Phyre^2

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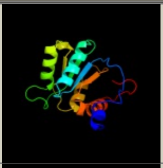
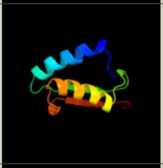
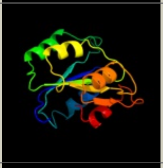
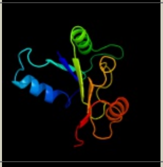
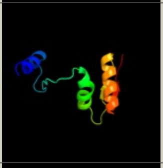
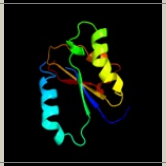
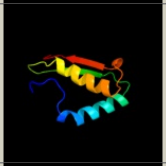
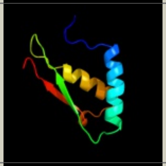
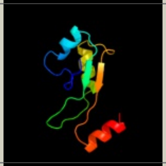
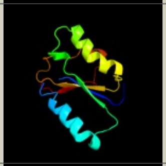
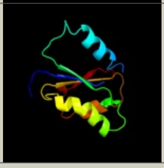
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ca8B_	 Alignment		99.9	20	**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
2	d1c7qa_	 Alignment		92.8	18	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
3	c2q8nB_	 Alignment		92.2	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
4	c2zf8A_	 Alignment		91.1	25	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
5	d2aizp1	 Alignment		89.9	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
6	c2h9aA_	 Alignment		89.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase corrinoid/iron- **PDBTitle:** corrinoid iron-sulfur protein
7	d2hqsc1	 Alignment		86.6	20	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
8	c1zzgB_	 Alignment		86.2	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of hypothetical protein tt0462 from thermus2 thermophilus hb8
9	c3ff1B_	 Alignment		85.1	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structure of glucose 6-phosphate isomerase from staphylococcus aureus
10	c3m5uA_	 Alignment		84.9	7	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase; **PDBTitle:** crystal structure of phosphoserine aminotransferase from2 campylobacter jejuni
11	c3k13A_	 Alignment		84.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron

12	c2wu8A_	Alignment		83.4	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
13	d1u0fa_	Alignment		81.7	16	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
14	c3khnB_	Alignment		81.3	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
15	c1t10A_	Alignment		80.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** phosphoglucose isomerase from leishmania mexicana in complex with2 substrate d-fructose-6-phosphate
16	c2kgwA_	Alignment		80.3	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
17	c3tr9A_	Alignment		78.4	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** structure of a dihydropteroate synthase (folp) in complex with pteroic2 acid from coxiella burnetii
18	c2h9aB_	Alignment		77.7	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase, iron- **PDBTitle:** corrinoid iron-sulfur protein
19	d1q50a_	Alignment		77.6	17	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
20	c2o2cB_	Alignment		77.6	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
21	c1r1mA_	Alignment	not modelled	77.2	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein class 4; **PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis
22	d1r1ma_	Alignment	not modelled	77.2	17	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
23	c2x5sB_	Alignment	not modelled	74.8	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
24	c3oonA_	Alignment	not modelled	74.0	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein (tpn50); **PDBTitle:** the structure of an outer membrance protein from borrelia burgdorferi2 b31
25	c3f0hA_	Alignment	not modelled	73.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (rer070207000802) from2 eubacterium rectale at 1.70 a resolution
26	c3hjbA_	Alignment	not modelled	73.6	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.
27	c2l26A_	Alignment	not modelled	72.9	24	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
28	c2k1sA_	Alignment	not modelled	72.9	20	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad; **PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics

						consortium target3 er553.
29	c2xdqA_	Alignment	not modelled	72.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase subunit n; **PDBTitle:** dark operative protochlorophyllide oxidoreductase (chln-2 chlb)2 complex
30	c3nbuC_	Alignment	not modelled	69.7	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
31	c3islA_	Alignment	not modelled	68.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine catabolism protein pucg; **PDBTitle:** crystal structure of ureidoglycine-glyoxylate aminotransferase (pucg)2 from bacillus subtilis
32	d1iata_	Alignment	not modelled	67.7	14	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
33	c2rgyA_	Alignment	not modelled	67.5	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of transcriptional regulator of laci family from2 burkhoderia phymatum
34	c3p1tB_	Alignment	not modelled	67.5	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of a putative aminotransferase (bpsl1724) from2 burkholderia pseudomallei k96243 at 2.60 a resolution
35	d1m32a_	Alignment	not modelled	67.0	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
36	d2ioja1	Alignment	not modelled	66.8	24	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
37	c3ez1A_	Alignment	not modelled	66.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase mocr family; **PDBTitle:** crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
38	c2vsnB_	Alignment		66.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**xcogt; **PDBTitle:** structure and topological arrangement of an o-glcnac2 transferase homolog: insight into molecular control of3 intracellular glycosylation
39	c3clkB_	Alignment	not modelled	66.2	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcription regulator; **PDBTitle:** crystal structure of a transcription regulator from lactobacillus2 plantarum
40	d1iuga_	Alignment	not modelled	65.5	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
41	c3brqA_	Alignment	not modelled	65.5	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator ascg; **PDBTitle:** crystal structure of the escherichia coli transcriptional repressor2 ascg
42	c2vefB_	Alignment	not modelled	64.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** dihydropteroate synthase from streptococcus pneumoniae
43	c3pe3D_	Alignment	not modelled	64.0	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
44	d1hm5a_	Alignment	not modelled	63.8	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
45	d2ch1a1	Alignment	not modelled	63.1	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
46	c3e3mA_	Alignment	not modelled	62.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of a laci family transcriptional2 regulator from silicibacter pomeroyi
47	c2yrrA_	Alignment	not modelled	62.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aminotransferase, class v; **PDBTitle:** hypothetical alanine aminotransferase (tth0173) from thermus2 thermophilus hb8
48	c3pr3B_	Alignment	not modelled	61.7	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
49	d1vjoa_	Alignment	not modelled	60.9	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
50	d1i60a_	Alignment	not modelled	60.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
51	d1f6ya_	Alignment	not modelled	59.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
52	d1ad1a_	Alignment	not modelled	58.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase

53	c2z9wA_	Alignment	not modelled	58.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of pyridoxamine-pyruvate aminotransferase complexed2 with pyridoxal
54	c3ljkA_	Alignment	not modelled	58.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
55	c2yciX_	Alignment	not modelled	57.7	14	**PDB header:**transferase **Chain:** X: **PDB Molecule:**5-methyltetrahydrofolate corrinoid/iron sulfur protein **PDBTitle:** methyltransferase native
56	d1gzda_	Alignment	not modelled	57.4	15	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
57	d1ru8a_	Alignment	not modelled	57.3	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
58	d1w23a_	Alignment	not modelled	57.2	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
59	c3ldtA_	Alignment	not modelled	57.0	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein, ompa family protein; **PDBTitle:** crystal structure of an outer membrane protein(ompa)from2 legionella pneumophila
60	c2vp8A_	Alignment	not modelled	56.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase 2; **PDBTitle:** structure of mycobacterium tuberculosis rv1207
61	d1bjna_	Alignment	not modelled	56.1	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
62	c2zy3A_	Alignment	not modelled	55.6	6	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-aspartate beta-decarboxylase; **PDBTitle:** dodecameric l-aspartate beta-decarboxylase
63	c3h5oB_	Alignment	not modelled	55.5	12	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator gntr; **PDBTitle:** the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
64	c3egcF_	Alignment	not modelled	55.3	15	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative ribose operon repressor; **PDBTitle:** crystal structure of a putative ribose operon repressor from2 burkholderia thailandensis
65	c3nnkC_	Alignment	not modelled	55.0	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ureidoglycine-glyoxylate aminotransferase; **PDBTitle:** biochemical and structural characterization of a ureidoglycine2 aminotransferase in the klebsiella pneumoniae uric acid catabolic3 pathway
66	c3cs3A_	Alignment	not modelled	53.7	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sugar-binding transcriptional regulator, laci family; **PDBTitle:** crystal structure of sugar-binding transcriptional regulator (laci2 family) from enterococcus faecalis
67	d2c0ra1	Alignment	not modelled	53.0	17	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
68	d2nvma1	Alignment	not modelled	52.7	19	**Fold:**Xisl-like **Superfamily:**Xisl-like **Family:**Xisl-like
69	d1p5dx1	Alignment	not modelled	51.8	11	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
70	d2nlva1	Alignment	not modelled	51.5	33	**Fold:**Xisl-like **Superfamily:**Xisl-like **Family:**Xisl-like
71	c2h0aA_	Alignment	not modelled	50.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of probable transcription regulator from2 thermus thermophilus
72	d1eyea_	Alignment	not modelled	50.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
73	d2fug61	Alignment	not modelled	50.2	31	**Fold:**HydA/Nqo6-like **Superfamily:**HydA/Nqo6-like **Family:**Nq06-like
74	c3d8uA_	Alignment	not modelled	49.7	5	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**purr transcriptional regulator; **PDBTitle:** the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimd 2210633
75	d2nwva1	Alignment	not modelled	49.5	29	**Fold:**Xisl-like **Superfamily:**Xisl-like **Family:**Xisl-like
76	c3k4hA_	Alignment	not modelled	49.4	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator laci from2 bacillus cereus subsp. cytotoxis nvh 391-98
77	d2ix4a2	Alignment	not modelled	49.2	18	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
78	c3gv0A_	Alignment	not modelled	48.8	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family; **PDBTitle:** crystal structure of laci family transcription regulator

						from2 agrobacterium tumefaciens
79	d1cqxa3	Alignment	not modelled	48.6	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
80	c3d7qB_	Alignment	not modelled	47.8	14	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**xisi protein-like; **PDBTitle:** crystal structure of a xisi-like protein (npun_ar114) from nostoc2 punctiforme pcc 73102 at 2.30 a resolution
81	c2e1mA_	Alignment	not modelled	47.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-glutamate oxidase; **PDBTitle:** crystal structure of l-glutamate oxidase from streptomyces sp. x-119-6
82	c3hcwB_	Alignment	not modelled	46.4	9	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maltose operon transcriptional repressor; **PDBTitle:** crystal structure of probable maltose operon transcriptional repressor2 malr from staphylococcus areus
83	d3bofa1	Alignment	not modelled	46.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Methyltetrahydrofolate-utiluzing methyltransferases
84	d1vk3a3	Alignment	not modelled	45.5	16	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
85	d1t3ta6	Alignment	not modelled	45.4	17	**Fold:**PurM C-terminal domain-like **Superfamily:**PurM C-terminal domain-like **Family:**PurM C-terminal domain-like
86	d1a3xa3	Alignment	not modelled	44.6	18	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**Pyruvate kinase, C-terminal domain
87	d1ajza_	Alignment	not modelled	43.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
88	c2r6hC_	Alignment	not modelled	43.7	29	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
89	c3ly1C_	Alignment	not modelled	42.7	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution
90	d1wyua1	Alignment	not modelled	42.7	18	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
91	c1tx2A_	Alignment	not modelled	42.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
92	d1tx2a_	Alignment	not modelled	42.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
93	c1y89B_	Alignment	not modelled	42.0	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
94	c3gybB_	Alignment	not modelled	41.7	9	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulators (laci-family **PDBTitle:** crystal structure of a laci-family transcriptional2 regulatory protein from corynebacterium glutamicum
95	c3d6kB_	Alignment	not modelled	41.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative aminotransferase; **PDBTitle:** the crystal structure of a putative aminotransferase from2 corynebacterium diphtheriae
96	c2j5tF_	Alignment	not modelled	40.5	20	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
97	c2huuA_	Alignment	not modelled	40.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alanine glyoxylate aminotransferase; **PDBTitle:** crystal structure of aedes aegypti alanine glyoxylate2 aminotransferase in complex with alanine
98	d2bkwa1	Alignment	not modelled	39.4	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Cystathionine synthase-like
99	c3getA_	Alignment	not modelled	39.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histidinol-phosphate aminotransferase; **PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (np_281508.1) from campylobacter jejuni at 2.01 a resolution
100	d1e5ma2	Alignment	not modelled	39.0	10	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Thiolase-related
101	c3pplB_	Alignment	not modelled	38.8	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** crystal structure of an aspartate transaminase (ncgl0237, cgl0240)2 from corynebacterium glutamicum atcc 13032 kitasato at 1.25 a3 resolution
102	d2ji7a1	Alignment	not modelled	38.3	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
						Fold: Thiolase-like

103	d2gfva2	Alignment	not modelled	37.4	17	**Superfamily:**Thiolase-like **Family:**Thiolase-related
104	c3nwyB_	Alignment	not modelled	37.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
105	c3qk7C_	Alignment	not modelled	36.8	6	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulators; **PDBTitle:** crystal structure of putative transcriptional regulator from yersinia2 pestis biovar microtus str. 91001
106	d1xhca2	Alignment	not modelled	36.2	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
107	c2vlbC_	Alignment	not modelled	36.2	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**arylmalonate decarboxylase; **PDBTitle:** structure of unliganded arylmalonate decarboxylase
108	c2e7pC_	Alignment	not modelled	36.1	16	**PDB header:**electron transport **Chain:** C: **PDB Molecule:**glutaredoxin; **PDBTitle:** crystal structure of the holo form of glutaredoxin c1 from populus2 tremula x tremuloides
109	d1k77a_	Alignment	not modelled	36.0	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Hypothetical protein YgbM (EC1530)
110	d1v77a_	Alignment	not modelled	35.8	12	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**RNase P subunit p30
111	c3td4D_	Alignment	not modelled	35.7	16	**PDB header:**membrane protein,peptide binding protein **Chain:** D: **PDB Molecule:**outer membrane protein omp38; **PDBTitle:** crystal structure of ompa-like domain from acinetobacter baumannii in2 complex with diaminopimelate
112	c2pjrF_	Alignment	not modelled	34.7	13	**PDB header:**hydrolase/dna **Chain:** F: **PDB Molecule:**protein (helicase pcra); **PDBTitle:** helicase product complex
113	c3dc1A_	Alignment	not modelled	34.0	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**kynurenine/alpha-aminoadipate aminotransferase **PDBTitle:** crystal structure of kynurenine aminotransferase ii complex with2 alpha-ketoglutarate
114	d2nzug1	Alignment	not modelled	33.5	14	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like
115	d1o1ya_	Alignment	not modelled	33.4	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
116	c2y5sA_	Alignment	not modelled	33.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydropteroate synthase; **PDBTitle:** crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
117	d1wyub1	Alignment	not modelled	33.2	11	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**Glycine dehydrogenase subunits (GDC-P)
118	d5mdha1	Alignment	not modelled	33.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
119	d1ozha1	Alignment	not modelled	32.8	5	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
120	c3g85A_	Alignment	not modelled	32.7	7	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (laci family); **PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum