Phyre2

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Description	P64479
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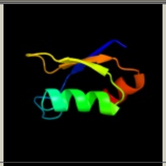
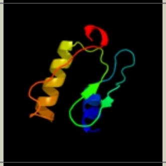
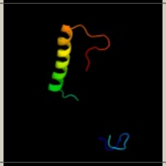
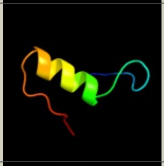
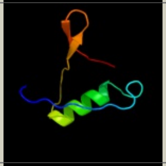
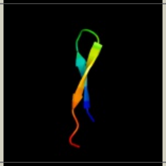
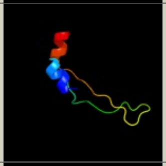
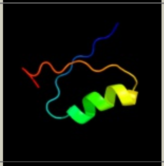
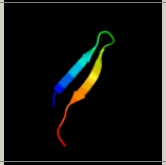
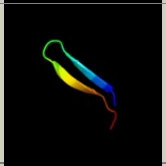
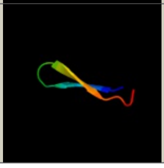
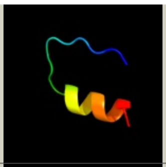
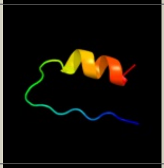
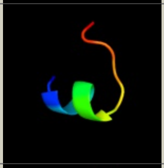
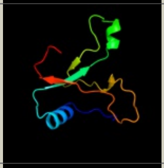
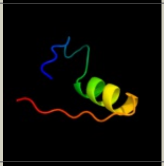
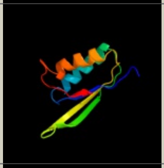
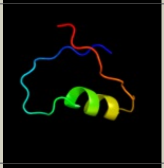
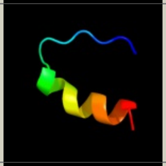
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1spbp_	Alignment		61.2	13	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
2	d2hiya1	Alignment		35.3	20	**Fold:**SP0830-like **Superfamily:**SP0830-like **Family:**SP0830-like
3	d2f5va2	Alignment		22.4	10	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GMC oxidoreductases
4	d2aw0a_	Alignment		18.4	30	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
5	d2bkfa1	Alignment		16.2	4	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
6	c1ajnA_	Alignment		14.6	18	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** penicillin acylase complexed with p-nitrophenylacetic acid
7	c3cueH_	Alignment		14.4	9	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**transport protein particle 31 kda subunit; **PDBTitle:** crystal structure of a trapp subassembly activating the rab2 ypt1p
8	d1kn6a_	Alignment		14.4	12	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Prohormone convertase 1 pro-domain
9	c1cp9A_	Alignment		12.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin amidohydrolase; **PDBTitle:** crystal structure of penicillin g acylase from the bro12 mutant strain of providencia rettgeri
10	c1gk9A_	Alignment		12.0	18	**PDB header:**antibiotic resistance **Chain:** A: **PDB Molecule:**penicillin g acylase alpha subunit; **PDBTitle:** crystal structures of penicillin acylase enzyme-substrate2 complexes: structural insights into the catalytic mechanism
11	c3k3wA_	Alignment		11.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**penicillin g acylase; **PDBTitle:** thermostable penicillin g acylase from alcaligence faecalis2 in orthorhombic form

12	d1pkxa1	Alignment		10.9	25	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
13	d1g8ma1	Alignment		10.9	18	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
14	c3kowH_	Alignment		10.8	33	**PDB header:**metal binding protein **Chain:** H: **PDB Molecule:**d-ornithine aminomutase s component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase backsoaked complex
15	d1oeyj_	Alignment		10.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
16	c2kt2A_	Alignment		10.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** structure of nmera, the n-terminal hma domain of tn501 mercuric2 reductase
17	c3ce8A_	Alignment		9.4	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
18	d1s6ua_	Alignment		9.2	18	**Fold:**Ferredoxin-like **Superfamily:**HMA, heavy metal-associated domain **Family:**HMA, heavy metal-associated domain
19	d1zcza1	Alignment		9.1	20	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Inosicase
20	c2wybA_	Alignment		9.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-homoserine lactone acylase pvdq subunit **PDBTitle:** the quorum quenching n-acyl homoserine lactone acylase pvdq2 with a covalently bound dodecanoic acid
21	d1m32a_	Alignment	not modelled	9.1	19	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
22	c2dunA_	Alignment	not modelled	9.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** solution structure of brct domain of dna polymerase mu
23	c1zr6A_	Alignment	not modelled	8.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
24	d1wxia1	Alignment	not modelled	8.5	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
25	c3q4gA_	Alignment	not modelled	8.5	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
26	d1kjqa2	Alignment	not modelled	8.2	13	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
27	c3hbxB_	Alignment	not modelled	7.8	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**glutamate decarboxylase 1; **PDBTitle:** crystal structure of gad1 from arabidopsis thaliana
28	c3dpiA_	Alignment	not modelled	7.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
						PDB header:transferase **Chain:** A: **PDB Molecule:**2-amino-3-ketobutyrate coenzyme a

29	c3tqxA_	Alignment	not modelled	7.0	11	ligase; **PDBTitle:** structure of the 2-amino-3-ketobutyrate coenzyme a ligase (kbl) from2 coxiella burnetii
30	d1d0na4	Alignment	not modelled	6.9	17	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
31	d1tiba_	Alignment	not modelled	6.9	6	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
32	c1thzA_	Alignment	not modelled	6.7	20	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of avian aicar transformylase in complex2 with a novel inhibitor identified by virtual ligand3 screening
33	c2gcfA_	Alignment	not modelled	6.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cation-transporting atpase pacs; **PDBTitle:** solution structure of the n-terminal domain of the coppper(i) atpase2 pacs in its apo form
34	c4a1oB_	Alignment	not modelled	6.5	24	**PDB header:**transferase-hydrolase **Chain:** B: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of mycobacterium tuberculosis purh complexed with2 aicar and a novel nucleotide cfair, at 2.48 a resolution.
35	c2ae3A_	Alignment	not modelled	6.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glutaryl 7-aminocephalosporanic acid acylase; **PDBTitle:** glutaryl 7-aminocephalosporanic acid acylase: mutational study of2 activation mechanism
36	d1q5ya_	Alignment	not modelled	6.3	33	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Nickel responsive regulator NikR, C-terminal domain
37	d1wj6a_	Alignment	not modelled	6.0	4	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
38	d2fg9a1	Alignment	not modelled	5.9	19	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
39	c2jz7A_	Alignment	not modelled	5.8	23	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
40	c3flpJ_	Alignment	not modelled	5.7	14	**PDB header:**sugar binding protein **Chain:** J: **PDB Molecule:**sap-like pentraxin; **PDBTitle:** crystal structure of native heptameric sap-like pentraxin2 from limulus polyphemus
41	c3hqtB_	Alignment	not modelled	5.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cai-1 autoinducer synthase; **PDBTitle:** plp-dependent acyl-coa transferase cqsa
42	c2rmlA_	Alignment	not modelled	5.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**copper-transporting p-type atpase copa; **PDBTitle:** solution structure of the n-terminal soluble domains of2 bacillus subtilis copa
43	d1scjb_	Alignment	not modelled	5.4	16	**Fold:**Ferredoxin-like **Superfamily:**Protease propeptides/inhibitors **Family:**Subtilase propeptides/inhibitors
44	d1jmsa4	Alignment	not modelled	5.4	10	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
45	c3uowB_	Alignment	not modelled	5.3	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
46	c1zczA_	Alignment	not modelled	5.2	16	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**bifunctional purine biosynthesis protein purh; **PDBTitle:** crystal structure of phosphoribosylaminoimidazolecarboxamide2 formyltransferase / imp cyclohydrolase (tm1249) from thermotoga3 maritima at 1.88 a resolution
47	d2fh1a1	Alignment	not modelled	5.2	17	**Fold:**Gelsolin-like **Superfamily:**Actin depolymerizing proteins **Family:**Gelsolin-like
48	d1kqpa_	Alignment	not modelled	5.2	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
49	d2o3aa1	Alignment	not modelled	5.2	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
50	d1r7ma2	Alignment	not modelled	5.1	24	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease