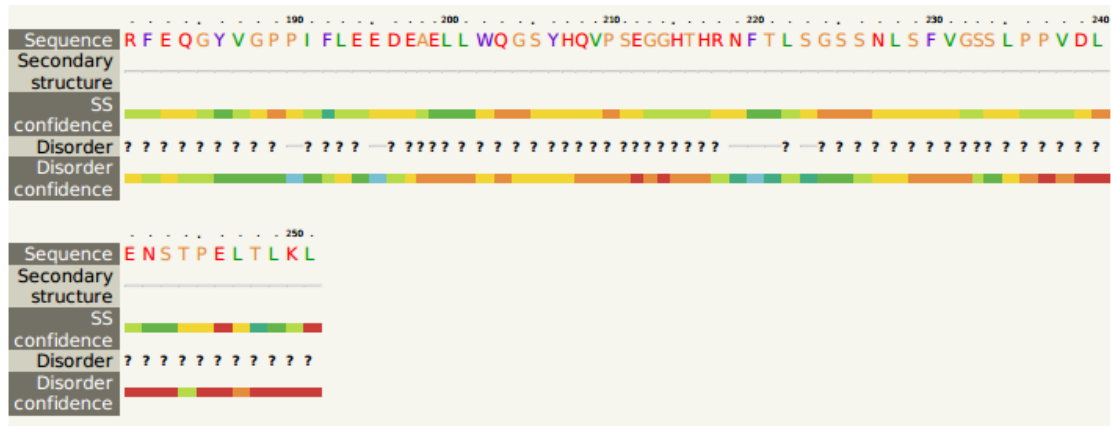


Supplementary data

Sequences producing significant alignments									
<div> Download New Select columns Show 100 </div>									
<input checked="" type="checkbox"/> select all 79 sequences selected <div> GenBank Graphics Distance tree of results New MSA Viewer </div>									
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Glycine max zinc finger protein mRNA, complete cds	Glycine max	1397	1397	100%	0.0	100.00%	940	MK045991.1
<input checked="" type="checkbox"/>	Glycine max zinc finger protein 4-like (LOC100815175) mRNA	Glycine max	1386	1386	100%	0.0	99.74%	1715	NM_00125238.3
<input checked="" type="checkbox"/>	PREDICTED: Glycine max zinc finger protein 4-like (LOC100815175) transcript variant X5 mRNA	Glycine max	1386	1386	100%	0.0	99.74%	1500	XM_006601778.4
<input checked="" type="checkbox"/>	PREDICTED: Glycine max zinc finger protein 4-like (LOC100815175) transcript variant X4 mRNA	Glycine max	1386	1386	100%	0.0	99.74%	1986	XM_041011635.1
<input checked="" type="checkbox"/>	PREDICTED: Glycine max zinc finger protein 4-like (LOC100815175) transcript variant X3 mRNA	Glycine max	1386	1386	100%	0.0	99.74%	1494	XM_006601777.3
<input checked="" type="checkbox"/>	PREDICTED: Glycine max zinc finger protein 4-like (LOC100815175) transcript variant X2 mRNA	Glycine max	1386	1386	100%	0.0	99.74%	1939	XM_006601779.4
<input checked="" type="checkbox"/>	PREDICTED: Glycine max zinc finger protein 4-like (LOC100815175) transcript variant X1 mRNA	Glycine max	1386	1386	100%	0.0	99.74%	1557	XM_006601775.3

Sequences producing significant alignments									
<div> Download Select columns Show 100 </div>									
<input checked="" type="checkbox"/> select all 100 sequences selected <div> GenPept Graphics Distance tree of results Multiple alignment MSA Viewer </div>									
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	zinc finger protein [Glycine max]	Glycine max	516	516	100%	0.0	100.00%	251	GQP72003.1
<input checked="" type="checkbox"/>	zinc finger protein 4-like [Glycine max]	Glycine max	511	511	100%	0.0	99.20%	251	NP_001242167.2
<input checked="" type="checkbox"/>	zinc finger protein 4-like [Glycine soja]	Glycine soja	508	508	100%	0.0	98.80%	251	XP_028215696.1
<input checked="" type="checkbox"/>	unknown [Glycine max]	Glycine max	507	507	100%	0.0	98.41%	251	ACU21215.1
<input checked="" type="checkbox"/>	Zinc finger protein 4 [Spatholobus suberectus]	Spatholobus suberectus	432	432	100%	1e-151	86.10%	258	TKY47376.1
<input checked="" type="checkbox"/>	zinc finger protein 4 [Cajanus cajan]	Cajanus cajan	430	430	100%	1e-150	83.40%	258	XP_020212769.1
<input checked="" type="checkbox"/>	hypothetical protein PHAVU_001G228400q [Phaseolus vulgaris]	Phaseolus vulgaris	422	422	100%	9e-148	80.38%	256	XP_007163363.1

Figure 1: Schematic representation of the protein structure of the human protein. The figure shows three segments of the protein structure, each with a sequence, secondary structure, and confidence scores. The segments are labeled 1, 2, and 3. Segment 1 (residues 1-60) shows a sequence of MKQHFDLLEVVASAEY ESEVSSSKVASNISIQETYAGPCSDNLTNSSNVTNPIELHLHSDAI. Segment 2 (residues 70-120) shows a sequence of SLDLTLKFNNDFSFSSTSESSNGPLSQTNLAANPRVFS CNYCKRKFFSS QALGGHQNAAH. Segment 3 (residues 130-180) shows a sequence of KRERTIAKRAMRMGIF SERYASLASLPFHGSFRSLGIKAHSLSLHHGFSPTRPPEMKSSA. The secondary structure is represented by blue arrows for alpha-helices and green cylinders for beta-sheets. The confidence scores are shown as a bar chart below the sequence, with colors indicating different levels of confidence.



D

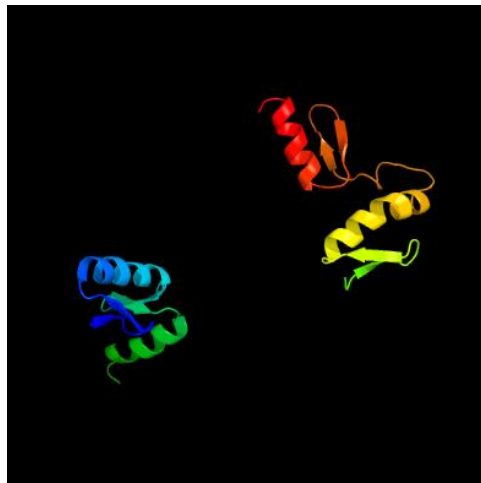


Fig. S1: Systemic bioinformatics analyses of *GmC2H24-like*. (A) BLASTn results between *GmC2H24-like* and other genes in NCBI (B) BLASTp results between *GmC2H24-like* and other proteins in NCBI (C) Secondary structure and disorder prediction of *GmC2H24-like* protein. (D) Tertiary structure model of *GmC2H24-like* protein. Image was coloured by rainbow N to C terminus. Model dimensions: X: 48.238, Y: 51.799, Z: 74.825.