

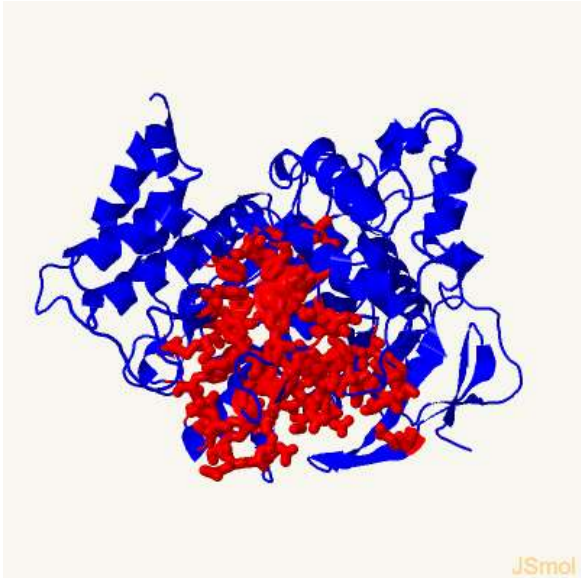


Job Description	AcetylCholinesterase		
Confidence	100.00%	Date	Thu Dec 31 02:48:20 GMT 2020
Rank	1	Aligned Residues	536
% Identity	91%	Template	d1dx4a_
SCOP info	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like		
Resolution	2.70		

Beta testing - Please contact [Lawrence Kelley](#) with problems/suggestions

Pocket detection
Large pockets are frequently found to be the location of active sites. The largest pocket as detected by the [fpocket2](#) program are shown in wireframe mode, coloured red.
[Download raw data](#)

Largest pocket
Pocket



Analyses

Quality

Conservation

Catalytic Sites

Pocket detection

Mutational sensitivity

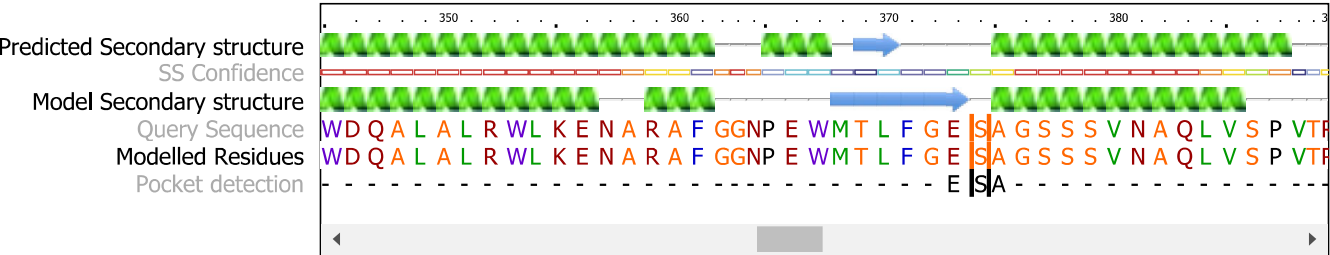
Residue: SER 374

Sequence profile

Mutations

ARNDQCQEGHILKMFSTWYV ARNDQCQEGHILKMFSTWYV

Take JMol snapshot Show All analyses Hide All analyses Clear Selection Hover over a residue below to see info. Click to spacefill.



Please cite: The Phyre2 web portal for protein modeling, prediction and analysis
Kelley LA et al. Nature Protocols 10, 845-858 (2015)[[paper](#)][[Citation link](#)]
For mutational analysis, please cite: SuSPect: Enhanced Prediction of Single Amino Acid Variant (SAV) Phenotype Using Network Features
Yates et al. J Mol Biol. 426(14): 2692-2701 (2014)[[paper](#)][[SuSPect Server](#)]