






















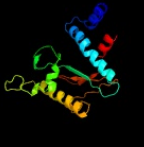


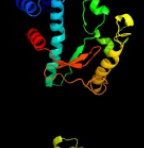



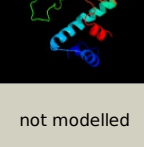


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1105_(-)_1232316_1232831
Date	Wed Jul 31 22:05:18 BST 2019
Unique Job ID	ee7106f692d3ad93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3biwD_</a>	 Alignment		100.0	28	<b>PDB header:</b> cell adhesion/cell adhesion <b>Chain:</b> D: <b>PDB Molecule:</b> neuroigin-1; <b>PDBTitle:</b> crystal structure of the neuroigin-1/neurexin-1beta synaptic adhesion2 complex
2	<a href="#">d1p0ia_</a>	 Alignment		100.0	21	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
3	<a href="#">c6i2tC_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
4	<a href="#">c2pm8A_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cholinesterase; <b>PDBTitle:</b> crystal structure of recombinant full length human2 butyrylcholinesterase
5	<a href="#">c1f8uA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
6	<a href="#">d1f8ua_</a>	 Alignment		100.0	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
7	<a href="#">d1ea5a_</a>	 Alignment		100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
8	<a href="#">c4bdtA_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> human acetylcholinesterase in complex with huprine w and fasciculin 2
9	<a href="#">c5x61A_</a>	 Alignment		100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of acetylcholinesterase catalytic subunit of the2 malaria vector anopheles gambiae, 3.4 a
10	<a href="#">c4qwwA_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> crystal structure of the fab410-bfache complex
11	<a href="#">c2w6cX_</a>	 Alignment		100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> acetylcholinesterase; <b>PDBTitle:</b> ache in complex with a bis(-)-nor-meptazinol derivative

12	<a href="#">d2ha2a1</a>	Alignment		100.0	23	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
13	<a href="#">d2h7ca1</a>	Alignment		100.0	31	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
14	<a href="#">c2ogsA</a>	Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable carboxylesterase est50; <b>PDBTitle:</b> crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
15	<a href="#">d1dx4a</a>	Alignment		100.0	19	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
16	<a href="#">d1ukca</a>	Alignment		100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
17	<a href="#">c5a2gB</a>	Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
18	<a href="#">d1qe3a</a>	Alignment		100.0	32	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
19	<a href="#">c4fg5B</a>	Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> e3 alpha-esterase-7 caboxylesterase; <b>PDBTitle:</b> crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
20	<a href="#">d1f6wa</a>	Alignment		100.0	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
21	<a href="#">d2bcea</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
22	<a href="#">c2fj0A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> crystal structure of juvenile hormone esterase from manduca sexta,2 with otfp covalently attached
23	<a href="#">c5w1uA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylic ester hydrolase; <b>PDBTitle:</b> culex quinquefasciatus carboxylesterase b2
24	<a href="#">d1thga</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
25	<a href="#">d1k4ya</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
26	<a href="#">c4be4A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sterol esterase; <b>PDBTitle:</b> closed conformation of o. piceae sterol esterase
27	<a href="#">c5thmA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase-6; <b>PDBTitle:</b> esterase-6 from drosophila melanogaster
28	<a href="#">d1llfa</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
29	<a href="#">d1gz7a</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases

					<b>Family:</b> Fungal lipases
30	<a href="#">d1crla_</a>	Alignment	not modelled	99.9	17 <b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
31	<a href="#">c4j0dB_</a>	Alignment	not modelled	20.8	19 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tannase; <b>PDBTitle:</b> tannin acyl hydrolase from lactobacillus plantarum (cadmium)
32	<a href="#">c6dk9l_</a>	Alignment	not modelled	7.3	8 <b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> dna damage-inducible protein; <b>PDBTitle:</b> yeast ddi2 cyanamide hydratase
33	<a href="#">c1nwdB_</a>	Alignment	not modelled	6.6	25 <b>PDB header:</b> binding protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase