Phyre^2

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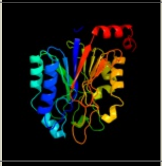
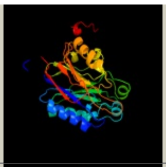
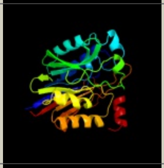
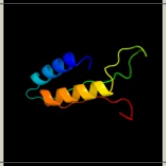
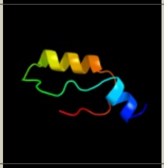
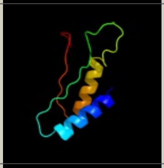
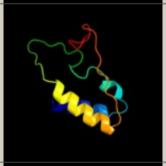
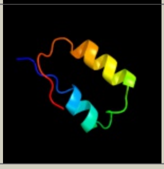
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2e11B_	Alignment		100.0	48	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrolase; **PDBTitle:** the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
2	c2vhiG_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**cg3027-pa; **PDBTitle:** crystal structure of a pyrimidine degrading enzyme from2 drosophila melanogaster
3	c1emsB_	Alignment		100.0	26	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**nit-fragile histidine triad fusion protein; **PDBTitle:** crystal structure of the c. elegans nitfhit protein
4	c2plqA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aliphatic amidase; **PDBTitle:** crystal structure of the amidase from geobacillus pallidus rapc8
5	c2e2kC_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formamidase; **PDBTitle:** helicobacter pylori formamidase amif contains a fine-tuned cysteine-2 glutamate-lysine catalytic triad
6	c2w1vA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
7	d1emsa2	Alignment		100.0	25	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
8	d1uf5a_	Alignment		100.0	23	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
9	d1f89a_	Alignment		100.0	23	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
10	c3dlaD_	Alignment		100.0	17	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
11	d1j31a_	Alignment		100.0	22	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase

12	c3hkxA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidase; **PDBTitle:** crystal structure analysis of an amidase from nesterenkonia sp.
13	c3n05B_	Alignment		100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
14	c3ilvA_	Alignment		100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
15	d1o60a_	Alignment		82.6	4	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
16	c3rqzC_	Alignment		75.1	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
17	d1d9ea_	Alignment		70.0	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
18	c3sz8D_	Alignment		54.8	6	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
19	c2qw5B_	Alignment		51.1	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
20	c3qfnA_	Alignment		38.9	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
21	c3stgA_	Alignment	not modelled	36.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase; **PDBTitle:** crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
22	c1s3mA_	Alignment	not modelled	36.9	16	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
23	d1s3la_	Alignment	not modelled	36.9	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
24	d3c9ua1	Alignment	not modelled	31.5	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
25	d1uf3a_	Alignment	not modelled	31.0	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
26	c2o14A_	Alignment	not modelled	30.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yxim; **PDBTitle:** x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
27	c2ei9A_	Alignment	not modelled	29.5	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein; **PDBTitle:** crystal structure of r1bm endonuclease domain
28	d1q7ra_	Alignment	not modelled	28.6	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family: Class I glutamine amidotransferases (GAT)
29	c1su1A_	Alignment	not modelled	24.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
30	d1su1a_	Alignment	not modelled	24.8	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
31	d1gpma2	Alignment	not modelled	24.4	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
32	d1wdua_	Alignment	not modelled	23.2	7	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
33	c2fu3A_	Alignment	not modelled	19.7	13	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
34	d1yx1a1	Alignment	not modelled	17.7	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**KguE-like
35	c1wu8B_	Alignment	not modelled	16.8	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph0463; **PDBTitle:** crystal structure of project ph0463 from pyrococcus horikoshii ot3
36	d3ck2a1	Alignment	not modelled	15.4	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
37	c3pzvB_	Alignment	not modelled	15.2	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endoglucanase; **PDBTitle:** c2 crystal form of the endo-1,4-beta-glucanase from bacillus subtilis2 168
38	d1hd7a_	Alignment	not modelled	15.1	7	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
39	c3ju2A_	Alignment	not modelled	14.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein smc04130; **PDBTitle:** crystal structure of protein smc04130 from sinorhizobium meliloti 1021
40	d1ydga_	Alignment	not modelled	13.8	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
41	c3o3cD_	Alignment	not modelled	13.4	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glycogen synthase basal state udp complex
42	d4pgaa_	Alignment	not modelled	13.0	11	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
43	d1vyba_	Alignment	not modelled	12.6	14	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
44	d1oi7a1	Alignment	not modelled	11.9	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
45	d1i60a_	Alignment	not modelled	11.4	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
46	d2abwa1	Alignment	not modelled	11.2	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
47	d1clib1	Alignment	not modelled	11.1	13	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
48	c2q8uA_	Alignment	not modelled	10.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
49	c2issF_	Alignment	not modelled	10.4	16	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
50	d2q02a1	Alignment	not modelled	10.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
51	d1z7da1	Alignment	not modelled	10.2	22	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
52	d1sffa_	Alignment	not modelled	10.0	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
53	c3ngoA_	Alignment	not modelled	9.9	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ccr4-not transcription complex subunit 6-like; **PDBTitle:** crystal structure of the human cnot6l nuclease domain in complex with2 poly(a) dna
54	d1xi3a_	Alignment	not modelled	9.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
55	c3tebA_	Alignment	not modelled	9.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase;

55	c3lebA_	Alignment	not modelled	9.4	10	**PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
56	d1jfla1	Alignment	not modelled	9.4	18	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
57	c3qxbB_	Alignment	not modelled	8.1	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative xylose isomerase; **PDBTitle:** crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
58	c3n0lA_	Alignment	not modelled	8.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine hydroxymethyltransferase; **PDBTitle:** crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
59	d2imqx1	Alignment	not modelled	7.8	20	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
60	d1nlfa_	Alignment	not modelled	7.6	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
61	c3bgwD_	Alignment	not modelled	7.6	5	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
62	c2ou4C_	Alignment	not modelled	7.5	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
63	c3nb0A_	Alignment	not modelled	7.4	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycogen [starch] synthase isoform 2; **PDBTitle:** glucose-6-phosphate activated form of yeast glycogen synthase
64	d2zoda1	Alignment	not modelled	7.3	6	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
65	d1f06a1	Alignment	not modelled	7.3	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c3t9aA_	Alignment	not modelled	7.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inositol pyrophosphate kinase; **PDBTitle:** crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
67	c2zsmA_	Alignment	not modelled	7.1	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate-1-semialdehyde 2,1-aminomutase; **PDBTitle:** crystal structure of glutamate-1-semialdehyde 2,1-2 aminomutase from aeropyrum pernix, hexagonal form
68	c1chmA_	Alignment	not modelled	7.1	15	**PDB header:**creatinase **Chain:** A: **PDB Molecule:**creatine amidinohydrolase; **PDBTitle:** enzymatic mechanism of creatine amidinohydrolase as deduced2 from crystal structures
69	c3pnxF_	Alignment	not modelled	7.0	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
70	c3bh0A_	Alignment	not modelled	6.8	5	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
71	c3iacA_	Alignment	not modelled	6.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucuronate isomerase; **PDBTitle:** 2.2 angstrom crystal structure of glucuronate isomerase from2 salmonella typhimurium.
72	d2z1ea1	Alignment	not modelled	6.4	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
73	c2rb9D_	Alignment	not modelled	6.3	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hype protein; **PDBTitle:** crystal structure of e.coli hype
74	c2wltA_	Alignment	not modelled	6.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
75	c1e9nB_	Alignment	not modelled	6.2	7	**PDB header:**dna repair **Chain:** B: **PDB Molecule:**dna-(apurinic or apyrimidinic site) lyase; **PDBTitle:** a second divalent metal ion in the active site of a new2 crystal form of human apurinic/apyrimidinic endonuclease,3 ape1, and its implications for the catalytic mechanism
76	d2zaua1	Alignment	not modelled	6.2	8	**Fold:**Bacillus chorismate mutase-like **Superfamily:**PurM N-terminal domain-like **Family:**PurM N-terminal domain-like
77	c2exuA_	Alignment	not modelled	6.0	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription initiation protein spt4/spt5; **PDBTitle:** crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
78	c1vqvB_	Alignment	not modelled	6.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thiamine monophosphate kinase; **PDBTitle:** crystal structure of thiamine monophosphate kinase (thil)2 from aquifex aeolicus
79	d1muwa_	Alignment	not modelled	6.0	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
80	c2i63B_	Alignment	not modelled	5.9	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ap-endonuclease;

80	c2j63B_	Alignment	not modelled	5.9	17	**PDBTitle:** crystal structure of ap endonuclease lmap from leishmania2 major
81	c3dx5A_	Alignment	not modelled	5.7	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
82	c3gfgB_	Alignment	not modelled	5.4	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
83	c1ezaA_	Alignment	not modelled	5.4	9	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
84	c3cwcB_	Alignment	not modelled	5.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
85	c3tr9A_	Alignment	not modelled	5.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
86	d1prxa_	Alignment	not modelled	5.1	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like