Phyre^2

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Description	P0A8X4
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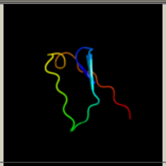
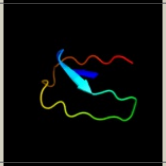
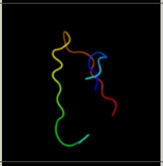
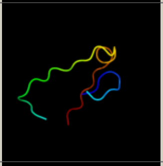
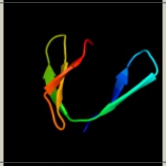
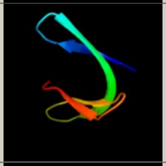
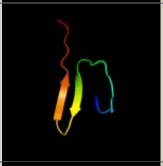
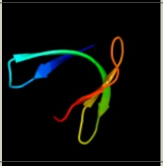
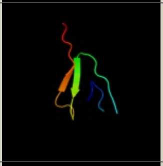
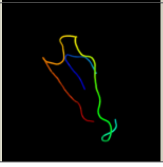
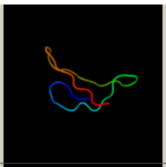
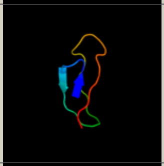
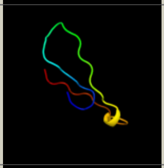
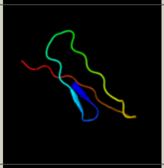
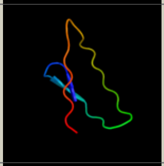
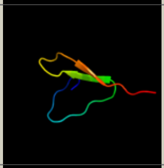
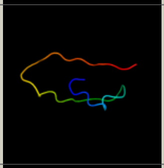
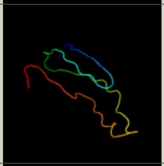
Unique Job ID	be2d28f6d30e00ce

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1yq2a3	Alignment		68.8	32	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
2	d1jz8a3	Alignment		67.9	28	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
3	c1yj5C_	Alignment		54.7	26	**PDB header:**transferase **Chain:** C: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase fha domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
4	c3bgaB_	Alignment		53.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of beta-galactosidase from bacteroides2 thetaiotaomicron vpi-5482
5	d2je8a4	Alignment		52.4	15	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
6	c3qhsD_	Alignment		50.0	23	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of full-length hfq from escherichia coli
7	d1hk9a_	Alignment		49.9	23	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
8	c3poaA_	Alignment		47.6	21	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** structural and functional analysis of phosphothreonine-dependent fha2 domain interactions
9	d1u1sa1	Alignment		47.4	23	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq
10	d1yjma1	Alignment		43.5	26	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
11	c2je8B_	Alignment		42.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-mannosidase; **PDBTitle:** structure of a beta-mannosidase from bacteroides2 thetaiotaomicron

12	c1jz6C_	Alignment		40.3	28	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
13	c3obaA_	Alignment		40.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-galactosidase; **PDBTitle:** structure of the beta-galactosidase from kluyveromyces lactis
14	c1yq2C_	Alignment		39.4	34	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-galactosidase; **PDBTitle:** beta-galactosidase from arthrobacter sp. c2-2 (isoenzyme c2-2 2-1)
15	c3pe9B_	Alignment		35.8	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
16	c3mv14_	Alignment		34.8	28	**PDB header:**hydrolase **Chain:** 4: **PDB Molecule:**beta-galactosidase; **PDBTitle:** e.coli (lacz) beta-galactosidase (r599a) in complex with guanidinium
17	d1ujxa_	Alignment		32.4	25	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
18	d2vzsa4	Alignment		25.9	26	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
19	d1tg7a2	Alignment		25.5	3	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Beta-galactosidase LacA, domains 4 and 5
20	c3u7zA_	Alignment		25.0	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative metal binding protein rumgna_00854; **PDBTitle:** crystal structure of a putative metal binding protein rumgna_008542 (zp_02040092.1) from ruminococcus gnavus atcc 29149 at 1.30 a3 resolution
21	c3gm8A_	Alignment	not modelled	22.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycoside hydrolase family 2, candidate beta-glycosidase; **PDBTitle:** crystal structure of a beta-glycosidase from bacteroides vulgatus
22	c2qguA_	Alignment	not modelled	21.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
23	c2gtqA_	Alignment	not modelled	21.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of aminopeptidase n from human pathogen neisseria2 meningitidis
24	d2nqda1	Alignment	not modelled	19.2	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like
25	c2h0eA_	Alignment	not modelled	18.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transthyretin-like protein pucm; **PDBTitle:** crystal structure of pucm in the absence of substrate
26	d1lgpa_	Alignment	not modelled	18.1	24	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
27	d1bhga2	Alignment	not modelled	17.9	13	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
28	d2jnaa1	Alignment	not modelled	16.9	23	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like

						Family: YdgH-like
29	c2w1wB_	Alignment	not modelled	16.1	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipolytic enzyme, g-d-s-l; **PDBTitle:** native structure of a family 35 carbohydrate binding module2 from clostridium thermocellum
30	d2c34a1	Alignment	not modelled	16.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ICP-like **Family:**ICP-like
31	d3bvua3	Alignment	not modelled	15.2	0	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
32	c3pe9C_	Alignment	not modelled	15.0	10	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
33	c2h1xB_	Alignment	not modelled	13.8	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
34	c2gpzC_	Alignment	not modelled	13.6	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** transthyretin-like protein from salmonella dublin
35	c3pe9A_	Alignment	not modelled	13.6	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
36	c1htyA_	Alignment	not modelled	13.6	0	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase ii; **PDBTitle:** golgi alpha-mannosidase ii
37	d1w9sa_	Alignment	not modelled	13.2	3	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
38	d1oo2a_	Alignment	not modelled	13.2	9	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
39	d2g1la1	Alignment	not modelled	12.7	33	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
40	c3ff6D_	Alignment	not modelled	12.6	32	**PDB header:**ligase **Chain:** D: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** human acc2 ct domain with cp-640186
41	c3qvaB_	Alignment	not modelled	12.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** structure of klebsiella pneumoniae 5-hydroxyisourate hydrolase
42	d1ttaa_	Alignment	not modelled	12.2	9	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
43	c3htxA_	Alignment	not modelled	11.9	64	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1
44	c2x24B_	Alignment	not modelled	11.8	28	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** bovine acc2 ct domain in complex with inhibitor
45	c2ow7A_	Alignment	not modelled	11.8	0	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
46	d2oeza1	Alignment	not modelled	11.7	27	**Fold:**YacF-like **Superfamily:**YacF-like **Family:**YacF-like
47	c3u2bC_	Alignment	not modelled	11.5	27	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription factor sox-4; **PDBTitle:** structure of the sox4 hmg domain bound to dna
48	c2wgnB_	Alignment	not modelled	11.5	7	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**inhibitor of cysteine peptidase compnd 3; **PDBTitle:** pseudomonas aeruginosa icp
49	c3hx1B_	Alignment	not modelled	11.2	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**slr1951 protein; **PDBTitle:** crystal structure of the slr1951 protein from synechocystis sp.2 northeast structural genomics consortium target sgr167a
50	c2v4vA_	Alignment	not modelled	11.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gh59 galactosidase; **PDBTitle:** crystal structure of a family 6 carbohydrate-binding module2 from clostridium cellulolyticum in complex with xylose
51	d1od3a_	Alignment	not modelled	10.7	14	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
52	d1i11a_	Alignment	not modelled	10.6	9	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
53	c3fm8A_	Alignment	not modelled	10.5	30	**PDB header:**transport protein/hydrolase activator **Chain:** A: **PDB Molecule:**kinesin-like protein kif13b; **PDBTitle:** crystal structure of full length centaurin alpha-1 bound with the fha2 domain of kif13b (capri target)
54	d1kq1a_	Alignment	not modelled	10.4	14	**Fold:**Sm-like fold **Superfamily:**Sm-like ribonucleoproteins **Family:**Pleiotropic translational regulator Hfq

55	d1uy4a_	Alignment	not modelled	10.2	18	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
56	c3cmgA_	Alignment	not modelled	9.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-galactosidase; **PDBTitle:** crystal structure of putative beta-galactosidase from bacteroides2 fragilis
57	d2g82a1	Alignment	not modelled	9.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
58	d1f86a_	Alignment	not modelled	9.5	9	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
59	c3d0wD_	Alignment	not modelled	9.4	24	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**yflh protein; **PDBTitle:** crystal structure of yflh protein from bacillus subtilis.2 northeast structural genomics consortium target sr326
60	c3lpgA_	Alignment	not modelled	8.9	8	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**beta-glucuronidase; **PDBTitle:** structure of e. coli beta-glucuronidase bound with a novel, potent2 inhibitor 3-(2-fluorophenyl)-1-(2-hydroxyethyl)-1-((6-methyl-2-oxo-1,3 2-dihydroquinolin-3-yl)methyl)urea
61	c3kcmC_	Alignment	not modelled	8.6	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**thioredoxin family protein; **PDBTitle:** the crystal structure of thioredoxin protein from geobacter2 metallireducens
62	d1tfpa_	Alignment	not modelled	8.6	9	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
63	d2d6fc3	Alignment	not modelled	8.6	9	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**GatB/GatE catalytic domain-like
64	c2crjA_	Alignment	not modelled	8.6	21	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
65	c3pe9D_	Alignment	not modelled	8.2	10	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
66	d1sr3a_	Alignment	not modelled	8.1	14	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
67	d1hsma_	Alignment	not modelled	7.9	15	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
68	d1wlna1	Alignment	not modelled	7.8	20	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
69	c1d0rA_	Alignment	not modelled	7.8	33	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**glucagon-like peptide-1-(7-36)-amide; **PDBTitle:** solution structure of glucagon-like peptide-1-(7-36)-amide2 in trifluoroethanol/water
70	d1uxxx_	Alignment	not modelled	7.8	23	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
71	c2co9A_	Alignment	not modelled	7.7	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
72	d1n67a1	Alignment	not modelled	7.4	10	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Fibrinogen-binding domain
73	c2bgpA_	Alignment	not modelled	7.4	27	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**endo-b1,4-mannanase 5c; **PDBTitle:** mannan binding module from man5c in bound conformation
74	d1k1fa_	Alignment	not modelled	7.3	13	**Fold:**Bcr-Abl oncoprotein oligomerization domain **Superfamily:**Bcr-Abl oncoprotein oligomerization domain **Family:**Bcr-Abl oncoprotein oligomerization domain
75	c1yq1A_	Alignment	not modelled	7.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutathione s-transferase; **PDBTitle:** structural genomics of caenorhabditis elegans: glutathione2 s-transferase
76	c1hrzA_	Alignment	not modelled	7.2	24	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**human sry; **PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multi-dimensional heteronuclear-edited and-filtered nmr
77	d2gzka2	Alignment	not modelled	7.2	24	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
78	c1hryA_	Alignment	not modelled	7.2	24	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**human sry; **PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multid-dimensional heteronuclear-edited and-filtered nmr
79	c2vzvB_	Alignment	not modelled	7.2	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** substrate complex of amycolatopsis orientalis exo-2 chitosanase csxa e541a with chitosan
80	d2noca1	Alignment	not modelled	7.1	39	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like

81	c2cdpC_	Alignment	not modelled	7.0	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-agarase 1; **PDBTitle:** structure of a cbm6 in complex with neoagarohexaose
82	d1uxza_	Alignment	not modelled	6.9	24	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Family 6 carbohydrate binding module, CBM6
83	c1hmfA_	Alignment	not modelled	6.8	15	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein fragment-b; **PDBTitle:** structure of the hmg box motif in the b-domain of hmg1
84	d1hmfa_	Alignment	not modelled	6.8	15	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
85	d1kgia_	Alignment	not modelled	6.8	7	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
86	c3kzeA_	Alignment	not modelled	6.8	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**t-lymphoma invasion and metastasis-inducing protein 1; **PDBTitle:** crystal structure of t-cell lymphoma invasion and metastasis-1 pdz in2 complex with ssrkeyya peptide
87	c1z5hB_	Alignment	not modelled	6.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tricorn protease interacting factor f3; **PDBTitle:** crystal structures of the tricorn interacting factor f32 from thermoplasma acidophilum
88	c2kklA_	Alignment	not modelled	6.7	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mb1858; **PDBTitle:** solution nmr structure of fha domain of mb1858 from2 mycobacterium bovis. northeast structural genomics3 consortium target mbr243c (24-155).
89	d1z0mb1	Alignment	not modelled	6.7	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
90	d1zzoa1	Alignment	not modelled	6.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
91	c3hsbB_	Alignment	not modelled	6.6	17	**PDB header:**rna binding protein/rna **Chain:** B: **PDB Molecule:**protein hfq; **PDBTitle:** crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
92	c3k1rA_	Alignment	not modelled	6.6	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**harmonin; **PDBTitle:** structure of harmonin npdz1 in complex with the sam-pbm of2 sans
93	c1kq1W_	Alignment	not modelled	6.4	14	**PDB header:**translation **Chain:** W: **PDB Molecule:**host factor for q beta; **PDBTitle:** 1.55 a crystal structure of the pleiotropic translational2 regulator, hfq
94	c3cynC_	Alignment	not modelled	6.3	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**probable glutathione peroxidase 8; **PDBTitle:** the structure of human gpx8
95	c2vr3B_	Alignment	not modelled	6.3	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**clumping factor a; **PDBTitle:** structural and biochemical characterization of fibrinogen2 binding to clfa from staphylocccus aureus
96	c2vzqA_	Alignment	not modelled	6.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exo-beta-d-glucosaminidase; **PDBTitle:** c-terminal cbm35 from amycolatopsis orientalis exo-2 chitosanase csxa in complex with digalacturonic acid
97	c2p5qA_	Alignment	not modelled	6.2	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione peroxidase 5; **PDBTitle:** crystal structure of the poplar glutathione peroxidase 5 in2 the reduced form
98	d2ff4a3	Alignment	not modelled	6.2	20	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
99	d1j3da_	Alignment	not modelled	6.2	21	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box