Phyre2

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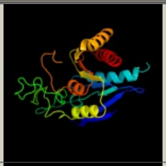
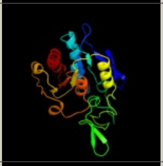
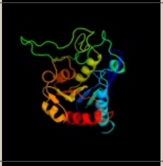
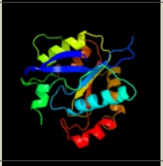
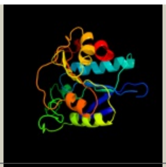
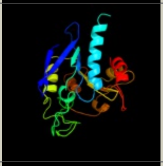
Description	P0ACV6
Date	Thu Jan 5 11:19:10 GMT 2012
Unique Job ID	5f77e12444d7f585

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dgvB_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxypeptidase b2; **PDBTitle:** crystal structure of thrombin activatable fibrinolysis inhibitor2 (tafi)
2	c2nsmA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase n catalytic chain; **PDBTitle:** crystal structure of the human carboxypeptidase n (kininase i)2 catalytic domain
3	c1ayeA_	Alignment		100.0	18	**PDB header:**serine protease **Chain:** A: **PDB Molecule:**procarboxypeptidase a2; **PDBTitle:** human procarboxypeptidase a2
4	c2boaB_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxypeptidase a4; **PDBTitle:** human procarboxypeptidase a4.
5	c1nsaA_	Alignment		100.0	21	**PDB header:**serine protease **Chain:** A: **PDB Molecule:**procarboxypeptidase b; **PDBTitle:** three-dimensional structure of porcine procarboxypeptidase2 b: a structural basis of its inactivity
6	c1jqgA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase a; **PDBTitle:** crystal structure of the carboxypeptidase a from2 helicoverpa armigera
7	c1uwyA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxypeptidase m; **PDBTitle:** crystal structure of human carboxypeptidase m
8	c1h8lA_	Alignment		100.0	23	**PDB header:**carboxypeptidase **Chain:** A: **PDB Molecule:**carboxypeptidase gp180 residues 503-882; **PDBTitle:** duck carboxypeptidase d domain ii in complex with gemsa
9	c3mn8A_	Alignment		100.0	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lp15968p; **PDBTitle:** structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
10	d1ayea1	Alignment		100.0	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
11	d1nsaa1	Alignment		100.0	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases

12	d1uwya2	Alignment		100.0	26	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
13	d1obra_	Alignment		100.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Carboxypeptidase T
14	d1kwma1	Alignment		100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
15	d1jqga1	Alignment		100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
16	d1z5ra1	Alignment		100.0	19	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
17	d1m4la_	Alignment		100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
18	d2bo9a1	Alignment		100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
19	c3d4uA_	Alignment		100.0	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**carboxypeptidase b2; **PDBTitle:** bovine thrombin-activatable fibrinolysis inhibitor (tafia) in complex2 with tick-derived carboxypeptidase inhibitor.
20	d2c1ca1	Alignment		100.0	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
21	d1h8la2	Alignment	not modelled	100.0	24	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Pancreatic carboxypeptidases
22	c3k2kA_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxypeptidase; **PDBTitle:** crystal structure of putative carboxypeptidase (yp_103406.1) from2 burkholderia mallei atcc 23344 at 2.49 a resolution
23	c3l2nA_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase m14, carboxypeptidase a; **PDBTitle:** crystal structure of putative carboxypeptidase a (yp_562911.1) from2 shewanella denitrificans os-217 at 2.39 a resolution
24	c1cpbB_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase (c-terminal peptidase) **Chain:** B: **PDB Molecule:**carboxypeptidase b; **PDBTitle:** structure of carboxypeptidase b at 2.8 angstroms resolution
25	c3cdxB_	Alignment	not modelled	100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**succinylglutamatedesuccinylase/aspartoacylase; **PDBTitle:** crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
26	c3b2yB_	Alignment	not modelled	99.9	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**metallopeptidase containing co-catalytic metalloactive **PDBTitle:** crystal structure of a putative metallopeptidase (sden_2526) from2 shewanella denitrificans os217 at 1.74 a resolution
						PDB header:hydrolase **Chain:** A: **PDB Molecule:**succinylglutamate

27	c3na6A_	Alignment	not modelled	99.9	21	desuccinylase/aspartoacylase; **PDBTitle:** crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
28	c2qvpC_	Alignment	not modelled	99.9	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative metallopeptidase (sama_0725) from2 shewanella amazonensis sb2b at 2.00 a resolution
29	c3fmcC_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**putative succinylglutamate desuccinylase / aspartoacylase; **PDBTitle:** crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
30	c2qj8B_	Alignment	not modelled	99.9	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mlr6093 protein; **PDBTitle:** crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
31	d1yw4a1	Alignment	not modelled	99.8	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
32	d2gu2a1	Alignment	not modelled	99.8	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
33	d2i3ca1	Alignment	not modelled	99.8	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
34	c3nh8A_	Alignment	not modelled	99.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aspartoacylase-2; **PDBTitle:** crystal structure of murine aminoacylase 3 in complex with n-acetyl-s-2 1,2-dichlorovinyl-l-cysteine
35	d1yw6a1	Alignment	not modelled	99.8	25	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
36	d2g9da1	Alignment	not modelled	99.8	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
37	d2bcoa1	Alignment	not modelled	99.7	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**AstE/AspA-like
38	c1cpbA_	Alignment		99.1	16	**PDB header:**hydrolase (c-terminal peptidase) **Chain:** A: **PDB Molecule:**carboxypeptidase b; **PDBTitle:** structure of carboxypeptidase b at 2.8 angstroms resolution
39	d2odfa1	Alignment	not modelled	93.2	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FGase-like
40	c1xovA_	Alignment	not modelled	86.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ply protein; **PDBTitle:** the crystal structure of the listeria monocytogenes bacteriophage psa2 endolysin plypsa
41	d1jwqa_	Alignment	not modelled	82.2	10	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
42	d1xova2	Alignment	not modelled	82.0	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**N-acetylmuramoyl-L-alanine amidase-like
43	d2q7sa1	Alignment	not modelled	80.5	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**FGase-like
44	c3czxA_	Alignment	not modelled	78.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of the putative n-acetylmuramoyl-l-2 alanine amidase from neisseria meningitidis
45	c1jd7A_	Alignment	not modelled	76.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
46	c3qayC_	Alignment	not modelled	69.1	6	**PDB header:**lyase **Chain:** C: **PDB Molecule:**endolysin; **PDBTitle:** catalytic domain of cd27l endolysin targeting clostridia difficile
47	c1jaeA_	Alignment	not modelled	50.2	17	**PDB header:**glycosidase **Chain:** A: **PDB Molecule:**alpha-amylase; **PDBTitle:** structure of tenebrio molitor larval alpha-amylase
48	c1bdeA_	Alignment	not modelled	36.0	26	**PDB header:**aids **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** helical structure of polypeptides from the c-terminal half2 of hiv-1 vpr, nmr, 20 structures
49	d1g94a2	Alignment	not modelled	34.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
50	c1dsjA_	Alignment	not modelled	31.0	28	**PDB header:**viral peptide **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** nmr solution structure of vpr50_75, 20 structures
51	c3gaaB_	Alignment	not modelled	30.9	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ta1441; **PDBTitle:** the crystal structure of the protein with unknown function

						from2 thermoplasma acidophilum
52	d1jaea2	Alignment	not modelled	23.0	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
53	d1g5ba_	Alignment	not modelled	19.4	15	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Protein serine/threonine phosphatase
54	c2wamB_	Alignment	not modelled	17.3	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical alanine and leucine rich **PDBTitle:** crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
55	d1mtza_	Alignment	not modelled	17.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Proline iminopeptidase-like
56	c3ne8A_	Alignment	not modelled	14.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** the crystal structure of a domain from n-acetylmuramoyl-l-alanine2 amidase of bartonella henselae str. houston-1
57	c2xt0A_	Alignment	not modelled	14.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
58	c3mnfA_	Alignment	not modelled	14.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pac2 family protein; **PDBTitle:** crystal structure of pac2 family protein from streptomyces avermitilis2 ma
59	d2p90a1	Alignment	not modelled	13.0	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Cgl1923-like **Family:**Cgl1923-like
60	c3blpX_	Alignment	not modelled	11.6	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase 1; **PDBTitle:** role of aromatic residues in human salivary alpha-amylase
61	d1b6ga_	Alignment	not modelled	11.4	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
62	c1tjnA_	Alignment	not modelled	10.5	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
63	d1tjna_	Alignment	not modelled	10.5	33	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
64	d1v6ta_	Alignment	not modelled	9.5	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
65	d2b3ya2	Alignment	not modelled	8.4	16	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
66	c3dddA_	Alignment	not modelled	8.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure of a putative acetyltransferase (np_142035.1) from2 pyrococcus horikoshii at 2.25 a resolution
67	c2xnsC_	Alignment	not modelled	8.3	31	**PDB header:**hydrolase/peptide **Chain:** C: **PDB Molecule:**regulator of g-protein signaling 14; **PDBTitle:** crystal structure of human g alpha i1 bound to a designed helical2 peptide derived from the goloco motif of rgs14
68	d1uf3a_	Alignment	not modelled	8.2	12	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
69	c1m8lA_	Alignment	not modelled	7.8	32	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** nmr structure of the hiv-1 regulatory protein vpr
70	d3ck2a1	Alignment	not modelled	7.5	9	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**YfcE-like
71	c3d3kD_	Alignment	not modelled	7.1	13	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
72	d1e6ua_	Alignment	not modelled	6.8	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
73	c2e2xA_	Alignment	not modelled	6.6	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**neurofibromin; **PDBTitle:** sec14 homology module of neurofibromin in complex with2 phosphatidylethanolamine
74	c3qfnA_	Alignment	not modelled	6.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of streptococcal asymmetric ap4a hydrolase and2 phosphodiesterase spr1479/saph in complex with inorganic phosphate
75	d1z6za1	Alignment	not modelled	6.1	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
76	c1n7gB_	Alignment	not modelled	6.1	26	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gdp-d-mannose-4,6-dehydratase; **PDBTitle:** crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
77	c3e35A_	Alignment	not modelled	6.1	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sco1997; **PDBTitle:** actinobacteria-specific protein of unknown function, sco1997

78	c1zoiC_	Alignment	not modelled	5.8	9	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**esterase; **PDBTitle:** crystal structure of a stereoselective esterase from2 pseudomonas putida ifo12996
79	c2x0dA_	Alignment	not modelled	5.8	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**wsaf; **PDBTitle:** apo structure of wsaf
80	c2p90B_	Alignment	not modelled	5.6	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
81	d1n7ha_	Alignment	not modelled	5.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
82	c2qjcA_	Alignment	not modelled	5.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**diadenosine tetraphosphatase, putative; **PDBTitle:** crystal structure of a putative diadenosine tetraphosphatase
83	c2ockA_	Alignment	not modelled	5.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**valacyclovir hydrolase; **PDBTitle:** crystal structure of valacyclovir hydrolase d123n mutant