Phyre2

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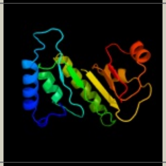
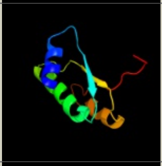
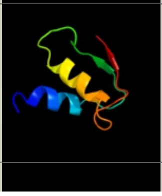
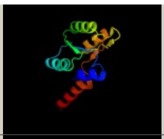
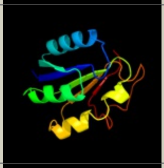
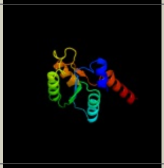
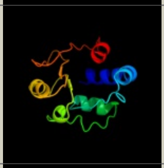
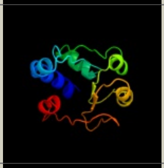
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z1dA_	Alignment		100.0	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hydrogenase expression/formation protein hypd; **PDBTitle:** crystal structure of [nife] hydrogenase maturation protein, hypd from2 thermococcus kodakaraensis
2	d7reqa2	Alignment		95.1	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
3	d1gqna_	Alignment		90.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
4	c3bicA_	Alignment		88.5	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase, mitochondrial precursor; **PDBTitle:** crystal structure of human methylmalonyl-coa mutase
5	c2yxbA_	Alignment		87.1	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
6	c2k8sA_	Alignment		86.4	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europea: northeast structural3 genomics target net6
7	c3l2iB_	Alignment		86.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.85 angstrom crystal structure of the 3-dehydroquinate dehydratase2 (arod) from salmonella typhimurium lt2.
8	c3js3C_	Alignment		83.9	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
9	c2yr1B_	Alignment		81.5	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of 3-dehydroquinate dehydratase from geobacillus2 kaustophilus hta426
10	c2q5cA_	Alignment		78.1	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
11	d1poib_	Alignment		73.5	22	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like

12	c2pjuD_	Alignment		72.4	13	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
13	d1ccwa_	Alignment		70.8	14	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
14	d2pjua1	Alignment		69.8	13	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
15	c3fldA_	Alignment		67.4	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** crystal structure of the trai c-terminal domain
16	d1oaoa_	Alignment		61.7	17	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
17	c1e1cA_	Alignment		60.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylmalonyl-coa mutase alpha chain; **PDBTitle:** methylmalonyl-coa mutase h244a mutant
18	d1su7a_	Alignment		60.3	13	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
19	c1jqkE_	Alignment		56.6	15	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase; **PDBTitle:** crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
20	c3lteH_	Alignment		55.9	13	**PDB header:**transcription **Chain:** H: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator (signal receiver domain) from2 bermanella marisrubri
21	d2pl1a1	Alignment	not modelled	54.1	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
22	d1jqka_	Alignment	not modelled	54.1	15	**Fold:**Prismane protein-like **Superfamily:**Prismane protein-like **Family:**Carbon monoxide dehydrogenase
23	d1sfla_	Alignment	not modelled	53.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
24	c2axoA_	Alignment	not modelled	53.1	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein atu2684; **PDBTitle:** x-ray crystal structure of protein agr_c_4864 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr35.
25	d2fug61	Alignment	not modelled	49.0	28	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
26	d1iloa_	Alignment	not modelled	45.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
27	d1olta_	Alignment	not modelled	44.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
28	c1e5dA_	Alignment	not modelled	43.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
29	c1e5lA_	Alignment	not modelled	42.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase;

						PDBTitle: apo saccharopine reductase from magnaporthe grisea
30	d2axoa1	Alignment	not modelled	40.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Atu2684-like
31	c3gt7A_	Alignment	not modelled	39.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
32	c2qs0A_	Alignment	not modelled	38.6	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**quinolinate synthetase a; **PDBTitle:** quinolinate synthase from pyrococcus furiosus
33	d1rjda_	Alignment	not modelled	36.2	27	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Leucine carboxy methyltransferase Ppm1
34	d1mb6a_	Alignment	not modelled	36.0	31	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
35	d1niya_	Alignment	not modelled	35.9	46	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
36	c3c3mA_	Alignment	not modelled	35.8	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of the n-terminal domain of response regulator2 receiver protein from methanoculleus marisnigri jr1
37	d1fmfa_	Alignment	not modelled	34.6	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
38	d1mvoa_	Alignment	not modelled	34.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
39	c2jk1A_	Alignment	not modelled	33.3	12	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**hydrogenase transcriptional regulatory protein hupr1; **PDBTitle:** crystal structure of the wild-type hupr receiver domain
40	d1nixa_	Alignment	not modelled	32.9	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
41	c2zayA_	Alignment	not modelled	32.8	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator from desulfuromonas2 acetoxidans
42	c3cnbC_	Alignment	not modelled	32.7	14	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna-binding response regulator, merr family; **PDBTitle:** crystal structure of signal receiver domain of dna binding response2 regulator protein (merr) from colwellia psychrerythraea 34h
43	d1mxsa_	Alignment	not modelled	32.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
44	d2pw9a1	Alignment	not modelled	31.1	10	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**FdhD/NarQ
45	d2dvta1	Alignment	not modelled	30.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**PP1699/LP2961-like
46	d1zesa1	Alignment	not modelled	29.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
47	d1i5ea_	Alignment	not modelled	29.0	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
48	d1wyza1	Alignment	not modelled	28.9	17	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
49	d1xcfa_	Alignment	not modelled	27.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
50	c3bo9B_	Alignment	not modelled	27.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nitroalkan dioxygenase; **PDBTitle:** crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
51	d2c4va1	Alignment	not modelled	27.1	14	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
52	d1dcfa_	Alignment	not modelled	27.1	13	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
53	d1efpb_	Alignment	not modelled	26.9	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
54	c1iclA_	Alignment	not modelled	26.5	100	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
55	c3h31A_	Alignment	not modelled	26.4	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**high potential iron-sulfur protein; **PDBTitle:** structure of rhodothermus marinus hipip at 1.0 a resolution
						PDB header:oxidoreductase

56	c3bw2A_	Alignment	not modelled	26.1	16	**Chain:** A: **PDB Molecule:**2-nitropropane dioxygenase; **PDBTitle:** crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
57	c2nt3A_	Alignment	not modelled	24.4	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator homolog; **PDBTitle:** receiver domain from myxococcus xanthus social motility protein frzs2 (y102a mutant)
58	d1xtta1	Alignment	not modelled	24.0	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
59	c2qzjC_	Alignment	not modelled	23.8	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of a two-component response regulator from2 clostridium difficile
60	c3ktoA_	Alignment	not modelled	23.7	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulator receiver protein; **PDBTitle:** crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
61	c2e55D_	Alignment	not modelled	23.6	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
62	c3epmB_	Alignment	not modelled	23.4	38	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**thiamine biosynthesis protein thic; **PDBTitle:** crystal structure of caulobacter crescentus thic
63	d1v9sa1	Alignment	not modelled	22.7	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
64	c2p2vA_	Alignment	not modelled	22.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-2,3-sialyltransferase; **PDBTitle:** crystal structure analysis of monofunctional alpha-2,3-2 sialyltransferase cst-i from campylobacter jejuni
65	d1o58a_	Alignment	not modelled	22.3	22	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
66	c2o7qA_	Alignment	not modelled	22.3	16	**PDB header:**oxidoreductase,transferase **Chain:** A: **PDB Molecule:**bifunctional 3-dehydroquinate dehydratase/shikimate **PDBTitle:** crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
67	c1q68A_	Alignment	not modelled	20.5	47	**PDB header:**membrane protein/transferase **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
68	c1e8cB_	Alignment	not modelled	20.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamate--2,6- **PDBTitle:** structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
69	c2jtbA_	Alignment	not modelled	20.1	42	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hainantoxin-3; **PDBTitle:** three dimensional solution structure of hainantoxin-iii by2 2d 1h-nmr
70	c3o3nB_	Alignment	not modelled	20.1	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
71	d7odca2	Alignment	not modelled	20.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
72	c2oczA_	Alignment	not modelled	19.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** the structure of a putative 3-dehydroquinate dehydratase from2 streptococcus pyogenes.
73	c3kwpA_	Alignment	not modelled	19.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**predicted methyltransferase; **PDBTitle:** crystal structure of putative methyltransferase from lactobacillus2 brevis
74	c2g40A_	Alignment	not modelled	19.5	4	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
75	d2g40a1	Alignment	not modelled	19.5	4	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**YkgG-like
76	d1uqra_	Alignment	not modelled	19.4	16	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
77	d1gtza_	Alignment	not modelled	19.2	20	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
78	c2qsjB_	Alignment	not modelled	19.0	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-binding response regulator, luxr family; **PDBTitle:** crystal structure of a luxr family dna-binding response2 regulator from silicibacter pomeroyi
79	c3hdgE_	Alignment	not modelled	19.0	13	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinella3 succinogenes
80	d1k3sa_	Alignment	not modelled	18.5	19	**Fold:**Secretion chaperone-like **Superfamily:**Type III secretory system chaperone-like **Family:**Type III secretory system chaperone
						PDB header:oxidoreductase

81	c3ju3A_	Alignment	not modelled	18.1	13	**Chain:** A: **PDB Molecule:**probable 2-oxoacid ferredoxin oxidoreductase, alpha chain; **PDBTitle:** crystal structure of alpha chain of probable 2-oxoacid ferredoxin2 oxidoreductase from thermoplasma acidophilum
82	c2iv0A_	Alignment	not modelled	17.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
83	c2fgxA_	Alignment	not modelled	17.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
84	d3clsc1	Alignment	not modelled	17.3	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
85	c2nvwB_	Alignment	not modelled	17.2	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
86	c3kcnA_	Alignment	not modelled	17.1	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**adenylate cyclase homolog; **PDBTitle:** the crystal structure of adenylate cyclase from2 rhodopirellula baltica
87	d1s4da_	Alignment	not modelled	16.6	15	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
88	d1o5oa_	Alignment	not modelled	16.5	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
89	c3shoA_	Alignment	not modelled	16.4	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, rpir family; **PDBTitle:** crystal structure of rpir transcription factor from sphaerobacter2 thermophilus (sugar isomerase domain)
90	d1j6ua2	Alignment	not modelled	16.2	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
91	c2yswB_	Alignment	not modelled	16.1	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
92	c3myrE_	Alignment	not modelled	16.0	23	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**hydrogenase (nife) small subunit hyda; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
93	d1ey1a_	Alignment	not modelled	15.8	16	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
94	c3h5iA_	Alignment	not modelled	15.7	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator/sensory box protein/ggdef **PDBTitle:** crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3 carboxydothermus hydrogenoformans
95	c3hdvB_	Alignment	not modelled	15.6	15	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** crystal structure of response regulator receiver protein from2 pseudomonas putida
96	d1e8ca2	Alignment	not modelled	15.5	17	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
97	d2bb3a1	Alignment	not modelled	15.2	20	**Fold:**Tetrapyrrole methylase **Superfamily:**Tetrapyrrole methylase **Family:**Tetrapyrrole methylase
98	d1l0sa_	Alignment	not modelled	15.0	63	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**An insect antifreeze protein **Family:**An insect antifreeze protein
99	c1o5zA_	Alignment	not modelled	14.9	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution