


























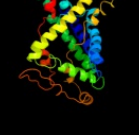
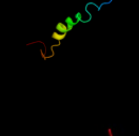
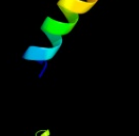
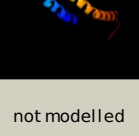


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ldaA_</a>	 Alignment		100.0	100	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol uptake facilitator protein; <b>PDBTitle:</b> crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
2	<a href="#">d1fx8a_</a>	 Alignment		100.0	100	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
3	<a href="#">c3c02A_</a>	 Alignment		100.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaglyceroporin; <b>PDBTitle:</b> x-ray structure of the aquaglyceroporin from plasmodium falciparum
4	<a href="#">c2f2bA_</a>	 Alignment		100.0	36	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin aqpm; <b>PDBTitle:</b> crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
5	<a href="#">c2w2eA_</a>	 Alignment		100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin; <b>PDBTitle:</b> 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
6	<a href="#">d1j4na_</a>	 Alignment		100.0	29	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
7	<a href="#">c3llqB_</a>	 Alignment		100.0	30	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aquaporin z 2; <b>PDBTitle:</b> aquaporin structure from plant pathogen agrobacterium tumefaciens
8	<a href="#">c1ymgA_</a>	 Alignment		100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein; <b>PDBTitle:</b> the channel architecture of aquaporin o at 2.2 angstrom resolution
9	<a href="#">d1ymga1</a>	 Alignment		100.0	27	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
10	<a href="#">c2d57A_</a>	 Alignment		100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin-4; <b>PDBTitle:</b> double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
11	<a href="#">c3d9sB_</a>	 Alignment		100.0	31	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> aquaporin-5; <b>PDBTitle:</b> human aquaporin 5 (aqp5) - high resolution x-ray structure

12	<a href="#">c3gd8A_</a>	Alignment		100.0	27	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin-4; <b>PDBTitle:</b> crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
13	<a href="#">d1h6ia_</a>	Alignment		100.0	30	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
14	<a href="#">d1rc2a_</a>	Alignment		100.0	29	<b>Fold:</b> Aquaporin-like <b>Superfamily:</b> Aquaporin-like <b>Family:</b> Aquaporin-like
15	<a href="#">c3iyzA_</a>	Alignment		100.0	28	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin-4; <b>PDBTitle:</b> structure of aquaporin-4 s180d mutant at 10.0 a resolution from2 electron micrograph
16	<a href="#">c2b5fD_</a>	Alignment		100.0	29	<b>PDB header:</b> transport protein,membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> aquaporin; <b>PDBTitle:</b> crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
17	<a href="#">c3kcvG_</a>	Alignment		72.7	12	<b>PDB header:</b> transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> probable formate transporter 1; <b>PDBTitle:</b> structure of formate channel
18	<a href="#">c2kncA_</a>	Alignment		58.1	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
19	<a href="#">d1f0ka_</a>	Alignment		33.6	33	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Peptidoglycan biosynthesis glycosyltransferase MurG
20	<a href="#">c3qngD_</a>	Alignment		27.6	12	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
21	<a href="#">d1pn3a_</a>	Alignment	not modelled	21.5	28	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
22	<a href="#">d1rrva_</a>	Alignment	not modelled	19.2	22	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
23	<a href="#">d1iira_</a>	Alignment	not modelled	18.5	22	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> Gtf glycosyltransferase
24	<a href="#">c3orgB_</a>	Alignment	not modelled	11.6	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cmclC; <b>PDBTitle:</b> crystal structure of a eukaryotic clC transporter
25	<a href="#">c1s4iC_</a>	Alignment	not modelled	9.4	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> superoxide dismutase-like protein yojm; <b>PDBTitle:</b> crystal structure of a sod-like protein from bacillus subtilis
26	<a href="#">c3d0qB_</a>	Alignment	not modelled	9.2	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein calg3; <b>PDBTitle:</b> crystal structure of calg3 from micromonospora echinospora determined2 in space group i222
27	<a href="#">d1lesoa_</a>	Alignment	not modelled	8.3	67	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
28	<a href="#">d1eqwa_</a>	Alignment	not modelled	8.1	57	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
29	<a href="#">d1oala_</a>	Alignment	not modelled	7.4	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like

						<b>Family:</b> Cu,Zn superoxide dismutase-like
30	<a href="#">c2aqmA_</a>	Alignment	not modelled	7.2	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase [cu-zn]; <b>PDBTitle:</b> cu/zn superoxide dismutase from brucella abortus
31	<a href="#">d2apsa_</a>	Alignment	not modelled	6.9	50	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
32	<a href="#">d1yrra2</a>	Alignment	not modelled	6.5	40	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
33	<a href="#">c1qupA_</a>	Alignment	not modelled	6.2	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase 1 copper chaperone; <b>PDBTitle:</b> crystal structure of the copper chaperone for superoxide2 dismutase
34	<a href="#">c1jk9D_</a>	Alignment	not modelled	6.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> copper chaperone for superoxide dismutase; <b>PDBTitle:</b> heterodimer between h48f-ysoD1 and yccs
35	<a href="#">d1f1ga_</a>	Alignment	not modelled	6.0	57	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
36	<a href="#">d1to4a_</a>	Alignment	not modelled	6.0	71	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
37	<a href="#">d1un7a2</a>	Alignment	not modelled	5.9	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> N-acetylglucosamine-6-phosphate deacetylase, NagA, catalytic domain
38	<a href="#">d2c9va1</a>	Alignment	not modelled	5.8	57	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
39	<a href="#">d1ej8a_</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
40	<a href="#">c2qvtA_</a>	Alignment	not modelled	5.8	38	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> avr1567-d; <b>PDBTitle:</b> structure of melampsora lini avirulence protein, avr1567-d
41	<a href="#">d1jk9b1</a>	Alignment	not modelled	5.8	17	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
42	<a href="#">c2q21B_</a>	Alignment	not modelled	5.7	57	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> superoxide dismutase; <b>PDBTitle:</b> crystal structure of superoxide dismutase from p.2 atrosanguina
43	<a href="#">c2jlpA_</a>	Alignment	not modelled	5.6	67	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular superoxide dismutase (cu-zn); <b>PDBTitle:</b> crystal structure of human extracellular copper-zinc2 superoxide dismutase.
44	<a href="#">d1do5a_</a>	Alignment	not modelled	5.6	57	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Cu,Zn superoxide dismutase-like <b>Family:</b> Cu,Zn superoxide dismutase-like
45	<a href="#">c3ia7A_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> calg4; <b>PDBTitle:</b> crystal structure of calg4, the calicheamicin glycosyltransferase
46	<a href="#">c3klzE_</a>	Alignment	not modelled	5.3	14	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> putative formate transporter 1; <b>PDBTitle:</b> pentameric formate channel with formate bound
47	<a href="#">c3iaaB_</a>	Alignment	not modelled	5.3	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> calg2; <b>PDBTitle:</b> crystal structure of calg2, calicheamicin glycosyltransferase, tdp2 bound form