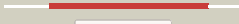



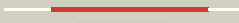



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1268c_(-)_1417664_1418362
Date	Wed Jul 31 22:05:36 BST 2019
Unique Job ID	acc68a3920bf75b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ervA_</a>	 Alignment		99.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative c39-like peptidase; <b>PDBTitle:</b> crystal structure of an putative c39-like peptidase from bacillus2 anthracis
2	<a href="#">c6mpzA_</a>	 Alignment		99.1	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> double glycine motif protease domain from ams/pcat <b>PDBTitle:</b> crystal structure of a double glycine motif protease from ams/pcat2 transporter in complex with the leader peptide
3	<a href="#">c3k8uA_</a>	 Alignment		99.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative abc transporter, atp-binding protein coma; <b>PDBTitle:</b> crystal structure of the peptidase domain of streptococcus coma, a bi-2 functional abc transporter involved in quorum sensing pathway
4	<a href="#">c3zuaA_</a>	 Alignment		98.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-hemolysin translocation atp-binding protein hlyb; <b>PDBTitle:</b> a c39-like domain
5	<a href="#">c4ry2A_</a>	 Alignment		97.8	23	<b>PDB header:</b> transport protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> abc-type bacteriocin transporter; <b>PDBTitle:</b> crystal structure of the peptidase-containing abc transporter pcat1
6	<a href="#">d2bu3a1</a>	 Alignment		97.8	16	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Phytochelatin synthase
7	<a href="#">d1cv8a_</a>	 Alignment		97.5	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
8	<a href="#">c2btwA_</a>	 Alignment		97.2	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> alr0975 protein; <b>PDBTitle:</b> crystal structure of alr0975
9	<a href="#">c3b79A_</a>	 Alignment		97.2	19	<b>PDB header:</b> nucleotide binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> toxin secretion atp-binding protein; <b>PDBTitle:</b> crystal structure of the n-terminal peptidase c39 like2 domain of the toxin secretion atp-binding protein from3 vibrio parahaemolyticus
10	<a href="#">c2c0yA_</a>	 Alignment		96.8	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> procathepsin s; <b>PDBTitle:</b> the crystal structure of a cys25ala mutant of human procathepsin s
11	<a href="#">d7pcka_</a>	 Alignment		96.6	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like

12	<a href="#">c3qt4A_</a>	Alignment		96.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cathepsin-I-like midgut cysteine proteinase; <b>PDBTitle:</b> structure of digestive procathepsin I 3 of tenebrio molitor larval2 midgut
13	<a href="#">c3qj3B_</a>	Alignment		96.3	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cathepsin I-like protein; <b>PDBTitle:</b> structure of digestive procathepsin I2 proteinase from tenebrio2 molitor larval midgut
14	<a href="#">c2o6xA_</a>	Alignment		96.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted cathepsin I 1; <b>PDBTitle:</b> crystal structure of procathepsin I1 from fasciola hepatica
15	<a href="#">d1vsna1</a>	Alignment		96.1	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
16	<a href="#">c3hhiB_</a>	Alignment		95.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cathepsin b-like cysteine protease; <b>PDBTitle:</b> crystal structure of cathepsin b from t. brucei in complex with ca074
17	<a href="#">c6hqzB_</a>	Alignment		95.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> avrprt2; <b>PDBTitle:</b> crystal structure of the type iii effector protein avrrpt2 from2 erwinia amylovora, a c70 family cysteine protease
18	<a href="#">d3pbha_</a>	Alignment		95.9	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
19	<a href="#">d1cs8a_</a>	Alignment		95.6	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
20	<a href="#">c6czkA_</a>	Alignment		95.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pro-cathepsin h; <b>PDBTitle:</b> crystal structure of wild-type human pro-cathepsin h
21	<a href="#">c3bwkD_</a>	Alignment	not modelled	95.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine protease falcipain-3; <b>PDBTitle:</b> crystal structure of falcipain-3 with its inhibitor, k11017
22	<a href="#">d1mira_</a>	Alignment	not modelled	94.9	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
23	<a href="#">d2r6na1</a>	Alignment	not modelled	94.8	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
24	<a href="#">c1icfA_</a>	Alignment	not modelled	94.8	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (cathepsin I: heavy chain); <b>PDBTitle:</b> crystal structure of mhc class ii associated p41 ii fragment in2 complex with cathepsin I
25	<a href="#">d1me4a_</a>	Alignment	not modelled	94.4	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
26	<a href="#">d2h7ja1</a>	Alignment	not modelled	94.4	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
27	<a href="#">c1jqpA_</a>	Alignment	not modelled	94.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dipeptidyl peptidase i; <b>PDBTitle:</b> dipeptidyl peptidase i (cathepsin c), a tetrameric cysteine protease2 of the papain family
28	<a href="#">d1fh0a_</a>	Alignment	not modelled	94.3	21	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
29	<a href="#">d1gmya_</a>	Alignment	not modelled	94.2	22	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like

30	<a href="#">c4yywA</a>	Alignment	not modelled	94.0	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> ficin isoform d; <b>PDBTitle:</b> ficin d2
31	<a href="#">c6a0qA</a>	Alignment	not modelled	93.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lpg2622; <b>PDBTitle:</b> the crystal structure of lpg2622_e64 complex
32	<a href="#">c3ch3X</a>	Alignment	not modelled	93.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> X; <b>PDB Molecule:</b> serine-repeat antigen protein; <b>PDBTitle:</b> crystal structure analysis of sera5e from plasmodium falciparum
33	<a href="#">c4ci7A</a>	Alignment	not modelled	93.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cell surface protein (putative cell surface-associated) <b>PDBTitle:</b> the crystal structure of the cysteine protease and lectin-like2 domains of cwp84, a surface layer associated protein of clostridium3 difficile
34	<a href="#">d1deua</a>	Alignment	not modelled	93.2	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
35	<a href="#">c2b1nA</a>	Alignment	not modelled	93.2	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> spe31; <b>PDBTitle:</b> crystal structure of a papain-fold protein without the catalytic2 cysteine from seeds of pachyrhizus erosus
36	<a href="#">d1cqda</a>	Alignment	not modelled	92.7	15	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
37	<a href="#">c5fpwC</a>	Alignment	not modelled	92.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> C; <b>PDB Molecule:</b> pro cathepsin b s9; <b>PDBTitle:</b> procathepsin b s9 from trypanosoma congolense
38	<a href="#">c4hwyA</a>	Alignment	not modelled	92.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine peptidase c (cpc); <b>PDBTitle:</b> trypanosoma brucei procathepsin b solved from 40 fs free-electron2 laser pulse data by serial femtosecond x-ray crystallography
39	<a href="#">d1dkia</a>	Alignment	not modelled	92.2	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
40	<a href="#">c1csbE</a>	Alignment	not modelled	91.8	18	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> E; <b>PDB Molecule:</b> cathepsin b heavy chain; <b>PDBTitle:</b> crystal structure of cathepsin b inhibited with ca030 at 2.1 angstroms2 resolution: a basis for the design of specific epoxysuccinyl3 inhibitors
41	<a href="#">d1m6da</a>	Alignment	not modelled	91.7	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
42	<a href="#">c3bbaB</a>	Alignment	not modelled	91.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> interpain a; <b>PDBTitle:</b> structure of active wild-type prevotella intermedia interpain a2 cysteine protease
43	<a href="#">c2jtcA</a>	Alignment	not modelled	91.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> streptopain; <b>PDBTitle:</b> 3d structure and backbone dynamics of spe b
44	<a href="#">c3oisA</a>	Alignment	not modelled	91.5	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> crystal structure xylellain, a cysteine protease from xylella2 fastidiosa
45	<a href="#">d1ef7a</a>	Alignment	not modelled	91.3	19	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
46	<a href="#">d1pvja</a>	Alignment	not modelled	90.7	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
47	<a href="#">c1nb3D</a>	Alignment	not modelled	90.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> cathepsin h; <b>PDBTitle:</b> crystal structure of stefin a in complex with cathepsin h: n-terminal2 residues of inhibitors can adapt to the active sites of endo-and3 exopeptidases
48	<a href="#">c3bb7A</a>	Alignment	not modelled	89.8	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> interpain a; <b>PDBTitle:</b> structure of prevotella intermedia prointerpain a fragment 39-3592 (mutant c154a)
49	<a href="#">d1jqpa2</a>	Alignment	not modelled	89.8	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
50	<a href="#">d2dcca1</a>	Alignment	not modelled	87.8	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
51	<a href="#">c3qsdA</a>	Alignment	not modelled	87.7	15	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> cathepsin b-like peptidase (c01 family); <b>PDBTitle:</b> structure of cathepsin b1 from schistosoma mansoni in complex with2 ca074 inhibitor
52	<a href="#">c5jt8B</a>	Alignment	not modelled	86.8	17	<b>PDB header:</b> allergen <b>Chain:</b> B; <b>PDB Molecule:</b> blo t 1 allergen; <b>PDBTitle:</b> structural basis for the limited antibody cross reactivity between the2 mite allergens blo t 1 and der p 1
53	<a href="#">d1thea</a>	Alignment	not modelled	85.8	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
54	<a href="#">d1ppoa</a>	Alignment	not modelled	85.5	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
55	<a href="#">c2tva</a>	Alignment	not modelled	84.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> papain;

55	<a href="#">c3u1aA</a>	Alignment	not modelled	84.0	15	<b>PDBTitle:</b> structure of the precursor of a thermostable variant of papain at 2.62 angstrom resolution
56	<a href="#">c1y4hA</a>	Alignment	not modelled	84.0	16	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> wild type staphopain-staphostatin complex
57	<a href="#">d1o0ea</a>	Alignment	not modelled	83.2	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
58	<a href="#">d1gece</a>	Alignment	not modelled	79.5	16	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
59	<a href="#">c3hwnC</a>	Alignment	not modelled	79.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> cathepsin I1; <b>PDBTitle:</b> cathepsin I with az13010160
60	<a href="#">d1iwda</a>	Alignment	not modelled	77.6	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
61	<a href="#">d2acta</a>	Alignment	not modelled	75.9	16	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
62	<a href="#">d2as8a1</a>	Alignment	not modelled	73.7	22	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
63	<a href="#">d2oula1</a>	Alignment	not modelled	73.2	16	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
64	<a href="#">c1x9yD</a>	Alignment	not modelled	72.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine proteinase; <b>PDBTitle:</b> the prostaphopain b structure
65	<a href="#">c5ef4A</a>	Alignment	not modelled	72.6	15	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> 2.05 a crystal structure of the amb a 11 cysteine protease, a major2 ragweed pollen allergen, in its proform
66	<a href="#">d1pcia</a>	Alignment	not modelled	70.5	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
67	<a href="#">d1aeca</a>	Alignment	not modelled	68.3	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
68	<a href="#">c5a24A</a>	Alignment	not modelled	54.3	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dionain-1; <b>PDBTitle:</b> crystal structure of dionain-1, the major endopeptidase in2 the venus flytrap digestive juice
69	<a href="#">c3pw3E</a>	Alignment	not modelled	49.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> aminopeptidase c; <b>PDBTitle:</b> crystal structure of a cysteine protease (bdi_2249) from2 parabacteroides distasonis atcc 8503 at 2.23 a resolution
70	<a href="#">d1pxva</a>	Alignment	not modelled	49.0	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
71	<a href="#">c3f55A</a>	Alignment	not modelled	47.7	17	<b>PDB header:</b> hydrolase, allergen <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,3-glucanase; <b>PDBTitle:</b> crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
72	<a href="#">c5t1oB</a>	Alignment	not modelled	45.8	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate-protein phosphotransferase ptsp; <b>PDBTitle:</b> solution-state nmr and saxs structural ensemble of npr (1-85) in2 complex with ein-ntr (170-424)
73	<a href="#">c3f75A</a>	Alignment	not modelled	45.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cathepsin I protease; <b>PDBTitle:</b> activated toxoplasma gondii cathepsin I (tgcp1) in complex with its2 propeptide
74	<a href="#">d1ghsa</a>	Alignment	not modelled	44.4	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
75	<a href="#">d1khqa</a>	Alignment	not modelled	43.8	19	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
76	<a href="#">c2bdzA</a>	Alignment	not modelled	42.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mexicain; <b>PDBTitle:</b> mexicain from jacarattia mexicana
77	<a href="#">c4yyqA</a>	Alignment	not modelled	42.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ficin isoform a; <b>PDBTitle:</b> ficin a
78	<a href="#">d3gcba</a>	Alignment	not modelled	40.7	18	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
79	<a href="#">d1vbga2</a>	Alignment	not modelled	40.7	23	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> Phosphohistidine domain <b>Family:</b> Pyruvate phosphate dikinase, central domain
80	<a href="#">d1s4va</a>	Alignment	not modelled	39.3	14	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
81	<a href="#">d1cmxa</a>	Alignment	not modelled	37.0	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase UCH-L
						<b>Fold:</b> TIM beta/alpha-barrel

82	<a href="#">d2cyga1</a>	Alignment	not modelled	36.4	15	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
83	<a href="#">c6mirA</a>	Alignment	not modelled	35.5	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ananain; <b>PDBTitle:</b> native ananain from ananas comosus
84	<a href="#">c5segwA</a>	Alignment	not modelled	35.3	15	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine protease; <b>PDBTitle:</b> 2.70 a crystal structure of the amb a 11 cysteine protease, a major2 ragweed pollen allergen, in its proform
85	<a href="#">c5msmD</a>	Alignment	not modelled	35.2	18	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> sister chromatid cohesion protein dcc1; <b>PDBTitle:</b> structure of the dcc1-ctf8-ctf18c trimer
86	<a href="#">d1yala</a>	Alignment	not modelled	35.1	17	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Papain-like
87	<a href="#">d2etla1</a>	Alignment	not modelled	34.3	13	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase UCH-L
88	<a href="#">c5msnA</a>	Alignment	not modelled	34.0	18	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> dcc1 protein; <b>PDBTitle:</b> structure of the dcc1 protein
89	<a href="#">c3a7sA</a>	Alignment	not modelled	32.2	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase isozyme I5; <b>PDBTitle:</b> catalytic domain of uch37
90	<a href="#">c3ffvA</a>	Alignment	not modelled	32.1	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> protein syd; <b>PDBTitle:</b> crystal structure analysis of syd
91	<a href="#">c3qfwB</a>	Alignment	not modelled	30.1	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose-1,5-bisphosphate carboxylase/oxygenase large <b>PDBTitle:</b> crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
92	<a href="#">c4ig7A</a>	Alignment	not modelled	29.6	11	<b>PDB header:</b> hydrolase/signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin c-terminal hydrolase 37; <b>PDBTitle:</b> crystal structure of trichinella spiralis uch37 bound to ubiquitin2 vinyl methyl ester
93	<a href="#">d1qo2a</a>	Alignment	not modelled	29.1	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
94	<a href="#">d1xd3a</a>	Alignment	not modelled	28.8	20	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Ubiquitin carboxyl-terminal hydrolase UCH-L
95	<a href="#">c2wdtA</a>	Alignment	not modelled	28.3	11	<b>PDB header:</b> hydrolase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase I3; <b>PDBTitle:</b> crystal structure of plasmodium falciparum uchI3 in complex2 with the suicide inhibitor ubvme
96	<a href="#">d1euza2</a>	Alignment	not modelled	27.3	18	<b>Fold:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Superfamily:</b> Aminoacid dehydrogenase-like, N-terminal domain <b>Family:</b> Aminoacid dehydrogenases
97	<a href="#">d1e9yb2</a>	Alignment	not modelled	27.1	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> alpha-subunit of urease, catalytic domain
98	<a href="#">c2r8rB</a>	Alignment	not modelled	26.8	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> sensor protein; <b>PDBTitle:</b> crystal structure of the n-terminal region (19..243) of sensor protein2 kdpd from pseudomonas syringae pv. tomato str. dc3000
99	<a href="#">d1ejxc2</a>	Alignment	not modelled	26.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> alpha-subunit of urease, catalytic domain
100	<a href="#">c6cgaC</a>	Alignment	not modelled	26.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase calypso; <b>PDBTitle:</b> structure of the pr-dub complex
101	<a href="#">d1l0oc</a>	Alignment	not modelled	25.2	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
102	<a href="#">c1l0oC</a>	Alignment	not modelled	25.2	24	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> sigma factor; <b>PDBTitle:</b> crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoIIab with the sporulation sigma factor3 sigmaf
103	<a href="#">c4zhjA</a>	Alignment	not modelled	24.2	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mg-chelatase subunit chlH; <b>PDBTitle:</b> crystal structure of the catalytic subunit of magnesium chelatase
104	<a href="#">c3ihrA</a>	Alignment	not modelled	24.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ubiquitin carboxyl-terminal hydrolase isozyme I5; <b>PDBTitle:</b> crystal structure of uch37
105	<a href="#">c1v9lA</a>	Alignment	not modelled	23.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> l-glutamate dehydrogenase from pyrobaculum islandicum2 complexed with nad
106	<a href="#">c1kblA</a>	Alignment	not modelled	23.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate phosphate dikinase; <b>PDBTitle:</b> pyruvate phosphate dikinase
107	<a href="#">d1aq0a</a>	Alignment	not modelled	23.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases <b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 40s ribosomal protein s13;

108	<a href="#">c3u5cN_</a>	Alignment	not modelled	22.4	38	<b>PDBTitle:</b> the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
109	<a href="#">c1hrdA_</a>	Alignment	not modelled	21.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate dehydrogenase; <b>PDBTitle:</b> glutamate dehydrogenase