Phyre^2

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Description	P37177
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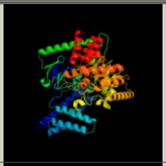
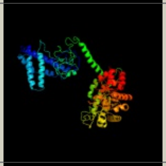
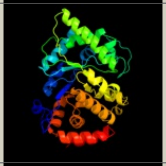
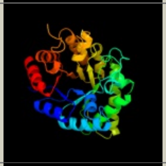
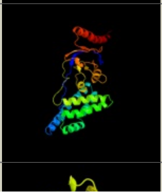
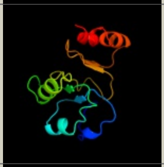
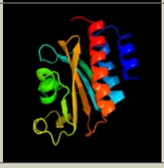
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hwgA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
2	c2hroA_	Alignment		100.0	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the full-lenght enzyme i of the pts system from2 staphylococcus carnosus
3	c1h6zA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** 3.0 a resolution crystal structure of glycosomal pyruvate2 phosphate dikinase from trypanosoma brucei
4	c2bg5C_	Alignment		100.0	38	**PDB header:**transferase **Chain:** C: **PDB Molecule:**phosphoenolpyruvate-protein kinase; **PDBTitle:** crystal structure of the phosphoenolpyruvate-binding enzyme2 i-domain from the thermoanaerobacter tengcongensis pep:3 sugar phosphotransferase system (pts)
5	c1kblA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
6	c1vbhA_	Alignment		100.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
7	c2olsA_	Alignment		100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
8	d1vbga1	Alignment		100.0	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
9	d1h6za1	Alignment		100.0	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
10	d1kbla1	Alignment		100.0	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate phosphate dikinase, C-terminal domain
11	c1ezaA_	Alignment		100.0	26	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**enzyme i; **PDBTitle:** amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
						

12	c3trcA_	Alignment		99.9	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
13	d1dxea_	Alignment		99.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
14	d1zyma2	Alignment		99.9	23	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
15	c3ci6B_	Alignment		99.9	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
16	c3qz6A_	Alignment		99.9	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
17	d2o9ca1	Alignment		99.8	11	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
18	c3mmhA_	Alignment		99.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
19	d2veaa1	Alignment		99.8	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
20	c3p01C_	Alignment		99.8	16	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
21	d1izca_	Alignment	not modelled	99.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
22	c1izcA_	Alignment	not modelled	99.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
23	c3k2nB_	Alignment	not modelled	99.8	14	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sigma-54-dependent transcriptional regulator; **PDBTitle:** the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum tls
24	c3p01A_	Alignment	not modelled	99.8	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
25	d1zyma1	Alignment	not modelled	99.8	29	**Fold:**SAM domain-like **Superfamily:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain **Family:**Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain
26	c2zmfA_	Alignment	not modelled	99.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
27	c3oovA_	Alignment	not modelled	99.8	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
28	d2oola1	Alignment	not modelled	99.8	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like

						Family:GAF domain
29	c2qybA_	Alignment	not modelled	99.8	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein, putative; **PDBTitle:** crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
30	d1vhma_	Alignment	not modelled	99.8	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
31	c2v5jB_	Alignment	not modelled	99.8	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
32	c1vhmB_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
33	c3e0yA_	Alignment	not modelled	99.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
34	c3hcyB_	Alignment	not modelled	99.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
35	c2vjwA_	Alignment	not modelled	99.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
36	c3eeaB_	Alignment	not modelled	99.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
37	c2vwtA_	Alignment	not modelled	99.8	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yfau, 2-keto-3-deoxy sugar aldolase; **PDBTitle:** crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
38	c3o5yA_	Alignment	not modelled	99.8	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
39	c1mc0A_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a; **PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
40	c3ksiA_	Alignment	not modelled	99.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
41	c2w3gA_	Alignment	not modelled	99.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component sensor histidine kinase devs (gaf **PDBTitle:** air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
42	c3dbaB_	Alignment	not modelled	99.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
43	c3ibjB_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
44	c2lb5A_	Alignment	not modelled	99.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
45	c3mf0A_	Alignment	not modelled	99.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
46	d3c2wa1	Alignment	not modelled	99.7	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
47	c1ykdB_	Alignment	not modelled	99.7	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the tandem gaf domains from a cyanobacterial2 adenylyl cyclase: novel modes of ligand-binding and dimerization
48	d2k2na1	Alignment	not modelled	99.7	23	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
49	c2k31A_	Alignment	not modelled	99.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
50	d1h6za2	Alignment	not modelled	99.6	24	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
51	d1vbga2	Alignment	not modelled	99.6	28	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
52	d1mc0a1	Alignment	not modelled	99.6	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
						PDB header:signaling protein

53	c2oolA_	Alignment	not modelled	99.6	13	**Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
54	d1kbla2	Alignment	not modelled	99.6	27	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
55	d1mc0a2	Alignment	not modelled	99.6	21	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
56	c3c2wB_	Alignment	not modelled	99.6	13	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
57	d1f5ma_	Alignment	not modelled	99.6	17	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
58	c2o9bA_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
59	c2veaA_	Alignment	not modelled	99.5	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phytochrome-like protein cph1; **PDBTitle:** the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
60	c2xssB_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
61	c3e98B_	Alignment	not modelled	99.4	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**gaf domain of unknown function; **PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
62	c3qqwC_	Alignment	not modelled	99.3	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**putative citrate lyase; **PDBTitle:** crystal structure of a hypothetical lyase (reut_b4148) from ralstonia2 eutropha jmp134 at 2.44 a resolution
63	c1sgjB_	Alignment	not modelled	99.2	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase, beta subunit; **PDBTitle:** crystal structure of citrate lyase beta subunit
64	d2g50a2	Alignment	not modelled	99.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
65	d1sgja_	Alignment	not modelled	99.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
66	d1e0ta2	Alignment	not modelled	99.1	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
67	d1a3xa2	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
68	c3t07D_	Alignment	not modelled	99.1	17	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
69	d1pkla2	Alignment	not modelled	99.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
70	d1liua2	Alignment	not modelled	98.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Pyruvate kinase
71	c2e28A_	Alignment	not modelled	98.9	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
72	c3r4iB_	Alignment	not modelled	98.8	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of a citrate lyase (bxe_b2899) from burkholderia2 xenovorans lb400 at 2.24 a resolution
73	c1u5vA_	Alignment	not modelled	98.8	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cite; **PDBTitle:** structure of cite complexed with triphosphate group of atp2 form mycobacterium tuberculosis
74	d1u5ha_	Alignment	not modelled	98.7	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
75	c3qllB_	Alignment	not modelled	98.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**citrate lyase; **PDBTitle:** crystal structure of ripc from yersinia pestis
76	c3cuzA_	Alignment	not modelled	98.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase a; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
77	c2vgbB_	Alignment	not modelled	98.1	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase isozymes r/l; **PDBTitle:** human erythrocyte pyruvate kinase
78	c3ma8A_	Alignment	not modelled	98.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of cgd1_2040, a pyruvate kinase from cryptosporidium2 parvum
						PDB header:transcription

79	c2gx5B_	Alignment	not modelled	98.0	14	**Chain:** B: **PDB Molecule:**gtp-sensing transcriptional pleiotropic repressor cody; **PDBTitle:** n-terminal gaf domain of transcriptional pleiotropic repressor cody
80	c2w1rA_	Alignment	not modelled	98.0	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of the c-terminal domain of b. subtilis2 spovt
81	c3pugA_	Alignment	not modelled	97.8	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** haloferax volcanii malate synthase native at 3mm glyoxylate
82	c1e0tD_	Alignment	not modelled	97.5	15	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
83	c2w1tB_	Alignment	not modelled	97.5	17	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
84	c3cuxA_	Alignment	not modelled	97.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**malate synthase; **PDBTitle:** atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
85	c1a3wB_	Alignment	not modelled	97.4	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from saccharomyces cerevisiae complexed with fbp, pg,2 mn2+ and k+
86	c3e0vB_	Alignment	not modelled	97.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
87	c1t5aB_	Alignment	not modelled	97.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
88	c1pklB_	Alignment	not modelled	97.4	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
89	c1aqfB_	Alignment	not modelled	97.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
90	c3eoeC_	Alignment	not modelled	97.3	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
91	d1d8ca_	Alignment	not modelled	96.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
92	c2avxA_	Alignment	not modelled	96.8	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein sdia; **PDBTitle:** solution structure of e coli sdia1-171
93	c3khdC_	Alignment	not modelled	96.8	14	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pff1300w.
94	c3qp1A_	Alignment	not modelled	96.3	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir ligand-binding domain bound to the native2 ligand c6-hsl
95	c3qp5C_	Alignment	not modelled	95.6	9	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
96	d1l3la2	Alignment	not modelled	94.2	13	**Fold:**Profilin-like **Superfamily:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors **Family:**Pheromone-binding domain of LuxR-like quorum-sensing transcription factors
97	d1eepa_	Alignment	not modelled	92.6	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
98	c2a7rD_	Alignment	not modelled	90.4	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
99	c3odmE_	Alignment	not modelled	89.9	13	**PDB header:**lyase **Chain:** E: **PDB Molecule:**phosphoenolpyruvate carboxylase; **PDBTitle:** archaeal-type phosphoenolpyruvate carboxylase
100	d1vrda1	Alignment	not modelled	88.2	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
101	d1jr1a1	Alignment	not modelled	87.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
102	c2uv0G_	Alignment	not modelled	87.3	14	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcriptional activator protein lasr; **PDBTitle:** structure of the p. aeruginosa lasr ligand-binding domain2 bound to its autoinducer
103	c1h0mD_	Alignment	not modelled	86.5	11	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
104	c1vrdA_	Alignment	not modelled	85.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine-5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine-5'-monophosphate

						dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
105	d1j93a_	Alignment	not modelled	85.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
106	c3lciA_	Alignment	not modelled	84.6	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** the d-sialic acid aldolase mutant v251w
107	c2vc6A_	Alignment	not modelled	84.5	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
108	d1zfja1	Alignment	not modelled	84.2	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
109	c3femB_	Alignment	not modelled	84.0	9	**PDB header:**biosynthetic protein, transferase **Chain:** B: **PDB Molecule:**pyridoxine biosynthesis protein snz1; **PDBTitle:** structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
110	c2zbtB_	Alignment	not modelled	84.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
111	c2nv2U_	Alignment	not modelled	83.3	15	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
112	c3r2gA_	Alignment	not modelled	83.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
113	c2v9dB_	Alignment	not modelled	83.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
114	c1v8bA_	Alignment	not modelled	82.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
115	d2hi6a1	Alignment	not modelled	82.2	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
116	d1hl2a_	Alignment	not modelled	82.2	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
117	c3citB_	Alignment	not modelled	82.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of the gaf domain of a putative sensor histidine2 kinase from pseudomonas syringae pv. tomato
118	c1jpkA_	Alignment	not modelled	81.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
119	c1jcnA_	Alignment	not modelled	81.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine monophosphate dehydrogenase i; **PDBTitle:** binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
120	d1n8ia_	Alignment	not modelled	80.8	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G