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Description [AcetylCholinesterase](#)

Date Thu Dec 31 01:04:51 GMT 2020

Unique Job ID 9a8664f55b7717b5

Sequence [MARFITSSSL ...](#)  
[Download FASTA](#)

Job Type **intensive**

Job Expiry **30 days**

# Phyre2

Final Model

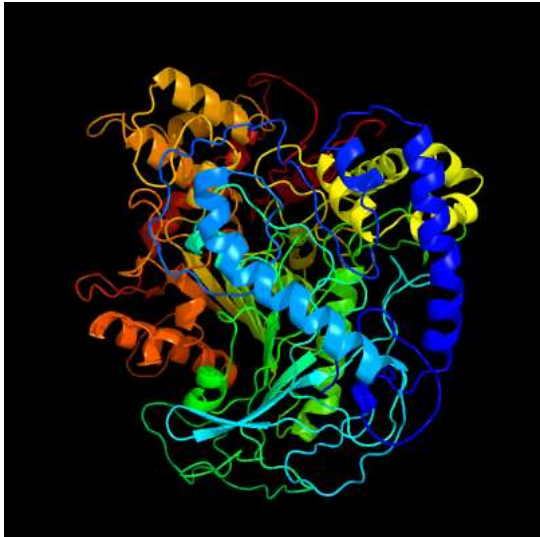
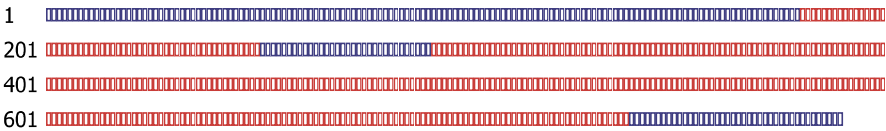


Image coloured by rainbow N → C terminus  
Model dimensions (Å): **X**:66,144 **Y**:73,548 **Z**:72,151

Download Model

Download all models



Confidence Key  
High(9) Low (0)

72% of residues modelled at >90% confidence ([Details](#))

[Hi-Res image](#) (black background)  
[Hi-Res image](#) (white background)

[Interactive 3D view in JSmol](#)

Sequence analysis

[View PSI-Blast Pseudo-Multiple Sequence Alignment](#) [Download FASTA version](#)


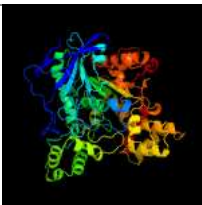

Secondary structure and disorder prediction [\[Show\]](#)

Domain analysis [\[Show\]](#)

Detailed template information [\[Hide\]](#)



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Info
1	<a href="#">d1dx4a</a> <input type="radio"/> <input type="checkbox"/>	 <a href="#">Alignment</a>		100.0	91	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like <a href="#">Run I</a>
2	<a href="#">c6i2tC</a> <input type="radio"/> <input type="checkbox"/>	 <a href="#">Alignment</a>		100.0	40	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cholinesterase <b>PDBTitle:</b> cryoem reconstruction of full butyrylcholinesterase tetramer <a href="#">Run I</a>
3	<a href="#">c4bdtA</a> <input type="radio"/> <input type="checkbox"/>	 <a href="#">Alignment</a>		100.0	38	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> acetylcholine <b>PDBTitle:</b> human acetylcholinesterase fasciculin 2

					<div>Run I</div>	
4	<div>c5x61A</div> <div><div></div><div></div></div>	<div>Alignment</div>		100.0	40	<div>PDB header:hydrolase</div> <div>Chain: A: PDB Molecule:acetylcholine</div> <div>PDBTitle: crystal structure of acetylcholinesterase from malaria vector anopheles gambiae, 3.4 Å resolution</div> <div>Run I</div>
5	<div>d1ea5a</div> <div><div></div><div></div></div>	<div>Alignment</div>		100.0	40	<div>Fold:alpha/beta-Hydrolases</div> <div>Superfamily:alpha/beta-Hydrolases</div> <div>Family:Acetylcholinesterase-like</div> <div>Run I</div>
6	<div>c2pm8A</div> <div><div></div><div></div></div>	<div>Alignment</div>		100.0	41	<div>PDB header:hydrolase</div> <div>Chain: A: PDB Molecule:cholinesterase</div> <div>PDBTitle: crystal structure of recombinant human butyrylcholinesterase</div>
<div>Generate superposition of selected models</div>						

Binding site prediction

Multi-template and ab initio information

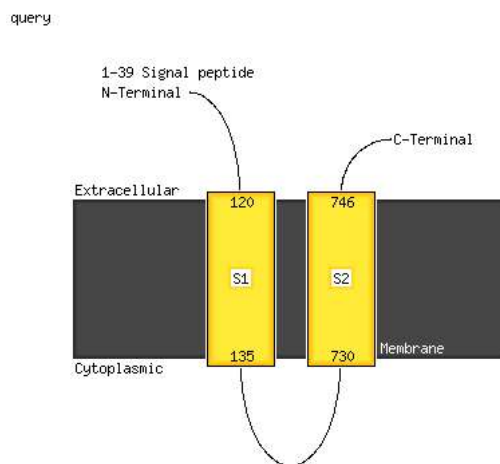
1 template was selected to model your protein based on heuristics to maximise confidence, percentage identity and alignment coverage. Below is a table indicating where your sequence was covered by each template, colour-coded by the confidence of the match to that template overall.

213 residues were modelled by ab initio. Please note: ab initio modelling is **highly** unreliable.

Template	Confidence	1	.....
d1dx4a	100%		.....
Template	Confidence	101	.....
d1dx4a	100%		.....
Template	Confidence	201	.....
d1dx4a	100%		.....
Template	Confidence	301	.....
d1dx4a	100%		.....
Template	Confidence	401	.....
d1dx4a	100%		.....
Template	Confidence	501	.....
d1dx4a	100%		.....
Template	Confidence	601	.....
d1dx4a	100%		.....
Template	Confidence	701	.....
d1dx4a	100%		.....

Transmembrane helix prediction

Transmembrane helices have been predicted in your sequence to adopt the topology shown below



Phyre is **now FREE for commercial users!**

All images and data generated by Phyre2 are free to use in any publication with acknowledgement

**Please cite:** The Phyre2 web portal for protein modeling, prediction and analysis.  
Kelley LA et al.. Nature Protocols 10, 845-858 (2015)[[pdf](#)] [[Citation link](#)]

If you use the binding site predictions from 3DLigandSite, **please also cite:**  
3DLigandSite: predicting ligand-binding sites using similar structures.  
Wass MN, Kelley LA and Sternberg MJ Nucleic Acids Research 38, W469-73 (2010)  
[[PubMed](#)]

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#### Component software

Template detection: [HHpred 1.51](#)  
Secondary structure prediction: [Psi-pred 2.5](#)  
Disorder prediction: [Disopred 2.4](#)  
Transmembrane prediction: [Memsat\\_SVM](#)  
Multi-template modelling and ab initio: [Poing 1.0](#)

