Supplemental Data
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Development and Validation of a Computational Method for Assessment of Missense Variants in Hypertrophic Cardiomyopathy

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Table S1. The 74 Gold Standard Variants

This table shows the 74 HCM variants we used as our gold standard.

Gene	NCBI mRNA accession	NCBI protein accession	cDNA change	Amino acid change	Classification
MYBPC3	NM_000256.3	NP_000247.2	c.440C>T	p.Pro147Leu	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.472G>A	p.Val158Met	Benign
MYBPC3	NM_000256.3	NP_000247.2	c.565G>A	p.Val189Ile	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.706A>G	p.Ser236Gly	Benign
MYBPC3	NM_000256.3	NP_000247.2	c.772G>A	p.Glu258Lys	Pathogenic
MYBPC3	NM_000256.3	NP_000247.2	c.833G>A	p.Gly278Glu	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.842G>A	p.Arg281Gln	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.977G>A	p.Arg326Gln	Benign
MYBPC3	NM_000256.3	NP_000247.2	c.1144C>T	p.Arg382Trp	Benign
MYBPC3	NM_000256.3	NP_000247.2	c.1147C>G	p.Leu383Val	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.1246G>A	p.Gly416Ser	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.1351G>C	p.Glu451Gln	Pathogenic
MYBPC3	NM_000256.3	NP_000247.2	c.1484G>A	p.Arg495Gln	Pathogenic
MYBPC3	NM_000256.3	NP_000247.2	c.1505G>A	p.Arg502Gln	Pathogenic
MYBPC3	NM_000256.3	NP_000247.2	c.1504C>T	p.Arg502Trp	Pathogenic
MYBPC3	NM_000256.3	NP_000247.2	c.1519G>A	p.Gly507Arg	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.1564G>A	p.Ala522Thr	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.1633C>A	p.Leu545Met	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.2063C>A	p.Thr688Lys	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.2265C>A	p.Asn755Lys	Pathogenic
MYBPC3	NM_000256.3	NP_000247.2	c.2410C>A	p.Leu804Met	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.2498C>T	p.Ala833Val	Benign
MYBPC3	NM_000256.3	NP_000247.2	c.2686G>A	p.Val896Met	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.3004C>T	p.Arg1002Trp	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.3142C>T	p.Arg1048Cys	Likely Benign
MYBPC3	NM_000256.3	NP_000247.2	c.3413G>A	p.Arg1138His	Likely Benign
MYH7	NM_000257.2	NP_000248.2	c.8A>C	p.Asp3Ala	Likely Benign
MYH7	NM_000257.2	NP_000248.2	c.321T>G	p.Asp107Glu	Likely Benign
MYH7	NM_000257.2	NP_000248.2	c.438G>T	p.Lys146Asn	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.767G>A	p.Gly256Glu	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.1208G>A	p.Arg403Gln	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.1207C>T	p.Arg403Trp	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.1357C>T	p.Arg453Cys	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.1750G>C	p.Gly584Arg	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.1816G>A	p.Val606Met	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.1988G>A	p.Arg663His	Pathogenic

MYH7	NM_000257.2	NP_000248.2	c.2146G>A	p.Gly716Arg	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2156G>A	p.Arg719Gln	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2155C>T	p.Arg719Trp	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2167C>T	p.Arg723Cys	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2167C>G	p.Arg723Gly	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2221G>T	p.Gly741Trp	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2389G>A	p.Ala797Thr	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2609G>A	p.Arg870His	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2717A>G	p.Asp906Gly	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2722C>G	p.Leu908Val	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2770G>A	p.Glu924Lys	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.2788G>A	p.Glu930Lys	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.3981C>A	p.Asn1327Lys	Likely Benign
MYH7	NM_000257.2	NP_000248.2	c.4135G>A	p.Ala1379Thr	Pathogenic
MYH7	NM_000257.2	NP_000248.2	c.4472C>G	p.Ser1491Cys	Benign
MYH7	NM_000257.2	NP_000248.2	c.4555A>T	p.Ser1519Cys	Likely Benign
MYL2	NM_000432.3	NP_000423.2	c.64G>A	p.Glu22Lys	Pathogenic
MYL2	NM_000432.3	NP_000423.2	c.173G>A	p.Arg58Gln	Pathogenic
TNNI3	NM_000363.4	NP_000354.4	c.235C>T	p.Arg79Cys	Likely Benign
TNNI3	NM_000363.4	NP_000354.4	c.244C>T	p.Pro82Ser	Likely Benign
TNNI3	NM_000363.4	NP_000354.4	c.244C>A	p.Pro82Thr	Likely Benign
TNNI3	NM_000363.4	NP_000354.4	c.253T>A	p.Leu85Met	Likely Benign
TNNI3	NM_000363.4	NP_000354.4	c.257C>A	p.Ala86Asp	Likely Benign
TNNI3	NM_000363.4	NP_000354.4	c.433C>G	p.Arg145Gly	Pathogenic
TNNI3	NM_000363.4	NP_000354.4	c.433C>T	p.Arg145Trp	Pathogenic
TNNI3	NM_000363.4	NP_000354.4	c.470C>T	p.Ala157Val	Pathogenic
TNNI3	NM_000363.4	NP_000354.4	c.485G>A	p.Arg162Gln	Pathogenic
TNNI3	NM_000363.4	NP_000354.4	c.557G>A	p.Arg186Gln	Pathogenic
TNNI3	NM_000363.4	NP_000354.4	c.575G>A	p.Arg192His	Pathogenic
TNNT2	NM_001001430.1	NP_001001430.1	c.236T>A	p.Ile79Asn	Pathogenic
TNNT2	NM_001001430.1	NP_001001430.1	c.275G>A	p.Arg92Gln	Pathogenic
TNNT2	NM_001001430.1	NP_001001430.1	c.274C>T	p.Arg92Trp	Pathogenic
TNNT2	NM_001001430.1	NP_001001430.1	c.421C>T	p.Arg141Trp	Pathogenic
TNNT2	NM_001001430.1	NP_001001430.1	c.682C>G	p.Gln228Glu	Likely Benign
TNNT2	NM_001001430.1	NP_001001430.1	c.758A>G	p.Lys253Arg	Benign
TNNT2	NM_001001430.1	NP_001001430.1	c.805A>T	p.Asn269Tyr	Likely Benign
TPM1	NM_000366.5	NP_000357.3	c.523G>A	p.Asp175Asn	Pathogenic
TPM1	NM_000366.5	NP_000357.3	c.688G>A	p.Asp230Asn	Pathogenic

Table S2. The Four Classification Scores

This table shows the 74 gold standard variants with the four scores described in the text.

Protien variant	Classification	PolyPhen score	MrBayes score	COILS score	Structure score
NP_000247.2:p.Pro147Leu	Likely Benign	0.364	1.773516		
NP_000247.2:p.Val158Met	Benign	0.038	1.831546		
NP_000247.2:p.Val189Ile	Likely Benign	0.206	1.162951		
NP_000247.2:p.Ser236Gly	Benign	0.001	1.430759		
NP_000247.2: p.Glu258Lys	Pathogenic	0.196	1.118029		
NP_000247.2:p.Gly278Glu	Likely Benign	0.66	1.212166		
NP_000247.2:p.Arg281Gln	Likely Benign	0.049	1.654965		
NP_000247.2:p.Arg326Gln	Benign	0.054	0.827841		
NP_000247.2:p.Arg382Trp	Benign	0.894	1.103284		
NP_000247.2:p.Leu383Val	Likely Benign	0.562	0.590754		
NP_000247.2:p.Gly416Ser	Likely Benign	0.989	0.186616		
NP_000247.2:p.Glu451Gln	Pathogenic	0.935	0.190564		
NP_000247.2:p.Arg495Gln	Pathogenic	0.994	0.187814		
NP_000247.2:p.Arg502Gln	Pathogenic	0.994	0.187814		
NP_000247.2:p.Arg502Trp	Pathogenic	0.997	0.187814		
NP_000247.2:p.Gly507Arg	Likely Benign	0.994	0.186616		
NP_000247.2:p.Ala522Thr	Likely Benign	0.006	2.367328		
NP_000247.2:p.Leu545Met	Likely Benign	0.919	0.1892		
NP_000247.2:p.Thr688Lys	Likely Benign	0.008	2.221069		
NP_000247.2:p.Asn755Lys	Pathogenic	0.997	0.185634		
NP_000247.2:p.Leu804Met	Likely Benign	0.207	0.826993		
NP_000247.2:p.Ala833Val	Benign	0.424	0.60121		
NP_000247.2:p.Val896Met	Likely Benign	0.004	1.020041		
NP_000247.2:p.Arg1002Trp	Likely Benign	0.998	0.187814		
NP_000247.2:p.Arg1048Cys	Likely Benign	0.791	1.075026		
NP_000247.2:p.Arg1138His	Likely Benign	0.993	0.187856		
NP_000248.2:p.Asp3Ala	Likely Benign	0.985	0.40412		
NP_000248.2:p.Asp107Glu	Likely Benign	0.011	0.817473		0.723684666666667
NP_000248.2:p.Lys146Asn	Pathogenic	0.578	0.349745		0.607340166666667

NP_000248.2:p.Gly256Glu	Pathogenic	0.999	0.064077		0.805175055555556
NP_000248.2:p.Arg403Gln	Pathogenic	0.99	0.232634		0.636061055555556
NP_000248.2:p.Arg403Trp	Pathogenic	0.999	0.232634		0.636061055555556
NP_000248.2:p.Arg453Cys	Pathogenic	0.999	0.259414		0.652296277777778
NP_000248.2:p.Gly584Arg	Pathogenic	0.998	0.064077		0.668971
NP_000248.2:p.Val606Met	Pathogenic	0.959	0.578037		0.703636944444445
NP_000248.2:p.Arg663His	Pathogenic	0.434	0.658202		0.768424666666667
NP_000248.2:p.Gly716Arg	Pathogenic	0.996	1.240913		0.886859833333333
NP_000248.2:p.Arg719Gln	Pathogenic	0.383	0.251198		0.919598
NP_000248.2:p.Arg719Trp	Pathogenic	0.888	0.251198		0.919598
NP_000248.2:p.Arg723Cys	Pathogenic	1	0.675437		0.926584944444444
NP_000248.2:p.Arg723Gly	Pathogenic	0.999	0.675437		0.926584944444444
NP_000248.2:p.Gly741Trp	Pathogenic	0.612	0.462298		0.934061166666667
NP_000248.2:p.Ala797Thr	Pathogenic	0.02	0.842704		0.891727611111111
NP_000248.2:p.Arg870His	Pathogenic	0.531	0.450972	0.049	
NP_000248.2:p.Asp906Gly	Pathogenic	0.465	0.922319	0.188	
NP_000248.2:p.Leu908Val	Pathogenic	0.917	0.13996	0.124	
NP_000248.2:p.Glu924Lys	Pathogenic	0.96	0.267061	0.042	
NP_000248.2:p.Glu930Lys	Pathogenic	0.96	0.065827	0.078	
NP_000248.2:p.Asn1327Lys	Likely Benign	0.373	0.570145	0.02	
NP_000248.2:p.Ala1379Thr	Pathogenic	0.153	0.268716	0.125	
NP_000248.2:p.Ser1491Cys	Benign	0.001	2.133482	0.003	
NP_000248.2:p.Ser1519Cys	Likely Benign	0.218	2.130523	0.002	
NP_000423.2:p.Glu22Lys	Pathogenic	0.381			0.639643
NP_000423.2:p.Arg58Gln	Pathogenic	0.47			0.703765333333333
NP_000354.4:p.Arg79Cys	Likely Benign	0.874	1.560826		0.590948
NP_000354.4:p.Pro82Ser	Likely Benign	0.995	0.214355		0.519521
NP_000354.4:p.Pro82Thr	Likely Benign	0.995	0.214355		0.519521
NP_000354.4:p.Leu85Met	Likely Benign	0.373	0.679624		0.603625
NP_000354.4:p.Ala86Asp	Likely Benign	0.198	0.973472		0.597456
NP_000354.4:p.Arg145Gly	Pathogenic	0.954	0.63085		0.84635
NP_000354.4:p.Arg145Trp	Pathogenic	0.971	0.63085		0.84635

NP_000354.4:p.Ala157Val	Pathogenic	0.887	0.399959		
NP_000354.4:p.Arg162Gln	Pathogenic	0.421	0.645396		
NP_000354.4:p.Arg186Gln	Pathogenic	0.794	0.465974		
NP_000354.4:p.Arg192His	Pathogenic	0.984	0.247463		
NP_001001430.1:p.Ile79Asn	Pathogenic	0.985	0.151537		
NP_001001430.1:p.Arg92Gln	Pathogenic	0.982	0.09613	0.091	
NP_001001430.1:p.Arg92Trp	Pathogenic	0.997	0.09613	0.201	
NP_001001430.1:p.Arg141Trp	Pathogenic	0.995	0.043148	0.232	
NP_001001430.1:p.Gln228Glu	Likely Benign	0.024	0.319379		0.7008
NP_001001430.1:p.Lys253Arg	Benign	0.009	0.497708		0.612637
NP_001001430.1:p.Asn269Tyr	Likely Benign	0.599	0.507608		0.672594
NP_000357.3:p.Asp175Asn	Pathogenic	0.896	0.354401	0.031	
NP_000357.3:p.Asp230Asn	Pathogenic	0.832	0.386874	0.038	

Table S3. List of Sequences in the MYH7 Alignment

This table shows the 68 sequences chosen for the MYH7 alignment and the UniProt or UniParc accessions used to refer to them in figure S2, ordered by sequence similarity to human MYH7. “MyH” in the description column indicates myosin heavy chain.

	Accession	Species	Description
1	P12883	Homo sapiens (human)	beta cardiac MyH
2	UPI0000D9BB5C	Macaca mulatta (Rhesus macaque)	alpha cardiac MyH
3	Q91973	Coturnix coturnix (quail)	slow muscle MyH
4	Q910C5	Gallus gallus (chicken)	chick atrial MyH
5	Q5EC16	Xenopus laevis (African clawed frog)	alpha cardiac MyH
6	UPI00015A4B13	Danio rerio (zebrafish)	slow muscle MyH
7	UPI00015A67FC	Danio rerio (zebrafish)	hypothetical protein
8	B6IDE0	Danio rerio (zebrafish)	slow muscle MyH
9	UPI00016278FC	Danio rerio (zebrafish)	ventricular MyH
10	B6IDE1	Danio rerio (zebrafish)	slow MyH
11	Q2HX56	Cyprinus carpio (common carp)	embryonic muscle MyH
12	B8JLS3	Danio rerio (zebrafish)	alpha cardiac MyH
13	UPI0000EB3EAF	Canis lupus (dog)	adult skeletal muscle MyH
14	UPI0000DA357F	Rattus norvegicus (rat)	perinatal skeletal muscle MyH
15	Q6DIX8	Xenopus tropicalis (Western clawed frog)	adult skeletal muscle MyH
16	Q4T2B5	Tetraodon nigroviridis	hypothetical protein
17	Q6DFQ6	Xenopus tropicalis (Western clawed frog)	extrocular skeletal muscle MyH
18	B4F6Y1	Xenopus tropicalis (Western clawed frog)	hypothetical protein
19	UPI00006A2578	Xenopus tropicalis (Western clawed frog)	extraocular skeletal muscle MyH
20	A6QPA6	Bos taurus (cattle)	embryonic skeletal muscle MyH
21	Q076A8	Canis lupus (dog)	embryonic skeletal muscle MyH
22	UPI0000D9E164	Macaca mulatta (Rhesus macaque)	embryonic skeletal muscle MyH
23	Q75UE1	Lampetra japonica (lamprey)	unspecified MyH
24	UPI0000E81268	Gallus gallus (chicken)	extraocular skeletal muscle MyH

	Accession	Species	Description
25	Q90339	Cyprinus carpio (common carp)	fast muscle MyH
26	Q6NX33	Xenopus tropicalis (Western clawed frog)	unspecified MyH
27	UPI0000D9E163	Macaca mulatta (Rhesus macaque)	embryonic skeletal muscle MyH
28	A8R0Q4	Hypophthalmichthys molitrix (silver carp)	fast muscle MyH
29	UPI00015A3FB7	Danio rerio (zebrafish)	fast muscle MyH
30	UPI0001761474	Danio rerio (zebrafish)	fast muscle MyH
31	B1AR69	Mus musculus (mouse)	extraocular skeletal muscle MyH
32	UPI00015A3FF2	Danio rerio (zebrafish)	skeletal muscle MyH
33	UPI0000D9E161	Macaca mulatta (Rhesus macaque)	extraocular skeletal muscle MyH
34	Q9GJP9	Oryctolagus cuniculus (rabbit)	extraocular skeletal muscle MyH
35	UPI0000DA3582	Rattus norvegicus (rat)	extraocular skeletal muscle MyH
36	B8A569	Danio rerio (zebrafish)	unspecified MyH
37	Q05K05	Oryzias latipes (Japanese rice fish)	smooth muscle MyH
38	UPI00015A7E7F	Danio rerio (zebrafish)	fast muscle MyH
39	Q9UKX3	Homo sapiens (human)	extraocular skeletal muscle MyH
40	Q508P7	Danio rerio (zebrafish)	fast muscle MyH
41	B8A561	Danio rerio (zebrafish)	unspecified MyH
42	UPI000175F75C	Danio rerio (zebrafish)	skeletal muscle MyH
43	O42352	Cyprinus carpio (common carp)	unspecified MyH
44	UPI00015A7E8A	Danio rerio (zebrafish)	fast muscle MyH
45	Q2HX58	Cyprinus carpio (common carp)	embryonic muscle MyH
46	A4GWV4	Siniperca kneri (Chinese perch)	skeletal muscle MyH
47	UPI0000EBDD42	Bos taurus (cattle)	extraocular skeletal muscle MyH
48	UPI0000DA33E7	Rattus norvegicus (rat)	extraocular skeletal muscle MyH

	Accession	Species	Description
49	Q6SNT2	Siniperca chuatsi (Chinese perch)	fast muscle MyH
50	Q05K10	Oryzias latipes (Japanese rice fish)	fast muscle MyH
51	Q90YF6	Paracirrhites forsteri (freckled hawkfish)	unspecified MyH
52	UPI0001796E5B	Equus caballus (horse)	extraocular skeletal muscle MyH
53	Q90337	Cyprinus carpio (common carp)	unspecified MyH
54	Q5NTZ3	Cyprinus carpio (common carp)	unspecified MyH
55	Q05K07	Oryzias latipes (Japanese rice fish)	fast muscle MyH
56	Q98TQ4	Notothenia coriiceps (black rockcod)	unspecified MyH
57	Q05K11	Oryzias latipes (Japanese rice fish)	fast muscle MyH
58	A4PDX4	Saurida undosquamis (brushtooth lizardfish)	fast muscle MyH
59	Q9DGD5	Pennahia argentata (silver croaker)	unspecified MyH
60	B2Z9Y7	Xenopus laevis (African clawed frog)	laryngeal skeletal muscle MyH
61	A8R0Q7	Hypophthalmichthys molitrix (silver carp)	fast muscle MyH
62	Q98TQ6	Notothenia coriiceps (black rockcod)	unspecified MyH
63	Q8JIP5	Oncorhynchus keta (chum salmon)	unspecified MyH
64	UPI000180BC7B	Ciona intestinalis (sea squirt)	embryonic muscle MyH
65	Q25142	Halocynthia roretzi (sea pineapple)	embryonic muscle MyH
66	B2RFJ0	Oikopleura dioica	embryonic muscle MyH
67	UPI0000E47670	Strongylocentrotus purpuratus (sea urchin)	unspecified MyH
68	B1PS43	Homo sapiens (human)	smooth muscle MyH

Table S4. List of Sequences in the MYBPC3 Alignment

This table shows the 50 sequences chosen for the MYBPC3 alignment and the UniProt or UniParc accessions used to refer to them in figure S2, ordered by sequence similarity to human MYBPC3. “MyBP-C” in the description column indicates myosin binding protein C.

	Accession	Species	Description
1	A8MXZ9	Homo sapiens (human)	cardiac MyBP-C
2	Q2Q1P6	Canis lupus (dog)	cardiac MyBP-C
3	UPI0001796E3C	Equus caballus (horse)	cardiac MyBP-C
4	UPI0000EB1703	Canis lupus (dog)	cardiac MyBP-C
5	A2AGQ1	Mus musculus (mouse)	cardiac MyBP-C
6	B2FDF4	Mus musculus (mouse)	cardiac MyBP-C
7	A9JR55	Mus musculus (mouse)	cardiac MyBP-C
8	Q3UIK0	Mus musculus (mouse)	cardiac MyBP-C
9	Q0VD56	Bos taurus (cattle)	cardiac MyBP-C
10	UPI000179E0E8	Bos taurus (cattle)	cardiac MyBP-C
11	UPI0000DC0477	Rattus norvegicus (rat)	cardiac MyBP-C
12	UPI000154D9A3	Rattus norvegicus (rat)	cardiac MyBP-C
13	O70468	Mus musculus (mouse)	cardiac MyBP-C
14	UPI0000F2DAC3	Monodelphis domestica (opossum)	hypothetical protein
15	UPI0000ECB979	Gallus gallus (chicken)	cardiac MyBP-C
16	Q90688	Gallus gallus (chicken)	cardiac MyBP-C
17	UPI0000ECB97A	Gallus gallus (chicken)	cardiac MyBP-C
18	Q90688-2	Gallus gallus (chicken)	cardiac MyBP-C
19	B7ZS41	Xenopus laevis (African clawed frog)	hypothetical protein
20	Q6IP30	Xenopus laevis (African clawed frog)	hypothetical protein
21	UPI00006A19A0	Xenopus tropicalis (Western clawed frog)	cardiac MyBP-C
22	Q90X86	Xenopus laevis (African clawed frog)	cardiac MyBP-C
23	Q498L6	Xenopus laevis (African clawed frog)	hypothetical protein
24	UPI0001722DB9	Danio rerio (zebrafish)	cardiac MyBP-C

	Accession	Species	Description
25	A9JTS4	Xenopus tropicalis (Western clawed frog)	cardiac MyBP-C
26	UPI00015A7ACC	Danio rerio (zebrafish)	hypothetical protein
27	UPI00015A7ACB	Danio rerio (zebrafish)	hypothetical protein
28	Q4SI34	Tetraodon nigroviridis (pufferfish)	hypothetical protein
29	UPI00015A7ACA	Danio rerio (zebrafish)	hypothetical protein
30	Q0IJ38	Danio rerio (zebrafish)	fast MyBP-C
31	UPI00015A7A35	Danio rerio (zebrafish)	hypothetical protein
32	UPI00015A7A37	Danio rerio (zebrafish)	hypothetical protein
33	UPI0000D8BC93	Danio rerio (zebrafish)	hypothetical protein
34	P16419	Gallus gallus (chicken)	fast MyBP-C
35	Q4T9D9	Tetraodon nigroviridis (pufferfish)	hypothetical protein
36	Q5BJ14	Danio rerio (zebrafish)	fast MyBP-C
37	UPI00015A4C30	Danio rerio (zebrafish)	hypothetical protein
38	UPI00015A4C2E	Danio rerio (zebrafish)	hypothetical protein
39	UPI000059FDA5	Canis lupus (dog)	fast MyBP-C
40	UPI000059FDA7	Canis lupus (dog)	fast MyBP-C
41	UPI00015A4C4C	Danio rerio (zebrafish)	hypothetical protein
42	UPI00015A4C31	Danio rerio (zebrafish)	hypothetical protein
43	UPI0000EB459A	Canis lupus (dog)	fast MyBP-C
44	UPI000154F1E6	Rattus norvegicus (rat)	fast MyBP-C
45	A1L4G9	Homo sapiens (human)	fast MyBP-C
46	Q14324	Homo sapiens (human)	fast MyBP-C
47	UPI0000D617F3	Homo sapiens (human)	fast MyBP-C
48	Q5XKE0	Mus musculus (mouse)	fast MyBP-C

	Accession	Species	Description
49	UPI00015DF070	Mus musculus (mouse)	fast MyBP-C
50	UPI00006A07B4	Xenopus tropicalis (Western clawed frog)	fast MyBP-C

Table S5. Pairwise Distances between Sequences in the MYH7 Alignment

This table shows the pairwise alignment distances between sequences in the manual MYH7 alignment. Sequences are ordered and numbered as in table S2.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	1.00	0.93	0.89	0.88	0.88	0.87	0.86	0.86	0.86	0.86	0.85	0.83	0.82	0.81	0.80	0.80	0.80
2	0.93	1.00	0.90	0.90	0.89	0.86	0.86	0.86	0.86	0.86	0.85	0.83	0.81	0.81	0.82	0.80	0.80
3	0.89	0.90	1.00	0.98	0.86	0.83	0.83	0.83	0.83	0.84	0.83	0.81	0.79	0.79	0.79	0.79	0.78
4	0.88	0.90	0.98	1.00	0.86	0.83	0.83	0.83	0.83	0.84	0.83	0.81	0.79	0.79	0.79	0.79	0.78
5	0.88	0.89	0.86	0.86	1.00	0.85	0.86	0.85	0.85	0.85	0.84	0.83	0.79	0.79	0.80	0.80	0.79
6	0.87	0.86	0.83	0.83	0.85	1.00	0.90	0.97	0.90	0.93	0.92	0.83	0.80	0.80	0.80	0.80	0.80
7	0.86	0.86	0.83	0.83	0.86	0.90	1.00	0.90	1.00	0.89	0.88	0.83	0.80	0.79	0.80	0.80	0.80
8	0.86	0.86	0.83	0.83	0.85	0.97	0.90	1.00	0.90	0.95	0.92	0.83	0.80	0.80	0.80	0.80	0.80
9	0.86	0.86	0.83	0.83	0.85	0.90	1.00	0.90	1.00	0.89	0.87	0.83	0.79	0.79	0.79	0.80	0.80
10	0.86	0.86	0.84	0.84	0.85	0.93	0.89	0.95	0.89	1.00	0.95	0.84	0.79	0.79	0.80	0.80	0.80
11	0.85	0.85	0.83	0.83	0.84	0.92	0.88	0.92	0.87	0.95	1.00	0.83	0.80	0.79	0.80	0.80	0.80
12	0.83	0.83	0.81	0.81	0.83	0.83	0.83	0.83	0.83	0.84	0.83	1.00	0.77	0.77	0.78	0.84	0.78
13	0.82	0.81	0.79	0.79	0.79	0.80	0.80	0.80	0.79	0.79	0.80	0.77	1.00	0.94	0.88	0.74	0.84
14	0.81	0.81	0.79	0.79	0.79	0.80	0.79	0.80	0.79	0.79	0.79	0.77	0.94	1.00	0.87	0.74	0.84
15	0.80	0.82	0.79	0.79	0.80	0.80	0.80	0.80	0.79	0.80	0.80	0.78	0.88	0.87	1.00	0.75	0.86
16	0.80	0.80	0.79	0.79	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.84	0.74	0.74	0.75	1.00	0.77
17	0.80	0.80	0.78	0.78	0.79	0.80	0.80	0.80	0.80	0.80	0.80	0.78	0.84	0.84	0.86	0.77	1.00
18	0.80	0.81	0.78	0.78	0.80	0.80	0.79	0.80	0.79	0.80	0.80	0.78	0.86	0.86	0.90	0.75	0.86
19	0.80	0.80	0.78	0.78	0.79	0.80	0.80	0.79	0.80	0.79	0.80	0.77	0.83	0.83	0.85	0.76	0.99
20	0.79	0.80	0.78	0.78	0.78	0.79	0.78	0.79	0.78	0.78	0.79	0.76	0.85	0.85	0.83	0.74	0.83
21	0.79	0.80	0.78	0.78	0.78	0.79	0.78	0.79	0.78	0.79	0.79	0.76	0.86	0.85	0.84	0.74	0.83
22	0.79	0.80	0.78	0.78	0.78	0.79	0.78	0.79	0.78	0.78	0.79	0.76	0.86	0.85	0.83	0.73	0.83
23	0.79	0.79	0.78	0.77	0.79	0.78	0.78	0.78	0.78	0.79	0.79	0.77	0.79	0.78	0.81	0.76	0.80
24	0.79	0.79	0.77	0.77	0.78	0.78	0.78	0.78	0.78	0.79	0.79	0.77	0.84	0.84	0.85	0.74	0.83

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
25	0.79	0.79	0.76	0.76	0.77	0.79	0.78	0.79	0.78	0.80	0.79	0.76	0.83	0.82	0.84	0.74	0.83
26	0.78	0.80	0.77	0.77	0.79	0.79	0.79	0.78	0.78	0.79	0.79	0.77	0.83	0.82	0.84	0.75	0.91
27	0.78	0.79	0.77	0.76	0.77	0.78	0.77	0.78	0.77	0.77	0.78	0.75	0.84	0.84	0.82	0.73	0.82
28	0.78	0.78	0.76	0.76	0.77	0.79	0.78	0.79	0.78	0.79	0.79	0.76	0.83	0.82	0.83	0.73	0.82
29	0.78	0.78	0.76	0.76	0.77	0.79	0.78	0.79	0.78	0.79	0.79	0.76	0.83	0.82	0.84	0.74	0.83
30	0.78	0.78	0.76	0.76	0.77	0.79	0.78	0.79	0.78	0.79	0.79	0.76	0.83	0.82	0.84	0.74	0.83
31	0.78	0.78	0.76	0.76	0.77	0.77	0.77	0.76	0.77	0.77	0.77	0.75	0.83	0.83	0.82	0.73	0.82
32	0.78	0.78	0.76	0.76	0.77	0.79	0.78	0.79	0.78	0.79	0.79	0.76	0.83	0.82	0.84	0.74	0.83
33	0.78	0.78	0.76	0.76	0.77	0.76	0.77	0.76	0.77	0.76	0.77	0.75	0.82	0.83	0.82	0.72	0.81
34	0.78	0.78	0.76	0.76	0.77	0.76	0.77	0.76	0.77	0.76	0.77	0.75	0.83	0.83	0.82	0.73	0.82
35	0.78	0.78	0.76	0.76	0.77	0.77	0.77	0.76	0.77	0.76	0.77	0.75	0.83	0.83	0.82	0.73	0.82
36	0.78	0.78	0.76	0.76	0.77	0.78	0.78	0.78	0.78	0.79	0.79	0.76	0.82	0.82	0.83	0.74	0.83
37	0.78	0.78	0.76	0.76	0.77	0.78	0.78	0.79	0.78	0.79	0.79	0.76	0.83	0.81	0.83	0.74	0.83
38	0.77	0.78	0.76	0.76	0.77	0.78	0.78	0.78	0.78	0.79	0.79	0.76	0.82	0.82	0.83	0.74	0.83
39	0.77	0.77	0.76	0.76	0.76	0.76	0.77	0.76	0.76	0.76	0.77	0.74	0.82	0.82	0.82	0.72	0.81
40	0.77	0.78	0.76	0.76	0.77	0.78	0.78	0.78	0.78	0.79	0.79	0.76	0.82	0.82	0.83	0.74	0.83
41	0.77	0.78	0.76	0.76	0.77	0.78	0.78	0.79	0.78	0.79	0.79	0.76	0.82	0.82	0.83	0.74	0.83
42	0.77	0.78	0.76	0.76	0.77	0.78	0.78	0.78	0.78	0.79	0.79	0.76	0.82	0.82	0.83	0.74	0.83
43	0.77	0.77	0.74	0.75	0.76	0.77	0.77	0.78	0.77	0.78	0.78	0.74	0.81	0.80	0.83	0.73	0.82
44	0.77	0.78	0.75	0.75	0.77	0.78	0.77	0.78	0.77	0.78	0.78	0.76	0.82	0.81	0.83	0.74	0.83
45	0.77	0.78	0.76	0.75	0.77	0.78	0.78	0.78	0.77	0.79	0.79	0.75	0.82	0.82	0.83	0.74	0.83
46	0.77	0.77	0.75	0.75	0.76	0.78	0.77	0.78	0.77	0.78	0.78	0.75	0.81	0.81	0.82	0.73	0.82
47	0.77	0.77	0.76	0.76	0.76	0.76	0.77	0.76	0.76	0.76	0.76	0.74	0.82	0.82	0.81	0.72	0.81
48	0.77	0.77	0.76	0.76	0.77	0.76	0.77	0.76	0.77	0.76	0.77	0.74	0.82	0.82	0.82	0.72	0.81

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
49	0.77	0.77	0.75	0.75	0.76	0.78	0.77	0.78	0.77	0.78	0.78	0.75	0.81	0.81	0.82	0.73	0.82
50	0.77	0.77	0.75	0.75	0.77	0.78	0.78	0.78	0.77	0.79	0.79	0.75	0.82	0.81	0.83	0.73	0.81
51	0.77	0.77	0.75	0.75	0.76	0.78	0.77	0.78	0.77	0.79	0.79	0.76	0.82	0.81	0.83	0.73	0.82
52	0.77	0.77	0.76	0.75	0.76	0.76	0.77	0.75	0.76	0.76	0.76	0.74	0.82	0.82	0.82	0.72	0.81
53	0.77	0.77	0.74	0.74	0.76	0.77	0.77	0.78	0.77	0.78	0.78	0.74	0.81	0.80	0.82	0.73	0.81
54	0.77	0.77	0.74	0.74	0.76	0.77	0.77	0.77	0.77	0.77	0.77	0.74	0.81	0.80	0.82	0.72	0.81
55	0.77	0.77	0.75	0.75	0.76	0.78	0.77	0.78	0.77	0.79	0.79	0.75	0.82	0.80	0.83	0.73	0.82
56	0.77	0.77	0.75	0.75	0.76	0.77	0.77	0.77	0.76	0.77	0.77	0.75	0.81	0.80	0.82	0.72	0.80
57	0.77	0.77	0.75	0.75	0.76	0.78	0.77	0.78	0.77	0.78	0.78	0.75	0.81	0.80	0.83	0.73	0.82
58	0.76	0.77	0.74	0.74	0.76	0.77	0.77	0.78	0.77	0.78	0.78	0.75	0.81	0.80	0.82	0.73	0.82
59	0.76	0.77	0.74	0.74	0.76	0.77	0.77	0.77	0.77	0.78	0.78	0.75	0.81	0.80	0.82	0.73	0.82
60	0.76	0.76	0.75	0.74	0.75	0.76	0.76	0.75	0.76	0.76	0.76	0.74	0.78	0.78	0.80	0.72	0.84
61	0.75	0.76	0.74	0.73	0.75	0.76	0.76	0.76	0.76	0.77	0.77	0.74	0.81	0.80	0.81	0.72	0.80
62	0.75	0.76	0.73	0.73	0.75	0.76	0.76	0.77	0.76	0.77	0.77	0.74	0.79	0.79	0.81	0.72	0.80
63	0.75	0.75	0.73	0.73	0.74	0.75	0.75	0.76	0.75	0.76	0.76	0.73	0.79	0.78	0.80	0.72	0.80
64	0.69	0.71	0.67	0.67	0.69	0.69	0.69	0.69	0.69	0.69	0.69	0.67	0.69	0.67	0.68	0.67	0.69
65	0.69	0.71	0.67	0.68	0.69	0.70	0.69	0.70	0.69	0.70	0.70	0.68	0.68	0.67	0.68	0.67	0.69
66	0.56	0.57	0.56	0.56	0.55	0.56	0.55	0.56	0.55	0.56	0.56	0.56	0.56	0.55	0.56	0.55	0.57
67	0.55	0.55	0.54	0.54	0.54	0.55	0.54	0.55	0.54	0.55	0.54	0.54	0.54	0.53	0.54	0.54	0.54
68	0.42	0.40	0.41	0.41	0.41	0.41	0.41	0.41	0.41	0.41	0.40	0.40	0.42	0.41	0.41	0.41	0.41

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
1	0.80	0.80	0.79	0.79	0.79	0.79	0.79	0.79	0.78	0.78	0.78	0.78	0.78	0.78	0.78	0.78	0.78
2	0.81	0.80	0.80	0.80	0.80	0.79	0.79	0.79	0.80	0.79	0.78	0.78	0.78	0.78	0.78	0.78	0.78
3	0.78	0.78	0.78	0.78	0.78	0.78	0.77	0.76	0.77	0.77	0.76	0.76	0.76	0.76	0.76	0.76	0.76
4	0.78	0.78	0.78	0.78	0.78	0.77	0.77	0.76	0.77	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.76
5	0.80	0.79	0.78	0.78	0.78	0.79	0.78	0.77	0.79	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77
6	0.80	0.80	0.79	0.79	0.79	0.78	0.78	0.79	0.79	0.78	0.79	0.79	0.79	0.77	0.79	0.76	0.76
7	0.79	0.80	0.78	0.78	0.78	0.78	0.78	0.78	0.79	0.77	0.78	0.78	0.78	0.77	0.78	0.77	0.77
8	0.80	0.79	0.79	0.79	0.79	0.78	0.78	0.79	0.78	0.78	0.79	0.79	0.79	0.76	0.79	0.76	0.76
9	0.79	0.80	0.78	0.78	0.78	0.78	0.78	0.78	0.78	0.77	0.78	0.78	0.78	0.77	0.78	0.77	0.77
10	0.80	0.79	0.78	0.79	0.78	0.79	0.79	0.80	0.79	0.77	0.79	0.79	0.79	0.77	0.79	0.76	0.76
11	0.80	0.80	0.79	0.79	0.79	0.79	0.79	0.79	0.79	0.78	0.79	0.79	0.79	0.77	0.79	0.77	0.77
12	0.78	0.77	0.76	0.76	0.76	0.77	0.77	0.76	0.77	0.75	0.76	0.76	0.76	0.75	0.76	0.75	0.75
13	0.86	0.83	0.85	0.86	0.86	0.79	0.84	0.83	0.83	0.84	0.83	0.83	0.83	0.83	0.83	0.82	0.83
14	0.86	0.83	0.85	0.85	0.85	0.78	0.84	0.82	0.82	0.84	0.82	0.82	0.82	0.83	0.82	0.83	0.83
15	0.90	0.85	0.83	0.84	0.83	0.81	0.85	0.84	0.84	0.82	0.83	0.84	0.84	0.82	0.84	0.82	0.82
16	0.75	0.76	0.74	0.74	0.73	0.76	0.74	0.74	0.75	0.73	0.73	0.74	0.74	0.73	0.74	0.72	0.73
17	0.86	0.99	0.83	0.83	0.83	0.80	0.83	0.83	0.91	0.82	0.82	0.83	0.83	0.82	0.83	0.81	0.82
18	1.00	0.85	0.82	0.83	0.83	0.80	0.87	0.85	0.86	0.82	0.84	0.85	0.85	0.84	0.85	0.83	0.83
19	0.85	1.00	0.82	0.82	0.82	0.79	0.82	0.83	0.90	0.81	0.82	0.83	0.83	0.81	0.83	0.81	0.81
20	0.82	0.82	1.00	0.98	0.97	0.78	0.81	0.80	0.82	0.97	0.80	0.80	0.80	0.80	0.80	0.79	0.79
21	0.83	0.82	0.98	1.00	0.98	0.79	0.81	0.81	0.81	0.98	0.81	0.81	0.80	0.80	0.80	0.80	0.80
22	0.83	0.82	0.97	0.98	1.00	0.78	0.81	0.81	0.81	1.00	0.81	0.80	0.80	0.80	0.80	0.79	0.79
23	0.80	0.79	0.78	0.79	0.78	1.00	0.78	0.79	0.79	0.77	0.78	0.78	0.78	0.77	0.79	0.77	0.77
24	0.87	0.82	0.81	0.81	0.81	0.78	1.00	0.82	0.82	0.80	0.80	0.82	0.82	0.85	0.82	0.85	0.85

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
25	0.85	0.83	0.80	0.81	0.81	0.79	0.82	1.00	0.84	0.79	0.91	0.95	0.95	0.80	0.97	0.79	0.80
26	0.86	0.90	0.82	0.81	0.81	0.79	0.82	0.84	1.00	0.80	0.82	0.84	0.84	0.80	0.84	0.80	0.80
27	0.82	0.81	0.97	0.98	1.00	0.77	0.80	0.79	0.80	1.00	0.80	0.79	0.79	0.79	0.79	0.78	0.79
28	0.84	0.82	0.80	0.81	0.81	0.78	0.80	0.91	0.82	0.80	1.00	0.92	0.92	0.80	0.92	0.79	0.79
29	0.85	0.83	0.80	0.81	0.80	0.78	0.82	0.95	0.84	0.79	0.92	1.00	1.00	0.80	0.97	0.80	0.80
30	0.85	0.83	0.80	0.80	0.80	0.78	0.82	0.95	0.84	0.79	0.92	1.00	1.00	0.80	0.98	0.80	0.80
31	0.84	0.81	0.80	0.80	0.80	0.77	0.85	0.80	0.80	0.79	0.80	0.80	0.80	1.00	0.80	0.96	0.97
32	0.85	0.83	0.80	0.80	0.80	0.79	0.82	0.97	0.84	0.79	0.92	0.97	0.98	0.80	1.00	0.79	0.80
33	0.83	0.81	0.79	0.80	0.79	0.77	0.85	0.79	0.80	0.78	0.79	0.80	0.80	0.96	0.79	1.00	0.96
34	0.83	0.81	0.79	0.80	0.79	0.77	0.85	0.80	0.80	0.79	0.79	0.80	0.80	0.97	0.80	0.96	1.00
35	0.84	0.81	0.80	0.80	0.80	0.77	0.85	0.80	0.80	0.79	0.80	0.81	0.80	0.99	0.80	0.96	0.97
36	0.85	0.83	0.80	0.81	0.80	0.79	0.82	0.90	0.84	0.79	0.88	0.91	0.91	0.80	0.91	0.80	0.80
37	0.84	0.83	0.80	0.81	0.81	0.78	0.81	0.93	0.83	0.80	0.91	0.93	0.93	0.79	0.93	0.79	0.79
38	0.85	0.83	0.80	0.80	0.80	0.79	0.81	0.90	0.83	0.79	0.88	0.91	0.91	0.80	0.91	0.80	0.80
39	0.83	0.81	0.79	0.80	0.79	0.76	0.85	0.79	0.80	0.78	0.79	0.80	0.80	0.96	0.79	0.98	0.96
40	0.84	0.83	0.80	0.80	0.80	0.78	0.81	0.90	0.83	0.79	0.88	0.90	0.90	0.80	0.91	0.79	0.80
41	0.84	0.83	0.80	0.80	0.80	0.78	0.81	0.90	0.83	0.79	0.88	0.91	0.90	0.80	0.91	0.80	0.80
42	0.84	0.83	0.80	0.80	0.80	0.78	0.81	0.90	0.83	0.79	0.88	0.90	0.90	0.80	0.91	0.80	0.80
43	0.83	0.81	0.78	0.79	0.78	0.78	0.80	0.94	0.82	0.77	0.89	0.93	0.93	0.78	0.93	0.78	0.78
44	0.84	0.83	0.80	0.80	0.80	0.78	0.81	0.90	0.83	0.79	0.88	0.90	0.90	0.80	0.91	0.80	0.80
45	0.84	0.82	0.80	0.80	0.80	0.78	0.81	0.90	0.83	0.79	0.87	0.90	0.90	0.80	0.90	0.79	0.79
46	0.84	0.81	0.79	0.79	0.79	0.78	0.80	0.93	0.83	0.78	0.90	0.92	0.93	0.79	0.93	0.78	0.79
47	0.82	0.81	0.79	0.79	0.79	0.76	0.84	0.79	0.80	0.78	0.79	0.80	0.79	0.95	0.79	0.94	0.95
48	0.83	0.81	0.79	0.80	0.79	0.76	0.84	0.79	0.80	0.79	0.80	0.80	0.80	0.98	0.79	0.95	0.95

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
49	0.84	0.81	0.79	0.79	0.79	0.78	0.80	0.93	0.83	0.78	0.90	0.93	0.93	0.79	0.93	0.78	0.79
50	0.84	0.81	0.80	0.80	0.80	0.78	0.80	0.92	0.82	0.79	0.90	0.92	0.92	0.79	0.92	0.78	0.78
51	0.84	0.82	0.79	0.79	0.79	0.78	0.80	0.93	0.83	0.78	0.90	0.92	0.92	0.79	0.93	0.78	0.78
52	0.83	0.81	0.79	0.79	0.79	0.76	0.84	0.79	0.80	0.78	0.79	0.80	0.79	0.96	0.79	0.95	0.96
53	0.83	0.81	0.78	0.79	0.78	0.78	0.80	0.94	0.82	0.77	0.89	0.93	0.93	0.78	0.93	0.77	0.78
54	0.83	0.81	0.78	0.79	0.78	0.78	0.80	0.94	0.81	0.77	0.88	0.92	0.92	0.78	0.93	0.77	0.78
55	0.84	0.81	0.79	0.80	0.80	0.78	0.80	0.92	0.82	0.79	0.89	0.92	0.92	0.79	0.93	0.78	0.79
56	0.82	0.80	0.79	0.79	0.79	0.78	0.80	0.88	0.81	0.78	0.88	0.89	0.88	0.78	0.88	0.77	0.77
57	0.84	0.81	0.79	0.79	0.80	0.78	0.80	0.92	0.82	0.78	0.89	0.92	0.92	0.79	0.92	0.78	0.78
58	0.83	0.81	0.78	0.78	0.78	0.78	0.80	0.90	0.82	0.77	0.87	0.89	0.89	0.79	0.90	0.78	0.78
59	0.83	0.82	0.78	0.78	0.78	0.78	0.80	0.89	0.82	0.77	0.87	0.89	0.89	0.79	0.89	0.78	0.78
60	0.81	0.84	0.77	0.77	0.77	0.75	0.78	0.79	0.86	0.76	0.77	0.79	0.79	0.77	0.79	0.77	0.77
61	0.82	0.80	0.78	0.78	0.78	0.76	0.79	0.88	0.81	0.77	0.86	0.88	0.88	0.78	0.88	0.77	0.77
62	0.82	0.80	0.77	0.77	0.77	0.77	0.79	0.88	0.81	0.76	0.86	0.88	0.88	0.77	0.88	0.76	0.76
63	0.81	0.80	0.76	0.77	0.77	0.76	0.77	0.86	0.80	0.76	0.84	0.86	0.86	0.76	0.86	0.76	0.76
64	0.68	0.68	0.67	0.67	0.68	0.68	0.66	0.68	0.69	0.67	0.68	0.68	0.68	0.66	0.68	0.65	0.65
65	0.68	0.68	0.67	0.67	0.68	0.69	0.67	0.68	0.69	0.67	0.67	0.68	0.68	0.66	0.68	0.66	0.66
66	0.56	0.57	0.55	0.55	0.55	0.56	0.55	0.56	0.57	0.54	0.56	0.56	0.56	0.54	0.57	0.54	0.55
67	0.54	0.54	0.53	0.53	0.53	0.54	0.53	0.54	0.54	0.53	0.54	0.54	0.54	0.53	0.54	0.53	0.53
68	0.40	0.41	0.41	0.41	0.41	0.41	0.40	0.41	0.40	0.41	0.41	0.41	0.41	0.40	0.41	0.40	0.41

	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51
1	0.78	0.78	0.78	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77
2	0.78	0.78	0.78	0.78	0.77	0.78	0.78	0.78	0.77	0.78	0.78	0.77	0.77	0.77	0.77	0.77	0.77
3	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.74	0.75	0.76	0.75	0.76	0.76	0.75	0.75	0.75
4	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.75	0.75	0.75	0.75	0.76	0.76	0.75	0.75	0.75
5	0.77	0.77	0.77	0.77	0.76	0.77	0.77	0.77	0.76	0.77	0.77	0.76	0.76	0.77	0.76	0.77	0.76
6	0.77	0.78	0.78	0.78	0.76	0.78	0.78	0.78	0.77	0.78	0.78	0.78	0.76	0.76	0.78	0.78	0.78
7	0.77	0.78	0.78	0.78	0.77	0.78	0.78	0.78	0.77	0.77	0.78	0.77	0.77	0.77	0.77	0.78	0.77
8	0.76	0.78	0.79	0.78	0.76	0.78	0.79	0.78	0.78	0.78	0.78	0.78	0.76	0.76	0.78	0.78	0.78
9	0.77	0.78	0.78	0.78	0.76	0.78	0.78	0.78	0.77	0.77	0.77	0.77	0.76	0.77	0.77	0.77	0.77
10	0.76	0.79	0.79	0.79	0.76	0.79	0.79	0.79	0.78	0.78	0.79	0.78	0.76	0.76	0.78	0.79	0.79
11	0.77	0.79	0.79	0.79	0.77	0.79	0.79	0.79	0.78	0.78	0.79	0.78	0.76	0.77	0.78	0.79	0.79
12	0.75	0.76	0.76	0.76	0.74	0.76	0.76	0.76	0.74	0.76	0.75	0.75	0.74	0.74	0.75	0.75	0.76
13	0.83	0.82	0.83	0.82	0.82	0.82	0.82	0.82	0.81	0.82	0.82	0.81	0.82	0.82	0.81	0.82	0.82
14	0.83	0.82	0.81	0.82	0.82	0.82	0.82	0.82	0.80	0.81	0.82	0.81	0.82	0.82	0.81	0.81	0.81
15	0.82	0.83	0.83	0.83	0.82	0.83	0.83	0.83	0.83	0.83	0.83	0.82	0.81	0.82	0.82	0.83	0.83
16	0.73	0.74	0.74	0.74	0.72	0.74	0.74	0.74	0.73	0.74	0.74	0.73	0.72	0.72	0.73	0.73	0.73
17	0.82	0.83	0.83	0.83	0.81	0.83	0.83	0.83	0.82	0.83	0.83	0.82	0.81	0.81	0.82	0.81	0.82
18	0.84	0.85	0.84	0.85	0.83	0.84	0.84	0.84	0.83	0.84	0.84	0.84	0.82	0.83	0.84	0.84	0.84
19	0.81	0.83	0.83	0.83	0.81	0.83	0.83	0.83	0.81	0.83	0.82	0.81	0.81	0.81	0.81	0.81	0.82
20	0.80	0.80	0.80	0.80	0.79	0.80	0.80	0.80	0.78	0.80	0.80	0.79	0.79	0.79	0.79	0.80	0.79
21	0.80	0.81	0.81	0.80	0.80	0.80	0.80	0.80	0.79	0.80	0.80	0.79	0.79	0.80	0.79	0.80	0.79
22	0.80	0.80	0.81	0.80	0.79	0.80	0.80	0.80	0.78	0.80	0.80	0.79	0.79	0.79	0.79	0.80	0.79
23	0.77	0.79	0.78	0.79	0.76	0.78	0.78	0.78	0.78	0.78	0.78	0.78	0.76	0.76	0.78	0.78	0.78
24	0.85	0.82	0.81	0.81	0.85	0.81	0.81	0.81	0.80	0.81	0.81	0.80	0.84	0.84	0.80	0.80	0.80

	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51
25	0.80	0.90	0.93	0.90	0.79	0.90	0.90	0.90	0.94	0.90	0.90	0.93	0.79	0.79	0.93	0.92	0.93
26	0.80	0.84	0.83	0.83	0.80	0.83	0.83	0.83	0.82	0.83	0.83	0.83	0.80	0.80	0.83	0.82	0.83
27	0.79	0.79	0.80	0.79	0.78	0.79	0.79	0.79	0.77	0.79	0.79	0.78	0.78	0.79	0.78	0.79	0.78
28	0.80	0.88	0.91	0.88	0.79	0.88	0.88	0.88	0.89	0.88	0.87	0.90	0.79	0.80	0.90	0.90	0.90
29	0.81	0.91	0.93	0.91	0.80	0.90	0.91	0.90	0.93	0.90	0.90	0.92	0.80	0.80	0.93	0.92	0.92
30	0.80	0.91	0.93	0.91	0.80	0.90	0.90	0.90	0.93	0.90	0.90	0.93	0.79	0.80	0.93	0.92	0.92
31	0.99	0.80	0.79	0.80	0.96	0.80	0.80	0.80	0.78	0.80	0.80	0.79	0.95	0.98	0.79	0.79	0.79
32	0.80	0.91	0.93	0.91	0.79	0.91	0.91	0.91	0.93	0.91	0.90	0.93	0.79	0.79	0.93	0.92	0.93
33	0.96	0.80	0.79	0.80	0.98	0.79	0.80	0.80	0.78	0.80	0.79	0.78	0.94	0.95	0.78	0.78	0.78
34	0.97	0.80	0.79	0.80	0.96	0.80	0.80	0.80	0.78	0.80	0.79	0.79	0.95	0.95	0.79	0.78	0.78
35	1.00	0.80	0.80	0.80	0.96	0.80	0.80	0.80	0.78	0.80	0.80	0.79	0.95	0.99	0.79	0.78	0.78
36	0.80	1.00	0.90	0.98	0.80	0.98	0.99	0.99	0.88	0.98	0.96	0.89	0.80	0.80	0.89	0.89	0.89
37	0.80	0.90	1.00	0.90	0.79	0.90	0.90	0.90	0.90	0.90	0.90	0.94	0.79	0.79	0.94	0.96	0.94
38	0.80	0.98	0.90	1.00	0.79	0.98	0.98	0.98	0.88	0.98	0.96	0.90	0.79	0.80	0.90	0.90	0.90
39	0.96	0.80	0.79	0.79	1.00	0.79	0.80	0.80	0.77	0.80	0.79	0.78	0.94	0.95	0.78	0.78	0.78
40	0.80	0.98	0.90	0.98	0.79	1.00	0.97	0.97	0.88	0.98	0.96	0.89	0.79	0.80	0.90	0.89	0.89
41	0.80	0.99	0.90	0.98	0.80	0.97	1.00	1.00	0.88	0.97	0.96	0.89	0.79	0.80	0.89	0.89	0.89
42	0.80	0.99	0.90	0.98	0.80	0.97	1.00	1.00	0.88	0.97	0.96	0.89	0.79	0.80	0.89	0.89	0.89
43	0.78	0.88	0.90	0.88	0.77	0.88	0.88	0.88	1.00	0.88	0.88	0.90	0.77	0.78	0.90	0.90	0.90
44	0.80	0.98	0.90	0.98	0.80	0.98	0.97	0.97	0.88	1.00	0.96	0.89	0.79	0.80	0.89	0.89	0.89
45	0.80	0.96	0.90	0.96	0.79	0.96	0.96	0.96	0.88	0.96	1.00	0.89	0.79	0.79	0.89	0.89	0.89
46	0.79	0.89	0.94	0.90	0.78	0.89	0.89	0.89	0.90	0.89	0.89	1.00	0.78	0.79	1.00	0.93	0.95
47	0.95	0.80	0.79	0.79	0.94	0.79	0.79	0.79	0.77	0.79	0.79	0.78	1.00	0.94	0.78	0.78	0.78
48	0.99	0.80	0.79	0.80	0.95	0.80	0.80	0.80	0.78	0.80	0.79	0.79	0.94	1.00	0.79	0.79	0.78

	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51
49	0.79	0.89	0.94	0.90	0.78	0.90	0.89	0.89	0.90	0.89	0.89	1.00	0.78	0.79	1.00	0.93	0.95
50	0.78	0.89	0.96	0.90	0.78	0.89	0.89	0.89	0.90	0.89	0.89	0.93	0.78	0.79	0.93	1.00	0.93
51	0.78	0.89	0.94	0.90	0.78	0.89	0.89	0.89	0.90	0.89	0.89	0.95	0.78	0.78	0.95	0.93	1.00
52	0.95	0.79	0.79	0.79	0.95	0.79	0.79	0.79	0.77	0.79	0.79	0.78	0.95	0.94	0.78	0.78	0.77
53	0.78	0.88	0.90	0.89	0.77	0.88	0.88	0.88	0.97	0.88	0.88	0.90	0.77	0.78	0.90	0.90	0.90
54	0.78	0.88	0.90	0.88	0.77	0.87	0.88	0.88	0.99	0.87	0.87	0.89	0.77	0.77	0.90	0.89	0.89
55	0.79	0.89	0.96	0.90	0.78	0.89	0.89	0.89	0.90	0.89	0.89	0.93	0.78	0.79	0.93	0.95	0.93
56	0.78	0.85	0.88	0.85	0.77	0.85	0.85	0.85	0.87	0.85	0.85	0.88	0.77	0.78	0.88	0.88	0.87
57	0.79	0.89	0.95	0.89	0.78	0.89	0.89	0.89	0.90	0.89	0.89	0.93	0.78	0.79	0.93	0.95	0.93
58	0.79	0.92	0.90	0.93	0.78	0.93	0.92	0.92	0.88	0.92	0.92	0.90	0.78	0.78	0.90	0.89	0.90
59	0.79	0.92	0.90	0.92	0.78	0.91	0.92	0.92	0.87	0.91	0.91	0.89	0.78	0.78	0.89	0.89	0.89
60	0.77	0.79	0.78	0.78	0.77	0.78	0.79	0.79	0.77	0.78	0.78	0.78	0.76	0.77	0.78	0.77	0.78
61	0.78	0.93	0.88	0.94	0.77	0.93	0.93	0.93	0.86	0.93	0.93	0.88	0.77	0.78	0.88	0.88	0.87
62	0.77	0.90	0.88	0.90	0.76	0.90	0.90	0.90	0.86	0.90	0.89	0.88	0.76	0.77	0.89	0.88	0.88
63	0.76	0.88	0.87	0.88	0.76	0.88	0.88	0.88	0.85	0.88	0.87	0.87	0.75	0.76	0.88	0.87	0.87
64	0.66	0.68	0.68	0.68	0.65	0.68	0.68	0.68	0.68	0.68	0.68	0.68	0.65	0.66	0.68	0.69	0.69
65	0.66	0.68	0.68	0.68	0.65	0.68	0.68	0.68	0.67	0.68	0.67	0.68	0.65	0.66	0.68	0.68	0.68
66	0.54	0.56	0.56	0.56	0.54	0.56	0.56	0.56	0.56	0.56	0.55	0.56	0.54	0.54	0.56	0.56	0.56
67	0.53	0.54	0.54	0.54	0.53	0.54	0.54	0.54	0.53	0.54	0.53	0.53	0.52	0.52	0.53	0.53	0.53
68	0.40	0.41	0.41	0.41	0.40	0.40	0.41	0.41	0.41	0.40	0.41	0.41	0.40	0.39	0.41	0.41	0.40

	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68
1	0.77	0.77	0.77	0.77	0.77	0.77	0.76	0.76	0.76	0.75	0.75	0.75	0.69	0.69	0.56	0.55	0.42
2	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.76	0.76	0.76	0.75	0.71	0.71	0.57	0.55	0.40
3	0.76	0.74	0.74	0.75	0.75	0.75	0.74	0.74	0.75	0.74	0.73	0.73	0.67	0.67	0.56	0.54	0.41
4	0.75	0.74	0.74	0.75	0.75	0.75	0.74	0.74	0.74	0.73	0.73	0.73	0.67	0.68	0.56	0.54	0.41
5	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.76	0.75	0.75	0.75	0.74	0.69	0.69	0.55	0.54	0.41
6	0.76	0.77	0.77	0.78	0.77	0.78	0.77	0.77	0.76	0.76	0.76	0.75	0.69	0.70	0.56	0.55	0.41
7	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.77	0.76	0.76	0.76	0.75	0.69	0.69	0.55	0.54	0.41
8	0.75	0.78	0.77	0.78	0.77	0.78	0.78	0.77	0.75	0.76	0.77	0.76	0.69	0.70	0.56	0.55	0.41
9	0.76	0.77	0.77	0.77	0.76	0.77	0.77	0.77	0.76	0.76	0.76	0.75	0.69	0.69	0.55	0.54	0.41
10	0.76	0.78	0.77	0.79	0.77	0.78	0.78	0.78	0.76	0.77	0.77	0.76	0.69	0.70	0.56	0.55	0.41
11	0.76	0.78	0.77	0.79	0.77	0.78	0.78	0.78	0.76	0.77	0.77	0.76	0.69	0.70	0.56	0.54	0.40
12	0.74	0.74	0.74	0.75	0.75	0.75	0.75	0.75	0.74	0.74	0.74	0.73	0.67	0.68	0.56	0.54	0.40
13	0.82	0.81	0.81	0.82	0.81	0.81	0.81	0.81	0.78	0.81	0.79	0.79	0.69	0.68	0.56	0.54	0.42
14	0.82	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.78	0.80	0.79	0.78	0.67	0.67	0.55	0.53	0.41
15	0.82	0.82	0.82	0.83	0.82	0.83	0.82	0.82	0.80	0.81	0.81	0.80	0.68	0.68	0.56	0.54	0.41
16	0.72	0.73	0.72	0.73	0.72	0.73	0.73	0.73	0.72	0.72	0.72	0.72	0.67	0.67	0.55	0.54	0.41
17	0.81	0.81	0.81	0.82	0.80	0.82	0.82	0.82	0.84	0.80	0.80	0.80	0.69	0.69	0.57	0.54	0.41
18	0.83	0.83	0.83	0.84	0.82	0.84	0.83	0.83	0.81	0.82	0.82	0.81	0.68	0.68	0.56	0.54	0.40
19	0.81	0.81	0.81	0.81	0.80	0.81	0.81	0.82	0.84	0.80	0.80	0.80	0.68	0.68	0.57	0.54	0.41
20	0.79	0.78	0.78	0.79	0.79	0.79	0.78	0.78	0.77	0.78	0.77	0.76	0.67	0.67	0.55	0.53	0.41
21	0.79	0.79	0.79	0.80	0.79	0.79	0.78	0.78	0.77	0.78	0.77	0.77	0.67	0.67	0.55	0.53	0.41
22	0.79	0.78	0.78	0.80	0.79	0.80	0.78	0.78	0.77	0.78	0.77	0.77	0.68	0.68	0.55	0.53	0.41
23	0.76	0.78	0.78	0.78	0.78	0.78	0.78	0.78	0.75	0.76	0.77	0.76	0.68	0.69	0.56	0.54	0.41
24	0.84	0.80	0.80	0.80	0.80	0.80	0.80	0.80	0.78	0.79	0.79	0.77	0.66	0.67	0.55	0.53	0.40

	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68
25	0.79	0.94	0.94	0.92	0.88	0.92	0.90	0.89	0.79	0.88	0.88	0.86	0.68	0.68	0.56	0.54	0.41
26	0.80	0.82	0.81	0.82	0.81	0.82	0.82	0.82	0.86	0.81	0.81	0.80	0.69	0.69	0.57	0.54	0.40
27	0.78	0.77	0.77	0.79	0.78	0.78	0.77	0.77	0.76	0.77	0.76	0.76	0.67	0.67	0.54	0.53	0.41
28	0.79	0.89	0.88	0.89	0.88	0.89	0.87	0.87	0.77	0.86	0.86	0.84	0.68	0.67	0.56	0.54	0.41
29	0.80	0.93	0.92	0.92	0.89	0.92	0.89	0.89	0.79	0.88	0.88	0.86	0.68	0.68	0.56	0.54	0.41
30	0.79	0.93	0.92	0.92	0.88	0.92	0.89	0.89	0.79	0.88	0.88	0.86	0.68	0.68	0.56	0.54	0.41
31	0.96	0.78	0.78	0.79	0.78	0.79	0.79	0.79	0.77	0.78	0.77	0.76	0.66	0.66	0.54	0.53	0.40
32	0.79	0.93	0.93	0.93	0.88	0.92	0.90	0.89	0.79	0.88	0.88	0.86	0.68	0.68	0.57	0.54	0.41
33	0.95	0.77	0.77	0.78	0.77	0.78	0.78	0.78	0.77	0.77	0.76	0.76	0.65	0.66	0.54	0.53	0.40
34	0.96	0.78	0.78	0.79	0.77	0.78	0.78	0.78	0.77	0.77	0.76	0.76	0.65	0.66	0.55	0.53	0.41
35	0.95	0.78	0.78	0.79	0.78	0.79	0.79	0.79	0.77	0.78	0.77	0.76	0.66	0.66	0.54	0.53	0.40
36	0.79	0.88	0.88	0.89	0.85	0.89	0.92	0.92	0.79	0.93	0.90	0.88	0.68	0.68	0.56	0.54	0.41
37	0.79	0.90	0.90	0.96	0.88	0.95	0.90	0.90	0.78	0.88	0.88	0.87	0.68	0.68	0.56	0.54	0.41
38	0.79	0.89	0.88	0.90	0.85	0.89	0.93	0.92	0.78	0.94	0.90	0.88	0.68	0.68	0.56	0.54	0.41
39	0.95	0.77	0.77	0.78	0.77	0.78	0.78	0.78	0.77	0.77	0.76	0.76	0.65	0.65	0.54	0.53	0.40
40	0.79	0.88	0.87	0.89	0.85	0.89	0.93	0.91	0.78	0.93	0.90	0.88	0.68	0.68	0.56	0.54	0.40
41	0.79	0.88	0.88	0.89	0.85	0.89	0.92	0.92	0.79	0.93	0.90	0.88	0.68	0.68	0.56	0.54	0.41
42	0.79	0.88	0.88	0.89	0.85	0.89	0.92	0.92	0.79	0.93	0.90	0.88	0.68	0.68	0.56	0.54	0.41
43	0.77	0.97	0.99	0.90	0.87	0.90	0.88	0.87	0.77	0.86	0.86	0.85	0.68	0.67	0.56	0.53	0.41
44	0.79	0.88	0.87	0.89	0.85	0.89	0.92	0.91	0.78	0.93	0.90	0.88	0.68	0.68	0.56	0.54	0.40
45	0.79	0.88	0.87	0.89	0.85	0.89	0.92	0.91	0.78	0.93	0.89	0.87	0.68	0.67	0.55	0.53	0.41
46	0.78	0.90	0.89	0.93	0.88	0.93	0.90	0.89	0.78	0.88	0.88	0.87	0.68	0.68	0.56	0.53	0.41
47	0.95	0.77	0.77	0.78	0.77	0.78	0.78	0.78	0.76	0.77	0.76	0.75	0.65	0.65	0.54	0.52	0.40
48	0.94	0.78	0.77	0.79	0.78	0.79	0.78	0.78	0.77	0.78	0.77	0.76	0.66	0.66	0.54	0.52	0.39

	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68
49	0.78	0.90	0.90	0.93	0.88	0.93	0.90	0.89	0.78	0.88	0.89	0.88	0.68	0.68	0.56	0.53	0.41
50	0.78	0.90	0.89	0.95	0.88	0.95	0.89	0.89	0.77	0.88	0.88	0.87	0.69	0.68	0.56	0.53	0.41
51	0.77	0.90	0.89	0.93	0.87	0.93	0.90	0.89	0.78	0.87	0.88	0.87	0.69	0.68	0.56	0.53	0.40
52	1.00	0.77	0.77	0.78	0.77	0.78	0.78	0.77	0.76	0.77	0.76	0.75	0.65	0.65	0.54	0.53	0.40
53	0.77	1.00	0.96	0.90	0.87	0.90	0.88	0.87	0.77	0.86	0.86	0.85	0.67	0.67	0.56	0.53	0.40
54	0.77	0.96	1.00	0.89	0.87	0.89	0.87	0.87	0.77	0.85	0.85	0.85	0.67	0.67	0.56	0.53	0.41
55	0.78	0.90	0.89	1.00	0.87	0.99	0.90	0.89	0.78	0.88	0.88	0.87	0.69	0.68	0.56	0.54	0.41
56	0.77	0.87	0.87	0.87	1.00	0.87	0.85	0.85	0.76	0.83	0.85	0.84	0.67	0.66	0.55	0.53	0.40
57	0.78	0.90	0.89	0.99	0.87	1.00	0.90	0.89	0.77	0.88	0.88	0.87	0.68	0.67	0.56	0.54	0.41
58	0.78	0.88	0.87	0.90	0.85	0.90	1.00	0.93	0.77	0.91	0.91	0.88	0.68	0.67	0.56	0.53	0.40
59	0.77	0.87	0.87	0.89	0.85	0.89	0.93	1.00	0.77	0.90	0.92	0.88	0.67	0.67	0.56	0.53	0.40
60	0.76	0.77	0.77	0.78	0.76	0.77	0.77	0.77	1.00	0.75	0.76	0.75	0.65	0.66	0.54	0.52	0.40
61	0.77	0.86	0.85	0.88	0.83	0.88	0.91	0.90	0.75	1.00	0.89	0.86	0.67	0.66	0.55	0.53	0.40
62	0.76	0.86	0.85	0.88	0.85	0.88	0.91	0.92	0.76	0.89	1.00	0.88	0.67	0.67	0.55	0.53	0.40
63	0.75	0.85	0.85	0.87	0.84	0.87	0.88	0.88	0.75	0.86	0.88	1.00	0.67	0.66	0.55	0.52	0.39
64	0.65	0.67	0.67	0.69	0.67	0.68	0.68	0.67	0.65	0.67	0.67	0.67	1.00	0.87	0.57	0.54	0.40
65	0.65	0.67	0.67	0.68	0.66	0.67	0.67	0.67	0.66	0.66	0.67	0.66	0.87	1.00	0.58	0.54	0.40
66	0.54	0.56	0.56	0.56	0.55	0.56	0.56	0.56	0.54	0.55	0.55	0.55	0.57	0.58	1.00	0.47	0.37
67	0.53	0.53	0.53	0.54	0.53	0.54	0.53	0.53	0.52	0.53	0.53	0.52	0.54	0.54	0.47	1.00	0.43
68	0.40	0.40	0.41	0.41	0.40	0.41	0.40	0.40	0.40	0.40	0.40	0.39	0.40	0.40	0.37	0.43	1.00

Table S6. Pairwise Distances between Sequences in the MYBPC3 Alignment

This table shows the pairwise alignment distances between sequences in the manual MYBPC3 alignment. Sequences are ordered and numbered as in table S3.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	1.00	0.92	0.92	0.92	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.90	0.89	0.87	0.72	0.71	0.71
2	0.92	1.00	0.94	0.99	0.91	0.91	0.91	0.91	0.92	0.92	0.91	0.91	0.90	0.87	0.72	0.72	0.72
3	0.92	0.94	1.00	0.94	0.91	0.91	0.91	0.91	0.91	0.91	0.90	0.90	0.90	0.87	0.73	0.73	0.73
4	0.92	0.99	0.94	1.00	0.91	0.91	0.91	0.91	0.91	0.91	0.90	0.90	0.90	0.86	0.72	0.71	0.71
5	0.90	0.91	0.91	0.91	1.00	1.00	1.00	1.00	0.88	0.88	0.97	0.97	0.99	0.87	0.72	0.72	0.72
6	0.90	0.91	0.91	0.91	1.00	1.00	1.00	1.00	0.88	0.88	0.97	0.97	0.99	0.88	0.72	0.72	0.72
7	0.90	0.91	0.91	0.91	1.00	1.00	1.00	1.00	0.88	0.88	0.97	0.97	0.99	0.88	0.72	0.72	0.72
8	0.90	0.91	0.91	0.91	1.00	1.00	1.00	1.00	0.88	0.88	0.97	0.97	0.99	0.88	0.72	0.72	0.72
9	0.90	0.92	0.91	0.91	0.88	0.88	0.88	0.88	1.00	1.00	0.88	0.88	0.88	0.86	0.72	0.72	0.72
10	0.90	0.92	0.91	0.91	0.88	0.88	0.88	0.88	1.00	1.00	0.88	0.88	0.88	0.86	0.72	0.72	0.72
11	0.90	0.91	0.90	0.90	0.97	0.97	0.97	0.97	0.88	0.88	1.00	1.00	0.96	0.88	0.72	0.72	0.72
12	0.90	0.91	0.90	0.90	0.97	0.97	0.97	0.97	0.88	0.88	1.00	1.00	0.96	0.88	0.72	0.72	0.72
13	0.89	0.90	0.90	0.90	0.99	0.99	0.99	0.99	0.88	0.88	0.96	0.96	1.00	0.87	0.71	0.72	0.71
14	0.87	0.87	0.87	0.86	0.87	0.88	0.88	0.88	0.86	0.86	0.88	0.88	0.87	1.00	0.73	0.73	0.72
15	0.72	0.72	0.73	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.71	0.73	1.00	1.00	1.00
16	0.71	0.72	0.73	0.71	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.73	1.00	1.00	0.99
17	0.71	0.72	0.73	0.71	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.71	0.72	1.00	0.99	1.00
18	0.71	0.72	0.73	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.72	0.71	0.73	1.00	1.00	0.99
19	0.68	0.68	0.69	0.68	0.69	0.70	0.70	0.70	0.68	0.68	0.69	0.69	0.69	0.69	0.77	0.77	0.76
20	0.68	0.68	0.69	0.67	0.70	0.70	0.70	0.70	0.68	0.67	0.69	0.69	0.69	0.69	0.76	0.76	0.75
21	0.68	0.69	0.70	0.69	0.70	0.70	0.70	0.70	0.68	0.68	0.69	0.69	0.69	0.70	0.77	0.76	0.76
22	0.68	0.68	0.69	0.68	0.69	0.69	0.70	0.70	0.67	0.67	0.69	0.69	0.69	0.69	0.76	0.76	0.76
23	0.68	0.68	0.69	0.68	0.69	0.69	0.70	0.70	0.67	0.67	0.69	0.69	0.69	0.69	0.77	0.76	0.76
24	0.67	0.68	0.67	0.67	0.67	0.67	0.68	0.68	0.66	0.66	0.67	0.67	0.67	0.68	0.72	0.72	0.72

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
25	0.67	0.67	0.68	0.67	0.69	0.69	0.69	0.69	0.66	0.66	0.68	0.68	0.68	0.71	0.77	0.77	0.77
26	0.66	0.67	0.67	0.67	0.66	0.66	0.66	0.66	0.65	0.65	0.66	0.66	0.66	0.67	0.71	0.71	0.71
27	0.65	0.66	0.66	0.66	0.65	0.65	0.65	0.65	0.64	0.64	0.65	0.65	0.65	0.66	0.70	0.70	0.70
28	0.64	0.65	0.65	0.64	0.64	0.64	0.64	0.64	0.63	0.64	0.64	0.64	0.63	0.66	0.71	0.70	0.70
29	0.63	0.63	0.63	0.63	0.63	0.63	0.63	0.63	0.62	0.62	0.63	0.63	0.62	0.66	0.71	0.70	0.70
30	0.59	0.59	0.58	0.59	0.59	0.59	0.59	0.59	0.58	0.58	0.59	0.59	0.58	0.59	0.61	0.61	0.61
31	0.59	0.59	0.58	0.59	0.59	0.59	0.59	0.59	0.58	0.58	0.59	0.59	0.58	0.59	0.61	0.61	0.61
32	0.59	0.59	0.58	0.59	0.59	0.59	0.59	0.59	0.58	0.58	0.59	0.59	0.58	0.59	0.61	0.61	0.61
33	0.58	0.59	0.58	0.59	0.59	0.59	0.59	0.59	0.58	0.58	0.58	0.58	0.58	0.59	0.61	0.61	0.61
34	0.57	0.58	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.58	0.57	0.57	0.56
35	0.57	0.58	0.57	0.58	0.58	0.58	0.58	0.58	0.57	0.57	0.58	0.58	0.57	0.59	0.60	0.60	0.60
36	0.57	0.58	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.58	0.61	0.61	0.61
37	0.57	0.58	0.58	0.58	0.58	0.58	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.58	0.61	0.60	0.60
38	0.57	0.58	0.58	0.58	0.58	0.58	0.58	0.58	0.57	0.56	0.57	0.57	0.57	0.58	0.61	0.60	0.60
39	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.57	0.57	0.56	0.57	0.58	0.58	0.58
40	0.57	0.57	0.56	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.57	0.57	0.56	0.56	0.58	0.58	0.57
41	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.57	0.57	0.56	0.57	0.60	0.60	0.60
42	0.56	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.57	0.57	0.56	0.57	0.60	0.60	0.60
43	0.56	0.57	0.56	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.57	0.57	0.56	0.56	0.58	0.58	0.57
44	0.56	0.56	0.56	0.56	0.56	0.57	0.57	0.57	0.56	0.56	0.57	0.57	0.56	0.56	0.58	0.58	0.57
45	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.57	0.57	0.57
46	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.57	0.57	0.57
47	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.56	0.56	0.56	0.56	0.57	0.57	0.57
48	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.55	0.56	0.56	0.55	0.56	0.57	0.57	0.57

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
49	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.55	0.56	0.56	0.55	0.56	0.57	0.57	0.57
50	0.55	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.56	0.59	0.59	0.58

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
1	0.71	0.68	0.68	0.68	0.68	0.68	0.67	0.67	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.58	0.57
2	0.72	0.68	0.68	0.69	0.68	0.68	0.68	0.67	0.67	0.66	0.65	0.63	0.59	0.59	0.59	0.59	0.58
3	0.73	0.69	0.69	0.70	0.69	0.69	0.67	0.68	0.67	0.66	0.65	0.63	0.58	0.58	0.58	0.58	0.58
4	0.72	0.68	0.67	0.69	0.68	0.68	0.67	0.67	0.67	0.66	0.64	0.63	0.59	0.59	0.59	0.59	0.58
5	0.72	0.69	0.70	0.70	0.69	0.69	0.67	0.69	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.59	0.57
6	0.72	0.70	0.70	0.70	0.69	0.69	0.67	0.69	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.59	0.57
7	0.72	0.70	0.70	0.70	0.70	0.70	0.68	0.69	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.59	0.57
8	0.72	0.70	0.70	0.70	0.70	0.70	0.68	0.69	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.59	0.57
9	0.72	0.68	0.68	0.68	0.67	0.67	0.66	0.66	0.65	0.64	0.63	0.62	0.58	0.58	0.58	0.58	0.57
10	0.72	0.68	0.67	0.68	0.67	0.67	0.66	0.66	0.65	0.64	0.64	0.62	0.58	0.58	0.58	0.58	0.57
11	0.72	0.69	0.69	0.69	0.69	0.69	0.67	0.68	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.58	0.57
12	0.72	0.69	0.69	0.69	0.69	0.69	0.67	0.68	0.66	0.65	0.64	0.63	0.59	0.59	0.59	0.58	0.57
13	0.71	0.69	0.69	0.69	0.69	0.69	0.67	0.68	0.66	0.65	0.63	0.62	0.58	0.58	0.58	0.58	0.56
14	0.73	0.69	0.69	0.70	0.69	0.69	0.68	0.71	0.67	0.66	0.66	0.66	0.59	0.59	0.59	0.59	0.58
15	1.00	0.77	0.76	0.77	0.76	0.77	0.72	0.77	0.71	0.70	0.71	0.71	0.61	0.61	0.61	0.61	0.57
16	1.00	0.77	0.76	0.76	0.76	0.76	0.72	0.77	0.71	0.70	0.70	0.70	0.61	0.61	0.61	0.61	0.57
17	0.99	0.76	0.75	0.76	0.76	0.76	0.72	0.77	0.71	0.70	0.70	0.70	0.61	0.61	0.61	0.61	0.56
18	1.00	0.77	0.76	0.76	0.77	0.77	0.72	0.77	0.71	0.70	0.70	0.71	0.61	0.61	0.61	0.61	0.57
19	0.77	1.00	1.00	0.95	1.00	1.00	0.74	0.95	0.73	0.72	0.70	0.72	0.62	0.62	0.62	0.62	0.59
20	0.76	1.00	1.00	0.95	1.00	1.00	0.73	0.95	0.71	0.70	0.70	0.71	0.62	0.62	0.62	0.61	0.58
21	0.76	0.95	0.95	1.00	0.95	0.95	0.74	0.99	0.72	0.71	0.72	0.72	0.63	0.63	0.63	0.62	0.59
22	0.77	1.00	1.00	0.95	1.00	1.00	0.74	0.95	0.72	0.71	0.70	0.72	0.62	0.62	0.62	0.62	0.58
23	0.77	1.00	1.00	0.95	1.00	1.00	0.74	0.95	0.72	0.71	0.70	0.72	0.62	0.62	0.62	0.62	0.58
24	0.72	0.74	0.73	0.74	0.74	0.74	1.00	0.73	0.99	0.99	0.82	0.99	0.63	0.63	0.63	0.63	0.57

	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34
25	0.77	0.95	0.95	0.99	0.95	0.95	0.73	1.00	0.74	0.73	0.69	0.70	0.62	0.62	0.62	0.62	0.59
26	0.71	0.73	0.71	0.72	0.72	0.72	0.99	0.74	1.00	1.00	0.83	0.98	0.64	0.64	0.64	0.63	0.57
27	0.70	0.72	0.70	0.71	0.71	0.71	0.99	0.73	1.00	1.00	0.82	0.97	0.63	0.63	0.63	0.63	0.57
28	0.70	0.70	0.70	0.72	0.70	0.70	0.82	0.69	0.83	0.82	1.00	0.80	0.62	0.62	0.62	0.62	0.58
29	0.71	0.72	0.71	0.72	0.72	0.72	0.99	0.70	0.98	0.97	0.80	1.00	0.63	0.63	0.63	0.63	0.57
30	0.61	0.62	0.62	0.63	0.62	0.62	0.63	0.62	0.64	0.63	0.62	0.63	1.00	1.00	1.00	1.00	0.62
31	0.61	0.62	0.62	0.63	0.62	0.62	0.63	0.62	0.64	0.63	0.62	0.63	1.00	1.00	1.00	1.00	0.62
32	0.61	0.62	0.62	0.63	0.62	0.62	0.63	0.62	0.64	0.63	0.62	0.63	1.00	1.00	1.00	1.00	0.62
33	0.61	0.62	0.61	0.62	0.62	0.62	0.63	0.62	0.63	0.63	0.62	0.63	1.00	1.00	1.00	1.00	0.62
34	0.57	0.59	0.58	0.59	0.58	0.58	0.57	0.59	0.57	0.57	0.58	0.57	0.62	0.62	0.62	0.62	1.00
35	0.60	0.61	0.61	0.62	0.61	0.61	0.63	0.63	0.62	0.62	0.63	0.61	0.78	0.78	0.78	0.78	0.63
36	0.61	0.62	0.61	0.62	0.62	0.62	0.62	0.62	0.62	0.62	0.60	0.61	0.75	0.75	0.75	0.74	0.60
37	0.60	0.62	0.62	0.62	0.61	0.61	0.61	0.62	0.61	0.61	0.61	0.61	0.74	0.74	0.74	0.74	0.60
38	0.60	0.62	0.62	0.62	0.61	0.61	0.61	0.62	0.61	0.61	0.61	0.61	0.74	0.74	0.74	0.74	0.60
39	0.58	0.59	0.57	0.60	0.58	0.58	0.60	0.59	0.60	0.60	0.58	0.60	0.64	0.64	0.64	0.64	0.71
40	0.58	0.59	0.57	0.60	0.58	0.58	0.60	0.59	0.60	0.60	0.58	0.59	0.64	0.64	0.64	0.64	0.71
41	0.60	0.61	0.61	0.61	0.61	0.61	0.61	0.61	0.61	0.61	0.59	0.60	0.73	0.73	0.73	0.73	0.59
42	0.60	0.61	0.62	0.61	0.61	0.61	0.61	0.61	0.61	0.61	0.60	0.61	0.74	0.74	0.74	0.74	0.59
43	0.58	0.58	0.57	0.60	0.58	0.58	0.60	0.59	0.60	0.59	0.57	0.59	0.64	0.64	0.64	0.64	0.71
44.00	0.58	0.59	0.57	0.60	0.58	0.58	0.59	0.59	0.59	0.59	0.57	0.59	0.65	0.65	0.65	0.65	0.72
45.00	0.57	0.58	0.56	0.59	0.58	0.58	0.59	0.58	0.60	0.59	0.57	0.59	0.64	0.64	0.64	0.64	0.72
46.00	0.57	0.58	0.56	0.59	0.57	0.57	0.59	0.58	0.60	0.59	0.57	0.59	0.64	0.64	0.64	0.64	0.72
47.00	0.57	0.58	0.56	0.59	0.57	0.57	0.59	0.58	0.60	0.59	0.57	0.59	0.64	0.64	0.64	0.64	0.72

	18	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**	**28**	**29**	**30**	**31**	**32**	**33**	**34**
48.00	0.57	0.58	0.57	0.59	0.58	0.58	0.59	0.58	0.59	0.59	0.57	0.59	0.64	0.64	0.64	0.65	0.72
49.00	0.57	0.58	0.57	0.59	0.58	0.58	0.59	0.58	0.59	0.59	0.57	0.59	0.64	0.64	0.64	0.65	0.72
50.00	0.59	0.60	0.58	0.61	0.59	0.59	0.61	0.61	0.61	0.60	0.60	0.60	0.66	0.66	0.66	0.67	0.66

	35	**36**	**37**	**38**	**39**	**40**	**41**	**42**	**43**	**44**	**45**	**46**	**47**	**48**	**49**	**50**
1	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55
2	0.58	0.58	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56
3	0.57	0.58	0.58	0.58	0.57	0.56	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56
4	0.58	0.58	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56
5	0.58	0.57	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56
6	0.58	0.57	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56
7	0.58	0.57	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56
8	0.58	0.57	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56
9	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.55	0.56
10	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.55	0.55	0.56
11	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56
12	0.58	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56
13	0.57	0.57	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.55	0.55	0.55
14	0.59	0.58	0.58	0.58	0.57	0.56	0.57	0.57	0.56	0.56	0.56	0.56	0.56	0.56	0.56	0.56
15	0.60	0.61	0.61	0.61	0.58	0.58	0.60	0.60	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.59
16	0.60	0.61	0.60	0.60	0.58	0.58	0.60	0.60	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.59
17	0.60	0.61	0.60	0.60	0.58	0.57	0.60	0.60	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.58
18	0.60	0.61	0.60	0.60	0.58	0.58	0.60	0.60	0.58	0.58	0.57	0.57	0.57	0.57	0.57	0.59
19	0.61	0.62	0.62	0.62	0.59	0.59	0.61	0.61	0.58	0.59	0.58	0.58	0.58	0.58	0.58	0.60
20	0.61	0.61	0.62	0.62	0.57	0.57	0.61	0.62	0.57	0.57	0.56	0.56	0.56	0.57	0.57	0.58
21	0.62	0.62	0.62	0.62	0.60	0.60	0.61	0.61	0.60	0.60	0.59	0.59	0.59	0.59	0.59	0.61
22	0.61	0.62	0.61	0.61	0.58	0.58	0.61	0.61	0.58	0.58	0.58	0.57	0.57	0.58	0.58	0.59
23	0.61	0.62	0.61	0.61	0.58	0.58	0.61	0.61	0.58	0.58	0.58	0.57	0.57	0.58	0.58	0.59
24	0.63	0.62	0.61	0.61	0.60	0.60	0.61	0.61	0.60	0.59	0.59	0.59	0.59	0.59	0.59	0.61

	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
25	0.63	0.62	0.62	0.62	0.59	0.59	0.61	0.61	0.59	0.59	0.58	0.58	0.58	0.58	0.58	0.61
26	0.62	0.62	0.61	0.61	0.60	0.60	0.61	0.61	0.60	0.59	0.60	0.60	0.60	0.59	0.59	0.61
27	0.62	0.62	0.61	0.61	0.60	0.60	0.61	0.61	0.59	0.59	0.59	0.59	0.59	0.59	0.59	0.60
28	0.63	0.60	0.61	0.61	0.58	0.58	0.59	0.60	0.57	0.57	0.57	0.57	0.57	0.57	0.57	0.60
29	0.61	0.61	0.61	0.61	0.60	0.59	0.60	0.61	0.59	0.59	0.59	0.59	0.59	0.59	0.59	0.60
30	0.78	0.75	0.74	0.74	0.64	0.64	0.73	0.74	0.64	0.65	0.64	0.64	0.64	0.64	0.64	0.66
31	0.78	0.75	0.74	0.74	0.64	0.64	0.73	0.74	0.64	0.65	0.64	0.64	0.64	0.64	0.64	0.66
32	0.78	0.75	0.74	0.74	0.64	0.64	0.73	0.74	0.64	0.65	0.64	0.64	0.64	0.64	0.64	0.66
33	0.78	0.74	0.74	0.74	0.64	0.64	0.73	0.74	0.64	0.65	0.64	0.64	0.64	0.65	0.65	0.67
34	0.63	0.60	0.60	0.60	0.71	0.71	0.59	0.59	0.71	0.72	0.72	0.72	0.72	0.72	0.72	0.66
35	1.00	0.75	0.74	0.74	0.65	0.65	0.74	0.74	0.65	0.65	0.65	0.65	0.65	0.65	0.65	0.65
36	0.75	1.00	0.98	0.98	0.63	0.63	0.97	0.98	0.63	0.63	0.63	0.63	0.63	0.63	0.63	0.64
37	0.74	0.98	1.00	1.00	0.63	0.63	0.98	1.00	0.62	0.63	0.63	0.63	0.63	0.62	0.62	0.63
38	0.74	0.98	1.00	1.00	0.62	0.63	0.98	1.00	0.62	0.63	0.63	0.62	0.63	0.62	0.62	0.63
39	0.65	0.63	0.63	0.62	1.00	1.00	0.62	0.62	1.00	0.92	0.91	0.91	0.91	0.92	0.92	0.71
40	0.65	0.63	0.63	0.63	1.00	1.00	0.62	0.62	1.00	0.92	0.91	0.91	0.91	0.92	0.92	0.71
41	0.74	0.97	0.98	0.98	0.62	0.62	1.00	0.98	0.62	0.62	0.62	0.62	0.62	0.62	0.62	0.63
42	0.74	0.98	1.00	1.00	0.62	0.62	0.98	1.00	0.62	0.62	0.62	0.62	0.62	0.62	0.62	0.63
43	0.65	0.63	0.62	0.62	1.00	1.00	0.62	0.62	1.00	0.92	0.91	0.91	0.91	0.92	0.91	0.71
44	0.65	0.63	0.63	0.63	0.92	0.92	0.62	0.62	0.92	1.00	0.93	0.93	0.93	0.98	0.98	0.71
45	0.65	0.63	0.63	0.63	0.91	0.91	0.62	0.62	0.91	0.93	1.00	1.00	1.00	0.93	0.93	0.71
46	0.65	0.63	0.63	0.62	0.91	0.91	0.62	0.62	0.91	0.93	1.00	1.00	1.00	0.93	0.93	0.71
47	0.65	0.63	0.63	0.63	0.91	0.91	0.62	0.62	0.91	0.93	1.00	1.00	1.00	0.93	0.93	0.71
48	0.65	0.63	0.62	0.62	0.92	0.92	0.62	0.62	0.92	0.98	0.93	0.93	0.93	1.00	1.00	0.71

	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
49	0.65	0.63	0.62	0.62	0.92	0.92	0.62	0.62	0.91	0.98	0.93	0.93	0.93	1.00	1.00	0.71
50	0.65	0.64	0.63	0.63	0.71	0.71	0.63	0.63	0.71	0.71	0.71	0.71	0.71	0.71	0.71	1.00

Figure S1. Age at Diagnostic Testing
This figure (on the next page) shows the distribution of age of diagnostic testing among HCM patients. Age at testing is used as a proxy for age of onset, which is indicative of phenotypic severity. Black indicates all patients, while red indicates patients with variants classified “Pathogenic” by the manual classification process we used to generate our training set. Both have a similar distribution. If our manual classification process picked out the most phenotypically severe variants, we would expect the red distribution to be skewed towards the left compared to the black distribution.

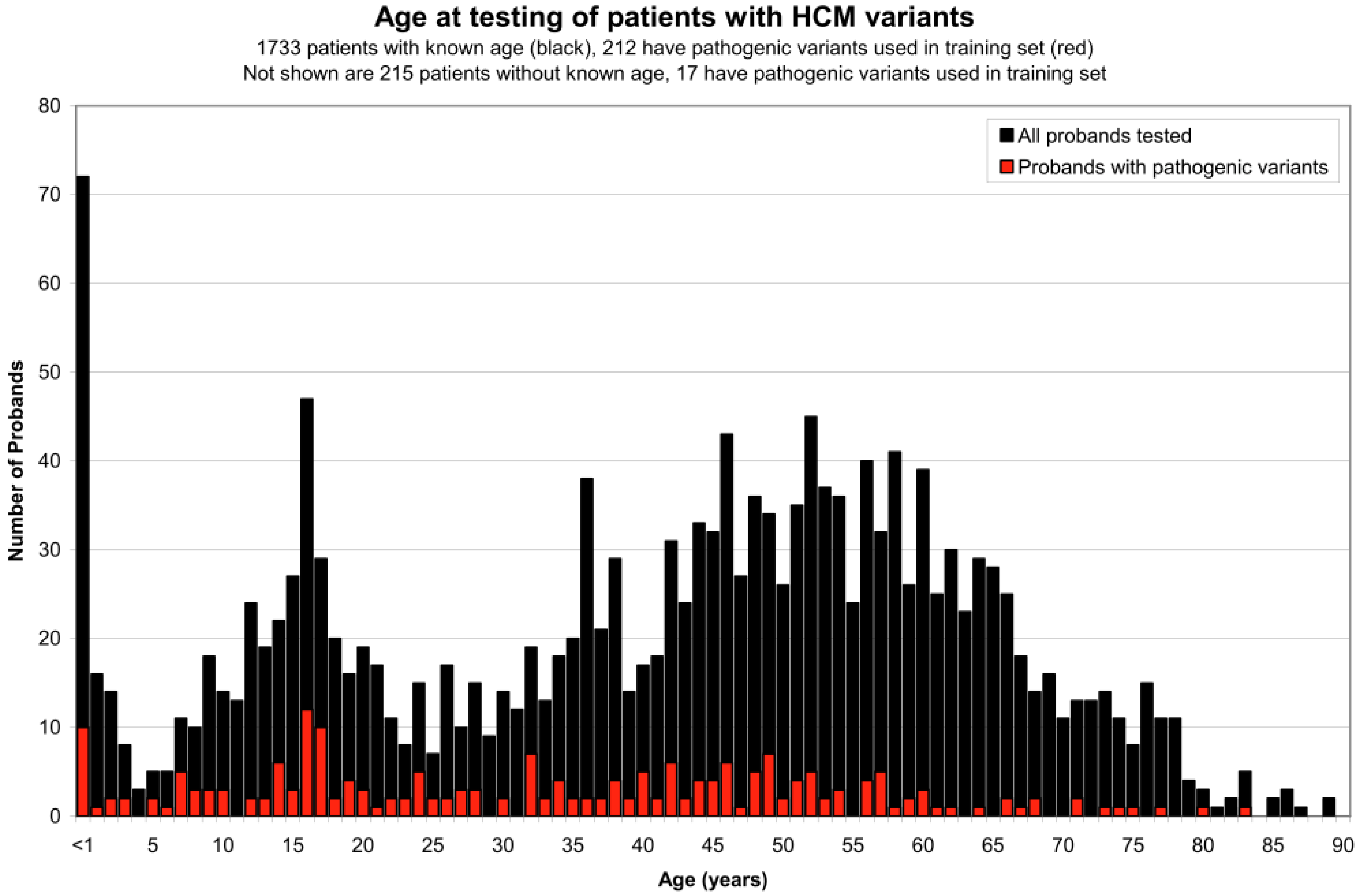
Age at testing of patients with HCM variants
1733 patients with known age (black), 212 have pathogenic variants used in training set (red)
Not shown are 215 patients without known age, 17 have pathogenic variants used in training set
All probands tested
Probands with pathogenic variants
Number of Probands
0
10
20
30
40
50
60
70
80
<1
5
10
15
20
25
30
35
40
45
50
55
60
65
70
75
80
85
90
Age (years)

Figure S2. MrBayes Control File

This control file was used in MrBayes to produce the MrBayes score. The file “sequences.nex” referenced in this file contains the multiple sequence alignment for the desired gene, in MrBayes Nexus file format.

```
begin mrbayes;
    execute sequences.nex;
    prset aamodelpr=fixed(equalin);
    lset rates=gamma;
    report siterates=yes;
    mcmc ngen=1000000 filename=mybpc3_tree;
    sump printtofile=yes;
    sumt showtreeprobs=yes;
end;
```

Figure S3. Multiple Sequence Alignments

These are the three custom alignments we used, in FASTA format. The first is an alignment of MYBPC3 used with PSIC, in ClustalW format. The second and third are alignments of MYBPC3 and MYH7 used with MrBayes, in MrBayes Nexus file format. All other alignments were produced using the PolyPhen-2 alignment pipeline.

Alignment 1 (MYBPC3 for PSIC)

```
CLUSTAL W (1.83) multiple sequence alignment


gi|172072588|ref|NP_0 myosin binding protein C, cardiac [Danio
reri   ---------------------------------------------------------
---------
MPEPTKKIVSAFSKKPKSQTAEIGARVIFEAETEKPGVKVKWQRESKDILPSHKYTISAEDNKH
SLTINNIIQEDAVGYAVIAGMSKVKFELKIKESEVKG---------
VEKAKSPDPAAVEHKPEESKPEESKPEPKEPPPAPTENSAPESTGPPSDGVAPEALPESHQPDT
RQDLTGLFTEKPHSGEVNVGENIIFIARVCGESLLKKPTVKWFKGKWMDLASKSGKHLQLKEHY
DRNT------------------------
KVYTFEMHIIAAKANFAGAYRCEVSSRDKFDSCNFDLIVHEART-TEGFDIRTAFRRTST----
----------DAGDDSGELDFSALLKKRDSFVKTG-Q-RAVHVSTEPDVDVWDILQK-
APPSEYEKIAFQYGITDLRGMLKRLKKMKKEEKKSAAFLKKLDPAYQVEKGHKIKLEIEVANPD
AEVKWLKNGQEIHPTGS--
KYIFESVGNKRFLTINNCSLSDDAAYMCVVGDEKTVTELFVKEPPVLIVRNLEDQMAMKGDRVE
FECEVSEEGAQVKWEKDGVELTRDESFK--
YRFKKDGCKHVLIINDVTKEDCGHYRVKTNGGQSLAELMVQEKQLEVYQSIADLTVKAKDQAVF
KCEVSDENVKGIWYKNGVEVKPDARTLITHIGRIHKLTIDDVKPEDEGDYTFVPEGFAF-
NLSAKLNFLEVKIDFVPRQDPPKIHLDCMGRTAESTILVVAGNKLRLDVPITGDPAPTVIWTK-
---------------------------
GEKVLTDSDGRVHVESTKGHCIFTIEGAERQDEGVYSVIVRNPAGEDTADINVKVVDVPDPPEA
PRILSVGEDSCVVQWDAPRFDGGQPVIGYVLERKKKKSYRWMRLNFDPYKETTFEAKKMIEGVP
YEMRVYAVNAIGMSRPSAASQPFVPVAPTSEPIGLCVDDISDTTISLKWRTPERIGSAELEGYG
VEYCKEG------------------
SDEWIPAFSGLTERTSVIIRDLPTGEKMQFRVRAYNMAGPSAPATLQQAVTIREIMQRPKIWLP
RNLRQTLIKKVGETINLVIPFQ-----
GKPRPQVSWTKNDEPLDPKSVSIRNSDTDTILFIRRSERKDSGKYDVQVQIENVEDKASVNIQI
V--------------------------
DVPGPPQNLKVMDVWGFNVALEWKPPKDNGNCDITGYNIQKADKKTMEWYTVFEQYRRTNCVVS
DLIMGNEYVFRVYAANMVGLSPEPCLSKDSAYIQKTG-----------
IVYKPPSYKDHDFSEAPKFTHPLKSRSVIAGYNATLSCSVRGIPKPKITWYKNKMDITNEAKYR
MFSNQGVLTLEIRKPCPFDGGVYMCKAVNDSGEDLVECKLEVRLPQVTKEDIKK----------
--------------------------------------------------------------
gi|47230505|emb|CAF99 unnamed protein product [Tetraodon
nigrovirid   ---------------------------------------------------
---------------
MPETLKKAVSAFTKKPKTLEAAAGSSVVFEAETEKPDAKVKWQCNAKDIANGNKYTIAADGSKH
SLSIKAVTHQDANIYAVISGGSKVKFELKV----------------VSKPEAP----------
ADGPEEPGVQPEQAPAASTQN--------QSVAAGPEAPPAE----------------------
```

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--
GQNITFVAKVNEESLLKKPSVKWFKGKWMDLASKSGKHLQLKESYDRNTKVADSQTSGNPVFLP
AYSVFLHLVQVYTFEMQILAAKANFAGAYRCEVSSKDKFDSCNFTLTVHDVCV-
EEGLDIRAAFRRTST---------------DGKEDSGELDFSTLLKKR------------
AVHVSSEPEVDVWEILSK-
APSSEYEKIAFQHGITDLRGMLKRLKKMKKEEKKSAAFLRKLDPAYQVTKGHKIRLAVEVANAD
ADVKWLKNGQEFHPTG---
RYIFESVGNMRYLTINNCSLADDAAYCCVVGEEKSTSELFVKEPPVLIVKNLEDQMVMKGDRVE
LECEVSEEGANVKWEKDGVELTRDESFK--
YRFKKDGCKHILIINDATKEDCGHYKVKTNGGESMAELLVQEKELEIYQSIADLTVKAKDQALF
KCEVSDENVRGTWYKNGAEVKPDARINITHIGRIHKLTIDDVKPGDEGDYTFVPDGYAY-
NLSAKLNFLEVKIDYVPRQDPPKIHLDCMGRTAESTIVVVAGNKLRLDVPITGDPAPTVIWTK-
----------------------------
GEKVVTEGDGRVHVESTKGHCIFTIEGAERQDEGIYSVVVRNAAGEDTADINVKVVDVPDPPQE
VKILSVGEESCVVQWDPPAFDGGQPIIGYVLERKKKKSYRWMRLNFDPYPETTYEAKRMIEGVA
YEMRVYAVNSIGMSRHSQASQPFVPVAPTSEPVGLCVDDISDTSIVLKWRPPERMGSVDLEGYG
VEYCKEG------------------
TDEWIPAAQGLTERTSLIIRNLTTGDRLQFRVRAYNMAGPSPAATLAQPITIREIMQRPKILLP
RNLRQTLIRRVGDTVNLVIPFQ-----
GKPRPKVTWSKNGEPLSSTLASIRNSEGDTILFIRKTEKTHSGKYDLQVQIENVEDTASVTLQV
VGRSDSRVWTSGGGSTGTLIFLLIRVLDLPGPPEVLKIVDVWGFNVALEWKPPKDDGNCEITGY
TVQKADKKTMEWFTVYDQYRRTHCIVSDLIMGNEYVFRVFANNLVGPSPEPCGTKDSAYIQKTG
GQQPHVVTSSGVVYKPPTHKEHDLSEAPKFTRPLVSRSVIAGYTATLSCSVRGVPKPKVTWYKN
KMDLSNEAKYRMLSNHGVLTLEIRKPCPFDGGVYTCKAVNDSGEDTVECKLEVRS-
QIIKEDKKEESKKETHPAA-----------------------------------------------
-----------------
gi|224051064|ref|XR_0 PREDICTED: Taeniopygia guttata misc_RNA
(LOC1   ----------------------------------------------------------
----------
MPEPVKKTVSAFTKKPKTTEVTAGNTAVFEAETEKSGIKVKWQRAGTEITESEKYVIKTEGNKH
SLTINNVGKEDDVTYAVIAGSSKVKFELKVKE----------------
PEKSETVTPAEAVPAPAASESPAPPAESSQNT---------------EVSSAETQ------
PEEPLDPIGLFVARPQDGEVTVGGNITFTAKVAGESLLKKPSVKWFKGKWMDLGSKVGKHLQLH
DSYDRNT-------------------------
KVYTFEMEIIEANMTFAGGYRCEVSTKDKFDSSNFSLTVNEAPV-
SGDLDIRAAFRRTSLAGGGRRMTSAFLSTEGHDDGAEFNFSSLLKKRDSFLRPS-
NRGEGKSESQSDVDVWDILRK-
APPTEYEKIAFQYGITDLRGMLKRLKRIKKEEKKSTAFLKKLDPAYQVDKGQKIKLMVEVANPD
ADVKWLKNGQEIQVSGS--
KYIFEAVGNKRILTINHCSLADDAAYECVVGDEKSFTELFVKEPPILIIHPLEDQMVMVGERVE
FECEVSEEGATVKWEKDGIELTREETFK--
YRFKKDGKKQYLIINESTKEDSGHYTVKTNGGVSVAELIVQEKKLEVYQSIADLTVKARDQAVF
KCEVSDENVKGIWLKNGKEVIPDERIKISHIGRIHKLIIEDVTPEDEADYSFIPQGFAY-
NLSAKLQFLEVKIDFVPREEPPKIHLDCLGQSPD-TIVVVAGNKLRLDVPVSGDPTPTVIWQK-
VNKRNDLLRNS-
EDSMTPSENSSDLNTDNKLLFESEGRVRVEMHEDHCVFIIEGAEKEDEGVYRVILKNPVGEDKA
DITVKVIDVPDPPEAPTISNIGEDYCTVQWQPPKYDGGQPVLGYILERKKKKSYRWMRLNFDLL
```

```
KELTYEAKRMIEGVVYEMRIYAVNSIGMSRPSPASQPFMPIAPPSEPTHFTVEDVSDSTVSLKW
RPPERIGAGGLDGYMVEYCKDG------------------
STEWIPALPGLTERTSALIKDLVTGDKLYFRVKAVNLAGESGAATIKEPVTVQEILQRPKFWLP
RQLRQTLVKKVGETINIVIPFQ-----
GKPRPKITWLKDGQTLDSKDVGIRNSNTDTILFIRKAELHHSGAYEVTLQIENMSDKVAITIQI
I--------------------------
DKPGPPQNIKLVDVWGFNAALEWTPPQDDGNAQILGYTVQKADKKTMEWYTVFDHYRRTNCIVS
DLIMGNEYFFRIFSENLCGLSETAATTKNPAHIQKTG-----------
TTYKPPCYKEHDFSEAPKFTHPLVNRSVIAGYNTTLSCAVRGIPKPKIFWFKNKMDLSGDAKYR
MFSKQGVLTLEIRKPTPFDGGIYTCKAVNECGEAEIECRLDVRGNQMNPMDNPNKAMKRVMGS-
--------------------------------------------------------------
sp|Q90688|MYPC3_CHICK Myosin-binding protein C, cardiac-type
OS=Gal   -------------------------------------------------------
-----------
MPEPAKKAVSAFTKKPKTTEVAAGSTAVFEAETEKTGIKVKWQRAGTEITDSEKYAIKAEGNKH
SLTISNVGKDDEVTYAVIAGTSKVKFELKVKE---------------
PEKSEPVAPAEASPAPAASELPAPPVESNQNP--------------EVPPAETQ------
PEEPVDPIGLFVTRPQDGEVTVGGNITFTAKVAGESLLKKPSVKWFKGKWMDLASKVGKHLQLH
DNYDRNN------------------------
KVYTFEMEIIEANMTFAGGYRCEVSTKDKFDSSNFNLIVNEAPV-
SGEMDIRAAFRRTSLAGGGRRMTSAFLSTEGLEESGELNFSALLKKRDSFLRTA-
NRGDGKSDSQPDVDVWEILRK-
APPSEYEKIAFQYGITDLRGMLKRLKRIKKEEKKSTAFLKKLDPAYQVDKGQKIKLMVEVANPD
ADVKWLKNGQEIQVSGS--
KYIFEAIGNKRILTINHCSLADDAAYECVVAEEKSFTELFVKEPPILITHPLEDQMVMVGERVE
FECEVSEEGATVKWEKDGVELTREETFK--
YRFKKDGKKQYLIINESTKEDSGHYTVKTNGGVSVAELIVQEKKLEVYQSIADLTVKARDQAVF
KCEVSDENVKGIWLKNGKEVVPDERIKISHIGRIHKLTIEDVTPGDEADYSFIPQGFAY-
NLSAKLQFLEVKIDFVPREEPPKIHLDCLGQSPD-TIVVVAGNKLRLDVPISGDPTPTVIWQK-
VNKKGELVHQSNEDSLTPSENSSDLSTDSKLLFESEGRVRVEKHEDHCVFIIEGAEKEDEGVYR
VIVKNPVGEDKADITVKVIDVPDPPEAPKISNIGEDYCTVQWQPPTYDGGQPVLGYILERKKKK
SYRWMRLNFDLLKELTYEAKRMIEGVVYEMRIYAVNSIGMSRPSPASQPFMPIAPPSEPTHFTV
EDVSDTTVALKWRPPERIGAGGLDGYIVEYCKDG------------------
SAEWTPALPGLTERTSALIKDLVTGDKLYFRVKAINLAGESGAAIIKEPVTVQEIMQRPKICVP
RHLRQTLVKKVGETINIMIPFQ-----
GKPRPKISWMKDGQTLDSKDVGIRNSSTDTILFIRKAELHHSGAYEVTLQIENMTDTVAITIQI
I--------------------------
DKPGPPQNIKLADVWGFNVALEWTPPQDDGNAQILGYTVQKADKKTMEWYTVYDHYRRTNCVVS
DLIMGNEYFFRVFSENLCGLSETAATTKNPAYIQKTG-----------
TTYKPPSYKEHDFSEPPKFTHPLVNRSVIAGYNTTLSCAVRGIPKPKIFWYKNKVDLSGDAKYR
MFSKQGVLTLEIRKPTPLDGGFYTCKAVNERGEAEIECRLDVRVPQ------------------
--------------------------------------------------------------
tr|A9JTS4|A9JTS4_XENT Mybpc3 protein OS=Xenopus tropicalis
GN=mybpc   -----------------------------------------------------
-------------MPEPVKK--
SAFTKKPKSEEVSVGGTVTFAAETDKPGLKVKWQRNNVDITANERFAIKSEGKQHSLTISNATA
EDEVVYAVIAGTSKVKFELKVKE---------------QEKTE-
```

```
EAPAPAPAAPEASEAPAPPAPDSSAPPPTETAEGEAKPPESAEATAIQ------
PEPPKDEIGLFLERPKDAEITVGSNIKFTARIAGANLIKKPVVKWFKGKWMDLTSKVGKHLQLH
EIYDRNT------------------------
KIYTFEIQIIQAKTTYAGGYRCEVSSKDKFDSCNFNLAVHEVST-SGEVDIRAAFRRTG-----
----------DGAEEAGELDFSALLKKRD---------NEPKQGAEPDVDVWDILKK-
APPSEYEKIAFQYGITDLRGLLKRLKKMKKEEKKSEAFLKKMDPAYQIDKGQKMKLVVEVANPD
AEVKWLKNGQEIRVSGS--
KYIFESIGNKRILTINNCSLADDAAYQCVIGEEKCFTELFVREPPVQILHSLEDQMVMVGERVE
FECEVSEEGAQVKWEKDGVELTREETFK--
YRFKKDGKKHFLIINETTLEDGGNYKVKTNGGESVAELMVQEKQLEVLQDVADLTVKAKEQAVF
KCEVSDETVTGIWVKNGKEVIPNNRIKITHIGRVHKLTIDDVVPQDEGDYSFIPNGFAF-
SLSAKLHFMEVKIDFVPRQEPPKIKLDCMSQCAD-TIIVVAGNKLRLDVPISGDPAPTVVWMK-
GDK---------------------------
LISEVDGRVHVETHADHCVFIIEGAEKSDEGAYTVLVKNEAGEDKANINVKVIEVPDPPESPKI
SNIGEDFCTVQWDPPKYDGGQPVLGYILERKKKKSYRWMRLNYDLVKELTYESKRMIEGVVYEM
RIYAVNSIGMSLPSQPSQPFMPIAPTSEPTQLVVEDVSDTSISLKWRPPERIGAGGLDGYTVEY
CKEG------------------
STEWVPALQGLTERNSVMIRDLPTGERLTFRVRAINLAGPSEPCTMKEPVTIREIMQRPKIWLP
RYLRQKLIKKVGETVNIVIPFQ-----
GKPRPVVTWLKDGQPVDPKQVGIRNSEADTILFIRKAERDHSGEYKVQIQIENCEDSATICIQI
V--------------------------
DKPSASQKLKIVEIWGFNVALEWAPPQDDGNTEITGYTVQKADKKTMEWFTVFEHYRRTHCVVS
DLIMGNEYYFRVFSENMCGLSEKPCTTKNSAYIQKTG-----------
TAYKPPTYKDHEFDEAPKFTHPLNDRSVVAGYNATLSCAVRGIPKPKITWYKNKMDLSMEARYR
SFSKQGVLTLEVRKPSPFDGGLYTCKAVNEHGVAETECRLEVRVPQ------------------
--------------------------------------------------------------
tr|A8MXZ9|A8MXZ9_HUMA Putative uncharacterized protein MYBPC3
OS=Ho   --------------------------------------------------------
----------
MPEPGKKPVSAFSKKPRSVEVAAGSPAVFEAETERAGVKVRWQRGGSDISASNKYGLATEGTRH
TLTVREVGPADQGSYAVIAGSSKVKFDLKVIE---------------AEKAEPML------
APAPAPAEATGAPGEAPAPAAELGESAPSPKGSSSAALNGPT----
PGAPDDPIGLFVMRPQDGEVTVGGSITFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQLH
DSYDRAS------------------------
KVYLFELHITDAQPAFTGSYRCEVSTKDKFDCSNFNLTVHEAMG-
TGDLDLLSAFRRTSLAGGGRRIS------DSHEDTGILDFSSLLKKSSSFRTP----
RDSKLEAPAEEDVWEILRQ-
APPSEYERIAFQYGVTDLRGMLKRLKGMRRDEKKSTAFQKKLEPAYQVSKGHKIRLTVELADHD
AEVKWLKNGQEIQMSGS--
KYIFESIGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRPLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGQRHHLIINEAMLEDAGHYALCTSGGQALAELIVQEKKLEVYQSIADLMVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRIPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKAITQGNKAPARPAPDAPEDTGDSDEWVFDKKLLCET
EGRVRVETTKDRSIFTVEGAEKEDEGVYTVTVKNPVGEDQVNLTVKVIDVPDAPAAPKISNVGE
DSCTVQWEPPAYDGGQPILGYILERKKKKSYRWMRLNFDLIQELSHEARRMIEGVVYEMRVYAV
```

```
NAIGMSRPSPASQPFMPIGPPSEPTHLAVEDVSDTTVSLKWRPPERVGAGGLDGYSVEYCPEG-
-----------------
CSEWVAALQGLTEHTSILVKDLPTGARLLFRVRAHNMAGPGAPVTTTEPVTVQEILQRPRLQLP
RHLRQTIQKKVGEPVNLLIPFQ-----
GKPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAARRVHSGTYQVTVRIENMEDKATLVLQV
V--------------------------
DKPSPPQDLRVTDAWGLNVALEWKPPQDVGNTELWGYTVQKADKKTMEWFTVLEHYRRTHCVVP
ELIIGNGYYFRVFSQNMVGFSDRAATTKEPVFIPRPG-----------
ITYEPPNYKALDFSEAPSFTQPLVNRSVIAGYTAMLCCAVRGSPKPKISWFKNGLDLGEDARFR
MFSKQGVLTLEIRKPCPFDGGIYVCRATNLQGEARCECRLEVRVPQ------------------
--------------------------------------------------------------
gi|114637607|ref|XP_5 PREDICTED: protein C, cardiac [Pan
troglodyte   ---------------------------------------------------
---------------
MPEPGKKPVSAFSKKPRSVEVAAGSPAVFEAETERAGVKVRWQRGGSDISASNKYGLATEGTRH
TLTVREVGPADQGSYAVIAGSSKVKFDLKVIE---------------AEKAEPML------
APAPAPAEATGAPGEAPAPAAELGESAPSPKGSSSAALNGPT----
PGAPDDPIGLFVMRPQDGEVTVGGSITFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQLH
DSYDRAS------------------------
KVYLFELHITDAQPAFAGGYRCEVSTKDKFDCSNFNLTVHEAMG-TGDLDLLSAFRRT------
---------------------------------------DSKLEAPAEEDVWEILRQ-
APPSEYERIAFQYGVTDLRGMLKRLKGMRRDEKKS-------------
TEACLLPLSTCVSLTRFPATSLR-------PPP--
RYIFESIGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRPLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGRRHHLIINEATLEDAGHYALCTSGGQALAELIVQEKKLEVYQSIADLMVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRIPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKAITQGNKAPARPAPDAPEDTGDSDEWVFDKKLLCET
EGRVRVETTKDRSIFTVEGAEKEDEGVYTVTVKNPVGEDQVNLTVKVIDVPDAPAAPKISNVGE
DSCTVQWEPPAYDGGQPILGYILERKKKKSYRWMRLNFDLIQELSHEARRMIEGVVYEMRVYAV
NAIGMSRPSPASQPFMPIGPPSEPTHLAVEDVSDTTVSLKWRPPERVGAGGLDGYSVEYCPEG-
-----------------
CSEWVAALQGLTEHTSILVKDLPTGARLLFRVRAHNMAGPGAPVTTTEPVTVQEILQRPRLQLP
RHLRQTIQKKVGEPVNLLIPFQ-----
GKPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAARRVHSGTYQVTVRIENMEDKATLVLQV
V--------------------------
DKPSPPQDLRVTDAWGLNVALEWKPPQDVGNTELWGYTVQKADKKTMEWFTVLEHYRRTHCVVP
ELIIGNGYYFRVFSQNMVGFSDRAATTKEPVFIPRPG-----------
ITYEPPNYKALDFSEAPSFTQPLVNRSIIAGYTAMLCCAVRGSPKPKISWFKNGLDLGEDARFR
MFSKQGVLTLEIRKPCP-----------------------------------------------
--------------------------------------------------------------
gi|109106380|ref|XR_0 PREDICTED: Macaca mulatta protein C,
cardiac    -----------------------------------------------------
-------------
MPEPGKKPVSAFSKKPRSVEVAAGSPAVFEVETERAGVKVRWQRGGSDIGASSKYGLATEGTRH
TLTVREVGPADQGSYAVIAGSSKVKFDLKVTE---------------AEKAEPVL------
```

```
APAPAPAEATGTPGETLAPAAELGESAPSPEGSSSAARNDPT----
PGAPDDPIGLFVMRPQDGEVTVGGSITFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQLH
DSYDRAS------------------------
KVYLFELHITDAQPAFTGGYRCEVSTKDKFDCSNFNLTVHEAVG-
TGDLDLLSSFRRTSLAGGGRRIS------DSHEDAGILDFSSLLKKSSSFRTP----
RDSKLEAPAEEDVWEILRQ-
APPSEYERIAFQYGVTDLRGMLKRLKGMRRDEKKSTAFQKKLEPAYQVSKGHKIRLTVELADPD
AEVKWLKNGQEIQMSGS--
KYIFESIGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRPLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGRRHRLIINEATLEDMGHYALRTSGGQALAELIVQEKKLEVYQSIADLTVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRIPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKAITQGNKSPARPAPDAPEDAGDSDEWVFDKKLLCET
EGRVRVETTKDRSIFTVEGAEKEDEGVYTVTVKNPVGEDRVNLTVKVIDVPDAPAAPKVSNVGE
DSCTVQWEPPAYDGGQPVLGYILERKKKKSYRWMRLNFDLIQELSHEARRMIEGVVYEMRVYAV
NAIGMSRPSPASQPFMPIGPPSEPTHLAVEDASDTTVSLKWRPPERVGAGGLDGYSVEYCPEGG
E----------------
CSEWVAALRGLTEHTSILVKDLPTGARLLFRVRAHNMAGPGAPVTTTEPVTVQEILQRPRLQLP
RHLRQTIQKKVREPVNLLIPFQLFLPSGQPRPQVTWTKEGQPLA-------------------
ARR-------------------------------------------------------------
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tr|Q2Q1P6|Q2Q1P6_CANF Cardiac myosin binding protein C OS=Canis
fam   ----------------------------------------------------------
--------
MPEPGKKPVSAFSKKPRSAEVAAGSPAVFEAETERSGVKVRWQRGGSDISASDKYGLAAEGTRH
TLTVRDVGPADQGSYAVIAGSSKVKFDLKVIE---------------
AEKAETVPGPASVPAPAPAPAEAPGAPGEALASATEEKGGSSSPEGSSSAAPDG------
SGAPDDPIGLFVMRPQDGEVTAGGSITFSARVAGASLLKPPTVKWFKGKWVDLSSKAGQHLQLH
SSYDRTS------------------------
KVYLFELHITDAQPTSAGGYRCEVSTKDKFDSCNFNLTVHEAVG-
PGDLDLRSAFRRTSLAGSGRRIS------DSHEDAGTLDFSSLLKKRDSFR------
RDSRLEAPAEEDVWEILRQ-
ASPSEYERIAFQHGVTDLRGMLKRLKGMKRDEKKSTAFQKKLEPAYQVSKGHKIRLTVELADPD
ADVKWLKNGQEIQMSGS--
KYIFESVGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRPLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGQRHHLIINEATLEDAGHYALRTSGGQALAELIVQEKKLEVYQSIADLTVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRKPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKTITQKNKVPAGPAPDASGDAAASDEWVFDKKLLCET
EGRVRVETTKDRSIFTVEGAEKEDEGVYVVTVKNPVGEDQVNLTVKVIDVPDAPAAPKISNVGE
DSCTVQWEPPAYDGGQPVLGYILERKKKKSYRWMRLNFDLLRELSHEARRMIEGVVYEMRVYAV
```

```
NAIGMSRPSPASQPFMPIGPPSEPTHLAVEDVTDTTVSLKWRPPERAGAGGLDGYSVEYCRED-
-----------------
CSEWVTALQGLTEHTAVLVKDLPTGARLQFRVRAHNMAGPGAPVTTQEPVTVQEILQRPRLQLP
RHLRQTIQRKVGEPVNLLIPFQ-----
GKPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAAHRAHSGTYQVMLRIENMEDKATLVLQI
V--------------------------
DKPSPPQDIRVAEAWGFNVALEWKPPQDYGNTEIWGYTVQKADTKTMEWFTVLEHYRRTHCVVS
ELIIGNGYYFRVFSHNMVGPSDKAATTKEPVFIPRPG-----------
ITYEPPSYKALDFSEAPSFTRPLVNRSVIAGYNATLCCAVRGSPKPKISWFKNGLDLGKDARFR
MFSKQGVLTLEIRKPCPFDGGIYVCRAINLQGEAQCECRLEVR-------------VPQ-----
--------------------------------------------------------------
gi|194217890|ref|XP_0 PREDICTED: similar to cardiac myosin
binding    -----------------------------------------------------
-------------
MPEPGKKPVSAFSKKPRSAEVAAGSPAVFEAETERAGLKVRWQRAGSDISASDKYGLAAEGTRH
TLTVRDVGPADQGSYAVIAGSSKVKFDLKVIE---------------PEKTEPVP------
SPAPTPAEAPGAPREALASATEAEGGSPSPEGSSSAAPDG------
PGAPDDPIGLFVMRPQDGEVTVGGSITFSARVAGASLLKPPMVKWFKGKWVDLSSKVGQHLQLH
DSYDRAS------------------------
KVYLFELHITDAQATFTGGYRCEVSTKDKFDSCNFNLTVHEAIG-PGDLDLRSAFRRT------
---------------------------------------DSRLEAPAEEDVWEILRQ-
APPSEYERIAFQHGITDLRGMLKRLKGMRRDEKKSTAFQKKLEPAYQVSKGHKIRLTVELANPD
AEVKWLKNGQEIQMSGS--
KYIFESIGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRPLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGQRHHLIINEATLEDAGHYALHTSGGQALAELIVQEKKLEVYQSIADLTVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAS-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRVPD-
TIVVVAGNKLRLDVPISGDPAPTVTWQKTITQGNKVPAGPAPDAPGDAGASDEWVFDKKLLCET
EGRVRVETTKDRSVFTLEGAEKEDEGVYIVTVKNPVGEDQVNLTVKVIDVPDAPAAPKISNVGE
DSCTVQWEPPAYDGGQPILGYILERKKKKSYRWMRLNFDLLRELSLEAKRMIEGVVYEMRVYAV
NAIGMSRPSPASQPFMPIGPPSEPTHLAVEDVSDTTVSLKWRPPERVGAGGLDGYSVEYCREG-
-----------------
GSEWVAALQGLTEHTSLLVKDLPTGARLLFRVRAHNVAGPGAPVTTKEPVTVQEILQRPRLQLP
RHLRQTIHRRVGEPVNLLIPFQ-----
GRPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAARRTHSGTYQVTLRIENMEDEATLVLQI
V--------------------------
DKPSPPQDIRVAEAWGFNVALEWKPPQDDGNTEIWGYTVQKADKKTMEWFTVLEHYRRTHCVVS
ELIIGNGYYFRVFSHNMVGPSDKAATTKEPVFIPKAG-----------
ITYESPSYKALDFLEAPSFTRPLVNRSVIAGYNATLSCAVRGSPKPNISWFKNGLDLRDDARFR
TFSKQGLLTLEIRKPCPFDGGIYVCRATNLQGEAQCECRLEVRGVKAQVGAPSSGQFPEEQPPG
GPEVP---------------------------------------------------------
tr|Q0VD56|Q0VD56_BOVI Myosin binding protein C, cardiac OS=Bos
taur   ---------------------------------------------------------
---------
MPEPGKKPVSAFSKKPRSAEVAAGSSAVFEAETERAGLKVRWQRAGSDISASDKYSLAAEGTRH
TLTVRDVGPADQGSYAVIAGSSKVKFDLKVVD---------------AGKAEPVS------
```

```
APAPAPTEAPGAPGEAPTSAPEVEAGAPSPEESSSAAPEG------
PSAPGDPIGLFVMRPQDGEVTVGGTITFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQLH
DSYDRTS------------------------
KVYLFELRIMDAQTTFAGGYRCEVSTKDKFDSCNFNLTVHEAVG-
PGDVDLRSTFRRTSLAGGSRRIS------DSHEDAGTLDFSSLLRKSS----L----
RTPRLEAPAEEDVWEILRQ-
APPSEYERIAFQHGVTDLRGMLKRLKGIKRDEKKSTAFQKKLQPAYQVSKGHKIRLMVELADPD
AEVKWLKNGQEIQMSGS--
KYIFESIGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRPLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGQKHHLIINEATLEDAGHYALRTSGGQALAELIVQEKKLEVYQSIADLTVGSKDQAVF
KCEVSDENVRGVWLKNGKELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRVPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKAITKGNKVPAGPAPDASEESGAGDEWVFDKKLLCET
EGRVRVETTKDRSIFTVEGAEREDEGVYVVTVKNPVGEDQVSLTVKVIDVPDAPAAPEISKVGE
DSCTVCWEPPAYDGGQPVLGYILERKKKKSYRWMRLNFDLLRELSHEARRMIEGVIYEMRVYAV
NAVGMSRPSPASQPFMPIGPPSEPTHLAVEDISDTTVSLKWRPPERAGAGGLDGYSVEYRREGS
-----------------
GSAWVSALPGLIERTSLLVKDLPTGARVLFRVRAHNLAGAGPPVTTKEPVTVQELLQRPRLQLP
RHLRQTIQKKVGEPVNLLIPFQ-----
GKPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAAHRAHSGTYQVTLRVEDMEDKAQLVLQV
V--------------------------
DKPSPPQDIQVAEAWGFNVALEWKPPQDDGNTELWGYTVQKADKKTMEWFTVLEHYRHTHCVVS
ELIIGNSYYFRVFSHNTVGPSDTAATTKEPVLIPRPG-----------
ITYELPKYKALDFSEAPSFTRPLVNRSVIAGYNTTLCCAVRGSPKPKISWFKNGLDLGKDARFR
MFSKQGVLTLEIRKPCPFDGGIYACRATNLEGEAQCECRLEVRVPQ------------------
--------------------------------------------------------------
gi|157824043|ref|NP_0 myosin binding protein C, cardiac [Rattus
nor   ----------------------------------------------------------
--------
MPEPGKRPVSAFTKKPRSVEVTAGSAAVFEAETERSGLKVQWQRDGSDIAANDKYGLAAEGKRH
TLTVRDVGPDDQGSYAVIAGSSKVKFDLKVTE---------------PAPPEKAES-----
AVAPTSMEAPETPKEVPALATQLEGNVSSPEGSVSVTQDGSVAGS-
QGAPDDPIGLFLMRPQDGEVTVGGSIVFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQLH
DSYDRAS------------------------
KVYLFELHITDAQATSAGGYRCEVSTKDKFDSCNFNLTVHEAIG-
SGDLDLRSAFRRTSLAGTGRRTS------DSHEDAGTLDFSSLLKK-SSFR------
RDSKLEAPAEEDVWEILRQ-
APPSEYERIAFQHGVTDLRGMLKRLKGMKHDEKKSTAFQKKLEPAYQVNKGHKIRLTVELADPD
AEVKWLKNGQEIQMSG---
RYIFESIGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRSLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGRKHHLIINEATLEDAGHYAVRTSGGQALAELIVQEKKLEVYQSIADLAVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDNRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGSTPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKTITQGKKASAGPPPGAPEDAGADEEWVFDKKLLCET
EGRVRVETTKDRSVFTVEGAEKEDEGVYTVTVKNPVGEDQVNLTVKVIDVPDAPAAPKISNVGE
```

```
DSCIVQWEPPAYDGGQPVLGYILERKKKKSYRWMRLNFDLLRELSHEARRMIEGVAYEMRVYAV
NAVGMSRPSPASQPFMPIGPPGEPTHLTVEDVSDTTVSLKWRPPERVGAGGLDGYSVEYCQEG-
-----------------
CSEWVTALQGLTERTSLLVKDLPTGARLLFRVRAHNVAGPGGPIITKEPVTVQEILQRPRLQLP
RHLRQTIQKKVGEPVNLLIPFQ-----
GKPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAAHRTHSGTYQVTVRIENMEDKATLVLQI
V--------------------------
DKPSPPLDIRVVETWGFSVALEWKPPQDDGNTEIWGYTVQKADKKTMEWFTVLEHYRQTHCVVS
ELIIGNGYYFRVFSHNMVGSSDRAAATKEPIFIPRPG-----------
ITYEPPKYKALDFSEAPSFTQPLTNRSIIAGYNAILCCAVRGSPKPKISWFKNGLDLGEDARFR
MFCKQGVLTLEIRKPCPYDGGVYVCRATNLQGEAQCECRLEVRVPQ------------------
--------------------------------------------------------------
sp|O70468|MYPC3_MOUSE Myosin-binding protein C, cardiac-type
OS=Mus   -------------------------------------------------------
-----------
MPEPGKKPVSAFNKKPRSAEVTAGSAAVFEAETERSGVMVRWQRDGSDITANDKYGLAAEGKRH
TLTVRDASPDDQGSYAVIAGSSKVKFDLKVTE---------------PAPPEKAES-----
EVAPG------APEEVPAPATELEESVSSPEGSVSVTQDGSAAEH-
QGAPDDPIGLFLMRPQDGEVTVGGSIVFSARVAGASLLKPPVVKWFKGKWVDLSSKVGQHLQLH
DSYDRAS------------------------
KVYLFELHITDAQTTSAGGYRCEVSTKDKFDSCNFNLTVHEAIG-
SGDLDLRSAFRRTSLAGAGRRTS------DSHEDAGTPDFSSLLKKRDSFR------
RDSKLEAPAEEDVWEILRQ-
APPSEYERIAFQHGVEACHRPLKRLKGMKQDEKKSTAFQKKLEPAYQVNKGHKIRLTVELADPD
AEVKWLKNGQEIQMSGS--
KYIFESVGAKRTLTISQCSLADDAAYQCVVGGEKCSTELFVKEPPVLITRSLEDQLVMVGQRVE
FECEVSEEGAQVKWLKDGVELTREETFK--
YRFKKDGRKHHLIINEATLEDAGHYAVRTSGGQSLAELIVQEKKLEVYQSIADLAVGAKDQAVF
KCEVSDENVRGVWLKNGKELVPDNRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGSTPD-
TIVVVTGNKLRLDVPISGDPAPTVVWQKTVTQGKKASAGPHPDAPEDAGADEEWVFDKKLLCET
EGRVRVETTKDRSVFTVEGAEKEDEGVYTVTVKNPVGEDQVNLTVKVIDVPDAPAAPKISNVGE
DSCTVQWEPPAYDGGQPVLGYILERKKKKSYRWMRLNFDLLRELSHEARRMIEGVAYEMRVYAV
NAVGMSRPSPASQPFMPIGPPGEPTHLAVEDVSDTTVSLKWRPPERVGAGGLDGYSVEYCQEG-
-----------------
CSEWTPALQGLTERRSMLVKDLPTGARLLFRVRAHNVAGPGGPIVTKEPVTVQEILQRPRLQLP
RHLRQTIQKKVGEPVNLLIPFQ-----
GKPRPQVTWTKEGQPLAGEEVSIRNSPTDTILFIRAARRTHSGTYQVTVRIENMEDKATLILQI
V--------------------------
DKPSPPQDIRIVETWGFNVALEWKPPQDDGNTEIWGYTVQKADKKTMEWFTVLEHYRRTHCVVS
ELIIGNGYYFRVFSHNMVGSSDKAAATKEPVFIPRPG-----------
ITYEPPKYKALDFSEAPSFTQPLANRSIIAGYNAILCCAVRGSPKPKISWFKNGLDLGEDARFR
MFCKQGVLTLEIRKPCPYDGGVYVCRATNLQGEAQCECRLEVRVPQ------------------
--------------------------------------------------------------
gi|126332728|ref|XP_0 PREDICTED: hypothetical protein
[Monodelphis    ------------------------------------------------
------------------
```

```
MPEPGKKAVSAFSKKPKSAEAAVGSSALFEAETERAGLKLRWQRAGSDISASDKYVLTSEGTRH
TLTVQDVQPDDQGLYAAIAGTSKVKFELKVKE---------------AAPGLSLG-----
QEAAPWAPKDTPSPGEGLLPSGPPVPGDASGPGSEGCPPNS------
EEASGDPIGLFVSRPQDGEVTVGDSITFSAQVAGASLLKPPVVKWFKGKWMDLSGKVGKNLQLH
DSYDRAS------------------------
KVYLFELHISEVQAAYAGGYRCEVSTKDKFDSCNFNLTVHEAIG-
PADLDLRSAFRRPSLPGGNRRTSG-----DGHDDAGSLDFSSLLKKRDLFRLVG-A-
RDPKLEAPAEEDVWEILRT-
APPSEYERIAFQHGVTDLRGMLKRLKGMKKDEKKSAAFLKKLEPAYQVNKGQKIRLVVEVADPD
AEVKWLKNGQPIQMSGS--
KYIFESAGNKRMLTISQCSLADDAAYQCMVGGDKCSTELFVKEPPVLITRGLEDQMVTVGQRVE
FECEVSEEGAPVKWLKDGVELTREETFK--
YRFKKDGRKHHLIINEATLEDSGHYAIRTSGGQALAELIVQEKTLEVYQNIADLTVGARDQAVF
KCEVSDENVKGVWLKNGRELVPDSRIKVSHIGRVHKLTIDDVTPADEADYSFVPEGFAC-
NLSAKLHFMEVKIDFVPRQEPPKIHLDCPGRTPD-
TIVVVAGNKLRLDVPISGDPAPTVIWQKASQESK------
TPDPATEVGDSSEWVFEKKLLCETEGRVRVETHKDRSIFTVEGAEKEDEGVYTVTVKNPVGEDQ
VNITVKVIDVPDPPAAPKISNVGEDSCTVQWQPPAYDGGQPILGYILERKKKKSYRWMRLNFDL
LRELSHEARRMIEGVVYEMRVYAVNAIGMSRPSPASQPFMPIGPPSEPTHLGVEDISDSSVTLK
WRPPERVGAGGLDGYSVEYCREG------------------
SSEWVSALQSLTERTSLLVKELPTGARLLFRVRAHNLAGPSAPAITKEAITVQEILERPRLRLP
RHLRQTVQRKVGEPVNILIPFQ-----
GKPRPQVTWTKEGQPLAGNDVSIRNSPTDTILFIRTAHRAHSGTYQVAVQIENMEDTATLVLQI
V--------------------------
DRPSPPQEVRVTETWGFNVALEWKPPQDDGNTELWGYTVQKADKKTMEWFTVLEHYRRTHCVVS
ELIMGNNYYFRVFSHNMVGASEKAATTKEPVFIPKIG-----------
LTYQPPTYKALDFSEAPSFTQPLVNRSVIAGYNAVLCCSVRGSPKPKISWFKNGLDLGEDARFR
MFSKQGVLTLEIRKPCPFDGGAYVCRATNAQGEAQCECRLEVRGKDVV----------------
--------------------------------------------------------------
gi|157823379|ref|NP_0 myosin binding protein C, fast-type
[Rattus n   ----------------------------------------------------
--------------MPEAKPAAKKAP-KGKDAPKEAPA--------------------------
-----------------AKQTPP-----------------------------------------
-------------AEPPKEAPPEDQSPTVE--------------------------------
EPTGLFLKKPDSVSVETGKDTVILAKVNGKELPGKPSIKWFKGKWQELGSKSGARFTFKESHDS
ASNVRPPT---------
GPEPGLATEPVYTVELHIGKVVLGDRGDYRLEVKAKDVCDSCPFNVDVEAPRQ-
DSSGQSLESFKRSGD--------------GKSEDAGELDFSGLLKKREVVEEEKKKKK-
DDDDLGIPPEIWELLKG-
AKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVKKSAAFTKKLDPAYQVDRGNKIKLVVEISDPD
LPLKWFKNGQEIKPSS---
KYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFVKEPPVLIVTPLEDQQVFVGDRVE
MSVEVSEEGAQVMWMKDGVEMTREDSYKARYRFKKDGKRHILIYSDVAQEDGGRYQVITNGGQC
EAELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYKNGVEVRPSKRITISHVGRF
HKLVIDDVRPEDEGDYTFVPDGYAL-
SLSAKLNFLEIKVEYVPKQEPPKIHLDCSGKTSDNSIVVVAGNKLRLDVAITGEPPPTATWLK-
---------------------------
```

```
GDEVFTVSEGRTRIEQRPDCSSFVIESAERSDEGRYTIKVTNPAGEDVASIFLRVVDVPDPPEA
VRVTSVGEDWAILVWEPPKYDGGQPVTGYLMERKKKGSHRWMKLNFEVFTDTTYESTKMIEGVL
YEMRVFAVNAIGVSQPSMNTKPFMPIAPTSAPQHLTVEDVTDTTTTLKWRPPDRIGAGGIDGYL
VEYCLEG------------------
SEEWVSANKEPVERCGFTVKDLPTGARILFRVVGVNIAGRSEPATLLQPVTIREIVEQPKIRLP
RHLRQTYIRKVGEALNLVIPFQ-----
GKPRPQVVWTKGGAPLDTSRVNVRTSDFDTVFFVRQAARSDSGEYELSVQIENMKDTATIRIRV
V--------------------------
EKAGPAENVMVKEVWGTNALVEWQPPKDDGNSEITGYFVQKADKKTMEWFNVYEHNRHTSCTVS
DLIVGNEYYFRVFSENICGLSDSPGVSKNTARILKTG-----------
ITLKPMEYKEHDFRTAPKFLTPLMDRVVVAGYAAALNCAVRGHPKPKVVWMKNKMEIHEDPKFL
ITNYQGILTLNIRRPSPFDAGTYSCRAFNELGEALAECKLDVRVPQ------------------
--------------------------------------------------------------
gi|81910387|sp|Q5XKE0 RecName: Full=Myosin-binding protein C,
fast-   --------------------------------------------------------
----------MPEAKPAAKKAS-KGKDAPKEAP-------------------------------
-------------AKQTP----------------------------------------------
---------EEPPKEAPPEDQSPTAE--------------------------------
EPTGIFLKKPDSVSVETGKDAVILAKVNGKELPGKPTIKWFKGKWQELGSKSGARFIFKESHDS
TSN------------------------
VYTVELHIGKVVLGDRGDYRLEIKAKDVCDSCSFNVDVEAPRQ-DSSGQSLESFKRSGD-----
---------GKSEDAGELDFSGLLKKREVVEEEKKKKK-DDDDLGIPPEIWELLKG-
AKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVKKSAAFTKKLDPAYQVDRGNKIKLVVEISDPD
LPLKWFKNGQEIKPSS---
KYVFENVGKKRILTINKCTLADDAAYEVAVQDEKCFTELFVKEPPVLIVTPLEDQQVFVGDRVE
MSVEVSEEGAQVMWMKDGVEMTREDSYKARYRFKKDGKRHILIYSDVAQEDGGRYQVITNGGQC
EAELIVEEKQLEVLQDIADLTVKAAEQAVFKCEVSDEKVTGKWYKNGVEVRPSKRITISHVGRF
HKLVIDDVRPEDEGDYTFVPDGYAL-
SLSAKLNFLEIKVEYVPKQEPPKIHLDCSGKTSDNSIVVVAGNKLRLDVAITGEPPPTATWLR-
---------------------------
GDEVFTATEGRTHIEQRPDCSSFVIESAERSDEGRYTIKVTNPVGEDVASIFLRVVDVPDPPEA
VRVTSVGEDWAILVWEPPKYDGGQPVTGYLMERKKKGSQRWMKINFEVFTDTTYESTKMIEGVL
YEMRVFAVNAIGVSQPSMNTKPFMPIAPTSAPQHLTVEDVTDTTTTLKWRPPDRIGAGGIDGYL
VEYCLEG------------------
SEEWVPANKEPVERCGFTVKDLPTGARILFRVVGVNIAGRSEPATLLQPVTIREIVEQPKIRLP
RHLRQTYIRKVGEALNLVIPFQ-----
GKPRPQVVWTKGGAPLDTSRVNVRTSDFDTVFFVRQAARSDSGEYELSVQIENMKDTATIRIRV
V--------------------------
EKAGPAENVMVKEVWGTNALVEWQPPKDDGNSEITGYFVQKADKKTMEWFNVYEHNRHTSCTVS
DLIVGNEYYFRIFSENICGLSDSPGVSKNTARILKTG-----------
ITLKPLEYKEHDFRTAPKFLTPLMDRVVVAGYTAALNCAVRGHPKPKVVWMKNKMEIHEDPKFL
ITNYQGILTLNIRRPSPFDAGTYSCRAFNELGEALAECKLDVRVPQ------------------
--------------------------------------------------------------
gi|6093456|sp|Q14324. RecName: Full=Myosin-binding protein C,
fast-   --------------------------------------------------------
----------MPEAKPAAKKAP-KGKDAPKGAP-------------------------------
--------------KEAPPKE-------------------------------------------
```

```
-------APAEAPKEAPPEDQSPTAE--------------------------------
EPTGVFLKKPDSVSVETGKDAVVVAKVNGKELPDKPTIKWFKGKWLELGSKSGARFSFKESHNS
ASN------------------------
VYTVELHIGKVVLGDRGYYRLEVKAKDTCDSCGFNIDVEAPRQ-DASGQSLESFKRTSE-----
---------KKSDTAGELDFSGLLKKREVVEEEKKKKKDDDDLGIPPEIWELLKG-
AKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVKKSAAFTKKLDPAYQVDRGNKIKLMVEISDPD
LTLKWFKNGQEIKPSS---
KYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFVKEPPVLIVTPLEDQQVFVGDRVE
MAVEVSEEGAQVMWMKDGVELTREDSFKARYRFKKDGKRHILIFSDVVQEDRGRYQVITNGGQC
EAELIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYKNGVEVRPSKRITISHVGRF
HKLVIDDVRPEDEGDYTFVPDGYALGSLSAKLNFLEIKVEYVPKQEPPKIHLDCSGKTSENAIV
VVAGNKLRLDVSITGEPPPVATWLK----------------------------
GDEVFTTTEGRTRIEKRVDCSSFVIESAQREDEGRYTIKVTNPVGEDVASIFLQVVDVPDPPEA
VRITSVGEDWAILVWEPPMYDGGKPVTGYLVERKKKGSQRWMKLNFEVFTETTYESTKMIEGIL
YEMRVFAVNAIGVSQPSMNTKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGYL
VEYCLEG------------------
SEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVNIAGRTEPATLAQPVTIREIAEPPKIRLP
RHLRQTYIRKVGEQLNLVVPFQ-----
GKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAARSDSGEYELSVQIENMKDTATIRIRV
V--------------------------
EKAGPPINVMVKEVWGTNALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSCTVS
DLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTG-----------
ITFKPFEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKVVWMKNKMEIREDPKFL
ITNYQGVLTLNIRRPSPFDAGTYTCRAVNELGEALAECKLEVRVPQ------------------
--------------------------------------------------------------
gi|73946990|ref|XP_53 PREDICTED: similar to myosin binding
protein    -----------------------------------------------------
-------------MPEAKPVAKKAPAKGKDAAQPAP----------------------------
-----------------KEAPPEA----------------------------------------
----------APAQPPEEAPPEDQSPTAE--------------------------------
EPTGIFLKKPDSVSVENGKDTHIVAKVNGKELPGKPTIKWFKGKWLELGSKSGARFSFKESHDS
ASN------------------------
VYTVELHIGKVVLGDRGNYRLEVKAKDFCDSCAFNIDVEAPRH-NTSVQGLESFKRTGE-----
---------GKSEDGGELDFSSLLKKREVVEEEKKKKK-DDDDLGIPPEIWELLKG-
AKKSEYEKIAFQYGITDLRGMLKRLKKAKVEVKKSAAFTKKLDPAYQVDRGNKIKLVVEISDPD
LPLKWYKNGQEIKPSS---
KYVFENVGKKRILTINKCTLADDAAYEVAVKDEKCFTELFVKEPPVLIVKPLEDQQVFVGDRVE
MSVEVSEDGAQVMWMKDGVELTREDSFKARYRFKKDGKRHILIYSDVTLEDGGRYQVMTNGDQC
EADLIVEEKQLEVLQDIADLTVKASEQAVFKCEVSDEKVTGKWYKNGIEVRPSKRITISHVGRF
HKLVIDDVRPEDEGDYTFVPDGYAL-
SLSAKLNFLEIKVEYVPKQEPPKIHLDCSGKTSENSLVVVAGNKLRLDVSITGEPRPVATWLK-
---------------------------
GDEVFTATEGRIRLEHQTDSSSFVIESADRADEGRYTIKVTNPVGEDVASIFLRVVDVPDPPEA
VRVTSVGEDWAILVWEPPKYDGGQPVTGYLLERKKKGSQRWMKLNFEVFTETTYESTKMIEGIL
YEMRVFAVNAIGVSQPSMNTKPFMPIAPTSEPLHLMVEDVTDTTTTLKWRPPDRIGAGGIDGYL
VEYCLEG------------------
SEDWVPANTELTERCGFTVKNLPTGAKILFRVVAINIAGRSQPASLFQPVTIREIVQQPKIRLP
```

```
RHLRQTYIRKVGEHLNLVIPFQ-----
GKPRPQVVWTKGGAPVDPARVHVRTSDFDTVFFVRQAARSDSGEYELTVQIENMKDTATIHIQV
V--------------------------
EKAGPAENVMVKEVWGTNALVEWQPPKDNGNSEITGYFVQKADKKTMEWFTVYEHNRHTSCTVP
DLIVGNEYYFRVFSENICGLSDSPGVSKNTARILKTG-----------
ITFKPLEYKEHDFRTPPKFLTPLPDRVVVAGYAAALNCAVRGYPKPKVVWMKNQMEIREDPKFL
MTNYQGVLTLNIRRPSPFDAGTYSCRAVNELGEALAECKLEVRVPQ------------------
--------------------------------------------------------------
gi|194215816|ref|XP_0 PREDICTED: similar to Myosin binding
protein    -----------------------------------------------------
-------------MPEAKPAAKKAP-EKKDAAKPAP----------------------------
-----------------KEAPPKE----------------------------------------
----------APAEPPKEAPPEDQSPTAE--------------------------------
EPTGIFLKKPDSVSVENGKDTVIVAKVNGKELQGKPTFKWIKGKWLELGSKSGARFTFKESHDP
ASN------------------------
VYTLELHIGKVVLGDRGDYRLEVKAKDFSDSCGFNIDVEAPRQ-DSSGQSLESFKRSGE-----
---------GKMKDAGELDFSGLLRKREVVEEENKKKKKDDDDLGIPPEVWELLKG-
AKKSEYERIAFQYGITDLRGMLKRLKKAKVEVKKSAAFTKKLDPAYQVDKGNKIKLVVEISDPD
LPLKWFKNGQEIKPSS---
KYVFENVGKKRILTINKCTLADDAAYEVVVKDEKCFTELFVREPPVLIITPLEDQQVFVGDRVE
MSVEVSEEGAQVMWMKDGVEMTREDSYKAQYRFKKDGKRHILIYSEVTLEDKGRYRVMTNGGQC
EADLIVEEKQLEVLQDIADLTVKASEQAEFKCEVSDEKVTGKWYKNGVEVRPSKRITISHIGRV
HKLVIDDVRPEDEGDYMFVPDGYAL-
SLSAKLNFLEIKVEYVPKQEPPKIHLDCSGKTSENAIVVVAGNKLRLDVSITGEPLPVATWLK-
---------------------------
EDQVFSATEGRVRIEQREGSSSFLIESAERGDEGRYTIKVTNPAGEDVASIFLRVVDVPDPPEA
VRVTSVGEDWAVLVWEPPKYDGGQPLT-------------------------------------
----------------------------------------------------------------
----------------------------------------------------------------
-----------------EQPKIRLPRHLRETYVRKVGEHLNLVIPFQ-----
GKPRPQVVWTKGGAPVDTSRVHVRTSDFDTVFFVREAARSDSGEYELSVQIENMKDTATIRIRV
V--------------------------
EKAGPPEHVMVKEVWGTNALVEWQPPKDDGNSEITGYLVQKADKKTMEWFTVYEHNRHTCCTVS
DLIMGNEYYFRVYSENFCGLSDLPGVSKNTARIVKTG-----------
ITFKPFEYKEHDFRMAPRFLTPLPDRVVVAGYAAALNCAVRGHPKPKVVWMKNNMEIREDPKFL
MTNYQGVLTLNIRRPSPFDAGTYSCRAVNELGEALAECKLEVRVIPGTMMLVDRPPETRAGRGA
AEGDLGSLLCRSETVFRLPRLVAAESYPDPPRCVPFRSCH----------------------
gi|113206110|ref|NP_0 myosin binding protein C, fast type
[Gallus g   ----------------------------------------------------
--------------MPEPSKAAPKKEAKKKEEKKEEK---------------------------
------------------KEAPP-----------------------------------------
------------PQEHKDEAPDDVHPPETP--------------------------------
DPEGLFLSKPQNVMVESGRDVTVSARVAGAALPCAPAVKWFKGKWAELGDKS-ARCRLRHSVD-
DDK------------------------
VHTFELTITKVAMGDRGDYRCEVTAKEQKDSCSFSIDVEAPR--SSEGNVLQAFKRTGE-----
---------GKDDTAGELDFSGLLKKREVQVEEKKKKK-DEDDQ-
FPPEIWELLKGVTKKSEYERIAFQYGITDLRGMLKRLKKVHVEPKKSEAFIRKLDPAYQVDKGN
```

```
KIKLVVELSDPDLPLKWYKNGQLLKPST---
KYVFENVGLKRILTIHKCSLADDAAYECRVNDEKCFTEVFVKEPPVTVVRGLEDQQVVVGDRVV
LEAEVSEEGAQVMWLKDGVDVTRDDAFK--
YRFKKDGKKHFLIINEAELSDSAHYKIMTNGGESEAELSVEEKQLEVLQDMADLTVKASEQAVF
KCEVSDEKVTGRWFRNGVEVKPSKRIHISHNGRFHKLVIDDVRPEDEGDYTFIPDGYAL-
SLSAKLNFLEIKVEYVPKQEPPKIHLDCSGKAAENTIVVVAGNKVRLDVPISGEPAPTVTWKR-
---------------------------
GDQLFTATEGRVHIDSQADLSSFVIESAERSDEGRYCITVTNPVGEDSATLHVRVVDVPDPPQS
VRVTSVGEDWAVLSWEAPPFDGGMPITGYLMERKKKGSMRWMKLNFEVFPDTTYESTKMIEGVF
YEMRVFAVNAIGVSQPSLNTQPFMPIAPTSEPTHVVLEDVTDTTATIKWRPPERIGAGGVDGYL
VEWCREG------------------
SNEWVAANTELVERCGLTARGLPTGERLLFRVISVNMAGKSPPATMAQPVTIREIVERPKIRLP
RHLRQTYIRRVGEQVNLVIPFQ-----GKPRPQVTWSREGGALP-
AEVQTRTSDVDSVFFIRSAARPLSGNYEMRVRIDNMEDCATLRLRVV-----------------
---------
ERPGPPQAVRVMEVWGSNALLQWEPPKDDGNAEISGYTVQKADTRTMEWFTVLEHSRPTRCTVS
ELVMGNEYRFRVYSENVCGTSQEPATSHNTARIAKEG-----------
LTLKMVPYKERDLRAAPQFLTPLVDRSVVAGYTVTLNCAVRGHPKPKVTWLKNSVEIGADPKFL
SRHGLGVLSLLIRRPGPFDGGTYGCRAVNEMGEATTECRLDVRVPQ------------------
--------------------------------------------------------------
gi|6166597|sp|Q00872. RecName: Full=Myosin-binding protein C,
slow-   --------------------------------------------------------
----------MPEPT----------KKE--------------------------ENE--
VPAPAPPPEEPSKEKEAGTTPAKD----------------------------------------
---------------WTLVETPPG-EEQAKQNA----------------------------
NSQLSILFIEKPQGGTVKVGEDITFIAKVKAEDLLRKPTIKWFKGKWMDLASKAGKHLQLKETF
ERHS------------------------
RVYTFEMQIIKAKDNFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REVKQQEEEPQVDVWELLKN-
AKPSEYEKIAFQYGITDLRGMLKRLKRMRREEKKSAAFAKILDPAYQVDKGGRVRFVVELADPK
LEVKWYKNGQEIRPS---
TKYIFEHKGCQRILFINNCQMTDDSEYYVTAGDEKCSTELFVREPPIMVTKQLEDTTAYCGERV
ELECEVSEDDANVKWFKNGEEIIPGPKSR--
YRIRVEGKKHILIIEGATKADAAEYSVMTTGGQSSAKLSVDLKPLKILTPLTDQTVNLGKEICL
KCEIS-ENIPGKWTKNGLPVQESDRLKVVHKGRIHKLVIANALTEDEGDYVFAPDAYNV-
TLPAKVHVID----------PPKIILDG-LDA-DNTVTVIAGNKLRLEIPISGEPPPKAMWSR-
---------------------------
GDKAIMEGSGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIKVKVVDFPDPPVA
PTVTEVGDDWCIMNWEPPAYDGGSPILGYFIERKKKQSSRWMRLNFDLCKETTFEPKKMIEGVA
YEVRIFAVNAIGISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHIGAAGLDGYV
LEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKDLIDKTKFTITGLPTDAKIFVRVKAVNAAG
ASEPKYYSQPILVKEIIEPPKIRIPRHLKQTYIRRVGEAVNLVIPFQ-----
GKPRPELTWKKDGAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVETASIDIQI
I--------------------------
DRPGPPQIVKIEDVWGENVALTWTPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTSATIT
ELVIGNEYYFRVFSENMCGLSEDATMTKESAVIARDG-----------
KIYKNPVYEDFDFSEAPMFTQPLVNTYAIAGYNATLNCSVRGNPKPKITWMKNKVAIVDDPRYR
```

```
MFSNQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVK-------VIAQ----------
--------------------------------------------------------------
gi|160425243|ref|NP_0 myosin binding protein C, slow type [Bos
taur    --------------------------------------------------------
---------MPEPT----------KKE--------------------------
ENEVLAPAPAPPPEEPNKEKEAGTAPVKEPNKEKEAGTAPAKEPNKEKEAGTAPAKEPNKEKEA
GTSPGKDEEDASPPGGLPPEWSIGESPAG-EEQDKQNA--------------------------
--
NSQLSILFVEKPQGGTVKVGENITFIAKVKAEDLLRKPTVKWFKGKWMDLASKAGKHLQLKETF
ERHS------------------------
RVYTFEMQIIKAKENYAGNYRCEVTYKDKFDSCSFDLEVLESTGTTPNIDIRSAFKRSGE----
-----------GQDDAGELDFSGLLKR----------REVKPQEEQPEVDVWELLKN-
AKPSEYEKIAFQYGITDLRGMLRRLKRMRRVEKKSAAFARILDPAYQVDKGGRVRFVVELADPK
LEVKWYKNGQEIRPS---
TKYIFEHKGCERIMFINNCVLTDDSEYYVTAGDEKCSTELFVREPPVMVTKQLEDTKAYCGERV
ELECEVSEDDANVKWFKNGEEIIPGPKSR--
YHIRVEGKKHILIIDGATKADSAEYSVMTTGGQSSAKLSVDLKPLKILTPLTDQTVNLGKEICL
KCEVS-ENITGKWTKNGLPVQETDHLKIVHKGRIHKLVIANALVEDEGDYVFTPDDYSV-
TLPAKVHVVD----------PPKINLDG-LDA-DNTVTVIAGNKLRLEIPISGEPPPKALWSR-
---------------------------
ADKAIMEGSGRIRSENYPDSTTLVIDIAEKDDSGVYHINLKNEAGEAHASIKIKVVDIPDPPVA
PNVTDVGDDWCIMTWDPPLYDGGSPILGYFIERKKKQSSRWMRLNFDLCKETIFEPKKMIEGVA
YEVRIFAVNAVGISKPSMPSKPFVPLAVTSPPTLLTVDSVTDTTVTMKWRPPDQIGAAGLDGYV
LEYCFEGSTSAKQSDENGEAAYDLPADDWIAANTELIEKTKFTITGLPTDSRIYVRVKAVNAAG
ASEPKYYSQPILVKEIIEAPKIRIPRHLKQTYIRRVGEAINLVIPFQ-----
GKPRPELIWTKDGAPIDKNQINIRNSETDTIVFIRKAERSHSGKYDLQVKVEKFVETASIDIRV
I--------------------------
DRPGPPQLVKIEDVWGENVALSWTPPRDDGNTAITGYTIQKADKKSMEWFTVIEHYHRTSATIT
ELVIGNEYYFRVFAENMCGLSEDATMTKESAVIAKDG-----------
KIYKNPVYEDFDFTEAPMFTQPLVNTYAVAGYNATLNCSVRGNPKPKITWMKNKVVIKDDPRYR
MFSNQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVK-------VVAQ----------
--------------------------------------------------------------
gi|194226708|ref|XP_0 PREDICTED: myosin binding protein C, slow
typ  -----------------------------------------------------------
--------MPEPT----------KKE--------------------------ENE--
APAPAPAPAEPNKEKEAGTAPAKDEEETFPPSALPPGLGSRALERKDS----------------
--------------EWSLGDSPAG-EDQDKQNA----------------------------
NSQLSTLLVEKPQSGAVKVGENITFIAKVKAEDLLRKPTIKWFKGKWMDLASKAGKHLQLKETF
ERHS------------------------
RVYTFEMQIIKAKENFAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REVKQQEETPEVDVWELLKN-
AKPSEYEKIAFQYGITDLRGMLKRLKRMRRVEKKSAAFARILDPAYQVDKGGRVRFVVELADPK
LEVKWYKNGQEIRPS---
TKYIFEHKGCERIMFINNCLLTDDSEYYVTAGDEKCSTELFVREPPVMVTKQLEDTKAYCGERV
ELECEVSEDDANVKWFKNGEEIIPGPKSR--
YRIKVDGKKHILIIEGATKADTAEYSVMTTGGQSSAKLSVDLKPLKVLTPLTDQTVKLGNEICL
KCEIS-ENITGKWTKNGLPIQESDRLKVVHKGRIHKLVIANALVEDEGDYVFTPDSYSI-
```

```
TLPAKVHVVD----------PPRIILDG-LDA-DNTVTVIAGNKLRLEIPISGEPPPKALWSR-
---------------------------
ADKAIMEGSGRIRAESYPDSSTLVIDVAEKEDSGVYHINLKNEAGEAHASIRIKVVDIPDPPVA
PTVTEVGDDWCIMNWEPPAYDGGSPILGYFIERKKKQSSRWMRLNFDLIKETTFEPKKMIEGVA
YEVRIFAVNAVGISKPSTPSRPFVPLAVTSPPTLLAVDSVTDNSVTMKWRPPDHIGAAGLDGYV
LEYCFEGS------------------
DNWLAANKDLIDKTKFTITDLPTDAKIFVRVKAVNKAGASEPKYYSQPILVKQIIEPPKIRIPR
HLKQTYIRRVGEAVNLVIPFQ-----
GKPKPELTWKKDGAEIDKNQVNIRNSETDTIIFIRKAERSHSGKYDLQVKVEKFVERATIDIQI
I--------------------------
DRPGPPQVVKIEDVWGENVALSWTPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTSATIS
ELVIGNEYYFRVFAENMCGLSEDATMTKESAVIAKDG-----------
KIYKNPVYEDFDFTEAPMFTQPLVNTYAVAGYNATLNCSVRGNPKPKITWMKNKVTIVDDPRYR
MFSNQGVCTLEIRKPSPYDGGTYSCKAVNDLGTVEIECKLEVK-------VVAQ----------
--------------------------------------------------------------
gi|109481744|ref|XP_0 PREDICTED: similar to myosin binding
protein    -----------------------------------------------------
-------------MPEPT----------KKE----------------------------
ENEVPAPAPPPEEPNKDKEAGTTPAKEEDEASPPSALPPGLGSRALERKDS-------------
-----------------EWSLGESPAGGEEQDKQNA----------------------------
NSQLSTLFVEKPQTGSVKVGANITFIAKVKAEDLLRKPTVKWFKGKWMDLASKAGKHLQLKETF
ERQT------------------------
RIYTFEMQIIKAKENYAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REVKQQEEEPEIDVWELLKN-
ANPNEYEKIAFQYGITDLRGMLKRLKRMRRVEKKSAAFAKILDPAYQIDKGGRVRFVVELADPK
LEVKWFKNGQEIRPS---
TKYIFEHKGNERIMFINNCALTDDSEYYVTAGDEKCSTELFVREPPIMVTKQLEDMNAYCGERV
ELEVEVSEDDANVKWFKNGEEIVPGPKSR--
YRIKVEGKKHTLIIEGATKADSAEYSVMTTGGQSSAKLSVDLRPLKITTPLTDQTVKLGKEVCL
KCEIS-ENVPGKWTKNGLPVQEGERLKVVHKGRIHKLVIANALIEDEGEYVFTPDAYNV-
PLSAKVHVID----------PPKIILDG-LDA-DNTVTVIAGSKLRLEIPVTGEPPPKAIWSR-
---------------------------
ADKAIMEGSGRIRAESYPDSSTLVIDVAERDDSGVYNINLKNEAGEAHASIKIKVVDIPDPPVA
PNVTEVGDDWCIMNWEPPVYDGGSPILGYFIERKKKQSSRWMRLNFDLCKETTFEPKKMIEGVA
YEVRIFAVNAIGISKPSMPSKPFVPLAVTSPPTLLAVDSVTDSSVTMKWRPPDQIGAAGLDGYV
LEYCFEGT------------------
EDWITANTDLIDKTKFTITGLPTDAKIFVRVKAINAAGASEPKYYSQPILVKEIIEPPKIRIPR
HLKQTYIRRVGEAVNLVIPFQ-----
GKPRPELTWKKDGAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLEVKVDKYVENASIDIQI
V--------------------------
DRPGPPQAVTIEDVWGENVALTWTPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTNATIT
ELVIGNEYYFRVFAENMCGLSEDATMTKESAVIAKDG-----------
KIYKNPVYEDFDFTEAPMFTQPLVNTYAIAGYNATLNCSVRGNPKPKITWMKNKVAIVDDPRYR
MFSNQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKGGLSFCRLLLQGVPPNIIDSY
LRDLQSSNPEEY--------------------------------------------------
gi|40254303|ref|NP_78 myosin binding protein C, slow type [Mus
musc   ---------------------------------------------------------
```

```
---------MPEPT----------KKE----------------------------
ENEVSAPAPPPEEPNKEKEAGTAPAK--------------------------------------
-----------------EWSLGESPAGGEEQDKQNA----------------------------
NSQLSTLFVEKPQTGSVKVGANITFVAKVRAEDLLRKPTVKWFKGKWMDLASKAGKHLQLKETF
ERQT------------------------
RVYTFEMQIIKAKENYAGNYRCEVTYKDKFDSCSFDLEVHESTGTTPNIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REVKQQEEEPEIDVWELLKN-
ANPNEYEKIAFQYGITDLRGMLKRLKRMRRVEKKSAAFAKILDPAYQVDKGGKVRFVVELADPK
LEVKWFKNGQEIRPS---
TKYIFEHKGNERIMFINNCSLTDDSEYYVTAGDEKCSTELFVREPPIMVTKQLEDMNAYCGERV
EMEVEVSEDDANVKWFKNGEEIFPGPKSR--
YKIKVEGKKHTLIIEGATKADSAEYSAMTTGGQSSAKLSVDLRPLKITTPLTDQTVKLGKEVCL
KCEIS-ENVPGKWTKNGLPVQEGERLKVVHKGRIHKLVIANALIEDEGEYVFTPDAYNV-
PLSAKVHVID----------PPKIILDG-LDA-DNTVTVIAGSKLRLEIPVTGEPPPKAIWSR-
---------------------------
ADKAIMEGSGRIRAESYPDSSTLVIDVAERDDSGVYNINLKNEAGEAHASIKIKVVDIPDPPVA
PNVTEVGDDWCIMNWEPPAYDGGSPILGYFIERKKKQSSRWMRLNFDLCKETTFEPKKMIEGVA
YEVRIFAVNAIGISKPSMPSKPFVPLAVTSPPTLLAVDSVTDSSVTMKWRPPDQIGAAGLDGYV
LEYCFEGT------------------
EDWIVANTDLIDKTKFTINGLPTDAKIFVRVKAINAAGASEPKYYSQPILVKEIIEPPKIRIPR
HLKQTYIRRVGEAVNLVIPFQ-----
GKPRPELTWKKDGEEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKYVENASIDIQI
V--------------------------
DRPGPPQTVTIEDVWGENVALTWTPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTNATIT
ELVIGNEYYFRVFAENMCGLSEDATMTKESAVIAKDG-----------
KIYKNPVYEDFNFTEAPMFTQPLVNTYAIAGYNATLNCSVRGNPKPKITWMKNKVAIVDDPRYR
MFSNQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVK-------VVAQ----------
--------------------------------------------------------------
gi|126339738|ref|XP_0 PREDICTED: similar to RIKEN cDNA
8030451F13 g   ---------------------------------------
MDTFTSQWSVGGLLWNDDNINKNKTITMMEDN----------
DNDEFSQHPDNKLAELFRFRCGNGKVYDDNSEPENEAPAPPPEEPSKEKEGGSGPPKGEGDVSP
PSALPADINARALARKDS------------------------------EWSLGESPVG-
EEQDKQNS----------------------------
NTSQSALFVEKPQNGTVKVGENITFIAKVEAKDLLRKPTVKWFKGKWMDLASKAGKHLQLKETF
ERQT------------------------
RMYTFEMQIIKAKENYAGNYRCEVSYKDKFDSCSFDLEVHESTGTTPNIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REVKQQEEEPEIDVWELLKN-
ANPNEYEKIAFQYGITDLRGMLKRLKRMRRVEKKSAAFSKILDPAYQVDKGGKVRFVVELADPK
LEVKWYKNGQEIRPS---
TKYIFEHKGNQRIMFINNCQMTDDSEYYVTAGDEKCSTELFVREPPIMVTKQLEDTNAYCGERI
ELECEVSEDDANVKWFKNGEEIVIGPKSR--
YKVKVEGKKHTLIIEGATKADSAEYSVMTTGGQSSCKLSVDLRPLKILQPLTDVTVKLGKEICL
KCEIS-ENISGKWTKNGLPVQEGERLKVVHKGKIHKLVIANALIEDEGEYVFAPDAYTV-
TLPAKVHVID----------PPKIYLDG-LEA-DNTVTVIAGSKLRLEIPVSGEPAPKALWSR-
---------------------------
ADKAIAEGGGRIRAESYPDSSTLVIDVAEREDSGVYNINLKNEAGEAHASIKIKVVDIPDPPLA
```

```
PNVSDVGDDWCIMNWEPPANDGGSPILGYFIERKKKQSSRWMRLNFDLIKETTFEPKKMIEGVA
YEVRIFAVNAIGISKPSMPSKPFVPLAVTSPPTLLAVDSVTDSTVTMKWRPPDQIGAAGLDGYV
LEYCFEGT------------------
EDWIVANPELTDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYGQPILVKEIIEPPKIRIPR
HLKQTYLRRVGEAVNLVIPFQ-----
GKPRPELTWKKDGADIDKNQINIRNSETDTIIFIRKAERSHSGKYDLEVKVDKYVDSASIDIQI
V--------------------------
DRPGPPQSVKIEDVWGENAALVWTPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTNATIT
ELVIGNEYYFRVFAENMCGLSEEATMTKESAVIAKDG-----------
KVYKNPVYDDFDFTEAPMFTQPLVNTYAIAGYNATLNCSVRGNPKPKITWMKNKVAIVNDPRYR
MFSNQGVCTLEIRKPSPYDGGTYCCKAVNELGTVEIECKLEVK-------VVAQ----------
--------------------------------------------------------------
gi|149637879|ref|XP_0 PREDICTED: similar to myosin binding
protein
MAVTNRYSPLHPLCDWGSWNDPAAKLWGEIPCRWQEMPLCHWGRVAPPLSPSAWLKILISQGSG
SSSPSPAGLSPPPFHGLQKE------------------------
GRLKNEAPPAPPAPPEGQNKEKEGGSGQAKDEDEATPPNALPKDGNLQSLERKDS---------
---------------------EWSLGEGPPA-EEQDKQNA------------------------
----
NSQLSTLFVEKPQSGTVKVGGDITFLAKVEAKDLLRKPTVKWFKGKWMDLASKAGKHLQLKETF
ERQT------------------------
RMYTFEMQIIKAKENYAGNYRCEVSYKDKFDSCSFDLEVKESTGTTPSIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REIK-QEEEPDIDVWELLKN-
ANPNEYEKIAFQYGITDLRGMLKRLKRMRRVEKKSAAFAKILDPAYQVDKGGKVRFVVELTDPK
VELKWYKNGQEIRPS---
TKYIFEHKGNQRILFINNCTLADDSEYYVSAGDEKCSTELFVREPPILVTKQLEDTNTYCGERV
ELDCEVSEEGANVKWFKNGEEIDTGPRSR--
YKVKVDGKKHILIIDGATKADNAEYSVMTTGGQSSAKLSVDLRPLKIVQPLTDTTVKLGKEITL
RCELS-ENITGKWTKNGLPVQESDRLKIQHKGRIHKLVIGTSAVEDEGEYVFTPDAYSV-
TLSAKVHVID----------PPKLYLDG-LDA-DNTVTVVAGSKLRLEIPVTGEPPPKAIWSR-
---------------------------
ADKCIMESGGRIRAESYPDSSTLVIDVAEREDSGIYKINLKNEAGEAQASIKIKVVDIPDPPVA
PSVADVGDDWCIMNWEPPVNDGGSPILGYFIERKKKQSSRWMRLNFDLCKETTFEPKKMIEGVA
YEVRIFAVNAIGISKPSMPSKPFVPLAVTSPPTLLAVDSITDTTVTMKWRPPDQIGAAGLDGYV
VEYCLEGS------------------
EEWIVANPELTDKTKYTITGLQTDSRIFVRVKAVNAAGASEPKYYAQPILVKEIIEHPKIRIPR
HLKQTYIRRVGEAVNLVIPFQ-----
GKPRPKLSWNKNGVPVDKNEINIRNSETDTIIFIRKAERSHSGKYDLKVEVDTFVDSASIDIQI
V--------------------------
DRPGPPQVVKIEDVWGENVALTWTPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTNATIT
ELVIGNEYYFRVFAENMCGLSEEVTMTKESAVIAKDG-----------
KVYKNPIYEDFNFTEAPMFTQPLVNTYAIAGYNATLNCSVRGNPKPKITWMKNKVAILNDPRYR
MFSNQGVCTLEIRKPSPYDGGTYSCKAVNELGEEEIECKLEVK-------VVAQ----------
--------------------------------------------------------------
gi|118082876|ref|XP_4 PREDICTED: similar to Myosin-binding
protein    -----------------------------------------------------
-------------MPEPT----------KKD-----------------------------
```

```
ETETENALPPPEQKTPQDGGTEKGK---------------------------------------
----------------VWSIGETAPE--EAEKRD-----------------------------
DSQRSTLFIEKPQSGTVSVGGNITFIAKVEAKDLLRKPNVKWFKGKWMDLASKAGKHLQLKESF
ERHT------------------------
KIHTFEMHIIQAKENYAGNYRCEVSYKDKFDSCSFDLEVTESSQAAPSIDIRSAFKRSGD----
-----------GQDDAGELDFSGLLKR----------REVKQQEEEPEVDVWELLKN-
ANPSEYEKIAFQYGITDLRGMLKRLKRMRREVKKSAAFAKGLDPAYQVDKGGKVRFMVELADPT
VELKWYKNGQEIRPS---
AKYIFEHKGNQRILFINNCTMTDDARYYVTAGDEKCSTELFVRDPPILVTKGLEDTSTYVGERV
ELSCEVSEDDANVKWFKNGVELTNEPKSR--
YRIKVEGKKHTLIIEEAAKNDNATYSVMTTGGQSEAKLSVDLRPLKISLALEDQTVRLGQEIHL
KCEIS-ENVEGKWYKNGQLVEASDRVKLYHKGRIHRFIIASAAVDDEGEYMFVPDAYNI-
NIPCKVHVVD----------PPKLHLDG-LGE-NNTVTVVAGTKLRLEIPITGEPTPKVMWSK-
---------------------------GDKWITD-
SGRIRAETYSDSSCLVIDTAEREDSGPFRITLKNEAGEDSALINIKVVDVPDPPQAPNVTEVGE
DWCVMTWDPPANDGGSPILGYFIERKKKQSSRWMRLNFELCKETTFEPKKMIEGVAYEVRVFAV
NAIGTSKPSMPSKSFVPLAVTSPPTLLAVDSVTDTSVTMKWRPPDHIGAAGLDGYVVEYCFEGS
ISTDQSEELMEPPFNLEADEWIVANPELTDKTKFTITGLPTGSKILVRVKAVNAAGESEPRYHP
QPILVKEVIEPPKIRLPRHLKQTYTRRVGETVNLVIPFQ-----
GRPRAKVSWQKNGSPIDKNQINIRNTENDTIIFIRKAERSHSGEYDMKVEVENLVDKATIDIQI
V--------------------------
DRPGPPEVVTIEDVWGENVNLSWKPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTSATIN
ELVIGNEYYFRVFAENMCGLSEDATMTKESALIAKDG-----------
KVYKYPVYDDFDFTERPLFTQPLVNTFAVAGYNATLNCSVRGNPKPKITWLKNKVAILNDPRYR
MFGNQGVCTLEIRKPSPYDGGTYTCRAVNELGEAEVDCKLEVK-------VIAR---------
TLS---QVIKW----------------------------------------------------
gi|224095487|ref|XP_0 PREDICTED: myosin binding protein C, slow
typ   ----------------------------------------------------------
--------MPEPT----------KKD-----------------------------
ETENESAPPPPEQKTPQEGGNEKGK---------------------------------------
----------------VWSLGEGAPE--ESEKRD-----------------------------
DSQRSTLFVEKPQSGTVSVGGNITFIAKVEAKDLLRKPNVKWFKGKWMDLASKAGKHLQLKESF
ERHT------------------------
KIHTFEMQIIKAKENYAGNYRCEVSYKDKFDSCSFDLEVTESSQAAPSIDIRSAFKRSGE----
-----------GQEDAGELDFSGLLKR----------REVKQQEEEPEVDVWDLLKN-
ANPSEYEKIAFQYGITDLRGMLKRLKRMRREPKKSAAFAKGLDPAYQVDKGGKVRFMVELADPT
VELKWYKNGQEIRPS---
AKYIFEHKGNQRILFINNCTMTDDARYYVTAGDEKCSTELFVRDPPILVTKGLEDTSTYVGERV
ELSCEVSEDDANVKWFRNGVELSNDPKSR--
YRIKVEGKKHTLVIEEAAKNDTATYSVMTTGGQSEAKLSVDLRPLKISLALEDQTVRLGQEIHL
KCEIS-ENVEGKWYKNGQLIEASDRVKLYHKGRIHRFVIPVSAVDDEGEYMFVPDAYNI-
NIPCKVHIVD----------PPKLHLDG-LGE-NNTVTVVAGNKLRLEIPITGEPPPKVFWSR-
---------------------------
GDKVPCHYSGRIRAESYPDSSCLVIDAAEREDSGPFRITLKNEAGEDTALINIKVVDVPDPPQA
PNVTEVGEDWCIMTWEPPANDGGSPILGYFIERKKKQSSRWMRLNFELCKETTFEPKKMIEGVA
YEVRVFAVNAIGMSKPSMPSKSFVPLAVTSPPTMLAVDSVTDTSVTMKWRPPDQIGAAGLDGYV
VEYCFEGSISTDLSEDLGEPPFNLEADEWIVANPELTDKTKFTINGLPTGSKILVRVKAVNAAG
```

```
ESEPKYHPQPILVKEVIEPPKIRLPRHLKQTYTRRVGETVNLVIPFQ-----
GKPRAKVSWEKNGSPIDKNDINIRNTEQDTIIFIRKAERGHSGEYDMKVEVENLVDKATIDIQI
I--------------------------
DRPGPPEVVTIEDVWGENVNLSWKPPKDDGNAAITGYTIQKADKKSMEWFTVIEHYHRTSATIN
ELVIGNEYYFRVFAENMCGLSEDATMTKESALIAKDG-----------
KVYKYPVYDDFDFSERPLFTQPLVNTFAVAGYNATLNCSVRGNPKPKITWMKNKVLIMNDPRYR
MFSNQGVCTLEIRKPSPYDGGTYTCRAVNELGEAEVDCKLEVR-------
VIYHGVINPGEPLSLAGDNQVYNAPFGVSQKKLRSHYVHDKTCERGVSGTRQGAGESGTRSPRR
DERGAHGRLSPG
gi|55925504|ref|NP_00 myosin binding protein C, slow type [Danio
re   -----------------------------------------------------------
-------MPEPT----------KKD----------------------------
DGQPEEDGSTPKKLSIDLPNDSDPESTRGRKDS-------------------------------
-----------------VWSLGDGQPP-EEIDKQTE----------------------------
NPPLSTLLIEKPQSGSITVGGDITFIAKVEAKDLLRKPTVKWFKGKWMDLASKTGKHLQLKESF
ERLS------------------------
KIHTFEMHIIKAKENYAGNYRCEVTYKDKFDSCSFDLEVKEVPEVSQSIDIRSAFKRSSE----
-----------GQDDAGELDFSGLLKHRHG-------REVK-QEETPEVDVWEILKN-
ARPDEYEKIAFTYGITDLRGLLKRLKKTKKEEKKSEAFAKRLEPAYQVDKGGKIRLIVDLADPT
VELKWYKNGQEIRPTPNNRKFIFEHKGTQRIMVINNCQMSDDAAYSVTAGEEKCTTELFVKELP
VNIVKELEPVKTTVNERIELECEVSEEGAKVKWMKNGVEVPTGVRSR--
YRVKSEGTKHWLIIDDASKDDTGTYSLMATGGTSQAHVQVDLKPLKVLMDLQSVTVLLGQPLKL
NCEIYPGNVPGRWYKNGQLVQPNDRISITHKTKNHSLDVESSTIHDAGDYTFVPEGYTQ-
TLSAKVHIID----------PPRVHLEA-LNVQDNTVTIVAGNKLRLEIPISGEPAPRVVWMK-
---------------------------
GERVILDTGSRVHAETFADHTCLTIDITEREDTGNYKIVLQNEAGEDTASVKVKVVDIPDPPEA
PLVTEVGGDWCTMTWEPPRYDGGSPILGYFIERKKKQSSRWMRLNFDLCKETTFEPKKMIEGVP
YEVRIFAVNAIGVSKPSEPSKPFIPLAVTSEPTMLVVDDVTDTTVTMKWRPPDTIGAAGLDGYQ
IEYCIEGT------------------
DDWIVANKELTKKTKYTITGLPVEAKILVRVKAINAAGASQPRTTQHSILVKEVIEPPKIRIPR
HLKQTYIRKVGEVVNLVVPFV-----GKPRPKVTWLKEGQPIDP-
TISIRNSDCDSIMFIRKAERKHSGKYELSVQVENHIDTAMLDIQIV------------------
--------
DLPGPPQAVKIEEIWGNNVALDWSPPKDSGNAPITGYTIQKADKKTMEWYTCVEHYHRTCITIS
DLVVGNEYFFRIYSENMVGLSEDATATKDSALIVKEG-----------
LHLKNPEYNDRDFTEPPRFTQPLINTFAIAGYNATLNCSVRANPRPKVVWMKNKITIIDDPRYR
MFHNQGVCTLEIRKPSPFDGGVYTCKAVNDLGEAQVDCKLEVKGGFTFFELMKRGVPLHLIDKY
MNESKTSESEKKGSD-----------------------------------------------
```

Alignment 2 (MYBPC3 for MrBayes)

```
#NEXUS

begin data;
     dimensions ntax=50 nchar=1274;
     format datatype=protein missing=? gap=- matchchar=.;

matrix
     Human_cardiac_myosin_bin
MPEPGKKPVSAFSKKPRSVEVAAGSPAVFEAETERAGVKVRWQRGGSDISASNKYGLATEGTRH
TLTVREVGPADQGSYAVIAGSSKVKFDLKVIEAEKAEPMLAPAPAPAEATGAPGEAPAPAAELG
ESAPSPKGSSSAALNGPTPGAPDDPIGLFVMRPQDGEVTVGGSITFSARVAGASLLKPPVVKWF
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Alignment 3 (MYH7 for MrBayes)

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------
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QRINANRRKLQRELDEATESNEAMGREVNALKSKLR----------
```

```
          ;
end;
```

Figure S4. Training Algorithm

The algorithm creates a 3-way classifier that wraps an SVR classifier. The SVR classifier M, for every x, gives a prediction M(x) and probability estimates for both possible targets p(x,Pathogenic) and p(x,Benign). The classifier uses the Radial Basis Function (RBF) kernel, which requires two parameters: C and gamma. The training algorithm performs an exhaustive search to find these parameters, as recommended by the SVR library, libSVM (Chang and Lin).

```
input: training data D (consists of 90% of full data set
for each cross-validation run, 100% for creation of final
classifier), minimum coverage threshold tCov
output: 3-way classifier K

  1. search (exhaustively within a range of values) for
     kernel parameters C and gamma that maximize accuracy on
     D
  2. train SVR model M on D using C, gamma
  3. compute predictions and probability estimates for data
     D using M
  4. set thresholds tPathogenic, tBenign that maximize
     accuracy of M on D while keeping coverage above tCov.
  5. Return the following 3-way classifier K:
       1. K(x) = 'Benign' if M(x) = Benign and p(x,Benign) >
          tBenign,
       2.   else 'Pathogenic' if M(x) = Pathogenic and
          p(x,Pathogenic)>tPathogenic,
       3.   else 'NoCall'
```

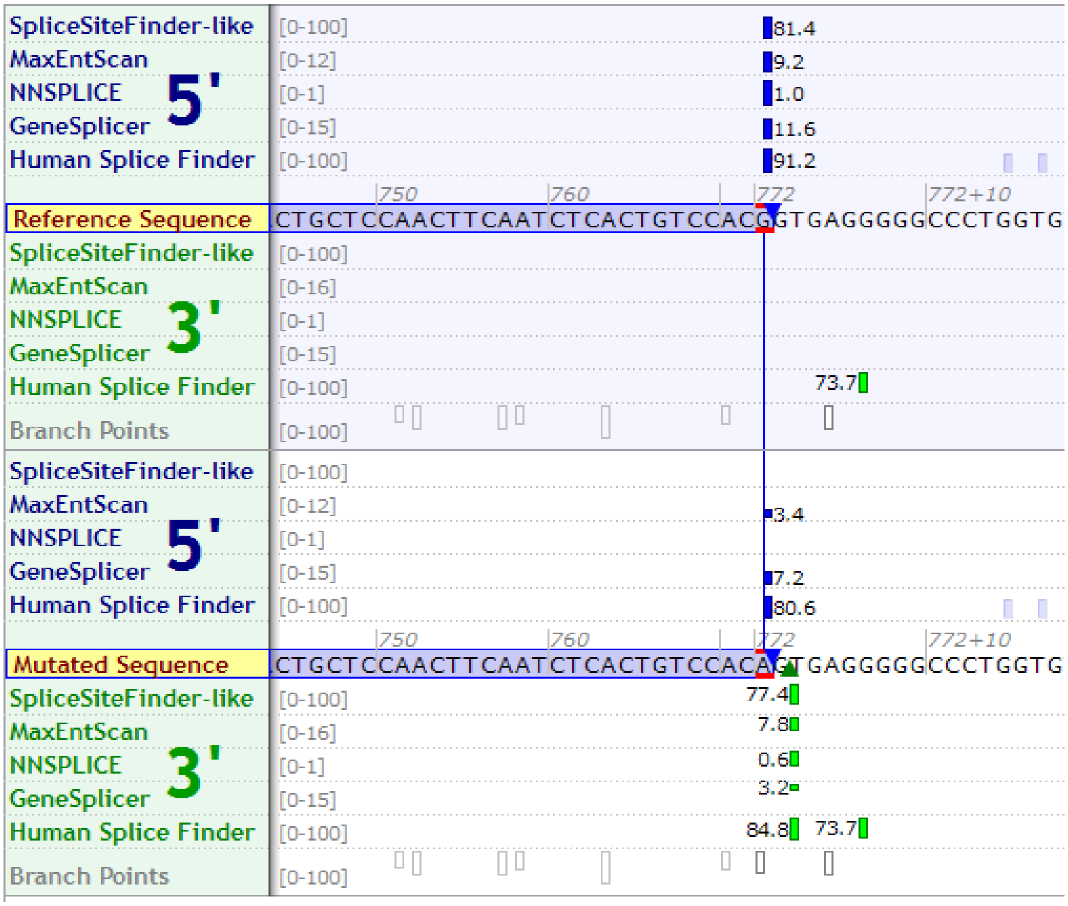
Figure S5. Validation Algorithm

Ten-fold cross-validation algorithm for the variant classifier.

```
input: all data D, minimum coverage threshold tCov
output: average accuracy of the 10-fold cross-validation A_average
1. Split D randomly into 10 parts (D_train_i)
2. For i = 1..10:
  2.1 train classifier using D_train_i, tCov to create trained classifier K_i (procedure in Supplementary Figure S3)
  2.2 apply K_i to the rest of the data (D - D_test_i), compute accuracy A_i
3. Return average(A_i)
```

Figure S6. Splice Site Inference

A screenshot of Alamut 1.5 (Interactive Biosoftware, 2009), standard software used for interpreting mutations in clinical laboratories. This shows that the variant MYBPC3 Glu258Lys is predicted to affect splicing. This is an example of the interface clinical laboratories typically use to view splice site predictions.



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