Phyre2

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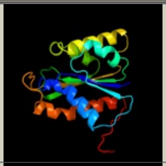
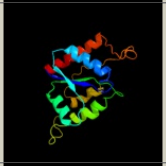
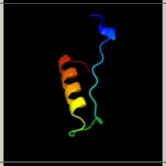
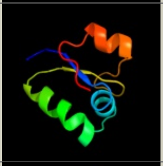
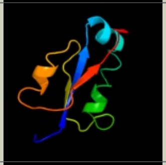
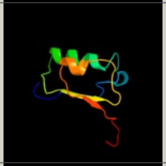
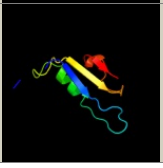
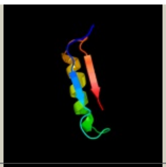
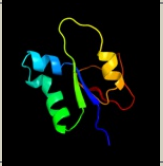
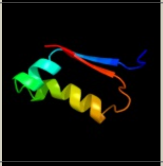
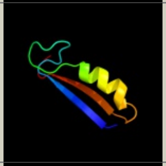
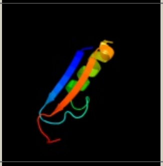
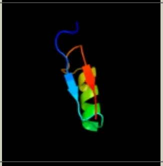
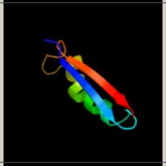
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cfza_	Alignment		100.0	38	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Hydrogenase maturating endopeptidase HybD
2	c2e85B_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrogenase 3 maturation protease; **PDBTitle:** crystal structure of the hydrogenase 3 maturation protease
3	c3pu6A_	Alignment		100.0	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of an uncharacterized protein from wolinella2 succinogenes
4	d1c8ba_	Alignment		96.9	28	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
5	c3fvwA_	Alignment		90.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
6	d9ldta1	Alignment		85.1	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
7	c2z2jA_	Alignment		84.2	34	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from mycobacterium2 tuberculosis
8	c2cukC_	Alignment		83.4	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
9	d1fmfa_	Alignment		81.7	11	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
10	c2ph5A_	Alignment		80.2	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**homospermidine synthase; **PDBTitle:** crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
11	d1a9xa3	Alignment		79.8	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like

12	d2ldxa1	Alignment		78.9	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
13	c2vhyB_	Alignment		78.2	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
14	d1i0za1	Alignment		77.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
15	d1jf8a_	Alignment		77.2	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
16	d5pnta_	Alignment		76.9	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
17	d5ldha1	Alignment		76.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
18	d1dg9a_	Alignment		76.0	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
19	d2c42a3	Alignment		75.4	15	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
20	d1i10a1	Alignment		74.1	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
21	c3d0oA_	Alignment	not modelled	73.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lactate dehydrogenase 1; **PDBTitle:** crystal structure of lactate dehydrogenase from2 staphylococcus aureus
22	d1pjca1	Alignment	not modelled	72.5	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
23	d2gv8a1	Alignment	not modelled	69.0	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
24	c3ggpA_	Alignment	not modelled	68.6	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
25	c4a26B_	Alignment	not modelled	67.1	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative c-1-tetrahydrofolate synthase, cytoplasmic; **PDBTitle:** the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
26	c1wwkA_	Alignment	not modelled	67.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
27	c3b1fA_	Alignment	not modelled	66.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans
28	d2jfga1	Alignment	not modelled	66.8	24	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain

29	c3gucB_	Alignment	not modelled	66.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ubiquitin-like modifier-activating enzyme 5; **PDBTitle:** human ubiquitin-activating enzyme 5 in complex with amppnp
30	d2dlda1	Alignment	not modelled	64.8	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
31	c2gi4A_	Alignment	not modelled	64.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**possible phosphotyrosine protein phosphatase; **PDBTitle:** solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
32	d1gdha1	Alignment	not modelled	64.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
33	c1d4fD_	Alignment	not modelled	63.6	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
34	d1qp8a1	Alignment	not modelled	62.6	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
35	c3dapB_	Alignment	not modelled	62.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
36	c2rirA_	Alignment	not modelled	60.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase, a chain; **PDBTitle:** crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
37	c2yxbA_	Alignment	not modelled	60.6	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**coenzyme b12-dependent mutase; **PDBTitle:** crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
38	d1wu2a3	Alignment	not modelled	60.4	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
39	d1np3a2	Alignment	not modelled	60.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
40	c1gdhA_	Alignment	not modelled	60.0	17	**PDB header:**oxidoreductase(choh (d)-nad(p)+ (a)) **Chain:** A: **PDB Molecule:**d-glycerate dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
41	c3tovB_	Alignment	not modelled	59.3	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase family 9; **PDBTitle:** the crystal structure of the glycosyl transferase family 9 from2 veillonella parvula dsm 2008
42	c1ez4B_	Alignment	not modelled	59.0	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of non-allosteric l-lactate dehydrogenase2 from lactobacillus pentosus at 2.3 angstrom resolution
43	d1ygya1	Alignment	not modelled	58.8	32	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
44	c3gvxA_	Alignment	not modelled	58.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerate dehydrogenase related protein; **PDBTitle:** crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
45	d1hyha1	Alignment	not modelled	57.7	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
46	d2ptha_	Alignment	not modelled	57.4	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
47	d1n1ea2	Alignment	not modelled	56.1	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
48	c2g5cD_	Alignment	not modelled	56.1	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
49	d1mx3a1	Alignment	not modelled	56.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
50	c3vh1A_	Alignment	not modelled	55.7	31	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of saccharomyces cerevisiae atg7 (1-595)
51	d1f0ya2	Alignment	not modelled	55.3	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
52	c1m6vE_	Alignment	not modelled	55.3	15	**PDB header:**ligase **Chain:** E: **PDB Molecule:**carbamoyl phosphate synthetase large chain; **PDBTitle:** crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
53	c3d64A_	Alignment	not modelled	55.2	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei

54	c3d1lB_	Alignment	not modelled	55.2	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
55	c3fi9B_	Alignment	not modelled	55.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from porphyromonas2 gingivalis
56	c3neaA_	Alignment	not modelled	54.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of peptidyl-trna hydrolase from francisella2 tularensis
57	c3v2iA_	Alignment	not modelled	54.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structure of a peptidyl-trna hydrolase (pth) from burkholderia2 thailandensis
58	c2g76A_	Alignment	not modelled	54.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
59	c2dbqA_	Alignment	not modelled	54.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
60	c1np3B_	Alignment	not modelled	54.1	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
61	c3d4oA_	Alignment	not modelled	54.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
62	d1a9xa4	Alignment	not modelled	53.8	14	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
63	d2ftsa3	Alignment	not modelled	53.7	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
64	c2fnzA_	Alignment	not modelled	53.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactate dehydrogenase; **PDBTitle:** crystal structure of the lactate dehydrogenase from cryptosporidium2 parvum complexed with cofactor (b-nicotinamide adenine dinucleotide)3 and inhibitor (oxamic acid)
65	c3h9gA_	Alignment	not modelled	53.4	24	**PDB header:**transferase/antibiotic **Chain:** A: **PDB Molecule:**mccb protein; **PDBTitle:** crystal structure of e. coli mccb + mcca-n7isoasn
66	d1f06a1	Alignment	not modelled	52.2	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	d1e5qa1	Alignment	not modelled	52.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
68	c3vh3A_	Alignment	not modelled	51.7	17	**PDB header:**metal binding protein/protein transport **Chain:** A: **PDB Molecule:**ubiquitin-like modifier-activating enzyme atg7; **PDBTitle:** crystal structure of atg7ctd-atg8 complex
69	c2ldxA_	Alignment	not modelled	51.7	26	**PDB header:**oxidoreductase(choh(d)-nad(a)) **Chain:** A: **PDB Molecule:**apo-lactate dehydrogenase; **PDBTitle:** characterization of the antigenic sites on the refined 3-2 angstroms resolution structure of mouse testicular lactate3 dehydrogenase c4
70	c3ktdC_	Alignment	not modelled	51.4	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
71	d1sc6a1	Alignment	not modelled	50.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
72	c1vqwB_	Alignment	not modelled	50.4	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein with similarity to flavin-containing **PDBTitle:** crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
73	c3k96B_	Alignment	not modelled	50.4	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
74	d1li4a1	Alignment	not modelled	50.3	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
75	c2xdoC_	Alignment	not modelled	50.1	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tetx2 protein; **PDBTitle:** structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
76	d1ez4a1	Alignment	not modelled	49.6	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
77	d1j4aa1	Alignment	not modelled	49.4	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
78	c3gznB_	Alignment	not modelled	49.3	27	**PDB header:**protein binding/ligase **Chain:** B: **PDB Molecule:**nedd8-activating enzyme e1 catalytic subunit;

						PDBTitle: structure of nedd8-activating enzyme in complex with nedd82 and mln4924
79	c3kboB_	Alignment	not modelled	49.1	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate/hydroxypyruvate reductase a; **PDBTitle:** 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
80	c2eklA_	Alignment	not modelled	48.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
81	c3n58D_	Alignment	not modelled	48.8	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
82	c2q1uA_	Alignment	not modelled	48.7	16	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmf in2 complex with nad+ and udp
83	c2cwdA_	Alignment	not modelled	48.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight phosphotyrosine protein phosphatase; **PDBTitle:** crystal structure of tt1001 protein from thermus thermophilus hb8
84	c3n7uD_	Alignment	not modelled	47.5	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
85	d2g5ca2	Alignment	not modelled	47.1	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
86	d1ryba_	Alignment	not modelled	46.9	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Peptidyl-tRNA hydrolase-like **Family:**Peptidyl-tRNA hydrolase-like
87	d1dxya1	Alignment	not modelled	46.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
88	c2uyyD_	Alignment	not modelled	46.7	28	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
89	c2x2oA_	Alignment	not modelled	46.6	27	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
90	c1hyhA_	Alignment	not modelled	46.3	31	**PDB header:**oxidoreductase (choh(d)-nad+(a)) **Chain:** A: **PDB Molecule:**l-2-hydroxyisocaproate dehydrogenase; **PDBTitle:** crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
91	d1rlja_	Alignment	not modelled	46.3	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
92	c1j4aA_	Alignment	not modelled	45.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
93	d1uz5a3	Alignment	not modelled	45.3	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
94	d2vapa1	Alignment	not modelled	44.9	27	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
95	d1p8aa_	Alignment	not modelled	44.6	27	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
96	d2qwxa1	Alignment	not modelled	44.2	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
97	d1llca1	Alignment	not modelled	43.9	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
98	c3dzbA_	Alignment	not modelled	43.4	25	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
99	d2hmva1	Alignment	not modelled	43.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
100	d1leha1	Alignment	not modelled	42.5	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
101	d1b0aa1	Alignment	not modelled	42.4	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
102	d1t0ia_	Alignment	not modelled	42.2	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
						Fold:NAD(P)-binding Rossmann-fold domains

103	d1uxja1	Alignment	not modelled	41.8	22	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
104	d1a4ia1	Alignment	not modelled	41.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
105	d1v8ba1	Alignment	not modelled	41.6	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
106	d1hdoa_	Alignment	not modelled	41.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
107	d2bkaa1	Alignment	not modelled	41.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
108	d1d4aa_	Alignment	not modelled	41.0	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
109	c2g1uA_	Alignment	not modelled	40.8	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
110	c3gviB_	Alignment	not modelled	40.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of lactate/malate dehydrogenase from2 brucella melitensis in complex with adp
111	c2omeA_	Alignment	not modelled	40.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**c-terminal-binding protein 2; **PDBTitle:** crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
112	d1jl3a_	Alignment	not modelled	40.5	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
113	c3nklA_	Alignment	not modelled	40.1	26	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
114	c3lcmB_	Alignment	not modelled	40.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
115	c2gcgB_	Alignment	not modelled	40.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
116	c3oetF_	Alignment	not modelled	38.9	25	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
117	c2j6iC_	Alignment	not modelled	38.7	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
118	c3jviA_	Alignment	not modelled	38.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
119	d1fcda1	Alignment	not modelled	38.4	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
120	c1cjcA_	Alignment	not modelled	38.3	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (adrenodoxin reductase); **PDBTitle:** structure of adrenodoxin reductase of mitochondrial p4502 systems