

Align human vs mouse vs zf colxix protein
 CLUSTAL W (1.83) multiple sequence alignment

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human -----MRLTGPWKLWLWMSIFLLPASTSVTVRDKTEESCPILRIEGHQLTQYD 47
mouse -----MRHTGSWKLWTVWVTFLLPACTCLTVRDKPETTCPTLRTERYQ---D 44
zf MFSRGPFSACKDDMIHYLRWTVFLWIVN-SIPFASGMVNERIDHTCPPLKLEDKWHNTV 59
      *      * . : : * :      : * . : : * . : : : * * * : *

human NINKLEVSGFDLGDSEFLRR-AFCESDKTCFKLGSALLIRDTIKIFPKGLPEEYSVAAMF 106
mouse DRNKSELSGFDLGEFALRH-AFCEGDKTCFKLGSVLLIRDTVKIFPKGLPEEYAIAMVF 103
zf NLHR-EFTGFDLAEKFLLRKGTVTDSDFLFRLGSKPLFKPTESVFPNGLXHEYSIVATF 118
      : : : * . : * * * . : . * * : . . : * . . * : * * * * : : : * . : * * * : * * * : * * * : *

human RVRRNAKKERWFLWQVLNQONIPQISIVVDGGKKVVEFMFQATEGDVNLNIFRNRELRLPL 166
mouse RVRRSTKKERWFLWKILNQONMAQISVVIDGTTKKVVEFMFQAEGLLNIVFKNRELRLPL 163
zf RIRKTTKKDRWVFXQIFDKGGTSQVSLIVDGAKKSVFLALGFLKNSXLYVFKNRDLHAL 178
      * : * : * : * * * : : : : . * : * : * * * * : . : * : * * * : * : *

human FDRQWHKLGISIQSQVISLYMDCNLIARRQTDEKDTVDFHGRVTVIATRSDGKPVDIELH 226
mouse FDRQWHKLGIGVQSRVLSLYMDCNLIASRHTEEKNSVDFQGRITIIAARASDGKPVDIELH 223
zf FDRQFHKLGVSVESNAVSIYLDCELIERQVTAERSGIDVSGRTFITRLEDGKPVDELQ 238
      * * * * : * * * : . : : * . . : * : * * * * : * * . . : * . * * * . * : * . * * * * : * :

human QLKIYCSANLIAQETCCIEISDTKCPEQDGFNGIASSWVTAHASKMSSYLPAKQELKDQCQ 286
mouse QLRIYCNANFLAEESCCNLSPTKCPEQDDFGSTTSSWGTSNMGKSSYLPGKQELKDTQC 283
zf EILVFCDSRIADLRCCDSPGAMCEPTVTHNPTAIPLVGTGLQKMLSMP--AQLPTDRCH 296
      : : : * . : : : * * : . : * . . : . * . * * * * * * * * * * * * :

human CIPNKGAGLPGAPGSPGQKGHKGEPEENGLHGAPGFPGQKGEQGFEGSKGETGKEGEGG 346
mouse CIPNKEAGLPGTLRSIGHKGDKGEPEHGLDGTPLPGQKGEQGLEGIKGEIGKEGEPG 343
zf CPALKGLKGDPPGQGLPGLKGDKGDGPP---PGPGTSLVEKQAQ----KGDQGSPTPG 348
      * . * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * * *

human EKGDPALAGLNGENGLKGD LGPHGPPGPKGEKGDTPPPALPGSLGIQGPQGGPPGKEG 406
mouse AKGDSGLDGLNGQDGLKGDSPGQGGPPGPKGDKGDMPGPPALPALTGSIIGIQQGPPGKEG 403
zf EKGDVGGPPGQPGAPGKEGKRGRGKTGEPGTPGLQGGPPGTCDAETVKGMKGDQGVAGERG 408
      * * * . * * * * : * . * : * . * * * * * * * * * * * * * * * * * * *

human QGRRGKTGPPGKPPPPPPGPPGIQGIHQTLGGYYNKDNKGNDEHEAGGLKGDKGETGL 466
mouse QGRRGKTGPPGNPFPFPFPFPGLQGLQPPGGYFN---KGTGEHGASGPKGEKGDGTGL 460
zf QKDRGDSGLPGLG-----AGGMKQKQKEEGP 436
      * : * * * : * * * * * * * * * * * * * * * * * * * * * * * * *

human PGFPGSVGPKGQKGEPEPFTKGEKDRGEPGVIGSQGVKGEPPGDPGPPGLIGSPGLKGG 526
mouse PGFPGSVGPKGHKGEPEPLTKGEKDRGEPGLLGPQGIKGEPPGDPGPPGLIGSPGLKGG 520
zf RGGPPVMTAHLRLSGPEEGSEKQKGEKGDQGEKGAEGSQGLQGPAGLTGPPGLEGK 496
      * * * * * . * * * * * * * * * * * * * * * * * * * * * * * * *

human QGSAGSMGPRGPPGDVGLPGEHGIPGKQGIKGEKDPGGIIGPPGLPGLKGEAGPPGKSL 586
mouse QGPAGSMGPRGPPGDVGLPGEHGIPGKQGVKGEKDPGGRIGPPGLPGLKGDAGPPGISL 580
zf VGGPPVGPRLGLQDGPAGLIGLPGKDMKGEKGDGGAPGAPGPPGLKGEPEP-CSV 555
      * . . . : * * * * * * * * * * * * * * * * * * * * * * * * *

human PGEPGLDGNPGAPGRGPKGERGLPGVHGSFGDIGPQIGIPRTGAQGPAGEPPIQGPR 646

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mouse      PGKPGLDGNPGSPGPRGPKGERGLPGLHGSFGDTGPPGVGIPGRTGSQGPAGEPPIQGPR 640
zf         GLCGGEEVASGLRGLRGPKEGRRVPGVPGDAGEKKEPFGFITGPPGLTGPKGEPGSQGPL 615
          * : . * * *****:** : * . * : * * * * * * * *
human     GLPGLPGTPTGTPGNDGVPGRDQKPGPLPGPPGDPIALPLLGDIGALLKNFCGNCQASVPGL 706
mouse     GLPGLPGTPTGMPGNDGAPGKDGKPGPLPGPPGDPIALPLLGDIGALLKNFCGNCQANVPGL 700
zf        GPQ---GPIGVPGIEGPPPGQRRPGLPGPPGEPALPMVGDMDGTLMKNACSVQTRVPGL 672
          *      * * * * : * * * : : ***** : * * * * : * * * : * * * *
human     KSNKGEEGGAGEPGKYDSMARKGDIGPRGPPGIPGREGPKGSKGERGYPIGPEKGDDEGL 766
mouse     KSIKDDGSTGEPGKYDPAARKGDVGRGPPGFPGREGPKGSKGERGYPIHGEKGDDEGL 760
zf        PGQKGEKSGPASPIMPMDGEKGDQQLRGPAGNPGKEGPKGVKGERGFPPGMDKDEGS 732
          . * * : * . * . * . * * * * * * * * * * * * * * * * * *
human     QGIPGIPGAPGPTGPPGLMGRGTGHPGPTGAEKGSDDGPPGKPGPPGPPGIPFNERNGMS 826
mouse     QGIPGLSGAPGPTGPPGLTGRGTGHPGPTGAEKDGSEGGPPGKPGPPGPPVPLNEGNMS 820
zf        PGPVPLPGSTGTGTSQMNRRPFAVGPQQQVDRGSEGGPPGQPPPPGPPGAPYSEGNMS 792
          * : * * : * : * * * * * * * * * * * * * * * * * * * * * *
human     SLYKIKGGVNVPSYPGPPGPPGPKGDPGVPVEPGAMGLPGLGFPVKGDRGPAGPPGIA 886
mouse     SLYKIQGGVNVPGYPGPPGPPGPKGDPGVPVEPGAMGLPGLGFPVKGDRGPAGPPGIA 880
zf        SIYKLNQAANGGQPPGPPGPPGPKGDEGRMGEPGLMGLPGLGLTGAKGDFPLPGLN 852
          * : * * : * . * . * * * * * * * * * * * * * * * * * * * *
human     GMSGKPGAPPPGVPGEPEEIPVVDIGFPPGEPGSGKPGINGKDGIPGAQGIMGKPGDR 946
mouse     GISGKPGAPPPGVPGEQEEIPIGDTGFPPEGPGSGKPGINGKDLPGAQGIMGKPGDR 940
zf        PVPKPGPRGETGIPGEPEEIPVGETGFPPEGPPGAPRPRKDGVPYEGATGRPGDR 912
          * * * * * * * * * * * * * * * * * * * * * * * * * * * *
human     GPKGERGDQGIPGDRGSQGERKPKGLTGMKGAIGPMGPPGNKSGMSGPHGQPPGSPGIP 1006
mouse     GPKGERGDQGIPGDRGPQGERKPKGLTGMKGAIGVGPAGSKGSTGPPGHGQPPGNPGIP 1000
zf        GTKGERGDPGIPGERGVQGERK---TGDKGTIGPQPPGQKGEPPGSLTSPGS---V 966
          * . * * * * * * * * * * * * * * * * * * * * * * * * * *
human     GIPADAVSFEEIKKYINQEVLRIFEERMAVFLSQLK-LPAAMLAAQAY-GRPFGPKDGL 1064
mouse     GTPADAVSFEEIKHYINQEVLRIFEERMAVFLSQLK-LPAAMLSAQAH-GRPFGPKDGL 1058
zf        KLLSDTAALLEEIKTFIRNEVLRVFEKFSDSQTLQKTPAAAILAAQGRQPPGPPGNDGS 1026
          : * : : * * * * : * . * * * * * * * * * : : * : * * * * * * * *
human     PPGPDGPP---QGYRGQKGERGEPGIGLPGSPGLPGTSALGLPGSPGAPGFPQPPGPGS 1121
mouse     PPGPDGPP---QGYRGQKGERGEPGIGLPGSPGLPGSSAVGLPGSPGAPGFPQPPGPGS 1115
zf        PPGPEGPPGPGSQGYRGQKGERGMGLGLPGAPGAPGQPVGLPGQPSGPPGPPGPHG 1086
          * * * * * * * * * * * * * * * * * * * * * * * * * * * *
human     RCNPEDCLYPVSHAHQRTGNG 1142
mouse     RCNPEDCLYPAPPPHQAGGK 1136
zf        RCNPSDCFHPYG---RRDG-- 1102
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