Phyre^2

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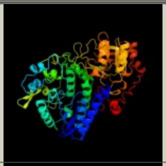
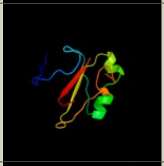
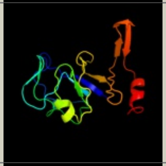
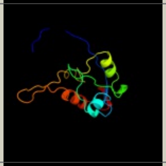
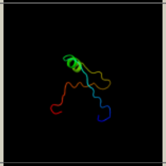
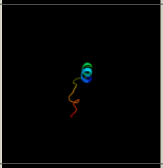
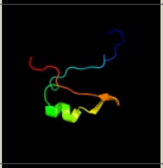
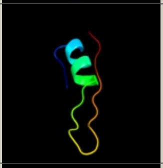
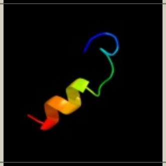
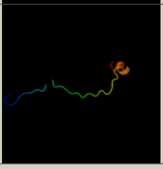
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gp4A_	Alignment		100.0	28	**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	28	**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	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
4	c2pcnA_	Alignment		76.7	13	**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
5	d1zyma2	Alignment		73.8	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
6	d1ujva_	Alignment		66.9	30	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
7	c2jv2A_	Alignment		60.6	45	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph1500; **PDBTitle:** solution structure of the n-terminal domain of ph1500
8	d1fjca_	Alignment		46.0	27	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
9	d1od5a1	Alignment		45.2	25	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
10	d1q5xa_	Alignment		45.0	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
11	d1dm9a_	Alignment		42.6	10	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Heat shock protein 15 kD

12	c1dm9A_	Alignment		42.6	10	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical 15.5 kd protein in mrca-pcka **PDBTitle:** heat shock protein 15 kd
13	d1pl8a1	Alignment		41.4	21	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**Alcohol dehydrogenase-like, N-terminal domain
14	c3soeA_	Alignment		41.0	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the 3rd pdz domain of the human membrane-2 associated guanylate kinase, ww and pdz domain-containing protein 33 (magi3)
15	d2npta1	Alignment		40.0	53	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
16	d1rk8a_	Alignment		36.5	21	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
17	d1wi0a_	Alignment		36.3	53	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
18	c1rkjA_	Alignment		35.9	21	**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
19	d1r31a1	Alignment		33.8	29	**Fold:**Ferredoxin-like **Superfamily:**NAD-binding domain of HMG-CoA reductase **Family:**NAD-binding domain of HMG-CoA reductase
20	c2k8iA_	Alignment		33.5	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
21	d1wsaa_	Alignment	not modelled	32.5	16	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
22	d2et1a1	Alignment	not modelled	31.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
23	c1nxjA_	Alignment	not modelled	31.3	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable s-adenosylmethionine:2- **PDBTitle:** structure of rv3853 from mycobacterium tuberculosis
24	d1nxja_	Alignment	not modelled	31.3	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
25	d1wl8a1	Alignment	not modelled	31.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
26	d1fxza2	Alignment	not modelled	30.5	13	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
27	c1ezaA_	Alignment	not modelled	29.9	18	**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
28	c1sddA_	Alignment	not modelled	29.3	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor v; **PDBTitle:** crystal structure of bovine factor vai
29	d1r61a_	Alignment	not modelled	29.3	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase

						Family: Putative cyclase
30	d1lcya1	Alignment	not modelled	29.2	41	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
31	d2hi6a1	Alignment	not modelled	28.1	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
32	c2e5hA_	Alignment	not modelled	27.7	23	**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
33	d1rgra_	Alignment	not modelled	27.6	25	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
34	d1agxa_	Alignment	not modelled	27.0	14	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
35	d1a8ya3	Alignment	not modelled	26.9	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
36	d2csja1	Alignment	not modelled	26.6	21	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
37	c1wa1X_	Alignment	not modelled	25.3	11	**PDB header:**reductase **Chain:** X: **PDB Molecule:**dissimilatory copper-containing nitrite **PDBTitle:** crystal structure of h313q mutant of alcaligenes2 xylosoxidans nitrite reductase
38	c1yq4A_	Alignment	not modelled	24.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate dehydrogenase flavoprotein subunit; **PDBTitle:** avian respiratory complex ii with 3-nitropropionate and ubiquinone
39	d2etna2	Alignment	not modelled	24.5	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
40	d1kola2	Alignment	not modelled	24.5	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
41	d2hgaa1	Alignment	not modelled	24.1	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**MTH1368 C-terminal domain-like
42	c3kw8A_	Alignment	not modelled	23.7	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative copper oxidase; **PDBTitle:** two-domain laccase from streptomyces coelicolor at 2.3 a resolution
43	c3c8oB_	Alignment	not modelled	23.4	17	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1
44	d2bu3a1	Alignment	not modelled	23.3	18	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Phytochelatin synthase
45	d1v7la_	Alignment	not modelled	23.2	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
46	d1k78a1	Alignment	not modelled	22.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
47	c1yw7A_	Alignment	not modelled	22.3	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
48	d2f23a2	Alignment	not modelled	21.9	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
49	d1gtta2	Alignment	not modelled	21.6	19	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
50	d1od5a2	Alignment	not modelled	21.4	17	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
51	d1x5ta1	Alignment	not modelled	21.2	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
52	d6paxa1	Alignment	not modelled	21.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
53	c3fm3B_	Alignment	not modelled	20.6	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
54	d1wi2a_	Alignment	not modelled	20.4	26	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
55	c2kl1A_	Alignment	not modelled	20.3	28	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ylbl protein; **PDBTitle:** solution structure of gtr34c from geobacillus thermodenitrificans.2 northeast structural genomics consortium target gtr34c
						PDB header:isomerase

56	c3u7jA_	Alignment	not modelled	20.1	17	**Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
57	c2joaA_	Alignment	not modelled	19.9	54	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**serine protease htra1; **PDBTitle:** htra1 bound to an optimized peptide: nmr assignment of pdz2 domain and ligand resonances
58	d1sdda1	Alignment	not modelled	19.8	21	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Multidomain cupredoxins
59	c3lzkC_	Alignment	not modelled	19.6	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
60	d1ry4a_	Alignment	not modelled	19.3	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
61	c3cdzA_	Alignment	not modelled	19.1	21	**PDB header:**blood clotting **Chain:** A: **PDB Molecule:**coagulation factor viii heavy chain; **PDBTitle:** crystal structure of human factor viii
62	c2krgA_	Alignment	not modelled	18.6	30	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**na(+)/h(+) exchange regulatory cofactor nhe-rf1; **PDBTitle:** solution structure of human sodium/ hydrogen exchange2 regulatory factor 1(150-358)
63	c3bpuA_	Alignment	not modelled	18.3	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane-associated guanylate kinase, ww and pdz domain- **PDBTitle:** crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant
64	c2ka9A_	Alignment	not modelled	18.3	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**disks large homolog 4; **PDBTitle:** solution structure of psd-95 pdz12 complexed with cypin2 peptide
65	d1rzxa_	Alignment	not modelled	17.6	19	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
66	c1fuiB_	Alignment	not modelled	17.6	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**l-fucose isomerase; **PDBTitle:** l-fucose isomerase from escherichia coli
67	c3t6oA_	Alignment	not modelled	17.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter/antisigma-factor antagonist stas; **PDBTitle:** the structure of an anti-sigma-factor antagonist (stas) domain protein2 from planctomyces limnophilus.
68	c3fijD_	Alignment	not modelled	17.5	18	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
69	d1ueba3	Alignment	not modelled	17.3	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
70	c2dhgA_	Alignment	not modelled	17.3	11	**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
71	c2kvcA_	Alignment	not modelled	17.2	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
72	d1jb0k_	Alignment	not modelled	17.1	44	**Fold:**Photosystem I reaction center subunit X, PsaK **Superfamily:**Photosystem I reaction center subunit X, PsaK **Family:**Photosystem I reaction center subunit X, PsaK
73	c1jb0K_	Alignment	not modelled	17.1	44	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem 1 reaction centre subunit x; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
74	c1p1dA_	Alignment	not modelled	17.1	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutamate receptor interacting protein; **PDBTitle:** structural insights into the inter-domain chaperoning of2 tandem pdz domains in glutamate receptor interacting3 proteins
75	c2vfjA_	Alignment	not modelled	17.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tumor necrosis factor; **PDBTitle:** structure of the a20 ovarian tumour (otu) domain
76	c2k6pA_	Alignment	not modelled	16.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein hp_1423; **PDBTitle:** solution structure of hypothetical protein, hp1423
77	d1vi4a_	Alignment	not modelled	16.5	13	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
78	d1j3la_	Alignment	not modelled	16.2	12	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
79	d2fug21	Alignment	not modelled	16.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
80	c2pkpA_	Alignment	not modelled	16.1	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)

81	d1qdlb_	Alignment	not modelled	15.9	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
82	c3prdA_	Alignment	not modelled	15.8	24	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
83	d2vbua1	Alignment	not modelled	15.8	46	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**CTP-dependent riboflavin kinase-like
84	c2qv5A_	Alignment	not modelled	15.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
85	d1obxa_	Alignment	not modelled	15.4	23	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
86	c1obyB_	Alignment	not modelled	15.4	23	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 a syndecan-4 peptide.
87	c1obxA_	Alignment	not modelled	15.4	23	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**syntenin 1; **PDBTitle:** crystal structure of the complex of pdz2 of syntenin with2 an interleukin 5 receptor alpha peptide.
88	c3mvnA_	Alignment	not modelled	15.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
89	c2d92A_	Alignment	not modelled	15.4	28	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
90	c3f43A_	Alignment	not modelled	15.2	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative anti-sigma factor antagonist tm1081; **PDBTitle:** crystal structure of a putative anti-sigma factor antagonist (tm1081)2 from thermotoga maritima at 1.59 a resolution
91	c2kfwA_	Alignment	not modelled	15.2	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
92	c3i18A_	Alignment	not modelled	15.1	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
93	c2p4vA_	Alignment	not modelled	15.1	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
94	d1a9xb2	Alignment	not modelled	15.1	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
95	d2b0aa1	Alignment	not modelled	15.0	29	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Putative cyclase **Family:**Putative cyclase
96	c2zpmA_	Alignment	not modelled	15.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of sigma e protease; **PDBTitle:** crystal structure analysis of pdz domain b
97	c2cdqB_	Alignment	not modelled	15.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
98	d1ky9a1	Alignment	not modelled	14.9	42	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**HtrA-like serine proteases
99	c3cgnA_	Alignment	not modelled	14.9	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd