Phyre^2

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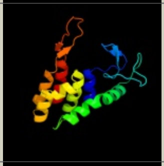
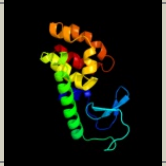
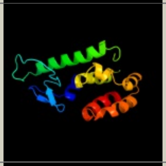
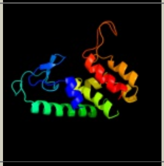
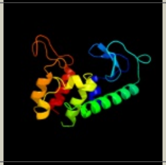
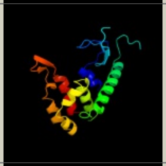
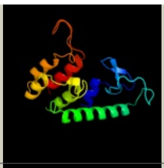
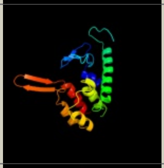
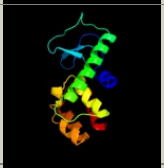
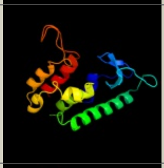
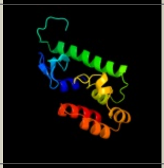
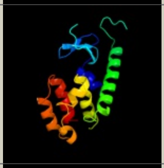
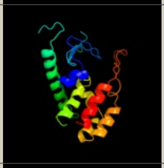
Description	P76159
Date	Thu Jan 5 12:19:52 GMT 2012
Unique Job ID	246caff990cef516

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hdeA_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of full-length endolysin r21 from phage 21
2	d1xjta_	Alignment		100.0	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
3	c3hdfA_	Alignment		100.0	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of truncated endolysin r21 from phage 21
4	c2anxB_	Alignment		100.0	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of bacteriophage p22 lysozyme mutant l87m
5	d1xjua_	Alignment		100.0	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
6	d1lpya_	Alignment		100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
7	d176la_	Alignment		100.0	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
8	d1jtma_	Alignment		100.0	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
9	d191la_	Alignment		100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
10	d169la_	Alignment		100.0	18	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
11	d1swya_	Alignment		100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme

12	d1p37a_	Alignment		100.0	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
13	d1t8fa_	Alignment		100.0	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
14	d146la_	Alignment		100.0	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
15	d157la_	Alignment		100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
16	d2f2qa1	Alignment		100.0	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
17	d1l64a_	Alignment		100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
18	d189la_	Alignment		100.0	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
19	c2o4wA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** t4 lysozyme circular permutant
20	d1k28a3	Alignment		100.0	19	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
21	d1p5ca_	Alignment	not modelled	100.0	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
22	c2qb0D_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase regulator **Chain:** D: **PDB Molecule:**telsam domain - lysozyme chimera; **PDBTitle:** structure of the 2tel crystallization module fused to t4 lysozyme with2 an ala-gly-pro linker.
23	c3sn6R_	Alignment	not modelled	99.9	21	**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
24	c1pdlC_	Alignment	not modelled	99.9	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**tail-associated lysozyme; **PDBTitle:** fitting of gp5 in the cryoem reconstruction of the2 bacteriophage t4 baseplate
25	c2o7aA_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** t4 lysozyme c-terminal fragment
26	d2ikba1	Alignment	not modelled	46.9	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
27	d1xima_	Alignment	not modelled	37.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
28	d2nr7a1	Alignment	not modelled	24.4	16	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
						Fold:TIM beta/alpha-barrel

29	d1xlma_	Alignment	not modelled	19.2	21	**Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
30	d1thqa_	Alignment	not modelled	14.8	15	**Fold:**Transmembrane beta-barrels **Superfamily:**OMPA-like **Family:**Outer membrane enzyme PagP
31	c2qvwA_	Alignment	not modelled	14.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glp_546_48378_50642; **PDBTitle:** structure of giardia dicer refined against twinned data
32	c3gabC_	Alignment	not modelled	11.4	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** c-terminal domain of bacillus subtilis mutl crystal form i
33	d2glka1	Alignment	not modelled	10.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
34	c1tolA_	Alignment	not modelled	9.7	18	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (fusion protein consisting of minor coat **PDBTitle:** fusion of n-terminal domain of the minor coat protein from2 gene iii in phage m13, and c-terminal domain of e. coli3 protein-tola
35	c2gboB_	Alignment	not modelled	9.0	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0358 protein ef2458; **PDBTitle:** protein of unknown function ef2458 from enterococcus faecalis
36	d2gboa1	Alignment	not modelled	9.0	10	**Fold:**Open three-helical up-and-down bundle **Superfamily:**EF2458-like **Family:**EF2458-like
37	c2bvbA_	Alignment	not modelled	8.6	16	**PDB header:**adhesion **Chain:** A: **PDB Molecule:**micronemal protein 1; **PDBTitle:** the c-terminal domain from micronemal protein 1 (mic1) from2 toxoplasma gondii
38	d1ulza1	Alignment	not modelled	8.4	13	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
39	d1w96c1	Alignment	not modelled	7.1	5	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
40	d1muwa_	Alignment	not modelled	7.0	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
41	c3cz6A_	Alignment	not modelled	6.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna-binding protein rap1; **PDBTitle:** crystal structure of the rap1 c-terminus
42	d1mqma_	Alignment	not modelled	6.4	23	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
43	d1a77a1	Alignment	not modelled	6.4	19	**Fold:**SAM domain-like **Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
44	d2viua_	Alignment	not modelled	5.9	23	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
45	c2x0kB_	Alignment	not modelled	5.8	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
46	d1qt1a_	Alignment	not modelled	5.7	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**Xylose isomerase
47	c3ncvB_	Alignment	not modelled	5.4	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** ngol