Phyre^2

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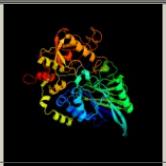
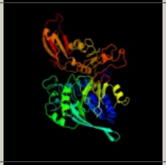
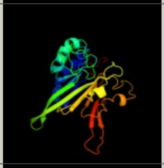
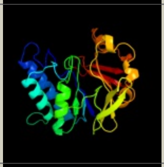
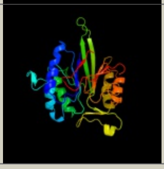
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wdfA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
2	c3qfkA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** 2.05 angstrom crystal structure of putative 5'-nucleotidase from2 staphylococcus aureus in complex with alpha-ketoglutarate
3	c2z1aA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase precursor from thermus2 thermophilus hb8
4	c3zu0A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nad nucleotidase; **PDBTitle:** structure of haemophilus influenzae nad nucleotidase (nadn)
5	c3ivdA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nucleotidase; **PDBTitle:** putative 5'-nucleotidase (c4898) from escherichia coli in2 complex with uridine
6	c1oidA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein usha; **PDBTitle:** 5'-nucleotidase (e. coli) with an engineered disulfide2 bridge (s228c, p513c)
7	c3jyfB_	Alignment		100.0	81	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- **PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
8	c3gveB_	Alignment		100.0	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
9	c3c9fB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5'-nucleotidase; **PDBTitle:** crystal structure of 5'-nucleotidase from candida albicans sc5314
10	d2z1aa2	Alignment		100.0	27	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
11	d1usha2	Alignment		100.0	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain

12	d3c9fa2	Alignment		100.0	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
13	d2z1aa1	Alignment		100.0	19	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
14	d1usha1	Alignment		100.0	20	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
15	d1t71a_	Alignment		100.0	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
16	d1t70a_	Alignment		100.0	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DR1281-like
17	d2z06a1	Alignment		100.0	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TTHA0625-like
18	d3c9fa1	Alignment		99.8	9	**Fold:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Superfamily:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain
19	d1ii7a_	Alignment		99.5	18	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**DNA double-strand break repair nuclease
20	d1uf3a_	Alignment		99.4	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
21	c2xmoB_	Alignment	not modelled	99.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
22	d2yvta1	Alignment	not modelled	99.2	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
23	c3auzA_	Alignment	not modelled	99.2	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
24	c3ib7A_	Alignment	not modelled	99.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**icc protein; **PDBTitle:** crystal structure of full length rv0805
25	c3t1iC_	Alignment	not modelled	99.1	19	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**double-strand break repair protein mre11a; **PDBTitle:** crystal structure of human mre11: understanding tumorigenic mutations
26	c3av0A_	Alignment	not modelled	99.1	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
27	c3qg5D_	Alignment	not modelled	99.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mre11; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
28	d1utea_	Alignment	not modelled	98.8	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like

29	d3d03a1	Alignment	not modelled	98.8	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
30	d1s3la_	Alignment	not modelled	98.8	23	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
31	c1s3mA_	Alignment	not modelled	98.8	23	**PDB header:**phosphodiesterase **Chain:** A: **PDB Molecule:**hypothetical protein mj0936; **PDBTitle:** structural and functional characterization of a novel2 archaeal phosphodiesterase
32	d2nxfa1	Alignment	not modelled	98.7	14	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**ADPRibase-Mn-like
33	c2hy1A_	Alignment	not modelled	98.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rv0805; **PDBTitle:** crystal structure of rv0805
34	d2hy1a1	Alignment	not modelled	98.7	17	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
35	c2q8uA_	Alignment	not modelled	98.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease, putative; **PDBTitle:** crystal structure of mre11 from thermotoga maritima msb8 (tm1635) at2 2.20 a resolution
36	d1qhwa_	Alignment	not modelled	98.6	12	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
37	c1qhwA_	Alignment	not modelled	98.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (purple acid phosphatase); **PDBTitle:** purple acid phosphatase from rat bone
38	c1kbpB_	Alignment	not modelled	98.5	15	**PDB header:**hydrolase (phosphoric monoester) **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** kidney bean purple acid phosphatase
39	d2qfra2	Alignment	not modelled	98.5	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
40	c3qfnA_	Alignment	not modelled	98.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
41	c1xzwB_	Alignment	not modelled	98.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purple acid phosphatase; **PDBTitle:** sweet potato purple acid phosphatase/phosphate complex
42	d3ck2a1	Alignment	not modelled	98.3	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
43	d1xzwa2	Alignment	not modelled	98.3	13	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Purple acid phosphatase-like
44	c3rl4A_	Alignment	not modelled	98.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
45	d1su1a_	Alignment	not modelled	98.2	20	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
46	c1su1A_	Alignment	not modelled	98.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yfce; **PDBTitle:** structural and biochemical characterization of yfce, a2 phosphoesterase from e. coli
47	c2kknA_	Alignment	not modelled	98.0	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of themotoga maritima protein tm1076:2 northeast structural genomics consortium target vt57
48	c3rqzC_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of metallophosphoesterase from sphaerobacter2 thermophilus
49	d1z2wa1	Alignment	not modelled	97.9	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
50	d1nnwa_	Alignment	not modelled	97.9	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Phosphoesterase-related
51	d2a22a1	Alignment	not modelled	97.9	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
52	d1xm7a_	Alignment	not modelled	97.6	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
53	c2qjcA_	Alignment	not modelled	96.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase
54	c2dfjA_	Alignment	not modelled	95.9	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosinetetraphosphatase; **PDBTitle:** crystal structure of the diadenosine tetraphosphate2 hydrolase from shigella flexneri 2a
55	d1g5ba_	Alignment	not modelled	95.9	26	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase

56	c2zbmA_	Alignment	not modelled	93.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine-phosphatase; **PDBTitle:** crystal structure of i115m mutant cold-active protein2 tyrosine phosphatase
57	c3icfB_	Alignment	not modelled	88.9	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase t; **PDBTitle:** structure of protein serine/threonine phosphatase from saccharomyces2 cerevisiae with similarity to human phosphatase pp5
58	d3c5wc1	Alignment	not modelled	88.4	25	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
59	c3d6nB_	Alignment	not modelled	87.3	16	**PDB header:**hydrolase/transferase **Chain:** B: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
60	d1jk7a_	Alignment	not modelled	86.1	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
61	c2jogA_	Alignment	not modelled	83.6	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** structure of the calcineurin-nfat complex
62	d1s70a_	Alignment	not modelled	82.6	21	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
63	c2cunA_	Alignment	not modelled	82.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
64	c1vlvA_	Alignment	not modelled	81.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
65	c1a1sA_	Alignment	not modelled	80.2	14	**PDB header:**transcarbamylase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine carbamoyltransferase from pyrococcus furiosus
66	c2p2gD_	Alignment	not modelled	79.8	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
67	c2w37A_	Alignment	not modelled	79.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, catabolic; **PDBTitle:** crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
68	d1s95a_	Alignment	not modelled	78.9	25	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
69	c1wao4_	Alignment	not modelled	77.8	22	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**serine/threonine protein phosphatase 5; **PDBTitle:** pp5 structure
70	c3updA_	Alignment	not modelled	77.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
71	d1ltka_	Alignment	not modelled	77.3	13	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
72	c1fvoB_	Alignment	not modelled	76.4	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
73	d1hdia_	Alignment	not modelled	73.6	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
74	d1qopa_	Alignment	not modelled	73.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
75	c1ml4A_	Alignment	not modelled	72.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
76	d1vjda_	Alignment	not modelled	72.6	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
77	c2at2B_	Alignment	not modelled	72.5	19	**PDB header:** **PDB COMPND:**
78	c1ortD_	Alignment	not modelled	71.8	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
79	d2p6ba1	Alignment	not modelled	71.4	22	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
80	c1zq2A_	Alignment	not modelled	70.4	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
81	d1vpea_	Alignment	not modelled	70.2	21	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase

82	d1qpga_	Alignment	not modelled	70.0	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
83	c3sdsA_	Alignment	not modelled	69.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
84	d1phpa_	Alignment	not modelled	67.9	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
85	c1jvnB_	Alignment	not modelled	66.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
86	c2rgwD_	Alignment	not modelled	64.3	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
87	c1js1Z_	Alignment	not modelled	63.0	11	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**transcarbamylase; **PDBTitle:** crystal structure of a new transcarbamylase from the2 anaerobic bacterium bacteroides fragilis at 2.0 a3 resolution
88	c2ef0A_	Alignment	not modelled	62.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
89	d1dlja3	Alignment	not modelled	62.4	7	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain **Family:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
90	c2eq5D_	Alignment	not modelled	62.2	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**228aa long hypothetical hydantoin racemase; **PDBTitle:** crystal structure of hydantoin racemase from pyrococcus horikoshii ot3
91	c2p6bC_	Alignment	not modelled	62.0	21	**PDB header:**hydrolase/hydrolase regulator **Chain:** C: **PDB Molecule:**calmodulin-dependent calcineurin a subunit alpha **PDBTitle:** crystal structure of human calcineurin in complex with2 pvivit peptide
92	c2pjuD_	Alignment	not modelled	61.0	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
93	c3q3vA_	Alignment	not modelled	59.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
94	d1o94c_	Alignment	not modelled	58.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
95	d2zdra2	Alignment	not modelled	57.0	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
96	d2pjua1	Alignment	not modelled	56.7	16	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
97	c2q5cA_	Alignment	not modelled	56.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
98	d1v6sa_	Alignment	not modelled	53.9	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
99	c1auiA_	Alignment	not modelled	53.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine phosphatase 2b; **PDBTitle:** human calcineurin heterodimer
100	d1auia_	Alignment	not modelled	53.5	24	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
101	d1vp8a_	Alignment	not modelled	52.0	25	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
102	c1pg5A_	Alignment	not modelled	49.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
103	c2otcA_	Alignment	not modelled	49.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
104	c3gd5D_	Alignment	not modelled	48.7	19	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
105	c2e77B_	Alignment	not modelled	46.3	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lactate oxidase; **PDBTitle:** crystal structure of l-lactate oxidase with pyruvate complex
106	d1tb3a1	Alignment	not modelled	43.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases

						Family:FMN-linked oxidoreductases
107	d1p4ca_	Alignment	not modelled	41.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
108	c1zmrA_	Alignment	not modelled	41.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
109	c1xuzA_	Alignment	not modelled	40.8	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
110	c2p10D_	Alignment	not modelled	40.7	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
111	c3q98A_	Alignment	not modelled	40.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
112	d3clsc1	Alignment	not modelled	38.5	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
113	d1efvb_	Alignment	not modelled	38.1	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
114	c3ih5A_	Alignment	not modelled	37.2	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**electron transfer flavoprotein alpha-subunit; **PDBTitle:** crystal structure of electron transfer flavoprotein alpha-2 subunit from bacteroides thetaiotaomicron
115	d1t57a_	Alignment	not modelled	36.2	25	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
116	c3lxmC_	Alignment	not modelled	35.6	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** 2.00 angstrom resolution crystal structure of a catalytic2 subunit of an aspartate carbamoyltransferase (pyrb) from3 yersinia pestis co92
117	d1djqa1	Alignment	not modelled	34.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
118	c2a7nA_	Alignment	not modelled	33.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l(+)-mandelate dehydrogenase; **PDBTitle:** crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
119	c3tpfF_	Alignment	not modelled	33.7	20	**PDB header:**transferase **Chain:** F: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
120	d16pka_	Alignment	not modelled	32.7	17	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase