

Protein Profiling

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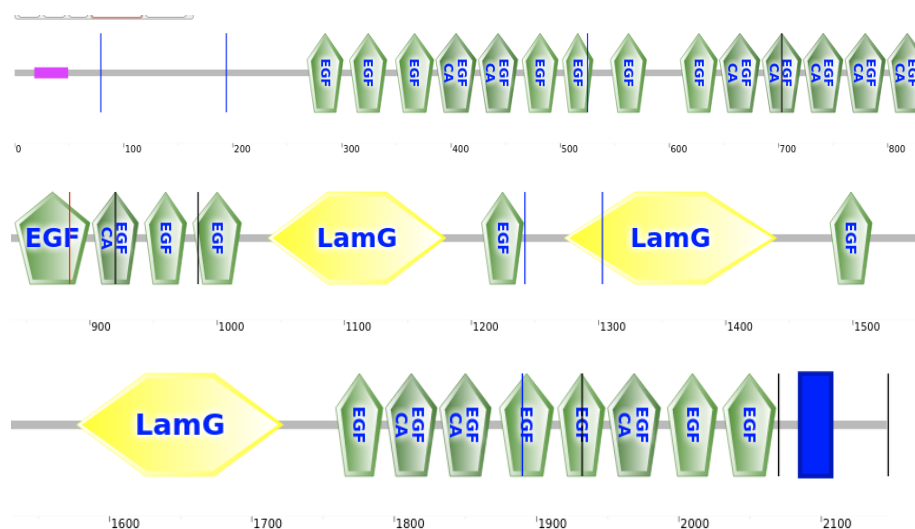
Introduction

Methods

1. From uniprot.org find the sequence of *Drosophila* Crbm UniProtKB-P10040(CRB_DROME). Then use SMART (<http://smart.embl-heidelberg.de/>) to predict domain organization of *Drosophila* Crumbs.
2. Use the Scansite(<http://scansite.mit.edu/>) to predict functional motifs in Crumbs with sequence of CRB_DROME.
3. Using T-Coffee to align cytoplasmic domains from human Crb1 and Crb2 with
4. *Drosophila* Crumbs.

Results

1. Here are the domain organization predicted by SMART.



2. Here are some predicted motif sites with high score.

Predicted Motif Sites (Table)			
Please allow popups in your browser settings to make links in the table work properly!			
▼ Score	Percentile	Motif	Motifgroup
0.948	4.151%	PDK1 Binding (PDK1_Bind)	Kinase binding site group (Kin_bind)
0.943	3.803%	PDK1 Binding (PDK1_Bind)	Kinase binding site group (Kin_bind)
0.940	3.671%	PDK1 Binding (PDK1_Bind)	Kinase binding site group (Kin_bind)
0.933	3.363%	PDK1 Binding (PDK1_Bind)	Kinase binding site group (Kin_bind)
0.917	2.576%	PDK1 Binding (PDK1_Bind)	Kinase binding site group (Kin_bind)
0.858	4.617%	Cbl-Associated protein C-SH3 (CapC_SH3)	Src homology 3 group (SH3)
0.809	3.488%	PIP3-binding PH (PIP3_PH)	Lipid binding group (Lip_bind)
0.800	3.013%	PIP3-binding PH (PIP3_PH)	Lipid binding group (Lip_bind)
0.786	2.089%	Cbl-Associated protein C-SH3 (CapC_SH3)	Src homology 3 group (SH3)
0.785	2.602%	Clk2 Kinase (Clk2_Kin)	Basophilic serine/threonine kinase (Baso_ST_kin)
0.780	2.455%	Clk2 Kinase (Clk2_Kin)	Basophilic serine/threonine kinase (Baso_ST_kin)
0.762	1.796%	PIP3-binding PH (PIP3_PH)	Lipid binding group (Lip_bind)
0.752	1.795%	Clk2 Kinase (Clk2_Kin)	Basophilic serine/threonine kinase (Baso_ST_kin)
0.742	4.865%	Aurora B (AuroB)	Basophilic serine/threonine kinase (Baso_ST_kin)
0.734	3.827%	Erk1 Binding (Erk1_Bind)	Kinase binding site group (Kin_bind)
0.732	3.935%	Erk D-domain (ErkDD)	Kinase binding site group (Kin_bind)
0.730	3.886%	Erk D-domain (ErkDD)	Kinase binding site group (Kin_bind)
0.727	3.758%	Erk D-domain (ErkDD)	Kinase binding site group (Kin_bind)

3. Alignment result of 3 sequences.

MSA			
The multiple sequence alignment result as produced by T-coffee.			
T-COFFEE, Version_11.00.d625267 (2016-01-11 15:25:41 - Revision d625267 - Build 507)			
Cedric Notredame			
SCORE=988			
* BAD AVG GOOD			
* SD P10040 2110- : 98 SD P82279 1369- : 100 sp Q5IJ48 1246- : 94 cons : 98			
sp P10040 2110- --RNKRATRGTYSPSAOEYCNPRLEMDNVLKPPPEERLI sp P82279 1369- --TSNKRATOGTYSPSROEKEGSRVEMWNLMPPPAMERLI sp Q5IJ48 1246- LAARKRRQSEGTYSPSQEVAGARLEMDSVLKVPPEERLI			
cons : : * : : ***** ** . . * . * . : : * . ****			

4.

Conclusions