



results of BLAST

BLASTP 2.2.13 [Nov-27-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1141625112-6143-132542853548.BLASTQ4

Database: Non-redundant SwissProt sequences
192,554 sequences; 71,789,263 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Query=

Length=12

Sequences producing significant alignments:			Score (Bits)	E Value
sp O96PK2 MACF4_HUMAN	Microtubule-actin crosslinking factor 1, i		18.5	243
sp Q9UBV4 WNT16_HUMAN	Wnt-16 protein precursor		18.1	318
sp O14669 TRIPC_HUMAN	Thyroid receptor-interacting protein 12 (T		18.1	318
sp O16760 DGKD_HUMAN	Diacylglycerol kinase delta (Diglyceride...		18.1	318
sp P54296 MYOM2_HUMAN	Myomesin-2 (M-protein) (165 kDa titin-a...		18.1	318
sp Q13614 MTMR2_HUMAN	Myotubularin-related protein 2		18.1	318
sp Q9UIQ6 LCAP_HUMAN	Leucyl-cystinyl aminopeptidase (Cystinyl...		17.7	415
sp P49619 DGKG_HUMAN	Diacylglycerol kinase, gamma (Diglycerid...		17.7	415
sp Q9Y6T7 DGKB_HUMAN	Diacylglycerol kinase, beta (Diglyceride...		17.7	415
sp Q969S2 NEIL2_HUMAN	Endonuclease VIII-like 2 (Nei-like 2) (...		17.3	542
sp Q8WUM9 S20A1_HUMAN	Sodium-dependent phosphate transporter ...		17.3	542
sp O75912 DGKI_HUMAN	Diacylglycerol kinase, iota (Diglyceride...		17.3	542
sp P52429 DGKE_HUMAN	Diacylglycerol kinase, epsilon (Diglycer...		17.3	542
sp P52824 DGKO_HUMAN	Diacylglycerol kinase, theta (Diglycerid...		17.3	542
sp Q9NZ20 PA2G3_HUMAN	Group III secretory phospholipase A2 pr...		17.3	542
sp Q13574 DGKZ_HUMAN	Diacylglycerol kinase, zeta (Diglyceride...		17.3	542
sp Q9P232 CNTN3_HUMAN	Contactin-3 precursor (Brain-derived im...		17.3	542
sp Q8IY67 RAVR1_HUMAN	Protein raver-1		16.9	708
sp Q14653 IRF3_HUMAN	Interferon regulatory factor 3 (IRF-3)		16.9	708
sp P10809 CH60_HUMAN	60 kDa heat shock protein, mitochondrial...		16.9	708
sp P23743 DGKA_HUMAN	Diacylglycerol kinase, alpha (Diglycerid...		16.9	708
sp P46977 STT3_HUMAN	Oligosaccharyl transferase STT3 subunit ...		16.9	708
sp Q12788 TBL3_HUMAN	WD-repeat protein SAZD (Transducin beta-lik		16.9	708
sp O14924 RGS12_HUMAN	Regulator of G-protein signaling 12 (RGS12		16.9	708
sp O8TE59 ATS19_HUMAN	ADAMTS-19 precursor (A disintegrin and ...		16.5	925
sp P58215 LOXL3_HUMAN	Lysyl oxidase homolog 3 precursor (Lysy...		16.5	925
sp Q9NQ84 GPC5C_HUMAN	G-protein coupled receptor family C gro...		16.5	925
sp Q9Y570 PPME1_HUMAN	Protein phosphatase methylesterase 1 (PME-		16.5	925
sp Q08397 LOXL1_HUMAN	Lysyl oxidase homolog 1 precursor (Lysy...		16.5	925
sp Q92522 H1X_HUMAN	Histone H1x		16.5	925
sp Q04756 HGFA_HUMAN	Hepatocyte growth factor activator precu...		16.5	925
sp P04150 GCR_HUMAN	Glucocorticoid receptor (GR)		16.5	925
sp Q9UBY8 CLN8_HUMAN	Protein CLN8		16.5	925
sp Q92747 ARC1A_HUMAN	Actin-related protein 2/3 complex subun...		16.2	1208

sp P0C0L4 CO4A_HUMAN	Complement C4-A precursor (Acidic comple...	16.2	1208
sp P14923 PLAK_HUMAN	Junction plakoglobin (Desmoplakin-3) (Desmo	16.2	1208
sp Q6VVB1 NHLC1_HUMAN	NHL repeat containing protein 1 (Malin)	16.2	1208
sp Q14576 ELAV3_HUMAN	ELAV-like protein 3 (Hu-antigen C) (HuC...	16.2	1208
sp Q9UKQ2 ADA28_HUMAN	ADAM 28 precursor (A disintegrin and me...	16.2	1208
sp O8TDB6 DTX3L_HUMAN	Deltex 3-like protein (B-lymphoma- and ...	16.2	1208
sp Q15413 RYR3_HUMAN	Ryanodine receptor 3 (Brain-type ryanodi...	16.2	1208
sp Q86XX4 FRAS1_HUMAN	Extracellular matrix protein FRAS1 precurs	16.2	1208
sp Q9Y6I9 TX264_HUMAN	Testis expressed sequence 264 protein p...	16.2	1208
sp Q9NUD5 ZCHC3_HUMAN	Zinc finger CCHC domain-containing protein	16.2	1208
sp O75420 PERO1_HUMAN	PERO amino acid rich with GYF domain prote	16.2	1208
sp Q9P296 C5ARL_HUMAN	C5a anaphylatoxin chemotactic receptor ...	16.2	1208
sp P17174 AATC_HUMAN	Aspartate aminotransferase, cytoplasmic ...	16.2	1208
sp P35222 CTNB1_HUMAN	Beta-catenin	16.2	1208
sp Q9UKY4 POMT2_HUMAN	Protein O-mannosyl-transferase 2 (Dolic...	16.2	1208
sp Q8NDV7 TNR6A_HUMAN	Trinucleotide repeat-containing gene 6A...	16.2	1208
sp P0C0L5 CO4B_HUMAN	Complement C4-B precursor (Basic complem...	16.2	1208
sp Q92545 RW1_HUMAN	RW1 protein	16.2	1208
sp O60716 CTND1_HUMAN	Catenin delta-1 (p120 catenin) (p120(ct...	16.2	1208
sp Q9NRD9 DUOX1_HUMAN	Dual oxidase 1 precursor (NADPH thyroid...	15.8	1578
sp Q95136 EDG5_HUMAN	Sphingosine 1-phosphate receptor Edg-5 (...	15.8	1578
sp Q95932 TGM3L_HUMAN	Protein-glutamine gamma-glutamyltransfe...	15.8	1578
sp P09237 MMP7_HUMAN	Matrilysin precursor (Pump-1 protease) (...	15.8	1578
sp P22681 CBL_HUMAN	CBL E3 ubiquitin protein ligase (Signal t...	15.8	1578
sp P12111 CO6A3_HUMAN	Collagen alpha-3(VI) chain precursor	15.8	1578
sp Q12772 SRBP2_HUMAN	Sterol regulatory element-binding prote...	15.8	1578
sp P15976 GATA1_HUMAN	Erythroid transcription factor (GATA-bi...	15.8	1578
sp Q6UVK1 CSPG4_HUMAN	Chondroitin sulfate proteoglycan 4 prec...	15.8	1578
sp P59046 NAL12_HUMAN	NACHT-, LRR- and PYD-containing protein...	15.8	1578
sp P02788 TRFL_HUMAN	Lactotransferrin precursor (Lactoferrin)...	15.8	1578
sp O15067 PUR4_HUMAN	Phosphoribosylformylglycinamide syntha...	15.8	1578
sp P12259 FA5_HUMAN	Coagulation factor V precursor (Activated...	15.8	1578
sp O15013 ARHGA_HUMAN	Rho guanine nucleotide exchange factor 10	15.8	1578
sp O75122 CLAP2_HUMAN	CLIP-associating protein 2 (Cytoplasmic...	15.8	1578
sp P17658 KCNA6_HUMAN	Potassium voltage-gated channel subfami...	15.4	2060
sp P29322 EPHA8_HUMAN	Ephrin type-A receptor 8 precursor (Tyr...	15.4	2060
sp O7Z401 MYCPP_HUMAN	C-myc promoter-binding protein	15.4	2060
sp Q8NHY2 RFWD2_HUMAN	Ring finger and WD repeat domain protei...	15.4	2060
sp Q9Y4C8 RBM19_HUMAN	Probable RNA-binding protein 19 (RNA-bindi	15.4	2060
sp Q96PE3 INP4A_HUMAN	Type I inositol-3,4-bisphosphate 4-phos...	15.4	2060
sp P31942 HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein...	15.4	2060
sp Q9Y2T3 GUAD_HUMAN	Guanine deaminase (Guanase) (Guanine ami...	15.4	2060
sp P25440 BRD2_HUMAN	Bromodomain-containing protein 2 (RING3 pro	15.4	2060
sp Q9NRA2 S17A5_HUMAN	Sialin (Solute carrier family 17 member...	15.4	2060
sp O5JSP0 FGD3_HUMAN	FYVE, RhoGEF and PH domain-containing pr...	15.4	2060
sp Q8N349 OR2LD_HUMAN	Olfactory receptor 2L13	15.4	2060
sp O43187 IRAK2_HUMAN	Interleukin-1 receptor-associated kinase-1	15.4	2060
sp P78367 NKX32_HUMAN	Homeobox protein Nkx-3.2 (Bagpipe homeobox	15.4	2060
sp Q14721 KCNB1_HUMAN	Potassium voltage-gated channel subfami...	15.4	2060
sp Q6UWN8 ISK6_HUMAN	Serine protease inhibitor Kazal-type 6 prec	15.4	2060
sp Q9NYQ7 CELR3_HUMAN	Cadherin EGF LAG seven-pass G-type rece...	15.4	2060
sp Q9ULK4 CRSP3_HUMAN	CRSP complex subunit 3 (Cofactor requir...	15.4	2060
sp O15143 ARC1B_HUMAN	Actin-related protein 2/3 complex subun...	15.4	2060
sp Q9BZR6 RTN4R_HUMAN	Reticulon-4 receptor precursor (Nogo re...	15.4	2060
sp Q9Y2U8 MAN1_HUMAN	Inner nuclear membrane protein Man1 (LEM...	15.4	2060
sp O14511 NRG2_HUMAN	Pro-neuregulin-2, membrane-bound isoform...	15.4	2060
sp P01574 IFNB_HUMAN	Interferon beta precursor (IFN-beta) (Fibro	15.4	2060
sp Q75355 ENP3_HUMAN	Ectonucleoside triphosphate diphosphohyd...	15.4	2060
sp P55084 ECHB_HUMAN	Trifunctional enzyme beta subunit, mitoc...	15.4	2060
sp P78426 NKX61_HUMAN	Homeobox protein Nkx-6.1	15.4	2060
sp Q14004 CD2L5_HUMAN	Cell division cycle 2-like protein kina...	15.4	2060
sp Q8NE62 CHDH_HUMAN	Choline dehydrogenase, mitochondrial precu	15.4	2060
sp Q92887 MRP2_HUMAN	Canalicular multispecific organic anion ...	15.4	2060
sp Q03828 EVX2_HUMAN	Homeobox even-skipped homolog protein 2 (EV	15.4	2060
sp Q8WXH0 SYNE2_HUMAN	Nesprin-2 (Nuclear envelope spectrin re...	15.4	2060

[sp|O14154|K0141_HUMAN](#) Protein KIAA0141[15.4](#)

2060

Alignments

>[sp|Q96PK2|MACF4_HUMAN](#) Microtubule-actin crosslinking factor 1, isoform 4
Length=5938

Score = 18.5 bits (36), Expect = 243
Identities = 6/11 (54%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
VK+ G+ S GW
Sbjct 465 VKISGTFSSGW 475

>[sp|O9UBV4|WNT16_HUMAN](#) Wnt-16 protein precursor
Length=365

Score = 18.1 bits (35), Expect = 318
Identities = 6/8 (75%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GG+S GW
Sbjct 156 GGSASEGW 163

>[sp|O14669|TRIPC_HUMAN](#) Thyroid receptor-interacting protein 12 (TRIP12)
Length=1992

Score = 18.1 bits (35), Expect = 318
Identities = 6/10 (60%), Positives = 6/10 (60%), Gaps = 0/10 (0%)

Query 3 KVGSSSLGW 12
K GGSS W
Sbjct 253 KTGSSSKFDW 262

>[sp|O16760|DGKD_HUMAN](#) Diacylglycerol kinase delta (Diglyceride kinase delta) (DGK-delta) (DAG kinase delta) (130 kDa diacylglycerol kinase)
Length=1214

Score = 18.1 bits (35), Expect = 318
Identities = 5/12 (41%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
++ GG S+GW
Sbjct 374 ILVCGGDGSGVW 385

>[sp|P54296|MYOM2_HUMAN](#) Myomesin-2 (M-protein) (165 kDa titin-associated protein) (165 kDa connectin-associated protein)
Length=1465

Score = 18.1 bits (35), Expect = 318
Identities = 4/11 (36%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
+++GGS + W
Sbjct 1277 MRIGGSEEMAW 1287

Score = 14.2 bits (25), Expect = 4590
Identities = 5/8 (62%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GGS LG+
Sbjct 738 GGSPILGY 745

>[sp|O13614|MTMR2_HUMAN](#) Myotubularin-related protein 2
Length=643

Score = 18.1 bits (35), Expect = 318
Identities = 7/11 (63%), Positives = 9/11 (81%), Gaps = 0/11 (0%)

Query 1 VVKVGGSSSLG 11
V K+GG+SS G
Sbjct 135 VEKIGGASSRG 145

>[sp|O9UIO6|LCAP_HUMAN](#) Leucyl-cystinyl aminopeptidase (Cystinyl aminopeptidase) (Oxytocinase) (OTase) (Insulin-regulated membrane aminopeptidase) (Insulin-responsive aminopeptidase) (IRAP) (Placental leucine aminopeptidase) (P-LAP)
Length=1025

Score = 17.7 bits (34), Expect = 415
Identities = 6/12 (50%), Positives = 7/12 (58%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
V KVG + GW
Sbjct 863 VFKVGAKTDKGW 874

>[sp|P49619|DGKG_HUMAN](#) Diacylglycerol kinase, gamma (Diglyceride kinase) (DGK-gamma) (DAG kinase gamma)
Length=791

Score = 17.7 bits (34), Expect = 415
Identities = 5/12 (41%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
V+ GG ++GW
Sbjct 487 VLACGGDGTVGW 498

>[sp|O9Y6T7|DGKB_HUMAN](#) Diacylglycerol kinase, beta (Diglyceride kinase) (DGK-beta) (DAG kinase beta) (90 kDa diacylglycerol kinase)
Length=804

Score = 17.7 bits (34), Expect = 415
Identities = 5/12 (41%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
V+ GG ++GW
Sbjct 491 VLACGGDGTVGW 502

>[sp|O969S2|NEIL2_HUMAN](#) Endonuclease VIII-like 2 (Nei-like 2) (DNA glycosylase/AP lyase Neil2) (DNA-(apurinic or apyrimidinic site) lyase Neil2) (NEH2)
Length=332

Score = 17.3 bits (33), Expect = 542
Identities = 7/8 (87%), Positives = 7/8 (87%), Gaps = 0/8 (0%)

Query 1 VVKVGGSS 8
VVK GGSS
Sbjct 22 VVKTTGGSS 29

>[sp|O8WUM9|S20A1_HUMAN](#) Sodium-dependent phosphate transporter 1 (Solute carrier family 20 member 1) (Phosphate transporter 1) (PiT-1) (Gibbon ape leukemia virus receptor 1) (GLVR-1) (Leukemia virus receptor 1 homolog)
Length=679

Score = 17.3 bits (33), Expect = 542
Identities = 6/10 (60%), Positives = 7/10 (70%), Gaps = 0/10 (0%)

Query 3 KVGSSSLGW 12
KVG S+GW
Sbjct 626 KVGSVSVGW 635

>[sp|O75912|DGKI_HUMAN](#) Diacylglycerol kinase, iota (Diglyceride kinase) (DGK-iota) (DAG kinase iota)
Length=1065

Score = 17.3 bits (33), Expect = 542
Identities = 4/12 (33%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGSSSLGW 12
++ GG ++GW
Sbjct 429 ILACGGDGTVGW 440

Score = 15.4 bits (28), Expect = 2060
Identities = 6/7 (85%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 5 GGSSSLG 11
GGSSS G
Sbjct 67 GGSSSSG 73

>[sp|P52429|DGKE_HUMAN](#) Diacylglycerol kinase, epsilon (Diglyceride kinase) (DGK-epsilon) (DAG kinase epsilon)
Length=567

Score = 17.3 bits (33), Expect = 542
Identities = 5/12 (41%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGSSSLGW 12
V+ GG ++GW
Sbjct 274 VLVCGGDGTVGW 285

>[sp|P52824|DGKO_HUMAN](#) Diacylglycerol kinase, theta (Diglyceride kinase) (DGK-theta) (DAG kinase theta)
Length=942

Score = 17.3 bits (33), Expect = 542
Identities = 5/12 (41%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGSSSLGW 12
V+ GG ++GW
Sbjct 641 VLVCGGDGTVGW 652

>[sp|O9NZ20|PA2G3_HUMAN](#) Group III secretory phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase GIII) (GIII sPLA2)
Length=509

Score = 17.3 bits (33), Expect = 542
Identities = 6/11 (54%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
V +GGS +L W
Sbjct 16 VALGGSPALRW 26

>[sp|Q13574|DGKZ_HUMAN](#) Diacylglycerol kinase, zeta (Diglyceride kinase) (DGK-zeta) (DAG kinase zeta)
Length=1117

Score = 17.3 bits (33), Expect = 542
Identities = 4/12 (33%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
++ GG ++GW
Sbjct 537 ILACGGDGTVGW 548

>[sp|Q9P232|CNTN3_HUMAN](#) Contactin-3 precursor (Brain-derived immunoglobulin superfamily protein 1) (BIG-1) (Plasmacytoma-associated neuronal glycoprotein)
Length=1028

Score = 17.3 bits (33), Expect = 542
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 3 KVGGS 9
KVGGS
Sbjct 553 KVGGS 559

>[sp|Q8IY67|RAVR1_HUMAN](#) Protein raver-1
Length=606

Score = 16.9 bits (32), Expect = 708
Identities = 5/11 (45%), Positives = 6/11 (54%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
V+ GG GW
Sbjct 536 VRAGGGDMQGW 546

>[sp|Q14653|IRF3_HUMAN](#) Interferon regulatory factor 3 (IRF-3)
Length=427

Score = 16.9 bits (32), Expect = 708
Identities = 6/10 (60%), Positives = 9/10 (90%), Gaps = 0/10 (0%)

Query 1 VVKVGGSSSL 10
+ +VGG+SSL
Sbjct 378 MARVGGASSL 387

Score = 13.1 bits (22), Expect = 10225
Identities = 4/10 (40%), Positives = 6/10 (60%), Gaps = 0/10 (0%)

Query 3 KVGGS 12
+VG + GW
Sbjct 232 EVGDRTLPGW 241

>[sp|P10809|CH60_HUMAN](#) 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein) (HuCHA60)
Length=573

Score = 16.9 bits (32), Expect = 708

Identities = 6/10 (60%), Positives = 9/10 (90%), Gaps = 0/10 (0%)

Query 1 VVKVGGSSSL 10
V+KVGG+S +
Sbjct 403 VLKVGGTSDV 412

>[sp|P23743|DGKA_HUMAN](#) Diacylglycerol kinase, alpha (Diglyceride kinase) (DGK-alpha)
(DAG kinase alpha) (80 kDa diacylglycerol kinase)
Length=735

Score = 16.9 bits (32), Expect = 708
Identities = 4/12 (33%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
++ GG ++GW
Sbjct 429 ILVCGDGTVGW 440

>[sp|P46977|STT3_HUMAN](#) Oligosaccharyl transferase STT3 subunit homolog (B5) (Integral
membrane protein 1) (TMC)
Length=705

Score = 16.9 bits (32), Expect = 708
Identities = 5/11 (45%), Positives = 9/11 (81%), Gaps = 0/11 (0%)

Query 1 VVKVGGSSSLG 11
+V++GGS+ G
Sbjct 599 MVRIGGSTDTG 609

>[sp|Q12788|TBL3_HUMAN](#) WD-repeat protein SAZD (Transducin beta-like 3 protein)
Length=519

Score = 16.9 bits (32), Expect = 708
Identities = 7/11 (63%), Positives = 7/11 (63%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
V G SSSL W
Sbjct 408 VASGASSLPW 418

>[sp|O14924|RGS12_HUMAN](#) Regulator of G-protein signaling 12 (RGS12)
Length=1447

Score = 16.9 bits (32), Expect = 708
Identities = 7/9 (77%), Positives = 8/9 (88%), Gaps = 0/9 (0%)

Query 1 VVKVGGSSS 9
VV +GGSSS
Sbjct 440 VVDLGGSSS 448

>[sp|Q8TE59|ATS19_HUMAN](#) ADAMTS-19 precursor (A disintegrin and metalloproteinase with
thrombospondin motifs 19) (ADAM-TS 19) (ADAM-TS19)
Length=1207

Score = 16.5 bits (31), Expect = 925
Identities = 5/8 (62%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GGS+ GW
Sbjct 55 GGSADPGW 62

>[sp|P58215|LOXL3_HUMAN](#) Lysyl oxidase homolog 3 precursor (Lysyl oxidase-like protein 3)

Length=753

Score = 16.5 bits (31), Expect = 925
Identities = 5/11 (45%), Positives = 7/11 (63%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
V++GG L W
Sbjct 432 VQIGGPGPLRW 442

>[sp|O9NO84|GPC5C_HUMAN](#) G-protein coupled receptor family C group 5 member C precursor (Retinoic acid-induced gene 3 protein) (RAIG-3)
Length=441

Score = 16.5 bits (31), Expect = 925
Identities = 5/7 (71%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 6 GSSSLGW 12
G+SS GW
Sbjct 190 GNSSAGW 196

>[sp|O9Y570|PPME1_HUMAN](#) Protein phosphatase methylesterase 1 (PME-1)
Length=386

Score = 16.5 bits (31), Expect = 925
Identities = 5/8 (62%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GG S+L W
Sbjct 85 GGHSALSW 92

>[sp|O08397|LOXL1_HUMAN](#) Lysyl oxidase homolog 1 precursor (Lysyl oxidase-like protein 1) (LOL)
Length=574

Score = 16.5 bits (31), Expect = 925
Identities = 5/8 (62%), Positives = 5/8 (62%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GG LGW
Sbjct 302 GGDPRLGW 309

>[sp|O92522|H1X_HUMAN](#) Histone H1x
Length=213

Score = 16.5 bits (31), Expect = 925
Identities = 6/10 (60%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

Query 1 VVKVGGSSSL 10
V K GGS++L
Sbjct 21 VTKAGGSAAL 30

>[sp|O04756|HGFA_HUMAN](#) Hepatocyte growth factor activator precursor (HGF activator) (HGFA) [Contains: Hepatocyte growth factor activator short chain; Hepatocyte growth factor activator long chain]
Length=655

Score = 16.5 bits (31), Expect = 925
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 4 VGGSSSL 10
+GGSSSL
Sbjct 409 IGGSSSL 415

>[sp|P04150|GCR_HUMAN](#) Glucocorticoid receptor (GR)
Length=777

Score = 16.5 bits (31), Expect = 925
Identities = 6/12 (50%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
+VK G+SS W
Sbjct 701 IVKREGNSSQNW 712

>[sp|O9UBY8|CLN8_HUMAN](#) Protein CLN8
Length=286

Score = 16.5 bits (31), Expect = 925
Identities = 6/12 (50%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
++K G S SL W
Sbjct 179 LLKAGWSESLFW 190

>[sp|O92747|ARC1A_HUMAN](#) Actin-related protein 2/3 complex subunit 1A (SOP2-like protein)
Length=370

Score = 16.2 bits (30), Expect = 1208
Identities = 5/8 (62%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GGS + GW
Sbjct 199 GSGTG GW 206

>[sp|P0C0L4|CO4A_HUMAN](#) Complement C4-A precursor (Acidic complement C4) [Contains: Complement C4 beta chain; Complement C4-A alpha chain; C4a anaphylatoxin; C4b-A; C4d-A; Complement C4 gamma chain]
Length=1744

Score = 16.2 bits (30), Expect = 1208
Identities = 6/7 (85%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 2 VKVGGSS 8
VKVGG+S
Sbjct 1368 VKVGGNS 1374

>[sp|P14923|PLAK_HUMAN](#) Junction plakoglobin (Desmoplakin-3) (Desmoplakin III)
Length=744

Score = 16.2 bits (30), Expect = 1208
Identities = 5/11 (45%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

Query 1 VVKVGGSSSLG 11
+V+ GG +LG
Sbjct 347 IVEAGGMQALG 357

>[sp|O6VVB1|NHL1_HUMAN](#) NHL repeat containing protein 1 (Malin)
Length=395

Score = 16.2 bits (30), Expect = 1208
Identities = 5/9 (55%), Positives = 6/9 (66%), Gaps = 0/9 (0%)

Query 4 VGGSSSLGW 12
+GG SL W
Sbjct 211 IGGQFSLPW 219

>[sp|O14576|ELAV3_HUMAN](#) ELAV-like protein 3 (Hu-antigen C) (HuC) (Paraneoplastic cerebellar degeneration-associated antigen) (Paraneoplastic limbic encephalitis antigen 21)
Length=367

Score = 16.2 bits (30), Expect = 1208
Identities = 4/8 (50%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GG++ GW
Sbjct 277 GGAAGAGW 284

>[sp|Q9UKQ2|ADA28_HUMAN](#) ADAM 28 precursor (A disintegrin and metalloproteinase domain 28) (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein-L) (MDC-L) (eMDC II) (ADAM23)
Length=775

Score = 16.2 bits (30), Expect = 1208
Identities = 5/8 (62%), Positives = 6/8 (75%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GGS +L W
Sbjct 568 GGSDNLPW 575

>[sp|Q8TDB6|DTX3L_HUMAN](#) Deltex 3-like protein (B-lymphoma- and BAL-associated protein) (Rhysin-2) (Rhysin2)
Length=740

Score = 16.2 bits (30), Expect = 1208
Identities = 7/10 (70%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

Query 1 VVKVGGSSSL 10
V+K GG SSL
Sbjct 506 VLKGGGMSSL 515

>[sp|O15413|RYR3_HUMAN](#) Ryanodine receptor 3 (Brain-type ryanodine receptor) (RyR3) (RYR-3) (Brain ryanodine receptor-calcium release channel)
Length=4870

Score = 16.2 bits (30), Expect = 1208
Identities = 5/11 (45%), Positives = 6/11 (54%), Gaps = 0/11 (0%)

Query 2 VKVGGSSSLGW 12
V GG +GW
Sbjct 1093 VVTGGDMRVGW 1103

>[sp|Q86XX4|FRAS1_HUMAN](#) Extracellular matrix protein FRAS1 precursor
Length=4007

Score = 16.2 bits (30), Expect = 1208
Identities = 6/10 (60%), Positives = 8/10 (80%), Gaps = 0/10 (0%)

Query 2 VKVGGSSSLG 11

V GGS+S+G
Sbjct 1605 VSPGGSTSVG 1614

>[sp|O9Y6I9|TX264_HUMAN](#) Testis expressed sequence 264 protein precursor (Secreted protein ZSIG11)
Length=313

Score = 16.2 bits (30), Expect = 1208
Identities = 5/7 (71%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 6 GSSSLGW 12
G+SS GW
Sbjct 246 GASSRGW 252

>[sp|O9NUD5|ZCHC3_HUMAN](#) Zinc finger CCHC domain-containing protein 3
Length=404

Score = 16.2 bits (30), Expect = 1208
Identities = 4/8 (50%), Positives = 5/8 (62%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GG +GW
Sbjct 33 GREKMGW 40

>[sp|O75420|PERO1_HUMAN](#) PERO amino acid rich with GYF domain protein 1
Length=817

Score = 16.2 bits (30), Expect = 1208
Identities = 5/8 (62%), Positives = 5/8 (62%), Gaps = 0/8 (0%)

Query 5 GGSSSLGW 12
GG S GW
Sbjct 143 GPRSAGW 150

>[sp|O9P296|C5ARL_HUMAN](#) C5a anaphylatoxin chemotactic receptor C5L2 (G-protein coupled receptor 77)
Length=337

Score = 16.2 bits (30), Expect = 1208
Identities = 7/9 (77%), Positives = 7/9 (77%), Gaps = 0/9 (0%)

Query 1 VVKVGGSSS 9
VV GGSSS
Sbjct 187 VVDYGGSSS 195

>[sp|P17174|AATC_HUMAN](#) Aspartate aminotransferase, cytoplasmic (Transaminase A) (Glutamate oxaloacetate transaminase 1)
Length=413

Score = 16.2 bits (30), Expect = 1208
Identities = 6/9 (66%), Positives = 7/9 (77%), Gaps = 0/9 (0%)

Query 3 KVGSSSLG 11
+VGG SLG
Sbjct 100 RVGGVQSLG 108

>[sp|P35222|CTNB1_HUMAN](#) Beta-catenin
Length=781

Score = 16.2 bits (30), Expect = 1208
 Identities = 5/11 (45%), Positives = 8/11 (72%), Gaps = 0/11 (0%)

Query 1 VVKVGGSSSLG 11
 +V+ GG +LG
 Sbjct 357 IVEAGGMQALG 367

>[sp|O9UKY4|POMT2_HUMAN](#) Protein O-mannosyl-transferase 2 (Dolichyl-phosphate-mannose--protein mannosyltransferase 2)
 Length=750

Score = 16.2 bits (30), Expect = 1208
 Identities = 5/12 (41%), Positives = 8/12 (66%), Gaps = 0/12 (0%)

Query 1 VVKVGGSSSLGW 12
 +++ GG LGW
 Sbjct 636 LLRGGGQVLLGW 647

>[sp|O8NDV7|TNR6A_HUMAN](#) Trinucleotide repeat-containing gene 6A protein (CAG repeat protein 26) (Glycin-tryptophan protein of 182 kDa) (GW182 autoantigen) (GW1 protein) (EMSY interactor protein)
 Length=1962

Score = 16.2 bits (30), Expect = 1208
 Identities = 5/7 (71%), Positives = 6/7 (85%), Gaps = 0/7 (0%)

Query 6 GSSSLGW 12
 GSSS+ W
 Sbjct 1602 GSSSVNW 1608

Database: Non-redundant SwissProt sequences

Posted date: Mar 4, 2006 8:15 AM

Number of letters in database: 7,391,856

Number of sequences in database: 13,628

Lambda K H
 0.310 0.132 0.421

Gapped

Lambda K H
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 13628

Number of Hits to DB: 59382

Number of extensions: 208

Number of successful extensions: 207

Number of sequences better than 100000: 192

Number of HSP's better than 100000 without gapping: 0

Number of HSP's gapped: 207

Number of HSP's successfully gapped: 207

Length of query: 12

Length of database: 7391856

Length adjustment: 0

Effective length of query: 12

Effective length of database: 7391856

Effective search space: 88702272

Effective search space used: 88702272

T: 11

A: 40

X1: 14 (6.3 bits)

X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 14 (10.0 bits)
S2: 14 (10.0 bits)