Phyre^2

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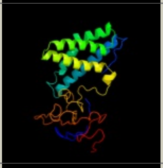
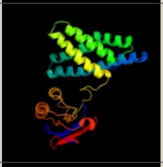
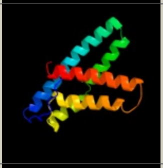
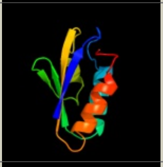
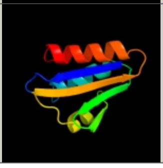
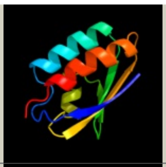
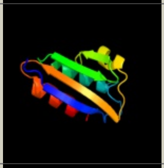
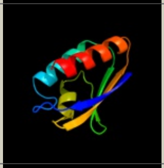
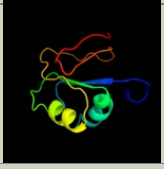
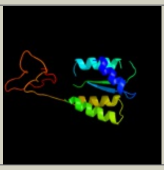
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ezaA_	Alignment		100.0	28	**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
2	c2hroA_	Alignment		100.0	24	**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	c2hwgA_	Alignment		100.0	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of phosphorylated enzyme i of the2 phosphoenolpyruvate:sugar phosphotransferase system
4	d3ct6a1	Alignment		100.0	30	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
5	d1zyma1	Alignment		99.9	30	**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
6	d3b48a1	Alignment		99.9	30	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
7	d2hpra_	Alignment		99.9	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
8	c3gdwA_	Alignment		99.8	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
9	d1ka5a_	Alignment		99.8	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
10	d1pcha_	Alignment		99.8	24	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
11	c3le1B_	Alignment		99.8	38	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, hpr-related proteins; **PDBTitle:** crystal structure of apohpr monomer from thermoanaerobacter2 tengcongensis

12	d1qr5a_	Alignment		99.8	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
13	d1mo1a_	Alignment		99.8	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
14	c3ihsB_	Alignment		99.8	32	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**phosphocarrier protein hpr; **PDBTitle:** crystal structure of a phosphocarrier protein hpr from2 bacillus anthracis str. ames
15	d1zyma2	Alignment		99.8	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
16	d2nzul1	Alignment		99.8	31	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
17	d1ptfa_	Alignment		99.8	30	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
18	d1cm3a_	Alignment		99.8	23	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
19	d1zvvj1	Alignment		99.8	29	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
20	c1h6zA_	Alignment		99.7	21	**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
21	c1kblA_	Alignment	not modelled	99.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate phosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase
22	d1h6za2	Alignment	not modelled	99.7	22	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
23	d1kbla2	Alignment	not modelled	99.7	28	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
24	d1vbga2	Alignment	not modelled	99.7	26	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
25	c1vbhA_	Alignment	not modelled	99.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
26	c3gx1A_	Alignment	not modelled	99.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
27	c2olsA_	Alignment	not modelled	99.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate synthase; **PDBTitle:** the crystal structure of the phosphoenolpyruvate synthase from2 neisseria meningitidis
28	c3iprC_	Alignment	not modelled	99.4	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
						PDB header:transferase/transferase inhibitor

29	c3t07D_	Alignment	not modelled	99.2	19	**Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
30	c2e28A_	Alignment	not modelled	99.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from bacillus2 stearothermophilus
31	d1pdoa_	Alignment	not modelled	98.5	14	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
32	c3mtqA_	Alignment	not modelled	97.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphoenolpyruvate-dependent sugar **PDBTitle:** crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
33	c3lfhF_	Alignment	not modelled	97.1	14	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
34	d3beda1	Alignment	not modelled	97.1	14	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
35	d1un8a4	Alignment		96.9	18	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
36	c3ct4B_	Alignment	not modelled	96.2	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts-dependent dihydroxyacetone kinase, **PDBTitle:** structure of dha-kinase subunit dhak from l. lactis
37	c1un9B_	Alignment	not modelled	96.2	18	**PDB header:**kinase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
38	d1oi2a_	Alignment	not modelled	96.2	23	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
39	c2iu6B_	Alignment	not modelled	95.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** regulation of the dha operon of lactococcus lactis
40	d2hi6a1	Alignment	not modelled	87.1	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
41	c3nyiA_	Alignment	not modelled	84.0	11	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fat acid-binding protein; **PDBTitle:** the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
42	d1eepa_	Alignment	not modelled	78.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
43	c3navB_	Alignment	not modelled	76.1	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
44	c2a7rD_	Alignment	not modelled	76.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gmp reductase 2; **PDBTitle:** crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
45	c2px0D_	Alignment	not modelled	70.0	13	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
46	d1ivsa1	Alignment	not modelled	69.3	15	**Fold:**Long alpha-hairpin **Superfamily:**tRNA-binding arm **Family:**Valyl-tRNA synthetase (ValRS) C-terminal domain
47	c3jr7A_	Alignment	not modelled	62.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized egv family protein cog1307; **PDBTitle:** the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
48	c1mgpA_	Alignment	not modelled	62.0	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
49	d1mgpa_	Alignment	not modelled	62.0	21	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
50	d2auna1	Alignment	not modelled	61.3	18	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LD-carboxypeptidase A C-terminal domain-like **Family:**LD-carboxypeptidase A C-terminal domain-like
51	c3thaB_	Alignment	not modelled	59.8	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** tryptophan synthase subunit alpha from campylobacter jejuni.
52	d1vrda1	Alignment	not modelled	57.4	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
						Fold: The "swivelling" beta/beta/alpha domain

53	d2gp4a1	Alignment	not modelled	57.0	11	**Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
54	c1nw3A_	Alignment	not modelled	56.7	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone methyltransferase dot1l; **PDBTitle:** structure of the catalytic domain of human dot1l, a non-set2 domain nucleosomal histone methyltransferase
55	d1nw3a_	Alignment	not modelled	56.7	28	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
56	d1jr1a1	Alignment	not modelled	56.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
57	c2g7zB_	Alignment	not modelled	56.0	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein spy1493; **PDBTitle:** conserved degv-like protein of unknown function from streptococcus2 pyogenes m1 gas binds long-chain fatty acids
58	d1oi7a2	Alignment	not modelled	54.9	18	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
59	c1u2zC_	Alignment	not modelled	54.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**histone-lysine n-methyltransferase, h3 lysine-79 **PDBTitle:** crystal structure of histone k79 methyltransferase dot1p2 from yeast
60	c2dt8A_	Alignment	not modelled	54.2	21	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** fatty acid binding of a degv family protein from thermus thermophilus
61	c2jgqB_	Alignment	not modelled	53.9	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
62	c3iz5H_	Alignment	not modelled	52.6	24	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l7a (l7ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
63	c1vrdA_	Alignment	not modelled	52.0	11	**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
64	c1w2wJ_	Alignment	not modelled	50.6	19	**PDB header:**isomerase **Chain:** J: **PDB Molecule:**5-methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of yeast ypr118w, a methylthioribose-1-2 phosphate isomerase related to regulatory eif2b subunits
65	c4a1eF_	Alignment	not modelled	48.0	24	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**rpl7a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
66	d1u2za_	Alignment	not modelled	47.8	18	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Catalytic, N-terminal domain of histone methyltransferase Dot1l
67	d1zfja1	Alignment	not modelled	47.7	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
68	d2fzva1	Alignment	not modelled	47.6	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
69	c3pl5A_	Alignment	not modelled	46.5	14	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** fatty acid binding protein
70	d2nu7a2	Alignment	not modelled	45.7	21	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
71	c2fzvC_	Alignment	not modelled	44.6	16	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
72	d1qopa_	Alignment	not modelled	44.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
73	c2zkrf_	Alignment	not modelled	43.8	28	**PDB header:**ribosomal protein/rna **Chain:** F: **PDB Molecule:**rna expansion segment es7 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
74	c3khjE_	Alignment	not modelled	43.8	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**inosine-5-monophosphate dehydrogenase; **PDBTitle:** c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
75	c2yvkA_	Alignment	not modelled	43.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**methylthioribose-1-phosphate isomerase; **PDBTitle:** crystal structure of 5-methylthioribose 1-phosphate2 isomerase product complex from bacillus subtilis
76	c2ekcA_	Alignment	not modelled	43.3	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
						PDB header:ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein rpl8 (l7ae);

77	c3izcH_	Alignment	not modelled	43.2	26	**PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
78	c2gp4A_	Alignment	not modelled	41.5	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
79	d1cf7b_	Alignment	not modelled	39.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Cell cycle transcription factor e2f-dp
80	c3r2gA_	Alignment	not modelled	38.9	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**inosine 5'-monophosphate dehydrogenase; **PDBTitle:** crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
81	d1pzxa_	Alignment	not modelled	38.1	10	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
82	d1vzwa1	Alignment	not modelled	36.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
83	c2jpiA_	Alignment	not modelled	34.5	13	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
84	d1y0ea_	Alignment	not modelled	34.1	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**NanE-like
85	d1g0da4	Alignment	not modelled	33.2	29	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
86	d1tuba1	Alignment	not modelled	33.2	13	**Fold:**Tubulin nucleotide-binding domain-like **Superfamily:**Tubulin nucleotide-binding domain-like **Family:**Tubulin, GTPase domain
87	d1piia2	Alignment	not modelled	33.1	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
88	d1j5ta_	Alignment	not modelled	32.1	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
89	c1jcnA_	Alignment	not modelled	32.0	10	**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
90	d1hg3a_	Alignment	not modelled	31.7	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
91	d2csua2	Alignment	not modelled	31.7	19	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
92	c3dmaA_	Alignment	not modelled	31.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
93	d1tb3a1	Alignment	not modelled	31.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
94	c1oi7A_	Alignment	not modelled	30.1	18	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**succinyl-coa synthetase alpha chain; **PDBTitle:** the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
95	d2btma_	Alignment	not modelled	30.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
96	c2fpgA_	Alignment	not modelled	29.1	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
97	d1pvna1	Alignment	not modelled	27.5	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
98	c3lupA_	Alignment	not modelled	27.1	10	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae
99	d1wv2a_	Alignment	not modelled	26.5	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
100	d1o8bb1	Alignment	not modelled	25.7	29	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
101	d1v7la_	Alignment	not modelled	25.6	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
102	d1aopa2	Alignment	not modelled	25.4	18	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
						PDB header:lyase

103	c2rkbE_	Alignment	not modelled	25.1	25	**Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells
104	d1a53a_	Alignment	not modelled	24.8	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
105	d1i4na_	Alignment	not modelled	24.8	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
106	d2cu0a1	Alignment	not modelled	24.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Inosine monophosphate dehydrogenase (IMPDH) **Family:**Inosine monophosphate dehydrogenase (IMPDH)
107	c2k8hA_	Alignment	not modelled	24.3	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**small ubiquitin protein; **PDBTitle:** solution structure of sumo from trypanosoma brucei
108	c2nu8D_	Alignment	not modelled	23.9	20	**PDB header:**ligase **Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase
109	c1ypfB_	Alignment	not modelled	23.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
110	c3fdjA_	Alignment	not modelled	23.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.
111	c2ekeC_	Alignment	not modelled	23.6	8	**PDB header:**ligase/protein binding **Chain:** C: **PDB Molecule:**ubiquitin-like protein smt3; **PDBTitle:** structure of a sumo-binding-motif mimic bound to smt3p-2 ubc9p: conservation of a noncovalent ubiquitin-like3 protein-e2 complex as a platform for selective4 interactions within a sumo pathway
112	d1geqa_	Alignment	not modelled	23.5	28	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
113	c3no4A_	Alignment	not modelled	23.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**creatinine amidohydrolase; **PDBTitle:** crystal structure of a creatinine amidohydrolase (npun_f1913) from2 nostoc punctiforme pcc 73102 at 2.00 a resolution
114	c2dy0A_	Alignment	not modelled	23.0	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
115	c2rbfB_	Alignment	not modelled	22.8	13	**PDB header:**oxidoreductase/dna **Chain:** B: **PDB Molecule:**bifunctional protein puta; **PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
116	d1ka9f_	Alignment	not modelled	22.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
117	d2pw9a1	Alignment	not modelled	22.4	13	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**FdhD/NarQ
118	c3m3hA_	Alignment	not modelled	22.2	10	**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'
119	d1h41a1	Alignment	not modelled	22.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**alpha-D-glucuronidase/Hyaluronidase catalytic domain
120	c3edlA_	Alignment	not modelled	21.8	15	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**alpha-tubulin; **PDBTitle:** kinesin13-microtubule ring complex