



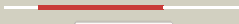












































#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1xqba_	 Alignment		100.0	48	Fold: YaeB-like Superfamily: YaeB-like Family: YaeB-like
2	c3okxA_	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: yaeb-like protein rpa0152; PDBTitle: crystal structure of yaeb-like protein from rhodopseudomonas palustris
3	c2nv4A_	 Alignment		100.0	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0066 protein af_0241; PDBTitle: crystal structure of upf0066 protein af0241 in complex with2 s-adenosylmethionine. northeast structural genomics3 consortium target gr27
4	c3g5oC_	 Alignment		97.4	17	PDB header: toxin/antitoxin Chain: C: PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
5	c3bpqD_	 Alignment		97.0	14	PDB header: toxin Chain: D: PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
6	d1wmia1	 Alignment		96.6	26	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
7	c2kheA_	 Alignment		95.6	24	PDB header: hydrolase Chain: A: PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
8	c3kixy_	 Alignment		93.6	14	PDB header: ribosome Chain: Y: PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome2 (postcleavage state; part 3 of 4)
9	d2a6sa1	 Alignment		91.9	13	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
10	c3oeiH_	 Alignment		89.0	14	PDB header: toxin, protein binding Chain: H: PDB Molecule: relk (toxin rv3358); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
11	c3kxeB_	 Alignment		71.6	16	PDB header: protein binding Chain: B: PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex

12	c2otrA_	Alignment		58.2	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hp0892; PDBTitle: solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
13	dlx6oa1	Alignment		55.3	15	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: elF5a N-terminal domain-like
14	dlz8ma1	Alignment		46.5	13	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
15	d1bkba1	Alignment		34.4	18	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: elF5a N-terminal domain-like
16	dliz6a1	Alignment		27.8	15	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: elF5a N-terminal domain-like
17	d2eifa1	Alignment		19.8	9	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: elF5a N-terminal domain-like
18	d1b74a2	Alignment		16.0	40	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
19	d1veha_	Alignment		15.5	23	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
20	c3butA_	Alignment		13.9	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af_0446; PDBTitle: crystal structure of protein af_0446 from archaeoglobus fulgidus
21	d1ixsa_	Alignment	not modelled	13.4	28	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
22	d1p2za1	Alignment	not modelled	12.7	20	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
23	c2vakF_	Alignment	not modelled	12.3	29	PDB header: viral protein Chain: F: PDB Molecule: sigma a; PDBTitle: crystal structure of the avian reovirus inner capsid2 protein sigmaa
24	c3cu2A_	Alignment	not modelled	12.1	26	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
25	d1xo8a_	Alignment	not modelled	11.9	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
26	c2vlcB_	Alignment	not modelled	11.6	9	PDB header: hydrolase Chain: B: PDB Molecule: type 2 ribosome-inactivating protein cinnamomin PDBTitle: crystal structure of natural cinnamomin (isoform iii)
27	d3etja3	Alignment	not modelled	11.6	27	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
28	c3k1qE_	Alignment	not modelled	11.5	14	PDB header: virus Chain: E: PDB Molecule: vp6a and vp6b, the clamping proteins; PDBTitle: backbone model of an aquareovirus virion by cryo-electron2 microscopy and bioinformatics

29	c1yycA	 Alignment	not modelled	11.4	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative late embryogenesis abundant protein; PDBTitle: solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
30	c2inyA	 Alignment	not modelled	10.8	27	PDB header: viral protein Chain: A: PDB Molecule: hexon protein; PDBTitle: nanoporous crystals of chicken embryo lethal orphan (celo) adenovirus2 major coat protein, hexon
31	d1p30a1	 Alignment	not modelled	8.9	36	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
32	c1ej6D	 Alignment	not modelled	8.3	29	PDB header: virus Chain: D: PDB Molecule: sigma2; PDBTitle: reovirus core
33	c3c9fB	 Alignment	not modelled	8.3	30	PDB header: hydrolase Chain: B: PDB Molecule: 5'-nucleotidase; PDBTitle: crystal structure of 5'-nucleotidase from candida albicans sc5314
34	d3c9fa2	 Alignment	not modelled	8.3	28	Fold: Metallo-dependent phosphatases Superfamily: Metallo-dependent phosphatases Family: 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
35	d1jfla2	 Alignment	not modelled	8.2	33	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
36	d1kjqaz	 Alignment	not modelled	8.1	25	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
37	d2j9ga3	 Alignment	not modelled	7.6	9	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
38	c2pn1A	 Alignment	not modelled	7.2	9	PDB header: ligase Chain: A: PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exigubacterium sp. 255-15 at 2.00 a3 resolution
39	d1u46a	 Alignment	not modelled	7.2	22	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit
40	c3k54A	 Alignment	not modelled	7.1	10	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase btk; PDBTitle: structures of human bruton's tyrosine kinase in active and inactive2 conformations suggests a mechanism of activation for tec family3 kinases.
41	c3i38L	 Alignment	not modelled	7.1	14	PDB header: chaperone Chain: L: PDB Molecule: putative chaperone dnaj; PDBTitle: structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
42	c3etjB	 Alignment	not modelled	7.0	30	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
43	d2qi2a1	 Alignment	not modelled	6.9	5	Fold: Sm-like fold Superfamily: Dom34/Pelota N-terminal domain-like Family: Dom34/Pelota N-terminal domain-like
44	d1fgka	 Alignment	not modelled	6.8	28	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit
45	c3dtcA	 Alignment	not modelled	6.7	22	PDB header: transferase Chain: A: PDB Molecule: mitogen-activated protein kinase kinase kinase 9; PDBTitle: crystal structure of mixed-lineage kinase mlk1 complexed2 with compound 16
46	c3sd2A	 Alignment	not modelled	6.6	26	PDB header: unknown function Chain: A: PDB Molecule: putative member of duf3244 protein family; PDBTitle: crystal structure of a putative member of duf3244 protein family2 (bt_3571) from bacteroides thetaiotaomicron vpi-5482 at 1.40 a3 resolution
47	c1y56A	 Alignment	not modelled	6.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
48	d1b64a	 Alignment	not modelled	6.5	25	Fold: Ferredoxin-like Superfamily: eEF-1beta-like Family: eEF-1beta-like
49	c1pyaD	 Alignment	not modelled	6.5	44	PDB header: carboxy-lyase Chain: D: PDB Molecule: pyruvoyl-dependent histidine decarboxylase (l- PDBTitle: refined structure of the pyruvoyl-dependent histidine2 decarboxylase from lactobacillus 30a
50	d1rjba	 Alignment	not modelled	6.4	19	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit
51	d1vkza3	 Alignment	not modelled	6.4	9	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
52	d2fhqa1	 Alignment	not modelled	6.0	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
53	c2hviK	 Alignment	not modelled	5.9	36	PDB header: virus Chain: K: PDB Molecule: hexon protein;

53	c2uvrk_	Alignment	not modelled	5.9	30	PDBTitle: the quasi-atomic model of human adenovirus type 52 capsid (part 2)
54	d2dx7a1	Alignment	not modelled	5.8	36	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
55	c3kl8C_	Alignment	not modelled	5.8	28	PDB header: transferase/ transferase inhibitor kinase ii; PDB Molecule: calcium/calmodulin dependent protein PDBTitle: camkiintide inhibitor complex
56	c3qd2B_	Alignment	not modelled	5.7	39	PDB header: gene regulation Chain: B: PDB Molecule: eukaryotic translation initiation factor 2- PDBTitle: crsytal structure of mouse perk kinase domain
57	d1a9xa6	Alignment	not modelled	5.6	23	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
58	c2c47D_	Alignment	not modelled	5.6	24	PDB header: transferase Chain: D: PDB Molecule: casein kinase 1 gamma 2 isoform; PDBTitle: structure of casein kinase 1 gamma 2
59	c3dfaA_	Alignment	not modelled	5.6	28	PDB header: transferase Chain: A: PDB Molecule: calcium-dependent protein kinase PDBTitle: crystal structure of kinase domain of calcium-dependent protein kinase2 cgd3_920 from cryptosporidium parvum
60	d1xhja_	Alignment	not modelled	5.3	23	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
61	c3lheA_	Alignment	not modelled	5.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: gntr family transcriptional regulator; PDBTitle: the crystal structure of the c-terminal domain of a gntr2 family transcriptional regulator from bacillus anthracis3 str. Sterne
62	c3cc6A_	Alignment	not modelled	5.2	29	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase 2 beta; PDBTitle: crystal structure of kinase domain of protein tyrosine kinase 2 beta2 (ptk2b)
63	c3p2aA_	Alignment	not modelled	5.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative thioredoxin-like protein; PDBTitle: crystal structure of thioredoxin 2 from yersinia pestis
64	d2q3nb2	Alignment	not modelled	5.2	15	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
65	d3bu3a1	Alignment	not modelled	5.2	28	Fold: Protein kinase-like (PK-like) Superfamily: Protein kinase-like (PK-like) Family: Protein kinases, catalytic subunit
66	d1f60b_	Alignment	not modelled	5.2	25	Fold: Ferredoxin-like Superfamily: eEF-1beta-like Family: eEF-1beta-like