

T-COFFEE, Version_7.38 Thu Nov 20 17:26:38 WEST 2008

Cedric Notredame

CPU TIME: 20 sec.

SCORE = 82

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BAD AVG GOOD

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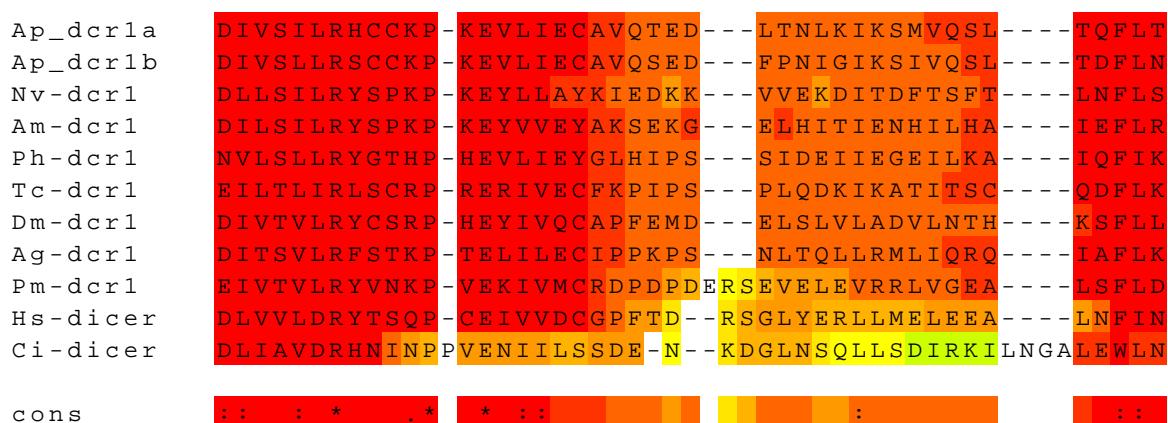
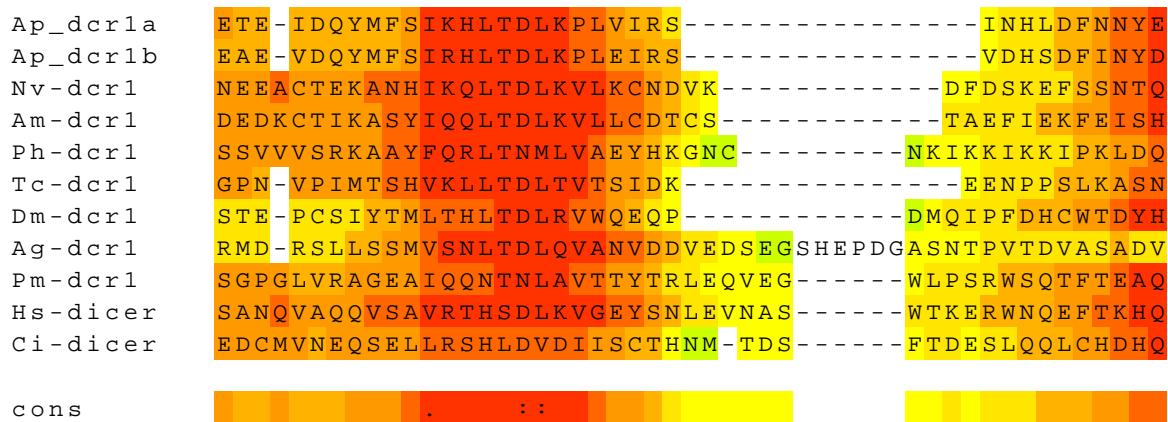
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Ap_dcrlb	:	84
Nv-dcrl	:	85
Am-dcrl	:	84
Ph-dcrl	:	81
Tc-dcrl	:	85
Dm-dcrl	:	80
Ag-dcrl	:	79
Pm-dcrl	:	80
Hs-dicer	:	80
Ci-dicer	:	76
cons	:	82

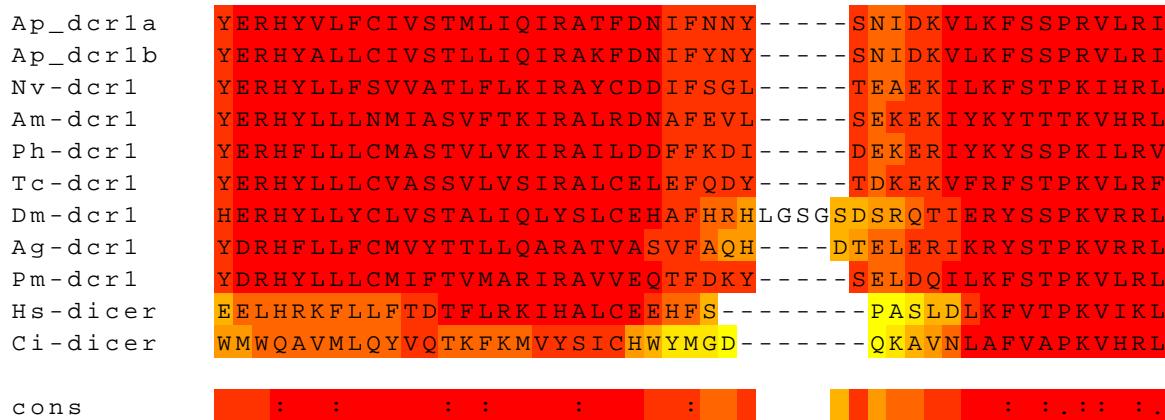
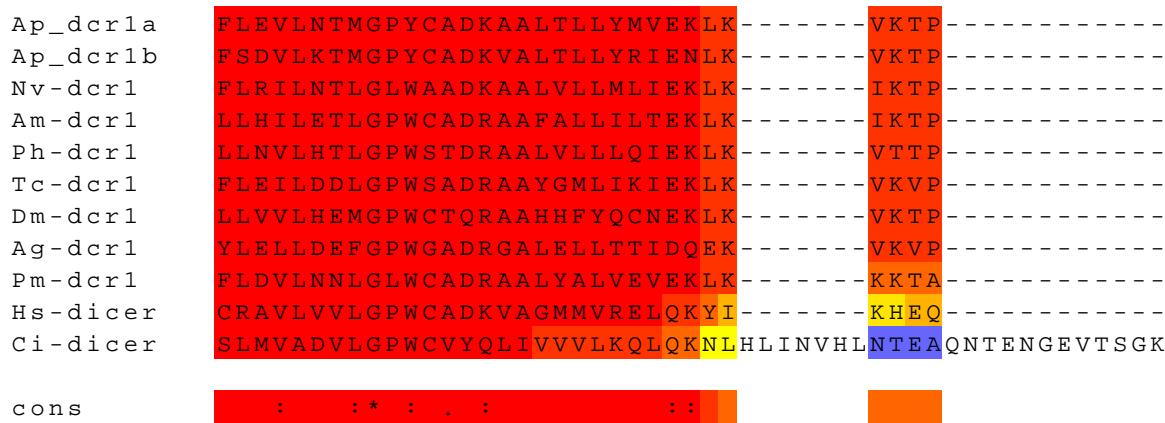
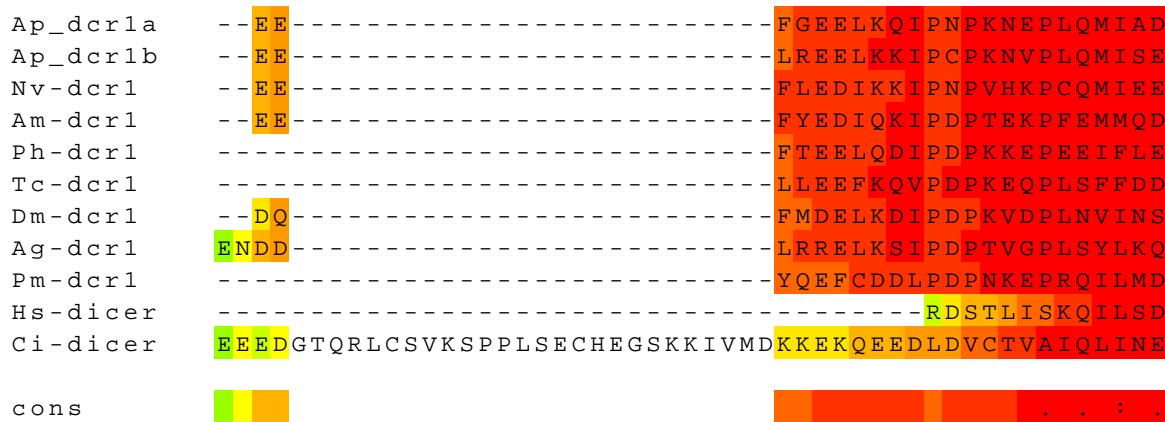
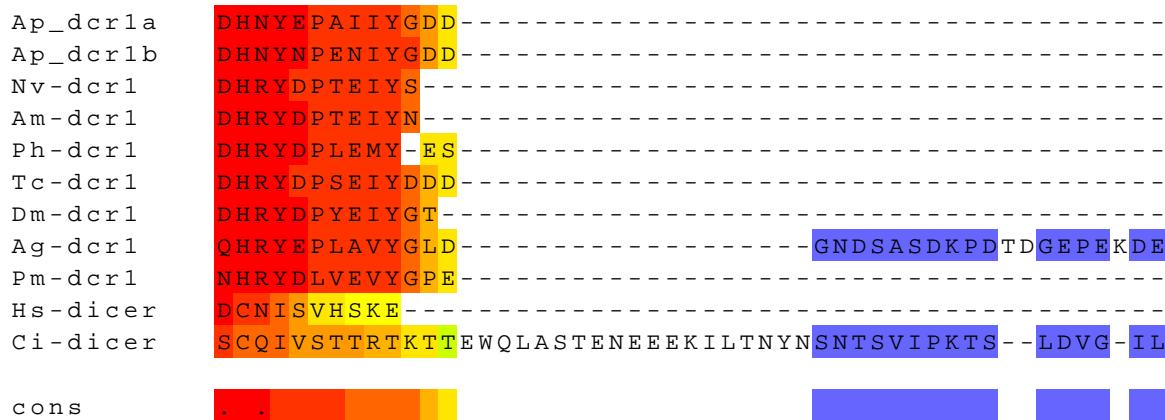
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Ap_dcrlb MAL-----TF-DDYVNTKTFTPQEYQVEL
Nv-dcrl MAF-----FF-NDHIHTKSFTPREHQVEL
Am-dcrl MAF-----PL-NDQIYTKSFTPREYQVEL
Ph-dcrl MAY-----HL-IDNVHSKSLTPKEPNVEL
Tc-dcrl MAC-----YL-NENVYHTHTFTPREYQVEL
Dm-dcrl MAF-----HWCDNNLHTTVFTPQVEL
Ag-dcrl MSL-----FHWTDGNIHTTALTQTEL
Pm-dcrl MMN-----RVQPENVHSTIFTPREYQVEL
Hs-dicer MKSPALQPLSMAGLQLMTPASSPMGPFGLPWQQEAIHDNIYTPRKYQVEL
Ci-dicer MLSSGSSSQE-----PGKPSWTSNSQCNSFIPRKYQIEL

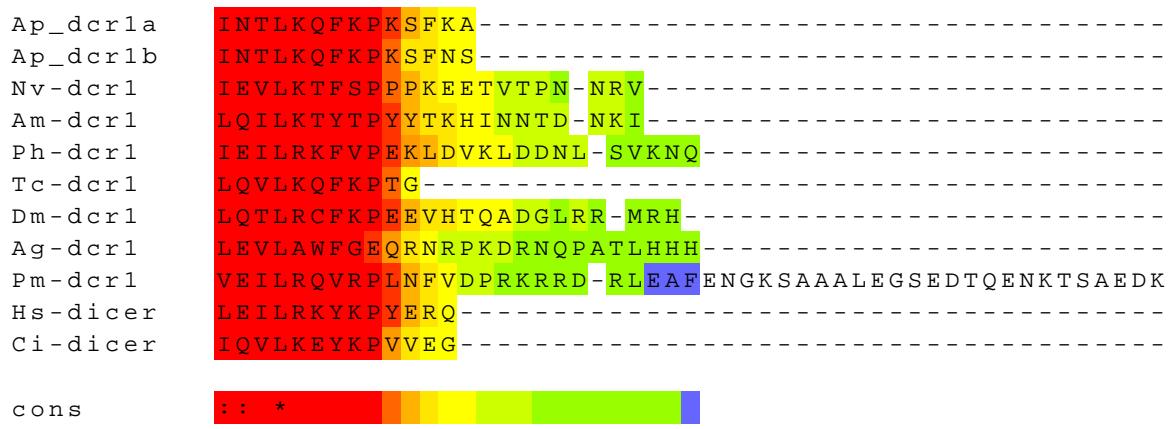
cons * : * :

Ap_dcrla LSSAKKNVIIISLEGITNKVFVILKLIRELAFKIHRSKSEK--RKWTLLVLE
Ap_dcrlb LSSAKKNVIIISLEGITNKVFVILKLIQELAFKMHRKSEK--RKWTLLVLE
Nv-dcrl LYSAKEKNIIICLGKITEQTFLIVTKVIQELAINNRRTLS-HDGKRTIYLLE
Am-dcrl FYAAKDKDIIVCLGKNYEQTFLIVIKLIQEFATNSRRLLS-QGGKRSLYILT
Ph-dcrl LDASCVRNIIIVCLGNНИGKTFIASKLQNTSNNISV--NN--GTITLYVAD
Tc-dcrl LDSAKKRNTIVCSSASSAKAFITIKLLQEFSHKMRV--PH--GKQALFVLD
Dm-dcrl LATAYERNTIICLGHRSSKEFIALKLLQELSRRARRHGR-VSVYLSCEVGT
Ag-dcrl LATAREENLIVCIAHNSAKEFLAVKLIQSMRTNRWSSHPEAPGKAIYL-T
Pm-dcrl VDACLKGNTLSVLASRSTRFLITMVTRMAHLTRSKEQGGKGQRTLTTGW
Hs-dicer LEAALDHNTIVCLNTGSGKTFIAVLLTKELSYQIRGDFS-RNGKRTVFLVN
Ci-dicer LECAAKQNTIICLNGDFGKCFMYTMFLREVIIKHNGKLN-NAPKFAVLLK

cons . . : : : * : . . : :







Sequence alignment of dicer proteins from various species. The sequences are color-coded based on amino acid conservation.

Species	Sequence
Ap_dcr1a	-----
Ap_dcr1b	-----
Nv-dcr1	-----
Am-dcr1	-----
Ph-dcr1	-----
Tc-dcr1	-----
Dm-dcr1	-----
Ag-dcr1	-----
Pm-dcr1	NVHEDPTKLATDGGNTENLQGSASKSETEMSCEGSEEPSDTTLCVQGSIYG-----
Hs-dicer	-----
Ci-dicer	-----

Sequence alignment of dicer proteins from various species. The sequences are color-coded based on amino acid conservation.

Species	Sequence
Ap_dcr1a	-----
Ap_dcr1b	-----
Nv-dcr1	-----
Am-dcr1	-----
Ph-dcr1	-----SNK LSDAS KTISKAI ET SAEKCS-----
Tc-dcr1	-----
Dm-dcr1	-----Q-----
Ag-dcr1	-----Q Q-----
Pm-dcr1	ISEIPLVSSGDGANDPNN-----ECEVN SGNAMPDLKAMEE-----
Hs-dicer	-----
Ci-dicer	-----

cons

Sequence alignment of dicer proteins from various species. The sequences are color-coded based on amino acid conservation.

Species	Sequence
Ap_dcr1a	-----
Ap_dcr1b	-----
Nv-dcr1	-----
Am-dcr1	-----
Ph-dcr1	-----T I L N-----
Tc-dcr1	-----
Dm-dcr1	-----
Ag-dcr1	-----
Pm-dcr1	LSEGHSQIHGT EPASEDPFLADENS TEDKSEL SHGAPS NMFCGSSIEDSSE-----
Hs-dicer	-----
Ci-dicer	-----

cons

Ap_dcr1a -----
Ap_dcr1b -----
Nv-dcr1 -----
Am-dcr1 -----
Ph-dcr1 ----- ESEMKKQCLNCD
Tc-dcr1 -----
Dm-dcr1 -----
Ag-dcr1 -----
Pm-dcr1 VVDISTDGYYFTA VSDVSPKCTS KAVSDSYTNDIE DCMIKANCNNHEVNVS
Hs-dicer -----
Ci-dicer -----

cons [redacted]

Ap_dcr1a -----
Ap_dcr1b -----
Nv-dcr1 -----
Am-dcr1 -----
Ph-dcr1 CTI -----
Tc-dcr1 -----
Dm-dcr1 -----
Ag-dcr1 -----
Pm-dcr1 RMTEVNTE NFCAE VTDKHSY LQDS LEDGVDF TKHS MKERS ADDM HITV QTC
Hs-dicer -----
Ci-dicer -----

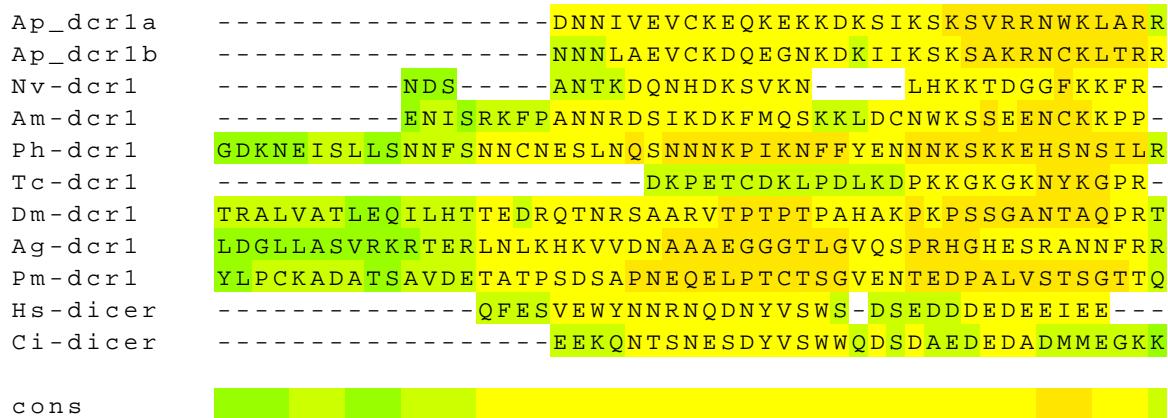
cons [blue]

Ap_dcr1a -----
Ap_dcr1b -----
Nv-dcr1 -----
Am-dcr1 -----
Ph-dcr1 MT EYLLKR -----
Tc-dcr1 -----
Dm-dcr1 -----
Ag-dcr1 -----
Pm-dcr1 PETTQYCSNA CEDVAAKTNDE DGSTLED SLCRLNIKE SSCTDGCD TESI KS
Hs-dicer -----
Ci-dicer -----

cons [blue] [green]

Ap_dcr1a -----
Ap_dcr1b -----
Nv-dcr1 -----
Am-dcr1 -----
Ph-dcr1 -----
Tc-dcr1 -----
Dm-dcr1 -----
Ag-dcr1 -----
Pm-dcr1 CDLHNGVLSAKNDLLDTAMIQN VKNMTLCNGFEHGSKDDIMDSEKDITSKM
Hs-dicer -----
Ci-dicer -----

cons



Ap_dcr1a	YLFLDLKNSNKEDFGWIQPQYTVDKEA-DPITEPKFEIEHKKQEETLRRF
Ap_dcr1b	HLFLDLKNSNEEDFGWIEPQYMVDNNA-DPITEPEEFIEIRKTQENILKRF
Nv-dcr1	YLLNEMSKC-EESLHFLSPLFTSEKSND-ELFCGRDLELEYRKQEEVLKKF
Am-dcr1	YLLNEISMH-DEELHFLSPLYTIEKNID-DISYSKDLIEEHRKQEEVLKRF
Ph-dcr1	HVLNDLQKA-DEDFSFLNVQFTVGKV-VDGTKDPKGAEHEHKQELMLKRF
Tc-dcr1	ALLCVMSKS-DEEYWVWSVSFSVNKI-ADPVREPRAESEHKRQEEVLRKY
Dm-dcr1	ELLAEIFSRR-DPDLKFLRCQYTTDRVAD-PTTEPKAEALEHRRQEEVLKRF
Ag-dcr1	VLLYEVSRS-QREFEFISPQYTVDKVATNPQNCLKQTTIEHRKQEEVLKRF
Pm-dcr1	RLLKELSDI-GGDFAWIFPQYTVEAK-ESVKEDPRAAEAEHKQEEVLRRF
Hs-dicer	RLIKEAGKQ-DPELAYISSNIFTGHGIGKNQPRNKQMEEAEFRKQEEVLRKF
Ci-dicer	RLLRELSKE-DKNLKHVSSSHLTPGV-EGERRGVDPASMDQSKQEEVLRKF

cons :: . : . : . : : * * * : : :

Ap_dcr1a	RQRECNVLIGTKVLEAGI
Ap_dcr1b	RQRNCNVLIGTKELETGI
Nv-dcr1	RIHECNLLLISTAILEEGI
Am-dcr1	RIHECNILISTSILEEGI
Ph-dcr1	RIRACNLLIGTSFLEEGI
Tc-dcr1	RSHECNIMIATSALEQGC
Dm-dcr1	RMHDCNVLIGTSVLEEGI
Ag-dcr1	RMHECNLLIGTSVLEEGI
Pm-dcr1	RHHECNILVSTRVLEEGI
Hs-dicer	RAHETNLLIATSIVEEGV
Ci-dicer	RSHESNLLICTGDLEDCA

cons * : * : : * : *

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Cedric Notredame

CPU TIME: 103 sec.

SCORE = 82

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BAD **AVG** **GOOD**

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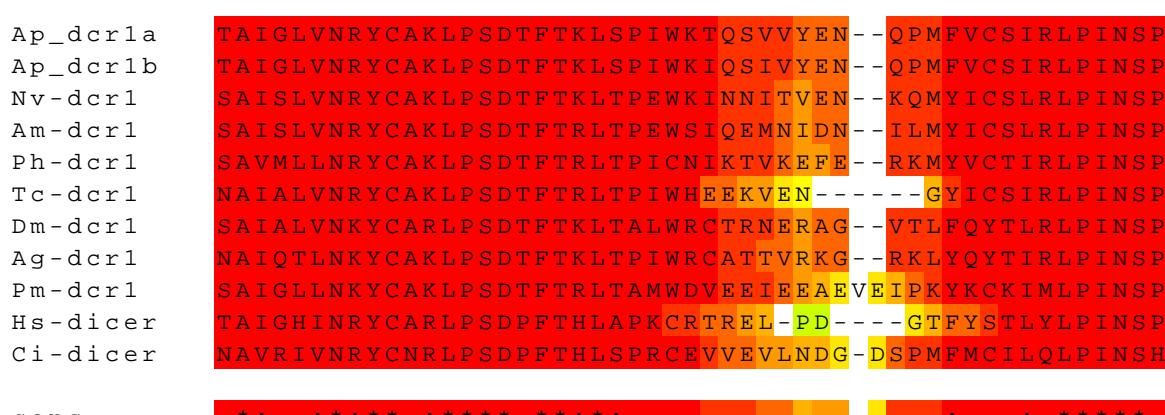
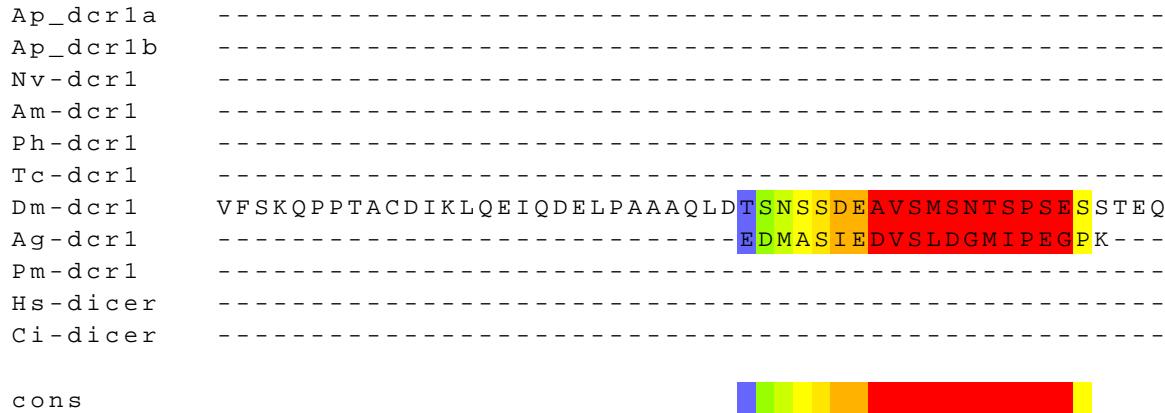
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Ap-dcrlb	:	8 5
Nv-dcrl	:	8 3
Am-dcrl	:	8 3
Ph-dcrl	:	8 2
Tc-dcrl	:	8 4
Dm-dcrl	:	8 1
Ag-dcrl	:	8 0
Pm-dcrl	:	8 1
Hs-dicer	:	8 0
Ci-dicer	:	7 8
cons	:	8 2

Ap-dcrla	DLPRCNLVINYNIPLSYKSYLRSKSRAKTLDAYHILMFDEDA
Ap-dcrlb	NLPRCNLVINYNLPLSYKSYLMSKSKARTLDAYVLMFDEHA
Nv-dcrl1	DIPKCNFVMRFEFPKNYQSYVQCKSRARATDALHVLLVPEIE
Am-dcrl1	DIPKCNFVMRYDFPKTYQSYVQCKSRARAPDALYVLLVSQEM
Ph-dcrl1	ELPKCNLVI RDFVKHYRSYINTKERARAANSLFCLLVGPNE
Tc-dcrl1	DLPKCNLVI RDFLPQSFH SYIHSKARARANEAHFL LANENE
Dm-dcrl1	DVPKCNLVVRWDPPTTYRSYVQCKGRARAA PAYHVILVAPS YKSPTVGGSVQ
Ag-dcrl1	ELPKCNLVI RWNSP ANYRSYAQCKGRAKAPGAYHVLFTPENAA SRSNEQQ
Pm-dcrl1	DVPQCNLVLRFDPPTDYRSYVHSCGRARGHDTFYFHLLITKNO
Hs-dicer	DIPKCNLVVRFDLPT EYRSYVQSKGRARAPI SNYIMLA DTK
Ci-dicer	YMPKCNLIMRFDVPKSYRSYAESKSRARA QTSAYVMLVRETE

cons : * * * : * : * * : * :

Ap_dcrla	-----
Ap_dcrlb	-----
Nv-dcrl	-----
Am-dcrl	-----
Ph-dcrl	-----
Tc-dcrl	-----
Dm-dcrl	LTDRSHRYICATGDTTEADSDSDDSAMPNSSGSDPYTFFGTARGTVKILNPE
Ag-dcrl	-----
Pm-dcrl	-----
Hs-dicer	-----
Ci-dicer	-----

cons



Ap_dcr1a IKHDIHGHPMPCEILAKRIAALEVCRQLHSHGELDDTLQPIKESFHAFN
 Ap_dcr1b IKHEIHGHMPMPCEILAKRIAALEVCRQIYSQGQLDDTLQPIKESFHAFN
 Nv-dcr1 LKYSISSYPMPNPKALAKRMAALQMCVCLHKENEIDDYLLPVGKENFKAHPE
 Am-dcr1 VKYIVSSYPMPNPKAMARRMAALQLCIDLHRKNEIDDNLPIGKENFKAKPE
 Ph-dcr1 IKQEIEGCPMPTRVLAKRFAAFQCCQLLHLSGELDDTLQPIKESFWIREE
 Tc-dcr1 VKKTVTSPPMINTLLARRAAAFMICQCLLHKAGELDDNLQPIGKENFKVNEE
 Dm-dcr1 LKHDIVGLPMPTQTLARRLAALQACVELHRIHELDDQLQPIGKEGFRALEP
 Ag-dcr1 WKEDIL
 Pm-dcr1 LKGTIEGPWQSKVSLAKMAAALECCRRLHQMEELDDQLQPVGKESMKLDDH
 Hs-dicer LRASIVGPPMSCVRLAERVVALICCEKLHKIGELDDHLMPPVGKETVKYEEE
 Ci-dicer VREPVQGIVMPMTLQLAQQAVALCCKVLYEAGELDENLMPIGKETVKYAAE

cons : : :

Ap_dcr1a ADEVL-PDAEDALIPPWDTEEPRPGTNKRRQYYYYKRIAELNDCRPVENKPC
 Ap_dcr1b TDEII-PDTEDSLITCKTKDSMPGTYKRRQHYYKRTAEALNDCRPVEGKPC
 Nv-dcr1 DSEVPAL-PDENM--DLTEARP GTTKRRQYYYYKKIADALIDCKPELEEP
 Am-dcr1 DAEVPAL-PDESKV--DFSEARPGTTKRRQYYYYKKTAEALTD CRPIIGVPS
 Ph-dcr1 GRLTVTNDETEEIVSRDSLEPRPGTTKRRQYYYYKKIADSLTDCLPMADKPS
 Tc-dcr1 DWNSSALEEESDE---ENLDPRPGTTKRRQYYYYKKVADALLDCHPPIIGQPT
 Dm-dcr1 DWECFELEPEDEQIVQLSDEPRPGTTKRRQYYYYKRIASEFCDCR PVAGAPC
 Ag-dcr1 -----IASVFNECRPDAETVA
 Pm-dcr1 --LCA-P-PADDQV--PEGMPRP GTTKRRQYC YKKVAVCLTGEQPKQGLDL
 Hs-dicer --L-D-LH--DEEE--TSVPGRPGSTKRRQCYPKAIPECLRDSYPRPDQPC
 Ci-dicer --L-D-PW--KREV--SSITGRPGSTKKRQTYNKDSPQILRSCLPQPDINL

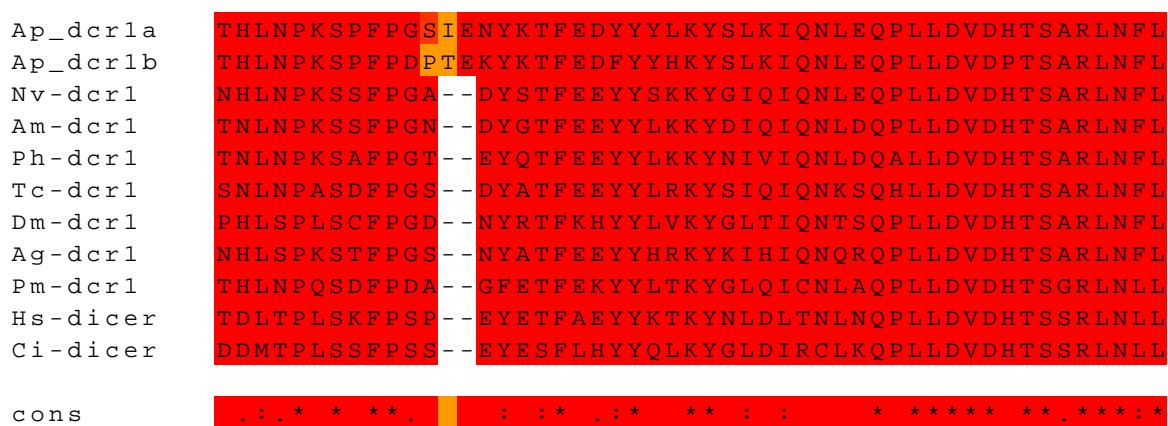
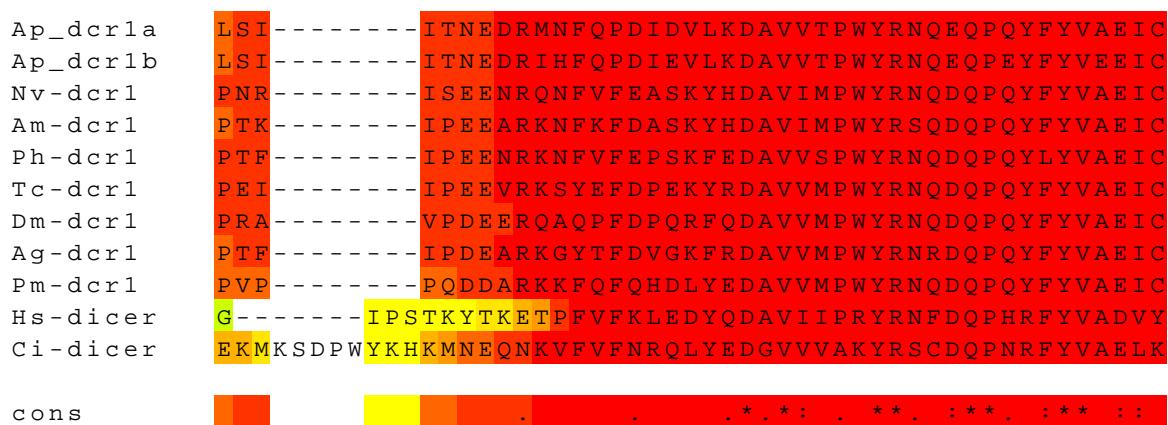
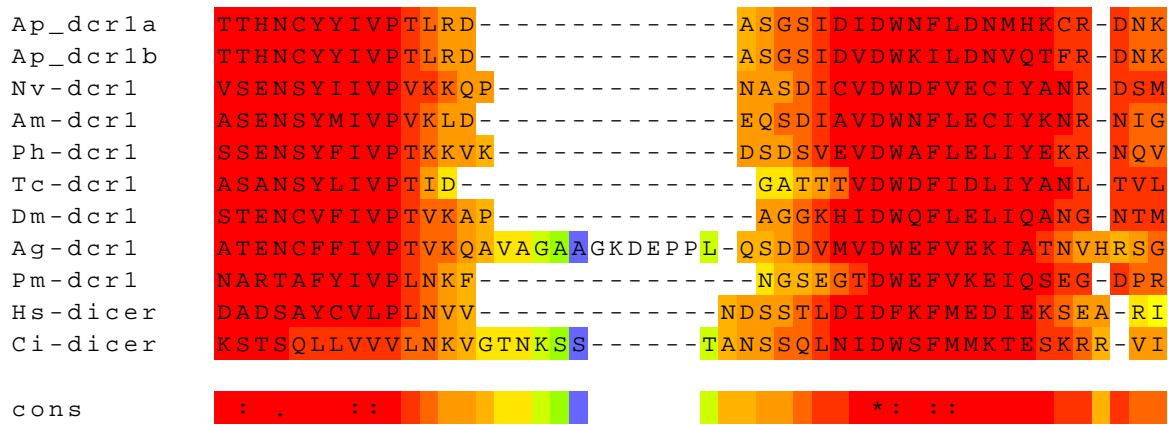
cons : . : * :

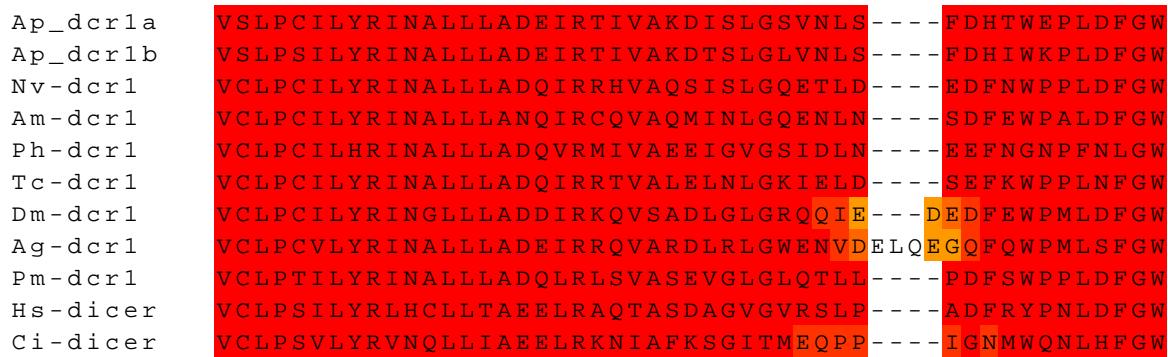
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 Nv-dcr1 YLYHINMVLSCLPPEEQNTRGRKIYPPEESDIGFGILTRKKIPKVC PFP
 Am-dcr1 YLYHINLVLSCCLPPEEQNTRGRKIYPPEESAIGFGIITLKEIPKLC PFP
 Ph-dcr1 FLYDISMVLSCCLPPEEQNTRGRKIHPPEENSSQFGILTKRIPKIGPF
 Tc-dcr1 YFYKIVMKLTCPLPEEQNTRGRKIYPPESPQGF GILTSKEIPKISAFPIF
 Dm-dcr1 YLYFIQLTLQCPipeEQNTRGRKIYPPEDAQQGF GILTTKRIPKLSAFSIF
 Ag-dcr1 YLYHIRMELICPIPEEQNTRGRKIYAPEESAQGF GILTTKLI PKISSFP
 Pm-dcr1 FVYKLDMLVLTCPPIPDEQNTRGRKIYRPEQSSRSFGIITTKPISQVSGFP
 Hs-dicer YLYVIGMVLTTPLPDELNFRRKLYPPEDTTRCFGILTAKPIPQIPHFP
 Ci-dicer FIYEIEMKIKNPLLDELNVRRKLFPEETSRCFGILT KPIPQIPGFPIF

cons : . * : : : * : : * : : * : : * : : * : : * : : * . : :

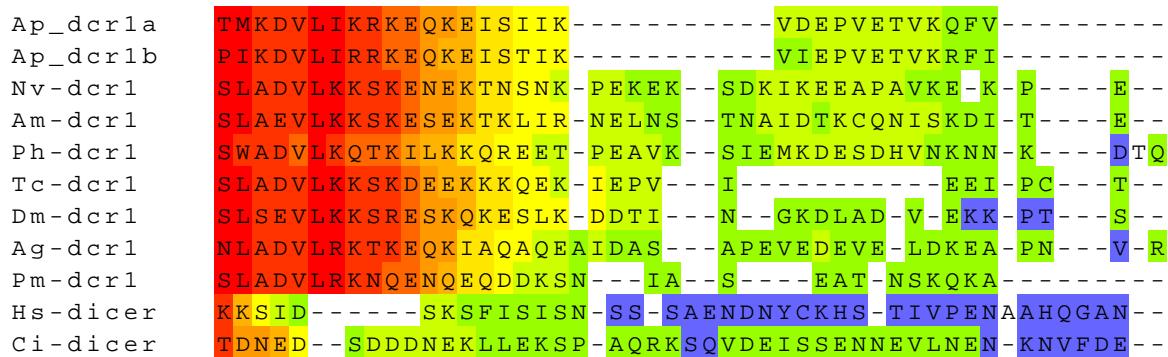
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 Ap_dcr1b PRCGEVYVRLKRIKTD MFLTQHQLDNIATFLNYTFNSVLCFKCRVEFNPT
 Nv-dcr1 TRSGEVRVDLKLSKETVVLDESKIDKVVSFLNYTFTNVRLQKYLMLFD
 Am-dcr1 TRSGEVHVKLKLTQKTIILNEMQVEKIATFLNYTFTNVRLQQYLM
 Ph-dcr1 TRSGEVQVKLKAQTTVQLTEIEINKIVAFIHYTFTSVLRLQKYLMMFD
 Tc-dcr1 TRSGEVSVDLQLCSQ-LIVTENQICKIREFLNYTFTSVLRLQKYLTL
 Dm-dcr1 TRSGEVKVSLELAKERVILTSEQIVCINGFLNYTFTNVRLQKFLML
 Ag-dcr1 TRSGEVKVSLDLCPQRVKLSAHQLEMVNCFVKYTFTKVLRLQKSLML
 Pm-dcr1 TRSGEVVVHVQEIERKVNVTQDQLSALQYFHKFTFTHVLRLK
 Hs-dicer TRSGEVTISIELKKSGFMLS LQM LE LITRLHQYI FSHILR
 Ci-dicer TRSGEESAKLKFCRGFVQLSAQQIKLVRIFHRYVFSDMLRVDRVPLSFQPE

cons : . * . ** : . . : : : : : : * : : * . : . :

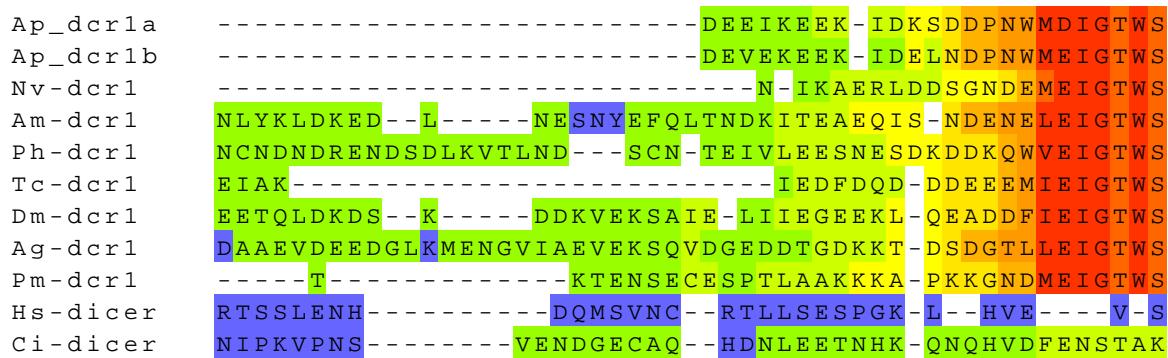




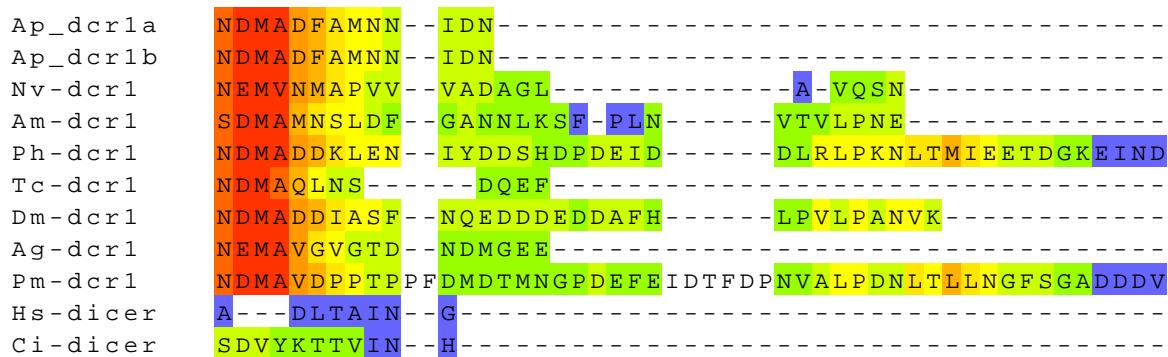
cons



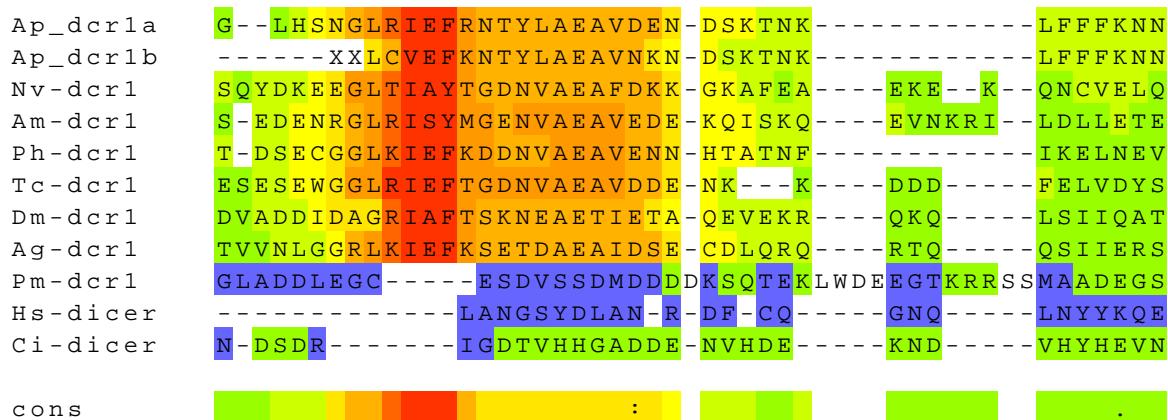
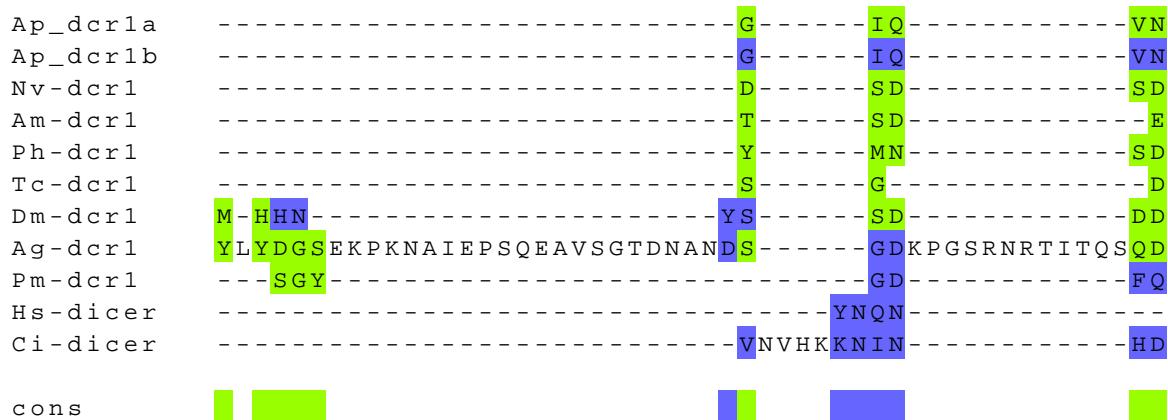
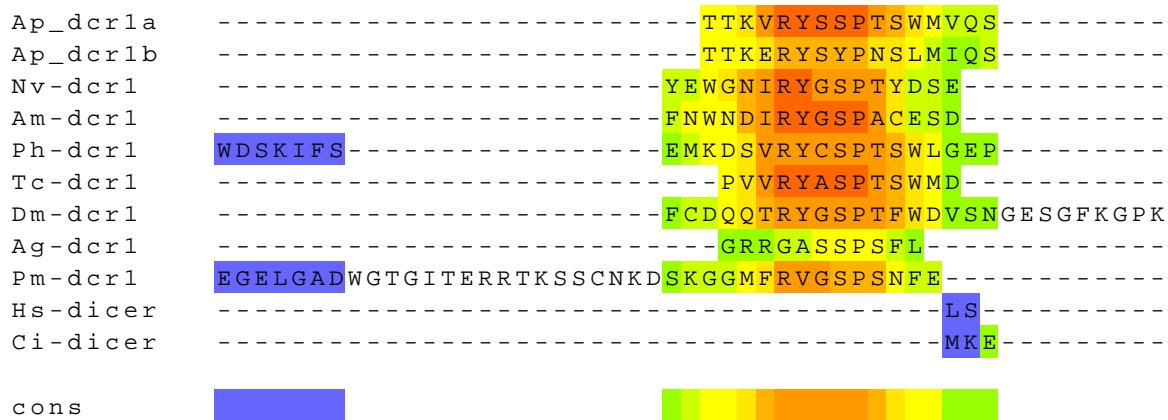
cons

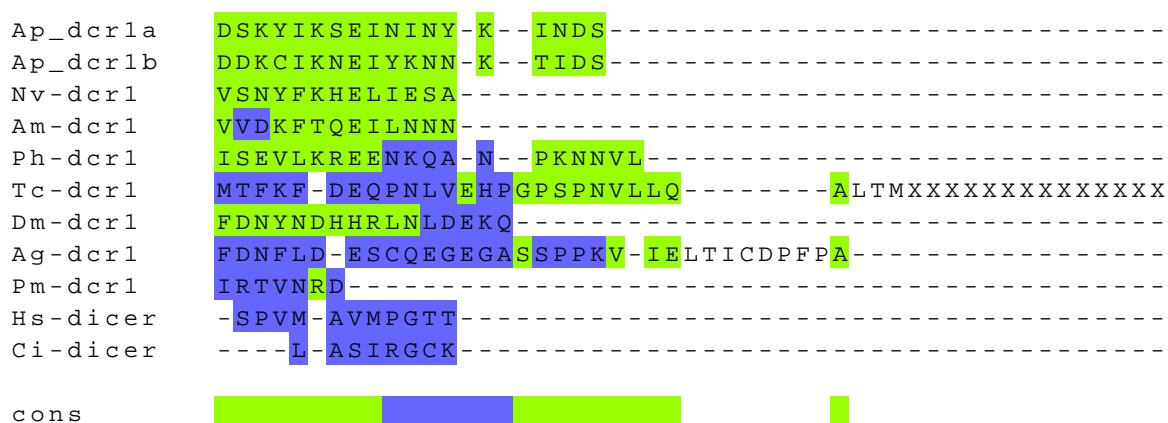
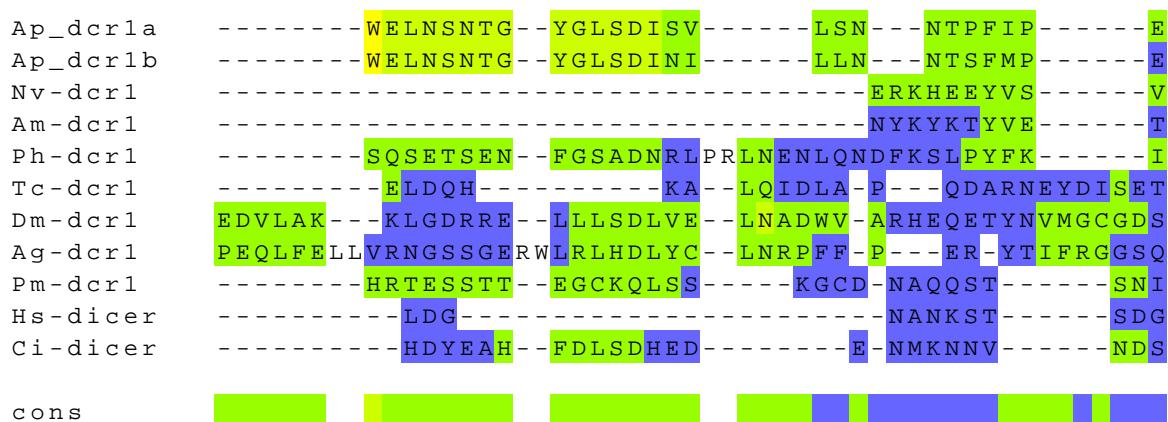
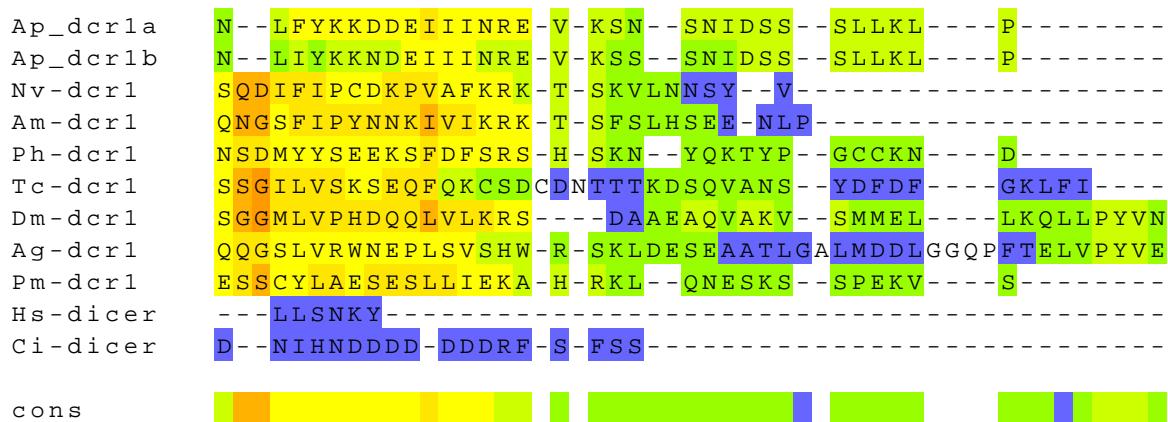
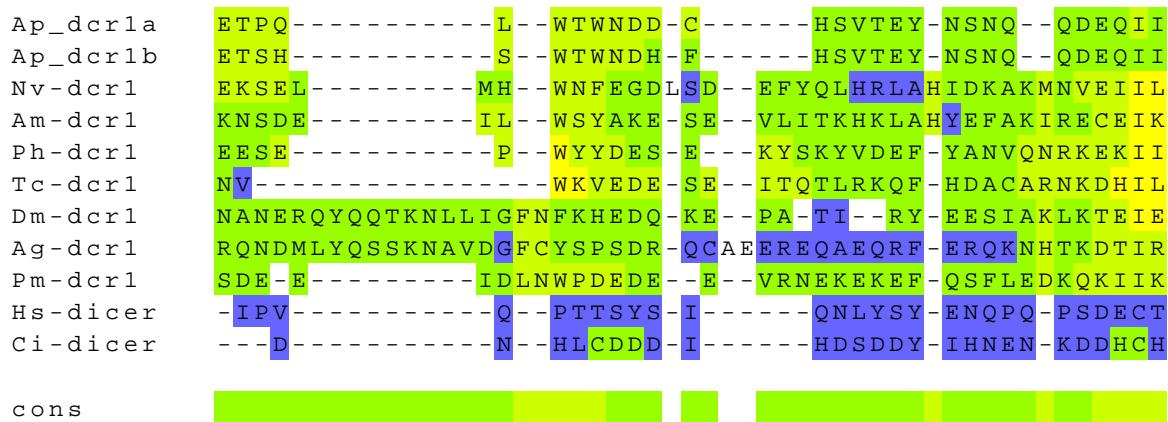


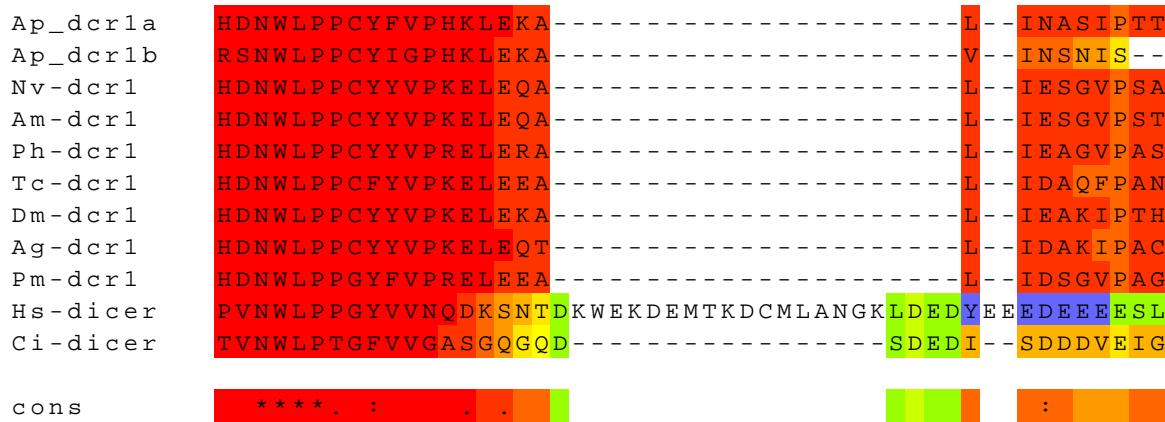
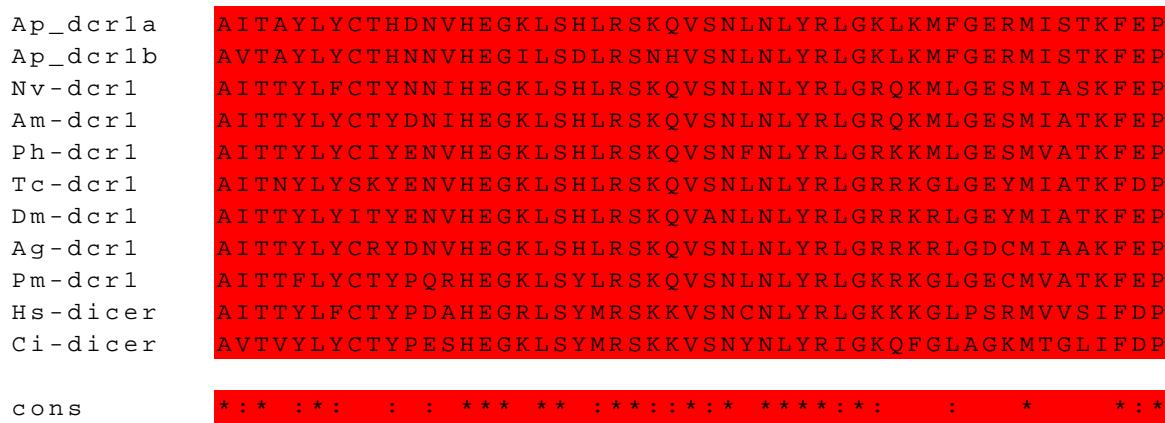
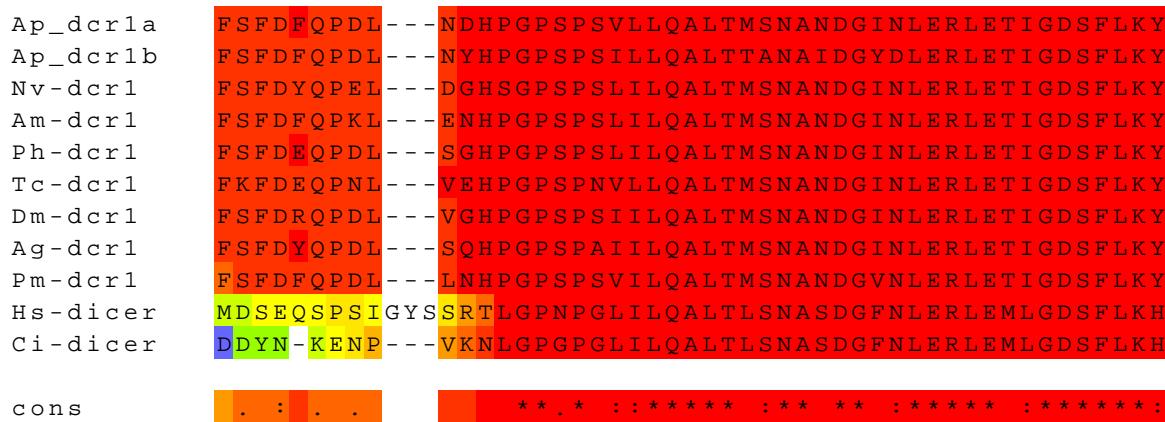
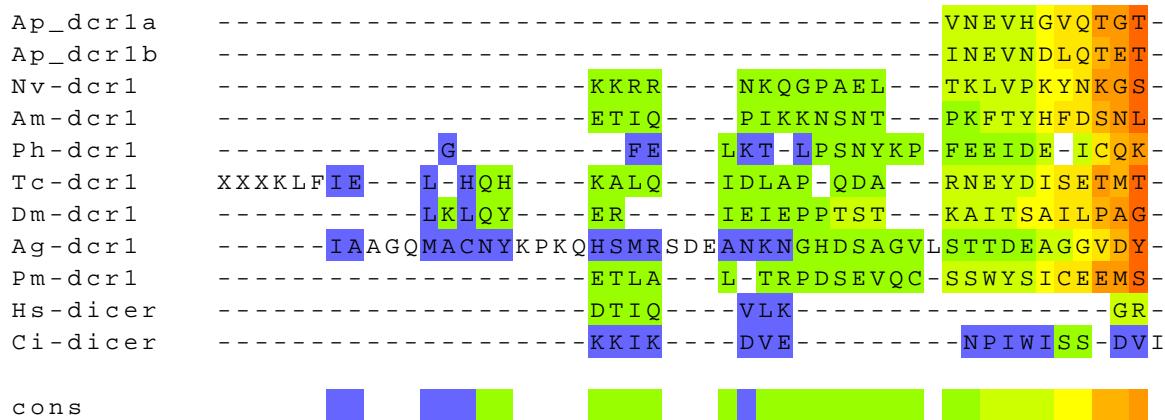
cons

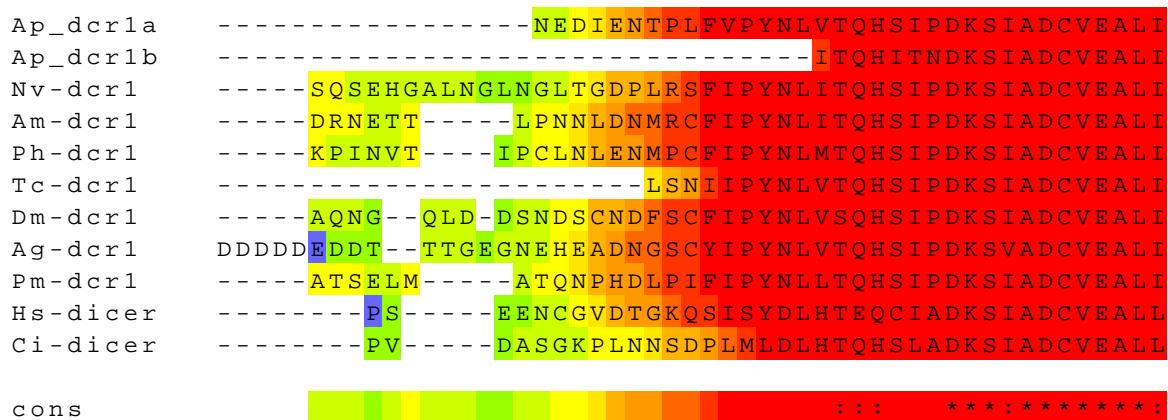
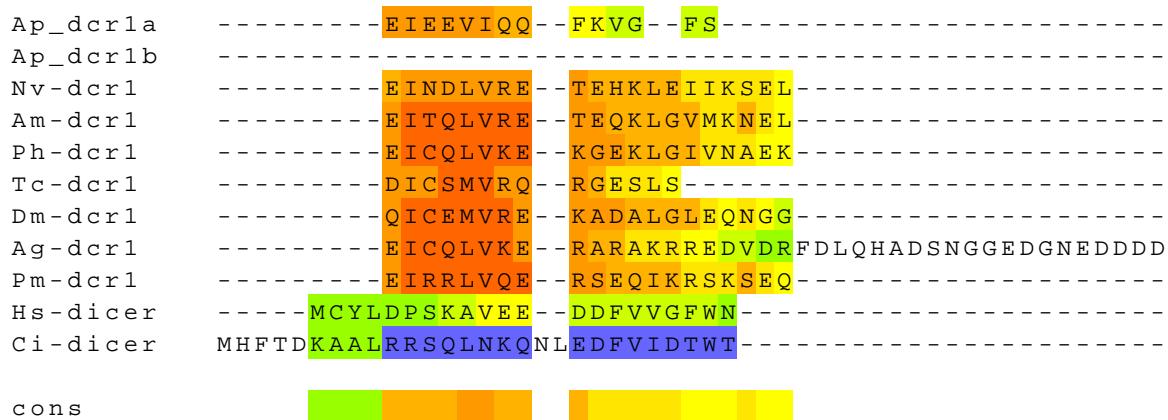
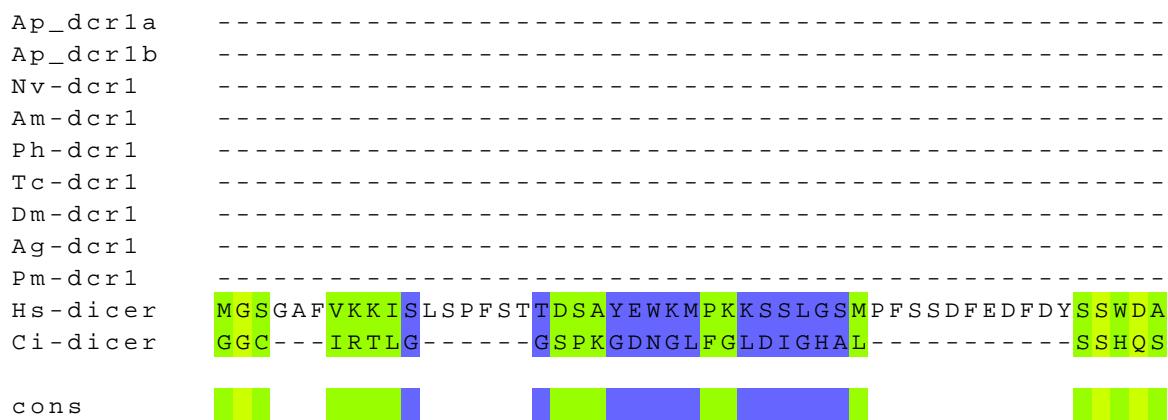
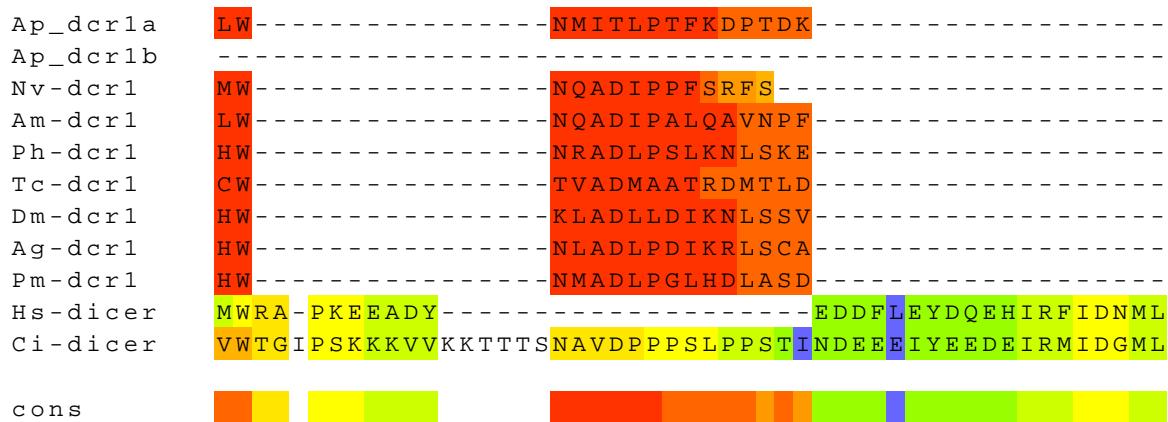


cons









Ap_dcr1a GAYLISCGARGALLFMSWLGI
 Ap_dcr1b GAYLISCGTRGALLFMSWLGI
 Nv-dcr1 GAYLIACGPRGALLFMSWLGI
 Am-dcr1 GAYLIACGPRGALLFMAWLGI
 Ph-dcr1 GAYLVACGPRGALLFMSWLGI
 Tc-dcr1 GAYLIECGPRGALLFMAWLGI
 Dm-dcr1 GAYLIECGPRGALLFMAWLGV
 Ag-dcr1 GAYLIECGPRGALLFMAWLGI
 Pm-dcr1 GAYLTTCGPRGALLFMSWLGI
 Hs-dicer GCYL
 Ci-dicer GAYLTTCGHRS

 cons * . ** * * . * : : . * * : * *

Ap_dcr1a DSKLGYLKPPSSPLL
 Ap_dcr1b DSKLGYLKLPSP
 Nv-dcr1 EGGSTKWTQLRYKKLQE
 Am-dcr1 NEKGETIWTQIRY
 Ph-dcr1 RPIKVMTNNGEVTF
 Tc-dcr1 GTYGEIELPKSPLSNH
 Dm-dcr1 STKPN-AENVV
 Ag-dcr1 TGQNDGPLSTGV
 Pm-dcr1 EASELITYGH
 Hs-dicer QKNLSVSCA
 Ci-dicer ETSKTVD

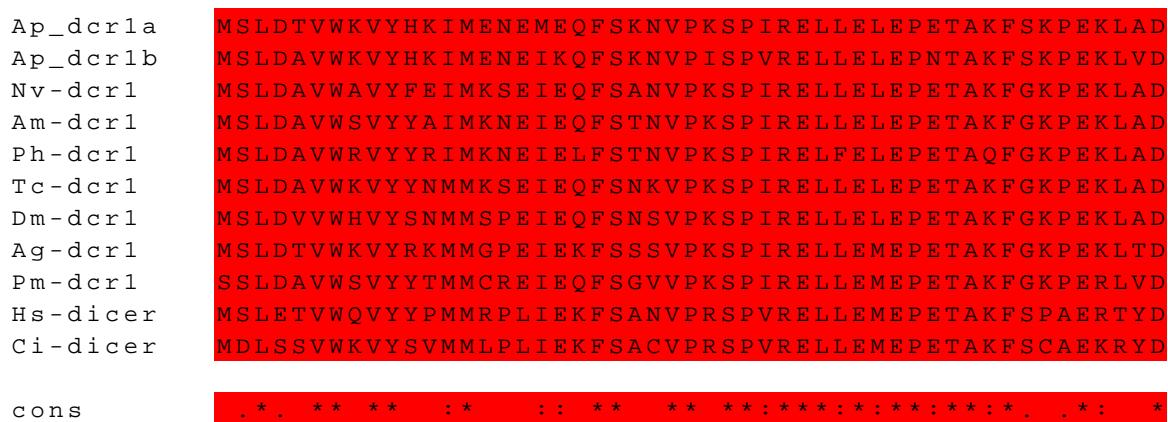
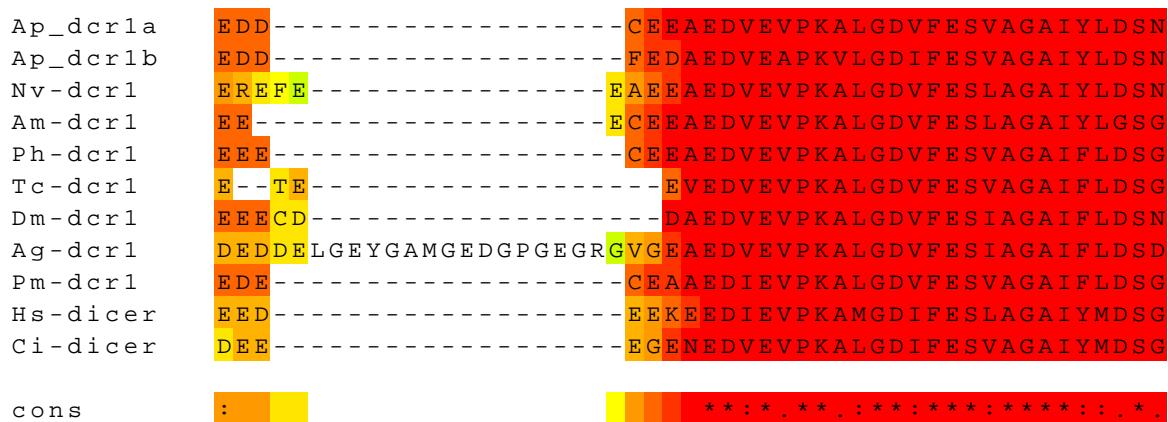
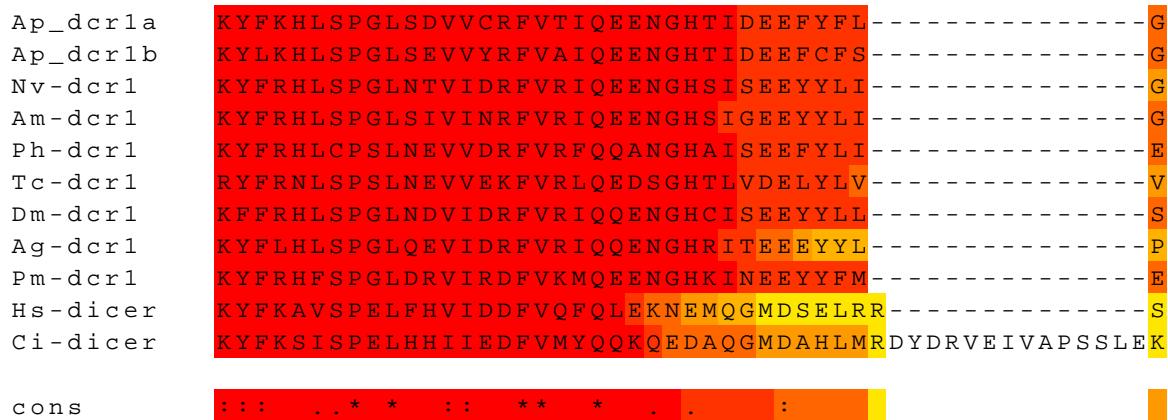
 cons *

Ap_dcr1a DPEGE
 Ap_dcr1b DPEGE
 Nv-dcr1 QPEIE
 Am-dcr1 DPEEE
 Ph-dcr1 NPEGE
 Tc-dcr1 YPREEL
 Dm-dcr1 NATELD
 Ag-dcr1 ATSRELAR
 Pm-dcr1 DTRKE
 Hs-dicer DADKT
 Ci-dicer NQQNK

 cons *

Ap_dcr1a EFLGDAVLDYL
 Ap_dcr1b EFLGDAVLDYL
 Nv-dcr1 EFLGDAVLDYL
 Am-dcr1 EFLGDAVLDYL
 Ph-dcr1 EFLGDAVLDYL
 Tc-dcr1 EFLGDAVLDYL
 Dm-dcr1 EFLGDAVLDYL
 Ag-dcr1 EFLGD
 Pm-dcr1 EFLGD
 Hs-dicer EFLGD
 Ci-dicer EFLGD

 cons ****



Ap_dcr1a	- - - I K K
Ap_dcr1b	- - - I K K
Nv-dcr1	- I K G R K
Am-dcr1	- - - Q Y
Ph-dcr1	G Y M K S F
Tc-dcr1	- K I D E S
Dm-dcr1	- - A K K D
Ag-dcr1	- H H K R R
Pm-dcr1	- A N Q G I
Hs-dicer	- - V P N S
Ci-dicer	- - - I Y

cons



T-COFFEE, Version_7.38 Thu Nov 20 17:26:38 WEST 2008

Cedric Notre Dame

CPU TIME : 26 sec.

SCORE = 96

*

BAD **AVG** **GOOD**

*

Ap-drosha	:	9 6
Am-drosha	:	9 7
Nv-drosha	:	9 7
Tc-drosha	:	9 7
Ag-drosha	:	9 6
Dm-drosha	:	9 6
Ph-drosha	:	9 6
Hs-drosha	:	9 5
Ci-drosha	:	9 2
cons	:	9 6

Ap-drosha	KKKWSRSAPSIDIYYKKPDDD	--SEVTFGNKIALDICDEFENTLGKRVSKM
Am-drosha	RKVWTRTAPADLYYTRDENN	--PKIMRGQTQKLHELCEFKKILLDRAAAA
Nv-drosha	RKIWTTRTAPADLYYSRDEKN	--NKLMKATGKLVQLCDDFKKILIDRASSA
Tc-drosha	KNIWTRSTPSDLYYRKDESNN	--ARVTRATKRLTQLCDKFNDCLVMRAAKV
Ag-drosha	RTLWVRSSPAELYYKRVSD	--KVVESTARLDALCTLFEEELIKRAERI
Dm-drosha	VESWVRSSPAELYYERTKSE	--NEVRGRARLQKLCTLFDEELLQRAKRV
Ph-drosha	NKVWIRSAPAYCYYERDPND	--LRRMKPTPKLDELCERFKYELVDRGKRI
Hs-drosha	KPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKA	
Ci-drosha	KK-WK----SDITLTRHO--OVKSST--IVKKLLESSKNLNLTGEYIDOT	

consensus

Sequence logo showing the conservation of amino acids across various Drosha orthologs. The x-axis represents the sequence position, and the y-axis lists the orthologs. The color scale indicates conservation: black (most conserved), yellow (moderate), and red (least conserved).

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
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cons

Ap-drosha KELDRKCSHPDRLHSELWYNEFGEMNDGPMCKCSVKSQRSGIRHNLYVGE
Am-drosha EELMAKKQHPQRHLPEMWFDNPGEMNDGPLCRCSAKSRRSGIRHGIYAGEG
Nv-drosha EELMAKKQHPQRHLPEMWFDNPGEMNDGPLCRCSAKSRRSGIRHGIYAGEG
Tc-drosha EELQRKQQHPDRLHPEMWYNDPGEMNDGPLCRCSEIKSRKSGIRHGIYPGEK
Ag-drosha EELTAKIKHPLRLHVLDLWYNDPGEMNDGPLCRCSEARSRRTGIRHGKYPGE
Dm-drosha EELSRKVQHPQRVHADLWHDAGEMNDGPLCRCSAKSRRIGIRHGIYPGET
Ph-drosha EELQRKQKHPYRLHSELWYNDPGEMNDGPLCRCSAKARRSGIRHGFYAGEN
Hs-drosha AEIKRKKAHPDRLHDELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGE
Ci-drosha SSIRKLKAHKDRLHEELWYNEPGOANDGPLCRCSSGSRDKGIRHNIYPGEV

cons

Ap-drosha
 Am-drosha
 Nv-drosha
 Tc-drosha
 Ag-drosha
 Dm-drosha
 Ph-drosha
 Hs-drosha
 Ci-drosha

```

PFEPCLPNSNNSDKLHYRITITPPTNFLLKPTVIECNE SKYTFEGFSLL
AINKCDLNSNNADKLYHYRITISPPTNFLLKPTI IKHDEHEFIFEGFSML
AIEKCD SHTNNADKLYHYRITISPPTNFLLKPTI IKHDEHEFIFEGFSMF
HLEKCV PDSNNAERLYHYRITISPPTNFLLKPTI IKHDEHEFIFEGFSMF
GFPK CIPNSNNADKLYHYRITISPPTNFLLKPTI IKHDQHEFLFEGFSLL
GYKL CDPNSNNAGKLHYRISISPPTNFLLKPTI IKHDEHEFIFEGFSLL
QKIC CDVKSNNAGNLYCYRITISPPTNFLTRPTIINYDDHEFIFEGFSLI
AIKPCRPMTNNA GRLHYRITVSPTNFLLDRPTVIEYDDHEYIFEGFSMF
PTAPYDPMKNNIGKMHHYRITVGP AVNYMISQPTTIEYSGHDYMFEGFSIF
  
```

cons . ** . : . * * : : * . * : : * * * : :

Ap-drosha
 Am-drosha
 Nv-drosha
 Tc-drosha
 Ag-drosha
 Dm-drosha
 Ph-drosha
 Hs-drosha
 Ci-drosha

```

SHYPI PILPTCKVIRFNTNYA ILYIEEKIPDNFIVKELQLFYDYLFDILE
SHFPLVKLPTCKVIRFNIEYTILYIDEKL PENFIIRELDEFQTYLFKEVLE
SHFPLVKLPTCKVIRFNIEYTILYMEEKMPENFTIQE LDYFQDYL FNEILE
SHFPL EKLPTCKVIRFNIEYTILYIEEKIPDNFTVRELDLFHDYL FRELLE
AHEPI GELPTCKVIRFNIEYTILYIEEQMPENFTIRELNLFDRYLFRELLE
SHVRLSDLPVCKVIRFNIEYTIEYE EKMPENFTIHELDIFFKYL FH ELL
SHYPI QKLPTCKVIRFNIEYI ILYVEEKL PENFSILELDLFY EYVFKEILE
AHAPLTNIPLCKVIRFNIDYTIHFIEEMMPENFCVKGLELFSLFLFRDILE
SDEPLDKIPLCDIIRFH IRYTIYLIEETPPESFCIRGLDLFDEYL FRELLE
  
```

cons : . : : * * . : * * : * * : : * : * : : * . : * *

Ap-drosha
 Am-drosha
 Nv-drosha
 Tc-drosha
 Ag-drosha
 Dm-drosha
 Ph-drosha
 Hs-drosha
 Ci-drosha



```

LVDDLHG----IGNKNGCPQFHFM PRFVKDLS DNGKEVLSMNEV LKYLLK
LIDFDLQA----AQNKSGCGQFHFM PRFVRDLADNGQEILSMNEV LNYLIK
LVDFDLQA----AQDKKGCAQFHFM PRFVRDLPDNGQEILSMNEV LSYLIK
LV DDFKA----AGDV DGCSQFHFM PRFV RELPDNGKEILAMNEV LQYLLD
LVDFTVQPS---GSGEDSSCP CYHFLPRFVRDLPDNGKEV LAMSEV LRYLLD
LVDFNLMPNLP SGNVEE S CPAFHFFPRFVRDLPDNGKEV LAMVEV LRYLLD
LVDFDLKN---SSHPE NCPQFHFM PRFV RELPDNGRELLPMCEV LKYLLS
LYDWNLKGPL-FEDSPPCCP RHFHM PRFVRFLPDGGKEVLSMHQ ILLYLLR
LYDWQGDTP-PSEALAKNKRKF RFFPRFVRSLPDNGKEILSLCKVLEYLLD
  
```

cons * * : : * : * * : * . * . : * : * : : * * :

Ap-drosha
 Am-drosha
 Nv-drosha
 Tc-drosha
 Ag-drosha
 Dm-drosha
 Ph-drosha
 Hs-drosha
 Ci-drosha



```

SNKLLFEESSLSALQ EPMNEWQNI VDEYKGMIVTNP GTKPYSIRVDQLDR
SSKLLIDPDDLPLRVEMPQYK WQNFADEVKGMI VT FPGKKPCSVR DQLDR
CSTLLIDPDELPLVEMPQFQWQNFADEVKG MVV TYPGKKPCSVR DQLDR
SSVSLIEEKDLED MIKMTQYEWQSYADEIKGMVV TYPGKKPCSVR DQLDR
NSGPLVPPDMLKEMMDMSQNEWQDYV D YVKGMVVSNPGM KPCSVR DQLDR
NSAQLVERQQLLHLNQISQSEWQNYVDFIKGMLVT KPGYKPCSLR DQLDR
SNKKLIEDGTLDLSLHKMTSSEWQDFADLVKG MVV TNP GMKPCSLR DQLDR
CSKALVP EEEIANMLQWEELEWQKYAE ECKGMIVTNP GTKPSSVR IDQLDR
SDKPLVDEKDLDWLMKCSHDEWLDHTDAIRGSI VTHPGKRPSSLRV DQLDR
  
```

cons . * . : : . : * . . : * : * : * : * : * : * : * :

Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

DSVNEATEK	-	-	-	NVNDGYPVLVHFGIRPPQLSYAGNP	-	DYQKGWRDY
NQTDQPP	-	-	-	GVIAYPEIVHFGIRPPQLSYAGNA	-	DYQKAWRDY
NQADQPP	-	-	-	GVIAYPEIVHFGIRPPQLSYAEIPS	DYQRRAWRDY	
NIDLQKP	-	-	-	GDYKFPEIVHFGIRPPQLSYAGNP	-	DYQKAWRDY
NVGDVPEANAI	-	-	-	DENGIVHPVIVHFGIRPPQLSYAGNP	-	EYQKAWREY
NNSDLPECVD	-	-	-	RETGISHPAIVHFGICHCPQLSYAGNP	-	EYQKAWREY
DTDESVKKKENAKSCSMENYYYYPEIVHFGIRPPQLSYAGNP	-	-	-	-	-	EYQRRAWRKY
EQFN--P	-	-	-	DVITFPIIVHFGIRPAQLSYAGDP	-	QYQKLWKSY
YDRKPVESTT	-	-	-	QHCPQVDERYPMIIHFGIRPANLSYAGDP	-	TYQRIWRAY

cons

Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

VKFRHLLANMPKPSFEDKRKLEIKERALQEMRSHNKMKGRTAVASSKGFF						
VKFRHLLANMPKPSFEDKRKLEAKENKLQELRTQSCKMKGRTDVSSSEGFY						
VKFRHLLANMPKPSFEDKRKLEAKENKLQELRTQSCKMKGRTDVDTSEGFY						
VKFRHLLANMSKPTFEDKRKLESKENKLQEMRTQGKMKRDITVAVSAEGFY						
IKFRHLIANMSKPSFEDKRKLEAKENRLLEMERMQGRMKRNITIAVSAKAFH						
VKYRHLMANMSKPSFKDKRKLEEKEQRLQEMRTQGRMKRNITVAISSEGFY						
VKFRHLLANMPKPTAEDKQKLAAKENSLHSMRAHSCKMKGRTVTVSSKGFY						
VKLRHLLANSPLVKQTDKQKLAQREEALQKIRQKNTMRREVTELSSQGFW						
LKQRHLMANSPLVKQSDKKLRRERENALQKIKRAKDMQREVTELSSHGFR						

cons

Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

KTGLMCDIVQHAMLLPVLVCHFRFHKSLEYLEDTIEYKFKNKYLQLALTH						
RTGIMCDIVQHAMLIPLVLVCHLRFHKSLDNLERTLGYEFKNRYLLQLALTH						
RTGIMCDIVQHAMLIPLVLVCHLRFHKSLDMLEQTLDYKFKKNRYLLQLALTH						
RTGIMCDIIQHAMLIPLVLVCHLRFHHSLNILEESVNYKFKNRALLQLALTH						
RTGIMCDMVQHAMLIPLVLTGHLRFHRSLNVLERYIGYTFTNRYTLQLALTH						
RTGIMCDVVQHAMLIPLVLTGHLRFHKSLDLLEESIGYRFKNRYLLQLALTH						
QTGLMCDVVQHAMLIPLVLVCHLRFHRSLVVLEEKINYKFKNKFLQLALTH						
KTGIRSDVCQHAMMLPVLTHHIRYHQCLMHLDKLIGYTFQDRCLLQLAMTH						
RTGLRSDDVCQHAMLLPVLSHHRLYHLCRLTLEKKIGYEFKERKWLSHAMNH						

cons

Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

PSYRENFGTNPDHARNTLTNCGIRQPEYGDERRIHYNTRKRGINTLINIMS						
PSYRENFGTNPDHARNSLTNCGIRQPEYGDERRIHYNTRKRGINTLINIMS						
PSYRENFGTNPDHARNSLTNCGIRQPEYGDERRIHYNTRKRGINTLINIMS						
PSYRENFGTNPDHARNSLTNCGIRQPEYGDERRIHYNTRKRGINTLINIMS						
PSYKENFGTNPDHARNSLTNCGIRQPEYGDERRIHYNTRKRGINTLISIMS						
PSYRENFGTNPDHARNSLTNCGIRQPEYGDERRIHYNTRKRGINTLVSIMS						
PSHHLNFGMNPDHARNSLSNCGIRQPKYGDRAVHHMHMRKKGINTLINIMS						
PSCQMNFGGLNPDHVRNTLSNCGLRLPRYGDSSIHYKYTRKRGITTLIRIMA						

cons

Ap-drosha RFGKKSEMESNIMHNERLEFLGDAVVEFVSSIHLFNMFPDIEEGGLATFRA
Am-drosha RFGARTETESSIAHNERLEFLGDAVVEFLTSIHLFHMFPDLEEGGLATYRA
Nv-drosha RFGAKKETESSIAHNERLEFLGDAVVEFLTSIHLFHMFPDLEEGGLATYRA
Tc-drosha RFGKQQETESENITHNERLEFLGDAVVEFLSSIHLFYTFPDLEEGGLATYRA
Ag-drosha RFGKEHETDSNITHNERLEFLGDAVVEFITSIHLFHMFPDLEEGGLATYRA
Dm-drosha RFGKEHETVSNIHNERLEFLGDAVVEFLSSIHLFFMPELEEGGLATYRA
Ph-drosha RFGRKNETQSNIYHNERLEFLGDAVVEFITSIHLFHIFRDLEEGGLATYRA
Hs-drosha RLGGDDPTPSRINHNERLEFLGDAVVEFLTSVHLYLFPSLEEGGLATYRT
Ci-drosha RLGGQRPVLPVLEHNERLEFLGDAVVGYFTSVHLFLFPDLSEGALTTFR

cons * : * * * * * * * * * : . : * : * : * . . . * . * : * : * :

Ap-drosha AIVQNQHLAVLAKTLKLDDFMLYAHGSDLCHDSELKHAMANCFEALMGALF
Am-drosha AIVQNQHLAVLAKLNLEEYMLYAHGSDLCHDLELRHAMANCFEALMGSLF
Nv-drosha AIVQNQHLAVLAKLNLEQYMLYAHGSDLCHDLELRHAMANCFEALMGALF
Tc-drosha AIVQNQHLAVLAKTLKLDQFMLYAHGSDLCHDLELRHAMANCFEALMGALF
Ag-drosha AIVQNQHLAVLAKKLHLEEFMLYAHGSDLCHELELRHALANCFEALMGALL
Dm-drosha AIVQNQHLALLAKKLQLEEFMLYAHGSDLCHELELRHAMANCFEALMGALL
Ph-drosha ALVQNQHLSVLAKKLDEFMLYAHGSDLCHDLELKHAMANCFEALMGALF
Hs-drosha AIVQNQHЛАMLAKKLELDRFMLYAHGPDLCRESDLRHAMANCFEALIGAVY
Ci-drosha VLVNNQHЛАLLAERLQLDEFMLYAHGPDLCRKADLRHAMANCFEALMGAIY

cons . : * : * * * : : * * : * . * : : * * * * . * * : . : * : * : * * * * : * :

Ap-drosha LDGGIEVADRVFGKTFYRDSPEYLDIWNYPYRHPPLQQQEPEGDRKWIKKLP
Am-drosha LDGGIEVADRVFGETLFKDEEDLAKVWVNYPKHPPLQQEPTGDRQWIPSFE
Nv-drosha LDGGIRIADTVFGETLFKNESDLLNIWVNYPKHPPLQQEPTGDRQWIPSFE
Tc-drosha LDGGINVDRVFSETLFKVNPDLLEVWMNLPPHPLQQEPTGDREWIPKFE
Ag-drosha LDGGIEVADRVFAYALFQEDDTLRGIWVNYPSPHPLQQEPLGDRHHIDSFE
Dm-drosha LDGGIKVADEVFTDALFRQDEKLLSIWKNLPEHPLQQEPLGDRSCIDSYR
Ph-drosha LDGGIESADKVFGMTLYGDDEDCSDVWFNYPPHPLQQEPLGDRKWISHFP
Hs-drosha LEGSLEEAKQLFGRLLFN-DPDLREVWLNYPLHPLQLQEPNTDRQLIETSP
Ci-drosha MEAGLERAQRLFGEFLWE-TEALQRVWRSLPLHQLEEEPVSDRRCIKDVP

cons : : . : . . : * : : : * . * * * : * * * * * *

Ap-drosha LLQKLTNFEDSIGIKFTHIRLLARAFTDRSVGFTNLTLGSNQRLEFLGDTV
Am-drosha LLQKLTKFEESIGIEFTHIRLLARAFTDRSIGYTNLTLSNQRLEFLGDTV
Nv-drosha LLQKLTKFEEGIGVEFSHIRLLARAFTDRSIGYTNLTLSNQRLEFLGDTV
Tc-drosha LLQNLTKFEESVGLQFNHIRLLARAFTDRSVGTYTNLTLSNQRLEFLGDTV
Ag-drosha MLKTLTRFEDSIGVQFNHIRLLARAFTDRSIGFTNLTLGSNQRLEFLGDTV
Dm-drosha VLKELTKFEDSIGIKFKHIRLLARAFTDRSIGFTHLTLGSNQRLEFLGDTV
Ph-drosha LLQNLTKFEEATGIEFKHIRLLARAFTDRSVGTYTNLTLSNQRLEFLGDSV
Hs-drosha VLQKLTEFEEAIGVIFTHVRLARAFTLRTVGFNFHHTLGHNQRMEFLGDSI
Ci-drosha ILQKLTKFEDSIGVKFNHIRLLAKAFTWRNVHENILTHGHNQRLEFLGDSV

cons : * : * * . * * : . * : * . * : * * * : * * * * : .

Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

```

LQLIASDYLYKYFPEHHEGHLSSLRSSLVNNRTQSVVCDDLGMVSYALYAN
LQLIVSEYLYKYFPEHHEGHLSSLRSSLVNNKTQAVVCDDLGMTQYALYGN
LQLIVSEYLYKFFPEHHEGHLSSLRSSLVNNKTQAVVCDDLGMTQYALYGN
LQLIASEYLYKYFPEHHEGHLSSLRSSLVNNRTQAVVCDDLGMNSNYAVYNN
LQLICSEYLYRHFPEHHEGHLSSLRSSLVNNRTQAVVCDDLGMTQYAVYSN
LQLICSEYLYRHFPEHHEGHLSSLRSSLVNNRTQAVVCDDLGMKYAVYAN
LQLIASEYLYKYFPEHHEGHLSSLRSSLVNNKTQSVVCDDLGMTQYAVYAN
MQLVATEYLFIFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITND
CNLVASAYLFKLYPTTHEGHLTLLRATVVNGRTQSLVATELGMPPEYVICL
  
```

cons : * : : * * : : * * * * * : * * : : * : * . : * * * . * . :



Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

```

--P----KAELTKDRADLLEAFLGALYIDKGLTFCQAFCNVCFFPRLHDF
--P----KAELTKDRADLLEAFLGALYVDKGLEYCRVFCDVCFPPRLQDF
--P----KAELTKDRADLLEAFLGALYVDKGGLHQCVCFFPRLQDF
--P----KAELTKDRADLLEAFLGALYVDQGLEFCEVFCQVTLFPRLQDF
--P----KADLTKDRADLLEAFLGALYVDKGLEYCEMFCHVCLFPRLQDF
--P----KADLTKDRADLLEAFLGALYVDKGGLYCEQFCHVCLFPRLQDF
--P----KVELVKDRADLLEAFLGALYVDNGLDICRVFCDVCFPPRLQIF
--K-TKRPVALRTKTLADLLESFIAALYIDKDEYVHTFMNVCFPPRLKEF
DNDSSTERVPEWREKNLADLLEAFVAALFIDKGLKYVKTFMKICFFPRLKEF
  
```

cons : * : * * * * : * : * * : : * : * . : * * * : *



Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

```

ILKQDWNDPKSKLQQCCLTLRSVDGGEPDIPVYKVIEC--MGPTNGRKYTV
IMNQDWNDPKSKLQQCCLTLRTMDGGEPDIPVYKVIEC--KGPTNTRVYTV
IMNQDWNDPKSKLQQCCLTLRTMDGGEPDIPVYKVIEC--KGPTNTRVYTV
IMNQDWNDPKSKLQQCCLTLRTMDGGEPDIPVYKVIECFTNSEVNTRVYTV
IMNQDWNDPKSKLQQCCLTLRTMDGGEPDIPVYKVIEC--TGPTNTRVYSV
IMNQDWNDPKSKLQQCCLTLRTMDGGEPDIPYYKVVEA--SGPTNTRVYKV
IMNQDWNDPKSKLQQCCLTLRTMDNVEPDIPYKVVEC--KGPTNTRVYTV
ILNQDWNDPKSQLQQCCLTLRT-EGKEPDIPLYKTLQT--VGPSHARTYTV
ILTQEWNNDPKSCLQQCCLTLRQ-EGKEPQLPTYEISHQ--TGPSHSRKYVV
  
```

cons * : . * ; * * * * * * * * : . * * : * * : . : . : * * * : * * :



Ap-drospha
 Am-drospha
 Nv-drospha
 Tc-drospha
 Ag-drospha
 Dm-drospha
 Ph-drospha
 Hs-drospha
 Ci-drospha

```

AVYFKSVRLSQATGHSIQRAEMNAANSALEVSKDLFPQLDHQRRAISRSLN
AVYFQGKRLAKASGHSIQEAEMNSAKEALEKSQDLFPQLDHQKRVIAKS-M
AVYFQGKRLAKASGHSIQEAEMNSAKEALEKSQDLFPQLDHQKRVIAKS-M
AVYFRGRRLASAMGHSIQQAEMNAAKKALEISQDLFPQLDHQRRVIAQS-L
AVYFRGKRLACADGHSIQQAEMNAAKQALENSKDLFPQLDHQKRVIAKS-M
AVYFRSKRLATSSGSSIQQAEAMNAAKQALENSRDLFPQLDHQKRVIAKS-I
AVYFRNKRLAKATGHSIQQAEMNAAKQAMEVSGPLFPQLDHQKRVIAKS-L
AVYFKGERIGCGKGPSIQQAEMGAAMDALEY--NFPQMAHQKRFIERK-Y
TVHFKGEEIGKGTGESIQRAERNAARTALNQ--YNFPQLEWQRRYVAEK-H
  
```

cons : * : * : * * * . * * . : * * : * : * : . . : .



T-COFFEE, Version_7.38 Thu Nov 20 17:26:38 WEST 2008

Cedric Notre Dame

CPU TIME: 11 sec.

SCORE = 88

*

BAD **AVG** **GOOD**

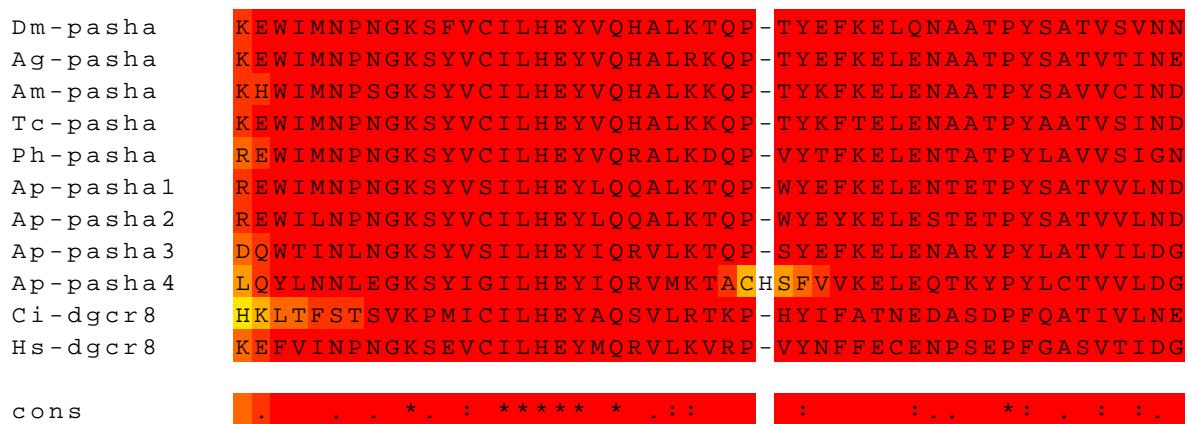
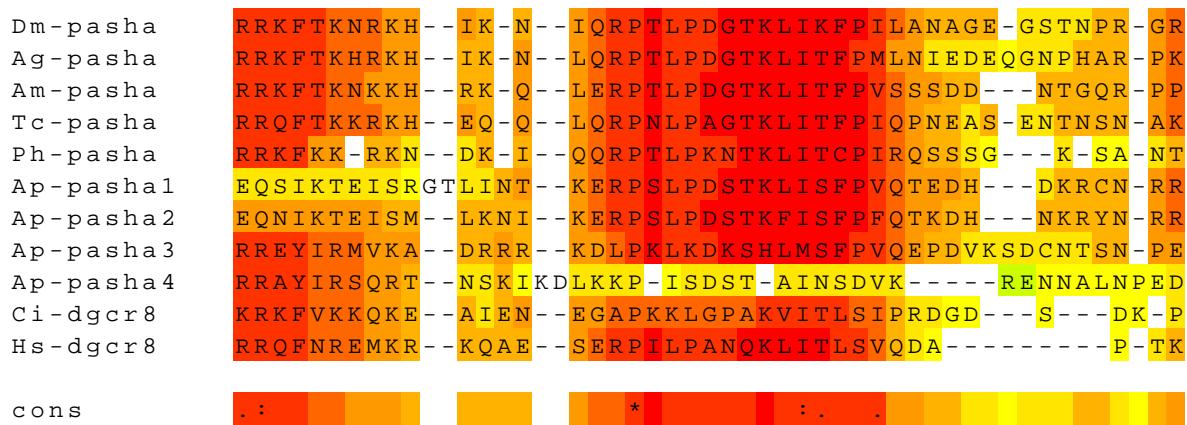
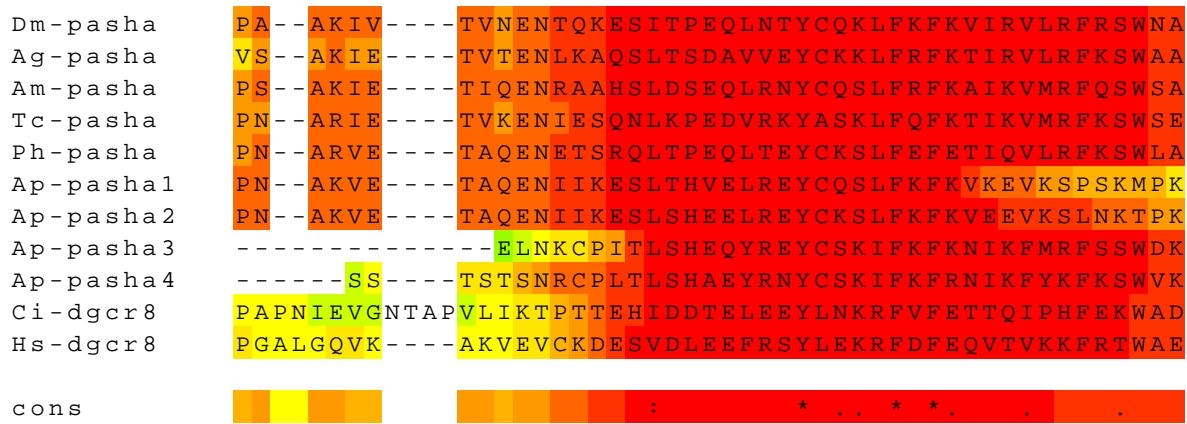
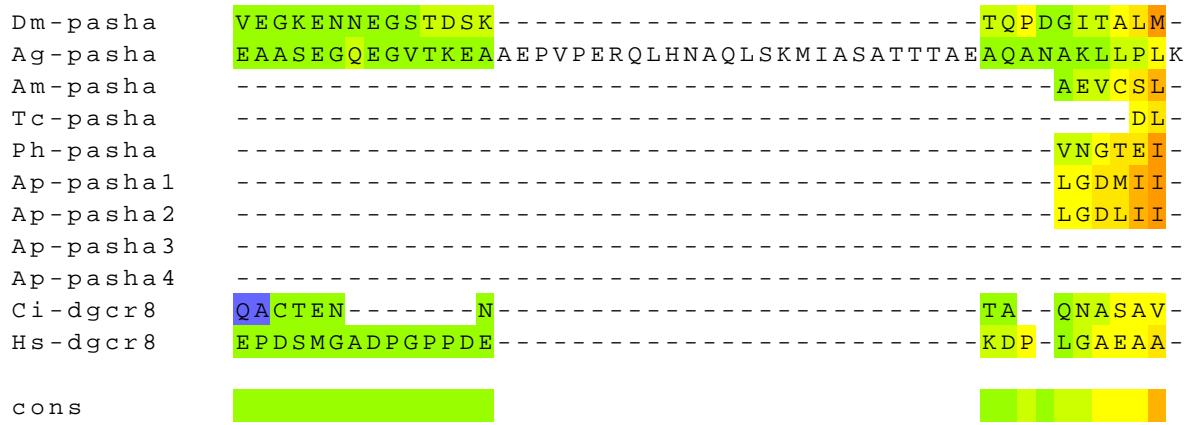
*

Dm-pasha	:	8 8
Ag-pasha	:	8 8
Am-pasha	:	9 0
Tc-pasha	:	9 0
Ph-pasha	:	8 9
Ap-pasha1	:	8 7
Ap-pasha2	:	8 8
Ap-pasha3	:	8 9
Ap-pasha4	:	8 4
Ci-dgcr8	:	8 6
Hs-dgcr8	:	8 5
cons	:	8 8

Dm-pasha	EKRLNHFEVLPEGWVQVTNSGMPFLHRKTRVCCASRPYFLGTTGSARKHA
Ag-pasha	EKGGRNHFEVLPEGWVQATHMSGMPLYLHKASRVCTASRPYFLGPGGSVRKHE
Am-pasha	EIGHHNHFVDLPEGWVQVTNSGMPLYLHKQSRVCTLAKPYFLGPGGSVRKHE
Tc-pasha	EKSQNHNFDVLPEGWIQVTNSGMPLYLHKNSRVCTLSKPYFLGPGGSVRKHE
Ph-pasha	EKVKNHNHFEDVLPDGWVTLTHNSGMPLYLHRTTRVCTLSKPYCLGPGGSARKHA
Ap-pasha1	EVCKNHFDILPENWIEATHKSGMPIYLNKKSRVVTLSRPyFLGPGDPKSHL
Ap-pasha2	QLSKNHFDILPENWIETIHKSGMPIYLNKKSRVVTLSRPyFLGPGDPKSHL
Ap-pasha3	DEDECIDDDLPPEGWIKCNHDSGMPVYLNEEMKVCFSKPYFLGVNSLKNHN
Ap-pasha4	DENSCSNNNDLPKGWKKIDHDSGMPIYMNTETRVCSFSKPYFLGVNSLKNHE
Ci-dgcr8	QCPISSLEPLPEDWMMVSHKSGIPVYLNKKTKVVTLSPYVVAGNVKHN
Hs-dgcr8	SRGRPPTEPLPDGWIMTFHNSGPVYLNHRSPYVVAGNVKHN

Dm-pasha
Ag-pasha
Am-pasha
Tc-pasha
Ph-pasha
Ap-pasha1
Ap-pasha2
Ap-pasha3
Ap-pasha4
Ci-dgcr8
Hs-dgcr8

cons * : . : : * * . .



Dm-pasha Ag-pasha Am-pasha Tc-pasha Ph-pasha Ap-pasha1 Ap-pasha2 Ap-pasha3 Ap-pasha4 Ci-dgcr8 Hs-dgcr8

```

LKYGTGYGTSKKQAKSEAARETLEILIPDVKDKitGNNKDO-K-----
LKYGTGYGTSKKQAKSEAARETLEILIPDMKDKitGKDAKG-----
MEYGSFGSSKKQAKANAARKTLEILIPQMRDKISGDNGGDTVSGNNNRMI
MQYGVGYGTSKKQAKSEAARATLEILIPEMKSKitTDAKTG-S-----
IQQYGTGVGSSKKQAKHAAKATLEILIPEMKDKitDQDEKLRL-G-----
VQYGVGLGNSKKQAKLNAAQATLDILIPEMKNKIDSNIK-----
VQYGVGLGNSKKQAKLNAAQATLDILLPEIKNKIDSNIK-----
MQYGIGIGSSKKQAKLDAARATLEILLPSVKNHJQINRRHA-M-----
IQQYIGITGSTKKQAKVDAARATLQILLPNVKYFQTDNSSET-K-----
KNYGTASGINKKSAKNKAALLTMEMLVPGFKEQVESL-----
VTYGSGTASSKKLAKNKAARATLEILIPDFVKQTSEEKP-----

```

cons * . . . * * . * * : : : * .



Dm-pasha Ag-pasha Am-pasha Tc-pasha Ph-pasha Ap-pasha1 Ap-pasha2 Ap-pasha3 Ap-pasha4 Ci-dgcr8 Hs-dgcr8

```

SGT-AKKAQSDFLSVFDDIRIEDPRVTEFCNKTTEPSPNAILLTCLQRNYGS
-AS-NGGGAAILSVFDEIKIEDPRVAEFCAKTTEPSPHAILLTCLQRNFGL
KAS-RANSADALSFDFEISITDPRVAEFCAKTTEPSPHAILITCLQRNYGL
S-A-SRDQDQDLSFFDEIRIEDPRVAEFCAKTTEPSPHDILLTCLQRNFGL
HAG-YNRGNTDLSFFDGKIEDPRVTEFCAKTTEPLPHEILLTCLQRNFGL
-----NQRDPVIFDQIKVTDPRVTEFCAKTTEPSPYAMLLVCLQRNFGE
-----NQRDPVIFDQIKVTDPRVTEFCAKTTEPSPYAMLLVCLQRNFGE
NERQGCSNFDGDLVFDKLNKDSRIPEFCQAQAEESMPYDMLQICVKRNFGE
NEIQDINHLEQYKIFDKLTVKDTMIPQICAQSTESTPYEMLKLCVKRNFGE
-----SNDQSLEYFDEVSIIDPRVHELKVHAGNFLPHQLLTECLKRNQGI
-----KDSEELEYFNHISIEDSRVYELTSKAGLLSPYQILHECLKRNHGM

```

cons * : : : * . : : : : * : * * : * * *



Dm-pasha Ag-pasha Am-pasha Tc-pasha Ph-pasha Ap-pasha1 Ap-pasha2 Ap-pasha3 Ap-pasha4 Ci-dgcr8 Hs-dgcr8

```

-DVQISQEINRT-----ANNKNEFTMTVGKHTAKVVCKNREGKQLASQAI
GEVHINYEVNTM-----KHRKNEFTMTVGKHATVVCKNKRDGKQRASQAI
GDMHINYSVNTL-----KHQRNEFTMRVGKHEATVVCRNKKDGKQRASQAI
NDLQISYQGNTL-----KNKKNQFTMTVGKHTATVVCKNKRDGKQRASQAI
SQMNIKYETTP-----KHCKNEFTMTVGNHTAKVICRNRDGKQKASQAI
CEIGIEYKLNNR-----RRMLNQCTMMVGKHTASVACKNRDGKQKASQVI
CEIGIEFKLNTN-----HRMLNQCTMTVGKHTASVACKNRDGKQKASQII
D-ACVKCEMQSMQSGSDSDIFYRCTMTVKEHSATVICKNKREGRQKGQAQAL
G-TNLLCEMEQMOSGSDDTNNYFRCTMTVEKYSATVICKDKLDGRQKGQAQAL
ADTAQFDVQVG-----KSKMIEYKMTCGHVVTGTAKKKVVGKQLASQQI
GDTSIKFVVPG-----KNQKSEYVMACGKHTVRGWCKNKRVGKQLASQKI

```

cons : . : . * : : . . : * * : * . : * :



Dm-pasha Ag-pasha Am-pasha Tc-pasha Ph-pasha Ap-pasha1 Ap-pasha2 Ap-pasha3 Ap-pasha4 Ci-dgcr8 Hs-dgcr8

```

LQILHPHIQTWGSLLRLYGNNSIKTFKEKKLEEQEITVLO-----
LQILHPHIKTWGSLLRLYGNRSVKSYKEKKQEEQEITVLO-----
LQLMHPHIQSWGSLLRLYGSRSVKSFKKEKKQLEQEITLLQ-----
LQALHPHITSWGSLLRLYGNGSVKSFKKEKKLEEQEITLLQ-----
LQALHPQIPSWSLRLYGNNTSVKTVKEKKIEEQEITLLQ-----
LGLLHPHIDNWGSLLRLYGNRSIKNAKEKKQEEQEITQLQ-----
LGLLHPHIDNWGSLLRLYGNRSIKNAKEKKQEEQEITQLQ-----
LKVLHPHIKYFGSLLRLYSHQNVGSGCEKKLDEPGN--Q-----
LKVLHPHIHYFGSLLRLYSHQHFETY-ENKPNEDKP--K-----
LKLLHPNMQTWGELIHAYGTSVAEKRARKKNIQEIEFELKQRRNLDSQKS
LQLLHPHVKNWGSLLRMYGRESSKMKVQETS-DKSVIELQ-----

```

cons * : * * : : : * . * : : * . : . : :



Dm-pasha Ag-pasha Am-pasha Tc-pasha Ph-pasha Ap-pasha1 Ap-pasha2 Ap-pasha3 Ap-pasha4 Ci-dgcr8 Hs-dgcr8

```

-----S K A A V N Q P N Y A I L D K L K S E M L K L C A K Q E S V L T M G T F V P P
-----S K A A I N Q P N Y A I L E K L K Q E M S K L E E R Q R N V R V I G K F V P P
-----G K A A V N Q P N H A I L S K L R Q E M R K L A E Q R Q A I Q P I G K F V P P
-----S K A A I N S P N F A I L D K L K L E L S K L R D K R T Q I K P I G V F I P T
-----S R G N S H S P N Y A I L N K L R E E M K K F K A M K S A I R P I G K F I P P
-----S K A A V N Q P N F A I L N K L K E E M L K I R D Q R K L K E -T N E M L G L
-----S K A A A N Q P N F A I L N K L K E E M L K I R D Q R K L K E -T N E M L G L
-----S P K P R S G P N Y E I L K K L R A E M S K -----
-----A E Q C R T H P D V E L L K K L R K A M L K L E S Q T N D L K -----
-----S N K D E E A D G D S Q E K K N A L A P N P E L L N K L R D M M M A L E Q E S S S K K R P G E -----
-----Q Y A K K N K P N L H I L S K L Q E E M K R L A E E R E E T R K K P K M -----

```

cons

The color scale shows a gradient from light yellow (0%) to dark red (100%). It includes labels: cons, *, :, ., **, :, :.

Dm-pasha Ag-pasha Am-pasha Tc-pasha Ph-pasha Ap-pasha1 Ap-pasha2 Ap-pasha3 Ap-pasha4 Ci-dgcr8 Hs-dgcr8

```

S D V D L P T S S G -----S N L N N V E L
S D V D L P T G A G -----A N L K N V D L
-----D L P T G S A -----A N L N N V D L
E S D S L P K L S S -----S N L K N V D L
D D V E L P A E S G -----T D L S N V L M
P Q T M L A T T C P Y T I A I P S S S T S P N
S P T M L A T T C P Y T I V N P S S S T S H N
-----L
-----K M
P D T D Q P S K K R -----N K L L L I D V
S I V A S A Q P G G -----E P L C T V D V

```

cons

The color scale shows a gradient from light yellow (0%) to dark red (100%).

T-COFFEE, Version_7.38 Thu Nov 20 17:26:38 WEST 2008

Cedric Notredame

CPU TIME: 36 sec.

SCORE = 90

*

BAD AVG GOOD

*

Hs-exp5	:	90
Ap-exp5	:	88
Am-exp5	:	91
Ag-exp5	:	91
Ph-exp5	:	90
Tc-exp5	:	91
Dm-exp5	:	91
Ci-exp5	:	85
cons	:	90

Hs-exp5	MAMD--QVNALCEQLVKAVTVMMDPNSTQRYRLEALKFCEEKEKCPI
Ap-exp5	MNLD-TPIETVVQQQLANAVDLTMDSMSQEKRHEAYRLCDSFKN
Am-exp5	MEFGVGNVAQISALEAQVVEVMMSPNVPQEQRLEVYNACERFK
Ag-exp5	MEMA-HDVVELANELARAVKITMDPEATQQARMDAYVACERFK
Ph-exp5	MATE-EIMIDQITGELIRALEITMNPVAEQSARQEAYTAYENFKDN
Tc-exp5	MAGP-DVAALAAADLARAVELTMSTGASQTDRLKAYNACESFK
Dm-exp5	MSQH-GGTEALAAELASAIDLVMNPMTQQQARLEAYMACERFKE
Ci-exp5	MDQN-Q----TQQIILALQTLLDPSATQCMRTEALNLCESYKS-NPHCAE
cons	* : : : . : : . * * . : : * . * .

Hs-exp5	C--GLRLAEK-T-QVAIVRHFGQLQILEHVVKFRWNSMSRLEKVYLKNSVME
Ap-exp5	CQCALYFTSDSAQYTDIVRHFGQLQLMEHCIKFRWYQMVQEDKL
Am-exp5	C--GLYLAQKAPNRSSVVRHFGLQLMEHCIKYRWTQISQSEKIFI
Ag-exp5	A--GLSLVTG-N-YPPIVRHFGQLQLMEHTVKFNWNSISQQEKI
Ph-exp5	V--GLYLVQL-NTPHGYIVHFGLQLMEHCVKFRWNQISQPEKI
Tc-exp5	A--GLYLAAG-TQHSLISRHFGLQLMEHTVKYRWTQISQQEKI
Dm-exp5	V--GLFLASS-PQSNNQVRFHFGQLIEYTIKYRWNCITHEEKVYIKDNAI
Ci-exp5	I--GFELLGH-RSLDAHVRYFGLQLIKHRVRHHWVNMESTEQNAVQSLTLE
cons	: :

Hs-exp5	LIANGTLNIL-EEENHIKDALSRRIVVEMIKREWPKHQWPDM
Ap-exp5	LVNSASP-S-LQINYLKDALARVVVEMIKREWPKHQWPGLN
Am-exp5	LLQEGTEPLL-QEEAHIKDALSRRVVEMIKREWPKQWP
Ag-exp5	LLQAGVGEAQDQSLAHIKDGVSRIIIVEMIKREWPKQWP
Ph-exp5	LLMDGK----QKETYVKGDSRIIIVEMIKREWPKQWP
Tc-exp5	LLAAGG-I-SDEPHMKDALSRRVIVEMVKREWPKQWPGL
Dm-exp5	MLNVGVGPAAEDRSLLPTKDALSRRIIIVEMIKREWPKQWP
Ci-exp5	MVNTCP-G-NEVTYIKTGLAGVLTEIVKHTWPQQWPNMEEVVIANKNS
cons	: : : : : : : : * . : : : : * : : * : * * : * . : : * : .

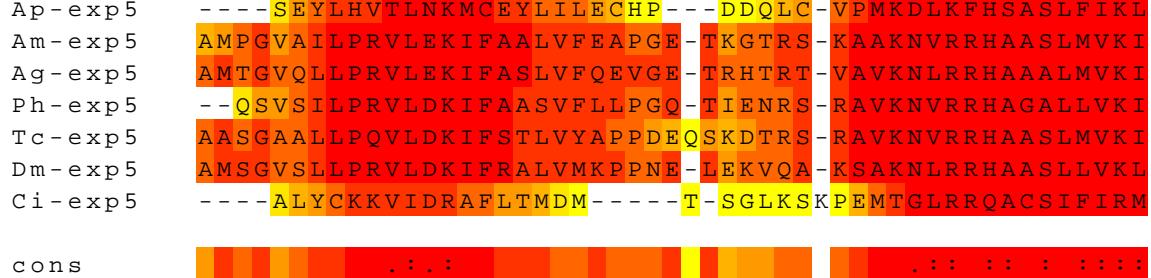
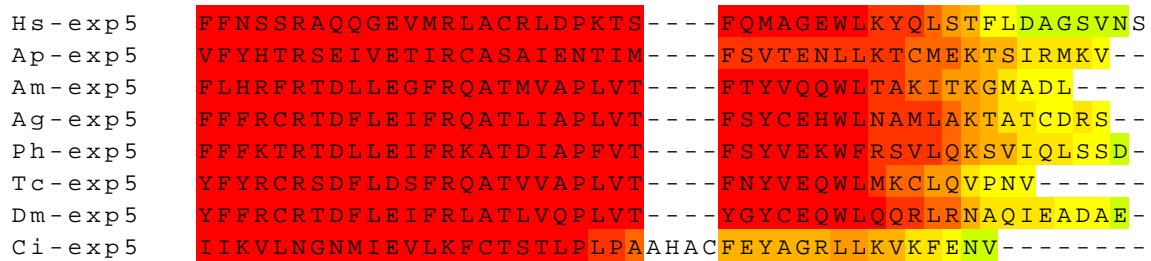
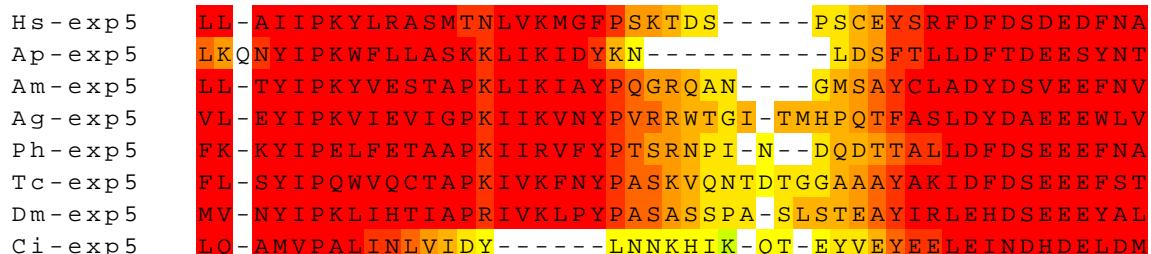
Hs-exp5	ET	-QTELVVMFILLRLAEDVVTFQTLP- PQR RRDIQQTLTQNMERIFSLL
Ap-exp5	CC	-QTETVMLIFLRLIEDVVLLQTVDNAARRRDISKEI QMSMSK IFPFFIN
Am-exp5	ES	-QTELVLLVFLRLVEDVALLQTLESNQRRKDIYQALNTNMAE IFSFFLR
Ag-exp5	MA	-QTELVLLVFLRLVEDVALLQTIESNQRRKDIYQALTVNMS EIFTFFLR
Ph-exp5	PT	-QSEIVLLIFLRLCEDAVLQTLESTQRRRDIYQALT TNMQD IFSFLIQ
Tc-exp5	EI	-QTELVLLVFLRLVEDVALLQTLESNQRRKDIYHALTANMAV IFDFFLR
Dm-exp5	EA	-QTELVLLVFLRLVEDVALLQTIESNQRRKD MYQALNNNMND FEFFLR
Ci-exp5	EVGTTEII EOMLLDLAEDVALLONVSNRTRGRDLR OALGLSAPN ILAFLLG	

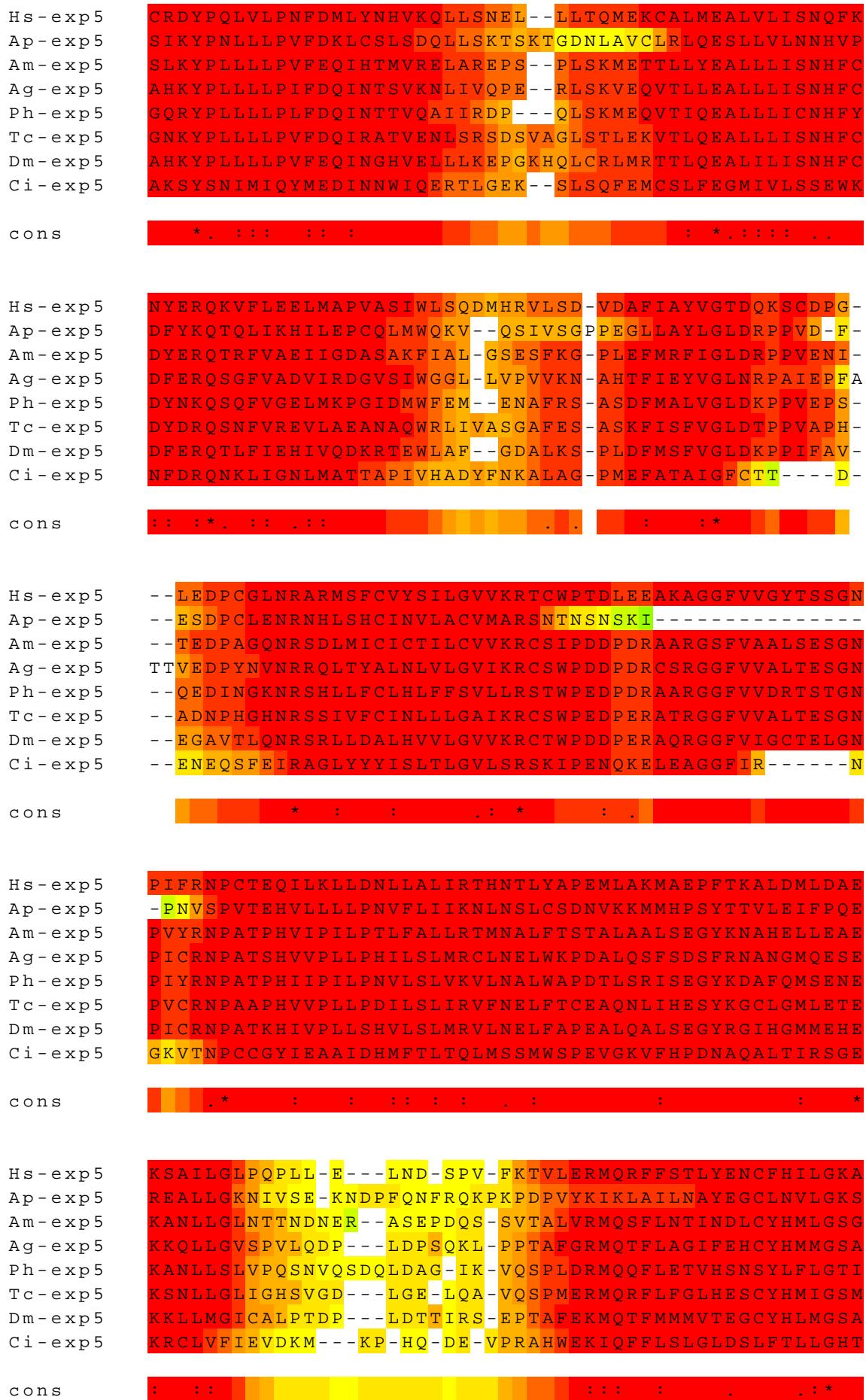
Hs-exp5	TLQENVNKYQQVKT	DTSQE SKAQANC RVGVAALNTLAGYIDWVSMSHITA
Ap-exp5	VIDNYCRQYLEFL	-SRNEQNAATALVRVIQLALANIGELFEFIQLSHVNFK
Am-exp5	LMEQHFSEFQKKN	-SLGCTSEAAAHSKVVQVVLSTLTGFVEWISINHVMAE
Ag-exp5	LIELHVGEFRSAT	-TGGDEHKAHGHSRVVQVALQTLTGFVEWVSINHIMA
Ph-exp5	IITCHIDLFKSI	--GNLEAGNQHFRRVVQTGLTTLSSFLEWASYTHFTNN
Tc-exp5	LIELHVNQFRICG	-ETNNTPKSTAHRVVQVVLLTGTGFVEWVSMSHIMAQ
Dm-exp5	LVEQHVTAFRETT	-RLCNYTKANAHSRVVEMVLLTSGFVEWVSIQHIMSS
Ci-exp5	ALKKQISVLYDD	-----ASPENIHLAGTTLRTISTYAEWVKLDHIFMN

cons : . : * . : * . : * .

	Hs-exp5	Ap-exp5	Am-exp5	Ag-exp5	Ph-exp5	Tc-exp5	Dm-exp5	Ci-exp5
N	C K L L E I L C L L L N E Q E L Q L G A A E C L L I A V S R K G K L E D R K P L M V L F G D V A M H	D C Y I I T V L C S L L D H F N F R Q S A V D C L L V L L S R K C K N E E R E C V V Q L L D Q - P L Q	D G R L L Q I L C L L L G D P I F Q C S A A E C L L Q I V N R K G K A E D R K Q L M I L F S E D A L R	N G R L L Q I L C I L L T D V E F Q Q P A A E C L G Q I T N R R G Q L K D R K P L L L F E D A P V E	D N A L L K I L C A L L E D E H F Q I N A V D C L L Q V V S R K G N P E E K K F F I E W F D L K V L Q	N G R L L H I L C L L L N D L A F Q Y P A A E C L S Q I V N R K G K V D E R K P L L L F N D E P I Q	N G K L M H F L C I L L N D K A F Q C N A A E C L A Q I T N R K G Q T K E R K P L L Q L F N E E P L R	D G I L I E V I F G L L N N S E L Q L P S A E C L L S I A N R K G T S E - R K R L L I L T T D F F V E

Sequence logo showing the conservation of amino acids at each position of the alignment. The x-axis represents the sequence position, and the y-axis lists the proteins: Hs-exp5, Ap-exp5, Am-exp5, Ag-exp5, Ph-exp5, Tc-exp5, Dm-exp5, Ci-exp5.





Hs-exp5 GPSMQQDFYTVEDLATQLLSSAFVNLLNNIPDYRLRPMRVVKPLVLFCPP
 Ap-exp5 CLLLGDQFYALQNFAPSFEATIMSDADSLPHVRIRTVMKNFIKPFLINCSS
 Am-exp5 CHMIGRDFYQLPGLAPALINSVFSNMEMIPDYRLPRIIRVFMKPFIYSCPP
 Ag-exp5 GPSLGRDLYALPGIANAIVGSVFASLEYVPDFRLRTIVRVFLKPFIYSCPP
 Ph-exp5 GPSLGKDFYQIPQLGLALINSLFSNLEFVPDFKLRAVIRTFFKSFIPSCPK
 Tc-exp5 GPSLGRDLYTLPDIGLAIINSVLAACLQCIPDYRMRIIRVFLKPFIYSCPT
 Dm-exp5 GPSLGRDLYQLMGLSDAIVTNVFSRMDLVPDYRLPRIIRVFFKPFVYSCPP
 Ci-exp5 **GVVLGESFYKIP**TLQHTINTKALGYVVNVPI~~T~~RLKCLLRQFLAKILKSCPL

cons : . : * : : : . : : * : : : : * . : : * .

Hs-exp5 EHYEALVSPILGPLFTYLHMRLSQKWQVINQRSSLG-----G-----EDEAA
 Ap-exp5 KYYDTVLIPILNSFLAHMLIRLSITWKNIPE-----EEYD
 Am-exp5 AFYESVLPVLAHVSTHMCQRLSAKWQYIAHLY-----E-----SGGLD
 Ag-exp5 VFHEAVLLPIFAHFVFPMLTRLTARWHYITALY-----E-----SGELG
 Ph-exp5 VCYKDVLVPVLISFMPYMLTRLKKWEHISQLR-----Q-----ESTNS
 Tc-exp5 PFYEAVLLPIVAHIAPLMLSRLHAKWLQVNEFR-----N-----R-----EGQ
 Dm-exp5 SFYDSVLVPLFAHLAPLMCERLTRRWIYIASLY-----E-----SGQLD
 Ci-exp5 DMVHEFTSPILFTYCRFMLERLGAWEAYGKREAERLVIQRGRGSIGYTSE

cons . . * : . : : * * * : : : : : : : : : : : : : : : :

Hs-exp5 DENPESQEMLEEQLVRMLTREVMDLITVCCVSKKGA-----DHSSAP
 Ap-exp5 NKGDGSEELLEDMMIRLLTREYLDLVRSSSLTSSNES-----KTSP--
 Am-exp5 EENTDTQEVIADMLNRNLTRDFVDVLKVALVGGAAS-----DATPPD
 Ag-exp5 EDVNDTQEVLLEDMLNRTLTREYIDVLKVALVGSTIDP---TANSTS DATMAG
 Ph-exp5 EESSDAQEVVDEKLTHIITKEYSDVINICLVGGNSD-----SVLDSD
 Tc-exp5 EDNADTQEVLLEDILTRALTREYLDVLKVALVGGGLT-----PETNTE
 Dm-exp5 GEVNDTQEVLLEDQLNRTLTREYLDVLKIALVGGQIGADHVAAGANANSNSV
 Ci-exp5 QEQQEEEEMLEEQLLRSITREHLELIINLCVNKTP-----

cons . : : * : : : : : : : : * : : : : : : : : : : : : : : :

Hs-exp5 PADGDDEEMMATE-----VTPSAMAE-----ELTDLGKCLMKHEDVCTALLITAF
 Ap-exp5 -----HGSVEEIPNSDLSELGIKLLRNEQSRLIVESIL
 Am-exp5 TMEQDSSGM-AIDF-----PSSRGNSIVAEVVSELGAVVLRHPSTCHSVLCVL
 Ag-exp5 GMDQDDQSMDGTPQALTRAQSAMTSEVISDLGGKLLRNQYTSNPIVMTVL
 Ph-exp5 AMEQDDLTES----S---GQRNVNQAFETVSEGLMLIRNESTQHVIIITLL
 Tc-exp5 NMETEDLSMDSPTP-----PPPTRSNTMTEVISDLGLVLLRSEKTCQSIVLAVL
 Dm-exp5 AMENEHHSMDSAPQ-----SRAIQSALLSDIISDLGGKLLRNGLIGNYVLMTL
 Ci-exp5 -QKDDEHSQ-----STSLGSHHL-AQLTDLGAVLAVSPA-CENMLPCVL

cons :

Hs-exp5 NSLAWK-----DTLSCQRTTSQLCWPLLKQV
 Ap-exp5 NGLSWNTSISQFWKTCQIFQWDNRSVSHPWCDSQSSFKATSLSQIVVKHL
 Am-exp5 GALAWN-----DSNASLKA-TMLTGPVVRAL
 Ag-exp5 SVLSWN-----DSNSSLKA-TLLSGPIIRFL
 Ph-exp5 RFISWS-----DGCAIYKA-PVLLHCVLRQL
 Tc-exp5 GALSWI-----DSNASLKA-TFLTGPIVRQL
 Dm-exp5 KAIAWN-----DGMCSMKA-VNIAAPVMRFL
 Ci-exp5 AALAWH-----DTSSCYKA-AQILWPLLKML

cons : : * * :

Hs-exp5 LS--GTL-L-ADAVTWLFTSVLKGLQMHGQHDGCMASLVHLAFQIYEALRP
Ap-exp5 AT--EDERTAMTIAPDLLIAVLESLHWFGHHDSNMGPLLATCLNIYETYRS
Am-exp5 AA--DGS-LTPDMAAHIMVAILQQLQLHGQHDANQGSLITLGAQVYECLRP
Ag-exp5 AA--EQL-ITEALASNIIIAVLKALQLHGQHESNQTSPLITLGVQAYEILRP
Ph-exp5 SN--DGI-LNEEIANHVMTTQLQALQIQGHQEAMQGLLTGAQLYELLRP
Tc-exp5 VS--DSS-LNGEMAHHIMASVNLNALMLHGQHEANQGSLTLGAQMYEMLRP
Dm-exp5 AA--EKL-MDENKAVTAFTAFLQGMQVHGQHEANQGLVTLGQFYELLRP
Ci-exp5 MNVKENI-FNPDPITRAVFEAMLRGLHRHGQHDGCESQLLSSLMFIQPLHT

cons : . : : * . . : * : : . : : .

Hs-exp5 RYLEIRA--VMEQIPEIQQKDSLQFDCKLLNPS---LQKVADKRRKDQFK
Ap-exp5 KNNQLLE--VLKKLPEinLETLERFDKWVMSEDP---LNNKVNKGKREMLK
Am-exp5 KFPNIIIE--VMOQIIPGVNLTDLQRFDEKMAVVST---KGNKVEKGKKDLFK
Ag-exp5 KFPNILE--VLQQIIPNVNSAGDIQKLDEKISSGST---KGNKIDKAKKDLFK
Ph-exp5 KFPSIVK--ILMQIIPNVNQQDLQKFDEKIIILSSQNFKTSYKLDKSTKDLFK
Tc-exp5 TFLEVLG--VMOQIIPGVNPVDLQKLDERISGSTS---KGNKVEKVKKDLFR
Dm-exp5 QFPILSE--VLQHIPSVAADIQKFDEKIAVAPV---KGNKVDRACKDIFK
Ci-exp5 KHAALFTSIMLQAAPDADQALVHKFFVN---FEK---TSEKQRKSALK

cons : : : * . . : . : : : : : . : :

Hs-exp5 RLIAGCIGKPLGEQFRKEVHIKNLPSLFKKTP---MLETEVLD-NDGGGL
Ap-exp5 KILAGCIGKDVQTHKCKAELRDLPRVLVPKICT---TDLLENGDDLN
Am-exp5 KITNQLIGRSVGQLFRKEVKIDNLPIEVFGKQQAV-RVDEISENSTDSGF
Ag-exp5 KITTNIIGRNIGQHGRKEVKILNLQPIVPPPNNHR-PNAFNLIIESNQETGL
Ph-exp5 KITHPLIGRNISQLFKKEIKIMDLPKLNLPKKGTKEVDFNYGQEL
Tc-exp5 KITGNLIGRSMGQLFKKEVKIHDLPSLAFSKKPQPK-EVT-P-----DL
Dm-exp5 KLTAQLVGRSVNQLFRHEVQIANLPPMQSHAKGSMGTTADIMDSNQNASL
Ci-exp5 EMLSGIIEQHVSQOFKEIPKMNILEPLQIKKRNQK---SKPEDS-YTGL

cons . : : : : : : . : * : : : : :

Hs-exp5 ATIF--EP
Ap-exp5 NKLQEYKL
Am-exp5 AALFAGPT
Ag-exp5 AHLFTNRS
Ph-exp5 NKL---LS
Tc-exp5 QN---VFS
Dm-exp5 ARLFGPPEK
Ci-exp5 AQLF--QP

cons : : : : : : : : : : : : : : :

T-COFFEE, Version_7.38 Thu Nov 20 17:26:38 WEST 2008

Cedric Notredame

CPU TIME: 27 sec.

SCORE = 94

*

BAD AVG GOOD

*

Ap-agola	:	9 4
Ap-agolb	:	9 5
Am-agol	:	9 4
Dm-agol	:	9 4
Tc-agol	:	9 4
Ph-agol	:	9 4
Pm-agol	:	9 4
Is-agol	:	9 4
Ci-ago	:	9 5
Hs-eIF2C2	:	9 4
cons	:	9 4

Ap-agola	V F N C P R R P N L G R E G R P I V L R A N H F Q	I S M P R G Y V H H D I N I Q P D K C P R K V N
Ap-agolb	V F N H P C R P N L G R E G R P I R L R T N H F Q	- V S M P R S Y I Q H Y V I Y I K P E N C P R R V N
Am-agol	M F S C P R R P N I G R E G R P I V L R A N H F Q	- I T M P R G Y V H H D I N I Q P D K C P R K V N
Dm-agol	V F T C P R R P N L G R E G R P I V L R A N H F Q	- V T M P R G Y V H H D I N I Q P D K C P R K V N
Tc-agol	V F Q C P R R P N L G R E G R P I G L K A N H F Q	- V T M P R G F V H H D V S I Q P D K C P R K V N
Ph-agol	M F C C P R R P S L G R E G R P I A L R A N H F Q	- I S M P R G Y V H H D I N I Q P D K C P R K V N
Pm-agol	A F V A P R R P N L G R E G R P I T L R A N H F Q	- I S M P R G Y I H H Y D I S I T P D K C P R K V N
Is-agol	M F V C P R R P N V G T E G R P I L L R A N H F Q	- I S M P R G Y L H H D V T I T P D K C P R K V N
Ci-ago	D F Q A P P R P N Q G Q V G K P I W L K A N Y F K	- V S I P N G D I H H Y D I D I K P D K C P R R V N
Hs-eIF2C2	V F D G - - R K N L Y T - A M P L P I G R D K V E L	M D I P K I D I Y H Y E L D I K P E K C P R R V N
cons	* : : : . : : * . : * * : * * : * * : * * :	

Ap-agola	R E I I E T M V H A Y	- S K L F G N L R P V F D G R N N L Y T R D P L P I G N D R M E L E V T L P G E
Ap-agolb	R E I I K I M V N A Y	- S K L F G N L R P A F D G R Q N L Y T R D P L P I G R K Q V E L E V K L P G Q
Am-agol	R E I I E T M V H A Y	- T K I F G T L K P V F D G R N N L Y T R D P L P I G T D K I E L E V T L P G E
Dm-agol	R E I I E T M V H A Y	- S K I F G V L K P V F D G R N N L Y T R D P L P I G N E R L E L E V T L P G E
Tc-agol	R E I I E T M V H A Y	- G K I F G N L K P V F D G R N N L Y T R D P L P I G N S R E E L E V T L P G E
Ph-agol	R E I I E T M V H A Y	- S K I F G S L K P V F D G R Q N L Y T R D P L P I G N D R V E L E V T L P G E
Pm-agol	R E I I E T M V H A F	- P R I F G T L K P V F D G R S N L Y T R D P L P I G N E K M E L E V T L P G E
Is-agol	R E I I E T M V Q S Y	- S K I F G Q Q K P V F D G R K N M Y T R D D I P I G K D K A E L E V T L P G E
Ci-ago	R E I I I N T M V E N F R S A I F Q D R K P V F D G R K N L Y T A Q P L P I D K Q K L E V E V T L P G E	
Hs-eIF2C2	R E I V E H M V Q H F K T Q I F G D R K P V F D G R K N L Y T A M P L P I G R D K V E L E V T L P G E	
cons	* * * : : * * . : : * : * . * * * . * : * * : * * . . : * : * * . * * * :	

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

GKDRVFRVNWKWLAQVSLFALEEALEGRTRQIPYDAILALDVVMRHLPSMT
CKDGVFHVYIKWLAQISLFDLEEAQGSRRPIPYDAVLALDVVMRHLASMT
GKDRVFRVVIKWLAQVSLFALEEALEGRTRQIPYDAILALDVVMRHLPSMT
GKDRIFRVTIKWQAQVSLFNLEEALEGRTRQIPYDAILALDVVMRHLPSMT
GKDRIFRVTIKWVAQVSLYGLEEALEGRTRQIPYEAIALALDVVMRHLPSMS
GKDRVFRVTIKWVAQVSLFALEEALEGRTRQIPFDTILALDVVMRHLPSMT
GRDRVFKVAMKWLAQVNLYTLEEALEGRTRTIPYDAIQALDVVMRHLPSMT
GKDRVFRVAIKWVAQVSLYALEEVLEGRSRHIPMDAVQALDVVMRHLPSMT
GRDRTFTVAIKWASRVSLYSLLAKLEGKMHGIPFETVQSLDVVMRHLPSLR
GKDRIFKVSIAKWVSCVSLQALHDALSGRLPSVPFETIQALDVVMRHLPSMR

```

cons : * * * : * * : . * * . * : * : : : * * * * * . * :

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

YTPVGRSFFSSPEGYYHPLGGGREVWFGFHQSVRPSQWKMMLNIDVSATAF
YTSVGKSFSPPESYHPLGGGREVWYGFHQSMQPSKWKMMLNLDVSASAF
YTPVGRSFFSPDGYYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFSSPEGYYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFSSPDGYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFSSPDGYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFSSPDGYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFSSPDGYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFSSPDGYHPLGGGREVWFHQSVRPSQWKMMLNIDVSATAF
YTPVGRSFFTASEGCSNPLGGGREVWFHQSVRPSLWKMMLNIDVSATAF

```

cons ** . * : * * : . : . * * * * * * : * * * * * : * * * : * *

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

YKAQPVIEFMCEVLDI RDIG-EQRKPLTDSQRVKFTKEIKGLKIEITHCGA
YKSQLVPEFMCEVLDI KDIS-EQKKPLTDSQRVKFTREIKGLKIEITHWGE
YKAQPVIEFMCEVLDI RDIG-DQKRPLTDSQRVKFTKEIKGLKIEITHCGT
YKAQPVIDFMCEVLDI RDIN-EQRKPLTDSQRVKFTKEIKGLKIEITHCGQ
YKAQPVIEFMCEVLDI RDIN-EQRKPLTDSQRVKFTKEIKGLKIEITHCGT
YKAQPVIDFMCEVLDI REIN-EQRKTLTDSQRVKFTKEIKGLKIEITHCGT
YKAQAVIEFMCEVLDI REIG-EQRKPLTDSQRVKFTKEIKGLKIEITHCGA
YKAQPVTEFMCEVLELRDIN-EQRKPLTDSQRVKFTKEIKGLKIEITHCGT
YRAQSCVQFLCDVLELRDIELDLRLIRGLTDSQRVKFTKEIRGLKVEITHCGT
YKAQPVIEFVCEVLDFKSIE-EQQKPLTDSQRVKFTKEIKGLKVEITHCGQ

```

cons : * : * : * : * : * : : : : : : : * : * * * * * * : * * : * * : * * * * *

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

MRRKYRVCNVTRRPAQMOSFPLQLENGQTVECTVAKYFLDKYKMKLRYPHL
MRRKYKVRNVTRKPAQTQTFPLQEKN-NVVECTVAKYFLDKHNMKLRYPNL
MRRKYRVCNVTRKPAQMOSFPLQLENGQTVECTVAKYFLDKYKMKLRYPHL
MRRKYRVCNVTRRPAQMOSFPLQLENGQTVECTVAKYFLDKYKRMKLRYPHL
MRRKYRVCNVTRRPAQMOSFPLQLENGQTVECTVAKYFLDKYKMKLRYPHL
MRRKYRVCNVTRRPAHMOSFPLQLENGQTVECTVAKYFLDKYKMKLRYPHL
MRRKYRVCNVTRRPAQMOSFPLQLENGQTVECTVAKYFLDKYKMKLRFPHL
MRRKYRVCNVTRRPAQLOSFPLQLENGQTVECTVAKYFLDKYKMKLRYPHL
MRRKYRVCNVTRRAASTQTFPLQLESQGTIECSVARYFQEKSCTLQFPFL
MRRKYRVCNVTRRPASHQTFPLQQESGQTVECTVAQYFKDRHKLVLRYPHL

```

cons * : * * : * * * : . * : * * * : . : : : : * : * : * : * : : : * : . * *

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLHVGEKHNNHIYLPLEVCKIVKSQRCARKLTDMQTSTMKETVRSA
PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEHKHTYLPLEVCNIVPGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEHKHTYLPLEVCNIVAGQRCIKKLTDMQTSTMKATARSAPDRE
PCLQVGQEQKHTYLPievCNIVQGQRCIKKLTDSDQTSTMKATARSAPDRE
PCLQVGQEQKHTYLPievCNIVAGQRCIKKLTDNQTSTMIRATARSAPDRQ
  
```

cons

```
****:***::: : * ***:***:*** . *** :**** * ****: * . ***: * :
```

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

REINSLVRRADFNNDSYVQEFGLTISNSMMEVGRVLPPPKLQYGGRTLP-
QDINSLVRQADFKNNPYVKEFGLTVDSDMIELGRVLPPPKLQYGGQTLPLP-
REINNLVRRADFNNDSYVQEFGLTISNNMMEVGRVLPPPKLQYGGRT---_
REINNLVKKRADFNNDSYVQEFGLTISNSMMEVGRVLPPPKLQYGGRVSTG_
REINNLVRRADFNNDPYVQEFGLTISNNMMEVGRVLPPPKLQYGGRVASL_
KEINSLVRRADFNNDAYVQEFGLTISNNMMEVGRVLPPPKLQYGGRSSLL_
REINNLVRKADFNNDPYMQEFGLTISTAMMEVGRVLPPPKLQYGGRT---_
REINNLVRKADFNTPYVQEGLSISNTMMEVGRRLILPPPKLQYGGRT---_
KEIAQLVRKAQFNNDPYVKEFGIQVIDEMTEVGRVLPPPKIQYGGDV---_
EEISKLMRSASFNTDPYVREFGIMVKDEMTDVTGRVLQPPSILYGGRN---
  
```

cons

```
. :* . * : * . * : . * : * : * : * : * : * . : * : * : * :
```

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

---NQGGLNVQQTKQQALPNQGVWDMRGKQFFTGVIEIRNWAIACF-----
---NQKILNAQQTKQQTLPSHGVWDMRGKQFFFGVKITNWAIACF-----
-----KQQAIPNGGVWDMRGKQFFTGVIEIRVWAIACF-----
LT-GQQLFPPQNKVSLASPNQGVWDMRGKQFFTGVIEIRIWAIACF-----
-----SGQQAMPNQGVWDMRGKQFFTGVIEIRVWAIACF-----
SSDEFAIRNSFHAKQQAMPIGGVWDMRGKQFFSGIEIRVWAIACF-----
-----KQQALPNQGVWDMRGKQFFTGVIEIRVWAVACF-----
-----KQQAIPNQGVWDMRGKQFHTGVIEIRIWAIACFAPQRTS-----
-----SSTPNQGVWDMRGKQFHSGISIDVWAIACF-----
-----KAIATPVQGVWDMRNRNKQFHTGIEIKVWAIACF-----
  
```

cons

```
: * * **** . * . * : * : * : * : * :
```

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

-----APQRTVREDALRNFTTQLQKISSDAGMPIVGQPCFCKYATGPD
-----ASQFSVRDDAIKNFTEQLQRISNEAGMPIVDAPCYCKYVTGLD
-----APQRTVRRDAIRNFIAQLQRISNDAGMPIIGQPCFCKYATGPD
-----APQRTVREDALRNFTQQLQKISNDAGMPIIGQPCFCKYATGPD
-----APQRTVREDALRNFTQQLQKISNDAGMPIIGQPCFCKYATGPD
-----APQRTVREDALRNFTQQLQKISNDAGMPIIGQPCFCKYATGPD
-----APQRTVREDALRNFTQQLQKISNDAGMPIIGQPCFCKYANGPD
ASGAIACFAPQRTCREDALRNFTQQLQKISNDAGMPIIGQPCFCKYATGPD
-----AHQRMCSDQHLRTFIKSLQRISEDAGMPIRGTPVFCKYAQGSE
-----APQRQCCTEVHLKSFTEQLRKISRDAGMPIQGQPCFCKYAQGAD
  
```

cons

```
* * : : * . * : * : * : * : * : * : :
```

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

QVEPMFRYLKSTFTGLQLVVVVLPGKTPVYAEVKRVRGDTVLGMATQCVQAK
QVEPMFNYLIKFKTLQLIIVILPGKTPVYAEVKRVRGDTVLGMATQCVQAK
QVEPMFRYLKATFSSLQLVCILPGKTPVYAEVKRVRGDTLLGMATQCVQAK
QVEPMFRYLKITFPGLQLVVVVLPGKTPVYAEVKRVRGDTVLGMATQCVQAK
QVEPMFRYLKSTFQSLQLVVVVLPGKTPVYAEVKRVRGDTVLGMATQCVQAK
QVEPMFRYLKSSFHALQLVVVVLPGKTPVYAEVKRVRGDTLLGMATQCVQAK
QVEPMFRYLKSTFTGLQLVCVLPGKTPVYAEVKRVRGDTVLGMATQCVQAK
QVEPMFRYLKSTFQGLQLVVVVLPGKTPVYAEVKRVRGDTVLGMATQCVQAK
HVEPLFRHLCDEFRALQLIVVILPGKTPVYAEVKRVRGDTLLGIATQCVQVK
SVEPMFRHLKNTYAGLQLVVVILPGKTPVYAEVKRVRGDTVLGMATQCVQMK
  
```

cons * * : * . : * : * * : * : * * * * * : * * * * * * ; * * ; * * * * * * *

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

NVNKTSPQTLNLCLKINVKLGGINSILVPSIRPKVFNEPVIFLGADVTHP
NVNKLSIQALSNLCLKINVKLGGTNTILVPSVRPKVFNEPLIILGADITHA
NVNKTSPQTLNLCLKINVKLGGINSILVPTIRPKVFDEPVIFFGADVTHP
NVNKTSPQTLNLCLKINVKLGGINSILVPSIRPKVFNEPVIFLGADVTHP
NVNKTSPQTLNLCLKINVKLGGINSILVPSIRPKIFNEPVIFLGADVTHP
NVIKTSPQTLNLCLKINVKLGGINSILVPSIRPKVFNEPVIFLGADVTHP
NVNKTSPQTLNLCLKINVKLGGINSILVPGIRPKVFNEPVIFLGADVTHP
NVNKTSPQTLNLCLKINVKLGGINSILVPSIRPKVFNEPVIFLGADVTHP
NVVKTSPQTLNLCLKINVKLGGVNNILVPSLRPKVFNDPVIFLGADVTHP
NVQRTTPQTLNLCLKINVKLGGVNNILLPQGRPPVFQQPVIFLGADVTHP
  
```

cons ** : : * : * * * * * * * * * . * : * * * : * : * : * : * * : * *,

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

PAGDNKKPSIAAVVGSMDAHPSRYAATVRVQQHQ-----R
TSNDDKISSIAAVGSMDAHPSTRYAAAMVRIQQHQ-----R
PAGDNKKPSIAAVVASMDAHPSTRYAAATVRVQQHQ-----R
PAGDNKKPSIAAVVGSMDAHPSRYAATVRVQQHQ-----R
PAGDNKKPSIAAVVGSMDAHPSRYAATVRVQQHQ-----R
PAGDNKKPSIAAVVGSMMDGHPSRYAATVRVQQHQ-----R
PAGDNKKPSIAAVVGSMDAHPSRYAATVRVQQHQ-----RNGSTTQGQSASDGSRP
PAGDNKKPSIAAVVGSMDAHPSRYAATVRVQQHQ-----R
PAGDTRKPSIAAVVGSMDAHPSRYSATVRVQQHRE-----R
PAGDGKKPSIAAVVGSMDAHPNRYCATVRVQQHQ-----R
  
```

cons . : * : . * * * : * . * * . * . * . * * : * * * :

Ap-ago1a
 Ap-ago1b
 Am-ago1
 Dm-ago1
 Tc-ago1
 Ph-ago1
 Pm-ago1
 Is-ago1
 Ci-ago
 Hs-eIF2C2

```

-----EIIQELSSMVRELLIMFYKSTGGYKPHRIILYRDGVSEGQ
-----EIQELSSMVRELLIMFYKSTRGYKPHRIILYRDGVSEGQ
-----EIQELSSMVRELLLMFYKSTGGYKPLRIILYRDGVSEGQ
-----EIQELSSMVRELLIMFYKSTGGYKPHRIILYRDGVSEGQ
-----EIQELSSMVRELLLMFYKSTRGGYKPHRIILYRDGVSEGQ
-----EIQELSSMVRELLMFYKSTRGGYKPHRIIMYRDGVSEGQ
-----RQLTFARTAHDEVIQELSSMVKELEIQFYKSTRFKPNRIILYRDGVSEGQ
-----EIQDLASMVKELLIQFYKSTRFKPNRIIFYRDGVSEGQ
-----EIRDLAIMVRDLMVEFYKATHYKPVRVIMYRDGVSEGQ
-----KIQDLAAMVRELLIQFYKSTRFKPTRIIFYRDGVSEGQ
  
```

cons : . * : : * : * * : : * : : * * : * : * * : * : * : * : * : * : * : * : * :

Ap-ago1a	FPH	-VLQHELT	AI	REACIKLEGDYKPGITFIIIVQKRHHTRLFCADKKEQSG		
Ap-ago1b	LSN	-VFNYE	LM	AI	REACIKLEGGYKPGITFISVQKRHHTRLFC	DKTEQCG
Am-ago1	FLH	-VLQHELT	AI	REACIKLEAEYRPGITFVVVQKRHHTRLFC	SEKRDQSG	
Dm-ago1	FPH	-VLQHELT	AI	REACIKLEPEYRPGITFIVVQKRHHTRLFC	CAEKKEQSG	
Tc-ago1	FLQ	-LLQHELT	AI	REACIKLESDYKPGITFIVVQKRHHTRLFC	ADKKEQSG	
Ph-ago1	FLHV	V	LQHELT	AVREACIQLEGDYKPGITFIVVQKRHHTRLFC	ADKKEQSG	
Pm-ago1	FQT	-VLQHELT	AM	REACIKLEADYKPGITYIAVQKRHHTRLFC	CSDKKEQSG	
Is-ago1	FQQ	-VLH	HELLA	V	REACMKLEADYKPGITFVVVQKRHHTRLFC	RNSHEDRSG
Ci-ago	FQQ	-VL	STELRA	I	REACTMLEVGYQPGITFIVVQKRHHTRLFC	CRN
Hs-eIF2C2	FQQ	-VLH	HELLA	I	REACIKLEYQPGITFIVVQKRHHTRLFC	KNERVG

cons : : * * : * : * : * : * : * : * : * : * : *

Ap-ago1a	KSGNI	PAGTTVDVGITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDNFES	
Ap-ago1b	KSGNI	PAGTTVDGITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDNNFKS	
Am-ago1	KSGNI	PAGTTVDVCITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDNRFES	
Dm-ago1	KSGNI	PAGTTVDVGITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDNFDS	
Tc-ago1	KSGNI	PAGTTVDVGITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDSHLDS	
Ph-ago1	KSGNI	PAGTTVDVGITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDNRFDs	
Pm-ago1	KSGNI	PAGTTVDVGITHPTE	FDFYLCSHQGIQGTSRP	SHYHVLWDDNFDS	
Is-ago1	KSGNI	PAGTTVDLGITHPTE	FDFYLCSHAGI	QGTSRP	SHYHVLWDDNQFSA
Ci-ago	KSGNI	PAGTTVDGICHPTEFDFYLCSHAGI	QGTSRP	SHYHVLWDDNNFMA	
Hs-eIF2C2	KSGNI	PAGTTVDTKITHPTE	FDFYLCSHAGI	QGTSRP	SHYHVLWDDNRFSS

cons : * : * : * : * : * : * : * : * : * : * : * : :

Ap-ago1a	DELQCLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVEKEHDS	GEG
Ap-ago1b	DELQRLTYQLC	TYVRCTRSISIPAPAYYAH	LVAQRAKYHMVEKEHDS	SEG
Am-ago1	DELQSLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVEKEHDS	GEG
Dm-ago1	DELQCLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVEKEHDS	GEG
Tc-ago1	DELQCLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVEKEHDS	GEG
Ph-ago1	DELQCLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVEKEHDS	AEG
Pm-ago1	DELQCLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVEKEHDS	GEG
Is-ago1	DELQCLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVDKDHD	SGE
Ci-ago	DELQVLTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVDKEHDS	GEG
Hs-eIF2C2	DELQILTYQLC	HTYVRCTRSVSIPAPAYYAH	LVAFRARYHLVDKEHDS	AEG

cons : * : * : * : * : * : * : * : * : * : * : * : * : *

Ap-ago1a	SHQSGCS	---	EDRTPGAMARAITVHADTKV	MYFA	
Ap-ago1b	SHISGCS	---	EDQTVDELARA	ITVHPNANKV	MYFA
Am-ago1	SHQSGCS	---	EDRTPGAMARAITVHANT	KRV	MYFA
Dm-ago1	SHQSGCS	---	EDRTPGAMARAITVHADTKV	MYFA	
Tc-ago1	SHQSGSS	---	EDRTPGAMARAITVHADTKV	MYFA	
Ph-ago1	SHQSSCS	---	EDRTPGAMARAITVHPET	KKV	MYFA
Pm-ago1	SHQSGNS	---	EDRTPSAMARAVTVHVD	TNRV	MYFA
Is-ago1	SHQSSNG	---	DDRTVVVALARAVTIH	PETLK	MYFA
Ci-ago	SLQSGHT	QHDQDAQLQAMS	KAVVVHEN	TVRN	MYFA
Hs-eIF2C2	SHTSGQS	---	NGRDHQALAKAVQVHQ	DLRT	MYFA

cons * . : . : : * : * : : : * : : : ***

T-COFFEE, Version_7.38 Thu Nov 20 17:26:38 WEST 2008

Cedric Notredame

CPU TIME: 1 sec.

SCORE = 99

*

BAD AVG GOOD

*

Ap-dcrla	:	9 9
Ak-dcrla	:	9 9
Ap-dcrlb	:	9 9
Ak-dcrlb	:	9 9
Mp	:	9 9
Rp	:	9 9
Ag	:	9 9
cons	:	9 9

Ap-dcrla	LSNNTPFIPEDSKYIKSEININYKINDSVNEVHGVQTGTFQPDLNHD
Ak-dcrla	LSNNTPFKPEDSKSIKSEININYKIIDSUVNNVNGVQTETFSFDYQPDLNHD
Ap-dcrlb	LLNNTSFMPEDDKCIKNEIYKNNKTIDSINEVNDLQTEFTSFDFQPDLNHYH
Ak-dcrlb	LSNNTSFMPEDNKCIKNEIHKNKTIDSINKVNDAQTEFTSFDFQPDLNHYH
Mp	LLNKTTSFMPEDSEYIKSETYIDSKTIDSUVNVHGVTETFSFDYQPDLNHD
Rp	LSNNTSFVPVKDKICIKNGVHLNNKAIDNINKV-DIQNETFSFDFQPDLNHH
Ag	LSNNTSFVPKDEKCIKNEIHINKKTIDNINKVHDIQNETFSFDFQPDLDNH

cons * * : * . * * : * . * * . : * * . : * . : * * * * : * * * : *

Ap-dcrla	PGPSPSVLLQALTMSNANDGINLERLETIGDSFLKYAITAYLYCTHDNVHE
Ak-dcrla	PGPSPSVLLQALTMSNANDGINLERLETIGDSFLKYAITAYLYCTHDNVHE
Ap-dcrlb	PGPSPSILLQALTANAIIDGYDLERLETIGDSFLKYAVTAYLYCTHNNVHE
Ak-dcrlb	PGPSPSILLQALTTSNANDGINLERLETIGDSFLKYAVTAYLYCTHNNVHE
Mp	PGPSPSVLLQALTMSNANDGINLERLETIGDSFLKYAITAYLYCTHDNVHE
Rp	PGPSPSVLLQALTMSNANDGINLERLETIGDSFLKYAITAYLYCTHDNVHE
Ag	PGPSPSVILQALTMSNANDGINLERLETIGDSFLKYAITAYLYCTHDNVHE

cons * * * * : * * * * : * * * : * * : * * * * * * * * * : * * * * * : * * * *

Ap-dcrla	GKLSHLRSKQVSNLNLRYRLGKLKMFGERMISTKFEPHDNWLPYCYFVPHKL
Ak-dcrla	GKLSHLRSKQVSNLNLRYRLGKLKMFGERMISTKFEPHDNWLPYCYFVPHKL
Ap-dcrlb	GILSDLRSNHVSNLNLRYRLGKLKMFGERMISTKFEPRSNWLPYCIGPHKL
Ak-dcrlb	GILSDLRSNHVSNLNLRYRLGKLKMFGERMISTKFEPRSNWLPCCIEPHKL
Mp	GKLSHLRSKQVSNLNLRYRLGKLKMFGERMISTKFEPHDNWLPYCYFVPHKL
Rp	GKLSHLRSKQVSNLNLRYRLGKLKMFGERMISTKFEPHDNWLPYCYFVPHKL
Ag	GKLSHLRSKQVSNLNLRYRLGKLKMFGERMISTKFEPHDNWLPYCYFVPHKL

cons * * . * * : * * * * * * * * * * : * * * * : * * * *

Ap-dcrla	EKALINASIPTTLWNMITLPTFKDPTDKEIEEVIQQFKVGFSNEDIENTPL
Ak-dcrla	EKALINASIPTTLWNMITLPTFKDPTDKEIEEVIQQFKNGFSNEDVENTPL
Ap-dcrlb	EKAVINSNIS-----
Ak-dcrlb	EKAVINSNIS-----
Mp	EKALINASIPTTLWNMITLPTFKDPTDKEIEEVIQQFKVGFSNENIENTPL
Rp	EKALINASIPTSLWNMITLPTFKDPTDKEIEEVIQQFKVGFSNDDLENTPL
Ag	EKALINASIPTSLWNMITLPTFKDPTDKEIEEVIQQFKVGFSNEDLESTPL

cons * * : * * : * . *

Ap-dcr1a FVPYNLVTQHSIPDKSIADCVEALIGAYLISCGARGALLFMSWLGI
RVLPT
Ak-dcr1a FVPYNLVTQHSIPDKSIADCVEALIGAYLISCGARGALLFMSWLGI
RVLPT
Ap-dcr1b -----ITQHITNDKSIADCVEALIGAYLISCGTRGALLFMSWLGI
TVLNT
Ak-dcr1b -----ITQHIINDKSIADCVEALIGAYLISCGNRGALLFMSWLGI
RVLNT
Mp FVPYNLVTQHSIPDKSIADCVEALIGAYLISCGARGALLFMSWLGI
RVLPS
Rp FVPYNLVTQHSIPDKSIADCVEALIGAYLISCGARGALLFMSWLGI
RVLPS
Ag FVPYNLVTQHSIPDKSIADCVEALIGAYLISCGARGALLFMSWLGI
KVLPS

cons : * :

Ap-dcr1a LDDSKLGYLKPPSSPLLRNVDDPEGEELTKLMDGFESFEQHLGYHFQDRSYL
Ak-dcr1a LDDSKLGYLKPPSSPLLRNVDDPEGEELTKLMDGFESFEQHLGYRFQD-----
Ap-dcr1b LDDSKLGYLKLPSPPLLRNVNDPEGEELTKLMDGFESFEQHLGYYYFQDRSYL
Ak-dcr1b LDDSKLGYLKPPSSSILHNINDSEGEELTKLMDGFESFEQHLGYCFQDRSYL
Mp LDDSKLGYLKPPSSPLLRNVDDPEGEELIKLMDGFESFEQHLGYRFQDRSYL
Rp LDNSKLGYLKPPSSPLLRNVHDPEGEELAKLMNGFESFEQHLGYRFQDRSYX
Ag LDCSKLGYLKPPSSPLLRNVHNPEGEELTKLMDGFESFEQHLGYHFQDRSYX

cons * * * * * * * * . . . : * : * : . . . * * * * * * * * * * * * :

Ap-dcr1a LQAMTHASYYPN
Ak-dcr1a -----
Ap-dcr1b LQAMTHASYYPN
Ak-dcr1b LQAMTHASYYPN
Mp LQAMTHASYYPN
Rp -----
Ag -----

cons