

Detailed template information

into	rmation					
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4uisB_	Alignment	AND ENTE	71.1	12	PDB header:hydrolase Chain: B: PDB Molecule:gamma-secretase; PDBTitle: the cryoem structure of human gamma-secretase complex PDB Entry: PDBe RCSB PDBj
2	<u>dldnpal</u>	Alignment		36.0	15	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBi
3	d1rrza_	Alignment		34.8	55	Fold: Spectrin repeat-like Superfamily: Glycogen synthesis protein GlgS Family: Glycogen synthesis protein GlgS PDB entry: PDBe RCSB PDBj
4	<u>c1rrzA</u>	Alignment		34.8	55	PDB header:structural genomics,biosynthetic protein Chain: A: PDB Molecule:glycogen synthesis protein glgs; PDBTitle: solution structure of glgs protein from e. coli PDB Entry: PDBe RCSB PDBj
5	<u>c7k82A</u> _	Alignment	<b>E</b>	30.4	35	PDB header:gene regulation Chain: A: PDB Molecule:swi/snf and rsc complexes subunit ssr4; PDBTitle: the x-ray crystal structure of ssr4, an s. pombe chromatin remodelling2 protein: sulfur sad PDB Entry: PDBe RCSB PDBj
6	c5zm0A_	Alignment	com	25.4	17	PDB header:flavoprotein Chain: A: PDB Molecule:cryptochrome photoreceptor; PDBTitle: x-ray structure of animal-like cryptochrome from chlamydomonas2 reinhardtii PDB Entry: PDBe RCSB PDBj
7	c1tezB_	Alignment	and the	24.6	26	PDB header:lyase/dna Chain: B: PDB Molecule:deoxyribodipyrimidine photolyase; PDBTitle: complex between dna and the dna photolyase from anacystis nidulans PDB Entry: PDBe RCSB PDBj
8	c3cvyA_	Alignment		23.3	21	PDB header:lyase/dna Chain: A: PDB Molecule:re11660p; PDBTitle: drosophila melanogaster (6-4) photolyase bound to repaired ds dna PDB Entry: PDBe RCSB PDBj
9	<u>c6ptzA_</u>	Alignment		22.3	12	PDB header:circadian clock protein Chain: A: PDB Molecule:cryptochrome-1; PDBTitle: crystal structure of pigeon cryptochrome 4 mutant y319d in complex2 with flavin adenine dinucleotide PDB Entry: PDBe RCSB PDBj
10	c3fy4C_	Alignment	6	20.0	13	PDB header:lyase Chain: C: PDB Molecule:6-4 photolyase; PDBTitle: (6-4) photolyase crystal structure PDB Entry: PDBe RCSB PDBj
11	c6zz6D_	Alignment	Control of the contro	19.6	19	PDB header:cell cycle Chain: D: PDB Molecule:sister chromatid cohesion protein 2; PDBTitle: cryo-em structure of s.cerevisiae cohesin-scc2-dna complex PDB Entry: PDBe RCSB PDBj

12	clnp7A_	Alignment		18.7	PDB header:lyase Chain: A: PDB Molecule:dna photolyase; 17 PDBTitle: crystal structure analysis of synechocystis sp. pcc6803 cryptochrome PDB Entry: PDBe RCSB PDBj
13	dlowla1	Alignment	Samo	18.6	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
14	dlnp7al	Alignment		18.0	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
15	d1u3da1	Alignment	Gunn.	16.2	Fold: Cryptochrome/photolyase FAD-binding domain Superfamily: Cryptochrome/photolyase FAD-binding domain Family: Cryptochrome/photolyase FAD-binding domain PDB entry: PDBe RCSB PDBj
16	<u>c4i6gA_</u>	Alignment		16.0	PDB header:transcription Chain: A: PDB Molecule:cryptochrome-2; PDBTitle: a vertebrate cryptochrome with fad PDB Entry: PDBe RCSB PDBj
17	c4ln0C_	Alignment	5	16.0	PDB header:transcription Chain: C: PDB Molecule:transcription cofactor vestigial-like protein 4; PDBTitle: crystal structure of the vgll4-tead4 complex PDB Entry: PDBe RCSB PDBj
18	c6kiiA_	Alignment		16.0	PDB header:dna binding protein, lyase Chain: A: PDB Molecule:deoxyribopyrimidine photolyase; PDBTitle: photolyase from arthrospira platensis PDB Entry: PDBe RCSB PDBj
19	d1ni5a4	Alignment		13.6	Fold: MesJ substrate recognition domain-like Superfamily: MesJ substrate recognition domain-like Family: MesJ substrate recognition domain-like PDB entry: PDBe RCSB PDBj
20	c4didB_	Alignment		13.5	PDB header:hydrolase/hydrolase Chain: B: PDB Molecule:inositol phosphate phosphatase sopb;  PDBTitle: crystal structure of salmonella effector n-terminal domair sopb in2 complex with cdc42 PDB Entry: PDBe RCSB PDBj
21	<u>c6cfwl</u>	Alignment	not modelled	13.4	PDB header:membrane protein Chain: I: PDB Molecule:mbh subunit; 46 PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase PDB Entry: PDBe RCSB PDBj
22	c6hyeF_	Alignment	not modelled	13.2	PDB header:plant protein Chain: F: PDB Molecule:pyridoxal 5'-phosphate synthase subunit pdx1.3; PDBTitle: pdx1.2/pdx1.3 complex (pdx1.3:k97a) PDB Entry: PDBe RCSB PDBi
23	c3imoC_	Alignment	not modelled	13.0	PDB header:unknown function Chain: C: PDB Molecule:integron cassette protein; 24 PDBTitle: structure from the mobile metagenome of vibrio cholerae. integron2 cassette protein vch_cass14 PDB Entry: PDBe RCSB PDBi
24	c3femB_	Alignment	not modelled	12.8	PDB header:biosynthetic protein, transferase Chain: B: PDB Molecule:pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae PDB Entry: PDBe RCSB PDBj
25	c6hxgE_	Alignment	not modelled	12.7	PDB Entry: PDBe RCSB PDBj  PDB header:plant protein Chain: E: PDB Molecule:pyridoxal 5'-phosphate synthase-like subunit pdx1.2; PDBTitle: pdx1.2/pdx1.3 complex (intermediate) PDB Entry: PDBe RCSB PDBj
26	c2zbtB_	Alignment	not modelled	12.6	PDB header:lyase Chain: B: PDB Molecule:pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8 PDB Entry: PDBe RCSB PDBj
27	c2ejeA_	Alignment	not modelled	12.6	PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i;  PDBTitle: solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna

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Alignment not modelled 9.6 15 Chain: A: PDB Molecules:cryptochrome-1; PDB Entry: PDB RCSB PDB; PDB RCMB PDB PROBECULEX.							
Alignment not modelled 9.5 PDB Entry: PDBR RCSR PDBi PDB REMERTED							PDB header:signaling protein
PDB Entry: PDBe RCSB PDB   PDB header:transferase Chain: A: PDB Molecule:lipopolysaccharide core biosynthesis protein rfag: PDB rittle: structure of an n-terminal membrane-anchoring region of the 2 glycosyltransferase waag PDB Entry: PDBe RCSB PDB  PDB header:cell cycle Chain: D: PDB Molecule:protein caf40; PDBTittle: structure of an n-terminal membrane-anchoring region of the 2 glycosyltransferase waag PDB Entry: PDBe RCSB PDB  PDB header:cell cycle Chain: D: PDB Molecule:protein caf40; PDBTittle: yeast not1 cn9bd-caf40 complex PDB Entry: PDBE RCSB PDB  PDB header:de novo protein Chain: C: PDB Molecule:cc-hept-bmecys-his-glu; PDBTittle: a de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 l25e PDB Entry: PDBE RCSB PDB  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDBTittle: a de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 l25e PDB Entry: PDBE RCSB PDB  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB Entry: PDBE RCSB PDB  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBE RCSB PDB  PDB header:transcription Chain: A: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBE RCSB PDB  PDB header:transcription factor ii-i repeat domain- pDB Tittle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBE RCSB PDB  PDB header:lyase (carbon-carbon) Chain: A: PDB Moleculedran photolyase;	41	c3tvsA_	Alignment	not modelled	9.6	15	
Alignment not modelled 9.5 60 Chain: A: PDB Molecule: (ipopolysaccharide core biosynthesis protein frag: PDBTitle: structure of an n-terminal membrane-anchoring region of the 2 glycosyltransferase waag PDB Entry: PDB excSB PDB; PDB header: Cell cycle Chain: D: PDB Molecule: protein caf40; PDBTitle: yeast not 1 cn9bd-caf40 complex PDB Entry: PDB excSB PDB; PDB header: Cell cycle Chain: D: PDB Molecule: protein caf40; PDBTitle: yeast not 1 cn9bd-caf40 complex PDB Entry: PDB excSB PDB; PDB header: de novo protein Chain: C: PDB Molecule: cc-hept-bmecys-his-glu; PDB reader: de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 l25e PDB Entry: PDB excSB PDB; PDB header: de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 l25e PDB Entry: PDB RCSB PDB; PDB header: de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 l25e PDB Entry: PDB RCSB PDB; PDB header: de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 l25e PDB Entry: PDB RCSB PDB; PDB header: chovo protein Chain: E: PDB Molecule: cc-hept-hcys-h-e; PDB Entry: PDB RCSB PDB; PDB header: coiled coil cc-hept-homocys-h-e PDB Entry: PDB RCSB PDB; PDB header: coiled coil cc-hept-homocys-h-e PDB Entry: PDB RCSB PDB; PDB header: coiled coil cc-hept-homocys-h-e PDB Entry: PDB RCSB PDB; PDB header: significant in human 2 cdna PDB Entry: PDB RCSB PDB; PDB header: significant in human 2 cdna PDB Entry: PDB RCSB PDB; PDB header: significant in human 2 cdna PDB Entry: PDB RCSB PDB; PDB header: significant in hot modelled PDB Entry: PDB RCSB PDB; PDB header: significant in hot modelled PDB Entry: PDB RCSB PDB; PDB header: significant in hot post modelled PDB Entry: PDB RCSB PDB; PDB header: significant in hot pDB Entry: PDB RCSB PDB; PDB header: significant in hot pDB Entry: PDB RCSB PDB; PDB header: significant in hot pDB Entry: PDB RCSB PDB; PDB header: significant in hot pDB Entry: PDB RCSB PDB; PDB Header: significant in hot post post post post post post pDB Entry: PDB RCSB PDB; PDB Header: significant in hot post							PDB Entry: PDBe RCSB PDBj
42 C2n58A Alignment not modelled 9.5 60 protein rfag; pDBTitle: structure of an n-terminal membrane-anchoring region of the pDB thrust; PDB RCSB PDBj PDB Entry: PDB E							
### PDB Inter: structure of an n-terminal membrane-anchoring region of the glycosyltransferase waag PDB Entry: PDB RCSB PDB    ### PDB Hader:de novo protein Caf40;  ### PDB Hader:de novo protein Caf40;  ### PDB Hader:de novo protein Chain: C: PDB Molecule:cc-hept-bmecys-his-glu;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hept-pDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:co-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:co-hept-hcys-h-e;  ### PDB Hader:de novo protein Chain: E: PDB Molecule:general transcription factor ii-i repeat domain:  ### PDB Hader:de novo protein Chain: A: PDB Molecule:de novo protein Chain: A: PD	42	c2n58A	Alianment	not modelled	9.5	60	protein rfag;
PDB Entry: PDBe RCSB PDB]  PDB Meader:cell cycle Chain: D: PDB Molecule:protein caf40; PDBTitle: yeast not1 cn9bd-caf40 complex PDB Entry: PDBe RCSB PDBi  PDB header:de novo protein Chain: C: PDB Molecule:cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBi  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 i25e PDB Entry: PDB RCSB PDBi  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBe RCSB PDBi  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBE RCSB PDBi PDB header:de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBE RCSB PDBi PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBE RCSB PDBi PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:carbon-potolyase;		_	3				the2 glycosyltransferase waag
Alignment not modelled 9.2 21 Chain: D: PDB Moiecule:protein caf40; PDBTitle: yeast not1 cn9bd-caf40 complex PDB Entry: PDBe RCSB PDB; PDB Header:de novo protein Chain: C: PDB Molecule:cc-hept-bmecys-his-glu; PDB Entry: PDBe RCSB PDB; PDB header:de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDB; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB Header:de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDB; PDB header:de novo designed heptameric coiled coil cc-hept-li8betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDB; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Intry: PDBe RCSB PDB; PDB header:de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDB; PDB header:de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDB; PDB header:de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDB; PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain-PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDB; PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase; Chain: A: PDB Molecule:dna photolyase;							PDB Entry: PDBe RCSB PDBj
PDB Inte: yeast not cropac-car4u complex PDB Entry: PDBE RCSB PDBj PDB header:de novo protein Chain: C: PDB Molecule:c-hept-bmecys-his-glu; PDB Entry: PDBE RCSB PDBj PDB header:de novo designed heptameric coiled coil cc-hept- il8betamecys-l22h-2 i25e PDB Entry: PDBE RCSB PDBj PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB header:de novo designed heptameric coiled coil cc-hept- il8betamecys-l22h-2 i25e PDB Entry: PDBE RCSB PDBj PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB resder:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB resder:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBE RCSB PDBj PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- pDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBE RCSB PDBj PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:don-carbon)	43	c4cv5D	Alianment	not modelled	9.2	21	Chain: D: PDB Molecule:protein caf40;
PDB header:de novo protein Chain: C: PDB Molecule:cc-hept-bmecys-his-glu; PDBTitle: a de novo designed heptameric coiled coil cc-hept- il 8betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBi PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBe RCSB PDBi PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Title: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBi PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBi PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;	7.5	<u>C +C \ 2D _</u>	Alignment	nocmodelled	3.2	21	
Alignment not modelled 9.1 37 PDBTitle: a de novo designed heptameric coiled coil cc-hept- il 18betamecys-122h-2 i25e PDB Entry: PDBe RCSB PDBj  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  37 PDBTitle: a de novo designed heptameric coiled coil cc-hept- il 18betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-homecys-his-glu;  Alignment not modelled 9.1 37 PDBTitle: a de novo designed heptameric coiled coil cc-hept- homocys-h-e PDB Entry: PDBe RCSB PDBj  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  PDB Entry: PDBe RCSB PDBj  PDB header:de novo designed heptameric coiled coil cc-hept- homocys-h-e PDB Entry: PDBe RCSB PDBj  PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDB Entry: PDBe RCSB PDBj  PDB Header:lyase (carbon-carbon) Chain: A: PDB Molecule:de pDB intry: PDBe RCSB PDBj  PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;							PDB header:de novo protein
i18betamecys-!22h-2 i25e PDB Entry: PDBe RCSB PDBj PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu; PDB header:de novo designed heptameric coiled coil cc-hept-i18betamecys-!22h-2 i25e PDB Entry: PDBe RCSB PDBj PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Entry: PDBe RCSB PDBj PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDB Title: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj PDB header:lyse (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;	44	c5ezeC	Alignment	not modelled	9.1	37	
PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  37 PDBTitle: a de novo designed heptameric coiled coil cc-hept- il 8betamecys-122h-2 i25e PDB Entry: PDBe RCSB PDBj  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;  Alignment  not modelled  9.1 37 PDBTitle: a de novo designed heptameric coiled coil cc-hept- homocys-h-e PDB Entry: PDBe RCSB PDBj  PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj  PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;			Augiment			J,	i18betamecys-l22h-2 i25e
Alignment not modelled 9.1 37 PDBTitle: a de novo designed heptameric coiled coil cc-heptil8betamecys-l22h-2 i25e PDB Entry: PDBe RCSB PDBj PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Molecule:cc-hept-hcys-h-e; PDB Title: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBj PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;							
i18betamecys-I22h-2 i25e PDB Entry: PDBe RCSB PDBi PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Title: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBi PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBi PDB Header:tysee (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;	45	cForeF	Allerance	not modelled	0.1	27	Chain: E: PDB Molecule:cc-hept-bmecys-his-glu;
PDB Entry: PDBe RCSB PDBj  PDB header:de novo protein Chain: E: PDB Molecule:cc-hept-hcys-h-e;  Alignment not modelled 9.1 37 PDBTitle: a de novo designed heptameric coiled coil cc-hept-homocys-h-e PDB Entry: PDBe RCSB PDBj  PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj  PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;	45	csezet_	Alignment	not modelled	9.1	3/	i18betamecys-l22h-2 i25e
Alignment not modelled 9.1 Chain: E: PDB Molecule:cc-hept-hcys-h-e; PDB Title: a de novo designed heptameric coiled coil cc-hept-homocys-he PDB Entry: PDBe RCSB PDBj PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj PDB Header:ty-PDBe RCSB PDBj PDB Header:ty-PDB Molecule:dna photolyase;							PDB Entry: PDBe RCSB PDBj
homocys-h-e PDB Entry: PDBe RCSB PDBj  PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj  PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;			_				Chain: E: PDB Molecule:cc-hept-hcys-h-e;
PDB Entry: PDBe RCSB PDBj  PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj  PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;	46	c5f2yE_	Alignment	not modelled	9.1	37	PDBTitle: a de novo designed heptameric coiled coil cc-hept-
Chain: A: PDB Molecule:general transcription factor ii-i repeat domain- PDB Title: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj PDB header:lyase (carbon-carbon)  Chain: A: PDB Molecule:dna photolyase;							PDB Entry: PDBe RCSB PDBj
47 c2d99A Alignment not modelled 9.1 20 domain-PDBTitle: solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna PDB Entry: PDBe RCSB PDBj PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;							
PDB Intel: solution structure of rsgi run-048, a gtt2l domain in human2 cdna PDB Entry: PDBe RCSB PDBj PDB header:lyase (carbon-carbon) Chain: A: PDB Molecule:dna photolyase;	47	c2d994	Alianment	not modelled	9.1	20	domain-
PDB Entry: PDBe RCSB PDBj  PDB header:lyase (carbon-carbon)  Chain: A: PDB Molecule:dna photolyase;		<u> </u>	Alignment			_~	
48 c1dppA pot modelled pot modelled 15 Chain: A: PDB Molecule:dna photolyase;							PDB Entry: PDBe RCSB PDBj
	40	c1dan^	7.11	not modelled	0.0	15	
	40	CTUIIDA_	Alignment	not modelled	9.0	13	

						DDD Follows DDD - DCCD DDD'
						PDB Entry: PDBe RCSB PDBj  PDB header:transcription
						Chain: A: PDB Molecule:general transcription factor ii-i repeat
49	c2dn5A_	Alignment	not modelled	9.0	25	domain- <b>PDBTitle:</b> solution structure of rsgi ruh-057, a gtf2i domain in
						human2 cdna
						PDB Entry: PDBe RCSB PDBj  PDB header:hydrolase
50	c3ih9A	Alignment	not modelled	8.9	27	Chain: A: PDB Molecule:salt-tolerant glutaminase;
		Alignment				PDBTitle: crystal structure analysis of mglu in its tris form PDB Entry: PDBe RCSB PDBi
			_			PDB header:signaling protein
51	c1u3cA	Alignment	not modelled	8.6	14	Chain: A: PDB Molecule:cryptochrome 1 apoprotein; PDBTitle: crystal structure of the phr domain of cryptochrome 1
J.	<u>crusert_</u>	Alignment	not modelied	0.0		from2 arabidopsis thaliana
						PDB Entry: PDBe RCSB PDBj  PDB header:dna binding protein
52	c2j4dA_	Alimmus aut	not modelled	8.6	20	Chain: A: PDB Molecule:cryptochrome dash;
J2	<u>czj4uA_</u>	Alignment	not modelled	0.0	20	PDBTitle: cryptochrome 3 from arabidopsis thaliana PDB Entry: PDBe RCSB PDBj
						PDB header:transcription
						Chain: A: PDB Molecule:rcd1 required for cell differentiation1 homolog;
53	c2fv2A_	Alignment	not modelled	8.6	18	PDBTitle: crystal structure analysis of human rcd-1 conserved
						region PDB Entry: PDBe RCSB PDBi
						PDB header:transferase/transferase
E 4	c/adcE	Alleman	not modelled	0.2	64	Chain: F: PDB Molecule:pyridoxine biosynthetic enzyme pdx1
54	<u>c4adsF_</u>	Alignment	not modelled	8.2	64	homologue, putative;  PDBTitle: crystal structure of plasmodial plp synthase complex
						PDB Entry: PDBe RCSB PDBj
						PDB header:hydrolase Chain: F: PDB Molecule:mazq-like nucleoside triphosphate
55	c2yf3F_	Alignment	not modelled	7.9	35	pyrophosphohydrolase;
	, <u></u>	Augminent				<b>PDBTitle:</b> crystal structure of dr2231, the mazg-like protein from deinococcus2 radiodurans, complex with manganese
						PDB Entry: PDBe RCSB PDBj
						PDB header:transcription Chain: A: PDB Molecule:general transcription factor ii-i;
56	c2dn4A_	Alignment	not modelled	7.9	20	PDBTitle: solution structure of rsgi ruh-060, a gtf2i domain in
						human2 cdna PDB Entry: PDBe RCSB PDBi
						PDB header:photosynthesis
57	c7d1tY_	Alignment	not modelled	7.7	40	Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12;
J,	<u> </u>	Alignment	not modelled	7.7	40	PDBTitle: cryo-em structure of psii at 1.95 angstrom resolution
						PDB Entry: PDBe RCSB PDBj PDB header:photosynthesis
						Chain: Y: PDB Molecule:photosystem ii reaction center protein
58	c7d1uY_	Alignment	not modelled	7.7	40	ycf12;
						PDBTitle: cryo-em structure of psii at 2.08 angstrom resolution PDB Entry: PDBe RCSB PDBi
			_			PDB header:photosynthesis
59	c7d1ty_	Alignment	not modelled	7.7	40	Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12;
		3				PDBTitle: cryo-em structure of psii at 1.95 angstrom resolution
						PDB Entry: PDBe RCSB PDBj  PDB header:electron transport, photosynthesis
60	-221/			7.7	40	Chain: Y: PDB Molecule:photosystem ii reaction center protein
60	<u>c3wu2Y_</u>	Alignment	not modelled	7.7	40	ycf12;  PDBTitle: crystal structure analysis of photosystem ii complex
						PDB Entry: PDBe RCSB PDBj
						PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein
61	c7d1uy_	Alignment	not modelled	7.7	40	ycf12;
						PDBTitle: cryo-em structure of psii at 2.08 angstrom resolution PDB Entry: PDBe RCSB PDBi
						PDB header:photosynthesis
						Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12;
62	<u>c5tisY_</u>	Alignment	not modelled	7.7	40	PDBTitle: room temperature xfel structure of the native, doubly-
						illuminated2 photosystem ii complex PDB Entry: PDBe RCSB PDBi
			_			PDB header:photosynthesis
63	c7edaY_	Alignment	not modelled	7.7	40	Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12;
	<u>0,2441_</u>	Alignment			,,,	PDBTitle: structure of monomeric photosystem ii
						PDB Entry: PDBe RCSB PDBj  PDB header:electron transport
		_				Chain: Y: PDB Molecule:photosystem ii reaction center protein
64	c5kaiY_	Alignment	not modelled	7.7	40	ycf12;  PDBTitle: nh3-bound rt xfel structure of photosystem ii 500 ms after
						the 2nd2 illumination (2f) at 2.8 a resolution
						PDB Entry: PDBe RCSB PDBj Fold: GTF2I-like repeat
65	d1g60a	Allerane	not modelled	7.5	20	Superfamily: GTF2I-like repeat
03	<u>d1q60a_</u>	Alignment	not modelled	7.5	20	Family: GTF2I-like repeat
			-			PDB entry: PDBe RCSB PDBj PDB header:viral protein
66	c5ipxA_	Alignment	not modelled	7.3	18	Chain: A: PDB Molecule:orf49 protein;
	_					PDBTitle: structure of orf49 from kshv PDB Entry: PDBe RCSB PDBj
						PDB header:oxidoreductase
67	•Ev2		mat word II I	7.0		Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12;
67	<u>c5mx2y_</u>	Alignment	not modelled	7.2	40	PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a
						resolution PDB Entry: PDBe RCSB PDBi
						PDB header:electron transport
68	c3a0by	Alignment	not modelled	6.9	40	Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12;
33	<u></u>	Alignment			,,,	PDBTitle: crystal structure of br-substituted photosystem ii complex
						PDB Entry: PDBe RCSB PDBj

69	c3a0bY_	Alignment	not modelled	6.9	40	PDB header:electron transport Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of br-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBj
70	<u>c4tnky</u>	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution PDB Entry: PDBe RCSB PDBj
71	<u>c7nhoy</u>	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule: PDBTitle: structure of psii-m PDB Entry: PDBe RCSB PDBj
72	<u>c4tnhy</u>	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution PDB Entry: PDBe RCSB PDBj
73	<u>c4tnkg</u>	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: G: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 250 microsec after the third2 illumination at 5.2 a resolution PDB Entry: PDBe RCSB PDBi
74	c4tnjy_	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution PDB Entry: PDBe RCSB PDBj
75	c3prry_	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein z; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer PDB Entry: PDBe RCSB PDBj
76	<u>c4fbyy</u>	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: fs x-ray diffraction of photosystem ii PDB Entry: PDBe RCSB PDBj
77	c4tniy_	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution PDB Entry: PDBe RCSB PDBi
78	<u>c7nhqy</u>	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule: PDBTitle: structure of psii-i prime (psii with psb28, and psb34) PDB Entry: PDBe RCSB PDBj
79	c4fbym_	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: M: PDB Molecule:photosystem ii reaction center protein m; PDBTitle: fs x-ray diffraction of photosystem ii PDB Entry: PDBe RCSB PDBj
80	c3bz1y_	Alignment	not modelled	6.9	40	PDB header:electron transport Chain: Y: PDB Molecule:photosystem ii protein y; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 1 of 2). this2 file contains first monomer of psii dimer PDB Entry: PDBe RCSB PDBj
81	<u>c4ixqg</u>	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: G: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state PDB Entry: PDBe RCSB PDBj
82	<u>c7nhpy</u>	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule: PDBTitle: structure of psii-i (psii with psb27, psb28, and psb34) PDB Entry: PDBe RCSB PDBj
83	c4ixrg_	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: G: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state PDB Entry: PDBe RCSB PDBj
84	c4ixry_	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, first illuminated state
85	<u>c4ixqy</u>	Alignment	not modelled	6.9	40	PDB Entry: PDBe RCSB PDBj PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt fs x-ray diffraction of photosystem ii, dark state PDB Entry: PDBe RCSB PDBj
86	c3a0hy_	Alignment	not modelled	6.9	40	PDB header:electron transport Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of i-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBj
87	c3a0hY_	Alignment	not modelled	6.9	40	PDB header:electron transport Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: crystal structure of i-substituted photosystem ii complex PDB Entry: PDBe RCSB PDBi
88	<u>c4tnhg</u>	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: G: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii in the dark state at 4.9 a2 resolution PDB Entry: PDBe RCSB PDBj
89	c4tnjg_	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: G: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the 2nd illumination2 (2f) at 4.5 a resolution PDB Entry: PDBe RCSB PDBj
90	<u>c3wu2y_</u>	Alignment	not modelled	6.9	40	PDB header:electron transport, photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: crystal structure analysis of photosystem ii complex

						PDB Entry: PDBe RCSB PDBj
91	c3bz2y_	Alignment	not modelled	6.9	40	PDB header:electron transport Chain: Y: PDB Molecule:photosystem ii protein y; PDBTitle: crystal structure of cyanobacterial photosystem ii (part 2 of 2). this2 file contains second monomer of psii dimer PDB Entry: PDBe RCSB PDBj
92	<u>c3kziy</u>	Alignment	not modelled	6.9	40	PDB header:electron transport Chain: Y: PDB Molecule: PDBTitle: crystal structure of monomeric form of cyanobacterial photosystem ii PDB Entry: PDBe RCSB PDBi
93	<u>c4tnig</u>	Alignment	not modelled	6.9	40	PDB header:electron transport,photosynthesis Chain: G: PDB Molecule:photosystem ii reaction center protein y; PDBTitle: rt xfel structure of photosystem ii 500 ms after the third2 illumination at 4.6 a resolution PDB Entry: PDBe RCSB PDBi
94	c3prqy_	Alignment	not modelled	6.9	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii psbx protein; PDBTitle: crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer PDB Entry: PDBe RCSB PDBj
95	<u>c3rgbG</u>	Alignment	not modelled	6.6	30	PDB header:oxidoreductase Chain: G: PDB Molecule:methane monooxygenase subunit c2; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylococcus capsulatus (bath) PDB Entry: PDBe RCSB PDBi
96	c6jloY_	Alignment	not modelled	6.6	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: xfel structure of cyanobacterial photosystem ii (2f state, dataset2) PDB Entry: PDBe RCSB PDBi
97	c7cjjY_	Alignment	not modelled	6.6	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: photosystem ii structure in the s2 state PDB Entry: PDBe RCSB PDBj
98	<u>c7cjjy</u> _	Alignment	not modelled	6.6	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: photosystem ii structure in the s2 state PDB Entry: PDBe RCSB PDBj
99	<u>c6jlnY_</u>	Alignment	not modelled	6.6	40	PDB header:photosynthesis Chain: Y: PDB Molecule:photosystem ii reaction center protein ycf12; PDBTitle: xfel structure of cyanobacterial photosystem ii (1f state, dataset2) PDB Entry: PDBe RCSB PDBj