Phyre^2

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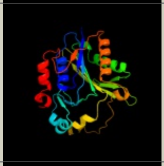
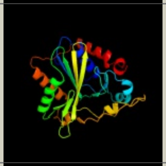
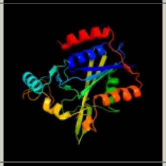
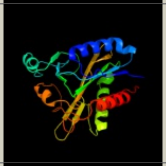
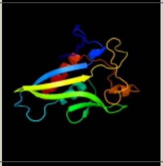
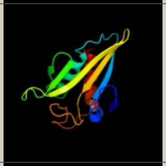
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x2gB_	Alignment		100.0	96	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lipoate-protein ligase a; **PDBTitle:** crystal structure of lipate-protein ligase a from2 escherichia coli
2	c1vqzA_	Alignment		100.0	31	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoate-protein ligase, putative; **PDBTitle:** crystal structure of a putative lipoate-protein ligase a (sp_1160)2 from streptococcus pneumoniae tigr4 at 1.99 a resolution
3	c2e5aA_	Alignment		100.0	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lipoyltransferase 1; **PDBTitle:** crystal structure of bovine lipoyltransferase in complex2 with lipoyl-amp
4	d1x2ga2	Alignment		100.0	99	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
5	d1vqza2	Alignment		100.0	36	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
6	d2c8ma1	Alignment		100.0	30	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
7	d2p5ia1	Alignment		100.0	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
8	d2p0la1	Alignment		100.0	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like
9	c2qhsA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
10	c2qhvA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoyltransferase; **PDBTitle:** structural basis of octanoic acid recognition by lipoate-protein2 ligase b
11	d1w66a1	Alignment		100.0	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**LplA-like

12	d1x2ga1	Alignment		99.9	98	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
13	d1vqza1	Alignment		99.8	18	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**SP1160 C-terminal domain-like
14	c2eayB_	Alignment		97.8	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin [acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from aquifex2 aeolicus
15	d2zgwa2	Alignment		97.8	19	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Biotin holoenzyme synthetase
16	c2ej9A_	Alignment		97.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative biotin ligase; **PDBTitle:** crystal structure of biotin protein ligase from2 methanococcus jannaschii
17	c2ewnA_	Alignment		97.4	18	**PDB header:**ligase, transcription **Chain:** A: **PDB Molecule:**bira bifunctional protein; **PDBTitle:** ecoli biotin repressor with co-repressor analog
18	c3bfmA_	Alignment		97.2	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**biotin protein ligase-like protein of unknown function; **PDBTitle:** crystal structure of a biotin protein ligase-like protein of unknown2 function (tm1040_0394) from silicibacter sp. tm1040 at 1.70 a3 resolution
19	c2dzcA_	Alignment		96.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin--[acetyl-coa-carboxylase] ligase; **PDBTitle:** crystal structure of biotin protein ligase from pyrococcus2 horikoshii, mutation r48a
20	c2cghB_	Alignment		96.6	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin ligase; **PDBTitle:** crystal structure of biotin ligase from mycobacterium2 tuberculosis
21	d1biaa3	Alignment	not modelled	95.4	23	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Biotin holoenzyme synthetase
22	c2qq4A_	Alignment	not modelled	90.5	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**iron-sulfur cluster biosynthesis protein iscu; **PDBTitle:** crystal structure of iron-sulfur cluster biosynthesis2 protein iscu (ttha1736) from thermus thermophilus hb8
23	d1t3qc1	Alignment	not modelled	84.0	9	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
24	d1jroa3	Alignment	not modelled	82.9	18	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
25	d1n62c1	Alignment	not modelled	80.1	14	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
26	d1ffvc1	Alignment	not modelled	80.1	16	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
27	d1v97a4	Alignment	not modelled	74.7	11	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like
28	d1rm6b1	Alignment	not modelled	73.7	17	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**CO dehydrogenase flavoprotein C-terminal domain-like **Family:**CO dehydrogenase flavoprotein C-terminal domain-like

29	c2w3rG_	Alignment	not modelled	67.0	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
30	d1knxa1	Alignment	not modelled	64.6	7	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
31	d1xjsa_	Alignment	not modelled	54.2	7	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
32	d1ko7a1	Alignment	not modelled	51.1	18	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
33	c1ybxA_	Alignment	not modelled	49.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** conserved hypothetical protein cth-383 from clostridium thermocellum
34	c3hrdC_	Alignment	not modelled	49.7	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
35	d1su0b_	Alignment	not modelled	48.1	10	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
36	c1knxF_	Alignment	not modelled	46.9	7	**PDB header:**transferase/hydrolase **Chain:** F: **PDB Molecule:**probable hpr(ser) kinase/phosphatase; **PDBTitle:** hpr kinase/phosphatase from mycoplasma pneumoniae
37	c1ko7B_	Alignment	not modelled	46.8	17	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution
38	d1yq9h1	Alignment	not modelled	46.6	25	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
39	d2brfa1	Alignment	not modelled	44.5	19	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
40	c2z7eB_	Alignment	not modelled	44.4	17	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
41	d1e3db_	Alignment	not modelled	43.3	18	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
42	d1cc1l_	Alignment	not modelled	43.3	19	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
43	d1frfl_	Alignment	not modelled	42.9	20	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
44	c1rm6E_	Alignment	not modelled	40.9	20	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
45	d1wuil1	Alignment	not modelled	40.3	21	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
46	d2ddza1	Alignment	not modelled	38.5	27	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**PH0223-like
47	c2grvC_	Alignment	not modelled	37.5	9	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**lpqw; **PDBTitle:** crystal structure of lpqw
48	c3myrB_	Alignment	not modelled	35.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nickel-dependent hydrogenase large subunit; **PDBTitle:** crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
49	d2a1ja1	Alignment	not modelled	34.9	20	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
50	c1ffuF_	Alignment	not modelled	33.0	18	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
51	c1t3qF_	Alignment	not modelled	32.6	8	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
52	c3o6uB_	Alignment	not modelled	32.4	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein cpe2226; **PDBTitle:** crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195
53	c3ry3B_	Alignment	not modelled	31.5	9	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**putative solute-binding protein; **PDBTitle:** putative solute-binding protein from yersinia pestis.
54	d1xoca1	Alignment	not modelled	31.2	17	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II

						Family: Phosphate binding protein-like
55	c3lvuB_	Alignment	not modelled	29.1	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
56	c2kzxA_	Alignment	not modelled	27.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a3dht5 from clostridium thermocellum,2 northeast structural genomics consortium target cmr116
57	d1u07a_	Alignment	not modelled	27.3	15	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
58	c1h2aL_	Alignment	not modelled	26.3	22	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**hydrogenase; **PDBTitle:** single crystals of hydrogenase from desulfovibrio vulgaris
59	d1p30a1	Alignment	not modelled	25.0	15	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Adenovirus hexon
60	c3uotB_	Alignment	not modelled	24.5	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
61	d1zlqa1	Alignment	not modelled	23.5	9	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
62	c2o7jA_	Alignment	not modelled	22.8	12	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic **PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose
63	c2kklA_	Alignment	not modelled	22.4	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
64	d1wh9a_	Alignment	not modelled	22.3	14	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Prokaryotic type KH domain (KH-domain type II) **Family:**Prokaryotic type KH domain (KH-domain type II)
65	c2wpnB_	Alignment	not modelled	22.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase2 from d. vulgaris hildenborough
66	c1n62C_	Alignment	not modelled	21.7	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
67	d1puga_	Alignment	not modelled	21.3	14	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
68	d1r9pa_	Alignment	not modelled	20.2	17	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
69	c2k9kA_	Alignment	not modelled	17.1	16	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**tonb2; **PDBTitle:** molecular characterization of the tonb2 protein from vibrio2 anguillarum
70	c3iz5s_	Alignment	not modelled	17.0	12	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l18a (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
71	d2gskb1	Alignment	not modelled	16.9	15	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
72	c3izcs_	Alignment	not modelled	16.3	16	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
73	c1wygA_	Alignment	not modelled	16.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
74	d1j8ba_	Alignment	not modelled	16.0	16	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
75	c1ztyA_	Alignment	not modelled	15.9	13	**PDB header:**sugar binding protein, signaling protein **Chain:** A: **PDB Molecule:**chitin oligosaccharide binding protein; **PDBTitle:** crystal structure of the chitin oligasaccharide binding2 protein
76	c2hw4A_	Alignment	not modelled	14.9	15	**PDB header:**structural genomics, hydrolase **Chain:** A: **PDB Molecule:**14 kda phosphohistidine phosphatase; **PDBTitle:** crystal structure of human phosphohistidine phosphatase
77	c2vqzB_	Alignment	not modelled	14.5	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**polymerase basic protein 2; **PDBTitle:** structure of the cap-binding domain of influenza virus2 polymerase subunit pb2 with bound m7gtp
78	d1pugb_	Alignment	not modelled	14.3	14	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
						PDB header:oxidoreductase

79	c2a5wC_	Alignment	not modelled	14.2	10	**Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma **PDBTitle:** crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
80	d1f0xa2	Alignment	not modelled	14.2	7	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
81	d2hw4a1	Alignment	not modelled	13.9	15	**Fold:**PHP14-like **Superfamily:**PHP14-like **Family:**Janus/Ocnus
82	c1vjqB_	Alignment	not modelled	13.9	19	**PDB header:**structural genomics, de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
83	d2gmha2	Alignment	not modelled	13.7	17	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**Electron transfer flavoprotein-ubiquinone oxidoreductase-like
84	c2jpeA_	Alignment	not modelled	13.7	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear inhibitor of protein phosphatase 1; **PDBTitle:** fha domain of nipp1
85	d1wfza_	Alignment	not modelled	13.3	22	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
86	c3t66A_	Alignment	not modelled	12.6	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
87	d1yjma1	Alignment	not modelled	12.3	18	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
88	c2kzwA_	Alignment	not modelled	12.1	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of q8psa4 from methanosarcina mazei, northeast2 structural genomics consortium target mar143a
89	c3ftoA_	Alignment	not modelled	11.8	10	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**oligopeptide-binding protein oppa; **PDBTitle:** crystal structure of oppa in a open conformation
90	d2ji7a1	Alignment	not modelled	11.6	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
91	c2x8xX_	Alignment	not modelled	11.1	21	**PDB header:**chaperone **Chain:** X: **PDB Molecule:**tlr1789 protein; **PDBTitle:** structure of the n-terminal domain of omp85 from the2 thermophilic cyanobacterium thermosynechococcus elongatus
92	d1b4ra_	Alignment	not modelled	11.0	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**PKD domain **Family:**PKD domain
93	d2q4ma1	Alignment	not modelled	10.9	15	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**At5g01750-like
94	c1zxuA_	Alignment	not modelled	10.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g01750 protein; **PDBTitle:** x-ray structure of protein from arabidopsis thaliana2 at5g01750
95	c2pmyB_	Alignment	not modelled	10.6	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ras and ef-hand domain-containing protein; **PDBTitle:** ef-hand domain of human rasef
96	c2grxC_	Alignment	not modelled	10.5	16	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
97	c3dclC_	Alignment	not modelled	10.3	27	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**tm1086; **PDBTitle:** crystal structure of tm1086
98	c1yj5C_	Alignment	not modelled	10.2	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
99	d2ihta1	Alignment	not modelled	9.5	12	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain