

Results Summary

ULTimate Y2H SCREEN

Drosophila melanogaster - Ras

vs Drosophila Whole Embryo_RP1 (0-12+12-24)

Thu, Apr 19, 2018 - 08:04 PM



Screen Parameters

Nature	cDNA
Reference Bait Fragment	Drosophila melanogaster - Ras (aa 1-164) ; hgx256v1
Prey Library	Drosophila Whole Embryo_RP1 (0-12+12-24)
Vector(s)	pB27 (N-LexA-bait-C fusion)
Processed Clones	164 (pB27_A)
Analyzed Interactions	68 millions (pB27_A)
3AT Concentration	0.0 mM (pB27_A)

Global PBS®

Global PBS (for Interactions represented in the Screen)		Nb	%
A	Very high confidence in the interaction	5	50.0%
B	High confidence in the interaction	1	10.0%
C	Good confidence in the interaction	0	0.0%
D	Moderate confidence in the interaction This category is the most difficult to interpret because it mixes two classes of interactions : - False-positive interactions - Interactions hardly detectable by the Y2H technique (low representation of the mRNA in the library, prey folding, prey toxicity in yeast)	2	20.0%
E	Interactions involving highly connected (or relatively highly connected) prey domains, warning of non-specific interaction. The total number of screens performed on each organism is taken into account to set this connectivity threshold: 20 interactions to different bait proteins in our entire database for Human, 10 for Mouse, Drosophila and Arabidopsis and 6 for all other organisms. They can be classified in different categories: - Prey proteins that are known to be highly connected due to their biological function - Proteins with a prey interacting domain that contains a known protein interaction motif or a biochemically promiscuous motif	0	0.0%
F	Experimentally proven technical artifacts	2	20.0%
Non Applicable			
N/A	The PBS is a score that is automatically computed through algorithms and cannot be attributed for the following reasons : - All the fragments of the same reference CDS are antisense - The 5p sequence is missing - All the fragments of the same reference CDS are either all OOF1 or all OOF2 - All the fragments of the same reference CDS lie in the 5' or 3' UTR		

Prey Fragment Analysis

Symbols	Means
✱	The fragment contains the full length ORF
	Fragment is fully in 5' UTR
	Fragment is fully in 3' UTR
x	Fragment contains at least one In Frame STOP codon in 5' UTR
x	Fragment contains at least one In Frame STOP codon in CDS
x	Fragment contains the natural STOP codon
[NR]	Fragment was found to be non relevant (poor quality, high N density)
IF OOF1 OOF2	With regard to the theoretical frame of each corresponding ORF (GenBank), fragments are cloned in frame (IF) if they are in the same frame as Gal4AD. In general, polypeptides synthesized from OOF fragments are not considered of biological interest, unless found together with another frame. However, some of the proteins expressed from an OOF fragment can be translated in the correct frame, due to the existence of natural frame-shift events during translation in yeast. No stop codons are displayed for OOF fragments.
??	Unidentified frame when : - The clone sequence is antisense - The 5p sequence is missing
N	Antisense
Start...Stop	Position of the 5p and 3p prey fragment ends, relative to the position of the ATG start codon (A=0)

Clone Name	Type Seq	Gene Name (Best Match)	Start..Stop (nt)	Frame	Sense	%Id 5p	%Id 3p	PBS
pB27_A-146	5p/3p	Drosophila melanogaster - BtbVII	1155..1954	IF		97.8	100.0	F
pB27_A-129	5p/3p	Drosophila melanogaster - CG8965	3..591	IF		96.2	99.2	A
pB27_A-27	5p/3p	Drosophila melanogaster - CG8965	3..591	IF		99.5	98.6	A
pB27_A-51	5p/3p	Drosophila melanogaster - CG8965	3..591	IF		99.5	92.8	A
pB27_A-43	5p/3p	Drosophila melanogaster - CG8965	3..591	IF		99.5	96.5	A
pB27_A-60	5p/3p	Drosophila melanogaster - CG8965	3..591	IF		99.5	98.9	A
pB27_A-132	5p/3p	Drosophila melanogaster - CG8965	9..583	IF		98.7	99.2	A
pB27_A-88	5p/3p	Drosophila melanogaster - CG8965	9..583	IF		99.5	100.0	A
pB27_A-156	5p/3p	Drosophila melanogaster - CG8965	9..583	IF		97.1	99.2	A
pB27_A-98	5p/3p	Drosophila melanogaster - CG8965	9..583	IF		97.5	99.2	A
pB27_A-126	5p	Drosophila melanogaster - CG8965	10	OOF1		98.5		A
pB27_A-135	5p/3p	Drosophila melanogaster - CG8965	10..917	OOF1		98.6	97.3	A
pB27_A-171	5p/3p	Drosophila melanogaster - CG8965	15..591	IF		96.1	99.2	A
pB27_A-30	5p/3p	Drosophila melanogaster - CG8965	15..591	IF		97.5	99.3	A
pB27_A-53	5p/3p	Drosophila melanogaster - CG8965	15..591	IF		99.3	98.7	A
pB27_A-159	5p/3p	Drosophila melanogaster - CG8965	15..591	IF		96.9	99.2	A
pB27_A-165	5p/3p	Drosophila melanogaster - CG8965	15..591	IF		96.8	99.2	A
pB27_A-122	5p/3p	Drosophila melanogaster - CG8965	15..591	IF		98.3	99.2	A
pB27_A-124	5p/3p	Drosophila melanogaster - CG8965	21..661	IF		97.9	98.9	A
pB27_A-143	5p/3p	Drosophila melanogaster - CG8965	21..661	IF		97.7	98.9	A
pB27_A-148	5p/3p	Drosophila melanogaster - CG8965	21..661	IF		97.9	98.9	A
pB27_A-42	5p	Drosophila melanogaster - CG8965	30	IF		97.8		A
pB27_A-79	5p/3p	Drosophila melanogaster - CG8965	33..778	IF		99.8	97.1	A
pB27_A-36	5p	Drosophila melanogaster - CG8965	58	OOF1		99.8		A
pB27_A-80	5p/3p	Drosophila melanogaster - CG8965	58..1142	OOF1		99.8	96.5	A
pB27_A-111	5p/3p	Drosophila melanogaster - CG8965	73..781	OOF1		97.8	97.3	A
pB27_A-33	5p/3p	Drosophila melanogaster - CG8965	73..781	OOF1		98.8	95.4	A

Clone Name	Type Seq	Gene Name (Best Match)	Start..Stop (nt)	Frame	Sense	%Id 5p	%Id 3p	PBS
pB27_A-4	5p/3p	Drosophila melanogaster - CG8965	73..781	OOF1		99.8	96.9	A
pB27_A-75	5p/3p	Drosophila melanogaster - CG8965	73..781	OOF1		99.8	95.7	A
pB27_A-161	5p/3p	Drosophila melanogaster - CG8965	73..781	OOF1		98.1	97.3	A
pB27_A-1	5p/3p	Drosophila melanogaster - CG8965	139..751	OOF1		99.5	97.0	A
pB27_A-63	5p/3p	Drosophila melanogaster - CG8965	139..751	OOF1		99.5	97.2	A
pB27_A-84	5p	Drosophila melanogaster - CG8965	141	IF		99.5		A
pB27_A-52	5p/3p	Drosophila melanogaster - CG8965	141..1191	IF		99.5	97.0	A
pB27_A-151	5p/3p	Drosophila melanogaster - CG8965	141..1191	IF		95.6	97.5	A
pB27_A-17	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		99.3	97.0	A
pB27_A-41	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		99.3	93.8	A
pB27_A-38	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		99.3	97.0	A
pB27_A-78	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		99.3	95.8	A
pB27_A-77	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		99.3	97.5	A
pB27_A-89	5p	Drosophila melanogaster - CG8965	168	IF		99.3		A
pB27_A-66	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		99.3	95.7	A
pB27_A-96	5p/3p	Drosophila melanogaster - CG8965	168..1193	IF		98.1	97.5	A
pB27_A-16	5p/3p	Drosophila melanogaster - CG8965	186..744	IF		99.2	98.2	A
pB27_A-99	5p/3p	Drosophila melanogaster - PI3K	-22..939	IF		96.2	100.0	A
pB27_A-40	5p/3p	Drosophila melanogaster - PI3K	72..942	IF		99.8	99.8	A
pB27_A-14	5p/3p	Drosophila melanogaster - PI3K	108..943	IF		99.8	100.0	A
pB27_A-57	5p/3p	Drosophila melanogaster - PI3K	108..943	IF		99.8	100.0	A
pB27_A-73	5p	Drosophila melanogaster - PI3K	108	IF		99.8		A
pB27_A-92	5p	Drosophila melanogaster - PI3K	108	IF		99.5		A
pB27_A-142	5p/3p	Drosophila melanogaster - PI3K	108..943	IF		98.3	100.0	A
pB27_A-20	5p	Drosophila melanogaster - PI3K	222	IF		99.5		A
pB27_A-119	5p/3p	Drosophila melanogaster - PI3K	222..994	IF		97.2	100.0	A
pB27_A-101	5p/3p	Drosophila melanogaster - PI3K	246..970	IF		98.3	100.0	A
pB27_A-120	5p/3p	Drosophila melanogaster - PI3K	294..940	IF		97.2	99.7	A
pB27_A-81	5p/3p	Drosophila melanogaster - PI3K	333..992	IF		99.8	97.0	A
pB27_A-21	5p/3p	Drosophila melanogaster - PI3K	360..939	IF		98.0	99.3	A
pB27_A-45	5p	Drosophila melanogaster - PI3K	360	IF		100.0		A
pB27_A-105	5p/3p	Drosophila melanogaster - PI3K	360..939	IF		98.5	100.0	A
pB27_A-162	5p/3p	Drosophila melanogaster - PI3K	360..939	IF		98.4	100.0	A
pB27_A-144	5p/3p	Drosophila melanogaster - PI3K	441..940	IF		95.6	91.9	A
pB27_A-56	5p/3p	Drosophila melanogaster - PI3K	441..940	IF		97.4	88.7	A
pB27_A-2	5p/3p	Drosophila melanogaster - PI3K	483..922	IF		100.0	99.3	A
pB27_A-164	5p/3p	Drosophila melanogaster - Raf Kinase	418..789	OOF1		97.7	100.0	B
pB27_A-104	5p/3p	Drosophila melanogaster - Raf Kinase	510..1045	IF		98.3	99.7	B
pB27_A-86	5p	Drosophila melanogaster - Raf Kinase	549	IF		99.7		B
pB27_A-29	5p/3p	Drosophila melanogaster - Raf Kinase	549..1278	IF		100.0	99.9	B
pB27_A-48	5p/3p	Drosophila melanogaster - Rgl	2172..3080	X	IF	99.8	95.3	A
pB27_A-115	5p/3p	Drosophila melanogaster - Rgl	2190..3249	X	IF	98.5	97.4	A
pB27_A-127	5p/3p	Drosophila melanogaster - Rgl	2265..2945	X	IF	98.7	99.7	A
pB27_A-44	5p/3p	Drosophila melanogaster - Rgl	2265..2945	X	IF	99.3	95.9	A
pB27_A-71	5p/3p	Drosophila melanogaster - Rgl	2265..2945	X	IF	99.3	100.0	A
pB27_A-9	5p/3p	Drosophila melanogaster - Rgl	2265		IF	99.3	75.8	A
pB27_A-167	5p/3p	Drosophila melanogaster - Rgl	2265..2945	X	IF	98.8	99.6	A
pB27_A-54	5p/3p	Drosophila melanogaster - Rgl	2334..3213	X	IF	99.5	96.4	A

HYBRIGENICS

SERVICES

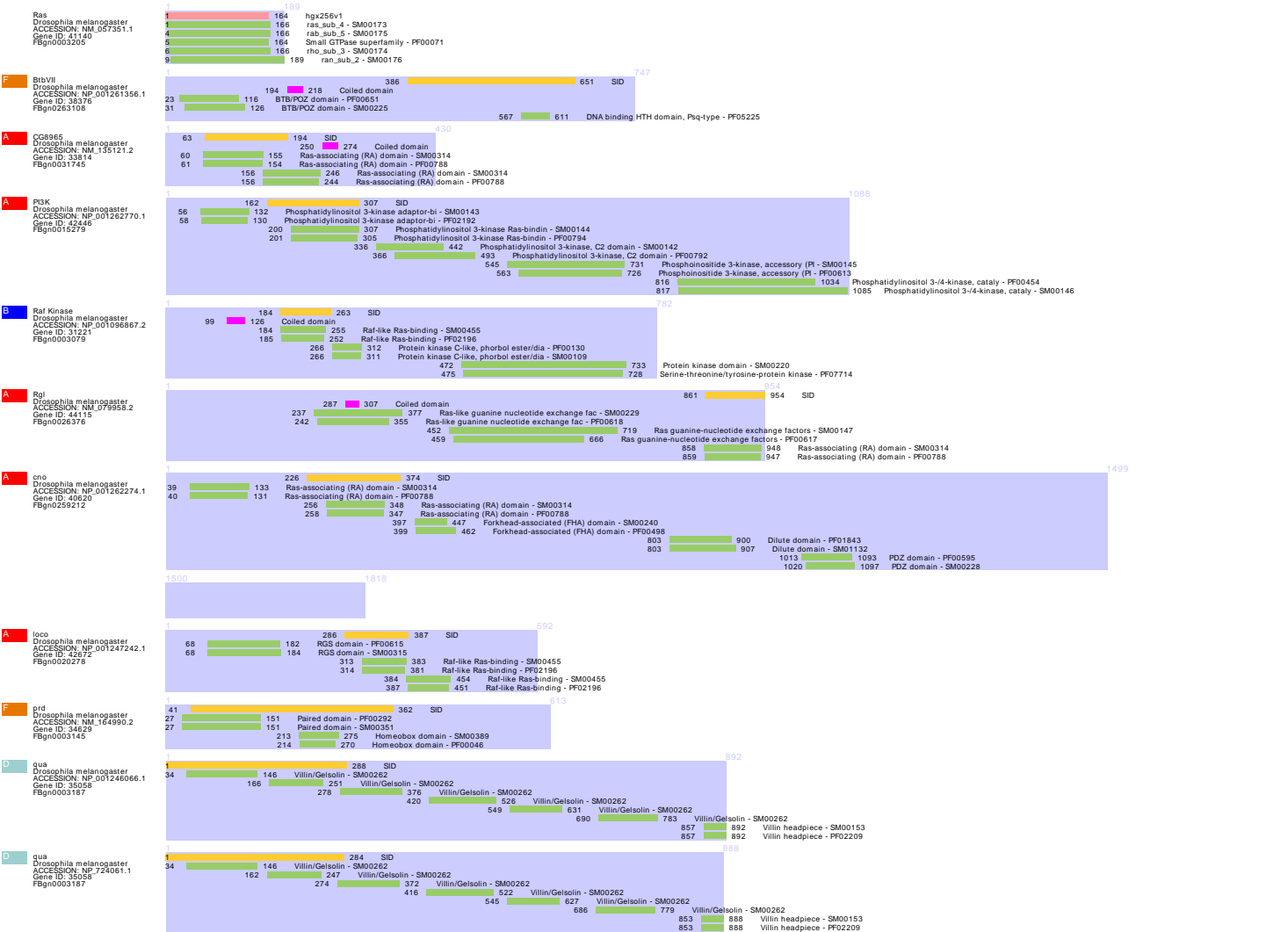
Clone Name	Type Seq	Gene Name (Best Match)	Start..Stop (nt)	Frame	Sense	%Id 5p	%Id 3p	PBS
pB27_A-19	5p/3p	Drosophila melanogaster - Rgl	2334..3213 X	IF		99.0	97.8	A
pB27_A-139	5p/3p	Drosophila melanogaster - Rgl	2334..3213 X	IF		97.7	97.4	A
pB27_A-131	5p	Drosophila melanogaster - Rgl	2334	IF		97.0		A
pB27_A-108	5p/3p	Drosophila melanogaster - Rgl	2361..2950 X	IF		97.9	99.7	A
pB27_A-117	5p/3p	Drosophila melanogaster - Rgl	2361..2950 X	IF		98.1	99.7	A
pB27_A-12	5p/3p	Drosophila melanogaster - Rgl	2361..3230 X	IF		87.9	90.9	A
pB27_A-154	5p/3p	Drosophila melanogaster - Rgl	2424..3263 X	IF		97.3	97.4	A
pB27_A-145	5p/3p	Drosophila melanogaster - Rgl	2511..3263 X	IF		96.6	97.2	A
pB27_A-8	5p/3p	Drosophila melanogaster - Rgl	2538..3259 X	IF		99.8	96.9	A
pB27_A-166	5p/3p	Drosophila melanogaster - Rgl	2580..3711 X	IF		95.8	98.9	A
pB27_A-18	5p/3p	Drosophila melanogaster - Rgl	2580..3711 X	IF		99.5	98.3	A
pB27_A-91	5p/3p	Drosophila melanogaster - Rgl	2580..3711 X	IF		99.9	91.3	A
pB27_A-147	5p/3p	Drosophila melanogaster - cno	-64..1418 X	IF		97.7	100.0	A
pB27_A-5	5p/3p	Drosophila melanogaster - cno	-25	IF		99.8	70.6	A
pB27_A-136	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		99.2	99.7	A
pB27_A-155	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		97.7	99.7	A
pB27_A-170	5p/3p	Drosophila melanogaster - cno	-25..1237	IF		97.6	99.7	A
pB27_A-13	5p	Drosophila melanogaster - cno	-25	IF		99.8		A
pB27_A-64	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		99.7	96.4	A
pB27_A-107	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		99.4	99.7	A
pB27_A-37	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		99.8	98.9	A
pB27_A-39	5p	Drosophila melanogaster - cno	-25	IF		98.4		A
pB27_A-25	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		99.8	99.5	A
pB27_A-65	5p/3p	Drosophila melanogaster - cno	-25..1163	IF		99.8	99.0	A
pB27_A-102	3p	Drosophila melanogaster - cno	..1258	??			99.7	A
pB27_A-158	5p/3p	Drosophila melanogaster - cno	288..1554	IF		98.4	100.0	A
pB27_A-138	5p/3p	Drosophila melanogaster - cno	318..1301	IF		93.8	99.4	A
pB27_A-118	5p/3p	Drosophila melanogaster - cno	318..1301	IF		98.5	99.5	A
pB27_A-113	5p/3p	Drosophila melanogaster - cno	366..1297	IF		96.8	99.7	A
pB27_A-24	5p/3p	Drosophila melanogaster - cno	411..1161	IF		99.8	97.7	A
pB27_A-149	5p/3p	Drosophila melanogaster - cno	414..1258	IF		98.0	99.7	A
pB27_A-157	5p/3p	Drosophila melanogaster - cno	414..1418	IF		98.1	100.0	A
pB27_A-103	5p/3p	Drosophila melanogaster - cno	414..1258	IF		96.8	99.7	A
pB27_A-85	5p/3p	Drosophila melanogaster - cno	414..1258	IF		99.8	96.4	A
pB27_A-112	5p/3p	Drosophila melanogaster - cno	414..1258	IF		97.6	99.7	A
pB27_A-134	5p/3p	Drosophila melanogaster - cno	420..1574	IF		98.0	100.0	A
pB27_A-116	5p/3p	Drosophila melanogaster - cno	420..1574	IF		97.0	100.0	A
pB27_A-62	5p/3p	Drosophila melanogaster - cno	420..1159	IF		99.8	99.4	A
pB27_A-163	5p/3p	Drosophila melanogaster - cno	429..1664	IF		97.8	99.7	A
pB27_A-3	5p/3p	Drosophila melanogaster - cno	429..1124	IF		99.8	98.3	A
pB27_A-87	5p	Drosophila melanogaster - cno	429	IF		99.8		A
pB27_A-125	5p/3p	Drosophila melanogaster - cno	429..1124	IF		98.5	99.4	A
pB27_A-49	5p/3p	Drosophila melanogaster - cno	429..1124	IF		99.8	99.3	A
pB27_A-31	5p/3p	Drosophila melanogaster - cno	429..1124	IF		98.6	99.3	A
pB27_A-61	5p/3p	Drosophila melanogaster - cno	429..1124	IF		99.8	99.5	A
pB27_A-55	5p/3p	Drosophila melanogaster - cno	445..1560	OOF1		97.9	99.1	A
pB27_A-95	5p	Drosophila melanogaster - cno	447	IF		99.8		A
pB27_A-137	5p/3p	Drosophila melanogaster - cno	459..1212	IF		99.0	99.7	A
pB27_A-22	5p/3p	Drosophila melanogaster - cno	465..1333	IF		99.2	99.0	A
pB27_A-28	5p/3p	Drosophila melanogaster - cno	465..1333	IF		99.8	99.0	A
pB27_A-82	5p/3p	Drosophila melanogaster - cno	465..1333	IF		99.8	98.9	A

Clone Name	Type Seq	Gene Name (Best Match)	Start..Stop (nt)	Frame	Sense	%Id 5p	%Id 3p	PBS
pB27_A-67	5p/3p	Drosophila melanogaster - cno	465..1333	IF		99.8	97.5	A
pB27_A-83	5p	Drosophila melanogaster - cno	471	IF		99.5		A
pB27_A-123	5p/3p	Drosophila melanogaster - cno	471..1541	IF		98.7	100.0	A
pB27_A-76	5p	Drosophila melanogaster - cno	471	IF		99.8		A
pB27_A-70	5p/3p	Drosophila melanogaster - cno	471..1541	IF		99.8	98.9	A
pB27_A-97	5p/3p	Drosophila melanogaster - cno	585..1297	IF		98.4	99.7	A
pB27_A-11	5p/3p	Drosophila melanogaster - cno	588..1554	IF		99.7	100.0	A
pB27_A-90	5p/3p	Drosophila melanogaster - cno	606..1156	IF		99.8	98.8	A
pB27_A-153	5p/3p	Drosophila melanogaster - cno	612..1154	IF		97.3	99.5	A
pB27_A-10	5p/3p	Drosophila melanogaster - cno	612..1154	IF		99.5	99.5	A
pB27_A-109	5p/3p	Drosophila melanogaster - cno	612..1154	IF		99.5	99.4	A
pB27_A-69	5p/3p	Drosophila melanogaster - cno	612..1154	IF		99.8	98.8	A
pB27_A-133	5p/3p	Drosophila melanogaster - cno	657..1296	IF		98.9	99.7	A
pB27_A-100	5p/3p	Drosophila melanogaster - cno	675..1503	IF		98.9	100.0	A
pB27_A-114	5p/3p	Drosophila melanogaster - eIF2B-epsilon	-23..490	OOF2		79.0	93.4	N/A
pB27_A-168	5p/3p	Drosophila melanogaster - loco	40..1247	OOF1		80.6	81.5	A
pB27_A-68	5p/3p	Drosophila melanogaster - loco	141..1247	IF		96.7	85.7	A
pB27_A-7	5p/3p	Drosophila melanogaster - loco	396..1818	X	IF	99.5	94.0	A
pB27_A-160	5p/3p	Drosophila melanogaster - loco	396..1818	X	IF	97.6	94.0	A
pB27_A-106	5p/3p	Drosophila melanogaster - loco	447..1172	IF		97.7	98.9	A
pB27_A-140	5p/3p	Drosophila melanogaster - loco	447..1172	IF		98.2	98.9	A
pB27_A-74	5p/3p	Drosophila melanogaster - loco	450..1163	IF		99.3	98.2	A
pB27_A-50	5p/3p	Drosophila melanogaster - loco	450..1163	IF		99.3	95.5	A
pB27_A-6	5p/3p	Drosophila melanogaster - loco	855..1785	X	IF	99.0	99.5	A
pB27_A-141	5p/3p	Drosophila melanogaster - loco	855..1785	X	IF	94.9	99.4	A
pB27_A-35	5p/3p	Drosophila melanogaster - No Match	-1..429 [NR]	X	IF	100.0	75.6	N/A
pB27_A-15	5p/3p	Drosophila melanogaster - prd	120..1086	IF		97.9	98.6	F
pB27_A-72	5p/3p	Drosophila melanogaster - prd	120..1086	IF		98.1	93.1	F
pB27_A-150	5p/3p	Drosophila melanogaster - qua	-1..865	IF		100.0	100.0	D
pB27_A-26	5p/3p	Drosophila melanogaster - qua	-1..853	IF		99.8	100.0	D
pB27_A-34	5p	Drosophila melanogaster - qua	-1	IF		99.8		D
pB27_A-59	5p	Drosophila melanogaster - qua	-1	IF		100.0		D
pB27_A-110	5p/3p	Drosophila melanogaster - qua	-1..853	IF		97.5	100.0	D
pB27_A-121	5p/3p	Drosophila melanogaster - qua	-1..853	IF		97.4	100.0	D
pB27_A-128	5p/3p	Drosophila melanogaster - qua	-1..853	IF		96.9	100.0	D
pB27_A-130	5p/3p	Drosophila melanogaster - qua	-1..853	IF		98.2	100.0	D
pB27_A-169	5p/3p	Drosophila melanogaster - qua	-1..853	IF		96.0	100.0	D
pB27_A-94	5p/3p	Drosophila melanogaster - qua	-1..853	IF		99.5	99.2	D

DomSight: DME_RP_hgx256v1 vs. Drosophila Whole Embryo_RP1 (0-12+ 12-24) (18 Apr 2019)
 (Bait plasmid(s): hgx256v1_pB27, hgx256v1_pB66)

Legend

- Bait fragment
- SID fragment
- Pfam or SMART domain
- Transmembrane domain (TMHMM)
- Coiled-coil domain (Ncolic)
- Signal peptide (SignalP)
- SID: Selected Interaction Domain**
 It is the amino acid sequence shared by all prey fragments matching the same reference protein. SIDs have been found in numerous cases to correspond to an identified structural or functional domain. GenMatch/NoMatch SIDs are shortened at the first in-frame stop codon. **Protein Display:** Proteins larger than 1500 aa are shown in sections of 1499 aa each. Only sections containing bait fragments, SIDs or predicted functional and structural domains are represented.



EXAMPLE OUTPUT FILE

Thu, Mar 29, 2018 - 05:50 PM HYBRIGENICS CONFIDENTIAL Program = DME_RP Screen = hgx256v1 Vector = pB27 (N-LexA-bait-C fusion)
Drosophila melanogaster - Ras (1-164) vs Drosophila Whole Embryo_RP1 (0-12+12-24)

Clone Name	Type Seq	Contig(s) Name	Gene Name (Best Match)	GiD	Global PBS	Additional Gene Notes	Start	Stop	Frame	Sense	UTR inclusion	% Id 5p/3p	Raw experimental 5p sequence	Post linker extraction 5p sequence	Raw Experimental 3p Ssequence	Post linker extraction 3p sequence
DME_RP_hgx256v1_pB27_A-27	5p 3p	6.3E+07	Droso - CG8965	FBgn0031745	A	CG8965; [CG8965-R	3	591	IF	Sense		99.5 / 98.6	TGGATGAGTG	GCTGAAGCA	TTTCANGTAT	CNTCAACGAG
DME_RP_hgx256v1_pB27_A-60	5p 3p	6.3E+07	Droso - CG8965	FBgn0031745	A	CG8965; [CG8965-R	3	591	IF	Sense		99.5 / 98.9	TGGATANTGN	GCTGAAGCA	TTTCANGCAT	GCCNACAATC
DME_RP_hgx256v1_pB27_A-99	5p 3p	6.3E+07	Droso - PI3K	GiD: 442620112	A	PI3K; [gij442620112]	-22	939	IF	Sense		96.2 / 100.0	TGGATATGAT	CGAACTTGAA	TTTCANGATC	GCTCTACGAG
DME_RP_hgx256v1_pB27_A-40	5p 3p	6.3E+07	Droso - PI3K	GiD: 442620112	A	PI3K; [gij442620112]	72	942	IF	Sense		99.8 / 99.8	TGGATATGNA	AGCGGAGCC	TTTCANGATC	CGGGCTGTAT
DME_RP_hgx256v1_pB27_A-164	5p 3p	6.3E+07	Droso - Raf kinase	FBgn0003079	B	Raf Kinase; [gij44261	418	789	OOF1	Sense		97.7 / 100.0	TGGATNNTGA	CACTATNAA	TTTCANGTAT	CAGCAACAAC
DME_RP_hgx256v1_pB27_A-104	5p 3p	6.3E+07	Droso - Raf kinase	FBgn0003079	B	Raf Kinase; [gij44261	510	1045	IF	Sense		98.3 / 99.7	TGGANANTGA	GCCGGGAC	TTTCANGTNT	CAACTCATTC
DME_RP_hgx256v1_pB27_A-86	5p	6.3E+07	Droso - Raf kinase	FBgn0003079	B	Raf Kinase; [gij44261	549	No Data	IF	Sense		99.7	TGGATGATGN	IGATCCTTTG		
DME_RP_hgx256v1_pB27_A-146	5p 3p	6.3E+07	Droso - BtbVII	GiD: 442629889	F	BtbVII; [gij442629889	1155	1954	IF	Sense		97.8 / 100.0	TGGANAGTGA	CTCGCNCTC	TTTCANGTAT	AGCGGGCAA

Global PBS: The PBS score is a computed technical parameter that gives the level of confidence one can have in the detected interaction. It varies from A to F.

A : very high confidence in the interaction

B : high confidence in the interaction

C : good confidence in the interaction

D : moderate confidence in the interaction identified through one unique prey fragment (singleton).

This category is the hardest to interpret because it mixes two classes of interactions:

(-) False-positive interactions (background noise): one singleton fragment has been selected by chance by the bait (non-specific because not interaction-dependent)

(-) Interactions hardly detectable by the two-hybrid technique because of the low representation of the mRNA in the library, bait or prey conformation, prey toxicity in yeast..

E : These interactions involve at least one interacting domain that is highly connected in our database, and therefore represents a potential false positive.

F : Experimentally proven technical artifacts

N/A : Non Applicable. The PBS is a score that is automatically computed through [algorithms](#) and cannot be attributed for the following reasons :

(-) All the fragments of the same reference CDS are antisense (see "Orientation" below)

(-) A singleton fragment is Out Of Frame (OOF1 or OOF2)

(-) The 5p sequence is missing

(-) All the fragments of the same reference CDS are either OOF1 or OOF2

(-) All the fragments of the same reference CDS lie in the **5p or 3p** UTR (Untranslated Region)

Start: Indicates the position of the 5p end of the prey fragment, relatively to the position of the start codon (in nucleotides)

Stop: Indicates the position of the 3p end of the prey fragment, relatively to the position of the start codon (in nucleotides)

Frame: With regard to the theoretical frame of the corresponding CDS (GeneBank), fragments are cloned in frame (IF) if they are in the same frame as the other polypeptidic moiety, Gal4 Activation Domain.

In general, polypeptides synthesized from OOF fragment are not considered of biological interest, unless found together with another frame. Indeed, some of the proteins expressed from an OOF fragment can be translated in the correct frame, due to the existence of natural frame-shift events during translation in yeast

Orientation: Antisense fragments correspond to DNA sequences from the opposite strand of a CDS and are therefore artefacts

UTR Inclusion: indicates if the prey found is fully in the 5p or 3p untranslated region (UTR)

% Id 5p/3p: Indicates the % identity of the prey sequences with the GenBank sequences. A sequence with a low identity score indicates a bad sequence or a low homology with the reference CDS (e.g. an alternative splice variant of the reference CDS)

Raw experimental 5p/3p sequence: Prey fragment, experimental sequences containing part of the vector

Post linker extraction 5p/3p sequence: Prey fragment, experimental sequences corresponding to insert sequence

Frag theoretical Sequence: This sequence shows the whole theoretical fragment sequence as deduced from GenBank data, according to the relative positions of the prey fragment (see "Start" and "Stop" above)