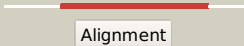

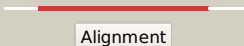

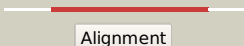







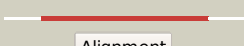








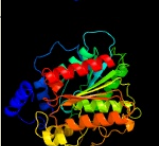


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2970c_(lipN)_3324583_3325713
Date	Thu Aug 8 16:20:13 BST 2019
Unique Job ID	46dbe37af856b214

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2zshA_</a>	 Alignment		100.0	29	<b>PDB header:</b> hormone receptor <b>Chain:</b> A: <b>PDB Molecule:</b> probable gibberellin receptor gid111; <b>PDBTitle:</b> structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
2	<a href="#">c4c87A_</a>	 Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> esterase lpest1 from lactobacillus plantarum wcfs1
3	<a href="#">c3ga7A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
4	<a href="#">c4krxB_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetyl esterase; <b>PDBTitle:</b> structure of aes from e. coli
5	<a href="#">c5jd5A_</a>	 Alignment		100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mgs-mile3; <b>PDBTitle:</b> crystal structure of mgs-mile3, an alpha/beta hydrolase enzyme from2 the metagenome of pyrene-phenanthrene enrichment culture with3 sediment sample of milazzo harbor, italy
6	<a href="#">c5jd4D_</a>	 Alignment		100.0	41	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> lae6; <b>PDBTitle:</b> crystal structure of lae6 ser161ala mutant, an alpha/beta hydrolase2 enzyme from the metagenome of lake arreo, spain
7	<a href="#">c3wj2A_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> crystal structure of estfa (fe-lacking apo form)
8	<a href="#">c3ed1E_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase receptor <b>Chain:</b> E: <b>PDB Molecule:</b> gibberellin receptor gid1; <b>PDBTitle:</b> crystal structure of rice gid1 complexed with ga3
9	<a href="#">c4ob7A_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase fold-3 domain protein; <b>PDBTitle:</b> crystal structure of esterase rppe mutant w187h
10	<a href="#">c3d7rB_</a>	 Alignment		100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a putative esterase from staphylococcus aureus
11	<a href="#">c4v2iB_</a>	 Alignment		100.0	35	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp

12	<a href="#">c4ypvA_</a>	Alignment		100.0	42	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> est8; <b>PDBTitle:</b> high-resolution structure of a metagenome-derived esterase est8
13	<a href="#">c4j7aB_</a>	Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of est25 - a bacterial homolog of hormone-sensitive2 lipase from a metagenomic library
14	<a href="#">c5miiD_</a>	Alignment		100.0	26	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> carboxyl esterase 2; <b>PDBTitle:</b> crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
15	<a href="#">d1lza_</a>	Alignment		100.0	36	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
16	<a href="#">c5hc4A_</a>	Alignment		100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipolytic enzyme; <b>PDBTitle:</b> structure of esterase est22
17	<a href="#">d1jkma_</a>	Alignment		100.0	26	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
18	<a href="#">c5l2pD_</a>	Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> arylesterase; <b>PDBTitle:</b> structure of arylesterase
19	<a href="#">d1jia_</a>	Alignment		100.0	35	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
20	<a href="#">c4wy8A_</a>	Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
21	<a href="#">c6aaeA_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of chloramphenicol-metabolizaing enzyme estdl136
22	<a href="#">c3dnmA_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> crystal structure hormone-sensitive lipase from a2 metagenome library
23	<a href="#">d1u4na_</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
24	<a href="#">c2wirB_</a>	Alignment	not modelled	100.0	37	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha/beta hydrolase fold-3 domain protein; <b>PDBTitle:</b> hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
25	<a href="#">c4wy5A_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
26	<a href="#">c3fakA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
27	<a href="#">c4xvcG_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> esterase e40; <b>PDBTitle:</b> crystal structure of an esterase from the bacterial hormone-sensitive2 lipase (hsl) family
28	<a href="#">c3qh4A_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase lipw; <b>PDBTitle:</b> crystal structure of esterase lipw from mycobacterium marinum

29	<a href="#">c2o7vA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cxe carboxylesterase; <b>PDBTitle:</b> carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
30	<a href="#">c2c7bA</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxylesterase; <b>PDBTitle:</b> the crystal structure of este1, a new thermophilic and2 thermostable carboxylesterase cloned from a metagenomic3 library
31	<a href="#">c4q3oB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mgs-mt1; <b>PDBTitle:</b> crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library
32	<a href="#">c3aikB</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 303aa long hypothetical esterase; <b>PDBTitle:</b> crystal structure of a hsl-like carboxylesterase from sulfolobus2 tokodaii
33	<a href="#">c4q05A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase e25; <b>PDBTitle:</b> crystal structure of an esterase e25
34	<a href="#">c4zrsA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
35	<a href="#">c4n5iX</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> esterase/lipase; <b>PDBTitle:</b> crystal structure of a c8-c4 sn3 inhibited esterase b from2 lactobacillus rhamnosis
36	<a href="#">c3bxpA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative lipase/esterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_2923) from2 lactobacillus plantarum wcf51 at 1.70 a resolution
37	<a href="#">c2ecfA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia
38	<a href="#">c2hu7A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acylamino-acid-releasing enzyme; <b>PDBTitle:</b> binding of inhibitors by acylaminoacyl peptidase
39	<a href="#">c4q3kB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mgs-m1; <b>PDBTitle:</b> crystal structure of mgs-m1, an alpha/beta hydrolase enzyme from a2 medee basin deep-sea metagenome library
40	<a href="#">c5oliA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase iv; <b>PDBTitle:</b> crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
41	<a href="#">c3azqA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> aminopeptidase; <b>PDBTitle:</b> crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
42	<a href="#">c5l8sD</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> amino acyl peptidase; <b>PDBTitle:</b> the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
43	<a href="#">c4e14A</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> kynurenine formamidase; <b>PDBTitle:</b> crystal structure of kynurenine formamidase conjugated with2 phenylmethylsulfonyl fluoride
44	<a href="#">c3bjrA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxylesterase; <b>PDBTitle:</b> crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcf51 at 2.09 a resolution
45	<a href="#">c4hxgJ</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> putative uncharacterized protein ph0594; <b>PDBTitle:</b> pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
46	<a href="#">c2eepA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl aminopeptidase iv, putative; <b>PDBTitle:</b> prolyl tripeptidyl aminopeptidase complexed with an inhibitor
47	<a href="#">c6a6oA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase/lipase-like protein; <b>PDBTitle:</b> crystal structure of acetyl ester-xyloside bifunctional hydrolase from2 caldicellulosiruptor lactoaceticus
48	<a href="#">c2qruA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
49	<a href="#">c1z68A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> fibroblast activation protein, alpha subunit; <b>PDBTitle:</b> crystal structure of human fibroblast activation protein alpha
50	<a href="#">c5t88B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase from pyrococcus furiosus
51	<a href="#">d1qfma2</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Prolyl oligopeptidase, C-terminal domain
52	<a href="#">c5yznA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-peptide hydrolase, putative; <b>PDBTitle:</b> crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
53	<a href="#">c6eoaC</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - apo
54	<a href="#">c2g5tA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> crystal structure of human dipeptidyl peptidase iv (dppiv)

						complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
55	<a href="#">c6eotG</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - slrflyeg, space group 19
56	<a href="#">c2qtbB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 4; <b>PDBTitle:</b> human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
57	<a href="#">c4wj1B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> inactive dipeptidyl peptidase 10; <b>PDBTitle:</b> structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels
58	<a href="#">c6eorD</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl peptidase 9; <b>PDBTitle:</b> dpp9 - 1g244
59	<a href="#">c4q1vA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dipeptidyl aminopeptidase iv; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl aminopeptidase iv2 (bacova_01349) from bacteroides ovatus atcc 8483 at 2.48 a resolution
60	<a href="#">c6eosB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl peptidase 8; <b>PDBTitle:</b> dpp8 - apo, space group 19
61	<a href="#">c1qfmA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (prolyl oligopeptidase); <b>PDBTitle:</b> prolyl oligopeptidase from porcine muscle
62	<a href="#">c5txeA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atxe2; <b>PDBTitle:</b> atxe2 isopeptidase - s527a variant with astexin3-dc4 bound
63	<a href="#">c3hxB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar hydrolase; <b>PDBTitle:</b> crystal structure of a sugar hydrolase (yeeb) from lactococcus lactis,2 northeast structural genomics consortium target kr108
64	<a href="#">c2bk1B</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> structural and mechanistic analysis of two prolyl2 endopeptidases: role of inter-domain dynamics in3 catalysis and specificity
65	<a href="#">c4bp9A</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b; <b>PDBTitle:</b> oligopeptidase b from trypanosoma brucei with covalently bound2 antipain - closed form
66	<a href="#">c4hvtA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> post-proline cleaving enzyme; <b>PDBTitle:</b> structure of a post-proline cleaving enzyme from rickettsia typhi
67	<a href="#">c2xe4A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> hydrolase/inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> oligopeptidase b; <b>PDBTitle:</b> structure of oligopeptidase b from leishmania major
68	<a href="#">d2hu7a2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acylamino-acid-releasing enzyme, C-terminal donain
69	<a href="#">d2pbla1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Carboxylesterase
70	<a href="#">c5aoaA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> the structure of a novel thermophilic esterase from the planctomycetes2 species, thermogutta terrifontis, est2-propionate bound
71	<a href="#">c1xfdD</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> dipeptidyl aminopeptidase-like protein 6; <b>PDBTitle:</b> structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
72	<a href="#">c5jr1C</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like <b>PDBTitle:</b> crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
73	<a href="#">c1yr2A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase; <b>PDBTitle:</b> structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
74	<a href="#">c3iumA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl endopeptidase; <b>PDBTitle:</b> appep_wtx opened state
75	<a href="#">d1vkha</a>	Alignment	not modelled	100.0	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Putative serine hydrolase Ydr428c
76	<a href="#">c5n4dA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> prolyl oligopeptidase; <b>PDBTitle:</b> prolyl oligopeptidase b from galerina marginata bound to 25mer2 macrocyclization substrate - d661a mutant
77	<a href="#">c5uzwD</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 g696insertion variant in complex with follower peptide and the2 covalent inhibitor zpp
78	<a href="#">c3k2iA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 4; <b>PDBTitle:</b> human acyl-coenzyme a thioesterase 4
						<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acyl-coenzyme a thioesterase 2,

79	<a href="#">c3hkB_</a>	Alignment	not modelled	99.9	17	mitochondrial; <b>PDBTitle:</b> crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
80	<a href="#">c3h04A_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of the protein with unknown function from2 staphylococcus aureus subsp. aureus mu50
81	<a href="#">d1orva2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
82	<a href="#">d2bgra2</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
83	<a href="#">c5uw7B_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> peptide cyclase 1; <b>PDBTitle:</b> pcy1 y481f variant in complex with follower peptide
84	<a href="#">c2i3dA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu1826; <b>PDBTitle:</b> crystal structure of protein of unknown function atu1826, a putative2 alpha/beta hydrolase from agrobacterium tumefaciens
85	<a href="#">d2i3da1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
86	<a href="#">c4zi5A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> p91; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
87	<a href="#">c4zv9E_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of an uncharacterized2 protein from escherichia coli o157:h7 str. sakai
88	<a href="#">d1xfda2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> DPP6 catalytic domain-like
89	<a href="#">c3f67A_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of putative dienelactone hydrolase from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
90	<a href="#">d1dina_</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Dienelactone hydrolase
91	<a href="#">d1ju3a2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> PepX catalytic domain-like
92	<a href="#">c2o2gA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dienelactone hydrolase; <b>PDBTitle:</b> crystal structure of dienelactone hydrolase (yp_324580.1) from2 anabaena variabilis atcc 29413 at 1.92 a resolution
93	<a href="#">c3ksrA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative serine hydrolase; <b>PDBTitle:</b> crystal structure of a putative serine hydrolase (xcc3885) from2 xanthomonas campestris pv. campestris at 2.69 a resolution
94	<a href="#">d1l7aa_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
95	<a href="#">c3trdA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha/beta hydrolase; <b>PDBTitle:</b> structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
96	<a href="#">d2fuka1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Atu1826-like
97	<a href="#">c3fnbB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acylaminoacyl peptidase smu_737; <b>PDBTitle:</b> crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
98	<a href="#">c3i6yA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase apc40077; <b>PDBTitle:</b> structure of an esterase from the oil-degrading bacterium oleispira2 antarctica
99	<a href="#">c3e4dD_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> esterase d; <b>PDBTitle:</b> structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
100	<a href="#">c5f2hA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
101	<a href="#">c4j0dB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tannase; <b>PDBTitle:</b> tannin acyl hydrolase from lactobacillus plantarum (cadmium)
102	<a href="#">d1vlqa_</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetyl xylan esterase-like
103	<a href="#">c3ls2D_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> s-formylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of an s-formylglutathione hydrolase from2 pseudoalteromonas haloplanktis tac125
104	<a href="#">c5g59A_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
105	<a href="#">c3fcxA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-formylglutathione hydrolase; <b>PDBTitle:</b> crystal structure of human esterase d



106	<a href="#">c3doiA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of a thermostable esterase complex with 2 paraoxon
107	<a href="#">c4h18D_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> cmt1; <b>PDBTitle:</b> three dimensional structure of corynomycoloyl tranferase c
108	<a href="#">c5cxcC_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ferulic acid esterase, amce1/fae1a; <b>PDBTitle:</b> structure of a ce1 ferulic acid esterase, amce1/fae1a, from 2 anaeromyces mucronatus in complex with ferulic acid
109	<a href="#">d2jbwa1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> 2,6-dihydropeseudooxynicotine hydrolase-like
110	<a href="#">c2uz0B_</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tributyryn esterase; <b>PDBTitle:</b> the crystal crystal structure of the esta protein, a2 virulence factor esta protein from streptococcus pneumonia
111	<a href="#">c1l7qA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cocaine esterase; <b>PDBTitle:</b> ser117ala mutant of bacterial cocaine esterase coce
112	<a href="#">c2jwbB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,6-dihydroxy-pseudo-oxynicotine hydrolase; <b>PDBTitle:</b> crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
113	<a href="#">c4b6gA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> the crystal structure of the neisserial esterase d.
114	<a href="#">c4eziA_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative hydrolase (lpg1103) from legionella2 pneumophila subsp. pneumophila str. philadelphia 1 at 1.15 a3 resolution
115	<a href="#">d1qe3a_</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Acetylcholinesterase-like
116	<a href="#">c5volA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative esterase; <b>PDBTitle:</b> bacint_04212 ferulic acid esterase
117	<a href="#">c5x6sB_</a>	Alignment	not modelled	99.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> acetylxytan esterase a; <b>PDBTitle:</b> acetyl xylan esterase from aspergillus awamori
118	<a href="#">c6ql5A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ferric enterobactin esterase; <b>PDBTitle:</b> crystal structure of the ferric enterobactin esterase (pfee) from 2 pseudomonas aeruginosa in complex with the tris-catechol vector
119	<a href="#">c3h2iA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> esterase; <b>PDBTitle:</b> crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
120	<a href="#">c3mveB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> upf0255 protein vv1_0328; <b>PDBTitle:</b> crystal structure of a novel pyruvate decarboxylase