




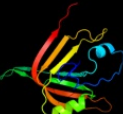











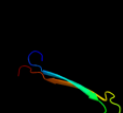







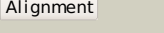
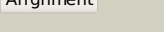


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3he1F_	 Alignment		100.0	28	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: major exported hcp3 protein; PDBTitle: secreted protein hcp3 from pseudomonas aeruginosa.
2	d1y12a1	 Alignment		100.0	17	Fold: Hcp1-like Superfamily: Hcp1-like Family: Hcp1-like
3	c3v4hA_	 Alignment		100.0	17	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a type vi secretion system effector from yersinia2 pestis
4	c3eaaB_	 Alignment		100.0	10	PDB header: unknown function Chain: B: PDB Molecule: evpc; PDBTitle: structure of a type six secretion system protein
5	d2gykb1	 Alignment		99.7	32	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
6	d2jb0b1	 Alignment		97.8	31	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
7	c7ceiB_	 Alignment		97.7	28	PDB header: immune system Chain: B: PDB Molecule: protein (colicin e7 immunity protein); PDBTitle: the endonuclease domain of colicin e7 in complex with its inhibitor2 im7 protein
8	c2qgpa_	 Alignment		92.5	23	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease; PDBTitle: x-ray structure of the hnh endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
9	c2joxA_	 Alignment		64.6	24	PDB header: transcription Chain: A: PDB Molecule: churchill protein; PDBTitle: embryonic neural inducing factor churchill is not a dna-2 binding zinc finger protein: solution structure reveals a3 solvent-exposed beta-sheet and zinc binuclear cluster
10	d1n9pa_	 Alignment		59.7	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
11	c1u3eM_	 Alignment		48.2	22	PDB header: dna binding protein/dna Chain: M: PDB Molecule: hnh homing endonuclease; PDBTitle: dna binding and cleavage by the hnh homing endonuclease i-hmui

12	c2gq1A_	Alignment		43.5	26	PDB header: hydrolase Chain: A: PDB Molecule: fructose-1,6-bisphosphatase; PDBTitle: crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
13	d1xl4a1	Alignment		41.6	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
14	c1u4fD_	Alignment		27.9	40	PDB header: allergen Chain: D: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: crystal structure of cytoplasmic domains of irk1 (kir2.1)2 channel
15	c2gixC_	Alignment		27.3	43	PDB header: metal transport Chain: C: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: cytoplasmic domain structure of kir2.1 containing2 andersen's mutation r218q and rescue mutation t309k
16	d1bk4a_	Alignment		27.0	25	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
17	d1nuwa_	Alignment		26.8	23	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
18	c2xkyl_	Alignment		26.0	43	PDB header: metal transport Chain: I: PDB Molecule: inward rectifier potassium channel 2; PDBTitle: single particle analysis of kir2.1nc_4 in negative stain
19	c2e4fA_	Alignment		25.0	12	PDB header: transport protein Chain: A: PDB Molecule: g protein-activated inward rectifier potassium channel 2; PDBTitle: crystal structure of the cytoplasmic domain of g-protein-gated inward2 rectifier potassium channel kir3.2
20	d1ftaa_	Alignment		24.5	23	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
21	c2fhyL_	Alignment	not modelled	24.2	23	PDB header: hydrolase Chain: L: PDB Molecule: fructose-1,6-bisphosphatase 1; PDBTitle: structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
22	d2ouwa1	Alignment	not modelled	22.8	13	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
23	d1p7ba1	Alignment	not modelled	20.3	43	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Cytoplasmic domain of inward rectifier potassium channel
24	d1u3em1	Alignment	not modelled	18.5	17	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Intron-encoded homing endonucleases
25	d1ne9a1	Alignment	not modelled	18.3	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: FemXAB nonribosomal peptidyltransferases
26	c3jycA_	Alignment	not modelled	15.8	17	PDB header: metal transport Chain: A: PDB Molecule: inward-rectifier k+ channel kir2.2; PDBTitle: crystal structure of the eukaryotic strong inward-rectifier2 k+ channel kir2.2 at 3.1 angstrom resolution
27	d1skye2	Alignment	not modelled	15.8	29	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
28	c2qp2A_	Alignment	not modelled	15.5	21	PDB header: unknown function Chain: A: PDB Molecule: unknown protein; PDBTitle: structure of a macpf/perforin-like protein
						PDB header: fluorescent protein

29	c3cfhB_	Alignment	not modelled	14.9	18	Chain: B: PDB Molecule: gfp-like photoswitchable fluorescent protein; PDBTitle: photoswitchable red fluorescent protein psrfp, off-state
30	c2gw4D_	Alignment	not modelled	14.8	21	PDB header: luminescent protein Chain: D: PDB Molecule: kaede; PDBTitle: crystal structure of stony coral fluorescent protein kaede, red form
31	c1zggA_	Alignment	not modelled	13.7	12	PDB header: hydrolase Chain: A: PDB Molecule: putative low molecular weight protein-tyrosine- PDBTitle: solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
32	c2otbB_	Alignment	not modelled	13.5	21	PDB header: fluorescent protein Chain: B: PDB Molecule: gfp-like fluorescent chromoprotein cfp484; PDBTitle: crystal structure of a monomeric cyan fluorescent protein2 in the fluorescent state
33	c1p7bB_	Alignment	not modelled	13.3	47	PDB header: metal transport Chain: B: PDB Molecule: integral membrane channel and cytosolic domains; PDBTitle: crystal structure of an inward rectifier potassium channel
34	c3lf4B_	Alignment	not modelled	13.3	21	PDB header: fluorescent protein Chain: B: PDB Molecule: fluorescent timer precursor blue102; PDBTitle: crystal structure of fluorescent timer precursor blue102
35	c2y7cA_	Alignment	not modelled	12.7	25	PDB header: transferase Chain: A: PDB Molecule: type-1 restriction enzyme ecoki specificity protein; PDBTitle: atomic model of the ocr-bound methylase complex from the2 type i restriction-modification enzyme ecoki (m2s1). based3 on fitting into em map 1534.
36	d2fzta1	Alignment	not modelled	12.3	26	Fold: Methionine synthase domain-like Superfamily: TM0693-like Family: TM0693-like
37	c2zo6A_	Alignment	not modelled	11.8	29	PDB header: luminescent protein Chain: A: PDB Molecule: cyan-emitting gfp-like protein, kusabira-cyan (kcy); PDBTitle: crystal structure of kusabira-cyan (kcy), a cyan-emitting gfp-like2 protein
38	d1xqma_	Alignment	not modelled	11.4	18	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
39	c2g3dB_	Alignment	not modelled	11.4	21	PDB header: luminescent protein Chain: B: PDB Molecule: green fluorescent protein; PDBTitle: structure of s65g y66a gfp variant after spontaneous2 peptide hydrolysis
40	c2ddcA_	Alignment	not modelled	11.4	29	PDB header: luminescent protein Chain: A: PDB Molecule: photoconvertible fluorescent protein; PDBTitle: unique behavior of a histidine responsible for an2 engineered green-to-red photoconversion process
41	d1ggxa_	Alignment	not modelled	11.1	21	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
42	d1d9qa_	Alignment	not modelled	10.9	20	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
43	c3l4hA_	Alignment	not modelled	10.9	16	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase hecw1; PDBTitle: helical box domain and second ww domain of the human e3 ubiquitin-2 protein ligase hecw1
44	c2zmcW_	Alignment	not modelled	10.8	25	PDB header: luminescent protein Chain: C: PDB Molecule: fluorescent protein; PDBTitle: crystal structure of monomeric kusabira-orange (mko),2 orange-emitting gfp-like protein, at ph 6.0
45	d1spia_	Alignment	not modelled	10.7	24	Fold: Carbohydrate phosphatase Superfamily: Carbohydrate phosphatase Family: Inositol monophosphatase/fructose-1,6-bisphosphatase-like
46	c2c9jG_	Alignment	not modelled	10.7	25	PDB header: luminescent protein Chain: G: PDB Molecule: green fluorescent protein fp512; PDBTitle: structure of the fluorescent protein cmfp512 at 1.35a from2 cerianthus membranaceus
47	d1fc2c_	Alignment	not modelled	10.4	22	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
48	c2zo7A_	Alignment	not modelled	10.3	29	PDB header: luminescent protein Chain: A: PDB Molecule: cyan/green-emitting gfp-like protein, kusabira-cyan mutant PDBTitle: crystal structure of a kusabira-cyan mutant (kcy-r1), a cyan/green-2 emitting gfp-like protein
49	c1olpB_	Alignment	not modelled	10.3	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-toxin; PDBTitle: alpha toxin from clostridium absonum
50	c2g9lA_	Alignment	not modelled	10.2	38	PDB header: antibiotic Chain: A: PDB Molecule: gaegurin-4; PDBTitle: the high-resolution solution conformation of an2 antimicrobial peptide gaegurin 4 and its mode of membrane3 interaction
51	d2rh7a1	Alignment	not modelled	10.0	21	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
52	c3cglE_	Alignment	not modelled	10.0	21	PDB header: fluorescent protein Chain: E: PDB Molecule: gfp-like fluorescent chromoprotein dsfp483; PDBTitle: crystal structure and raman studies of dsfp483, a cyan fluorescent2 protein from discosoma striata
						PDB header: luminescent protein Chain: B: PDB Molecule: gfp-like non-fluorescent chromoprotein;

53	c1yzwB_	Alignment	not modelled	9.9	18	PDBTitle: the 2.1a crystal structure of the far-red fluorescent2 protein hcred: inherent conformational flexibility of the3 chromophore
54	c2bjqA_	Alignment	not modelled	9.8	15	PDB header: motility Chain: A: PDB Molecule: mfp2a; PDBTitle: crystal structure of the nematode sperm cell motility2 protein mfp2
55	c3gb3B_	Alignment	not modelled	9.7	7	PDB header: fluorescent protein Chain: B: PDB Molecule: killerrred; PDBTitle: x-ray structure of genetically encoded photosensitizer2 killerrred in native form
56	c3simA_	Alignment	not modelled	9.4	25	PDB header: hydrolase Chain: A: PDB Molecule: protein, family 18 chitinase; PDBTitle: crystallographic structure analysis of family 18 chitinase from crocus2 vernus
57	c2kxB_	Alignment	not modelled	9.0	64	PDB header: protein binding Chain: B: PDB Molecule: peptide of far upstream element-binding protein 1; PDBTitle: solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
58	c3myuB_	Alignment	not modelled	8.8	20	PDB header: vib binding protein Chain: B: PDB Molecule: high affinity transport system protein p37; PDBTitle: mycoplasma genitalium mg289
59	c3sggA_	Alignment	not modelled	8.8	36	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical hydrolase; PDBTitle: crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
60	c2y50A_	Alignment	not modelled	8.7	23	PDB header: hydrolase Chain: A: PDB Molecule: collagenase; PDBTitle: crystal structure of collagenase g from clostridium2 histolyticum at 2.80 angstrom resolution
61	c2c9iG_	Alignment	not modelled	8.7	18	PDB header: luminescent protein Chain: G: PDB Molecule: green fluorescent protein asfp499; PDBTitle: structure of the fluorescent protein asfp499 from anemonia2 sulcata
62	c2ib5H_	Alignment	not modelled	8.7	14	PDB header: luminescent protein Chain: H: PDB Molecule: chromo protein; PDBTitle: structural characterization of a blue chromoprotein and its yellow2 mutant from the sea anemone cnidopus japonicus
63	c2z6zA_	Alignment	not modelled	8.6	25	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent protein dronpa; PDBTitle: crystal structure of a photoswitchable gfp-like protein2 dronpa in the bright-state
64	c2xfyA_	Alignment	not modelled	8.5	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-amylase; PDBTitle: crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
65	d1moua_	Alignment	not modelled	8.4	21	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
66	c2icrD_	Alignment	not modelled	8.4	25	PDB header: fluorescent protein Chain: D: PDB Molecule: red fluorescent protein zoanrfp; PDBTitle: red fluorescent protein zrpf574 from zoanthus sp.
67	c2hpwA_	Alignment	not modelled	8.3	21	PDB header: luminescent protein Chain: A: PDB Molecule: green fluorescent protein; PDBTitle: green fluorescent protein from clytia gregaria
68	c3eplA_	Alignment	not modelled	8.3	17	PDB header: transferase/rna Chain: A: PDB Molecule: trna isopentenyltransferase; PDBTitle: crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
69	d1deeg_	Alignment	not modelled	8.2	22	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
70	c1amlA_	Alignment	not modelled	8.1	50	PDB header: serine protease inhibitor Chain: A: PDB Molecule: amyloid a4; PDBTitle: the alzheimer`s disease amyloid a4 peptide (residues 1-40)
71	d2jwda1	Alignment	not modelled	7.8	22	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
72	c3nezB_	Alignment	not modelled	7.8	21	PDB header: fluorescent protein Chain: B: PDB Molecule: mrojoa; PDBTitle: mrojoa
73	d1uisa_	Alignment	not modelled	7.7	18	Fold: GFP-like Superfamily: GFP-like Family: Fluorescent proteins
74	d2cwqa1	Alignment	not modelled	7.5	14	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
75	c3uksB_	Alignment	not modelled	7.5	17	PDB header: hydrolase Chain: B: PDB Molecule: sedoheptulose-1,7 bisphosphatase, putative; PDBTitle: 1.85 angstrom crystal structure of putative sedoheptulose-1,72 bisphosphatase from toxoplasma gondii
76	d1hcra_	Alignment	not modelled	7.1	63	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
77	d1ijwc_	Alignment	not modelled	7.1	63	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
78	c2y6xA_	Alignment	not modelled	7.0	19	PDB header: photosynthesis Chain: A: PDB Molecule: photosystem ii 11 kd protein; PDBTitle: structure of psb27 from thermosynechococcus elongatus

79	c3t7hB_	 Alignment	not modelled	6.9	19	PDB header: ligase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: atg8 transfer from atg7 to atg3: a distinctive e1-e2 architecture and2 mechanism in the autophagy pathway
80	d1t3la2	 Alignment	not modelled	6.8	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
81	d1x9aa_	 Alignment	not modelled	6.7	22	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrH-like
82	d1lrza1	 Alignment	not modelled	6.7	35	Fold: Long alpha-hairpin Superfamily: tRNA-binding arm Family: Methicillin resistance protein FemA probable tRNA-binding arm
83	d1khoa2	 Alignment	not modelled	6.6	21	Fold: Lipase/lipoxygenase domain (PLAT/LH2 domain) Superfamily: Lipase/lipoxygenase domain (PLAT/LH2 domain) Family: Alpha-toxin, C-terminal domain
84	d1lp1b_	 Alignment	not modelled	6.6	22	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: Immunoglobulin-binding protein A modules
85	d1vyva2	 Alignment	not modelled	6.4	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
86	d1vyua2	 Alignment	not modelled	6.3	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
87	d1saza1	 Alignment	not modelled	6.2	29	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Acetokinase-like
88	c2qksA_	 Alignment	not modelled	6.2	19	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
89	d2pstx1	 Alignment	not modelled	6.2	20	Fold: MbtH/L9 domain-like Superfamily: MbtH-like Family: MbtH-like
90	c3nezA_	 Alignment	not modelled	6.2	16	PDB header: fluorescent protein Chain: A: PDB Molecule: mrojoa; PDBTitle: mrojoa
91	c3d3qB_	 Alignment	not modelled	6.0	12	PDB header: transferase Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
92	c1y2iC_	 Alignment	not modelled	6.0	39	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein s0862; PDBTitle: crystal structure of mcs9 target apc27401 from shigella2 flexneri
93	d1y2ia_	 Alignment	not modelled	6.0	39	Fold: Dodecin subunit-like Superfamily: YbjQ-like Family: YbjQ-like
94	d1ogmx1	 Alignment	not modelled	6.0	28	Fold: Dextranase, N-terminal domain Superfamily: Dextranase, N-terminal domain Family: Dextranase, N-terminal domain
95	c3akoG_	 Alignment	not modelled	6.0	24	PDB header: fluorescent protein Chain: G: PDB Molecule: venus; PDBTitle: crystal structure of the reassembled venus
96	c2yicC_	 Alignment	not modelled	5.7	12	PDB header: lyase Chain: C: PDB Molecule: 2-oxoglutarate decarboxylase; PDBTitle: crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
97	c2okrC_	 Alignment	not modelled	5.6	38	PDB header: transferase Chain: C: PDB Molecule: map kinase-activated protein kinase 2; PDBTitle: crystal structure of the p38a-mapkap kinase 2 heterodimer
98	c2okrF_	 Alignment	not modelled	5.6	38	PDB header: transferase Chain: F: PDB Molecule: map kinase-activated protein kinase 2; PDBTitle: crystal structure of the p38a-mapkap kinase 2 heterodimer
99	c3nb0A_	 Alignment	not modelled	5.5	19	PDB header: transferase Chain: A: PDB Molecule: glycogen [starch] synthase isoform 2; PDBTitle: glucose-6-phosphate activated form of yeast glycogen synthase