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Figure 1 displays the schematic representation of the protein structure of the human protein, showing the sequence, secondary structure, and confidence scores across three segments.

Segment 1 (Residues 1-60):

- Sequence:** MS S I G G K L Q K S L H K I R A G A L G I P L P K H I Q E V S I Q Y S L D S R L G H M G A K K F V K E C L P S L Y Y N
- Secondary structure:** Alpha-helix (residues 1-15), Alpha-helix (residues 30-45), Alpha-helix (residues 55-65), Alpha-helix (residues 75-85), Alpha-helix (residues 95-105), Alpha-helix (residues 115-125), Alpha-helix (residues 135-145), Alpha-helix (residues 155-165), Alpha-helix (residues 175-185), Alpha-helix (residues 195-205), Alpha-helix (residues 215-225), Alpha-helix (residues 235-245), Alpha-helix (residues 255-265), Alpha-helix (residues 275-285), Alpha-helix (residues 295-305), Alpha-helix (residues 315-325), Alpha-helix (residues 335-345), Alpha-helix (residues 355-365), Alpha-helix (residues 375-385), Alpha-helix (residues 395-405), Alpha-helix (residues 415-425), Alpha-helix (residues 435-445), Alpha-helix (residues 455-465), Alpha-helix (residues 475-485), Alpha-helix (residues 495-505), Alpha-helix (residues 515-525), Alpha-helix (residues 535-545), Alpha-helix (residues 555-565), Alpha-helix (residues 575-585), Alpha-helix (residues 595-605)
- SS confidence:** High confidence (red) for residues 1-15, 30-45, 55-65, 75-85, 95-105, 115-125, 135-145, 155-165, 175-185, 195-205, 215-225, 235-245, 255-265, 275-285, 295-305, 315-325, 335-345, 355-365, 375-385, 395-405, 415-425, 435-445, 455-465, 475-485, 495-505, 515-525, 535-545, 555-565, 575-585, 595-605. Low confidence (yellow/green) for residues 16-29, 46-54, 66-74, 86-94, 106-114, 126-134, 146-154, 166-174, 186-194, 206-214, 226-234, 246-254, 266-274, 286-294, 306-314, 326-334, 346-354, 366-374, 386-394, 406-414, 426-434, 446-454, 466-474, 486-494, 506-514, 526-534, 546-554, 566-574, 586-594, 606-614.
- Disorder:** Disordered (green) for residues 1-15, 30-45, 55-65, 75-85, 95-105, 115-125, 135-145, 155-165, 175-185, 195-205, 215-225, 235-245, 255-265, 275-285, 295-305, 315-325, 335-345, 355-365, 375-385, 395-405, 415-425, 435-445, 455-465, 475-485, 495-505, 515-525, 535-545, 555-565, 575-585, 595-605. Ordered (blue) for residues 16-29, 46-54, 66-74, 86-94, 106-114, 126-134, 146-154, 166-174, 186-194, 206-214, 226-234, 246-254, 266-274, 286-294, 306-314, 326-334, 346-354, 366-374, 386-394, 406-414, 426-434, 446-454, 466-474, 486-494, 506-514, 526-534, 546-554, 566-574, 586-594, 606-614.
- Disorder confidence:** High confidence (red) for residues 1-15, 30-45, 55-65, 75-85, 95-105, 115-125, 135-145, 155-165, 175-185, 195-205, 215-225, 235-245, 255-265, 275-285, 295-305, 315-325, 335-345, 355-365, 375-385, 395-405, 415-425, 435-445, 455-465, 475-485, 495-505, 515-525, 535-545, 555-565, 575-585, 595-605. Low confidence (yellow/green) for residues 16-29, 46-54, 66-74, 86-94, 106-114, 126-134, 146-154, 166-174, 186-194, 206-214, 226-234, 246-254, 266-274, 286-294, 306-314, 326-334, 346-354, 366-374, 386-394, 406-414, 426-434, 446-454, 466-474, 486-494, 506-514, 526-534, 546-554, 566-574, 586-594, 606-614.

Segment 2 (Residues 70-120):

- Sequence:** N Y G L K F N V N H R L P N D Q T P T F S I I S N N K V I Y S Y D M R S K Q L E T I S S D I Q K A L K E L H H E S S P E
- Secondary structure:** Alpha-helix (residues 70-85), Alpha-helix (residues 90-105), Alpha-helix (residues 110-125), Alpha-helix (residues 130-145), Alpha-helix (residues 150-165), Alpha-helix (residues 170-185), Alpha-helix (residues 190-205), Alpha-helix (residues 210-225), Alpha-helix (residues 230-245), Alpha-helix (residues 250-265), Alpha-helix (residues 270-285), Alpha-helix (residues 290-305), Alpha-helix (residues 310-325), Alpha-helix (residues 330-345), Alpha-helix (residues 350-365), Alpha-helix (residues 370-385), Alpha-helix (residues 390-405), Alpha-helix (residues 410-425), Alpha-helix (residues 430-445), Alpha-helix (residues 450-465), Alpha-helix (residues 470-485), Alpha-helix (residues 490-505), Alpha-helix (residues 510-525), Alpha-helix (residues 530-545), Alpha-helix (residues 550-565), Alpha-helix (residues 570-585), Alpha-helix (residues 590-605)
- SS confidence:** High confidence (red) for residues 70-85, 90-105, 110-125, 130-145, 150-165, 170-185, 190-205, 210-225, 230-245, 250-265, 270-285, 290-305, 310-325, 330-345, 350-365, 370-385, 390-405, 410-425, 430-445, 450-465, 470-485, 490-505, 510-525, 530-545, 550-565, 570-585, 590-605. Low confidence (yellow/green) for residues 86-89, 106-109, 126-129, 146-149, 166-169, 186-189, 206-209, 226-229, 246-249, 266-269, 286-289, 306-309, 326-329, 346-349, 366-369, 386-389, 406-409, 426-429, 446-449, 466-469, 486-489, 506-509, 526-529, 546-549, 566-569, 586-589, 606-609.
- Disorder:** Disordered (green) for residues 70-85, 90-105, 110-125, 130-145, 150-165, 170-185, 190-205, 210-225, 230-245, 250-265, 270-285, 290-305, 310-325, 330-345, 350-365, 370-385, 390-405, 410-425, 430-445, 450-465, 470-485, 490-505, 510-525, 530-545, 550-565, 570-585, 590-605. Ordered (blue) for residues 86-89, 106-109, 126-129, 146-149, 166-169, 186-189, 206-209, 226-229, 246-249, 266-269, 286-289, 306-309, 326-329, 346-349, 366-369, 386-389, 406-409, 426-429, 446-449, 466-469, 486-489, 506-509, 526-529, 546-549, 566-569, 586-589, 606-609.
- Disorder confidence:** High confidence (red) for residues 70-85, 90-105, 110-125, 130-145, 150-165, 170-185, 190-205, 210-225, 230-245, 250-265, 270-285, 290-305, 310-325

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand