Phyre^2

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Description	P0A9M2
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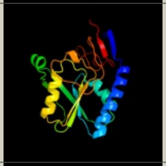
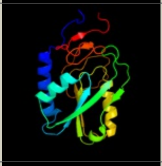
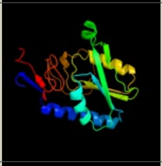
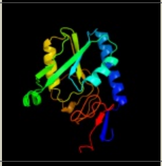
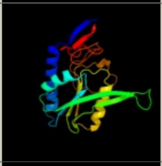
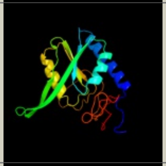
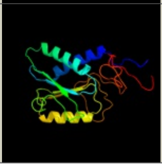
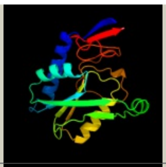
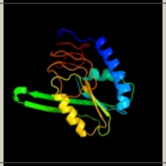
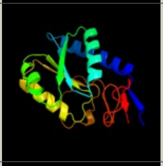
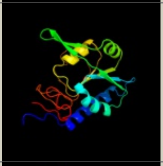
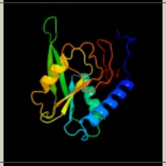
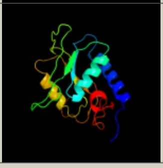
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1g9sa_	Alignment		100.0	99	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
2	d1fsga_	Alignment		100.0	31	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
3	c3kb8A_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
4	d1cjba_	Alignment		100.0	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
5	d1yfza1	Alignment		100.0	55	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
6	c1yfzA_	Alignment		100.0	55	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
7	d1p17b_	Alignment		100.0	36	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
8	d1j7ja_	Alignment		100.0	95	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
9	c2jbhA_	Alignment		100.0	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
10	d1tc1a_	Alignment		100.0	40	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
11	d1z7ga1	Alignment		100.0	31	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

12	c3o7mD_	Alignment		100.0	48	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
13	d1hgxa_	Alignment		100.0	39	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
14	c2ywtA_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
15	d1pzma_	Alignment		100.0	37	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
16	c1pzmB_	Alignment		100.0	34	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
17	d1dqna_	Alignment		100.0	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
18	d2igba1	Alignment		100.0	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
19	d1ufra_	Alignment		100.0	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
20	d1w30a_	Alignment		100.0	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
21	d1a3ca_	Alignment	not modelled	100.0	22	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
22	d1vdma1	Alignment	not modelled	100.0	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
23	c2jkzB_	Alignment	not modelled	100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** saccharomyces cerevisiae hypoxanthine-guanine2 phosphoribosyltransferase in complex with gmp (guanosine 5'3 -monophosphate) (orthorhombic crystal form)
24	d1nula_	Alignment	not modelled	99.9	18	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
25	d1wd5a_	Alignment	not modelled	99.9	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
26	d1g2qa_	Alignment	not modelled	99.8	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
27	d1ecfa1	Alignment	not modelled	99.8	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
28	d1gph11	Alignment	not modelled	99.8	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)

29	d1zn7a1	Alignment	not modelled	99.8	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
30	c1ecjB_	Alignment	not modelled	99.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
31	c1gph1_	Alignment	not modelled	99.7	15	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
32	d1vcha1	Alignment	not modelled	99.7	11	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
33	d1y0ba1	Alignment	not modelled	99.7	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
34	c2dy0A_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
35	d1o57a2	Alignment	not modelled	99.7	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
36	c1o57A_	Alignment	not modelled	99.7	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
37	d1l1qa_	Alignment	not modelled	99.6	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
38	c2wnsB_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** human orotate phosphoribosyltransferase (oprtase) domain of2 uridine 5'-monophosphate synthase (umps) in complex with3 its substrate orotidine 5'-monophosphate (omp)
39	c2p1zA_	Alignment	not modelled	99.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase; **PDBTitle:** crystal structure of phosphoribosyltransferase from corynebacterium2 diphtheriae
40	d1mzva_	Alignment	not modelled	99.6	14	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
41	d1qb7a_	Alignment	not modelled	99.5	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
42	d1lh0a_	Alignment	not modelled	99.5	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
43	c2yzkC_	Alignment	not modelled	99.5	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 aeropyrum pernix
44	c3dezA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** crystal structure of orotate phosphoribosyltransferase from2 streptococcus mutans
45	c3lpnB_	Alignment	not modelled	99.5	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of the phosphoribosylpyrophosphate (prpp) synthetase2 from thermoplasma volcanium in complex with an atp analog (ampcpp).
46	d2aeea1	Alignment	not modelled	99.5	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
47	c3n2lA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
48	c3mjdA_	Alignment	not modelled	99.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.9 angstrom crystal structure of orotate2 phosphoribosyltransferase (pyre) francisella tularensis.
49	c2przB_	Alignment	not modelled	99.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**orotate phosphoribosyltransferase 1; **PDBTitle:** s. cerevisiae orotate phosphoribosyltransferase complexed2 with omp
50	c3efhB_	Alignment	not modelled	99.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase 1; **PDBTitle:** crystal structure of human phosphoribosyl pyrophosphate2 synthetase 1
51	c2ehjA_	Alignment	not modelled	99.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of uracil phosphoribosyl transferase
52	c2c4kD_	Alignment	not modelled	99.4	20	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
53	c1dkrB_	Alignment	not modelled	99.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase; **PDBTitle:** crystal structures of bacillus subtilis

						phosphoribosylpyrophosphate2 synthetase: molecular basis of allosteric inhibition and activation.
54	d1o5oa_	Alignment	not modelled	99.4	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
55	d1i5ea_	Alignment	not modelled	99.3	17	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
56	d1dkua2	Alignment	not modelled	99.3	24	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
57	c3m3hA_	Alignment	not modelled	99.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 1.75 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase from bacillus anthracis str. 'ames3 ancestor'
58	d1u9ya2	Alignment	not modelled	99.3	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
59	d2c4ka2	Alignment	not modelled	99.3	21	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
60	c1u9yD_	Alignment	not modelled	99.3	20	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** crystal structure of phosphoribosyl diphosphate synthase2 from methanocaldococcus jannaschii
61	c2e55D_	Alignment	not modelled	99.3	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** structure of aq2163 protein from aquifex aeolicus
62	c3dahB_	Alignment	not modelled	99.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribose-phosphate pyrophosphokinase; **PDBTitle:** 2.3 a crystal structure of ribose-phosphate pyrophosphokinase from2 burkholderia pseudomallei
63	c3qw4B_	Alignment	not modelled	99.2	18	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**ump synthase; **PDBTitle:** structure of leishmania donovani ump synthase
64	d1xtta1	Alignment	not modelled	99.2	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
65	d1bd3a_	Alignment	not modelled	99.1	20	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
66	c3dmpD_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uracil phosphoribosyltransferase; **PDBTitle:** 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
67	d1v9sa1	Alignment	not modelled	99.0	16	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
68	d1u9ya1	Alignment	not modelled	94.8	9	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
69	d2c4ka1	Alignment	not modelled	91.6	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
70	d1dkua1	Alignment	not modelled	91.3	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosylpyrophosphate synthetase-like
71	d1vi2a1	Alignment	not modelled	76.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
72	c2hk8B_	Alignment	not modelled	74.6	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution
73	c3mmnA_	Alignment	not modelled	73.6	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidine kinase homolog; **PDBTitle:** crystal structure of the receiver domain of the histidine kinase cki12 from arabidopsis thaliana complexed with mg2+
74	c3o8qB_	Alignment	not modelled	72.5	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase i alpha; **PDBTitle:** 1.45 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae
75	c3fbtB_	Alignment	not modelled	70.2	17	**PDB header:**oxidoreductase, lyase **Chain:** B: **PDB Molecule:**chorismate mutase and shikimate 5-dehydrogenase **PDBTitle:** crystal structure of a chorismate mutase/shikimate 5-2 dehydrogenase fusion protein from clostridium3 acetobutylicum
76	d1vmea1	Alignment	not modelled	68.2	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
77	c3pgjB_	Alignment	not modelled	66.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.49 angstrom resolution crystal structure of shikimate 5-2 dehydrogenase (aroe) from vibrio cholerae o1 biovar eltor str. n169613 in complex with shikimate
78	c3pwzA_	Alignment	not modelled	66.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase 3; **PDBTitle:** crystal structure of an ael1 enzyme from pseudomonas putida
79	c3tozA_	Alignment	not modelled	66.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** 2.2 angstrom crystal structure of shikimate 5-

						dehydrogenase from2 listeria monocytogenes in complex with nad.
80	d1dcfa_	Alignment	not modelled	64.7	14	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**Receiver domain of the ethylene receptor
81	d1npya1	Alignment	not modelled	63.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
82	c3donA_	Alignment	not modelled	58.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from staphylococcus2 epidermidis
83	c1vi2B_	Alignment	not modelled	54.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase 2; **PDBTitle:** crystal structure of shikimate-5-dehydrogenase with nad
84	d1tk9a_	Alignment	not modelled	54.5	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
85	d1p77a1	Alignment	not modelled	53.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
86	d1u0sy_	Alignment	not modelled	52.1	28	**Fold:**Flavodoxin-like **Superfamily:**CheY-like **Family:**CheY-related
87	c3ej6D_	Alignment	not modelled	47.2	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
88	c2f00A_	Alignment	not modelled	47.1	7	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate--l-alanine ligase; **PDBTitle:** escherichia coli murc
89	c2eggA_	Alignment	not modelled	45.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate 5-dehydrogenase (aroe) from2 geobacillus kaustophilus
90	c1nytC_	Alignment	not modelled	45.5	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** shikimate dehydrogenase aroe complexed with nadp+
91	c1npyA_	Alignment	not modelled	43.1	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical shikimate 5-dehydrogenase-like **PDBTitle:** structure of shikimate 5-dehydrogenase-like protein hi0607
92	d1gtea3	Alignment	not modelled	42.6	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
93	d1nyta1	Alignment	not modelled	41.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
94	c1vmeB_	Alignment	not modelled	39.7	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
95	c3kwmC_	Alignment	not modelled	36.6	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a
96	d1h3da1	Alignment	not modelled	35.9	36	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
97	d2jfga1	Alignment	not modelled	34.4	33	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
98	c1gpjA_	Alignment	not modelled	34.3	23	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
99	d1x92a_	Alignment	not modelled	32.5	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**mono-SIS domain
100	d1nvta1	Alignment	not modelled	29.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
101	c2vd3B_	Alignment	not modelled	29.5	43	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
102	c1j6uA_	Alignment	not modelled	29.0	6	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate-alanine ligase murc; **PDBTitle:** crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
103	c1lkzB_	Alignment	not modelled	27.3	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose 5-phosphate isomerase a; **PDBTitle:** crystal structure of d-ribose-5-phosphate isomerase (rpia)2 from escherichia coli.
104	d1pjqa1	Alignment	not modelled	27.2	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
105	c3h5iA_	Alignment	not modelled	26.4	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator/sensory box protein/ggdef **PDBTitle:** crystal structure of the n-terminal domain of a response2 regulator/sensory box/ggdef 3-domain protein from3

						carboxydothermus hydrogenoformans
106	c1p74B_	Alignment	not modelled	26.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate 5-dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase (aroe) from2 haemophilus influenzae
107	c2d92A_	Alignment	not modelled	26.1	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**inad-like protein; **PDBTitle:** solution structure of the fifth pdz domain of inad-like2 protein
108	c1sy7B_	Alignment	not modelled	25.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**catalase 1; **PDBTitle:** crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
109	c2vsvB_	Alignment	not modelled	24.4	16	**PDB header:**protein-binding **Chain:** B: **PDB Molecule:**rhophilin-2; **PDBTitle:** crystal structure of the pdz domain of human rhophilin-2
110	d1o63a_	Alignment	not modelled	24.1	45	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
111	d1ve4a1	Alignment	not modelled	24.1	36	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
112	c3ca8B_	Alignment	not modelled	24.0	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
113	c2yvaB_	Alignment	not modelled	23.9	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dnaa initiator-associating protein diaa; **PDBTitle:** crystal structure of escherichia coli diaa
114	c2c1iA_	Alignment	not modelled	23.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
115	c3gl9B_	Alignment	not modelled	23.1	26	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**response regulator; **PDBTitle:** the structure of a histidine kinase-response regulator2 complex sheds light into two-component signaling and3 reveals a novel cis autophosphorylation mechanism
116	d1vaea_	Alignment	not modelled	22.8	13	**Fold:**PDZ domain-like **Superfamily:**PDZ domain-like **Family:**PDZ domain
117	d1nh8a1	Alignment	not modelled	22.5	55	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
118	c1m0sA_	Alignment	not modelled	22.3	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** northeast structural genomics consortium (nesg id ir21)
119	d1z7me1	Alignment	not modelled	21.8	64	**Fold:**Periplasmic binding protein-like II **Superfamily:**Periplasmic binding protein-like II **Family:**Phosphate binding protein-like
120	c3dfzB_	Alignment	not modelled	21.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase