

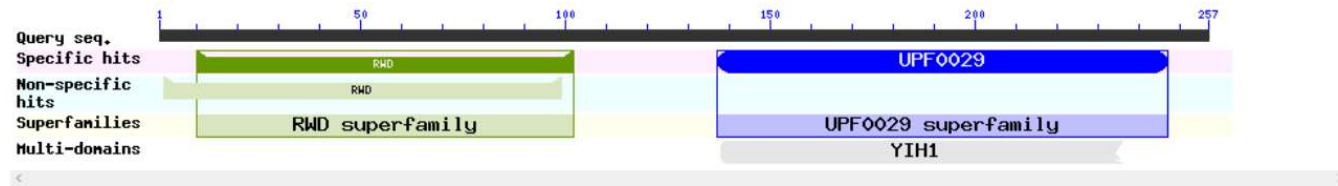
a

Range 1: 6 to 293 [GenPept](#) [Graphics](#)

▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps
167 bits(422)	7e-55	Compositional matrix adjust.	95/291(33%)	150/291(51%)	42/291(14%)
Query 1	MSDEEQRIAEIESLASIFPDLLLEETTDKQLVFKF-----DRDIGMTINLPEDYPSI				51
	+ + +++ EIE++A+I+ + + +F + + + LP +YP				
Sbjct 6	VGNSQRQSEEIEAMAAIYGEEWCVIDENAKIFCIRVTDFMDDPKWTLCLQVMLPSEYPGT				65
Query 52	SPPIFELSGPYLRREQEVLHNSLNDVYIENIGFPVIFNWISLVQDFIRDLP EEVAEP--				109
	+PP ++L+ P+L+ +++ L NSL ++Y+ N+G +++ W+ ++D + ++ EP				
Sbjct 66	APPSYQLNAPWLKQGERADLSNSLEEIYVHNMGESILYQWVEKIRDALIQ-KSQITEPDP				124
Query 110	-----SHVADDVVTPMAEEIDDMN-----IRHGEVLTDRKSA				141
	H ++ V + +I + + HG +TDR+S				
Sbjct 125	DVKKKTEEVEVESEEDPILEHPPENPVKTLDLKISEETQPETEELPPVAHGVPITDRRST				184
Query 142	FQAHLAEVRSKEDVDRVMRILKSNTKICRATHNITAYRYMTEINGKPIHHHDCVDDGEFG				201
	FQAH+A V E V V+ L N KI ATHNI AYR E K DC DDGE				
Sbjct 185	FQAHVAPVVCPEQVKLVLAKLYENKKIASATHNIYAYRIFCE--DKQTFLQDCEDDGETA				242
Query 202	ASSKMLELMDRMKADNMVVVSRWYGGIHLGPDRFRHINNLTROILSDNNY				252
	A ++L LM+ + NVMVVVSRWYGGI LGPDRF+HINN R IL + N+				
Sbjct 243	AGGRLHLHMEILNVKNMVVVSRWYGGILLGPDRFKHINNCARNILVEKNF				293

b



Name	Accession	Description	Interval	E-value
[+] UPF0029	pfam01205	Uncharacterized protein family UPF0029;	137-247	6.42e-36
[+] RWD	smart00591	domain in RING finger and WD repeat containing proteins and DEXDc-like helicases subfamily ...	10-102	7.62e-21
[+] RWD	pfam05773	RWD domain; This domain was identified in WD40 repeat proteins and Ring finger domain proteins. ...	2-99	7.88e-18
[+] YIH1	COG1739	Putative translation regulator, IMPACT (imprinted ancient) protein family [General function ...	138-236	2.08e-07