Phyre2

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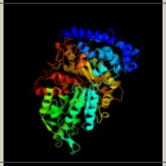
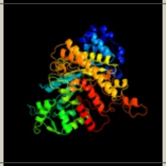
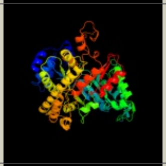
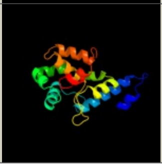
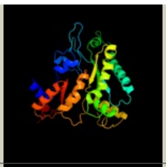
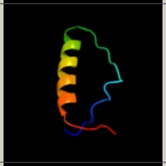
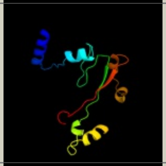
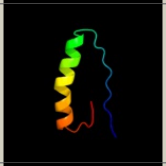
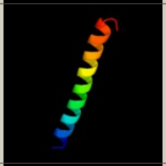
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pemA_	Alignment		100.0	90	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase 2 alpha **PDBTitle:** ribonucleotide reductase protein r1e from salmonella2 typhimurium
2	c3r1rB_	Alignment		100.0	23	**PDB header:**complex (oxidoreductase/peptide) **Chain:** B: **PDB Molecule:**ribonucleotide reductase r1 protein; **PDBTitle:** ribonucleotide reductase r1 protein with amppnp occupying2 the activity site from escherichia coli
3	c2wghA_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large **PDBTitle:** human ribonucleotide reductase r1 subunit (rrm1) in complex2 with datp and mg.
4	c3hnfA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large subunit; **PDBTitle:** crystal structure of human ribonucleotide reductase 1 bound to the2 effectors ttp and datp
5	c2cvuA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleoside-diphosphate reductase large chain **PDBTitle:** structures of yeast ribonucleotide reductase i
6	c1xjeA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribonucleotide reductase, b12-dependent; **PDBTitle:** structural mechanism of allosteric substrate specificity in a2 ribonucleotide reductase: dttp-gdp complex
7	d1rlra2	Alignment		100.0	26	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
8	d1peqa2	Alignment		100.0	91	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**R1 subunit of ribonucleotide reductase, C-terminal domain
9	d1l1la_	Alignment		100.0	19	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**B12-dependent (class II) ribonucleotide reductase
10	d1peqa1	Alignment		100.0	85	**Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain **Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain **Family:**R1 subunit of ribonucleotide reductase, N-terminal domain
11	d1rlra1	Alignment		100.0	14	**Fold:**R1 subunit of ribonucleotide reductase, N-terminal domain **Superfamily:**R1 subunit of ribonucleotide reductase, N-terminal domain **Family:**R1 subunit of ribonucleotide reductase, N-terminal domain

12	d1hk8a_	Alignment		95.0	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
13	c1hk8A_	Alignment		95.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
14	d1h16a_	Alignment		76.3	14	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
15	c3pg6D_	Alignment		53.3	25	**PDB header:**ligase **Chain:** D: **PDB Molecule:**e3 ubiquitin-protein ligase dtx3l; **PDBTitle:** the carboxyl terminal domain of human deltex 3-like
16	d1qhma_	Alignment		32.3	14	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
17	d2okqa1	Alignment		29.1	19	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YbaA-like
18	d1geqa_	Alignment		27.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
19	d1h3ob_	Alignment		22.9	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
20	d2ccqa1	Alignment		22.4	16	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
21	c2okqB_	Alignment	not modelled	20.1	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ybaa; **PDBTitle:** crystal structure of unknown conserved ybaa protein from2 shigella flexneri
22	d1jlia_	Alignment	not modelled	15.7	22	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
23	d1msza_	Alignment	not modelled	13.8	17	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
24	c1mszA_	Alignment	not modelled	13.8	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
25	d2b4va2	Alignment	not modelled	12.7	44	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**RNA editing terminal uridyl transferase 2, RET2, catalytic domain
26	c3pe0B_	Alignment	not modelled	12.7	24	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**plectin; **PDBTitle:** structure of the central region of the plakin domain of plectin
27	d1v93a_	Alignment	not modelled	12.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FAD-linked oxidoreductase **Family:**Methylenetetrahydrofolate reductase
28	c1pgjA_	Alignment	not modelled	12.0	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
						Fold: Four-helical up-and-down bundle

29	d1v74b_	Alignment	not modelled	11.6	18	**Superfamily:**Colicin D immunity protein **Family:**Colicin D immunity protein
30	d1vkna2	Alignment	not modelled	10.9	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
31	c2iz1C_	Alignment	not modelled	10.9	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
32	d1ic8a2	Alignment	not modelled	10.8	16	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**POU-specific domain
33	c3rcqA_	Alignment	not modelled	10.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartyl/asparaginyl beta-hydroxylase; **PDBTitle:** crystal structure of human aspartate beta-hydroxylase isoform a
34	c2v3sB_	Alignment	not modelled	10.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase osr1; **PDBTitle:** structural insights into the recognition of substrates and2 activators by the osr1 kinase
35	d2uyoa1	Alignment	not modelled	10.3	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**ML2640-like
36	d1vmha_	Alignment	not modelled	10.2	10	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
37	c2f3oB_	Alignment	not modelled	10.1	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyruvate formate-lyase 2; **PDBTitle:** crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus
38	d1vmfa_	Alignment	not modelled	9.7	10	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
39	c2p4qA_	Alignment	not modelled	9.5	44	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating 1; **PDBTitle:** crystal structure analysis of gnd1 in saccharomyces cerevisiae
40	c3fwnB_	Alignment	not modelled	9.2	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
41	d1vmja_	Alignment	not modelled	9.2	20	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
42	d1j09a2	Alignment	not modelled	8.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
43	d2d5ua1	Alignment	not modelled	8.6	16	**Fold:**PUG domain-like **Superfamily:**PUG domain-like **Family:**PUG domain
44	c2p6hB_	Alignment	not modelled	8.2	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
45	d1r9da_	Alignment	not modelled	7.7	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
46	d1gv2a2	Alignment	not modelled	7.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
47	c1pgqA_	Alignment	not modelled	7.6	39	**PDB header:**oxidoreductase (choh(d)-nadp+(a)) **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
48	c1idzA_	Alignment	not modelled	7.3	21	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**mouse c-myb dna-binding domain repeat 3; **PDBTitle:** structure of myb transforming protein, nmr, 20 structures
49	c2xrgA_	Alignment	not modelled	7.2	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ectonucleotide pyrophosphatase/phosphodiesterase family **PDBTitle:** crystal structure of autotaxin (enpp2) in complex with the2 ha155 boronic acid inhibitor
50	d1wiga2	Alignment	not modelled	7.2	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
51	d2d0ob1	Alignment	not modelled	7.1	16	**Fold:**Anticodon-binding domain-like **Superfamily:**B12-dependent dehydatase associated subunit **Family:**Dehydratase-reactivating factor beta subunit
52	c2p6cB_	Alignment	not modelled	6.9	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**aq_2013 protein; **PDBTitle:** crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
53	c3ng3A_	Alignment	not modelled	6.9	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of deoxyribose phosphate aldolase from mycobacterium2 avium 104 in a schiff base with an unknown aldehyde
						Fold:SAM domain-like

54	d2csba2	Alignment	not modelled	6.8	42	**Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
55	c3hm6X_	Alignment	not modelled	6.8	16	**PDB header:**signaling protein **Chain:** X: **PDB Molecule:**plexin-b1; **PDBTitle:** crystal structure of the cytoplasmic domain of human plexin b1
56	d2b3wa1	Alignment	not modelled	6.6	20	**Fold:**YbiA-like **Superfamily:**YbiA-like **Family:**YbiA-like
57	c2qlwA_	Alignment	not modelled	6.4	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
58	c2qlxA_	Alignment	not modelled	6.4	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
59	d1vpha_	Alignment	not modelled	6.3	16	**Fold:**YjbQ-like **Superfamily:**YjbQ-like **Family:**YjbQ-like
60	c2c1fA_	Alignment	not modelled	6.3	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bifunctional endo-1,4-beta-xylanase a; **PDBTitle:** the structure of the family 11 xylanase from neocallimastix2 patriciarum
61	d2g5ca2	Alignment	not modelled	6.2	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c3dzbA_	Alignment	not modelled	6.0	32	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
63	d1f0ya2	Alignment	not modelled	6.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
64	c3a9lB_	Alignment	not modelled	6.0	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
65	c2is9A_	Alignment	not modelled	5.9	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**defective in cullin neddylation protein 1; **PDBTitle:** structure of yeast dcn-1
66	d1mbja_	Alignment	not modelled	5.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
67	c1mbjA_	Alignment	not modelled	5.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**myb proto-oncogene protein; **PDBTitle:** mouse c-myb dna-binding domain repeat 3
68	c1obfO_	Alignment	not modelled	5.8	19	**PDB header:**glycolytic pathway **Chain:** O: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylosoxidans at 1.73 resolution.
69	d1k3ta2	Alignment	not modelled	5.7	22	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
70	d1jfla1	Alignment	not modelled	5.7	32	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
71	d1h4ga_	Alignment	not modelled	5.6	24	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
72	d1f5ja_	Alignment	not modelled	5.6	29	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
73	c2jr7A_	Alignment	not modelled	5.6	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**dph3 homolog; **PDBTitle:** solution structure of human desr1
74	c3ivuB_	Alignment	not modelled	5.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
75	c3iymA_	Alignment	not modelled	5.6	20	**PDB header:**virus **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** backbone trace of the capsid protein dimer of a fungal partitivirus2 from electron cryomicroscopy and homology modeling
76	d1x8da1	Alignment	not modelled	5.5	27	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
77	d1te1b_	Alignment	not modelled	5.4	29	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
78	d1m4wa_	Alignment	not modelled	5.4	29	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
79	d1wgea1	Alignment	not modelled	5.4	23	**Fold:**Rubredoxin-like **Superfamily:**CSL zinc finger **Family:**CSL zinc finger
80	d2awia2	Alignment	not modelled	5.4	10	**Fold:**alpha-alpha superhelix **Superfamily:**TPR-like **Family:**PrgX C-terminal domain-like

81	d1xyna_	Alignment	not modelled	5.4	24	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
82	c2dcjA_	Alignment	not modelled	5.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**xylanase j; **PDBTitle:** a two-domain structure of alkaliphilic xynj from bacillus sp. 41m-1
83	c2g5cD_	Alignment	not modelled	5.2	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
84	c2kzuA_	Alignment	not modelled	5.2	31	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death-associated protein 6; **PDBTitle:** daxx helical bundle (dhb) domain / rassf1c complex
85	d1t6gc_	Alignment	not modelled	5.1	18	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
86	d1xi8a3	Alignment	not modelled	5.1	28	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
87	d1at3a_	Alignment	not modelled	5.1	40	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
88	d1igoa_	Alignment	not modelled	5.1	18	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Xylanase/endoglucanase 11/12
89	c2p6uA_	Alignment	not modelled	5.1	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
90	c2pv7B_	Alignment	not modelled	5.0	28	**PDB header:**isomerase, oxidoreductase **Chain:** B: **PDB Molecule:**t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) **PDBTitle:** crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution