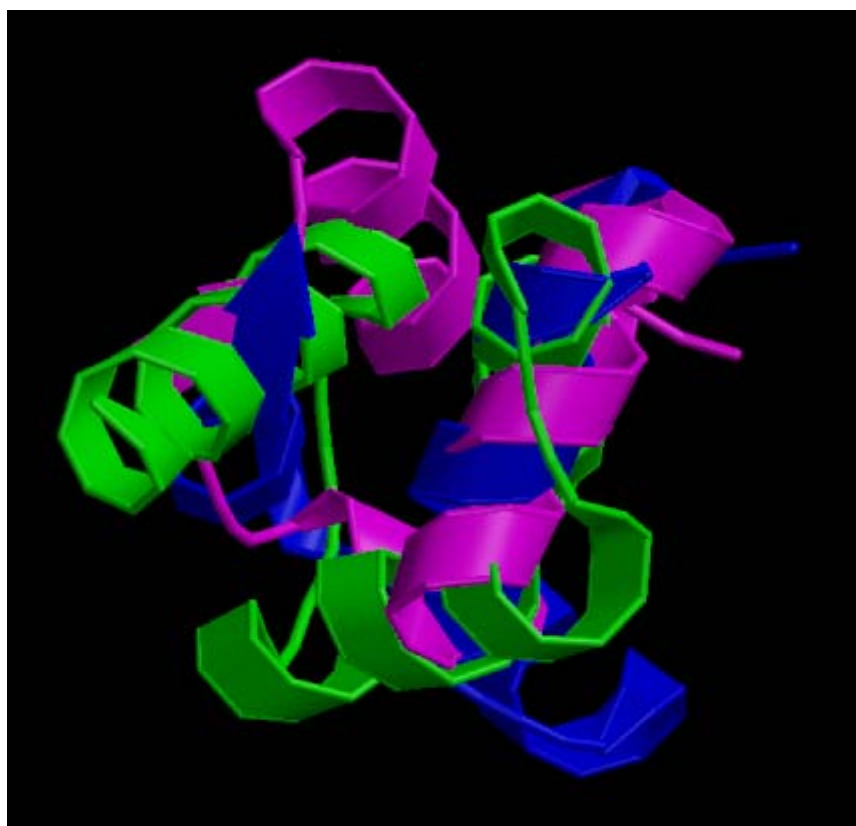


A



B

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1DGS:A 427/428 CPAKRFEAIRHYASRKAMDIEGLGE--KLIERLLE----KGLVRDVADLYHLRKEDLLGL
2BPG:A 22/23 -----LANFEKNVSQAIHKYNAYRKAASVIAKYPHKI-----KSGAE
1C7Y:A 63/64 FNNKQERTLFKELIK----TNGVGP--KLALAILS----GMSAQQFVNAVEREEVGVK

1DGS:A 481/482 ER-----MGEKSAQNL-----LRQIEESKHRGL-----
2BPG:A 59/60 AKKLPGVGTKIA--EKIDEFLATGKLRKLEKIRQDDT-----
1C7Y:A 113/114 LP-----GI--GKKA-----ERLIVEMKDRFKLHGDLFTPAADLVLTSPASPA

1DGS:A 504/505 -----ERLLYALGL-PGVGEVLARN----LARRFGTMDRLLEASLEELIEVEVGELTAR
2BPG:A 94/95 -----SSSINFLTRVTGIGPSARK----LVDEGIK---TLEDL-RKNEDK--LNHHQRI
1C7Y:A 156/157 TDDAE-----QE-AVAALVALGYKPEASRMVS----KIARPDASSETLIRE-----

1DGS:A 554/555 AILETLKDP
2BPG:A 139/140 GLKYFEDFE
1C7Y:A -----
    
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