Phyre^2

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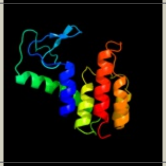
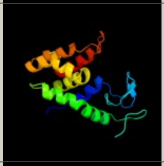
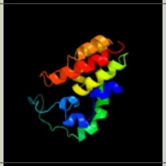
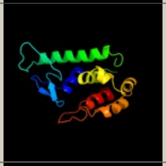
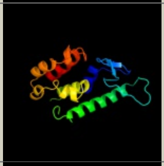
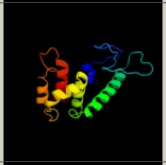
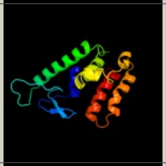
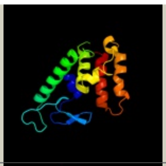
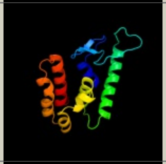
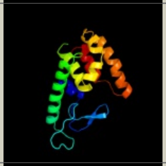
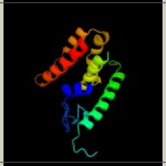
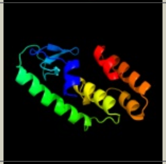
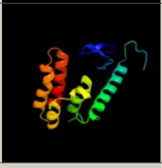
Description	P78285
Date	Thu Jan 5 12:33:12 GMT 2012
Unique Job ID	192565c258517e36

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hdeA_	Alignment		100.0	99	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of full-length endolysin r21 from phage 21
2	d1xjta_	Alignment		100.0	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
3	c3hdfA_	Alignment		100.0	98	**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 I87m
5	d1xjua_	Alignment		100.0	29	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
6	d1lpya_	Alignment		100.0	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
7	d176la_	Alignment		100.0	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
8	d1jtma_	Alignment		100.0	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
9	d169la_	Alignment		100.0	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
10	d191la_	Alignment		100.0	26	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
11	d1p37a_	Alignment		100.0	23	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme

12	d1swya_	Alignment		100.0	26	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
13	d1t8fa_	Alignment		100.0	26	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
14	d157la_	Alignment		100.0	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
15	d146la_	Alignment		100.0	24	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
16	d1l64a_	Alignment		100.0	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
17	d2f2qa1	Alignment		100.0	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
18	d189la_	Alignment		100.0	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
19	d1k28a3	Alignment		100.0	28	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
20	c2o4wA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** t4 lysozyme circular permutant
21	d1p5ca_	Alignment	not modelled	100.0	27	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Phage lysozyme
22	c2qb0D_	Alignment	not modelled	100.0	24	**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	100.0	26	**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	26	**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	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** t4 lysozyme c-terminal fragment
26	d2ikba1	Alignment	not modelled	63.9	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
27	c2qvwA_	Alignment	not modelled	59.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glp_546_48378_50642; **PDBTitle:** structure of giardia dicer refined against twinned data
28	d2nr7a1	Alignment	not modelled	36.8	21	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**NMB1012-like
						Fold:SAM domain-like

29	d1a77a1	Alignment	not modelled	13.5	16	**Superfamily:**5' to 3' exonuclease, C-terminal subdomain **Family:**5' to 3' exonuclease, C-terminal subdomain
30	c3gabC_	Alignment	not modelled	11.8	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** c-terminal domain of bacillus subtilis mutl crystal form i
31	c2bvbA_	Alignment	not modelled	10.3	40	**PDB header:**adhesion **Chain:** A: **PDB Molecule:**micronemal protein 1; **PDBTitle:** the c-terminal domain from micronemal protein 1 (mic1) from2 toxoplasma gondii
32	d2gboa1	Alignment	not modelled	10.3	16	**Fold:**Open three-helical up-and-down bundle **Superfamily:**EF2458-like **Family:**EF2458-like
33	c2gboB_	Alignment	not modelled	10.3	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**upf0358 protein ef2458; **PDBTitle:** protein of unknown function ef2458 from enterococcus faecalis
34	c2fmmE_	Alignment	not modelled	9.8	13	**PDB header:**transcription **Chain:** E: **PDB Molecule:**protein emsy; **PDBTitle:** crystal structure of emsy-hp1 complex