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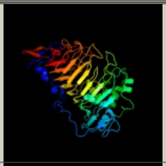
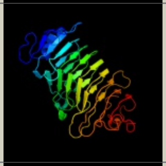
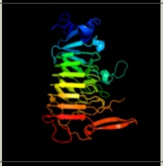
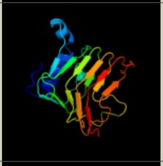
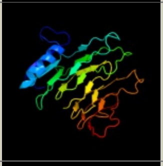
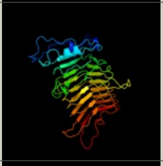
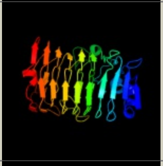
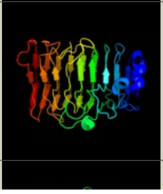
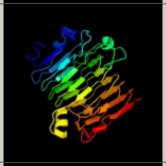
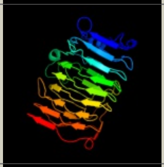
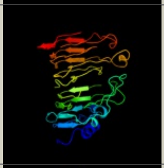
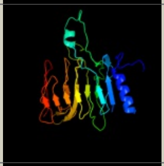
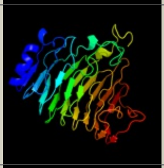
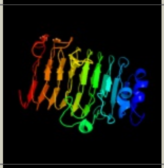
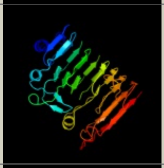
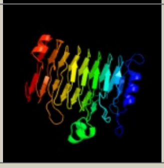
Description	P46130
Date	Thu Jan 5 12:04:05 GMT 2012
Unique Job ID	6be7df39e593cd44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3grhA_	Alignment		100.0	100	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acyl-coa thioester hydrolase ybgc; **PDBTitle:** crystal structure of escherichia coli ybhc
2	d1gq8a_	Alignment		100.0	30	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectin methylesterase
3	c1xg2A_	Alignment		100.0	29	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**pectinesterase 1; **PDBTitle:** crystal structure of the complex between pectin2 methylesterase and its inhibitor protein
4	d1qjva_	Alignment		100.0	26	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectin methylesterase
5	d1ofla_	Alignment		99.0	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
6	c1dbgA_	Alignment		98.9	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
7	d1ru4a_	Alignment		98.9	16	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate transeliminase
8	d1bhea_	Alignment		98.7	11	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
9	c3eqnB_	Alignment		98.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucan 1,3-beta-glucosidase; **PDBTitle:** crystal structure of beta-1,3-glucanase from phanerochaete2 chrysosporium (lam55a)
10	d1czfa_	Alignment		98.5	14	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
11	c1czfB_	Alignment		98.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polygalacturonase ii; **PDBTitle:** endo-polygalacturonase ii from aspergillus niger

12	c2pyhB_	Alignment		98.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4; **PDBTitle:** azotobacter vinelandii mannuronan c-5 epimerase alge4 a-module2 complexed with mannuronan trisaccharide
13	c2iq7D_	Alignment		98.2	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**endopolygalacturonase; **PDBTitle:** crystal structure of the polygalacturonase from colletotrichum lupini2 and its implications for the interaction with polygalacturonase-3 inhibiting proteins
14	d1nhca_	Alignment		98.0	13	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
15	c2uveA_	Alignment		98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exopolygalacturonase; **PDBTitle:** structure of yersinia enterocolitica family 282 exopolygalacturonase
16	c2inuC_	Alignment		98.0	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**insulin fructotransferase; **PDBTitle:** crystal structure of insulin fructotransferase in the absence of2 substrate
17	d1hg8a_	Alignment		98.0	15	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
18	d1ia5a_	Alignment		97.9	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
19	c3jurA_	Alignment		97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-poly-alpha-d-galacturonosidase; **PDBTitle:** the crystal structure of a hyperthermoactive exopolygalacturonase from2 thermotoga maritima
20	d1rmga_	Alignment		97.2	10	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
21	c3ggnA_	Alignment	not modelled	96.9	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the pre-mature bacteriophage phi29 gene product2 12
22	c3gq8A_	Alignment	not modelled	96.5	12	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**preneck appendage protein; **PDBTitle:** crystal structure of the bacteriophage phi29 gene product2 12 n-terminal fragment in complex with 2-(n-3 cyclohexylamino)ethane sulfonic acid (ches)
23	c2qy1B_	Alignment	not modelled	96.4	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pectate lyase ii; **PDBTitle:** pectate lyase a31g/r236f from xanthomonas campestris
24	d1idka_	Alignment	not modelled	96.0	28	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectin lyase
25	d1pcla_	Alignment	not modelled	95.6	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
26	d1qcxa_	Alignment	not modelled	95.2	25	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectin lyase
27	d1bn8a_	Alignment	not modelled	95.0	18	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
28	d1k5ca_	Alignment	not modelled	94.9	12	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Galacturonase
29	d1pe9a_	Alignment	not modelled	93.9	27	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like

						Family: Pectate lyase-like
30	d1ogmx2	Alignment	not modelled	93.4	11	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Dextranase, catalytic domain
31	d1o88a_	Alignment	not modelled	93.4	21	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
32	c2vjjA_	Alignment	not modelled	92.8	19	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike protein; **PDBTitle:** tailspike protein of e.coli bacteriophage hk620 in complex2 with hexasaccharide
33	c1vblA_	Alignment	not modelled	92.4	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**pectate lyase 47; **PDBTitle:** structure of the thermostable pectate lyase pl 47
34	c2z8gB_	Alignment	not modelled	85.1	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**isopullulanase; **PDBTitle:** aspergillus niger atcc9642 isopullulanase complexed with isopanose
35	d1pxza_	Alignment	not modelled	85.0	19	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Pectate lyase-like
36	c1ogoX_	Alignment	not modelled	41.2	13	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**dextranase; **PDBTitle:** dex49a from penicillium minioluteum complex with isomaltose
37	d1j83a_	Alignment	not modelled	18.8	23	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 17 carbohydrate binding module, CBM17
38	c3cegA_	Alignment	not modelled	18.1	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 6; **PDBTitle:** crystal structure of the ubc domain of baculoviral iap2 repeat-containing protein 6
39	d1acoa1	Alignment	not modelled	16.2	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
40	c2l02B_	Alignment	not modelled	12.3	45	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
41	c2p4gA_	Alignment	not modelled	10.9	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a pyrimidine reductase-like protein (dip1392)2 from corynebacterium diphtheriae nctc at 2.30 a resolution
42	c3owvA_	Alignment	not modelled	10.0	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna-entry nuclease; **PDBTitle:** structural insights into catalytic and substrate binding mechanisms of2 the strategic enda nuclease from streptococcus pneumoniae
43	c2vbeA_	Alignment	not modelled	9.9	29	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**tailspike-protein; **PDBTitle:** tailspike protein of bacteriophage sf6
44	d1dmla1	Alignment	not modelled	9.8	20	**Fold:**DNA clamp **Superfamily:**DNA clamp **Family:**DNA polymerase processivity factor
45	c2xz8A_	Alignment	not modelled	9.1	33	**PDB header:**immune system **Chain:** A: **PDB Molecule:**peptidoglycan-recognition protein lf; **PDBTitle:** crystal structure of the lfw ectodomain of the2 peptidoglycan recognition protein lf
46	c1dmlG_	Alignment	not modelled	8.9	20	**PDB header:**dna binding protein/transferase **Chain:** G: **PDB Molecule:**dna polymerase processivity factor; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-2 terminus of hsv pol
47	c2rfyB_	Alignment	not modelled	8.9	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** crystal structure of cellobiohydrolase from melanocarpus2 albomyces complexed with cellobiose
48	d2nn6h3	Alignment	not modelled	8.4	17	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
49	c2qyvB_	Alignment	not modelled	7.8	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xaa-his dipeptidase; **PDBTitle:** crystal structure of putative xaa-his dipeptidase (yp_718209.1) from2 haemophilus somnus 129pt at 2.11 a resolution
50	d1autl2	Alignment	not modelled	7.7	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
51	d1ckva_	Alignment	not modelled	7.6	50	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
52	c3b4qA_	Alignment	not modelled	7.5	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a conserved protein domain (unknown2 function) from corynebacterium diphtheriae
53	c3ep1B_	Alignment	not modelled	7.1	38	**PDB header:**immune system **Chain:** B: **PDB Molecule:**pgrp-hd - peptidoglycan recognition protein **PDBTitle:** structure of the pgrp-hd from alvinella pompejana
54	d2cu8a1	Alignment	not modelled	7.0	21	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain

55	c3gw6F_	Alignment	not modelled	6.6	21	**PDB header:**chaperone **Chain:** F: **PDB Molecule:**endo-n-acetylneuraminidase; **PDBTitle:** intramolecular chaperone
56	d1hqia_	Alignment	not modelled	6.0	67	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
57	d1ex4a1	Alignment	not modelled	5.8	37	**Fold:**SH3-like barrel **Superfamily:**DNA-binding domain of retroviral integrase **Family:**DNA-binding domain of retroviral integrase
58	d1el6a_	Alignment	not modelled	5.8	25	**Fold:**Baseplate structural protein gp11 **Superfamily:**Baseplate structural protein gp11 **Family:**Baseplate structural protein gp11
59	d2moba_	Alignment	not modelled	5.6	40	**Fold:**Monooxygenase (hydroxylase) regulatory protein **Superfamily:**Monooxygenase (hydroxylase) regulatory protein **Family:**Monooxygenase (hydroxylase) regulatory protein
60	c2mobA_	Alignment	not modelled	5.6	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (methane monooxygenase regulatory **PDBTitle:** methane monooxygenase component b
61	c3rlcA_	Alignment	not modelled	5.2	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**a1 protein; **PDBTitle:** crystal structure of the read-through domain from bacteriophage qbeta2 a1 protein, hexagonal crystal form
62	d1k4ia_	Alignment	not modelled	5.1	10	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
63	d1xpaa2	Alignment	not modelled	5.1	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain
64	c1s2jA_	Alignment	not modelled	5.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan recognition protein sa cg11709-pa; **PDBTitle:** crystal structure of the drosophila pattern-recognition2 receptor pgrp-sa
65	d1jb0d_	Alignment	not modelled	5.0	14	**Fold:**Photosystem I subunit PsaD **Superfamily:**Photosystem I subunit PsaD **Family:**Photosystem I subunit PsaD