Phyre^2

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Description	P0ACV2
Date	Thu Jan 5 11:19:08 GMT 2012
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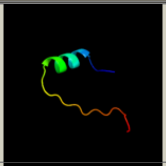
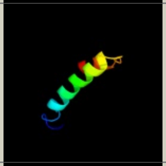
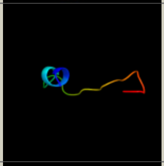
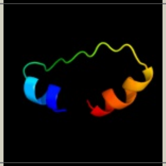
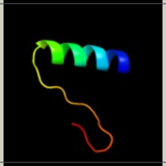
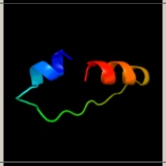
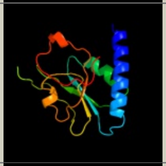
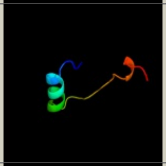
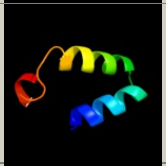
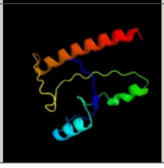
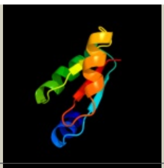
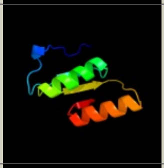
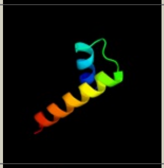
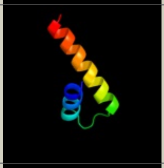
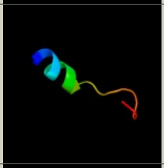
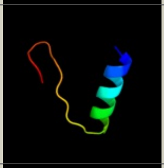
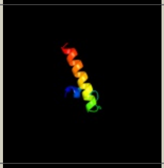
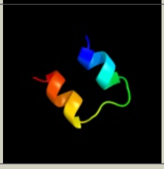
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j5bA_	Alignment		52.6	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
2	c1ltxA_	Alignment		42.3	22	**PDB header:**transferase/protein binding **Chain:** A: **PDB Molecule:**rab geranylgeranyltransferase alpha subunit; **PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
3	c3cwcB_	Alignment		41.5	5	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative glycerate kinase 2; **PDBTitle:** crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
4	c3lubE_	Alignment		36.9	17	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**putative creatinine amidohydrolase; **PDBTitle:** crystal structure of putative creatinine amidohydrolase2 (yp_211512.1) from bacteroides fragilis nctc 9343 at 2.11 a3 resolution
5	c3no4A_	Alignment		33.5	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
6	d1hrua_	Alignment		27.3	11	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
7	d1v7za_	Alignment		26.8	10	**Fold:**Creatininase **Superfamily:**Creatininase **Family:**Creatininase
8	d1g9sa_	Alignment		20.5	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
9	c2cycB_	Alignment		20.4	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
10	c2penE_	Alignment		18.2	30	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**orf134; **PDBTitle:** crystal structure of rbcx, crystal form i
11	c3khsB_	Alignment		18.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase

12	d1nkta4	Alignment		16.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
13	d1d7ya2	Alignment		16.3	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
14	c1fcuA_	Alignment		15.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
15	d1fcqa_	Alignment		14.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
16	d1tuwa_	Alignment		13.9	6	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Polyketide synthesis cyclase
17	d1k7ja_	Alignment		13.7	19	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
18	c2pe4A_	Alignment		13.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
19	c1r6uB_	Alignment		13.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
20	d1d8da_	Alignment		12.9	38	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
21	d2peqa1	Alignment	not modelled	12.2	30	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like
22	d1r6ta2	Alignment	not modelled	12.0	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
23	d1jcua_	Alignment	not modelled	12.0	22	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**YrdC-like
24	c2quiB_	Alignment	not modelled	11.9	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
25	d1pyfa_	Alignment	not modelled	11.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
26	d1p3qq_	Alignment	not modelled	11.4	11	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
27	c1tcvB_	Alignment	not modelled	11.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine-nucleoside phosphorylase; **PDBTitle:** crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
28	d1iyjb4	Alignment	not modelled	11.0	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
						PDB header:hydrolase

29	c2advB_	Alignment	not modelled	11.0	8	**Chain:** B: **PDB Molecule:**glutaryl 7- aminocephalosporanic acid acylase; **PDBTitle:** crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism
30	d1fl2a2	Alignment	not modelled	10.5	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
31	c2rjnA_	Alignment	not modelled	10.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**response regulator receiver:metal-dependent **PDBTitle:** crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
32	d1mn3a_	Alignment	not modelled	10.0	12	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
33	c2p4sA_	Alignment	not modelled	9.9	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
34	d1nj8a2	Alignment	not modelled	9.8	33	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
35	c2ip1A_	Alignment	not modelled	9.3	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
36	c2h3oA_	Alignment	not modelled	9.2	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**merf; **PDBTitle:** structure of merft, a membrane protein with two trans-2 membrane helices
37	d3eeqa2	Alignment	not modelled	9.2	13	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
38	c1xuzA_	Alignment	not modelled	8.9	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
39	c2l7kA_	Alignment	not modelled	8.3	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
40	d1a9xb1	Alignment	not modelled	8.3	16	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Carbamoyl phosphate synthetase, small subunit N-terminal domain **Family:**Carbamoyl phosphate synthetase, small subunit N-terminal domain
41	d1nj1a2	Alignment	not modelled	8.2	23	**Fold:**IF3-like **Superfamily:**C-terminal domain of ProRS **Family:**C-terminal domain of ProRS
42	d2py8a1	Alignment	not modelled	8.2	14	**Fold:**RbcX-like **Superfamily:**RbcX-like **Family:**RbcX-like
43	c1tnol_	Alignment	not modelled	8.2	36	**PDB header:**transferase **Chain:** I: **PDB Molecule:**geranylgeranyltransferase type i alpha subunit; **PDBTitle:** rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a kkksktkcvim peptide derived from k-3 ras4b
44	c1jzdA_	Alignment	not modelled	8.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
45	c3rpfB_	Alignment	not modelled	8.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**molybdopterin synthase catalytic subunit; **PDBTitle:** protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
46	c2ntxB_	Alignment	not modelled	8.0	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
47	c3g8rA_	Alignment	not modelled	8.0	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
48	d1c0ma1	Alignment	not modelled	7.9	6	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
49	d1gm5a4	Alignment	not modelled	7.9	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
50	d1cv8a_	Alignment	not modelled	7.9	12	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
51	c3tmgA_	Alignment	not modelled	7.6	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**glycine betaine, l-proline abc transporter, **PDBTitle:** crystal structure of glycine betaine, l-proline abc transporter,2 glycine/betaine/l-proline-binding protein (prox) from borrelia3 burgdorferi
52	d2pi8a1	Alignment	not modelled	7.6	20	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases

						Family:MLTA-like
53	d1iuqa_	Alignment	not modelled	7.5	13	**Fold:**Glycerol-3-phosphate (1)-acyltransferase **Superfamily:**Glycerol-3-phosphate (1)-acyltransferase **Family:**Glycerol-3-phosphate (1)-acyltransferase
54	c2khzB_	Alignment	not modelled	7.4	23	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**c-myc-responsive protein rcl; **PDBTitle:** solution structure of rcl
55	d2h6fa1	Alignment	not modelled	7.4	38	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
56	d1v4na_	Alignment	not modelled	7.2	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
57	c2b8eB_	Alignment	not modelled	7.2	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**cation-transporting atpase; **PDBTitle:** copa atp binding domain
58	d1vdca2	Alignment	not modelled	7.1	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
59	d1mkya3	Alignment	not modelled	7.1	13	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Probable GTPase Der, C-terminal domain **Family:**Probable GTPase Der, C-terminal domain
60	c3ggsA_	Alignment	not modelled	7.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
61	c3l6gA_	Alignment	not modelled	6.8	12	**PDB header:**glycine betaine-binding protein **Chain:** A: **PDB Molecule:**betaine abc transporter permease and substrate binding **PDBTitle:** crystal structure of lactococcal opuac in its open conformation
62	c3focB_	Alignment	not modelled	6.8	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
63	d1zj8a4	Alignment	not modelled	6.7	17	**Fold:**Nitrite and sulphite reductase 4Fe-4S domain-like **Superfamily:**Nitrite and sulphite reductase 4Fe-4S domain-like **Family:**Nitrite and sulphite reductase 4Fe-4S domain-like
64	c1t3bA_	Alignment	not modelled	6.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
65	c1w8xP_	Alignment	not modelled	6.6	43	**PDB header:**virus **Chain:** P: **PDB Molecule:**protein p16; **PDBTitle:** structural analysis of prd1
66	d1xhca2	Alignment	not modelled	6.5	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
67	c3f6tA_	Alignment	not modelled	6.4	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
68	c3hv0A_	Alignment	not modelled	6.4	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
69	d1vlia2	Alignment	not modelled	6.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
70	c3s29C_	Alignment	not modelled	6.2	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sucrose synthase 1; **PDBTitle:** the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
71	c2cyaA_	Alignment	not modelled	6.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
72	d2ocda1	Alignment	not modelled	6.1	7	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
73	c3t4cD_	Alignment	not modelled	6.1	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 1; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
74	d1v58a1	Alignment	not modelled	6.1	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
75	d2ae0x1	Alignment	not modelled	6.0	19	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**MLTA-like
76	d1pxva_	Alignment	not modelled	5.9	11	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Papain-like
77	c2omdB_	Alignment	not modelled	5.7	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**molybdopterin-converting factor subunit 2; **PDBTitle:** crystal structure of molybdopterin converting factor subunit 22 (aq_2181) from aquifex aeolicus vf5
78	d2nrqa1	Alignment	not modelled	5.6	14	**Fold:**RL5-like **Superfamily:**RL5-like

						Family:SSO1042-like
79	d1r71a_	Alignment	not modelled	5.5	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
80	c2nzzA_	Alignment	not modelled	5.5	56	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**penetratin conjugated gas (374-394) peptide; **PDBTitle:** nmr structure analysis of the penetratin conjugated gas2 (374-394) peptide
81	d1dcea1	Alignment	not modelled	5.4	29	**Fold:**alpha-alpha superhelix **Superfamily:**Protein prenylyltransferase **Family:**Protein prenylyltransferase
82	c3jxeB_	Alignment	not modelled	5.4	27	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
83	d1tf5a4	Alignment	not modelled	5.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	d1ur3m_	Alignment	not modelled	5.4	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
85	c2eqaA_	Alignment	not modelled	5.4	19	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein st1526; **PDBTitle:** crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
86	c2ou2A_	Alignment	not modelled	5.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase htatip; **PDBTitle:** acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
87	c3m8yC_	Alignment	not modelled	5.2	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
88	d1q1ra2	Alignment	not modelled	5.2	9	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
89	c3nurA_	Alignment	not modelled	5.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** crystal structure of a putative amidohydrolase from staphylococcus2 aureus
90	d1eeja1	Alignment	not modelled	5.1	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
91	c3ihjA_	Alignment	not modelled	5.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine aminotransferase 2; **PDBTitle:** human alanine aminotransferase 2 in complex with plp
92	c2pkaB_	Alignment	not modelled	5.0	19	**PDB header:**serine proteinase **Chain:** B: **PDB Molecule:**kallikrein a; **PDBTitle:** refined 2 angstroms x-ray crystal structure of porcine2 pancreatic kallikrein a, a specific trypsin-like serine3 proteinase. crystallization, structure determination,4 crystallographic refinement, structure and its comparison5 with bovine trypsin