

Supplementary Materials

Intrinsic Disorder of BAF Complex: Roles in Chromatin Remodeling and Disease Development

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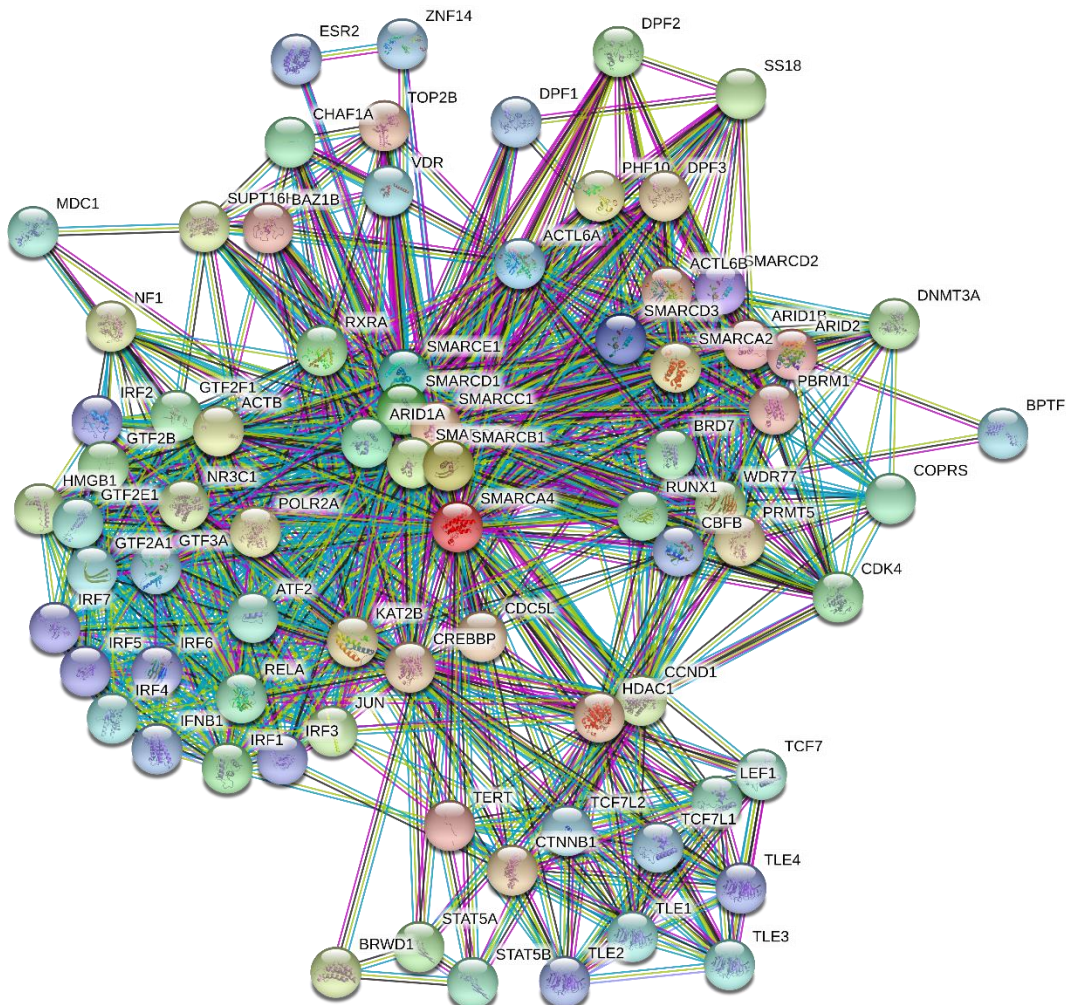
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* Author to whom correspondence should be addressed; E-Mail: vuversky@health.usf.edu; Tel.: 1-813-974-5816; Fax: 1-813-974-7357.

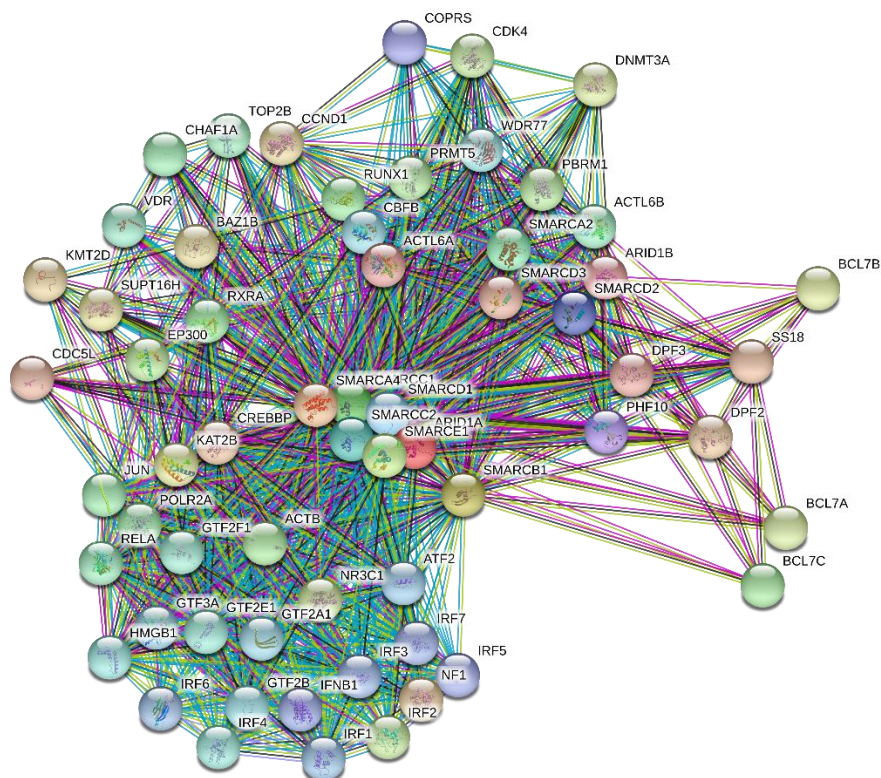
BRG1/SMARCA4 (UniProt ID: P51532; PPID=61.3%; 1,647 residues)

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LWAL
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KIVDAVIKYKSSSGRQLSEVFIQLPSRKELPEYYELIRKPVDFKKIKERIRNHKYRSLNDLEKDVMLLCQNAQT FN
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BAF250A/ARID1A (UniProt ID: O14497; PPID=75.8%; 2,285 residues)

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SMTSSKGGQEDMNLSLQSRPSSLPDLGSIIDLPMTGEGALSPGVSTSGISSSQGEQSNPAQSPFSPHTSPHLPGIR
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ICLPVL DGLLHWAVCPSAEAQDPFSTLGPNAVLSQRLVLETLSKLSIQDNNVDLILATPPFSRLEKLYSTMVRFLS
DRKNPVCREMAVLLANLAQGDSLAARAIQVQKSGIGNLLGFLEDSLAATQFQSSQASLLHMQNPPFEPTSVDMMRR
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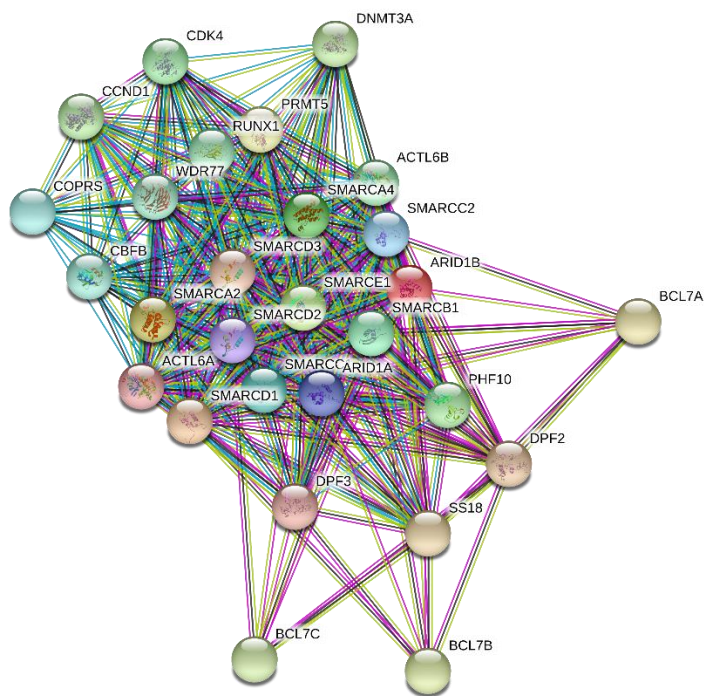


BAF250B/ARID1B (UniProt ID: Q8NFD5; PPID=76.9%; 2,236 residues)

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DMSPGESKLPLPLKADGKEEGTPQPESSKSSSSSTTTGEKITKVYELGNEPERKLWVDRLTFMEERGSVPVSLP
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IVTPEAWRVMSLSKGLLAESTWALDTINILLYDDSTVATFNLSQLSGFLELLVEYFRKCLIDIFGILMEYEVGDPS
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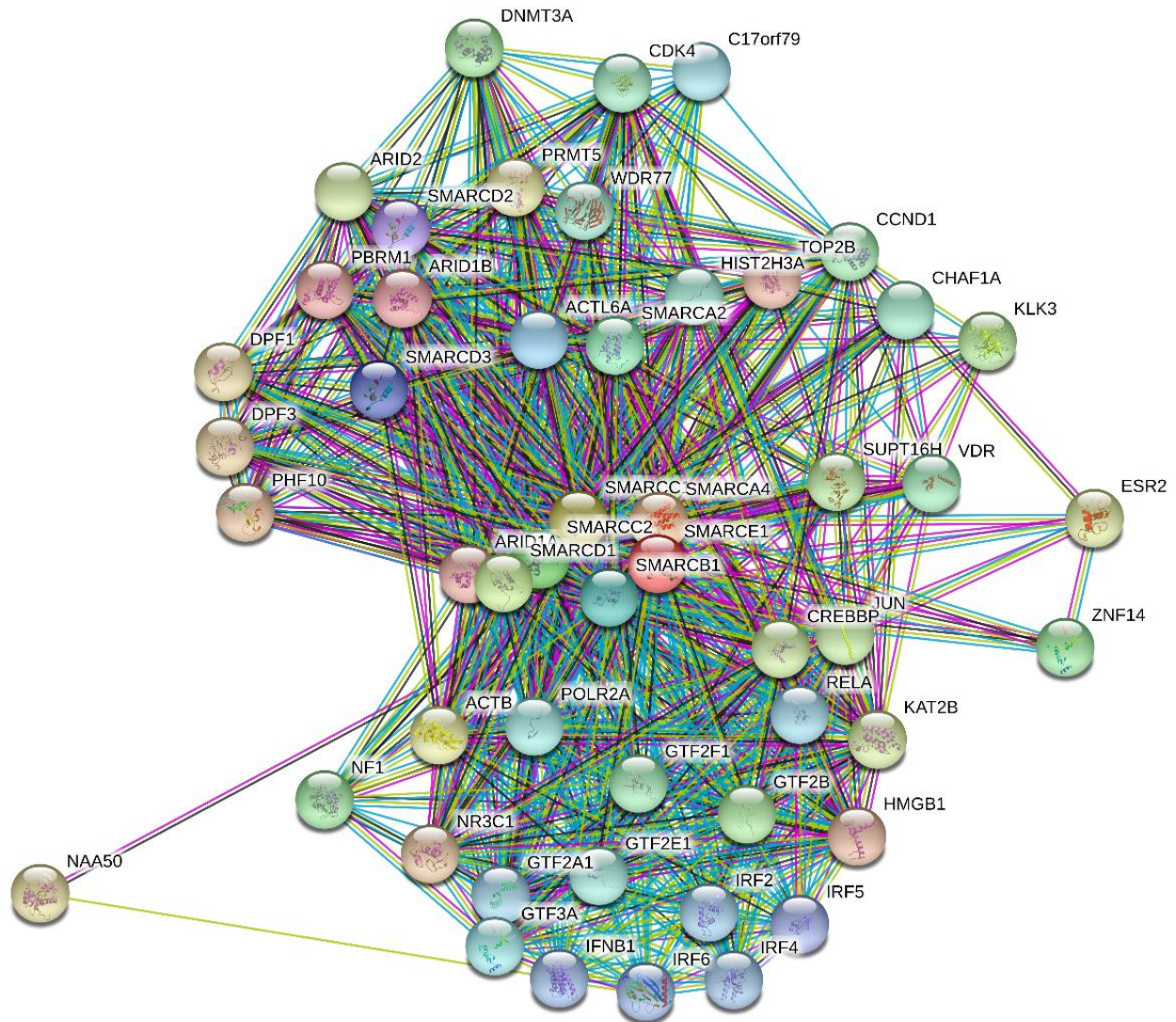
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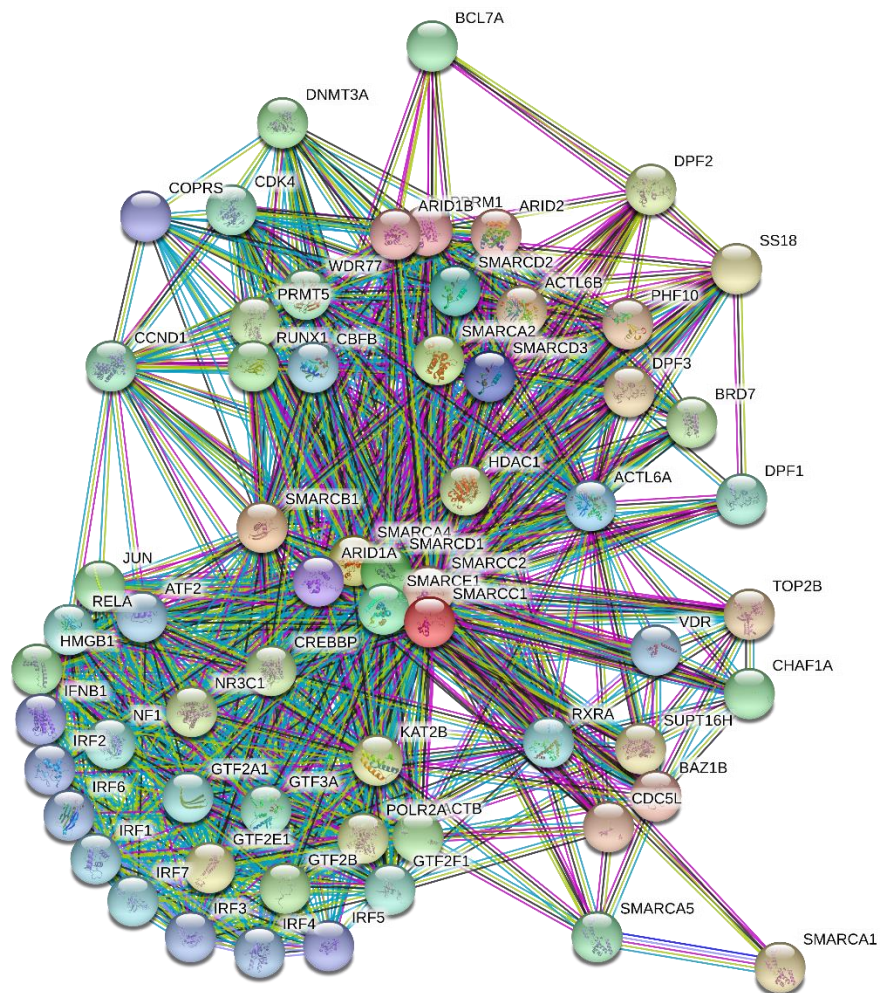
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regulator of chromatin subfamily E member 1 OS=Homo sapiens OX=9606
GN=SMARCE1 PE=1 SV=2

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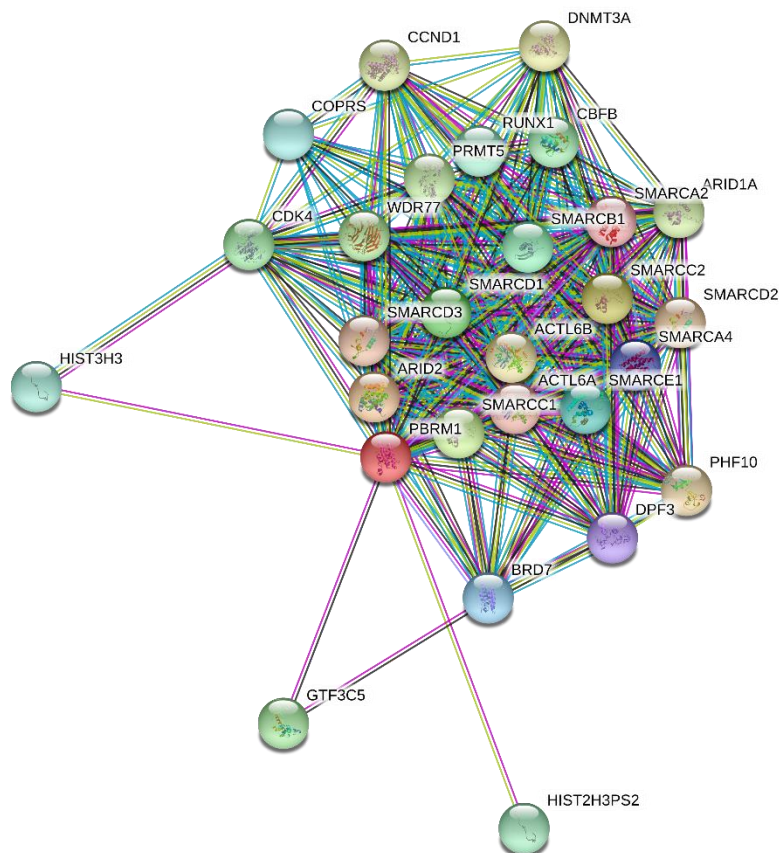
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OX=9606 GN=SMARCC1 PE=1 SV=3
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BAF180/PBRM1 (UniProt ID: Q86U86; PPID=43.2%; 1,689 residues)

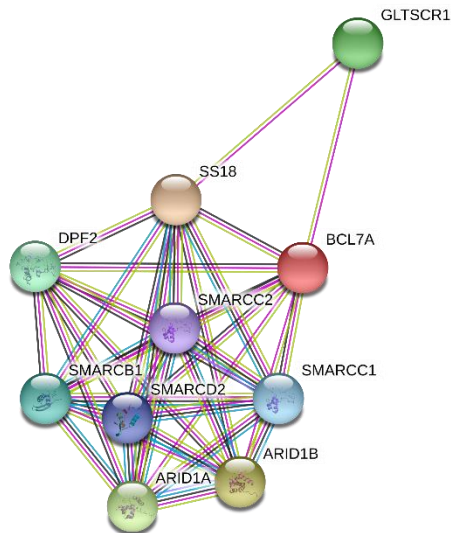
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PE=1 SV=1

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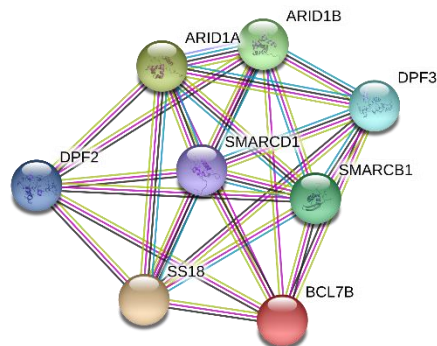
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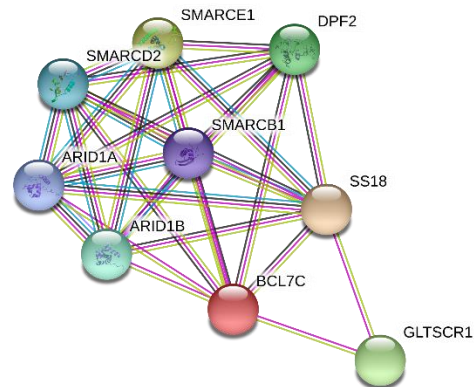
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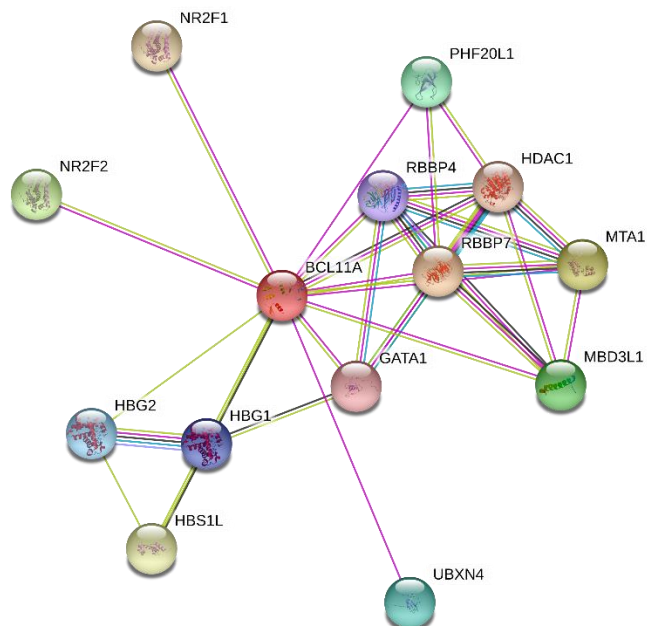
BCL7C (UniProt ID: Q8WUZ0; PPID=90.0%; 217 residues)

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BCL11A (UniProt ID: Q9H165; PPID=69.0%; 835 residues)

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AEYAPQGICKDEPSSYTCTTCKQPFTSAWFLQHAQNTGLRIYLESEHGSPLTPRVGIPSGLGAECPSQPPLHGIH
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NGSLRFSTPPGELDGGISGRSGTSGGSTPHISGPGPGRPSSKEGRSDTCEYCGKVFKNCNLTVHRSHTGERPY
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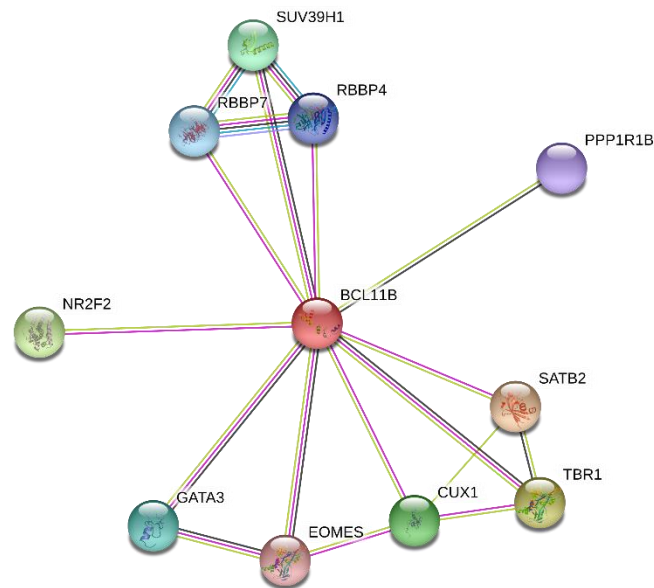


BCL11B (UniProt ID: Q9C0K0; PPID=69.8%; 894 residues)

>sp|Q9C0K0|BC11B_HUMAN B-cell lymphoma/leukemia 11B OS=Homo sapiens OX=9606

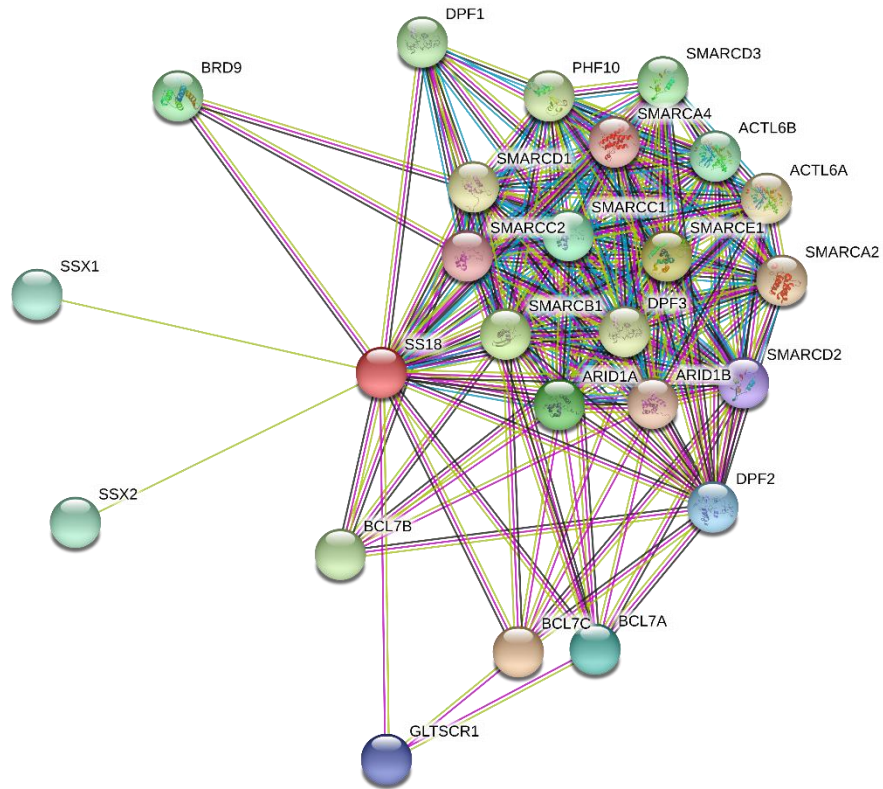
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KQKRGAFKRAAGGGDAGDDDDAGGCGDAGAGGAVNGRGGGFAPGTEFPGLFPRKPAPLPSPLNSAAKRIKVEKD
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ASGGSTPHLGGPGPRPSSKEGRRSDTCEYCGKVFKNCSNLTIVHRRSHTGERPYKCELCNYACAQSSKLTRHMKTHG
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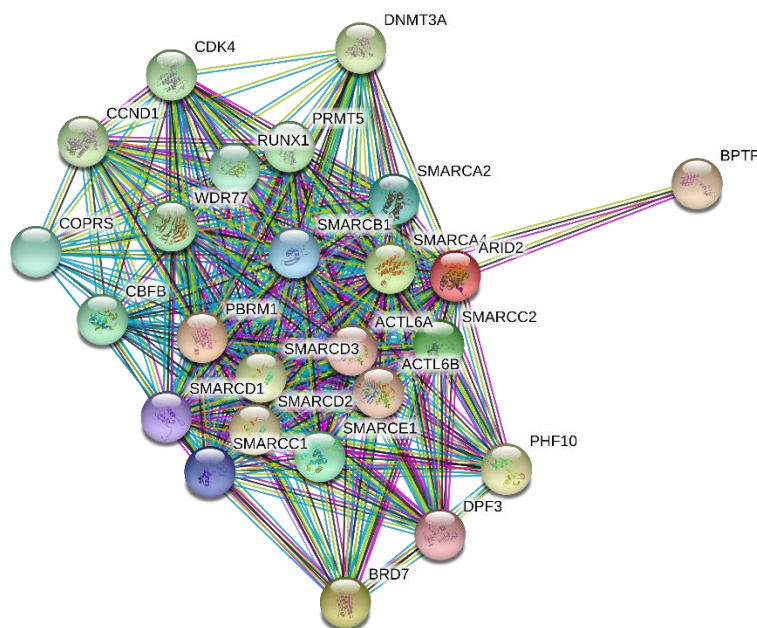


SSXT/SS18 (UniProt ID: Q15532; PPID= 84.1%; 418 residues)

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GYDRPYEDSSQHYYEGNSQYGGQQDAYQGPPQGGYPPQQQYPGQQGYPGQQGYGPSQGGPGPQYPNPQGGQ
QYGGYRPTQPGPPQPPQRPYGYDQGQYGNYYQ
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>sp|Q68CP9|ARID2_HUMAN AT-rich interactive domain-containing protein 2
OS=Homo sapiens OX=9606 GN=ARID2 PE=1 SV=2
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FPRSCSNAAFALKQYYLRYLEKYEKVHFFGEDDDEVPPGNPKPQLPIGAIPSSYNYQQHSVSDYLRQSYGLSMDFNS
PNDYNKLVLSLLSGLPNEVDFAINVCTLLSNESKHVMQLEKDPKIITLLLANAGVFDDTLGFSFSTVFGEWKEKTDR
DFVKFWKDIVDDNEVRDLISDRNKSHEGTSGEWIWESLFHPPRKLGINDEGQRVLQIAVILRNLSFEEGNVKLLAA
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AAVKLIEHPSSSHQMLSEIRPQAEIQVQTQTHVASAPASRAVVAQHVA PPPGIVEIDSEKFACQWLNAHFEVNPDCS
VSRAEMYSEYLSSTCSKLARGGILTSTGFYKCLRTVFPNHTVKRVEDSSSNGQAHIHVVGVKRRAIPLPIQMYYQQQP
VSTSVVRVDSVPDVPSPAPSPAGIPHSQITIGNHFQRTVPANQSSNLTAQSSMFPVQGVHTVAQTVVSRIPQNPSPH
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LPAPQIPPPNNARAPSPQVVYQVASNQAGFGVQGGTPAQQLLVGQQNVQLVPSAMPSPSGGVQTVPI SNLQILPGPL
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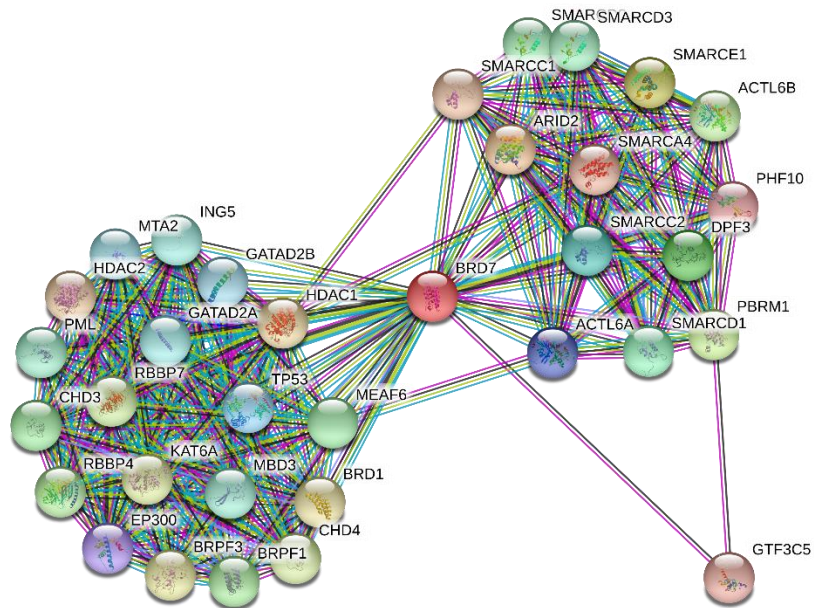


BRD7 (UniProt ID: Q9NPI1; PPID= 61.2%; 651 residues)

>sp|Q9NPI1|BRD7_HUMAN Bromodomain-containing protein 7 OS=Homo sapiens

OX=9606 GN=BRD7 PE=1 SV=1

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FFSFPVTDFIAPGYSMI IKHPMDFSTMKEKIKNNYQSI EELKDNFKLMCTNAMIYNKPETIYYKAAKLLHSGMKI
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LLDVLTGGHRSRTLQEMEMSLPEDEGHTRTLD TAKEMEITEVEPPGRLDSSTQDR LIALKAVTNFGVPVEVFDSEEA
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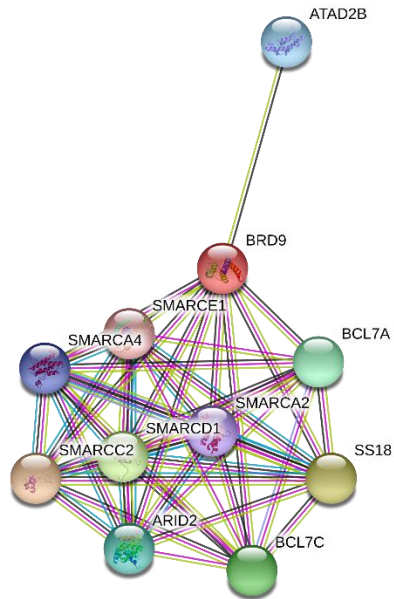


BRD9 (UniProt ID: Q9H8M2; PPID= 60.1%; 597 residues)

>sp|Q9H8M2|BRD9_HUMAN Bromodomain-containing protein 9 OS=Homo sapiens

OX=9606 GN=BRD9 PE=1 SV=2

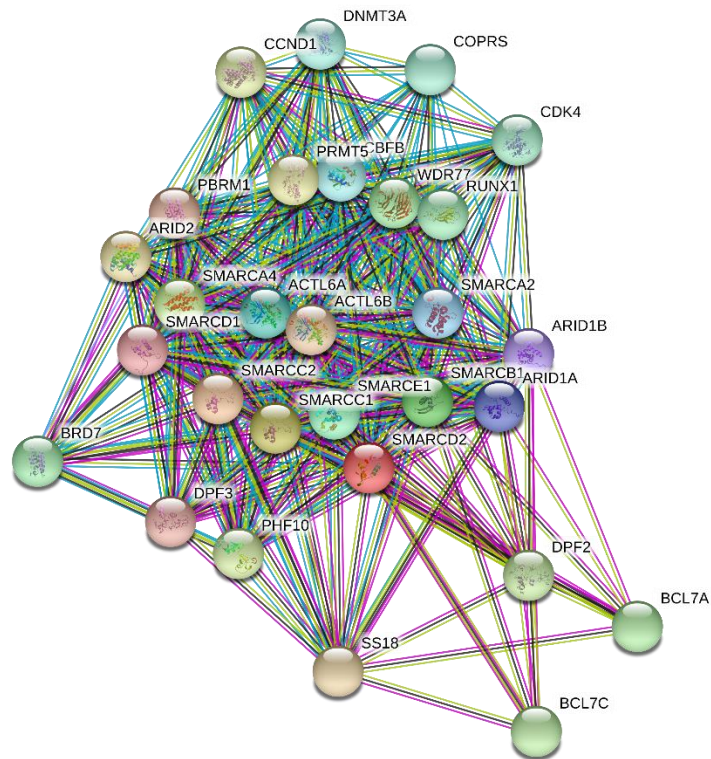
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EARDRINRFLPGGKMGYLKRNGDGSLLYSVNTAEPDADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLLSS
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RNVPMKPPDEAKVGDTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDSHLNLDETTKLLQDLHEAQA
ERGGSRPSSNLSLSNASERDQHHLGSPSRLSVGEQPDVTHDPYEFLLQSPPEAASAKT



BAF60A/SMARCD1 (UniProt ID: Q96GM5; PPID= 43.8%; 515 residues)

```
>sp|Q96GM5|SMRD1_HUMAN SWI/SNF-related matrix-associated actin-dependent  
regulator of chromatin subfamily D member 1 OS=Homo sapiens OX=9606  
GN=SMARCD1 PE=1 SV=2
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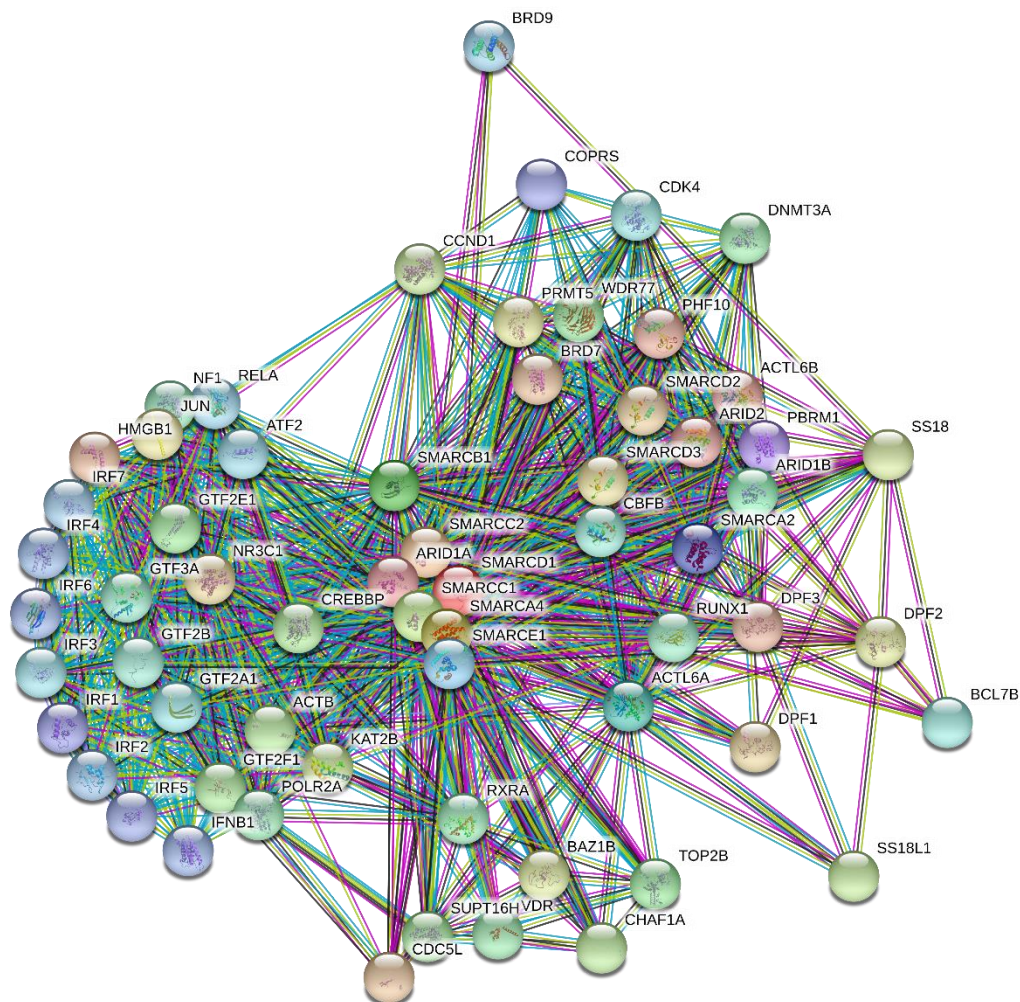
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BAF60B/SMARCD2 (UniProt ID: Q92925; PPID= 49.3%; 531 residues)

>sp|Q92925|SMRD2_HUMAN SWI/SNF-related matrix-associated actin-dependent
regulator of chromatin subfamily D member 2 OS=Homo sapiens OX=9606
GN=SMARCD2 PE=1 SV=3

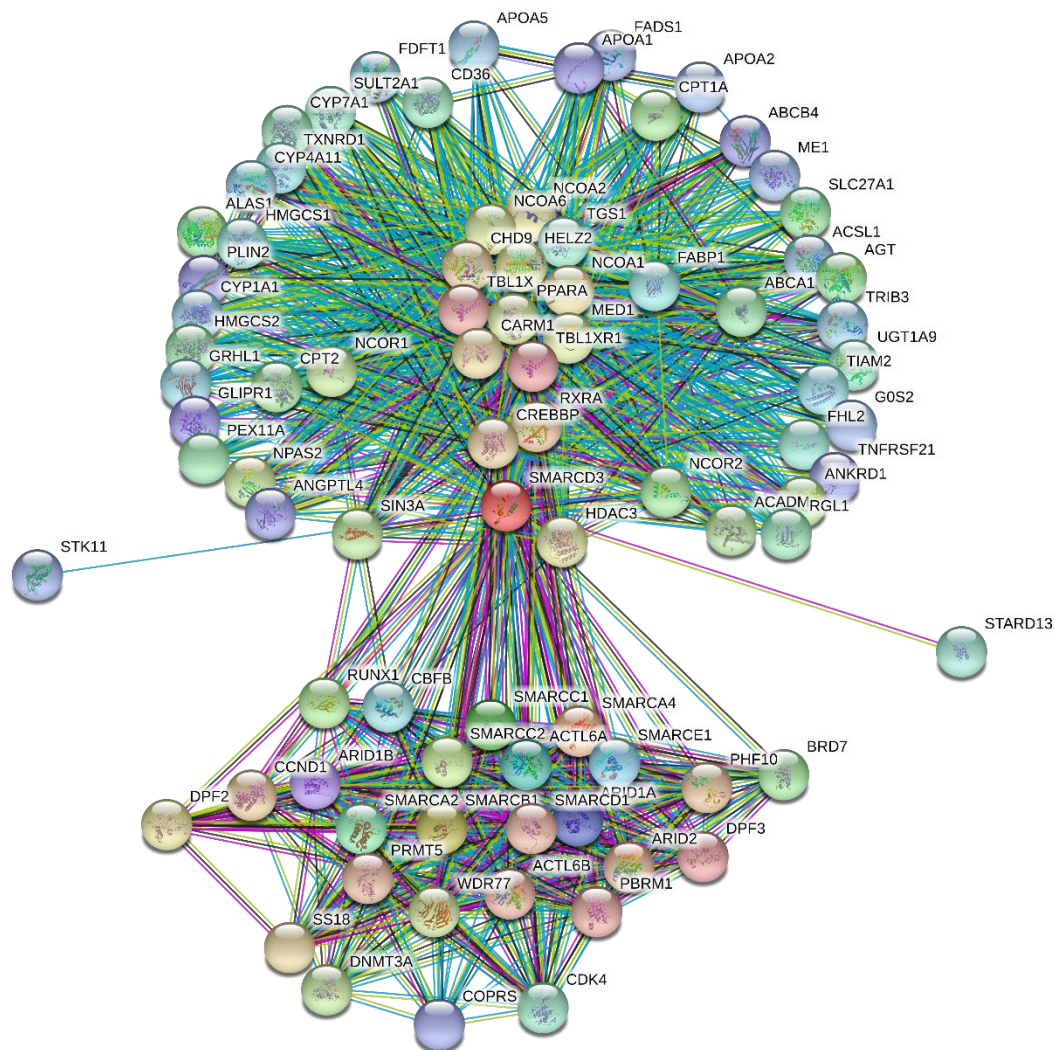
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PQRIRELV
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PIVINHVISVDPNDQKKTACYDIDVEVDDPLKAQMSNFLASTTNQOEIASLDVKIHETIESINQLKTQDFMLSFS
TDPQDFIQEWLRSQRRDLKIITDVIGNPEEERRAAFYHQPAQAEAVGRHIFAKVQRRQEQLEQVLGIRLT



BAF60C/SMARCD3 (UniProt ID: Q6STE5; PPID=50.5%; 483 residues)

>sp|Q6STE5|SMRD3_HUMAN SWI/SNF-related matrix-associated actin-dependent
regulator of chromatin subfamily D member 3 OS=Homo sapiens OX=9606
GN=SMARCD3 PE=1 SV=1

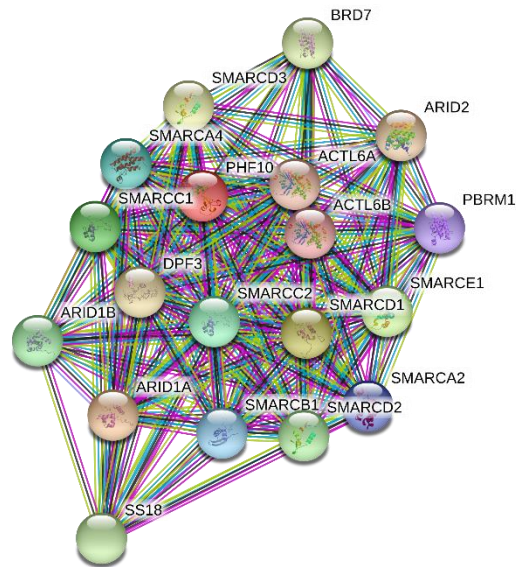
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RKLRLYISNTFNPAPKPAEDSDGSIASWELRVEGKLLDDPSKQKRKFSSFFKSLVIELDKDLYGPDNHLVEWHRTPT
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KYFQQIFDCPRLKFSEIPQRLTALLLPDPDIVINHVISVDPDSDQKKTACYDIDVEVEEPLKGQMSSFLLSTANQQEI
SALDSKIHETIESINQLKIQRDFMLSFSRDPKGYVQDLLRSQSRDLKVMTDVAGNPEEERRAEFYHQPWSEAVSRY
FYCKIQQRQEQLEQSLVVRNT



BAF45A/PHF10 (UniProt ID: Q8WUB8; PPID=53.3%; 498 residues)

>sp|Q8WUB8|PHF10_HUMAN PHD finger protein 10 OS=Homo sapiens OX=9606 GN=PHF10
PE=1 SV=3

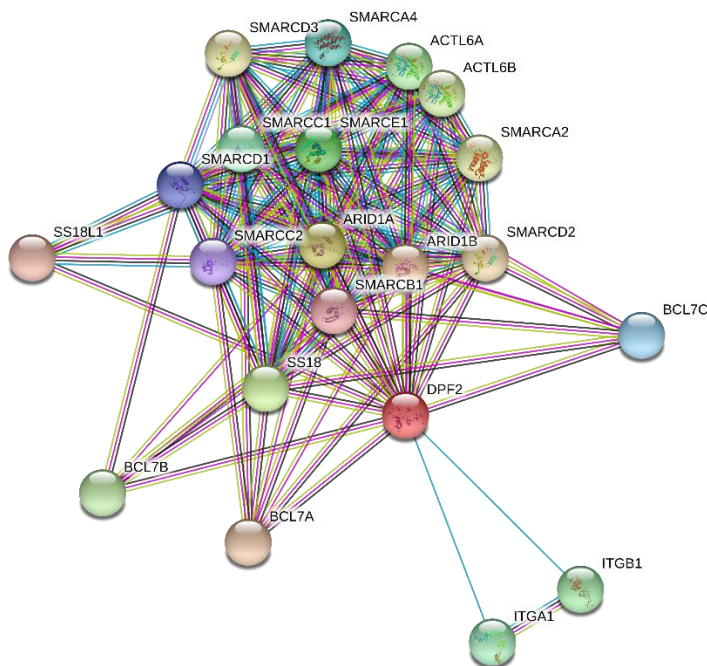
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VIQVPQGKYKVLPTERTKVSSYPVALIPGQFQEYYKRYSPDELRYLPLNTALYEPPLDPELPALDSGDSDDGEDGR
GDEKRKNKGTSDSSSGNVSEGESPPDSQEDSFQGRQKSKDKAATPRKDGPKRSVLSKSVPGYKPKVIPNAICGICLK
GKESNKKGKAESLIHCSQCENSGHPSCLDMTLMELVSMIKTYPWQCMECKTCIICGQPHHEEEMMFCDMCDRGYHTFC
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BAF45D/DPF2 (UniProt ID: Q92785; PPID= 59.7%; 391 residues)

>sp|Q92785|REQU_HUMAN Zinc finger protein ubi-d4 OS=Homo sapiens OX=9606
GN=DPF2 PE=1 SV=2

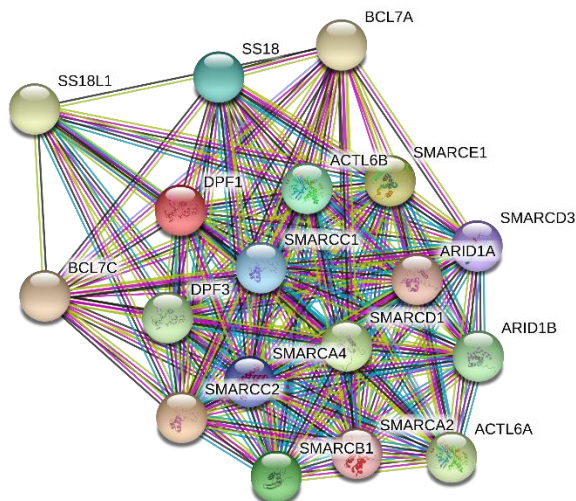
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HLAEEEGEDKEDSQPPTPVSQRSEEQKSKKGPDLALPNNYCDFCLGDSKINKKTGQPEELVSCSDCGRSGHPSCLO
FTPVMMAAVKTYRWQCIECKCCNICGTSENDQQLLFCDDCDRGYHMYCLTPSMSEPPEGSWSCHLCLDLLKEKASIY
QNQNSS



BAF45B/DPF1 (UniProt ID: Q92782; PPID=35.8%; 380 residues)

>sp|Q92782|DPF1_HUMAN Zinc finger protein neuro-d4 OS=Homo sapiens OX=9606
GN=DPF1 PE=1 SV=2

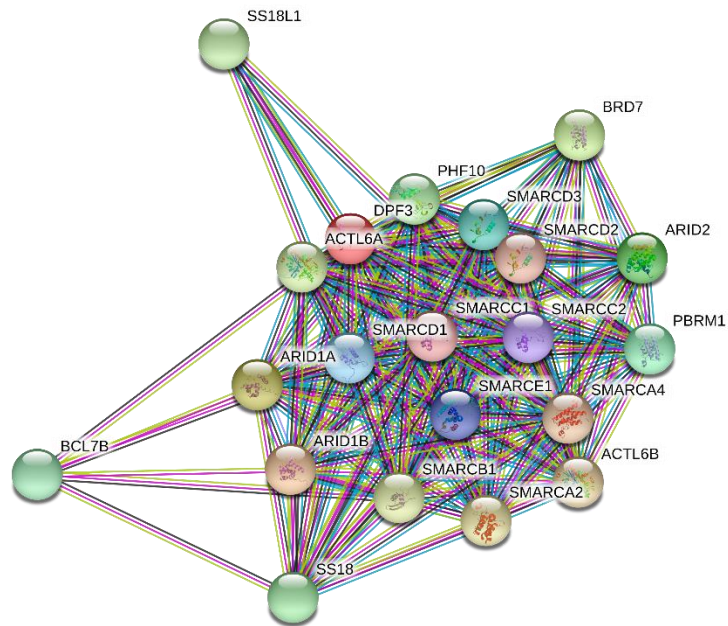
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BAF45C/DPF3 (UniProt ID: Q92784; PPID=50.5%; 378 residues)

>sp|Q92784|DPF3_HUMAN Zinc finger protein DPF3 OS=Homo sapiens OX=9606
GN=DPF3 PE=1 SV=3

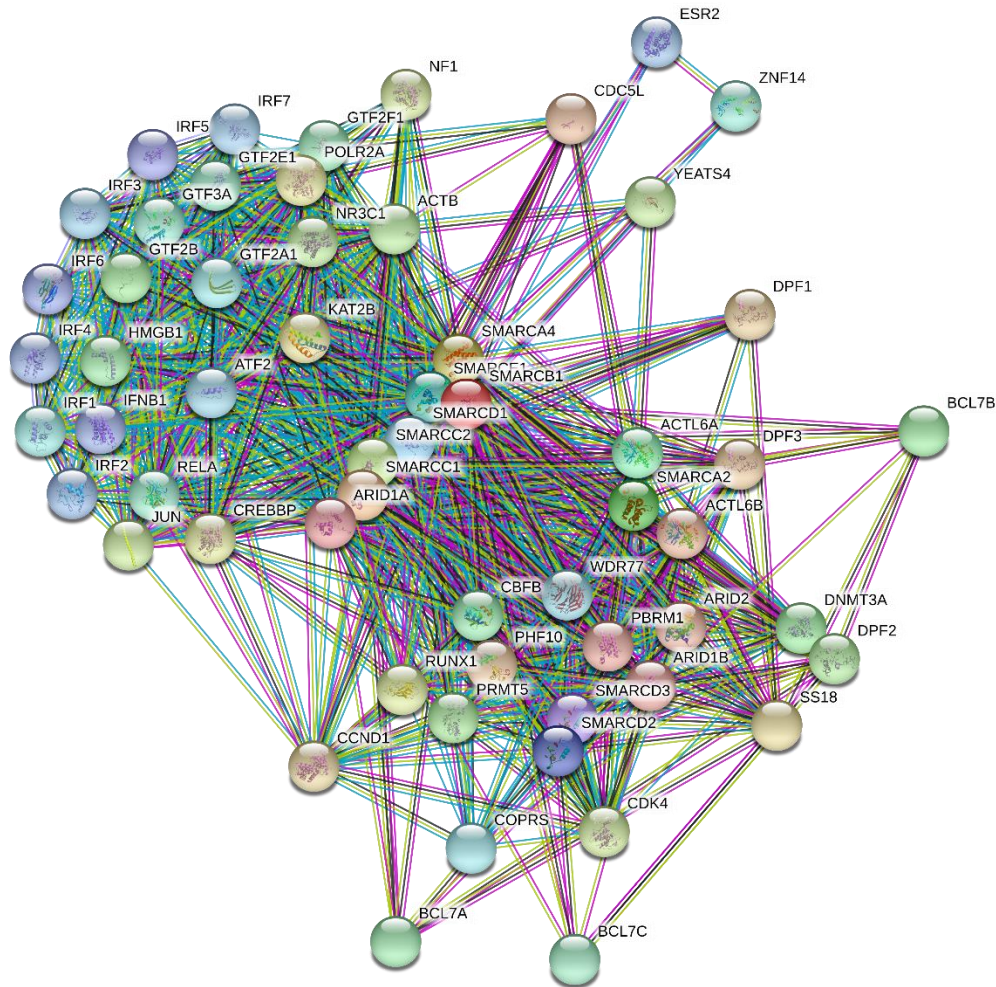
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BAF47/SMARCB1 (UniProt ID: Q12824; PPID=35.8%; 385 residues)

>sp|Q12824|SNF5_HUMAN SWI/SNF-related matrix-associated actin-dependent
regulator of chromatin subfamily B member 1 OS=Homo sapiens OX=9606
GN=SMARCB1 PE=1 SV=2

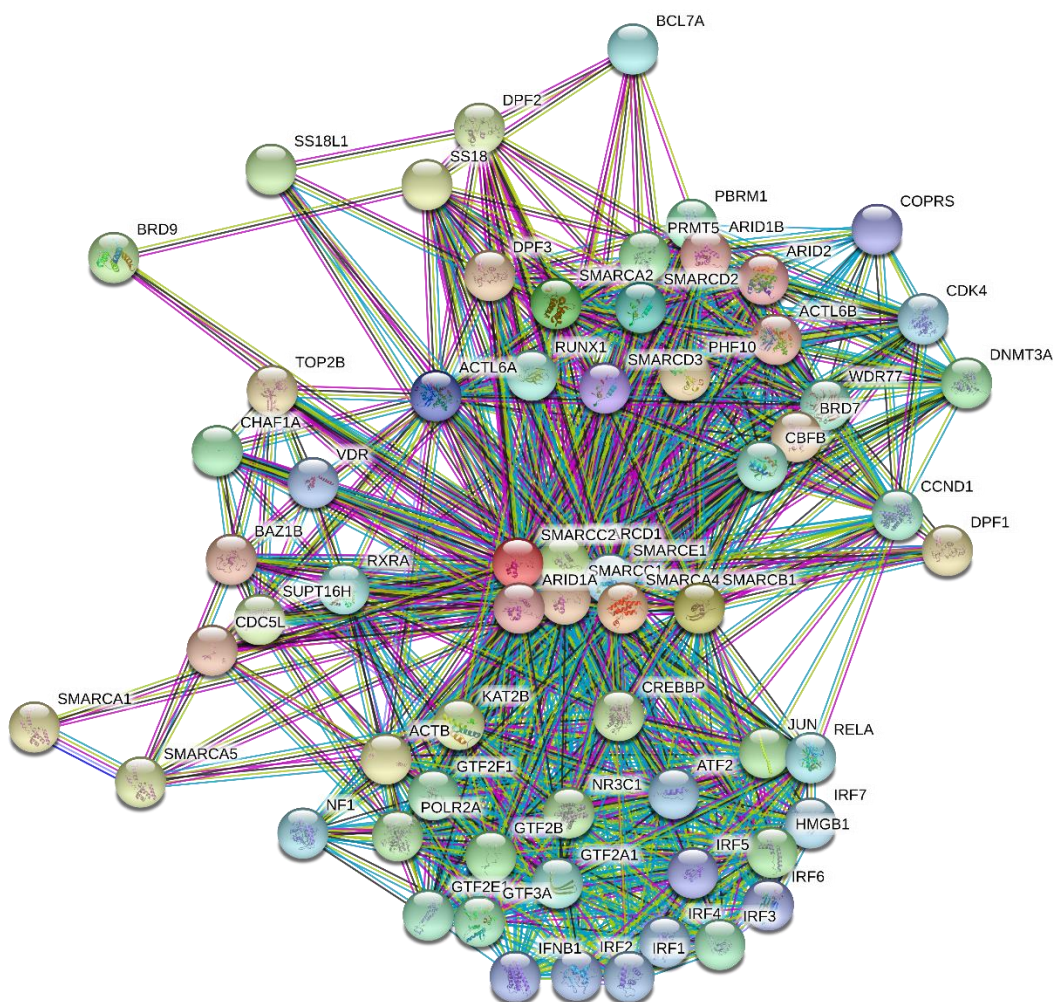
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RMGRDCKRRTFPLCFDDHDPAVIHENASQPEVLVPIRLDMEIDGQKLRFDAFTWNMNEKLMTPPEMFSEILCDDLNLNPL
TFVPAIASAIRQQIESYPTDSILEDQSDQRVIIKLNHVGNISLVDQFEWDMSEKENSPEKFALKLCELGLGGEFV
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BAF170/SMARCC2 (UniProt ID: Q8TAQ2; PPID=63.1%; 1,214 residues)

>sp|Q8TAQ2|SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens
OX=9606 GN=SMARCC2 PE=1 SV=1

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GLVPLQPKTPQQTSASQQMLNFPD KGEKPTDMQNFGLRTDMYTKKNVPSKSKAAASATREWTEQETLLLLLEALEMY
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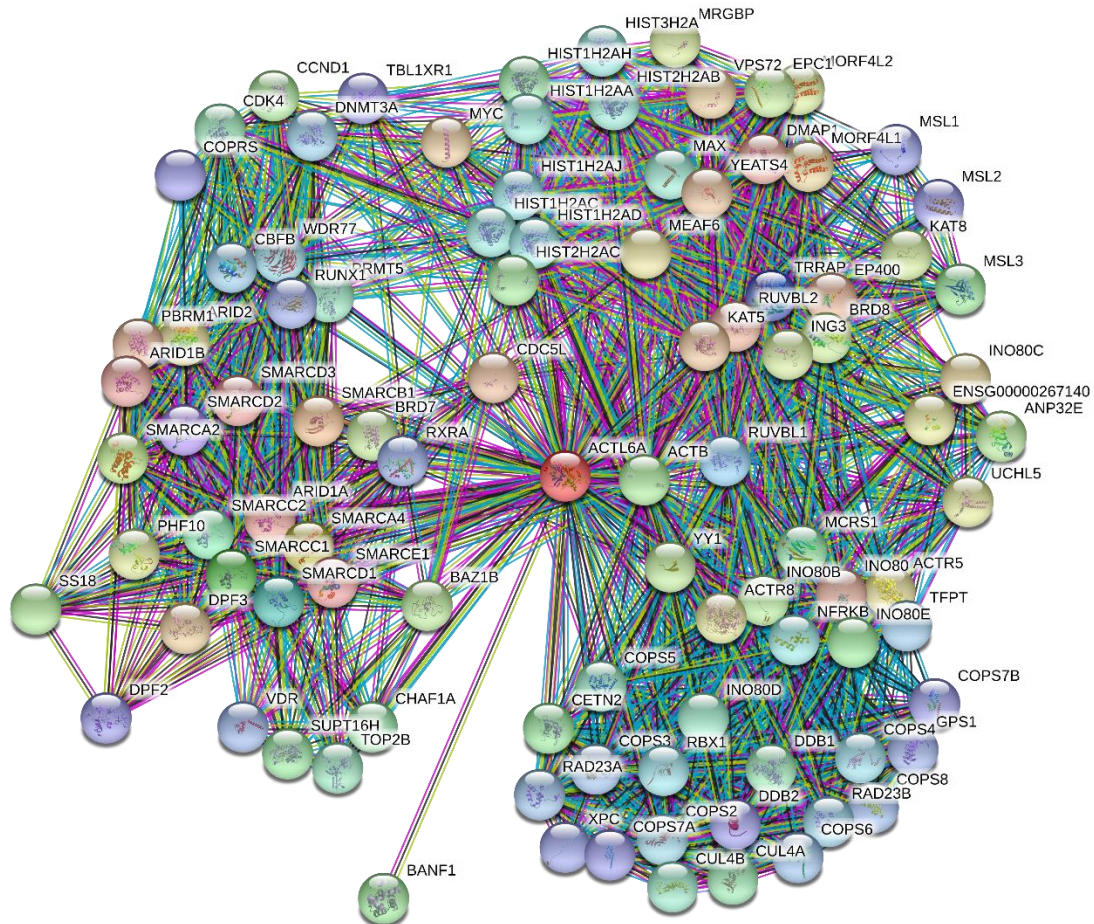


BAF53A/ACTL6A (UniProt ID: O96019; PPID=23.5%; 429 residues)

>sp|O96019|ACTL6A_HUMAN Actin-like protein 6A OS=Homo sapiens OX=9606

GN=ACTL6A PE=1 SV=1

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 AVLTAFANGRSTGLILDGATHTTAIPVHDGYVLQGGIVKSPLAGDFITMQCRELFQEMNIELVPPYMIASKEAVRE
 GSPANWKRKEKLPQVTRSWHNYMCNCVIQDFQASVLQVSDSTYDEQVAAQMPTVHYEFPNGYNCDFGAERLKIPEGL
 FDPSTNVKGLSGNTMLGVSHVVTTSVGMCDIDIRPGLYGSVIVAGGNTLIQSFTDRLNRELSQKTPPSMRLKLIANNT
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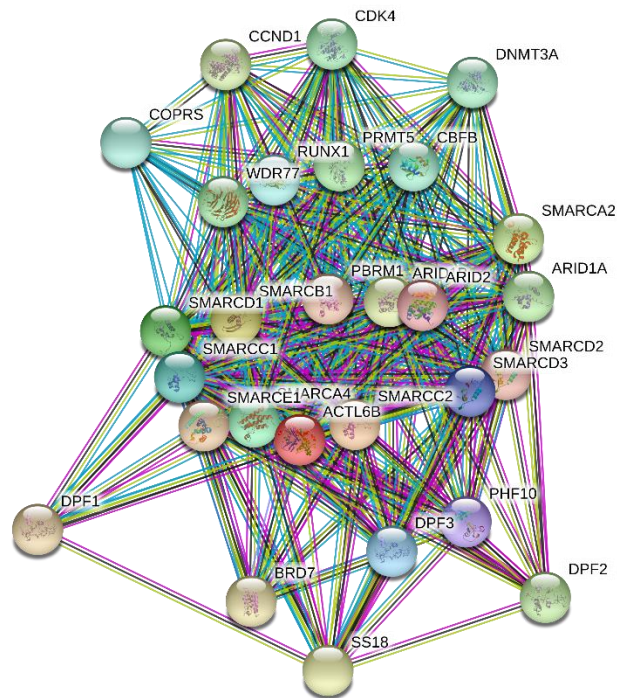


BAF53B/ACTL6B (UniProt ID: O94805; PPID=25.4%; 426 residues)

>sp|O94805|ACTL6B_HUMAN Actin-like protein 6B OS=Homo sapiens OX=9606

GN=ACTL6B PE=1 SV=1

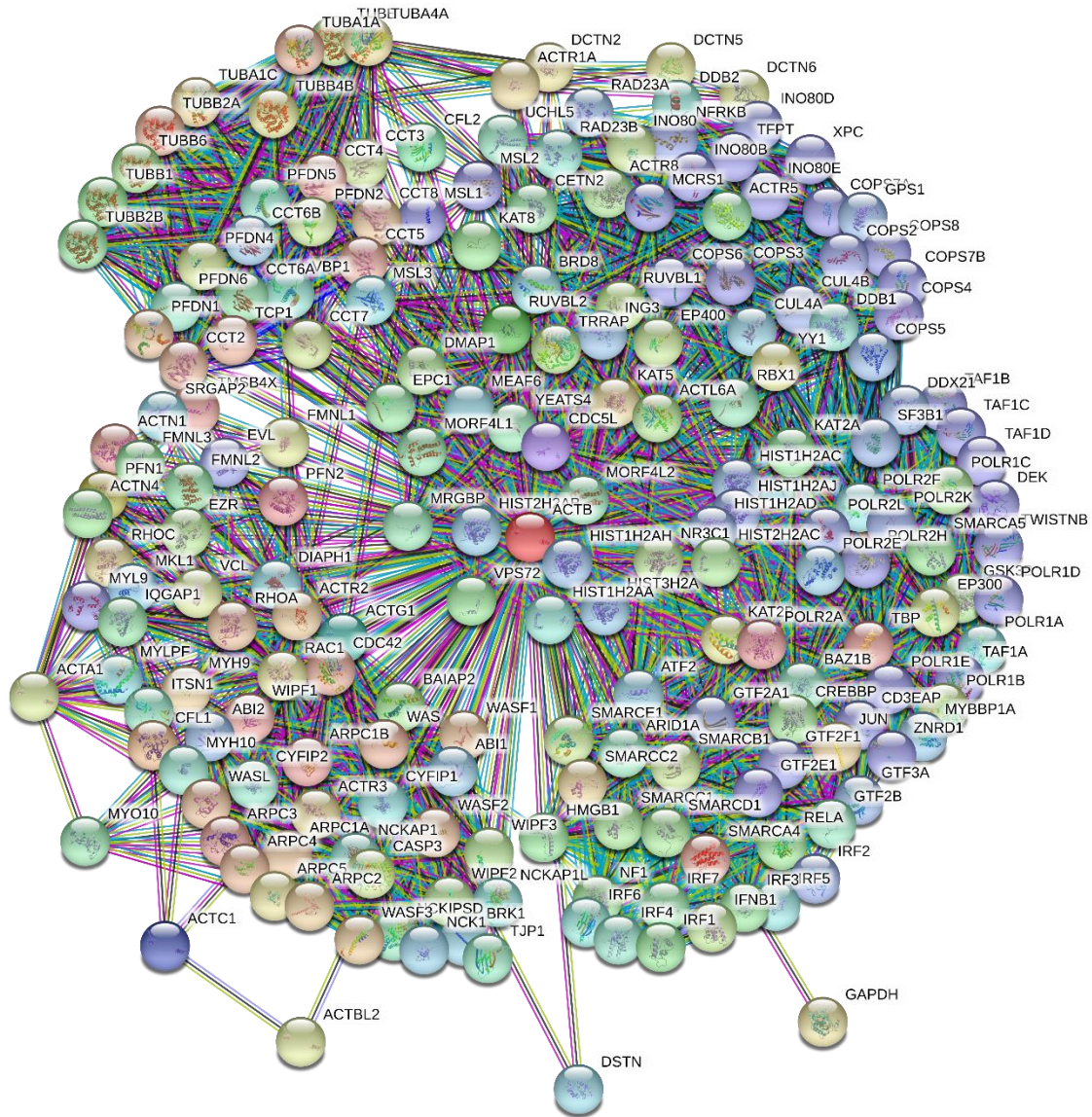
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TAFANGRSTGLVLD SGATHTTAIPVHDGYVLQQGIVKSPLAGDFISMQCRELFQEMAIIDIIPPYMIAAKEPVREGAP
PNWKKKEKLPQVSKSWHNYMCNEVIQDFQASVLQVSDSPYDEQVAAQMPTVHYEMPNGYNTDYGAERLRIPEGLFDP
SNVKGLSGNTMLGVGHVVTTSIGMCDIDIRPGLYGSVIVTGGNTLLQGFTDRLNRELSQKTPPSMRLKLIASNSTME
RKFS PWIGGSILASLGT FQQMWISKQEYEEGGKQCVERKCP



Actin- β /ACTB (UniProt ID: P60709; PPID=22.1%; 375 residues)

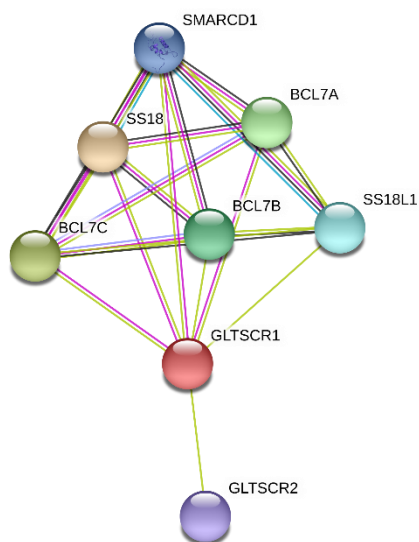
>sp|P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB
PE=1 SV=1

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NWDDMEKIWHHTFYNELRVAP E EHPVLLTEAPLNPKANREKMTQIMFETFNT PAMYVAIQAVLSLYASGR TTGIVMD
SGDGVTHTVPIYEGYALPHA I LRLDLAGRD L TDYLMKIL TERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAA
SSSSLEKSYELPDGQVITIGNERFRCP EALFQPSFLGMESCGIHETT FNSIMKCDVDIRKDL YANTVLSGGTTMYPG
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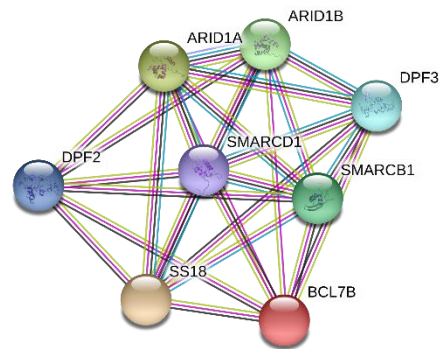
GLTSCR1/BICRA (UniProt ID: Q9NZM4; PPID=88.2%; 1,560 residues)

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GLTSCR1L/BICRAL (UniProt ID: Q6AI39; PPID=74.8%; 1,079 residues)

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C



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>sp|P51531|SMCA2_HUMAN Probable global transcription activator SNF2L2 OS=Homo
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