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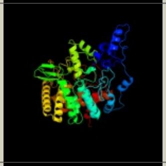
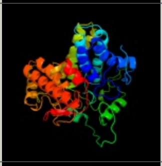
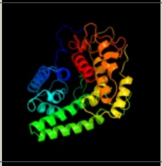
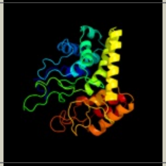
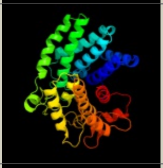
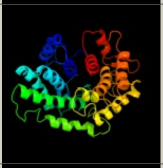
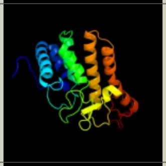
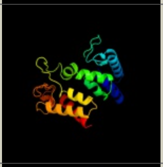
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2jg0a1	Alignment		100.0	51	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Trehalase-like
2	c2jg0A_	Alignment		100.0	51	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**periplasmic trehalase; **PDBTitle:** family 37 trehalase from escherichia coli in complex with 1-2 thiatrehazolin
3	c3c67B_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized protein ygjk; **PDBTitle:** escherichia coli k12 ygjk in a complexed with glucose
4	c2z07A_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ttha0978; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 thermus thermophilus hb8
5	c1v7wA_	Alignment		99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**chitobiose phosphorylase; **PDBTitle:** crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
6	c2okxB_	Alignment		99.9	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**rhamnosidase b; **PDBTitle:** crystal structure of gh78 family rhamnosidase of bacillus sp. gl1 at2 1.9 a
7	d1v7wa1	Alignment		99.9	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
8	c3cihA_	Alignment		99.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative alpha-rhamnosidase; **PDBTitle:** crystal structure of a putative alpha-rhamnosidase from2 bacteroides thetaiotaomicron
9	d1lf6a1	Alignment		99.8	14	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
10	c2cqtA_	Alignment		99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cellobiose phosphorylase; **PDBTitle:** crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
11	c1lf6A_	Alignment		99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** crystal structure of bacterial glucoamylase

12	d1ulva1	Alignment		99.3	19	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Bacterial glucoamylase C-terminal domain-like
13	d2fbaa1	Alignment		98.8	17	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
14	c2vn4A_	Alignment		98.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucoamylase; **PDBTitle:** glycoside hydrolase family 15 glucoamylase from hypocrea2 jecorina
15	c1ug9A_	Alignment		98.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glucodextranase; **PDBTitle:** crystal structure of glucodextranase from arthrobacter globiformis i42
16	d1gaia_	Alignment		98.6	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glucoamylase
17	d2nvpa1	Alignment		97.7	18	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
18	c2ww1B_	Alignment		97.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt39902 from bacteroides thetaiotaomicron vpi-5482 in complex with3 thiomannobioside
19	c3qspB_	Alignment		97.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** analysis of a new family of widely distributed metal-independent alpha2 mannosidases provides unique insight into the processing of n-linked3 glycans, streptococcus pneumoniae sp_2144 non-productive substrate4 complex with alpha-1,6-mannobiose
20	c2p0vA_	Alignment		97.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
21	d2p0va1	Alignment	not modelled	97.5	16	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
22	c2eacB_	Alignment	not modelled	97.3	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-fucosidase; **PDBTitle:** crystal structure of 1,2-a-l-fucosidase from2 bifidobacterium bifidum in complex with3 deoxyfuconojirimycin
23	c2wvyA_	Alignment	not modelled	97.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-1,2-mannosidase; **PDBTitle:** structure of the family gh92 inverting mannosidase bt21992 from bacteroides thetaiotaomicron vpi-5482
24	d1h54a1	Alignment	not modelled	96.9	13	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Glycosyltransferase family 36 C-terminal domain
25	c2rdyB_	Alignment	not modelled	94.6	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh0842 protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
26	c1h54B_	Alignment	not modelled	91.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**maltose phosphorylase; **PDBTitle:** maltose phosphorylase from lactobacillus brevis
27	c3gt5A_	Alignment	not modelled	85.8	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylglucosamine 2-epimerase; **PDBTitle:** crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
28	c3bhwA_	Alignment	not modelled	58.5	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from magnetospirillum2 magneticum
						Fold:SAM domain-like

29	d1nzpa_	Alignment	not modelled	42.0	11	**Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
30	d2afaa1	Alignment	not modelled	38.8	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
31	c3k7xA_	Alignment	not modelled	37.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin0763 protein; **PDBTitle:** crystal structure of the lin0763 protein from listeria2 innocua. northeast structural genomics consortium target3 lkr23.
32	c2q07A_	Alignment	not modelled	35.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein af0587; **PDBTitle:** crystal structure of af0587, a protein of unknown function
33	d1q79a3	Alignment	not modelled	33.6	12	**Fold:**Ferredoxin-like **Superfamily:**PAP/Archaeal CCA-adding enzyme, C-terminal domain **Family:**Poly(A) polymerase, PAP, C-terminal domain
34	c2gz6B_	Alignment	not modelled	29.1	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetyl-d-glucosamine 2-epimerase; **PDBTitle:** crystal structure of anabaena sp. ch1 n-acetyl-d-glucosamine 2-2 epimerase at 2.0 a
35	c2g2dA_	Alignment	not modelled	28.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:cobalamin adenosyltransferase; **PDBTitle:** crystal structure of a putative pduo-type atp:cobalamin2 adenosyltransferase from mycobacterium tuberculosis
36	c2qjxA_	Alignment	not modelled	27.9	9	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
37	d1aina_	Alignment	not modelled	26.5	12	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
38	d1wu7a2	Alignment	not modelled	24.5	25	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
39	d1fp3a_	Alignment	not modelled	21.9	15	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**N-acylglucosamine (NAG) epimerase
40	c1wy1B_	Alignment	not modelled	21.7	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein ph0671; **PDBTitle:** crystal structure of the ph0671 protein from pyrococcus horikoshii ot3
41	d2ovra1	Alignment	not modelled	20.8	13	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
42	c1wyoA_	Alignment	not modelled	19.8	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
43	d2qjza1	Alignment	not modelled	18.4	12	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
44	d2bcqa1	Alignment	not modelled	18.3	14	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
45	d1jmsa1	Alignment	not modelled	16.5	16	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
46	c3racA_	Alignment	not modelled	16.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**histidine-trna ligase; **PDBTitle:** crystal strucutre of histidine--trna ligase subunit from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446.
47	d1dm5a_	Alignment	not modelled	15.1	11	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
48	d2fmpa1	Alignment	not modelled	14.6	19	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
49	c3lhrA_	Alignment	not modelled	14.3	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**zinc finger protein 24; **PDBTitle:** crystal structure of the scan domain from human znf24
50	d1mcxa_	Alignment	not modelled	13.6	12	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
51	c1wvtA_	Alignment	not modelled	13.6	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st2180; **PDBTitle:** crystal structure of uncharacterized protein st2180 from sulfolobus2 tokodaii
52	c3ajfA_	Alignment	not modelled	13.5	22	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** structural insigths into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus
53	d1rutx4	Alignment	not modelled	12.7	71	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
54	c2idxA_	Alignment	not modelled	12.0	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cob(i)yrinic acid a,c-diamide **PDBTitle:** structure of human atp:cobalamin adenosyltransferase bound2 to atp.
55	d1iwpa_	Alignment	not modelled	11.8	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Cobalamin (vitamin B12)-dependent enzymes **Family:**Diol dehydratase, alpha subunit

56	d1zeta2	Alignment	not modelled	11.2	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
57	d1xg7a_	Alignment	not modelled	10.0	13	**Fold:**DNA-glycosylase **Superfamily:**DNA-glycosylase **Family:**AgoG-like
58	c1kdhA_	Alignment	not modelled	9.8	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**terminal deoxynucleotidyltransferase short **PDBTitle:** binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
59	c3qsjA_	Alignment	not modelled	9.7	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from alicyclobacillus2 acidocaldarius
60	d2ie7a1	Alignment	not modelled	9.7	13	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
61	c3lzzB_	Alignment	not modelled	9.7	78	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structures of cupin superfamily bbduf985 from branchiostoma2 belcheri tsingtauense in apo and gdp-bound forms
62	d1z3xa1	Alignment	not modelled	9.5	18	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
63	d1jq6a_	Alignment	not modelled	9.1	17	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
64	d1k8kd1	Alignment	not modelled	8.9	28	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits **Family:**Arp2/3 complex subunits
65	d1hvda_	Alignment	not modelled	8.9	13	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
66	c1nj2A_	Alignment	not modelled	8.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**proline-trna synthetase; **PDBTitle:** crystal structure of prolyl-trna synthetase from methanothermobacter2 thermautotrophicus
67	d1avca1	Alignment	not modelled	8.8	5	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
68	c2fllA_	Alignment	not modelled	8.6	20	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** ternary complex of human dna polymerase iota with dna and dttp
69	c2wseE_	Alignment	not modelled	8.5	33	**PDB header:**photosynthesis **Chain:** E: **PDB Molecule:**photosystem i reaction center subunit iv a, **PDBTitle:** improved model of plant photosystem i
70	c1w3wA_	Alignment	not modelled	8.4	10	**PDB header:**coagulation **Chain:** A: **PDB Molecule:**annexin a8; **PDBTitle:** the 2.1 angstroem resolution structure of annexin a8
71	c2bcuA_	Alignment	not modelled	8.3	14	**PDB header:**transferase, lyase/dna **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** dna polymerase lambda in complex with a dna duplex2 containing an unpaired damp and a t:t mismatch
72	d1fs1b1	Alignment	not modelled	8.2	9	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
73	d1w7ba_	Alignment	not modelled	8.2	5	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
74	d1m9ia2	Alignment	not modelled	8.1	5	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
75	c3k1qB_	Alignment	not modelled	8.1	31	**PDB header:**virus **Chain:** B: **PDB Molecule:**vp3a, the building block protein of inner shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
76	d1alaa_	Alignment	not modelled	8.1	13	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
77	c2doqD_	Alignment	not modelled	7.9	27	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**sfi1p; **PDBTitle:** crystal structure of sfi1p/cdc31p complex
78	d1nc7a_	Alignment	not modelled	7.8	47	**Fold:**Hypothetical protein TM1070 **Superfamily:**Hypothetical protein TM1070 **Family:**Hypothetical protein TM1070
79	d1dk2a_	Alignment	not modelled	7.7	19	**Fold:**SAM domain-like **Superfamily:**DNA polymerase beta, N-terminal domain-like **Family:**DNA polymerase beta, N-terminal domain-like
80	d1riqa1	Alignment	not modelled	7.5	28	**Fold:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Superfamily:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) **Family:**Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
81	d2g4ca2	Alignment	not modelled	7.4	22	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain

82	d1fs2b1	Alignment	not modelled	7.4	9	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
83	c1t94B_	Alignment	not modelled	7.4	25	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa
84	d1psea_	Alignment	not modelled	7.4	55	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
85	c2lmdA_	Alignment	not modelled	7.3	67	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prospero homeobox protein 1; **PDBTitle:** minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b
86	c2ah6B_	Alignment	not modelled	7.3	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bh1595, unknown conserved protein; **PDBTitle:** crystal structure of a putative cobalamin adenosyltransferase (bh1595)2 from bacillus halodurans c-125 at 1.60 a resolution
87	d1h6za3	Alignment	not modelled	7.2	6	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Pyruvate phosphate dikinase, N-terminal domain
88	d2bgxa1	Alignment	not modelled	7.2	29	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
89	d1z7ma1	Alignment	not modelled	7.2	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
90	c2r7aC_	Alignment	not modelled	7.1	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**bacterial heme binding protein; **PDBTitle:** crystal structure of a periplasmic heme binding protein2 from shigella dysenteriae
91	c3pg8B_	Alignment	not modelled	7.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phospho-2-dehydro-3-deoxyheptonate aldolase; **PDBTitle:** truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
92	d1gxie_	Alignment	not modelled	7.0	48	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
93	c1t3nB_	Alignment	not modelled	7.0	21	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**polymerase (dna directed) iota; **PDBTitle:** structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
94	c3k1qC_	Alignment	not modelled	7.0	31	**PDB header:**virus **Chain:** C: **PDB Molecule:**vp3b, the building block protein of inner shell; **PDBTitle:** backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics
95	d2q07a2	Alignment	not modelled	6.9	17	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**AF0587 domain-like
96	d1m9ia1	Alignment	not modelled	6.9	5	**Fold:**Annexin **Superfamily:**Annexin **Family:**Annexin
97	d1usya_	Alignment	not modelled	6.9	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
98	d1r8ea2	Alignment	not modelled	6.7	14	**Fold:**Probable bacterial effector-binding domain **Superfamily:**Probable bacterial effector-binding domain **Family:**Multidrug-binding domain of transcription activator BmrR
99	d1cfra_	Alignment	not modelled	6.5	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Cfr10I/Bse634I