Phyre^2

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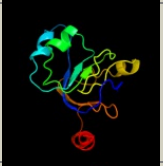
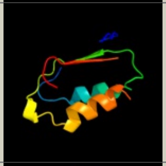
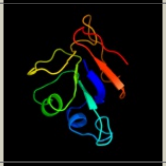
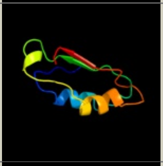
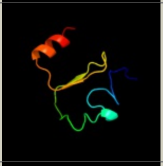
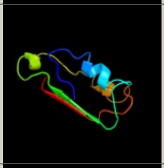
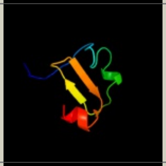
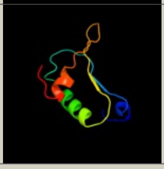
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gp4A_	Alignment		100.0	65	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
2	d2gp4a2	Alignment		100.0	65	**Fold:**IlvD/EDD N-terminal domain-like **Superfamily:**IlvD/EDD N-terminal domain-like **Family:**IvD/EDD N-terminal domain-like
3	d2gp4a1	Alignment		100.0	63	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
4	d1zyma2	Alignment		92.4	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
5	d1vbga2	Alignment		86.8	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
6	d1vi4a_	Alignment		77.0	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
7	d1h6za2	Alignment		75.2	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
8	c2pcnA_	Alignment		70.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:2-demethylmenaquinone **PDBTitle:** crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
9	c1ezaA_	Alignment		68.7	13	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
10	d1q5xa_	Alignment		66.0	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
11	c3l83A_	Alignment		64.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus

12	c2jv2A_	Alignment		58.3	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
13	d1nxja_	Alignment		57.8	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
14	c1nxjA_	Alignment		57.8	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable s-adenosylmethionine:2- **PDBTitle:** structure of rv3853 from mycobacterium tuberculosis
15	c2hwgA_	Alignment		57.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
16	c3c8oB_	Alignment		57.0	17	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1
17	d2hi6a1	Alignment		49.3	37	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
18	d1j3la_	Alignment		45.5	19	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
19	c3nxkE_	Alignment		43.8	11	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
20	d1a9xb2	Alignment		43.2	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
21	c2jz7A_	Alignment	not modelled	42.9	23	**PDB header:**selenium-binding protein **Chain:** A: **PDB Molecule:**selenium binding protein; **PDBTitle:** solution nmr structure of selenium-binding protein from2 methanococcus vannielii
22	d1wl8a1	Alignment	not modelled	41.2	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
23	d1kbla2	Alignment	not modelled	40.0	35	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
24	c3nojA_	Alignment	not modelled	39.2	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
25	d2npta1	Alignment	not modelled	37.1	44	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
26	d1rk8a_	Alignment	not modelled	36.0	23	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
27	c3rpfC_	Alignment	not modelled	35.3	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**molybdopterin converting factor, subunit 1 (moad); **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
28	d1v7la_	Alignment	not modelled	35.1	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like

29	c1dm9A_	Alignment	not modelled	34.8	20	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
30	d1dm9a_	Alignment	not modelled	34.8	20	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD
31	c2pkpA_	Alignment	not modelled	34.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
32	c3ahhA_	Alignment	not modelled	33.8	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**xylulose 5-phosphate/fructose 6-phosphate phosphoketolase; **PDBTitle:** h142a mutant of phosphoketolase from bifidobacterium breve complexed2 with acetyl thiamine diphosphate
33	d1pl8a1	Alignment	not modelled	33.6	16	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
34	d1wi0a_	Alignment	not modelled	33.0	44	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
35	d1wsaa_	Alignment	not modelled	32.6	10	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
36	d1fjca_	Alignment	not modelled	32.5	26	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
37	c1sddA_	Alignment	not modelled	32.4	26	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
38	d1r31a1	Alignment	not modelled	30.0	29	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
39	d1fuia2	Alignment	not modelled	29.3	11	**Fold:**FucI/AraA N-terminal and middle domains **Superfamily:**FucI/AraA N-terminal and middle domains **Family:**L-fucose isomerase, N-terminal and second domains
40	d1od5a1	Alignment	not modelled	28.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
41	d2cqaa1	Alignment	not modelled	27.8	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**TIP49 domain
42	d2a9va1	Alignment	not modelled	26.6	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
43	c1rkjA_	Alignment	not modelled	26.2	30	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**nucleolin; **PDBTitle:** solution structure of the complex formed by the two n-2 terminal rna-binding domains of nucleolin and a pre-rrna3 target
44	c1keeH_	Alignment	not modelled	25.9	17	**PDB header:**ligase **Chain:** H: **PDB Molecule:**carbamoyl-phosphate synthetase small chain; **PDBTitle:** inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
45	d1qdlb_	Alignment	not modelled	25.9	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
46	d1ueba3	Alignment	not modelled	25.6	44	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
47	c2e5hA_	Alignment	not modelled	24.6	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**zinc finger cchc-type and rna-binding motif- **PDBTitle:** solution structure of rna binding domain in zinc finger2 cchc-type and rna binding motif 1
48	c3kw8A_	Alignment	not modelled	24.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper oxidase; **PDBTitle:** two-domain laccase from streptomyces coelicolor at 2.3 a resolution
49	d1r61a_	Alignment	not modelled	24.5	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
50	c1gph1_	Alignment	not modelled	23.9	8	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
51	c2vriA_	Alignment	not modelled	23.8	16	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structure of the nsp3 x-domain of human coronavirus nl63
52	d2etna2	Alignment	not modelled	23.1	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
53	c2zpmA_	Alignment	not modelled	23.1	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
54	d1a8ya3	Alignment	not modelled	23.0	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin

55	d1sdda1	Alignment	not modelled	22.9	26	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
56	c3fm3B_	Alignment	not modelled	22.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
57	c3mvnA_	Alignment	not modelled	22.6	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
58	c2p4vA_	Alignment	not modelled	22.2	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
59	c1yw7A_	Alignment	not modelled	22.2	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
60	c2dhgA_	Alignment	not modelled	21.1	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**trna selenocysteine associated protein (secp43); **PDBTitle:** solution structure of the c-terminal rna recognition motif2 in trna selenocysteine associated protein
61	d2ieaa1	Alignment	not modelled	21.1	12	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
62	d1o1ya_	Alignment	not modelled	20.7	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
63	d2et1a1	Alignment	not modelled	20.7	10	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
64	c3gmiA_	Alignment	not modelled	20.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0348 protein mj0951; **PDBTitle:** crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
65	d1l5ja2	Alignment	not modelled	20.5	35	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
66	c3ex7B_	Alignment	not modelled	20.4	20	**PDB header:**hydrolase/rna binding protein/rna **Chain:** B: **PDB Molecule:**rna-binding protein 8a; **PDBTitle:** the crystal structure of ejc in its transition state
67	c2y0fD_	Alignment	not modelled	19.9	30	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; **PDBTitle:** structure of gcpe (ispg) from thermus thermophilus hb27
68	c2q8kA_	Alignment	not modelled	19.8	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** the crystal structure of ebp1
69	d1lcya1	Alignment	not modelled	19.3	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
70	d2f23a2	Alignment	not modelled	19.2	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
71	d1s1ma1	Alignment	not modelled	19.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
72	c2qv5A_	Alignment	not modelled	18.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
73	c2hcuA_	Alignment	not modelled	18.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
74	d1ofda3	Alignment	not modelled	18.5	15	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
75	c3k4iC_	Alignment	not modelled	18.4	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
76	c1wa1X_	Alignment	not modelled	18.4	21	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite **PDBTitle:** crystal structure of h313q mutant of alcaligenes2 xylosoxidans nitrite reductase
77	d1x87a_	Alignment	not modelled	18.0	22	**Fold:**Urocanase **Superfamily:**Urocanase **Family:**Urocanase
78	c1nriA_	Alignment	not modelled	17.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein hi0754; **PDBTitle:** crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
79	d1nria_	Alignment	not modelled	17.8	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
80	c1gpmD_	Alignment	not modelled	17.7	17	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp

						and pyrophosphate
81	d2j5wa4	Alignment	not modelled	17.4	16	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
82	c3fijD_	Alignment	not modelled	17.4	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
83	d2q07a1	Alignment	not modelled	17.4	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**PUA domain
84	d2b0aa1	Alignment	not modelled	17.2	14	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
85	c1b6aA_	Alignment	not modelled	17.2	32	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
86	c3u7jA_	Alignment	not modelled	17.2	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
87	c3lzkC_	Alignment	not modelled	16.9	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
88	d2fug21	Alignment	not modelled	16.8	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
89	c3cdzA_	Alignment	not modelled	16.7	11	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
90	c2dgtA_	Alignment	not modelled	16.7	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna-binding protein 30; **PDBTitle:** solution structure of the second rna binding domain in rna-2 binding protein 30
91	d1p3da2	Alignment	not modelled	16.6	3	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
92	d1kv7a1	Alignment	not modelled	16.5	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
93	d1oe1a1	Alignment	not modelled	15.9	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
94	c2vefB_	Alignment	not modelled	15.9	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
95	d2j5wa3	Alignment	not modelled	15.9	32	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
96	c2f3jA_	Alignment	not modelled	15.8	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**rna and export factor binding protein 2; **PDBTitle:** the solution structure of the ref2-i mrna export factor2 (residues 1-155).
97	c3l7nA_	Alignment	not modelled	15.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
98	d1ujva_	Alignment	not modelled	15.5	22	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
99	d1e8ca2	Alignment	not modelled	15.5	23	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain