**The Crystal Structure of JNK from *Drosophila melanogaster* Reveals an Evolutionarily Conserved Topology with that of Mammalian JNK Proteins.**

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DJNK QHYTVEVGDTNFTIHSRYINLRPIG*SGAQ*GIVCAAYDTITQQNVAIKKLSRPFQNVTHAK 66

JNK1 NFYSVEIGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAILERNVAIKKLSRPFQNQTHAK 68

JNK2 QFYSVQVADSTFTVLKRYQQLKPIGSGAQGIVCAAFDTVLGINVAVKKLSRPFQNQTHAK 68

JNK3 QFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQTHAK 106

 

DJNK RAYREFKLMKLVNHKNIIGLLNAFTPQRNLEEFQDVYLVMELMDANLCQVIQMDLDHDRM 126

JNK1 RAYRELVLMKCVNHKNIIGLLNVFTPQKSLEEFQDVYIVMELMDANLCQVIQMELDHERM 128

JNK2 RAYRELVLLKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIHMELDHERM 128

JNK3 RAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQMELDHERM 166

 

DJNK SYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKADCTLKILDFGLARTAGTTFMM*TPY*VVT 186

JNK1 SYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGL*ARTAGTSFMMTPYVVT* 188

JNK2 SYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTASTNFMMTPYVVT 188

JNK3 SYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLA*RTAGT*SFMMTPYVVT 226

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DJNK RYYRAPEVILGMGYTENVDIWSVGCIMGEMIRGGVLFPGTDHIDQWNKIIEQLGTPSPSF 246

JNK1 *R*YYRAPEVILGMGYKENVDIWSVGCIMGEMIKGGVLFPGTDHIDQWNKVIEQLGTPCPEF 248

JNK2 RYYRAPEVILGMGYKENVDIWSVGCIMGELVKGSVIFQGTDHIDQWNKVIEQLGTPSAEF 248

JNK3 RYYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQWNKVIEQLGTPCPEF 286

 

DJNK MQRLQPTVRNYVENRPRYTGYSFDRLFPDGLFPND*NN*QNSRRKASDARNLLSKMLVIDPEQ 307

JNK1 MKKLQPTVRTYVENRPKYAGYSFEKLFPDVLFP*ADSEH*N-KLKASQARDLLSKMLVIDASK 308

JNK2 MAALQPTVRNYVENRPAYPGIAFEELFPDWIFP*SE*SERD-KIKTSQARDLLSKMLVIDPDK 308

JNK3 MKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHN-KLKASQARDLLSKMLVIDPAK 346

 

DJNK RISVDEALKHEYINVWYDAEEVDAPAPEPYDHSV*DE*REHTVEQWKELIYEEVMDY 362

JNK1 RISVDEALQHPYINVWYDPSEAEAPPPK*IPDKQLDEREHT*IEEWKELIYKEVMDL 361

JNK2 RISVDEALRHPYITVWYDPAEAEAPPPQI*YDAQLEERE*HAIEEWKELIYKEVM 361

JNK3 RISVDDALQHPYINVWYDPAEVEAPPP*QIYDK*QLDEREHTIEEWKELIYKEVMN 400

**Additional file 1.** Structure-based sequence alignment of DJNK, mammalian JNK1, JNK2, and JNK3. The amino acid sequences of DJNK, JNK1 [PDB:1UKH 13], JNK2 [PDB:3E7O 14] and JNK3 [PDB:1JNK 15] are aligned based on structural comparisons. The secondary structure elements for DJNK are indicated above the sequences with open boxes designating *α* and 310 helices and open arrows designating *β* strands. Residues in *italic letters* are not included in the models. Phosphorylation sites are denoted by asterisks. Conserved amino acids crucial for the ATP binding, catalytic activity and peptide binding are highlighted.