Phyre²

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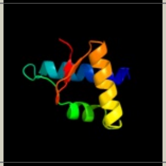
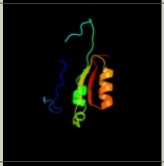
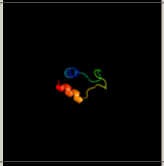
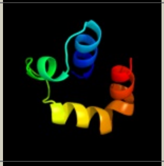
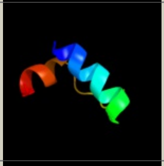
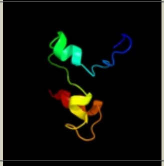
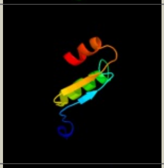
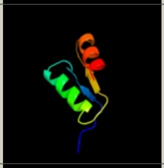
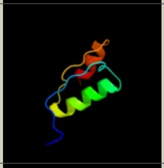
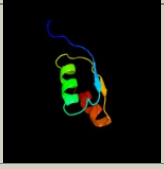
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2v9va2	Alignment		82.8	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
2	c2v9vA_	Alignment		67.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** crystal structure of moorella thermoacetica selb(377-511)
3	d1musa_	Alignment		65.8	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
4	d1b7ea_	Alignment		59.1	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Transposase inhibitor (Tn5 transposase)
5	c6paxA_	Alignment		57.1	24	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**homeobox protein pax-6; **PDBTitle:** crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
6	c3hefB_	Alignment		49.7	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
7	d2ezha_	Alignment		47.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
8	d2ezia_	Alignment		46.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
9	d1pdnc_	Alignment		24.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
10	d1mpga1	Alignment		23.1	12	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**DNA repair glycosylase, 2 C-terminal domains
11	c2plyB_	Alignment		21.9	8	**PDB header:**translation/rna **Chain:** B: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna binding fragment of elongation factor2 selb in complex with secis rna.

12	c2pfsA_	Alignment		21.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
13	c3r1iB_	Alignment		20.6	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain type dehydrogenase/reductase; **PDBTitle:** crystal structure of a short-chain type dehydrogenase/reductase from2 mycobacterium marinum
14	c3ctmH_	Alignment		16.4	20	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
15	d1osna_	Alignment		15.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
16	c3emkA_	Alignment		15.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
17	d1ajza_	Alignment		15.5	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
18	c3ak4C_	Alignment		14.9	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-dependent quinuclidinone reductase; **PDBTitle:** crystal structure of nadh-dependent quinuclidinone reductase from2 agrobacterium tumefaciens
19	c2kvcA_	Alignment		14.1	23	**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
20	c3pk0B_	Alignment		14.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of short-chain dehydrogenase/reductase sdr from2 mycobacterium smegmatis
21	c2vp8A_	Alignment	not modelled	13.4	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
22	d1cyda_	Alignment	not modelled	13.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
23	d3bpya1	Alignment	not modelled	12.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
24	c2y5sA_	Alignment	not modelled	11.5	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
25	d6paxa2	Alignment	not modelled	11.4	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
26	d1dlwa_	Alignment	not modelled	11.3	9	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
27	c2z1nA_	Alignment	not modelled	11.3	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of ape0912 from aeropyrum pernix k1
28	c3gk0H_	Alignment	not modelled	11.1	24	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
29	c2vdaA_	Alignment	not modelled	10.9	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca;

						PDBTitle: solution structure of the seca-signal peptide complex
30	c2rfpA_	Alignment	not modelled	10.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ntp pyrophosphohydrolase; **PDBTitle:** crystal structure of putative ntp pyrophosphohydrolase2 (yp_001813558.1) from exiguobacterium sibiricum 255-15 at 1.74 a3 resolution
31	d1rh6a_	Alignment	not modelled	10.8	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
32	c3ol4B_	Alignment	not modelled	10.6	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
33	d1k78a2	Alignment	not modelled	10.6	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Paired domain
34	c2k27A_	Alignment	not modelled	10.0	23	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**paired box protein pax-8; **PDBTitle:** solution structure of human pax8 paired box domain
35	c3co7C_	Alignment	not modelled	9.8	14	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**forkhead box protein o1; **PDBTitle:** crystal structure of foxo1 dbd bound to dbe2 dna
36	d1iyxa1	Alignment	not modelled	9.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
37	d3orca_	Alignment	not modelled	9.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
38	d1bdba_	Alignment	not modelled	9.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
39	c2kzvA_	Alignment	not modelled	9.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
40	c3mx7A_	Alignment	not modelled	9.1	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
41	d1pm6a_	Alignment	not modelled	9.0	15	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Excisionase-like
42	d2o23a1	Alignment	not modelled	8.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	c2o2sA_	Alignment	not modelled	8.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acyl carrier reductase; **PDBTitle:** the structure of t. gondii enoyl acyl carrier protein reductase in2 complex with nad and triclosan
44	c3fmtF_	Alignment	not modelled	8.7	13	**PDB header:**replication inhibitor/dna **Chain:** F: **PDB Molecule:**protein seqa; **PDBTitle:** crystal structure of seqa bound to dna
45	d1ae1a_	Alignment	not modelled	8.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	d1m5wa_	Alignment	not modelled	8.4	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
47	c3aq8A_	Alignment	not modelled	8.4	4	**PDB header:**oxygen binding **Chain:** A: **PDB Molecule:**group 1 truncated hemoglobin; **PDBTitle:** crystal structure of truncated hemoglobin from tetrahymena pyriformis,2 q46e mutant, fe(iii) form
48	c3gafF_	Alignment	not modelled	8.4	15	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**7-alpha-hydroxysteroid dehydrogenase; **PDBTitle:** 2.2a crystal structure of 7-alpha-hydroxysteroid2 dehydrogenase from brucella melitensis
49	c3gdfA_	Alignment	not modelled	8.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable nadp-dependent mannitol dehydrogenase; **PDBTitle:** crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladosporium herbarum.
50	c3l1pA_	Alignment	not modelled	8.2	20	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**pou domain, class 5, transcription factor 1; **PDBTitle:** pou protein:dna complex
51	c3rihB_	Alignment	not modelled	7.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain dehydrogenase or reductase; **PDBTitle:** crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
52	c1e17A_	Alignment	not modelled	7.7	9	**PDB header:**dna binding domain **Chain:** A: **PDB Molecule:**afx; **PDBTitle:** solution structure of the dna binding domain of the human2 forkhead transcription factor afx (foxo4)
53	c2wdzD_	Alignment	not modelled	7.5	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
54	c3rkrC_	Alignment	not modelled	7.4	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
						Fold:NAD(P)-binding Rossmann-fold domains

55	d1h5qa_	Alignment	not modelled	7.3	11	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
56	d1d7oa_	Alignment	not modelled	7.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
57	c2ixsB_	Alignment	not modelled	7.0	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sdai restriction endonuclease; **PDBTitle:** structure of sdai restriction endonuclease
58	d1s69a_	Alignment	not modelled	6.9	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
59	d1xi8a3	Alignment	not modelled	6.8	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
60	d1vl8a_	Alignment	not modelled	6.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	d1vi7a1	Alignment	not modelled	6.6	19	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
62	c3afnC_	Alignment	not modelled	6.6	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of aldose reductase a1-r complexed with nadp
63	d1xb4a2	Alignment	not modelled	6.6	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
64	c3k6qB_	Alignment	not modelled	6.6	14	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative ligand binding protein; **PDBTitle:** crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
65	d1idra_	Alignment	not modelled	6.5	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Truncated hemoglobin
66	d1g31a_	Alignment	not modelled	6.5	20	**Fold:**GroES-like **Superfamily:**GroES-like **Family:**GroES
67	c3iccA_	Alignment	not modelled	6.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative 3-oxoacyl-(acyl carrier protein) reductase; **PDBTitle:** crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
68	d2c6ya1	Alignment	not modelled	6.4	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
69	c3cxtA_	Alignment	not modelled	6.4	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
70	c1qcrD_	Alignment	not modelled	6.3	8	**PDB header:** **PDB COMPND:**
71	d1fmca_	Alignment	not modelled	6.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	c3rf7A_	Alignment	not modelled	6.2	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**iron-containing alcohol dehydrogenase; **PDBTitle:** crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
73	d1d1la_	Alignment	not modelled	6.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
74	c3ksuA_	Alignment	not modelled	6.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-acyl carrier protein reductase; **PDBTitle:** crystal structure of short-chain dehydrogenase from2 oenococcus oeni psu-1
75	c3f9iB_	Alignment	not modelled	6.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-oxoacyl-[acyl-carrier-protein] reductase; **PDBTitle:** crystal structure of 3-ketoacyl-(acyl-carrier-protein) reductase2 rickettsia prowazekii
76	d1ejxa_	Alignment	not modelled	5.9	13	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
77	c3hluA_	Alignment	not modelled	5.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein duf2179; **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
78	d4croa_	Alignment	not modelled	5.6	22	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
79	d2giab1	Alignment	not modelled	5.5	50	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Guide RNA binding protein gBP
80	c2giaB_	Alignment	not modelled	5.5	50	**PDB header:**translation **Chain:** B: **PDB Molecule:**mitochondrial rna-binding protein 1; **PDBTitle:** crystal structures of trypanosoma bruciei mrp1/mrp2
						PDB header:hydrolase

81	c1iszA_	Alignment	not modelled	5.5	5	**Chain:** A: **PDB Molecule:**endo-1,4-beta-d-xylanase; **PDBTitle:** crystal structure of xylanase from streptomyces2 olivaceoviridis e-86 complexed with galactose
82	d1un2a_	Alignment	not modelled	5.5	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
83	d2i7pa1	Alignment	not modelled	5.5	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
84	c1vi2B_	Alignment	not modelled	5.5	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
85	c2kl8A_	Alignment	not modelled	5.4	8	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
86	c2pijB_	Alignment	not modelled	5.4	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
87	c2b4qB_	Alignment	not modelled	5.4	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rhamnolipids biosynthesis 3-oxoacyl-[acyl- **PDBTitle:** pseudomonas aeruginosa rhlg/nadp active-site complex
88	d1sbya1	Alignment	not modelled	5.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	d2cvea1	Alignment	not modelled	5.4	16	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**YigZ N-terminal domain-like
90	d2abka_	Alignment	not modelled	5.3	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**Endonuclease III
91	d1w6ta1	Alignment	not modelled	5.3	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
92	c3cwbQ_	Alignment	not modelled	5.2	8	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
93	d1ja9a_	Alignment	not modelled	5.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	d1xsea_	Alignment	not modelled	5.2	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	d4ubpa_	Alignment	not modelled	5.1	12	**Fold:**Urease, gamma-subunit **Superfamily:**Urease, gamma-subunit **Family:**Urease, gamma-subunit
96	d2ptza1	Alignment	not modelled	5.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**Enolase
97	c1yb1B_	Alignment	not modelled	5.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**17-beta-hydroxysteroid dehydrogenase type xi; **PDBTitle:** crystal structure of human 17-beta-hydroxysteroid dehydrogenase type2 xi
98	d1q7ba_	Alignment	not modelled	5.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases