Phyre^2

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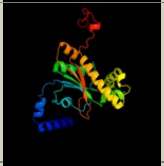
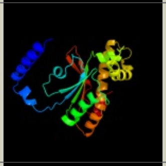
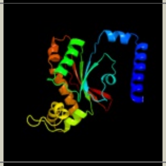
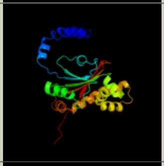
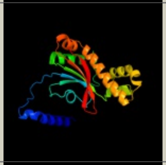
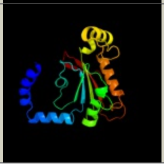
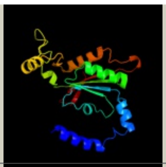
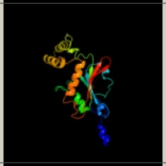
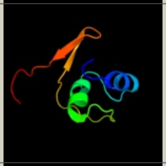
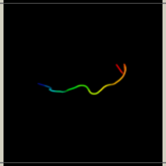
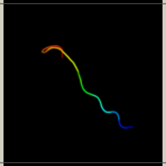
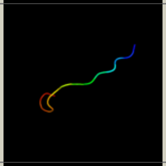
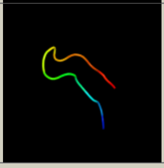
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i6pa_	Alignment		100.0	100	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
2	c2a8cE_	Alignment		100.0	63	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** haemophilus influenzae beta-carbonic anhydrase
3	d1ddza1	Alignment		100.0	48	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
4	d1ddza2	Alignment		100.0	45	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
5	c1ddzA_	Alignment		100.0	47	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** x-ray structure of a beta-carbonic anhydrase from the red2 alga, porphyridium purpureum r-1
6	c3ucoB_	Alignment		100.0	39	**PDB header:**lyase/lyase inhibitor **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide
7	c2w3nA_	Alignment		100.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
8	d1ekja_	Alignment		100.0	25	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
9	c3eyxB_	Alignment		100.0	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase nce103 from2 saccharomyces cerevisiae
10	c2a5vB_	Alignment		100.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase (carbonate dehydratase) (carbonic **PDBTitle:** crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
11	c3lasA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carbonic anhydrase; **PDBTitle:** crystal structure of carbonic anhydrase from streptococcus mutans to2 1.4 angstrom resolution

12	c1ylkA_	Alignment		100.0	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv1284/mt1322; **PDBTitle:** crystal structure of rv1284 from mycobacterium tuberculosis in complex2 with thiocyanate
13	d1g5ca_	Alignment		100.0	24	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
14	c2hwkA_	Alignment		62.6	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**helicase nsp2; **PDBTitle:** crystal structure of venezuelan equine encephalitis2 alphavirus nsp2 protease domain
15	d1j2ra_	Alignment		36.5	19	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
16	c3degC_	Alignment		30.9	21	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
17	c2h5eB_	Alignment		28.9	21	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
18	c3i8sC_	Alignment		28.7	27	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** structure of the cytosolic domain of e. coli feob, nucleotide-free2 form
19	d1n0ua2	Alignment		28.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
20	d1fqta_	Alignment		28.2	14	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
21	c2de7E_	Alignment	not modelled	28.0	31	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ferredoxin component of carbazole; **PDBTitle:** the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
22	d1zo0a1	Alignment	not modelled	27.4	21	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Ornithine decarboxylase antizyme-like
23	c3d89A_	Alignment	not modelled	27.3	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rieske domain-containing protein; **PDBTitle:** crystal structure of a soluble rieske ferredoxin from mus musculus
24	d1nrjb_	Alignment	not modelled	26.8	42	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
25	d1z01a1	Alignment	not modelled	26.0	29	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
26	d2de6a1	Alignment	not modelled	25.7	50	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
27	c2ywfA_	Alignment	not modelled	25.2	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
28	d2fh5b1	Alignment	not modelled	24.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
						PDB header:hydrolase

29	c3trkA_	Alignment	not modelled	24.5	16	**Chain:** A: **PDB Molecule:**nonstructural polyprotein; **PDBTitle:** structure of the chikungunya virus nsp2 protease
30	c3ibyA_	Alignment	not modelled	24.5	33	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** structure of cytosolic domain of l. pneumophila feob
31	c3gceA_	Alignment	not modelled	24.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin component of carbazole 1,9a- **PDBTitle:** ferredoxin of carbazole 1,9a-dioxygenase from nocardioides2 aromaticivorans ic177
32	d1rkba_	Alignment	not modelled	24.2	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
33	c1d2eA_	Alignment	not modelled	24.2	27	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**elongation factor tu (ef-tu); **PDBTitle:** crystal structure of mitochondrial ef-tu in complex with gdp
34	c2qu8A_	Alignment	not modelled	23.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nucleolar gtp-binding protein 1; **PDBTitle:** crystal structure of putative nucleolar gtp-binding protein 1 pff0625w2 from plasmodium falciparum
35	d2jo6a1	Alignment	not modelled	23.2	25	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
36	c3p27A_	Alignment	not modelled	22.9	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**elongation factor 1 alpha-like protein; **PDBTitle:** crystal structure of a translational gtpase (gdp form)
37	c3k53B_	Alignment	not modelled	22.5	15	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b; **PDBTitle:** crystal structure of nfeob from p. furiosus
38	c1mj1A_	Alignment	not modelled	22.4	27	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**elongation factor tu; **PDBTitle:** fitting the ternary complex of ef-tu/trna/gtp and ribosomal proteins2 into a 13 a cryo-em map of the coli 70s ribosome
39	d1s0ua3	Alignment	not modelled	22.3	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
40	c3izyP_	Alignment	not modelled	21.8	29	**PDB header:**rna, ribosomal protein **Chain:** P: **PDB Molecule:**translation initiation factor if-2, mitochondrial; **PDBTitle:** mammalian mitochondrial translation initiation factor 2
41	c3tr5C_	Alignment	not modelled	21.3	21	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
42	c2bvnB_	Alignment	not modelled	21.1	27	**PDB header:**elongation factor **Chain:** B: **PDB Molecule:**elongation factor tu; **PDBTitle:** e. coli ef-tu:gdpnp in complex with the antibiotic2 enacyloxin iia
43	d1r5ba3	Alignment	not modelled	21.1	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
44	c2dy1A_	Alignment	not modelled	21.0	29	**PDB header:**signaling protein, translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus
45	c1zunB_	Alignment	not modelled	20.7	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylate transferase, subunit **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
46	d1efca3	Alignment	not modelled	20.1	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
47	c2qagC_	Alignment	not modelled	20.0	27	**PDB header:**cell cycle, structural protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of human septin trimer 2/6/7
48	c3oqpB_	Alignment	not modelled	19.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
49	d1g7sa4	Alignment	not modelled	19.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
50	c2rauA_	Alignment	not modelled	19.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative esterase; **PDBTitle:** crystal structure of a putative lipase (np_343859.1) from sulfolobus2 solfataricus at 1.85 a resolution
51	c1r5nA_	Alignment	not modelled	19.3	36	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic peptide chain release factor gtp- **PDBTitle:** crystal structure analysis of sup35 complexed with gdp
52	c2zxrA_	Alignment	not modelled	19.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**single-stranded dna specific exonuclease recj; **PDBTitle:** crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
53	c3hb7G_	Alignment	not modelled	19.1	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**isochorismatase hydrolase; **PDBTitle:** the crystal structure of an isochorismatase-like hydrolase from2 alkaliphilus metalliredigens to 2.3a
54	d1ulra_	Alignment	not modelled	19.0	14	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like

55	c3t5dC_	Alignment	not modelled	18.9	27	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of septin 7 in complex with gdp
56	c2qpzA_	Alignment	not modelled	18.8	15	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**naphthalene 1,2-dioxygenase system ferredoxin **PDBTitle:** naphthalene 1,2-dioxygenase rieske ferredoxin
57	d1svia_	Alignment	not modelled	18.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
58	c2xexA_	Alignment	not modelled	18.4	29	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
59	d2ih2a2	Alignment	not modelled	18.2	24	**Fold:**DNA methylase specificity domain **Superfamily:**DNA methylase specificity domain **Family:**TaqI C-terminal domain-like
60	c3br8A_	Alignment	not modelled	17.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
61	c3pqcA_	Alignment	not modelled	17.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtp-binding protein engb; **PDBTitle:** crystal structure of thermotoga maritima ribosome biogenesis gtp-2 binding protein engb (ysxc/yiha) in complex with gdp
62	c2i7fB_	Alignment	not modelled	17.5	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin component of dioxygenase; **PDBTitle:** sphingomonas yanoikuyae b1 ferredoxin
63	c1s0uA_	Alignment	not modelled	17.3	36	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** eif2gamma apo
64	d3c0da1	Alignment	not modelled	17.1	9	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
65	c3a1vB_	Alignment	not modelled	17.0	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**iron(ii) transport protein b; **PDBTitle:** crystal structue of the cytosolic domain of t. maritima feob2 iron iransporter in apo form
66	c1z01D_	Alignment	not modelled	17.0	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**2-oxo-1,2-dihydroquinoline 8-monooxygenase, **PDBTitle:** 2-oxoquinoline 8-monooxygenase component: active site2 modulation by rieske-[2fe-2s] center oxidation/reduction
67	d1egaa1	Alignment	not modelled	16.9	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
68	d1vm9a_	Alignment	not modelled	16.8	27	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Rieske iron-sulfur protein (ISP)
69	c2wjjB_	Alignment	not modelled	16.5	27	**PDB header:**metal transport **Chain:** B: **PDB Molecule:**ferrous iron transport protein b homolog; **PDBTitle:** structure and function of the feob g-domain from2 methanococcus jannaschii
70	d2bv3a2	Alignment	not modelled	16.5	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
71	c1zo1I_	Alignment	not modelled	16.3	29	**PDB header:**translation/rna **Chain:** I: **PDB Molecule:**translation initiation factor 2; **PDBTitle:** if2, if1, and trna fitted to cryo-em data of e. coli 70s2 initiation complex
72	d2jzaa1	Alignment	not modelled	16.2	18	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**NirD-like
73	c1g7cA_	Alignment	not modelled	16.1	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor 1-alpha; **PDBTitle:** yeast eef1a:eef1ba in complex with gdpnp
74	c3oqpA_	Alignment	not modelled	16.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
75	d1udxa2	Alignment	not modelled	15.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
76	c2plfA_	Alignment	not modelled	15.6	36	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor 2 gamma subunit; **PDBTitle:** the structure of aif2gamma subunit from the archaeon2 sulfolobus solfataricus in the nucleotide-free form.
77	c2x2fD_	Alignment	not modelled	15.6	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**dynamin-1; **PDBTitle:** dynamin 1 gtpase dimer, short axis form
78	c2zovA_	Alignment	not modelled	15.4	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** structure of the periplasmic domain of motb from salmonella2 (crystal form i)
79	d1apsa_	Alignment	not modelled	14.8	21	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
80	d1w2ia_	Alignment	not modelled	14.7	24	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like

						Family: Acylphosphatase-like
81	d1viaa_	Alignment	not modelled	14.6	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
82	c2r8bA_	Alignment	not modelled	14.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2452; **PDBTitle:** the crystal structure of the protein atu2452 of unknown function from2 agrobacterium tumefaciens str. c58
83	c1kk3A_	Alignment	not modelled	14.4	36	**PDB header:**translation **Chain:** A: **PDB Molecule:**eif2gamma; **PDBTitle:** structure of the wild-type large gamma subunit of2 initiation factor eif2 from pyrococcus abyssi complexed3 with gdp-mg2+
84	c1wb1C_	Alignment	not modelled	14.4	36	**PDB header:**protein synthesis **Chain:** C: **PDB Molecule:**translation elongation factor selb; **PDBTitle:** crystal structure of translation elongation factor selb2 from methanococcus maripaludis in complex with gdp
85	d1wf3a1	Alignment	not modelled	14.1	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
86	c3lxwA_	Alignment	not modelled	13.5	33	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 1; **PDBTitle:** crystal structure of human gtpase imap family member 1
87	d2gc6a1	Alignment	not modelled	13.3	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
88	c3a1wA_	Alignment	not modelled	13.2	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**iron(ii) transport protein b; **PDBTitle:** crystal structue of the g domain of t. maritima feob iron2 iransporter
89	c3lx8A_	Alignment	not modelled	13.0	30	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**ferrous iron uptake transporter protein b; **PDBTitle:** crystal structure of gdp-bound nfeob from s. thermophilus
90	c2elfA_	Alignment	not modelled	13.0	27	**PDB header:**translation **Chain:** A: **PDB Molecule:**protein translation elongation factor 1a; **PDBTitle:** crystal structure of the selb-like elongation factor ef-pyl2 from methanosarcina mazei
91	c4proD_	Alignment	not modelled	12.9	10	**PDB header:**serine protease **Chain:** D: **PDB Molecule:**alpha-lytic protease; **PDBTitle:** alpha-lytic protease complexed with pro region
92	c3o93A_	Alignment	not modelled	12.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes
93	c3dukD_	Alignment	not modelled	12.7	10	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**ntf2-like protein of unknown function; **PDBTitle:** crystal structure of a ntf2-like protein of unknown function2 (mfla_0564) from methylobacillus flagellatus kt at 2.200 a resolution
94	c3hynA_	Alignment	not modelled	12.6	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative signal transduction protein; **PDBTitle:** crystal structure of a putative signal transduction protein2 (eubrec_0645) from eubacterium rectale atcc 33656 at 1.20 a3 resolution
95	c3gkqB_	Alignment	not modelled	12.6	47	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**terminal oxygenase component of carbazole 1,9a- **PDBTitle:** terminal oxygenase of carbazole 1,9a-dioxygenase from2 novosphingobium sp. ka1
96	c1qgeD_	Alignment	not modelled	12.6	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**protein (triacylglycerol hydrolase); **PDBTitle:** new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
97	c2wsmB_	Alignment	not modelled	12.5	29	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**hydrogenase expression/formation protein (hypb); **PDBTitle:** crystal structure of hydrogenase maturation factor hypb from2 archaeoglobus fulgidus
98	d2hh8a1	Alignment	not modelled	12.5	13	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like
99	c3snhA_	Alignment	not modelled	12.5	27	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**dynamin-1; **PDBTitle:** crystal structure of nucleotide-free human dynamin1