Phyre^2

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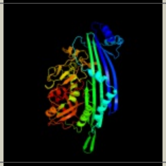
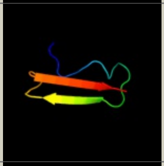
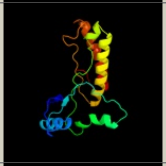
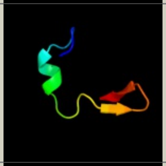
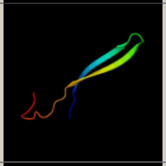
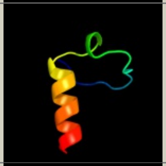
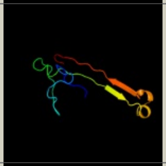
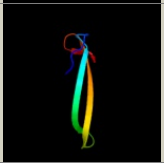
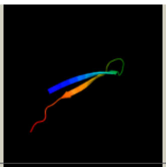
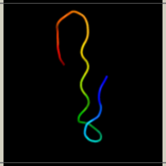
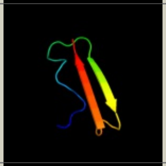
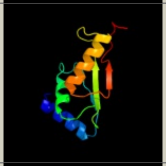
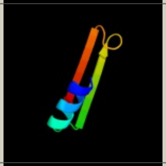
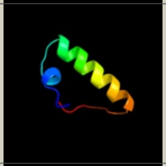
Description	P0AGG8
Date	Thu Jan 5 11:29:05 GMT 2012
Unique Job ID	5989de5b2aa84641

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qtdC_	 Alignment		100.0	21	**PDB header:**gene regulation **Chain:** C: **PDB Molecule:**pmba protein; **PDBTitle:** crystal structure of putative modulator of gyrase (pmba) from2 pseudomonas aeruginosa pao1
2	d1vpba_	 Alignment		100.0	21	**Fold:**Putative modulator of DNA gyrase, PmbA/TldD **Superfamily:**Putative modulator of DNA gyrase, PmbA/TldD **Family:**Putative modulator of DNA gyrase, PmbA/TldD
3	d1vl4a_	 Alignment		100.0	20	**Fold:**Putative modulator of DNA gyrase, PmbA/TldD **Superfamily:**Putative modulator of DNA gyrase, PmbA/TldD **Family:**Putative modulator of DNA gyrase, PmbA/TldD
4	c1bknA_	 Alignment		35.7	6	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**mutl; **PDBTitle:** crystal structure of an n-terminal 40kd fragment of e. coli2 dna mismatch repair protein mutl
5	c3kwsB_	 Alignment		32.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
6	d1o12a1	 Alignment		30.3	43	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
7	c3onrI_	 Alignment		30.3	0	**PDB header:**metal binding protein **Chain:** I: **PDB Molecule:**protein transport protein sece2; **PDBTitle:** crystal structure of the calcium chelating immunodominant antigen,2 calcium dodecin (rv0379),from mycobacterium tuberculosis with a novel3 calcium-binding site
8	d1vlva1	 Alignment		28.3	23	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
9	c1w7vD_	 Alignment		24.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**xaa-pro aminopeptidase; **PDBTitle:** znmg substituted aminopeptidase p from e. coli
10	d2q02a1	 Alignment		18.7	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
11	c3ff0A_	 Alignment		15.9	12	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**phenazine biosynthesis protein phzb 2; **PDBTitle:** crystal structure of a phenazine biosynthesis-related protein (phzb2)2 from pseudomonas aeruginosa at 1.90 a resolution

12	c3oqtP_	Alignment		14.9	16	**PDB header:**flavoprotein **Chain:** P: **PDB Molecule:**rv1498a protein; **PDBTitle:** crystal structure of rv1498a protein from mycobacterium tuberculosis
13	d1m1ha1	Alignment		14.5	28	**Fold:**N-utilization substance G protein NusG, insert domain **Superfamily:**N-utilization substance G protein NusG, insert domain **Family:**N-utilization substance G protein NusG, insert domain
14	d1bkna2	Alignment		14.4	6	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
15	c2iv0A_	Alignment		13.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**isocitrate dehydrogenase; **PDBTitle:** thermal stability of isocitrate dehydrogenase from2 archaeoglobus fulgidus studied by crystal structure3 analysis and engineering of chimers
16	c2bp1C_	Alignment		13.6	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aflatoxin b1 aldehyde reductase member 2; **PDBTitle:** structure of the aflatoxin aldehyde reductase in complex2 with nadph
17	c1ea6A_	Alignment		13.3	9	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**pms1 protein homolog 2; **PDBTitle:** n-terminal 40kda fragment of nhpms2 complexed with adp
18	d1ydua1	Alignment		13.0	18	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
19	c2qw5B_	Alignment		12.4	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**xylose isomerase-like tim barrel; **PDBTitle:** crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
20	d1tuha_	Alignment		12.1	8	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Hypothetical protein egc068 from a soil-derived mobile gene cassette
21	c1tuhA_	Alignment	not modelled	12.1	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein egc068; **PDBTitle:** structure of bal32a from a soil-derived mobile gene cassette
22	c1vlvA_	Alignment	not modelled	11.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
23	d1c75a_	Alignment	not modelled	10.8	23	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
24	d351ca_	Alignment	not modelled	10.2	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
25	d1fi3a_	Alignment	not modelled	10.2	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
26	d1dvva_	Alignment	not modelled	9.8	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
27	c3gknA_	Alignment	not modelled	9.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** insights into the alkyl peroxide reduction activity of xanthomonas2 campestris bacterioferritin comigratory protein from the trapped3 intermediate/ligand complex structures
28	c3ezjA_	Alignment	not modelled	8.9	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**general secretion pathway protein gspd; **PDBTitle:** crystal structure of the n-terminal domain of the secretin gspd from2 etec determined with the assistance of a nanobody

29	d1cora_	Alignment	not modelled	8.8	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
30	c3tr9A_	Alignment	not modelled	8.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
31	c3updA_	Alignment	not modelled	8.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
32	d7odca2	Alignment	not modelled	8.3	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
33	c2on3A_	Alignment	not modelled	8.2	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and2 leishmania donovani ornithine decarboxylases by 3-aminooxy-3 1-aminopropane
34	d1ynra1	Alignment	not modelled	8.2	0	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
35	c3l23A_	Alignment	not modelled	8.1	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
36	c2xrfA_	Alignment	not modelled	8.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
37	d1otha1	Alignment	not modelled	8.0	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
38	c3f7xA_	Alignment	not modelled	8.0	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of a putative polyketide cyclase (pp0894) from2 pseudomonas putida kt2440 at 1.24 a resolution
39	d1h7sa2	Alignment	not modelled	8.0	9	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
40	d1b63a2	Alignment	not modelled	7.9	6	**Fold:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Superfamily:**ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase **Family:**DNA gyrase/MutL, N-terminal domain
41	d1ix2a_	Alignment	not modelled	7.8	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
42	d2pjua1	Alignment	not modelled	7.8	21	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
43	d2ds5a1	Alignment	not modelled	7.8	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
44	c1ovxB_	Alignment	not modelled	7.7	20	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
45	c3cjlA_	Alignment	not modelled	7.7	31	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**domain of unknown function; **PDBTitle:** crystal structure of a protein of unknown function (eca1910) from2 pectobacterium atrosepticum scri1043 at 2.20 a resolution
46	c3ixrA_	Alignment	not modelled	7.6	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bacterioferritin comigratory protein; **PDBTitle:** crystal structure of xylella fastidiosa prxq c47s mutant
47	c3h4lB_	Alignment	not modelled	7.2	12	**PDB header:**dna binding protein, protein binding **Chain:** B: **PDB Molecule:**dna mismatch repair protein pms1; **PDBTitle:** crystal structure of n terminal domain of a dna repair protein
48	d1dxha1	Alignment	not modelled	7.2	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
49	d1w0da_	Alignment	not modelled	7.0	14	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
50	d2a5yb1	Alignment	not modelled	7.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**CED-4 C-terminal domain-like
51	d2k54a1	Alignment	not modelled	6.7	21	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0742-like
52	d1d7ka2	Alignment	not modelled	6.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
53	d1pvva1	Alignment	not modelled	6.7	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
						PDB header:protein binding

54	c3na3A_		Alignment	not modelled	6.6	3	**Chain:** A: **PDB Molecule:**dna mismatch repair protein mlh1; **PDBTitle:** mutl protein homolog 1 isoform 1 from homo sapiens
55	c2kk4A_		Alignment	not modelled	6.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af_2094; **PDBTitle:** solution nmr structure of protein af2094 from archaeoglobus2 fulgidus. northeast structural genomics consotium (nesg)3 target gt2
56	c1htrP_		Alignment	not modelled	6.5	19	**PDB header:**aspartyl protease **Chain:** P: **PDB Molecule:**progastricsin (pro segment); **PDBTitle:** crystal and molecular structures of human progastricsin at 1.622 angstroms resolution
57	d1s5aa_		Alignment	not modelled	6.5	13	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PhzA/PhzB-like
58	d1kfia4		Alignment	not modelled	6.5	16	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
59	c3fuyC_		Alignment	not modelled	6.4	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative integron gene cassette protein; **PDBTitle:** structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass1
60	c3e8vA_		Alignment	not modelled	6.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible transglutaminase-family protein; **PDBTitle:** crystal structure of a possible transglutaminase-family2 protein proteolytic fragment from bacteroides fragilis
61	d1ajza_		Alignment	not modelled	6.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
62	c3k30B_		Alignment	not modelled	6.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
63	c2ds8A_		Alignment	not modelled	6.3	20	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit **PDBTitle:** structure of the zbd-xb complex
64	d2c9qa1		Alignment	not modelled	6.2	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Copper resistance protein C (CopC, PcoC)
65	d1ud9a1		Alignment	not modelled	6.2	16	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
66	c3o6cA_		Alignment	not modelled	6.2	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
67	c2l4dA_		Alignment	not modelled	6.2	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**sco1/senc family protein/cytochrome c; **PDBTitle:** cytochrome c domain of pp3183 protein from pseudomonas putida
68	d1dl6a_		Alignment	not modelled	6.1	17	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
69	c2ideE_		Alignment	not modelled	6.0	11	**PDB header:**biosynthetic protein **Chain:** E: **PDB Molecule:**molybdenum cofactor biosynthesis protein c; **PDBTitle:** crystal structure of the molybdenum cofactor biosynthesis protein c2 (ttha1789) from thermus theromophilus hb8
70	d1m5wa_		Alignment	not modelled	6.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
71	c3r8wC_		Alignment	not modelled	5.9	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-isopropylmalate dehydrogenase 2, chloroplastic; **PDBTitle:** structure of 3-isopropylmalate dehydrogenase isoform 2 from2 arabidopsis thaliana at 2.2 angstrom resolution
72	d1pb1a_		Alignment	not modelled	5.9	13	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
73	d1hqsa_		Alignment	not modelled	5.9	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
74	d1ekxa1		Alignment	not modelled	5.8	27	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
75	c2h90A_		Alignment	not modelled	5.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
76	c3jvvA_		Alignment	not modelled	5.8	10	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
77	d1ad1a_		Alignment	not modelled	5.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
78	c3blxM_		Alignment	not modelled	5.7	14	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**isocitrate dehydrogenase [nad] subunit 1; **PDBTitle:** yeast isocitrate dehydrogenase (apo form)
79	c3mhsE_		Alignment	not modelled	5.7	8	**PDB header:**hydrolase/transcription regulator/protei **Chain:** E: **PDB Molecule:**saga-associated factor 73; **PDBTitle:** structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde

80	d1cm7a_	Alignment	not modelled	5.7	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
81	c3g0kA_	Alignment	not modelled	5.6	15	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**putative membrane protein; **PDBTitle:** crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
82	d1xaca_	Alignment	not modelled	5.6	16	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
83	d1sjwa_	Alignment	not modelled	5.6	17	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
84	d1a05a_	Alignment	not modelled	5.5	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
85	d1e42a2	Alignment	not modelled	5.5	24	**Fold:**Subdomain of clathrin and coatomer appendage domain **Superfamily:**Subdomain of clathrin and coatomer appendage domain **Family:**Clathrin adaptor appendage, alpha and beta chain-specific domain
86	c3gk0H_	Alignment	not modelled	5.4	17	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
87	d1hyua4	Alignment	not modelled	5.3	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
88	c1yj7A_	Alignment	not modelled	5.3	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**escj; **PDBTitle:** crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
89	c3hz4A_	Alignment	not modelled	5.3	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
90	d1luza_	Alignment	not modelled	5.3	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
91	d1cnza_	Alignment	not modelled	5.3	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
92	d1unld_	Alignment	not modelled	5.2	12	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
93	c1unhD_	Alignment	not modelled	5.2	12	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**cyclin-dependent kinase 5 activator 1; **PDBTitle:** structural mechanism for the inhibition of cdk5-p25 by2 roscovitine, aloisine and indirubin.
94	d1ddwa_	Alignment	not modelled	5.2	13	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Enabled/VASP homology 1 domain (EVH1 domain)
95	d1iz5a1	Alignment	not modelled	5.2	14	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
96	c3b4oB_	Alignment	not modelled	5.2	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**phenazine biosynthesis protein a/b; **PDBTitle:** crystal structure of phenazine biosynthesis protein phza/b2 from burkholderia cepacia r18194, apo form
97	d1wgka_	Alignment	not modelled	5.1	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**C9orf74 homolog
98	d1g2ua_	Alignment	not modelled	5.1	15	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
99	d1yhta1	Alignment	not modelled	5.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain