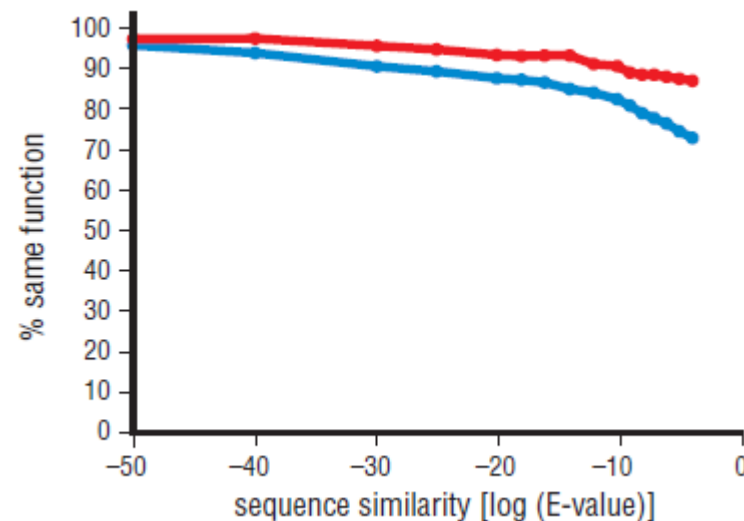


EXPERIMENT 2: Protein profiling

Dr. Zhiyi Wei
SUSTC

Sequence comparison

- Sequence comparison provides a measure of the relationship between genes

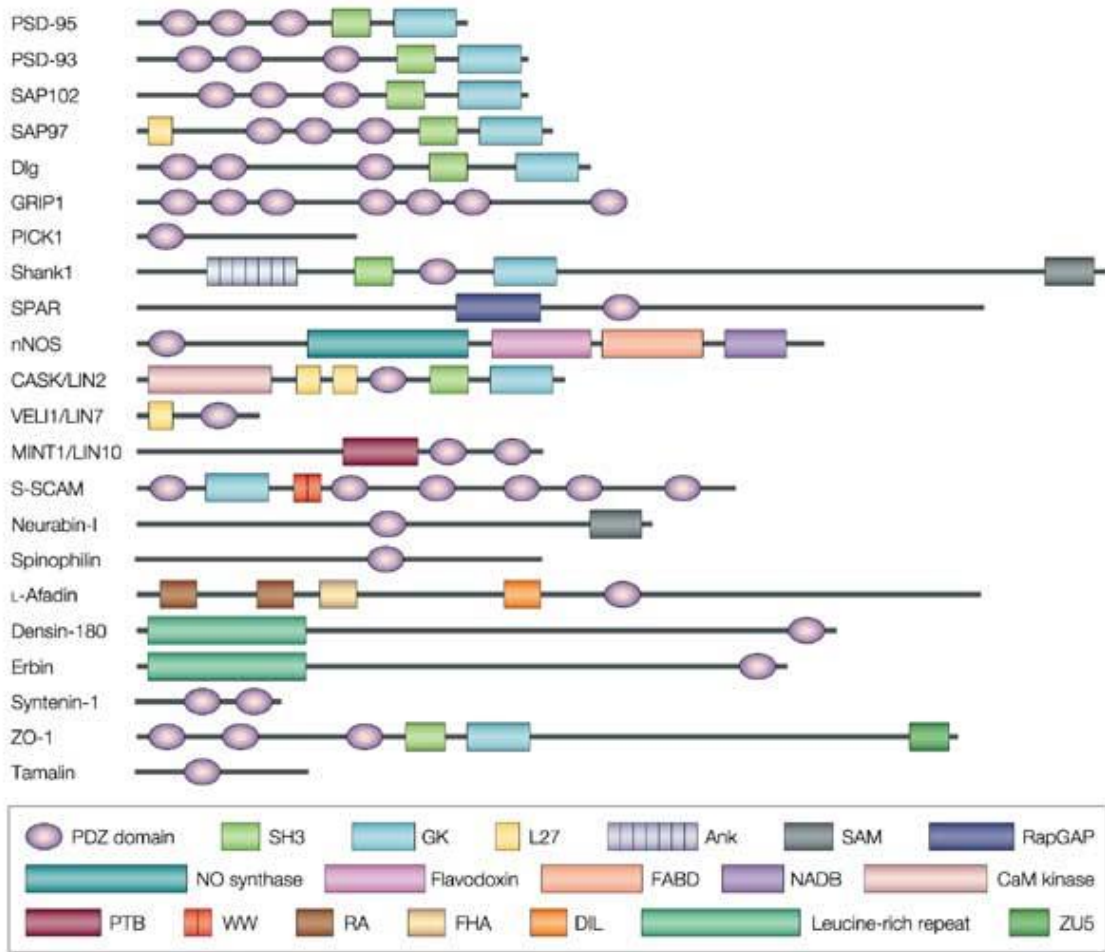


Sequence alignment

H.s. Wee1 409-457
 H.s. Ttk 614-659
 S.c. Ste7 313-358
 S.c. Mkk1 332-376
 S.p. Byr1 168-213
 S.c. St20 722-767
 S.c. Cc15 129-172
 S.p. Byr2 505-553
 S.c. Spk1 302-348
 S.p. Kin1 249-293
 S.p. Cdr1 111-156
 M.m. K6a1 507-556
 R.n. Kpbh 136-180
 H.s. Erk2 132-176
 S.c. Kss1 137-182

	Motif 1															Motif 2																																					
	Q	V	G	R	G	L	R	Y	I	H	S	M	S	-	L	V	H	M	D	I	K	P	S	N	I	F	I	S	R	T	S	I	P	N	A	A	S	E	E	G	D	E	D	D	W	A	S	N	K	-	-	-	-
	N	M	L	E	A	V	H	T	I	H	Q	H	G	-	I	V	H	S	D	L	K	P	A	N	F	L	I	V	D	G	-	-	-	-	-	M	L	K	L	I	D	F	G	I	A	N	Q	M	Q	P	D	-	-
	G	V	L	N	G	L	D	H	L	Y	R	Q	Y	K	I	I	H	R	D	I	K	P	S	N	V	L	I	N	S	K	-	-	-	-	G	Q	I	K	L	C	D	F	G	V	S	K	K	L	I	-	-	-	-
	A	V	L	R	G	L	S	Y	L	H	E	K	K	-	V	I	H	R	D	I	K	P	Q	N	I	L	L	N	E	N	-	-	-	-	G	Q	V	K	L	C	D	F	G	V	S	G	E	A	V	-	-	-	-
	S	M	V	K	G	L	I	Y	L	N	V	L	H	I	I	H	R	D	L	K	P	S	N	V	V	V	N	S	R	-	-	-	-	G	E	I	K	L	C	D	F	G	V	S	G	E	L	V	-	-	-	-	
	E	T	L	S	G	L	E	F	L	H	S	K	G	-	V	L	H	R	D	I	K	S	D	N	I	L	L	S	M	E	-	-	-	-	G	D	I	K	L	T	D	F	G	F	C	A	Q	I	N	E	-	-	-
	Q	T	L	L	G	L	K	Y	L	H	G	E	G	-	V	I	H	R	D	I	K	A	A	N	I	L	L	S	A	D	-	-	-	-	N	T	V	K	L	A	D	F	G	V	S	T	I	V	-	-	-	-	
	Q	T	L	K	G	L	E	Y	L	H	S	R	G	-	I	V	H	R	D	I	K	G	A	N	I	L	V	D	N	K	-	-	-	-	G	K	I	K	I	S	D	F	G	I	S	K	K	L	E	L	N	S	T
	Q	I	L	T	A	I	K	Y	I	H	S	M	G	-	I	S	H	R	D	L	K	P	D	N	I	L	I	E	Q	D	D	-	-	P	V	L	V	K	I	T	D	F	G	L	A	K	V	Q	G	-	-	-	-
	Q	I	G	S	A	L	S	Y	L	H	Q	N	S	-	V	V	H	R	D	L	K	I	E	N	I	L	I	S	K	T	-	-	-	-	G	D	I	K	I	I	D	F	G	L	S	N	L	Y	R	-	-	-	-
	Q	I	L	D	A	V	A	H	C	H	R	F	R	-	F	R	H	R	D	L	K	L	E	N	I	L	I	K	V	N	-	-	-	-	E	Q	Q	I	K	I	A	D	F	G	M	A	T	V	E	P	-	-	-
	T	I	S	K	T	V	E	Y	L	H	S	Q	G	-	V	V	H	R	D	L	K	P	S	N	I	L	Y	V	D	E	S	G	N	P	E	C	L	R	I	C	D	F	G	F	A	K	Q	L	R	A	-	-	-
	S	L	L	E	A	V	N	F	L	H	V	N	N	-	I	V	H	R	D	L	K	P	E	N	I	L	L	D	D	N	-	-	-	-	M	Q	I	R	L	S	D	F	G	F	S	C	H	L	E	-	-	-	-
	Q	I	L	R	G	L	K	Y	I	H	S	A	M	-	V	L	H	R	D	L	K	P	S	N	L	L	L	N	T	T	-	-	-	-	C	L	S	C	K	I	C	D	F	G	L	A	R	V	A	-	-	-	-
	Q	I	L	R	A	L	K	S	I	H	S	A	Q	-	V	I	H	R	D	I	K	P	S	N	L	L	L	N	S	N	-	-	-	-	-	C	K	V	C	D	F	G	L	A	R	C	L	A	S	S	S	-	

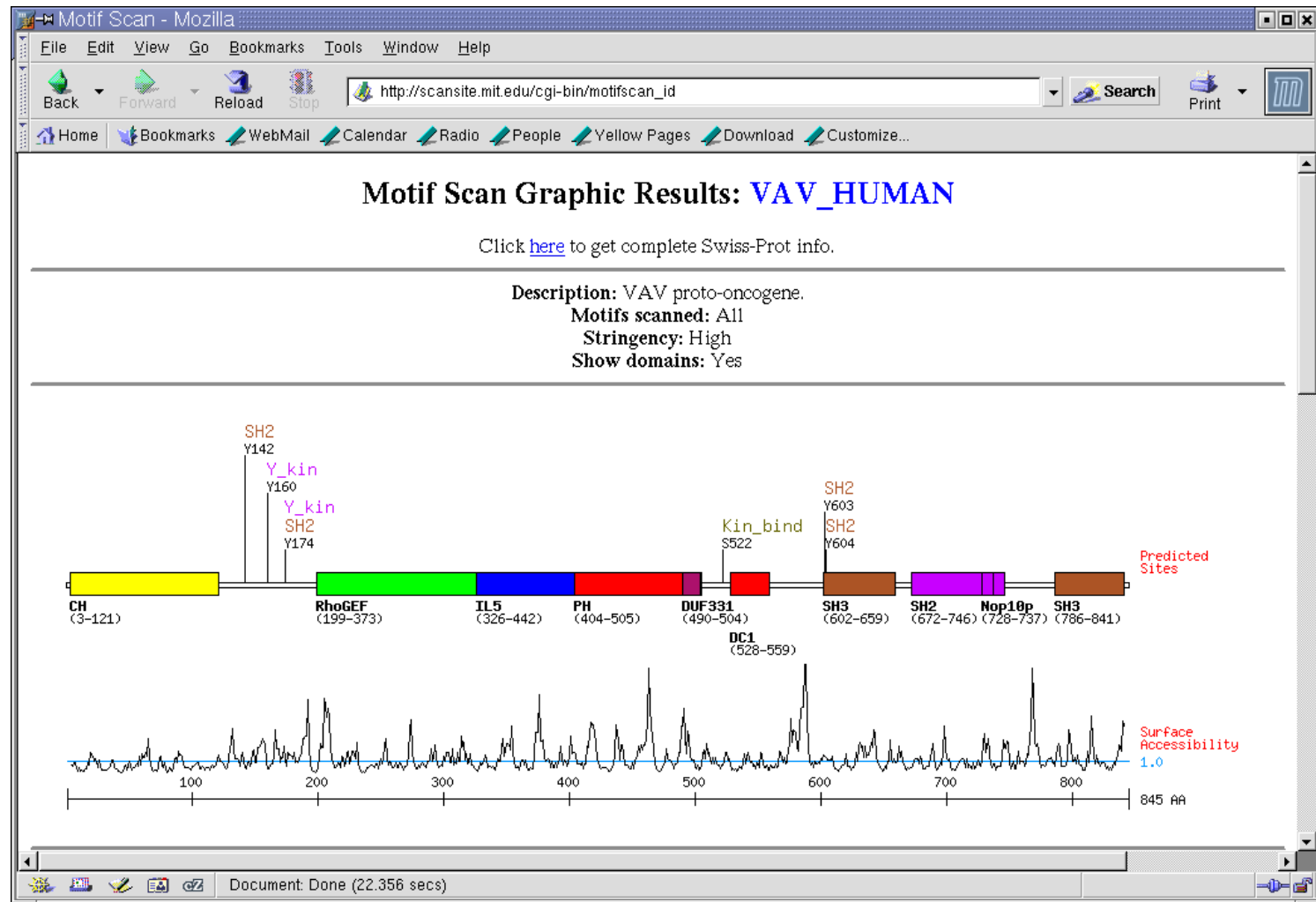
Protein domain



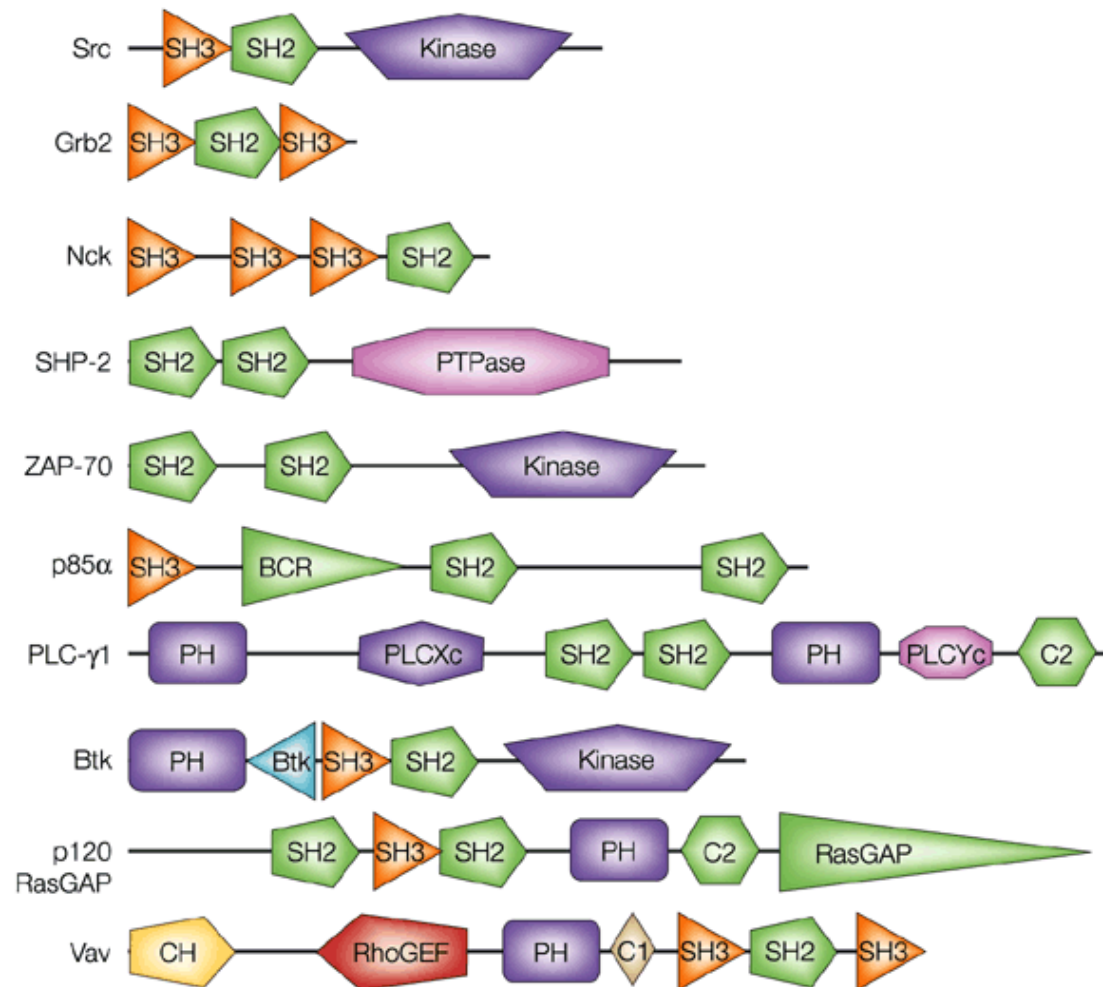
Protein motif

Contiguous motif	Consensus sequence	Function
Walker (P loop)	[A/G]XXXXGK[S/T]	binds ATP or GTP
Zn finger	CX ₂₋₄ CX ₁₂ HX ₃₋₅ H	binds Zn in a DNA-binding domain
Osteonectin	CX[D/N]XXCXXG[K/R/H]XCX ₆₋₇ PXCXCX ₃₋₅ CP	binds calcium and collagen
DEAD box helicase	XXDEAD[R/K/E/N]X	ATP-dependent RNA unwinding
MARCKS	GQENGNV[K/R]	substrate for protein kinase C
Calsequestrin	[E/Q][D/E]GL[D/N]FPXYDGXDRV	binds calcium

Motif prediction by Scansite



Domain prediction by SMART



Tasks

1. Predict domain organization of ***Drosophila* Crumbs**
 - Using SMART (<http://smart.embl-heidelberg.de/>)
2. Predict functional motifs in Crumbs
 - Using Scansite (<http://scansite.mit.edu/>)
3. Align cytoplasmic domains from human Crb1 and Crb2 with *Drosophila* Crumbs
 - Getting conserved sequence profile of the C-terminal last 9 residues
4. Find another protein having the similar C-terminal end
 - Based on the sequence profile
5. Justify whether this protein can bind with the same PDZ domain

Lab report format

- Title
- Your name and student No.
- Introduction
- Methods
- Results
- Conclusions