



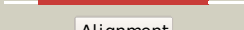

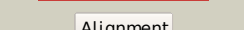

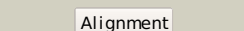





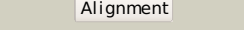

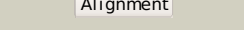

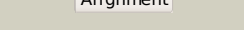

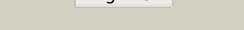

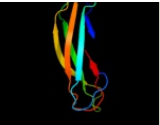





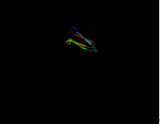




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ac0B_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-glucosidase i; <b>PDBTitle:</b> crystal structure of beta-glucosidase from kluyveromyces marxianus in2 complex with glucose
2	<a href="#">c2x41A_</a>	 Alignment		100.0	30	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
3	<a href="#">c3f93D_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> beta-glucosidase; <b>PDBTitle:</b> crystal structure of exo-1,3/1,4-beta-glucanase (exop) from2 pseudoalteromonas sp. bb1
4	<a href="#">c1ex1A_</a>	 Alignment		100.0	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein (beta-d-glucan exohydrolase isoenzyme exo1); <b>PDBTitle:</b> beta-d-glucan exohydrolase from barley
5	<a href="#">c3bmxB_</a>	 Alignment		100.0	25	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized lipoprotein ybbd; <b>PDBTitle:</b> beta-n-hexosaminidase (ybbd) from bacillus subtilis
6	<a href="#">c3lk6A_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lipoprotein ybbd; <b>PDBTitle:</b> beta-n-hexosaminidase n318d mutant (ybbd_n318d) from bacillus subtilis
7	<a href="#">c3sqlB_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glycosyl hydrolase family 3; <b>PDBTitle:</b> crystal structure of glycoside hydrolase from synechococcus
8	<a href="#">d1x38a1</a>	 Alignment		100.0	32	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> NagZ-like
9	<a href="#">c3tevA_</a>	 Alignment		100.0	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> glycosyl hydrolase, family 3; <b>PDBTitle:</b> the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
10	<a href="#">d1tr9a_</a>	 Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> NagZ-like
11	<a href="#">d1x38a2</a>	 Alignment		100.0	35	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Beta-D-glucan exohydrolase, C-terminal domain <b>Family:</b> Beta-D-glucan exohydrolase, C-terminal domain

12	<a href="#">c2kl6A_</a>	Alignment		97.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
13	<a href="#">d1w8oa1</a>	Alignment		97.3	19	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> E-set domains of sugar-utilizing enzymes
14	<a href="#">c2l0dA_</a>	Alignment		97.1	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell surface protein; <b>PDBTitle:</b> solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
15	<a href="#">c2kutA_</a>	Alignment		96.9	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
16	<a href="#">d2vzsa2</a>	Alignment		96.2	27	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
17	<a href="#">c1l9mB_</a>	Alignment		95.9	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein-glutamine glutamyltransferase e3; <b>PDBTitle:</b> three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
18	<a href="#">d2q3za2</a>	Alignment		95.8	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
19	<a href="#">c2x3bB_</a>	Alignment		95.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> toxic extracellular endopeptidase; <b>PDBTitle:</b> asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
20	<a href="#">d1ex0a2</a>	Alignment		94.4	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
21	<a href="#">d1g0da2</a>	Alignment	not modelled	94.0	12	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
22	<a href="#">c3isyA_</a>	Alignment	not modelled	93.5	22	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> intracellular proteinase inhibitor; <b>PDBTitle:</b> crystal structure of an intracellular proteinase inhibitor (ipi,2 bsu11130) from bacillus subtilis at 2.61 a resolution
23	<a href="#">d1vjja2</a>	Alignment	not modelled	93.2	14	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Transglutaminase, two C-terminal domains <b>Family:</b> Transglutaminase, two C-terminal domains
24	<a href="#">c3rgbA_</a>	Alignment	not modelled	90.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methane monooxygenase subunit b2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath)
25	<a href="#">d4ubpb_</a>	Alignment	not modelled	89.1	22	<b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
26	<a href="#">d2co7b1</a>	Alignment	not modelled	88.8	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
27	<a href="#">c1yewl_</a>	Alignment	not modelled	88.7	25	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> I: <b>PDB Molecule:</b> particulate methane monooxygenase, b subunit; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
28	<a href="#">c3fn9B_</a>	Alignment	not modelled	88.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative beta-galactosidase; <b>PDBTitle:</b> crystal structure of putative beta-galactosidase from bacteroides2 fragilis
29	<a href="#">c2e6jA_</a>	Alignment	not modelled	87.8	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hydin protein; <b>PDBTitle:</b> solution structure of the c-terminal papd-like domain

					from2 human hydin protein
30	<a href="#">d1ejxb</a>	Alignment	not modelled	87.6	24 <b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
31	<a href="#">d1e9ya1</a>	Alignment	not modelled	86.0	26 <b>Fold:</b> beta-clip <b>Superfamily:</b> Urease, beta-subunit <b>Family:</b> Urease, beta-subunit
32	<a href="#">c2cqtA</a>	Alignment	not modelled	86.0	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cellobiose phosphorylase; <b>PDBTitle:</b> crystal structure of cellvibrio gilvus cellobiose phosphorylase2 crystallized from sodium/potassium phosphate
33	<a href="#">c1kv3F</a>	Alignment	not modelled	85.1	17 <b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> human tissue transglutaminase in gdp bound form
34	<a href="#">c3qgaD</a>	Alignment	not modelled	84.4	20 <b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> fusion of urease beta and gamma subunits; <b>PDBTitle:</b> 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae
35	<a href="#">c1g0dA</a>	Alignment	not modelled	83.7	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein-glutamine gamma-glutamyltransferase; <b>PDBTitle:</b> crystal structure of red sea bream transglutaminase
36	<a href="#">c1f13A</a>	Alignment	not modelled	83.5	12 <b>PDB header:</b> coagulation factor <b>Chain:</b> A: <b>PDB Molecule:</b> cellular coagulation factor xiii zymogen; <b>PDBTitle:</b> recombinant human cellular coagulation factor xiii
37	<a href="#">d1v7wa2</a>	Alignment	not modelled	81.8	15 <b>Fold:</b> Supersandwich <b>Superfamily:</b> Galactose mutarotase-like <b>Family:</b> Glycosyltransferase family 36 N-terminal domain
38	<a href="#">c1iq8B</a>	Alignment	not modelled	80.6	9 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> archaeosine trna-guanine transglycosylase; <b>PDBTitle:</b> crystal structure of archaeosine trna-guanine2 transglycosylase from pyrococcus horikoshii
39	<a href="#">d1jz8a1</a>	Alignment	not modelled	80.1	16 <b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
40	<a href="#">c1e9zA</a>	Alignment	not modelled	80.0	26 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> urease subunit alpha; <b>PDBTitle:</b> crystal structure of helicobacter pylori urease
41	<a href="#">c2a74B</a>	Alignment	not modelled	79.5	14 <b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement component c3c; <b>PDBTitle:</b> human complement component c3c
42	<a href="#">d2ccwa1</a>	Alignment	not modelled	78.9	18 <b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
43	<a href="#">c3rfr1</a>	Alignment	not modelled	78.5	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> pmob; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase (pmmo) from2 methylocystis sp. strain m
44	<a href="#">c3eoeC</a>	Alignment	not modelled	77.8	17 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
45	<a href="#">c3qisA</a>	Alignment	not modelled	77.0	20 <b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1; <b>PDBTitle:</b> recognition of the f&h motif by the lowe syndrome protein ocr1
46	<a href="#">c2h47C</a>	Alignment	not modelled	76.6	26 <b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> azurin; <b>PDBTitle:</b> crystal structure of an electron transfer complex between2 aromatic amine dehydrogenase and azurin from alcaligenes3 faecalis (form 1)
47	<a href="#">c3qbtH</a>	Alignment	not modelled	75.5	15 <b>PDB header:</b> protein transport/hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1; <b>PDBTitle:</b> crystal structure of ocr1 540-678 in complex with rab8a:gppnhp
48	<a href="#">c2qsvA</a>	Alignment	not modelled	75.2	19 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein of unknown function from porphyromonas2 gingivalis w83
49	<a href="#">c1v7wA</a>	Alignment	not modelled	74.9	17 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> chitobiose phosphorylase; <b>PDBTitle:</b> crystal structure of vibrio proteolyticus chitobiose phosphorylase in2 complex with glcnac
50	<a href="#">c3hs0B</a>	Alignment	not modelled	74.6	13 <b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cobra venom factor; <b>PDBTitle:</b> cobra venom factor (cvf) in complex with human factor b
51	<a href="#">d2g50a2</a>	Alignment	not modelled	74.4	18 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
52	<a href="#">c5mdhB</a>	Alignment	not modelled	73.2	24 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of ternary complex of porcine cytoplasmic malate2 dehydrogenase alpha-ketomalonate and tnad at 2.4 angstroms resolution
53	<a href="#">d1azca</a>	Alignment	not modelled	72.9	18 <b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
54	<a href="#">d1civa1</a>	Alignment	not modelled	72.8	19 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like

55	<a href="#">d7mdha1</a>	Alignment	not modelled	72.5	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
56	<a href="#">d1liua2</a>	Alignment	not modelled	72.3	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
57	<a href="#">c2co7B_</a>	Alignment	not modelled	72.1	18	<b>PDB header:</b> fibril protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative fimbriae assembly chaperone; <b>PDBTitle:</b> salmonella enterica safra pilin in complex with the safb2 chaperone (type ii)
58	<a href="#">c3g6jB_</a>	Alignment	not modelled	71.9	15	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement c3 alpha chain; <b>PDBTitle:</b> c3b in complex with a c3b specific fab
59	<a href="#">c1mldA_</a>	Alignment	not modelled	71.7	21	<b>PDB header:</b> oxidoreductase(nad(a)-choh(d)) <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> refined structure of mitochondrial malate dehydrogenase2 from porcine heart and the consensus structure for3 dicarboxylic acid oxidoreductases
60	<a href="#">d1y7ta1</a>	Alignment	not modelled	71.6	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
61	<a href="#">d5mdha1</a>	Alignment	not modelled	71.5	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
62	<a href="#">c1b8vA_</a>	Alignment	not modelled	71.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> malate dehydrogenase from aquaspirillum arcticum
63	<a href="#">c3fcsA_</a>	Alignment	not modelled	69.7	15	<b>PDB header:</b> cell adhesion/blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> integrin, alpha 2b; <b>PDBTitle:</b> structure of complete ectodomain of integrin aiiib3
64	<a href="#">d1b8pa1</a>	Alignment	not modelled	69.1	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
65	<a href="#">c3t07D_</a>	Alignment	not modelled	68.8	23	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
66	<a href="#">c1e0tD_</a>	Alignment	not modelled	68.6	14	<b>PDB header:</b> phosphotransferase <b>Chain:</b> D: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> r292d mutant of e. coli pyruvate kinase
67	<a href="#">c2ys4A_</a>	Alignment	not modelled	68.3	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hydrocephalus-inducing protein homolog; <b>PDBTitle:</b> solution structure of the n-terminal papd-like domain of2 hydin protein from human
68	<a href="#">c2a73B_</a>	Alignment	not modelled	67.8	14	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> complement c3; <b>PDBTitle:</b> human complement component c3
69	<a href="#">c7mdhA_</a>	Alignment	not modelled	66.6	21	<b>PDB header:</b> chloroplastic malate dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> structural basis for light activation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form
70	<a href="#">d1cc3a_</a>	Alignment	not modelled	66.5	16	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
71	<a href="#">c1sevA_</a>	Alignment	not modelled	66.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal precursor; <b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
72	<a href="#">c1smkD_</a>	Alignment	not modelled	66.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase, glyoxysomal; <b>PDBTitle:</b> mature and translocatable forms of glyoxysomal malate2 dehydrogenase have different activities and stabilities3 but similar crystal structures
73	<a href="#">d1cuoa_</a>	Alignment	not modelled	66.1	20	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
74	<a href="#">d1llda1</a>	Alignment	not modelled	65.7	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
75	<a href="#">c2rdo7_</a>	Alignment	not modelled	65.5	15	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> elongation factor g; <b>PDBTitle:</b> 50s subunit with ef-g(gdpnp) and rrf bound
76	<a href="#">d1ldma1</a>	Alignment	not modelled	64.3	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
77	<a href="#">d1o6za1</a>	Alignment	not modelled	64.1	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
78	<a href="#">d1e0ta2</a>	Alignment	not modelled	64.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
79	<a href="#">d1nbca_</a>	Alignment	not modelled	63.3	18	<b>Fold:</b> Common fold of diphtheria toxin/transcription factors/cytochrome f <b>Superfamily:</b> Carbohydrate-binding domain <b>Family:</b> Cellulose-binding domain family III
80	<a href="#">d1a5za1</a>	Alignment	not modelled	62.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

						<b>Family:</b> LDH N-terminal domain-like
81	<a href="#">d1l1aa3</a>	Alignment	not modelled	61.7	16	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> Arthropod hemocyanin, C-terminal domain
82	<a href="#">c2b39B</a>	Alignment	not modelled	61.7	14	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> c3; <b>PDBTitle:</b> structure of mammalian c3 with an intact thioester at 3a resolution
83	<a href="#">c1wziA</a>	Alignment	not modelled	60.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structural basis for alteration of cofactor specificity of2 malate dehydrogenase from thermus flavus
84	<a href="#">c1ogoX</a>	Alignment	not modelled	60.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> dextranase; <b>PDBTitle:</b> dex49a from penicillium minioluteum complex with isomaltose
85	<a href="#">c2dfdD</a>	Alignment	not modelled	60.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of human malate dehydrogenase type 2
86	<a href="#">c3cu7A</a>	Alignment	not modelled	60.1	13	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> complement c5; <b>PDBTitle:</b> human complement component 5
87	<a href="#">d2l1dx1</a>	Alignment	not modelled	59.5	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
88	<a href="#">c2pwzG</a>	Alignment	not modelled	59.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo form of e.coli malate dehydrogenase
89	<a href="#">d1i0za1</a>	Alignment	not modelled	58.7	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
90	<a href="#">c2pn5A</a>	Alignment	not modelled	58.5	17	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> thioester-containing protein i; <b>PDBTitle:</b> crystal structure of tep1r
91	<a href="#">c8ldhA</a>	Alignment	not modelled	58.5	19	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
92	<a href="#">c1hyhA</a>	Alignment	not modelled	58.2	20	<b>PDB header:</b> oxidoreductase (choh(d)-nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-2-hydroxyisocaproate dehydrogenase from2 lactobacillus confusus at 2.2 angstroms resolution-an example of3 strong asymmetry between subunits
93	<a href="#">d1jv2a2</a>	Alignment	not modelled	56.9	22	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Integrin domains <b>Family:</b> Integrin domains
94	<a href="#">d1p5va1</a>	Alignment	not modelled	55.8	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
95	<a href="#">c2qv2A</a>	Alignment	not modelled	55.7	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol polyphosphate 5-phosphatase ocr1-1; <b>PDBTitle:</b> a role of the lowe syndrome protein ocr1 in early steps of2 the endocytic pathway
96	<a href="#">c1jz6C</a>	Alignment	not modelled	55.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> beta-galactosidase; <b>PDBTitle:</b> e. coli (lacz) beta-galactosidase in complex with galacto-2 tetrazole
97	<a href="#">c3H2A</a>	Alignment	not modelled	54.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of bacillus anthracis str. ames malate dehydrogenase2 in closed conformation.
98	<a href="#">d5ldha1</a>	Alignment	not modelled	54.7	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
99	<a href="#">d1nwpA</a>	Alignment	not modelled	53.8	21	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
100	<a href="#">c2hjrK</a>	Alignment	not modelled	53.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum malate2 dehydrogenase
101	<a href="#">d1l4ia1</a>	Alignment	not modelled	53.1	15	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> Pilus chaperone
102	<a href="#">c2o14A</a>	Alignment	not modelled	52.6	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yxim; <b>PDBTitle:</b> x-ray crystal structure of protein yxim_bacsu from bacillus2 subtilis. northeast structural genomics consortium target3 sr595
103	<a href="#">c2l8aA</a>	Alignment	not modelled	52.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endoglucanase; <b>PDBTitle:</b> structure of a novel cbm3 lacking the calcium-binding site
104	<a href="#">d1i10a1</a>	Alignment	not modelled	52.5	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
105	<a href="#">c2v6bB</a>	Alignment	not modelled	52.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from deinococcus2 radiodurans (apo form)
106	<a href="#">c2jbxA</a>	Alignment	not modelled	51.9	55	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor iie subunit



						<b>PDBTitle:</b> nmr structure of the tfiie-alpha carboxyl terminus
107	<a href="#">c1lldA</a>	Alignment	not modelled	51.2	14	<b>PDB header:</b> oxidoreductase(choh (d)-nad (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> molecular basis of allosteric activation of bacterial l-lactate2 dehydrogenase
108	<a href="#">c3mpbA</a>	Alignment	not modelled	51.1	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar isomerase; <b>PDBTitle:</b> z5688 from e. coli o157:h7 bound to fructose
109	<a href="#">d1a3xa2</a>	Alignment	not modelled	50.3	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
110	<a href="#">d9ldta1</a>	Alignment	not modelled	50.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
111	<a href="#">c2rngA</a>	Alignment	not modelled	49.5	55	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor iie subunit <b>PDBTitle:</b> solution structure of the c-terminal acidic domain of tfiie2 alpha
112	<a href="#">c1a5zA</a>	Alignment	not modelled	49.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> lactate dehydrogenase from thermotoga maritima (tml dh)
113	<a href="#">d1hya1</a>	Alignment	not modelled	48.8	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
114	<a href="#">c1t5aB</a>	Alignment	not modelled	48.7	17	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate kinase, m2 isozyme; <b>PDBTitle:</b> human pyruvate kinase m2
115	<a href="#">c3q48B</a>	Alignment	not modelled	48.6	13	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone cupb2; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa cupb2 chaperone
116	<a href="#">c1z9sA</a>	Alignment	not modelled	47.9	16	<b>PDB header:</b> chaperone/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein caf1m; <b>PDBTitle:</b> crystal structure of the native chaperone:subunit:subunit2 caf1m:caf1:caf1 complex
117	<a href="#">d1iq8a1</a>	Alignment	not modelled	47.5	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> tRNA-guanine transglycosylase <b>Family:</b> tRNA-guanine transglycosylase
118	<a href="#">c3p7mC</a>	Alignment	not modelled	47.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> structure of putative lactate dehydrogenase from francisella2 tularensis subsp. tularensis schu s4
119	<a href="#">d1joia</a>	Alignment	not modelled	47.1	18	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Plastocyanin/azurin-like
120	<a href="#">c2e28A</a>	Alignment	not modelled	46.9	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate kinase; <b>PDBTitle:</b> crystal structure analysis of pyruvate kinase from bacillus2 steartothermophilus