Phyre^2

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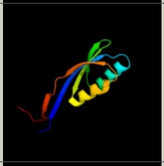
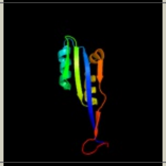
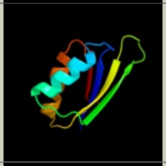
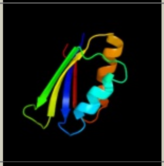
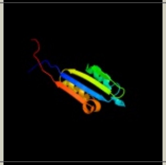
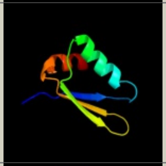
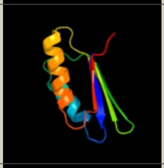
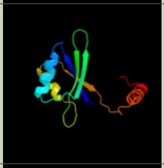
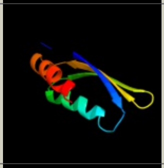
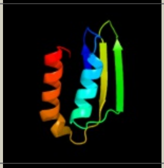
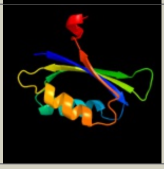
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pc6C_	Alignment		100.0	57	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
2	c2f1fA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
3	c2fgcA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
4	d2f1fa2	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
5	d2fgca2	Alignment		100.0	44	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
6	d2pc6a1	Alignment		100.0	52	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
7	d2pc6a2	Alignment		100.0	62	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
8	d2f1fa1	Alignment		100.0	100	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
9	d2fgca1	Alignment		100.0	33	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
10	d2f06a2	Alignment		99.5	25	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
11	d1sc6a3	Alignment		99.3	23	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain

12	d1ygya3	Alignment		99.2	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
13	c3ibwA_	Alignment		98.8	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gtp pyrophosphokinase; **PDBTitle:** crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
14	c2f06B_	Alignment		98.3	22	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
15	c1ygyA_	Alignment		97.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
16	c2nyiB_	Alignment		97.7	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**unknown protein; **PDBTitle:** crystal structure of an unknown protein from galdieria2 sulphuraria
17	d1u8sa1	Alignment		97.4	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
18	d1u8sa2	Alignment		97.4	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Glycine cleavage system transcriptional repressor
19	d1zpva1	Alignment		97.4	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**SP0238-like
20	c1y7pB_	Alignment		97.3	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein af1403; **PDBTitle:** 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
21	c3n0vD_	Alignment	not modelled	97.2	7	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
22	d2qmwa2	Alignment	not modelled	97.2	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
23	c1ybaC_	Alignment	not modelled	97.1	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
24	c3mwbA_	Alignment	not modelled	97.1	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
25	c2qmxB_	Alignment	not modelled	97.0	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum tls
26	c3nrbD_	Alignment	not modelled	97.0	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (puru,2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
27	c1u8sB_	Alignment	not modelled	97.0	11	**PDB header:**transcription **Chain:** B: **PDB Molecule:**glycine cleavage system transcriptional **PDBTitle:** crystal structure of putative glycine cleavage system2 transcriptional repressor
28	c3luyA_	Alignment	not modelled	96.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis

29	c3mtjA_	Alignment	not modelled	96.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
30	c3k5pA_	Alignment	not modelled	96.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
31	c3obiC_	Alignment	not modelled	96.7	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
32	c2qmwA_	Alignment	not modelled	96.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
33	c3o1lB_	Alignment	not modelled	96.6	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
34	c3louB_	Alignment	not modelled	96.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase; **PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
35	d1phza1	Alignment	not modelled	96.5	24	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
36	d2f06a1	Alignment	not modelled	96.2	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**BT0572-like
37	c2dtjA_	Alignment	not modelled	95.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
38	c2re1A_	Alignment	not modelled	95.2	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase, alpha and beta subunits; **PDBTitle:** crystal structure of aspartokinase alpha and beta subunits
39	d2hmfa3	Alignment	not modelled	94.2	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
40	c2zhoB_	Alignment	not modelled	93.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
41	d2nzca1	Alignment	not modelled	93.5	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
42	d2cdqa2	Alignment	not modelled	92.8	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
43	c3mahA_	Alignment	not modelled	92.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartokinase; **PDBTitle:** a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
44	d2hmfa2	Alignment	not modelled	91.6	22	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
45	c3l76B_	Alignment	not modelled	90.6	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
46	c1tdjA_	Alignment	not modelled	88.3	13	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
47	c2rjzA_	Alignment	not modelled	88.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pilo protein; **PDBTitle:** crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
48	d2j0wa2	Alignment	not modelled	87.4	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
49	d2cdqa3	Alignment	not modelled	85.5	20	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
50	c3ab4K_	Alignment	not modelled	84.9	15	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
51	c2phmA_	Alignment	not modelled	84.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
52	c3c1nA_	Alignment	not modelled	81.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
53	c2zw2B_	Alignment	not modelled	77.0	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**putative uncharacterized protein sts178; **PDBTitle:** crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)

54	c3mgjA_	Alignment	not modelled	76.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj1480; **PDBTitle:** crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
55	d3dhxa1	Alignment	not modelled	72.7	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
56	d2qswa1	Alignment	not modelled	69.8	19	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
57	c2cdqB_	Alignment	not modelled	69.7	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
58	d1gtda_	Alignment	not modelled	68.7	20	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
59	c2dgbA_	Alignment	not modelled	66.9	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein purs; **PDBTitle:** structure of thermus thermophilus purs in the p21 form
60	c3p96A_	Alignment	not modelled	66.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase serb; **PDBTitle:** crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
61	c2gv1A_	Alignment	not modelled	65.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** nmr solution structure of the acylphosphatase from2 eschaerichia coli
62	d2j0wa3	Alignment	not modelled	64.6	18	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
63	d1apsa_	Alignment	not modelled	62.9	16	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
64	d1urra_	Alignment	not modelled	54.4	13	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
65	c2j0wA_	Alignment	not modelled	52.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
66	d1w2ia_	Alignment	not modelled	51.3	13	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
67	d1tdja2	Alignment	not modelled	50.4	15	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
68	d1vq3a_	Alignment	not modelled	48.8	11	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
69	c1rwuA_	Alignment	not modelled	45.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
70	d1rwua_	Alignment	not modelled	45.8	15	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
71	d2acya_	Alignment	not modelled	42.3	14	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
72	d1o51a_	Alignment	not modelled	40.1	14	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
73	c2dclB_	Alignment	not modelled	36.7	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
74	d2qrra1	Alignment	not modelled	36.0	14	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**NIL domain-like
75	c3crnA_	Alignment	not modelled	34.3	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator receiver domain protein, chey-like; **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
76	d1t4aa_	Alignment	not modelled	30.5	13	**Fold:**PurS-like **Superfamily:**PurS-like **Family:**PurS subunit of FGAM synthetase
77	c1jqsC_	Alignment	not modelled	29.8	16	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**elongation factor g; **PDBTitle:** fitting of l11 protein and elongation factor g (domain g'2 and v) in the cryo-em map of e. coli 70s ribosome bound3 with ef-g and gmppcp, a nonhydrolysable gtp analog
78	c3br8A_	Alignment	not modelled	28.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
79	c2jrlA_	Alignment	not modelled	28.3	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** solution structure of the beryllofluoride-activated ntrc4 receiver2 domain dimer
						Fold: Ferredoxin-like

80	d1n0ua5	Alignment	not modelled	28.0	21	**Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
81	d1ln4a_	Alignment	not modelled	27.5	14	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
82	d1ulra_	Alignment	not modelled	27.1	16	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
83	c3i42A_	Alignment	not modelled	26.8	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey- **PDBTitle:** structure of response regulator receiver domain (chey-like)2 from methylobacillus flagellatus
84	c3cg4A_	Alignment	not modelled	26.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**response regulator receiver domain protein (chey-like); **PDBTitle:** crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
85	c3eodA_	Alignment	not modelled	24.5	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein hnr; **PDBTitle:** crystal structure of n-terminal domain of e. coli rssb
86	d1xjca_	Alignment	not modelled	24.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
87	d1jo0a_	Alignment	not modelled	23.6	11	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
88	c2dnrA_	Alignment	not modelled	23.2	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**synaptojanin-1; **PDBTitle:** solution structure of rna binding domain in synaptojanin 1
89	c2cveA_	Alignment	not modelled	22.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1053; **PDBTitle:** crystal structure of a conserved hypothetical protein tt1547 from2 thermus thermophilus hb8
90	d1zj8a1	Alignment	not modelled	22.6	22	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
91	c2bjeA_	Alignment	not modelled	22.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acylphosphatase; **PDBTitle:** acylphosphatase from sulfolobus solfataricus. monclinic p212 space group
92	d1qkka_	Alignment	not modelled	22.5	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
93	c3cfyA_	Alignment	not modelled	20.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative luxo repressor protein; **PDBTitle:** crystal structure of signal receiver domain of putative luxo2 repressor protein from vibrio parahaemolyticus
94	c2yx5A_	Alignment	not modelled	20.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0062 protein mj1593; **PDBTitle:** crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
95	d2a9pa1	Alignment	not modelled	19.6	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
96	d1ixra2	Alignment	not modelled	19.4	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA helicase RuvA subunit, N-terminal domain
97	d1dcfa_	Alignment	not modelled	19.3	12	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
98	d1rq8a_	Alignment	not modelled	19.3	23	**Fold:**IF3-like **Superfamily:**YhbY-like **Family:**YhbY-like
99	c2jsxA_	Alignment	not modelled	18.7	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein napd; **PDBTitle:** solution structure of the e. coli tat proofreading2 chaperone protein napd