























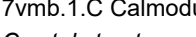

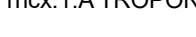

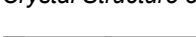





All Projects

2QAC mutated.fasta Created: today at 08:34









































Summary    Templates 50    Models 1    Project Data ▾

Template Results ⓘ

Templates		Quaternary Structure	Sequence Similarity	Alignment	More ▾		
↓↑Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/> ✓	2qac.1.A Myosin A tail domain interacting protein MTIP <i>The closed MTIP-MyosinA-tail complex from the malaria parasite invasion machinery</i>						
▼	<div><div></div></div>	0.93	-	99.31	X-ray, 1.7Å	hetero-dimer 	None
<input type="checkbox"/>	4mzj.1.A Myosin A tail domain interacting protein <i>Crystal Structure of MTIP from Plasmodium falciparum in complex with pGly[801,805], a stapled myoA tail peptide</i>						
▼	<div><div></div></div>	0.93	-	99.31	X-ray, 1.5Å	hetero-dimer 	None
<input type="checkbox"/>	4aom.1.A MYOSIN A TAIL DOMAIN INTERACTING PROTEIN <i>MTIP and MyoA complex</i>						
▼	<div><div></div></div>	0.92	-	99.31	X-ray, 1.9Å	hetero-dimer 	None
<input type="checkbox"/>	6zn3.1.B Myosin A tail domain interacting protein <i>Plasmodium faciparum glideosome trimeric sub-complex</i>						
▼	<div><div></div></div>	0.92	-	99.31	X-ray, 2.5Å	hetero-trimer 	None
<input type="checkbox"/>	4mzl.1.A Myosin A tail domain interacting protein <i>Crystal Structure of MTIP from Plasmodium falciparum in complex with HBS myoA, a hydrogen bond surrogate myoA helix mimetic</i>						
▼	<div><div></div></div>	0.91	-	99.31	X-ray, 2.0Å	hetero-dimer 	None
<input type="checkbox"/>	A0A6V7T2F7.1.A Calmodulin <i>AlphaFold DB model of A0A6V7T2F7_PLAVN (gene: A0A6V7T2F7_PLAVN, organism: Plasmodium vinckei brucechwatti)</i>						
▼	<div><div></div></div>	0.90	-	71.72	AlphaFold v2	monomer ✓	None
<input type="checkbox"/>	6ycz.1.B Myosin A tail domain interacting protein <i>Plasmodium falciparum Myosin A delta-Nter, Post-Rigor state</i>						
▼	<div><div></div></div>	0.88	-	99.31	X-ray, 3.3Å	hetero-trimer 	1 x MG  , 1 x ADP 
<input type="checkbox"/>	6ycx.1.C Myosin A tail domain interacting protein <i>Plasmodium falciparum Myosin A full-length, pre-powerstroke state</i>						
▼	<div><div></div></div>	0.88	-	99.31	X-ray, 4.0Å	hetero-hexamer 	2 x ADP  , 2 x VO4  , 2 x MG 
<input type="checkbox"/>	6ycx.1.F Myosin A tail domain interacting protein <i>Plasmodium falciparum Myosin A full-length, pre-powerstroke state</i>						

↓↑Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
▼		0.85	-	99.31	X-ray, 4.0Å	hetero-hexamer 	2 x ADP  , 2 x VO4  , 2 x MG 
<input type="checkbox"/>	4ggn.1.A Myosin A tail domain interacting protein MTIP <i>Malaria invasion machinery protein complex</i>						
▼		0.78	-	78.57	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	4ggn.3.A Myosin A tail domain interacting protein MTIP <i>Malaria invasion machinery protein complex</i>						
▼		0.78	-	78.57	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	4ggn.2.A Myosin A tail domain interacting protein MTIP <i>Malaria invasion machinery protein complex</i>						
▼		0.77	-	78.57	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	4ggn.1.A Myosin A tail domain interacting protein MTIP <i>Malaria invasion machinery protein complex</i>						
▼		0.77	-	80.49	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	4ggn.2.A Myosin A tail domain interacting protein MTIP <i>Malaria invasion machinery protein complex</i>						
▼		0.76	-	80.49	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	2auc.1.A Myosin A Tail Interacting Protein <i>Structure of the Plasmodium MTIP-MyoA complex, a key component of the parasite invasion motor</i>						
▼		0.69	0.46	79.20	X-ray, 2.6Å	hetero-tetramer 	None
<input type="checkbox"/>	2auc.1.C Myosin A Tail Interacting Protein <i>Structure of the Plasmodium MTIP-MyoA complex, a key component of the parasite invasion motor</i>						
▼		0.67	0.48	79.20	X-ray, 2.6Å	hetero-tetramer 	None
<input type="checkbox"/>	2auc.1.B Myosin A Tail Interacting Protein <i>Structure of the Plasmodium MTIP-MyoA complex, a key component of the parasite invasion motor</i>						
▼		0.63	0.45	79.20	X-ray, 2.6Å	hetero-tetramer 	None
<input type="checkbox"/>	7vmb.1.C Calmodulin-1 <i>Crystal structure of IQSEC1-IQ motif, Sec7PH tandem in complex with calmodulin</i>						
▼		0.51	-	20.31	X-ray, 2.0Å	hetero-trimer 	None
<input type="checkbox"/>	1ncx.1.A TROPONIN C						
▼		0.51	-	22.66	X-ray, 1.8Å	monomer 	2 x CD 
<input type="checkbox"/>	3sg5.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin-1 chimera <i>Crystal Structure of Dimeric GCaMP3-D380Y, QP(linker 1), LP(linker 2)</i>						
▼		0.50	0.13	19.38	X-ray, 1.9Å	homo-dimer 	8 x CA 
<input type="checkbox"/>	2w49.1.A TROPONIN C, SKELETAL MUSCLE <i>ISOMETRICALLY CONTRACTING INSECT ASYNCHRONOUS FLIGHT MUSCLE</i>						

↓Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
▼		0.50	-	22.66	EM, 35.0Å	hetero-36-mer 	16 x CA 
<input type="checkbox"/>	1ytz.1.C Troponin C <i>Crystal structure of skeletal muscle troponin in the Ca<sup>2+</sup>-activated state</i>						
▼		0.50	-	22.66	X-ray, 3.0Å	hetero-trimer 	3 x DR6  , 4 x CA 
<input type="checkbox"/>	3sg4.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin-1 chimera <i>Crystal Structure of GCaMP3-D380Y, LP(linker 2)</i>						
▼		0.50	-	19.23	X-ray, 2.4Å	monomer ✓	4 x CA 
<input type="checkbox"/>	3wld.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin <i>Crystal structure of monomeric GCaMP6m</i>						
▼		0.50	-	19.23	X-ray, 2.7Å	monomer ✓	4 x CA 
<input type="checkbox"/>	9k8x.1.A Calcium indicator GCaMP6s-BrUS-145, Calmodulin-1 <i>Crystal structure of the calcium indicator GCaMP6s-BrUS-145 in calcium-bounded state</i>						
▼		0.50	-	19.38	X-ray, 2.0Å	monomer ✓	4 x CA 
<input type="checkbox"/>	8zlw.1.B Calmodulin <i>Crystal Structure of RDGC IQ motif/dCaM Complex</i>						
▼		0.49	-	19.53	X-ray, 2.2Å	hetero-trimer 	4 x CA 
<input type="checkbox"/>	6u2m.1.A HaloCaMP V2 <i>Crystal structure of a HaloTag-based calcium indicator, HaloCaMP V2, bound to JF635</i>						
▼		0.49	-	23.70	X-ray, 2.0Å	monomer ✓	1 x PUJ  , 4 x CA 
<input type="checkbox"/>	3wlc.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin <i>Crystal structure of dimeric GCaMP6m</i>						
▼		0.49	0.12	19.23	X-ray, 2.5Å	homo-dimer 	8 x CA 
<input type="checkbox"/>	1tnw.1.A TROPONIN C <i>NMR SOLUTION STRUCTURE OF CALCIUM SATURATED SKELETAL MUSCLE TROPONIN C</i>						
▼		0.48	-	21.88	NMR	monomer ✓	None
<input type="checkbox"/>	4i2y.2.A RGECO1 <i>Crystal Structure of the genetically encoded calcium indicator RGECO1</i>						
▼		0.48	-	23.70	X-ray, 2.2Å	monomer ✓	4 x CA 
<input type="checkbox"/>	3evr.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin-1 chimera <i>Crystal structure of Calcium bound monomeric GCaMP2</i>						
▼		0.48	-	20.16	X-ray, 2.0Å	monomer ✓	4 x CA 
<input type="checkbox"/>	3ewt.1.A Calmodulin <i>Crystal Structure of calmodulin complexed with a peptide</i>						
▼		0.48	-	20.31	X-ray, 2.4Å	hetero-dimer 	4 x CA 

↓↑Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	9mod.1.H Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament variant I79N in troponin T at pCa=5.8 in Ca<sup>2+</sup>-free tilted state (upper strand)</i>						
▼		0.47	-	22.66	EM	hetero-15-mer 	7 x ADP  , 7 x MG 
<input type="checkbox"/>	9mo7.1.G Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament at pCa=5.8 in Ca<sup>2+</sup>-bound fully activated state (lower strand)</i>						
▼		0.47	-	22.66	EM	hetero-14-mer 	6 x ADP  , 6 x MG  , 3 x CA 
<input type="checkbox"/>	9moc.1.H Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament variant I79N in troponin T at pCa=5.8 in Ca<sup>2+</sup>-free rotated state (upper strand)</i>						
▼		0.47	-	22.66	EM	hetero-15-mer 	7 x ADP  , 7 x MG 
<input type="checkbox"/>	9v59.1.A WHaloCaMP1a <i>Crystal structure of calcium indicator WHaloCaMP1a labeled with BD566-HTL substrate</i>						
▼		0.47	-	23.70	X-ray, 2.2Å	monomer ✓	5 x GLC  , 4 x CA  , 1 x 01
<input type="checkbox"/>	4i2y.1.A RGECO1 <i>Crystal Structure of the genetically encoded calcium indicator RGECO1</i>						
▼		0.47	-	23.70	X-ray, 2.2Å	monomer ✓	4 x CA 
<input type="checkbox"/>	9mo8.1.H Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament at pCa=5.8 in Ca<sup>2+</sup>-free state (upper strand)</i>						
▼		0.46	-	22.66	EM	hetero-15-mer 	7 x ADP  , 7 x MG 
<input type="checkbox"/>	9mo9.1.G Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament variant I79N in troponin T at pCa=5.8 in Ca<sup>2+</sup>-free rotated state (lower strand)</i>						
▼		0.46	-	22.66	EM	hetero-14-mer 	6 x ADP  , 6 x MG 
<input type="checkbox"/>	6u3b.1.A Calmodulin-1 <i>1.7 Angstrom crystal structure of the Q135P Ca-CaM:CaV1.2 IQ domain complex</i>						
▼		0.46	-	20.47	X-ray, 1.7Å	hetero-dimer 	5 x CA 
<input type="checkbox"/>	5oeo.1.A Calmodulin-1 <i>Solution structure of the complex of TRPV5(655-725) with a Calmodulin E32Q/E68Q double mutant</i>						
▼		0.45	-	21.26	NMR	hetero-dimer 	2 x CA 
<input type="checkbox"/>	9mo5.1.G Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament at pCa=5.8 in Ca<sup>2+</sup>-bound partially activated state (lower strand)</i>						
▼		0.45	-	22.66	EM	hetero-14-mer 	6 x ADP  , 6 x MG  , 3 x CA 
<input type="checkbox"/>	6u39.1.A Calmodulin-1 <i>2.4 Angstrom crystal structure of the D129G Ca-CaM:CaV1.2 IQ domain complex</i>						
▼		0.45	-	23.70	X-ray, 2.4Å	hetero-dimer 	3 x CA 
<input type="checkbox"/>	6u39.2.A Calmodulin-1 <i>2.4 Angstrom crystal structure of the D129G Ca-CaM:CaV1.2 IQ domain complex</i>						

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
▼		0.44	-	23.70	X-ray, 2.4Å	hetero-dimer	3 x CA
<input type="checkbox"/>	9mo4.1.G Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament at pCa=5.8 in Ca2+-free state (lower strand)</i>						
▼		0.44	-	22.66	EM	hetero-14-mer	6 x ADP , 6 x MG
<input type="checkbox"/>	9mo6.1.G Troponin C, slow skeletal and cardiac muscles <i>Structure of native murine cardiac thin filament at pCa=5.8 in Ca2+-free tilted state (lower strand)</i>						
▼		0.44	-	22.66	EM	hetero-14-mer	6 x ADP , 6 x MG
<input type="checkbox"/>	6u39.5.A Calmodulin-1 <i>2.4 Angstrom crystal structure of the D129G Ca-CaM:CaV1.2 IQ domain complex</i>						
▼		0.42	-	23.70	X-ray, 2.4Å	hetero-dimer	2 x CA
<input type="checkbox"/>	5tp6.1.A Calmodulin <i>Solution structure of the CaM34 with the iNOS CaM binding domain peptide</i>						
▼		0.42	-	23.70	NMR	hetero-dimer	None
<input type="checkbox"/>	5tp6.1.A Calmodulin <i>Solution structure of the CaM34 with the iNOS CaM binding domain peptide</i>						
▼		0.39	-	19.69	NMR	hetero-dimer	None
<input type="checkbox"/>	1yv0.1.C Troponin C, skeletal muscle <i>Crystal structure of skeletal muscle troponin in the Ca2+-free state</i>						
▼		0.39	-	22.66	X-ray, 7.0Å	hetero-trimer	2 x MG

The full list of templates matching your target sequence includes the following templates which are not in the list above. The full template list is available in text or html format.

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