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Description	P21369
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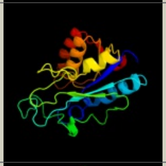
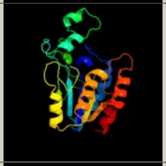
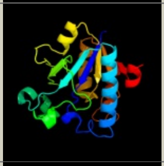
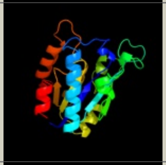
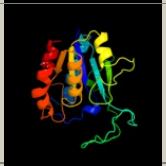
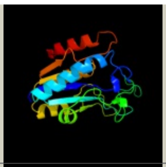
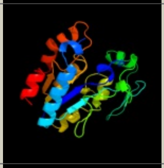
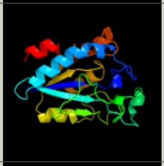
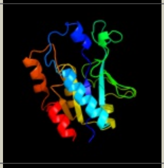
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2h0rD_	Alignment		100.0	34	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
2	c2wtaA_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
3	d1nbaa_	Alignment		100.0	20	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
4	c3hu5B_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein from desulfovibrio2 vulgaris subsp. vulgaris str. hildenborough
5	c2fq1A_	Alignment		100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**isochorismatase; **PDBTitle:** crystal structure of the two-domain non-ribosomal peptide synthetase2 entb containing isochorismate lyase and aryl-carrier protein domains
6	c3r2jC_	Alignment		100.0	37	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha/beta-hydrolase-like protein; **PDBTitle:** crystal structure of pnc1 from l. infantum in complex with nicotinate
7	c3irvA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cysteine hydrolase; **PDBTitle:** crystal structure of cysteine hydrolase pspph_2384 from pseudomonas2 syringae pv. phaseolicola 1448a
8	d1nf9a_	Alignment		100.0	21	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
9	c3oqpA_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
10	d1j2ra_	Alignment		100.0	22	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
11	c3ot4F_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**putative isochorismatase; **PDBTitle:** structure and catalytic mechanism of bordetella bronchiseptica nicf

12	d1im5a_	Alignment		100.0	42	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
13	c3oqpB_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
14	c3kl2K_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** K: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase from streptomyces2 avermitilis
15	c3gbcA_	Alignment		100.0	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pyrazinamidase/nicotinamidas pnca; **PDBTitle:** determination of the crystal structure of the pyrazinamidase from2 m.tuberculosis : a structure-function analysis for prediction3 resistance to pyrazinamide
16	c3hb7G_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
17	c3eefA_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-carbamoylsarcosine amidase related protein; **PDBTitle:** crystal structure of n-carbamoylsarcosine amidase from thermoplasma2 acidophilum
18	c3mcwA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
19	c3o93A_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
20	c3lqyA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase; **PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
21	c2a67C_	Alignment	not modelled	100.0	24	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
22	c1yzvA_	Alignment	not modelled	100.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** hypothetical protein from trypanosoma cruzi
23	d1yaca_	Alignment	not modelled	100.0	26	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
24	c2b34C_	Alignment	not modelled	100.0	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**mar1 ribonuclease; **PDBTitle:** structure of mar1 ribonuclease from caenorhabditis elegans
25	d1x9ga_	Alignment	not modelled	100.0	24	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
26	d1cmwa2	Alignment	not modelled	83.4	19	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
27	d1tfra2	Alignment	not modelled	67.4	14	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
28	c2ihnA_	Alignment	not modelled	66.9	12	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ribonuclease h; **PDBTitle:** co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
						Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes

29	d1tyza_	Alignment	not modelled	63.6	16	**Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
30	d1xdpa3	Alignment	not modelled	55.7	18	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
31	d1xp8a1	Alignment	not modelled	54.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
32	c1xdoB_	Alignment	not modelled	53.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
33	d1a9xa3	Alignment	not modelled	53.5	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
34	d1f2da_	Alignment	not modelled	50.6	14	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
35	c1cmwA_	Alignment	not modelled	47.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** crystal structure of taq dna-polymerase shows a new2 orientation for the structure-specific nuclease domain
36	c3fkjA_	Alignment	not modelled	45.1	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerases; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution
37	d1vp8a_	Alignment	not modelled	39.4	21	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
38	c2b4qB_	Alignment	not modelled	38.9	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
39	d1oi7a1	Alignment	not modelled	38.7	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
40	c3euaD_	Alignment	not modelled	38.4	10	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative fructose-aminoacid-6-phosphate deglycase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (bsu32610) from2 bacillus subtilis at 1.90 a resolution
41	d1xu9a_	Alignment	not modelled	38.2	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
42	d1qsga_	Alignment	not modelled	38.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	d2dt5a1	Alignment	not modelled	36.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional repressor Rex, N-terminal domain
44	c1xp8A_	Alignment	not modelled	36.1	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
45	c2nm0B_	Alignment	not modelled	35.5	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
46	c2f06B_	Alignment	not modelled	35.3	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of protein bt0572 from bacteroides thetaiotaomicron
47	c1x1qA_	Alignment	not modelled	34.3	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
48	d1nhpa2	Alignment	not modelled	33.5	25	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
49	d1gz6a_	Alignment	not modelled	32.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
50	d2bd0a1	Alignment	not modelled	32.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
51	c3toxG_	Alignment	not modelled	31.9	21	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
52	c3nugA_	Alignment	not modelled	31.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** crystal structure of wild type tetrameric pyridoxal 4-dehydrogenase2 from mesorhizobium loti
53	c2recB_	Alignment	not modelled	30.1	8	**PDB header:**helicase **PDB COMPND:**
						Fold:NAD(P)-binding Rossmann-fold domains

54	d2ae2a_	Alignment	not modelled	28.6	15	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
55	c3g8rA_	Alignment	not modelled	27.9	12	**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
56	c2ptgA_	Alignment	not modelled	27.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** crystal structure of eimeria tenella enoyl reductase
57	d1ooea_	Alignment	not modelled	27.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
58	d2bs2a2	Alignment	not modelled	27.7	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
59	d1qopb_	Alignment	not modelled	26.7	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
60	d1duvg2	Alignment	not modelled	26.5	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
61	d1pv8a_	Alignment	not modelled	26.3	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
62	d1ae1a_	Alignment	not modelled	25.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
63	c3v2hB_	Alignment	not modelled	25.9	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**d-beta-hydroxybutyrate dehydrogenase; **PDBTitle:** the crystal structure of d-beta-hydroxybutyrate dehydrogenase from2 sinorhizobium meliloti
64	c3rd5A_	Alignment	not modelled	24.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mypaa.01249.c; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium paratuberculosis
65	c3i1jB_	Alignment	not modelled	24.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short chain **PDBTitle:** structure of a putative short chain dehydrogenase from2 pseudomonas syringae
66	d1o5wa1	Alignment	not modelled	24.7	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
67	c2dy0A_	Alignment	not modelled	24.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
68	c3d3kD_	Alignment	not modelled	24.2	5	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
69	d1mg5a_	Alignment	not modelled	23.5	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
70	d1v8za1	Alignment	not modelled	23.4	17	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
71	d1dxha2	Alignment	not modelled	23.2	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
72	c2p68A_	Alignment	not modelled	23.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of aq_1716 from aquifex aeolicus vf5
73	c3grkE_	Alignment	not modelled	23.0	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
74	d1ulsa_	Alignment	not modelled	22.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
75	c2cfcB_	Alignment	not modelled	22.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-(r)-hydroxypropyl-com dehydrogenase; **PDBTitle:** structural basis for stereo selectivity in the (r)- and2 (s)-hydroxypropylethane thiosulfonate dehydrogenases
76	c3rkrC_	Alignment	not modelled	22.3	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**short chain oxidoreductase; **PDBTitle:** crystal structure of a metagenomic short-chain oxidoreductase (sdr) in2 complex with nadp
77	c1vlvA_	Alignment	not modelled	22.0	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
78	c2vyeA_	Alignment	not modelled	22.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex

79	d1c0pa1	Alignment	not modelled	21.8	21	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**D-aminoacid oxidase, N-terminal domain
80	d1ulua_	Alignment	not modelled	21.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
81	d2pd4a1	Alignment	not modelled	21.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	c3edmD_	Alignment	not modelled	21.2	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short chain dehydrogenase; **PDBTitle:** crystal structure of a short chain dehydrogenase from agrobacterium2 tumefaciens
83	d1pr9a_	Alignment	not modelled	21.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
84	c2ntnB_	Alignment	not modelled	21.1	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of maba-c60v/g139a/s144l
85	c3m1aF_	Alignment	not modelled	21.1	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** the crystal structure of a short-chain dehydrogenase from2 streptomyces avermitilis to 2a
86	c2nwqA_	Alignment	not modelled	20.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable short-chain dehydrogenase; **PDBTitle:** short chain dehydrogenase from pseudomonas aeruginosa
87	d1xsea_	Alignment	not modelled	20.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	d2a4ka1	Alignment	not modelled	20.6	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	c3ek2D_	Alignment	not modelled	20.1	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of eonyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
90	c2ha8A_	Alignment	not modelled	20.1	6	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**tar (hiv-1) rna loop binding protein; **PDBTitle:** methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
91	c3l77A_	Alignment	not modelled	19.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain alcohol dehydrogenase; **PDBTitle:** x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
92	d1k2wa_	Alignment	not modelled	19.8	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
93	c2ehdB_	Alignment	not modelled	19.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, short-chain dehydrogenase/reductase family; **PDBTitle:** crystal structure analysis of oxidoreductase
94	d1ubea1	Alignment	not modelled	19.4	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
95	c2w37A_	Alignment	not modelled	19.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
96	c2pd6D_	Alignment	not modelled	19.2	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**estradiol 17-beta-dehydrogenase 8; **PDBTitle:** structure of human hydroxysteroid dehydrogenase type 8, hsd17b8
97	d1xq1a_	Alignment	not modelled	19.2	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
98	d2o8ra3	Alignment	not modelled	19.1	17	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
99	c3g68A_	Alignment	not modelled	19.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative phosphosugar isomerase; **PDBTitle:** crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution