Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P45546
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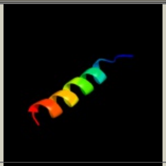
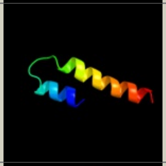
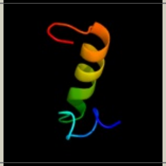
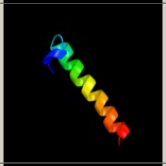
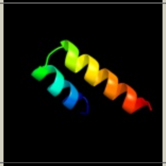
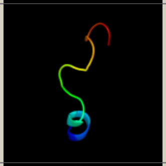
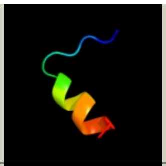
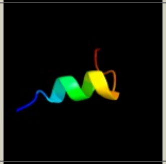
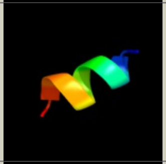
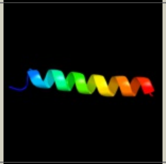
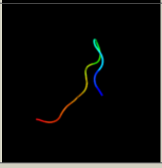
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ww9B_	Alignment		32.7	30	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the2 yeast 80s ribosome
2	c2jx0A_	Alignment		29.5	15	**PDB header:**cell adhesion, signaling protein **Chain:** A: **PDB Molecule:**arf gtpase-activating protein git1; **PDBTitle:** the paxillin-binding domain (pbd) of g protein coupled2 receptor (gpcr)-kinase (grk) interacting protein 1 (git1)
3	d1y9ia_	Alignment		26.6	28	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
4	d1rfza_	Alignment		26.1	28	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
5	c3thgA_	Alignment		20.5	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribulose bisphosphate carboxylase/oxygenase activase 1, **PDBTitle:** crystal structure of the creosote rubisco activase c-domain
6	c2vy2A_	Alignment		18.8	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**protein leafy; **PDBTitle:** structure of leafy transcription factor from arabidopsis2 thaliana in complex with dna from ag-i promoter
7	c2b99A_	Alignment		17.6	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of an archaeal pentameric riboflavin2 synthase complex with a substrate analog inhibitor
8	c3rlbA_	Alignment		16.5	13	**PDB header:**thiamine-binding protein **Chain:** A: **PDB Molecule:**thit; **PDBTitle:** crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter
9	c3dh4A_	Alignment		16.3	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
10	d1qgta_	Alignment		15.8	39	**Fold:**Hepatitis B viral capsid (hbcag) **Superfamily:**Hepatitis B viral capsid (hbcag) **Family:**Hepatitis B viral capsid (hbcag)
11	d1o82a_	Alignment		15.4	29	**Fold:**Saposin-like **Superfamily:**Bacteriocin AS-48 **Family:**Bacteriocin AS-48

12	c2kbcB_	Alignment		15.1	31	**PDB header:**hormone **Chain:** B: **PDB Molecule:**insl5_b-chain; **PDBTitle:** solution structure of human insulin-like peptide 5 (insl5)
13	d1zs3a1	Alignment		14.6	4	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
14	c2xq2A_	Alignment		14.5	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
15	d1ufya_	Alignment		14.5	33	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
16	c2o01I_	Alignment		14.2	55	**PDB header:**photosynthesis **Chain:** I: **PDB Molecule:**photosystem i reaction center subunit viii; **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
17	c3lw5I_	Alignment		14.2	55	**PDB header:**photosynthesis **Chain:** I: **PDB Molecule:**photosystem i reaction center subunit viii; **PDBTitle:** improved model of plant photosystem i
18	c2wseI_	Alignment		14.2	55	**PDB header:**photosynthesis **Chain:** I: **PDB Molecule:**photosystem i reaction center subunit viii; **PDBTitle:** improved model of plant photosystem i
19	c2l81A_	Alignment		14.1	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**enhancer of filamentation 1; **PDBTitle:** solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
20	d2hjqa2	Alignment		13.6	25	**Fold:**GINS/PriA/YqbF domain **Superfamily:**PriA/YqbF domain **Family:**YqbF N-terminal domain-like
21	c1unuB_	Alignment	not modelled	13.5	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
22	c1unuA_	Alignment	not modelled	13.5	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
23	d1xmec1	Alignment	not modelled	13.3	26	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa
24	d1xhoa_	Alignment	not modelled	13.1	43	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
25	c1uo3B_	Alignment	not modelled	13.0	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
26	c2cceA_	Alignment	not modelled	12.5	23	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
27	c2cceB_	Alignment	not modelled	12.5	23	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
28	c2ccfA_	Alignment	not modelled	12.5	23	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel configuration of pli e20s
29	c2rrhA	Alignment	not modelled	12.2	36	**PDB header:**hormone **Chain:** A: **PDB Molecule:**vip peptides;

						methanol
30	c2v8wA_	Alignment	not modelled	11.8	33	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 4e; **PDBTitle:** crystallographic and mass spectrometric characterisation of2 eif4e with n7-cap derivatives
31	d1r0ka1	Alignment	not modelled	11.7	16	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
32	c2la2A_	Alignment	not modelled	11.7	12	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cecropin; **PDBTitle:** solution structure of papiliocin isolated from the swallowtail2 butterfly, papilio xuthus
33	c2ky5A_	Alignment	not modelled	11.3	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**platelet endothelial cell adhesion molecule; **PDBTitle:** solution structure of the pecam-1 cytoplasmic tail with dpc
34	c1gcmA_	Alignment	not modelled	11.0	23	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
35	c1piqA_	Alignment	not modelled	10.8	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein (general control protein gcn4-piq); **PDBTitle:** crystal structure of gcn4-piq, a trimeric coiled coil with buried2 polar residues
36	c1ij1C_	Alignment	not modelled	10.8	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
37	c1ij1B_	Alignment	not modelled	10.8	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
38	c1ij1A_	Alignment	not modelled	10.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvlt coiled-coil trimer with threonine at the d(12)2 position
39	d2j9ga2	Alignment	not modelled	10.8	22	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
40	d2pyqa1	Alignment	not modelled	10.7	24	**Fold:**Jann4075-like **Superfamily:**Jann4075-like **Family:**Jann4075-like
41	c1z23A_	Alignment	not modelled	10.7	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**crk-associated substrate; **PDBTitle:** the serine-rich domain from crk-associated substrate2 (p130cas)
42	c2q7cC_	Alignment	not modelled	10.7	23	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**fusion protein between yeast variant gcn4 and **PDBTitle:** crystal structure of iqn17
43	c2npsA_	Alignment	not modelled	10.5	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**vesicle-associated membrane protein 4; **PDBTitle:** crystal structure of the early endosomal snare complex
44	c2affB_	Alignment	not modelled	10.4	29	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mki67 fha domain interacting nucleolar phosphoprotein; **PDBTitle:** the solution structure of the ki67fha/hnifk(226-269)3p complex
45	c1gcmB_	Alignment	not modelled	10.4	23	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
46	c3aqpB_	Alignment	not modelled	10.4	20	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**probable secdf protein-export membrane protein; **PDBTitle:** crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus
47	d1zy9a2	Alignment	not modelled	10.3	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**YicI catalytic domain-like
48	c1xhoB_	Alignment	not modelled	10.3	43	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase; **PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
49	c1uo5B_	Alignment	not modelled	10.2	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
50	c1uo5A_	Alignment	not modelled	10.2	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
51	c2wpzA_	Alignment	not modelled	10.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
52	d1q0qa1	Alignment	not modelled	10.1	6	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
53	c1gcmC_	Alignment	not modelled	10.0	23	**PDB header:**transcription regulation **Chain:** C: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li

54	c2jo1A_	Alignment	not modelled	9.9	24	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
55	c1gclD_	Alignment	not modelled	9.9	27	**PDB header:**leucine zipper **Chain:** D: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
56	c1gclA_	Alignment	not modelled	9.9	27	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
57	c1gclC_	Alignment	not modelled	9.9	27	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
58	c1gclB_	Alignment	not modelled	9.9	27	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
59	c3iz6T_	Alignment	not modelled	9.9	17	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**40s ribosomal protein s21 (s21e); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
60	c2d2pA_	Alignment	not modelled	9.8	36	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**pituitary adenylate cyclase activating **PDBTitle:** the solution structure of micelle-bound peptide
61	c1untA_	Alignment	not modelled	9.7	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
62	c2wpzB_	Alignment	not modelled	9.7	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
63	c1t0oA_	Alignment	not modelled	9.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** the structure of alpha-galactosidase from trichoderma reesei complexed2 with beta-d-galactose
64	c1unxA_	Alignment	not modelled	9.6	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
65	c3a23A_	Alignment	not modelled	9.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative secreted alpha-galactosidase; **PDBTitle:** crystal structure of beta-l-arabinopyranosidase complexed with d-2 galactose
66	c1unwB_	Alignment	not modelled	9.4	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
67	c1uo2A_	Alignment	not modelled	9.4	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
68	c1w5iA_	Alignment	not modelled	9.4	27	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
69	c2wpzC_	Alignment	not modelled	9.4	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4 leucine zipper mutant with two vxxnxxx motifs2 coordinating chloride
70	c1untB_	Alignment	not modelled	9.3	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
71	c2voyG_	Alignment	not modelled	9.3	17	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
72	d2cs0a1	Alignment	not modelled	9.2	29	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
73	c3kinA_	Alignment	not modelled	9.2	29	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**kinesin heavy chain; **PDBTitle:** kinesin (dimeric) from rattus norvegicus
74	c2kncB_	Alignment	not modelled	9.2	27	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
75	c2jgcA_	Alignment	not modelled	9.2	28	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 4e type **PDBTitle:** structure of the human eif4e homologous protein, 4ehp2 without ligand bound
76	c3lrmB_	Alignment	not modelled	9.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-galactosidase 1; **PDBTitle:** structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
77	d2bz1a1	Alignment	not modelled	9.0	18	**Fold:**RibA-like **Superfamily:**RibA-like **Family:**RibA-like
78	c1uo2B_	Alignment	not modelled	9.0	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
79	c1w5iB_	Alignment	not modelled	9.0	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.

80	c1rb1C_	Alignment	not modelled	9.0	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
81	c3k7zC_	Alignment	not modelled	9.0	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
82	c1ij0C_	Alignment	not modelled	8.9	19	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** coiled coil trimer gcn4-pvls ser at buried d position
83	c1ij0A_	Alignment	not modelled	8.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** coiled coil trimer gcn4-pvls ser at buried d position
84	c1ij0B_	Alignment	not modelled	8.9	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** coiled coil trimer gcn4-pvls ser at buried d position
85	d1chma1	Alignment	not modelled	8.9	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Creatinase/prolidase N-terminal domain **Family:**Creatinase/prolidase N-terminal domain
86	c2f7nA_	Alignment	not modelled	8.9	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding stress response protein, dps family; **PDBTitle:** structure of d. radiodurans dps-1
87	d1xrda1	Alignment	not modelled	8.9	27	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
88	c1rb4C_	Alignment	not modelled	8.8	19	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
89	d1w2fa_	Alignment	not modelled	8.7	21	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**Inositol polyphosphate kinase (IPK)
90	c1unxB_	Alignment	not modelled	8.7	27	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
91	c1zy9A_	Alignment	not modelled	8.7	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-galactosidase; **PDBTitle:** crystal structure of alpha-galactosidase (ec 3.2.1.22) (melibiase)2 (tm1192) from thermotoga maritima at 2.34 a resolution
92	c1swiB_	Alignment	not modelled	8.6	19	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
93	c1rb4A_	Alignment	not modelled	8.6	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal automatic solution
94	c1swiC_	Alignment	not modelled	8.6	19	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4p1; **PDBTitle:** gcn4-leucine zipper core mutant as n16a complexed with2 benzene
95	c1l2aD_	Alignment	not modelled	8.6	43	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**cellobiohydrolase; **PDBTitle:** the crystal structure and catalytic mechanism of2 cellobiohydrolase cels, the major enzymatic component of3 the clostridium thermocellum cellulosome
96	d1l1ya_	Alignment	not modelled	8.6	43	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**Cellulases catalytic domain
97	c2ysxA_	Alignment	not modelled	8.5	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signaling inositol polyphosphate phosphatase **PDBTitle:** solution structure of the human ship sh2 domain
98	c3nfqA_	Alignment	not modelled	8.4	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor iws1; **PDBTitle:** crystal structure of the conserved central domain of yeast spn1/iws1
99	c1l6nA_	Alignment	not modelled	8.4	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**gag polyprotein; **PDBTitle:** structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein