



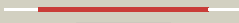
















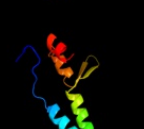













#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1m56G_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
2	<a href="#">d3dtua1</a>	 Alignment		100.0	38	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
3	<a href="#">dlv54a_</a>	 Alignment		100.0	39	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
4	<a href="#">dlar1a_</a>	 Alignment		100.0	39	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
5	<a href="#">dlftta_</a>	 Alignment		100.0	100	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
6	<a href="#">c1fftF_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> ubiquinol oxidase; <b>PDBTitle:</b> the structure of ubiquinol oxidase from escherichia coli
7	<a href="#">c3eh4A_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase subunit 1; <b>PDBTitle:</b> structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
8	<a href="#">dlxmea1</a>	 Alignment		100.0	20	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
9	<a href="#">c3mk7K_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit n; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
10	<a href="#">c3o0rB_</a>	 Alignment		100.0	15	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitric oxide reductase subunit b; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
11	<a href="#">dlm56c_</a>	 Alignment		95.2	11	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like

12	<a href="#">d1v54c_</a>	Alignment		94.3	10	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
13	<a href="#">d1qlec_</a>	Alignment		93.8	10	<b>Fold:</b> Cytochrome c oxidase subunit III-like <b>Superfamily:</b> Cytochrome c oxidase subunit III-like <b>Family:</b> Cytochrome c oxidase subunit III-like
14	<a href="#">d1fftb2</a>	Alignment		33.9	16	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
15	<a href="#">c3mk7F_</a>	Alignment		17.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase
16	<a href="#">c3chxG_</a>	Alignment		16.4	23	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> pmoc; <b>PDBTitle:</b> crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
17	<a href="#">c1jauA_</a>	Alignment		16.4	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane glycoprotein (gp41); <b>PDBTitle:</b> nmr solution structure of the trp-rich peptide of hiv gp412 bound to dpc micelles
18	<a href="#">c2kncA_</a>	Alignment		13.5	11	<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="#">d2hf5a1</a>	Alignment		12.3	30	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
20	<a href="#">d1l9bh2</a>	Alignment		11.9	43	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
21	<a href="#">d3pvia_</a>	Alignment	not modelled	11.8	47	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Restriction endonuclease-like <b>Family:</b> Restriction endonuclease PvulI
22	<a href="#">c3ke2A_</a>	Alignment	not modelled	11.6	50	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein yp_928783.1; <b>PDBTitle:</b> crystal structure of a duf2131 family protein (sama_2911) from shewanella amazonensis sb2b at 2.50 a resolution
23	<a href="#">d1rzhh2</a>	Alignment	not modelled	11.4	44	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
24	<a href="#">d2ghvc1</a>	Alignment	not modelled	11.3	20	<b>Fold:</b> SARS receptor-binding domain-like <b>Superfamily:</b> SARS receptor-binding domain-like <b>Family:</b> SARS receptor-binding domain-like
25	<a href="#">d1n7za_</a>	Alignment	not modelled	10.7	23	<b>Fold:</b> Baseplate structural protein gp8 <b>Superfamily:</b> Baseplate structural protein gp8 <b>Family:</b> Baseplate structural protein gp8
26	<a href="#">d2rcrh2</a>	Alignment	not modelled	9.4	43	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
27	<a href="#">c1yewC_</a>	Alignment	not modelled	8.5	13	<b>PDB header:</b> oxidoreductase, membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> particulate methane monooxygenase subunit c2; <b>PDBTitle:</b> crystal structure of particulate methane monooxygenase
						<b>PDB header:</b> viral protein <b>Chain:</b> F: <b>PDB Molecule:</b> fusion complex of hiv-1 envelope

28	<a href="#">c3g9rF_</a>	Alignment	not modelled	8.3	38	glycoprotein <b>PDBTitle:</b> structure of the hiv-1 gp41 membrane-proximal ectodomain2 region in a putative prefusion conformation
29	<a href="#">d1y5ic1</a>	Alignment	not modelled	8.3	20	<b>Fold:</b> Heme-binding four-helical bundle <b>Superfamily:</b> Respiratory nitrate reductase 1 gamma chain <b>Family:</b> Respiratory nitrate reductase 1 gamma chain
30	<a href="#">c1javA_</a>	Alignment	not modelled	8.2	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane glycoprotein (gp41); <b>PDBTitle:</b> average nmr solution structure of the trp-rich peptide of2 hiv gp41 bound to dpc micelles
31	<a href="#">c2pv6A_</a>	Alignment	not modelled	8.0	38	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein; <b>PDBTitle:</b> hiv-1 gp41 membrane proximal ectodomain region peptide in2 dpc micelle
32	<a href="#">c3ir3B_</a>	Alignment	not modelled	7.3	28	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-thioester dehydratase 2; <b>PDBTitle:</b> crystal structure of human 3-hydroxyacyl-thioester dehydratase 22 (htd2)
33	<a href="#">d2qf3a1</a>	Alignment	not modelled	6.7	27	<b>Fold:</b> Trypsin-like serine proteases <b>Superfamily:</b> Trypsin-like serine proteases <b>Family:</b> Prokaryotic proteases
34	<a href="#">c3kskA_</a>	Alignment	not modelled	6.7	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> type-2 restriction enzyme pvuii; <b>PDBTitle:</b> crystal structure of single chain pvuii
35	<a href="#">c2l2lB_</a>	Alignment	not modelled	6.5	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> methyl-cpg-binding domain protein 2; <b>PDBTitle:</b> solution structure of the coiled-coil complex between mbd2 and2 p66alpha
36	<a href="#">c1odqA_</a>	Alignment	not modelled	6.5	9	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 3.7, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
37	<a href="#">c1odpA_</a>	Alignment	not modelled	6.5	9	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.6, 37 degrees celsius and peptide:sds mole ratio3 of 1:40
38	<a href="#">c1odrA_</a>	Alignment	not modelled	6.5	9	<b>PDB header:</b> lipid transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i peptide; <b>PDBTitle:</b> peptide of human apoa-i residues 166-185. nmr, 5 structures2 at ph 6.0, 37 degrees celsius and peptide:dpc mole ratio3 of 1:40
39	<a href="#">c2yupA_</a>	Alignment	not modelled	6.4	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> vinexin; <b>PDBTitle:</b> solution structure of the second sh3 domain of human vinexin
40	<a href="#">d1dzfa1</a>	Alignment	not modelled	6.3	24	<b>Fold:</b> Restriction endonuclease-like <b>Superfamily:</b> Eukaryotic RPB5 N-terminal domain <b>Family:</b> Eukaryotic RPB5 N-terminal domain
41	<a href="#">c2fu4B_</a>	Alignment	not modelled	5.9	19	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ferric uptake regulation protein; <b>PDBTitle:</b> crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
42	<a href="#">c2kncB_</a>	Alignment	not modelled	5.9	24	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
43	<a href="#">d1ihwa_</a>	Alignment	not modelled	5.9	30	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> DNA-binding domain of retroviral integrase <b>Family:</b> DNA-binding domain of retroviral integrase
44	<a href="#">d1okkd1</a>	Alignment	not modelled	5.6	21	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins
45	<a href="#">d2e74g1</a>	Alignment	not modelled	5.5	33	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
46	<a href="#">c2yu6A_</a>	Alignment	not modelled	5.5	24	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> yth domain-containing protein 2; <b>PDBTitle:</b> solution structure of the yth domain in yth domain-2 containing protein 2
47	<a href="#">c1izlJ_</a>	Alignment	not modelled	5.5	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> J: <b>PDB Molecule:</b> photosystem ii: subunit psba; <b>PDBTitle:</b> crystal structure of photosystem ii
48	<a href="#">d1ctda_</a>	Alignment	not modelled	5.5	21	<b>Fold:</b> EF Hand-like <b>Superfamily:</b> EF-hand <b>Family:</b> Calmodulin-like
49	<a href="#">d1vf5g_</a>	Alignment	not modelled	5.5	33	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> PetG subunit of the cytochrome b6f complex <b>Family:</b> PetG subunit of the cytochrome b6f complex
50	<a href="#">c1vf5G_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> photosynthesis <b>Chain:</b> G: <b>PDB Molecule:</b> protein pet g; <b>PDBTitle:</b> crystal structure of cytochrome b6f complex from m.laminosus
51	<a href="#">c1yybA_</a>	Alignment	not modelled	5.5	33	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 5; <b>PDBTitle:</b> solution structure of 1-26 fragment of human programmed2 cell death 5 protein
52	<a href="#">d1ehkb2</a>	Alignment	not modelled	5.4	22	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
53	<a href="#">d2j7pe1</a>	Alignment	not modelled	5.3	21	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Domain of the SRP/SRP receptor G-proteins <b>Family:</b> Domain of the SRP/SRP receptor G-proteins

54	<a href="#">d2jioa1</a>	 Alignment	not modelled	5.2	25	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
55	<a href="#">c3a1gD</a>	 Alignment	not modelled	5.0	42	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> polymerase basic protein 2; <b>PDBTitle:</b> high-resolution crystal structure of rna polymerase pb1-pb22 subunits from influenza a virus