Interpro ID	**Motif Name**	**A**	**B**
IPR000504	RNA-binding region RNP-1 (RNA recognition r	49	246
IPR001650	Helicase, C-terminal	39	98
IPR001410	DEAD/DEAH box helicase	39	100
IPR001680	G-protein beta WD-40 repeat	36	330
IPR008938	ARM repeat fold	24	365
IPR007124	Histone-fold/TFIID-TAF/NF-Y	15	53
IPR000629	ATP-dependent helicase, DEAD-box	14	17
IPR009072	Histone-fold	13	71
IPR007125	Histone core	12	36
IPR003593	AAA ATPase	9	141
IPR001159	Double-stranded RNA binding (DsRBD) domai	8	23
IPR008994	Nucleic acid-binding OB-fold	8	82
IPR000795	Protein synthesis factor, GTP-binding	7	15
IPR009000	Translation factor	7	16
IPR004038	Ribosomal protein L7Ae/L30e/S12e/Gadd45	6	7
IPR005818	Histone H1/H5	6	10
IPR005824	KOW	6	10
IPR000558	Histone H2B	6	13
IPR002464	ATP-dependent helicase, DEAH-box	6	13
IPR004161	Elongation factor Tu, domain 2	6	15
IPR002119	Histone H2A	6	16
IPR000953	Chromo	6	30
IPR001878	Zn-finger, CCHC type	6	46
IPR003439	ABC transporter	6	70
IPR007109	Brix domain	5	1
IPR005819	Histone H5	5	4
IPR001247	3' exoribonuclease	5	5
IPR001208	MCM	5	7
IPR003034	DNA-binding SAP	5	24
IPR000330	SNF2 related domain	5	42
IPR004087	KH	5	42
IPR003395	SMC protein, N-terminal	4	3
IPR004037	Ribosomal protein L7AE	3	1
IPR008251	Chromo shadow	3	1
IPR008921	DNA polymerase III clamp loader subunit, C-t	3	1
IPR004589	ATP-dependent DNA helicase RecQ	3	2
IPR000988	Ribosomal protein L24E	2	1
IPR002121	HRDC domain	2	1
IPR002415	High mobility group-like nuclear protein	2	1
IPR005612	CBF/Mak21 family	2	1
IPR005825	Ribosomal protein L24/L26	2	1
IPR009018	Signal recognition particle, 9 kDa and 14 kDa	2	1

Absence of a specific IPR motif	C	D

Replace the number below with the above IPR id to know more about the motif
http://www.ebi.ac.uk/interpro/DisplayIproEntry?ac=IPRnnnnnnn

Statistics:
If the frequency of any cell is less than 5, Fisher exact test was employed showing two

C	D	Odd ratio	P value (Fis	Chi square test
642	27989	8.68387027		p<0.001 (chisq=252.377239999527)
652	28137	17.1738919		p<0.001 (chisq=390.310401575334)
652	28135	16.8292178		p<0.001 (chisq=383.678300842524)
655	27905	4.64760583		p<0.001 (chisq=84.9626679913749)
667	27870	2.74744819		p<0.001 (chisq=22.5563050016568)
676	28182	11.7988724		p<0.001 (chisq=104.799136540015)
677	28218	34.3254844		p<0.001 (chisq=225.465020664709)
678	28164	7.60588309		p<0.001 (chisq=56.3798595012)
679	28199	13.8433972		p<0.001 (chisq=95.9296239945199)
682	28094	2.62937543		p<0.01 (chisq=6.94749614551515)
683	28212	14.3673054		p<0.001 (chisq=63.2758949763662)
683	28153	4.02142628		p<0.001 (chisq=13.6815214389727)
684	28220	19.2534113		p<0.001 (chisq=69.6329567548056)
684	28219	18.0494335		p<0.001 (chisq=66.0761508970337)
685	28228	35.3217935		p<0.001 (chisq=88.8802533373617)
685	28225	24.7226277		p<0.001 (chisq=70.2417008249432)
685	28225	24.7226277		p<0.001 (chisq=70.2417008249432)
685	28222	19.0153846		p<0.001 (chisq=57.5118624023301)
685	28222	19.0153846		p<0.001 (chisq=57.5118624023301)
685	28220	16.4788321		p<0.001 (chisq=51.0574040717789)
685	28219	15.4483577		p<0.001 (chisq=48.2735429971323)
685	28205	8.2350365		p<0.001 (chisq=25.6795585958955)
685	28189	5.36762932		p<0.001 (chisq=14.9781666942395)
685	28165	3.52429614		p<0.01 (chisq=7.6805109946311)
686	28234	205.787172	4.51E-08	
686	28231	51.4413265	8.92E-07	
686	28230	41.1516035		p<0.001 (chisq=77.8946288723723)
686	28228	29.39192		p<0.001 (chisq=63.469105421065)
686	28211	8.56748056		p<0.001 (chisq=21.4569155046897)
686	28193	4.89257948		p<0.005 (chisq=10.4242004257588)
686	28193	4.89257948		p<0.005 (chisq=10.4242004257588)
687	28232	54.792819	1.07E-05	
688	28234	123.113372	5.33E-05	
688	28234	123.113372	5.33E-05	
688	28234	123.113372	5.33E-05	
688	28233	61.5545058	0.00013095	
689	28234	81.9564586	0.00168242	
689	28234	81.9564586	0.00168242	
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689	28234	81.9564586	0.00168242	
689	28234	81.9564586	0.00168242	

P-tail value; otherwise, chi-square test with Yates' correction value was employed to calculate th

with Yates' cor

Interpro ID	**Motif Name**	**A**	**B**
IPR007109	Brix domain	5	1
IPR004037	Ribosomal protein L7AE	3	1
IPR008251	Chromo shadow	3	1
IPR008921	DNA polymerase III clamp loader subunit, C-t	3	1
IPR000988	Ribosomal protein L24E	2	1
IPR002121	HRDC domain	2	1
IPR002415	High mobility group-like nuclear protein	2	1
IPR005612	CBF/Mak21 family	2	1
IPR005825	Ribosomal protein L24/L26	2	1
IPR009018	Signal recognition particle, 9 kDa and 14 kDa	2	1
IPR004589	ATP-dependent DNA helicase RecQ	3	2
IPR003395	SMC protein, N-terminal	4	3
IPR005819	Histone H5	5	4
IPR001247	3' exoribonuclease	5	5
IPR004038	Ribosomal protein L7Ae/L30e/S12e/Gadd45	6	7
IPR000629	ATP-dependent helicase, DEAD-box	14	17
IPR001208	MCM	5	7
IPR005818	Histone H1/H5	6	10
IPR005824	KOW	6	10
IPR000795	Protein synthesis factor, GTP-binding	7	15
IPR000558	Histone H2B	6	13
IPR002464	ATP-dependent helicase, DEAH-box	6	13
IPR009000	Translation factor	7	16
IPR001650	Helicase, C-terminal	39	98
IPR001410	DEAD/DEAH box helicase	39	100
IPR004161	Elongation factor Tu, domain 2	6	15
IPR002119	Histone H2A	6	16
IPR001159	Double-stranded RNA binding (DsRBD) domai	8	23
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IPR004087	KH	5	42
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IPR003439	ABC transporter	6	70
IPR008938	ARM repeat fold	24	365
IPR003593	AAA ATPase	9	141

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C	**D**	**Odd ratio**	**P value (Fis**	**Chi square test**
686	28234	205.787172	4.51E-08	
688	28234	123.113372	5.33E-05	
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689	28234	81.9564586	0.00168242	
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689	28234	81.9564586	0.00168242	
688	28233	61.5545058	0.00013095	
687	28232	54.792819	1.07E-05	
686	28231	51.4413265	8.92E-07	
686	28230	41.1516035		p<0.001 (chisq=77.8946288723723)
685	28228	35.3217935		p<0.001 (chisq=88.8802533373617)
677	28218	34.3254844		p<0.001 (chisq=225.465020664709)
686	28228	29.39192		p<0.001 (chisq=63.469105421065)
685	28225	24.7226277		p<0.001 (chisq=70.2417008249432)
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684	28220	19.2534113		p<0.001 (chisq=69.6329567548056)
685	28222	19.0153846		p<0.001 (chisq=57.5118624023301)
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684	28219	18.0494335		p<0.001 (chisq=66.0761508970337)
652	28137	17.1738919		p<0.001 (chisq=390.310401575334)
652	28135	16.8292178		p<0.001 (chisq=383.678300842524)
685	28220	16.4788321		p<0.001 (chisq=51.0574040717789)
685	28219	15.4483577		p<0.001 (chisq=48.2735429971323)
683	28212	14.3673054		p<0.001 (chisq=63.2758949763662)
679	28199	13.8433972		p<0.001 (chisq=95.9296239945199)
676	28182	11.7988724		p<0.001 (chisq=104.799136540015)
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685	28165	3.52429614		p<0.01 (chisq=7.6805109946311)
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