Εργασία στο μάθημα ΔΟΜΙΚΗ ΒΙΟΧΗΜΕΙΑ ΚΑΙ ΣΤΟΙΧΕΙΑ ΒΙΟΠΛΗΡΟΦΟΡΙΚΗΣ
Ομάδα: Δούκα Ματίνα(8299), Στάμου Παρασκευή(8379)
Υπεύθυνη καθηγήτρια: Χολή-Παπαδοπούλου Θεοδώρα
Όνομα πρωτεΐνης: 1CLL

FASTA(από UniProtKB):
>sp|P62158|CALM_HUMAN Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2
MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG
NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE
EVDEMIREADIDGDGQVNYEEFVQMMTAK

PROTPARAM:

User-provided sequence:

```
      10        20        30        40        50        60
MADQLTEEQI AEFKEAFSLF DKDGDGTITT KELGTVMRSL GQNPTEAELQ DMINEVDADG

      70        80        90       100       110       120
NGTIDFPEFL TMMARKMKDT DSEEEIREAF RVFDKDGNGY ISAAELRHVM TNLGEKLTDE

     130       140
EVDEMIREAD IDGDGQVNYE EFVQMMTAK
```

Number of amino acids: 149

Molecular weight: 16837.5

Theoretical pI: 4.09

Amino acid composition:

Ala (A)	11	7.4%	Tyr (Y)	2	1.3%
Arg (R)	6	4.0%	Val (V)	7	4.7%
Asn (N)	6	4.0%	Pyl (O)	0	0.0%
Asp (D)	17	11.4%	Sec (U)	0	0.0%
Cys (C)	0	0.0%			
Gln (Q)	6	4.0%			
Glu (E)	21	14.1%	(B)	0	0.0%
Gly (G)	11	7.4%	(Z)	0	0.0%
His (H)	1	0.7%	(X)	0	0.0%
Ile (I)	8	5.4%			
Leu (L)	9	6.0%			
Lys (K)	8	5.4%			
Met (M)	10	6.7%			
Phe (F)	8	5.4%			
Pro (P)	2	1.3%			
Ser (S)	4	2.7%			
Thr (T)	12	8.1%			
Trp (W)	0	0.0%			

Total number of negatively charged residues (Asp + Glu): 38
Total number of positively charged residues (Arg + Lys): 14

Atomic composition:

Carbon	C	719
Hydrogen	H	1129
Nitrogen	N	189
Oxygen	O	256
Sulfur	S	10

Formula: $C_{719}H_{1129}N_{189}O_{256}S_{10}$
Total number of atoms: 2303

Extinction coefficients:

This protein does not contain any Trp residues. Experience shows that
this could result in more than 10% error in the computed extinction coefficient.

Extinction coefficients are in units of M^{-1} cm^{-1}, at 280 nm measured in water.

Ext. coefficient 2980
Abs 0.1% (=1 g/l) 0.177

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).
>20 hours (yeast, in vivo).
>10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 28.21
This classifies the protein as stable.

Aliphatic index: 65.50

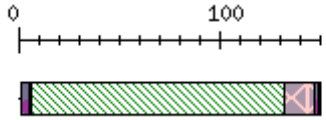
Grand average of hydropathicity (GRAVY): -0.654

PRODOM:

database:	multiple alignments
Program:	ncbi-blastp
Matrix:	BLOSUM62
Expect:	0.01
Filter:	seg

Graphical results and forms to other applications

The following is the graphical representation of the HSP found by BLAST.
Please note that HSPs are sorted from highest to lowest scores, so that lower scoring HSPs may be hidden.



Align subsequence with ProDom domains, using Multalin

Domain ID	BEGIN	END	
PD000012	6	131	Submit
PD002799	5	74	Submit
PD002799	82	146	Submit
PDB5J7H4	5	144	Submit
PDB7J4K1	25	115	Submit
PDC5T3X2	43	148	Submit
PD002827	54	142	Submit

PDE0F6H4	5	144	Submit
PDB8B462	5	140	Submit
PDA1F114	90	148	Submit
PDB6L323	1	147	Submit
PDC768N7	88	147	Submit
PDC0A1I3	10	110	Submit
PDC6C600	4	56	Submit
PDB1M9U6	5	143	Submit
PDB381W0	61	147	Submit
PD851386	81	147	Submit
PDD6Y0J8	44	148	Submit
PDD873Q2	74	146	Submit
PDD7V6N9	94	146	Submit
PDB8K817	82	146	Submit
PDD86432	56	81	Submit
PDB2C2O0	85	143	Submit
PDA5C7J8	8	93	Submit

PDC5T3F8	7	144	Submit
PDB2P1E2	63	143	Submit
PDD78077	86	148	Submit
PDA4R9E5	70	143	Submit
PDB7S5E8	7	140	Submit
PDC947T1	127	147	Submit
PDC732F4	84	131	Submit
PDC7X3O5	70	144	Submit
PDB7I003	7	131	Submit
PDB0D2H1	36	121	Submit
PDD343M4	7	99	Submit
PDC7D0O4	89	142	Submit
PD061537	67	144	Submit
PDA1F114	17	73	Submit
PDB213K1	90	142	Submit
PDB2C2O0	14	78	Submit
PDA1J8Z2	84	147	Submit

PDB173A7	84	140	Submit
PDD0S5L8	5	56	Submit
PDC44543	86	145	Submit
PDB0N4G0	84	147	Submit
PDD9K0I4	4	105	Submit
PDD2R1N0	85	147	Submit
PDB565C4	26	143	Submit
PDA2A364	89	146	Submit
PDE0T3U8	13	149	Submit
PDA0A3M7	73	144	Submit
PD498404	37	78	Submit
PD003407	84	147	Submit
PDB1O9S5	52	113	Submit
PDB693L4	15	126	Submit
PDC87651	90	145	Submit
PDB015Z3	82	124	Submit
PDB2B3P0	94	148	Submit

PD465777	70	147	Submit
PDB1D8B3	94	144	Submit
PDA5L972	72	142	Submit
PDB2O3R4	90	146	Submit
PDB0X1Z3	86	142	Submit
PDA2T7T5	90	146	Submit
PDB1N646	11	70	Submit
PDD1F4C8	87	143	Submit
PDC8J846	62	143	Submit
PDA2D7H7	59	125	Submit
PDB0M3G7	92	146	Submit
PDD349V3	89	146	Submit
PDD0T2M4	12	68	Submit
PDB6A9B6	16	76	Submit
PD312936	57	109	Submit
PD406130	57	113	Submit
PDA96187	87	142	Submit

PDC5M9V7	90	142	Submit
PDD5B3Q3	33	107	Submit
PDC999J9	59	102	Submit
PDD2X1S1	83	149	Submit
PDC768N7	15	73	Submit
PDC123P6	16	68	Submit
PD721888	73	143	Submit
PDB167A9	16	70	Submit
PDC6A9F9	52	99	Submit
PDC4P118	83	130	Submit

Domain 3D modelling using Swiss-Model

Domain ID	BEGIN	END	
PD000012	6	131	Submit
PD002799	5	74	Submit
PD002799	82	146	Submit
PDA1F114	90	148	Submit
PD851386	81	147	Submit

PDD86432	56	81	Submit
PDC947T1	127	147	Submit
PDC123P6	16	68	Submit

Domain 3D modelling using Geno3D

Domain ID	BEGIN	END	
PD000012	6	131	Submit
PD002799	5	74	Submit
PD002799	82	146	Submit
PDA1F114	90	148	Submit
PD851386	81	147	Submit
PDD86432	56	81	Submit
PDC947T1	127	147	Submit
PDC123P6	16	68	Submit

HSP Results

Warning: Original output has been filtered to yield non-redundant similarities

blastp 2.2.26 [Sep-21-2011]

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

Query: unkwown
(149 letters)

Database: prodom2010.1 multiple alignments
45,292,438 sequences; 2,147,483,647 total letters

ProDom domains producing High-scoring Segment Pairs:

Position	ProDom domain	Score	E value
1-147	#PDB6L323	143	2e-09
4-56	#PDC6C600	132	2e-08
4-105	#PDD9K0I4	102	0.002
5-143	#PDB1M9U6	131	9e-08
5-144	#PDB5J7H4	252	3e-24
5-56	#PDD0S5L8	102	0.0004
5-140	#PDB8B462	145	1e-09
5-144	#PDE0F6H4	163	1e-11
5-74	#PD002799	346	8e-40
6-131	#PD000012	645	2e-84
7-144	#PDC5T3F8	117	6e-06
7-140	#PDB7S5E8	112	4e-05
7-99	#PDD343M4	105	0.0003
7-131	#PDB7I003	107	0.0002
8-93	#PDA5C7J8	118	3e-06
10-110	#PDC0A1I3	136	1e-08
11-70	#PDB1N646	96	0.002
12-68	#PDD0T2M4	94	0.005
13-149	#PDE0T3U8	100	0.004
14-78	#PDB2C2O0	102	0.0003
15-126	#PDB693L4	98	0.007
15-73	#PDC768N7	93	0.004
16-68	#PDC123P6	92	0.006
16-76	#PDB6A9B6	94	0.004
16-70	#PDB167A9	92	0.006
17-73	#PDA1F114	103	0.0001
25-115	#PDB7J4K1	178	1e-14
26-143	#PDB565C4	101	0.003
33-107	#PDD5B3Q3	93	0.009
36-121	#PDB0D2H1	106	0.0001
37-78	#PD498404	100	0.0003
43-148	#PDC5T3X2	175	8e-14
44-148	#PDD6Y0J8	129	1e-07
52-113	#PDB1O9S5	99	0.0007
52-99	#PDC6A9F9	91	0.006
54-142	#PD002827	167	5e-13
56-81	#PDD86432	120	8e-07
57-113	#PD406130	93	0.004
57-109	#PD312936	94	0.003
59-125	#PDA2D7H7	95	0.005
59-102	#PDC999J9	93	0.003

61-147	#PDB381W0	130	4e-08
62-143	#PDC8J846	95	0.003
63-143	#PDB2P1E2	116	4e-06
67-144	#PD061537	104	0.0002
70-144	#PDC7X3O5	107	6e-05
70-147	#PD465777	97	0.001
70-143	#PDA4R9E5	112	2e-05
72-142	#PDA5L972	96	0.006
73-143	#PD721888	92	0.007
73-144	#PDA0A3M7	100	0.0005
74-146	#PDD873Q2	125	3e-07
81-147	#PD851386	129	5e-08
82-124	#PDB015Z3	98	0.001
82-146	#PDB8K817	123	3e-07
82-146	#PD002799	332	7e-38
83-149	#PDD2X1S1	93	0.005
83-130	#PDC4P118	90	0.01
84-147	#PDA1J8Z2	102	0.0002
84-140	#PDB173A7	102	0.0002
84-131	#PDC732F4	108	3e-05
84-147	#PDB0N4G0	102	0.0002
84-147	#PD003407	100	0.0005
85-143	#PDB2C2O0	118	2e-06
85-147	#PDD2R1N0	102	0.0006
86-142	#PDB0X1Z3	96	0.002
86-145	#PDC44543	102	0.0002
86-148	#PDD78077	115	1e-05
87-143	#PDD1F4C8	95	0.002
87-142	#PDA96187	93	0.004
88-147	#PDC768N7	142	7e-10
89-146	#PDA2A364	100	0.0004
89-142	#PDC7D0O4	105	8e-05
89-146	#PDD349V3	95	0.005
90-145	#PDC87651	98	0.0009
90-142	#PDB213K1	102	0.0002
90-146	#PDB2O3R4	96	0.001
90-142	#PDC5M9V7	93	0.003
90-146	#PDA2T7T5	96	0.001
90-148	#PDA1F114	143	5e-10
92-146	#PDB0M3G7	95	0.002
94-146	#PDD7V6N9	124	8e-07
94-144	#PDB1D8B3	97	0.001
94-148	#PDB2B3P0	98	0.001
127-147	#PDC947T1	109	2e-05

>**PD000012** (Closest domain: B5XCM2_SALSA 6-133)
Number of domains in family: 10473
Commentary (automatic):
SUBNAME: CALCIUM REFERENCE FULL=PUTATIVE REPEAT UNCHARACTERIZED KINASE ATP-BINDING NUCLEOTIDE-BINDING RECNAME:

Length = 128
Score = 645 (253.1 bits), Expect = 2e-84
Identities = 126/126 (100%), Positives = 126/126 (100%)

```
Query:   6 TEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTID 65
         TEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTID
Sbjct:   6 TEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTID 65

Query:   66 FPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEM 125
         FPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEM
Sbjct:   66 FPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEM 125

Query:   126 IREADI 131
         IREADI
Sbjct:   126 IREADI 131
```

>**PD002799** (Closest domain: G7MLA5_MACMU 5-74)
Number of domains in family: 1817
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED REFERENCE CALCIUM MEMBRANE DOMAIN
RECNAME: SH3 FULL=ACTIN
Length = 70
Score = 346 (137.9 bits), Expect = 8e-40
Identities = 68/70 (97%), Positives = 68/70 (97%), Gaps = 2/70 (2%)

```
Query:   5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI 64
         LTEEQIAEFKEAFSLFDKDGDGTITTKELG VM SLGQNPTEAELQDMINEVDADGNGTI
Sbjct:   5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGAVMTSLGQNPTEAELQDMINEVDADGNGTI 64

Query:   65 DFPEFLTMMA 74
         DFPEFLTMMA
Sbjct:   65 DFPEFLTMMA 74
```

>**PD002799** (Closest domain: E3TEM4_ICTPU 82-146)
Number of domains in family: 1817
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED REFERENCE CALCIUM MEMBRANE DOMAIN
RECNAME: SH3 FULL=ACTIN
Length = 65
Score = 332 (132.5 bits), Expect = 7e-38
Identities = 65/65 (100%), Positives = 65/65 (100%), Gaps = 1/65 (1%)

```
Query:   82 SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEE 141
         SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEE
Sbjct:   82 SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEE 141

Query:   142 FVQMM 146
         FVQMM
Sbjct:   142 FVQMM 146
```

>**PDB5J7H4** (Closest domain: A5AVZ9_VITVI 21-233)

Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM
Length = 213
Score = 252 (101.7 bits), Expect = 3e-24
Identities = 64/177 (36%), Positives = 90/177 (50%), Gaps = 37/177 (20%)

```
Query:    5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQD---------- 51
          L + +  E KEAF LFD DG GTI  +EL   MR+LG   TE  L++
Sbjct:   37 LPQRKRQEIKEAFDLFDTDGSGTIDARELNVAMRALGFEMTEEYLRELSGVTFLFILNSF 96

Query:   52 ------------------------MINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIR 87
                                    MI +VD +G+G IDF EF  MM  K+ + DS+EE+
Sbjct:   97 RNLQIFVILMANTCFAMSFQQITQMIADVDKNGSGAIDFDEFAHMMTAKIGERDSKEELM 156

Query:   88 EAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQ 144
          +AF + D+D NG IS+ +++ +   LGEK +  E++EMIREAD D      +E F+
Sbjct:  157 KAFHIIDQDQNGKISSMDIKRITEELGEKFSTREIEEMIREADQDYMDLFMFEIFLH 213
```

>**PDB7J4K1** (Closest domain: A6XN13_PRUPE 64-153)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: REFERENCE FULL=PUTATIVE UNCHARACTERIZED FULL=CALMODULIN
Length = 90
Score = 178 (73.2 bits), Expect = 1e-14
Identities = 33/91 (36%), Positives = 53/91 (58%), Gaps = 2/91 (2%)

```
Query:   25 DGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKMKDTDSEE 84
         DG I   ELG +MR LG N T+A+ + +  E        +FP FL +M + MK T  +
Sbjct:   65 DGKIVPSELGNLMRLLGVNSTQAQHKSIAAEEKL--TAPFNFPHFLDLMGKHMKPTPFDH 122

Query:   85 EIREAFRVFDKDGNGYISAAELRHVMTNLGE 115
          ++   F+V DKD  G++  +ELRH++T++ +
Sbjct:  123 QLCNTFKVLDKDSTGFVFVSELRHILTSINK 153
```

>**PDC5T3X2** (Closest domain: A7RJ54_NEMVE 1-147)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FULL=PREDICTED
Length = 147
Score = 175 (72.0 bits), Expect = 8e-14
Identities = 42/107 (39%), Positives = 66/107 (61%), Gaps = 3/107 (2%)

```
Query:   43 NPTEAELQDMINEVD-ADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYI 101
         NP E ELQD+ NE+D   G GTIDF +F+ MM  + K ++ EEEIR AF VFD D   +I
Sbjct:   31 NPGEQELQDITNEIDYGKGGGTIDFEDFVKMMEDQKKPSE-EEEIRTAFDVFDSDHKEFI 89

Query:  102 SAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTA 148
          + ++R  +  +   E++EM+ + D+  D +  +EEF +++T
Sbjct:   90 ESGDIRGALHRVN-TIPPRELEEMLVDLDLVRDRKFTFEEFKKLVTT 135
```

>**PD002827** (Closest domain: G0MQV0_CAEBE 42-134)
Number of domains in family: 890
Commentary (automatic):
SUBNAME: CALCIUM PROTEASE ALTNAME: HYDROLASE REFERENCE THIOL FULL=PUTATIVE UNCHARACTERIZED FULL=CALPAIN
Length = 93
Score = 167 (68.9 bits), Expect = 5e-13
Identities = 35/91 (38%), Positives = 57/91 (62%), Gaps = 3/91 (3%)

```
Query:    54 NEVDADGNGTIDFPEFLTMM--ARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMT 111
          N+VDADGNG IDF EF   M  ++ +  + +EE IRE F +FD+D NG I+  E +++
Sbjct:    45 NQVDADGNGEIDFEEFCACMKKSQNIVKSTNEELIRECFEIFDQDRNGIITENEFKYIAK 104

Query:   112 NLGEKLTDEEVDEMIREADIDGDGQVNYEEF 142
            G+   DE  +++ RE D+  +G ++ ++F
Sbjct:   105 EFGD-FDDELAEKVFRELDVSANGHLSADQF 134
```

>**PDE0F6H4** (Closest domain: G7YUF6_CLOSI 1285-1580)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=ANOSMIN-1
Length = 296
Score = 163 (67.4 bits), Expect = 1e-11
Identities = 41/143 (28%), Positives = 74/143 (51%), Gaps = 4/143 (2%)

```
Query:     5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI 64
           L+E ++A   +AF LFD    G I + +LG  +R L   P+ AE+  ++  ++    G I
Sbjct:  1435 LSEFEVANITKAFRLFDPRNTGFIRSSQLGNALRWLKLIPSNAEIASLLEVINPSKTGLI 1494

Query:    65 DFPEFLTMMARKMKD--TDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLG-EKLTDEE 121
             FL         T+ E E+ +AF  FDK   GY+S+ ++  ++T  G E + ++E
Sbjct:  1495 SLELFLAAAVELWYGPITNLELELWKAFEKFDKRLCGYVSSDKMYDILTRFGCEPIPEQE 1554

Query:   122 VDEMIREADIDGDGQVNYEEFVQ 144
           ++I+  + D + ++ Y E V+
Sbjct:  1555 AIKLIKRFE-DKNQRIYYAEMVR 1576
```

>**PDB8B462** (Closest domain: A9UYW5_MONBE 560-747)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FULL=PREDICTED
Length = 188
Score = 145 (60.5 bits), Expect = 1e-09
Identities = 46/160 (28%), Positives = 70/160 (43%), Gaps = 30/160 (18%)

```
Query:     5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI 64
           L+ E  A   EAF L  +  G ++   G V+R +G NP+E E+  +        T+
Sbjct:   589 LSAEDRAVLAEAFQL-HESSPGQLSAASFGEVVRIVGANPSEEEV---LAHCGNKTTFTL 644

Query:    65 DFPEFLTMMARKMKDTDSEEEIREAFRVFDK----------------------DGNGY 100
           D  +    +A +    D  + +R+AF +FD                       +G G
```

Sbjct: 645 D--DVANYLATQKLHEDPVQTLRDAFAMFDPWRPLALSATARAQALMVVMPPVFSEGKGS 702

Query: 101 ISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYE 140
I A E R VM NLGE+ E++EM+R + DGQ+ YE
Sbjct: 703 IDATEFRTVMHNLGERFQMYEIEEMMRVPETTADGQIVYE 742

>**PDA1F114** (Closest domain: B3GQ31_ORYSI 16-76)
Number of domains in family: 233
Commentary (automatic):
SUBNAME: CALCIUM REPEAT FULL=PUTATIVE REFERENCE UNCHARACTERIZED TRANSMEMBRANE MEMBRANE HELIX OXIDOREDUCTASE
Length = 61
Score = 143 (59.7 bits), Expect = 5e-10
Identities = 30/60 (50%), Positives = 41/60 (68%), Gaps = 1/60 (1%)

Query: 90 FRVFDKDGNGYISAAELRHVM-TNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTA 148
F FD DG+G ISAAELR M T LGE+++DEE +++ D DGDG + EFV+++ A
Sbjct: 16 FATFDHDGDGRISAAELRLCMKTTLGEEVSDEEAGQLVASVDADGDGLLCEAEFVRLVQA 75

>**PDB6L323** (Closest domain: Q38C77_TRYB2 1-172)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED
Length = 172
Score = 143 (59.7 bits), Expect = 2e-09
Identities = 40/156 (25%), Positives = 71/156 (45%), Gaps = 10/156 (6%)

Query: 1 MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADG 60
M LT + +++ +EAF LFD +G I + ++ SL E +++ +G
Sbjct: 5 MKCTLTHDVVSDLQEAFRLFDSADEGVIAMSRVRSLAFSLVPKLNEGMFSRVLSTTKLEG 64

Query: 61 NGTIDFPEFLTMMARKMKDTDSE------EEIREAFRVFDKDGNGYISAAELRHVMTNLG 114
I+FP+F+ + + + D + +E+ E F +D + GYI +M G
Sbjct: 65 CDVINFPQFVVLFS-TLSDVSTRAENFGVDELVEVFSHYDTNRTGYIDLNCFLQIMMEEG 123

Query: 115 EKLTDEEVDEMI---READIDGDGQVNYEEFVQMMT 147
E L+ E E++ R +VNY +FVQ +
Sbjct: 124 ELLSAVEGSELVLHLRRFGCVHLNKVNYCKFVQRLV 159

>**PDC768N7** (Closest domain: C5LU89_PERM5 324-382)
Number of domains in family: 11
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE UNCHARACTERIZED KINASE NUCLEOTIDE-BINDING FULL=CALCIUM-DEPENDENT KINASE ATP-BINDING FULL=PREDICTED
Length = 59
Score = 142 (59.3 bits), Expect = 7e-10
Identities = 30/60 (50%), Positives = 41/60 (68%), Gaps = 3/60 (5%)

Query: 88 EAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMT 147
+AFR D+DG+G IS LR T LGE ++E+I+E DI+GDGQ+ YEEFV ++T
Sbjct: 325 DAFRKMDRDGSGSISLENLR---TILGEDYMGTRIEEIIKECDINGDGQIQYEEFVALVT 381

>**PDC0A1I3** (Closest domain: A0DBN0_PARTE 337-450)
Number of domains in family: 5
Commentary (automatic):
SUBNAME: CALCIUM REPEAT REFERENCE FULL=CHROMOSOME SHOTGUN GENOME SEQUENCE WHOLE UNDETERMINED
Length = 114
Score = 136 (57.0 bits), Expect = 1e-08
Identities = 35/102 (34%), Positives = 63/102 (61%), Gaps = 6/102 (5%)

```
Query:   10 IAEFKEAFSLFDKDGDGTITTKELGTV-MRSLGQNPTEAELQDMINEVDADGNGTIDFPE 68
         +AEFK+    DKDG+G I+  EL  V ++   +  + + D+ ++VD + +G +DF E
Sbjct:  354 LAEFKK----IDKDGNGQISKDELVQVYLKQYDEIKAKQMVDDIFDKVDTNKSGYVDFTE 409

Query:   69 FLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVM 110
         F+T  A + K  + ++ +++AF +FD +G+G IS  EL+ +M
Sbjct:  410 FITSAANEEKLLN-KQRLQQAFNMFDTNGDGQISRDELQEIM 450
```

>**PDC6C600** (Closest domain: D5GKQ9_TUBMM 41-99)
Number of domains in family: 44
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE UNCHARACTERIZED FULL=CALMODULIN REFERENCE FULL=CALMODULIN FULL=PREDICTED ION SHOTGUN
Length = 59
Score = 132 (55.5 bits), Expect = 2e-08
Identities = 25/53 (47%), Positives = 36/53 (67%), Gaps = 2/53 (3%)

```
Query:    4 QLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEV 56
          QL+  QI E KE+F + DKDGDG I  ++LG ++ SLGQ+PT A +   ++ V
Sbjct:   44 QLSSTQIQELKESFQMLDKDGDGIIGKQDLGAMLGSLGQDPTPAVINAHLSSV 96
```

>**PDB1M9U6** (Closest domain: B9PNM5_TOXGO 114-282)
Number of domains in family: 6
Commentary (automatic):
BIOSYNTHESIS SYNTHASE SUBNAME: ALTNAME: ACID AMINO BRANCHED-CHAIN AMINO-ACID FATTY FULL=2-ISOPROPYLMALATE
Length = 169
Score = 131 (55.1 bits), Expect = 9e-08
Identities = 35/147 (23%), Positives = 74/147 (50%), Gaps = 8/147 (5%)

```
Query:    5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI 64
          LT+EQ+A  +  F+  D +  G +   ++  ++ +LG + TE ELQ  +++ D D    +
Sbjct:  119 LTDEQVASTRALFNEIDVEAKGLLDPNQICALLNTLGYHLTEEELQQAMDDYDVDYKNGL 178

Query:   65 DFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMT--------NLGEK 116
          +  + + ++      T  + ++ EAF + D D +G +  A L+ ++         ++ EK
Sbjct:  179 NEDDLIQLVEEVEASTVQKRKVVEAFALMDVDSSGIVDVARLQALLCGTEGGGAEDVPDP 238

Query:  117 LTDEEVDEMIREADIDGDGQVNYEEFV 143
          L++ E    + EA    DG+ +Y +FV
Sbjct:  239 LSESEFAYFMLEARAMKDGRFDYRKFV 265
```

>**PDB381W0** (Closest domain: F1L7U2_ASCSU 125-211)
Number of domains in family: 14
Commentary (automatic):
SUBNAME: REFERENCE FULL=PUTATIVE UNCHARACTERIZED CALCIUM FULL=CHROMOSOME SHOTGUN FAMILY GENOME SEQUENCE
Length = 87
Score = 130 (54.7 bits), Expect = 4e-08
Identities = 23/87 (26%), Positives = 47/87 (54%), Gaps = 2/87 (2%)

```
Query:   61 NGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDE 120
         N  +DF  FL ++   +  D   EI  A R  D    G+I+  E   +++++GE+++ E
Sbjct:  125 NKKVDFASFLEILHADSEKGDPMVEIIAALRGIDPKNQGWITVPEFVSILSSVGERISRE 184

Query:  121 EVDEMIREADIDGDGQVNYEEFVQMMT 147
         E+D ++ + D+   +V Y + +Q ++
Sbjct:  185 EIDNILLQLDLKSSSRVPYAKLIQSLS 211
```

>**PD851386** (Closest domain: F7C5K1_MACMU 94-162)
Number of domains in family: 94
Commentary (automatic):
SUBNAME: LIGHT CALCIUM CHAIN FULL=MYOSIN REGULATORY SKELETAL 2 MUSCLE REFERENCE
Length = 69
Score = 129 (54.3 bits), Expect = 5e-08
Identities = 25/67 (37%), Positives = 39/67 (58%), Gaps = 3/67 (4%)

```
Query:   81 DSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYE 140
         D EE I  AF+VFD +G G + A  +R ++T   E+ + EE+D+M      D  G +NY+
Sbjct:   94 DPEETILNAFKVFDPEGKGVLKADYVRDMLTTQAERFSKEEIDQMFAAFPPDVTGNLNYK 153

Query:  141 EFVQMMT 147
          V ++T
Sbjct:  154 NLVHIIT 160
```

>**PDD6Y0J8** (Closest domain: D7FLY0_ECTSI 1-150)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED
Length = 150
Score = 129 (54.3 bits), Expect = 1e-07
Identities = 34/108 (31%), Positives = 55/108 (50%), Gaps = 6/108 (5%)

```
Query:   44 PTEAELQDMINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGY--I 101
         PT+AEL  + +++D+D  G +DF  F   MA  MK     E++    R FD+   G   I
Sbjct:   41 PTKAELSSLTSKMDSDKTGKVDFGSFFAAMAAFMKPKYGREKLD---RAFDEISGGLDEI 97

Query:  102 SAAELRHVMTNLGEK-LTDEEVDEMIREADIDGDGQVNYEEFVQMMTA 148
          A  L   M +LG+  +   + + MI E D +G G+++  +F  + T
```

Sbjct: 98 DATFLHRTMVHLGQSTIRYADCEAMICEVDRNGHGRISKRDFHHLQTC 145

>**PDD873Q2** (Closest domain: C1EC04_MICSR 179-279)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=PREDICTED CALCIUM
Length = 101
Score = 125 (52.8 bits), Expect = 3e-07
Identities = 27/73 (36%), Positives = 46/73 (63%), Gaps = 1/73 (1%)

Query: 74 ARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDG 133
AR+MKD DS+ ++ AF + D DG+G +S L +V+ L +K+T E++E++ EA G
Sbjct: 179 ARQMKDHDSDLILQRAFDLLDSDGSGKVSKGALCYVLGALCDKMTCAEIEELVDEAGGGG 238

Query: 134 DGQVNYEEFVQMM 146
D + +F+ +M
Sbjct: 239 D-ALTLSQFMGIM 250

>**PDD7V6N9** (Closest domain: D8LAT5_ECTSI 1-181)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=CALMODULIN
Length = 181
Score = 124 (52.4 bits), Expect = 8e-07
Identities = 24/53 (45%), Positives = 36/53 (67%), Gaps = 1/53 (1%)

Query: 94 DKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM 146
D G Y++ AEL+ ++T GE LTDEEVDE++RE D G++ YE + +M+
Sbjct: 124 DSRGRPYVARAELQKILTREGEALTDEEVDELLRECRPDEVGRIVYEGYRRML 176

>**PDB8K817** (Closest domain: F0VNX6_NEOCL 130-194)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: REGULATORY LIGHT CHAIN FULL=MYOSIN CHAIN FULL=PUTATIVE FULL=PREDICTED MYOSIN CALCIUM
Length = 65
Score = 123 (52.0 bits), Expect = 3e-07
Identities = 22/65 (33%), Positives = 41/65 (63%), Gaps = 5/65 (7%)

Query: 82 SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEE 141
SE+ +R+AF++FD G +S+ +L+ ++ N GE L+ E DE++ A +DG +Y +
Sbjct: 130 SEKTLRQAFQLFDPKNTGKLSSQQLQDIVMNRGEPLSKAEFDELVLLAGLDGQKSFDYTQ 189

Query: 142 FVQMM 146
V+ +
Sbjct: 190 LVKRL 194

>**PDD86432** (Closest domain: G3I9A7_CRIGR 1-64)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=CALMODULIN CALCIUM

Length = 64
Score = 120 (50.8 bits), Expect = 8e-07
Identities = 22/26 (84%), Positives = 23/26 (88%), Gaps = 4/26 (15%)

```
Query:    56 VDADGNGTIDFPEFLTMMARKMKDTD 81
          +  GNGTIDFPEFLTMMARKMKDTD
Sbjct:    39 LGPSGNGTIDFPEFLTMMARKMKDTD 64
```

>**PDB2C2O0** (Closest domain: F2UMB7_SALS5 5598-5668)
Number of domains in family: 11
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE FULL=PREDICTED UNCHARACTERIZED DOMAIN-CONTAINING HAND FULL=EF SH3 EF
Length = 71
Score = 118 (50.1 bits), Expect = 2e-06
Identities = 25/60 (41%), Positives = 40/60 (66%), Gaps = 1/60 (1%)

```
Query:    85 EIREAFRVFDKDGNGYISAAELRHVMTNLGEKL-TDEEVDEMIREADIDGDGQVNYEEFV 143
          ++ +A   FD D NG +SA+EL  +  LG +L T ++V + +R  D+DGDGQ++Y EF+
Sbjct:  5608 KMYDACVFFDADKNGLVSASELMGAVLWLGLQLATPQDVLQAMRMYDVDGDGQLSYTEFL 5667
```

>**PDA5C7J8** (Closest domain: G0TRM6_TRYVI 392-523)
Number of domains in family: 11
Commentary (automatic):
NUCLEOTIDE-BINDING SUBNAME: ATP-BINDING FULL=PUTATIVE UNCHARACTERIZED KINASE FULL=PROTEIN KINASE REFERENCE TRANSFERASE
Length = 132
Score = 118 (50.1 bits), Expect = 3e-06
Identities = 31/90 (34%), Positives = 47/90 (52%), Gaps = 8/90 (8%)

```
Query:     8 EQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDAD--GNGTID 65
          E +AE + AF   D +G G ITT+     M  L  N T+AE+ +  N VD +  G GT+
Sbjct:   416 EYLAEVRRAFDAIDVNGTGLITTES----MAKLSPNCTKAEIVEFFNTVDPENAGRGTLS 471

Query:    66 FPEFLTMMARK--MKDTDSEEEIREAFRVF 93
          F +F+ + +R    KD    + +R   R+F
Sbjct:   472 FEQFVHLCSRYNVFKDHPLVQRLRHLERIF 501
```

>**PDC5T3F8** (Closest domain: A2DPY5_TRIVA 1-147)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FAMILY HAND FULL=EF
Length = 147
Score = 117 (49.7 bits), Expect = 6e-06
Identities = 36/138 (26%), Positives = 67/138 (48%), Gaps = 4/138 (2%)

```
Query:     7 EEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDF 66
          + QI   ++AF L  +   GT+T +++ + ++SL   P  +E  D I+++     T  F
Sbjct:     9 KRQIKTLRKAFDLRARKVSGTLTKEKMKSTIKSLRLIPAPSE--DEIDQMCCYEEVT--F 64

Query:    67 PEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMI 126
           +F+  +   M+  + E+  AF+ FDK  +G IS     ++ + G  L+  + + M
```

Sbjct: 65 EDFVMTIYMYMRAVSNSNELIRAFQFFDKTKSGLISFDTAIQILQSQGILLSTVQKEAMR 124

Query: 127 READIDGDGQVNYEEFVQ 144
E + DG V+Y F
Sbjct: 125 AELQVREDGMVDYVSFAH 142

>**PDB2P1E2** (Closest domain: C4A006_BRAFL 80-176)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FULL=PUTATIVE UNCHARACTERIZED CALCIUM
Length = 97
Score = 116 (49.3 bits), Expect = 4e-06
Identities = 21/83 (25%), Positives = 46/83 (55%), Gaps = 2/83 (2%)

Query: 63 TIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEV 122
I F FL++ KMKDT+ + + + + FD G G++ +++ + G++ +++E
Sbjct: 81 PISFQVFLSLFGNKMKDTNPVQALLDGMKQFDPKGKGFLPKLKVKEIFCERGDRFSEDEW 140

Query: 123 DEMIREAD--IDGDGQVNYEEFV 143
++M+ A ++ GQ N+ F+
Sbjct: 141 NKMLAGAPWAVNKKGQFNWVGFL 163

>**PDD78077** (Closest domain: D7FSY6_ECTSI 211-350)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: TRANSFERASE EC=2.7.11.1 FULL=N/A CALCIUM
Length = 140
Score = 115 (48.9 bits), Expect = 1e-05
Identities = 28/66 (42%), Positives = 41/66 (62%), Gaps = 3/66 (4%)

Query: 86 IREAFRVFDKDGNGYISAAELRHVMTNLGE-KLTDEEVDEMIREADIDGDGQ--VNYEEF 142
IR+AF FD++G G++SAA++ V+ GE L+DEE E+ + GQ VN E F
Sbjct: 282 IRQAFSSFDQEGKGFVSAADISRVLAESGEGTLSDEESLELDKAVASANRGQRGVNMESF 341

Query: 143 VQMMTA 148
+MMT+
Sbjct: 342 EKMMTS 347
>**PDA4R9E5** (Closest domain: C5LM50_PERM5 319-413)
Number of domains in family: 15
Commentary (automatic):
KINASE SUBNAME: NUCLEOTIDE-BINDING ATP-BINDING FULL=CALCIUM-DEPENDENT CALCIUM KINASE TRANSFERASE EC=2.7.11.1 EC=2.7.11.17
Length = 95
Score = 112 (47.8 bits), Expect = 2e-05
Identities = 30/76 (39%), Positives = 43/76 (56%), Gaps = 6/76 (7%)

Query: 70 LTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKL--TDEEVDEMIR 127
L ++A M T ++ E FRV DKDGNG I+ EL T L EKL T EE +
Sbjct: 338 LGLIAMTM-STPQVRQLEEQFRVLDKDGNGVITLEEL---TTALTEKLNMTREEARTVFS 393

Query: 128 EADIDGDGQVNYEEFV 143

+ D+ G+ +++Y EF+
Sbjct: 394 KLDVTGNHEIHYSEFL 409

>**PDB7S5E8** (Closest domain: A2EH13_TRIVA 6-184)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FAMILY HAND FULL=EF
Length = 179
Score = 112 (47.8 bits), Expect = 4e-05
Identities = 39/146 (26%), Positives = 73/146 (50%), Gaps = 12/146 (8%)

Query: 7 EEQIAE-FKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTI- 64
E Q+ E K ++++D D TI ++ +RSLG PT A+L+++ + D T
Sbjct: 26 EAQVKEMLKTLYAIYDPDETETIKEEDFNDFVRSLGLYPTNAKLKEIAAQCREDETNTFF 85

Query: 65 DFPEFLTMMARKMKD----------TDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLG 114
+ P+ +++ + D SEE++ A + D + G+++ + R ++++ G
Sbjct: 86 NCPKLESVLIPLVIDAMINPNSELAPPSEEKLLLALKSLDLEHKGHLTEGDFRTILSSNG 145

Query: 115 EKLTDEEVDEMIREADIDGDGQVNYE 140
EKL +E+D + EA G VN E
Sbjct: 146 EKLDPDELDPAVEEAVNPATGVVNLE 171

>**PDC947T1** (Closest domain: B9ENM0_SALSA 74-94)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: CALCIUM REFERENCE EC=1.3.1.74 OXIDOREDUCTASE FULL=PUTATIVE UNCHARACTERIZED FULL=CALMODULIN FULL=CALMODULIN
Length = 21
Score = 109 (46.6 bits), Expect = 2e-05
Identities = 21/21 (100%), Positives = 21/21 (100%), Gaps = 3/21 (14%)

Query: 127 READIDGDGQVNYEEFVQMMT 147
READIDGDGQVNYEEFVQMMT
Sbjct: 74 READIDGDGQVNYEEFVQMMT 94

>**PDC732F4** (Closest domain: E9HFR2_DAPPU 81-134)
Number of domains in family: 12
Commentary (automatic):
CALCIUM REGULATORY FULL=MYOSIN LIGHT SUBNAME: MUSCLE CHAIN REPEAT ADDUCTOR MOTOR
Length = 54
Score = 108 (46.2 bits), Expect = 3e-05
Identities = 22/48 (45%), Positives = 31/48 (64%), Gaps = 2/48 (4%)

Query: 84 EEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADI 131
E I AF F K+ G+++ LR + T +G++ TDE+VDEM REA I
Sbjct: 81 EVINNAFGCFVKENTGFLNEERLRELQTTMGDRFTDEDVDEMYREAPI 128

>**PDC7X3O5** (Closest domain: E1ZEC2_CHLVA 269-350)
Number of domains in family: 6

Commentary (automatic):
SUBNAME: FULL=PROLINE CALCIUM OXIDASE FULL=PUTATIVE UNCHARACTERIZED REFERENCE DEHYDROGENASE OXIDASE
Length = 82
Score = 107 (45.8 bits), Expect = 6e-05
Identities = 24/75 (32%), Positives = 40/75 (53%), Gaps = 8/75 (10%)

```
Query:   70 LTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREA 129
         L + A   + + S   I + FR FD DGNGY++  E  HV + L      E +DE+
Sbjct:  276 LGLPALLERTSSSLLAIGDLFRRFDTDGNGYMTHDEFAHVYSQLFVDDAPERIDEIFAHL 335

Query:  130 DIDGDGQVNYEEFVQ 144
         D+  D +V+Y ++++
Sbjct:  336 DVGKDARVDYVDWIK 350
```

>**PDB7I003** (Closest domain: C3YY99_BRAFL 1-154)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FULL=PUTATIVE UNCHARACTERIZED
Length = 154
Score = 107 (45.8 bits), Expect = 0.0002
Identities = 34/125 (27%), Positives = 54/125 (43%), Gaps = 43/125 (34%)

```
Query:    7 EEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDF 66
          E+Q A FK  F + DKD DG + ++ELG  M S+G  P  ++L        DGNG +D
Sbjct:   10 EKQKALFKRCFDMLDKDKDGFLLSRELGKAMTSVGIKPLPSDL------ALKDGNGVLD- 62

Query:   67 PEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMI 126
                    +EE++EA +                ++G   +D+ +D M+
Sbjct:   63 ----------KEELKEAIK--------------------SIGMVHSDKHIDFMV 86

Query:  127 READI 131
          + AD
Sbjct:   87 KAADC 91
```

>**PDB0D2H1** (Closest domain: Q001X6_TOXGO 57-142)
Number of domains in family: 10
Commentary (automatic):
SUBNAME: FULL=PUTATIVE CHAIN LIGHT UNCHARACTERIZED FULL=MYOSIN REFERENCE STRIATED MUSCLE TGMLC4
Length = 86
Score = 106 (45.4 bits), Expect = 0.0001
Identities = 26/86 (30%), Positives = 39/86 (45%), Gaps = 4/86 (4%)

```
Query:   36 VMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDK 95
         + R LG  P+E E+    + V    NG  D   F    +  + D D     RE F V+DK
Sbjct:   58 LARYLGLAPSEQEVDTFFHRV----NGRCDLAAFGRFCSLLVHDEDKAANFRELFLVYDK 113

Query:   96 DGNGYISAAELRHVMTNLGEKLTDEE 121
```

```
          +  G +    ++ +  NLGE L+  E
 Sbjct:   114 EHTGKLKKRVVKMIFCNLGEPLSAAE 139
```

>**PDD343M4** (Closest domain: C1E4U2_MICSR 1-152)
Number of domains in family: 2
Commentary (automatic):
KINASE NUCLEOTIDE-BINDING SERINE/THREONINE-PROTEIN SUBNAME: TRANSFERASE ATP-BINDING FULL=PREDICTED
Length = 152
Score = 105 (45.1 bits), Expect = 0.0003
Identities = 28/100 (28%), Positives = 45/100 (45%), Gaps = 9/100 (9%)

```
 Query:     7 EEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNP-------TEAELQDMINEVDAD 59
           E +  E ++ FSL+D DG G I+  +  +  G  P        AE+   + E   D
 Sbjct:    27 EHRFWEARDCFSLYDPDGKGRISGGVVAEALARFGARPDGAGDDEWAAEVATAMRECGCD 86

 Query:    60 GNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNG 99
            NGT++F  F  +        +E++ REA + F+  G G
 Sbjct:    87 ANGTVNFNSFKRVY--NHTKGLAEKDSREASKAFESIGPG 124
```

>**PDC7D0O4** (Closest domain: A0BVG6_PARTE 769-824)
Number of domains in family: 9
Commentary (automatic):
CALCIUM SUBNAME: REPEAT REFERENCE FULL=CHROMOSOME SENSOR SHOTGUN GENOME SEQUENCE WHOLE
Length = 56
Score = 105 (45.1 bits), Expect = 8e-05
Identities = 20/54 (37%), Positives = 32/54 (59%), Gaps = 1/54 (1%)

```
 Query:    89 AFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEF 142
           AF+ FD + +  IS A+++  +  +  K   + +D + R AD  GD Q+NYEEF
 Sbjct:   770 AFQAFDTNCDNVISKADMKEALLQMNIKHDQKAIDYIFRMADTSGDNQINYEEF 823
```

>**PD061537** (Closest domain: G0NPN1_CAEBE 94-179)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM F40F9.8 REFERENCE FULL=PROTEIN
Length = 86
Score = 104 (44.7 bits), Expect = 0.0002
Identities = 20/78 (25%), Positives = 42/78 (53%), Gaps = 2/78 (2%)

```
 Query:    67 PEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMI 126
           P  ++ +  +    D+ ++I  AF+V     N Y+    L  ++T++GE LT +EV + +
 Sbjct:    94 PRVVSAIQNEEWKDDTPKQIHAAFQVIT--SNNYVQKDTLLQLLTSIGEPLTPQEVKQFL 151

 Query:   127 READIDGDGQVNYEEFVQ 144
             I G+G +++  +V+
```

Sbjct: 152 NHVSIRGNGDIDWVAYVK 169

>**PDA1F114** (Closest domain: B3GQ31_ORYSI 16-76)
Number of domains in family: 233
Commentary (automatic):
SUBNAME: CALCIUM REPEAT FULL=PUTATIVE REFERENCE UNCHARACTERIZED TRANSMEMBRANE MEMBRANE HELIX OXIDOREDUCTASE
Length = 61
Score = 103 (44.3 bits), Expect = 0.0001
Identities = 22/58 (37%), Positives = 36/58 (62%), Gaps = 1/58 (1%)

Query: 17 FSLFDKDGDGTITTKELGTVMRS-LGQNPTEAELQDMINEVDADGNGTIDFPEFLTMM 73
F+ FD DGDG I+ EL M++ LG+ ++ E ++ VDADG+G + EF+ ++
Sbjct: 16 FATFDHDGDGRISAAELRLCMKTTLGEEVSDEEAGQLVASVDADGDGLLCEAEFVRLV 73

>**PDB213K1** (Closest domain: B6AAA3_CRYMR 154-208)
Number of domains in family: 12
Commentary (automatic):
SUBNAME: SCAFFOLD CALCIUM SHOTGUN GENOME FULL=WHOLE ASSEMBLY SET REFERENCE ALLELIC
Length = 55
Score = 102 (43.9 bits), Expect = 0.0002
Identities = 21/54 (38%), Positives = 35/54 (64%), Gaps = 1/54 (1%)

Query: 90 FRVFDKDGNGYISAAELRHVMTNLG-EKLTDEEVDEMIREADIDGDGQVNYEEF 142
FR+ D++ + YI+A EL+ ++ G LT +E DE++ AD + DG ++YEE
Sbjct: 154 FRLLDRNNSEYITALELKQMLITKGISPLTPDEADELLFIADQNNDGLISYEEI 207

>**PDB2C2O0** (Closest domain: F0Y683_AURAN 1278-1363)
Number of domains in family: 11
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE FULL=PREDICTED UNCHARACTERIZED DOMAIN-CONTAINING HAND FULL=EF SH3 EF
Length = 86
Score = 102 (43.9 bits), Expect = 0.0003
Identities = 24/65 (36%), Positives = 34/65 (52%), Gaps = 3/65 (4%)

Query: 14 KEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMM 73
+ F FD DG+GT+TT EL +R L T A + VDADG+ +I EF+
Sbjct: 1297 SDCFEAFDTDGNGTLTTGELAVGLRWLLSRATPATCLAVAVHVDADGDRSISKAEFVEAF 1356

Query: 74 ARKMK 78
A ++
Sbjct: 1357 AALVR 1361

>**PDA1J8Z2** (Closest domain: A7T520_NEMVE 29-93)
Number of domains in family: 55
Commentary (automatic):
SUBNAME: REFERENCE FULL=PROTEIN CALCIUM FULL=PUTATIVE UNCHARACTERIZED CARP ALTNAME: RECNAME: FAM188A
Length = 65
Score = 102 (43.9 bits), Expect = 0.0002

Identities = 17/64 (26%), Positives = 39/64 (60%), Gaps = 2/64 (3%)

```
Query:    84 EEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFV 143
          ++++++FR  D D  G++S  +L+ V+      L + E+  + R+ D+DG G++ Y++F+
Sbjct:    30 QQLQKSFRNLDPDNTGHVSFHQLKDVLVQHYVILNNNELLSLWRKHDVDGKGRIVYKDFL 89

Query:   144 QMMT 147
          +
Sbjct:    90 RHFV 93
```

>**PDB173A7** (Closest domain: C5LTX2_PERM5 456-510)
Number of domains in family: 5
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE FULL=PREDICTED UNCHARACTERIZED NUCLEOTIDE-BINDING REFERENCE KINASE ATP-BINDING KINASE
Length = 55
Score = 102 (43.9 bits), Expect = 0.0002
Identities = 21/57 (36%), Positives = 37/57 (64%), Gaps = 3/57 (5%)

```
Query:    84 EEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYE 140
          +++R+AF   D D +G IS + LR+V   LG++    V+++I+EAD + +G + YE
Sbjct:   456 QDVRDAFYRLDVDNSGVISLSNLRNV---LGDRFCGTRVEDLIKEADANNEGYITYE 509
```

>**PDD0S5L8** (Closest domain: C5KE42_PERM5 1-104)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: FULL=CALMODULIN
Length = 104
Score = 102 (43.9 bits), Expect = 0.0004
Identities = 20/52 (38%), Positives = 30/52 (57%), Gaps = 3/52 (5%)

```
Query:     5 LTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEV 56
          L E  I+  +  F L D DGDG IT KE   ++R+LG  PT+ +  + + E+
Sbjct:    10 LPESTISAIEATFRLCDGDGDGHITKKEATMLLRALGHIPTQKQCSEFLQEL 61
```

>**PDC44543** (Closest domain: Q22CZ0_TETTS 417-480)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: KINASE CALCIUM NUCLEOTIDE-BINDING FULL=CHROMOSOME SHOTGUN CONTAINING EC=2.7.11.17 DOMAIN SCAFFOLD_29
Length = 64
Score = 102 (43.9 bits), Expect = 0.0002
Identities = 24/63 (38%), Positives = 36/63 (57%), Gaps = 4/63 (6%)

```
Query:    86 IREAFRVFDKDGNGYISAAELRHVMTN---LGEKLTDEEVDEMIREADIDGDGQVNYEEF 142
          IR+AF++FDK+  G IS   L  +    +K  D  VD M++  D   DG ++YEEF
Sbjct:   419 IRQAFKIFDKNNIGKISPNHLNELFLDNAYYAKKKIDYWVD-MVKCCDFKNDGVIDYEEF 477

Query:   143 VQM 145
```

+M
Sbjct: 478 SKM 480

>**PDB0N4G0** (Closest domain: D8LUA6_ECTSI 776-839)
Number of domains in family: 12
Commentary (automatic):
SUBNAME: REFERENCE CALCIUM FULL=CHROMOSOME SHOTGUN FAMILY GENOME HAND FULL=EF SEQUENCE
Length = 64
Score = 102 (43.9 bits), Expect = 0.0002
Identities = 22/64 (34%), Positives = 36/64 (56%), Gaps = 8/64 (12%)

Query: 84 EEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFV 143
IRE F FD+ GY++ AE+R + +L KL+ E ++ +DG +++Y EFV
Sbjct: 776 RSIREVFGHFDRRRCGYVNVAEMRDALADLRIKLSAREATDLHSMMALDGGDRLSYAEFV 835

Query: 144 QMMT 147
+T
Sbjct: 836 VFVT 839

>**PDD9K0I4** (Closest domain: Q7UYM6_RHOBA 293-583)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: CALMODULIN REFERENCE FULL=PROBABLE CALCIUM
Length = 291
Score = 102 (43.9 bits), Expect = 0.002
Identities = 30/107 (28%), Positives = 53/107 (49%), Gaps = 5/107 (4%)

Query: 4 QLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMR-SLGQNPT-EAELQDMINEVDADGN 61
+ T ++ + ++ FD+DGD +IT E + +R +G PT EL ++ + + +
Sbjct: 468 RFTIRELRKLEQLLRTFDRDGDQSITRSEAASPIRVCIGLGPTAHRELANVRDTSQPETS 527

Query: 62 GTIDFPEFLTMMARKMKDTDSEEEIR---EAFRVFDKDGNGYISAAE 105
++ PE+ M R + + S E E FR D DG+ I A+E
Sbjct: 528 PSVTAPEWFQRMDRNLDNDLSRREFPGTDEQFRSLDADGDELIDASE 574

>**PDD2R1N0** (Closest domain: D7G7I0_ECTSI 1431-1566)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM
Length = 136
Score = 102 (43.9 bits), Expect = 0.0006
Identities = 22/65 (33%), Positives = 37/65 (56%), Gaps = 2/65 (3%)

Query: 85 EIREAFRVFDKDGNGYISAAELRHVMTNLG--EKLTDEEVDEMIREADIDGDGQVNYEEF 142
RE F D+D G+I+ A+ R V+ +L + LT++EVD + D GDG+V+Y
Sbjct: 1433 RFRERFVAVDRDKTGFINRAQFRAVLASLPGTQDLTEDEVDRLSTLLDDQGDGRVSYRSL 1492

Query: 143 VQMMT 147
+ ++

Sbjct: 1493 LDLLV 1497

>**PDB565C4** (Closest domain: E1Z602_CHLVA 59-271)
Number of domains in family: 7
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM REFERENCE FULL=PREDICTED
Length = 213
Score = 101 (43.5 bits), Expect = 0.003
Identities = 37/143 (25%), Positives = 59/143 (41%), Gaps = 25/143 (17%)

Query: 26 GTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMA--RKMKDTDSE 83
G ++ ++L SLG + EA L + D DG+ T++ EFL MA ++ + E
Sbjct: 119 GELSLEQLRPACASLGYHLDEATLHSIFAGADMDGSRTLNVHEFLATMAIVHSLRGPEDE 178

Query: 84 EEI----------REAFRVFDKDGNGYISAAEL----------RHVMTNLGEKLTDE 120
E + EAF F +G+I EL RH G
Sbjct: 179 ELVDPQILATWRTAEEAFMSFASSRDGFIEKDELTGLMHESATDQVRHSANGSGGDPIRS 238

Query: 121 EVDEMIREADIDGDGQVNYEEFV 143
+ E D++G G+V++ EF+
Sbjct: 239 IAQQRFEELDLNGSGRVSFLEFL 261

>**PDA2A364** (Closest domain: D8LY69_BLAHO 87-143)
Number of domains in family: 10
Commentary (automatic):
SUBNAME: FULL=CALMODULIN-LIKE REFERENCE FULL=PUTATIVE FULL=CALMODULIN SHOTGUN ASSEMBLY ISOLATE CALMODULIN-LIKE GENOME
Length = 57
Score = 100 (43.1 bits), Expect = 0.0004
Identities = 20/59 (33%), Positives = 39/59 (66%), Gaps = 4/59 (6%)

Query: 89 AFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQV-NYEEFVQMM 146
F++FDK+ +G + A++LRH++++LGE + ++E+D + G G V YE+F + +
Sbjct: 87 VFKMFDKNQDGTVLASDLRHILSHLGEVIPEDEIDALFHAL---GYGDVIKYEDFAKQL 142

>**PDE0T3U8** (Closest domain: D8LAY6_ECTSI 1068-1492)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=NEPHRORETININ CALCIUM
Length = 425
Score = 100 (43.1 bits), Expect = 0.004
Identities = 41/163 (25%), Positives = 69/163 (42%), Gaps = 27/163 (16%)

Query: 13 FKEAFSLFDKDGDGTITTKELGTV---MRSLGQNPTEAELQDMINEVDADGNGTIDFPEF 69
EAF D++ G I+T EL V M S G+ E L+ ++ +D G I E
Sbjct: 1200 LAEAFREMDQNRTGEISTHELEEVFWGMLSPGEMARE-HLRALVKGMDPGATGKIGLREL 1258

Query: 70 LTMMARK----------MKDTDSEEE-----IREAFRVFDKDGNGYISAAELRH 108
+T ++ + +K + E + EAF + DK G +S A+

Sbjct: 1259 VTFVSARQGGGGVGKAAKAAETGLKRALARAELGGSSVEEAFSLLDKKGTDSVSHADFWE 1318

Query: 109 VMTNLG--EKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTAK 149
+ +LG L ++D ++R D GDG+V+ ++ K
Sbjct: 1319 AVRDLGGVPGLVKSDLDPLLRRLDTAGDGRVSLPALMRWAERK 1361

>**PDA0A3M7** (Closest domain: C3ZQ19_BRAFL 272-350)
Number of domains in family: 37
Commentary (automatic):
CALCIUM SUBNAME: FULL=EF-HAND ALTNAME: REFERENCE DOMAIN-CONTAINING FULL=PUTATIVE UNCHARACTERIZED CALCIUM-BINDING RECNAME:
Length = 79
Score = 100 (43.1 bits), Expect = 0.0005
Identities = 20/72 (27%), Positives = 40/72 (55%), Gaps = 2/72 (2%)

Query: 73 MARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADID 132
+ +KMK S +++AF FD +GYIS +L+ V+ + ++D+ +++ I
Sbjct: 281 LRKKMKSNYSN--VKKAFLAFDATNSGYISIDDLKSVLVHFTIPMSDQLFSQLMDRLRIK 338

Query: 133 GDGQVNYEEFVQ 144
G+V +E F++
Sbjct: 339 ASGKVAWEHFLE 350

>**PD498404** (Closest domain: G7P8X1_MACFA 1-47)
Number of domains in family: 4
Commentary (automatic):
SUBNAME: FULL=CALMODULIN-LIKE FULL=PUTATIVE UNCHARACTERIZED
Length = 47
Score = 100 (43.1 bits), Expect = 0.0003
Identities = 19/42 (45%), Positives = 26/42 (61%), Gaps = 1/42 (2%)

Query: 37 MRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKMK 78
MR LG +PT E+Q + DGNG +DF FLT+M ++K
Sbjct: 4 MRCLGASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIK 45

>**PD003407** (Closest domain: A5B016_VITVI 17-80)
Number of domains in family: 279
Commentary (automatic):
CALCIUM SUBNAME: ALTNAME: REPEAT FULL=PROTEIN FULL=S100 RECNAME: CALCIUM-BINDING REFERENCE BINDING
Length = 64
Score = 100 (43.1 bits), Expect = 0.0005
Identities = 19/64 (29%), Positives = 33/64 (51%), Gaps = 1/64 (1%)

Query: 84 EEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFV 143
E+IR FR +D++G+ +S AEL+ +LG + AD + DG ++ EE
Sbjct: 17 EQIRGIFRKYDRBGDRRLSKAELKEAFKHLGSHFPXWRAXRALSRADANKDGYISEEELT 76

Query: 144 QMMT 147

++
Sbjct: 77 SLVN 80

>**PDB1O9S5** (Closest domain: F0VK07_NEOCL 64-153)
Number of domains in family: 8
Commentary (automatic):
SUBNAME: CALCIUM HAND FULL=EF REPEAT DOMAIN-CONTAINING NUCLEOTIDE-BINDING FULL=CHROMOSOME SHOTGUN REFERENCE
Length = 90
Score = 99 (42.7 bits), Expect = 0.0007
Identities = 21/62 (33%), Positives = 38/62 (61%), Gaps = 1/62 (1%)

Query: 52 MINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMT 111
+ + D G+G++D+ EFL +A + T S+ + F+VFD + +GYI +EL +++
Sbjct: 79 LFQKFDFKGSGSVDYEEFLIGIAVCCRGTKSDR-MYVLFQVFDLNSDGYIQKSELVAMLS 137

Query: 112 NL 113
NL
Sbjct: 138 NL 139

>**PDB693L4** (Closest domain: A2FK30_TRIVA 1-318)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: REFERENCE FAMILY HAND FULL=EF CALCIUM
Length = 318
Score = 98 (42.4 bits), Expect = 0.007
Identities = 24/112 (21%), Positives = 56/112 (50%), Gaps = 3/112 (2%)

Query: 15 EAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMA 74
+ F F + ++ ++L + SL + ++ ++D++ E + ID +F+ +
Sbjct: 10 DCFENFIDSPNEKVSIRKLPRLFSSLQRPFSKKYIKDLLKEEGLESEAAIDIKQFMKIFR 69

Query: 75 RKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMI 126
+ D + + ++F +FD + +G IS E +++N G T EE +++I
Sbjct: 70 VRKCDEADVQMLVDSFMIFDSNQDGKISIDEYNSIVSNYGLPFTSEEYEKII 121

>**PDC87651** (Closest domain: A0CIN3_PARTE 416-481)
Number of domains in family: 5
Commentary (automatic):
SUBNAME: CALCIUM FULL=CHROMOSOME SHOTGUN REFERENCE GENOME SEQUENCE WHOLE UNDETERMINED HAND
Length = 66
Score = 98 (42.4 bits), Expect = 0.0009
Identities = 16/56 (28%), Positives = 36/56 (64%), Gaps = 3/56 (5%)

Query: 90 FRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQM 145
F + D +G++ ++ ++M+++ K D+ +D I+ AD + DGQ++Y+E V++
Sbjct: 417 FDIIDSRCSGFLDWSQFLYLMSSVQAKTRDQRIDLFIKIADSNKDGQLSYQEVVRL 472

>**PDB015Z3** (Closest domain: E0VR32_PEDHC 84-171)

Number of domains in family: 135
Commentary (automatic):
TRANSMEMBRANE SUBNAME: MEMBRANE HELIX REPEAT CALCIUM CARRIER MITOCHONDRIAL FULL=MITOCHONDRIAL FULL=PUTATIVE
Length = 88
Score = 98 (42.4 bits), Expect = 0.001
Identities = 19/43 (44%), Positives = 28/43 (65%), Gaps = 3/43 (6%)

Query: 82 SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDE 124
EE EAFR FDKDG G+ISAA+ + +M ++ L +V++
Sbjct: 125 HEEYATEAFRRFDKDGTGFISAADFQDIMVSIKSHLLTPQVEQ 167

>**PDB2B3P0** (Closest domain: A0DEF2_PARTE 406-481)
Number of domains in family: 6
Commentary (automatic):
SUBNAME: CALCIUM FULL=CHROMOSOME SHOTGUN REFERENCE GENOME SEQUENCE WHOLE UNDETERMINED SCAFFOLD_34
Length = 76
Score = 98 (42.4 bits), Expect = 0.001
Identities = 21/56 (37%), Positives = 35/56 (62%), Gaps = 1/56 (1%)

Query: 94 DKDGNGYISAAELRHVMTNLGEKLTDE-EVDEMIREADIDGDGQVNYEEFVQMMTA 148
D+DGNGY+S EL+++ N DE E++E+ E D + DG ++ EF+Q++
Sbjct: 406 DQDGNGYLSKVELKNIFKNKILVPVDEFELNELFMEFDKNRDGHISISEFLQIVKP 461

>**PD465777** (Closest domain: C4JRC9_UNCRE 119-203)
Number of domains in family: 54
Commentary (automatic):
SUBNAME: SUPERFAMILY FULL=EF-HAND CA2-MODULATED FULL=PUTATIVE UNCHARACTERIZED REFERENCE FULL=CALMODULIN HAND FULL=PREDICTED
Length = 85
Score = 97 (42.0 bits), Expect = 0.001
Identities = 30/81 (37%), Positives = 46/81 (56%), Gaps = 6/81 (7%)

Query: 70 LTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREA 129
L + AR D EE+ A+R+F + +G I + LR V L E +++E + +MIREA
Sbjct: 122 LKLHARS--DDARSEEVEHAYRLFTRGTDGPILLSHLRRVARELKEDVSEELLRDMIREA 179

Query: 130 DIDGDG---QVNYEEFVQMMT 147
+ G+G VN E+F +MT
Sbjct: 180 N-GGEGLHAGVNVEQFGDVMT 199

>**PDB1D8B3** (Closest domain: G4VMH5_SCHMA 817-883)
Number of domains in family: 8
Commentary (automatic):
SUBNAME: REFERENCE FULL=PUTATIVE CALCIUM UNCHARACTERIZED SCAFFOLD DOMAIN-CONTAINING HAND FULL=PREDICTED FULL=EF
Length = 67
Score = 97 (42.0 bits), Expect = 0.001
Identities = 16/51 (31%), Positives = 32/51 (62%), Gaps = 4/51 (7%)

Query: 94 DKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQ 144
D G G+I+ +L ++ L +++D E+D++I + DI DG+++Y +Q
Sbjct: 829 DPKGTGFITPKQLNDILIELCLQVSDREIDDLIEKFDIHKDGKISYLALLQ 879

>**PDA5L972** (Closest domain: A4H5I7_LEIBR 94-249)
Number of domains in family: 14
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM REFERENCE TRANSMEMBRANE CONTAINING EF DOMAIN CALMODULIN-LIKE
Length = 156
Score = 96 (41.6 bits), Expect = 0.006
Identities = 19/71 (26%), Positives = 35/71 (49%), Gaps = 1/71 (1%)

Query: 72 MMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADI 131
++ R D EE++R F FD G I + +H N+G + V+++ D+
Sbjct: 164 LVPRGNADASPEEKLRVVFSEFDNKGTRMIDVDDFKHGFHNMGLDFSSATVEDLFERTDL 223

Query: 132 DGDGQVNYEEF 142
+ D +++Y EF
Sbjct: 224 NHDHRISYSEF 234

>**PDB2O3R4** (Closest domain: A0BIS8_PARTE 481-536)
Number of domains in family: 20
Commentary (automatic):
SUBNAME: CALCIUM REFERENCE FULL=CHROMOSOME SHOTGUN GENOME SEQUENCE WHOLE UNDETERMINED FULL=PUTATIVE
Length = 56
Score = 96 (41.6 bits), Expect = 0.001
Identities = 20/57 (35%), Positives = 36/57 (63%), Gaps = 3/57 (5%)

Query: 90 FRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM 146
F + D+DG GYIS +++ T T+ EV+ + ++ DID DG++N E+ V+++
Sbjct: 481 FNLIDQDGKGYISIEDMKKTFT---YGFTEREVENLFQQYDIDRDGKLNMEDLVRII 534

>**PDB0X1Z3** (Closest domain: A0E1G4_PARTE 98-168)
Number of domains in family: 53
Commentary (automatic):
SUBNAME: CALCIUM REFERENCE FULL=PUTATIVE UNCHARACTERIZED SHOTGUN GENOME REPEAT FULL=CHROMOSOME ALTNAME:
Length = 71
Score = 96 (41.6 bits), Expect = 0.002
Identities = 22/65 (33%), Positives = 40/65 (61%), Gaps = 8/65 (12%)

Query: 86 IREAFRVFDKDGNGYISAAELRHVM-TNLGEKLTDEEVDE-------MIREADIDGDGQV 137
+ +AFR FDK G+GYI+A +L+ V T + K+ + ++ E ++ D+D +GQ+
Sbjct: 104 VDQAFRKFDKTGDGYITADDLKGVYNTKMHPKVKNGQMTETQVFEEFLVNFGDVDKNGQL 163

Query: 138 NYEEF 142

Y+E+
Sbjct: 164 TYQEW 168

>**PDA2T7T5** (Closest domain: C1MLD1_MICPC 188-245)
Number of domains in family: 15
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE FULL=CALCIUM-BINDING UNCHARACTERIZED EF-HAND-CONTAINING REFERENCE FULL=PREDICTED CALCIUM-BINDING TRANSDUCTION
Length = 58
Score = 96 (41.6 bits), Expect = 0.001
Identities = 21/57 (36%), Positives = 31/57 (54%), Gaps = 2/57 (3%)

Query: 90 FRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM 146
F++FD DG+G IS E +T L L + V ++ D+DG G + EF+ MM
Sbjct: 190 FKLFDTDGDGLISFPEYLFFITLL--SLPESHVKTAFQQFDVDGSGHLCRNEFIDMM 244

>**PDB1N646** (Closest domain: F0VLW9_NEOCL 2-66)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: FULL=CALMODULIN 1 RELATED FULL=MYOSIN CHAIN FAMILY HAND LIGHT FULL=EF
Length = 65
Score = 96 (41.6 bits), Expect = 0.002
Identities = 25/64 (39%), Positives = 36/64 (56%), Gaps = 7/64 (10%)

Query: 11 AEF----KEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDF 66
AEF K F+L D+DGDG + +LGT++R LGQ + A + + NE+ GN +
Sbjct: 2 AEFQYLCKFCFTLMDEDGDGKVKVSQLGTMLRMLGQIWSYASILTVENEL---GNRPVTL 58

Query: 67 PEFL 70
FL
Sbjct: 59 DTFL 62

>**PDD1F4C8** (Closest domain: Q497J8_MOUSE 36-99)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: REFERENCE FULL=UNCHARACTERIZED CALCIUM FULL=NOVEL FULL=1700023F06RIK
Length = 64
Score = 95 (41.2 bits), Expect = 0.002
Identities = 17/57 (29%), Positives = 35/57 (61%), Gaps = 4/57 (7%)

Query: 87 REAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFV 143
++ F++F G + ++ + N G +L +E+ E +R AD+DGDG V++++F+
Sbjct: 42 QDIFKLFSCSPTGTVDMQSMKIALRNAGIQLGPQEMCEALRLADLDGDGIVSFKDFL 98

>**PDC8J846** (Closest domain: B9PRI1_TOXGO 58-147)
Number of domains in family: 4
Commentary (automatic):
SUBNAME: C FULL=PUTATIVE ISOTYPE FULL=TROPONIN UNCHARACTERIZED GAMMA GAMMA REFERENCE TROPONIN
Length = 90
Score = 95 (41.2 bits), Expect = 0.003

Identities = 29/85 (34%), Positives = 44/85 (51%), Gaps = 3/85 (3%)

Query: 62 GTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGE--KLTD 119
G F +F+T+ + D E + +A R G+ +S A LR + LG KLT+
Sbjct: 63 GDFSFEDFMTVASVVYNDVAIERGLVQALRQICPKGSKTVSTAILREHLLKLGMGIKLTE 122

Query: 120 EEVDEMIR-EADIDGDGQVNYEEFV 143
EEVD ++ E D + G V++E FV
Sbjct: 123 EEVDMFLQFECDPNRKGVVDFENFV 147

>**PDA2D7H7** (Closest domain: Q4Q1H8_LEIMA 121-235)
Number of domains in family: 8
Commentary (automatic):
SUBNAME: FULL=PUTATIVE CALTRACTIN REFERENCE FULL=CALTRACTIN CALCIUM CALTRACTIN UNCHARACTERIZED
Length = 115
Score = 95 (41.2 bits), Expect = 0.005
Identities = 24/68 (35%), Positives = 35/68 (51%), Gaps = 1/68 (1%)

Query: 59 DGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVF-DKDGNGYISAAELRHVMTNLGEKL 117
D + ID F M+ RK+K EEE+ F + DK G+I+ +R + GE L
Sbjct: 141 DSSDGIDLDVFEQMVLRKLKHRSYEEELTYTFALLEDKSYPGFITKESVRRIAAETGEPL 200

Query: 118 TDEEVDEM 125
T+ E+ EM
Sbjct: 201 TEAEIAEM 208

>**PDB0M3G7** (Closest domain: C5KBX2_PERM5 446-500)
Number of domains in family: 8
Commentary (automatic):
SUBNAME: NUCLEOTIDE-BINDING ATP-BINDING FULL=CHROMOSOME SHOTGUN REFERENCE GENOME SEQUENCE WHOLE UNDETERMINED
Length = 55
Score = 95 (41.2 bits), Expect = 0.002
Identities = 22/58 (37%), Positives = 34/58 (58%), Gaps = 6/58 (10%)

Query: 92 VFDK---DGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM 146
VFDK D GYIS LR V LG+ V++++R+ D +G++ Y+EFV+ +
Sbjct: 446 VFDKLDVDKTGYISVDNLRAV---LGDSFCGTSVEDLLRQVDYKCNGRIEYDEFVRAL 500

>**PDD349V3** (Closest domain: F2U0P1_SALS5 35-149)
Number of domains in family: 2
Commentary (automatic):
NUCLEOTIDE-BINDING SUBNAME: ATP-BINDING MOTOR MICROTUBULE C3 FULL=KIFC3 MEMBER FAMILY FULL=KINESIN
Length = 115
Score = 95 (41.2 bits), Expect = 0.005
Identities = 21/60 (35%), Positives = 37/60 (61%), Gaps = 2/60 (3%)

Query: 89 AFRVFDKDGNGYISAAELRHVMTN--LGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM 146
F+ D D NG + E V+++ L L+ +E++++ R AD DGDG+++YEEF+ +

Sbjct: 42 VFQNADADNNGVLDVDEFESVLSSDTLKLNLSKDEMEQIRRSADQDGDGKISYEEFIPVF 101

>**PDD0T2M4** (Closest domain: G4Z3C0_PHYSP 460-564)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM REFERENCE
Length = 105
Score = 94 (40.8 bits), Expect = 0.005
Identities = 22/57 (38%), Positives = 33/57 (57%), Gaps = 1/57 (1%)

Query: 12 EFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPE 68
E K AFS +D+DG G + +E +M G +E + +I+E+D D +GTI F E
Sbjct: 474 EVKAAFSKYDRDGSGELDYEEFRRMMHESGVKDSEV-IDALIDEIDRDRSGTISFNE 529

>**PDB6A9B6** (Closest domain: B9GPT4_POPTR 455-531)
Number of domains in family: 16
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED CALCIUM FULL=PREDICTED REFERENCE
TRANSMEMBRANE MEMBRANE REPEAT FULL=JD1
Length = 77
Score = 94 (40.8 bits), Expect = 0.004
Identities = 21/61 (34%), Positives = 33/61 (54%), Gaps = 1/61 (1%)

Query: 16 AFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMAR 75
AF+ D G G I+ +ELG +R QN E E+ ++ N D DG+G + F++ + R
Sbjct: 463 AFTECDTGGHGLISEQELGDTIRLAIQNLDEDEIHELFNVFDTDGDGIVSKDSFISCLRR 522

Query: 76 K 76

Sbjct: 523 N 523

>**PD312936** (Closest domain: A8JGI1_CHLRE 176-226)
Number of domains in family: 259
Commentary (automatic):
TRANSMEMBRANE SUBNAME: CALCIUM MEMBRANE REPEAT HELIX FULL=PUTATIVE
UNCHARACTERIZED CARRIER REFERENCE
Length = 51
Score = 94 (40.8 bits), Expect = 0.003
Identities = 21/53 (39%), Positives = 30/53 (56%), Gaps = 3/53 (5%)

Query: 57 DADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHV 109
D DG+G I +PEFL ++ + E +++ F V D DGNG I A E + V
Sbjct: 177 DVDGDGLISYPEFLLVLTLL---SIHERDVKTIFDVVDLDGNGQIDAEEFKAV 226

>**PD406130** (Closest domain: B6TKT3_MAIZE 70-137)
Number of domains in family: 50
Commentary (automatic):
SUBNAME: CALCIUM REPEAT FULL=CALCINEURIN B-LIKE FULL=PUTATIVE UNCHARACTERIZED BINDING
REFERENCE FULL=PREDICTED
Length = 68
Score = 93 (40.4 bits), Expect = 0.004

Identities = 21/57 (36%), Positives = 31/57 (54%), Gaps = 5/57 (8%)

```
Query:    57 DADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNL 113
          D   NG IDF EF+  ++      D+ E+   AF+++D  G GYI   ELR ++  L
Sbjct:    81 DLKRNGVIDFEEFVRSLSVFHPKADTSEKTAFAFKLYDLRGTGYIEKEELREMVLAL 137
```

>**PDA96187** (Closest domain: A0DTI2_PARTE 115-183)
Number of domains in family: 19
Commentary (automatic):
SUBNAME: CALCIUM REFERENCE FULL=PREDICTED CALCIUM-BINDING FULL=CHROMOSOME SHOTGUN
ALTNAME: GENOME FULL=PUTATIVE
Length = 69
Score = 93 (40.4 bits), Expect = 0.004
Identities = 21/62 (33%), Positives = 35/62 (56%), Gaps = 6/62 (9%)

```
Query:    87 REAFRVFDKDGNGYISAAELRHVMTNLGEKL------TDEEVDEMIREADIDGDGQVNYE 140
          R  FR FD+DG+G+I+  E+  ++     +      T E+V   +R  D++ DGQV+ E
Sbjct:    122 RRLFRKFDQDGSGFITENEVPQLLIETYRSMGIQYNPTQEDVKSWMRMTDLNDDGQVSLE 181

Query:    141 EF 142
          E+
Sbjct:    182 EY 183
```

>**PDC5M9V7** (Closest domain: A7S612_NEMVE 18-68)
Number of domains in family: 30
Commentary (automatic):
SUBNAME: CALCIUM REFERENCE CALCIUM-BINDING FULL=SARCOPLASMIC FULL=PUTATIVE
UNCHARACTERIZED PROTEIN FULL=CALCIUM REPEAT
Length = 51
Score = 93 (40.4 bits), Expect = 0.003
Identities = 19/53 (35%), Positives = 35/53 (66%), Gaps = 2/53 (3%)

```
Query:    90 FRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEF 142
          F  +D + +GYI  AEL+   ++L  +L++E++     E D+DGDG+++ E+F
Sbjct:    18 FHHWDINHSGYIEKAELKQCCSDL--RLSEEKLAITFNELDLDGDGKISLEDF 68
```

>**PDD5B3Q3** (Closest domain: G4NHL3_MAGO7 50-161)
Number of domains in family: 1
Commentary (automatic):
SUBNAME: FULL=PUTATIVE UNCHARACTERIZED
Length = 112
Score = 93 (40.4 bits), Expect = 0.009
Identities = 27/75 (36%), Positives = 40/75 (53%), Gaps = 5/75 (6%)

```
Query:    33 LGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRV 92
          LG+ +  L      AE   + N+VD DG G   + EFL       + DS EE++E F
Sbjct:    90 LGSSVAGLSAEERRAEDVKVFNQVDLDGKGFFTYGEFLDFSG----EPDS-EELKEYFAK 144

Query:    93 FDKDGNGYISAAELR 107
          +DK+G+G I+  E+R
```

Sbjct: 145 YDKNGDGGITVEEMR 159

>**PDC999J9** (Closest domain: A0BG74_PARTE 80-126)
Number of domains in family: 3
Commentary (automatic):
SUBNAME: FULL=CHROMOSOME SHOTGUN GENOME SEQUENCE WHOLE UNDETERMINED SCAFFOLD_121 SCAFFOLD_105 REFERENCE
Length = 47
Score = 93 (40.4 bits), Expect = 0.003
Identities = 18/44 (40%), Positives = 27/44 (61%), Gaps = 3/44 (6%)

Query: 59 DGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYIS 102
+ TIDF EFL +M KM +S+EEI AF +F + + +I+
Sbjct: 82 ENKNTIDFNEFLQIMTEKMNAKESQEEIERAFHLFSQGNDNFIT 125

>**PDD2X1S1** (Closest domain: G0QS00_ICHMG 318-400)
Number of domains in family: 2
Commentary (automatic):
SUBNAME: KINASE CALCIUM EC=3.4.22.53 HYDROLASE DOMAIN EC=3.1.21.5 FULL=PUTATIVE FULL=PROTEIN UNCHARACTERIZED
Length = 83
Score = 93 (40.4 bits), Expect = 0.005
Identities = 17/67 (25%), Positives = 35/67 (52%), Gaps = 8/67 (11%)

Query: 83 EEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEF 142
EE++ F+ FD YIS +L+ + G ++ E++ M++E + Q+++ EF
Sbjct: 328 EEKLCSLFKYFDPSDTNYISVLDLKEIFLRNGRDVSIEDIKSMLKEIKLKNQDQISFTEF 387

Query: 143 VQMMTAK 149
+ M +
Sbjct: 388 KKFMIGQ 394

>**PDC768N7** (Closest domain: C5LU89_PERM5 324-382)
Number of domains in family: 11
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE UNCHARACTERIZED KINASE NUCLEOTIDE-BINDING FULL=CALCIUM-DEPENDENT KINASE ATP-BINDING FULL=PREDICTED
Length = 59
Score = 93 (40.4 bits), Expect = 0.004
Identities = 19/59 (32%), Positives = 37/59 (62%), Gaps = 3/59 (5%)

Query: 15 EAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMM 73
+AF D+DG G+I+ + L T+ LG++ ++++I E D +G+G I + EF+ ++
Sbjct: 325 DAFRKMDRDGSGSISLENLRTI---LGEDYMGTRIEEIIKECDINGDGQIQYEEFVALV 380

>**PDC123P6** (Closest domain: OBL_OBEGE 118-173)
Number of domains in family: 23
Commentary (automatic):
CALCIUM SUBNAME: FULL=MODIFIED AEQUORIN REPEAT PRECURSOR LUMINESCENCE FLAGS: RECNAME: PHOTOPROTEIN
Length = 56

Score = 92 (40.0 bits), Expect = 0.006
Identities = 20/53 (37%), Positives = 27/53 (50%), Gaps = 3/53 (5%)

```
Query:    16 AFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPE 68
           F +FDKDG GTIT  E     R  G +P+E + +      D D +G +D  E
Sbjct:   118 VFDIFDKDGSGTITLDEWKAYGRISGISPSEEDCEKTFQHCDLDNSGELDVDE 170
```

>**PD721888** (Closest domain: G3HGD2_CRIGR 41-120)
Number of domains in family: 5
Commentary (automatic):
SUBNAME: REFERENCE C17ORF57 DOMAIN-CONTAINING FULL=EF-HAND FULL=UNCHARACTERIZED FIS POLYMORPHISM TESTI2032768 REPEAT
Length = 80
Score = 92 (40.0 bits), Expect = 0.007
Identities = 24/71 (33%), Positives = 41/71 (57%), Gaps = 4/71 (5%)

```
Query:    73 MARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADID 132
           M + +K  D +E I EA    +K    YIS  EL+  +  LG  L+DE++ +++ E +I+
Sbjct:    42 MRQVLKTVDIDESILEAV---NKLQGSYISLEELQSALPTLGITLSDEDIQKIVSEINIE 98

Query:   133 GDGQVNYEEFV 143
            G VN ++F+
Sbjct:    99 S-GMVNLDDFI 108
```

>**PDB167A9** (Closest domain: E0VNM9_PEDHC 20-86)
Number of domains in family: 16
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE UNCHARACTERIZED REFERENCE FULL=PYRAZINAMIDASE/NICOTINAMIDASE FULL=PREDICTED FULL=NICOTINAMIDASE EC=2.7.11.17 EXONUCLEASE
Length = 67
Score = 92 (40.0 bits), Expect = 0.006
Identities = 21/62 (33%), Positives = 35/62 (56%), Gaps = 7/62 (11%)

```
Query:    16 AFSLFDKDGDGTITTKELGTVMRSLGQNPT-------EAELQDMINEVDADGNGTIDFPE 68
           F+ FDK+GDG++  KE  ++ R+L +N          +L+D+    D +G+G ID  E
Sbjct:    23 CFTAFDKNGDGSLDMKEFNSLCRALFRNDRGKIYALDSEKLRDIFEVFDHNGDGLIDRNE 82

Query:    69 FL 70
           F+
Sbjct:    83 FV 84
```

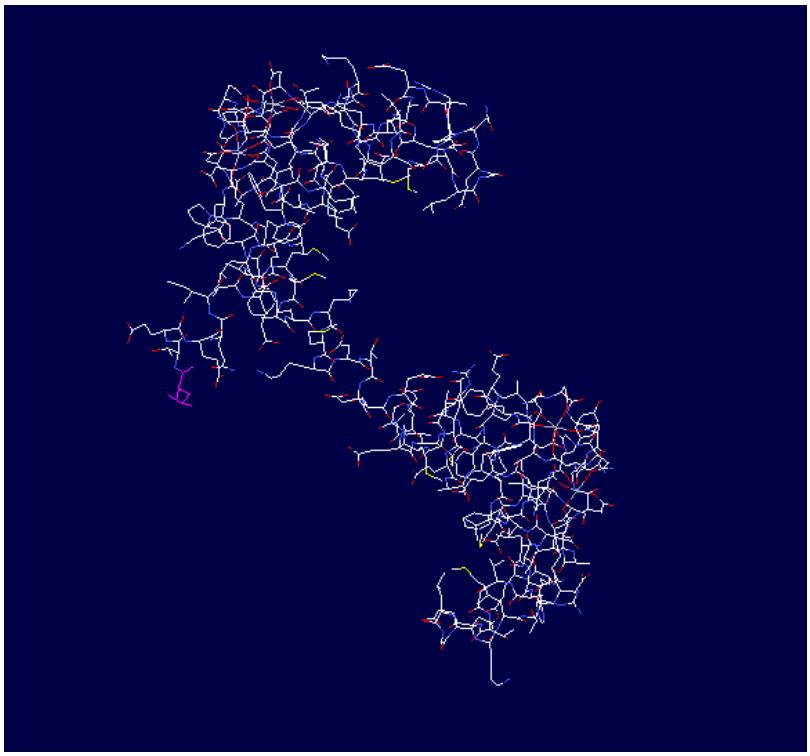
>**PDC6A9F9** (Closest domain: D7G458_ECTSI 386-433)
Number of domains in family: 52
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE UNCHARACTERIZED HAND FULL=EF DOMAIN-CONTAINING REPEAT HYDROLASE REFERENCE
Length = 48
Score = 91 (39.7 bits), Expect = 0.006
Identities = 21/48 (43%), Positives = 29/48 (60%), Gaps = 2/48 (4%)

Query: 52 MINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNG 99
M + D DGNGT+D+ EFL MA K T ++ +R F ++D DG G
Sbjct: 388 MFDLFDTDGNGTVDYGEFLAGMA-SFKHT-GDKALRFCFDIYDLDGGG 433

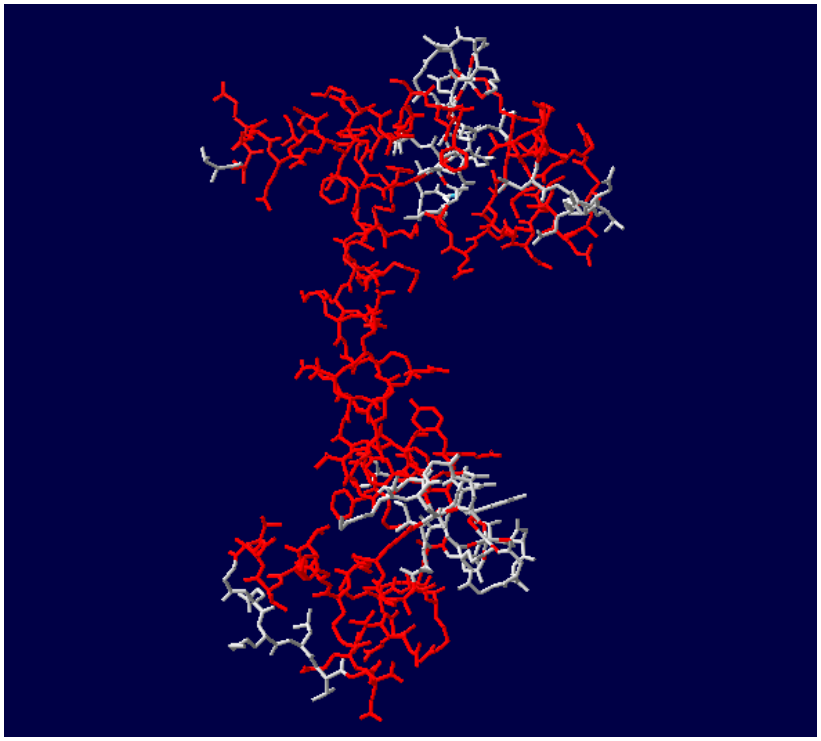
>**PDC4P118** (Closest domain: A0BDK2_PARTE 386-443)
Number of domains in family: 4
Commentary (automatic):
SUBNAME: CALCIUM FULL=PUTATIVE UNCHARACTERIZED NUCLEOTIDE-BINDING FULL=CHROMOSOME REPEAT SHOTGUN FULL=CALCIUM-DEPENDENT REFERENCE
Length = 58
Score = 90 (39.3 bits), Expect = 0.01
Identities = 19/48 (39%), Positives = 28/48 (58%), Gaps = 2/48 (4%)

Query: 83 EEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREAD 130
+E + +AF++FD DG+G IS ELR V+ G D +I +AD
Sbjct: 395 QERLFQAFKMFDLDGSGKISREELRQVLGKTGSGFDDNTFKALIADAD 442

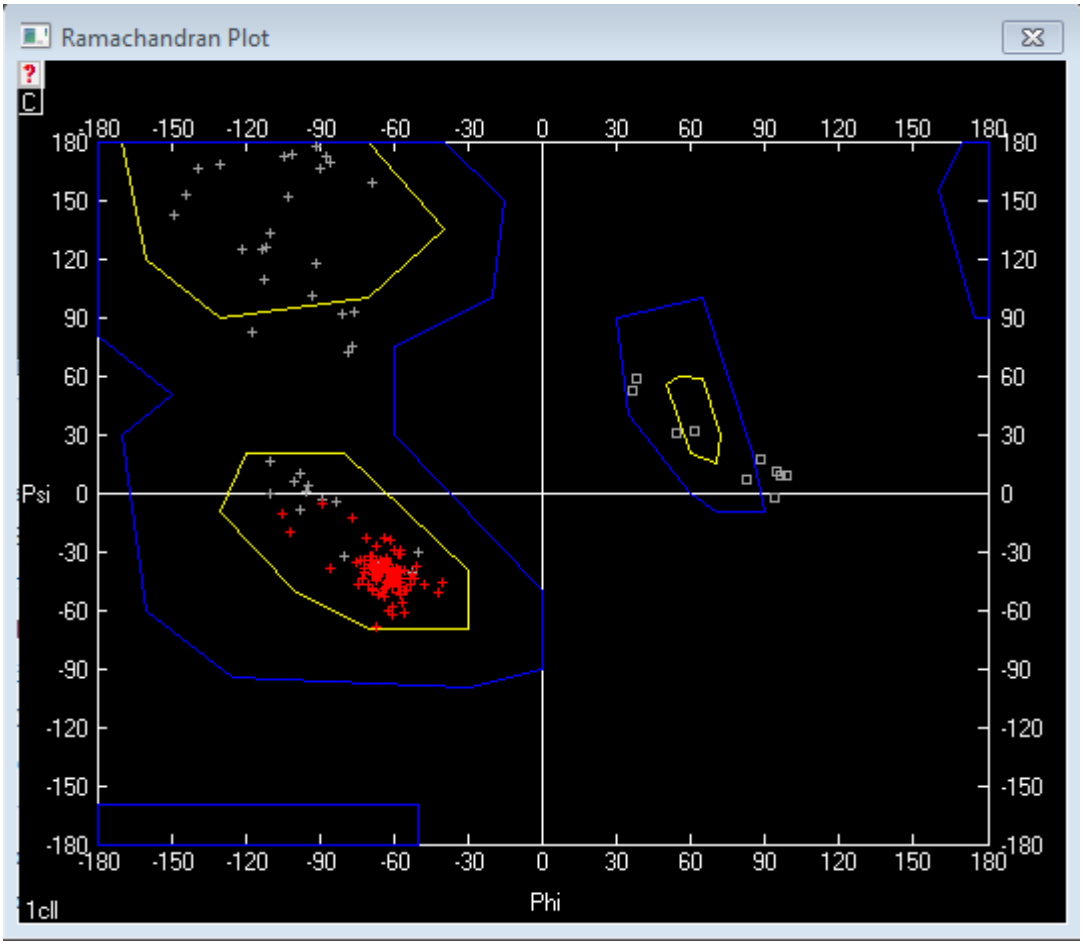
ΜΕΤΑ ΑΠΟ ΧΡΗΣΗ ΤΟΥ ΛΟΓΙΣΜΙΚΟΥ SPDBV, παίρνουμε την ακόλουθη εικόνα για τη δομή της πρωτεΐνης.



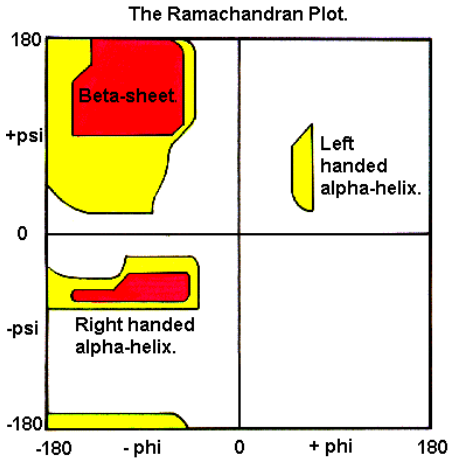
RENDER IN SOLID 3D/ COLOR BY SECONDARY STRUCTURE(χρωματισμός αυτής με βάση τη δευτεροταγή δομή). Το κόκκινο χρώμα αναπαριστά τις περιοχές τύπου α-έλικας.



RAMACHANDRAN PLOT



Σε ένα πολυπεπτίδιο, οι δεσμοί N-Cα και Cα-C είναι σχετικώς ελεύθεροι να περιστρέφονται. Αυτές οι περιστροφές εκπροσωπούνται από τις γωνίες στρέψης φ και ψ, αντίστοιχα. Η περιστροφή γύρω από τον πεπτιδικό δεσμό , αντίθετα, είναι αδύνατη, καθώς αυτός έχει εν μέρει χαρακτήρα διπλού δεσμού. Το διάγραμμα Ramachandran, λοιπόν, είναι ένα διάγραμμα το οποίο δείχνει τις τιμές των γωνιών που μπορεί να υιοθετήσει ένα αμινοξύ , κατά την περιστροφή μιας πολυπεπτιδικής αλυσίδας.



Σύμφωνα με το διάγραμμα όπως δίνεται στην εικόνα, η περιοχή στο πάνω αριστερά τεταρτημόριο αντιστοιχεί σε γωνίες που συναντώνται σε β-κλώνους. Η περιοχή στο κάτω αριστερά τεταρτημόριο αντιστοιχεί σε δεξιόστροφες α-έλικες. Η περιοχή στο πάνω δεξιά τεταρτημόριο αντιστοιχεί στις πιο σπάνιες αριστερόστροφες α-έλικες, που σπάνια παρατηρούνται σε πρωτείνες.

Στο δικό μας παράδειγμα, εκτός των επιτρεπτών διαμορφώσεων, λόγω έλλειψης πλευρικής αλυσίδας στο μόριο τους (μειωμένη στερεοχημική παρεμπόδιση) εμφανίζονται γλυκίνες.
Συγκεκριμένα, τα αμινοξέα που βρίσκονται εκτός των επιτρεπτών ορίων είναι τα εξής(φαίνονται στην παρακάτω εικόνα με το γαλάζιο χρώμα):

Gly 25
Gly 40
Gly 61
Gly 98
Gly 113