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 Created: today at 13:08


Template Results

Templates	Quaternary Structure		Sequence Similarity		Alignment	More ▾	
↓↑Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/> ✓	Q65ZC9.1.A Single-chain Fv <i>AlphaFold DB model of Q65ZC9_HUMAN (gene: scFv, organism: Homo sapiens (Human))</i>						
▼	<div><div></div></div>	0.88	-	86.19	AlphaFold v2	monomer ✓	None
<input type="checkbox"/> ⚙	8dy0.1.A spFv GLK1 HL <i>Crystal Structure of spFv GLK1 HL</i>						
▼	<div><div></div></div>	0.83	-	88.75	X-ray, 2.1Å	monomer ✓	None
<input type="checkbox"/>	6g8r.1.A single-chain variable fragment <i>SP140 PHD-Bromodomain complex with scFv</i>						
▼	<div><div></div></div>	0.82	-	91.67	X-ray, 2.7Å	hetero-dimer ⚠	2 x ZN <a href="#">🔗</a>
<input type="checkbox"/>	6g8r.1.A single-chain variable fragment <i>SP140 PHD-Bromodomain complex with scFv</i>						
▼	<div><div></div></div>	0.82	-	92.08	X-ray, 2.7Å	hetero-dimer ⚠	2 x ZN <a href="#">🔗</a>
<input type="checkbox"/>	8dy0.1.A spFv GLK1 HL <i>Crystal Structure of spFv GLK1 HL</i>						
▼	<div><div></div></div>	0.82	-	89.12	X-ray, 2.1Å	monomer ✓	None
<input type="checkbox"/>	6y6c.1.B Single chain variable <i>TREM2 extracellular domain (19-174) in complex with single-chain variable fragment (scFv-4)</i>						
▼	<div><div></div></div>	0.82	-	94.14	X-ray, 2.3Å	hetero-octamer ⚠	4 x NAG <a href="#">🔗</a>
<input type="checkbox"/>	7yue.1.A Single chain variable Fragment <i>Epitope-directed anti-SARS CoV 2 scFv engineered against the key spike protein region.</i>						
▼	<div><div></div><div></div></div>	0.82	-	91.21	X-ray, 2.3Å	hetero-dimer ⚠	None
<input type="checkbox"/>	7yue.1.A Single chain variable Fragment <i>Epitope-directed anti-SARS CoV 2 scFv engineered against the key spike protein region.</i>						
▼	<div><div></div><div></div></div>	0.82	-	88.38	X-ray, 2.3Å	hetero-dimer ⚠	None
<input type="checkbox"/>	6ymq.2.A Single-chain variable 4 <i>TREM2 extracellular domain (19-131) in complex with single-chain variable 4 (scFv-4)</i>						
▼	<div><div></div></div>	0.81	-	94.14	X-ray, 3.1Å	hetero-dimer ⚠	1 x NAG <a href="#">🔗</a>
<input type="checkbox"/>	6y6c.1.B Single chain variable <i>TREM2 extracellular domain (19-174) in complex with single-chain variable fragment (scFv-4)</i>						
▼	<div><div></div></div>	0.81	-	94.12	X-ray, 2.3Å	hetero-octamer ⚠	4 x NAG <a href="#">🔗</a>

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	6ymq.2.A Single-chain variable 4 <i>TREM2 extracellular domain (19-131) in complex with single-chain variable 4 (scFv-4)</i>						
▼		0.81	-	94.12	X-ray, 3.1Å	hetero-dimer 	1 x NAG 
<input type="checkbox"/>	2ghw.1.B anti-sars scFv antibody, 80R <i>Crystal structure of SARS spike protein receptor binding domain in complex with a neutralizing antibody, 80R</i>						
▼		0.81	-	77.59	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	6yye.1.B TREM2 Single chain variable 2 <i>TREM2 extracellular domain (19-131) in complex with single-chain variable fragment (scFv-2)</i>						
▼		0.81	-	92.47	X-ray, 3.4Å	hetero-dimer 	1 x NAG 
<input type="checkbox"/>	7w7q.1.A 1F11S antibody <i>Crystal structure of 1F11S antibody(ScFv)</i>						
▼		0.81	0.47	89.92	X-ray, 2.0Å	homo-dimer 	None
<input type="checkbox"/>	7w7q.1.A 1F11S antibody <i>Crystal structure of 1F11S antibody(ScFv)</i>						
▼		0.80	0.47	89.50	X-ray, 2.0Å	homo-dimer 	None
<input type="checkbox"/>	2ghw.1.B anti-sars scFv antibody, 80R <i>Crystal structure of SARS spike protein receptor binding domain in complex with a neutralizing antibody, 80R</i>						
▼		0.80	-	78.66	X-ray, 2.3Å	hetero-dimer 	None
<input type="checkbox"/>	7tzh.1.A scFvF7 <i>Structure of human LAG3 domains 3-4 in complex with antibody single chain-variable fragment</i>						
▼		0.80	-	86.61	X-ray, 2.4Å	hetero-dimer 	1 x NAG 
<input type="checkbox"/>	7u9w.1.B 230AS-88 <i>Pfs230 D1 domain in complex with 230AS-88</i>						
▼		0.80	-	80.17	X-ray, 2.8Å	hetero-dimer 	None
<input type="checkbox"/>	7tzh.1.A scFvF7 <i>Structure of human LAG3 domains 3-4 in complex with antibody single chain-variable fragment</i>						
▼		0.80	-	87.39	X-ray, 2.4Å	hetero-dimer 	1 x NAG 
<input type="checkbox"/>	6yye.1.B TREM2 Single chain variable 2 <i>TREM2 extracellular domain (19-131) in complex with single-chain variable fragment (scFv-2)</i>						
▼		0.80	-	92.86	X-ray, 3.4Å	hetero-dimer 	1 x NAG 
<input type="checkbox"/>	6zqk.1.A 841 heavy chain <i>HER2-binding scFv-Fab fusion 841</i>						
▼		0.80	-	81.74	X-ray, 2.2Å	hetero-dimer 	None
<input type="checkbox"/>	7ucq.1.B 230AS-18 <i>Pfs230 D1 domain in complex with 230AS-18</i>						
▼		0.80	-	74.38	X-ray, 2.5Å	hetero-dimer 	None
<input type="checkbox"/>	7u9w.1.B 230AS-88 <i>Pfs230 D1 domain in complex with 230AS-88</i>						
▼		0.80	-	80.83	X-ray, 2.8Å	hetero-dimer 	None

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	6zqk.2.A 841 heavy chain <i>HER2-binding scFv-Fab fusion 841</i>						
▼		0.79	-	81.74	X-ray, 2.2Å	hetero-dimer 	None
<input type="checkbox"/>	5f72.1.B Single chain Fv from a Fab <i>De novo design and crystallographic validation of antibodies targeting a pre-selected epitope</i>						
▼		0.79	-	83.75	X-ray, 1.8Å	hetero-dimer 	None
<input type="checkbox"/>	7tzg.1.B scFvF7 <i>Structure of human LAG3 in complex with antibody single-chain variable fragment</i>						
▼		0.79	-	86.25	X-ray, 3.7Å	hetero-tetramer 	7 x NAG 
<input type="checkbox"/>	5b3n.1.A anti-H4K20me1_scFv <i>The crystal structure of anti-H4K20me1_scFv, 15F11</i>						
▼		0.79	-	75.42	X-ray, 1.9Å	monomer 	None
<input type="checkbox"/>	6dsi.1.A Anti-TN-C scFv <i>Anti recombinant prolactin receptor scFv</i>						
▼		0.79	-	87.82	X-ray, 2.5Å	monomer 	None
<input type="checkbox"/>	7tzg.1.B scFvF7 <i>Structure of human LAG3 in complex with antibody single-chain variable fragment</i>						
▼		0.79	-	87.39	X-ray, 3.7Å	hetero-tetramer 	7 x NAG 
<input type="checkbox"/>	6zqk.1.A 841 heavy chain <i>HER2-binding scFv-Fab fusion 841</i>						
▼		0.79	-	81.51	X-ray, 2.2Å	hetero-dimer 	None
<input type="checkbox"/>	7url.1.A anti-HIV scFv <i>The crystal structure of anti-HIV_scFv</i>						
▼		0.79	-	74.18	X-ray, 1.5Å	monomer 	None
<input type="checkbox"/>	5f72.1.B Single chain Fv from a Fab <i>De novo design and crystallographic validation of antibodies targeting a pre-selected epitope</i>						
▼		0.79	-	83.40	X-ray, 1.8Å	hetero-dimer 	None
<input type="checkbox"/>	6zqk.2.A 841 heavy chain <i>HER2-binding scFv-Fab fusion 841</i>						
▼		0.79	-	81.51	X-ray, 2.2Å	hetero-dimer 	None
<input type="checkbox"/>	7tzg.1.A scFvF7 <i>Structure of human LAG3 in complex with antibody single-chain variable fragment</i>						
▼		0.79	-	87.39	X-ray, 3.7Å	hetero-tetramer 	7 x NAG 
<input type="checkbox"/>	7tzg.1.A scFvF7 <i>Structure of human LAG3 in complex with antibody single-chain variable fragment</i>						
▼		0.79	-	86.25	X-ray, 3.7Å	hetero-tetramer 	7 x NAG 
<input type="checkbox"/>	7ucq.1.B 230AS-18 <i>Pfs230 D1 domain in complex with 230AS-18</i>						
▼		0.79	-	75.00	X-ray, 2.5Å	hetero-dimer 	None

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	6dsi.1.A Anti-TN-C scFv <i>Anti recombinant prolactin receptor scFv</i>						
▼		0.78	-	90.34	X-ray, 2.5Å	monomer ✓	None
<input type="checkbox"/>	7ui1.2.A 230AL-37 <i>Pfs230 D1D2 domain in complex with 230AL-37</i>						
▼		0.78	-	73.97	X-ray, 3.3Å	monomer ✓	None
<input type="checkbox"/>	7vmu.1.A scFv E4 <i>Crystal Structure of SARS-CoV Spike Receptor-Binding Domain Complexed with Neutralizing Antibody</i>						
▼		0.78	-	83.54	X-ray, 2.9Å	hetero-dimer ⚠	None
<input type="checkbox"/>	7vmu.1.A scFv E4 <i>Crystal Structure of SARS-CoV Spike Receptor-Binding Domain Complexed with Neutralizing Antibody</i>						
▼		0.77	-	84.39	X-ray, 2.9Å	hetero-dimer ⚠	None
<input type="checkbox"/>	6kn9.1.B scFv <i>Crystal structure of human interleukin 18 receptor beta extracellular domain in complex with an antagonistic scFv</i>						
▼		0.74	-	83.68	X-ray, 3.3Å	hetero-dimer ⚠	1 x NAG <a href="#">↗</a>
<input type="checkbox"/>	6kn9.1.B scFv <i>Crystal structure of human interleukin 18 receptor beta extracellular domain in complex with an antagonistic scFv</i>						
▼		0.74	-	82.50	X-ray, 3.3Å	hetero-dimer ⚠	1 x NAG <a href="#">↗</a>
<input type="checkbox"/>	7zce.1.F scFv76 single chain fragment <i>SARS-CoV-2 Spike protein in complex with the single chain fragment scFv76</i>						
▼		0.67	0.04	79.17	EM	hetero-hexamer ⚠	12 x NAG-NAG, 27 x NAG <a href="#">↗</a>
<input type="checkbox"/>	7zce.1.E scFv76 single chain fragment <i>SARS-CoV-2 Spike protein in complex with the single chain fragment scFv76</i>						
▼		0.67	0.04	79.17	EM	hetero-hexamer ⚠	12 x NAG-NAG, 27 x NAG <a href="#">↗</a>
<input type="checkbox"/>	7zce.1.D scFv76 single chain fragment <i>SARS-CoV-2 Spike protein in complex with the single chain fragment scFv76</i>						
▼		0.66	0.04	79.17	EM	hetero-hexamer ⚠	12 x NAG-NAG, 27 x NAG <a href="#">↗</a>
<input type="checkbox"/>	7zce.1.F scFv76 single chain fragment <i>SARS-CoV-2 Spike protein in complex with the single chain fragment scFv76</i>						
▼		0.66	0.03	78.69	EM	hetero-hexamer ⚠	12 x NAG-NAG, 27 x NAG <a href="#">↗</a>
<input type="checkbox"/>	7zce.1.E scFv76 single chain fragment <i>SARS-CoV-2 Spike protein in complex with the single chain fragment scFv76</i>						
▼		0.66	0.03	78.69	EM	hetero-hexamer ⚠	12 x NAG-NAG, 27 x NAG <a href="#">↗</a>
<input type="checkbox"/>	7zce.1.D scFv76 single chain fragment <i>SARS-CoV-2 Spike protein in complex with the single chain fragment scFv76</i>						
▼		0.65	0.03	78.69	EM	hetero-hexamer ⚠	12 x NAG-NAG, 27 x NAG <a href="#">↗</a>
<input type="checkbox"/>	6kn9.2.B scFv <i>Crystal structure of human interleukin 18 receptor beta extracellular domain in complex with an antagonistic scFv</i>						
▼		0.42	-	83.68	X-ray, 3.3Å	hetero-dimer ⚠	1 x NAG-NAG

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	6kn9.2.B scFv <i>Crystal structure of human interleukin 18 receptor beta extracellular domain in complex with an antagonistic scFv</i>						
<input checked="" type="checkbox"/>		0.42	-	82.50	X-ray, 3.3Å	hetero-dimer <a href="#">⚠</a>	1 x NAG-NAG

1z2e.1.A, 1z2e8.1.B, 1z2e8.2.B, 1z5c8.A, 1z5c8.1.B, 1a0q.1.A, 1a0q.1.B, 1a14.1.A, 1a14.1.C, 1a3l.1.A, 1a3l.1.B, 1a3r.1.A, 1a3r.1.B, 1a4j.1.A, 1a4j.1.B, 1a4k.1.A, 1a4k.1.B, 1a4k.2.B, 1a5f.1.A, 1a5f.1.B, 1a6t.1.A, 1a6t.1.B, 1a6t.2.B, 1a6u.1.A, 1a6v.1.A, 1a6v.1.B, 1a6v.2.A, 1a6v.3.B, 1a6v.3.B, 1a6w.1.B, 1a7n.1.B, 1a7q.1.B, 1a8j.1.A, 1a8j.1.B, 1ac6.1.A, 1ac6.1.B, 1acy.1.A, 1acy.1.B, 1ad0.1.A, 1ad0.1.B, 1ad9.1.A, 1ad9.1.B, 1ad9.2.B, 1adq.1.B, 1adq.1.C, 1ae6.1.A, 1ae6.1.B, 1afv.1.C, 1afv.1.D, 1ah1.1.A, 1ahw.1.A, 1ahw.1.B, 1aif.1.B, 1aj7.1.A, 1aj7.1.B, 1akj.1.C, 1ao7.1.C, 1ap2.1.A, 1ap2.1.B, 1ap2.2.B, 1aqk.1.A, 1aqk.1.B, 1ar2.1.A, 1axs.1.A, 1axs.1.B, 1axs.2.B, 1axt.1.A, 1axt.1.B, 1ay1.1.A, 1ay1.1.B, 1b2w.1.A, 1b2w.1.B, 1b4j.1.A, 1b4j.1.B, 1b6d.1.A, 1b6d.1.B, 1b88.1.A, 1b88.1.B, 1baf.1.A, 1baf.1.B, 1bbd.1.A, 1bbd.1.B, 1bbj.1.A, 1bbj.1.B, 1bd2.1.C, 1bec.1.A, 1bey.1.A, 1bey.1.B, 1bfo.1.A, 1bfo.1.B, 1bfo.2.B, 1bgx.1.B, 1bgx.1.C, 1bj1.1.A, 1bj1.1.B, 1bjm.1.A, 1bjm.1.B, 1bln.1.A, 1bln.1.B, 1bln.2.B, 1bln.2.B, 1bm3.1.A, 1bm3.1.B, 1bog.1.A, 1bog.1.B, 1bql.1.B, 1bvk.2.B, 1bvl.1.A, 1bvl.2.A, 1bwm.1.A, 1bww.1.A, 1bz7.1.A, 1bz7.1.B, 1bzq.1.B, 1c08.1.B, 1c12.1.A, 1c12.1.B, 1c1e.1.A, 1c1e.1.B, 1c5b.1.A, 1c5b.1.B, 1c5c.1.B, 1c5d.1.B, 1c5d.1.D, 1cbv.1.A, 1cbv.1.B, 1cd8.1.A, 1ce1.1.A, 1ce1.1.B, 1cf8.1.A, 1cf8.1.B, 1cfq.1.A, 1cfq.1.B, 1cfs.1.A, 1cfs.1.B, 1cft.1.A, 1cgs.1.A, 1cgs.1.B, 1cic.1.A, 1cic.1.B, 1cic.1.C, 1cic.1.D, 1ck0.1.A, 1ck0.1.B, 1cl7.1.A, 1cl7.1.B, 1clo.1.A, 1clo.1.B, 1cl.1.A, 1cl.1.B, 1clz.1.A, 1clz.1.B, 1cr9.1.A, 1cr9.1.B, 1ct8.1.A, 1ct8.1.B, 1ct8.1.C, 1ct8.1.D, 1cu4.1.A, 1cu4.1.B, 1cz8.1.C, 1cz8.1.D, 1cz8.1.E, 1cz8.1.F, 1d5b.1.A, 1d5b.1.B, 1d5i.1.A, 1d5i.1.B, 1d6v.1.A, 1d6v.1.B, 1d9k.1.B, 1dba.1.B, 1dbb.1.B, 1dbk.1.B, 1dbm.1.B, 1dcl.1.A, 1dcl.1.B, 1dee.1.A, 1dee.1.B, 1dfb.1.A, 1dfb.1.B, 1dl7.1.A, 1dl7.1.B, 1dlf.1.A, 1dlf.1.B, 1dn0.1.B, 1dn0.2.A, 1dn0.2.B, 1dq.1.A, 1dq.1.B, 1dqj.1.B, 1dqj.1.B, 1dq.1.A, 1dq.1.B, 1dqm.1.A, 1dqm.1.B, 1dq.1.A, 1dq.1.B, 1dq.2.B, 1dq.1.A, 1dq.1.B, 1dsf.1.A, 1dsf.1.B, 1dvf.1.B, 1dvf.1.C, 1dvf.1.D, 1dz.1.A, 1e4w.1.A, 1e4w.1.B, 1e4x.1.A, 1e4x.1.B, 1e4x.2.A, 1e4x.2.B, 1e6j.1.A, 1e6j.1.B, 1e6o.1.A, 1e6o.1.B, 1eap.1.A, 1eap.1.B, 1eeq.1.A, 1eeu.1.A, 1efq.1.A, 1egj.1.B, 1egj.1.C, 1ehl.1.A, 1ehl.1.B, 1ejo.1.A, 1ejo.1.B, 1ek3.1.A, 1emt.1.A, 1emt.1.B, 1e08.1.C, 1e08.1.D, 1etz.1.A, 1etz.1.B, 1etz.2.A, 1etz.2.B, 1f11.1.A, 1f11.1.B, 1f2x.1.A, 1f3d.1.A, 1f3d.1.B, 1f3d.1.C, 1f3d.1.D, 1f3r.1.B, 1f4w.1.A, 1f4w.1.B, 1f4y.1.A, 1f58.1.A, 1f58.1.B, 1f6l.1.A, 1f8t.1.A, 1f8t.1.B, 1f90.1.A, 1f90.1.B, 1fai.1.A, 1fai.1.B, 1fbi.1.A, 1fbi.1.B, 1fbi.2.A, 1fbi.2.B, 1fdl.1.A, 1fdl.1.B, 1fe8.1.B, 1fe8.1.C, 1fe8.2.B, 1fe8.2.C, 1fgv.1.A, 1fgv.1.B, 1fh5.1.A, 1fh5.1.B, 1fig.1.A, 1fig.1.B, 1fj1.1.A, 1fj1.1.B, 1fj3.1.A, 1fj3.1.B, 1fj3.2.A, 1fj3.2.B, 1fj5.1.A, 1fj5.1.B, 1fj6.1.A, 1fj6.1.B, 1flr.1.A, 1flr.1.B, 1fn4.1.A, 1fn4.1.B, 1fn4.1.C, 1fns.1.A, 1fns.1.B, 1fo0.1.C, 1fo0.1.D, 1for.1.A, 1for.1.B, 1fpt.1.C, 1fgr.1.A, 1fgr.1.B, 1fsk.1.B, 1fsk.1.C, 1fvc.1.B, 1fvd.1.A, 1fvd.1.B, 1fvd.2.B, 1fve.1.B, 1fve.2.B, 1fyt.1.E, 1g6r.1.A, 1g6v.1.B, 1g7h.1.B, 1g9e.1.A, 1g9m.1.C, 1g9m.1.D, 1g9n.1.C, 1g9n.1.D, 1gaf.1.A, 1gaf.1.B, 1gc1.1.C, 1gc1.1.D, 1gg.1.A, 1gg.1.B, 1gg.2.A, 1gg.2.B, 1ghf.1.A, 1ghf.1.B, 1gig.1.A, 1gig.1.B, 1gpo.1.A, 1gpo.1.B, 1gpo.2.A, 1gpo.2.B, 1h0d.1.A, 1h0d.1.B, 1h3p.1.A, 1h3p.1.B, 1h5b.1.B, 1h5b.2.A, 1h5b.2.B, 1h8n.1.A, 1h8o.1.A, 1hcv.1.A, 1hez.1.A, 1hez.1.B, 1hez.1.C, 1hez.1.D, 1hi6.1.A, 1hi6.1.B, 1hil.1.A, 1hil.1.B, 1him.1.A, 1hin.1.A, 1hin.1.B, 1hkl.1.A, 1hkl.1.B, 1hq4.1.A, 1hq4.1.B, 1hxm.1.A, 1hxm.1.B, 1hys.1.E, 1hys.1.F, 1hzh.1.A, 1hzh.1.B, 1hzh.1.C, 1hzh.1.D, 1i3g.1.A, 1i3g.1.B, 1i3u.1.A, 1i3v.1.A, 1i7z.1.A, 1i7z.1.B, 1i7z.2.B, 1i85.1.C, 1i85.1.D, 1i8i.1.A, 1i8i.1.B, 1i8k.1.A, 1i8l.1.B, 1i8m.1.A, 1i8m.1.B, 1i8m.2.A, 1i8m.2.B, 1i9e.1.A, 1i9i.1.A, 1i9i.1.B, 1i9j.1.A, 1i9j.1.B, 1i9r.1.D, 1i9r.1.E, 1iai.1.A, 1iai.1.B, 1iai.1.D, 1ibg.1.A, 1ibg.1.B, 1ic4.1.B, 1ic5.1.B, 1ic7.1.B, 1ieh.1.A, 1ifh.1.A, 1ifh.1.B, 1igc.1.A, 1igc.1.B, 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Build Models 0

Clear Selection

No templates selected



Surface ▲

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