



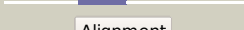



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0514 (-) _606152_606451
Date	Fri Jul 26 01:50:06 BST 2019
Unique Job ID	7675dae264950e65

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3ci0k1	 Alignment		20.2	67	Fold: SAM domain-like Superfamily: GspK insert domain-like Family: GspK insert domain-like
2	c2lorA	 Alignment		20.2	27	PDB header: membrane protein Chain: A; PDB Molecule: transmembrane protein 141; PDBTitle: backbone structure of human membrane protein tmem141
3	c5zhbB	 Alignment		14.5	35	PDB header: hydrolase Chain: B; PDB Molecule: inositol-1-monophosphatase; PDBTitle: structure of inositol monophosphatase from anabaena (nostoc) sp. pcc2 7120
4	d1isua	 Alignment		11.8	58	Fold: HIPIP (high potential iron protein) Superfamily: HIPIP (high potential iron protein) Family: HIPIP (high potential iron protein)
5	c5z62N	 Alignment		9.5	38	PDB header: electron transport Chain: N; PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase
6	d1vdwa	 Alignment		8.5	30	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
7	c2pcrA	 Alignment		8.2	35	PDB header: hydrolase Chain: A; PDB Molecule: inositol-1-monophosphatase; PDBTitle: crystal structure of myo-inositol-1(or 4)-monophosphatase (aq_1983)2 from aquifex aeolicus vf5
8	d1f5ma	 Alignment		8.2	16	Fold: Profilin-like Superfamily: GAF domain-like Family: GAF domain
9	d2pkha1	 Alignment		8.0	11	Fold: Chorismate lyase-like Superfamily: Chorismate lyase-like Family: UTRA domain
10	c2gk2B	 Alignment		7.9	41	PDB header: cell adhesion Chain: B; PDB Molecule: carcinoembryonic antigen-related cell adhesion molecule 1; PDBTitle: crystal structure of the n terminal domain of human ceacam1
11	c5eq9A	 Alignment		7.4	25	PDB header: biosynthetic protein Chain: A; PDB Molecule: inositol monophosphatase; PDBTitle: crystal structure of medicago truncatula histidinol-phosphate2 phosphatase (mthpp) in complex with l-histidinol phosphate and mg2+

12	c4lduA_	Alignment		7.2	60	PDB header: dna binding protein Chain: A: PDB Molecule: auxin response factor 5; PDBTitle: crystal structure of the dna binding domain of arabidopsis thaliana2 auxin response factor 5
13	c3s9vD_	Alignment		7.1	40	PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
14	c4ldxB_	Alignment		7.0	56	PDB header: transcription/dna Chain: B: PDB Molecule: auxin response factor 1; PDBTitle: crystal structure of the dna binding domain of arabidopsis thaliana2 auxin response factor 1 (arf1) in complex with protomor-like sequence3 er7
15	c2dksA_	Alignment		6.9	31	PDB header: cell adhesion Chain: A: PDB Molecule: carcinoembryonic antigen-related cell adhesion PDBTitle: solution structure of the first ig-like domain of human2 carcinoembryonic antigen related cell adhesion molecule 8
16	d1rk8C_	Alignment		6.7	57	Fold: WW domain-like Superfamily: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain Family: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
17	c1rk8C_	Alignment		6.7	57	PDB header: translation Chain: C: PDB Molecule: within the bgcn gene intron protein; PDBTitle: structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
18	c2jijA_	Alignment		6.6	25	PDB header: hydrolase Chain: A: PDB Molecule: prolyl-4 hydroxylase; PDBTitle: crystal structure of the apo form of chlamydomonas2 reinhardtii prolyl-4 hydroxylase type i
19	c3pybB_	Alignment		5.9	40	PDB header: isomerase Chain: B: PDB Molecule: ent-copalyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate
20	c4qycA_	Alignment		5.8	41	PDB header: cell adhesion Chain: A: PDB Molecule: carcinoembryonic antigen-related cell adhesion molecule 1, PDBTitle: crystal structure of the chimeric protein human ceacam1: human tim32 membrane distal amino terminal (n)-domain
21	d1l6za1	Alignment	not modelled	5.7	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
22	c2czhB_	Alignment	not modelled	5.7	20	PDB header: hydrolase Chain: B: PDB Molecule: inositol monophosphatase 2; PDBTitle: crystal structure of human myo-inositol monophosphatase 22 (impa2) with phosphate ion (orthorhombic form)
23	c3u6gB_	Alignment	not modelled	5.5	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein duf4425; PDBTitle: crystal structure of a domain of unknown function, duf4425 (bvj_3708)2 from bacteroides vulgatus atcc 8482 at 1.35 a resolution
24	c3p5rB_	Alignment	not modelled	5.4	44	PDB header: lyase Chain: B: PDB Molecule: taxadiene synthase; PDBTitle: crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
25	c5bp8A_	Alignment	not modelled	5.3	42	PDB header: isomerase Chain: A: PDB Molecule: ent-copalyl diphosphate synthase; PDBTitle: ent-copalyl diphosphate synthase from streptomyces platensis
26	d1c3pa_	Alignment	not modelled	5.2	50	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Histone deacetylase, HDAC
27	d1mpga2	Alignment	not modelled	5.1	21	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: DNA repair glycosylase, N-terminal domain