

Additional File A1: multiple sequence alignment of full-length *Drosophila* RD proteins.

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DmeRun      1 AAAAAAATAAAGGPGPQ-Q-SSNAT-----TASAIAINPAQS-----LANSTHSAASSTGSS-TP
DvirGJ19252 1 QVLAATAAATAAATAATNVSC-GNISTH-----SASSTGSSSTPDN-----NSSNNNNNSSNSS---
DanaGF15983 1 MHLTTTSSNSTASNANNNNNNNNNNT-----TNNNNNS-----SSNNNNNSSQTN
DvirGJ18917* 1 MHLTTTSGNSTASNANNNNNN-----SNNNNN-----TANNNSSSSNN
DseGM22662/63* 1 MHLTTTSSNSTASNANNNNN-----TANNNN-----TSSNNNTTNG
DpseGA13742/42* 1 MHISAEVSSSTTSNQIQQQQQQQQQQQHQL-----HQQHQHQQHQQTTPTATT-TGGSTTKRRNAES
DyakGE17890 1 MHISAEVSSSTTSNQIQQQQQHQQQ--HQQQ-----QQQQQQQLLQQQQQ--TATTTTKRRNAES
DvirGJ19245/46* 1 MHISAEVSSSTTSNQTAHQQQQQQQHQQH-----QQQQQSTQQQLQHTAATTTGSTTKRRNAES
DyakGE17788 1 MVTSSSTSPGTGNGWSSSTGDFKGITALATATGG-----GAGGATQGATASTGATTAEVLA VSSSA-VGSSSPTGGASNG
DpseGA22609 1 SMVTSSSTSPGTGNG-WSTPGDYKGATAATAPAPSVV---TAATASTAAAAAASVMCEVLPSSS-ASVGSSSPTGGASNG
DwilGK25373 1 SMVTSSSTSPGTAGWTTTG DYKVAT-----VSGSGSSAATAVAMCDVLPVSSNA-VGSSSPTGGASNG
DperGL15806 1 QVLAATAAATAAATAAVNSGSSGVSAQSTSLAN-----TSTHSASSTGSS-----TPDISAANTTANSSSSSS
DyakGE15340/41* 1 MHLTTTSSNSTASNANNNNN-----NTANNNN-----TSSNNNTTNG
DgriGH17774/75* 1 MHLTTTSSNSTASNANNNNN-----NNNNNNNNNNNTANNNNSSSSNN
DsimGD15530* 1 MHLTTTSSNSTASNANNNNN-----TANNNN-----TSSNNNTTNG
DmeCG42267 1 MHISAEVSSSTTSNQIQ-----QQQQ-----HQQQQHQLLQHQHQQ--TATTTTKRRNAES
DperGL15800/02* 1 MHISAEVSSSTTSNQIQQQQ-----L-----HQQHQHQQHQQTTPTATT-TGGSTTKRRNAES
DwilGK19810/11* 1 MHISAEVSSSTTSNQIQHQHQQ-----QHNP-----SATATAAAATTTTSTTPTT-TGSSNTKRRNAET
DereGG19698 1 AAAAAAATAAAGGPGPQ-Q-SSNAASA-----TASAIAINPAQS-----LANSTHSAASSTGSS-TP
DmojGI15491 1 QVLAATAAATAAATAATNVSC-GNISTH-----SASSTGSSSTPDNSHHSSNNNNNNSSSTNNNNSSSSNN
DereGG18309 1 MVTSSSTSPGTGNGWSSSTGDFKGITAVATATGG-----GAGGATQGATASTGATAEVMAVSSSA-VGSSSPTGGASNG
DgriGH11831* 1 -MVTSSASPTGTG-WSSPGDYKSAS-----TAVAAAAAATAAASVMCEVLPSSS-ASVGSSSPTGGASNG
DperGL16499 1 SMVTSSSTSPGTGNG-WSTPGDYKGATAATAPAPSVV---TAATASTAAAAAASVMCEVLPSSS-ASVGSSSPTGGASNG
DwilGK19815 1 TQAIAATAAATAAATAAVTQVLAATAAATAAATAAVNSASSTASSTGSSSTPDN-INNSSNNNNNNNNSHSSNNNNSSNN
DereGG17578 1 MHLTTTSSNSTASNANNNNN-----TANNNN-----TSSNNNTTNG
DmojGI11519 1 MHLTTTSSNSTASNANNNNNTNNN-----NNNNNN-----TANNNTASNN
DpseGA25684 1
DanaGF15967 1 MHISAEVSSSTTSNQIQHQHQQQQQQQQHQQ-----QQQQQQQQHQLLQHQHQQTTNTTTKRRNAES
DsiGD17495 1 MHISAEVSSSTTSNQIQQQ-----QQQQ-----HQQQQHQLLQHQHQQ--TATTTTKRRNAES
DgriGH17737/38* 1 MHISAEVSSSTTSNQTHQQQQHQQHQLLQHQH-----QQQQQVTHQQHTTATTTT-TTSSSTTKRRNVES
DseGM22478 1 MVTSSSTSPGTGNGWSSSTGDFKGITAVATATGG-----GASGATQGATASTGATAAEVLA VSSSA-VGSSSPTGGASNG
DanaGF21771 1 MVTSSASPTGTGNGWTS-TGDFKGLTAVPAVVAA-----TGASGGN-----SAGGTAKVLAISSSA-VGSSSPTGGASNG
DvirGJ18742 1 -MVTSSASPTGTG-WSAPADYKSAT-----TAAAAA-----AAAVMCEVIPSSS-ASVGSSSPTGGASNG
DseGM23050 1 AAAAAAATAAATAAAGGPGPQ-Q-SNNVA-----TASAIAINPAQS-----LANSTHSAASSTGSS-TP
DanaGF15970 1 SSHAQVLAATAAATAAATAAISG-----ASSAGSSAANN-----QANTSTHSAASSTGSS-TP
DpseGA14956 1 QVLAATAAATAAATAAVNSGSSGVSAQSTSLAN-----TSTHSASSTGSS-----TPDISAANTTANSSSSSS
DperGL15927 1 ---MANNNNNNSTNNNNNST-----TNNNNNS-----STANNNTSNG
DwilGK20052/54* 1 MHLTTTSSNSTTSSTVNNNN-----NNNNNTS-----SNNNNNTSNG
DseGM23044/45* 1 MHISAEVSSSTTSNQIQHQ-----QQQQ-----HQLLQ-----QQQQQ--TATTTTKRRNAES
DereGG19691 1 MHISAEVSSSTTSNQIHQQQQQQQQQQHQQ-----QQQQQQHQLLQHQHQQTTATTTT-TTKRRNAES
DmeCG34145 1 MHLTTTSSNSTASNANNNNN-----TANNNN-----TSSNNNTTNG
DmojGI15484/86* 1 MHISAEVSSSTTSNQTHQQQQQQQQQQPT-----QQQQ-----HPAAATTTT-TTASTTK-----
DsiGD17500 1 AAAAAAATAAATAAAGGPGPQ-Q-SSNVA-----SASAIAINPAQS-----LANSTHSAASSTGSS-TP
DyakGE17894 1 AAAAAAATAAATAAAGGPGPQQSSNAATATAT-----ATASAIAINPAQS-----LANSTHSAASSTGSS-TP
Dmelz 1 MVTSSSTSPGTGNGWSSSTGDFKGITAVATATGG-----GVGGATQGATASTGATAAEVLA VSSSA-VGSSSPTGGASNG
DsiGD16951* 1
DgriGH17740 1 QVLAATAAATAAATAATNVGHPGNISTH-----SASSTGSSSTPDN-----TNNSSNTSSNNNTSSSSNN
DmojGI14398 1 AMVTSSASPTGTG-WSAPAEYKSAN-----TAVAAATAGGSAAAAMCEVLPSSS-ASVGSSSPTGGASNG

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DmeRun	57	DLSTNNISSSS-----NATTSPONS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DvirGJ19252	54	--SSNNNNNNS-----NS---NAANL-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DanaGF15983	47	GSNNNNNNT-----SSNNNNNNNNNNTEQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DvirGJ18917*	42	NN-TSNTNG-----SNNNSSSSNNN--TEQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DseGM22662/63*	40	SSNN--TSG-----NNNNSSGNN--SNTQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DpseGA13742/42*	66	SSNNNNNNNSNN---NNNNNSTTNNNNNNNNNNNNSSNNAKTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DyakGE17890	61	SASNNNNNTS---TNNNNNNNNNNSTTNNNNNNNN--VTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DvirGJ19245/46*	64	NNNNNNNNNSN---SNNNN---NNNNNNNNNNNTSSSKNKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DyakGE17788	75	TAHSGHSGHTGG-----HSSSTASNNNNIGASNSNSNSN---NNNNNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DpseGA22609	76	TAHSGHSGGGNS---SSTTIATTNNNNNNNNNNNNNNNNNN---NNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DwilGK25373	65	TANSGHSGGGGG---GNGGNSNNNNNNNNNNNNNNNNNN---NNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DperGL15806	67	NSNTTANSTA-----NNGSSNSNS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DyakGE15340/41*	41	SSNNNNTSG-----NNNNNNSSGNNNSNTQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DgriGH17774/75*	47	NNNTSNTNG-----SNNNSSSSNNNNSTEQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DsmGD15530*	40	SSNNN--TSG-----NNNNSSGNN--SNTQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DmeCG42267	52	SASNNNNNNN--TSTNNNNNTNNNNSTTNNNNNNNNVTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DperGL15800/02*	57	SSNNNNNNSSS---NNNNN---NNNNNNNNSSSNAKTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DwilGK19810/11*	60	NNNNNNNNNN---NNNNN---NNNNNNNAKTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DereGG19698	59	DLSTNNISSSS-----NATTSPONS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DmojGI15491	68	NTSSNNNNNS---NS---SNANA-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DereGG18309	75	TAHSGHSGHTGG-----HSSSSASHNNNNIGASNSNSNSNNNNNNNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DgriGH1831*	61	TANSAHSASGNK-----NNSNNNNNN---NNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DperGL16499	76	TAHSGHSGGGGQ---QQHHYCHHHQHNNN---NNNNN---NNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DwilGK19815	80	NNNNSSSTSSS---ASSSSASSS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DereGG17578	41	SSNNN--TSGG---NNNNNNSSGNN--SNTQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DmojGI11519	44	NNNNSNTNG-----SNNNNSSSSNNNNTEQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DpseGA25684	1	-----MTSDILAERTLGDFLTEHPGELVRTSSPLF
DanaGF15967	66	SSNNNNNNNTTNNNKNNNNNSNNNNNNNNNTNNNNNNNNVTKAVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DsiGD17495	54	SASNNNNNN--TSTNNNNNTNNNNSTTNNNNNNNN--VTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DgriGH17737/38*	64	NNNNNSTTNN---NNNNN---NNNNN---SSKSKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DseGM22478	75	TAHSGHSGHTGG-----HSSSTASNNNNIGASNSN---NNNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DanaGF21771	70	TAHSGHSGST-----TSNSGNNNNNSNSNNNSNSN---NNNNALHQDLKMERLQKRQOEHPGELVRTSNPYF
DvirGJ18742	60	TANSTHSGS-----NKNNNNNNNNSRN--NNNNNS---NNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DseGM23050	57	DLSTNNISSSS-----NATTSPONS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DanaGF15970	51	DLNTANISTSTTSSSSSTASSANNSSSTNS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DpseGA14956	67	NS--NTANNTA-----NNGSSNSNS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DperGL15927	38	TNNNN-----TNNNNTEQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DwilGK20052/54*	44	SSNNNNNNNS-----SSNNNNNNNNNNTEQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DseGM23044/45*	49	SASNNNNN-----TNNNNNSTTNNNNNNNN--VTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DereGG19691	65	SASNNNNNTS--TNNNNNTSNNNNNNNNNNSTTNNNNNN--VTKPVDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHV
DmeCG34145	40	SSNNN--TSG-----NNNNSSGNN--SNTQNTPTTPAQLLNEAYTKMSTDILAERTLGDFLTEHPGELVRTSSPLF
DmojGI15484/86*	53	-----LDTSPLYTPENLERTVDVLLAEHPGELVKTGSPHI
DsiGD17500	57	DLSTNNISSSS-----NATTSPONS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DyakGE17894	64	DLSTNNISSSS-----NATTSPONS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
Dmelz	75	TAHSGHSGHTGG-----HSSSTASNNNNIGASNSNSN---NNNAVHQDLLMERLQKRQOEHPGELVRTSNPYF
DsiGD16951*	1	-----LVRTSNPYF
DgriGH17740	62	SSNSNNNNSSS-----NTSAASAANS-----AKMPSMTDMFASLHEMLQBYHGELAQTGSPSI
DmojGI14398	65	TANSGHSGGNKININNNNNNSNNNNNNNTNSRNNNNNS---NNAVHQDLLMERLQKRQOEHPGELVRTSNPYF

DmeRun	110	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DvirGJ19252	103	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DanaGF15983	118	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DvirGJ18917*	111	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DseGM22662/63*	107	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DpseGA13742/42*	143	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKES	QVD		
DyakGE17890	136	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DvirGJ19245/46*	137	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DyakGE17788	146	LCSALPAHWSNKTLP	MAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DpseGA22609	148	LCSALPSHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNCTAQMKNQAKFNDLRFVGRSGRGKSFTLTI			
DwilGK25373	132	LCSALPSHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNCTAQMKNQAKFNDLRFVGRSGRGKSFTLTI			
DperGL15806	120	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DyakGE15340/41*	113	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DgriGH17774/75*	119	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGR-----	
DsimGD15530*	108	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDL-----SVGKSFTLTI	
DmeCG42267	131	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DperGL15800/02*	128	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGR--KDS	PVA		
DwilGK19810/11*	119	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DereGA25698	112	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DmojGI15491	119	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DereGG18309	148	LCSALPAHWSNKTLP	MAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DgriGH11831*	116	LCSALPTHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRLR	CTQWSRNGSDRRR		
DperGL16499	143	LCSALPSHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DwilGK19815	136	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DereGG17578	114	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DmojGI11519	115	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DpseGA25684	31	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DanaGF15967	146	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DsiGD17495	130	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DgriGH17737/38*	128	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DseGM22478	140	LCSALPAHWSNKTLP	MAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DanaGF21771	137	LCSALPSHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNCTAQMKNQAKFNDLRFVGRSGRGKSFTLTI			
DvirGJ18742	122	LCSALPSHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DseGM23050	110	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DanaGF15970	115	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DpseGA14956	118	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DperGL15927	97	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DwilGK20052/54*	116	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGASNT	HWL
DseGM23044/45*	116	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DereGG19691	143	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DmeCG34145	108	VCTVLP	PHWSNKTLPVAFKVVS	SLGDI	MDGTMVTIRAGNDENYCAELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI	
DmojGI15484/86*	89	VCTVLP	THWSNKTLPVAFKVLALGEVMDGTIVTIRAGNDENFCGELRNCTAVMKNQAKFNDLRFVGRSGRGKSFTLTI			
DsiGD17500	110	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DyakGE17894	117	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
Dmelz	142	LCSALPAHWSNKTLP	MAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DsiGD16951*	10	LCSALPAHWSNKTLP	MAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			
DgriGH17740	116	LCSALPNHWSNKS	LPGAFKVTALDDVPDGTIVSIKCGNDENYCGELRNCTTTMKNQAKFNDLRFVGRSGRGKSFTLTI			
DmojGI14398	140	LCSALPSHWSNKTLP	LAFKVVALAEVGDGTIVTIRAGNDENCCAELRNFTTQMKNDVAKFNDLRFVGRSGRGKSFTLTI			

DmeRun	190	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAAQAAQVHHHPAL
DvirGJ19252	183	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQQA--AAAVHHHPAL
DanaGF15983	198	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DvirGJ18917*	191	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DseGM22662/63*	187	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DpseGA13742/42*	223	VIPTNQHEIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DyakGE17890	216	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DvirGJ19245/46*	217	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLP-----
DyakGE17788	226	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFPSTKALHELETLRSAKVAAVTTAAAAA
DpseGA22609	228	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFP--KTLHELETLRSAKVAATTTAAAAA
DwilGK25373	212	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYR-ICLT-----LGFP--KTLHELESLSAKVAATTTAVASV
DperGL15806	200	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAA-QAAVHHHPAL
DyakGE15340/41*	193	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DgriGH1774/75*	191	-----ATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DsimGD15530*	182	TVSTNPPHIATYNKAIKVTVDGPREPRSKTSKQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DmeCG42267	211	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DperGL15800/02*	207	VVPTNKNEIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DwilGK19810/11*	199	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPDVS-----
DereGD15698	192	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAAQAAQVHHHPAL
DmojGI15491	199	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQQA--AAAVHHHPAL
DereGG18309	228	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFPSTKALHELETLRSAKVAAVTTAAAAA
DgriGH11831*	196	RMDRLDQQRVDQAAEARLLSSQVAHQ-----IHKFLN-RQNGKLAEIAKQVADF
DperGL16499	223	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFP--KTLHELETLRSAKVAATTTAAAAA
DwilGK19815	216	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAA--AAVHHHPAL
DereGG17578	194	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DmojGI11519	195	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DpseGA25684	111	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DanaGF15967	226	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DsiGD17495	210	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DgriGH17737/38*	208	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DseGM22478	220	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFPSTKALHELETLRSAKVAAVTTAAAAA
DanaGF21771	217	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFP--KSLHELEALRR--AVTTAAAAA
DvirGJ18742	202	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPPGGPOYRAICLGQRPIIDGFP--KTFHELETLRSAKVAATTTAAAAA
DseGM23050	190	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAAQAAQVHHHPAL
DanaGF15970	195	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAAQAAQVHHHPAL
DpseGA14956	198	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAA-QAAVHHHPAL
DperGL15927	177	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DwilGK20052/54*	196	SSCTTPTSAQFNNFALGFTCSSPMLPSTASDLQHLSSLVGSTSGQMTHHSLLCATGQTSISSTVNGASANVHSSQNGA
DseGM23044/45*	196	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DereGG19691	223	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DmeCG34145	188	TVSTNPPHIATYNKAIKVTVDGPREPRSKT-RQQQQFHFAFGQRFHFSTDPDLSGFR-MPPIG-----NCQS-----A
DmojGI15484/86*	169	VISTNPIQIATYTKAIKVTVDGPREPRSKV-RHQGFHPFAFG--PQRFQPDPLMAGLPFKLPGFAHLVGMShLHAPDWR
DsiGD17500	190	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAAQAAQVHHHPAL
DyakGE17894	197	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQAAAQAAQVHHHPAL
Dmelz	222	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFPSTKALHELESLSAKVAAVTTAAAAA
DsiGD16951*	90	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPHYRAICLGQRPIIDGFPSTKALHELETLRSAKVAAVTTAAAAA
DgriGH17740	196	TIATYFVQIASYSKAIKVTVDGPREPRSKOS--YGYPHPGAFNPFMLNPAWLDAAYMTYGYADYFRQQA--AAAVHHHPAL
DmojGI14398	220	TVATSEPPQVATYAKAIKVTVDGPREPRSKTSPTGGPOYRAICLGQRPIIDGFP--KTFHELETLRSAKVAATTTAAAAA

DmeRun	269	AKSSASSVSPNPNPSVATSS-----SSAVQP-----SEYPHPAAAVAAAA-----CQPAAMMPSPPGAAPA
DvirGJ19252	261	SKAATSPNGSASGVVSPGTA-----AAGAAVPAAAA-----ADYPPPPSSVGVGVG-----AVAPGSMMPSPPGGPPA
DanaGF15983	264	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DvirGJ18917*	257	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DseGM22662/63*	253	RYTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DpseGA13742/42*	300	AHMAIGGRPAFTTAAFFFCCHH-----AAFPASGLRGLSDGQQQQQHQQQQ--HQQLATVGAHSTTSPEGSPTTTT
DyakGE17890	293	AHMAIGGRPAFTTAAFFFCCHH-----AAFPASGLRGLSD-----NQHQQQQQ--QLATVGAHSTTSPEGSPTTTT
DvirGJ19245/46*	276	-----DNOQLPTVGAHSTTSPEGSPTTTT
DyakGE17788	306	ATAASAANAVAAAAAVTPTGGGVG---GVGGVAGGQAGVGVGAGLVQQLSSYSSP-----NSTINSDCQVYKPN
DpseGA22609	306	ATAATAATAVAAAAASVALPGSTTTTG---GVGVGVGVGSGSSGSGAGLVQQLSSYSSP-----NSTINSDCQVYKPN
DwilGK155373	285	A-----AASVVTAAAVSTTSG-----STSTSLVQQLSSYSSS-----NSTINSDCPGYKPN
DperGL15806	278	SKASPSSSSSIVSPSASAPASSG-----AGNGAAGP-----ADYHHVSQITPPPSRG-TNCRWPTGCHDALAAQEPL
DyakGE15340/41*	259	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DgriGH17774/75*	248	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DsimGD15530*	249	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVPAVLPDSTA
DmeCG42267	288	AHMAIGGRPAFTTAAFFFCCHH-----AAFPASGLRGLSD-----SQHQQQQQQHQLATVGAHSTTSPEGSPTTTT
DperGL15800/02*	284	AHMAIGGRSACFPAGPFFCCHH-----AAFPASGLRGLSDGQQQQQHQQQQQHQLATVGAHSTTSPEGSPTTTT
DwilGK19810/11*	261	-----QEQQQQQQQHQLATVGAHSTTSPEGSPTTAPT
DereG19698	271	AKSSASSVSPNPNPSVATSS-----SSAVQP-----SEYPHPAAAVAAAA-----CQPAAMMPSPPGAAPA
DmojGI15491	277	SKAATSPNGSNSGVISPGAGGAAMPTAASAVVAAAA-----ADYPPVPVGVGVGVG---VVPASMMPSPPGGPPA
DereG18309	308	ATAASAANAVAAAAAVAPAGGGVA---GGVAGG-----AGAGLVQLSSYSSP-----NSTINSDCQVYKPN
DgriGH11831*	246	E-----RESN-----ALTEELGEVPSKQ-----LCPL-ADWRWLSSQ
DperGL16499	301	ATAATAATAVAAAAASVALPGSTTTGGVGVGVGVGVGVGSGSSGSGAGLVQQLSSYSSP-----NSTINSDCQVYKPN
DwilGK19815	293	AKTSPGGGAPPPSGGGGAP-----TPP-----DYHHVSQITPPAPAG-----APSNQPATGSATALA
DereG17578	260	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DmojGI11519	261	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DpseGA25684	177	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DanaGF15967	303	AHMAIGGRPAFTTAAFFFCCHHAAAAAAAFPTASGLRGLSDA-----DNQQQQQQ--QQQQQLAHSSTTSPEGSPTTTT
DsiGD17495	287	AHMAIGGRPAFTTAAFFFCCHH-----AAFPASGLRGLSD-----SQHQQQQQ--HLATVGAHSTTSPEGSPTTTT
DgriGH17737/38*	285	AHMAIGGRPAFTTAAFFFCCHH-----HGAAFPATAA-----SGIRLSENQPLATVGAHSTTSPEGSPTTTT
DseGM22478	300	ATAASAANAVAAAAAVTPTGGGGG---AGGVAGG-----AGAGLVQQLSSYSSP-----NSTINSDCQVYKPN
DanaGF21771	293	ATAATAATAVAAAAAVSPAGGGGG---GTVGVGVG-----SGAGLVQQLNSYSSP-----NSTINSDCQVYKPN
DvirGJ18742	280	A-----VSVASAGNTLTTN-----ASIAQQLGSSYSSS-----NSTINSDCQGYKPN
DseGM23050	269	AKSSASSVSPNPNPSVATSS-----SSAVQP-----SEYPHPAAAVAAAA-----CQPAAMMPSPPGAAPA
DanaGF15970	274	AKAAAQVSPVSGSNSIPT-----AASVGAGPGAGNVAPPPTGGDYHSGGA---PCQPAAMMPSPPGAAPA
DpseGA14956	276	SKASPSSSSSIVSPSASAPASSG-----AGNGAAGP-----ADYHHVSQITPPPSGAPTAACQPAAMMPSPPGAAPA
DperGL15927	243	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DwilGK20052/54*	276	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DseGM23044/45*	273	AHMAIGGRPAFTTAAFFFCCHH-----AAFPASGLRGLSD-----SQHQQQQQ--HLATVGAHSTTSPEGSPTTTT
DereG19691	300	AHMAIGGRPAFTTAPFFCCHH-----AAFPAGGLRGLSD-----SQHQQQQQQHQLATVGAHSTTSPEGSPTTTT
DmeCG34145	254	SNTHWGYGSAASAYSPLYASSG-----LSSCTTPTSQFNNPALGFTCSSNDQNNQDFGGATNRDCVP-MLPDSTA
DmojGI15484/86*	246	AHMAIGGRPAFTTAAFFFCCHH-----HGASFPGGAT-----GGLRGLSDNQQMATVGAHSTTSPEGSPTTTT
DsiGD17500	269	AKSSASSVSPNPNPSVATSS-----SSAVQP-----SEYPHPAAAVAAAA-----CQPAAMMPSPPGAAPA
DyakGE17894	276	AKSSASSVSPNPNPSVATSS-----SSAVQP-----AEYHPHPAAAVAAAAA---ACQPAAMMPSPPGAAPA
Dmelz	302	ATAASAANAVAAAAAVTPTGGGGGV---AAGGVAGG-----AGAGLVQQLSSYSSP-----NSTINSDCQVYKPN
DsiGD16951*	170	ATAASAANAVAAAAAVTPTGGGGG---AGGVAGG-----AGAGLVQQLSSYSSP-----NSTINSDCQVYKPN
DgriGH17740	274	SKAATSPNGSVSGVSPAMP-----NAGAS-----SDYPPPMPSASSSSSS---IVPPASMMPSPPGGAPA
DmojGI14398	298	A-----VSVASAGNALTNTN-----ASIAQQLGSSYSSS-----NSTINSDCQGYKPN

DmeRun 325 --TPYAIPOPFNHFVAAAAAKA-----ATPHAFHPYNFA--AAAGLRARN--AALHHQSEP-----VHVSPAS
DvirGJ19252 324 --SAYAMPOPFNHFVAAAAAAHQNQ----KSTPHAFHPYNFA--AAAGLRARNAAALHHGGLSA--EAAHMSPAS
DanaGF15983 335 SDLDQHLSSLVGSTSCQMTHHSL-----LGATGQTSISSTVNGASGGGAGGAGGGAGAAGAGGGGNSILVP
DvirGJ18917* 328 SDLDQHLSSLVGSSSQMSHHSL-----LGASGQTSISSTVNGAGAGSGAT-----AGSATAGGGGGANSILVP
DseGM22662/63* 324 SDLDQHLSSLVGSTSCQMTHHSL-----LGAGGQTSISSTVNGASGGGSAG--AGTAGGGAGSGGGAGGAGGNSILVP
DpseGA13742/42* 373 GT----LSAFVQPAIHCPPLGS-----PRSPPTILTSLQHDNNNN--SSNIDAGFESDSISVTGSPRKSISPLTH
DyakGE17890 362 SG--TQLSAFVQPPMTSSPP-----PVTSLQHDNNNNNNNNNNSSSHIDAGFESDSISVTGSPRKSLSPLTH
DvirGJ19245/46* 303 AT----LSAFVQPPA-CNASA-----GGSPLTLTSLMQHHDNNNNNNSSNIDAGFESDSISVTGSPRKSIS-LTH
DyakGE17788 377 APHIQGADMMGAGEWT-GSSSS-----AAAYYHSHA-HHPH-HHHAHHLQ-----HQMLPPPPPPPA
DpseGA22609 377 APHIQETDLMGAGEWTGSSSS-----AAAYYHSHAHHHPH-HH-HAHAHAHHAHHLQHMLPPPPPPPA
DwilGK15373 333 APHIQETE---SGEWTGSASSS-----NVAYTVGVGVPTTHHATH---HTHPHSHSHAHAHHLQH-HHQMTPPPPPPA
DperGL15806 344 RQPPYAIPOPFNHFVAAAAAAQQQQHHAKSTPHAFHPYNFA--AAAGLRARNAAAVLHHGGDATG---ISHISPAS
DyakGE15340/41* 330 SDLDQHLSSLVGSTSCQMTHHSL-----LGAGGQTSISSTVNGASGGGSAG--AGTAGGGAGSGGGAGGAGGNSILVP
DgrIGH17774/75* 319 SDLDQHLSSLVGSTSCQMTHHSL-----LGASGQTSISSTVNGASAGSGAT-----AGSAAGAGSGGGGNSILVP
DsimGD15530* 321 SDLDQHLSSLVGSTSCQMTHHSL-----LGAGGQTSISSTVNGASGGGSAG--AGTAGGGAGSGGGAGGAGGNSILVP
DmeCG42267 359 SG--TQLSAFVQPPMTSSPP-----PVTSLQHDNNNNNNNNNNSSSHIDAGFESDSISVTGSPRKSLSPLTH
DperGL15800/02* 359 GT----LSAFVQPAIHCPPLGS-----PRSPPTILTSLQHDNNNN--SSNIDAGFESDSISVTGSPRKSISPLTH
DwilGK19810/11* 294 TT-TTSSAFVQPNSSSLGLGLGVGVGLGAGSPTVLTSLSSQDDNN--HNIDAGFESDSISVTGSPRKSLS-LTQ
DereGA19698 329 --TPYAMPOPFNHFVAAAAAKA-----ATPHAFHPYNFA--AAAGLRARN--AALHHQSEP-----VHVSPAS
DmojGI15491 348 --SAYAMPOPFNHFVAAAAAAHQSQ----KATPHAFHPYNFA--AAAGLRARNAAALHHGGLSA--ETAHMSPAS
DereGG18309 371 APHIQGADMMGAGEWT-GSSSS-----AAAYYHSHA-HHP-----HHLQ-----HQMLPPPPPPPA
DgrIGH11831* 277 ALSVLQQTQ-----
DperGL16499 375 APHIQETDLMGAGEWTGSSSS-----AAAYYHSHAHHHPH-HHA-HAHAHHAHHAHHLQHMLPPPPPPPA
DwilGK19815 345 -----STPQQPQHHPHAASSGMMP-----SPPGAAAVFPV-----ATAAAA
DereGG17578 331 SDLDQHLSSLVGSTSCQMTHHSL-----LGAGGQTSISSTVNGASGGGSAG--AGTAGGGAGSGGGAGGAGGNSILVP
DmojGI11519 332 SDLDQHLNSLP-----
DpseGA25684 248 SDLDQHLSSLVGSTSCQMTHHSL-----LGATGQTSISSTVNGASAGSAGT--GGTAGGAGS-----GAGGNSILVP
DanaGF15967 375 TSGHTQLSAFVQPPICSSPV-----LAPLTLQ-DNENDNNNTNNNSNIDAGFESDSISVTGSPRKSLSPLTH
DsiGD17495 355 SG--TQLSAFVQPPMTSSPP-----PVTSLQHDNNNNNNNNNNSSSHIDAGFESDSISVTGSPRKSLSPLTH
DgrIGH17737/38* 349 AT----LSAFVQPAA-CNASV-----GSSPLTLTSLMQHHDNNNNNNSSNIDAGFESDSISVTGSPRKSIS-LTH
DseGM22478 364 APHIQAAEMMGAGEWTNGSSSS-----AAAYYHSHA-HHPH-HHHAHHLQ-----HQMLPPPPPPPA
DanaGF21771 358 APHIQETDLMGAGEWT-GSTST-----AAAYYHSHAHHHPH-HHPH-HPHA-----HLHQHMLPPPPPPPA
DvirGJ18742 322 APQIQETDLIGAAEWTGSASSGANVAYPVGVGVGVYHHAHSHTHSHTHGSAHH---HHAHHLQHMLPPPPPPPA
DseGM23050 325 --TPYAIPOPFNHFVAAAAAKA-----ATPHAFHPYNFA--AAAGLRARN--AALHHQSEP-----VHVSPAS
DanaGF15970 339 --AAYAMPOPFNHFVAAAAAAHQHP---KATPHAFHPYNFATAAAVGLRARN--AALHHQSEAQVPLNHVSPAS
DpseGA14956 343 --AAYAIPOPFNHFVAAAAAAQQQQHHAKSTPHAFHPYNFA--AAAGLRARNAAAVLHHGGDATG---ISHISPAS
DperGL15927 314 SDLDQHLSSLVGSTSCQMTHHSL-----LGATGQTSISSTVNGASAGSAGT--GGTAGGAGS-----GAGGNSILVP
DwilGK20052/54* 347 SDLDQHLSSLVGSTSCQMTHHSL-----LGATGQTSISSTVNGASAGGATAG-SVTGGGTAGTGGSGGGATNSILVP
DseGM23044/45* 342 SG--TQLSAFVQPPMTSSPP-----PVTSLQHDNNNNNNNNNNSSSHIDAGFESDSISVTGSPRKSLSPLTH
DereGG19691 371 SG--TQLSAFVQPPMTSSPP-----PVTSLQHDNNNNNNNNNNISSHIDAGFESDSISVTGSPRKSLSPLTH
DmeCG34145 325 SDLDQHLSSLVGSTSCQMTHHSL-----LGAGGQTSISSTVNGASGGGSAG--AGTAGGGAGSGGGAGGAGGNSILVP
DmojGI15484/86* 310 AT----LSAFVQPPA-CNASA-----GGSPLMLTSLQHDNNNNNNSSNIDAGFESDSISVTGSPRKSIS-LTH
DsiGD17500 325 --TPYAMPOPFNHFVAAAAAKA-----ATPHAFHPYNFA--AAAGLRARN--AALHHQSEP-----VHVSPAS
DyakGE17894 335 --TPYAMPOPFNHFVAAAAAKA-----ATPHAFHPYNFA--AAAGLRARN--AALHHQSEP-----VHVSPAS
Dmelz 368 APHIQAAEMMGAGEWTNGSSSS-----AAAYYHSHA-HHPH-HHHAHHLQ-----HQMLPPPPPPPA
DsiGD16951* 234 APHIQDLIQEPR---VSKAST-----TTAFFAIT-----
DgrIGH17740 332 --AAYAMPOPFNHFVAAAAAAHQSQ----KSTPHAFHPYNFA--AAAGLRARNAAALHHGGVP---ADAHMSPAS
DmojGI14398 340 APQIQETDLIGAAEWTGSASSGANIAYPVGVGVGVYHHAHHTHSHSHSHSHSHSHSHAHHHHHLQHMLPPPPPPPA

DmeRun	383	SRPSSSSPT-----	-QQHVLLK NT	
DvirGJ19252	394	SRPSSSSPT--PTPTS-----	-MPHVLLK NT	
DanaGF15983	409	RYHTNTSN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLSTNTPNLGS----	-TCAAGANGG
DvirGJ18917*	393	RYHTNASN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLSTNTPNLGS-----	-CSGAGASN
DseGM22662/63*	396	RYHTNASN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLTTNTPNLGS-----	-TAGGGGAANG
DpseGA13742/42*	437	DEEEAADAEEAEAAEAEAPD----	GEAAEAAGTQLSGDARSLATISGRSAAGSL-----	TETAPGSG GAFTAI IQ
DyakGE17890	428	DEE---EAEAEAEADADAEA-----	EEAEVGGLSLNGGGIQTTHSESSPGS-----	-GGAFTAI IQ
DvirGJ15845/46*	368	DEEEDPD-----	EAGRSRSPDLLSADASSVATLPAPGS-----	-GGAFTAI IQ
DyakGE17788	433	AAPVSVGVGGNGATMG--MGMGVG---	MGMNHYG---GGYDSANSEAGQYAA-----	-HLPEVLPE HG
DpseGA22609	442	AAPVTNGAG--GMGVGVGMGVGMGMVGMMSMNHYG--	SGYETASSEADAGNYA-----	-HLPEVLPE HG
DwilGK25373	403	ATPVAMGGQASGMGMGMGMGMGMTNMNHYGSTMGGYDASY-----	DTS-----	-HLP TVLQD HG
DperGL15806	419	SRPSSSSPT-----	-QQHVLLK NT	
DyakGE15340/41*	402	RYHTNASN-EYNVHSSQNXXXXVHSSQNGPRSLSDSSQAESPQVEDLTTNTPNLGS-----	-TAGGGGAANG	
DgriGH17774/75*	384	RYHTNASN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLSTNTPNLGS-----	-CSGGGATN
DsimGD15530*	393	RYHTNASN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLTTNTPNLGS-----	-TAGGGGAANG
DmcCG42267	425	DEEEAEEAEAEAEAEAEAE-----	EEAEVGGLSRNGGGIQTTHSESSPGS-----	-GGAFTAI IQ
DperGL15800/02*	423	DEEEAEEADAEEAEAEAEAEAPD----	GEAAEAEPGTQLSGDARSLATISGRS-----	-GGAFTAI IQ
DwilGK19810/11*	370	EDE-----	EADADGDGTEAESTLLGHQTEFSSGS-----	-GGAFTAI IQ
DereGG19698	387	SRPSSSSPT-----	-QQHVLLK NT	
DmojGI15491	418	SRPSSSSPT--PTPTS-----	-MPHVLLK NT	
DereGG18309	422	AAPVSVGVGGNGATMG--MGMGMGVGMGMGNHYG---	GGYDSANSEAGQYAA-----	-HLP TVLPE HG
DgriGH11831*	285	-----	-----	-AKYLETHS
DperGL16499	442	AAPVTNGAGGMGVGVGMGVGMGMVGMMSMNHYG--	SGYETASSEADAGNYA-----	-HLPEVLPE HG
DwilGK19815	382	AAAAMAMPQ-----	-----	-FFPN
DereGG17578	403	RYHTNASN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLTTNTPNLGS-----	-TAGGGGAANG
DmojGI11519	343	-----	-----	-TAGGGGAANG
DpseGA25684	315	RYHTNASN-DYNVHSSQN-----	GPRSLSDSSQAESPQVEDLSTNTPNLGSG-----	-TCGGGGGAN
DanaGF15967	445	DEE-----ETDSIS-----	REENTN---HNNGMAGSUG-ESSPGS-----	-GGAFTAI IQ
DsiGD17495	421	DEE---EAEAEAEAEAEAEAE-----	EEAEVGGLSLNGGGIQTTHSESSPGS-----	-GGAFTAI IQ
DgriGH17737/38*	414	DDEESQPNDPEAETDAEA-----	EAGRSRSPDLLSADASSVATPTEPAPGS-----	-GGAFTAI IQ
DseGM22478	421	AAPVSVGVGGNGATMG--MGMGVGV--	GMGMNHYG---GGYDSANSEAGQYAA-----	-HLPEVLPE HG
DanaGF21771	420	AAPVSV--TGNGATMG--VGMGMGVGMGMGMANP-Y	GGYDATNSSEAGNYA-----	-HLPEVLPE HG
DvirGJ18742	398	AA-----	PVPVPVATASAMNHYSSAMGGYDTTTHDAGNY-----	-HISSVLPD H-
DseGM23050	383	SRPSSSSPT-----	-QQHVLLK NT	
DanaGF15970	410	SRPSSSSPT-----	-QQHVLLK NT	
DpseGA14956	416	SRPSSSSPT-----	-QQHVLLK NT	
DperGL15927	381	RYHTNASN-DYNVHSSQN-----	GPRSLSDSSQAESPQVEDLSTNTPNLGSG-----	-TCGGGGGTAN
DwilGK20052/54*	420	RYHTNASNNNDYNVHSSQN-----	GPRSLSDSSQAESPQVEDLSTNTPNLGG-----	-SETGAANGG
DseGM23044/45*	408	DEE---EAEAEAEAEAEAEAE-----	EEAEVGGLSLNGGGIQTTHSESSPGS-----	-GGAFTAI IQ
DereGG19691	437	DEE---EAEAEAEAEAEAEAE-----	EEAEVGGLSLNGGGIQTTHSESSPGS-----	-GGAFTAI IQ
DmeCG34145	397	RYHTNASN-EYNVHSSQN-----	GPRSLSDSSQAESPQVEDLTTNTPNLGS-----	-TAGGGGAANG
DmojGI15484/86*	375	DEEEDPD-----	EAGRSRSPDLLSADASSVATLVPAFGAGSGALDGTGTSGSGGGG GAFTAI IQ	
DsiGD17500	383	SRPSSSSPT-----	-QQHVLLK NT	
DyakGE17894	393	SRPSSSSPT-----	-QQHVLLK NT	
Dmelz	425	AAPVSVGVGGNGATMG--MGMGVGV--	GMGMNHYG---GGYDSANSEAGQYAA-----	-HLPEVLPE HG
DsiGD16951*	-----	-----	-----	-----
DgriGH17740	401	SRPSSSSPTPMPTPTA-----	-----	-TPHVLLK NT
DmojGI14398	420	AAPV-----	PVPVPVGTASAMNHYSSAMSGETTTTHDAANY-----	-HISTVLPD H

DmeRun	402	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	F	DL	DKSLD	-----
DvirGJ19252	418	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DanaGF15983	464	AANAGSGGA	AGT	GSSSGA	-----	G	AAI	PAGNP	-S	MLGANQN	FPGIVNQAQHAS-ASAYGGGAGVG
DvirGJ18917*	447	GGAANGAASA	AGAGSG	ASA	-----	G	ASAGAGNP	-A	MLGANQN	FPGIVNQAQHAS-ASAYGGGAGVG--	
DseGM22662/63*	451	GAGSNAGSGA	AGSG	AGGAG	-----	V	ASSAVGNP	-A	MLGANQN	FPGIVNQAQHAS-ASAYGG--GTGV-	
DpseGA13742/42*	505	RS-KNPSELF	GGFA	ACAGN	-----	H	FAP-SHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DyakGE17890	481	RSGKNPTELF	GGFA	ACAGN	-----	H	FAHSGHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DvirGJ19245/46*	412	RS-KNPSELF	GGFA	ACAG	-----	H	FAPAAHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DyakGE17788	489	HGFATDPYQT	AG	-Y	CGGN	-----	T	AGGS	-----	A	SKSELDYGGGYNQAWSNGYQNY-QYGSCLATA--
DpseGA22609	501	HGFATDPYQT	AGGY	CTCAGA	-----	G	KSDLENL	GGGGYGAG	---	G	YNNAAAWSNGYNNY-QYCNCSAS--A
DwilGK25373	462	HGIATDPYQM	AGGY	CSASGNPG	-----	K	TTELETLN	VTGYGSGAGSGYNN	--	A	WSNGYNNYPQYGS
DperGL15806	438	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DyakGE15340/41*	467	GAGSNAGSGA	AGSG	AGGAG	-----	G	ASSAVGNP	-S	MLGANQN	FPGIVNQAQHAS-ASAYGG--GTGV-	
DgrIGH17774/75*	438	GGAANGSGSA	AVAGSV	ASS	-----	V	ASAGAGNP	-G	MLGTNQN	FPGIVNQAQHAS-ASAYGGGAGVG--	
DsimGD15530*	448	GAGSNAGSGA	AGSG	AGGAG	-----	G	ASSAVGNP	-K	GLGANQN	FPGI	-----
DmeCG42267	480	RSGKNPTELF	GGFA	-AGGN	-----	H	FAPSGHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DperGL15800/02*	470	-----	-----	-----	-----	L	FMO	SP	-L	LPQSSQ	WLYTQLYGSYS
DwilGK19810/11*	408	RS-KNHTDLF	GGFS	NC	SASGAAGGGGAGNFP	PSSTPHTPTFNPALAAQLFLOSP	A	LPQSSQ	WLYS	QLYGSYS	TDHLPW
DereGG19698	406	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSLD	-----
DmojGI15491	442	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DereGG18309	482	HGFATDPYQT	AG	-Y	CGGN	-----	A	AGGS	-----	A	SKSELDYGGGYNQAWSNGYQNY-QYGSCLATA--
DgrIGH11831*	293	HSLLPKLVQ	AST	-----	-----	-----	-----	-----	-----	-----	-----
DperGL16499	503	HGFATDPYQT	AGGY	CTCAGA	-----	G	KSDLENL	GGGGYGAG	---	G	YNNAAAWSNGYNNY-QYCNCSAS--A
DwilGK19815	395	-----	-----	-----	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DereGG17578	458	GAGTNAGSGA	AGSG	AGGAG	-----	G	AA	AVGNP	-S	MLGANQN	FPGIVNQAQHAS-ASAYGG--GTGV-
DmojGI11519	343	-----	-----	-----	-----	A	GRQRN	FPGIVNQAQHAS-ASAYGG--G	V	G	V
DpseGA25684	371	GGAANGGAGA	AGAG	GSASSA	-----	G	AAA	AVGVGNP	G	AMLGANQN	FPGIVNQAQHAS-ASAYGG--GAG--
DanaGF15967	485	RS-KNPTELF	GGFA	ACSGN	-----	H	FPP-AHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYS
DsiGD17495	474	RSGKNPTELF	GGFA	-AGGN	-----	H	FAPSGHS	FNPAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DgrIGH17737/38*	470	RS-KNPTELF	GGFA	ACAAS	-----	H	FAPAAHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DseGM22478	479	HGFATDPYQT	AG	-Y	CGGN	-----	T	GGGS	-----	A	SKSELDYGGGYNQAWSNGYQNY-QYGSCLATA--
DanaGF21771	480	HGFATDPYQT	AG	-Y	TGTGGVA	-----	T	GGGNA	VGNAGGSKSELDYGGGYNQAWSNGYQNY-QYGS	CSATS--	
DvirGJ18742	442	-GFSADPYQT	AAAS	YCGTS	-----	S	KSDLESIN	-ASYGATP	-A	AYNNPAAWSNGYNNY-QYGS	CSATA-A
DseGM23050	402	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSLD	-----
DanaGF15970	429	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DpseGA14956	435	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DperGL15927	437	GGAANGGAGA	AGG	GSASSA	-----	G	AAA	AVGVGNP	G	AMLGANQN	FPGIVNQAQHAS-ASAYGG--GAG--
DwilGK20052/54*	476	SGATGGGTAGT	CGS	GISSPG	-----	S	GA	VAGG	VASMLVGSNQ	NFQA	HVSQHV
DseGM23044/45*	461	RSGKNPTELF	GGFA	-AGGN	-----	H	FAPSGHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DereGG19691	490	RSGKNPTELF	GGFA	-AGGN	-----	H	FAPSGHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DmeCG34145	452	GAGSNAGSGA	AGSG	AGGAG	-----	G	ASSAVGNP	-A	MLGANQN	FPGIVNQAQHAS-ASAYGG--GTGV-	
DmojGI15484/86*	435	RS-KNPSELF	GGFA	AGG	-----	H	FAPTAHS	FNPALAAQLFLOSP	-L	LPQSSQ	WLYTQLYGSYS
DsiGD17500	402	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSLD	-----
DyakGE17894	412	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSLD	-----
Dmelz	483	HGFATDPYQT	AG	-Y	CGGN	-----	T	GGGS	-----	A	SKSELDYGGGYNQAWSNGYQNY-QYGSCLATA--
DsiGD16951*	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
DgrIGH17740	427	SIETSSIHEQSA	SD	DSDD	-----	Q	DVVKSE	Y	EL	DKSID	STRSSP--
DmojGI14398	466	-GFSADPYQT	AAAS	YCGTS	-----	S	KSDLETN	-ASYGATP	-T	AYNNAAWSNGYNNY-QYGS	CSATA-A

DmeRun 438 -----VAPLRMRCDLKAPSAMKPLYHES-----GPCAVANSRQP
DvirGJ19252 460 -----TQQISVPLRMRCDLKAPSALKPLYHET-----ASAAAVAAPRQA
DanaGF15983 526 VGVGVGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DvirGJ18917* 506 ----VGGGHS-AAAAAAG-----CNGSLYPAYLT-----
DseGM22662/63* 509 ----VGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DpseGA13742/42* 566 LRSAAAAAASAVPAQVQAQTQAQPQ---DSATSLMSSGGDHDGWN--LIKRCVTLITH---NPPDAENANPNS--SP
DyakGE17890 545 LRNAAAAAAN-INPGQENAG-----VPPLGSPNDHDGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DvirGJ19245/46* 474 LRSAAAAAANTAPQQHQQQQESG-----SVLPAAAN--DADGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DyakGE17788 543 QYGPQAAPPPQPPP--PPPVV-----LCPQLYSTVNQNQIHLHLHSSEKLEQYLGATG---ADHLTIQSLTGSSRS
DpseGA22609 561 QYGGTGGAAPPPPPPPV-----LYPQLYSTVNQNQIHLHLHSSEKLEQYLGASD---QQLTISSLTGS-RS
DwilGK25373 529 QYGGATAAPPPP--PPPVV-----LYPQLYSTVNQNQIHLHLHSSEKLEQYLGATD---QQLTISSLTGS-RS
DperGL15806 480 -----LAQHSVPLRMRCDLKAPSALKPLYHES-----AAATNRQA
DyakGE15340/41* 525 ----VGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DgriGH17774/75* 497 ----VAGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DsimGD15530* -----
DmeCG42267 543 LRNAAAAAAN-INPGQENSG-----IPPLGSPNDHDGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DperGL15800/02* 498 LRSAAAAAASAVPAQVQAQTQAQPQ---DSATSLMSSGGDHDGWN--LIKRCVTLITH---NPPDAENANPNS--SP
DwilGK19810/11* 487 LRSAAAAAASSSSSSSSSQQLTTLTVPAASTPAGASGGAVAWASDLIKRCVTLITH---NPPDVENSNPNA--ASP
DereGG125698 442 -----VAPLRMRCDLKAPSAMKPLYHES-----GPCAVANSRQP
DmojGI15491 484 -----TQQISVPLRMRCDLKAPSALKPLYHES-----SAAA-AAAAAVAAVHAPRQA
DereGG18309 536 QYGPQAAPPPQPPP--PPPVV-----LCPQLYSTVNQNQIHLHLHSSEKLEQYLGATG---AEHLTIQSLTGSSRS
DgriGH11831* 305 -----VKQFKEDLQLAQHYEASFRLGLATAERR---PELLPMSMAIAN---
DperGL16499 563 QYGGTGGSAPPPPPPPV-----LYPQLYSTVNQNQIHLHLHSSEKLEQYLGASD---QQLTISSLTGS-RS
DwilGK19815 425 -----TQQISMLRMRCDLKAPSSLKPLYHES-----TSTSPTAGLLQT
DereGG17578 516 ----VGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DmojGI11519 372 VGVGVGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DpseGA25684 433 ----VGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DanaGF15967 547 LRNAAAAAASNLNPNTTPTP-----EGVPPSSQDHDGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DsiGD17495 537 LRNAAAAAAN-INPGQENPG-----VPTLGSNPDHDGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DgriGH17737/38* 533 LRSAAAAAASSTTPQQQQQQQQQQQLQDSVPLVASG-DADGWN--LVKRCVTLITH---NPPDAENANPNA--SP
DseGM22478 533 QYGPQAAPPPQPPP--PPPVV-----LCPQLYSTVNQNQIHLHLHSSEKLEQYLGATG---ADHLTIQSLTGSSRS
DanaGF21771 545 QYGPQTAAPPPPP--PPPVV-----LYPQLYSTVNQNQIHLHLHSSEKLEQYLGTAAGG---GEQLTISSLTGSSRS
DvirGJ18742 503 QYGGAGAHATAP---PPPVV-----LYPQLYSTVNQNQIHLHLHSSEKLEQYL--ATD---QQLTISSLASN-RS
DseGM23050 438 -----VAPLRMRCDLKAPSAMKPLYHES-----GPCAVANSRQP
DanaGF15970 472 -----VAHHHLGPLRMRCDLKAPSAMKPLYHEP-----SVVAVN-PRQA
DpseGA14956 477 -----LAQHSVPLRMRCDLKAPSALKPLYHES-----AAATNRQA
DperGL15927 499 ----VGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DwilGK20052/54* 540 GGGGGGGGGGGGGSGAGGNVQHGSTN-GGGSLYPVLPAASLLYSQLYTAANQSAHGFSHTLAAAHSNPSSVHGAELO
DseGM23044/45* 524 LRNAAAAAAN-INPGQENPG-----VPPVGSNPDHDGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DereGG19691 553 LRNAAAAAAN-INPGQENHG-----APPLGSPNDHDGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DmeCG34145 510 ----VGGGHS-AAAAAAG-----CNGSLYPVLPASLLYSQLYTAANQSAHGFSHTLP-AHASPNSSVHG-ELQ
DmojGI15484/86* 497 LRSAAAAAASSTAAPQQQPQQQSLPQQHEPSMLAAAAAGADADGWN--LIKRCVTLITH---NPPDAENANPNA--SP
DsiGD17500 438 -----VAPLRMRCDLKAPSAMKPLYHES-----GPCAVANSRQP
DyakGE17894 448 -----VAPLRMRCDLKAPSAMKPLYHES-----GPCAVASSRQP
Dmelz 537 QYGPQAAPPPQPPP--PPPVV-----LCPQLYSTVNQNQIHLHLHSSEKLEQYLGATG---ADHLTIQSLTGSSRS
DsiGD16951* -----
DgriGH17740 469 -----THHISVPLRMRCDLKAPSALKPLYHET-----SAAA-AAAAAAVAAVPRQA
DmojGI14398 527 QYGGAGAHATAP---PPPVV-----LYPQLYSTVNQNQIHLHLHSSEKLEQYL--ATD---QQLTISSLASN-RS

DmeRun	472	SPETT-----
DvirGJ19252	500	SPETTL-----
DanaGF15983	593	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DvirGJ18917*		-----
DseGM22662/63*	572	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DpseGA13742/42*	636	PVSTTRRSPSPS-----PVETIDLDDVSTTSRSASGSASG-----
DyakGE17890	607	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASGSSGL-----G
DvirGJ19245/46*	538	PVSSRRRSPSP-----VETIDLDDVSTTSRSASGSSG-----
DyakGE17788	610	SIEIGQD-----QYHQVVHHAQQQQQQQQQ---VHHPQQQQQQ---QVESAGEVG---
DpseGA22609	628	SIEIGPAGGLLGLTGEQEQ-HQHQNQHQQQQQLQQQPLEQSSEASNQS-YHLSHHQQHPHQ-----QQQQQQQQQ---
DwilGK25373	593	SIEIGLGGGGTVGGGVGG--AGALTVSSQDQDQQVAVSNEAVANQS-YHLASQEVQ-----QQQQQEVG---
DperGL15806	517	SPETTL-----
DyakGE15340/41*	588	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DgriGH17774/75*	561	SVMDHISNVGV-----RQQHNIM---AGGGVAHPGDLTLIGNCGASVRNIEDGNT-----
DsimGD15530*		-----
DmeCG42267	602	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASGSS-----G
DperGL15800/02*	568	PVSTTRRSPSPS-----PVETIDLDDVSTTSRSASGSASG-----
DwilGK19810/11*	564	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASVSGSS-----
DereGG19698	476	SPETT-----
DmojGI15491	530	SPETTL-----
DereGG18309	603	SIEIGQD-----QYHQVVHHSQQQQQQQQQ---VHHPQQQQQQ---QVESAGEVG---
DgriGH11831*		-----
DperGL16499	630	SIEIGPAGGLLGLTGEQEH-HQHQQQQQQHLQQQPLEQSSEASNQS-YHLSHHQQHPHQ-----QQQQQQQQQQ---
DwilGK19815	464	SPETTSLT-----
DereGG17578	579	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DmojGI11519	440	SVMDHISNVGV-----RQQHNIM---AGGGVAHPGDLTLIGNCGASVRNIEDGNT-----
DpseGA25684	496	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DanaGF15967	607	PVSSRRRSPSPS-----VETIDLDDVSTTSRSASGASSGEAGGGASG-----G
DsiGD17495	596	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASGSS-----G
DgriGH17737/38*	605	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASGSSG-----
DseGM22478	600	SIEIGQD-----QYHQVVHHAQQQQQQQ---VHHPQQQQ---VESAGEVG---
DanaGF21771	613	SIEIAQD-----PYQ---HHQQQQHHQHP-----HPQQTEQQ-----VVPGGGGTG---
DvirGJ18742	564	SIEIGLGTGVCGGGGGSSVSGGVALGEQEQAASVIAEQAAEGASQN-YHLHHHHH-----ETQRQMEAQ---
DseGM23050	472	SPETT-----
DanaGF15970	510	SPETTIP-----
DpseGA14956	514	SPETTL-----
DperGL15927	562	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DwilGK20052/54*	619	SVMDHISNVGVGVVRHQHHHNIMSAAGGGGLTHPGDLTLIGNCGASVRNIEDGNVT-----
DseGM23044/45*	583	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASGSS-----G
DereGG19691	612	PVSTTRRSPSPS-----VETIDLDDVSTTSRSASGSS-----G
DmeCG34145	573	SVMDHISNVGV-----RQQHNIM---AGGGVTHPGDLTLIGNCGASVRNIEDGNS-----
DmojGI15484/86*	570	PVSSRRRSPSPS-----VETIDLDDVSTTSRSASGSSG-----
DsiGD17500	472	SPETT-----
DyakGE17894	482	SPETT-----
Dmelz	604	SIEIGQD-----QYHQVVHHAQQQQQQQQQVVHHPQQQQ---VESAGEVG---
DsiGD16951*		-----
DgriGH17740	515	SPETTL-----
DmojGI14398	588	SIEIGLGTGLSGG-----VSLGEQDQQAASVIAEQAAEGASQNNYHLHHHHHQQQQQQQQQLEAQRQLEAQHQQQ

DmeRun	477	-----TKIKSAAVQQKT	VWRPY
DvirGJ19252	507	-----AATKLKNAVQQKT	VWRPY
DanaGF15983	640	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DvirGJ18917*		-----	
DseGM22662/63*	619	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DpseGA13742/42*	671	-----SGSSGGGP	TRTPKPSADVWRPY
DyakGE17890	641	LGGGVGGMGVGGAVG	--PI--TRTPKPSADVWRPY
DvirGJ19245/46*	570	-----AGGP	TRTPKPTADVWRPY
DyakGE17788	655	-----GSVAGG	--VESAEEDVGDLTQVWRPY
DpseGA22609	696	----AVEQVQQGEGV	CVEAP--DEDVGDLTQVWRPY
DwilGK25373	655	-----CEVST	QED--DLTQVWRPY
DperGL15806	524	-----AATKLKNSAVQQKT	VWRPY
DyakGE15340/41*	635	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DgriGH17774/75*	608	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DsimGD15530*		-----	
DmeCG42267	634	HGGGVG----GGGAVG	--PI--TRTPKPSADVWRPY
DperGL15800/02*	603	-----SGSSGGGP	TRTPKPSADVWRPY
DwilGK19810/11*	597	-----GGGPGS	GGGP--TRTPKPTADVWRPY
DereGG19698	481	-----	TKIKSAAVQQKT
DmojGI15491	537	-----AATKLKNAVQQKT	VWRPY
DereGG18309	647	-----GSGAGG	--VESAEEDVGDLTQVWRPY
DgriGH11831*		-----	
DperGL16499	699	----AVEQVQQGEGV	CVEAP--DEDVGDLTQVWRPY
DwilGK19815	472	-----TAAATKLKSAAVQQKT	VWRPY
DereGG17578	626	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DmojGI11519	487	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DpseGA25684	543	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DanaGF15967	649	LAGGVGGAAAAAVS	GGGP--NRTPKPSADVWRPY
DsiGD17495	628	HGGGVG----VGGAVG	--PI--TRTPKPSADVWRPY
DgriGH17737/38*	637	-----AGGP	TRTPKPTSDVWRPY
DseGM22478	639	-----GSGAGG	--VESAEEDVGDLSQVWRPY
DanaGF21771	651	-----GGGGSGDVVES	PEEDVGDLTQVWRPY
DvirGJ18742	629	-----QQHQSDVSNEAA	PEEDVGDMTQVWRPY
DseGM23050	477	-----TKIKSAAVQQKT	VWRPY
DanaGF15970	517	-----AATKLKSASVQQKT	VWRPY
DpseGA14956	521	-----AATKLKNSAVQQKT	VWRPY
DperGL15927	609	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DwilGK20052/54*	676	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DseGM23044/45*	615	HGGGVG----VGGAVG	--PI--TRTPKPSADVWRPY
DereGG19691	644	HGGGVG-----GAVG	--PI--TRTPKPSADVWRPY
DmeCG34145	620	-----NRQVAALAAHRC	HNPTDNGGSVWRPY
DmojGI15484/86*	602	-----AGGP	TRTPKPTADVWRPY
DsiGD17500	477	-----TKIKSAAVQQKT	VWRPY
DyakGE17894	487	-----TKIKSAAVQQKT	VWRPY
Dmelz	648	-----GSGAGG	--VESAEEDVGDLSQVWRPY
DsiGD16951*		-----	
DgriGH17740	522	-----AATKLKNAVQQKT	VWRPY
DmojGI14398	658	QQQQHQQQQHP	SDVSNEAAPEEDVGDMTQVWRPY