













































































































2DN1 mutated,fasta Created: today at 18:20




























Template Results ⓘ

Templates							
Quaternary Structure							
Sequence Similarity							
Alignment							
More ▼							
↕Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	P63112.1.A Hemoglobin subunit alpha <i>AlphaFold DB model of HBA_PAPCY (gene: HBA, organism: Papio cynocephalus (Yellow baboon))</i>						
▼	<div></div>	0.98	-	91.49	AlphaFold v2	monomer ✓	None
<input type="checkbox"/> ✓	2dn2.1.C Hemoglobin alpha subunit <i>1.25A resolution crystal structure of human hemoglobin in the deoxy form</i>						
▼	<div></div>	0.94	0.69	99.29	X-ray, 1.3Å	hetero-tetramer ⚠	4 x HEM ⓘ
<input type="checkbox"/>	8dov.2.A Hemoglobin subunit alpha <i>Crystal structure of the Shr Hemoglobin Interacting Domain 2 (HID2) in complex with Hemoglobin</i>						
▼	<div></div>	0.94	-	99.29	X-ray, 2.1Å	hetero-pentamer ⚠	4 x HEM ⓘ
<input type="checkbox"/>	1k1k.1.A HEMOGLOBIN ALPHA CHAIN <i>Structure of Mutant Human Carbonmonoxyhemoglobin C (beta E6K) at 2.0 Angstrom Resolution in Phosphate Buffer.</i>						
▼	<div></div>	0.94	-	99.29	X-ray, 2.0Å	hetero-tetramer ⚠	4 x HEM ⓘ
<input type="checkbox"/>	1ird.1.C Hemoglobin alpha chain <i>Crystal Structure of Human Carbonmonoxy-Haemoglobin at 1.25 A Resolution</i>						
▼	<div></div>	0.93	0.46	99.29	X-ray, 1.3Å	hetero-tetramer ⚠	4 x HEM ⓘ
<input type="checkbox"/>	2yrs.1.A Hemoglobin subunit alpha <i>Human hemoglobin D Los Angeles: crystal structure</i>						
▼	<div></div>	0.93	0.66	99.29	X-ray, 2.3Å	hetero-tetramer ⚠	4 x HEM ⓘ
<input type="checkbox"/>	1yff.1.A Hemoglobin alpha chain <i>STRUCTURE OF HUMAN CARBONMONOXYHEMOGLOBIN C (BETA E6K): TWO QUATERNARY STATES (R2 and R3) IN ONE CRYSTAL</i>						
▼	<div></div>	0.93	0.28	99.29	X-ray, 2.4Å	hetero-tetramer ⚠	4 x HEM ⓘ
<input type="checkbox"/>	1lfq.1.A Hemoglobin alpha chain <i>OXY HEMOGLOBIN (93% RELATIVE HUMIDITY)</i>						
▼	<div></div>	0.92	-	99.29	X-ray, 2.6Å	hetero-tetramer ⚠	4 x HEM ⓘ

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	1hda.1.C HEMOGLOBIN (DEOXY) (ALPHA CHAIN) <i>A NOVEL ALLOSTERIC MECHANISM IN HAEMOGLOBIN. STRUCTURE OF BOVINE DEOXYHAEMOGLOBIN, ABSENCE OF SPECIFIC CHLORIDE-BINDING SITES AND ORIGIN OF THE CHLORIDE-LINKED BOHR EFFECT IN BOVINE AND HUMAN HAEMOGLOBIN</i>						
▼		0.92	0.70	87.23	X-ray, 2.2Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	6ihx.1.A Hemoglobin subunit alpha <i>Crystal Structure Analysis of bovine Hemoglobin modified by SNP</i>						
▼		0.92	-	87.14	X-ray, 1.5Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	1g09.1.A HEMOGLOBIN ALPHA CHAIN <i>CARBONMONOXY LIGANDED BOVINE HEMOGLOBIN PH 7.2</i>						
▼		0.92	0.48	87.23	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	1fsx.1.A HEMOGLOBIN ALPHA CHAIN <i>THE X-RAY STRUCTURE DETERMINATION OF BOVINE CARBONMONOXY HB AT 2.1 Å RESOLUTION AND ITS RELATIONSHIP TO THE QUATERNARY STRUCTURE OF OTHER HB CRYSTAL FORMS</i>						
▼		0.92	0.76	87.23	X-ray, 2.1Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	1g09.1.C HEMOGLOBIN ALPHA CHAIN <i>CARBONMONOXY LIGANDED BOVINE HEMOGLOBIN PH 7.2</i>						
▼		0.92	0.48	87.23	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	2qsp.1.C Hemoglobin subunit alpha <i>Bovine Hemoglobin at pH 5.7</i>						
▼		0.92	0.37	87.23	X-ray, 1.8Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	5c6e.1.C Hemoglobin subunit alpha <i>Joint X-ray/neutron structure of equine cyanomet hemoglobin in R state</i>						
▼		0.92	0.59	87.23	neutron diff., 2.0Å	hetero-tetramer 	4 x HEM  , 4 x CYN 
<input type="checkbox"/>	1iwh.1.A Hemoglobin alpha chain <i>Crystal Structure of Horse Carbonmonoxyhemoglobin-Bezafibrate Complex at 1.55Å Resolution: A Novel Allosteric Binding Site in R-State Hemoglobin</i>						
▼		0.91	-	87.23	X-ray, 1.5Å	hetero-tetramer 	4 x HEM  , 2 x PEM 
<input type="checkbox"/>	1fsx.1.C HEMOGLOBIN ALPHA CHAIN <i>THE X-RAY STRUCTURE DETERMINATION OF BOVINE CARBONMONOXY HB AT 2.1 Å RESOLUTION AND ITS RELATIONSHIP TO THE QUATERNARY STRUCTURE OF OTHER HB CRYSTAL FORMS</i>						
▼		0.91	0.76	87.23	X-ray, 2.1Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	7uvb.1.A Hemoglobin subunit alpha <i>CRYSTAL STRUCTURE OF CARBONMONOXY HEMOGLOBIN S (LIGANDED SICKLE CELL HEMOGLOBIN) COMPLEXED WITH GBT021601</i>						
▼		0.91	0.57	99.29	X-ray, 2.0Å	hetero-tetramer 	4 x HEM  , 4 x FOR  , 2 x OHF 

Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	3d1a.1.C Hemoglobin subunit alpha-1/2 <i>Crystal Structure Determination of Goat Hemoglobin at 2.61 Angstrom Resolution</i>						
▼		0.91	0.21	85.82	X-ray, 2.6Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3pi8.1.A Hemoglobin subunit alpha <i>Site-specific Glycosylation of Hemoglobin Utilizing Oxime Ligation Chemistry as a Viable Alternative to PEGylation</i>						
▼		0.91	0.60	87.23	X-ray, 2.2Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3cy5.1.A Hemoglobin subunit alpha-2 <i>Crystal structure determination of buffalo (Bubalus bubalis) hemoglobin at 2 angstrom resolution</i>						
▼		0.91	-	85.82	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	4h2l.1.A Alpha-globin <i>Deer mouse hemoglobin in hydrated format</i>						
▼		0.91	-	84.40	X-ray, 1.8Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	2zlt.1.C Hemoglobin subunit alpha <i>Horse methemoglobin high salt, pH 7.0</i>						
▼		0.91	0.51	86.52	X-ray, 1.9Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3d1a.1.A Hemoglobin subunit alpha-1/2 <i>Crystal Structure Determination of Goat Hemoglobin at 2.61 Angstrom Resolution</i>						
▼		0.91	0.21	85.82	X-ray, 2.6Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3d4x.1.A Hemoglobin subunit alpha <i>Crystal structure determination of cat (Felis silvestris catus) hemoglobin at 2.2 angstrom resolution</i>						
▼		0.91	0.52	84.40	X-ray, 2.2Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3cy5.1.C Hemoglobin subunit alpha-2 <i>Crystal structure determination of buffalo (Bubalus bubalis) hemoglobin at 2 angstrom resolution</i>						
▼		0.91	-	85.82	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	4yu4.1.C hemoglobin <i>Crystal structure of Mongoose (Helogale parvula) hemoglobin at pH 7.0</i>						
▼		0.91	0.53	87.23	X-ray, 2.8Å	hetero-tetramer 	4 x HEM  , 4 x OXY 
<input type="checkbox"/>	2qu0.1.A Hemoglobin subunit alpha-1/2 <i>Crystal structure determination of sheep methemoglobin at 2.7 Angstrom resolution</i>						
▼		0.91	0.52	85.82	X-ray, 2.7Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	4yu4.1.A hemoglobin <i>Crystal structure of Mongoose (Helogale parvula) hemoglobin at pH 7.0</i>						
▼		0.90	0.53	87.23	X-ray, 2.8Å	hetero-tetramer 	4 x HEM  , 4 x OXY 
<input type="checkbox"/>	6r2o.1.A Hemoglobin subunit alpha <i>Hemoglobin structure from serial crystallography with a 3D-printed nozzle.</i>						

↓↑Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
▼		0.90	0.51	87.23	X-ray, 2.5Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3gqr.1.A Hemoglobin subunit alpha <i>Crystal structure determination of cat (Felis silvestris catus) hemoglobin at 2.4 angstrom resolution</i>						
▼		0.90	0.33	84.40	X-ray, 2.4Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3gqr.2.C Hemoglobin subunit alpha <i>Crystal structure determination of cat (Felis silvestris catus) hemoglobin at 2.4 angstrom resolution</i>						
▼		0.90	-	84.40	X-ray, 2.4Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3gdj.1.A Hemoglobin subunit alpha <i>Crystal structure determination of camel(Camelus dromedarius)hemoglobin at 2 angstrom resolution</i>						
▼		0.90	0.47	83.69	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3gqp.1.C Hemoglobin subunit alpha <i>Crystal structure determination of cat (Felis silvestris catus) hemoglobin at 2.0 angstrom resolution</i>						
▼		0.90	0.76	84.40	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	1y8h.1.A Hemoglobin alpha chains <i>HORSE METHEMOGLOBIN LOW SALT, PH 7.0</i>						
▼		0.90	0.40	86.52	X-ray, 3.1Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	2rao.1.A Hemoglobin subunit alpha-1/2 <i>X ray crystal structure of rabbit hemoglobin (oxy form) at 2.0 angstrom resolution</i>						
▼		0.89	0.62	81.56	X-ray, 2.0Å	hetero-tetramer 	4 x HEM  , 4 x OXY 
<input type="checkbox"/>	2zlw.1.A Hemoglobin subunit alpha <i>Horse methemoglobin high salt, pH 7.0 (75% relative humidity)</i>						
▼		0.89	0.54	86.52	X-ray, 2.9Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3fh9.1.A Hemoglobin alpha chain <i>Crystal structure determination of indian flying fox (Pteropus giganteus) at 1.62 A resolution</i>						
▼		0.89	0.60	85.82	X-ray, 1.6Å	hetero-tetramer 	4 x HEM  , 4 x OXY 
<input type="checkbox"/>	2ri4.1.A Hemoglobin subunit alpha-1/2 <i>Crystal Structure determination of Goat Methemoglobin at 2.7 Angstrom</i>						
▼		0.88	0.23	85.82	X-ray, 2.7Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3lqd.1.A Hemoglobin subunit alpha <i>Crystal structure determination of Lepus europaeus 2.8 A resolution</i>						
▼		0.88	0.65	82.27	X-ray, 2.8Å	hetero-tetramer 	4 x HEM  , 4 x OXY 
<input type="checkbox"/>	3hrw.1.A Hemoglobin subunit alpha <i>Crystal structure of hemoglobin from mouse (Mus musculus)at 2.8</i>						
▼		0.88	-	85.11	X-ray, 2.8Å	hetero-tetramer 	4 x HEM 

↓↑Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
<input type="checkbox"/>	2zlx.2.A Hemoglobin subunit alpha <i>Horse methemoglobin high salt, pH 7.0 (66% relative humidity)</i>						
▼		0.88	-	86.52	X-ray, 2.8Å	hetero-dimer 	2 x HEM 
<input type="checkbox"/>	1ns6.1.A Hemoglobin alpha subunit <i>The 2.1A Structure of Horse (alpha hemichrome/beta met) Hemoglobin at pH 5.4</i>						
▼		0.88	-	86.52	X-ray, 2.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3gqr.2.A Hemoglobin subunit alpha <i>Crystal structure determination of cat (Felis silvestris catus) hemoglobin at 2.4 angstrom resolution</i>						
▼		0.88	-	84.40	X-ray, 2.4Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3eu1.1.A Hemoglobin subunit alpha-1/2 <i>Crystal Structure determination of goat hemoglobin (Capra hircus) at 3 angstrom resolution</i>						
▼		0.88	0.21	85.82	X-ray, 3.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	2ri4.2.C Hemoglobin subunit alpha-1/2 <i>Crystal Structure determination of Goat Methemoglobin at 2.7 Angstrom</i>						
▼		0.88	0.24	85.82	X-ray, 2.7Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	2ri4.1.C Hemoglobin subunit alpha-1/2 <i>Crystal Structure determination of Goat Methemoglobin at 2.7 Angstrom</i>						
▼		0.87	0.23	85.82	X-ray, 2.7Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3eu1.1.C Hemoglobin subunit alpha-1/2 <i>Crystal Structure determination of goat hemoglobin (Capra hircus) at 3 angstrom resolution</i>						
▼		0.87	0.21	85.82	X-ray, 3.0Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	3hrw.1.C Hemoglobin subunit alpha <i>Crystal structure of hemoglobin from mouse (Mus musculus)at 2.8</i>						
▼		0.87	-	85.11	X-ray, 2.8Å	hetero-tetramer 	4 x HEM 
<input type="checkbox"/>	5eui.1.A HBA protein <i>Structure of predicted ancestral pika hemoglobin</i>						
▼		0.85	-	89.36	X-ray, 1.4Å	hetero-dimer 	2 x HEM 

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.

105m.1.A, 1a3o.1.A, 1a4f.1.A, 1a4f.1.D, 1a9w.1.B, 1aby.1.A, 1aby.1.B, 1aj9.1.A, 1aj9.1.D, 1all.1.A, 1ash.1.A, 1b0b.1.A, 1b33.1.A, 1b33.2.E, 1b8d.1.A, 1b8d.1.B, 1bab.1.A, 1bij.1.A, 1bij.1.B, 1bin.1.A, 1bje.1.A, 1bvc.1.A, 1bz1.1.C, 1bzb.1.A, 1c40.1.A, 1c40.1.B, 1c7b.1.B, 1c7b.1.C, 1c7c.1.A, 1c7c.1.B, 1c7d.1.A, 1cbl.1.A, 1cbl.1.D, 1cg5.1.A, 1cg5.1.B, 1cg8.1.A, 1cg8.1.B, 1ch1.1.A, 1ch2.1.A, 1ch3.1.A, 1ch4.1.A, 1ch4.1.C, 1ch5.1.A, 1ch7.1.A, 1ch9.1.A, 1cik.1.A, 1cio.1.A, 1cmy.1.B, 1co8.1.A, 1co9.1.A, 1cp0.1.A, 1cp5.1.A, 1cpw.1.A, 1cpw.1.A, 1cpw.1.A, 1d8u.1.A, 1d8u.1.B, 1dm1.1.A, 1dti.1.A, 1duk.1.A, 1dxt.1.B, 1dxv.1.B, 1ebt.1.A, 1eca.1.A, 1emy.1.A, 1eyx.1.A, 1eyx.1.B, 1f5o.1.A, 1f6h.1.A, 1f99.1.B, 1faw.1.A, 1faw.1.B, 1fcs.1.A, 1fdh.1.B, 1fhj.1.B, 1fhj.1.C, 1fhj.1.D, 1flp.1.A, 1fn3.1.A, 1fn3.1.B, 1fsl.1.A, 1fsl.2.A, 1fsx.1.A, 1fsx.1.C, 1fsx.1.D, 1g09.1.A, 1g09.1.C, 1g0a.1.B, 1g0a.1.D, 1gbu.1.B, 1gbv.1.B, 1gcv.1.A, 1gcv.1.B, 1gcw.1.A, 1gcw.1.B, 1gcw.1.C, 1gcw.1.D, 1gdk.1.A, 1gli.1.A, 1gvh.1.A, 1h1x.1.A, 1h97.1.A, 1ha7.1.B, 1hab.1.B, 1hba.1.B, 1hbg.1.A, 1hbb.1.B, 1hbb.1.C, 1hbb.1.D, 1hbr.1.A, 1hbr.1.B, 1hbs.1.A, 1hbs.1.B, 1hbs.1.C, 1hbs.1.D, 1hbs.2.A, 1hbs.2.B, 1hbs.2.C, 1hbs.2.D, 1hco.1.B, 1hda.1.B, 1hda.1.C, 1hdb.1.B, 1hds.1.A, 1hds.1.B, 1hds.1.C, 1hds.1.D, 1hdb.1.A, 1hlm.1.A, 1hrm.1.A, 1hv4.1.D, 1hv4.2.C, 1i3d.1.C, 1irc.1.A, 1ird.1.C, 1ird.1.D, 1it2.1.A, 1it2.2.A, 1it3.2.A, 1it3.4.A, 1ith.1.A, 1iwh.1.A, 1iwh.1.B, 1j3f.1.A, 1j52.1.A, 1j7y.1.B, 1jeb.1.A, 1jeb.1.B, 1jeb.1.C, 1jf3.1.A, 1jl6.1.A, 1jy7.3.C, 1jy7.3.D, 1jzk.1.B, 1jzl.1.A, 1k1k.1.A, 1k1k.1.B, 1kfr.1.A,

kn1.1.A, 1la6.1.C, 1lfq.1.A, 1lh7.1.A, 1lshs.1.A, 1lia.1.A, 1lia.1.B, 1ljw.1.A, 1llw.1.A, 1lue.1.A, 1m6c.1.A, 1m9p.1.B, 1mba.1.A, 1mbc.1.A, 1mbs.1.A, 1mcy.1.A, 1mg9.1.A, 1mko.1.A, 1mko.1.B, 1mko.1.D, 1mlf.1.A, 1mlk.1.A, 1mlm.1.A, 1mlq.1.A, 1mnh.1.A, 1mni.1.A, 1mni.2.A, 1mnj.1.A, 1mnk.1.A, 1mob.1.A, 1moc.1.A, 1mti.1.A, 1mtk.1.A, 1mwc.1.A, 1myf.1.A, 1myh.1.A, 1myi.1.A, 1myi.2.A, 1myj.1.A, 1myj.2.A, 1myt.1.A, 1n9x.1.A, 1nej.1.D, 1ngk.1.A, 1ngk.1.B, 1ngk.1.D, 1ngk.1.G, 1ngk.1.H, 1npf.1.A, 1nqp.1.A, 1nqp.1.D, 1ns6.1.A, 1ns6.1.B, 1ns9.1.D, 1nwi.1.B, 1nxf.1.B, 1nz2.1.A, 1nz3.1.A, 1o16.1.A, 1o1i.1.A, 1o1i.1.B, 1o1j.1.A, 1o1j.1.B, 1o1k.1.B, 1o1l.1.A, 1o1l.1.C, 1o1m.1.A, 1o1n.1.A, 1o1o.1.A, 1o1o.1.B, 1o1p.1.B, 1obm.1.A, 1ofj.1.A, 1ofk.1.A, 1oj6.1.A, 1oj6.2.A, 1oj6.4.A, 1or4.1.A, 1or4.1.B, 1or6.1.A, 1or6.1.B, 1out.1.A, 1out.1.B, 1ouu.1.B, 1pbx.1.D, 1phn.1.B, 1pmb.2.A, 1pgw.1.C, 1pgw.1.D, 1q8.1.A, 1qpw.1.A, 1qpw.1.B, 1qpw.1.D, 1qpw.1.D, 1qxd.2.C, 1r1x.1.A, 1r1x.1.D, 1r1y.1.A, 1r1y.1.B, 1rse.1.A, 1rvw.1.C, 1s0h.1.A, 1s0h.1.D, 1s5x.1.B, 1sdk.2.H, 1shr.1.B, 1shr.1.C, 1shr.1.D, 1spg.1.A, 1spg.1.B, 1tu9.1.A, 1uc3.1.A, 1ufp.1.A, 1umo.1.A, 1umo.1.A, 1umo.1.C, 1urv.1.A, 1urv.2.A, 1ury.1.A, 1ury.2.A, 1uvx.1.A, 1uvy.1.A, 1ux8.1.A, 1v07.1.A, 1v4u.1.B, 1v4u.1.C, 1v4w.1.C, 1v4w.1.D, 1v4x.1.C, 1v4x.1.D, 1v5h.1.A, 1vre.1.A, 1vrf.1.A, 1vwt.1.C, 1w92.1.D, 1wmu.1.A, 1wmu.1.B, 1wvp.1.A, 1x46.1.A, 1xch.1.A, 1xq5.1.A, 1xy0.1.A, 1xye.1.A, 1xz5.1.A, 1xz7.1.A, 1xzu.1.A, 1xzv.1.A, 1y01.1.B, 1y09.1.A, 1y0a.1.A, 1y0c.1.A, 1y0d.1.C, 1y22.1.B, 1y22.1.B, 1y31.1.B, 1y35.1.B, 1y45.1.B, 1y46.1.B, 1y4b.1.B, 1y4f.1.B, 1y4g.1.B, 1y4p.1.D, 1y4q.1.B, 1y4r.1.B, 1y4v.1.B, 1y5f.1.B, 1y5j.1.B, 1y5k.1.B, 1y7c.1.B, 1y7d.1.B, 1y7g.1.B, 1y7z.1.B, 1y83.1.B, 1y85.1.B, 1y8h.1.A, 1y8k.1.B, 1ycb.1.A, 1yeu.1.A, 1yff.1.A, 1yff.2.D, 1yhu.1.A, 1yhu.1.B, 1yhu.1.C, 1yhu.1.D, 1yie.1.D, 1yma.1.A, 1ymc.1.A, 1yzi.1.C, 1yzi.1.D, 1z8u.1.B, 1z8u.3.D, 2aa1.1.A, 2aa1.1.B, 2aa1.1.C, 2auo.1.A, 2auq.1.A, 2av0.1.A, 2b7h.1.A, 2b7h.1.B, 2bk9.1.A, 2bkm.1.A, 2bmm.1.A, 2bv8.1.B, 2bw9.1.F, 2c0k.1.A, 2c7j.1.B, 2cmm.1.A, 2d2m.1.J, 2d2m.1.T, 2d2m.1.U, 2d2m.1.W, 2d6c.1.A, 2d6c.2.A, 2dc3.1.A, 2dc3.1.B, 2dhh.1.A, 2dhh.1.B, 2dn2.1.C, 2dn2.1.D, 2e2y.1.A, 2eb8.1.A, 2eb9.1.A, 2ef2.1.A, 2ekt.1.A, 2eku.1.A, 2evp.1.A, 2fam.1.A, 2g10.1.A, 2g3h.1.A, 2gkm.1.A, 2gnv.1.A, 2gnv.1.B, 2gnw.1.A, 2gnw.1.B, 2grf.1.A, 2grh.1.B, 2gtl.1.I, 2gtl.1.J, 2gtl.2.C, 2gtl.2.H, 2h35.1.A, 2h35.1.D, 2hbf.1.D, 2hbs.1.D, 2hbs.2.B, 2hhe.1.B, 2in4.1.A, 2lhb.1.A, 2m6z.1.C, 2m6z.1.D, 2mgc.1.A, 2nrl.1.A, 2nx0.1.A, 2oh8.1.A, 2oh9.1.A, 2oha.1.A, 2ohh.1.A, 2oif.1.A, 2peg.1.B, 2peg.1.C, 2pgh.1.B, 2pgh.1.C, 2pgh.1.D, 2qf.1.A, 2qmb.1.A, 2qmb.1.B, 2qrw.1.A, 2qrw.1.B, 2qrw.2.A, 2qsp.1.A, 2qsp.1.C, 2qss.1.D, 2qu0.1.A, 2qu0.1.B, 2qu0.1.D, 2r4w.1.A, 2r4x.1.A, 2r4z.1.A, 2r50.1.A, 2r50.1.B, 2r50.2.A, 2r50.2.B, 2r80.1.A, 2r80.1.B, 2r80.1.C, 2rao.1.A, 2rao.1.B, 2ri4.1.A, 2ri4.1.C, 2ri4.1.D, 2ri4.2.C, 2ri4.2.D, 2spo.1.A, 2uul.1.D, 2uum.2.L, 2vee.2.B, 2vhh.1.A, 2vjt.1.A, 2vml.1.K, 2vml.1.L, 2vwo.1.A, 2vvy.1.A, 2vvy.1.A, 2w31.1.A, 2w31.1.B, 2w6x.1.A, 2w6y.1.A, 2w72.1.A, 2wth.1.A, 2wy4.1.A, 2xkg.1.A, 2xyk.1.A, 2xyk.2.A, 2yrs.1.A, 2yrs.1.B, 2zfb.1.A, 2zfb.1.B, 2zlt.1.C, 2zlv.1.A, 2zlv.1.B, 2zlw.1.A, 2zlw.1.D, 2zlx.1.B, 2zlx.2.A, 2zso.1.N, 2zsl.1.R, 2zsl.1.X, 2zwl.1.A, 3a0g.1.B, 3a2g.1.A, 3a59.1.A, 3a59.1.B, 3ag0.1.A, 3ag9.1.A, 3at5.1.A, 3at5.1.B, 3at6.1.B, 3at6.1.C, 3b75.1.C, 3b75.2.A, 3b75.2.B, 3b75.2.D, 3b75.3.C, 3b75.3.D, 3bcq.1.A, 3bcq.1.C, 3bcq.1.D, 3bj1.1.A, 3bj1.1.B, 3bj2.1.D, 3bj3.1.A, 3bom.1.A, 3bom.1.D, 3brp.2.D, 3cy5.1.A, 3cy5.1.B, 3cy5.1.C, 3d17.1.C, 3d17.1.D, 3d1a.1.A, 3d1a.1.B, 3d1a.1.C, 3d1k.1.A, 3d1k.1.D, 3d4x.1.A, 3d4x.1.B, 3dhr.1.A, 3dhr.2.B, 3dhr.2.C, 3dht.1.A, 3dht.1.B, 3djn.1.A, 3dju.1.A, 3dut.1.B, 3dut.1.D, 3e9v.1.A, 3eok.1.A, 3eok.1.B, 3eu1.1.A, 3eu1.1.C, 3fh9.1.A, 3fh9.1.B, 3gdj.1.A, 3gdj.1.B, 3glh.1.A, 3gou.1.A, 3gqp.1.C, 3gqr.1.A, 3gqr.1.D, 3gqr.2.A, 3gqr.2.B, 3gqr.2.C, 3h57.1.A, 3hen.1.A, 3hep.1.A, 3hrw.1.A, 3hrw.1.B, 3hrw.1.C, 3hrw.1.D, 3hyu.1.A, 3hyu.1.B, 3ia3.1.B, 3k8b.1.A, 3k8b.1.B, 3k8b.1.D, 3k9z.1.A, 3kun.1.A, 3kuo.1.A, 3kuo.2.A, 3lhb.4.B, 3lqd.1.A, 3lqd.1.B, 3m38.1.A, 3mjp.1.A, 3mjp.1.B, 3mjp.1.C, 3mjp.1.D, 3mju.1.A, 3mju.1.B, 3mkb.1.A, 3mkb.1.B, 3mn0.1.A, 3mnc.1.A, 3mnn.1.A, 3mnn.2.A, 3mym.1.A, 3myn.1.A, 3nfe.1.B, 3nl7.1.B, 3nml.1.A, 3nmm.1.A, 3o7n.1.B, 3o89.1.A, 3oj1.1.A, 3ok5.1.B, 3onz.1.B, 3ovu.1.C, 3ozu.1.A, 3ozv.1.A, 3ozv.2.A, 3pel.1.A, 3pel.1.B, 3pi2.3.B, 3pi3.3.A, 3pi4.3.D, 3pi8.1.A, 3pt7.1.B, 3pt8.1.B, 3qjb.1.A, 3qjc.1.B, 3qjd.1.A, 3qjd.1.B, 3qje.1.B, 3qm5.1.A, 3qma.1.A, 3qqq.1.A, 3qqq.1.B, 3qqr.1.A, 3qqr.2.A, 3qzx.1.B, 3qzz.1.A, 3rgk.1.A, 3rj6.1.A, 3rjn.1.A, 3s1i.1.A, 3s1i.1.B, 3s48.2.B, 3s65.1.B, 3s65.1.D, 3s66.1.A, 3s6n.1.A, 3szk.1.B, 3tld.1.A, 3tm3.1.A, 3tm9.1.A, 3ubc.1.A, 3ugy.1.A, 3ugz.1.A, 3uh3.1.A, 3uh5.1.A, 3uh6.1.A, 3uh7.1.A, 3uhb.1.A, 3uhc.1.A, 3uhd.1.A, 3uhe.1.A, 3uhg.1.A, 3uhh.1.A, 3uhi.1.A, 3v2v.1.A, 3vhh.1.B, 3vm9.1.A, 3vm9.1.B, 3vre.1.A, 3vre.1.B, 3vrf.1.B, 3vrf.1.C, 3vrg.1.A, 3w4u.1.A, 3w4u.2.A

7y4l.346.A, 7y4l.368.A, 7y4l.374.A, 7y4l.412.A, 7y4l.418.A, 7y4l.420.A, 7y4l.432.A, 7y4l.434.A, 7y4l.436.A, 7y4l.440.A, 7y4l.445.A, 7y4l.457.A, 7y4l.463.A, 7y4l.465.A, 7y4l.475.A, 7y4l.509.A, 7y4l.529.A, 7y4l.541.A, 7y4l.547.A, 7y4l.553.A, 7y4l.555.A, 7y4l.56.A, 7y4l.564.A, 7y4l.570.A, 7y4l.574.A, 7y4l.578.A, 7y4l.592.A, 7y4l.623.A, 7y4l.625.A, 7y4l.628.A, 7y4l.630.A, 7y4l.632.A, 7y4l.635.A, 7y4l.637.A, 7y4l.639.A, 7y4l.641.A, 7y4l.646.A, 7y4l.649.A, 7y4l.653.A, 7y4l.655.A, 7y4l.657.A, 7y4l.659.A, 7y4l.66.A, 7y4l.664.A, 7y4l.67.A, 7y4l.674.A, 7y4l.678.A, 7y4l.680.A, 7y4l.684.A, 7y4l.688.A, 7y4l.692.A, 7y4l.694.A, 7y4l.702.A, 7y4l.704.A, 7y4l.706.A, 7y4l.708.A, 7y4l.710.A, 7y4l.75.A, 7y4l.78.A, 7y4l.88.A, 7y4l.99.A, 7y5e.671.A, 7y5e.711.A, 7y5e.715.A, 7y7a.1155.A, 7y7a.1161.A, 7y7a.1163.A, 7ylk.1.A, 7z1u.1.A, 7z1u.1.B, 7zos.1.A, 8ddy.1.A, 8dov.2.A, 8dov.2.D, 8eao.1.A, 8eb7.1.F, 8eb7.1.L, 8ejn.1.A, 8ejn.2.A, 8eko.1.A, 8el3.1.B, 8el6.1.B, 8el6.1.D, 8ess.1.A, 8esu.1.A, 8eum.1.A, 8eun.1.A, 8f2r.1.D, 8f2r.1.G, 8f2u.1.D, 8f2u.1.G, 8f9h.1.A, 8f9i.1.A, 8f9i.2.A, 8fdj.1.A, 8fdk.1.B, 8fdn.1.B, 8fdn.1.D, 8grz.1.A, 8h17.1.A, 8hfq.1.1, 8hfq.1.3, 8hfq.1.L, 8hfq.1.R, 8imi.1.4, 8imi.1.9, 8imi.1.B, 8imi.1.C, 8imi.1.D, 8imi.1.E, 8imi.1.F, 8imi.1.G, 8imi.1.H, 8imi.1.I, 8imi.1.J, 8imi.1.L, 8imi.1.N, 8imi.1.O, 8imi.1.P, 8imi.1.Q, 8imi.1.R, 8imi.1.S, 8imi.1.T, 8imi.1.U, 8imi.1.V, 8imi.1.X, 8imi.1.f, 8imi.1.g, 8imi.1.i, 8imj.1.D, 8imj.1.N, 8imj.1.P, 8imj.1.d, 8imj.1.e, 8imj.1.l, 8imj.1.o, 8imk.1.5, 8imk.1.B, 8imk.1.C, 8imk.1.H, 8imk.1.S, 8imk.1.f, 8iml.1.2, 8iml.1.4, 8iml.1.6, 8iml.1.8, 8iml.1.9, 8iml.1.B, 8iml.1.D, 8iml.1.E, 8iml.1.H, 8iml.1.I, 8iml.1.K, 8iml.1.O, 8iml.1.P, 8iml.1.a, 8imm.1.2, 8imm.1.8, 8imm.1.9, 8imm.1.V, 8imm.1.b, 8imm.1.d, 8imm.1.1, 8imm.1.2, 8imm.1.3, 8imm.1.4, 8imm.1.5, 8imm.1.6, 8imm.1.7, 8imm.1.8, 8imm.1.9, 8imm.1.B, 8imm.1.C, 8imm.1.D, 8imm.1.E, 8imm.1.F, 8imm.1.H, 8imm.1.I, 8imm.1.J, 8imm.1.O, 8imm.1.Q, 8imm.1.R, 8imm.1.S, 8imm.1.U, 8imm.1.V, 8imm.1.W, 8imm.1.Y, 8imm.1.a, 8imm.1.b, 8imm.1.c, 8imo.1.6, 8imo.1.B, 8imo.1.I, 8imo.1.P, 8imo.1.Q, 8imo.1.T, 8imo.1.V, 8imo.1.a, 8kfh.1.A, 8kfh.2.A, 8kfi.1.A, 8kfi.2.A, 8kfj.1.A, 8kfj.2.A, 8or7.1.B, 8oup.1.A, 8oup.1.B, 8oup.2.B, 8p0w.1.D, 8p0w.1.G, 8puq.1.A, 8pur.1.C, 8qba.1.A, 8tls.1.A, 8to2.1.1, 8to2.1.D, 8to2.1.H, 8to2.1.N, 8to2.1.R, 8to2.1.T, 8to2.1.V, 8tpj.1.E, 8tpj.1.G, 8tpj.1.I, 8tpj.1.K, 8tpj.1.M, 8tpj.1.O, 8u0y.1.J, 8u0y.1.U, 8u10.1.k, 8u10.1.l, 8u10.1.m, 8u10.1.p, 8u10.1.t, 8u10.1.u, 8u11.1.3, 8u11.1.Z, 8u11.1.b, 8u5a.1.A, 8uhe.1.A, 8uhe.1.C, 8uhe.1.E, 8uhe.1.G, 8uhe.1.I, 8uhe.1.J, 8uhe.1.M, 8uhe.1.O, 8uhe.1.Q, 8vyl.1.C, 8vyl.1.D, 8wix.1.A, 8wix.1.B, 8wiz.1.A, 8wiz.1.B, 8wj1.1.D, 8wql.11.A, 8wql.13.A, 8wql.15.A, 8wql.166.A, 8wql.201.A, 8wql.203.A, 8wql.205.A, 8wql.206.A, 8wql.208.A, 8wql.211.A, 8wql.365.A, 8wql.367.A, 8wql.370.A, 8wql.373.A, 8wql.375.A, 8wql.379.A, 8wql.382.A, 8wql.384.A, 8wql.4.A, 8wql.6.A, 8wql.63.A, 8wql.65.A, 8wql.68.A, 8wql.70.A, 8wql.71.A, 8wql.73.A, 8wql.75.A, 8wql.77.A, 8wql.8.A, 8wql.80.A, 8wql.82.A, 8wql.83.A, 8wql.84.A, 8wql.86.A, 8wql.88.A, 8wub.1.A, 8xbj.1.A, 8xf1.1.B, 8xf3.1.B, 8xmp.1.E, 8xmq.1.D, 8xmw.1.E, 8z20.1.A, 9av9.1.B, 9ayz.1.B, 9ayz.1.D, 9fhh.1.B, 9fmu.1.A, 9fmu.1.B, 9fno.1.A, 9fno.1.B, 9hej.1.D, 9hek.1.D, 9hek.1.E, 9i1r.1.A, 9i1r.1.C, 9i1r.1.E, 9i1r.1.G, 9i1r.1.I, 9i1r.1.J, 9i1r.1.T, 9jg6.1.f, 9nb6.1.D, 9nb6.1.E, 9nb8.1.D, 9nb8.1.E, P63112.1.A

Build Models 0

Clear Selection

No templates selected



Cartoon ▲







