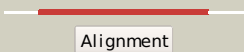

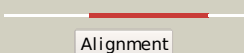

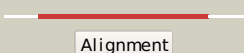

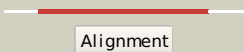

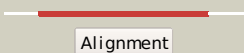
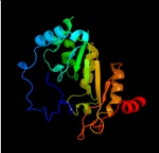
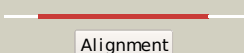

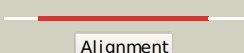

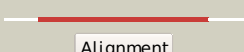

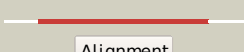

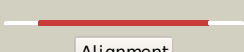

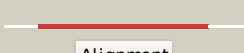








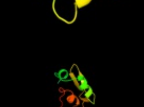



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8fA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
2	c3canA_	 Alignment		99.9	22	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
3	c3rfaA_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
4	c2yx0A_	 Alignment		99.9	20	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
5	d1tv8a_	 Alignment		99.7	20	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
6	c2z2uA_	 Alignment		99.6	19	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
7	c2a5hC_	 Alignment		99.4	15	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
8	d1r30a_	 Alignment		99.3	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
9	c1r30A_	 Alignment		99.3	17	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
10	c3t7vA_	 Alignment		99.2	11	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
11	c3cixA_	 Alignment		99.0	19	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate

12	d1olta_	Alignment		98.9	10	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
13	d1bc6a_	Alignment		98.6	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
14	d7fd1a_	Alignment		98.6	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
15	c1gx7A_	Alignment		98.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
16	c2gmhA_	Alignment		98.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
17	c1gthD_	Alignment		98.5	28	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
18	c2v2kB_	Alignment		98.5	16	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
19	c2v4jE_	Alignment		98.5	20	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
20	c1hfeL_	Alignment		98.5	21	PDB header: hydrogenase Chain: L: PDB Molecule: protein (fe-only hydrogenase (e.c.1.18.99.1) PDBTitle: 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
21	c2zvsB_	Alignment	not modelled	98.5	30	PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfh1; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
22	d2fug9l	Alignment	not modelled	98.4	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
23	c2fugG_	Alignment	not modelled	98.4	24	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase chain 9; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
24	d1h98a_	Alignment	not modelled	98.4	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
25	c2ivfB_	Alignment	not modelled	98.4	27	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
26	d1rgva_	Alignment	not modelled	98.3	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
27	d1y5ib1	Alignment	not modelled	98.3	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	c3c7bA_	Alignment	not modelled	98.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from

					archaeoglobus2 fulgidus
29	d1blua_	Alignment	not modelled	98.3	24 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
30	c3c7bE_	Alignment	not modelled	98.3	21 PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
31	d1fcaa_	Alignment	not modelled	98.3	33 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
32	c3gyxl_	Alignment	not modelled	98.3	29 PDB header: oxidoreductase Chain: J: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
33	c2fgoA_	Alignment	not modelled	98.2	21 PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
34	d2fdna_	Alignment	not modelled	98.2	35 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
35	c1ti2F_	Alignment	not modelled	98.2	22 PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
36	d1jnrb_	Alignment	not modelled	98.2	27 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
37	d1hfel2_	Alignment	not modelled	98.2	33 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
38	c2vpyB_	Alignment	not modelled	98.2	17 PDB header: oxidoreductase Chain: B: PDB Molecule: nrhc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
39	d1clfa_	Alignment	not modelled	98.2	32 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
40	c2v4jA_	Alignment	not modelled	98.2	25 PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
41	d1jb0c_	Alignment	not modelled	98.1	24 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
42	c1c4cA_	Alignment	not modelled	98.1	21 PDB header: oxidoreductase Chain: A: PDB Molecule: protein (fe-only hydrogenase); PDBTitle: binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
43	c2c3yA_	Alignment	not modelled	98.1	21 PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
44	d1kqfb1_	Alignment	not modelled	98.1	20 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
45	d1h0hb_	Alignment	not modelled	98.0	14 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
46	d1dura_	Alignment	not modelled	98.0	30 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
47	d1xera_	Alignment	not modelled	98.0	27 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
48	c1kqfB_	Alignment	not modelled	98.0	26 PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
49	d1gtea5_	Alignment	not modelled	98.0	26 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
50	c2qggF_	Alignment	not modelled	97.9	13 PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
51	d2gmha3_	Alignment	not modelled	97.9	25 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
52	d3c7bb1_	Alignment	not modelled	97.6	20 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
53	d2c42a5_	Alignment	not modelled	97.5	20 Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
					Fold: Ferredoxin-like

54	d3c8ya3	Alignment	not modelled	97.5	23	Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
55	d2fug34	Alignment	not modelled	97.4	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
56	d1vlfn2	Alignment	not modelled	97.4	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
57	d1vjwa	Alignment	not modelled	97.4	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
58	dliqza	Alignment	not modelled	97.4	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
59	c2fugC	Alignment	not modelled	96.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
60	d1sj1a	Alignment	not modelled	96.9	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
61	c3bk7A	Alignment	not modelled	96.6	29	PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
62	c1dwlA	Alignment	not modelled	96.0	27	PDB header: electron transfer Chain: A: PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
63	d1fxra	Alignment	not modelled	95.9	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
64	d1kf6b1	Alignment	not modelled	94.4	28	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
65	d2bs2b1	Alignment	not modelled	94.4	22	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
66	c3cf4A	Alignment	not modelled	94.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acids complex
67	c1nekB	Alignment	not modelled	93.7	20	PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
68	c2bs2E	Alignment	not modelled	93.5	23	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinetella succinogenes
69	d1nekb1	Alignment	not modelled	93.3	23	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
70	c2b76N	Alignment	not modelled	93.0	29	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
71	d2v4ja1	Alignment	not modelled	92.6	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
72	c2h89B	Alignment	not modelled	92.4	20	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
73	d3c7ba1	Alignment	not modelled	92.0	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
74	c1gcyA	Alignment	not modelled	90.9	17	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
75	c1jgiA	Alignment	not modelled	90.8	17	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of the active site mutant glu328gln of2 amylsucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
76	d1m53a2	Alignment	not modelled	90.1	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
77	d1g5aa2	Alignment	not modelled	89.5	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
78	d2v4jb1	Alignment	not modelled	89.4	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
79	c3a47A	Alignment	not modelled	89.2	19	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
						PDB header: transferase

80	c1m7xC_	Alignment	not modelled	88.8	21	Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
81	c1m53A_	Alignment	not modelled	88.1	21	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
82	c1ehaA_	Alignment	not modelled	87.5	15	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
83	c3k1dA_	Alignment	not modelled	87.2	31	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
84	c3czkA_	Alignment	not modelled	86.8	21	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
85	d1uoka2	Alignment	not modelled	86.8	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
86	c1cygA_	Alignment	not modelled	86.8	20	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
87	c1bagA_	Alignment	not modelled	86.8	7	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
88	c3k8kB_	Alignment	not modelled	86.5	19	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
89	c3blpX_	Alignment	not modelled	86.4	12	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
90	c1zjaB_	Alignment	not modelled	86.3	25	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
91	c1tcmB_	Alignment	not modelled	86.2	17	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
92	c1qhoA_	Alignment	not modelled	86.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
93	c2ze0A_	Alignment	not modelled	85.6	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
94	d1gcya2	Alignment	not modelled	85.5	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
95	c1uoka_	Alignment	not modelled	85.3	19	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
96	c3amkA_	Alignment	not modelled	85.2	24	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
97	d1ua7a2	Alignment	not modelled	84.9	7	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
98	c3m07A_	Alignment	not modelled	84.5	21	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhimurium.
99	c3bmwA_	Alignment	not modelled	84.4	13	PDB header: transferase Chain: A: PDB Molecule: cyclomaltoedextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
100	c2by0A_	Alignment	not modelled	84.4	28	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
101	d1gjwa2	Alignment	not modelled	84.4	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
102	c3amlA_	Alignment	not modelled	84.3	26	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
103	d2bhua3	Alignment	not modelled	83.8	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
104	d1m7xa3	Alignment	not modelled	83.6	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	c2dh3A_	Alignment	not modelled	82.7	13	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
						Fold: TIM beta/alpha-barrel

106	d1gvia3	Alignment	not modelled	82.1	16	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
107	c2ya0A_	Alignment	not modelled	82.0	15	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
108	d1wzla3	Alignment	not modelled	81.9	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
109	d1ea9c3	Alignment	not modelled	81.9	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
110	c1jaeA_	Alignment	not modelled	81.6	14	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
111	c1jd7A_	Alignment	not modelled	81.0	7	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of 2 pseudoalteromonas haloplanctis alpha-amylase
112	d1j0ha3	Alignment	not modelled	80.9	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
113	c2wskA_	Alignment	not modelled	80.8	16	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
114	c1jdaA_	Alignment	not modelled	80.6	17	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
115	c3zt5D_	Alignment	not modelled	80.6	16	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
116	c1jibA_	Alignment	not modelled	80.1	14	PDB header: hydrolase Chain: A: PDB Molecule: neopullulanase; PDBTitle: complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
117	d1h3ga3	Alignment	not modelled	79.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
118	c2zidA_	Alignment	not modelled	79.7	21	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
119	c3edeB_	Alignment	not modelled	79.2	20	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
120	c3bzjA_	Alignment	not modelled	78.8	18	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l