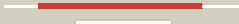








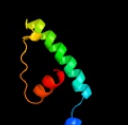

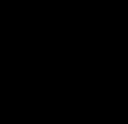
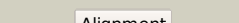


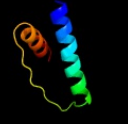






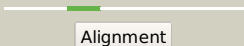
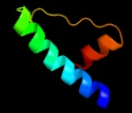
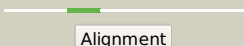
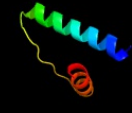
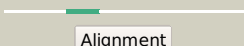

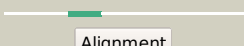

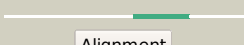

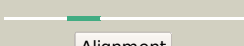

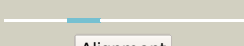
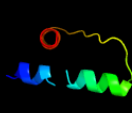





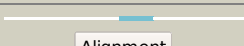

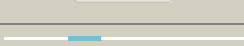
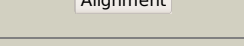
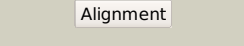




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4o5pB_	 Alignment		100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from pseudomonas2 aeruginosa
2	c4m0mA_	 Alignment		96.7	23	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the crystal structure of a functionally unknown protein lpg2422 from2 legionella pneumophila subsp. pneumophila str. philadelphia 1
3	d1ei9a_	 Alignment		69.7	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterases
4	c2vsgA_	 Alignment		67.3	19	PDB header: ligase Chain: A: PDB Molecule: surfactin synthetase subunit 3; PDBTitle: structure of surfactin a synthetase c (srfa-c), a2 nonribosomal peptide synthetase termination module
5	c3og9A_	 Alignment		67.2	20	PDB header: hydrolase Chain: A: PDB Molecule: protein yahd a copper inducible hydrolase; PDBTitle: structure of yahd with malic acid
6	d2h1ia1	 Alignment		64.2	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
7	c5f2hA_	 Alignment		63.1	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
8	c3ajaA_	 Alignment		62.8	24	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msme_6394
9	c2cbgA_	 Alignment		60.7	17	PDB header: hydrolase Chain: A: PDB Molecule: fengycin synthetase; PDBTitle: crystal structure of the pmsf-inhibited thioesterase domain2 of the fengycin biosynthesis cluster
10	c4zxiA_	 Alignment		53.7	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: tyrocidine synthetase 3; PDBTitle: crystal structure of holo-ab3403 a four domain nonribosomal peptide2 synthetase bound to amp and glycine
11	d1jmkc_	 Alignment		53.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases

12	d3b5ea1	 Alignment		51.5	11	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
13	c2zyiB	 Alignment		51.0	23	PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
14	c2h1iA	 Alignment		47.9	17	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of the bacillus cereus carboxylesterase
15	c2r8bA	 Alignment		46.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2452; PDBTitle: the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
16	c4ijsB	 Alignment		46.2	13	PDB header: rna binding protein/rna Chain: B: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of nucleocapsid protein encoded by the prototypic2 member of orthobunyavirus
17	c3lp5A	 Alignment		45.0	18	PDB header: hydrolase Chain: A: PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
18	d2r8ba1	 Alignment		38.2	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
19	c2jbwB	 Alignment		36.0	16	PDB header: hydrolase Chain: B: PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine2 hydrolase.
20	c3fleB	 Alignment		34.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
21	c3wydA	 Alignment	not modelled	33.3	14	PDB header: hydrolase Chain: A: PDB Molecule: lc-est1c; PDBTitle: c-terminal esterase domain of lc-est1
22	c3fewX	 Alignment	not modelled	32.2	45	PDB header: immune system Chain: X: PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a2 duplicated receptor binding domain
23	c4xbsA	 Alignment	not modelled	31.7	15	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
24	c4h0cA	 Alignment	not modelled	30.4	24	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase/carboxylesterase; PDBTitle: crystal structure of phospholipase/carboxylesterase from dyadobacter2 fermentans dsm 18053
25	c3g8yA	 Alignment	not modelled	30.0	23	PDB header: hydrolase Chain: A: PDB Molecule: susd/ragb-associated esterase-like protein; PDBTitle: crystal structure of a putative hydrolase (bvu_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
26	c4f21G	 Alignment	not modelled	29.8	33	PDB header: hydrolase/hydrolase inhibitor Chain: G: PDB Molecule: carboxylesterase/phospholipase family protein; PDBTitle: crystal structure of carboxylesterase/phospholipase family protein2 from francisella tularensis
27	c3mtvA	 Alignment	not modelled	29.6	19	PDB header: hydrolase Chain: A: PDB Molecule: papain-like cysteine protease; PDBTitle: the crystal structure of the prrsv nonstructural protein nsp1
28	dlcexa	 Alignment	not modelled	28.6	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like

29	c2i6oA_	Alignment	not modelled	28.1	9	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
30	c4kvvL_	Alignment	not modelled	27.8	53	PDB header: de novo protein Chain: L: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
31	c4kvvH_	Alignment	not modelled	27.8	53	PDB header: de novo protein Chain: H: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
32	d2jbwa1	Alignment	not modelled	26.7	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
33	d1lpbb2	Alignment	not modelled	25.3	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
34	c3e4dD_	Alignment	not modelled	24.8	23	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione2 hydrolase from agrobacterium tumefaciens
35	c5cxcC_	Alignment	not modelled	23.7	17	PDB header: hydrolase Chain: C: PDB Molecule: ferulic acid esterase, amce1/fae1a; PDBTitle: structure of a ce1 ferulic acid esterase, amce1/fae1a, from2 anaeromyces mucronatus in complex with ferulic acid
36	d1qoza_	Alignment	not modelled	22.9	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
37	c2czqB_	Alignment	not modelled	22.3	29	PDB header: hydrolase Chain: B: PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
38	c3fcxA_	Alignment	not modelled	22.1	24	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
39	d1tiba_	Alignment	not modelled	21.7	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
40	d1sfra_	Alignment	not modelled	21.7	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
41	d2d81a1	Alignment	not modelled	21.7	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: PHB depolymerase-like
42	c1mo2A_	Alignment	not modelled	21.5	23	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase2 (debs te), ph 8.5
43	d1mo2a_	Alignment	not modelled	21.5	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
44	c3gbsA_	Alignment	not modelled	21.2	29	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
45	c4b6gA_	Alignment	not modelled	21.1	21	PDB header: hydrolase Chain: A: PDB Molecule: putative esterase; PDBTitle: the crystal structure of the neisserial esterase d.
46	c3hkB_	Alignment	not modelled	21.1	22	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa2 thioesterase (acot2)
47	d1ispa_	Alignment	not modelled	20.8	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Bacterial lipase
48	c3trdA_	Alignment	not modelled	20.7	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase; PDBTitle: structure of an alpha-beta serine hydrolase homologue from coxiella2 burnetii
49	c3dd5F_	Alignment	not modelled	20.6	19	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
50	c3gzbc_	Alignment	not modelled	20.1	50	PDB header: lyase Chain: C: PDB Molecule: putative snoal-like polyketide cyclase; PDBTitle: crystal structure of putative snoal-like polyketide cyclase2 (yp_001182657.1) from shewanella putrefaciens cn-32 at 1.44 a3 resolution
51	d3tgla_	Alignment	not modelled	19.5	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
52	c3visB_	Alignment	not modelled	19.5	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of cutinase est119 from thermobifida alba ahk119
53	d1dqza_	Alignment	not modelled	18.7	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
54	c4bhHz_	Alignment	not modelled	18.6	22	PDB header: viral protein/rna Chain: Z: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of tetramer of la crosse virus nucleoprotein in2 complex with ssrna
						Fold: alpha/beta-Hydrolases

55	d1tcaa_	Alignment	not modelled	18.3	20	Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
56	d2h7xa1	Alignment	not modelled	17.8	25	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
57	d1lgva_	Alignment	not modelled	17.5	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
58	d1g66a_	Alignment	not modelled	17.5	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
59	d2idob1	Alignment	not modelled	17.0	21	Fold: DNA polymerase III theta subunit-like Superfamily: DNA polymerase III theta subunit-like Family: DNA polymerase III theta subunit-like
60	d1gp1a2	Alignment	not modelled	16.9	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
61	c3frrA_	Alignment	not modelled	16.7	26	PDB header: protein binding Chain: A: PDB Molecule: uncharacterized protein kiaa0174; PDBTitle: structure of human ist1(ntd) - (residues 1-189)(p21)
62	c2h7xA_	Alignment	not modelled	16.6	24	PDB header: hydrolase Chain: A: PDB Molecule: type i polyketide synthase pikaiv; PDBTitle: pikromycin thioesterase adduct with reduced triketide2 affinity label
63	c2n1dA_	Alignment	not modelled	16.4	23	PDB header: protein binding Chain: A: PDB Molecule: mrg/morf4l-binding protein; PDBTitle: solution structure of the mrg15-mrgbp complex
64	d1se7a_	Alignment	not modelled	16.4	20	Fold: DNA polymerase III theta subunit-like Superfamily: DNA polymerase III theta subunit-like Family: DNA polymerase III theta subunit-like
65	c4fleA_	Alignment	not modelled	16.4	26	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of the esterase yqia (ye3661) from yersinia2 enterocolitica, northeast structural genomics consortium target yer85
66	c1dnuB_	Alignment	not modelled	15.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: myeloperoxidase; PDBTitle: structural analyses of human myeloperoxidase-thiocyanate complex
67	c3nuzF_	Alignment	not modelled	15.9	29	PDB header: hydrolase Chain: F: PDB Molecule: putative acetyl xylan esterase; PDBTitle: crystal structure of a putative acetyl xylan esterase (bf1801) from2 bacteroides fragilis nctc 9343 at 2.30 a resolution
68	c2vtvA_	Alignment	not modelled	15.9	14	PDB header: hydrolase Chain: A: PDB Molecule: phb depolymerase phaz7; PDBTitle: phaz7 depolymerase from paucimonas lemoignei
69	d1uwca_	Alignment	not modelled	15.8	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
70	c4idxA_	Alignment	not modelled	15.3	13	PDB header: dna binding protein Chain: A: PDB Molecule: nucleocapsid protein; PDBTitle: hexameric crystal structure of schmallenberg virus nucleoprotein
71	c2f8vY_	Alignment	not modelled	15.0	17	PDB header: contractile protein/contractile protein Chain: Y: PDB Molecule: telethonin; PDBTitle: structure of full length telethonin in complex with the n-terminus of2 titin
72	c3g7nA_	Alignment	not modelled	14.4	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of the hypothetical protein from penicillium2 expansum at 1.3
73	c2dbhA_	Alignment	not modelled	14.1	30	PDB header: signaling protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
74	d2ae9a1	Alignment	not modelled	13.9	22	Fold: DNA polymerase III theta subunit-like Superfamily: DNA polymerase III theta subunit-like Family: DNA polymerase III theta subunit-like
75	c4z8zA_	Alignment	not modelled	13.9	11	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
76	c3nrtC_	Alignment	not modelled	13.8	23	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative ryanodine receptor; PDBTitle: the crystal structure of putative ryanodine receptor from bacteroides2 thetaiotaomicron vpi-5482
77	c4js0B_	Alignment	not modelled	13.8	33	PDB header: signaling protein/signaling protein Chain: B: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: complex of cdc42 with the crib-pr domain of irsp53
78	c3lcrA_	Alignment	not modelled	13.8	22	PDB header: hydrolase Chain: A: PDB Molecule: tautomycin biosynthetic pks; PDBTitle: thioesterase from tautomycin biosynthetic pathway
79	c1ya5T_	Alignment	not modelled	13.8	17	PDB header: structural protein Chain: T: PDB Molecule: telethonin; PDBTitle: crystal structure of the titin domains z1z2 in complex with telethonin
80	c4em8A_	Alignment	not modelled	13.8	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase b; PDBTitle: the structure of ribose 5-phosphate isomerase b from anaplasma2 phagocytophilum
81	c3dc8A_	Alignment	not modelled	13.6	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin2722 protein;

81	c3us8A_	Alignment	not modelled	13.8	41	PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
82	c4ip8B_	Alignment	not modelled	13.5	33	PDB header: protein binding Chain: B: PDB Molecule: serum amyloid a-1 protein; PDBTitle: structure of human serum amyloid a1
83	c3d0kA_	Alignment	not modelled	13.4	16	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
84	c4g4gA_	Alignment	not modelled	13.2	20	PDB header: hydrolase Chain: A: PDB Molecule: 4-o-methyl-glucuronoyl methylesterase; PDBTitle: crystal structure of recombinant glucuronoyl esterase from2 sporotrichum thermophile determined at 1.55 a resolution
85	d1cuka3	Alignment	not modelled	12.7	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
86	d1f0na_	Alignment	not modelled	12.6	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
87	d1yl7a1	Alignment	not modelled	12.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	c2vg2C_	Alignment	not modelled	12.1	13	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
89	d1n7ka_	Alignment	not modelled	12.1	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
90	c4kvvF_	Alignment	not modelled	12.0	50	PDB header: de novo protein Chain: F: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
91	c4kvvD_	Alignment	not modelled	12.0	50	PDB header: de novo protein Chain: D: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
92	c4kvvA_	Alignment	not modelled	12.0	50	PDB header: de novo protein Chain: A: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
93	c4kvvI_	Alignment	not modelled	12.0	50	PDB header: de novo protein Chain: I: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
94	c4kvvK_	Alignment	not modelled	12.0	50	PDB header: de novo protein Chain: K: PDB Molecule: 6-helix coiled coil cc-hex-l24c peptide with an alkylated PDBTitle: crystal structure of an alkylated cys mutant of cc-hex
95	c4j1jA_	Alignment	not modelled	12.0	16	PDB header: viral protein/dna Chain: A: PDB Molecule: nucleocapsid; PDBTitle: leanyer orthobunyavirus nucleoprotein-ssdna complex
96	c3fnbB_	Alignment	not modelled	11.8	20	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
97	c4j37A_	Alignment	not modelled	11.7	31	PDB header: rna binding protein Chain: A: PDB Molecule: trna pseudouridine synthase a, mitochondrial; PDBTitle: crystal structure of the catalytic domain of human pus1
98	c3rqrA_	Alignment	not modelled	11.5	21	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of the ryr domain of the rabbit ryanodine receptor
99	c3uuuA_	Alignment	not modelled	11.3	22	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa