Phyre^2

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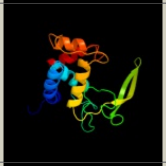
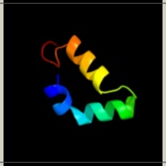
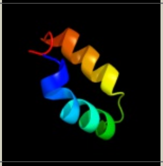
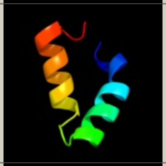
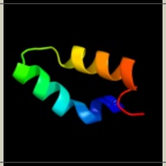
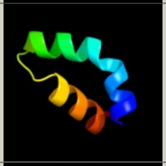
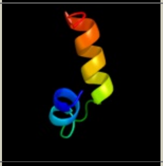
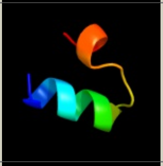
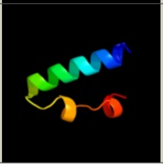
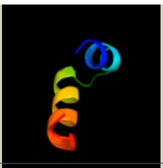
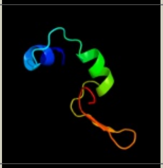
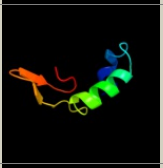
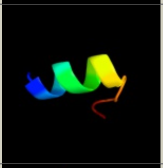
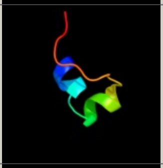
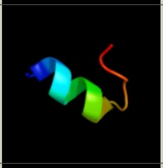
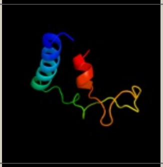
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zycA_	Alignment		100.0	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
2	c3fi7A_	Alignment		100.0	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
3	d1qusa_	Alignment		96.9	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
4	c3mgwA_	Alignment		95.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
5	c3gxkB_	Alignment		95.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod2 (gadus morhua l.) in complex with nag oligomers sheds new3 light on substrate binding and the catalytic mechanism.4 native structure to 1.9
6	d1gbsa_	Alignment		95.1	14	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
7	c2y8pA_	Alignment		95.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
8	d1qsaa2	Alignment		94.8	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
9	c3bkhA_	Alignment		89.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
10	d1nvma1	Alignment		60.7	21	**Fold:**RuvA C-terminal domain-like **Superfamily:**post-HMGL domain-like **Family:**DmpG/LeuA communication domain-like
11	d1yt3a2	Alignment		36.7	6	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNase D C-terminal domains

12	c1slyA_	Alignment		27.3	21	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
13	c2k0nA_	Alignment		27.1	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription **PDBTitle:** solution structure of yeast gal11p kix domain
14	c2fbdB_	Alignment		25.9	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysozyme 1; **PDBTitle:** the crystallographic structure of the digestive lysozyme 1 from musca2 domestica at 1.90 ang.
15	d1yroa1	Alignment		20.5	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
16	c2eq7C_	Alignment		18.9	27	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
17	c3l87A_	Alignment		18.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide deformylase; **PDBTitle:** the crystal structure of smu.143c from streptococcus mutans ua159
18	c2eq9C_	Alignment		18.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
19	d1t3ca_	Alignment		14.6	13	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Clostridium neurotoxins, catalytic domain
20	c2eq8C_	Alignment		14.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
21	d1bw6a_	Alignment	not modelled	13.7	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
22	d1h3ob_	Alignment	not modelled	13.2	17	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
23	c2cooA_	Alignment	not modelled	12.4	0	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
24	c3dv0I_	Alignment	not modelled	12.4	13	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
25	d1w85i_	Alignment	not modelled	12.4	13	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
26	d1w4ha1	Alignment	not modelled	12.2	0	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
27	d1gd6a_	Alignment	not modelled	12.1	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme

28	d1mp1a_	Alignment	not modelled	12.0	20	**Fold:**PWI domain **Superfamily:**PWI domain **Family:**PWI domain
29	d2p02a2	Alignment	not modelled	11.6	38	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
30	c3sn6R_	Alignment	not modelled	11.3	11	**PDB header:**signaling protein/hydrolase **Chain: R: PDB Molecule:**lysozyme, beta-2 adrenergic receptor; **PDBTitle:** crystal structure of the beta2 adrenergic receptor-gs protein complex
31	d2cyua1	Alignment	not modelled	11.2	0	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
32	c1ewrA_	Alignment	not modelled	10.7	21	**PDB header:**hydrolase **Chain: A: PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of taq muts
33	d1p35a_	Alignment	not modelled	10.7	67	**Fold:**Baculovirus p35 protein **Superfamily:**Baculovirus p35 protein **Family:**Baculovirus p35 protein
34	d1qm4a2	Alignment	not modelled	9.7	40	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
35	c1w3dA_	Alignment	not modelled	9.6	13	**PDB header:**transferase **Chain: A: PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
36	d1alca_	Alignment	not modelled	9.5	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
37	d1iiza_	Alignment	not modelled	9.0	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
38	d1lm4a_	Alignment	not modelled	8.9	29	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
39	d1lm6a_	Alignment	not modelled	8.9	29	**Fold:**Peptide deformylase **Superfamily:**Peptide deformylase **Family:**Peptide deformylase
40	d2bgxa2	Alignment	not modelled	8.7	12	**Fold:**N-acetylmuramoyl-L-alanine amidase-like **Superfamily:**N-acetylmuramoyl-L-alanine amidase-like **Family:**N-acetylmuramoyl-L-alanine amidase-like
41	d1wuda1	Alignment	not modelled	8.7	22	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
42	c2lmdA_	Alignment	not modelled	8.6	14	**PDB header:**transcription **Chain: A: PDB Molecule:**prospero homeobox protein 1; **PDBTitle:** minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b
43	d1yzma1	Alignment	not modelled	8.3	16	**Fold:**Long alpha-hairpin **Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
44	d1f6sa_	Alignment	not modelled	8.3	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
45	c1w4kA_	Alignment	not modelled	8.3	13	**PDB header:**transferase **Chain: A: PDB Molecule:**pyruvate dehydrogenase e2; **PDBTitle:** peripheral-subunit binding domains from mesophilic,2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
46	d1w7pd2	Alignment	not modelled	8.2	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
47	d1mxaa2	Alignment	not modelled	8.1	38	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
48	d1u5tb1	Alignment	not modelled	8.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
49	c1zwvA_	Alignment	not modelled	7.9	0	**PDB header:**transferase **Chain: A: PDB Molecule:**lipoamide acyltransferase component of branched- **PDBTitle:** solution structure of the subunit binding domain (hbsbd) of2 the human mitochondrial branched-chain alpha-ketoacid3 dehydrogenase
50	d1b9oa_	Alignment	not modelled	7.7	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
51	c1u1iC_	Alignment	not modelled	7.2	33	**PDB header:**isomerase **Chain: C: PDB Molecule:**myo-inositol-1-phosphate synthase; **PDBTitle:** myo-inositol phosphate synthase mips from a. fulgidus
52	c2bh7A_	Alignment	not modelled	7.2	15	**PDB header:**hydrolase **Chain: A: PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
						Fold: Long alpha-hairpin

53	d1z0kb1	Alignment	not modelled	7.0	18	**Superfamily:**Rabenosyn-5 Rab-binding domain-like **Family:**Rabenosyn-5 Rab-binding domain-like
54	d1fkqa_	Alignment	not modelled	6.8	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**C-type lysozyme
55	c1wx4B_	Alignment	not modelled	6.1	18	**PDB header:**oxidoreductase/metal transport **Chain:** B: **PDB Molecule:**melc; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
56	d1pjqa3	Alignment	not modelled	6.1	14	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
57	d2csba2	Alignment	not modelled	5.7	17	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
58	c2l69A_	Alignment	not modelled	5.7	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
59	d2coba1	Alignment	not modelled	5.6	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
60	d1bala_	Alignment	not modelled	5.4	0	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
61	d1tuka1	Alignment	not modelled	5.3	42	**Fold:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Superfamily:**Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin **Family:**Plant lipid-transfer and hydrophobic proteins
62	d2jn6a1	Alignment	not modelled	5.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Cgl2762-like
63	c3cymA_	Alignment	not modelled	5.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis