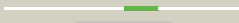
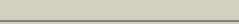
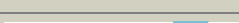
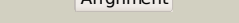
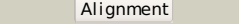
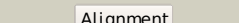
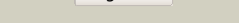
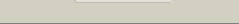
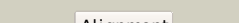
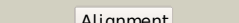
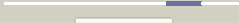
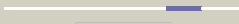
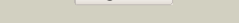


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zcdA_	 Alignment		99.9	14	PDB header: membrane protein Chain: A: PDB Molecule: na(+)/h(+) antiporter 1; PDBTitle: crystal structure of the na+/h+ antiporter nhaa
2	c3jxoB_	 Alignment		99.3	30	PDB header: transport protein Chain: B: PDB Molecule: trka-n domain protein; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
3	d1vcta2	 Alignment		98.8	21	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
4	c2bknA_	 Alignment		98.8	18	PDB header: membrane protein Chain: A: PDB Molecule: hypothetical protein ph0236; PDBTitle: structure analysis of unknown function protein
5	d2fy8a2	 Alignment		98.8	18	Fold: TrkA C-terminal domain-like Superfamily: TrkA C-terminal domain-like Family: TrkA C-terminal domain-like
6	c2fy8A_	 Alignment		98.5	18	PDB header: transport protein Chain: A: PDB Molecule: calcium-gated potassium channel mthk; PDBTitle: crystal structure of mthk rck domain in its ligand-free gating-ring2 form
7	c1lnqC_	 Alignment		98.5	18	PDB header: metal transport Chain: C: PDB Molecule: potassium channel related protein; PDBTitle: crystal structure of mthk at 3.3 a
8	c3l4bG_	 Alignment		98.2	32	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
9	d3deda1	 Alignment		97.9	23	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
10	d2o1ra1	 Alignment		97.8	24	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
11	d2plia1	 Alignment		97.8	25	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like

12	d2p13a1	Alignment		97.7	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
13	c3llbA	Alignment		97.7	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
14	c3dedB	Alignment		97.6	25	PDB header: membrane protein Chain: B: PDB Molecule: probable hemolysin; PDBTitle: c-terminal domain of probable hemolysin from chromobacterium violaceum
15	d2o3ga1	Alignment		97.6	23	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
16	d2pls1	Alignment		97.4	23	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
17	d2nqwa1	Alignment		97.4	21	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
18	d2oai1	Alignment		97.3	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
19	d2rk5a1	Alignment		97.2	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
20	d2r2za1	Alignment		97.1	15	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
21	c3mt5A	Alignment	not modelled	96.8	11	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: potassium large conductance calcium-activated channel, PDBTitle: crystal structure of the human bk gating apparatus
22	d2p3ha1	Alignment	not modelled	96.0	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
23	c3u6nC	Alignment	not modelled	95.4	10	PDB header: transport protein Chain: C: PDB Molecule: high-conductance ca2+-activated k+ channel protein; PDBTitle: open structure of the bk channel gating ring
24	d2p4pa1	Alignment	not modelled	93.8	9	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
25	c3eywA	Alignment	not modelled	92.3	11	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
26	c2l0eA	Alignment	not modelled	88.8	27	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm vi of the nhe1 isoform of the na+/h+ exchanger
27	d1lssa	Alignment	not modelled	88.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
28	c2g1uA	Alignment	not modelled	78.4	19	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution

29	c3llvA		Alignment	not modelled	78.2	16	PDB header: nad(p) binding protein Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: the crystal structure of the nad(p)-binding domain of an2 exopolyphosphatase-related protein from archaeoglobus fulgidus to3 1.7a
30	c3fwzA		Alignment	not modelled	74.4	10	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ybal; PDBTitle: crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
31	d1ld1a		Alignment	not modelled	65.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
32	c2kbvA		Alignment	not modelled	53.0	35	PDB header: membrane protein Chain: A: PDB Molecule: sodium/hydrogen exchanger 1; PDBTitle: structural and functional analysis of tm xi of the nhe12 isoform of the na+/h+ exchanger
33	c2khaA		Alignment	not modelled	48.2	12	PDB header: sugar binding protein Chain: A: PDB Molecule: beta-1,3-glucan-binding protein; PDBTitle: solution structure of a pathogen recognition domain from a2 lepidopteran insect, plodia interpunctella
34	c3ie4A		Alignment	not modelled	47.2	16	PDB header: immune system Chain: A: PDB Molecule: gram-negative binding protein 3; PDBTitle: b-glucan binding domain of drosophila gnbp3 defines a novel2 family of pattern recognition receptor
35	c2rqeA		Alignment	not modelled	44.9	12	PDB header: sugar binding protein Chain: A: PDB Molecule: beta-1,3-glucan-binding protein; PDBTitle: solution structure of the silkworm bgrp/gnbp3 n-terminal2 domain reveals the mechanism for b-1,3-glucan specific3 recognition
36	d2fy8a1		Alignment	not modelled	43.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
37	d2c5aa1		Alignment	not modelled	41.9	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	d1tygb		Alignment	not modelled	38.4	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
39	d1pjqa1		Alignment	not modelled	36.2	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
40	c1tygG		Alignment	not modelled	35.6	15	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/this complex
41	c3nafA		Alignment	not modelled	35.6	12	PDB header: ion transport Chain: A: PDB Molecule: calcium-activated potassium channel subunit alpha-1; PDBTitle: structure of the intracellular gating ring from the human high-2 conductance ca2+ gated k+ channel (bk channel)
42	d2hmva1		Alignment	not modelled	35.1	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
43	c3dqpA		Alignment	not modelled	29.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase ylbe; PDBTitle: crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
44	d1hdoa		Alignment	not modelled	29.1	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
45	d1e5qa1		Alignment	not modelled	28.5	4	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	c2kl0A		Alignment	not modelled	25.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
47	c3cwiA		Alignment	not modelled	21.1	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: thiamine-biosynthesis protein this; PDBTitle: crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
48	d1zud21		Alignment	not modelled	19.5	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
49	c3c85A		Alignment	not modelled	19.2	9	PDB header: transport protein Chain: A: PDB Molecule: putative glutathione-regulated potassium-efflux system PDBTitle: crystal structure of trka domain of putative glutathione-regulated2 potassium-efflux kefb from vibrio parahaemolyticus
50	d1b0aa1		Alignment	not modelled	18.8	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
51	d1x5qa1		Alignment	not modelled	18.4	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
52	d1edza1		Alignment	not modelled	17.1	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
53	d1g9oa		Alignment	not modelled	17.0	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain

54	c3r6dA	 Alignment	not modelled	16.9	8	PDB header: lyase, isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
55	c3bpuA	 Alignment	not modelled	16.1	19	PDB header: transferase Chain: A: PDB Molecule: membrane-associated guanylate kinase, ww and pdz domain- PDBTitle: crystal structure of the 3rd pdz domain of human membrane associated2 guanylate kinase, c677s and c709s double mutant
56	dlg7sa2	 Alignment	not modelled	15.6	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
57	c3icpA	 Alignment	not modelled	15.3	12	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
58	c3l77A	 Alignment	not modelled	15.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: short-chain alcohol dehydrogenase; PDBTitle: x-ray structure alcohol dehydrogenase from archaeon thermococcus2 sibiricus complexed with 5-hydroxy-nadp
59	c1edzA	 Alignment	not modelled	15.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate dehydrogenase; PDBTitle: structure of the nad-dependent 5,10-2 methylenetetrahydrofolate dehydrogenase from saccharomyces3 cerevisiae
60	d2cu3a1	 Alignment	not modelled	14.5	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
61	c3htrB	 Alignment	not modelled	14.5	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodopseudomonas palustris
62	c3k8hA	 Alignment	not modelled	14.2	14	PDB header: membrane protein Chain: A: PDB Molecule: 30k1p; PDBTitle: structure of crystal form i of tp0453
63	c2vspA	 Alignment	not modelled	14.1	15	PDB header: transport protein Chain: A: PDB Molecule: pdz domain-containing protein 1; PDBTitle: crystal structure of the fourth pdz domain of pdz domain-2 containing protein 1
64	c3r3sD	 Alignment	not modelled	13.2	8	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
65	c2pk3B	 Alignment	not modelled	13.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
66	c2x4gA	 Alignment	not modelled	13.1	9	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
67	d1yjma1	 Alignment	not modelled	13.1	36	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
68	d1tp5a1	 Alignment	not modelled	13.1	16	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
69	c2q1wC	 Alignment	not modelled	12.9	5	PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
70	d2piea1	 Alignment	not modelled	12.8	19	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
71	d2i0ia1	 Alignment	not modelled	12.5	18	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
72	c1yj5C	 Alignment	not modelled	12.3	38	PDB header: transferase Chain: C: PDB Molecule: 5' polynucleotide kinase-3' phosphatase fha domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
73	d1a4ia1	 Alignment	not modelled	12.3	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
74	d1wvga1	 Alignment	not modelled	12.1	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
75	c3dhnA	 Alignment	not modelled	11.9	19	PDB header: isomerase, lyase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
76	d2f1ka2	 Alignment	not modelled	11.8	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
77	c3ctmH	 Alignment	not modelled	11.5	8	PDB header: oxidoreductase Chain: H: PDB Molecule: carbonyl reductase; PDBTitle: crystal structure of a carbonyl reductase from candida2

						parapsilosis with anti-prelog stereo-specificity PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh-flavin reductase; PDBTitle: crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
78	c3h2sA	Alignment	not modelled	11.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nadh-flavin reductase; PDBTitle: crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
79	c2p5uC	Alignment	not modelled	11.0	8	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
80	c2nwqA	Alignment	not modelled	11.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable short-chain dehydrogenase; PDBTitle: short chain dehydrogenase from pseudomonas aeruginosa
81	d1rkxa	Alignment	not modelled	10.9	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
82	c3ew7A	Alignment	not modelled	10.8	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo0794 protein; PDBTitle: crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
83	d1be9a	Alignment	not modelled	10.8	16	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
84	d1hi9a	Alignment	not modelled	10.6	13	Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein
85	c2jxoA	Alignment	not modelled	10.5	18	PDB header: protein binding Chain: A: PDB Molecule: ezrin-radixin-moesin-binding phosphoprotein 50; PDBTitle: structure of the second pdz domain of nhrf-1
86	d2brfa1	Alignment	not modelled	10.4	32	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
87	d1dg6a	Alignment	not modelled	10.3	25	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
88	c1dg6A	Alignment	not modelled	10.3	25	PDB header: apoptosis Chain: A: PDB Molecule: apo2l/tnf-related apoptis inducing ligand (trail); PDBTitle: crystal structure of apo2l/trail
89	c3edmD	Alignment	not modelled	10.3	8	PDB header: oxidoreductase Chain: D: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase from agrobacterium2 tumefaciens
90	d2q8oa1	Alignment	not modelled	10.3	20	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
91	c3kt9A	Alignment	not modelled	10.3	23	PDB header: hydrolase Chain: A: PDB Molecule: aprataxin; PDBTitle: aprataxin fha domain
92	c2qq5A	Alignment	not modelled	10.2	5	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase/reductase sdr family member 1; PDBTitle: crystal structure of human sdr family member 1
93	d1xu9a	Alignment	not modelled	10.1	6	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
94	d2q1ma1	Alignment	not modelled	9.9	26	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
95	d1lgpa	Alignment	not modelled	9.8	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
96	c2q30C	Alignment	not modelled	9.8	13	PDB header: unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a rmlc-like cupin protein (dde_2303) from2 desulfovibrio desulfuricans subsp. at 1.94 a resolution
97	c3iusB	Alignment	not modelled	9.6	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: the structure of a functionally unknown conserved protein2 from silicibacter pomeroyi dss
98	c3oh8A	Alignment	not modelled	9.5	17	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sula family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
99	d1ujxa	Alignment	not modelled	9.5	41	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain