Phyre^2

Email	l.a.kelley@imperial.ac.uk
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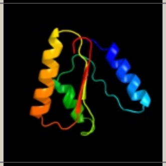
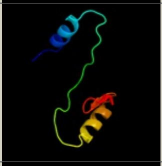
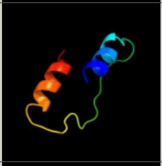
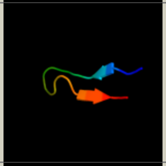
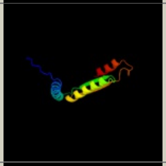
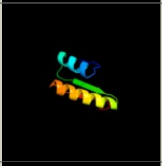
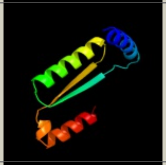
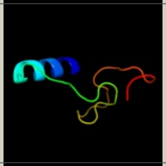
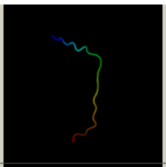
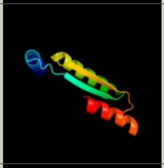
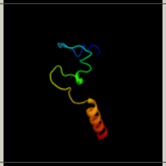
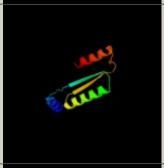
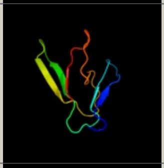
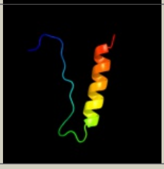
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2isba1	Alignment		100.0	31	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**FumA C-terminal domain-like **Family:**FumA C-terminal domain-like
2	d1ed7a_	Alignment		58.8	12	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
3	c1k98A_	Alignment		53.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
4	c3fpnA_	Alignment		51.0	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**geobacillus stearothermophilus uvra interaction **PDBTitle:** crystal structure of uvra-uvrb interaction domains
5	c2xmoB_	Alignment		38.2	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmo2642 protein; **PDBTitle:** the crystal structure of lmo2642
6	d1ei5a2	Alignment		37.1	25	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
7	c3l07B_	Alignment		36.5	17	**PDB header:**oxidoreductase,hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
8	d3bula2	Alignment		36.4	25	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
9	c3p2oA_	Alignment		35.8	18	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
10	d12asa_	Alignment		34.3	18	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
11	c3p2oB_	Alignment		32.4	18	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni

12	c2zoeA_	Alignment		31.2	23	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemagglutinin components ha3; **PDBTitle:** ha3 subcomponent of clostridium botulinum type c progenitor2 toxin, complex with n-acetylneuramic acid
13	c2d49A_	Alignment		28.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase c; **PDBTitle:** solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
14	c2c2xB_	Alignment		28.4	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase- **PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis
15	c2e0iD_	Alignment		28.3	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**432aa long hypothetical deoxyribodipyrimidine photolyase; **PDBTitle:** crystal structure of archaeal photolyase from sulfolobus tokodaii with2 two fad molecules: implication of a novel light-harvesting cofactor
16	d1a4ia2	Alignment		26.5	16	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
17	d1aiwa_	Alignment		25.7	7	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
18	d2piea1	Alignment		25.4	21	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
19	d1vkza2	Alignment		24.2	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
20	d1yqea1	Alignment		24.1	8	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
21	c2gfqC_	Alignment	not modelled	23.6	9	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
22	c3lzkC_	Alignment	not modelled	23.4	18	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fumarylacetoacetate hydrolase family protein; **PDBTitle:** the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
23	c3cr8C_	Alignment	not modelled	22.7	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
24	d1b8aa1	Alignment	not modelled	22.6	6	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
25	d1goia1	Alignment	not modelled	21.8	18	**Fold:**WW domain-like **Superfamily:**Carbohydrate binding domain **Family:**Carbohydrate binding domain
26	d1o6aa_	Alignment	not modelled	21.5	13	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
27	d1v58a1	Alignment	not modelled	21.3	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
28	d2gqba1	Alignment	not modelled	21.2	35	**Fold:**RPA2825-like **Superfamily:**RPA2825-like **Family:**RPA2825-like
						PDB header:isomerase,biosynthetic protein

29	c3orsD_	Alignment	not modelled	21.1	14	**Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
30	d2gfqa1	Alignment	not modelled	20.5	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
31	c2crvA_	Alignment	not modelled	19.6	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of c-terminal domain of mitochondrial2 translational initiationfactor 2
32	d1vjea_	Alignment	not modelled	19.3	25	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
33	d1ooya2	Alignment	not modelled	19.2	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
34	d1muja2	Alignment	not modelled	18.4	35	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
35	d1ni9a_	Alignment	not modelled	18.1	23	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**GlpX-like bacterial fructose-1,6-bisphosphatase
36	c3trhI_	Alignment	not modelled	17.8	10	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
37	c2j7pA_	Alignment	not modelled	17.4	17	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
38	c3uotB_	Alignment	not modelled	17.3	6	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
39	d2piaa1	Alignment	not modelled	17.1	0	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
40	c2qv6D_	Alignment	not modelled	17.0	9	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**gtp cyclohydrolase iii; **PDBTitle:** gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
41	d1edza2	Alignment	not modelled	17.0	10	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Tetrahydrofolate dehydrogenase/cyclohydrolase
42	d2cp6a1	Alignment	not modelled	16.5	15	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
43	d2oz4a1	Alignment	not modelled	16.2	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C2 set domains
44	d1j98a_	Alignment	not modelled	16.1	45	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
45	d2vzsa5	Alignment	not modelled	16.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
46	d1g3ga_	Alignment	not modelled	16.0	17	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
47	d1fnda1	Alignment	not modelled	15.8	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
48	c3ff4A_	Alignment	not modelled	15.6	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
49	d2eyqa1	Alignment	not modelled	15.5	6	**Fold:**SH3-like barrel **Superfamily:**CarD-like **Family:**CarD-like
50	c3c00B_	Alignment	not modelled	15.1	11	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**escu; **PDBTitle:** crystal structural of the mutated g247t escu/spas c-terminal domain
51	c3eeqB_	Alignment	not modelled	15.0	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cobalamin biosynthesis protein g **PDBTitle:** crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
52	d1jr2a_	Alignment	not modelled	14.8	21	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
53	c1jr2A_	Alignment	not modelled	14.8	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
54	d1n0ua3	Alignment	not modelled	14.7	10	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
						PDB header:structural genomics, unknown function

55	c2l9dA_	Alignment	not modelled	14.7	17	**Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
56	d1uhta_	Alignment	not modelled	14.4	13	**Fold:**SMAD/FHA domain **Superfamily:**SMAD/FHA domain **Family:**FHA domain
57	d1sf8a_	Alignment	not modelled	14.0	23	**Fold:**HSP90 C-terminal domain **Superfamily:**HSP90 C-terminal domain **Family:**HSP90 C-terminal domain
58	c2iheA_	Alignment	not modelled	13.9	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
59	c3kw0D_	Alignment	not modelled	13.4	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cysteine peptidase; **PDBTitle:** crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
60	d1a5ra_	Alignment	not modelled	13.4	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
61	c3qq5A_	Alignment	not modelled	13.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**small gtp-binding protein; **PDBTitle:** crystal structure of the [fefe]-hydrogenase maturation protein hydf
62	d1owla1	Alignment	not modelled	13.0	14	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
63	c3fmxX_	Alignment	not modelled	13.0	17	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**tartrate dehydrogenase/decarboxylase; **PDBTitle:** crystal structure of tartrate dehydrogenase from pseudomonas2 putida complexed with nadh
64	c1tezB_	Alignment	not modelled	12.9	14	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from anacystis nidulans
65	d1es0a2	Alignment	not modelled	12.8	35	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
66	c3mxnB_	Alignment	not modelled	12.6	24	**PDB header:**replication **Chain:** B: **PDB Molecule:**recq-mediated genome instability protein 2; **PDBTitle:** crystal structure of the rmi core complex
67	c3cyyA_	Alignment	not modelled	12.5	22	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** the crystal structure of zo-1 pdz2 in complex with the cx43 peptide
68	c2jlhA_	Alignment	not modelled	12.5	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** crystal structure of the cytoplasmic domain of yersinia2 pestis yscu n263a mutant
69	c3en2A_	Alignment	not modelled	12.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
70	d2gc6a1	Alignment	not modelled	12.4	18	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
71	d1u3da1	Alignment	not modelled	12.3	20	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
72	c3chvA_	Alignment	not modelled	12.3	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim **PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
73	c1a4iB_	Alignment	not modelled	12.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
74	c3ibgF_	Alignment	not modelled	12.0	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
75	c2oqjF_	Alignment	not modelled	11.9	71	**PDB header:**immune system **Chain:** F: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
76	d2coza1	Alignment	not modelled	11.8	16	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
77	c3o59X_	Alignment	not modelled	11.6	46	**PDB header:**transferase **Chain:** X: **PDB Molecule:**dna polymerase ii large subunit; **PDBTitle:** dna polymerase d large subunit dp2(1-300) from pyrococcus horikoshii
78	c3t7yB_	Alignment	not modelled	11.6	11	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**yop proteins translocation protein u; **PDBTitle:** structure of an autocleavage-inactive mutant of the cytoplasmic domain2 of ct091, the yscu homologue of chlamydia trachomatis
79	d2f2ab1	Alignment	not modelled	11.5	19	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
						Fold:OB-fold

80	d1c0aa1	Alignment	not modelled	11.5	21	**Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
81	d2cnda1	Alignment	not modelled	11.4	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
82	d4ubpb_	Alignment	not modelled	11.1	17	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
83	d1o9ya_	Alignment	not modelled	11.1	20	**Fold:**Surface presentation of antigens (SPOA) **Superfamily:**Surface presentation of antigens (SPOA) **Family:**Surface presentation of antigens (SPOA)
84	d1e9ya1	Alignment	not modelled	11.0	12	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
85	d2ew0a1	Alignment	not modelled	11.0	22	**Fold:**VC0467-like **Superfamily:**VC0467-like **Family:**VC0467-like
86	c3d8tB_	Alignment	not modelled	10.9	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
87	c2oqjL_	Alignment	not modelled	10.8	71	**PDB header:**immune system **Chain:** L: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
88	c2oqjI_	Alignment	not modelled	10.8	71	**PDB header:**immune system **Chain:** I: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
89	c2oqjC_	Alignment	not modelled	10.8	71	**PDB header:**immune system **Chain:** C: **PDB Molecule:**peptide 2g12.1 (acppshvldmrsgtclaaegk); **PDBTitle:** crystal structure analysis of fab 2g12 in complex with peptide 2g12.1
90	d1e32a1	Alignment	not modelled	10.8	10	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
91	d1pcfa_	Alignment	not modelled	10.6	47	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
92	c3rfuC_	Alignment	not modelled	10.4	15	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**copper efflux atpase; **PDBTitle:** crystal structure of a copper-transporting pib-type atpase
93	c1zgxA_	Alignment	not modelled	10.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**guanyl-specific ribonuclease sa; **PDBTitle:** crystal structure of ribonuclease mutant
94	c2ihfA_	Alignment	not modelled	10.3	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
95	d1sm4a1	Alignment	not modelled	10.2	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
96	d1qx4a1	Alignment	not modelled	10.2	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
97	d1xnea_	Alignment	not modelled	10.2	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
98	d1krha1	Alignment	not modelled	10.1	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
99	c3op0B_	Alignment	not modelled	10.1	58	**PDB header:**signaling protein/signaling protein regu **Chain:** B: **PDB Molecule:**signal transduction protein cbl-c; **PDBTitle:** crystal structure of cbl-c (cbl-3) tkb domain in complex with egfr2 py1069 peptide