Phyre2

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Description	P0A8T7
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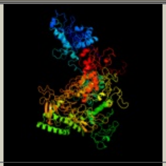
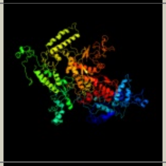
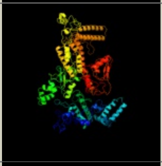
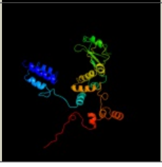
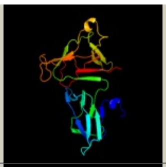
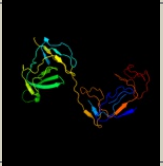
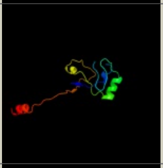
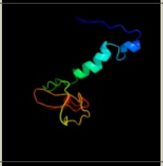
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iydD_	Alignment		100.0	100	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
2	c3h0gA_	Alignment		100.0	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb1; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
3	d1twfa_	Alignment		100.0	24	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
4	d1smyd_	Alignment		100.0	52	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
5	c1i6hA_	Alignment		100.0	24	**PDB header:**transcription/dna-rna hybrid **Chain:** A: **PDB Molecule:**dna-directed rna polymerase ii largest subunit; **PDBTitle:** rna polymerase ii elongation complex
6	d1i6vd_	Alignment		100.0	51	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
7	c1i6vD_	Alignment		100.0	51	**PDB header:**transcription **Chain:** D: **PDB Molecule:**dna-directed rna polymerase; **PDBTitle:** thermus aquaticus core rna polymerase-rifampicin complex
8	d1ynjd1	Alignment		100.0	58	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
9	c2pmzQ_	Alignment		100.0	31	**PDB header:**translation, transferase **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase subunit a; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
10	c3qqcA_	Alignment		100.0	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit b, dna-directed rna **PDBTitle:** crystal structure of archaeal spt4/5 bound to the rnap clamp domain
11	c2pmzG_	Alignment		100.0	27	**PDB header:**translation, transferase **Chain:** G: **PDB Molecule:**dna-directed rna polymerase subunit a"; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus

12	c2aukA_	Alignment		98.0	98	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of e. coli rna polymerase beta' g/g' insert
13	c2aujD_	Alignment		97.7	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna-directed rna polymerase beta' chain; **PDBTitle:** structure of thermus aquaticus rna polymerase beta'-subunit2 insert
14	c3e7hA_	Alignment		96.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor
15	c2j7nA_	Alignment		89.8	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-dependent rna polymerase; **PDBTitle:** structure of the rnai polymerase from neurospora crassa
16	c3ky9B_	Alignment		62.5	12	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** autoinhibited vav1
17	d1nvmb2	Alignment		56.4	15	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
18	d2f9yb1	Alignment		48.4	21	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Biotin dependent carboxylase carboxyltransferase domain
19	c2f9yB_	Alignment		48.4	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl transferase subunit **PDBTitle:** the crystal structure of the carboxyltransferase subunit of acc from2 escherichia coli
20	c1nvmB_	Alignment		47.0	15	**PDB header:**lyase/oxidoreductase **Chain:** B: **PDB Molecule:**acetaldehyde dehydrogenase (acylating); **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
21	d1odha_	Alignment	not modelled	46.7	21	**Fold:**GCM domain **Superfamily:**GCM domain **Family:**GCM domain
22	c2f9iD_	Alignment	not modelled	45.7	16	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acetyl-coenzyme a carboxylase carboxyl **PDBTitle:** crystal structure of the carboxyltransferase subunit of acc2 from staphylococcus aureus
23	c3hcjB_	Alignment	not modelled	42.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase; **PDBTitle:** structure of msrb from xanthomonas campestris (oxidized2 form)
24	d1l1da_	Alignment	not modelled	41.1	18	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
25	d1xm0a1	Alignment	not modelled	41.1	18	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**SelR domain
26	c2lcqA_	Alignment	not modelled	40.8	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative toxin vapc6; **PDBTitle:** solution structure of the endonuclease nob1 from p.horikoshii
27	c3cezA_	Alignment	not modelled	40.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** crystal structure of methionine-r-sulfoxide reductase from2 burkholderia pseudomallei
28	c2l1uA_	Alignment	not modelled	40.6	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b2, mitochondrial; **PDBTitle:** structure-functional analysis of mammalian msrb2 protein

29	c1dvbA_	Alignment	not modelled	40.6	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
30	c3e0mB_	Alignment	not modelled	37.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peptide methionine sulfoxide reductase msra/msrb **PDBTitle:** crystal structure of fusion protein of msra and msrb
31	c3a44D_	Alignment	not modelled	37.2	33	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**hydrogenase nickel incorporation protein hypa; **PDBTitle:** crystal structure of hypa in the dimeric form
32	d2dk5a1	Alignment	not modelled	36.6	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RPO3F domain-like
33	c2k8dA_	Alignment	not modelled	36.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peptide methionine sulfoxide reductase msrb; **PDBTitle:** solution structure of a zinc-binding methionine sulfoxide reductase
34	d2g9ha2	Alignment	not modelled	34.6	71	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
35	c3bbnR_	Alignment	not modelled	34.3	17	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**ribosomal protein s18; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
36	d1s9va2	Alignment	not modelled	33.4	57	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
37	c2vrwB_	Alignment	not modelled	31.7	19	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** critical structural role for the ph and c1 domains of the2 vav1 exchange factor
38	d2vnud2	Alignment	not modelled	31.7	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
39	c2kc1A_	Alignment	not modelled	31.5	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**mkiaa1027 protein; **PDBTitle:** nmr structure of the f0 domain (residues 0-85) of the talin2 ferm domain
40	d2eppa1	Alignment	not modelled	30.9	35	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
41	d1fnga2	Alignment	not modelled	30.3	71	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
42	d1nmla1	Alignment	not modelled	29.8	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
43	c3alrA_	Alignment	not modelled	28.1	26	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**nanos protein; **PDBTitle:** crystal structure of nanos
44	d1eb7a1	Alignment	not modelled	28.1	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
45	c3bjiA_	Alignment	not modelled	27.4	20	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** structural basis of promiscuous guanine nucleotide exchange2 by the t-cell essential vav1
46	c2kaoA_	Alignment	not modelled	26.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b1; **PDBTitle:** structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
47	d1x64a2	Alignment	not modelled	26.8	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
48	c3mkrB_	Alignment	not modelled	26.7	31	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of yeast alpha/epsilon-cop subcomplex of the copi2 vesicular coat
49	d1dw0a_	Alignment	not modelled	26.5	15	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
50	d1jk8a2	Alignment	not modelled	26.3	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
51	d1ekea_	Alignment	not modelled	26.2	24	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
52	d1es0a2	Alignment	not modelled	25.0	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
53	d1muja2	Alignment	not modelled	24.9	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
54	c3mv2A_	Alignment	not modelled	24.9	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
55	c3imkA_	Alignment	not modelled	23.3	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein

						(yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
56	d1iqca1	Alignment	not modelled	23.0	33	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
57	c3t6pA_	Alignment	not modelled	22.8	16	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 2; **PDBTitle:** iap antagonist-induced conformational change in ciap1 promotes e32 ligase activation via dimerization
58	d1b12a_	Alignment	not modelled	22.4	12	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
59	d1x62a1	Alignment	not modelled	22.1	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
60	d1klua2	Alignment	not modelled	21.5	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
61	d2p24a2	Alignment	not modelled	21.4	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
62	d1iaka2	Alignment	not modelled	21.4	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
63	d2coba1	Alignment	not modelled	21.4	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
64	c3df1R_	Alignment	not modelled	21.3	20	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**30s ribosomal protein s18; **PDBTitle:** crystal structure of the bacterial ribosome from escherichia2 coli in complex with hygromycin b. this file contains the3 30s subunit of the first 70s ribosome, with hygromycin b4 bound. the entire crystal structure contains two 70s5 ribosomes.
65	c3zyqA_	Alignment	not modelled	21.2	23	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution
66	c2yhoE_	Alignment	not modelled	21.0	31	**PDB header:**ligase **Chain:** E: **PDB Molecule:**e3 ubiquitin-protein ligase mylip; **PDBTitle:** the idol-ube2d complex mediates sterol-dependent degradation of the2 ldl receptor
67	d1zvpa2	Alignment	not modelled	20.0	42	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**VC0802-like
68	d1uvqa2	Alignment	not modelled	19.9	50	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
69	d2qalr1	Alignment	not modelled	19.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein S18 **Family:**Ribosomal protein S18
70	c3nijA_	Alignment	not modelled	19.3	21	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase ubr1; **PDBTitle:** the structure of ubr box (hiaa)
71	c1nltA_	Alignment	not modelled	19.2	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial protein import protein mas5; **PDBTitle:** the crystal structure of hsp40 ydj1
72	c3d33B_	Alignment	not modelled	19.0	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**domain of unknown function with an immunoglobulin-like **PDBTitle:** crystal structure of a duf3244 family protein with an immunoglobulin-2 like beta-sandwich fold (bvu_0276) from bacteroides vulgatus atcc3 8482 at 1.70 a resolution
73	c1w8xN_	Alignment	not modelled	19.0	57	**PDB header:**virus **Chain:** N: **PDB Molecule:**protein p31; **PDBTitle:** structural analysis of prd1
74	c3fl2A_	Alignment	not modelled	18.9	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the ring domain of the e3 ubiquitin-2 protein ligase uhrf1
75	c2ftcP_	Alignment	not modelled	18.6	32	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**mitochondrial ribosomal protein l33 isoform a; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
76	d1ew4a_	Alignment	not modelled	18.6	27	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
77	d1hk8a_	Alignment	not modelled	18.4	17	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
78	c1hk8A_	Alignment	not modelled	18.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
79	d2uubr1	Alignment	not modelled	16.5	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein S18 **Family:**Ribosomal protein S18

80	c2yu3A_	Alignment	not modelled	16.3	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii 39 kda **PDBTitle:** solution structure of the domain swapped wingedhelix in dna-2 directed rna polymerase iii 39 kda polypeptide
81	c3npeA_	Alignment	not modelled	16.1	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; **PDBTitle:** structure of vp14 in complex with oxygen
82	c2ysaA_	Alignment	not modelled	16.1	29	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6; **PDBTitle:** solution structure of the zinc finger cchc domain from the2 human retinoblastoma-binding protein 6 (retinoblastoma-3 binding q protein 1, rbq-1)
83	c2kkeA_	Alignment	not modelled	15.4	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
84	d1i94r_	Alignment	not modelled	15.4	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Ribosomal protein S18 **Family:**Ribosomal protein S18
85	c2riqA_	Alignment	not modelled	15.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
86	d1wiia_	Alignment	not modelled	15.0	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
87	d1gu2a_	Alignment	not modelled	14.9	11	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**monodomain cytochrome c
88	d2fug21	Alignment	not modelled	14.9	19	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**NQO2-like
89	c2kdxA_	Alignment	not modelled	14.7	14	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
90	c3fybA_	Alignment	not modelled	14.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein of unknown function (duf1244); **PDBTitle:** crystal structure of a protein of unknown function (duf1244) from2 alcanivorax borkumensis
91	d2dula1	Alignment	not modelled	14.3	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**TRM1-like
92	c3fzeA_	Alignment	not modelled	14.2	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein ste5; **PDBTitle:** structure of the 'minimal scaffold' (ms) domain of ste52 that cocatalyzes fus3 phosphorylation by ste7
93	c2kmaA_	Alignment	not modelled	14.2	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**talin 1; **PDBTitle:** nmr structure of the f0f1 double domain (residues 1-202) of2 the talin ferm domain
94	c3p04B_	Alignment	not modelled	14.1	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized bcr; **PDBTitle:** crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
95	d1jb0j_	Alignment	not modelled	13.9	50	**Fold:**Single transmembrane helix **Superfamily:**Subunit IX of photosystem I reaction centre, PsaJ **Family:**Subunit IX of photosystem I reaction centre, PsaJ
96	c2kn9A_	Alignment	not modelled	13.9	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubredoxin; **PDBTitle:** solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
97	d1umua_	Alignment	not modelled	13.8	14	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**LexA-related
98	d1a8ra_	Alignment	not modelled	13.8	12	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**GTP cyclohydrolase I
99	c1x65A_	Alignment	not modelled	13.7	9	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**unr protein; **PDBTitle:** solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)