Phyre^2

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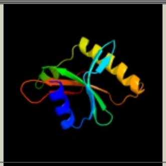
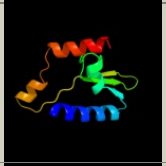
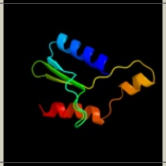
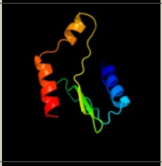
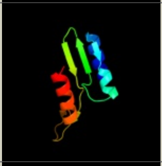
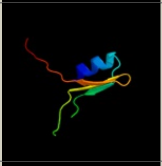
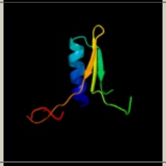
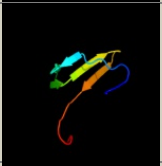
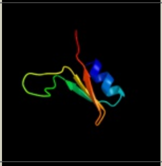
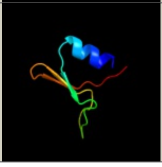
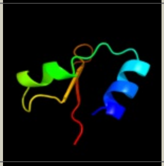
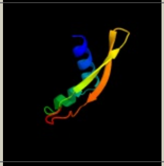
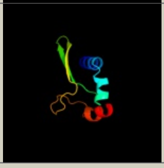
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fovA_	Alignment		100.0	37	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
2	d1gefa_	Alignment		97.8	22	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
3	d1ob8a_	Alignment		97.3	21	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
4	c2wj0B_	Alignment		96.8	21	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**archaeal hjc; **PDBTitle:** crystal structures of holliday junction resolvases from2 archaeoglobus fulgidus bound to dna substrate
5	d1hh1a_	Alignment		96.3	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
6	c1y88A_	Alignment		95.9	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1548; **PDBTitle:** crystal structure of protein of unknown function af1548
7	d1y88a2	Alignment		95.9	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**MRR-like
8	c2vldA_	Alignment		93.3	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
9	c3dnxA_	Alignment		92.1	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spo1766; **PDBTitle:** spo1766 protein of unknown function from silicibacter pomeroyi.
10	d1xmxa_	Alignment		92.0	17	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hypothetical protein VC1899
11	d2inba1	Alignment		90.5	19	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XisH-like

12	d2okfa1	Alignment		89.7	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XisH-like
13	d1cw0a_	Alignment		79.5	30	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
14	d1w36b3	Alignment		70.4	23	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Exodeoxyribonuclease V beta chain (RecB), C-terminal domain
15	d1e4ea2	Alignment		68.0	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
16	c1w36E_	Alignment		56.9	23	**PDB header:**recombination **Chain:** E: **PDB Molecule:**exodeoxyribonuclease v beta chain; **PDBTitle:** recbcd:dna complex
17	d1iowa2	Alignment		51.3	13	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
18	d1uc8a2	Alignment		38.3	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Lysine biosynthesis enzyme LysX ATP-binding domain
19	d1vsra_	Alignment		32.8	28	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
20	c3se7A_	Alignment		32.5	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
21	d2j9ga3	Alignment	not modelled	25.6	21	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
22	c3tqtB_	Alignment	not modelled	24.8	6	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
23	d1kjqa3	Alignment	not modelled	24.2	18	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
24	c3e5nA_	Alignment	not modelled	23.4	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
25	d1miua5	Alignment	not modelled	21.6	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
26	d1ulza3	Alignment	not modelled	20.4	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
27	c3bpqD_	Alignment	not modelled	19.1	33	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
28	c3h1tA_	Alignment	not modelled	18.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i site-specific restriction-modification **PDBTitle:** the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016

29	c2dlnA_	Alignment	not modelled	17.6	13	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
30	d1ehia2	Alignment	not modelled	17.5	11	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
31	d1m0da_	Alignment	not modelled	16.9	25	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Endonuclease I (Holliday junction resolvase)
32	d1tx3a1	Alignment	not modelled	16.9	10	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease HincII
33	d1y0ka1	Alignment	not modelled	16.3	60	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**PA4535-like
34	d1iyjb5	Alignment	not modelled	15.9	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
35	d1puza_	Alignment	not modelled	15.1	55	**Fold:**YgfY-like **Superfamily:**YgfY-like **Family:**YgfY-like
36	d1fy7a_	Alignment	not modelled	14.9	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
37	c3i12A_	Alignment	not modelled	14.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
38	c1x6iB_	Alignment	not modelled	14.4	36	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ygfy; **PDBTitle:** crystal structure of ygfy from escherichia coli
39	d3etja3	Alignment	not modelled	14.1	10	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
40	c2jr5A_	Alignment	not modelled	14.0	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0350 protein vc_2471; **PDBTitle:** solution structure of upf0350 protein vc_2471. northeast2 structural genomics target vcr36
41	d1j6ua1	Alignment	not modelled	13.7	10	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
42	c2pvpB_	Alignment	not modelled	13.3	5	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
43	c2cl2A_	Alignment	not modelled	13.1	63	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative laminarinase; **PDBTitle:** endo-1,3(4)-beta-glucanase from phanerochaete chrysosporium,2 solved using native sulfur sad, exhibiting intact3 heptasaccharide glycosylation
44	d2ozua1	Alignment	not modelled	13.0	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
45	d2fiwa1	Alignment	not modelled	12.8	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
46	c3r23B_	Alignment	not modelled	12.6	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
47	c2givA_	Alignment	not modelled	12.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable histone acetyltransferase myst1; **PDBTitle:** human myst histone acetyltransferase 1
48	d2giva1	Alignment	not modelled	12.3	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
49	d2r85a2	Alignment	not modelled	11.6	13	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
50	d2r7ka2	Alignment	not modelled	11.1	13	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
51	c1ulzA_	Alignment	not modelled	11.1	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
52	d1xdfa1	Alignment	not modelled	10.7	9	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
53	c3hrlA_	Alignment	not modelled	10.6	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**endonuclease-like protein; **PDBTitle:** crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
54	c2p0aA_	Alignment	not modelled	9.9	13	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin-3; **PDBTitle:** the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
55	c2duwA_	Alignment	not modelled	9.6	15	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein;

55	c2duwA_	Alignment	not modelled	9.6	15	**PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
56	c3fqiA_	Alignment	not modelled	9.6	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein dom3z; **PDBTitle:** crystal structure of the mouse dom3z
57	c1uc8B_	Alignment	not modelled	9.6	15	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**lysine biosynthesis enzyme; **PDBTitle:** crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
58	d1zhva2	Alignment	not modelled	9.4	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Atu0741-like
59	d2o8ra3	Alignment	not modelled	9.3	36	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
60	d1p9oa_	Alignment	not modelled	9.2	21	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
61	c3u9sE_	Alignment	not modelled	9.1	23	**PDB header:**ligase **Chain:** E: **PDB Molecule:**methylcrotonyl-coa carboxylase, alpha-subunit; **PDBTitle:** crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
62	d2jfga1	Alignment	not modelled	9.1	11	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
63	c1ehiB_	Alignment	not modelled	9.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine:d-lactate ligase; **PDBTitle:** d-alanine:d-lactate ligase (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides
64	c2k7hA_	Alignment	not modelled	8.7	12	**PDB header:**allergen **Chain:** A: **PDB Molecule:**stress-induced protein sam22; **PDBTitle:** nmr solution structure of soybean allergen gly m 4
65	c2ou2A_	Alignment	not modelled	8.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone acetyltransferase htatip; **PDBTitle:** acetyltransferase domain of human hiv-1 tat interacting2 protein, 60kda, isoform 3
66	d2naca2	Alignment	not modelled	8.6	27	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
67	d1p3da1	Alignment	not modelled	8.3	18	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
68	c3uvzB_	Alignment	not modelled	8.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
69	c3s5pA_	Alignment	not modelled	8.2	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose 5-phosphate isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase b rpib from giardia2 lamblia
70	c1e4eB_	Alignment	not modelled	8.1	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
71	c3koxA_	Alignment	not modelled	8.0	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**d-ornithine aminomutase e component; **PDBTitle:** crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
72	c3dfuB_	Alignment	not modelled	7.8	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein from 6-phosphogluconate **PDBTitle:** crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
73	d1gsoa3	Alignment	not modelled	7.8	19	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
74	c3cqyA_	Alignment	not modelled	7.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of a functionally unknown protein (so_1313) from2 shewanella oneidensis mr-1
75	d2jdca1	Alignment	not modelled	7.6	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
76	c3orqA_	Alignment	not modelled	7.5	6	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
77	c3ey5A_	Alignment	not modelled	7.3	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase-like, gnat family; **PDBTitle:** putative acetyltransferase from gnat family from bacteroides2 thetaiotaomicron.
78	c3bt3B_	Alignment	not modelled	7.3	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**glyoxalase-related enzyme, arac type; **PDBTitle:** crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
79	d1pk8a2	Alignment	not modelled	7.3	13	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
80	c2x7bA_	Alignment	not modelled	7.3	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase sso0209;

80	c2x7bA_	Alignment	not modelled	7.3	16	**PDBTitle:** crystal structure of the n-terminal acetylase ard1 from2 sulfolobus solfataricus p2
81	c3qbwA_	Alignment	not modelled	7.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anhydro-n-acetylmuramic acid kinase; **PDBTitle:** crystal structure of pseudomonas aeruginosa 1,6-anhydro-n-2 actetylmuramic acid kinase (anmk) bound to adenosine diphosphate
82	c3g3oA_	Alignment	not modelled	7.0	36	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**vacuolar transporter chaperone 2; **PDBTitle:** crystal structure of the cytoplasmic tunnel domain in yeast2 vtc2p
83	c1y7eA_	Alignment	not modelled	7.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable m18-family aminopeptidase 1; **PDBTitle:** the crystal structure of aminopeptidase i from borrelia burgdorferi2 b31
84	d1u7za_	Alignment	not modelled	6.9	17	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
85	c2i80B_	Alignment	not modelled	6.5	11	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
86	c2qb5B_	Alignment	not modelled	6.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**inositol-tetrakisphosphate 1-kinase; **PDBTitle:** crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
87	c3g8cB_	Alignment	not modelled	6.4	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
88	d1jiwi_	Alignment	not modelled	6.3	23	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Metalloprotease inhibitor
89	c3gidB_	Alignment	not modelled	6.2	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
90	c3q2oB_	Alignment	not modelled	6.2	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
91	c3ie5A_	Alignment	not modelled	6.2	16	**PDB header:**plant protein, biosynthetic protein **Chain:** A: **PDB Molecule:**phenolic oxidative coupling protein hyp-1; **PDBTitle:** crystal structure of hyp-1 protein from hypericum perforatum2 (st john's wort) involved in hypericin biosynthesis
92	c2rdyB_	Alignment	not modelled	6.2	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**bh0842 protein; **PDBTitle:** crystal structure of a putative glycoside hydrolase family2 protein from bacillus halodurans
93	d1jg5a_	Alignment	not modelled	6.1	25	**Fold:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Superfamily:**GTP cyclohydrolase I feedback regulatory protein, GFRP **Family:**GTP cyclohydrolase I feedback regulatory protein, GFRP
94	d1dcja_	Alignment	not modelled	6.0	14	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
95	c2pn1A_	Alignment	not modelled	5.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoylphosphate synthase large subunit; **PDBTitle:** crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
96	c1pk8D_	Alignment	not modelled	5.9	14	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**rat synapsin i; **PDBTitle:** crystal structure of rat synapsin i c domain complexed to2 ca.atp
97	c1upsB_	Alignment	not modelled	5.9	50	**PDB header:**glycosyl hydrolase **Chain:** B: **PDB Molecule:**glcnac-alpha-1,4-gal-releasing endo-beta- **PDBTitle:** glcnac[alpha]1-4gal releasing endo-[beta]-galactosidase2 from clostridium perfringens
98	c1w96B_	Alignment	not modelled	5.8	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase; **PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
99	c3juuA_	Alignment	not modelled	5.7	38	**PDB header:**hydrolase/carbohydrate **Chain:** A: **PDB Molecule:**porphyranase b; **PDBTitle:** crystal structure of porphyranase b (porb) from zobellia2 galactanivorans