

 All Projects

>7LYH_1|Chain A|3C-like proteinase|Severe acute respiratory syndrome coronavirus 2 (2697049) mutated.fasta

Created: today at 10:03











Summary

Templates 8

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"/> ✓	9du3.1.A 3C-like proteinase nsp5 SARS-CoV-2 Mpro in complex with compound 1						
▼		1.00	1.00	99.67	X-ray, 2.1Å	homo-dimer ✓	2 x 01
<input type="checkbox"/>	9du4.1.A 3C-like proteinase nsp5 SARS-CoV-2 Mpro in complex with compound 3						
▼		1.00	1.00	99.67	X-ray, 2.4Å	homo-dimer ✓	2 x 01
<input type="checkbox"/>	7jr3.1.B 3C-like proteinase SARS-CoV-2 3CL protease crystallized under reducing conditions						
▼		1.00	1.00	99.67	X-ray, 1.5Å	homo-dimer ✓	None
<input type="checkbox"/>	9dtz.1.B 3C-like proteinase nsp5 SARS-CoV-2 Mpro in complex with compound 5						
▼		1.00	1.00	99.67	X-ray, 2.2Å	homo-dimer ✓	2 x 01
<input type="checkbox"/>	9dtz.1.A 3C-like proteinase nsp5 SARS-CoV-2 Mpro in complex with compound 5						
▼		1.00	1.00	99.67	X-ray, 2.2Å	homo-dimer ✓	2 x 01
<input type="checkbox"/>	7n8c.1.A 3C-like proteinase Joint X-ray/neutron structure of SARS-CoV-2 main protease (Mpro) in complex with Mcule5948770040						
▼		1.00	0.98	99.67	neutron diff., 2.5Å	homo-dimer ✓	2 x YD1 
<input type="checkbox"/>	8zq8.1.A 3C-like proteinase nsp5 SARS-Cov-2 3CL protease in complex with macrocyclic inhibitor CG-1039						
▼		1.00	0.95	99.67	X-ray, 1.8Å	homo-dimer ✓	2 x 01
<input type="checkbox"/>	7mhf.1.B 3C-like proteinase Crystal Structure of SARS-CoV-2 Main Protease (Mpro) at 100 K						
▼		1.00	0.93	99.67	X-ray, 1.5Å	homo-dimer ✓	2 x ZN 

1b1b.1.A, 1bib.1.A, 1fst.1.C, 1fst1.D, 1fc3.1.A, 1fc3.1.B, 1fc3.1.C, 1hxd.1.A, 1hxd.2.A, 1iig.1.A, 1iig.1.B, 1j75.1.A, 1ku9.1.A, 1lj9.1.A, 1lj9.1.B, 1lnw.1.A, 1lnw.1.B, 1lnw.2.A, 1lnw.2.B, 1lnw.3.A, 1lnw.3.B, 1lnw.4.A, 1lnw.4.B, 1lq1.1.C, 1lq1.1.D, 1lq1.2.D, 1lvb.1.A, 1lvo.1.A, 1lvo.1.B, 1lvo.2.B, 1lvo.4.D, 1mkm.1.A, 1mkm.1.B, 1nex.2.A, 1oyi.1.A, 1p4x.1.A, 1p9s.1.A, 1q2w.1.A, 1q2w.1.B, 1r7.1.A, 1s3j.1.A, 1s3j.1.B, 1sfu.1.A, 1sfu.1.B, 1ub9.1.A, 1uj1.1.A, 1uj1.1.B, 1uk2.1.B, 1uk3.1.A, 1wi9.1.A, 1xd7.1.A, 1xn7.1.A, 1ylf.1.A, 1ylf.1.B, 1yjf.1.C, 1z1i.1.A, 1z1j.1.A, 1z1j.1.B, 1z67.1.A, 2a5k.1.A, 2a5k.1.B, 2a61.1.A, 2a61.1.B, 2alv.1.A, 2amp.1.A, 2amq.1.A, 2amq.1.B, 2bx3.1.B, 2bx4.1.A, 2c3s.1.A, 2cfx.1.A, 2cg4.1.A, 2cyv.1.A, 2d1h.1.A, 2d1h.1.B, 2dbb.1.A, 2dbb.1.B, 2du9.1.B, 2duc.1.A, 2duc.1.B, 2e1c.1.D, 2e7w.1.A, 2e7x.1.A, 2efn.1.A, 2efo.1.A, 2efp.1.A, 2efq.1.A, 2ek5.1.A, 2ek5.3.B, 2ek5.4.A, 2ek5.4.D, 2eth.1.A, 2eth.1.B, 2ewn.1.A, 2ewn.1.B, 2fbh.1.A, 2fbi.1.A, 2fnp.1.A, 2fnp.1.B, 2frh.1.A, 2frh.1.B, 2gt8.1.B, 2gz9.1.A, 2heo.1.A, 2heo.1.B, 2htj.1.A, 2ivm.1.A, 2ivm.1.B, 2jt1.1.A, 2k02.1.A, 2k53.1.A, 2k7x.1.A, 2l02.1.A, 2l02.1.B, 2l4a.1.A, 2l54.1.A, 2lfc.1.A, 2liz.1.A, 2lnb.1.A, 2mlg.1.A, 2obp.1.A, 2op9.1.A, 2op9.1.B, 2p6s.1.B, 2p6s.1.C, 2p6s.1.D, 2p6s.1.F, 2p6s.1.H, 2p6t.1.A, 2p6t.1.D, 2p6t.1.E, 2p6t.1.G, 2pfb.1.A, 2pfb.1.B, 2pmh.1.A, 2pn6.1.A, 2pwx.1.A, 2q6d.1.A, 2q6d.1.B, 2q6d.2.A, 2q6f.1.B, 2q6g.1.A, 2q6g.1.B, 2qc2.1.A, 2qc2.1.B, 2qcy.1.A, 2qiq.1.A, 2qz8.1.A, 2rv.1.A, 2v79.1.A, 2v79.1.B, 2vbx.1.A, 2vj1.1.A, 2vj1.2.A, 2w24.1.F, 2w25.1.A, 2w25.1.B, 2w29.1.A, 2w29.1.B, 2xvc.1.A, 2y75.1.A, 2y75.1.B, 2yna.1.B, 2yr2.4.B, 2z9k.1.A, 2zny.3.B, 2zny.4.A, 2zny.4.B, 2zny.5.A, 2zny.5.B, 2zny.5.D, 2zny.5.E, 2znz.1.A, 2znz.1.D, 2znz.5.A, 2zu2.1.B, 3atw.1.B, 3aw1.1.A, 3aw1.1.B, 3bj6.1.A, 3bpx.1.A, 3bpx.1.B, 3cdh.1.A, 3cdh.1.B, 3d23.1.A, 3d23.1.C, 3d62.1.A, 3dpi.1.A, 3dqv.1.B, 3dqv.3.B, 3e6m.1.A, 3e6m.1.B, 3e6m.2.B, 3e6m.3.B, 3e6m.4.A, 3ea7.1.A, 3ea7.1.B, 3ea8.1.B, 3ea9.1.A, 3ebn.1.A, 3ebn.2.A, 3ech.1.A, 3ech.1.B, 3eco.1.A, 3eco.1.B, 3f9e.1.A, 3f9f.1.A, 3f9g.1.A, 3f9g.1.B, 3f9h.1.B, 3fzd.1.A, 3g3z.1.A, 3g3z.1.B, 3gf2.1.B, 3gfi.1.A, 3gfi.1.B, 3gfi.1.A, 3gfi.1.A, 3i4p.1.A, 3i71.1.A, 3i71.1.B, 3iwm.1.C, 3iwm.1.E, 3iwm.1.F, 3iwm.1.H, 3k69.1.A, 3lwf.1.A, 3m3s.1.A, 3m3t.1.A, 3m3v.1.A, 3m3v.1.B, 3mex.1.A, 3mex.1.B, 3mks.1.C, 3mks.2.A, 3mmg.1.A, 3mmg.2.A, 3ov8.1.A, 3q5f.1.A, 3qph.1.A, 3qpt.1.A, 3s2w.1.A, 3s2w.1.B, 3s2w.2.B, 3s2w.3.B, 3s2w.3.B, 3s2w.4.A, 3s2w.4.B, 3sna.1.A, 3t8r.1.B, 3tlo.1.B, 3v7d.1.A, 3v7d.2.A, 3vb2.1.A, 3vb2.1.D, 3vb3.1.B, 3vb3.1.A, 3vod.1.A, 3vod.1.B, 3vai.1.A, 4aih.1.A, 4aih.2.A, 4aih.2.B, 4aih.2.B, 4aih.3.A, 4aih.3.B, 4aij.1.A, 4aij.1.B, 4aik.1.B, 4awx.1.B, 4b8x.1.A, 4ch7.1.A, 4egz.1.A, 4egz.1.B, 4f49.1.A, 4f52.1.A, 4f52.2.A, 4fht.1.A, 4fht.1.B, 4g9y.1.A, 4ham.1.A, 4hf0.1.A, 4hf0.1.B, 4hi3.1.A, 4hi3.1.B, 4hob.1.A, 4hob.1.B, 4hob.2.A, 4hx4.1.A, 4hx8.1.A, 4hx8.1.B, 4jba.1.A, 4kmf.1.A, 4l9n.1.A, 4l9n.1.B, 4l9t.1.A, 4l9t.1.B, 4l9v.1.A, 4mds.1.A, 4pcq.1.A, 4pcq.1.B, 4pcq.2.A, 4pcq.2.B, 4pq1.1.A, 4pq1.1.B, 4pt7.1.A, 4rsp.1.A, 4uoY.1.A, 4uoY.1.B, 4uoY.1.D, 4un1.1.B, 4un1.2.B, 4wmf.2.C, 4xfq.1.A, 4xfq.1.B, 4yo9.1.B, 4yog.1.A, 4zro.1.A, 4zro.1.B, 4zro.1.C, 4zro.1.D, 4zuh.1.A, 4zuh.1.B, 4zzl.1.A, 4zzl.1.B, 5aip.1.A, 5aip.1.B, 5aiq.1.A, 5aiq.1.B, 5aiq.2.A, 5aiq.2.B, 5b6o.1.A, 5b6o.1.B, 5box.1.A, 5box.1.C, 5bpd.1.A, 5bpd.1.C, 5bpi.1.A, 5bpi.1.B, 5bpi.1.D, 5bqt.1.A, 5bqt.1.B, 5bqt.1.C, 5bqt.1.D, 5coT.1.A, 5coT.2.A, 5c17.1.A, 5c3n.1.A, 5c3n.1.B, 5cyy.1.A, 5cyy.1.B, 5d4r.1.A, 5d4r.1.B, 5d4s.1.A, 5eu8.1.A, 5fb2.1.A, 5gwy.1.A, 5gwy.1.B, 5gwz.1.A, 5hs5.1.A, 5hsm.1.A, 5hso.1.C, 5hyc.1.A, 5hyo.1.B, 5kbj.1.A, 5kbj.1.B, 5kbj.1.C, 5kbj.1.D, 5kbj.2.A, 5kbj.2.B, 5kbj.2.C, 5kbj.2.D, 5kvr.1.A, 5n07.1.B, 5nh0.1.A, 5x7z.1.B, 5x80.1.A, 5x80.1.B, 5x80.2.A, 5x80.2.B, 5yhx.1.A, 5yhx.1.B, 5yhx.3.A, 5yhx.3.B, 5yhy.1.A, 5yi0.1.A, 5yi1.1.A, 5yi2.1.A, 5yi2.1.B, 5yi2.2.A, 5yi2.2.B, 5yi2.3.A, 5yi2.3.B, 5yi2.4.A, 5yi2.4.B, 5yi3.1.A, 5yi3.1.B, 5yi3.2.A, 5yi3.2.A, 5yi3.2.A, 5yi3.2.A, 5yi3.3.A, 5yi3.3.A, 5yi3.4.A, 5yi3.4.A, 5yiq.1.A, 5zqq.1.A, 5zqq.1.B, 6ep3.1.A, 6ep3.1.B, 6fi9.1.A, 6fv1.2.A, 6fv1.3.A, 6hsd.1.B, 6hsm.1.B, 6hsm.2.A, 6hsm.3.A, 6hsm.3.B, 6hsm.4.B, 6jj1.1.A, 6jj1.2.A, 6k8e.1.A, 6lze.1.A, 6m0k.1.A, 6nrr.1.B, 6ns1.1.A, 6tey.1.A, 6w2a.1.A, 6w2a.1.B, 6w81.1.A, 6w81.1.B, 6wtj.1.B, 6wtk.1.B, 6wtt.1.A, 6wtt.2.A, 6wtt.2.B, 6xa4.1.B, 6xbg.1.B, 6xbi.1.A, 6xhm.1.B, 6xhn.1.A, 6xhn.1.B, 6xoa.1.A, 6xoa.1.B, 6xoa.2.A, 6xoa.2.B, 6y2g.1.B, 6y42.1.A, 6y42.1.B, 6y45.1.A, 6y45.1.B, 6yb7.1.B, 7aku.1.B, 7aol.1.A, 7avd.1.A, 7avd.1.B, 7boC.1.A, 7b5t.1.A, 7b5t.1.B, 7b5t.1.C, 7b5t.1.D, 7b5y.1.A, 7b5y.1.B, 7b5y.1.C, 7b5y.1.D, 7bb2.1.A, 7bhY.1.C, 7bhY.1.D, 7bhy.2.A, 7bro.1.B, 7czq.1.A, 7czY.1.A, 7cam.1.B, 7cam.1.B, 7cb7.1.B, 7cb7.1.B, 7cbt.1.A, 7cbt.1.B, 7cwc.1.A, 7cwc.1.B, 7d1m.1.A, 7d1m.1.B, 7d3c.1.A, 7d3c.1.B, 7dg6.1.A, 7dgh.1.B, 7dgi.1.B, 7dpp.1.A, 7dpu.1.A, 7dqz.1.A, 7dqz.1.B, 7dr9.1.B, 7dvp.1.A, 7dvt.1.A, 7dvu.1.A, 7dvv.1.A, 7e5x.1.A, 7e5x.1.B, 7e6k.1.A, 7e6n.1.A,

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