Phyre^2

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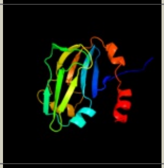
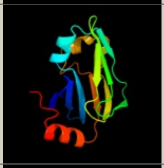
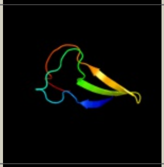
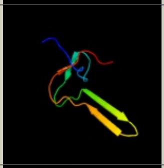
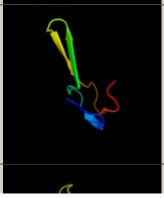
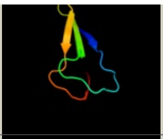
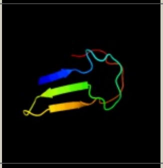
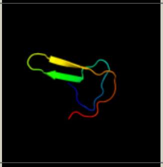
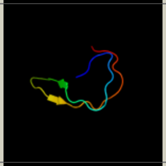
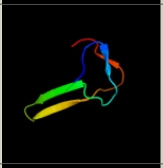
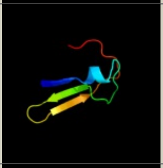
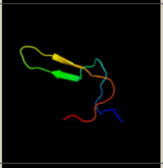
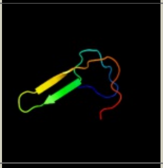
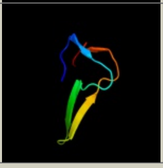
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a8jF_	Alignment		100.0	100	**PDB header:**transferase/transport protein **Chain:** F: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of et-ehred complex
2	c3iftA_	Alignment		100.0	48	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
3	d1onla_	Alignment		100.0	56	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
4	c2edgA_	Alignment		100.0	44	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** solution structure of the gcv_h domain from mouse glycine
5	d1hpca_	Alignment		100.0	50	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
6	c2ka7A_	Alignment		100.0	57	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** nmr solution structure of tm0212 at 40 c
7	c3mxuA_	Alignment		100.0	53	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycine cleavage system h protein; **PDBTitle:** crystal structure of glycine cleavage system protein h from bartonella2 henselae
8	c2b8gA_	Alignment		97.8	30	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**biotin/lipoyl attachment protein; **PDBTitle:** solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
9	d1dcza_	Alignment		97.7	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
10	d1k8ma_	Alignment		97.7	30	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
11	d1bdoa_	Alignment		97.6	34	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains

12	c3n6rK_	Alignment		97.6	32	**PDB header:**ligase **Chain:** K: **PDB Molecule:**propionyl-coa carboxylase, alpha subunit; **PDBTitle:** crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
13	c2ejmA_	Alignment		97.6	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methylcrotonoyl-coa carboxylase subunit alpha; **PDBTitle:** solution structure of ruh-072, an apo-biotnyl domain form2 human acetyl coenzyme a carboxylase
14	d1ghja_	Alignment		97.6	18	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
15	c2l5tA_	Alignment		97.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase; **PDBTitle:** solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
16	c2dneA_	Alignment		97.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** solution structure of rsgi ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
17	d1iyua_	Alignment		97.5	23	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
18	d1qjoa_	Alignment		97.5	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
19	c2q8iB_	Alignment		97.5	26	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase component of **PDBTitle:** pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
20	c2ejgD_	Alignment		97.5	29	**PDB header:**ligase **Chain:** D: **PDB Molecule:**149aa long hypothetical methylmalonyl-coa decarboxylase **PDBTitle:** crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
21	c2dncA_	Alignment	not modelled	97.4	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase protein x component; **PDBTitle:** solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
22	d1y8ob1	Alignment	not modelled	97.4	27	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
23	d2pnrc1	Alignment	not modelled	97.4	26	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
24	d1o78a_	Alignment	not modelled	97.4	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
25	d1laba_	Alignment	not modelled	97.3	24	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
26	d1gjxa_	Alignment	not modelled	97.3	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif **Family:**Biotinyl/lipoyl-carrier proteins and domains
27	c2kccA_	Alignment	not modelled	97.2	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
28	c2dn8A_	Alignment	not modelled	97.1	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
29	d1pmra_	Alignment	not modelled	97.0	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Single hybrid motif

						Family: Biotinyl/lipoyl-carrier proteins and domains
30	c3d4rE_	Alignment	not modelled	96.6	31	**PDB header:**unknown function **Chain:** E: **PDB Molecule:**domain of unknown function from the pfam-b_34464 family; **PDBTitle:** crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
31	c2k33A_	Alignment	not modelled	93.8	32	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**acra; **PDBTitle:** solution structure of an n-glycosylated protein using in2 vitro glycosylation
32	c2qf7A_	Alignment	not modelled	93.3	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
33	c2qj8B_	Alignment	not modelled	91.7	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
34	c3na6A_	Alignment	not modelled	88.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
35	c3fmcC_	Alignment	not modelled	86.7	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
36	c3cdxB_	Alignment	not modelled	81.2	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
37	c2jkuA_	Alignment	not modelled	68.2	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**propionyl-coa carboxylase alpha chain, **PDBTitle:** crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
38	d1brwa3	Alignment	not modelled	61.2	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
39	c3h9iB_	Alignment	not modelled	58.3	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cation efflux system protein cusb; **PDBTitle:** crystal structure of the membrane fusion protein cusb from escherichia2 coli
40	d1uoua3	Alignment	not modelled	57.6	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
41	d2tpta3	Alignment	not modelled	51.9	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
42	d2gpra_	Alignment	not modelled	44.7	21	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
43	c2aukA_	Alignment	not modelled	40.8	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
44	d2f3ga_	Alignment	not modelled	36.5	17	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
45	c3lnnB_	Alignment	not modelled	36.2	32	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**membrane fusion protein (mfp) heavy metal cation efflux **PDBTitle:** crystal structure of zneb from cupriavidus metallidurans
46	d1glaf_	Alignment	not modelled	35.9	33	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Glucose permease-like
47	c2f1mA_	Alignment	not modelled	34.0	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acriflavine resistance protein a; **PDBTitle:** conformational flexibility in the multidrug efflux system protein acra
48	c3h5qA_	Alignment	not modelled	32.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
49	c1t5eB_	Alignment	not modelled	32.2	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**multidrug resistance protein mexa; **PDBTitle:** the structure of mexa
50	c2dsjA_	Alignment	not modelled	31.7	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
51	c1brwB_	Alignment	not modelled	31.1	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
52	c2j0fC_	Alignment	not modelled	30.3	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
53	d1gpra_	Alignment	not modelled	30.2	20	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif

						Family: Glucose permease-like
54	c1otpA_	Alignment	not modelled	29.9	19	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
55	d1vf7a_	Alignment	not modelled	29.6	20	**Fold:**HlyD-like secretion proteins **Superfamily:**HlyD-like secretion proteins **Family:**HlyD-like secretion proteins
56	d1ci3m2	Alignment	not modelled	26.7	32	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
57	d2p84a1	Alignment	not modelled	26.6	20	**Fold:**YopX-like **Superfamily:**YopX-like **Family:**YopX-like
58	d1m1fa_	Alignment	not modelled	19.8	21	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
59	c3fppB_	Alignment	not modelled	18.5	22	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**macrolide-specific efflux protein maca; **PDBTitle:** crystal structure of e.coli maca
60	c2xhaB_	Alignment	not modelled	15.8	28	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
61	c1vdzA_	Alignment	not modelled	15.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atpase subunit a; **PDBTitle:** crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
62	d1d7qa_	Alignment	not modelled	10.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
63	c2b44A_	Alignment	not modelled	10.5	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycyl-glycine endopeptidase lytm; **PDBTitle:** truncated s. aureus lytm, p 32 2 1 crystal form
64	d1v95a_	Alignment	not modelled	9.4	35	**Fold:**Anticodon-binding domain-like **Superfamily:**Class II aaRS ABD-related **Family:**Anticodon-binding domain of Class II aaRS
65	d1e2wa2	Alignment	not modelled	8.6	34	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**Cytochrome f, small domain
66	c2xhcA_	Alignment	not modelled	7.5	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
67	d1ne8a_	Alignment	not modelled	7.5	38	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
68	d2vv5a1	Alignment	not modelled	7.1	19	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Mechanosensitive channel protein MscS (YggB), middle domain
69	d1qapa2	Alignment	not modelled	6.8	18	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
70	c2hsiB_	Alignment	not modelled	6.3	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative peptidase m23; **PDBTitle:** crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
71	c2gu1A_	Alignment	not modelled	6.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**zinc peptidase; **PDBTitle:** crystal structure of a zinc containing peptidase from2 vibrio cholerae
72	d1jt8a_	Alignment	not modelled	6.1	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
73	c3pajA_	Alignment	not modelled	5.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase, carboxylating; **PDBTitle:** 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
74	d1qwya_	Alignment	not modelled	5.8	40	**Fold:**Barrel-sandwich hybrid **Superfamily:**Duplicated hybrid motif **Family:**Peptidoglycan hydrolase LytM
75	d1o4ua2	Alignment	not modelled	5.3	16	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**NadC N-terminal domain-like
76	c3fggA_	Alignment	not modelled	5.3	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bce2196; **PDBTitle:** crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
77	c3tqvA_	Alignment	not modelled	5.0	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.