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MAX-PLANCK-GESELLSCHAFT

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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

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HHpred

HHsenser

HMMER3

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New job

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Resubmit_HMM

Resubmit/HHsenser

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HHpred - Results

Job-ID: p152_26993

Date: 00:21 on Apr 23 2015

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Results

Histogram

Reduced alignment

Representative alignment

Full alignment

Create model

Merge Q/T alignments

Forward to PCoils

Forward MSA

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Export

Color alignments

☐ color only SS

☒ color alignments

☐ color alignments

View alignment

Activate Jalview

Note: click PDBalert to upload your query sequence and get alerted by email as soon as better PDB templates get available.

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99

100

Resubmit section

4u6t_A

4jgu_A

1b4r_A

4aqq_A

2dlg_A

4kdw_A

4uyp_A

4l9d_A

1fo0_B

2yr1_A

1i3g_L

3sd2_A

1sq2_N

3shs_A

4nkd_B

2jjv_A

2yuz_A

1dlf_L

4hgw_A

3u6r_L

2coq_A

3bik_B

2dia_A

4aj0_A

2d7t_L

3noq_A

4unu_A

3bp6_A

3rgh_A

1jhl_L

1i8k_A

1qfw_H

3r8b_B

2e27_L

2qc1_B

1nqk_L

2dnc_A

4kju_B

2d7p_A

4hbc_L

1p4b_L

1j05_L

4ffy_L

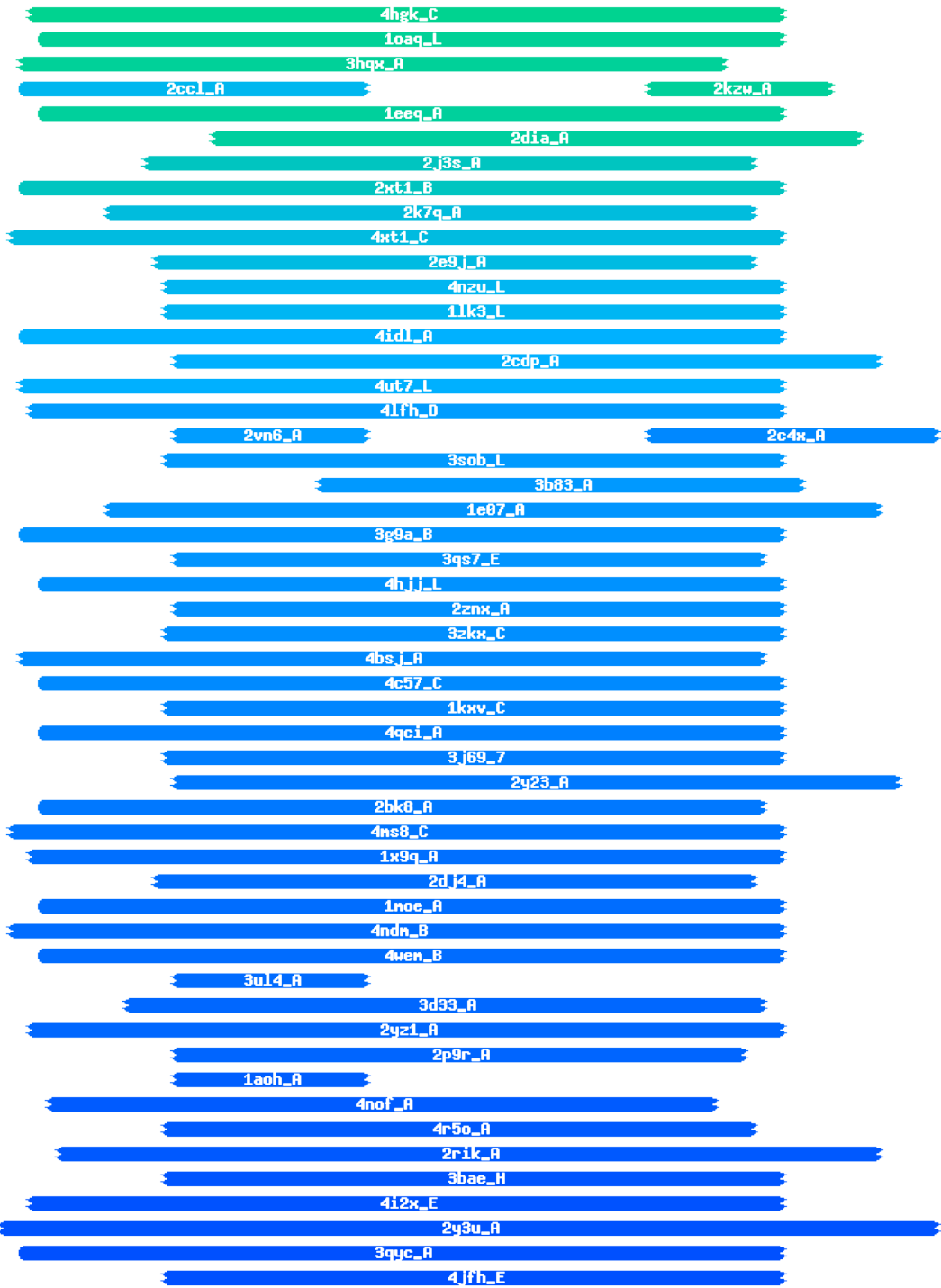
3r06_A

2d7n_A

4wnq_A

file:///Users/sjkim/Dropbox/NPC/POM152/HHPred/HHpred26993.webarchive

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Query Thu_Apr_23_00:21:36_+0200_2015 (seq=RVKPSASLKL...RDEGHHHHHH Len=111 Neff=5.5 Nseqs=93)
Parameters score SS:yes search:local realign with MAP:no

No Hit		Prob	E-value	P-value	Score	SS	Cols	Query	HMM	Template	HMM
<input type="checkbox"/>	1 4u6t_A	COLH protein, collagena	95.8	0.0083	2.4E-07	38.5	3.2	78	1-99	1-85	(86)
<input type="checkbox"/>	2 4jgu_A	COLH protein, collagena	95.7	0.024	7E-07	37.0	5.1	79	1-99	9-94	(95)
<input type="checkbox"/>	3 1b4r_A	Protein (PKD1_human); P	94.7	0.23	6.5E-06	31.7	7.3	69	6-87	1-69	(80)
<input type="checkbox"/>	4 4aqo_A	Collagenase, collagenas	94.2	0.11	3.2E-06	33.6	5.2	78	1-99	7-91	(92)
<input type="checkbox"/>	5 2dlg_A	Filamin-B; beta-sandwic	91.1	0.75	2.2E-05	30.6	5.9	63	15-79	12-74	(102)
<input type="checkbox"/>	6 4kdw_A	Antifreeze protein; bac	89.9	0.64	1.9E-05	32.2	5.0	55	25-86	46-109	(123)
<input type="checkbox"/>	7 419d_A	Protease; PKD domain, c	88.0	0.4	1.2E-05	30.8	2.6	29	68-98	56-84	(88)
<input type="checkbox"/>	8 1fo0_B	Protein (BM3.3 T cell r	85.6	3.2	9.1E-05	25.7	5.9	75	5-84	1-86	(112)
<input type="checkbox"/>	9 2yrl_A	KIAA1837 protein; PKD d	84.8	4.4	0.00013	26.3	6.5	55	25-87	23-83	(102)
<input type="checkbox"/>	10 1i3g_L	Antibody FV fragment; a	79.3	7.4	0.00021	23.4	5.7	73	4-82	3-82	(111)
<input type="checkbox"/>	11 3sd2_A	Putative member of DUF3	79.3	13	0.00038	24.9	8.8	60	16-80	30-89	(101)
<input type="checkbox"/>	12 1sq2_N	Novel antigen receptor;	78.8	5.7	0.00016	24.4	5.1	71	6-82	1-74	(113)
<input type="checkbox"/>	13 3shs_A	HOC head outer capsid p	78.2	13	0.00037	27.6	7.7	62	12-87	10-77	(304)
<input type="checkbox"/>	14 4nkd_B	Engineered SCFV light c	76.9	8.5	0.00024	24.5	5.7	74	3-82	4-89	(138)

<input type="checkbox"/>	15	2jju_A	Signal regulatory prote	76.8	6.8	0.0002	24.6	5.2	79	3-82	1-82	(127)
<input type="checkbox"/>	16	2yvw_A	NEW antigen receptor va	76.0	12	0.00035	22.7	6.4	71	6-82	1-74	(111)
<input type="checkbox"/>	17	1dlf_L	Anti-dansyl immunoglob	74.7	12	0.00034	22.4	5.7	72	5-82	1-84	(113)
<input type="checkbox"/>	18	4hgm_A	Shark V-NAR; IG-fold, h	74.6	8.4	0.00024	23.9	5.1	71	6-82	1-74	(112)
<input type="checkbox"/>	19	3u6r_L	Antibody 1:7 (light cha	74.1	10	0.0003	23.9	5.5	71	6-82	1-78	(143)
<input type="checkbox"/>	20	2coq_A	NEW antigen receptor va	74.1	11	0.00033	22.5	5.5	71	6-82	1-74	(108)
<input type="checkbox"/>	21	3bik_B	Programmed cell death p	73.1	16	0.00046	22.7	6.5	77	2-82	6-91	(134)
<input type="checkbox"/>	22	2dia_A	Filamin-B; beta-sandwic	72.6	20	0.00056	23.5	7.8	75	3-79	11-85	(113)
<input type="checkbox"/>	23	4aj0_A	Germinal LINE lambda 3	70.9	12	0.00034	22.3	5.0	72	5-82	1-78	(107)
<input type="checkbox"/>	24	2d7t_L	Anti polyhydroxybutyrat	70.6	14	0.00041	22.7	5.5	72	5-82	1-79	(116)
<input type="checkbox"/>	25	3moq_A	NEW antigen receptor va	69.6	21	0.0006	22.6	6.5	71	6-82	1-74	(126)
<input type="checkbox"/>	26	4unu_A	MCG, IG lambda chain V-	69.3	17	0.0005	21.6	5.5	73	4-82	1-82	(111)
<input type="checkbox"/>	27	3bp6_A	Programmed cell death p	69.3	18	0.00052	21.7	6.6	72	7-82	1-81	(117)
<input type="checkbox"/>	28	3rgh_A	Filamin-A; cell adhesio	69.0	22	0.00063	22.6	6.4	75	3-79	8-82	(100)
<input type="checkbox"/>	29	1jhl_L	IGG1-kappa D11.15 FV (1	68.6	18	0.00051	21.4	5.9	72	5-82	1-79	(108)
<input type="checkbox"/>	30	1i8k_A	Epidermal growth factor	67.6	17	0.0005	21.4	5.3	72	5-82	1-79	(107)
<input type="checkbox"/>	31	1qfw_M	FV, antibody (anti beta	67.5	18	0.00053	21.4	5.4	59	18-82	15-79	(108)
<input type="checkbox"/>	32	3r8b_B	G5-8, enterotoxin type	67.1	21	0.00062	21.8	5.8	74	4-82	4-87	(125)
<input type="checkbox"/>	33	2e27_L	Anti-ciguatoxin antibod	66.3	19	0.00055	22.2	5.4	74	3-82	1-81	(119)
<input type="checkbox"/>	34	2yc1_B	Single chain antibody f	66.3	18	0.00052	23.6	5.5	75	2-82	13-94	(146)
<input type="checkbox"/>	35	1mqk_L	Antibody 7E2 FV fragmen	66.2	20	0.00057	21.9	5.5	72	5-82	1-79	(120)
<input type="checkbox"/>	36	2dmc_A	Filamin-B; beta-sandwic	64.4	4.6	0.00013	27.0	2.2	62	15-78	26-87	(116)
<input type="checkbox"/>	37	4kjj_B	High-affinity sirpa var	64.0	21	0.0006	22.5	5.4	79	3-82	5-86	(133)
<input type="checkbox"/>	38	2d7p_A	Filamin-C; beta-sandwic	63.6	32	0.00093	22.6	6.5	74	3-79	11-84	(112)
<input type="checkbox"/>	39	4hbc_L	Antigen binding fragmen	63.3	21	0.00059	24.0	5.5	72	5-82	1-79	(213)
<input type="checkbox"/>	40	1p4b_L	Antibody variable light	63.2	29	0.00084	21.9	6.3	74	3-82	4-86	(135)
<input type="checkbox"/>	41	1j05_L	T84.66 antibody, anti-C	63.1	24	0.00068	20.9	5.3	59	18-82	15-83	(111)
<input type="checkbox"/>	42	4ffyl_L	DENV1-E111 single chain	62.9	18	0.00052	22.2	4.8	72	5-82	1-83	(126)
<input type="checkbox"/>	43	3r06_A	Anti-mouse CD3epsilon a	62.8	21	0.0006	24.0	5.4	59	18-82	15-79	(213)
<input type="checkbox"/>	44	2d7n_A	Filamin-C; beta-sandwic	62.3	28	0.0008	22.4	5.7	60	17-79	6-65	(93)
<input type="checkbox"/>	45	4wnq_A	TCR variable delta 1 ch	61.9	35	0.001	22.4	6.5	76	3-82	1-84	(207)
<input type="checkbox"/>	46	4hgk_C	Shark V-NAR antibody; I	61.5	22	0.00062	22.2	5.0	73	4-82	18-93	(128)
<input type="checkbox"/>	47	1oaq_L	Light chain; immune sys	61.1	28	0.0008	21.0	6.4	72	5-82	1-81	(120)
<input type="checkbox"/>	48	3hqx_A	UPF0345 protein aciad03	61.0	24	0.00069	24.3	5.4	64	3-76	17-89	(111)
<input type="checkbox"/>	49	2kzw_A	Uncharacterized protein	60.9	6.3	0.00018	27.6	2.5	19	68-87	110-128	(145)
<input type="checkbox"/>	50	1eeq_A	Kappa-4 immunoglobulin	60.8	22	0.00062	21.2	4.8	72	5-82	1-85	(114)
<input type="checkbox"/>	51	2dia_A	Filamin-B; beta-sandwic	60.6	36	0.001	22.2	6.8	67	23-90	43-112	(113)
<input type="checkbox"/>	52	2j3s_A	Filamin-A; cytoskeleton	58.7	14	0.00039	28.2	4.3	62	16-79	113-174	(288)
<input type="checkbox"/>	53	4uyp_A	SCAC, cellulosomal scaf	58.7	5.1	0.00015	28.8	1.7	21	19-39	14-41	(151)
<input type="checkbox"/>	54	2xt1_B	Camelid VHH 9; viral pr	58.7	34	0.00097	21.2	8.1	78	3-82	1-89	(121)
<input type="checkbox"/>	55	2k7q_A	Filamin-A; IG-like, ABP	57.0	13	0.00039	26.6	3.8	66	12-79	9-74	(191)
<input type="checkbox"/>	56	4xt1_C	Nanobody 7; GPCR, chemo	56.8	40	0.0012	21.5	6.9	79	2-82	2-90	(134)
<input type="checkbox"/>	57	2e9j_A	Filamin-B; beta-sandwic	56.7	21	0.00059	23.5	4.4	61	17-79	37-97	(119)
<input type="checkbox"/>	58	2ccl_A	Cellulosomal scaffoldin	55.9	4.4	0.00013	29.2	1.0	37	3-39	1-45	(158)
<input type="checkbox"/>	59	4nzu_L	13PL heavy chain; antib	55.8	32	0.00093	23.1	5.4	59	18-82	15-79	(211)
<input type="checkbox"/>	60	1lk3_L	9D7 light chain; antige	55.7	32	0.00092	23.0	5.4	59	18-82	14-78	(210)
<input type="checkbox"/>	61	4idl_A	Single domain antibody	54.9	43	0.0012	21.3	6.4	76	3-82	1-88	(136)
<input type="checkbox"/>	62	2cdp_A	Beta-agarase 1; carbohy	54.8	40	0.0011	23.6	5.9	73	19-92	66-154	(160)
<input type="checkbox"/>	63	4ut7_L	Broadly neutralizing hu	54.8	45	0.0013	21.5	6.2	74	3-82	2-84	(153)
<input type="checkbox"/>	64	4lfh_D	9C2 TCR delta chain; NK	53.2	56	0.0016	22.1	6.5	75	4-82	3-85	(236)
<input type="checkbox"/>	65	2vn6_A	Cohesin, scaffolding pr	53.2	7	0.0002	27.8	1.7	21	19-39	24-52	(151)
<input type="checkbox"/>	66	3sob_L	Antibody light chain; b	53.0	37	0.0011	23.2	5.4	59	18-82	38-102	(237)
<input type="checkbox"/>	67	3b83_A	Ten-D3; beta sheet, com	52.9	33	0.00095	20.6	4.7	47	34-84	32-78	(100)
<input type="checkbox"/>	68	1e07_A	Carcinoembryonic antige	52.6	51	0.0015	26.3	6.8	71	12-92	567-637	(642)
<input type="checkbox"/>	69	3g9a_B	Minimizer; antibody com	52.5	54	0.0015	21.7	6.1	76	3-82	1-88	(139)
<input type="checkbox"/>	70	3qs7_E	FL cytokine receptor; i	52.5	59	0.0017	24.8	7.0	57	19-80	341-399	(423)
<input type="checkbox"/>	71	4hjj_L	Anti-IL12 anti-IL18 DFA	52.3	36	0.001	24.1	5.4	72	5-82	1-79	(327)
<input type="checkbox"/>	72	2znx_A	SCFV; fluorotryptophan,	52.2	36	0.001	23.7	5.3	58	19-82	16-79	(242)
<input type="checkbox"/>	73	3zkk_C	XA4815; hydrolase; 2.37	52.1	47	0.0013	20.8	7.2	61	18-82	14-87	(122)
<input type="checkbox"/>	74	4bsj_A	Vascular endothelial gr	51.6	64	0.0018	22.3	6.9	71	3-80	3-76	(232)
<input type="checkbox"/>	75	4c57_C	Nanobody, cyclin-G-asso	51.6	49	0.0014	21.0	7.5	74	5-82	1-87	(141)
<input type="checkbox"/>	76	2c4x_A	Endoglucanase, ctcel19D-	51.5	11	0.00031	28.9	2.6	29	68-98	65-93	(260)
<input type="checkbox"/>	77	1kxv_C	Camelid VHH domain CAB1	51.3	43	0.0012	20.2	7.1	61	18-82	14-86	(121)
<input type="checkbox"/>	78	4qci_A	ANTI-PDGF-BB antibody -	50.8	22	0.00063	23.8	3.9	72	5-82	1-78	(209)
<input type="checkbox"/>	79	3j69_7	Nanobody VHH PVSP6A; pi	50.6	50	0.0014	20.7	6.0	63	18-82	14-87	(126)
<input type="checkbox"/>	80	2y23_A	Myomesin; structural pr	50.2	59	0.0017	22.9	6.2	72	19-94	236-311	(312)
<input type="checkbox"/>	81	2bk8_A	Connectin, M1, titin he	50.1	42	0.0012	19.7	7.8	71	5-80	1-79	(97)
<input type="checkbox"/>	82	4ms8_C	42F3 alpha; IG, TCR MHC	49.9	58	0.0017	21.3	5.9	77	2-82	2-86	(212)
<input type="checkbox"/>	83	1x9q_A	SCFV, 4M5.3 anti-fluore	49.4	42	0.0012	23.6	5.4	73	4-82	14-98	(268)
<input type="checkbox"/>	84	2dj4_A	Filamin-B; beta-sandwic	49.3	47	0.0013	21.4	5.2	61	17-79	26-86	(108)
<input type="checkbox"/>	85	1mo_e_A	Anti-CEA MAB T84.66; an	49.2	36	0.001	23.3	4.9	72	5-82	1-83	(240)
<input type="checkbox"/>	86	4ndm_B	AB18.1 TCR delta chain;	49.1	66	0.0019	21.7	7.4	77	2-82	9-93	(235)
<input type="checkbox"/>	87	4wem_B	Anti-F4+ETEC bacteria V	49.1	54	0.0015	20.6	7.1	76	5-82	1-86	(127)
<input type="checkbox"/>	88	3ul4_A	Cellulosome-anchoring p	49.0	9	0.00026	27.4	1.7	21	19-39	20-47	(157)
<input type="checkbox"/>	89	3d33_A	Domain of unknown funct	48.7	65	0.0019	21.5	9.1	64	14-80	31-95	(108)
<input type="checkbox"/>	90	2yz1_A	Tyrosine-protein phosph	48.7	26	0.00074	21.2	3.7	78	4-82	6-86	(120)
<input type="checkbox"/>	91	2p9r_A	Alpha-2-M, alpha-2-macr	48.5	55	0.0016	20.6	8.7	60	19-78	16-82	(102)
<input type="checkbox"/>	92	1aoh_A	Cellulosome-integrating	47.9	9.7	0.00028	26.8	1.7	21	19-39	18-45	(147)
<input type="checkbox"/>	93	4nof_A	Polymeric immunoglobuli	47.7	48	0.0014	19.9	4.9	68	6-75	4-92	(125)
<input type="checkbox"/>	94	4r5o_A	Quinonprotein alcohol d	47.5	43	0.0012	26.6	5.7	49	18-79	32-80	(427)
<input type="checkbox"/>	95	2rik_A	Titin; I-SET IG fold, p	47.5	67	0.0019	23.0	6.3	81	7-92	7-94	(284)
<input type="checkbox"/>	96	3bae_H	W02 IGG2A FAB fragment	47.1	62	0.0018	22.0	5.8	61	18-82	14-88	(228)
<input type="checkbox"/>	97	4i2x_E	Signal-regulatory prote	46.9	57	0.0016	23.6	5.9	78	4-82	2-82	(328)
<input type="checkbox"/>	98	2y3u_A	Collagenase, collagenas	46.9	4.8	0.00014	35.7	0.0	81	1-98	700-783	(785)
<input type="checkbox"/>	99	3qyc_A	VH domain of IGG molecu	46.8	65	0.0019	21.0	5.9	76	3-82	1-89	(146)
<input type="checkbox"/>	100	4jfh_E	BETA17 TCR allele; immu	46.8	44	0.0013	23.1	5.1	60	18-82	15-82	(244)

No 1



☐ >4u6t_A COLH protein, collagenase; calcium-binding protein, hydrolase; HET: P33; 1.76A {Clostridium histolyticum}
PDB: 4u7k_A

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T Consensus 75 ---L-I--v- 84 (113)
 T 1dlf_L 75 DFTLKISRVE 84 (113)
 T ss_dssp EEEEEECSCC
 T ss_pred eEEEECCCC

No 18    SCOPe   

☐ >4hgm_A Shark V-NAR; IG-fold, human albumin, V-NAR, immune system; 2.34A {Squalus acanthias} SCOP: **b.1.1.1**
 Probab=74.63 E-value=8.4 Score=23.91 Aligned_cols=71 Identities=11% Similarity=0.212 Sum_probs=0.0

Q ss_pred eEEeCC-CccecCCcCCeEEeEEeCC--CcEEEEEEeCCCCeEEEEeCcccccEEeCCcCCcCCeEEEEEE
 Q Thu_Apr_23_00: 6 ASLKLH-HDLKLCGLGHSSVPVAKGQG--PFTLYDIIETFSKRKTFEIKETNEYVIKTPVFTTGGDYILSLVSIK 82 (111)
 Q Consensus 6 A-F-----C-g--v-v-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG-y-v-L-sv- 82 (111)
 |.|... ..+.+.|++++.+.+.|+ +.+.|--- .|+.....+. .|+.+. .|+.+.|.|+|+
 T Consensus 1 a-i--p-----G--v-L-C-----v-W-k-----r-----L-I--v- 74 (112)
 T 4hgm_A 1 TRVDQSPSSLSASVGRVTITCVLTDTSYPLSYWYQK--PGSSNKEQISIS--GRYSESVN--KGTKSFTLTISLQ 74 (112)
 T ss_dssp CEEEEECSEEECTTCEEEEEEESSCCTCEEEEEEE--TTCCEEECCSC--TTEEEEEE--TTTEEEEEEESSC
 T ss_pred CeeEECCCCEEEEcCCCEEEEEcCCCCCCEEEEEEC--CCCCeEEEEEC--CcEEEEEc--CCCCEEEEEECCCC

No 19    SCOPe   

☐ >3u6r_L Antibody 1:7 (light chain); IG-like domain, neutralizing single chain FV, immune system; 2.67A {Homo sapiens} SCOP: **b.1.1.0**
 Probab=74.12 E-value=10 Score=23.87 Aligned_cols=71 Identities=14% Similarity=0.214 Sum_probs=0.0

Q ss_pred eEEeCC-CccecCCcCCeEEeEEeCCcCCeEEEEEEeCCCCeEEEEeCcc-----ccccEEeCCcCCcCCeEEEEEE
 Q Thu_Apr_23_00: 6 ASLKLH-HDLKLCGLGHSSVPVAKGQGPFLLTYDIETFSKRKTFEIKETNEYVIKTPVFTTGGDYILSL 78 (111)
 Q Consensus 6 A-F-----C-g--v-v-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG-y-v-L-sv- 78 (111)
 +.|... ..+.+.|++++.+.+.|+ +.+.|--- .|+.....+. .|+.+. .|+.+.|.|+|+
 T Consensus 1 P-i--p-----G--v-L-C-----v-W-k-----r-----L-I 74 (143)
 T 3u6r_L 1 AELTQSPATLSLSPGERATLSRASQSVNXYLAWYQK--PQAPRLIYDASNRATGIPARFSGS--GSGTDTFTLT 74 (143)
 T ss_dssp CEEEEECSEEECTTCEEEEEEESSCCTCEEEEEEE--TTCCEEEETTEECTTCCTTEEE--ETTEEEEEEE
 T ss_pred CccCcCCcEEEEcCCCCEEEEEEcCcCCcEEEEEc--CCCCEEEEEccccCccCcCCcEEEEE---eCCCEEEEE

Q ss_pred EEEE
 Q Thu_Apr_23_00: 79 VSIK 82 (111)
 Q Consensus 79 -sV- 82 (111)
 .|+|+
 T Consensus 75 --v- 78 (143)
 T 3u6r_L 75 SNLE 78 (143)
 T ss_dssp CCCC
 T ss_pred CCCC

No 20    SCOPe   

☐ >2coq_A NEW antigen receptor variable domain; IG VNAR, natural TYPE2, immune system; 2.10A {Orectolobus maculatus} SCOP: **b.1.1.1**
 Probab=74.12 E-value=11 Score=22.50 Aligned_cols=71 Identities=10% Similarity=0.076 Sum_probs=0.0

Q ss_pred eEEeCC-CccecCCcCCeEEeEEeCC--CcEEEEEEeCCCCeEEEEeCcccccEEeCCcCCcCCeEEEEEE
 Q Thu_Apr_23_00: 6 ASLKLH-HDLKLCGLGHSSVPVAKGQG--PFTLYDIIETFSKRKTFEIKETNEYVIKTPVFTTGGDYILSLVSIK 82 (111)
 Q Consensus 6 A-F-----C-g--v-v-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG-y-v-L-sv- 82 (111)
 +.|... ..+.+.|++++.+.+.|+ +.+.|--- .|+.....+. .|+.+. .|+.+.|.|+|+
 T Consensus 1 p-v--p-----G--v-L-C-----v-W-k-----r-----L-I--v- 74 (108)
 T 2coq_A 1 ARVDQTPRIATKETGESLTINCVLRDTACALDSTNWRVK--LGSTKEQITIS--IGGRYSETVD--EGSNSASLTIRDLR 74 (108)
 T ss_dssp CEEEEECSEEECTTCEEEEEEESSCCTCEEEEEEE--TTCCEEECC--CBTTEEEEEE--TTTEEEEEEESSC
 T ss_pred CeeEEcCceEEcCCCCEEEEEEcCCCCCCEEEEEEC--CCCCeEEEc--cCcEEEEEe--cCCcEEEEECCCC

No 21    SCOPe   

☐ >3bik_B Programmed cell death protein 1; CO-stimulation, receptor-ligand complex, immunoglobulin-like sandwich, T cell, B cell, programmed death; 2.65A {Mus musculus} SCOP: **b.1.1.1**
 Probab=73.13 E-value=16 Score=22.69 Aligned_cols=77 Identities=13% Similarity=0.242 Sum_probs=0.0

Q ss_pred CCCcEEeCC-CccecCCcCCeEEeEEeCC--CcEEEEEEeCCCCeEEEEe-----CcccccEEeCCcCCcCCc
 Q Thu_Apr_23_00: 2 VKPSASLKLH-HDLKLCGLGHSSVPVAKGQG--PFTLYDIIETFSKRKTFEIKETNEYVIKTPVFTTGG 72 (111)
 Q Consensus 2 --asA-F-----C-g--v-v-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG 72 (111)
 ..+.+.|... ..+.+.|++++.+.+.|+ +.+.|--- .|+.....+. .|+.+. .|+.+.|.|+|+
 T Consensus 6 --v--p-----G--v-L-C-----v-W-k-----r-----L-I--v- 81 (134)
 T 3bik_B 6 NGPWRSLTFYPAWLTVSEGANATFTCSLNSWEDLMLNWRLS--PSNQTEKQAASNGLSQPVQDARFQITQLP--NRH 81 (134)
 T ss_dssp ----CCEEEECSEEEETTSCEEEEEEESSCCTCEEEEEEE--TTCCEEEEEETTEEESSCTTEEEECT--TSS
 T ss_pred CCCCCEEECcEEeCCcCEEEEEeCCCCCCEEEEEEC--CCCCeEEEEcCCcCcccccCcEEEEEc--CCC







Q ss_pred eEEEEEEEEE
 Q Thu_Apr_23_00: 73 DYILSLVSIK 82 (111)
 Q Consensus 73 -y-v-L-sv- 82 (111)
 .|.|.|.+.|+|+
 T Consensus 82 ---L-I--v- 91 (134)
 T 3bik_B 82 DFHMNILDTR 91 (134)
 T ss_dssp EEEEEECSCC
 T ss_pred eEEEEECcCC

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fold, type II' beta turn., immune system; 1.80A {Mus musculus} SCOP: [b.1.1.1](#) PDB: [1i8i_A](#)
Probab=67.56 E-value=17 Score=21.45 Aligned_cols=72 Identities=13% Similarity=0.198 Sum_probs=0.0

```
Q ss_pred      ceEEeCC-CcceeccCCeEEeEEeCCcCEEEEEECCCCeEEEEEeCcc-----ccccEEeCCcCCcCEEE
Q Thu_Apr_23_00: 5 SASLKLH-HDLKLCGLDHSSVPVALKGQGPFTLTVDIETFSKRKTFEIKETI-----KTNEYVIKTPVFTTGGDYL 77 (111)
Q Consensus    5 sA-F-----C-g--v-v-V-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG-y-v- 77 (111)
               ...|... ..+..=..|+++..+..+..|..+..+..|---.. ..|+....+... ..+|..+.. ..++..+..|.
T Consensus    1 -----p-----G--v-L-C-----v-W-----r-----L----- 74 (107)
T 1i8k_A       1 DIELTQSPASLSVATGKVTIRCMSTTDIDDDMNWYQOK--PGEPPKFLISEGNTLRPGVPSRFSSS---GTGTFDFVFT 74 (107)
T ss_dssp      CCCEEECSEEECCCTTCCEEEEEESSCCTTCEEEEC--TTSCEEEETTTTECTTCTTEEE---ETTEEE
T ss_pred      CceeEEcCCeEEeCCCCEEEEeCCCCcEEEEEeC--CCCCEEEEEeCCcCCCCCCEEE---cCCCEEE
```

```
Q ss_pred      EEEEE
Q Thu_Apr_23_00: 78 LVSIK 82 (111)
Q Consensus    78 L-sV- 82 (111)
               |..+|+
T Consensus    75 I--v- 79 (107)
T 1i8k_A       75 IENTL 79 (107)
T ss_dssp      ESSCC
T ss_pred      ECCCC
```

No 31    SCOPe  PDB  NCBI  PubMed

☐ >1qfw_M FV, antibody (anti beta subunit) (light chain); glycoprotein hormone; HET: NAG; 3.50A {Mus musculus}
SCOP: [b.1.1.1](#)
Probab=67.50 E-value=18 Score=21.37 Aligned_cols=59 Identities=8% Similarity=0.179 Sum_probs=0.0







```
Q ss_pred      cCCCEeeEEeCCCCEEEEEeCCCCeEEEEEcCcc-----cccEEeCCcCCcCEEEEEEE
Q Thu_Apr_23_00: 18 LGDHSSVPVALKGQGPFTLTVDIETFSKRKTFEIKETI-----TNEYVIKTPVFTTGGDYL 82 (111)
Q Consensus    18 -g--v-v-V-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG-y-v-L-sV- 82 (111)
               ..|+++..+..+..|..+..+..|---.. ..|+....+... ..+|..+.. ..++..+..|.
T Consensus    15 -G--v-L-C-----v-W-----r-----L----- 79 (108)
T 1qfw_M       15 VGERVTLSCKASSETVDSFVSWYQOK--PEQSPKLLIFGASNRFSGVDRFTGS---GSATDFTLTISVQ 79 (108)
T ss_dssp      TTCEEEEEESSCCCEEEEC--TTSCEEEECSSCBCTTCTTEEC---BCSSEEEESSCC
T ss_pred      CCCCEEEeCCcCCcCEEEEC--CCCCEEEEEcCccCCCCCCEEE---eCCCEEEEC
```

No 32    SCOPe  PDB  NCBI  PubMed

☐ >3r8b_B G5-8, enterotoxin type B; immunoglobulin-like, OB-fold, toxin-immune system complex; 2.95A {Rattus norvegicus} SCOP: [b.1.1.1](#)
Probab=67.05 E-value=21 Score=21.77 Aligned_cols=74 Identities=8% Similarity=0.078 Sum_probs=0.0

```
Q ss_pred      CceEEeCC-CcceeccCCeEEeEEeCCcCEEEEEECCCCeEEEEEcCcc-----cccEEeCCcCCcCE
Q Thu_Apr_23_00: 4 PSASLKLH-HDLKLCGLDHSSVPVALKGQGPFTLTVDIETFSKRKTFEIKETI-----TNEYVIKTPVFTTGGD 73 (111)
Q Consensus    4 asA-F-----C-g--v-v-V-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG- 73 (111)
               +..+..|... ..+..=..|+++..+..+..|..+..+..|---.. ..|+....+... ..+|..+.. ..++..+..|.
T Consensus    4 -----v-p-----G--v-L-C-----v-W-----r-----L----- 78 (125)
T 3r8b_B       4 LEAAVTQSPRNKVAVTGKVTLSCKQNTSYFNMYWYQOD--TGHELRLIFMSHGIRNVEKGDIPDGYKASRP---SQEN 78 (125)
T ss_dssp      -CCEEEEECSEEEETTCCEEEEEEESSCCSEEEEC--TTSCEEEESSTTCCEECSSCTTEEE---ETTE
T ss_pred      cccceEEcCCcCEEEcCCcEEEEEeCCCCCCEEEEC--CCCCCEEEECcCccCCCCCCEEEc---CCc
```

```
Q ss_pred      EEEEEEE
Q Thu_Apr_23_00: 74 YLLSLVSIK 82 (111)
Q Consensus    74 y-v-L-sV- 82 (111)
               +..+..|..+|+
T Consensus    79 --L-I--v- 87 (125)
T 3r8b_B       79 FSLILELAT 87 (125)
T ss_dssp      EEEETTC
T ss_pred      EEEEEcCC
```

No 33    SCOPe  PDB  NCBI  PubMed

☐ >2e27_L Anti-ciguatoxin antibody, light chain; immunoglobulin fold, immune system; HET: AB0; 1.70A {Mus musculus}
SCOP: [b.1.1.0](#) PDB: [3iy1_A](#)
Probab=66.30 E-value=19 Score=22.24 Aligned_cols=74 Identities=12% Similarity=0.177 Sum_probs=0.0

```
Q ss_pred      CCceEEeCC-CcceeccCCeEEeEEeCCcCEEEEEECCCCeEEEEEcCcc-----ccccEEeCCcCCcCE
Q Thu_Apr_23_00: 3 KPSASLKLH-HDLKLCGLDHSSVPVALKGQGPFTLTVDIETFSKRKTFEIKETI-----KTNEYVIKTPVFTTGGD 75 (111)
Q Consensus    3 -asA-F-----C-g--v-v-V-l-G--PftL-yeiv---gk-----v-i-----I-tp---GG-y- 75 (111)
               +...|... ..+..=..|+++..+..+..|..+..+..|---.. ..|+....+... ..+|..+.. ..++..+..|.
T Consensus    1 -----v-p-----G--v-L-C-----v-W-k-----r-----L----- 74 (119)
T 2e27_L       1 MADIQMTQSPSSLASLGGKVTITCKANQDVKKIAWYQHK--PGKGPRLLIYYTSLKSGISRRFSGS---GSGRDYS 74 (119)
T ss_dssp      ---CCEEEEECSEEEETTCCEEEEEEESSCCTTCEEEEC--TTSCEEEETTTTECTTCTTEEE---ETTEEE
T ss_pred      CCcccEEcCceEEeCCcCEEEeCCCCcEEEEEc--CCCCEEEEEccccCCcCCcCEEE---cCCCEE
```

```
Q ss_pred      EEEEEEE
Q Thu_Apr_23_00: 76 LSLVSIK 82 (111)
Q Consensus    76 v-L-sV- 82 (111)
               |..+|+
T Consensus    75 L-I--v- 81 (119)
T 2e27_L       75 FSLINLE 81 (119)
T ss_dssp      EECCSCC
T ss_pred      EEECCC
```

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☐ >1e07_A Carcinoembryonic antigen; glycoprotein, CEA, tumour marker, immunoglobulin-fold; NMR {Homo sapiens} PDB: 2dks_A
Probab=52.62 E-value=51 Score=26.34 Aligned_cols=71 Identities=11% Similarity=0.097 Sum_probs=0.0

```
Q ss_pred          CcCecccCCCeEEeECCcCEEEEEECCCCCEEEEEECCCCcCEEEEEEcccCCccc
Q Thu_Apr_23_00:   12 HDLKLCLGDHSSVPVALKGQGPFTLTLDIETFSKKRKTFEIKETNEYVIKTPVFTTGGDYILSLVSIKSTGCVVGL 91 (111)
Q Consensus        12 -----C-g-v-v-V-l-G-PftL-yeiv-----gk-----v-i-----I-tp-----GG-y-v-L-s-V-D-GC---L 91 (111)
                   .....|+++..+...|.|-+++|..  +|+...  .+...|.---.....|.|.---+---+...|
T Consensus        567 ~-v-g~-l-C~-g-p~-v-W~-g-l-----L-i-----d-G-Y-C-a-N-G~-s~l 636 (642)
T 1e07_A           567 PDSSYLSGANLNLCHSASNPSPQYSWRI-----NGIPQQ-----HTQVLFIKAITPNNNGTYACFVSNLATGRNNSIVK 636 (642)
T ss_pred          CCcEEECcCEEEEEECCCCCCEEEEEE-----CCEEEc-----cCceEEEEcCccCCcCEEEEEEcccCccceEEE
```

```
Q ss_pred          C
Q Thu_Apr_23_00:   92 S    92 (111)
Q Consensus        92 ~    92 (111)
                   .
T Consensus        637 ~    637 (642)
T 1e07_A           637 S    637 (642)
T ss_pred          E
```

No 69        

☐ >3g9a_B Minimizer; antibody complex, chromophore, luminescence, photoprotein, fluorescent protein-immune system complex, nanobody; HET: GYS; 1.61A {Camelus dromedarius} SCOP: b.1.1.1
Probab=52.53 E-value=54 Score=21.66 Aligned_cols=76 Identities=12% Similarity=0.146 Sum_probs=0.0

```
Q ss_pred          CCcEEcCCcCCcCCcCEEEcCCc-----CCcEEEEEEcCCcCEEEc-----CccccEEEEcCCcCC
Q Thu_Apr_23_00:   3 KPSASLKLHHDHKLCLGDHSSVPVALKGQ--GPFTLTLDIETFSKKRKTFEI-----KEIKTNEYVIKTPVFTT 70 (111)
Q Consensus        3 -asA-F-----C-g-v-v-V-l-G---PftL-yeiv-----gk-----v-i-----I-tp----- 70 (111)
                   +|...+.+.+.+.+.|+++..+...+.+.  ++.+.|-...  .+.....+  ..-...+|+.+...  .
T Consensus        1 ~-v~-v~-v~-G~-VtL-C~-g-p~-v-W~-g-l-----L-i-----d-G-Y-C-a-N-G~-s~l 76 (139)
T 3g9a_B           1 MADVQLQESGGGSVQAGGSLRLSCAASGDTFSSYSMAWFRQA--PGKECELVSNILRDGTTTYAGSVKGRFTISRDD--A 76 (139)
T ss_dssp          ---CCEEEESEEECTTCEEEEEEESSCGGGSEEEEEEC--TSCEEEEEECTTCEEECTTTTTEEEET--T
T ss_pred          CCcEEECcCEEEcCCCEEEEcCccCCCCcCEEEEEEc-----CCcCEEEEEEcCCCEEEcCCcCceEEEEcC--C
```

```
Q ss_pred          CceEEEEEEEEE
Q Thu_Apr_23_00:   71 GGDYILSLVSIK 82 (111)
Q Consensus        71 GG-y-v-L-sV~ 82 (111)
                   .+.+.|.|.+.+
T Consensus        77 ~-sL-I~-v~ 88 (139)
T 3g9a_B           77 KNTVYLQMVNLK 88 (139)
T ss_dssp          TEEEEEECCSC
T ss_pred          CceEEEECCCC
```

No 70       

☐ >3qs7_E FL cytokine receptor; immunoglobulin-like domain, four-helical bundle cytokine, CY receptor complex, extracellular complex; HET: NAG; 4.30A {Homo sapiens}
Probab=52.46 E-value=59 Score=24.83 Aligned_cols=57 Identities=23% Similarity=0.203 Sum_probs=0.0

```
Q ss_pred          CCcEEEEEEcCCcCEEEEEECCCCCEEEEEECCCCcCEEEEEE--eCCCCcCCcCEEEEEE
Q Thu_Apr_23_00:   19 GDHSSVPVALKGQGPFTLTLDIETFSKKRKTFEIKETNEYVI--KTPVFTTGGDYILSLVS 80 (111)
Q Consensus        19 g-v-v-v-V-l-G--PftL-yeiv-----gk-----v-i-----I-tp-----GG-y-v-L-s 80 (111)
                   |+++..+...+.|.|-+++|..  +|+.....  ..+.|.  ..-...|.|.+++..+
T Consensus        341 G-----l-C~-g-p-p-i-W-k~-g~l-----D-G-Y-C-a-N 399 (423)
T 3qs7_E           341 YEECFSVRKAYPQIRCTWTF---SRKSFPCQKG-LDNGYSISKFCNHKHPGEYIFHAEN 399 (423)
T ss_dssp          TCCCCEEEEEEESCEEEEEE---TTEEEECBCB-CSSSSSEEEECCTTCCSEEEEEE
T ss_pred          CCcEEEEEEcCCCEEEEEE---CCccccCcccc-ccccEEEEEcCccCceEEEEEEc
```

No 71       

☐ >4hjj_L Anti-IL12 anti-IL18 DFAB light chain; DFAB complex, dual variable domain immunoglobulin, IM system; 2.10A {Homo sapiens} SCOP: b.1.1.0 b.1.1.0 b.1.1.0
Probab=52.25 E-value=36 Score=24.14 Aligned_cols=72 Identities=11% Similarity=0.221 Sum_probs=0.0

```
Q ss_pred          ceEEECc-CccecCCcCEEEcCEEEcCCCCCEEEEEECCCCCEEEEEECCCC-----cccEEEEcCCcCCcCEEEEEE
Q Thu_Apr_23_00:   5 SASLKLH-HDLKLCLGDHSSVPVALKGQGPFTLTLDIETFSKKRKTFEIKETNEYVIKTPVFTTGGDYILSLVS 77 (111)
Q Consensus        5 sA-F-----C-g-v-v-V-l-G--PftL-yeiv-----gk-----v-i-----I-tp-----GG-y-v- 77 (111)
                   .+|.  ..+.+.+.|+++..+...+.|.|-+++|..  +|+.....  ..+.|.  ..-...|.|.+++..+
T Consensus        1 ~-v~-p~-v~-G~-V-L-C~-p~-v-W-k~-g~l-----L-i-----d-G-Y-C-a-N 74 (327)
T 4hjj_L           1 DIVMTQSPDSLAVSLGERATINCKASQSVSNDVAWYQKQ--PGPPKLLIYYASNRYTGVPRFSGS---GSGTDFTLT 74 (327)
T ss_dssp          CCCEEEECSEEEECTTSCEEEEEESSCCTTCEEEEEEc--TSCCEEEETTEECTTCCTTEEEE---EETTEEEEEE
T ss_pred          CccecCCcCEEEcCCCCCEEEEEEcCCcCCcCEEEEEEc-----CCcCEEEEEEccccCccceEEEEE---CCcCEEEEEE
```

```
Q ss_pred          EEEEE
Q Thu_Apr_23_00:   78 LVSIK 82 (111)
Q Consensus        78 L~sV~ 82 (111)
                   |.+.+
T Consensus        75 i~-v~ 79 (327)
T 4hjj_L           75 ISSLE 79 (327)
T ss_dssp          ESSCC
T ss_pred          EccCC
```

Q ss pred ccCCceEEEEEEEEEcccCCccccCCCCeEE

Q Thu_Apr_23_00: 68 FTTGGDYILSLVSIKIDSTGCVVGLSQPDAKI 98 (111)
Q Consensus 68 ---GG-y-v-L-sV-D--GC---L---v-I 98 (111)
+..-|.|.|. |+|.|.|. .|. |
T Consensus 65 y---G-YtVtLt-Vtd--G-s-t-t---ItV 93 (260)
T 2c4x_A 65 YKNPGTYKVKLI-VTDNQGASSFTA-TIKV 93 (260)
T ss_dssp CSSCEEEEEEE-EEETTSCEEEEE-EEEE
T ss_pred eCCcCEEEEEEE-EEcCCCCCEEEEE-EEEE

No 77       

☐ >1kxy_C Camelid VHH domain CAB10; beta 8 alpha 8, beta barrel, hydrolase, immune system; 1.60A {Camelus dromedarius} SCOP: b.1.1.1
Probab=51.28 E-value=43 Score=20.24 Aligned_cols=61 Identities=15% Similarity=0.196 Sum_probs=0.0

Q ss_pred cCCcEEEEEEcC--CCcEEEEEEcCCcCEEEEEcCccc-----ccEEECcCCcCCcCEEEEEEE
Q Thu_Apr_23_00: 18 LGDHSSVPVALKGQ--GPFTLTyDIETfSSKRKTfEIKIKT-----NEYVIKTPVFTTGGDYILSLVSIK 82 (111)
Q Consensus 18 -g--v-v-V-l-G---PftL-yeiv--gk---v-i-----I-tp---GG-y-v-L-sV- 82 (111)
|.+++|.+++|. .+.+.|-.. .+.....+. .+.+. .+.+.|.|. |
T Consensus 14 -G--v-L-C---p--v-W-k-----r-----sL-I--v- 86 (121)
T 1kxy_C 14 AGGSLRLSCAASGNTLCTYDMSWYRRA--PGKGRDFVSGIDNDGTTTYVDVSVAGRFTISQGN--AKNTAYLQMDSLK 86 (121)
T ss_dssp TTCEEEEEEEESCCTCEEEEEEEc---TTSCEEEEEEcTCEEECGGBTTfEEEEECs--STfEEEEEEcSCC
T ss_pred CCCCEEEEEcCCcCccceEEEEEEc---CCCcEEEEEEcCCcCEEEcCcccccEEEEEEcC--CCcEEEEEEcCCC

No 78       

☐ >4qci_A ANTI-PDGF-BB antibody - light chain; growth factor cytokine fold, growth factor hormone, PDGFR-BE receptor, extracellular; 2.30A {Homo sapiens}
Probab=50.81 E-value=22 Score=23.76 Aligned_cols=72 Identities=10% Similarity=0.171 Sum_probs=0.0

Q ss_pred ceEEECcCccceccCCcEEEEEEcCCcCEEEEEEEcCCcCEEEEEcCcc-----ccccEEECcCCcCCcCEEEEEEE
Q Thu_Apr_23_00: 5 SASLKLHHDLLKCLGDHSSVPVALKGQGPFTLTyDIETfSSKRKTfEIKIKT-----KTNEYVIKTPVFTTGGDYILSLVSIK 78 (111)
Q Consensus 5 sA-F-----C-g--v-v-V-l-G---PftL-yeiv--gk---v-i-----I-tp---GG-y-v-L-sV- 78 (111)
|.+++|.+++|. .+.+.|-.. .+.....+. .+.+. .+.+.|.|. |
T Consensus 1 q--v--v--v--G--v-L-C---p--v-W-k-----r-----sL-I--v- 74 (209)
T 4qci_A 1 SYELTQPPSVVAPGQTARISCSGDSLSGSYFVHWYQK--PGQAPVLVIYDDSNRPSGIPERFSGSN--SGNTATLTI 74 (209)
T ss_dssp -CCBCCSEEEECCTSCEEEEEEcTGGGBcCEEEEEc---TTSCEEEEBTTCCTTCCTfEEEEE--ETfEEEEE
T ss_pred CCcEEECcEEECcCCcCEEEEEEEcCccceEEEEEEc---CCCcEEEEEEcCccCCcCccEEEEc---cCCcEEEEEE

Q ss_pred EEEE
Q Thu_Apr_23_00: 79 VSIK 82 (111)
Q Consensus 79 -sV- 82 (111)
|.+++|.+++|. .+.+.|-.. .+.....+. .+.+. .+.+.|.|. |
T Consensus 75 --v- 78 (209)
T 4qci_A 75 SGTQ 78 (209)
T ss_dssp SSCC
T ss_pred cccc

No 79       

☐ >3j69_7 Nanobody VHH PVSP6A; picornavirus, antibody, poliovirus, mechanism neutralization, virus-immune system complex; HET: MYR PLM; 4.80A {Camelus dromedarius}
Probab=50.57 E-value=50 Score=20.71 Aligned_cols=63 Identities=10% Similarity=0.056 Sum_probs=0.0

Q ss_pred cCCcEEEEEEcC--CcEEEEEEcCCcCEEEEEcCccc-----cccEEECcCCcCCcCEEEEEEE
Q Thu_Apr_23_00: 18 LGDHSSVPVALKGQ--PFTLTyDIETfSSKRKTfEIKIKT-----TNEYVIKTPVFTTGGDYILSLVSIK 82 (111)
Q Consensus 18 -g--v-v-V-l-G---PftL-yeiv--gk---v-i-----I-tp---GG-y-v-L-sV- 82 (111)
|.+++|.+++|. .+.+.|-.. .+.....+. .+.+. .+.+.|.|. |
T Consensus 14 -G--v-L-C---p--v-W-k-----r-----sL-I--v- 87 (126)
T 3j69_7 14 TGGSLRLSCAASGPTFSHGMAWFRQAPKEKEWVACVRTSGVSAYYADSVLGRFTISQDN--AKSTLYLQMNLLK 87 (126)
T ss_dssp TTCEEEEEEEcSCCSCSEEEEEcSSSScEEEEEEcSSCCfEECTTTTfEEEEEg--GfTfEEEEEcSCC
T ss_pred CCCCEEEEEcCCcCccceEEEEEEcCCCCCEEEEEEEcCCcCEEEcCcccccEEEEEEcC--CCCfEEEEEcCCC

No 80       

☐ >2y23_A Myomesin; structural protein, sarcomere, M-BAND, immunoglobulin-like; 2.50A {Homo sapiens} PDB: 4v10_A
Probab=50.15 E-value=59 Score=22.90 Aligned_cols=72 Identities=8% Similarity=0.108 Sum_probs=0.0

Q ss_pred CCcEEEEEEcC--CCcEEEEEEcCCcCEEEEE-eCcccccEEECcCCc--CCcEEEEEEEEccCcccccCCC
Q Thu_Apr_23_00: 19 GDHSSVPVALKG-QGPFTLTyDIETfSSKRKTfEIKIKTNEYVIKTPVFT--TGGDYILSLVSIKIDSTGCVVGLSQP 94 (111)
Q Consensus 19 g--v-v-V-l-G---PftL-yeiv--gk---v-i-----I-tp---GG-y-v-L-sV-D--GC--L- 94 (111)
|.+++|.+++|. .+.+.|-.. .+.....+. .+.+. .+.+.|.|. |
T Consensus 236 g--v-l-C---p--v-W-k-----L-i-v--d-G-Y-C-a-N--G--l-- 311 (312)
T 2y23_A 236 ECNVLLKCKVANIKKETHIVVYK---DEREISVDEKHDfKDGICTLLITfESKKGAGIYfVILKDDRGKDKSRLLKLVDE 311 (312)
T ss_dssp TTEEEEEEEESCSCSEEEEEc---TTEEEEEcCC---CEEEEEcSCSGGGCEEEEEEESTTCCEEEEEEEcSC
T ss_pred CCEEEEEEEcCCcCccceEEEEEEc---CCEECcCccCEEECEEEEEEEcCcccccEEEEEEEEcCEEEEEEEEEc

No 81       

☐ >2bk8_A Connectin, M1, titin heart isoform N2-B; IG domain, M-BAND, structural protein, muscle, antio; 1.69A {Homo sapiens}
Probab=50.10 E-value=42 Score=19.74 Aligned_cols=71 Identities=14% Similarity=0.169 Sum_probs=0.0

Q ss_pred ceEEEC--CccceccCCcEEEEEEcC--CCcEEEEEEcCCcCE---EEECcCcccccEEECcCCc--CCcEEEC
Q Thu_Apr_23_00: 5 SASLKLH-HDLKCLGDHSSVPVALKG-QGPFTLTyDIETfSSKRK---TFEIKIKTNEYVIKTPVFT--TGGDYIL 76 (111)

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2.60A {Mus musculus} SCOP: [b.1.1.1 b.1.1.1](#)

Probab=49.19 E-value=36 Score=23.32 Aligned_cols=72 Identities=11% Similarity=0.110 Sum_probs=0.0

```
Q ss_pred          ceEEeCC-CcEEccCCeEEeEEecCC----CcEEEEEEeCCCCeEEEEeCccc-----cccEEeCCcCCcCce
Q Thu_Apr_23_00:   5 SASLKLH-HDLKLCGLDHSSVPVAlKGQ---PFTLTyDIETfSSKRKTfEIKIK-----TNEYVVIKTPVFTTGGD 73 (111)
Q Consensus        5 sA-F-----C-g--v-v-V-l-G-----PftL-yeiv---gk-----v-i-----I-tp---GG- 73 (111)
                  .+|. .+.+. .|++++.+.+.|. | .+.+|---. +|+.....+... ..+|.+. .+.+.
T Consensus        1 -----p-----v-G--v-L-C-----v-W-k-----r----- 74 (240)
T lmoec_A           1 DIVLTQSPASLAVSLGQRATMSCRAGESVDIFGVGFLHWYQOK--PGQPPKLLIYRASNLGSGIPVRfSGT---GSRTD 74 (240)
T ss_dssp           CCCEEECSEEEECTTSCEEEEEESSCCETTECEEEEEEC---TTSCEEEETTTECTTCCTTEEE---ETTE
T ss_pred           CCcEEcCCeEEeCCcCEEEeCCcCCcCEEEEEEC---CCCCeEEEEECcCCcCCcCEEE---cCCCE
```

```
Q ss_pred          EEEEEEE
Q Thu_Apr_23_00:   74 YILSLVSIK 82 (111)
Q Consensus        74 y-v-L-sV~ 82 (111)
                  +|.|.+.+
T Consensus        75 --L-I--v~ 83 (240)
T lmoec_A           75 FTLLIDPVE 83 (240)
T ss_dssp           EEEEESSCC
T ss_pred           EEEEECCCC
```

No 86        

☐ >4ndm_B AB18.1 TCR delta chain; immunoglobulin, histocompatibility antigens, T cell receptor immunological, lymphocytes, T cell recognition, activation; 3.01A {Homo sapiens} SCOP: [b.1.1.2 b.1.1.0](#)
Probab=49.11 E-value=66 Score=21.68 Aligned_cols=77 Identities=9% Similarity=0.168 Sum_probs=0.0

```
Q ss_pred          CCCcEEeCC-CcEEccCCeEEeEEecC-CcEEEEEEeCCCCeEEEEeCccc-----cccEEeCCcCCcCCcCce
Q Thu_Apr_23_00:   2 VKPSASLKLH-HDLKLCGLDHSSVPVAlKGQ-GPFTLTyDIETfSSKRKTfEIKIK-----TNEYVVIKTPVFTTGGD 73 (111)
Q Consensus        2 --sA-F-----C-g--v-v-V-l-G-----PftL-yeiv---gk-----v-i-----I-tp---GG- 73 (111)
                  +.....|. .+.+. .|++++.+.+.|. |.+.+|.---. .+.+.+.+.+. .+.+.+.+.+.
T Consensus        9 -----v-----p-----G-v-L-C-----v-W-k-----r----- 84 (235)
T 4ndm_B            9 EDPAQKVTAQSSVSMPVRKAVTLNCLYETSWWSYYIFWYKQL--PSKEMIFLIHQGSDEQNAKSGRYSVNFK--KAAKS 84 (235)
T ss_dssp           ---CEEEECcCCcEEETTSCEEEEEEECCSSCEEEEEEEEC---TTCCEEEEEEESSCCCEETTEEEEEE---TTTTE
T ss_pred           CCCcCCcEEcCcEEEEeCCcEEEEeEEecCCcCEEEEEeC---CCCCeEEEEECcCCcCCcCEEEEEc---CCcCE
```

```
Q ss_pred          EEEEEEE
Q Thu_Apr_23_00:   74 YILSLVSIK 82 (111)
Q Consensus        74 y-v-L-sV~ 82 (111)
                  +|.|.+.+
T Consensus        85 --L-I--v~ 93 (235)
T 4ndm_B            85 VALTISALQ 93 (235)
T ss_dssp           EEEEESSCC
T ss_pred           EEEEEcCC
```

No 87       

☐ >4wem_B Anti-F4+ETEC bacteria VHH variable region; complex, llama single domain antibody, adhesin, nanobody, ST protein; 1.55A {Lama glama}
Probab=49.07 E-value=54 Score=20.65 Aligned_cols=76 Identities=9% Similarity=0.027 Sum_probs=0.0

```
Q ss_pred          ceEEeCCCCcEEccCCcEEeEEecC---CCeEEEEEEeCCCCeEEEEe-----CccccEEeCCcCCcCCcCeE
Q Thu_Apr_23_00:   5 SASLKLHHDHLKLCGLDHSSVPVAlKGQ--GPFTLTyDIETfSSKRKTfEIKIK-----KEIKTNEYVVIKTPVFTTGGDy 74 (111)
Q Consensus        5 sA-F-----C-g--v-v-V-l-G-----PftL-yeiv---gk-----v-i-----I-tp---GG-y 74 (111)
                  ..+.+.+.+.+. .|++++.+.+.+. .+.+.+|-----..... .+.+.+.+.+. .+.+.
T Consensus        1 -v-v-----v-v-G--v-L-C-----v-W-k-----i-----R----- 78 (127)
T 4wem_B            1 QVQLQESGGGLVQAGGSLRLSCEASGNVDRIDAMGFRQAPGKQRFVGYISEGGILNYGDFVKGRFTISRDN--AKNTV 78 (127)
T ss_dssp           CEEEEECCEEEETTCCEEEEEEESGGGCCCEEEECTTSCCEEEECTTCEEEECTTCCTTEEEEEG--GGTEE
T ss_pred           CcEEECcCCcEEeCCcCEEEEEeCCcCceEEEEEEeCCCCCCEEEEEeCCcEEeCccCceEEEEEc---CCcCE
```

```
Q ss_pred          EEEEEEE
Q Thu_Apr_23_00:   75 ILSLVSIK 82 (111)
Q Consensus        75 -v-L-sV~ 82 (111)
                  +|.|.+.+
T Consensus        79 sL-I--v~ 86 (127)
T 4wem_B            79 YLQMSNLK 86 (127)
T ss_dssp           EEEECSCC
T ss_pred           EEEECcCC
```

No 88        

☐ >3u14_A Cellulosome-anchoring protein; cohesin, type I cohesin-dockerin COMP protein-protein interaction, cell adhesion; HET: PEG; 1.95A {Clostridium thermocellum} SCOP: [b.2.2.0](#)
Probab=49.02 E-value=9 Score=27.40 Aligned_cols=21 Identities=48% Similarity=0.822 Sum_probs=0.0

```
Q ss_pred          CCcEEeEEEEcC-----CcEEEE
Q Thu_Apr_23_00:   19 GDHSSVPVAlKGQ-----PFTLTyD 39 (111)
Q Consensus        19 g--v-v-V-l-G-----PftL-ye 39 (111)
                  |+++++|.+.+| .+.+|
T Consensus        20 G-tf-V-v--nvp--gi-s--f-l-YD 47 (157)
T 3u14_A            20 GDRIEVPVSLKNVPDKGIVSSDFVIEYD 47 (157)
T ss_dssp           TCEEEEEEEESCCTTCEEEEEEEEC
T ss_pred           CCEEEEEEEEcCccCCEeEEEEEEEC
```

```

Q ss_pred          eEEeCC-CccceccCCCeeeeEEEEeCC-CcEEEEEEeCCCC-----cEEEEEEcccccccEEFeCC
Q Thu_Apr_23_00:  6 ASLKLH-HDLKLCIGDHSSVPALKGQG-PfTLTYDITFTSS          KRKFTEIKTKFNEVXIKTP    66 (111)
Q Consensus       C-g-v-v-V-L-G-PfTL-yeiv-g          -k-v-i-          I-tp    66 (111)
                  +.|... ..+.=.|+++|++=+.+|. + |.+|+---. .+          .|.....+.....+|.+.
T Consensus       -g-v-L-C          -W          -g-rakL-fmkgDlTVFYVNIS    81 (125)
T 4nof_A          4 GGLPSDTHVYTKDIGRNVITCEPFKRENAPSKKSLCKKT--NQSCELVIDSTEKVNPSYIGRAKLFMKGDTLVFYVNI    81 (125)
T ss_dssp          CCCTCTCEEEEEETTCCEEEEECCGGGTTCSEEEEEEC--SSCEEEEEETTSCBCTTTTTTEEEECCTCTTTEEEEEEC
T ss_pred          cccCCCCcCEEEECCEEEECCECCcccceCEEEEEEC--CCceEEECcCcccccCCCCcCEEEECcCCCTCCcCEEEEC

```


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