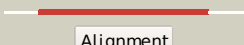

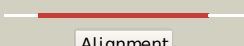
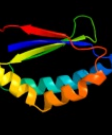
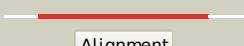

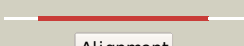











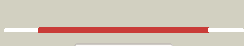





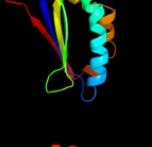
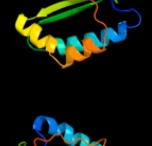
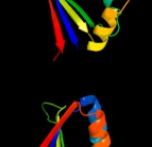
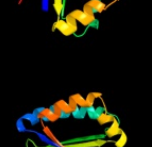

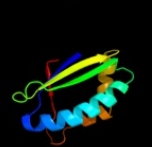
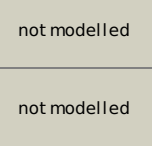


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2omoC_</a>	 Alignment		99.9	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> duf176; <b>PDBTitle:</b> putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
2	<a href="#">c2gffB_</a>	 Alignment		99.9	73	<b>PDB header:</b> sugar binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> lsrg protein; <b>PDBTitle:</b> crystal structure of yersinia pestis lsrg
3	<a href="#">d2omoa1</a>	 Alignment		99.9	42	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
4	<a href="#">c3bm7A_</a>	 Alignment		99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein of unknown function with ferredoxin-like fold; <b>PDBTitle:</b> crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
5	<a href="#">c3e8oB_</a>	 Alignment		99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein with ferredoxin-like fold; <b>PDBTitle:</b> crystal structure of a putative antibiotic biosynthesis monooxygenase2 (dr_2100) from deinococcus radiodurans at 1.40 a resolution
6	<a href="#">c2bbeA_</a>	 Alignment		99.9	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein so0527; <b>PDBTitle:</b> crystal structure of protein so0527 from shewanella oneidensis
7	<a href="#">c3gz7B_</a>	 Alignment		99.9	10	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_888398.1) from bordetella bronchiseptica3 at 2.15 a resolution
8	<a href="#">d1y0ha_</a>	 Alignment		99.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
9	<a href="#">d2pd1a1</a>	 Alignment		99.9	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
10	<a href="#">c2fb0A_</a>	 Alignment		99.9	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
11	<a href="#">c3fqvB_</a>	 Alignment		99.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein with ferredoxin-like fold; <b>PDBTitle:</b> crystal structure of a putative antibiotic biosynthesis monooxygenase2 (spo2313) from silicibacter pomeroyi dss-3 at 1.30 a resolution

12	<a href="#">d1tuva_</a>	Alignment		99.9	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
13	<a href="#">c3mcsB_</a>	Alignment		99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of putative monooxygenase (fn1347) from2 fusobacterium nucleatum subsp. nucleatum atcc 25586 at 2.55 a3 resolution
14	<a href="#">d1x7va_</a>	Alignment		99.9	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PA3566-like
15	<a href="#">c3kkfA_</a>	Alignment		99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of putative antibiotic biosynthesis2 monooxygenase (np_810307.1) from bacteriodes3 thetaiotaomicron vpi-5482 at 1.30 a resolution
16	<a href="#">d1iuja_</a>	Alignment		99.9	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
17	<a href="#">c3f44A_</a>	Alignment		99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative monooxygenase; <b>PDBTitle:</b> crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
18	<a href="#">c3kngA_</a>	Alignment		99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> snoab; <b>PDBTitle:</b> crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
19	<a href="#">c3hx9B_</a>	Alignment		99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein rv3592; <b>PDBTitle:</b> structure of heme-degrader, mhud (rv3592), from2 mycobacterium tuberculosis with two hemes bound in its3 active site
20	<a href="#">d1q8ba_</a>	Alignment		99.8	19	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YjCS
21	<a href="#">d2zdpal</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
22	<a href="#">c3fj2A_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase-like protein; <b>PDBTitle:</b> crystal structure of a monooxygenase-like protein (lin2316) from2 listeria innocua at 1.85 a resolution
23	<a href="#">c2riIA_</a>	Alignment	not modelled	99.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> antibiotic biosynthesis monooxygenase; <b>PDBTitle:</b> crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
24	<a href="#">d1xbwa_</a>	Alignment	not modelled	99.4	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
25	<a href="#">d1tz0a_</a>	Alignment	not modelled	99.3	12	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
26	<a href="#">d1lq9a_</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Actinorhodin biosynthesis monooxygenase ActVa-Orf6
27	<a href="#">d1tr0a_</a>	Alignment	not modelled	98.1	7	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Plant stress-induced protein
28	<a href="#">c3bn7A_</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (cc_2267) from2 caulobacter crescentus cb15 at 1.64 a resolution <b>PDB header:</b> unknown function

29	<a href="#">c2qycA</a>	Alignment	not modelled	98.0	13	<b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-like protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
30	<a href="#">c3hfkB</a>	Alignment	not modelled	97.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-methylmuconolactone methylisomerase; <b>PDBTitle:</b> crystal structure of 4-methylmuconolactone methylisomerase2 (h52a) in complex with 4-methylmuconolactone
31	<a href="#">d2cb2a1</a>	Alignment	not modelled	97.9	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> SOR-like
32	<a href="#">c3bguA</a>	Alignment	not modelled	97.7	8	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-like protein of unknown function; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
33	<a href="#">c3bdeA</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> mlI5499 protein; <b>PDBTitle:</b> crystal structure of a dabb family protein with a ferredoxin-like fold2 (mlI5499) from mesorhizobium loti maff303099 at 1.79 a resolution
34	<a href="#">d1q4ra</a>	Alignment	not modelled	97.7	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Plant stress-induced protein
35	<a href="#">c3bb5B</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> stress responsive alpha-beta protein; <b>PDBTitle:</b> crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
36	<a href="#">d1rja</a>	Alignment	not modelled	97.4	15	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Plant stress-induced protein
37	<a href="#">c3fmbA</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dimeric protein of unknown function and ferredoxin-like <b>PDBTitle:</b> crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
38	<a href="#">d1x8da1</a>	Alignment	not modelled	97.0	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> YiiL-like
39	<a href="#">d2fra1</a>	Alignment	not modelled	97.0	10	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> EthD-like
40	<a href="#">d2higa1</a>	Alignment	not modelled	96.9	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Hypothetical protein YdhR
41	<a href="#">d2go8a1</a>	Alignment	not modelled	96.7	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> PG130-like
42	<a href="#">c1wd6B</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein ydhr; <b>PDBTitle:</b> crystal structure of jw1657 from escherichia coli
43	<a href="#">c2qlwA</a>	Alignment	not modelled	96.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> rhau; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
44	<a href="#">c2qlxA</a>	Alignment	not modelled	96.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnose mutarotase; <b>PDBTitle:</b> crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
45	<a href="#">d1vqsa</a>	Alignment	not modelled	96.4	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> NIPSNAP
46	<a href="#">d1vqya1</a>	Alignment	not modelled	96.3	16	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> NIPSNAP
47	<a href="#">d2fiua1</a>	Alignment	not modelled	96.0	6	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Atu0297-like
48	<a href="#">c3lo3E</a>	Alignment	not modelled	95.7	5	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
49	<a href="#">c3a16C</a>	Alignment	not modelled	95.2	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> aldoxime dehydratase; <b>PDBTitle:</b> crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
50	<a href="#">c2jdjB</a>	Alignment	not modelled	95.0	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> redy-like protein; <b>PDBTitle:</b> crystal structure of hapk from hahella chejuensis
51	<a href="#">c3bf4B</a>	Alignment	not modelled	93.7	4	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ethyl tert-butyl ether degradation ethd protein; <b>PDBTitle:</b> crystal structure of an ethd-like protein (reut_b5694) from ralstonia2 eutropha jmp134 at 2.10 a resolution
52	<a href="#">c3dcaC</a>	Alignment	not modelled	92.4	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rpa0582; <b>PDBTitle:</b> crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
53	<a href="#">c3gn6B</a>	Alignment	not modelled	79.6	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> ct0912, orfan protein with a ferredoxin-like domain repeat;

53	<a href="#">c3gn0B_</a>	Alignment	not modelled	79.0	13	<b>PDBTitle:</b> crystal structure of ct0912, orfan protein from chlorobium tepidum2 with a ferredoxin-like domain repeat (np_661805.1) from chlorobium3 tepidum t1s at 1.80 a resolution
54	<a href="#">c2kl8A_</a>	Alignment	not modelled	70.1	12	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> or15; <b>PDBTitle:</b> solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
55	<a href="#">d2ifxa1</a>	Alignment	not modelled	67.1	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Mml1-like
56	<a href="#">c2e1aD_</a>	Alignment	not modelled	60.2	9	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> 75aa long hypothetical regulatory protein asnc; <b>PDBTitle:</b> crystal structure of ffrp-dm1
57	<a href="#">c2djwF_</a>	Alignment	not modelled	39.5	12	<b>PDB header:</b> unknown function <b>Chain:</b> F: <b>PDB Molecule:</b> probable transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of ttha0845 from thermus thermophilus hb8
58	<a href="#">d2cs4a1</a>	Alignment	not modelled	34.4	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
59	<a href="#">d1zr9a1</a>	Alignment	not modelled	23.1	16	<b>Fold:</b> beta-beta-alpha zinc fingers <b>Superfamily:</b> beta-beta-alpha zinc fingers <b>Family:</b> HkH motif-containing C2H2 finger
60	<a href="#">c1zr9A_</a>	Alignment	not modelled	23.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger protein 593; <b>PDBTitle:</b> solution structure of a human c2h2-type zinc finger protein
61	<a href="#">d2pbza2</a>	Alignment	not modelled	16.2	9	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> Glutathione synthetase ATP-binding domain-like <b>Family:</b> PurP ATP-binding domain-like
62	<a href="#">d2cfxa2</a>	Alignment	not modelled	10.7	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
63	<a href="#">c2uwqA_</a>	Alignment	not modelled	9.7	11	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis-stimulating of p53 protein 2; <b>PDBTitle:</b> solution structure of aspp2 n-terminus
64	<a href="#">d1i1ga2</a>	Alignment	not modelled	6.5	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> Lrp/AsnC-like transcriptional regulator C-terminal domain
65	<a href="#">c3anoA_</a>	Alignment	not modelled	5.8	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ap-4-a phosphorylase; <b>PDBTitle:</b> crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
66	<a href="#">c2kbrA_</a>	Alignment	not modelled	5.7	22	<b>PDB header:</b> structural protein/cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> harmonin; <b>PDBTitle:</b> solution structure of harmonin n terminal domain in complex2 with a internal peptide of cadherin23