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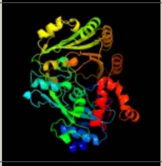
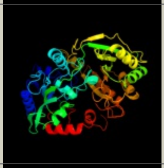
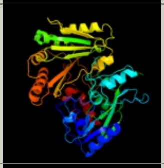
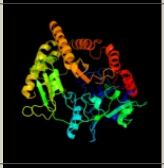
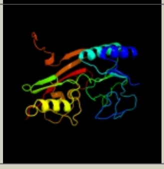
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pm9A_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
2	c1wveB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-cresol dehydrogenase [hydroxylating] **PDBTitle:** p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
3	c3bw7A_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1; **PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
4	c1ahuB_	Alignment		100.0	17	**PDB header:**flavoenzyme **Chain:** B: **PDB Molecule:**vanillyl-alcohol oxidase; **PDBTitle:** structure of the octameric flavoenzyme vanillyl-alcohol2 oxidase in complex with p-cresol
5	c2uuvC_	Alignment		100.0	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**alkyldihydroxyacetonephosphate synthase; **PDBTitle:** alkyldihydroxyacetonephosphate synthase in p1
6	c2exrA_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 7; **PDBTitle:** x-ray structure of cytokinin oxidase/dehydrogenase (ckx)2 from arabidopsis thaliana at5g21482
7	c2bvfA_	Alignment		100.0	14	**PDB header:**oxidase **Chain:** A: **PDB Molecule:**6-hydroxy-d-nicotine oxidase; **PDBTitle:** crystal structure of 6-hydoxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
8	c1zr6A_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucooligosaccharide oxidase; **PDBTitle:** the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
9	c3fwaA_	Alignment		100.0	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**reticuline oxidase; **PDBTitle:** structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
10	c3d2hA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**berberine bridge-forming enzyme; **PDBTitle:** structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
11	c1f0xA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-lactate dehydrogenase; **PDBTitle:** crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.

12	c3popD_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**gilr oxidase; **PDBTitle:** the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
13	c2wdwB_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative hexose oxidase; **PDBTitle:** the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
14	c2ipiD_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aclacinomycin oxidoreductase (aknox); **PDBTitle:** crystal structure of aclacinomycin oxidoreductase
15	c2vfvA_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xylitol oxidase; **PDBTitle:** alditol oxidase from streptomyces coelicolor a3(2): complex2 with sulphite
16	c2y3rC_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**taml; **PDBTitle:** structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase taml in p21 space group
17	c1i19B_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** crystal structure of cholesterol oxidase from b.sterolicum
18	c3js8A_	Alignment		100.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cholesterol oxidase; **PDBTitle:** solvent-stable cholesterol oxidase
19	d1wvfa2	Alignment		100.0	25	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
20	d1e8ga2	Alignment		100.0	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
21	d1f0xa2	Alignment	not modelled	100.0	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
22	d1w1oa2	Alignment	not modelled	100.0	18	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
23	d2i0ka2	Alignment	not modelled	100.0	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**FAD-linked oxidases, N-terminal domain
24	d1hska1	Alignment	not modelled	100.0	15	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
25	d1uxya1	Alignment	not modelled	100.0	12	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
26	c1hskA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** crystal structure of s. aureus murb
27	c1mbbA_	Alignment	not modelled	99.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uridine diphospho-n-acetylenolpyruvylglucosamine **PDBTitle:** oxidoreductase
28	c2yvsA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycolate oxidase subunit glce; **PDBTitle:** crystal structure of glycolate oxidase subunit glce from thermus2 thermophilus hb8
						PDB header:oxidoreductase

29	c3i99A_	Alignment	not modelled	99.9	14	**Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvoylglucosamine reductase; **PDBTitle:** the crystal structure of the udp-n-acetylenolpyruvoylglucosamine2 reductase from the vibrio cholerae o1 biovar tor
30	d1e8ga1	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
31	c2gquA_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-n-acetylenolpyruvylglucosamine reductase; **PDBTitle:** crystal structure of udp-n-acetylenolpyruvylglucosamine2 reductase (murb) from thermus caldophilus
32	d1wvfa1	Alignment	not modelled	99.7	14	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Vanillyl-alcohol oxidase-like
33	d1f0xa1	Alignment	not modelled	99.6	12	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**D-lactate dehydrogenase
34	d1w1oa1	Alignment	not modelled	99.1	10	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cytokinin dehydrogenase 1
35	d1ffvc2	Alignment	not modelled	97.0	14	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
36	c1ffuF_	Alignment	not modelled	96.8	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**cutm, flavoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
37	c1n62C_	Alignment	not modelled	96.7	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**carbon monoxide dehydrogenase medium chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
38	c1t3qF_	Alignment	not modelled	96.7	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**quinoline 2-oxidoreductase medium subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
39	d1n62c2	Alignment	not modelled	96.4	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
40	d1v97a6	Alignment	not modelled	96.4	10	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
41	d3b9jb2	Alignment	not modelled	96.0	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
42	d1t3qc2	Alignment	not modelled	96.0	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
43	c3etrM_	Alignment	not modelled	95.7	7	**PDB header:**oxidoreductase **Chain:** M: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of xanthine oxidase in complex with2 lumazine
44	c3hrdC_	Alignment	not modelled	95.7	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nicotinate dehydrogenase fad-subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
45	c3b9jJ_	Alignment	not modelled	95.7	7	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
46	c1rm6E_	Alignment	not modelled	95.2	13	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**4-hydroxybenzoyl-coa reductase beta subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
47	c2w3rG_	Alignment	not modelled	94.9	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
48	d2i0ka1	Alignment	not modelled	94.6	10	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cholesterol oxidase
49	d1jroa4	Alignment	not modelled	94.5	14	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
50	c1wygA_	Alignment	not modelled	93.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
51	d1rm6b2	Alignment	not modelled	93.1	10	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CO dehydrogenase flavoprotein N-terminal domain-like
52	c2uval_	Alignment	not modelled	71.9	25	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
						PDB header:transferase

53	c2vkzH_	Alignment	not modelled	69.8	28	**Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
54	d1jaka1	Alignment	not modelled	64.5	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
55	c3nsnA_	Alignment	not modelled	61.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylglucosaminidase; **PDBTitle:** crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
56	d1yhta1	Alignment	not modelled	61.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
57	c3gh7A_	Alignment	not modelled	59.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase; **PDBTitle:** crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
58	d1qbaa3	Alignment	not modelled	59.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
59	c2gvsA_	Alignment	not modelled	59.4	33	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**chemosensory protein csp-sg4; **PDBTitle:** nmr solution structure of cspsg4
60	d1kx9b_	Alignment	not modelled	57.7	25	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
61	c2yl8A_	Alignment	not modelled	56.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
62	d2gjxa1	Alignment	not modelled	56.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
63	d1nowa1	Alignment	not modelled	56.5	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-N-acetylhexosaminidase catalytic domain
64	c2ylaA_	Alignment	not modelled	56.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
65	d1n8va_	Alignment	not modelled	56.0	25	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
66	c1nouA_	Alignment	not modelled	55.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase beta chain; **PDBTitle:** native human lysosomal beta-hexosaminidase isoform b
67	c1jk9D_	Alignment	not modelled	55.2	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**copper chaperone for superoxide dismutase; **PDBTitle:** heterodimer between h48f-ysod1 and yccs
68	c2gjxE_	Alignment	not modelled	54.9	14	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**beta-hexosaminidase alpha chain; **PDBTitle:** crystallographic structure of human beta-hexosaminidase a
69	c1m04A_	Alignment	not modelled	54.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnac)
70	c3rcnA_	Alignment	not modelled	53.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetylhexosaminidase; **PDBTitle:** crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
71	c3lmyA_	Alignment	not modelled	51.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-hexosaminidase subunit beta; **PDBTitle:** the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
72	c3rpmA_	Alignment	not modelled	49.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-n-acetyl-hexosaminidase; **PDBTitle:** crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
73	c1qupA_	Alignment	not modelled	47.8	18	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**superoxide dismutase 1 copper chaperone; **PDBTitle:** crystal structure of the copper chaperone for superoxide2 dismutase
74	c1qbaA_	Alignment	not modelled	45.3	19	**PDB header:**glycosyl hydrolase **Chain:** A: **PDB Molecule:**chitobiase; **PDBTitle:** bacterial chitobiase, glycosyl hydrolase family 20
75	c3m7iA_	Alignment	not modelled	42.9	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of transketolase in complex with thiamine2 diphosphate, ribose-5-phosphate(pyranose form) and3 magnesium ion
76	c3s8sA_	Alignment	not modelled	42.2	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase setd1a; **PDBTitle:** crystal structure of the rrm domain of human setd1a
77	c2epoB_	Alignment	not modelled	41.0	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**n-acetyl-beta-d-glucosaminidase; **PDBTitle:** n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
78	d1itza2	Alignment	not modelled	40.6	4	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

79	d2r8oa1	Alignment	not modelled	40.5	0	**Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
80	c2yswB_	Alignment	not modelled	39.0	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** crystal structure of the 3-dehydroquinate dehydratase from aquifex2 aeolicus vf5
81	c3mhyC_	Alignment	not modelled	37.4	12	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
82	c2rd5D_	Alignment	not modelled	36.4	22	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
83	d1umdb1	Alignment	not modelled	35.1	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
84	d1ik6a1	Alignment	not modelled	32.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
85	d1r9ja1	Alignment	not modelled	32.3	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
86	d1w85b1	Alignment	not modelled	30.6	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
87	d1vfja_	Alignment	not modelled	29.7	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
88	c1ik6A_	Alignment	not modelled	28.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate dehydrogenase; **PDBTitle:** 3d structure of the e1beta subunit of pyruvate2 dehydrogenase from the archeon pyrobaculum aerophilum
89	d2piia_	Alignment	not modelled	28.0	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
90	c2rneA_	Alignment	not modelled	27.0	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**tia1 protein; **PDBTitle:** solution structure of the second rna recognition motif2 (rrm) of tia-1
91	d1gpua2	Alignment	not modelled	26.9	11	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**TK-like Pyr module
92	d2ozlb1	Alignment	not modelled	26.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase Pyr module
93	d1g7sa2	Alignment	not modelled	26.5	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
94	c2dgxA_	Alignment	not modelled	26.4	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kiaa0430 protein; **PDBTitle:** solution structure of the rna recognition motif in kiaa04302 protein
95	d1vm6a3	Alignment	not modelled	26.2	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d1poib_	Alignment	not modelled	26.1	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase beta subunit-like
97	d1ltka_	Alignment	not modelled	25.8	7	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
98	c1vm6B_	Alignment	not modelled	25.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
99	d2cqpa1	Alignment	not modelled	25.5	9	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
100	c2bp7F_	Alignment	not modelled	24.9	13	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**2-oxoisovalerate dehydrogenase beta subunit; **PDBTitle:** new crystal form of the pseudomonas putida branched-chain2 dehydrogenase (e1)
101	d1qy7a_	Alignment	not modelled	24.0	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
102	d1pama4	Alignment	not modelled	23.0	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
103	c1bplA_	Alignment	not modelled	22.0	14	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
104	d2ns1b1	Alignment	not modelled	22.0	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
105	c1ni4D_	Alignment	not modelled	21.6	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**pyruvate dehydrogenase e1 component: beta **PDBTitle:** human pyruvate dehydrogenase
						PDB header:oxidoreductase

106	c1yl7F_	Alignment	not modelled	20.9	20	**Chain:** F: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
107	d1rk8a_	Alignment	not modelled	20.7	11	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD