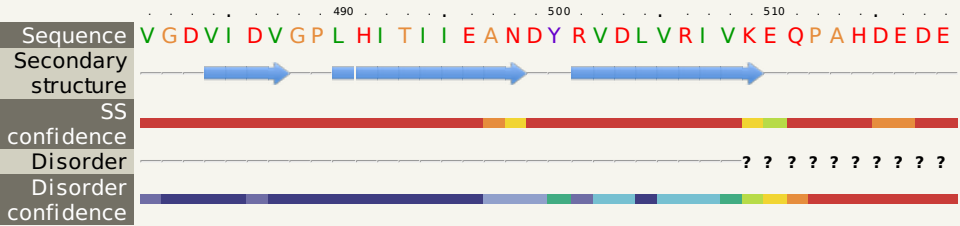
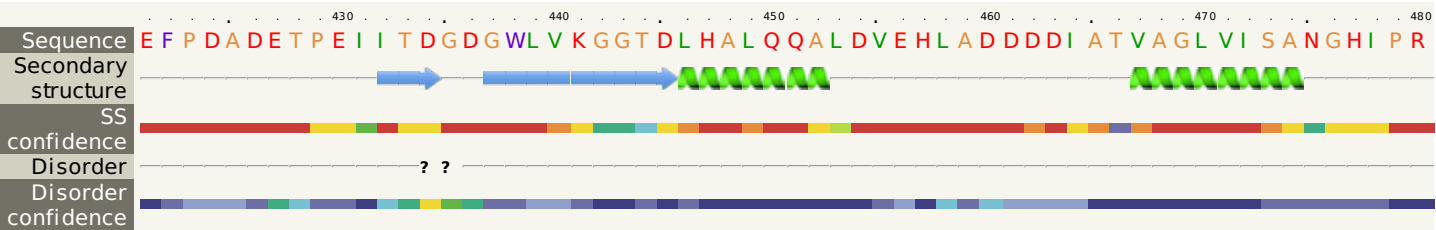


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Description	P0AEC0
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Protein structure and sequence analysis of the human protein (P05125). The figure displays the full-length protein sequence (1-420 residues) and its predicted secondary structure (alpha-helices and beta-strands). The sequence is color-coded by amino acid type. The secondary structure is shown as a green ribbon model. The protein is annotated with various domains and motifs, including a signal peptide (1-16), a transmembrane domain (17-21), a coiled-coil domain (22-31), a zinc finger domain (32-41), a helix-loop-helix domain (42-51), a helix-turn-helix domain (52-61), a helix-loop-helix domain (62-71), a helix-turn-helix domain (72-81), a helix-loop-helix domain (82-91), a helix-turn-helix domain (92-101), a helix-loop-helix domain (102-111), a helix-turn-helix domain (112-121), a helix-loop-helix domain (122-131), a helix-turn-helix domain (132-141), a helix-loop-helix domain (142-151), a helix-turn-helix domain (152-161), a helix-loop-helix domain (162-171), a helix-turn-helix domain (172-181), a helix-loop-helix domain (182-191), a helix-turn-helix domain (192-201), a helix-loop-helix domain (202-211), a helix-turn-helix domain (212-221), a helix-loop-helix domain (222-231), a helix-turn-helix domain (232-241), a helix-loop-helix domain (242-251), a helix-turn-helix domain (252-261), a helix-loop-helix domain (262-271), a helix-turn-helix domain (272-281), a helix-loop-helix domain (282-291), a helix-turn-helix domain (292-301), a helix-loop-helix domain (302-311), a helix-turn-helix domain (312-321), a helix-loop-helix domain (322-331), a helix-turn-helix domain (332-341), a helix-loop-helix domain (342-351), a helix-turn-helix domain (352-361), a helix-loop-helix domain (362-371), a helix-turn-helix domain (372-381), a helix-loop-helix domain (382-391), a helix-turn-helix domain (392-401), a helix-loop-helix domain (402-411), a helix-turn-helix domain (412-420).



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand