

Program: water
Rundate: Sun Nov 18 2005 19:23:24
Align_format: srspair
Report_file: fly-dscamL.water
#####

#=====

Aligned_sequences: 2
1: Fly
2: Human
Matrix: EBLOSUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 2181
Identity: 633/2181 (29.0%)
Similarity: 996/2181 (45.7%)
Gaps: 315/2181 (14.4%)
Score: 2523.5

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fly exon 4 and human Dscam-L homolog (exon 3), with Human Dscam-L Ig-like C2-type domain #2 underlined, and InterProScan predicted Fly IG PF00047.14 domain underlined

fly exon 6 and human Dscam=L homologous region (exon 5), Human Dscam-L Ig-like C2-type 3 underlined, and InterProScan fly predicted IG PF00047.14 underlined

fly exon 9.9 and human Dscam-L homolog (exon 9), with Human Dscam-L Ig-like C2-type 7 underlined, and InterProScan fly predicted IG PF00047.14 underlined

fly exon 17 and human Dscam=L homolog (exon 27), with predicted transmembrane domain underlined

Fly	10	WMLLFAAVALIACGSQTLAANPPDADQKGPVFLKEPTNRIDFSNSTGAEI	59
		: . . . : : : : : : . : . . . :	
Human	62	WLVTFLLLL-----DSLHKARPEDVG-TSLYFVNDSLQQVTFSSSVGVVV	105
Fly	60	ECKASGNPMPEIIWIRSDGTAVGDVPGLRQISSDGKLVFPFRAEDYRQE	109
		. . : : : : : : : : . . .	
Human	106	PCPAAGSPSAALRWYLATGDDIYDVPHIRHVHANGTLQLYPFSPSAFNSF	155

Fly	110	VHAQVYACLARNQFGSIISRDRVHRAVVAQYYEADVNDKEHVIRGNSAVIK	159
Human	156	IHDNDYFCTAENAAGKIRSPNIRVKAVFREPYTVRVEDQSRMRGNVAVFK	205
Fly	160	CLIPSFVADFVEVVSWHTDEEENYFPGAEDGKYLVLPSGELHIREVGPE	209
Human	206	CLIPSSVQEQYVSVVSWEKD-TVSIIP----EHRFFITYHGGLYISDVQKE	250
Fly	210	DGYKSYQCRTKHRLTGETRLSATKGRLVITEPVSSSPPKINALTYKPNIV	259
Human	251	DALSTYRCITKHKYSGETRQS-NGARLSVTDPAESIPTILDG--FHSQEV	297
Fly	260	ESMASTAILCPAQGYPAFSFRWYKFIEGTTTRKQAVVLNDR-VKQVSGTLI	308
Human	298	WAGHTVELPCTASGYPIPAIRWLK--DG---RPLPADSRWTKRITG-LT	340
Fly	309	IKDAVVEDSGKYLCVVNSVGGESVETVLTVTAPLSAKIDPPTQTVDfGR	358
Human	341	ISDLRTEDSGTYICEVTNTFGSAEATGILMVIDPLHVTLTTPKKLKTGIGS	390
Fly	359	PAVFTCQYTGNPiKTVSWMKDgKAI-----GHSEPVLRIESVKKED	399
Human	391	TVILSCALTGSPEFTIRWYRNTELVLpDEAISIRGLSNETLLITSAQKSH	440
Fly	400	KgMYQCFVRNDQESAEASAEKLKGGRFDPPVIRQAFQEETMEPGPSVFLK	449
Human	441	SGAYQCFATRKAQTAQDFAIIAL--EDGTPRIVSSFSEKVVNPGEQFSLM	488
Fly	450	CVAGGNPTPEISWELDGKKIANNDRYQVGQYVTVNGDVSYLNITSVHAN	499
Human	489	CAAKGAPPPTVTWALDDEPIVRDGSHTRNQYTMSDGTtISHMNVtGPQIR	538
Fly	500	DGGLYKCIaSKSVGVAEHSaKLNvYGLPYIRQMEKKAIVAGETLIVTCpV	549
Human	539	DGGVYRCTARNLVGSAEQARINVRGPPSIRAMRNITAVAGRDTLINCRV	588
Fly	550	AGYPIDSIvWERDNRALPINRKQKVFPNGTLIIENVERNSDQATyTCvAK	599
Human	589	IGYPYYSIKWYKDALLLPDNHROVVFENGTLKLTDVOKGMDEGEYLCSVL	638

Fly	600	NQEGYSARGSLEVQVM <u>VPPQVL</u> <u>PFSFGESAADVGD</u> <u>IASANCVVPKGD</u> <u>LPL</u>	649
		 : : : . . :	
Human	639	IQPQLSISQSVHVAVK <u>VPPLIQPFEF</u> -- <u>PPASIGQLLYIPC</u> <u>VVSSGDMPI</u>	686
Fly	650	<u>EIRWSLNSAPIVNGENGFTLVRLNKRTSL</u> <u>LNIDSLNAFH</u> <u>RGVYKCIATNP</u>	699
		 : . . : : . . : . .	
Human	687	<u>RITWRKDGQVIISG</u> - <u>SGVT</u> - <u>IESKEFMSS</u> <u>LQISSVSLKHNGNYTCIASNA</u>	734
Fly	700	<u>AGTSEYVAELQVN</u> VPPRWILEPTDKAFAQGSDAKVECKADGFPPKQVTWK	749
		 : : . . :	
Human	735	<u>AATVSRERQLIVR</u> VPPRFVVQPNNQDGIYGKAGVLNCSVDGYPPPKVMWK	784
Fly	750	KAVGD-TPGEYKDLKKSDNIRV-EEGTLHVDNIQKTNEGYLCEAINGIG	797
		 : : : . . :	
Human	785	HAKGSGNPQQYHPVPLTGRIQILPNSSLLIRHVLEEDIGYYLCQASNGVG	834
Fly	798	SGLSAVIMISVQAPPEFTEKLRNQ TARRGEPAVLQCEAKGEKPIGILWNM	847
		: . . : . . : . . : : . . : . . : . . : . . : . .	
Human	835	TDISKSMFLT VKIPAMITSHPNTTIAIKGHAKELNCTARGERPIIIRWEK	884
Fly	848	NNMRLDPKNDNRYTIREEILSTGVMSSLSIKRTERS DSALFTCVATNAFG	897
		. . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . .	
Human	885	GDTVIDPDRVMRYAIATKDNGDEVVSTLKLKPADRGDSVFFSCHAINS YG	934
Fly	898	SDDASINMIVQEVP EMPYALKVLDKSGRSVQLSWAQPYDGNSPLDRYIIE	947
		 : . . : . . : : . . : : . .	
Human	935	EDRGLIQLTVQEPPDPP-ELEIREVKARSMNLRWTQRF DGNSIITGFDIE	983
Fly	948	FKRSRASW--SEIDRVIVPGHTTEAQVQKLSPATTYNIRIVAENAIGTSQ	995
		: : : . . : . . : . . : . . : . .	
Human	984	YKNKSDSWDFKQSTRNISP-TINQANIVDLHPASVYSIRMYSFNKIGRSE	1032
Fly	996	SSEAVTIITAE EAPSGKPQNIKVEPVNQTTMRVTWKPPPRTEWNGEILGY	1045
		. : . . : . . : . . : . . : . . : . . : . . : . .	
Human	1033	PSKELTISTEEAAPDGPPMDVTLQPVTSSQSIQVTWKAPKKELQNGVIRGY	1082
Fly	1046	YVG YKLSNTNSSYVFETINFITEEGKEHNLELQNLRVYTQYSVVIQAFNK	1095
		: . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . :	
Human	1083	QIGYRENSPGSNGQYSIVE-MKATGDSEVYTLDNLKKFAQYGVVVQAFNR	1131
Fly	1096	IGAGPLSEEEKQFTAEGTPSQPPSDTACTTLTSQTIRVGWVSPPLESANG	1145
		. . . : : . . : . . : . .	
Human	1132	AGTGPSSSEINATTLEDVPSQPPENVRALSITSDVAVISWSEP PRSTLNG	1181

Fly	1146	VIKTYKVVY---APSDEWYDETKRHYKKTASSDTV-LHGLKKYTNYTMQV	1191
		: . : : : ... : : : : :	
Human	1182	VLKGYRVIFWSLYVDGEWGE---MQNITTTREVELRGMEKFTNYSVQV	1227
Fly	1192	LATTAGGDGVRSVPIHCQTEPDVPEAPTDVKALVMGNAAILVSWRPPAQP	1241
		: : :.....: . :	
Human	1228	LAYTQAGDGVRSSVLYIQTKEDVPGPPAGIKAVPSSASSVVVSWLPPTKP	1277
Fly	1242	NGIITQYTVYSKAEG-----AETETKTQKVPHYQMSFEATELEKNKPYE	1285
		: . : : : : . . : :..... . :..... .	
Human	1278	NGVIRKYTIFCSPGSGQPAPSEYETSPE-----QLFYRIAHLNRGQQYL	1322
Fly	1286	FWVTASTTIGEGQQSKSIVAMPSDQVPAKIASFDDTFTATFKEDAKMPCL	1335
		. . . : . .. :..... :..... :..... .	
Human	1323	LWVAAVTSAGRGNSSSEKVTIEPAGKAPAKIISFGGTVTTPWMKDVRLPCN	1372
Fly	1336	AVGAPQPEITW----KIKGVEFSANDMRVLPDGSLLIKSVNRQDAGDYS	1381
		: . . : . : :..... . :.....: : : : : : :	
Human	1373	SVGDPAPAVKWTKDSEDSAI PVSMDGHRLIHTNGTLLLRVKAEDSGYYT	1422
Fly	1382	CHAENSIAKDSITHKLIVLAPPQSPHVTLSATTTDALTVKLKPHEGDTAP	1431
		. . : : : ... : : : . : : :..... :.....:	
Human	1423	CTATNTGGFDTIIVNLLVQVPPDQPRLTVSKTSASSITLTWIPGDNGGSS	1472
Fly	1432	LHGYTLHYKPEFG-EWETSEVSVDSQKHNIEGLLCGSRYQVYATGFNNIG	1480
		:. : :.....: :.....: : : : : : :	
Human	1473	IRGFVLQYSVDNSEEWKDVFISSERSFKLDCLKGTWYKVKLAAKNSVG	1522
Fly	1481	AGEASDILNTRTKGQKPKL-PEKPRFIEVSSNSVSLHFKAWKDGGCPMSH	1529
		: . . : : : : : :.....: :..... : : : :	
Human	1523	SGRISEIIEAKTHGREPSFSKDQHLFTHINSTHARLNLQGWNNGGCPITA	1572
Fly	1530	FVVESKKRDQIEWNQISNNVKPDNNYVVDLEPATWYNLRITAHNSAGFT	1579
		. : : : :..... : : . :	
Human	1573	IVLEYRPKGTWAWQGLRAN--SSGEVFLTELREATWYELRMACNSAGCG	1620
Fly	1580	VAEYDFATLTVTGGTIAPSRDLPELSAE---DTIRIILSNLNLVVPVVA	1626
		 : : : : :.....: :.. :	
Human	1621	NETAQFATLDYDGSTIPPIK-----SAOGEGDDVKKLFT---IGCPVILA	1662

Fly	1627	LLVIIIAIV-----ICILRSKGNHHKDDVVYNQTMG	1658
		. .:.:.	
Human	1663	TLGVALLFIVRKKRKEKRLKRLDAKSLAEMLI SKNNR SFDTPVKGP PQG	1712
Fly	1659	PGATLDKRRPDL----RDELGYIAPPNRKLP-----	1685
		...: :...:.....:	
Human	1713	PRLHIDIPRVQLLIEDKEGIKQLGDDKATIPVTDAEFSQAVNPQS FCTGV	1762
Fly	1686	-----PV-----PGSNYNTCDRIKRGRGGLRSNHST-----	1711
		: : : .	
Human	1763	SLHHPTLIQSTGPLIDMSDIRPGTN-----PVSRKNV KSAHSTRN RYS	1805
Fly	1712	-----W-----DPRR	1716
		..	
Human	1806	SQWTLTKCQASTPARTLTSDWRTVG SQHGVT VTESDSYSASLSQDTDKGR	1855
Fly	1717	N-----PNLYEELKAPPVPMHGNHYGHAGNAECHYRH PGMEDE ICP	1758
		.:. ::: .	
Human	1856	NSMVSTESASSTYEELARA-----YEHA KLEEQL-Q	1885
Fly	1759	YATFHL-----LGFREEMDPTKAMNFQT FPHQNGHAGPVPG	1794
		: . .:. : : .	
Human	1886	HAKFEITECFISDSSSDQMTTGTNENADSM T SMS-----TPS	1922
Fly	1795	HAG----TMLPPGHPGHVHSRSGSQ SMP-RANR-----YQRKNSQGG	1831
		:~::~ : .:~::...	
Human	1923	EPGICRF TASPPKPQ DADR GKN VAVPI PHRANKSDYC NLPLYAKSEAFFR	1972
Fly	1832	QSSIYTPAPEYDDPANCAEEDQYRRYTRVNSQGGS L YSGPGPEYDD PANC	1881
		::~::... . .~. :~::... . ::~ :	
Human	1973	KADGREPCPVV-PPREASIRNLARTY--HTQARHL TL-----DPAS-	2010
Fly	1882	APEEDQYGSQYGGPY-GOPYDHYGSRGSMGRRSIGSARNPGNGSPE PPPP	1930
		 ::~ :~::... .~:: .~ .	
Human	2011	-----KSLGLPHPGAP--AAASTATLPQRTLAMP APPAGTAPPAPGP	2050
Fly	1931	PPRNHDMSNSSFND SKESNEISEAECDRDHGPRGNYGAVKRSP QPKDQRT	1980
		: :~ .~~:: .	
Human	2051	TPAEPPTAPSA-----APPAPSTEP PRAGGP HTKMGGSRDS-----	2086
Fly	1981	TEEMRKLIERNETGPKQLQLQQANGAGFTAY 2011	
		: .~:: .~:: .	
Human	2087	-----LLEMSTSGVGRSOKQ---GAG--AY 2106	