

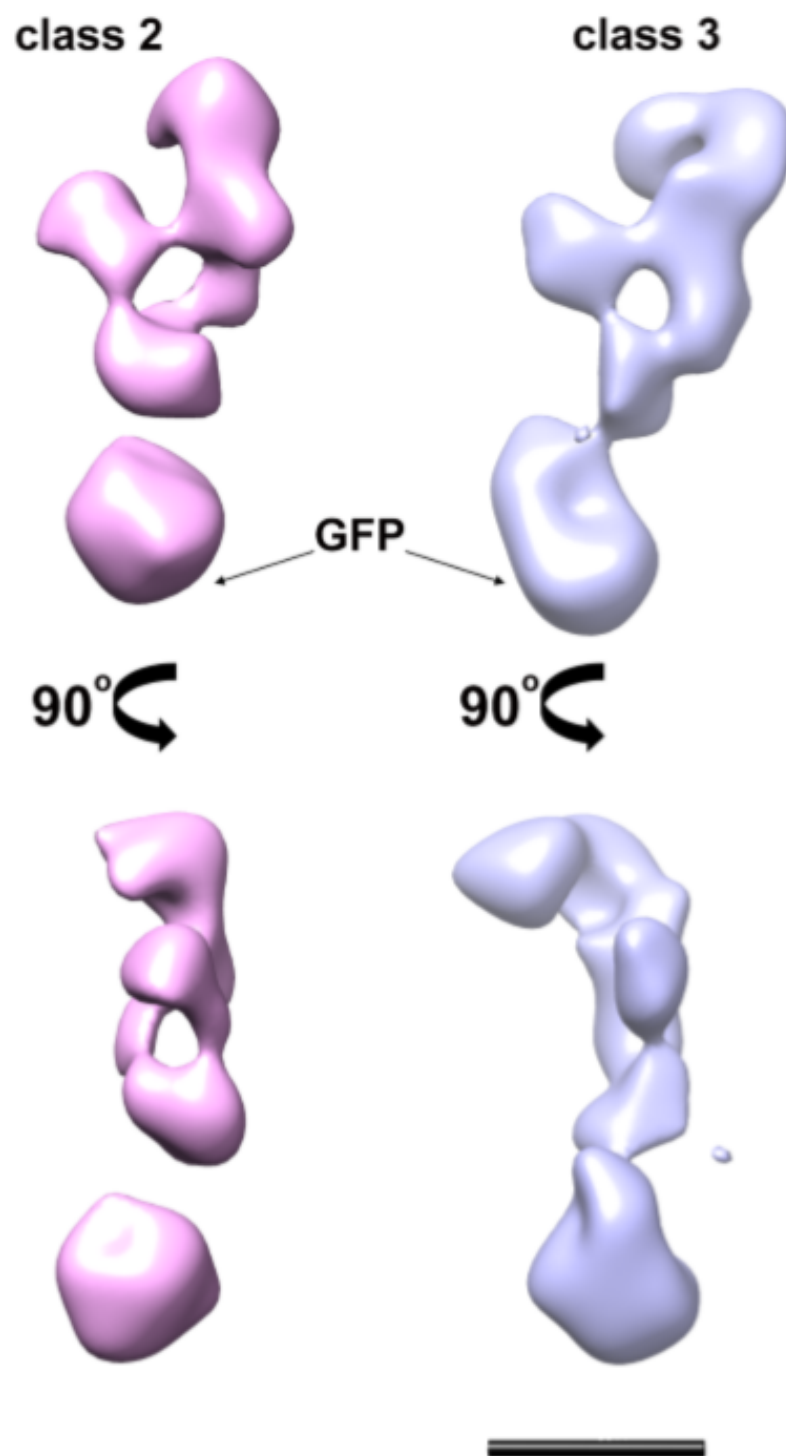


Figure S1: Additional 3D classes of Wsc1-GFP, calculated with RELION2.0 [43]. Two orientations are shown for each reconstruction, which differ by rotation for 90 degrees around the vertical axis. The size bar corresponds to 5 μm.

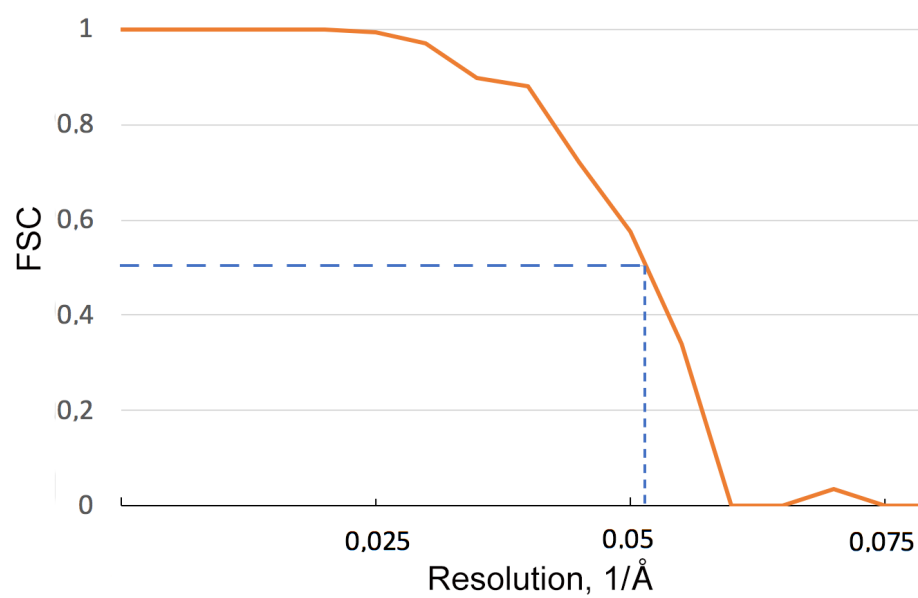


Figure S2. Fourier shell correlation plot for the 3D reconstruction in Fig. 4C.

COVID-19 is an emerging, rapidly evolving situation.Get the latest public health information from CDC: <https://www.coronavirus.gov>Get the latest research information from NIH: <https://www.nih.gov/coronavirus>Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>**BLAST®** » **blastp suite** » results for RID-ZHDZDEH6013

Job Title [gb|AJT71945.1|...](#)
RID [ZHDZDEH6013](#) Search expires on 01-10 02:52 am
Program PSI-BLAST Iteration 1
Database pdb
Query ID [AJT71945.1](#)
Description [Slg1p \[Saccharomyces cerevisiae YJM195\]...](#)
Molecule type amino acid
Query Length 378

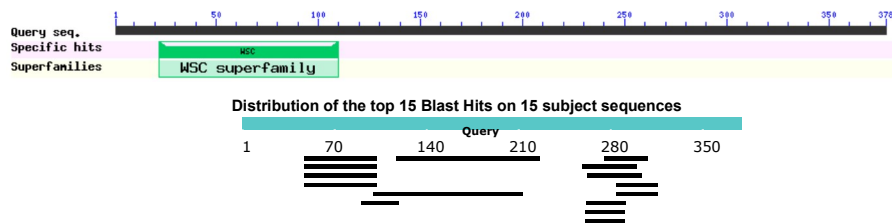
Run PSI-Blast iteration 2Number of sequences **Sequences with E-value BETTER than threshold**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	Select for PSI blast	Used to build PSSM	Newly added
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Run PSI-BLAST Iteration 2 with max number of sequences **Sequences with E-value WORSE than threshold**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	Select for PSI blast	Used to build PSSM	Newly added
Structure of Coxsackievirus A10 complexed with its receptor KREMEN1 (Homo sapiens)	Homo sapiens	36.5	36.5	14%	0.047	32.14%	378	6SNW_E (scored below threshold on previous iteration)	Select seq 6SNW_E for PSI blast		
Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 7.4 (Homo sapiens)	Homo sapiens	36.5	36.5	14%	0.048	32.14%	375	7BZT_E (scored below threshold on previous iteration)	Select seq 7BZT_E for PSI blast		
Wnt modulator Kremen crystal form I at 1.90Å (Homo sapiens)	Homo sapiens	36.2	36.2	14%	0.053	32.14%	406	5FWS_A (scored below threshold on previous iteration)	Select seq 5FWS_A for PSI blast		
Wnt modulator Kremen in complex with DKK1 (CRD2) and LRP6 (PE3PE4) (Homo sapiens)	Homo sapiens	34.8	34.8	14%	0.14	32.14%	293	5FWW_B (scored below threshold on previous iteration)	Select seq 5FWW_B for PSI blast		
Solution NMR Structure of the serine-rich domain of hEE1 (Enhancer of filamentation 1) from Homo sapiens. Northeast Structural Genomics Consortium Target HR5554A (Homo sapiens)	Homo sapiens	32.1	32.1	8%	0.56	46.88%	176	2L81_A (scored below threshold on previous iteration)	Select seq 2L81_A for PSI blast		
Structure of human voltage-gated sodium channel Nav1.7 in complex with auxiliary beta subunits, huwentoxin-IV and saxitoxin (Y1755 up) (Homo sapiens)	Homo sapiens	31.6	31.6	10%	1.2	32.50%	215	6J8G_C (scored below threshold on previous iteration)	Select seq 6J8G_C for PSI blast		
Solution structure of integrin b2 monomer transmembrane domain in bicelle (Homo sapiens)	Homo sapiens	28.6	28.6	10%	1.5	40.00%	52	5ZAZ_A (scored below threshold on previous iteration)	Select seq 5ZAZ_A for PSI blast		
Structure of Tra1 subunit within the chromatin modifying complex SAGA (Komagataella pastoris)	Komagataella pastoris	32.1	32.1	29%	1.8	22.12%	3825	5OEJ_B (scored below threshold on previous iteration)	Select seq 5OEJ_B for PSI blast		
The structure of an Allene Oxide Synthase reveals a novel use for a catalase fold (Plexaura homomalla)	Plexaura homomalla	30.4	30.4	7%	4.5	43.75%	374	1U5U_A (scored below threshold on previous iteration)	Select seq 1U5U_A for PSI blast		
RNA Polymerase II from Komagataella Pastoris (Type-1 crystal) (Komagataella phaffii GS115)	Komagataella phaffii GS115	30.4	30.4	28%	5.4	26.61%	1743	5X4Z_A (scored below threshold on previous iteration)	Select seq 5X4Z_A for PSI blast		
Allene oxide synthase 8R-lipoxygenase from Plexaura homomalla (Plexaura homomalla)	Plexaura homomalla	30.4	30.4	7%	5.4	43.75%	1066	3DY5_A (scored below threshold on previous iteration)	Select seq 3DY5_A for PSI blast		
Solution NMR Structure of APP TMD (Homo sapiens)	Homo sapiens	26.3	26.3	7%	6.8	41.38%	30	6YHF_A (scored below threshold on previous iteration)	Select seq 6YHF_A for PSI blast		
Allophanate Hydrolase Complex from Mycobacterium smegmatis. Msmeq0435-Msmeq0436 (Mycobacterium smegmatis MC2 155)	Mycobacterium smegmatis MC2 155	29.5	29.5	7%	7.3	40.74%	318	3MML_A (scored below threshold on previous iteration)	Select seq 3MML_A for PSI blast		
Solution NMR Structure of APP V44M mutant TMD (Homo sapiens)	Homo sapiens	26.0	26.0	7%	8.4	41.38%	30	6YHP_A (scored below threshold on previous iteration)	Select seq 6YHP_A for PSI blast		
Structure of amyloid precursor protein's transmembrane domain (Homo sapiens)	Homo sapiens	26.3	26.3	7%	8.5	41.38%	43	2LLM_A (scored below threshold on previous iteration)	Select seq 2LLM_A for PSI blast		

Graphic Summary



Alignments

Alignment view ☐ CDS feature

Structure of Coxsackievirus A10 complexed with its receptor KREMEN1 [Homo sapiens]

Sequence ID: **6SNW_E** Length: 378 Number of Matches: 1

Range 1: 130 to 184

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.5 bits(109)	0.047()	Compositional matrix adjust.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP---SGSESTSSSNTCCVFCFSGSNMCGGE					101
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 130	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD					184

Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 7.4 [Homo sapiens]

Sequence ID: **7BZT_E** Length: 375 Number of Matches: 1

Range 1: 127 to 181

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.5 bits(109)	0.048()	Compositional matrix adjust.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP---	101	---SGSESTSSSNCNCFGYSGMCCGGE			
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 127	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD	181				

Wnt modulator Kremen crystal form I at 1.90A [Homo sapiens]

Sequence ID: **5FWS_A** Length: 406 Number of Matches: 1

Range 1: 158 to 212

Score	Expect	Method	Identities	Positives	Gaps	Frame
36.2 bits(108)	0.053()	Compositional matrix adjust.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP---SGSESTSSSCNTCYFGYSSMPCGGE	101				
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 158	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD	212				

Wnt modulator Kremen in complex with DKK1 (CRD2) and LRP6 (PE3PE4) [Homo sapiens]

Sequence ID: **5FWW_B** Length: 293 Number of Matches: 1

Range 1: 118 to 172

Score	Expect	Method	Identities	Positives	Gaps	Frame
34.8 bits(103)	0.14()	Compositional matrix adjust.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP---	101	---SGSESTSSSCNTCYFCGYSMEPCGG			
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 118	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD	172				

Solution NMR Structure of the serine-rich domain of hEF1 (Enhancer of filamentation 1) from Homo sapiens, Northeast Structural

Genomics Consortium Target HR5554A [Homo sapiens]

Sequence ID: **2L81_A** Length: 176 Number of Matches: 1

Range 1: 79 to 110

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.1 bits(94)	0.56()	Compositional matrix adjust.	15/32(47%)	20/32(62%)	0/32(0%)	
Query 273	VVGAVAIACILLIVRHINMKREQDRMEKEYQ	304				
	V GAVA A C+ ++ H MKRE R+E +Q					
Sbjct 79	VGVAVANAACLPILILHNMRRELQRVEDSHQ	110				

Structure of human voltage-gated sodium channel Nav1.7 in complex with auxiliary beta subunits, huwentoxin-IV and saxitoxin (Y1755

up) [Homo sapiens]

Sequence ID: **6J8G_C** Length: 215 Number of Matches: 1

Range 1: 153 to 189

Score	Expect	Method	Identities	Positives	Gaps	Frame
31.6 bits(92)	1.2()	Compositional matrix adjust.	13/40(33%)	25/40(62%)	3/40(7%)	
Query 257	KKKANVGAIVGGVGGVVGVAIAICILLIVRHINMKREQ	296				
	++ + V IVG VGG +A+ + +L++V+ + K+E					
Sbjct 153	ERDSTVAVIVGASVGGF---LAVVILVLMVVKCVRRKEQ	189				

Solution structure of integrin b2 monomer transmembrane domain in bicelle [Homo sapiens]

Sequence ID: **5ZAZ_A** Length: 52 Number of Matches: 1

Range 1: 13 to 52

Score	Expect	Method	Identities	Positives	Gaps	Frame
28.6 bits(82)	1.5()	Composition-based stats.	16/40(40%)	22/40(55%)	0/40(0%)	
Query 261	NVGAIVGGVVGGVVGVAIAICILLIVRHINMKREQDRME	300				
	N+ AIVGG V G+V + L I + +H++ R E R E					
Sbjct 13	NIAAIVGGTVAGIVLIGILLVIWKALIHLSDLREYRFE	52				

Structure of Tra1 subunit within the chromatin modifying complex SAGA [Komagataella pastoris]

Sequence ID: **5OEJ_B** Length: 3825 Number of Matches: 1

Range 1: 3178 to 3290

Score	Expect	Method	Identities	Positives	Gaps	Frame
32.1 bits(94)	1.8()	Composition-based stats.	25/113(22%)	45/113(39%)	1/113(0%)	
Query 101	EDAVSVYQLSDTNSNISSSDSSTESTSASSSTTSSTTSSTTSSTTSSTSMAS	160				
	ED ++ + N SS+ S +T + + T T+ +T S					
Sbjct 3178	EDYQAIQRQAMAVNRAEEQSSNKQDTADSVLKNNTNPQPQTRTETSGTTAESDKKPSIPP	3237				
Query 161	STVQNSPESTQAAASISTSQSSSTVTSESLTSDTLATSSTSQS-QDATSII	212				

Sbjct 3238 Q SP+ ++ A + ++ Q+ S ESS ++ S Q QD I+ KEEQGSPQPSRFATTQASPQAQSQENGESSQKHPFEIPTTDSRQFPWQDVEEIM 3290

The structure of an Allene Oxide Synthase reveals a novel use for a catalase fold [Plexaura homomalla]
Sequence ID: **1U5U_A** Length: 374 Number of Matches: 1
Range 1: 238 to 269

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.4 bits(88)	4.5()	Compositional matrix adjust.	14/32(44%)	18/32(56%)	2/32(6%)	
Query 283	ILLIVRHINMKREQDRMEKEYQEAIK--PVEY		312			
	I + RH N KR D + KEY E ++ PV Y					
Sbjct 238	IWIFSRHENERFPDDYLRAKEYVERLQKGPVNY		269			

RNA Polymerase II from Komagataella Pastoris (Type-1 crystal) [Komagataella phaffii GS115]
Sequence ID: **5X4Z_A** Length: 1743 Number of Matches: 1
Range 1: 1631 to 1739

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.4 bits(88)	5.4()	Composition-based stats.	29/109(27%)	45/109(41%)	1/109(0%)	
Query 117	SISSSDSSTESTSASSSTTSSTTSSTTSSTTSSTTSSTSMASSTVQNSPESTQ-AAAS		175			
	S +S S S S S ++ + +S + +S S TS S ++ Q SP S Q + S					
Sbjct 1631	SPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTS		1690			
Query 176	ISTSQSSSTVTSESLTSDTLATSSSTSQSDATSIYSTTFHTEGGST		224			
	S +S + S S T S +S S YS + H+ G +					
Sbjct 1691	PQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTSPQYSPTS		1739			

Taxonomy

Reports

Lineage

Organism	Blast Name	Score	Number of Hits	Description
cellular organisms			51	
.Eukaryota	eukaryotes		47	
..Opisthokonta	eukaryotes		46	
...Eumetazoa	animals		23	
....Homo sapiens	primates	36.5	19	Homo sapiens hits
...Plexaura homomalla	soft corals	30.4	4	Plexaura homomalla hits
...Komagataella pastoris	budding yeasts	32.1	1	Komagataella pastoris hits
...Komagataella phaffii GS115	budding yeasts	32.1	22	Komagataella phaffii GS115 hits
..Linanthus concinnus	eudicots	30.4	1	Linanthus concinnus hits
.Mycolicibacterium smegmatis MC2 155	high_GC Gram+	29.5	4	Mycolicibacterium smegmatis MC2 155 hits

Organism

Description	Score	E value	Accession
Homo sapiens (human) [primates]			
Structure of Coxsackievirus A10 complexed with its receptor KREMEN1 [Homo sapiens]	36.5	0.047	6SNW_E
Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 7.4 [Homo sapiens]	36.5	0.048	7BZT_E
Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 5.5 [Homo sapiens]	36.5	0.048	7BZU_E
Wnt modulator Kremen crystal form I at 1.90A [Homo sapiens]	36.2	0.053	5FWS_A
Wnt modulator Kremen crystal form I at 2.10A [Homo sapiens]	36.2	0.053	5FWT_A
Wnt modulator Kremen crystal form II at 2.8A [Homo sapiens]	36.2	0.053	5FWU_A
Wnt modulator Kremen crystal form III at 3.2A [Homo sapiens]	36.2	0.053	5FWV_A
Wnt modulator Kremen in complex with DKK1 (CRD2) and LRP6 (PE3PE4) [Homo sapiens]	34.8	0.14	5FWW_B
Solution NMR Structure of the serine-rich domain of hEF1 (Enhancer of filamentation 1) from Homo sapiens, Northeast Structural Genomics Consortium Target HR5554A [Homo sapiens]	32.1	0.56	2L81_A
Structure of human voltage-gated sodium channel Nav1.7 in complex with auxiliary beta subunits, huwentoxin-IV and saxitoxin (Y1755 up) [Homo sapiens]	31.6	1.2	6J8G_C
Structure of human voltage-gated sodium channel Nav1.7 in complex with auxiliary beta subunits, huwentoxin-IV and saxitoxin (Y1755 down) [Homo sapiens]	31.6	1.2	6J8H_C
Structure of human voltage-gated sodium channel Nav1.7 in complex with auxiliary beta subunits, ProTx-II and tetrodotoxin (Y1755 up) [Homo sapiens]	31.6	1.2	6J8I_C
Structure of human voltage-gated sodium channel Nav1.7 in complex with auxiliary beta subunits, ProTx-II and tetrodotoxin (Y1755 down) [Homo sapiens]	31.6	1.2	6J8J_C
Solution structure of integrin b2 monomer tranmembrane domain in bicelle [Homo sapiens]	28.6	1.5	5ZAZ_A
Solution NMR Structure of APP TMD [Homo sapiens]	26.3	6.8	6YHF_A
Solution NMR Structure of APP V44M mutant TMD [Homo sapiens]	26.0	8.4	6YHP_A
Structure of amyloid precursor protein's transmembrane domain [Homo sapiens]	26.3	8.5	2LLM_A
Dimeric structure of transmembrane domain of amyloid precursor protein in micellar environment [Homo sapiens]	26.3	8.5	2LOH_A
Dimeric structure of transmembrane domain of amyloid precursor protein in micellar environment [Homo sapiens]	26.3	8.5	2LOH_B
Komagataella pastoris [budding yeasts]			
Structure of Tra1 subunit within the chromatin modifying complex SAGA [Komagataella pastoris]	32.1	1.8	5OEJ_B
Komagataella phaffii GS115 [budding yeasts]			
Structure of SAGA bound to TBP [Komagataella phaffii GS115]	32.1	1.8	6TB4_L
Structure of SAGA bound to TBP, including Spt8 and DUB [Komagataella phaffii GS115]	32.1	1.8	6TBM_L
RNA Polymerase II from Komagataella Pastoris (Type-1 crystal) [Komagataella phaffii GS115]	30.4	5.4	5X4Z_A
RNA Polymerase II from Komagataella Pastoris (Type-1 crystal) [Komagataella phaffii GS115]	30.4	5.4	5X4Z_M
RNA Polymerase II from Komagataella Pastoris (Type-2 crystal) [Komagataella phaffii GS115]	30.4	5.4	5X50_A
RNA Polymerase II from Komagataella Pastoris (Type-3 crystal) [Komagataella phaffii GS115]	30.4	5.4	5X51_A
RNA Polymerase II from Komagataella Pastoris (Type-3 crystal) [Komagataella phaffii GS115]	30.4	5.4	5X51_M
RNA Polymerase II elongation complex bound with Spt5 KOW5 and Elf1 [Komagataella phaffii GS115]	30.4	5.4	5XOG_A
RNA Polymerase II elongation complex bound with Spt4/5 and TFIIS [Komagataella phaffii GS115]	30.4	5.4	5XON_A
RNA polymerase II elongation complex stalled at SHL(-1) of the nucleosome, with foreign DNA [Komagataella phaffii GS115]	30.4	5.4	6A5L_A
RNA polymerase II elongation complex stalled at SHL(-6) of the nucleosome [Komagataella phaffii GS115]	30.4	5.4	6A5Q_A
RNA polymerase II elongation complex stalled at SHL(-5) of the nucleosome [Komagataella phaffii GS115]	30.4	5.4	6A5P_A
RNA polymerase II elongation complex stalled at SHL(-2) of the nucleosome [Komagataella phaffii GS115]	30.4	5.4	6A5R_A
RNA polymerase II elongation complex stalled at SHL(-1) of the nucleosome [Komagataella phaffii GS115]	30.4	5.4	6A5T_A
RNA polymerase II elongation complex stalled at SHL(-1) of the nucleosome, with foreign DNA, tilt conformation [Komagataella phaffii GS115]	30.4	5.4	6A5U_A
RNA polymerase II elongation complex stalled at SHL(-1) of the nucleosome, with foreign DNA (+1 position) [Komagataella phaffii GS115]	30.4	5.4	6INQ_A
RNA polymerase II elongation complex bound with Elf1 and Spt4/5, stalled at SHL(-5) of the nucleosome [Komagataella phaffii GS115]	30.4	5.4	6J4W_A
RNA polymerase II elongation complex bound with Elf1 and Spt4/5, stalled at SHL(-1) of the nucleosome (+1A) [Komagataella phaffii GS115]	30.4	5.4	6J4X_A

Description	Score	E value	Accession
RNA polymerase II elongation complex bound with Elf1 and Spt4/5, stalled at SHL(-1) of the nucleosome (+1B). [Komagataella phaffii GS115]	30.4	5.4	6J4Y_A
RNA polymerase II elongation complex bound with Spt4/5 and foreign DNA, stalled at SHL(-1) of the nucleosome [Komagataella phaffii GS115]	30.4	5.4	6J4Z_A
RNA polymerase II elongation complex bound with Spt4/5 and foreign DNA, stalled at SHL(-1) of the nucleosome (tilted conformation). [Komagataella phaffii GS115]	30.4	5.4	6J50_A
RNA polymerase II elongation complex bound with Spt4/5 and foreign DNA, stalled at SHL(-1) of the nucleosome, weak Elf1 (+1 position). [Komagataella phaffii GS115]	30.4	5.4	6J51_A
Plexaura homomalla [soft corals]			
The structure of an Allene Oxide Synthase reveals a novel use for a catalase fold [Plexaura homomalla]	30.4	4.5	1U5U_A
The structure of an Allene Oxide Synthase reveals a novel use for a catalase fold [Plexaura homomalla]	30.4	4.5	1U5U_B
Allene oxide synthase 8R-lipoxygenase from Plexaura homomalla [Plexaura homomalla]	30.4	5.4	3DY5_A
Allene oxide synthase 8R-lipoxygenase from Plexaura homomalla [Plexaura homomalla]	30.4	5.4	3DY5_C
Linanthus concinnus [eudicots]			
RNA polymerase II elongation complex bound with Elf1 and Spt4/5, stalled at SHL(-1) of the nucleosome [Linanthus concinnus]	30.4	5.4	6IR9_A
Mycolicibacterium smegmatis MC2 155 [high GC Gram+]			
Allophanate Hydrolase Complex from Mycobacterium smegmatis, Msmeg0435-Msmeg0436 [Mycolicibacterium smegmatis MC2 155]	29.5	7.3	3MML_A
Allophanate Hydrolase Complex from Mycobacterium smegmatis, Msmeg0435-Msmeg0436 [Mycolicibacterium smegmatis MC2 155]	29.5	7.3	3MML_C
Allophanate Hydrolase Complex from Mycobacterium smegmatis, Msmeg0435-Msmeg0436 [Mycolicibacterium smegmatis MC2 155]	29.5	7.3	3MML_E
Allophanate Hydrolase Complex from Mycobacterium smegmatis, Msmeg0435-Msmeg0436 [Mycolicibacterium smegmatis MC2 155]	29.5	7.3	3MML_G

Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
cellular organisms	51	6	
Eukaryota	47	5	
Opisthokonta	46	4	
Eumetazoa	23	2	
Homo sapiens	19	1	Homo sapiens hits
Plexaura homomalla	4	1	Plexaura homomalla hits
Komagataella	23	2	
Komagataella pastoris	1	1	Komagataella pastoris hits
Komagataella phaffii GS115	22	1	Komagataella phaffii GS115 hits
Linanthus concinnus	1	1	Linanthus concinnus hits
Mycolicibacterium smegmatis MC2 155	4	1	Mycolicibacterium smegmatis MC2 155 hits

Top

COVID-19 is an emerging, rapidly evolving situation.Get the latest public health information from CDC: <https://www.coronavirus.gov>Get the latest research information from NIH: <https://www.nih.gov/coronavirus>Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/sars-cov-2/>**BLAST®** » **blastp suite** » results for RID-ZGZWU4SH013

Informational Message: Frequency ratios for PSSM are all zeros, frequency ratios for BLOSUM62 will be used during traceback in composition based statistics

Informational Message: Query 'KAF1902179 Slg1p, partial..' (# 1): Warning: Frequency ratios for PSSM are all zeros, frequency ratios for BLOSUM62 will be used during traceback in composition based statistics

Job Title [gb|KAF1902179.1|...](#)
RID [ZGZWU4SH013](#) Search expires on 01-09 22:51 pm
Program PSI-BLAST Iteration 2
Database pdb
Query ID [KAF1902179.1](#)
Description [Slg1p_partial.\[Saccharomyces cerevisiae\]...](#)
Molecule type amino acid
Query Length 378

Run PSI-Blast iteration 3Number of sequences **Sequences with E-value BETTER than threshold**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	Select for PSI blast	Used to build PSSM	Newly added
Wnt modulator Kremen in complex with DKK1 (CRD2) and LRP6 (PE3PE4) (Homo sapiens)	Homo sapiens	43.0	43.0	14%	5e-04	32.14%	293	5FWW_B (scored below threshold on previous iteration)	Select seq 5FWW_B for PSI blast		
Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 7.4.(Homo sapiens)	Homo sapiens	43.0	43.0	14%	6e-04	32.14%	375	7BZT_E (scored below threshold on previous iteration)	Select seq 7BZT_E for PSI blast		
Structure of Coxsackievirus A10 complexed with its receptor KREMEN1 (Homo sapiens)	Homo sapiens	43.0	43.0	14%	6e-04	32.14%	378	6SNW_E (scored below threshold on previous iteration)	Select seq 6SNW_E for PSI blast		
Wnt modulator Kremen crystal form I at 1.90A (Homo sapiens)	Homo sapiens	43.0	43.0	14%	6e-04	32.14%	406	5FWS_A (scored below threshold on previous iteration)	Select seq 5FWS_A for PSI blast		

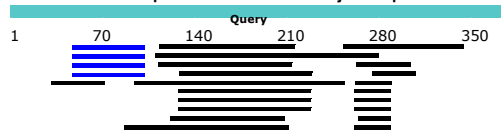
Run PSI-BLAST Iteration 3 with max number of sequences: **Sequences with E-value WORSE than threshold**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	Select for PSI blast	Used to build PSSM	Newly added
eIF2B:eIF2 complex_phosphorylated on eIF2 alpha serine 52 (Saccharomyces cerevisiae S288C)	Saccharomyces cerevisiae S288C	39.9	75.1	26%	0.006	28.18%	651	6I3M_C (scored below threshold on previous iteration)	Select seq 6I3M_C for PSI blast		
EBOV GP in complex with variable Fab domains of IgGs c2G4 and c13C6 (Ebola virus - Mayinga, Zaire, 1976)	Ebola virus - Mayinga, Zaire, 1976	38.3	38.3	44%	0.019	20.35%	469	5KEL_A (scored below threshold on previous iteration)	Select seq 5KEL_A for PSI blast		
PROTON NUCLEAR MAGNETIC RESONANCE AND DISTANCE GEOMETRY(SLASH)SIMULATED ANNEALING STUDIES ON THE VARIANT-1 NEUROTOXIN FROM THE NEW WORLD SCORPION CENTRUROIDES SCULPTURATUS EWING (Centruroides sculpturatus)	Centruroides sculpturatus	34.5	34.5	10%	0.027	41.46%	65	1VNA_A (scored below threshold on previous iteration)	Select seq 1VNA_A for PSI blast		
Bacteriophage T4 isometric capsid (Escherichia virus T4)	Escherichia virus T4	37.6	37.6	41%	0.028	23.93%	376	5VF3_Z (scored below threshold on previous iteration)	Select seq 5VF3_Z for PSI blast		
Structure of Tra1 subunit within the chromatin modifying complex SAGA (Komagataella pastoris)	Komagataella pastoris	35.6	35.6	26%	0.17	24.51%	3825	5OEJ_B (scored below threshold on previous iteration)	Select seq 5OEJ_B for PSI blast		
The solution NMR structure of the transmembrane C-terminal domain of the amyloid precursor protein (C99) (Homo sapiens)	Homo sapiens	32.9	32.9	23%	0.24	25.74%	122	2LP1_A (scored below threshold on previous iteration)	Select seq 2LP1_A for PSI blast		
Solution structure of integrin b2 monomer tranmembrane domain in bicelle (Homo sapiens)	Homo sapiens	31.0	31.0	10%	0.35	40.00%	52	5ZAZ_A (scored below threshold on previous iteration)	Select seq 5ZAZ_A for PSI blast		
Three-Dimensional Structure Of a Single Chain Fv Fragment Complexed With The peptide GCN4(7P-14P) (Mus musculus)	Mus musculus	32.6	32.6	26%	0.42	29.25%	135	1P4B_L (scored below threshold on previous iteration)	Select seq 1P4B_L for PSI blast		
Crystal structure of glycopeptide 22 in complex with scFv-SM3 (Mus musculus)	Mus musculus	33.3	33.3	26%	0.44	28.30%	244	5FXC_H (scored below threshold on previous iteration)	Select seq 5FXC_H for PSI blast		
Solution NMR Structure of the serine-rich domain of hEF1 (Enhancer of filamentation 1) from Homo sapiens, Northeast Structural Genomics Consortium Target HR5554A (Homo sapiens)	Homo sapiens	32.9	32.9	8%	0.48	46.88%	176	2L81_A (scored below threshold on previous iteration)	Select seq 2L81_A for PSI blast		

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession	Select for PSI blast	Used to build PSSM	Newly added
Application of anti-helix antibodies in protein structure determination (9014-1P4B) [Mus musculus]	Mus musculus	32.2	32.2	26%	0.48	29.25%	115	6K65_L (scored below threshold on previous iteration)	Select seq 6K65_L for PSI blast		
Crystal structure of scFv-SM3 in complex with APD-SGalNAc-RP [Mus musculus]	Mus musculus	32.9	32.9	26%	0.60	28.30%	244	5A2I_H (scored below threshold on previous iteration)	Select seq 5A2I_H for PSI blast		
Solution NMR Structure of APP TMD [Homo sapiens]	Homo sapiens	29.5	29.5	7%	0.65	44.44%	30	6YHF_A (scored below threshold on previous iteration)	Select seq 6YHF_A for PSI blast		
Solution NMR Structure of APP V44M mutant TMD [Homo sapiens]	Homo sapiens	29.1	29.1	7%	0.85	44.44%	30	6YHP_A (scored below threshold on previous iteration)	Select seq 6YHP_A for PSI blast		
Structure of amyloid precursor protein's transmembrane domain [Homo sapiens]	Homo sapiens	29.5	29.5	7%	0.86	44.44%	43	2LLM_A (scored below threshold on previous iteration)	Select seq 2LLM_A for PSI blast		
Candida albicans PKh Kinase Domain [Candida albicans SC5314]	Candida albicans SC5314	32.6	32.6	22%	1.1	29.41%	974	4C0T_A (scored below threshold on previous iteration)	Select seq 4C0T_A for PSI blast		
Recognition of the Amyloid Precursor Protein by Human gamma-secretase [Homo sapiens]	Homo sapiens	29.5	29.5	7%	3.0	44.44%	104	6IYC_E (scored below threshold on previous iteration)	Select seq 6IYC_E for PSI blast		
Solution NMR structure of transmembrane domain of amyloid precursor protein WT [Homo sapiens]	Homo sapiens	27.6	27.6	6%	3.4	45.83%	31	2LZ3_A (scored below threshold on previous iteration)	Select seq 2LZ3_A for PSI blast		
Solution NMR Structure of APP I45T mutant TMD [Homo sapiens]	Homo sapiens	27.6	27.6	7%	3.6	40.74%	30	6YHX_A (scored below threshold on previous iteration)	Select seq 6YHX_A for PSI blast		
Cryo-EM structure of a human spliceosome activated for step 2 of splicing (C' complex) [Homo sapiens]	Homo sapiens	30.6	30.6	32%	4.9	25.52%	2752	5MQF_S (scored below threshold on previous iteration)	Select seq 5MQF_S for PSI blast		
Crystal structure of the ligand binding region of staphylococcal adhesion SraP [Staphylococcus aureus subsp. aureus NCTC 8325]	Staphylococcus aureus subsp. aureus NCTC 8325	30.3	30.3	37%	6.0	18.88%	541	4M00_A (scored below threshold on previous iteration)	Select seq 4M00_A for PSI blast		

Graphic Summary

Distribution of the top 26 Blast Hits on 25 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

Wnt modulator Kremen in complex with DKK1 (CRD2) and LRP6 (PE3PE4) [Homo sapiens]

Sequence ID: **5FWW_B** Length: 293 Number of Matches: 1

Range 1: 118 to 172

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.0 bits(99)	5e-04()	Composition-based stats.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP----	SGSESTSSSCNTYCFGYSSEMCGGE	101			
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 118	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD	172				

Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 7.4 [Homo sapiens]

Sequence ID: **7BZT_E** Length: 375 Number of Matches: 1

Range 1: 127 to 181

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.0 bits(99)	6e-04()	Composition-based stats.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP----	SGSESTSSSCNTYCFGYSSEMCGGE	101			
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 127	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD	181				

Structure of Coxsackievirus A10 complexed with its receptor KREMEN1 [Homo sapiens]

Sequence ID: **6SNW_E** Length: 378 Number of Matches: 1

Range 1: 130 to 184

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.0 bits(99)	6e-04()	Composition-based stats.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP----	SGSESTSSSCNTYCFGYSSEMCGGE	101			
	C S C ++ + + + C+CG+ NP E+ S+ CN+ CFG ++ CGG+					
Sbjct 130	CISFCRSQRKFAGMESGYACFCGN-NPDYWKYGEAASTECNSVCFGDHTQPCGGD	184				

Wnt modulator Kremen crystal form I at 1.90A [Homo sapiens]

Sequence ID: **5FWS_A** Length: 406 Number of Matches: 1

Range 1: 158 to 212

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.0 bits(99)	6e-04()	Composition-based stats.	18/56(32%)	31/56(55%)	4/56(7%)	
Query 49	CNSECSAKGASYFALYNHSECYCGDTNP----	SGSESTSSSCNTYCFGYSSEMCGGE	101			

Sequence ID: 613M_
Range 1: 152 to 259

Range 2: 147 to 227

Sequence ID: 5KEL_1
Range 1: 301 to 461

Sequence ID: 1V
Range 1: 9 to 48

Sequence ID: 5VF3_
Range 1: 122 to 281

Sequence ID: **SOES_B**
Range 1: 3195 to 3290

Sequence ID: ZLF
Range 1: 9 to 103

Sequence ID: 52A
Range 1: 13 to 52

08.01.2021, 20:37

Score	Expect	Method	Identities	Positives	Gaps	Frame
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32.6 bits(72) 1.1() Composition-based stats. 25/85(29%) 36/85(42%) 11/85(12%)

Query 123 SSTSTSSASSSTTSSTTSSTTSSTTSSTTSSTSMASSTVQNSPESTQAAASISTSQSS 182
SS+ SS T S T ST + +S+A+ V N P +T+Q+S
Sbjct 598 SSSNGHKGSSTPEKEPSPATINNKSSTEKVSAA--YVLNKP-----ATNQNS 646

Query 183 STVTSESLTSDTLATSTSSSQSD 207
ST S +S++ T S QD
Sbjct 647 STSEDSKRSSNSNETRKLYSQSD 671

Recognition of the Amyloid Precursor Protein by Human gamma-secretase [Homo sapiens]
Sequence ID: 6IYC_E Length: 104 Number of Matches: 1
Range 1: 11 to 37

Score	Expect	Method	Identities	Positives	Gaps	Frame
29.5 bits(64)	3.0()	Composition-based stats.	12/27(44%)	20/27(74%)	0/27(0%)	
Query 260	ANVGAIVGGVGGVGAIAIALCILLI	286				
	+N GAI+G +VGGVV A I + ++++					
Sbjct 11	SNKGAIIGLMVGGVVIATVIVITLVML	37				

Solution NMR structure of transmembrane domain of amyloid precursor protein WT [Homo sapiens]
Sequence ID: 2LZ3_A Length: 31 Number of Matches: 1
Range 1: 5 to 28

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.6 bits(59)	3.4()	Composition-based stats.	11/24(46%)	18/24(75%)	0/24(0%)	
Query 263	GAIVGGVGGVGGVGAIAIALCILLI	286				
	GAI+G +VGGVV A I + ++++					
Sbjct 5	GAIIGLMVGGVVIATVIVITLVML	28				

Solution NMR Structure of APP I45T mutant TMD [Homo sapiens]
Sequence ID: 6YHX_A Length: 30 Number of Matches: 1
Range 1: 1 to 27

Score	Expect	Method	Identities	Positives	Gaps	Frame
27.6 bits(59)	3.6()	Composition-based stats.	11/27(41%)	19/27(70%)	0/27(0%)	
Query 260	ANVGAIVGGVGGVGAIAIALCILLI	286				
	+N GAI+G +VGGVV A + ++++					
Sbjct 1	SNKGAIIGLMVGGVVIATVIVITLVML	27				

Cryo-EM structure of a human spliceosome activated for step 2 of splicing (C* complex) [Homo sapiens]
Sequence ID: 6MQF_S Length: 2752 Number of Matches: 1
Range 1: 1034 to 1178

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.6 bits(67)	4.9()	Composition-based stats.	37/145(26%)	56/145(38%)	22/145(15%)	
Query 88	TYCFYSSSEMCGGEDAYSVMYQLD-----SDTNSNSISSSDSSTESTSASSSTT	135				
	+ C G S GE + V L SDT+S + S + S + S T+					
Sbjct 1034	SLCAGVKSSSTPFGESYFGVSSLQLKGQSQTSPDHRSDTSSPEVRQSHSESPSLQKSKQTS	1093				
Query 136	-----SSTTSSTTSSTTSSTTSSTSMASSTVQNSPESTQAAASISTSQSSSTVTSESS	190				
	S ++S T S + S+S + S + + S S S TV S S					
Sbjct 1094	PKGGRSSSSPVTELASRSPIRQDRGEFSAPMLKSGMSPEQSRFQSDSSSYPTVDSNSL	1153				
Query 191	LTSDTLATSTSSQ-----SQDATS	210				
	L L T+ + + +DAT+					
Sbjct 1154	LQQSRLETAESKERMALPPQEDATA	1178				

Crystal structure of the ligand binding region of staphylococcal adhesion SraP [Staphylococcus aureus subsp. aureus NCTC 8325]
Sequence ID: 4M00_A Length: 541 Number of Matches: 1
Range 1: 388 to 530

Score	Expect	Method	Identities	Positives	Gaps	Frame
30.3 bits(66)	6.0()	Composition-based stats.	27/143(19%)	63/143(44%)	0/143(0%)	
Query 113	TNSNSISSSDSSTESTSASSSTTSSTTSSTTSTTSTSTTSSTSMASSTVQNSPESTQA	172				
	T +++ + + ++T + S + S T+S T + ST + +++ S +					
Sbjct 388	TTTDMGTGTINTVTGLPSGLSYDSATNSIIIGTPKIGQSTVTVVSTDQANNKSTTTFTI	447				
Query 173	AASISTSQSSSTVTSESLTSDTLATSTSSSQSDATSIIVSTTFHTEGGSTIFVNTIT	232				
	+T+ + + + +SS ++ ++Q ++ + T G + NTI+					
Sbjct 448	NVVDTTAPTVTPIGDQSSEVYSPISPIKIATQDMSGNAVNTVTGLPSGLTFDSTNNTIS	507				
Query 233	ASAQNSGSATGTAGSDSTSGSKT	255				
	+ N G++T + S SG+KT					
Sbjct 508	GTFPTNIGTSTISIVSTDASGNKT	530				

Taxonomy

Reports

Lineage

o	Organism	Blast Name	Score	Number of Hits	Description
	root			71	
	.cellular organisms			67	
	..Opisthokonta	eukaryotes		66	
	...Bilateria	animals		46	
	Euarchontoglires	placentals		44	
	Homo sapiens	primates	43.0	30	Homo sapiens hits
	Mus musculus	rodents	32.6	14	Mus musculus hits
	Centruroides sculpturatus	scorpions	34.5	2	Centruroides sculpturatus hits
	...Saccharomyces cerevisiae S288C	budding yeasts	39.9	10	Saccharomyces cerevisiae S288C hits
	...Saccharomyces cerevisiae	budding yeasts	39.9	6	Saccharomyces cerevisiae hits
	...Komagataella pastoris	budding yeasts	35.6	1	Komagataella pastoris hits
	...Komagataella phaffii GS115	budding yeasts	35.6	2	Komagataella phaffii GS115 hits
	...Candida albicans SC5314	budding yeasts	32.6	1	Candida albicans SC5314 hits
	..Staphylococcus aureus subsp. aureus NCTC 8325	firmicutes	30.3	1	Staphylococcus aureus subsp. aureus NCTC 8325 hits
	.Ebola virus - Mayinga, Zaire, 1976	viruses	38.3	3	Ebola virus - Mayinga, Zaire, 1976 hits
	.Escherichia virus T4	viruses	37.6	1	Escherichia virus T4 hits

Organism

Description	Score	E	Accession
o			

			value	
Homo sapiens (human)	[primates]			
Wnt modulator Kremen in complex with DKK1 (CRD2) and LRP6 (PE3PE4) [Homo sapiens]		43.0	5e-04	5FWW_B
Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 7.4 [Homo sapiens]		43.0	6e-04	7BZT_E
Cryo-EM structure of mature Coxsackievirus A10 in complex with KRM1 at pH 5.5 [Homo sapiens]		43.0	6e-04	7BZU_E
Structure of Coxsackievirus A10 complexed with its receptor KREMEN1 [Homo sapiens]		43.0	6e-04	6SNW_E
Wnt modulator Kremen crystal form I at 1.90A [Homo sapiens]		43.0	6e-04	5FWS_A
Wnt modulator Kremen crystal form I at 2.10A [Homo sapiens]		43.0	6e-04	5FWT_A
Wnt modulator Kremen crystal form II at 2.8A [Homo sapiens]		43.0	6e-04	5FWU_A
Wnt modulator Kremen crystal form III at 3.2A [Homo sapiens]		43.0	6e-04	5FWV_A
The solution NMR structure of the transmembrane C-terminal domain of the amyloid precursor protein (C99) [Homo sapiens]		32.9	0.24	2LP1_A
Solution structure of integrin b2 monomer tranmembrane domain in bicelle [Homo sapiens]		31.0	0.35	5ZAZ_A
Solution NMR Structure of the serine-rich domain of hEF1 (Enhancer of filamentation 1) from Homo sapiens, Northeast Structural Genomics Consortium Target HR5554A [Homo sapiens]		32.9	0.48	2L81_A
Solution NMR Structure of APP TMD [Homo sapiens]		29.5	0.65	6YHF_A
Solution NMR Structure of APP V44M mutant TMD [Homo sapiens]		29.1	0.85	6YHP_A
Structure of amyloid precursor protein's transmembrane domain [Homo sapiens]		29.5	0.86	2LLM_A
Dimeric structure of transmembrane domain of amyloid precursor protein in micellar environment [Homo sapiens]		29.5	0.86	2LOH_A
Dimeric structure of transmembrane domain of amyloid precursor protein in micellar environment [Homo sapiens]		29.5	0.86	2LOH_B
Recognition of the Amyloid Precursor Protein by Human gamma-secretase [Homo sapiens]		29.5	3.0	6LYC_E
Solution NMR structure of transmembrane domain of amyloid precursor protein WT [Homo sapiens]		27.6	3.4	2LZ3_A
Solution NMR structure of transmembrane domain of amyloid precursor protein WT [Homo sapiens]		27.6	3.4	2LZ3_B
Solution NMR Structure of APP I45T mutant TMD [Homo sapiens]		27.6	3.6	6YHX_A
Cryo-EM structure of a human spliceosome activated for step 2 of splicing (C* complex) [Homo sapiens]		30.6	4.9	5MQF_S
Cryo-EM structure of the human spliceosome just prior to exon ligation at 3.6 angstrom [Homo sapiens]		30.6	4.9	5XJC_U
The Cryo-EM Structure of Human Catalytic Step I Spliceosome (C complex) at 4.1 angstrom resolution [Homo sapiens]		30.6	4.9	5YZG_U
cryo-EM structure of a human activated spliceosome (mature Bact) at 5.1 angstrom, [Homo sapiens]		30.6	4.9	5Z56_U
Cryo-EM structure of the human activated spliceosome (late Bact) at 6.5 angstrom [Homo sapiens]		30.6	4.9	5Z57_U
human Bact spliceosome core structure [Homo sapiens]		30.6	4.9	6FF4_S
human Bact spliceosome core structure [Homo sapiens]		30.6	4.9	6FF7_S
Cryo-EM structure of a human post-catalytic spliceosome (P complex) at 3.0 angstrom [Homo sapiens]		30.6	4.9	6IC2_U
Human C Complex Spliceosome - High-resolution CORE [Homo sapiens]		30.6	4.9	6ZYM_S
Human C Complex Spliceosome - Medium-resolution PERIPHERY [Homo sapiens]		30.6	4.9	7A5P_S
Saccharomyces cerevisiae S288C	[budding yeasts]			
eIF2B:eIF2 complex, phosphorylated on eIF2 alpha serine 52, [Saccharomyces cerevisiae S288C]		39.9	0.006	6I3M_C
eIF2B:eIF2 complex, phosphorylated on eIF2 alpha serine 52, [Saccharomyces cerevisiae S288C]		39.9	0.006	6I3M_D
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model 1) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG0_G
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model 1) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG0_H
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model 2) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG1_G
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model 2) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG1_H
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model A) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG2_G
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model A) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG2_H
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model B) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG3_G
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model B) [Saccharomyces cerevisiae S288C]		39.9	0.006	6QG3_H
Saccharomyces cerevisiae (baker's yeast)	[budding yeasts]			
eIF2B:eIF2 complex [Saccharomyces cerevisiae]		39.9	0.006	6I7T_C
eIF2B:eIF2 complex [Saccharomyces cerevisiae]		39.9	0.006	6I7T_D
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model C) [Saccharomyces cerevisiae]		39.9	0.006	6QG5_G
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model C) [Saccharomyces cerevisiae]		39.9	0.006	6QG5_H
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model D) [Saccharomyces cerevisiae]		39.9	0.006	6QG6_G
Structure of eIF2B:eIF2 (phosphorylated at Ser51) complex (model D) [Saccharomyces cerevisiae]		39.9	0.006	6QG6_H
Ebola virus - Mayinga, Zaire, 1976	[viruses]			
EBOV GP in complex with variable Fab domains of IgGs c2G4 and c13C6 [Ebola virus - Mayinga, Zaire, 1976]		38.3	0.019	5KEL_A
EBOV GP in complex with variable Fab domains of IgGs c2G4 and c13C6 [Ebola virus - Mayinga, Zaire, 1976]		38.3	0.019	5KEL_E
EBOV GP in complex with variable Fab domains of IgGs c2G4 and c13C6 [Ebola virus - Mayinga, Zaire, 1976]		38.3	0.019	5KEL_F
Centruroides sculpturatus (bark scorpion)	[scorpions]			
PROTON NUCLEAR MAGNETIC RESONANCE AND DISTANCE GEOMETRY (SLASH)SIMULATED ANNEALING STUDIES ON THE VARIANT-1 NEUROTOXIN FROM THE NEW WORLD SCORPION CENTRUROIDES SCULPTURATUS EWING [Centruroides sculpturatus]		34.5	0.027	1VNA_A
PROTON NUCLEAR MAGNETIC RESONANCE AND DISTANCE GEOMETRY (SLASH)SIMULATED ANNEALING STUDIES ON THE VARIANT-1 NEUROTOXIN FROM THE NEW WORLD SCORPION CENTRUROIDES SCULPTURATUS EWING [Centruroides sculpturatus]		34.5	0.027	1VNB_A
Escherichia virus T4	[viruses]			
Bacteriophage T4 isometric capsid [Escherichia virus T4]		37.6	0.028	5VF3_Z
Komagataella pastoris	[budding yeasts]			
Structure of Tra1 subunit within the chromatin modifying complex SAGA [Komagataella pastoris]		35.6	0.17	5OEJ_B
Komagataella phaffii GS115	[budding yeasts]			
Structure of SAGA bound to TBP [Komagataella phaffii GS115]		35.6	0.17	6TB4_L
Structure of SAGA bound to TBP, including Spt8 and DUB [Komagataella phaffii GS115]		35.6	0.17	6TBM_L
Mus musculus (house mouse)	[rodents]			
Three-Dimensional Structure Of a Single Chain Fv Fragment Complexed With The peptide GCN4(7P-14P). [Mus musculus]		32.6	0.42	1P4B_L
Crystal Structure of scFv against peptide GCN4 [Mus musculus]		32.6	0.42	1P4I_L
Crystal structure of glycopeptide 22 in complex with scFv-SM3 [Mus musculus]		33.3	0.44	5FXC_H
Understanding the singular conformational landscape of the Tn antigens: Sulfur-for- oxygen substitution in the glycosidic linkage provides new insights into molecular recognition by an antibody [Mus musculus]		33.3	0.44	5N7B_H
Crystal structure of glycopeptide 'GVTSAFPDT'RPAP' in complex with scFv-SM3 [Mus musculus]		33.3	0.44	5OWP_H
Crystal structure of scFv-SM3 in complex with APD-SeThrGalNAc-RP [Mus musculus]		33.3	0.44	6FRJ_H
Crystal structure of scFv-SM3 in complex with compound 3 [Mus musculus]		33.3	0.44	6FZO_H
Crystal structure of scFv-SM3 in complex with compound 2 [Mus musculus]		33.3	0.44	6FZR_H
scFv-1SM3 in complex with glycopeptide containing an sp2-imino sugar [Mus musculus]		33.3	0.44	6TGG_H
Application of anti-helix antibodies in protein structure determination (9014-1P4B) [Mus musculus]		32.2	0.48	6K65_L
Crystal structure of scFv-SM3 in complex with APD-SGalNAc-RP [Mus musculus]		32.9	0.60	5A2I_H
Crystal structure of scFv-SM3 in complex with the naked peptide APDTRP [Mus musculus]		32.9	0.60	5A2J_H
Crystal structure of scFv-SM3 in complex with APD-TGalNAc-RP [Mus musculus]		32.9	0.60	5A2K_H
Crystal structure of scFv-SM3 in complex with APD-CGalNAc-RP [Mus musculus]		32.9	0.60	5A2L_H
Candida albicans SC5314	[budding yeasts]			
Candida albicans PKh Kinase Domain [Candida albicans SC5314]		32.6	1.1	4C0T_A

Staphylococcus aureus subsp. aureus NCTC 8325	[firmicutes	]			
Crystal structure of the ligand binding region of staphylococcal adhesion SraP [Staphylococcus aureus subsp. aureus NCTC 8325]			30.3	6.0	4M00_A

Taxonomy

o	Taxonomy	Number of hits	Number of Organisms	Description
	root	71	11	
	.. cellular organisms	67	9	
	.. Opisthokonta	66	8	
	... Bilateria	46	3	
	 Euarchontoglires	44	2	
	 Homo sapiens	30	1	Homo sapiens hits
	 Mus musculus	14	1	Mus musculus hits
	 Centruroides sculpturatus	2	1	Centruroides sculpturatus hits
	... Saccharomycetales	20	5	
	 Saccharomyces	16	2	
	 Saccharomyces cerevisiae	6	2	Saccharomyces cerevisiae hits
	 Saccharomyces cerevisiae S288C	10	1	Saccharomyces cerevisiae S288C hits
	 Komagataella	3	2	
	 Komagataella pastoris	1	1	Komagataella pastoris hits
	 Komagataella phaffii GS115	2	1	Komagataella phaffii GS115 hits
	 Candida albicans SC5314	1	1	Candida albicans SC5314 hits
	.. Staphylococcus aureus subsp. aureus NCTC 8325	1	1	Staphylococcus aureus subsp. aureus NCTC 8325 hits
	.. Viruses	4	2	
	.. Ebola virus - Mayinga, Zaire, 1976	3	1	Ebola virus - Mayinga, Zaire, 1976 hits
	.. Escherichia virus T4	1	1	Escherichia virus T4 hits

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