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Figure 1 displays the protein structure and disorder analysis for the human protein encoded by the LOC101929 gene. The protein sequence is shown in three segments, with positions 1-60, 70-120, and 130-180. The secondary structure is predicted using a green helix and blue strand model. The disorder analysis includes SS confidence, Disorder, and Disorder confidence scores.

Position	Sequence	Secondary structure	SS confidence	Disorder	Disorder confidence
1-60	MKSLQALFGGTFDPVHYGHLKPVETLANLILGLTRVTIIPNNVPPHRPQPEANSVQRKHML	Helix (10-30), Helix (35-45), Helix (55-60)	Low confidence (red/orange)	Disordered (blue)	High confidence (dark blue)
70-120	ELAIADKPLFTLDERELKRNAPS YTAQTLKEWRQEQQPDVPLAFIIGQDSLTLTPTWY EY	Helix (70-80), Helix (85-95), Helix (100-110), Helix (115-120)	Low confidence (red/orange)	Disordered (blue)	High confidence (dark blue)
130-180	ETILDNAHLIVCRRPGYPLEMAQPQYQQWLEDHLTHNPEDLHLQPAGKIYLAETPWFNIS	Helix (130-140), Helix (145-155), Helix (160-170), Helix (175-180)	Low confidence (red/orange)	Disordered (blue)	High confidence (dark blue)
190-210	ATII RERLQNGESCEDLLPEPVLTYINQQGLYR	Helix (190-200), Helix (205-210)	Low confidence (red/orange)	Disordered (blue)	High confidence (dark blue)

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand