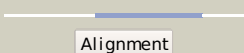
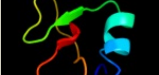
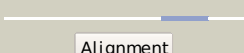

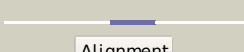

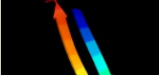


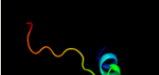



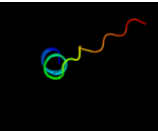

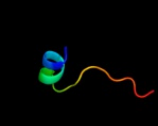
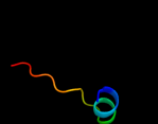




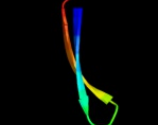
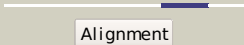
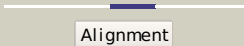
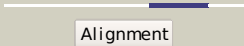
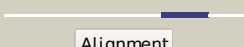


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3hwpA_</a>	 Alignment		40.6	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phlg; <b>PDBTitle:</b> crystal structure and computational analyses provide insights into the catalytic mechanism of 2, 4-diacetylphloroglucinol hydrolase phlg3 from pseudomonas fluorescens
2	<a href="#">d1fd3a_</a>	 Alignment		28.3	28	<b>Fold:</b> Defensin-like <b>Superfamily:</b> Defensin-like <b>Family:</b> Defensin
3	<a href="#">d2coha2</a>	 Alignment		22.1	18	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> cAMP-binding domain-like <b>Family:</b> cAMP-binding domain
4	<a href="#">c3k0zB_</a>	 Alignment		21.6	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
5	<a href="#">d1wk1a_</a>	 Alignment		19.6	29	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
6	<a href="#">d1rdl1_</a>	 Alignment		19.6	24	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
7	<a href="#">d2geya1</a>	 Alignment		17.6	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
8	<a href="#">d1mpua_</a>	 Alignment		16.3	16	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
9	<a href="#">d3bdwa1</a>	 Alignment		14.9	16	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
10	<a href="#">d1rl3a1</a>	 Alignment		14.7	24	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
11	<a href="#">d1zhva1</a>	 Alignment		14.4	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> ACT-like <b>Family:</b> Atu0741-like

12	<a href="#">c1hupA</a>	Alignment		13.9	6	<b>PDB header:</b> c-type lectin <b>Chain:</b> A: <b>PDB Molecule:</b> mannose-binding protein; <b>PDBTitle:</b> human mannose binding protein carbohydrate recognition domain2 trimerizes through a triple alpha-helical coiled-coil
13	<a href="#">d1hupa1</a>	Alignment		13.3	6	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
14	<a href="#">d1fifa1</a>	Alignment		12.6	18	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
15	<a href="#">d2msba</a>	Alignment		11.9	18	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
16	<a href="#">d1egga</a>	Alignment		11.8	24	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
17	<a href="#">c3kkgA</a>	Alignment		11.6	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of putative snoal-like polyketide cyclase2 (yp_509242.1) from jannaschia sp. ccs1 at 1.40 a resolution
18	<a href="#">d1ja3a</a>	Alignment		11.6	12	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
19	<a href="#">c3ehcA</a>	Alignment		11.4	6	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> snoal-like polyketide cyclase; <b>PDBTitle:</b> crystal structure of a snoal-like polyketide cyclase (atu3018) from2 agrobacterium tumefaciens str. c58 at 2.12 a resolution
20	<a href="#">c3cfwA</a>	Alignment		11.1	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> l-selectin; <b>PDBTitle:</b> l-selectin lectin and egf domains
21	<a href="#">d1byfa</a>	Alignment	not modelled	11.0	32	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
22	<a href="#">d1pwba1</a>	Alignment	not modelled	10.8	35	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
23	<a href="#">d1c9fa</a>	Alignment	not modelled	10.7	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> CAD domain
24	<a href="#">d2gexa1</a>	Alignment	not modelled	10.7	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-Like polyketide cyclase
25	<a href="#">c3ff7C</a>	Alignment	not modelled	10.5	12	<b>PDB header:</b> cell adhesion/immunue system <b>Chain:</b> C: <b>PDB Molecule:</b> killer cell lectin-like receptor subfamily g <b>PDBTitle:</b> structure of nk cell receptor klrg1 bound to e-cadherin
26	<a href="#">d1g1ta1</a>	Alignment	not modelled	10.5	47	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
27	<a href="#">d1rjha</a>	Alignment	not modelled	10.1	53	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
28	<a href="#">d1glsa1</a>	Alignment	not modelled	10.0	29	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
29	<a href="#">d2f99a1</a>	Alignment	not modelled	9.9	6	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> Snoal-Like polyketide cyclase

30	<a href="#">dltkeal</a>	Alignment	not modelled	9.9	33	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
31	<a href="#">c1rpuA</a>	Alignment	not modelled	9.3	43	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> A: <b>PDB Molecule:</b> 19 kda protein; <b>PDBTitle:</b> crystal structure of cirv p19 bound to sirna
32	<a href="#">d1rpua</a>	Alignment	not modelled	9.3	43	<b>Fold:</b> Tombusvirus P19 core protein, VP19 <b>Superfamily:</b> Tombusvirus P19 core protein, VP19 <b>Family:</b> Tombusvirus P19 core protein, VP19
33	<a href="#">c1r13A</a>	Alignment	not modelled	9.2	24	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pulmonary surfactant-associated protein a; <b>PDBTitle:</b> carbohydrate recognition and neck domains of surfactant protein a (sp-2 a)
34	<a href="#">c1kwwC</a>	Alignment	not modelled	8.7	18	<b>PDB header:</b> immune system, sugar binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> mannose-binding protein a; <b>PDBTitle:</b> rat mannose protein a complexed with a-me-fuc.
35	<a href="#">c3m9zA</a>	Alignment	not modelled	8.6	41	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> killer cell lectin-like receptor subfamily b member 1a; <b>PDBTitle:</b> crystal structure of extracellular domain of mouse nkr-p1a
36	<a href="#">c3f9sB</a>	Alignment	not modelled	8.3	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (Iferr_0659) from2 acidithiobacillus ferrooxidans atcc at 1.76 a resolution
37	<a href="#">c2eelA</a>	Alignment	not modelled	7.9	17	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> cell death activator cide-a; <b>PDBTitle:</b> solution structure of the cide-n domain of human cell death2 activator cide-a
38	<a href="#">d1qo3d</a>	Alignment	not modelled	7.3	18	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
39	<a href="#">c2vuvA</a>	Alignment	not modelled	7.1	41	<b>PDB header:</b> sugar-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> codakine; <b>PDBTitle:</b> crystal structure of codakine at 1.3a resolution
40	<a href="#">c3g8lD</a>	Alignment	not modelled	6.9	16	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> lectin-related nk cell receptor ly49l1; <b>PDBTitle:</b> crystal structure of murine natural killer cell receptor,2 ly49l4
41	<a href="#">c1eslA</a>	Alignment	not modelled	6.9	47	<b>PDB header:</b> cell adhesion protein <b>Chain:</b> A: <b>PDB Molecule:</b> human e-selectin; <b>PDBTitle:</b> insight into e-selectin(/slash)ligand interaction from the2 crystal structure and mutagenesis of the lec(/slash)egf3 domains
42	<a href="#">d1sjwa</a>	Alignment	not modelled	6.7	11	<b>Fold:</b> Cystatin-like <b>Superfamily:</b> NTF2-like <b>Family:</b> SnoaL-like polyketide cyclase
43	<a href="#">c1zhvA</a>	Alignment	not modelled	6.6	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein atu0741; <b>PDBTitle:</b> x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
44	<a href="#">c1wwtA</a>	Alignment	not modelled	6.6	44	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the tgs domain from human threonyl-2 trna synthetase
45	<a href="#">d3c8ja1</a>	Alignment	not modelled	6.4	18	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
46	<a href="#">d1hq8a</a>	Alignment	not modelled	6.3	11	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
47	<a href="#">c1fm5A</a>	Alignment	not modelled	6.0	29	<b>PDB header:</b> immune system <b>Chain:</b> A: <b>PDB Molecule:</b> early activation antigen cd69; <b>PDBTitle:</b> crystal structure of human cd69
48	<a href="#">c2jyvA</a>	Alignment	not modelled	6.0	29	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> granulin-2; <b>PDBTitle:</b> human granulin f
49	<a href="#">d1r62a</a>	Alignment	not modelled	5.9	18	<b>Fold:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Superfamily:</b> ATPase domain of HSP90 chaperone/DNA topoisomerase II/histidine kinase <b>Family:</b> Histidine kinase
50	<a href="#">d1qo3c</a>	Alignment	not modelled	5.8	18	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
51	<a href="#">c3bc6D</a>	Alignment	not modelled	5.8	24	<b>PDB header:</b> immune system <b>Chain:</b> D: <b>PDB Molecule:</b> c-type lectin domain family 4 member k; <b>PDBTitle:</b> the carbohydrate recognition domain of langerin reveals high2 structural similarity with the one of dc-sign but an additional,3 calcium-independent sugar-binding site
52	<a href="#">c3pzdB</a>	Alignment	not modelled	5.8	83	<b>PDB header:</b> motor protein/apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> netrin receptor dcc; <b>PDBTitle:</b> structure of the myosin x myth4-ferm/dcc complex
53	<a href="#">d1e87a</a>	Alignment	not modelled	5.8	29	<b>Fold:</b> C-type lectin-like <b>Superfamily:</b> C-type lectin-like <b>Family:</b> C-type lectin domain
54	<a href="#">c3g0kA</a>	Alignment	not modelled	5.8	19	<b>PDB header:</b> ca-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative membrane protein; <b>PDBTitle:</b> crystal structure of a protein of unknown function with a cystatin-2 like fold (saro_2880) from novosphingobium aromaticivorans dsm at3 1.30 a resolution
						<b>PDB header:</b> structural genomics, unknown function

55	<a href="#">c3g8zA_</a>	 Alignment	not modelled	5.6	6	<b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function with cystatin-like fold; <b>PDBTitle:</b> crystal structure of protein of unknown function with cystatin-like2 fold (np_639274.1) from xanthomonas campestris at 1.90 a resolution
56	<a href="#">c3dbzB_</a>	 Alignment	not modelled	5.4	35	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> pulmonary surfactant-associated protein d; <b>PDBTitle:</b> human surfactant protein d
57	<a href="#">dlibxa_</a>	 Alignment	not modelled	5.3	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> CAD & PB1 domains <b>Family:</b> CAD domain
58	<a href="#">c3i0yC_</a>	 Alignment	not modelled	5.1	6	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> putative polyketide cyclase; <b>PDBTitle:</b> crystal structure of a putative polyketide cyclase (xcc0381) from2 xanthomonas campestris pv. campestris at 1.50 a resolution