

A

19	EQARTESQAEPLNAQVN	36	Site Y32 = SH2-domain binding motif (SH2)
39	PREHRAQSSEETIYAPQN	56	
59	ETIYAEQKPLGNFDRLG	76	
79	PRNGRRAEKLVDPIAVTD	96	
101	DRGADFQTLNPLIEGVG	118	Site Y114 = PTB-domain binding motif (PTB)
121	AHGGPHPQEPHEHIAELE	138	
142	QSGRSFQKPFVESVAVTG	159	
163	EGGQDTQTLKNPLIEGVG	180	Site Y176 = PTB-domain binding motif (PTB)
199	EQARRAESQAEPLNAQVN	216	Site Y211 = SH2-domain binding motif (SH2)
218	PREHRAQSSEETIYAPQN	235	
238	ETIYAEQKPLGNFDRLG	255	
258	PRNGRRAEKLVDPIAVTD	275	
280	DRGADFQTLNPLIEGVG	297	Site Y293 = PTB-domain binding motif (PTB)
300	AHGGPHPQEPHEHIAELE	317	
321	QSGRSFQKPFVESVAVTG	338	
342	EGGQDTQTLKNPLIEGVG	359	Site Y355 = PTB-domain binding motif (PTB)

Consensus ergrrrqkpleplYAvvg

B

11	THSTEKQREPLTQSQS	24	
27	RAPSPQEPPLIYATV	40	Site Y37 = SH2-domain binding motif (SH2)
54	KPLSQQEEVVAAL	67	
81	PERNLESETIYTTV	94	Site Y91 = SH2-domain binding motif (SH2)
96	SQSTIQAEILVADV	109	
119	TRRDPASETIYAEV	132	

Consensus testpqsEtIYAtv

C

104	QSSQSTPLYATPLPQQ	120	
140	TAPODSTPLYATPSFQQ	156	Site Y149 = SH2-domain binding motif (SH2)
176	AAEQDSTPLYATPSFHK	192	Site Y185 = SH2-domain binding motif (SH2)
204	TSSQDSEPLYATPLPQR	220	Site Y213 = SH2-domain binding motif (SH2)
232	TSNQDSEPLYATPLPQR	248	Site Y241 = SH2-domain binding motif (SH2)
260	TSSQDSEPLYATPLPQR	276	Site Y269 = SH2-domain binding motif (SH2)
288	TSSQDNEPLYATPAFQQ	304	

Consensus tssqdstPLYATpLpqq