Phyre^2

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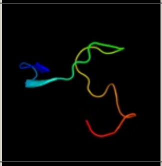
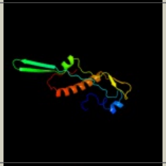
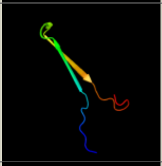
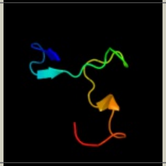
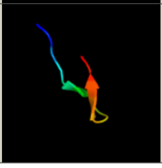
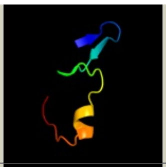
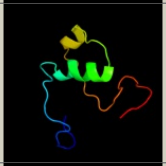
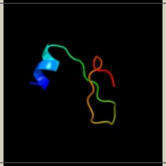
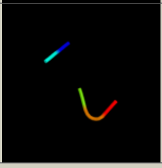
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oy7A_	Alignment		96.0	15	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer surface protein a; **PDBTitle:** the crystal structure of ospa mutant
2	c1n7dA_	Alignment		58.3	13	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** extracellular domain of the ldl receptor
3	d1adta1	Alignment		45.4	34	**Fold:**Domain of early E2A DNA-binding protein, ADDBP **Superfamily:**Domain of early E2A DNA-binding protein, ADDBP **Family:**Domain of early E2A DNA-binding protein, ADDBP
4	d1x3za1	Alignment		44.1	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
5	c3ib5A_	Alignment		41.3	18	**PDB header:**hormone **Chain:** A: **PDB Molecule:**sex pheromone precursor; **PDBTitle:** crystal structure of sex pheromone precursor (yp_536235.1)2 from lactobacillus salivarius subsp. salivarius ucc118 at3 1.35 a resolution
6	c2ivzD_	Alignment		37.7	13	**PDB header:**protein transport/hydrolase **Chain:** D: **PDB Molecule:**protein tolb; **PDBTitle:** structure of tolb in complex with a peptide of the colicin2 e9 t-domain
7	c3e5zA_	Alignment		26.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative gluconolactonase; **PDBTitle:** x-ray structure of the putative gluconolactonase in protein family2 pf08450. northeast structural genomics consortium target drr130.
8	c3mswA_	Alignment		25.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function (bf3112) from2 bacteroides fragilis nctc 9343 at 1.90 a resolution
9	c2w8bB_	Alignment		25.0	13	**PDB header:**protein transport/membrane protein **Chain:** B: **PDB Molecule:**protein tolb; **PDBTitle:** crystal structure of processed tolb in complex with pal
10	c3eswA_	Alignment		24.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
11	c3rwxA_	Alignment		24.6	21	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical bacterial outer membrane protein; **PDBTitle:** crystal structure of a hypothetical bacterial outer membrane protein2 (bf2706) from bacteroides fragilis nctc 9343 at 2.40 a resolution

12	d2f4ma1	Alignment		24.5	24	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
13	c1j5qB_	Alignment		22.5	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**major capsid protein; **PDBTitle:** the structure and evolution of the major capsid protein of a large,2 lipid-containing, dna virus.
14	d1ospo_	Alignment		22.1	17	**Fold:**open-sided beta-meander **Superfamily:**Outer surface protein **Family:**Outer surface protein
15	c2x12A_	Alignment		21.7	27	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimbriae-associated protein fap1; **PDBTitle:** ph-induced modulation of streptococcus parasanguinis2 adhesion by fap1 fimbriae
16	c3cbbA_	Alignment		19.7	18	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 4-alpha, dna binding **PDBTitle:** crystal structure of hepatocyte nuclear factor 4alpha in2 complex with dna: diabetes gene product
17	c3vh0C_	Alignment		19.0	9	**PDB header:**protein binding/dna **Chain:** C: **PDB Molecule:**uncharacterized protein ynce; **PDBTitle:** crystal structure of e. coli ynce complexed with dna
18	d1hraa_	Alignment		17.4	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
19	c2cokA_	Alignment		16.2	3	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of brct domain of poly(adp-ribose)2 polymerase-1
20	c1gibA_	Alignment		15.9	100	**PDB header:**neurotoxin **Chain:** A: **PDB Molecule:**mu-conotoxin giiib; **PDBTitle:** mu-conotoxin giiib, nmr
21	d1ss3a_	Alignment	not modelled	15.8	25	**Fold:**Toxic hairpin **Superfamily:**Pollen allergen ole e 6 **Family:**Pollen allergen ole e 6
22	c2vsaA_	Alignment	not modelled	15.8	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mosquitocidal toxin; **PDBTitle:** structure and mode of action of a mosquitocidal holotoxin
23	c2z48B_	Alignment	not modelled	15.4	20	**PDB header:**toxin **Chain:** B: **PDB Molecule:**hemolytic lectin cel-iii; **PDBTitle:** crystal structure of hemolytic lectin cel-iii complexed2 with galnac
24	d1bcoa1	Alignment	not modelled	15.0	17	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
25	c3ebqA_	Alignment	not modelled	14.9	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**molecule: pppde1 (permuted papain fold **PDBTitle:** crystal structure of human pppde1
26	d1ei5a1	Alignment	not modelled	14.9	32	**Fold:**Streptavidin-like **Superfamily:**D-aminopeptidase, middle and C-terminal domains **Family:**D-aminopeptidase, middle and C-terminal domains
27	c2envA_	Alignment	not modelled	14.1	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**peroxisome proliferator-activated receptor delta; **PDBTitle:** solution sturcture of the c4-type zinc finger domain from2 human peroxisome proliferator-activated receptor delta
28	c3bl9B_	Alignment	not modelled	14.1	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**scavenger mrna-decapping enzyme dcps; **PDBTitle:** synthetic gene encoded dcps bound to inhibitor dg157493

29	d1r0oa_	Alignment	not modelled	13.8	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
30	c3u4zB_	Alignment	not modelled	13.8	32	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**telomerase-associated protein 82; **PDBTitle:** crystal structure of the tetrahymena telomerase processivity factor2 teb1 ob-b
31	d1hcqa_	Alignment	not modelled	13.5	8	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
32	c2hwnF_	Alignment	not modelled	13.5	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**a kinase binding peptide; **PDBTitle:** crystal structure of rii alpha dimerization/docking domain of pka2 bound to the d-akap2 peptide
33	d2fs2a1	Alignment	not modelled	13.5	15	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**PaaI/YdiI-like
34	c1r4iA_	Alignment	not modelled	13.4	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**androgen receptor; **PDBTitle:** crystal structure of androgen receptor dna-binding domain2 bound to a direct repeat response element
35	d1r4ia_	Alignment	not modelled	13.4	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
36	c3bmxB_	Alignment	not modelled	13.4	42	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**uncharacterized lipoprotein ybbd; **PDBTitle:** beta-n-hexosaminidase (ybbd) from bacillus subtilis
37	d1r4ra_	Alignment	not modelled	13.3	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
38	d1o5ua_	Alignment	not modelled	13.2	8	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Hypothetical protein TM1112
39	c3cjhK_	Alignment	not modelled	13.2	50	**PDB header:**protein transport **Chain:** K: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** tim8-tim13 complex
40	d1lata_	Alignment	not modelled	13.1	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
41	c2eblA_	Alignment	not modelled	13.1	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**coup transcription factor 1; **PDBTitle:** solution structure of the zinc finger, c4-type domain of2 human coup transcription factor 1
42	c3jroA_	Alignment	not modelled	13.1	11	**PDB header:**transport protein, structural protein **Chain:** A: **PDB Molecule:**fusion protein of protein transport protein sec13 **PDBTitle:** nup84-nup145c-sec13 edge element of the npc lattice
43	c3swnA_	Alignment	not modelled	13.0	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u6 snrna-associated sm-like protein lsm5; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
44	d1r0na_	Alignment	not modelled	13.0	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
45	d2hanb1	Alignment	not modelled	13.0	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
46	d1pk6c_	Alignment	not modelled	12.9	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
47	d1glua_	Alignment	not modelled	12.8	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
48	c3dzuD_	Alignment	not modelled	12.8	18	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**peroxisome proliferator-activated receptor gamma; **PDBTitle:** intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with bvt.13, 9-cis retinoic acid and ncoa2 peptide
49	c2dg2D_	Alignment	not modelled	12.8	21	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**apolipoprotein a-i binding protein; **PDBTitle:** crystal structure of mouse apolipoprotein a-i binding2 protein
50	c3swnC_	Alignment	not modelled	12.8	13	**PDB header:**rna binding protein **Chain:** C: **PDB Molecule:**u6 snrna-associated sm-like protein lsm7; **PDBTitle:** structure of the lsm657 complex: an assembly intermediate of the lsm12 7 and lsm2 8 rings
51	d1dszb_	Alignment	not modelled	12.6	27	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
52	d1dsza_	Alignment	not modelled	12.5	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
53	c2bskD_	Alignment	not modelled	12.5	29	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the tim9 tim10 hexameric complex
54	c2ka3C_	Alignment	not modelled	12.5	36	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
						PDB header:viral protein

55	c2w2sA_	Alignment	not modelled	12.2	46	**Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** structure of the lagos bat virus matrix protein
56	d1brwa3	Alignment	not modelled	12.1	23	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
57	d1lo1a_	Alignment	not modelled	11.9	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
58	d1ynwa1	Alignment	not modelled	11.8	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
59	d1bcga_	Alignment	not modelled	11.7	38	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Long-chain scorpion toxins
60	d1kb6b_	Alignment	not modelled	11.7	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
61	c1xmlA_	Alignment	not modelled	11.6	17	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock-like protein 1; **PDBTitle:** structure of human dcps
62	d1pk6b_	Alignment	not modelled	11.6	27	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
63	c1t3dB_	Alignment	not modelled	11.5	32	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine acetyltransferase; **PDBTitle:** crystal structure of serine acetyltransferase from e.coli at 2.2a
64	d1a6ya_	Alignment	not modelled	11.4	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
65	d2tpta3	Alignment	not modelled	11.3	23	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
66	c2kx7A_	Alignment	not modelled	11.3	28	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sensor-like histidine kinase yojn; **PDBTitle:** solution structure of the e.coli rcsd-abl domain (residues 688-795)
67	d1pvza_	Alignment	not modelled	11.2	44	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
68	c3nzpA_	Alignment	not modelled	11.1	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
69	c3bp1A_	Alignment	not modelled	11.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph-dependent 7-cyano-7-deazaguanine reductase; **PDBTitle:** crystal structure of putative 7-cyano-7-deazaguanine2 reductase quef from vibrio cholerae o1 biovar eltor
70	c3dxrB_	Alignment	not modelled	11.0	29	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the yeast inter-membrane space2 chaperone assembly tim9.10
71	d2bskb1	Alignment	not modelled	11.0	29	**Fold:**Tim10-like **Superfamily:**Tim10-like **Family:**Tim10/DDP
72	d2nllb_	Alignment	not modelled	11.0	9	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
73	d1m3ya2	Alignment	not modelled	11.0	33	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Group II dsDNA viruses VP **Family:**Major capsid protein vp54
74	c2a66A_	Alignment	not modelled	10.9	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**orphan nuclear receptor nr5a2; **PDBTitle:** human liver receptor homologue dna-binding domain (hlrh-12 dbd) in complex with dsdna from the hcyp7a1 promoter
75	d2bska1	Alignment	not modelled	10.9	25	**Fold:**Tim10-like **Superfamily:**Tim10-like **Family:**Tim10/DDP
76	c2g9tT_	Alignment	not modelled	10.9	29	**PDB header:**viral protein **Chain:** T: **PDB Molecule:** **PDBTitle:** crystal structure of the sars coronavirus nsp10 at 2.1a
77	d1jofa_	Alignment	not modelled	10.8	13	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
78	c3dxrA_	Alignment	not modelled	10.7	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** crystal structure of the yeast inter-membrane space2 chaperone assembly tim9.10
79	c2hnbA_	Alignment	not modelled	10.7	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
80	d1xata_	Alignment	not modelled	10.5	26	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Galactoside acetyltransferase-like
						PDB header:transcription/dna

81	c1r0nB_	Alignment	not modelled	10.5	18	**Chain:** B: **PDB Molecule:**ecdysone receptor; **PDBTitle:** crystal structure of heterodimeric ecdsyone receptor dna2 binding complex
82	c1z7eC_	Alignment	not modelled	10.4	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
83	d1c3ha_	Alignment	not modelled	10.3	31	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
84	d2hana1	Alignment	not modelled	10.3	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
85	d1jnpa_	Alignment	not modelled	10.2	26	**Fold:**Oncogene products **Superfamily:**Oncogene products **Family:**Oncogene products
86	c3cjhJ_	Alignment	not modelled	10.2	38	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**mitochondrial import inner membrane translocase subunit **PDBTitle:** tim8-tim13 complex
87	d1f1sa3	Alignment	not modelled	10.1	18	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
88	d2nlla_	Alignment	not modelled	10.1	20	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
89	c3dzyA_	Alignment	not modelled	10.1	27	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**retinoic acid receptor rxr-alpha; **PDBTitle:** intact ppar gamma - rxr alpha nuclear receptor complex on dna bound2 with rosiglitazone, 9-cis retinoic acid and ncoa2 peptide
90	d1cita_	Alignment	not modelled	10.0	18	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
91	c2khbA_	Alignment	not modelled	9.9	30	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of linear kalata b1 (loop 6)
92	c1m4xC_	Alignment	not modelled	9.9	33	**PDB header:**virus **Chain:** C: **PDB Molecule:**pbcv-1 virus capsid; **PDBTitle:** pbcv-1 virus capsid, quasi-atomic model
93	c3cw1Z_	Alignment	not modelled	9.9	15	**PDB header:**splicing **Chain:** Z: **PDB Molecule:**small nuclear ribonucleoprotein f; **PDBTitle:** crystal structure of human spliceosomal u1 snrnp
94	d1w9pa2	Alignment	not modelled	9.8	18	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
95	d1t3da_	Alignment	not modelled	9.7	32	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**Serine acetyltransferase
96	c2e2wA_	Alignment	not modelled	9.7	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase 4; **PDBTitle:** solution structure of the first brct domain of human dna2 ligase iv
97	d2oqea2	Alignment	not modelled	9.7	25	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
98	c3fybA_	Alignment	not modelled	9.6	25	**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
99	c1i84V_	Alignment	not modelled	9.6	18	**PDB header:**contractile protein **Chain:** V: **PDB Molecule:**smooth muscle myosin heavy chain; **PDBTitle:** cryo-em structure of the heavy meromyosin subfragment of2 chicken gizzard smooth muscle myosin with regulatory light3 chain in the dephosphorylated state. only c alphas4 provided for regulatory light chain. only backbone atoms5 provided for s2 fragment.