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MAX-PLANCK-GESELLSCHAFT

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1617116

HHPR

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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

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New job

Resubmit

Resubmit_HMM

Resubmit/HHsenser

Realign

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HHpred - Results

Job-ID: 1617116

Date: 06:06 on Nov 08 2015

Help

Results

Histogram

Reduced alignment

Representative alignment

Full alignment

Create model

Merge Q/T alignments

Forward to PCoils

Forward MSA

Save

Export

Color alignments

☐ color only SS

☒ color alignments

☐ color alignments

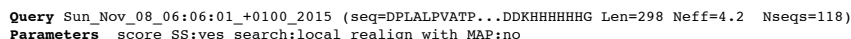
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Activate Jalview

13

252

Resubmit section



	No Hit		Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1	4xov_A	Rsgreen0.7; green fluor	100.0	2.2E-96	6E-101	681.9	32.8	238	13-252	33-270 (270)
2	2wur_A	Green fluorescent prote	100.0	5.2E-96	7E-101	670.5	32.2	236	15-252	1-236 (236)
3	4xgy_A	Green fluorescent prote	100.0	9.6E-95	2.7E-99	676.7	31.6	238	15-254	8-258 (303)
4	3vht_B	Green fluorescent prote	100.0	2.3E-91	6.4E-96	650.5	32.6	231	14-246	3-233 (271)
5	3ai4_A	Yeast enhanced green fl	100.0	5.5E-91	1.5E-95	648.9	32.5	228	15-244	4-231 (283)
6	4jrb_A	Green fluorescent prote	100.0	2E-88	5.6E-93	661.1	33.5	228	14-243	3-230 (313)
7	4u2v_B	Green fluorescent prote	100.0	2.7E-88	7.5E-93	640.5	32.4	227	15-243	4-230 (316)
8	2hpa_A	Green fluorescent prote	100.0	1.5E-87	4.1E-92	613.3	32.7	227	14-252	3-233 (233)
9	2jad_A	Yellow fluorescent prote	100.0	6.8E-86	1.9E-90	634.0	32.8	239	15-257	1-241 (362)
10	3ned_A	Pamcherry protein; RFP	100.0	7E-86	2E-90	604.9	32.3	220	19-252	18-242 (242)
11	4he4_A	Yellow fluorescent prot	100.0	3.6E-85	1E-89	601.2	32.8	232	16-259	2-239 (244)
12	4xb1_A	CLPB protein, putative,	100.0	9.4E-85	2.6E-89	627.3	32.2	225	19-245	154-378 (381)
13	3ai5_A	Yeast enhanced green fl	100.0	1.8E-84	5.1E-89	611.0	32.8	231	15-247	4-234 (307)
14	3ir8_A	Large stokes shift fluo	100.0	2.3E-84	6.5E-89	588.5	31.3	206	21-240	5-215 (221)

No 1       

[illegible][illegible][illegible]

11/7/2015 9:10 PM

[illegible]

>3ai4_A Yeast enhanced green fluorescent protein, DNA POL IOTA; UBM, ubiquitin-binding motif, GFP, fusion, fluorescent prote replication; HET: CR2; 1.60A {Aequorea victoria} PDB: 2kwu_A* 2ktf_B* 210g_A*
 Probab=100.00 E-value=5.5e-91 Score=648.89 Aligned cols=228 Identities=98% Similarity=1.494 Sum_probs=0.0

[illegible]

No 6      

>4jrb_A Green fluorescent protein, major allergen BLA G 1; asthma, NEW fold, proposed lipid binding protein, binding protein; HET: CR2 PGT D12; 2.41A [Aequorea victoria].
Probab=100.00 E-value=2e-88 Score=661.07 Aligned_cols=228 Identities=98% Similarity=1.489 Sum_probs=0.0

[illegible]

No 7    

>4u2v_b Green fluorescent protein,BCL-2 homologous antagonist/killer; apoptosis, BAK; HET: CR2 MPD; 2.30A [Aequorea victoria] PDB: 4bdu_A*

[illegible]

Q ss_pred		hcce	
Q Sun_Nov_08_06:	253	SGLSR	257 (298)
Q Consensus	253		257 (298)
		+++	
T Consensus	237		241 (362)
T 2jad_A	237	SGSGS	241 (362)
T ss_dssp		CCCC-	
T ss_pred		ccccc	



>3ned_A Pamcherry1 protein; RFP; beta barrel, fluorescent protein; HET: NRQ CH6 EYG; 0.95A {Discosoma SP} SCOP: d.22.1.1 PDB: 3kcs_A* 3kct_A* 3kf3_A* 3nez_A* 2h5q_A* 2h5o_A* 2h5p_A* 2h5r_A* 3nf0_A* 4q7r_A* 4h3l_A* 4h3m_A* 4h3n_A* 2ql1_A* 4q7u_A* 2qlg_A* 2qlh_A* 4kfd_A* 2vad_A* ...
 Probab=100.0 E-value=7e-86 Score=604.88 Aligned_cols=220 Identities=28% Similarity=0.542 Sum_probs=0.0

[illegible][illegible][illegible]

>**4he4_A** Yellow fluorescent protein; phiyfp, mutant variant of phiyfp Tyr-Gly chromophore, beta-barrel, biomarker, Thr-Tyr-Gly BI chromophore; HET: CRO; 2.05Å [Phalidius sp] SCOP: [d.22.1.0](#)
 Probab=100.0 E-value=3.6e-85 Score=601.21 Aligned cols=232 Identities=49% Similarity=0.845 Sum probs=0.0

[illegible][illegible][illegible]

Q ss_pred		hhhhcceecc	
Q Sun_Nov_08_06:	250	LYKSGRLSYD	259 (298)
Q Consensus	250		259 (298)
		++. - =	
T Consensus	230		239 (244)
T 4he4_A	230	TYDFDAGSGD	239 (244)
T ss_dssp		HTC-----	
T ss_pred		heeeccCCcC	



4xibi_A CLPB protein, putative, green fluorescent protein; CLP chaperone, AAA+ ATPase, refoldase, protein metabolism; HET: CRO; 2.01Å (Plasmodium falciparum)
Probab=100.0 E-value=9.4e-85 Score=627.25 Aligned_cols=225 Identities=95% Similarity=1.437 Sum_probs=0.0

```

Q ss_pred          hhhccCCcEEEEEeEEcCCCEEEEEEEcCCCCCHHHhhhcccccccCCCCCchhhh
Q Sun_Nov_08_06:  19  EELFTGVPVILVELDGDVGNGHKFVSAGEGDATYGLTKLFKICTTGKLPWPWLTVTTFYGVQCFSRYPDHMKRHDF 98 (298)
Q Consensus        19  ---k---meG-VNQH-F-I-GeG-G-q-k-vt-GpLFFS-dILs--f-YG-r-fITsY--I---DyF 98 (298)
                  +++|++|.++++|+||+||+|+|+|+|+++|+|+|||||++++| ||||+|-|++|+|+|
T Consensus        154  ---l-m---m-l-g-Vng-f---g-g-g-g-lpf-----f-yp-----d-f 231 (381)
T 4xibi_A          154  EELFTGVPVILVELDGDVGNGHKFVSAGEGDATNGKTLTKFKICTTGKLPWPWLTVTTL---XVQCFSRYPDHMKRHDF 231 (381)
T ss_dssp          cGGGSSEEEEEEEETTTEEEEEEEEGGTTEEEEEEECTTCSSSCGGGGTTTC---CGGSGSGGGGGGCHH
T ss_pred          cgggcceeeeeeccccccEEEEEccccCCCCCEEEEEEEcCCCCCHHHhhh----ccccccCCCCCcChH

Q ss_pred          HhhCCCcEEEEEeEcCCcEEFEeEEeEeCCCCCCCCccccccccCcCeEEecCCCCcCEEEe
Q Sun_Nov_08_06:  99  KSAMPEGYQERTIFPKDDGNLYKTRAEVKFGDTLVNRIELKGIDFKEDGNLLGHYLNINSHNVIMADQKNQIKVN 178 (298)
Q Consensus        99  KqsfPeGYswErT---PEDGv-t-----itleg-c-----v---G-nFP-dGPMAqktt-----e-----d---gi-g- 178 (298)
                  ||||||+|+|+|+|+|+|+|++++|+|++|+++|+|+|+|+|+|++|. |+|+|+|+++|++++++|+
T Consensus        232  k---p-g---r---Fed-g-----g-f---gpvm-----l--- 311 (381)
T 4xibi_A          99  KSAMPEGYQERTISFKDDGYTYKTRAEVKFGDTLVNRIELKGIDFKEDGNLLGHYLNINSHNVITADQNKGNIKAN 311 (381)
T ss_dssp          HHHTTTCEEEEEEEETTTEEEEEEEECTTCSSSTTSCTTSCBCSCCEEEEEEEGGGTTEEEe
T ss_pred          HhhCCCcEEEEEeEcCCcEEFEeEEeEeCCCCCCCCccccEEeCCcCcEEeccccCCcCEEEe

Q ss_pred          EEEEEEEcCCCCEEEEEEccCCcCCCCcCCCCEEEEEEeEcCCcCcCEEEEEEEecccc
Q Sun_Nov_08_06:  179  FKIRHNIEDGSQLADHYQQNTIGDGVLPLPDNHYLSTQSALSKDNPNEKRDMHVLEFVTAAGITH 245 (298)
Q Consensus        179  -----l-l-dGg---T-yk-kkPi-----v-mP-Hfi-----skD-E-rDhl--vE-A---A 245 (298)
                  ++|+++|+|+++|+|++++|++++|+|++|++|++|++|++|++|++|++|++|++|++|+|
T Consensus        312  -----g-----p-----p-h-----kd-e--dhI---E-a---A--- 378 (381)
T 4xibi_A          312  FKIRHNVEDGSVQLADHYQQNTIGDGVLPLPDNHYLSTQSVLSKDNPNEKRDMHVLEFVTAAGITL 378 (381)
T ss_dssp          EEEEEEBTTSCEEEEEEEEEESSSSCCCCCSCEEEEEEEECCTTCSSCEEEEEEEEECCCC
T ss_pred          EEEEEECcCCCCEEEEEEccccCCCCCCCCCEEEEEEEcCCCCCcCeEEEEEccccCccc

```

















No 13      

[illegible]

No 14

[illegible]

T 3ir8_A 157 DYMAIKLKGGGHYLCFCKSTYKAKK-----PVRMPGRHEIDRKLDVTSN-NRDYSVTEVQCEIATA 215 (221)
T ss_dssp EEEEEETCCCEEEEEEEEEEESS-----CCCCCCEEEEEEEEEEE-CTTSSEEEEEEEEEE
T ss_pred EEEEEETCCCEEEEEEEeeccCC-----CCCCCCEEEEEEEEEeecc-CCCCCEEEEEEEEE

No 15                 

>**3gb3_A** Killerred; fluorescent protein, genetically encoded photosensitizer, phototoxicity; HET: CRQ; 1.75Å
 (Anthemusdusa SP) SCOP: d.22.1.0 PDB: 3gl4_A* 4b30_A* 2wiq_A* 2wis_A* 3a8s_A*
 Probab=100.0 E-value=3.6e-84 Score=591.46 Aligned_cols=218 Identities=26% Similarity=0.548 Sum_probs=0.0

```

Q ssn_pred      cccchhhcccEEEEEHEEECCCEEEEEEEEEECCcCEEEEEECCCCCCCCHHHHhhhhccccccccccccCCCCC
Q Sun_Nov_08_06: 15 VSKGELEGTGVPLVLDGVNGHGFSGEGGATYGLFKCTGGLVPLVPTVLTFTTGYGCSFRSPYDHKMR 94 (298)
Q Consensus      15 -G--mEg-VNcH-F-IGeG-P-eG-q-k-vt-GPLPFS-dILs-f-YG-r-FtkYp-I-- 94 (298)
T Consensus      1 m-G--mEg-VNcH-F-IGeG-P-eG-q-k-l-vt-GPLPFS-dILs-f-r-FkYP-I-- 76 (235)
T 3gb3_A          1 MEGGPALFQSDMTKIFIDGVEQKFTIVADGSKFPGDGFNVHAVCTGKLPMSKICHLIX-EPFFARYPDGI 76 (235)
T ss_dssp         -CCSTTGGGGSCEEEEEEEETTEEEEEEEETCTTSCSEEEEEETTSSSSSCGGGGTTTC--CGGSGBCSTTS
T ss_dsp          cccchhhcccEEEEEHEEECCCEEEEEEEEEECCCCCEEEEEECCCCCCCCHHHHhhhhccccccccccccCCCCC

```

[illegible]

Q	ss_pred		eEEEEEEEEEeCCCCeEEEEEEcccccCcCCcCCCCcEEEEEEeeEeCccCCCcEEEEEEEEE		
Q	Sun_Nov_08_06:	174	GKYNFGRHRIHNIDGSGVLADHYQQONT-IGCGVLDLNDNHLYSLKQSALDKPEKKRDHMVLEFVTA	240	(298)
Q	Consensus	174	gi-g-l-dGg-T-yk-kKP-i-v-mP-Hfi-sKD-E-rDhi-vE-A	240	(298)
			+ + ++ + + + + +++++++ +++++ + + + + + + + + + + + + + + + +		
T	Consensus		-L-g-f-l-L-Gg-f-f-yakk-v-mP-hfv-hrl--v-L-E-a-	220	(235)
T	3gb3_A	155	RQLRAF-IGFTTGGGLMM-GHFDskMTFNRSRAIEPGPHVITLTQRMRDTSdkRDHVCRGVAYA	220	(235)
T	ss_dssp		EEEEEE-EEEEETTCSEEE-EEEEEEEEECSSSCCCCCCEEEEEEEERCCTTCSSEEEEEEEEEE		
T	ss_pred		EEEEEE-EEEEEECCcEE-EEEEccccccccCCCCCCCCcEEEEEEEEE		

No 16                             

▶ **4q9w_A** GFP-like fluorescent chromoprotein CFP484; beta barrel, fluorescent protein, artificial metalloenzyme, metalloenzyme, biocojugation; HET: PIA; 1.00Å {Clavularia SP} SCOP: d.22.1.0 PDB: 4q9w_A* 2hqk_A* 4r6d_A* 2ote_A* 2otb_A* 4dxi_A* 4dxo_A* 4j2c_A* 4dpx_A* 4gob_A* 4dxq_A* 4dxn_A* 2vzx_A* 3adf_A* 2g
 Probab=100.00 E-value=1e-83 Score=583.41 Aligned_cols=206 Identities=28% Similarity=0.566 Sum_probs=0.0

[illegible][illegible][illegible]

No 17       

▶ **3wck_A** Monomeric photosensitizing fluorescent protein SUP; GFP fold, genetically encoded photosens phototoxicity;
 HET: CRQ; 2.30A [Synthetic construct]
 Probab=100.0 E-value=8.8e-84 Score=597.92 Aligned_cols=219 Identities=25% Similarity=0.514 Sum_probs=0.0

[illegible]

```
Q ss_pred          chhhHhhhCCcCeEEEEEEccCcEeeEeEeeeCCEEEEEEeEEeeCCCCCccccccc--ccCCCceEeecccccC
Q Sun_Nov_08_06:   94 RHDFPKSAMPgGVQERTFFKDDGNGYKTRAEVKGFTLVNRIELKGDIFKEDGNLGHKL-EYNYNSHNvYIIMADKKQ
Q Consensus        -DyFYKqSPFeGYswert- FEDGEgv-t-isleg-v-G-nFP-dGPVMgkkt-
                   +|+|+|+|+|+|+|+|+|++++++||+|+|+++|+|+|+|+|+|+|+.+|+|+|+|-p-++
T Consensus        113 -DyFYKqSPFeGYswert- FEDGEgv-t-isleg-v-G-nFP-dGPVMgkkt-wePS-E-p--d-++
T 3wck_A           113 -SHfAQCPTPEGLSLIDRTVFENDGTTHSHYTBLDDTCVVSRITVNCDFGGPDPGRIMRDQLVDLPSTHMHPgh-PNI
T ss_dssp          -CCNNHHHCCTTTTEEEEEEEETECBEEEEEEEEETECBEEEEEEEEESCTTSSTTTTTTEEBECCEEEEEEECS--
```

T ss_pred -CCHHHhCCCCeEEEEEECCcEEEEEEEECCEEEEEEEECCCCCchhhccccCCCCeEEEEEEcc--CC

Q ss_pred CeEEEEEEEEeCCCCEEEEEEcc--CcCCcCCCCEEEEEEeEcCccCCcEEEEEEEE

Q Sun_Nov_08_06: 173 NGIKVNFKIRHNIEDGVSQADHYQONT-IGDGPVLLPDNHYLSTQSALSKDPNEKRDHMLVLEFVTA 240 (298)



Q Consensus 173 -gi-g-----l-l-dGg-----T-yk-kkP-i-----v-mP--Hfi-----sKD--E-rDhi--vE--A 240 (298)

T Consensus 190 g-L-g-----l-l-dGg-----fkt-y-akk-v-mP--HFv-hrl-----e--v-l-E-a-A 256 (271)

T 2lcr_A 190 AVROTAT-IGFTTADGGKMM-GHFDKMTFNGSRAIEIPGPHFVTITKQTRDTSKRDHVCQREYAYA 256 (271)

T ss_dssp EEEEEEE-EEEEETTSCEEE-EEEEEEEEECSSCCCCCCEEEEEEEEC-----CEEEEEEEEE

T ss_pred CEEEEEE-EEEEeCCCCEE-EEEEeccccccccCCCCCCEEEEEEEEcCccCCCCCEEEEEEE

No 18    SCOPe PDB PROTEIN DATA BANK  NCBI  PubMed

>2lcr_A RED fluorescent protein ZOANRFP; ZRFP574, chromophore structure, Cys-Phe LINK; HET: XYG; 1.51A {Zoanthus SP} SCOP: d.22.1.0 PDB: 2fl1_A* 2ojk_A* 2pxs_A* 2pxw_A* 1xa9_A* 2ogr_A* 1xae_A* Probab=100.00 E-value=1.3e-83 Score=587.97 Aligned_cols=211 Identities=22% Similarity=0.445 Sum_probs=0.0

Q ss_pred hhhccCCcEEEEEEEECCEEEEEEEEeCCcCeEEEEEEc-CCCCCHHHHHhhhhccccccccCCCCCchhh

Q Sun_Nov_08_06: 19 EELFTGVVPIVLVDGDNVGHKFSVSGEGDATYGLTKFICTT-GKLPVPWPTLVTTFTYGVQCFSTRYPDHMKRHD 97 (298)

Q Consensus 19 -----m-k--meG-VNCh-F-I-GeG-G-p-eG-q--k--vt--GpLPFS-dILs--f-YG-r-FtkYP--I--Dy 97 (298)

T Consensus 13 -----M--k--meG-VNCh-F-I-GeG-G-p-eG-q--kl-vtkGpLPFS-dILs--f--G-r-P-kYP--i--dy 88 (237)

T 2lcr_A 13 AHGLTDDMTMHRMGCVGDKHGVIEGNGNMPFKGQFINLCVIEGGPLPFSIDLSAAF--XNRLFTEYPEGI--VDY 88 (237)

T ss_dssp CTTCCSSEEEEEETTSCEEEEEEETTTTEEEEEEEEGGGTTEEEEEEEESCSCSSCGGGGGGCG--CTTSCBCCTTS--CCH

T ss_pred hhhcCCCCeEEEEEEEECCEEEEEEEEeCCCCEEEEEEcCCcCCCCCHHHHHhh--ccccccccCCCC--chh

Q ss_pred HHHhCCcCeEEEEEEcCCcEEEEEEeEe--eCEEEEEEEeCCCCCCCCcccc--ccCCcCeEeccccCCCCe

Q Sun_Nov_08_06: 98 FKSAMPEGVQERTIFFKDDGNKYTRAEVKF--EGDTLVNRIELKIDFKEDGNILGHKL--EYNYNHNVYIMADKQKNG 174 (298)

Q Consensus 98 FKqsfPeGYswert--FEDGGv-t-----itl-eg-c-----v--G-nFP-dGPMqkkt--e-----d-----g 174 (298)

T Consensus 89 FK-sfPeGys-eRt--FEDGGv-t-----isl-eg-----v--G-nFP-dGPMqkkt--wePs--E--yp-----dg- 166 (237)

T 2lcr_A 89 FKNSCPAGYTWHRSFREDGAVCISADITVNVRENCYHSTFYGVNFPADGPMKMTTNPECEKILPIN--SQKI 166 (237)

T ss_dssp HHHHTTTCEEEEEEEETTSCEEEEEEEETTTTEEEEEEEECCTTSTTTTTCCEEEECCEEEEEEEET--TTTE

T ss_pred HHHhCCcCeEEEEEEcCCcEEEEEEEEeCEEEEEEEEECCCCCCCCccccCCCCcCeEEEEEEc--CCCE

Q ss_pred EEEEEEEEECCCCe---EEEEEEccccCccc--CCCCCEEEEEEEeBecCccCceEEEEEEEE

Q Sun_Nov_08_06: 175 IGVNFKIRHNIEDGVS---QLADHYQONTPIGDGP-VLLPDNHYLSTQSALSKDPNEKRDHMLVLEFVTA 240 (298)

Q Consensus 175 i-g-----l-l-dGg-----T-yk-kkPi-----v-mP--Hfi-----sKD--E-rDhi--vE--A 240 (298)

T Consensus 167 L-g-----l-l-Gg-y-----T-y-akk-----v-mP--HFv-rie-----v-l-E-a-A 231 (237)

T 2lcr_A 167 LKGDVSMYLLKDKGRYRCQFDITYIAKT-----EPKEMPWHFIQHKLNREDRSDAKNQKQLEHAIA 231 (237)

T ss_dssp EEEEEEEEEETTSCEEEEEEEEEESS-----CCSSCCCCEEEEEEEECCCCSSCCEEEEEEE

T ss_pred EEEEEEEEECCCCEEEEEEeccccCC-----ccccCCCCEEEEEEEEcCccCCCCCEEEEEEE

No 19    SCOPe PDB PROTEIN DATA BANK  NCBI  PubMed

>2rh7_A Green fluorescent protein; HET: CRO; 1.50A {Renilla reniformis} SCOP: d.22.1.1 Probab=100.00 E-value=1e-83 Score=589.46 Aligned_cols=212 Identities=22% Similarity=0.461 Sum_probs=0.0

Q ss_pred cccchhhccCCcEEEEEEEECCEEEEEEEEeCCcCeEEEEEEc-CCCCCHHHHHhhhhccccccccCCCCC

Q Sun_Nov_08_06: 15 VSKGEELFTGVVPIVLVDGDNVGHKFSVSGEGDATYGLTKFICTTG-KLPVPWPTLVTTFTYGVQCFSTRYPDHMK 93 (298)

Q Consensus 15 ---G---m-k--meG-VNCh-F-I-GeG-G-p-eG-q--k--vt--GpLPFS-dILs--f-YG-r-FtkYP--I-- 93 (298)

T Consensus 1 -----M--k--meG-VNCh-F-I-GeG-G-p-eG-q--kl-vtkGpLPFS-dILs--f--G-r-P-kYP--i-- 77 (239)

T 2rh7_A 1 MDLAKLGLKEVMPKINLEGLVDGAFSMGVGEGNILEGTQEVKISVTKGAPLPFAFDIVSVAF--XNRYATGYPEEI- 77 (239)

T ss_dssp -----CCSSEEEEEEEETTSCEEEEEEEEEETTTTEEEEEEEESCSCSSCGGGGTTTC--CTTSCBCCTTS-

T ss_pred CcchhhCCCCeEEEEEEEECCEEEEEEEEeCCCCEEEEEEcCCCCCCCCCHHHHHhh--ccccccccCCCC-

Q ss_pred chhhHHhCCcCeEEEEEEcCCcEEEEEEeEeCEEEEEEEeCCCCCCCCcccc--ccCCcCeEeccccCCC

Q Sun_Nov_08_06: 94 RHDFPKSAMPEGVQERTIFFKDDGNKYTRAEVKFGDTLVNRIELKIDFKEDGNILGHKL--EYNYNHNVYIMADKQK 172 (298)

Q Consensus 94 --DyFKqsfPeGYswert--FEDGGv-t-----itleg-c-----v--G-nFP-dGPMqkkt--e-----d--- 172 (298)

T Consensus 78 --DyFK-sfPeGys-eRt--FEDGGv-t-----isleg-----v--G-nFP-dGPMqkkt--wePs--E--p-----d 152 (239)

T 2rh7_A 78 --SDYFLQSPFGFTYRNIRYQDGGTAIVKSDISLEDGKFINVDVFKAKDLRRMGPMQDILVMQPMYSYSMT--NV 152 (239)

T ss_dssp -CCTTGGGTTTCEEEEEEEETTSCEEEEEEEEEECCEEEEEEEEECCCTTSTTTTTCCEEEECCEEEEEEE-----ET

T ss_pred -chHHHHcCCcCeEEEEEEcCCcEEEEEEEEeCEEEEEEEEECCCCCceCccccCCCCeEEEEc-----C

Q ss_pred CeEEEEEEEECCCCe---EEEEEEccccCccc--CCCCCEEEEEEEeBecCccCceEEEEEEEE

Q Sun_Nov_08_06: 173 NGIKVNFKIRHNIEDGVS---QLADHYQONTPIGDGP-VLLPDNHYLSTQSALSKDPNEKRDHMLVLEFVTA 240 (298)


Q Consensus 173 -gi-g-----l-l-dGg-----T-yk-kkPi-----v-mP--Hfi-----sKD--E-rDhi--vE--A 240 (298)

T Consensus 153 g-L-g-----l-l-Gg-y-----T-y--kk-----v--LP--HFv-rie-----v-E-a-A 218 (239)

T 2rh7_A 153 TSVIGECIIAFKLTGKHFTHYHMRVYKSKK-----PVETMPLYHFIQHRLVKTNV-DTASGVYVQHETAIA 218 (239)

T ss_dssp TEEEEEEEEEEETTSCEEEEEEEEEESS-----CCSSCCCCEEEEEEEEEEEC-----CEEEEEEE

T ss_pred CEEEEEEEEEECCCCEEEEEEeccccCC-----chhhCCCCEEEEEEEEeC-CCCCCEEEEEEE

No 20    SCOPe PDB PROTEIN DATA BANK  NCBI  PubMed

>4ohs_A FAR-RED fluorescent protein Aq143; beta barrel, RFP, fluoresc protein; HET: CH6 NRQ; 2.19A {Actinia equina} SCOP: d.22.1.0 Probab=100.00 E-value=3.7e-83 Score=585.39 Aligned_cols=208 Identities=25% Similarity=0.452 Sum_probs=0.0

Q ss_pred chhhccCCcEEEEEEEECCEEEEEEEEeCCcCeEEEEEEc-CCCCCHHHHHhhhhccccccccCCCCCchh

Q Sun_Nov_08_06: 18 GEELFTGVVPIVLVDGDNVGHKFSVSGEGDATYGLTKFICTTG-KLPVPWPTLVTTFTYGVQCFSTRYPDHMKRHD 96 (298)

Q Consensus 18 G-----m-k--meG-VNCh-F-I-GeG-G-p-eG-q--k--vt--GpLPFS-dILs--f-YG-r-FtkYP--I--D 96 (298)

T Consensus 10 -----m--k--meG-VNCh-F-I-GeG-G-p-eG-q--kl-vtkGpLPFS-dILs--f--r-F-kYP--i--d 85 (237)

T 4ohs_A 10 GAPLVTEDMCKMTMEGTINGHHFKCVGEGKPFEGTQVEKIRITEGGLPFPAYDILAPCCX--SKFTKIHVSGI--PD 85 (237)







T ss_dssp CCCCCSSSEEEEEEEEEETTSCEEEEEEEEEETTTTEEEEEEEESCSCSSCGGGTGGCG--CTTSCBCTTC--CC

T ss_pred chhhcCCcCeEEEEEEEECCEEEEEEEEeCCCCEEEEEEcCCcCCCCCHHHHHhh--ccccccccCCCC--CC

Q ss_pred hHHHHCCcCeEEEEEEcCCcEEEEEEeEeCEEEEEEEeCCCCCCCCcccc--ccCCcCeEeccccCCCCe

Q ss_pred hccCCcEEEEEEECCEEEEEEEcCCcEEEEEEC-CCCCHHHHhhcccccECCCCCChhhhH
Q Sun_Nov_08_06 21 LFTGVPLDGVGHGSGEGEDATYGLTKLITCTG-KLPVWPPLVITFTYGVQCFSPYDHHRRKDF 99 (298)
Q Consensus 21 LFTGVPLDGVGHGSGEGEDATYGLTKLITCTG-KLPVWPPLVITFTYGVQCFSPYDHHRRKDF 99 (298)

		+ +++ ++++ + + + + + + ++ + +	
T Consensus	3	----m-k-meG-VNGH-F-i-G-G-G-p-e-q--kl-vtkg-plPPFs-dILs-f--r-F-KYP-i-+-dyFK	78 (223)
T 2c9j_A	3	QLDNNLSKSVKMGNVNGNVNHYBDGGDGPNSSGQSLTKLRGKGGLITMTGFX--FRAFTKYPEGI--ADYFK	78 (223)
T ss_dssp		-----CEEHEEEEEEETTEEEEEEEEEETTTTTEEEEEESSSSSCSSCGGGTTCCTTCTSCBCCTTS--CCTTG	
T ss_pred		cCCCCeEEEEEEEEEeCCCCEEEEEEECCECCCHHHhhcc--ceecCCCCc--CCHH	
Q ss_pred		hhCCCCeEEEEEEcCcCEEEeeEeeeCEEEeeEEEECCCCCCCCccccccc--cCCCeEEeccccCCCCeEEEE	
Q Sun_Nov_08_06:	100	SAMPEGVQERTTFKFDGGNYKTAEVKFGEDTLVNRIELKGDIFKDDNGILHGK--EYNYSNVIMADQKRNKIKYK	178 (298)
Q Consensus	100	qsfpPeGSyweRt--FEDGGv-t-----itleg-c---v--G-nFP-dGPVMqkkt-----e-----d-gi-q-	178 (298)
		+ +	
T Consensus	79	-sfpeGSy-eRt--FEDGGv-t-isleg-----v--G-nFP-dGPVMqkkt--weps-e--p---dg-L-g	154 (223)
T 2c9j_A	79	GSPFPAFWNRRLIEFDGGVINMSSDIYTKDKVLHGDFVWALGVNPFPGPVKNKEIWMVEPABETLTA-----KINGVLGF	154 (223)
T ss_dssp		GGTTTTTTCSEEEEEEEETTSEEEEEEEEETTCTGTATTTTTEEEEEECEEEEE-----ETTEEEEE	
T ss_pred		HhCCCCeEEEEEEcCcCEEEEEEEEEECCEEEEEEEEECCCCCccccccccCCCCEEEEe-----cCCCCEEEEE	
Q ss_pred		EEEEEEcCCCC---EEEEEEcccCccc--cCCCCEEEEEEeeEcCccCceEEEEEEEE	
Q Sun_Nov_08_06:	179	FKIRHNIEDSGS---QLADHYQNTPIKDGP-VLLDPNHISLTQSALSCKDPNKRRDHVILEVFVA	240 (298)
Q Consensus	179	--l-l-dgg-----T-yk-kkPI-----v-m-P-Hfi-----sKD-E-rdhvi-vE-A	240 (298)
		++ +	
T Consensus	155	--l-l-Gg-Y--T-y-ak-----vg-P-HFVrlvkv-----v-----E-a-A	214 (223)
T 2c9j_A	155	CPKAYLLKDGSYYYGHMTTFYRSKK-----SGQPLPFGFKHRLVKTKV-KPQGMVQEAYATA	214 (223)
T ss_dssp		EEEEEEETTSCEEEEEEEEEESS-----TTCCCESSEEEEEEEEEE--CGGSSEEEEEEEEEE	
T ss_pred		EEEEEEcCCCCEEEEEEEeeccc-----ccccCCCCEEEEEEEEEEc--CCCCEEEEEEEEE	

No 24    SCOPe   

>2a46_A GFP-like fluorescent chromoprotein AMFP486; beta barrel, luminescent protein; HET: CR7; 1.65A {Anemonia majano} SCOP: d.22.1.0 PDB: 2a48_A* 2a47_A*
Probab=100.00 E-value=9.2e-83 Score=582.92 Aligned_cols=206 Identities=27% Similarity=0.508 Sum_probs=0.0







```

Q ss_pred          hccCCcEEEEEEEEEECCcEEEEEEEEEEccCCcEcE-EEEEEEcC-CCCCCCHHHHHhhhhcccccCCcCCcCHhhh
Q Sun_Nov_08_06:  21 LTGTGVVPLVLDGVGDMGCGCGCGADATYKGLTLKLFCTTCKGLKLPVWPLVHTTGVGCGFYDFYDKHMRHDF 97 (298)
Q Consensus       21 +-----m-k-meg-VGNH-F-I-GeG-G-p-e-q-k-v-t-GpLPFS-dILs-f-YG-r-FtKYp-I-----+ 97 (298)
                  ++++++-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
T Consensus       18 -----M-k-meg-VGNH-F-I-GeG-G-p-e-q-k-v-klvtGgplPFS-dILs-f-YG-r-FtKYp-I-----+ 93 (238)
T 2a46_A          18 FTGDDMKTmHGCGVGNHGYFVtGCGNGKPYEGTGTSTFKVtMANGGLPAFSDILstfV-NRcRFTAYPTSM--PDY
T ss_dssp         TSCSSCEEEEEEEEEETTEEEEEEEEEEEEEETTEEEEEEEEEEEtCCSCCSCCTHHHHTTCT--CTTSSBCTCT--CCT
T ss_pred         hCCcCCcEEEEEEEEEEcCCEEEEEEEEEccCCCCcEEEEEEEEtCCcCCcCCCCHHHHHHhhhh-cccccccCCCCc---cH

```

[illegible]

Q	ss_pred		EEEEEEEEECCCCC-----EEEEEEccccCcCCCcCCCCCEEEEEEEeEcCccCcccEEEEEeEee	
Q	Sun_Nov_08_06:	177	VNFIRKHNIDGDSV--GLADHYQQNPITPIDGGFLPNNHLYSTQSALSKDKNPKRDLHMVEELFVTVA	240 (298)
Q	Consensus	177	g-+--+l-l-dgg-+T-yk-kkPi-v-mP-Hfi-sKD-E-RDhi-vE-+	240 (298)
T	Consensus	177	++++ ++ +++ + + ++++ ++++ +. .+-	
T	2a46_A	170	g-+--+l-l-Gg-gy-T-yakk-V-mP-Hfv-rie-vl-E-a+	230 (238)
T	2a46_A	170	GDTVFRLMLGGGNRYRCQFTSYKTKK---PVMPPNHYVEHRIARTDL-DKGNSGVQLTEPHAHA	230 (238)
T	ss_dssp		EEEEEEEEEETTSEEEEEEEEEEESS-----CCCCCSEEEEEEEEEEEC-STTSCSEEEEEEEEE	
T	ss_pred		EEEEEEEEECCCCC-----EEEEEEeEecCC-CccCCCCCEEEEEEEeEc-cCCCCCEEEEEEE	

No 25    SCOPe   
 >3cg1_A GFP-like fluorescent chromoprotein DSFP483; beta barrel, chromophore, luminescence, photoprotein, fluore
 protein; HET: CRQ; 2.09Å [Discosoma striata] SCOP: [d.22.1.1](#)
 Probab=100.00 E-value=1.2e-82 Score=582.93 Aligned cols=212 Identities=24% Similarity=0.500 Sum probs=0.0

[illegible][illegible][illegible]

No 26        

```

Q ss_pred          CCCCCCHHHHHHhhcccceeccccCCCCChhHHhhCCceEEEEEEeeCCEEEeeEeeCCEEEeeEEeeC
Q Sun_Nov_08_06:  64 TGKLPVPMPLTTTTFYGVGQFSRYPDHKRRDFFKSAMPBGVQERTIFFDGNYKTRAEVKFGDTLVNRIELKGD 143 (298)
Q Consensus       64 -GLPFS-dLS--f-YG-R-FtkYP--I--DyFKqsfePGYswert--FEDGGV-t--ileg-c--v--v--Gn 143 (298)
























```

No 31                       

Probab=100.00 E-value=3.1e-82 Score=582.16 Aligned_cols=208 Identities=26% Similarity=0.559 Sum_probs=0.0
























[illegible][illegible]

Q ss_pred		EEEEEEEEECCCCC-----EEEEEEEEEcccCcCCcCCCCCEEEEEEEeeEccCccCccCEEEEEEEeE	
Q sun_Nov_08_06:	177	VNFKRHHNIEDGSGV--QLADYQQNTPIGDGPVLPLLDNYHLSLQASLKSDPKRKHDMVLLFVTA	240 (298)
Q Consensus	177	[---]l-l dGG- T-yk-kkP[---]v-mP-Hfi-skD-E-rDhi--VE--A [+++][+][+][+][++ ++][+][+][+][+][+][+][+][+][+][+]	240 (298)
T Consensus	157	[---]l-l dGG-gyT-yakk-[---]v-mP-Hfv-rie[---]v-l-E-a-A	217 (249)
T t4za_c	157	GDVMALLLEGGHYRDFTKTYKAKK-DVRLPDHFVDHRIELILSH-DKDYNVKRVLYEHAEAA	217 (249)
T ss_dssp		EEEEEEEEETTSSEEEEEEEEEESS-----CCCCCEEEEEEEEEEEETTSSEEEEEEEEEEE	
T ss_psp		EEEEEEEEECCCCEEEEEEEEEccccc-----CccCCCCEEEEEEEEEEec-cCCCCEEEEEEEEEE	

No 32                       

[illegible][illegible]

Q	ss_nov	EEEEEEEEECCCCC-----EEEEEEEEcccCccCccCCCCCEEEEEEEEEccCccCccCCEEEEEEEFEE		
Q	sun_Pred_08_06:	179	PKRHHNIEDGVS---QLADHYQONTIGDGVLLPDNHYLSQTQALSKDPNKRKDDHVLHLEFVTA	240 (298)
Q	Consensus	179	---l-l-dGG---T-yk-kkPi-v-mP-Hfi-skD--E-rDhi-vE-A	240 (298)
			++ + + + + ++ ++ ++ ++ +..+-----+ _ _ _	
T	Consensus	188	---l-l-dGG-yr-T-yakk--v-lP-HFv-hrie-l-E-a-A	246 (255)
T	Zioiv_A	188	VNMALSLGGGHGYRDKFTTYKAKK---VVLDPDHYFHDIETKSH-DKYSYNVNLHLEHAEAA	246 (255)
T	ss_dssp		EEEEEEETTSCEEEEEEEEEEESS-----CCCCCCCEEEEEEEEEEF--CTTSSEEEEEEEEEE	
T	ss_dssp		EEEEEEEEECCCCEEEEEEEEcccC-----CccCCCCEEEEEEEEFeee-cCCCCEEEEEEEEEE	

No 33                       







[illegible][illegible]

```

Q ss_pred          EEEEEEEECCECEEEEEEEccCccCCCCCEEEEEeeEeCccCCcCEEEEEEE
Q Sun_Nov_08_06: 176 KVNFKIRHNEDVSGVQLADHYQNTPIGDGVLLPDNHYLSQSALSKDPNKRKHMLVEFVTA 240 (298)
Q Consensus        176 -g-----l-dg-----T-yk-kkPi-----v-mP-----Hfi-----sKD-----E-rDhi-----vE-----A 240 (298)
                    +|+++|+|+|+++++|+|+|+|+++++|+.|+|+|+.+++|.+.+.+.+.+.+.+.
T Consensus        159 -----g-----P-----H-i-----ri-----s-dl-e-m-----lLLlLlLl----- 223 (343)
T t4pe A           159 KANFKIRHNEDVSGVQLADHYQNTPIGDGVLLPDNHYLSQSALSKDPNKRKHMLVEFVTA 223 (343)

```


T ss_dssp EEEEEEEEBTSSCEEEEEEEEEEESSCSCCCCCCEEEEEEEECCTTCCSSEEEEEEEEEE
T ss_pred EEEEEEEECCECEEEEEEEEcCcccccCcccccCceEEEEEEecCccchhhhhhhHHHhC







No 34      

>4hvf_A Green fluorescent protein BLPF-Y6; LANGFP, beta-barrel, Gly-Tyr-Gly chromophore, biomarker, cephalochordate; HET: CR2; 1.70A {Branchiostoma lanceolatum} SCOP: d.22.1.0 PDB: 4jge_A* 4jee_A* 4jf9_A* Probab=100.00 E-value=2.1e-81 Score=570.52 Aligned_cols=205 Identities=20% Similarity=0.336 Sum_probs=0.0

Q ss_pred CceEEEEEEECCEEEEEEEEcCccCceEEEEEEcCCCCCHHHhhhhccccccccCCCCChhhHHhC
Q Sun_Nov_08_06: 25 VVPILVLDGVDVNGHKFSVSGEGEDATYGLTKLFICTTGKLPVWPPTLVTTFTYGVQCFSRYPDHMKRHDFFKSAMPE 104 (298)
Q Consensus 25 -m-k--meG-VNGH-F-I-GeG-G-p-eG-q--k-vt-GpLPFS-dILs--f-YG-r-FtkYP-I--DyFKqsFPe 104 (298)
T Consensus 12 ---k--meG-VNGH-F-i-G-G-G-p-eG---kl-vt-GpLPFS-dILs--f--G-r-F-kYP-i--DyFK-sfPe 87 (226)
T 4hvf_A 12 PATHELHIFGSLNLEFDLVGRGTGNPKGEYELHLKSTKSAQSPWILVPOI--XFYQYLPFPDGA--MSPFOAAMND 87 (226)
T ss_dssp CCEEEEEEEEBTTEEEEEEEETTTTEEEEEEESSSSCSCGGGGTTTC---CGGGBCSTTC--BCHHHHHHT
T ss_pred ceeEEEEEEECCEEEEEEEEcCCCCCEEEEEEEcCCCCCHHHhhhh--ccccccccCCCC--cChHHhCC

Q ss_pred --ceEEEEEEcCCEEEEEEEcCEEEEEEEcCCCCCCCCcccccc--ccCCceEEcCCcCCCEEEEEEE
Q Sun_Nov_08_06: 105 --GYVQRTIFPKDDGNKYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKL--EYNYNSHNVIMADKQNGIKVNFKI 181 (298)
Q Consensus 105 --GysweRt--FEDGGv-t-----itleg-c-----v--G-nFP-dGPVMqkkt-----e-----gi-g----- 181 (298)
T Consensus 88 G-Gys-eRt--FEDGGv-t-----itleg-----v--G-nFP-dGPVMqkkt--wePs-e--p-----dg-L-g----- 164 (226)
T 4hvf_A 88 GSGYQVHRMQFEDGATLTGIYRYTYGTHIKGEFVIGTGFPADGPMVMSLTAAWCVTKLVIP--NNTIIDKFPDW 164 (226)
T ss_dssp SCCEEEEEEEEBTSSCEEEEEEEETTEEEEEEEECCTTSTTTTTCCEEECEEEEEEE---ETTEEEEEEE
T ss_pred CCCcEEEEEEcCCEEEEEEEcCEEEEEEEcCCCCCCCCccccccceCCcCEEEEEEc---CCCEEEEEEE

Q ss_pred EEEcCCCE---EEEEEEcCccCccC-CcCCCCCEEEEEEEcCccCccCceEEEEEEc
Q Sun_Nov_08_06: 182 RHNIEDGSV---QLADHYQNTPIGDGPVLLPDNHYLSTQSAKSKDPNEKRDMVLLFVTAAG 242 (298)
Q Consensus 182 -l-l-dGg---T-yk-kkPi---v-mP--Hfi---sKD--E-rDhi--vE---A-- 242 (298)
T Consensus 165 -l-l-dGg-y-----t-y--kkpv-----P--hfV-rie-----kdhi--E--kAF- 223 (226)
T 4hvf_A 165 TYTTTSCKRYQSNVRSNFTFAKPIAANILKQKP--MFVFRKTELK---HSKTELFKEWQTAFS 223 (226)
T ss_dssp EEEETTSCEEEEEEEESSCCCHHHTSCS--EEEEEEEEE---ECSSEEEEEEEES
T ss_pred EEEcCCCCCEEEEEEEcCccCccCCCCC---EEEEEEEEE---cCCCEEEEEEEhhhh







No 35      

>2g6y_A Green fluorescent protein 2; natural chromophore, rapid matura beta-CAN, luminescent protein; HET: CR2; 1.60A {Pontellina plumata} SCOP: d.22.1.0 PDB: 2g6x_A* 2g3o_A* Probab=100.00 E-value=4.4e-81 Score=565.85 Aligned_cols=207 Identities=21% Similarity=0.339 Sum_probs=0.0

Q ss_pred CCceEEEEEEECCEEEEEEEEcCccCceEEEEEEcCCCCCHHHhhhhccccccccCCCCChhhHHhC
Q Sun_Nov_08_06: 24 GVVPILVLDGVDVNGHKFSVSGEGEDATYGLTKLFICTTGKLPVWPPTLVTTFTYGVQCFSRYPDHMKRHDFFKSAMPE 103 (298)
Q Consensus 24 --m-k--meG-VNGH-F-I-GeG-G-p-eG-q--k-vt-GpLPFS-dILs--f-YG-r-FtkYP-I--DyFKqsFPe 103 (298)
T Consensus 2 --m-k--meG-VNGH-F-i-G-G-G-p-eG-q--kl-vtkGpLPFS-dIL--f--r-F-kYP-i--d-Pkqs-p 77 (217)
T 2g6y_A 2 PAMEICRITGTLNGVFELVGGEGTPEQGRMTNMKSTKGALTFSPYLLSHVMX--FYHFGTYPSGY--ENPFLHAIN 77 (217)
T ss_dssp -CEEEEEEEEBTTEEEEEEEETTEEEEEEEEGGGTTEEEEEEESSSSCSCGGGGTTTC---CGGGBCSTTC--CCHHHHGGG
T ss_pred CcceeEEEEEEECCEEEEEEEEcCCCCCEEEEEEEcCCCCCHHHhhhhcc--ccccccccCCCC--CChHHhCC

Q ss_pred -CceEEEEEEcCCEEEEEEEcCEEEEEEEcCCCCCCCCcccccc--ccCCceEEcCCcCCCEEEEEEE
Q Sun_Nov_08_06: 104 -EGYVQRTIFPKDDGNKYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKL--EYNYNSHNVIMADKQNGIKVNFKI 181 (298)
Q Consensus 104 -eGYsweRt--FEDGGv-t-----itleg-c-----v--G-nFP-dGPVMqkkt-----e-----d-----gi-g----- 181 (298)
T Consensus 78 -eGys-eRt--fEDGGv-t-----isleg-----v--G-nFP-dGPVMqkkt--wePs-e--p-----dg-L-g----- 154 (217)
T 2g6y_A 78 NGGYTNRIEKYEDGGLVHVSFYSRYEAGRVIGDFVMTGFPEDSVIFTDKIRSNATVEHLHPM--GDNDLDGSFTR 154 (217)
T ss_dssp TTCEEEEEEEEBTSSCEEEEEEEETTEEEEEEEECCTTCGGGSSCEEECEEEEEEE---STTEEEEEEE
T ss_pred CCCEEEEEEEcCCEEEEEEEcCEEEEEEEcCCCCCCCCccccccCCEEEEEEc---CCCEEEEEEE

Q ss_pred EEEcCCCE---EEEEEEcCccCccC-CcCCCCCEEEEEEEcCccCccCceEEEEEEc
Q Sun_Nov_08_06: 182 RHNIEDGSV---QLADHYQNTPIGDGPVLLPDNHYLSTQSAKSKDPNEKRDMVLLFVTAAG 241 (298)
Q Consensus 182 -l-l-dGg---T-yk-kkPi---v-mP--Hfi---sKD--E-rDhi--vE---A-- 241 (298)
T Consensus 155 -l-l-dGg-y-----t-y--kkpi-----P--HFv-rie-----e-Af 213 (217)
T 2g6y_A 155 TFSLDGGYSSVDSHMHFKSAIHPSILQNGGPMFAFRVVEDHS---NTELGIVYQAHF 213 (217)
T ss_dssp EEEETTSCEEEEEEEESSCCCHHHTSSSCCEEEEEEECC---SSEEEEEEEEEE
T ss_pred EEEcCCCCCEEEEEEEcCccCccCCCCCEEEEEEEc---CCCEEEEEEE

No 36      

>2zmu_A Fluorescent protein; GFP-like protein, luminescent protein, structural genomics, structural genomics/proteomics initiative, RSGI, NPPSFA; HET: CFY; 1.65A {Fungia concinna} SCOP: d.22.1.0 PDB: 2zmu_A* 3mgf_A* Probab=100.00 E-value=1.3e-80 Score=564.34 Aligned_cols=207 Identities=25% Similarity=0.523 Sum_probs=0.0

Q ss_pred hccCceEEEEEEECCEEEEEEEEcCccCeE---EEEEEEc-CCCCCHHHhhhhccccccccCCCCChhh
Q Sun_Nov_08_06: 21 LFTGVVPIVLDGVDVNGHKFSVSGEGEDATYGLTKLFICTTGKLPVWPPTLVTTFTYGVQCFSRYPDHMKRHDFF 97 (298)
Q Consensus 21 -----m-k--meG-VNGH-F-I-GeG-G-p-eG-q--k-vt-GpLPFS-dILs--f-YG-r-FtkYP-I--Dy 97 (298)
T Consensus 4 -----m-k--meG-VNGH-F-i-GeG-G-p-eG-q--kl-vtkGpLPFS-dILs--f--r-F-kYP-i--dy 78 (223)
T 2zmu_A 4 VIKPBMKMYRYSYDGSVNGHEFTLEGEGTRPYEGHQMELRVMTAKGGPMPPAFDLVSHVX---HNPFTKYPEE---PDY 78 (223)
T ss_dssp TCSSSEEEEEEEEBTTEEEEEEEEGGGTTEEEEEEEETTCSSSSCTHHHTC---CTTSSBCTTS---CCH
T ss_pred ccCCcCEEEEEEEECCEEEEEEEcCCCCCEEEEEEEcCCcCCCHHHcccc--ceccccCCCC--CCH

Q ss_pred HhhhCCCEEEEEEEcCCEEEEEEEcCEEEEEEEcCCCCCCCCcccccc--ccCCceEEcCCcCCCEEE
Q Sun_Nov_08_06: 98 FKSAMPEGYVQRTIFPKDDGNKYKTRAEVKFEGDTLVNRIELKIDFKEDGNILGHKL--EYNYNSHNVIMADKQNGIK 176 (298)
Q Consensus 98 FKqsFPeGysweRt--FEDGGv-t-----itleg-c-----v--G-nFP-dGPVMqkkt-----e-----d-----gi-g----- 176 (298)
T Consensus 79 FK-sfPeGys-eRt--FEDGGv-t-----isleg-----v--G-nFP-dGPVMqkkt--wePs-e--p-----dg-L-g----- 154 (223)
T 2zmu_A 79 FKQAFPPEGLSWERSLEFDGGASVSAHISLRGNTFYHKSFTGVNFPADGPIMQNSVDWEPSTKITA---SDGVLK 154 (223)
T ss_dssp HHHHTTCEEEEEEEETTSCEEEEEEEETTEEEEEEEECCTTSTTTTTCCEEECEEEEEEE---ETTEEE
T ss_pred HHHhCCCEEEEEEEcCCEEEEEEEcCEEEEEEEcCCCCCCCCccccccCCEEEEEc---cCEEE

[illegible]

Q Consensus 99 KqsfPEGYsweRt--FEDGgv-t-----itleg-c-----v--G-nFP-dGPVMgkkt-----e-----d-----gi-g- 178 (298)

T Consensus 136 kq--p-G-----R-----fedgg-----g-----g-Fp-dgpm-----e-----l----- 215 (297)

T 4ndj_A 136 KSAMPEGQYQERTIFFKDDGNVYKTRAIEVFGPDGLVNIIRLEKGIQDFKEDGNIHLGKLESHNVHVIYATDQKNGIKLAN 215 (297)

T ss_dssp hHHTTTTCCEEEEEEEETTCCEEEEEEEETTEEEEEEEETSCCTTSTTTTCCSCCCCEEEEEEEGGGTEEEE 215 (297)

T ss_pred hhCCCCCcEEEEEEECcCEEEEEEEECcEEEEEEEEecCCCCCCCCcCccCccCceCccCccCCEEE

[illegible]

No 40       

>**4dkn_A** Amphioxus green fluorescent protein, GFPAL; chromophore, beta-CAN, fluorescence; HET: CR2; 1.35A
{Brachiostoma floridae} SCOP: [d.22.1.0](#)
Probab=100.0 E-value=1.6e-79 Score=556.86 Aligned_cols=204 Identities=23% Similarity=0.392 Sum_probs=0.0

[illegible][illegible]

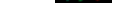
```
Q ss_prev      EEEEECCCCC-----EEEEEECCCcCCc-CCGCCCEEEEHEEHeEcCcKCCeEEEEEEEE
S Sun_Nov_08_06: 180 KIRHNIEDGVS----QLADHYQNQTIDCG-PVLLPNHYYLSTQSALKSGDKHMVLVEVTAA    241   (298)
T Consensus     180 -l-l-dgq                    T-yk-kkpI       v-mP-Hfi             sKD-E-Rdhi-vE-A    241   (298)
                +|+||++|+|+| ++|++++|+++ +++| |++|+|.... | |||+|+|++|+|
T Consensus     158 -l-l-dgg-qy              t-y kkvvp          P-hfvr-rie-s        kd-i-e-KAF    217   (221)
D 4dknA         158 DWSYNLNQGKKRYRARSYSHVDIGPKFSADLMKPQ--VFVVQRKHCHVKAT--KTEVIIDEREKAF    217   (221)
T ss_dssp        EEEEEETTSCEEHHHEEEESSSC---CCC-----EEEEEEEEEC---SSSEEEEEEEEE
T ss_ssnp        CEEEEEHCCEEEEEEEEEEEecCccccccCCCCCC-----EEEEEEHEEc-----cccEEEHhhhhh
```

No 41     

>**4kf5_C** Fluorescent protein sfcherry-GFP10-11; HET: CRO CH6; 2.60A {Synthetic construct}
 Probab=100.00 E-value=2.1e-79 Score=564.95 Aligned cols=202 Identities=38% Similarity=0.684 Sum probs=0.0

[illegible][illegible][illegible]







No 42                         


>2dd7_A Green fluorescent protein; luminescent protein; HET: CR2 CXS; 1.90A (Chiridius poppei) SCOP: **d.22.1.0**
 PDB: **2dd9_A***
 Probab=100.0 E-value=7.8e-79 Score=550.83 Aligned cols=204 Identities=17% Similarity=0.329 Sum probs=0.0

Q ss_pred		CCcCeEEEEEEECCEEEEEEEEcCcCceEEEEEEeCCCCCHHHhhhhhcccccceccccCCCChhHhHhCC	
Q Sun_Nov_08_06:	24	GVVIVLVLDDGVHGKFSFVSGEGDAtYgkLTfKTCTGGLPVPWTLTlTTFYtVGQCFSRYPDHMKRDFFKGSAMP	103 (298)
Q Consensus	24	-m~v-k-meG-VnGH-F-I-GeG-G-p-eG-q-k--vtG-LPFs-dLS--fg-YGR-fTkYp-I---DYDFKSqAP	103 (298)
T Consensus		++ ++++ + + + + + ++ + ++++ + + +++ ++ + ++ + + +	
T ddd7 A	1	m~-m~-k-meG-VnGH-F-I-G-G-G-eG~--kl-vt-gLPFs-dLS--fg~r-f-KfYp-Ikt-d-Fkgs-p	74 (216)
T ddd7 A	1	TTTFIKESRIHGNLGKFGELVLGGVG--EGRGLEIMETDKDLPLAFSPLLSHCMC--FYHFASFPKGt--KNLYIHHAAT	74 (216)

T	ss_dssp	CC	EEEEEEEEET	TEEEEEEEEE	---ET	TEEEEEEESS	CCSSCGGGGGGG	---CGGGE	CCCTTC	---CC	HHHHHT	
T	ss_pred	CC	ceEEEEEEEC	CEEEEEEEec	---cc	EEEEEEEC	CCCCCCH	HHhh	hc	---ce	ccccCCCC	---c
Q	ss_pred		-C	ceEEEEEEec	Cc	CEEEeeE	Eeee	CEEEEEeE	Eeee	CCCCC	Ccccccc	---cc
Q	Sun_Nov_08_104		-	EGVY	NR	TIF	FDK	GNV	KRA	EY	FGD	T
Q	Consensus	104		-e	Gysw	eRt	-	FDDG	v	-	l	isleg
T	Consensus	75		-e	Gys	eRt	-	FDDG	v	-	l	isleg
T	2dd7_A	151		NGGY	TN	TR	KI	EY	DG	GI	LV	NF
T	ss_dssp			TT	CCCC	EEEEEEEEET	TEEEEEEEEE	CCCC	THHH	TT	CEEE	EE
T	ss_pred			CC	Cee	EEEEEEEC	CC	EEEEEEEEEC	CCCC	CCCC	cccccccc	CC








[illegible]

No 43      

 >4zf5_A Green fluorescent protein; HET: 4NU; 1.70A {Aequorea victoria} PDB: [4zf4_A*](#) [4zf3_A*](#) [3p28_A*](#)
Probab=100.00 E-value=6.1e-70 Score=500.60 Aligned cols=188 Identities=90% Similarity=1.403 Sum probs=0.0

[illegible][illegible]

Q	ss_pred		EecCCcCcEeEEEEEEEEcccccchhhh	
Q	sun_Nov_08_06:	222	SKDPNFKRHDHVMVLEFVTAAGITGMDLEY	251 (298)
Q	Consensus	222	sKD- E-rDhi -vE-	251 (298)
T	Consensus	167	-d-e-kdhi -E-ka-	196 (252)
T	z4fs_A	167	SKDPNFKRHDHVMVLEFVTAAGITGMDLEY	196 (252)
T	ss_dssp		ECCTTCSSEEEEEEEEEEEC-----	
T	ss_pred		ecCCCCCcEEEEEEEEEcccccchhhh	

No 44                       

[illegible][illegible]

No 45      

 [3rwa_A](#) Fluorescent protein FP480; GFP-like fluorescent proteins, mkate, circularly permuted, FL protein; HET: NRQ; 1.67Å [Entomacaea quadricolor] PDB: [3rwt_A*](#)

Probab=100.00 E-value=5.9e-69 Score=490.23 Aligned cols=163 Identities=24% Similarity=0.516 Sum probs=0.0

[illegible]

[illegible]

Q ss_pred		CC EE EEEEEEEC	
Q Sun_Nov_08_06:	172	K NGIK VNFK R HNIE	186 (298)
Q Consensus	172	---g-i-g-+---l-l- +++ + +++ + + d+g-L-g-+---l-l-	186 (298)
T Consensus	219		233 (233)
T 3rwa_A	219	D GGLE GRSD M AL KLV	233 (233)
T ss_dssp		SSSEEEEEEEEEEC	
T ss_pred		CC EE EeEEEEEEcC	

No 46

>**3evp_A** Circular-permutated green fluorescent protein; EGFP, chromophore, luminescence, photoprotein, signaling protein; HET: CRO; 1.45A (Aequorea victoria)
 Probab=100.00 E-value=7e-66 Score=470.43 Aligned_cols=143 Identities=97% Similarity=1.535 Sum_probs=0.0

[illegible][illegible]

No 47     

► **4anJ_A** Unconventional myosin-VI, green fluorescent prote; motor protein-metal-binding protein complex, molecular motor, metal-binding protein, transition state; HET: CR2 ADP; 2.60Å {Sus scrofa}
 Probab=100.0 E-value=3.5e-63 Score=526.65 Aligned cols=229 Identites=98% Similarity=1.503 Sum_probs=0.0

[illegible][illegible][illegible]

No 48

>4pa0_A Myosin-7, green fluorescent protein; cardiac, motor, omeacantiv mercarbil, motor-fluoresce protein complex;
HET: CRO 20W; 2.25A {Homo sapiens}; PDB: 4p7h_A* 4db1_A* 2w4a_M 2w4g_M 2w4h_M 2mys_A* 1m8g_A* 1mwv_A* 1o18
1o19_A* 1o1a_A* 1o1b_A* 1o1c_A* 1o1d_A* 1o1e_A* 1o1f_A* 1o1g_A*
Probab=100.00 E-value=2.3e-60 Score=503.94 Aligned cols=225 Identities=97% Similarity=1.495 Sum probs=0.0

[illegible]

Q ss_pred EEEEEEEcCCcEEEEeEeeeCCEEEEeEEEEEcCCCCcccccccccCCcceeEecccCCcCEEEEEEEEEc
Q Sun Nov 08 06: 107 VQERTIFFKDDGNYKTRAEVVKFEGDTLVNRIELKGI~~DFKED~~GNILGHKLEYNYSN~~HN~~VYIMADKQKNGIKVNF~~KIRHNI~~E 186 (298)

Q ss_pred cceccccCCCCc

Q Sun_Nov_08_06: 81 GVQCFSRYPDHMKRHDFFKSAMPEGVGYQERTIFFKDDGNKYKTRAEVFKPGDTLVNRIELKGI~~DFKEDGNL~~GLK~~L~~-B~~Y~~NY 159 (298)

Q Consensus 81 G-r-FtkYP--I--DyFKqsfPeGYSwrE--FDGGV-t--itleg-c--v--G-nfP-dGPVMgkkt--~-- 159 (298)

T	Consensus		1	G-r-F-kY-P-i--dyFK-sfPeGys-eRtT-fEDGGv-t-----isleg-v---l-G-nP-dGPVMqk-t-weP	78	(168)
T	2a50_B		1	XSKXKFIKLVSQGI--PDYFQKGSPFGI-EETDDEGGVGLTAHQDDCLDGCVLYKVKKLNHNPADGVPMOKNAKRGEW	78	(168)
T	ss_dssp			-CTTCCEBECTTC-CCTTGCGTTCCEEEEEEETTSCEEEEEEEETTEEEEEEEEC CCTCSTTTTTCCCCC		
T	ss_pred			CccccccCCCCCC--cCHHHHCeEeeeeEECCCCEEEEEEEEcCEEEEEEEEC CCCCCCc ccccceCcC		
Q	ss_pred			CceeEFeccccCCCCCeEEEEEEEEEECCCEE--EEEEEEECcCcCCCC--cCCCCEEEEEEeeEcCcCccCceEf		
Q	Sun_Nov_08_06:	160	NSHNVVIIMADKDNGIKVFNFKRHNHTLGDGSV--QLADHYQQNTPTIGDP- -VLIPDNPHYLSTQSALKSDPKNRKHDM	233	(298)	
Q	Consensus	160	e- + -d-q-g-l-g-1-l-dGg-T-y-k-kKi-p-Hfi-SKD-E-RdhI-	233	(298)	
			+ ++ ++++ +++ + + ++ + + + + ++ +.++ +++++.			
T	Consensus	79	s-e-p----dg-L-g-----l-l-Cg-y-T-y-akk-----v-mP-HFV-rii-----v-	148	(168)	
T	2a50_B	79	A TEIVVE-----VDGVLRGQSLMA LCPGGRHLC HLTHTYSRK-----PASALMKPGFHFDHRRIIMEE-V EKGKY K	148	(168)	
T	ss_dssp			EEEEEE-----ETTEEEEEEEETTSCSEEEEEEEESS-----CGGSGCCCCSEEEEEEEEEEE-EBTTTT		
T	ss_pred			eFEFEeee-----CCCEEEEEEEEEEECCCCEEEEEEEccccCc-----cccccccCEEEEEEEeee-cCCCCCEE		

Q ss_pred		EEEEEEecccc	
Q Sun_Nov_08_06:	234	LELFVTAAGIT	244 (298)
Q Consensus	234	vVE---A	244 (298)
		. .++ .+.+	
T Consensus	149	--E-a-A	159 (168)
T 2a50_B	149	QYEAaVGRYCD	159 (168)
T ss_dssp		EEEEEEEECCCC	
T ss_pred		EEEEEEEEeEc	

No 52

> [4rh7_A](#) Green fluorescent protein/cytoplasmic dynein 2 HE 1; AAA+ protein, motor protein, dynein motor domain; HET: AOV ATP ADP; 3.41A [Synthetic construct]
 Probab=100.0 E-value=1.3e-50 Score=466.21 Aligned_cols=245 Identities=85% Similarity=1.287 Sum_probs=0.0

[illegible][illegible][illegible]

```
Q ss_pred          ---hhhhhccceccccch
Q Sun_Nov_08_06:  249   ---ELYKSLGRSYDLGDT    263 (298)
Q Consensus        249                               263 (298)
                    +.++.+.+.+++.+
T Consensus        237             HHHHHLf         254 (3450)
T 4rh7_A           237 VTRKKLVDDCHHFRLPEP      254 (3450)
T ss_dssp
T ss_pred          HHHHHHHHHHHHhCCCCC
```

No 53      

→ **3u0k_A** Roamp; fluorescent protein, calcium binding, EF-hand, genetically E calcium indicator; HET: NFA CRK;
 2.10A [Entacmaea quadricolor]
 Probab=100.00 E-value=1.1e-45 Score=360.83 Aligned_cols=148 Identities=31% Similarity=0.609 Sum_probs=0.0

```

Q ss_pred          cCCCCccccccchhhcccceEEEEEEEEEEcccCEEEEEEEcccCEEEEEEEc-CCCCccccccccccccccccccccccccc
Q Sun_Nov_08_06:  8 ATPGIPMVSGKEELFTGVPLVLDGVDFGKFEESVSGEGEDATYGKLTFLKFTCT -GKLPVHPHTLVLTITVYGVGCEFC 86 (298)
Q Consensus       .      -      m -k -meG-VNcH-F-I-GeG-G-p-e-G-q-k-vt-  GpLPS-dILs-l-F-YG-r-F-t 86 (298)
                  |      +      +      +      +      +      +      +      +      +      +      +      +      +      +      +      +
T Consensus       147      -      -      -      -      -      -      -      -      -      -      -      -      -      -      -      -
T 3u0kA           147 GTGG-SMNS-----LTKENMRMKVVLVSGVNGHGFCKTCEGEGFPMYGTQMTIRIKVLGGPLPAPFDILATSXX--SRTPF 219 (440)
T ss_dssp         TSSCC-CCCT--TSSCCSEEEEEEEEEETTEEEEEEEEEETTTTTTEEEEEEEEESSSSSSCGGGGTTC--CTTSC
T ss_pred         Ccch-hhhh--hcCCCCeEEEEEEcCEEEEEEEcccCEEEEEEECCCCCCCCcccccccccccc--hhhhh

```

```

Q ssn_pred      cCCCCcchhhhhhhCCcCeEEEEEEecCCcEEEEeeKeeCEEEEEEEKEEeCCCCcccccccccc-cCCcCeeE
Q Sun_Nov_08_06: 87 RYpDHMRKDFKSPFAMpGQYQERTFFKFDGNKTRAEVfKFGDITLVNRLEKIDGDKGNLGHGK-L-EYNNYSNN 164 (298)
Q Consensus      kYp- - -DyFKGfPeYKggvT- -FEDGGvT- - -itleg- - -v- -G-nfP-dpVMqkkt- - -e- 164 (298)
                  |+++++|+|++++|+|+|++++|+|++++|+|++++|+|++++|+|++++|+|++++|+|+++++
T Consensus      220 -y- -i- d- f- k- p- g- sW-er- fedgg- -v- isled- l- a- gvnfP- g- VmqKk- - -eps- e- 296 (440)
T 3u0kA          220 KYPkGI- -PDFFKQSPfPGFTVRVRYEDGGGVITVMQDITSLDGLGVYHAQVRGVNPSFNGAQMOKKTKGWEpTRDQL 296 (440)
T ss_dssp         BCCTTTS--CCNNHHHTTTTCEEEEEEEETTSCEEEEEEEEEEETTCEEEEEEEEEEECCTTSTTTTTCCEEECCBCCB
T ss_dsap         hCCcCcc- -cchhhhCccccceeeEEccCccCEEEecceeeCEEEEEhhhhCCcCccccchhhhhhhhhhhcchhhc

```

No 54       

 4i2y A Rgecol; calcium binding, sensor, fluorescent protein, mapple, fluore calcium indicator; HET: NRQ; 2.20A

[illegible]

Q ss_pred		hhCCCEEEEEEeEeeCCcEEEEeeEeeCCEEEEEEEeEeeCCCCccccccccc--ccCCChve	
Q sun_Nov_08_06:	100	SAMPGYGVQERTIFPKDNGKYNRAEVKFDGLTVLNRILKLGIDGKDLGLH--EYNNYSNNEF	164 (298)
Q Consensus	100	gsfpeGYswErT---FEDGGVt-----itleg-c-v--g-NFP-dgPVMqkkt-----e-	164 (298)
		+ + + ++ .++ + +.+++++++ ++++.+ . +..++ gg+... .++..+++	
T Consensus	210	sg-PegyswEr-dfg-gG-i--d-Lg-V-irLgrinEf--vmqkg-----e-s-ekl	275 (419)
T 4i2y_A	210	LSPFGFRWsvrVNFDCGIIHVNDSSLQDGVFYIKVKLRITFPFDGPVMQKKTMGWEATRDQL	275 (419)
T ss_dssp		HTTTTCCEEEEEEEETTSCEEEEEEEETTEEEEEEEECCTTSTTTTTCEEEECBCCC	
T ss_pred		hhCCCEEEEEEeEeeCCcEEEcCCCCcccccccceehhchCCcChHHHHHHHHhhhhhhhhh	

No 55     

>2a50_A ASPFP595, GFP-like non-fluorescent chromoprotein FP595 CHAI; ASCP, fluorescent protein, photochromic prote
reversible photoswitch; HET: NRQ; 1.30A {Anemonia sulcata} PDB: 2a52_A* 2a53_A* 2a54_A* 2a56_A* 3cfa_L*
3cff_L* 3cfh_L*
Probab=99.95 E-value=3.2e-28 Score=187.61 Aligned_cols=60 Identities=30% Similarity=0.592 Sum_probs=0.0

[illegible]

No 56     

>sevp_A1 Circular-permuted green fluorescent protein; EGFP, chromophore, luminescence, photoprotein, signaling protein; HET: CRO; 1.45A {Aqueorea victoria}
 Probab=99.77 E-value=2.8e-18 Score=157.49 Aligned_cols=111 Identities=78% Similarity=1.133 Sum_probs=0.0

Q	ss_pred		CCcCeEecccCCCCCEEEEEEEEEECCGCCEEEEEEccCcCccCCCCEEEEEEEEcCccCcCceEEHVVLE		
Q	Sun_Nov_08_06:	159	YNShNVYIMdAKDKNGIKANFVKIRHINIEDGGVQLAYHYQNQTfGDGVLPLDNDGYLSTQSKSLKDPNKKRDNHMVILFFV	238	(298)
Q	Consensus	159	-e-d-g-i-g-l-l-dGg-T-yk-kPi-v-mP-Hfi-sKD-E-RdhI-vE- +.+++.+ +++++ +.+.+.+.+ +.++++.+ +++++.+ +.+.+.+.+ +.++++.+ +.++++.	238	(298)
T	Consensus	1	-yi-pd-qkg-f-i-edg-qLa-Q-nPig-P-I-H-L-t-lskPd-e-Rdh-E-v	80	(243)
T	3evp_A	1	SSlENVYIMdAKDKNGIKANFVKIRHINIEDGGVQLAYHYQNQTfGDGVLPLDNDGYLSTQSKSLKDPNKKRDNHMVILFFV	80	(243)
T	ss_dssp		CCEEEEEEEEGGGTCEEEEEEEEBTTSCCEEEEEEEESSSSSSSSSSSCEEEEEEEECCTTCSSSEEEEEEE		
T	ss_pred		CcCcEeEeecccCCCCCEEEEEEEEcCccCcCEEEecCcccccCCCCccccCcCceEEeEecccCccccCcCEEEeEe		


Q ss_pred		Eeeeeccccchhhhhcceeccccchhhhccccccc	
Q Sun_Nov_08_06:	239	TAAAGTTHGMDELYKSLRSYDLGDTIERGRQDYKD	273 (298)
Q Consensus	239	-A----- +++++ ----- -.+. +.-.-.	273 (298)
T Consensus	81	-A-i-----y-----g-l-----	111 (243)
T 3evp_A	81	TAAAGITLGMDELYK-----GGTGGSMVSKGEEFLFTG	111 (243)
T ss_dssp		EEEEC-----CGGGGSS	
T ss_pred		eeeeccccchheee---cCccceecCchhhccc	

No 57              

>3osq_A Maltose-binding periplasmic protein, green fluore protein; engineered protein, sensor protein, fluorescent protein, MBP maltose sensor; HET: C12 MAL; 1.90A [Escherichia coli]
 Probab=99.6 E-value=1.2e-15 Score=155.59 Aligned cols=149 Identities=95% Similarity=1.499 Sum probs=0.0

[illegible][illegible]

No 58              


>42y_A Rgecol; calcium binding, sensor, fluorescent protein, mapple, fluore calcium indicator; HET: NRQ; 2.20A
 [Gallus gallus]
 Probab=99.41 E-value=1e-12 Score=127.78 Aligned cols=85 Identities=25% Similarity=0.385 Sum probs=0.0


```
Q ss_pred      CcccEeEcccCCCCeEEEEEEEEeCCCCE---EEEEEEcccCcCCCCCCCCEEEEEEeEcCcCcCeEEEE
Q Sun_Nov_08_0160 NSHNYIMADKQKNGIKVNFKRINRDNIGDSGV---QLADHYKKPIGIDGSPVLLPNNDYLSITQSAISKDNRHHRHMVLL 236 (298)
Q Consensus    160 e-----d-----g-----l-----l-----dgg-----T-yk-kqPti-v-m-----Hfi-----skD-E-rdHl-vE 236 (298)
```

Q ss_pred		EEEEccccccccchhhhhc	
Q Sun_Nov_08_06:	237	FVTAAGITGHGMDELYKSG	254 (298)
Q Consensus	237	A..... +++ ++	254 (298)
T Consensus	101	a..... +++ ++	118 (419)
T 4i2y_A	101	RAEGRHSTGGMDELYKGG	118 (419)
T ss_dssp		EEEEEC	
T ss_pred		EEEEECccccceeecc	

Q ss_pred		EEEEEEe	
Q Sun_Nov_08_06:	233	VLLVEFVA	240 (298)
Q Consensus	233	-v- +.	240 (298)
		· · +.	
T Consensus	130	-e-a	137 (440)
T 3u0k_A	130	VQREHAVA	137 (440)
T ss_dssp		EEEEEEEE	
T ss_pred		EEEEEEEE	

[illegible][illegible][illegible]

No 68



>4r03_A

Uncharacterized protein; PF12930 family protein, DUF3836, structural genomics, joint for structural genomics, JCSG; HET: MSE CIT; 1.50A {Parabacteroides distasonis atcc 8503}

Probab=37.36 E-value=2e+02 Score=23.63 Aligned_cols=70 Identities=14% Similarity=0.286 Sum_probs=0.0

Q ss_pred

Q Sun_Nov_08_06: 115

Q Consensus 115

T Consensus 10

T 4r03_A 10

T ss_dssp

T ss_pred

Q ss_pred

Q Sun_Nov_08_06: 194

Q Consensus 194


T Consensus 78

T 4r03_A 78

T ss_dssp

T ss_pred

No 69



>2k4v_A

Uncharacterized protein PA1076; structural genomics, unknown function, PSI-2, protein struct initiative; NMR {Pseudomonas aeruginosa}

Probab=35.61 E-value=35 Score=28.98 Aligned_cols=15 Identities=33% Similarity=0.931 Sum_probs=0.0

Q ss_pred

Q Sun_Nov_08_06: 28

Q Consensus 28




T Consensus 41

T 2k4v_A 41

T ss_dssp

T ss_pred

No 70



>2i9x_A

Putative septation protein spovg; APC86317.1, staphylococcus epidermidis ATCC 12228, ST genomics, PSI-2, protein structure initiative; 1.80A {Staphylococcus epidermidis} SCOP: d.366.1.1

Probab=23.52 E-value=2.1e+02 Score=22.50 Aligned_cols=34 Identities=12% Similarity=0.255 Sum_probs=0.0

Q ss_pred

Q Sun_Nov_08_06: 107

Q Consensus 107


T Consensus 7

T 2i9x_A 7

T ss_dssp

T ss_pred

No 71



>2ia9_A

Putative septation protein spovg; APC85465, bacillus subtilis subsp. subtilis STR. 168, structural genomics, PSI-2; 3.00A {Bacillus subtilis} SCOP: d.366.1.1

Probab=21.87 E-value=2.2e+02 Score=23.01 Aligned_cols=34 Identities=18% Similarity=0.294 Sum_probs=0.0

Q ss_pred

Q Sun_Nov_08_06: 107

Q Consensus 107



T Consensus 7

T 2ia9_A 7

T ss_dssp

T ss_pred

No 72



>3wxr_K

Proteasome subunit beta type-4; UPS, 20S proteasome, hydrolase, protease, 19S regulatory PAR multicatalytic protease; 3.15A {Saccharomyces cerevisiae S288C} SCOP: d.153.1.4

Probab=21.81 E-value=24 Score=31.44 Aligned_cols=13 Identities=85% Similarity=1.334 Sum_probs=0.0

Q ss_pred

Q Sun_Nov_08_06: 270

Q Consensus 270


T Consensus 224

T 3wxr_K 224

T ss_dssp

T ss_pred

No 73



>2i9z_A

Putative septation protein spovg; APC86317, staphylococcus epidermidis ATCC 12228, STRU genomics, PSI-2, protein structure initiative; 2.30A {Staphylococcus epidermidis} SCOP: d.366.1.1

Probab=21.44 E-value=2.3e+02 Score=23.11 Aligned_cols=34 Identities=12% Similarity=0.255 Sum_probs=0.0

Q ss_pred

Q Sun_Nov_08_06: 107

Q Consensus 107

T Consensus

T 2i9z_A

T ss_dssp

T ss_pred

7 TdVri~i~g-lkA-aSVt-d~fvI~IKVi

7 TDVRLRKIQTDGRMKALVSI~~TL~~DAFVIHDLRV

EEEEEECCSCSEEEEEETTEEEEEEE

EEEEEEeCCCCEEEEEEECEEEEeEEEE

40 (105)

40 (105)

Done!

Please cite as appropriate:

HHpred: Söding, J. (2005) Protein homology detection by HMM-HMM comparison. Bioinformatics 21: 951-960.

PSIPRED: Jones, D.T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. JMB 292: 195-202.

PDB: Bourne, PE. *et al.* (2004) The distribution and query systems of the RCSB Protein Data Bank. NAR 32: D223.