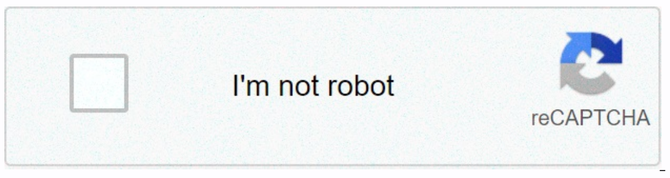

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Biochemistry ws

Biochemical genetics; studies on the molecular mechanism of transition is a complex genetic rearrangement process found in all living organisms. It is involved in the transformation of the genome, with the spread of antibiotic resistance in bacteria, and with chromosomal changes in some cancers. Biochemical decomposition is very similar to the combination of HIV virus prophylaxis 1. In addition, the transfer of molecules in the laboratory is likely to provide new tools for rearranging DNA molecules. Thus, this process is receiving considerable attention. My laboratory is to decipher the molecular details of the transfer by studying the bacterial transposon model, Tn5. Tn5 encoding a protein called transposase that stimulates all steps in transposition; transposase-transposon DNA binding, the formation of a transposon neoclaprotein compound, a defection of transposon DNA-free from the surrounding DNA sequence, inserttransposon DNA into a new genetic site. For Tn5, all these steps occur in a simple and specific system in the laboratory. This allows us to study the detailed biochemical effects of various target mutations at the site of the pylorisasse and DNA. In addition, in collaboration with Professor Ivan Rement's laboratory, we have identified the 3D structure of the nape. This, besides genetics and biochemistry, will generate a complete picture of the structure/function of the transposase and target DNA sequence. My laboratory is also interested in developing the Tn5 transfer system as a molecular genetic tool. Our long-term goal is to develop methods that will allow genetics in the collective laboratory to become a standard laboratory procedure. 1.Cater DB, NR Law: Some histochemical and biochemical observations on the Preen gland. J. Vesiol - London. 1950, 111: 231-243.PubMed CAS PubMed Central Article Google Finder 2.Haahti E, Lagerspetz K, Nikkari T, Fales HM: Fat from the office gland of birds. 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Fat. 2011, DOI 10.1007/s11745-011-3642-1 Google 68.Bradford MM: 3-90527(76)2697-10.1016/0003 .254-248 ,72 ,1976 ,كيمياء الشرح الحيوية .طريقة سريعة وحساسة لكمية الكميات ميكروغرام من البروتين باستخدام مبدأ البروتين الصبغة ملزمة.PubMed CAS مقالة جوجل الباحث صفحة 2 فيلوجينيتيك من synthases الشمع الطيور المفترضة بالمقارنة مع مختلف المآتيل من .يُظهر علاقة بروتينات الطيور التي تم تحليلها مع أسيل ترانسفيراسات من كائنات مختلفة phylogram الإنسان والنباتات والخميرة وتتراهيدينا والبكتيريا. The tree is based on the alignment of the following sequences (NCBI accession numbers are given): HsAWAT1 [Homo sapiens, NP_001013597.1], HsAWAT2 [H. sapiens, NP_001002254.1], HsMOGAT3 [H. sapiens, NP_835470], HsMOGAT2 [H. sapiens, NP_079374], HsMOGAT1 [H. sapiens, NP_477513.2], HsACAT1 [H. sapiens, NP_003092.4], HsACAT2 [H. sapiens, NP_003569.1], HsDGAT2 [H. sapiens, NP_115953.2], HsDGAT1 [H. sapiens, NP_036211.2], SchWS [Simmondsia chinensis, AF149919_1], EgWS [Euglena gracilis, ADI60058.1], PxhWS [Petunia x hybrida, AAZ08051.1], AcWS/DGAT [Acinetobacter sp. ADP1, YP_045555.1], GgWS1 [Gallus gallus, XP_424082.2], GgWS2 [G. gallus, JQ031643], GgWS4 [G. gallus, XP_419207.1], GgWS5 [G. gallus, NP_001026192.1], AdWS5 [Anser domesticus, JQ031647], TaWS5 [Tyto alba, JQ031646], AdWS4 [A. domesticus, JQ031643], TaWS4 [T. alba, JQ031645], HsTMEM68 [H. sapiens, Q96MH6.2] ، GgDGAT1 [G. جالوس، JQ031642]، تتراهيدمينا WS [تتراهيدمينا ترموفيليا، XP_001027910، XP_001026090، XP_001008104، XP_001019739] MhWS1 [مارينوباكتر هيدروكربونيكوس، ABO21021.1]، Arabidopsis WSD [Arabidopsis thaliana، NP_568547.1، NP_177356.1، NP_850307.1، NP_200151.2] MrDGAT2B [Umbelopsis ramannaian، AAK84180.1] ، MrDGAT2A [U. ramanniana, AAK84179.1], ScDGA1p [Saccharomyces cerevisiae, NP_014888.1], ScARE1p [S. cerevisiae, CAA 42296.1], ScARE2p [S. cerevisiae, CAA96298.1], Arabidopsis WS [A. ثالیانا، NP_200345.1, XP_002866091.1, NP_200349.1, NP_200346.1]. الأرقام في الفروع هي قيم موضعاً. 188 متوالية بمجموع 41 ويقابل المقياس بدائل الأحماض الأمينية لكل موقع في محاذاة bootstrap تم إنشاء 95 صحيحة. يمكن اعتبار القيم التي تزيد عن تشير إلى احتمال هذه العلاقة في %. dendrogram مع ClustalX2 و MEGA5 البرمجيات. البرمجيات.