Phyre2

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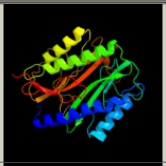
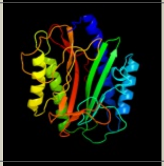
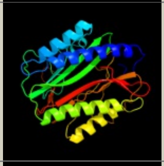
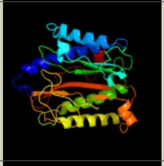
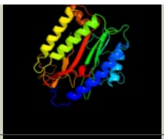
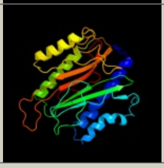
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2gg2a1	Alignment		100.0	100	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
2	c2g6pA_	Alignment		100.0	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
3	c2gz5A_	Alignment		100.0	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
4	c3s6bA_	Alignment		100.0	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
5	c3tavA_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of a methionine aminopeptidase from mycobacterium2 abscessus
6	c3mx6A_	Alignment		100.0	52	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase from rickettsia2 prowazekii bound to methionine
7	c1yj3A_	Alignment		100.0	51	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure analysis of product bound methionine2 aminopeptidase type 1c from mycobacterium tuberculosis
8	d1o0xa_	Alignment		100.0	43	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
9	c1w7vD_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
10	c2oknB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal strcture of human prolidase
11	d1qxya_	Alignment		100.0	33	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase

12	c3l24A_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of the nerve agent degrading2 organophosphate anhydrolase/prolidase in complex with3 inhibitors
13	c1chmA_	Alignment		100.0	18	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
14	c2zsgB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aminopeptidase p, putative; **PDBTitle:** crystal structure of x-pro aminopeptidase from thermotoga maritima2 msb8
15	d1chma2	Alignment		100.0	18	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
16	c3ig4E_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** structure of a putative aminopeptidase p from bacillus anthracis
17	c1wy2B_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-pro dipeptidase; **PDBTitle:** crystal structure of the prolidase from pyrococcus horikoshii ot3
18	c3q6dA_	Alignment		100.0	27	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**proline dipeptidase; **PDBTitle:** xaa-pro dipeptidase from bacillus anthracis.
19	c2howB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**356aa long hypothetical dipeptidase; **PDBTitle:** dipeptidase (ph0974) from pyrococcus horikoshii ot3
20	c3cb5A_	Alignment		100.0	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of the s. pombe peptidase homology domain of fact2 complex subunit spt16 (form a)
21	d1pv9a2	Alignment	not modelled	100.0	25	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
22	d2v3za2	Alignment	not modelled	100.0	26	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
23	d1b6aa2	Alignment	not modelled	100.0	21	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
24	c3ctzA_	Alignment	not modelled	100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xaa-pro aminopeptidase 1; **PDBTitle:** structure of human cytosolic x-prolyl aminopeptidase
25	c2v6cA_	Alignment	not modelled	100.0	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** crystal structure of erbb3 binding protein 1 (ebp1)
26	c2q8kA_	Alignment	not modelled	100.0	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** the crystal structure of ebp1
27	d1xgsa2	Alignment	not modelled	100.0	31	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
28	c3bitA_	Alignment	not modelled	100.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fact complex subunit spt16; **PDBTitle:** crystal structure of yeast spt16 n-terminal domain
29	c1xgnB_	Alignment	not modelled	100.0	30	**PDB header:**aminopeptidase **Chain:** B: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus

30	c1b6aA_	Alignment	not modelled	100.0	21	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
31	c3fm3B_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
32	c1yw7A_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
33	c1kp0B_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** the crystal structure analysis of creatine amidinohydrolase2 from actinobacillus
34	d1kp0a2	Alignment	not modelled	100.0	17	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
35	c3nojA_	Alignment	not modelled	68.2	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
36	c2c5qE_	Alignment	not modelled	66.3	16	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
37	d1wi0a_	Alignment	not modelled	28.9	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
38	c3innB_	Alignment	not modelled	27.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
39	d2npta1	Alignment	not modelled	27.1	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
40	c3prdA_	Alignment	not modelled	25.9	29	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
41	d1e4cp_	Alignment	not modelled	25.7	17	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
42	c2fk5B_	Alignment	not modelled	24.9	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
43	d1kt0a2	Alignment	not modelled	24.0	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
44	c2l25A_	Alignment	not modelled	21.3	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** np_888769.1
45	c3ds8A_	Alignment	not modelled	20.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from listeria2 innocua
46	c2y0oA_	Alignment	not modelled	20.3	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable d-lyxose ketol-isomerase; **PDBTitle:** the structure of a d-lyxose isomerase from the sigmab2 regulon of bacillus subtilis
47	c2ki0A_	Alignment	not modelled	19.8	14	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**ds119; **PDBTitle:** nmr structure of a de novo designed beta alpha beta
48	c2kw0A_	Alignment	not modelled	19.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
49	c2hl7A_	Alignment	not modelled	18.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
50	c2zyiB_	Alignment	not modelled	16.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
51	c2pc9B_	Alignment	not modelled	16.3	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate carboxykinase [atp]; **PDBTitle:** crystal structure of atp-dependent phosphoenolpyruvate carboxykinase2 from thermus thermophilus hb8
52	d1ex9a_	Alignment	not modelled	14.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
53	c3mpbA_	Alignment	not modelled	14.2	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar isomerase; **PDBTitle:** z5688 from e. coli o157:h7 bound to fructose
54	c3k4iC_	Alignment	not modelled	13.6	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
55	d1l1pa_	Alignment	not modelled	12.9	35	**Fold:**FKBP-like **Superfamily:**FKBP-like

						Family:FKBP immunophilin/proline isomerase
56	c2xs4A_	Alignment	not modelled	12.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**karilysin protease; **PDBTitle:** structure of karilysin catalytic mmp domain in complex with2 magnesium
57	c2opiB_	Alignment	not modelled	12.7	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
58	d1cvla_	Alignment	not modelled	12.6	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
59	d1ii2a1	Alignment	not modelled	12.5	18	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
60	c2vavL_	Alignment	not modelled	12.5	13	**PDB header:**transferase **Chain:** L: **PDB Molecule:**acetyl-coa--deacetylcephalosporin c **PDBTitle:** crystal structure of deacetylcephalosporin c2 acetyltransferase (dac-soak)
61	d1k8qa_	Alignment	not modelled	12.3	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Gastric lipase
62	c3i1iA_	Alignment	not modelled	11.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homoserine o-acetyltransferase; **PDBTitle:** x-ray crystal structure of homoserine o-acetyltransferase from2 bacillus anthracis
63	d2dsta1	Alignment	not modelled	10.8	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**TTHA1544-like
64	c1ahuB_	Alignment	not modelled	10.8	22	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
65	d1w26a3	Alignment	not modelled	10.7	21	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
66	c3lp5A_	Alignment	not modelled	10.7	21	**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
67	d4lipd_	Alignment	not modelled	10.4	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Bacterial lipase
68	c2k5nA_	Alignment	not modelled	10.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative cold-shock protein; **PDBTitle:** solution nmr structure of the n-terminal domain of protein2 eca1580 from erwinia carotovora, northeast structural3 genomics consortium target ewr156a
69	d1j3ba1	Alignment	not modelled	10.1	11	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
70	c2irpA_	Alignment	not modelled	10.0	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative aldolase class 2 protein aq_1979; **PDBTitle:** crystal structure of the l-fuculose-1-phosphate aldolase (aq_1979)2 from aquifex aeolicus vf5
71	d1tiaa_	Alignment	not modelled	9.8	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
72	d1m1fa_	Alignment	not modelled	9.3	12	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
73	d2vata1	Alignment	not modelled	9.2	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
74	d1t11a3	Alignment	not modelled	9.1	30	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
75	d3tgla_	Alignment	not modelled	9.0	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
76	c3fmyA_	Alignment	not modelled	9.0	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
77	c3ocrA_	Alignment	not modelled	8.9	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**class ii aldolase/adducin domain protein; **PDBTitle:** crystal structure of aldolase ii superfamily protein from pseudomonas2 syringae
78	d2pl5a1	Alignment	not modelled	8.8	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**O-acetyltransferase
79	d1rp1a2	Alignment	not modelled	8.5	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
80	d1tiba_	Alignment	not modelled	8.2	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
81	c2gacA_	Alignment	not modelled	8.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosylasparaginase; **PDBTitle:** t152c mutant glycosylasparaginase from

						flavobacterium2 meningosepticum
82	d1lgya_	Alignment	not modelled	8.1	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
83	d1cxva_	Alignment	not modelled	8.1	19	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Matrix metalloproteases, catalytic domain
84	c1t3mA_	Alignment	not modelled	8.0	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative l-asparaginase; **PDBTitle:** structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
85	d1uwca_	Alignment	not modelled	7.7	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
86	d1y7ma2	Alignment	not modelled	7.7	19	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
87	d1hpla2	Alignment	not modelled	7.7	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
88	c1kt0A_	Alignment	not modelled	7.7	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**51 kda fk506-binding protein; **PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
89	d1lpbb2	Alignment	not modelled	7.6	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
90	d2olra1	Alignment	not modelled	7.6	13	**Fold:**PEP carboxykinase-like **Superfamily:**PEP carboxykinase-like **Family:**PEP carboxykinase C-terminal domain
91	c3jr1A_	Alignment	not modelled	7.5	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative fructosamine-3-kinase; **PDBTitle:** crystal structure of putative fructosamine-3-kinase2 (yp_719053.1) from haemophilus somnus 129pt at 2.32 a3 resolution
92	d1g6pa_	Alignment	not modelled	7.3	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
93	c2zakB_	Alignment	not modelled	7.2	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**l-asparaginase precursor; **PDBTitle:** orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
94	c2pplA_	Alignment	not modelled	7.1	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pancreatic lipase-related protein 1; **PDBTitle:** human pancreatic lipase-related protein 1
95	d1etha2	Alignment	not modelled	7.1	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Pancreatic lipase, N-terminal domain
96	c2kxxA_	Alignment	not modelled	6.9	5	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
97	c2gezE_	Alignment	not modelled	6.8	9	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
98	d1tcaa_	Alignment	not modelled	6.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
99	c2k5jB_	Alignment	not modelled	6.7	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1