All Projects

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

Summary Templates 50 Models 1 Project Data

Template Results

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

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
	4ggn.1.A Myosin A tail domain interacting protein MTIP *Malaria invasion machinery protein complex*						
		0.78	-	78.57	X-ray, 2.3Å	hetero-dimer ⚠	None
	4ggn.3.A Myosin A tail domain interacting protein MTIP *Malaria invasion machinery protein complex*						
		0.78	-	78.57	X-ray, 2.3Å	hetero-dimer ⚠	None
	4ggn.2.A Myosin A tail domain interacting protein MTIP *Malaria invasion machinery protein complex*						
		0.77	-	78.57	X-ray, 2.3Å	hetero-dimer ⚠	None
	4ggn.1.A Myosin A tail domain interacting protein MTIP *Malaria invasion machinery protein complex*						
		0.77	-	80.49	X-ray, 2.3Å	hetero-dimer ⚠	None
	4ggn.2.A Myosin A tail domain interacting protein MTIP *Malaria invasion machinery protein complex*						
		0.76	-	80.49	X-ray, 2.3Å	hetero-dimer ⚠	None
	2auc.1.A Myosin A Tail Interacting Protein *Structure of the Plasmodium MTIP-MyoA complex, a key component of the parasite invasion motor*						
		0.69	0.46	79.20	X-ray, 2.6Å	hetero-tetramer ⚠	None
	2auc.1.C Myosin A Tail Interacting Protein *Structure of the Plasmodium MTIP-MyoA complex, a key component of the parasite invasion motor*						
		0.67	0.48	79.20	X-ray, 2.6Å	hetero-tetramer ⚠	None
	2auc.1.B Myosin A Tail Interacting Protein *Structure of the Plasmodium MTIP-MyoA complex, a key component of the parasite invasion motor*						
		0.63	0.45	79.20	X-ray, 2.6Å	hetero-tetramer ⚠	None
	7vmb.1.C Calmodulin-1 *Crystal structure of IQSEC1-IQ motif, Sec7PH tandem in complex with calmodulin*						
		0.51	-	20.31	X-ray, 2.0Å	hetero-trimer ⚠	None
	1ncx.1.A TROPONIN C						
		0.51	-	22.66	X-ray, 1.8Å	monomer ✓	2 x CD
	3sg5.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin-1 chimera *Crystal Structure of Dimeric GCaMP3-D380Y, QP(linker 1), LP(linker 2)*						
		0.50	0.13	19.38	X-ray, 1.9Å	homo-dimer ⚠	8 x CA
	2w49.1.A TROPONIN C, SKELETAL MUSCLE *ISOMETRICALLY CONTRACTING INSECT ASYNCHRONOUS FLIGHT MUSCLE*						

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
		0.50	-	22.66	EM, 35.0Å	hetero-36-mer ⚠	16 x CA
	1ytz.1.C Troponin C *Crystal structure of skeletal muscle troponin in the Ca2+-activated state*						
		0.50	-	22.66	X-ray, 3.0Å	hetero-trimer ⚠	3 x DR6, 4 x CA
	3sg4.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin-1 chimera *Crystal Structure of GCaMP3-D380Y, LP(linker 2)*						
		0.50	-	19.23	X-ray, 2.4Å	monomer ✓	4 x CA
	3wld.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin *Crystal structure of monomeric GCaMP6m*						
		0.50	-	19.23	X-ray, 2.7Å	monomer ✓	4 x CA
	9k8x.1.A Calcium indicator GCaMP6s-BrUS-145,Calmodulin-1 *Crystal structure of the calcium indicator GCaMP6s-BrUS-145 in calcium-bounded state*						
		0.50	-	19.38	X-ray, 2.0Å	monomer ✓	4 x CA
	8zlw.1.B Calmodulin *Crystal Structure of RDGC IQ motif/dCaM Complex*						
		0.49	-	19.53	X-ray, 2.2Å	hetero-trimer ⚠	4 x CA
	6u2m.1.A HaloCaMP V2 *Crystal structure of a HaloTag-based calcium indicator, HaloCaMP V2, bound to JF635*						
		0.49	-	23.70	X-ray, 2.0Å	monomer ✓	1 x PUJ, 4 x CA
	3wlc.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin *Crystal structure of dimeric GCaMP6m*						
		0.49	0.12	19.23	X-ray, 2.5Å	homo-dimer ⚠	8 x CA
	1tnw.1.A TROPONIN C *NMR SOLUTION STRUCTURE OF CALCIUM SATURATED SKELETAL MUSCLE TROPONIN C*						
		0.48	-	21.88	NMR	monomer ✓	None
	4i2y.2.A RGECO1 *Crystal Structure of the genetically encoded calcium indicator RGECO1*						
		0.48	-	23.70	X-ray, 2.2Å	monomer ✓	4 x CA
	3evr.1.A Myosin light chain kinase, Green fluorescent protein, Calmodulin-1 chimera *Crystal structure of Calcium bound monomeric GCAMP2*						
		0.48	-	20.16	X-ray, 2.0Å	monomer ✓	4 x CA
	3ewt.1.A Calmodulin *Crystal Structure of calmodulin complexed with a peptide*						
		0.48	-	20.31	X-ray, 2.4Å	hetero-dimer ⚠	4 x CA

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
	9mod.1.H Troponin C, slow skeletal and cardiac muscles *Structure of native murine cardiac thin filament variant I79N in troponin T at pCa=5.8 in Ca2+-free tilted state (upper strand)*						
		0.47	-	22.66	EM	hetero-15-mer ⚠	7 x ADP, 7 x MG
	9mo7.1.G Troponin C, slow skeletal and cardiac muscles *Structure of native murine cardiac thin filament at pCa=5.8 in Ca2+-bound fully activated state (lower strand)*						
		0.47	-	22.66	EM	hetero-14-mer ⚠	6 x ADP, 6 x MG, 3 x CA
	9moc.1.H Troponin C, slow skeletal and cardiac muscles *Structure of native murine cardiac thin filament variant I79N in troponin T at pCa=5.8 in Ca2+-free rotated state (upper strand)*						
		0.47	-	22.66	EM	hetero-15-mer ⚠	7 x ADP, 7 x MG
	9v59.1.A WHaloCaMP1a *Crystal structure of calcium indicator WHaloCaMP1a labeled with BD566-HTL substrate*						
		0.47	-	23.70	X-ray, 2.2Å	monomer ✓	5 x GLC, 4 x CA, 1 x 01
	4i2y.1.A RGECO1 *Crystal Structure of the genetically encoded calcium indicator RGECO1*						
		0.47	-	23.70	X-ray, 2.2Å	monomer ✓	4 x CA
	9mo8.1.H Troponin C, slow skeletal and cardiac muscles *Structure of native murine cardiac thin filament at pCa=5.8 in Ca2+-free state (upper strand)*						
		0.46	-	22.66	EM	hetero-15-mer ⚠	7 x ADP, 7 x MG
	9mo9.1.G Troponin C, slow skeletal and cardiac muscles *Structure of native murine cardiac thin filament variant I79N in troponin T at pCa=5.8 in Ca2+-free rotated state (lower strand)*						
		0.46	-	22.66	EM	hetero-14-mer ⚠	6 x ADP, 6 x MG
	6u3b.1.A Calmodulin-1 *1.7 Angstrom crystal structure of the Q135P Ca-CaM:CaV1.2 IQ domain complex*						
		0.46	-	20.47	X-ray, 1.7Å	hetero-dimer ⚠	5 x CA
	5oeo.1.A Calmodulin-1 *Solution structure of the complex of TRPV5(655-725) with a Calmodulin E32Q/E68Q double mutant*						
		0.45	-	21.26	NMR	hetero-dimer ⚠	2 x CA
	9mo5.1.G Troponin C, slow skeletal and cardiac muscles *Structure of native murine cardiac thin filament at pCa=5.8 in Ca2+-bound partially activated state (lower strand)*						
		0.45	-	22.66	EM	hetero-14-mer ⚠	6 x ADP, 6 x MG, 3 x CA
	6u39.1.A Calmodulin-1 *2.4 Angstrom crystal structure of the D129G Ca-CaM:CaV1.2 IQ domain complex*						
		0.45	-	23.70	X-ray, 2.4Å	hetero-dimer ⚠	3 x CA
	6u39.2.A Calmodulin-1 *2.4 Angstrom crystal structure of the D129G Ca-CaM:CaV1.2 IQ domain complex*						

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

1a03.1.A, 1a03.1.B, 1a29.1.A, 1a2x.1.A, 1a4p.1.H, 1a4p.2.D, 1a75.1.A, 1a75.2.A, 1ahr.1.A, 1aj4.1.A, 1aj5.1.A, 1aj5.2.A, 1ak8.1.A, 1alv.1.A, 1alv.1.B, 1alw.1.A, 1ap4.1.A, 1aui.1.B, 1avs.1.A, 1avs.2.A, 1b1g.1.A, 1b4c.1.A, 1b7t.1.B, 1b7t.1.C, 1b8c.1.A, 1b8l.1.A, 1b8r.1.A, 1b9a.1.A, 1bjf.1.A, 1blq.1.A, 1bmo.1.A, 1boc.1.A, 1bod.1.A, 1br4.4.B, 1bt6.2.B, 1bu3.1.A, 1c07.1.A, 1c7v.1.A, 1c7w.1.A, 1cb1.1.A, 1cdl.1.A, 1cdl.2.A, 1cdl.3.A, 1cdl.4.A, 1cdm.1.A, 1cdn.1.A, 1cdp.1.B, 1cfc.1.A, 1cfd.1.A, 1cff.1.A, 1cfp.1.B, 1ckk.1.A, 1clb.1.A, 1cll.1.A, 1clm.1.A, 1cm1.2.A, 1cm4.1.A, 1cmf.1.A, 1cmg.1.A, 1cnp.1.A, 1cnp.1.B, 1cta.1.A, 1cta.1.B, 1ctd.1.A, 1ctd.1.B, 1ctr.1.A, 1d1o.1.A, 1ddf.1.A, 1df0.1.A, 1df0.1.B, 1dfk.1.B, 1dfk.1.C, 1dgu.1.A, 1dgv.1.A, 1djg.2.A, 1dji.1.A, 1djx.2.A, 1dmo.1.A, 1dt7.1.A, 1dtl.1.A, 1dvi.1.A, 1e8a.1.A, 1e8a.1.B, 1eg3.1.A, 1eh2.1.A, 1ej3.1.A, 1el4.1.A, 1f4o.1.A, 1f54.1.A, 1f55.1.A, 1f70.1.A, 1f71.1.A, 1f8h.1.A, 1ff1.1.A, 1fi5.1.A, 1fi6.1.A, 1fpw.1.A, 1fw4.1.A, 1g33.1.A, 1g4y.1.D, 1g8i.1.A, 1g8i.2.A, 1ggw.1.A, 1ggz.1.A, 1gjy.1.A, 1gjy.1.B, 1gjy.2.A, 1gjy.2.B, 1gqm.1.A, 1gx3.1.A, 1h4b.1.A, 1h8b.1.A, 1hqv.1.A, 1ht9.1.A, 1ht9.1.B, 1i84.1.B, 1igv.1.A, 1ih0.1.A, 1ij5.1.A, 1iku.1.A, 1iq3.1.A, 1iq5.1.A, 1irj.1.A, 1irj.1.B, 1irj.2.A, 1irj.3.A, 1irj.3.B, 1irj.4.A, 1irj.4.B, 1iwq.1.A, 1j1d.1.A, 1j1d.2.A, 1j1e.1.A, 1j1e.2.A, 1j55.1.A, 1j7o.1.A, 1j7p.1.A, 1j7q.1.A, 1j7r.1.A, 1jba.1.A, 1jc2.1.A, 1jf0.1.A, 1jf2.1.A, 1jfj.1.A, 1jfk.1.A, 1jsa.1.A, 1juo.1.B, 1jwd.1.A, 1jwd.1.B, 1k2h.1.B, 1k8u.1.A, 1k90.1.F, 1k90.2.B, 1k90.4.B, 1k93.1.B, 1k94.1.A, 1k94.1.B, 1k95.1.A, 1k96.1.A, 1k9k.1.A, 1k9k.1.B, 1k9p.1.A, 1k9u.1.A, 1k9u.1.B, 1kcy.1.A, 1kfu.1.A, 1kfu.1.B, 1kfx.1.A, 1kfx.1.B, 1kk7.1.B, 1kk7.1.C, 1kk8.1.B, 1kk8.1.C, 1kqm.1.B, 1kqm.1.C, 1kqv.1.A, 1ksm.1.A, 1kso.1.A, 1kso.1.B, 1kwo.1.B, 1kwo.1.C, 1l2o.1.B, 1la0.1.A, 1la3.1.A, 1lkj.1.A, 1lvc.1.B, 1lxf.1.A, 1m31.1.A, 1m39.1.A, 1m45.1.A, 1m46.1.A, 1m5y.1.A, 1m5y.1.C, 1m63.1.B, 1m63.1.F, 1m8q.1.B, 1m8q.1.L, 1mho.1.A, 1mq1.1.A, 1mr8.1.A, 1mr8.1.B, 1mux.1.A, 1mwn.1.B, 1mxe.1.A, 1mxl.1.A, 1mzb.1.A, 1n0y.1.A, 1n0y.2.A, 1n2d.1.A, 1n2d.1.B, 1n65.1.A, 1ncx.1.A, 1niw.3.A, 1niw.5.C, 1niw.6.C, 1niw.6.G, 1np8.1.A, 1np8.1.B, 1npq.1.A, 1nsh.1.A, 1nub.1.A, 1nwd.1.A, 1nx0.1.A, 1nx0.1.B, 1nx1.1.A, 1nx2.1.B, 1nya.1.A, 1odb.1.A, 1odb.3.A, 1omd.1.A, 1omr.1.A, 1omv.2.D, 1ooj.1.A, 1oqp.1.A, 1osa.1.A, 1ozo.1.A, 1ozo.1.B, 1ozs.1.A, 1pk0.1.D, 1pon.1.A, 1pon.1.B, 1prw.1.A, 1psb.1.A, 1psb.1.B, 1pul.1.A, 1pva.1.A, 1pva.2.A, 1pvb.1.A, 1q80.1.A, 1qas.1.A, 1qat.2.A, 1qiv.1.A, 1qiw.1.A, 1qiw.2.A, 1qjt.1.A, 1qlk.1.A, 1qls.1.A, 1qs7.1.A, 1qs7.2.A, 1qtx.1.A, 1qv0.1.A, 1qvi.1.B, 1qvi.1.C, 1qx2.1.A, 1qx2.2.A, 1qx5.1.A, 1qx5.1.B, 1qx5.2.A, 1qx5.2.B, 1qx5.3.A, 1qx5.3.B, 1qx5.4.A, 1qx5.4.B, 1qx7.1.B, 1qx7.2.A, 1qx7.2.B, 1qx7.4.A, 1qxp.1.A, 1qxp.2.A, 1r2u.1.A, 1r6p.1.A, 1rec.1.A, 1rfj.1.A, 1rjv.1.A, 1rk9.1.A, 1rwy.1.A, 1rwy.2.A, 1rwy.3.A, 1s1e.1.A, 1s26.1.B, 1s3p.1.A, 1s5g.1.B, 1s5g.1.C, 1s6c.1.A, 1s6i.1.A, 1s6j.1.A, 1sbj.1.A, 1scm.1.B, 1scm.1.C, 1scv.1.A, 1sjj.1.A, 1sjj.1.B, 1sk6.2.B, 1sk6.3.B, 1skt.1.A, 1sl7.1.A, 1sl8.1.A, 1smg.1.A, 1snl.1.A, 1spy.1.A, 1sr6.1.B, 1sra.1.A, 1sw2.1.A, 1sw8.1.A, 1sy9.1.A, 1sym.1.A, 1tcf.1.A, 1tco.1.B, 1tiz.1.A, 1tn4.1.A, 1tnp.1.A, 1tnq.1.A, 1tnw.1.A, 1tnx.1.A, 1trf.1.A, 1ttx.1.A, 1tuz.1.A, 1u5i.1.A, 1uhi.1.A, 1uhk.1.A, 1uhn.1.A, 1up5.1.A, 1up5.2.A, 1uwo.1.A, 1uwo.1.B, 1v1f.1.A, 1vrk.1.A, 1w7j.1.B, 1wdc.1.B, 1wlm.1.A, 1wlz.1.A, 1wlz.2.A, 1wlz.4.A, 1wrk.1.A, 1wrk.1.B, 1wrz.1.A, 1wy9.1.A, 1x02.1.A, 1xa5.1.A, 1xfu.1.B, 1xfy.4.B, 1xk4.1.C, 1xk4.2.A, 1xo5.1.A, 1xo5.2.A, 1xvj.1.A, 1xyd.1.A, 1y0v.1.B, 1y1a.1.A, 1y1a.3.B, 1y1x.1.A, 1y1x.2.A, 1y6w.1.A, 1yr5.1.A, 1yrt.1.B, 1ytz.1.C, 1yur.1.A, 1yur.1.B, 1yus.1.A, 1yus.1.B, 1yut.1.A, 1yut.1.B, 1yuu.1.A, 1yuu.1.B, 1yv0.1.C, 1yx7.1.A, 1yx8.1.A, 1zac.1.A, 1zfs.1.A, 1zmz.1.A, 1zot.1.B, 1zuz.2.C, 2a4j.1.A, 2aao.1.A, 2aao.2.A, 2ahq.1.A, 2ami.1.A, 2auc.1.A, 2auc.1.B, 2auc.1.C, 2b1u.1.A, 2b59.1.B, 2bbm.1.A, 2bbn.1.A, 2bca.1.A, 2bcb.1.A, 2bcx.1.A, 2be4.1.A, 2be6.1.A, 2be6.3.A, 2be6.4.A, 2bec.1.A, 2bki.1.B, 2bki.1.C, 2bl0.1.B, 2bl0.1.C,

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