

SUPPLEMENTAL MATERIAL

SUPPLEMENTARY TABLES

Supplementary Table S1: Glycan array binding of EEA at a concentration of 200 μ g/ml: list of glycan structures ranked from highest relative fluorescence units (RFU) to lowest.

EEA3-Alexa488 at 200ug/ml cfg_rRequest_904 array-333211

Glycan Number	Glycan name	Avg RFU	StDev	SEM	%CV
198	Man α 1-6(Man α 1-3)Man α 1-6(Man α 1-3)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	50258	13085	6542	26
99	Gal α 1-3(Fuc α 1-2)Gal β -Sp8	49370	15825	7912	32
98	Gal α 1-3(Fuc α 1-2)Gal β 1-4Glc β -Sp0	47659	15351	7676	32
290	Gal α 1-3(Fuc α 1-2)Gal β -Sp18	45917	15683	7841	34
197	Man α 1-6(Man α 1-3)Man α 1-6(Man α 2Man α 1-3)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	40788	6906	3453	17
310	Man α 1-3(Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	37819	7060	3530	19
192	Man α 1-6(Man α 1-2Man α 1-3)Man α 1-6(Man α 2Man α 1-3)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	36914	8601	4301	23
97	Gal α 1-3(Fuc α 1-2)Gal β 1-4GlcNAc-Sp0	35329	1700	850	5
95	Gal α 1-3(Fuc α 1-2)Gal β 1-3GlcNAc β -Sp0	35176	4455	2228	13
50	Man α 1-3(Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp13	30930	20296	10148	66
61	Fuc α 1-2Gal β 1-3GlcNAc β 1-3Gal β 1-4Glc β -Sp10	24615	2171	1085	9
193	Man α 1-2Man α 1-6(Man α 1-3)Man α 1-6(Man α 2Man α 2Man α 1-3)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	24511	2120	1060	9
241	Gal β 1-4GlcNAc β 1-2Man α 1-3(Fuc α 1-3(Gal β 1-4)GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp20	23203	813	407	4
63	Fuc α 1-2Gal β 1-3GlcNAc β -Sp0	21920	14903	7452	68
312	Man α 1-6(Man α 1-3)Man α 1-6(Man α 1-3)Man β -Sp10	19915	2938	1469	15
69	Fuc α 1-2Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc-Sp0	19799	4998	2499	25
172	(GlcNAc β 1-4)5 β -Sp8	12800	894	447	7
201	Fuc α 1-3(Gal β 1-4)GlcNAc β 1-2Man α 1-3(Fuc α 1-3(Gal β 1-4)GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp20	11885	3324	1662	28
62	Fuc α 1-2Gal β 1-3GlcNAc β 1-3Gal β 1-4Glc β -Sp8	9804	11082	5541	113

52	Galβ1-4GlcNAcβ1-2Manα1-3(Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp13	9560	1937	968	20
64	Fuca1-2Galβ1-3GlcNAcβ-Sp8	7994	1204	602	15
173	GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ-Sp8	7530	882	441	12
79	GalNAcα1-3(Fuca1-2)Galβ1-3GlcNAcβ-Sp0	7512	1579	790	21
105	Galα1-3Galβ1-4GlcNAcβ-Sp8	6872	1670	835	24
171	(GlcNAcβ1-4)6β-Sp8	6402	574	287	9
51	GlcNAcβ1-2Manα1-3(GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp13	6356	733	366	12
87	GalNAcα1-4(Fuca1-2)Galβ1-4GlcNAcβ-Sp8	6044	860	430	14
313	Manα1-2Manα1-2Manα1-3(Manα1-2Manα1-6(Manα1-3)Manα1-6)Manα-Sp9	5900	683	342	12
70	Fuca1-2Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-Sp0	5641	1750	875	31
72	Fuca1-2Galβ1-4GlcNAcβ-Sp8	4881	3933	1967	81
103	Galα1-3Galβ1-4(Fuca1-3)GlcNAcβ-Sp8	4514	518	259	11
194	Manα1-2Manα1-2Manα1-3(Manα1-2Manα1-3(Manα1-2Manα1-6)Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp12	3896	1872	936	48
112	Galα1-4GlcNAcβ-Sp8	3204	1928	964	60
86	GalNAcα1-3Galβ-Sp8	2835	423	211	15
10	α-GalNAc-Sp8	2805	379	190	14
270	Fuca1-2Galβ1-4[6OSO3]GlcNAc-Sp8	2543	483	242	19
156	GlcNAcα1-3Galβ1-4GlcNAcβ-Sp8	2063	117	59	6
305	GlcNAcβ1-2Manα1-3(GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp12	1914	637	319	33
94	Galα1-2Galβ-Sp8	1900	343	171	18
307	GlcNAcβ1-4GlcNAcβ-Sp10	1852	243	121	13
309	HOOC(CH3)CH-3-O-GlcNAcβ1-4GlcNAcβ-Sp10	1786	175	87	10
314	Manα1-2Manα1-2Manα1-3(Manα1-2Manα1-6(Manα1-2Manα1-3)Manα1-6)Manα-Sp9	1775	201	100	11
319	Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-3(Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp12	1752	134	67	8
308	GlcNAcβ1-4GlcNAcβ-Sp12	1700	103	52	6
104	Galα1-3Galβ1-3GlcNAcβ-Sp0	1530	495	248	32
57	Fuca1-2Galβ1-3(Fuca1-4)GlcNAcβ-Sp8	1402	128	64	9
111	Galα1-4Galβ1-4Glcβ-Sp0	1337	252	126	19
300	GalNAcα-Sp15	1321	203	101	15
92	GalNAcβ1-4GlcNAcβ-Sp0	1277	217	109	17
176	GlcNAcβ1-6Galβ1-4GlcNAcβ-Sp8	1245	280	140	22
195	Manα1-3(Manα1-6)Manα-Sp9	1136	350	175	31

175	GlcNAc β 1-6GalNAc α -Sp8	1128	85	43	8
100	Gal α 1-3(Gal α 1-4)Gal β 1-4GlcNAc β -Sp8	1124	114	57	10
68	Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp8	992	197	98	20
91	GalNAc β 1-4(Fuc α 1-3)GlcNAc β -Sp0	991	974	487	98
85	GalNAc α 1-3GalNAc β -Sp8	937	384	192	41
190	Man α 1-2Man α 1-3(Man α 1-2Man α 1-6)Man α -Sp9	920	286	143	31
67	Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp0	866	145	72	17
93	GalNAc β 1-4GlcNAc β -Sp8	830	86	43	10
106	Gal α 1-3Gal β 1-4Glc β -Sp0	797	269	135	34
82	GalNAc α 1-3(Fuc α 1-2)Gal β 1-4GlcNAc β -Sp8	793	103	52	13
196	Man α 1-3(Man α 1-2Man α 1-2Man α 1-6)Man α -Sp9	723	187	93	26
65	Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp0	720	91	46	13
107	Gal α 1-3Gal β -Sp8	668	225	113	34
168	GlcNAc β 1-4MDPLys	657	62	31	9
155	Gal β 1-4Glc β -Sp8	651	157	79	24
301	GalNAc α 1-3(Fuc α 1-2)Gal β -Sp18	613	276	138	45
160	GlcNAc β 1-3(GlcNAc β 1-6)Gal β 1-4GlcNAc β -Sp8	594	168	84	28
297	Gal β 1-4GlcNAc β 1-3(GlcNAc β 1-6)Gal β 1-4GlcNAc-Sp0	590	95	48	16
151	Gal β 1-4GlcNAc β 1-6GalNAc α -Sp8	581	338	169	58
110	Gal α 1-4Gal β 1-4GlcNAc β -Sp8	543	145	73	27
128	Gal β 1-3GalNAc β 1-4(Neu5Ac α 2-3)Gal β 1-4Glc β -Sp0	525	300	150	57
157	GlcNAc α 1-6Gal β 1-4GlcNAc β -Sp8	522	122	61	23
167	GlcNAc β 1-3Gal β 1-4Glc β -Sp0	504	104	52	21
304	GlcNAc β 1-2Man α 1-3(Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	485	227	113	47
320	Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-3(GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	477	101	51	21
169	GlcNAc β 1-4(GlcNAc β 1-6)GalNAc α -Sp8	460	91	46	20
66	Fuc α 1-2Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp0	441	197	99	45
166	GlcNAc β 1-3Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp0	440	143	72	33
109	Gal α 1-4Gal β 1-4GlcNAc β -Sp0	432	247	123	57
164	GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp0	406	53	26	13
14	α -Neu5Ac-Sp8	383	172	86	45
139	Gal β 1-4[6OSO ₃]Glc β -Sp0	379	157	78	41

159	GlcNAc β 1-3(GlcNAc β 1-6)GalNAc α -Sp8	375	81	41	22
265	[3OSO3]Gal β 1-4(Fuca1-3)(6OSO3)Glc-Sp0	364	193	96	53
163	GlcNAc β 1-3Gal β 1-3GalNAc α -Sp8	359	149	74	41
293	Gal β 1-3(Neu5Ac α 2-3Gal β 1-4(Fuca1-3)GlcNAc β 1-6)GalNAc-Sp14	351	279	140	80
222	Neu5Ac α 2-3Gal β -Sp8	328	106	53	32
247	Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-3Gal β 1-4(Fuca1-3)GlcNAc β 1-3Gal β 1-4(Fuca1-3)GlcNAc β -Sp0	308	119	60	39
58	Fuca1-2Gal β 1-3GalNAc α -Sp8	307	106	53	34
81	GalNAc α 1-3(Fuca1-2)Gal β 1-4GlcNAc β -Sp0	306	135	68	44
191	Man α 1-2Man α 1-3Man α -Sp9	305	79	40	26
218	NeuAc α 2-3Gal β 1-3(Fuca1-4)GlcNAc β 1-3Gal β 1-4(Fuca1-3)GlcNAc β Sp0	287	27	13	9
272	Fuca1-2-(6OSO3)-Gal β 1-4Glc-Sp0	282	207	103	73
165	GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp8	272	82	41	30
71	Fuca1-2Gal β 1-4GlcNAc β -Sp0	272	107	53	39
142	Gal β 1-4GalNAc β 1-3(Fuca1-2)Gal β 1-4GlcNAc β -Sp8	271	67	34	25
126	Gal β 1-3GalNAc β -Sp8	269	54	27	20
36	[3OSO3]Gal β 1-4GlcNAc β -Sp0	267	195	97	73
96	Gal α 1-3(Fuca1-2)Gal β 1-4(Fuca1-3)GlcNAc β -Sp0	265	16	8	6
170	GlcNAc β 1-4Gal β 1-4GlcNAc β -Sp8	265	108	54	41
150	Gal β 1-4GlcNAc β 1-6(Gal β 1-3)GalNAc α -Sp8	262	81	40	31
5	Gal β 1-3GlcNAc β 1-2Man α 1-3(Gal β 1-3GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp19	261	175	87	67
130	Gal β 1-3Gal β -Sp8	255	150	75	59
143	Neu5Ac α 2-3Gal β 1-4GlcNAc β 1-2Man α 1-3(Neu5Ac α 2-3Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	255	23	12	9
243	Neu5Ac α 2-6GalNAc β 1-4GlcNAc β -Sp0	255	140	70	55
135	Gal β 1-4(Fuca1-3)GlcNAc β -Sp0	252	71	35	28
280	Gal β 1-4[Fuca1-3][6OSO3]GlcNAc-Sp0	252	78	39	31
59	Fuca1-2Gal β 1-3GalNAc β 1-4(Neu5Ac α 2-3)Gal β 1-4Glc β -Sp0	243	127	63	52
288	[6OSO3]Gal β 1-4[6OSO3]GlcNAc β -Sp0	242	114	57	47
45	[6OSO3]Gal β 1-4[6OSO3]Glc β -Sp8	240	78	39	33
202	Neu5Ac α 2-3Gal β 1-3GalNAc α -Sp8	239	48	24	20
129	Gal β 1-3GalNAc β 1-4Gal β 1-4Glc β -Sp8	239	43	22	18
84	GalNAc α 1-3(Fuca1-2)Gal β -Sp8	236	82	41	35

189	Man α 1-2Man α 1-2Man α 1-3Man α -Sp9	234	51	25	22
174	GlcNAc β 1-6(Gal β 1-3)GalNAc α -Sp8	234	30	15	13
76	Fuc α 1-3GlcNAc β -Sp8	231	135	68	58
44	[6OSO3]Gal β 1-4GlcNAc β -Sp8	230	150	75	65
267	[3OSO3]Gal β 1-4[Fuc α 1-3][6OSO3]GlcNAc-Sp8	230	122	61	53
136	Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp8	229	84	42	37
12	α -L-Fuc-Sp9	228	131	66	57
47	[6OSO3]GlcNAc β -Sp8	224	73	37	33
108	Gal α 1-4(Fuc α 1-2)Gal β 1-4GlcNAc β -Sp8	222	105	53	47
17	β -D-Gal-Sp8	220	77	38	35
258	Neu5Gca2-3Gal β 1-3GlcNAc β -Sp0	217	78	39	36
7	α -D-Gal-Sp8	217	62	31	29
260	Neu5Gca2-3Gal β 1-4GlcNAc β -Sp0	217	85	43	39
145	Gal β 1-4GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp0	216	102	51	47
232	Neu5Aca2-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β -Sp8	215	102	51	47
302	GalNAc β 1-3Gal β -Sp8	214	83	42	39
311	Man α 1-6Man β -Sp10	208	77	39	37
137	Gal β 1-4(Fuc α 1-3)GlcNAc β 1-4Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp0	208	84	42	41
158	GlcNAc β 1-2Gal β 1-3GalNAc α -Sp8	206	119	60	58
229	Neu5Aca2-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β 1-3Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp0	201	36	18	18
122	Gal β 1-3(Neu5Aca2-6)GalNAc α -Sp8	200	63	32	32
281	Gal β 1-4[Fuc α 1-3][6OSO3]Glc-Sp0	200	111	55	56
28	[3OSO3]Gal β 1-4Glc β -Sp8	199	55	27	27
34	[3OSO3]Gal β 1-4(Fuc α 1-3)GlcNAc β -Sp8	199	63	31	32
219	Neu5Aca2-3Gal β 1-3(Neu5Aca2-3Gal β 1-4)GlcNAc β -Sp8	199	68	34	34
263	Neu5Gca2-6Gal β 1-4GlcNAc β -Sp0	197	46	23	23
154	Gal β 1-4Glc β -Sp0	197	98	49	50
187	KDN α 2-3Gal β 1-3GlcNAc β -Sp0	195	32	16	16
249	Neu5Aca2-6Gal β 1-4Glc β -Sp0	194	80	40	41
235	Neu5Aca2-3Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp0	194	125	63	65
23	β -GlcN(Gc)-Sp8	193	63	31	32
148	Gal β 1-4GlcNAc β 1-3Gal β 1-4Glc β -Sp0	186	151	76	81

318	Neu5Ac α 2-3Gal β 1-4GlcNAc β 1-2Man α 1-3(Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	186	127	63	68
230	Neu5Ac α 2-3Gal β 1-4(Fuca1-3)GlcNAc β -Sp0	183	27	13	15
115	Gal β 1-3(Fuca1-4)GlcNAc β 1-3Gal β 1-4(Fuca1-3)GlcNAc β -Sp0	183	75	38	41
54	Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-3(Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp8	183	69	34	38
40	[4OSO3]Gal β 1-4GlcNAc β -Sp8	182	71	36	39
133	Gal β 1-3GlcNAc β -Sp0	182	99	50	54
292	Gal β 1-3GalNAc α -Sp16	181	141	70	78
226	Neu5Ac α 2-3Gal β 1-3GlcNAc β -Sp8	181	133	66	73
287	[3OSO3][4OSO3]Gal β 1-4GlcNAc β -SpSp0	181	55	27	30
20	β -GalNAc-Sp8	180	83	41	46
114	Gal β 1-2Gal β -Sp8	180	112	56	62
224	NeuAc α 2-3Gal β 1-3GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp0	179	111	56	62
120	Gal β 1-3(Gal β 1-4GlcNAc β 1-6)GalNAc α -Sp8	178	76	38	43
74	Fuca1-2Gal β -Sp8	176	96	48	55
162	GlcNAc β 1-3Gal β -Sp8	174	114	57	66
246	Neu5Ac α 2-6Gal β 1-4GlcNAc β -Sp8	171	120	60	70
113	Gal α 1-6Glc β -Sp8	170	87	43	51
88	GalNAc β 1-3GalNAc α -Sp8	170	134	67	79
271	Fuca1-2[6OSO3]Gal β 1-4[6OSO3]Glc-Sp0	170	35	17	20
83	GalNAc α 1-3(Fuca1-2)Gal β 1-4Glc β -Sp0	168	73	36	43
80	GalNAc α 1-3(Fuca1-2)Gal β 1-4(Fuca1-3)GlcNAc β -Sp0	168	53	26	31
276	Gal β 1-3(GlcNAc β 1-6)GalNAc-Sp14	166	80	40	48
24	(Gal β 1-4GlcNAc β)2-3,6-GalNAc α -Sp8	166	89	44	53
269	Fuca1-2[6OSO3]Gal β 1-4GlcNAc-Sp0	166	99	49	59
161	GlcNAc β 1-3GalNAc α -Sp8	166	78	39	47
26	[3OSO3][6OSO3]Gal β 1-4[6OSO3]GlcNAc β -Sp0	164	80	40	49
199	Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-3(Neu5Ac α 2-3Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	164	99	49	60
6	Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-3(Neu5Ac α 2-6Gal β 1-4GlcNAc β 1-2Man α 1-6)Man β 1-4GlcNAc β 1-4GlcNAc β -Sp12	162	82	41	51
39	[4OSO3][6OSO3]Gal β 1-4GlcNAc β -Sp0	161	45	22	28

134	Galβ1-3GlcNAcβ-Sp8	161	31	15	19
32	[3OSO3]Galβ1-3GalNAcα-Sp8	160	63	31	39
251	Neu5Acα2-6Galβ-Sp8	158	79	39	50
217	Neu5Acα2-3Galβ1-3(Fuca1-4)GlcNAcβ-Sp8	157	62	31	39
237	Neu5Acα2-3Galβ1-4GlcNAcβ-Sp8	156	56	28	36
299	Galβ1-4GlcNAcβ1-6Galβ1-4GlcNAcβ-Sp0	156	79	39	50
184	GlcAβ-Sp8	156	44	22	28
75	Fuca1-3GlcNAcβ-Sp8	154	84	42	54
264	Neu5Gcα-Sp8	153	46	23	30
31	[3OSO3]Galβ1-3(Fuca1-4)GlcNAcβ-Sp8	153	115	58	76
295	Galβ1-4GlcNAcβ1-2Mana1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-2Mana1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp12	152	98	49	64
118	Galβ1-3(Fuca1-4)GlcNAc-Sp8	151	23	12	15
256	Galβ1-4GlcNAcβ1-2Mana1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-2Mana1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp21	150	56	28	37
2	Neu5Acα2-8Neu5Acβ-Sp17	149	128	64	86
182	G-ol-Sp8	148	62	31	42
132	Galβ1-3GlcNAcβ1-3Galβ1-4Glcβ-Sp10	148	55	27	37
188	KDNα2-3Galβ1-4GlcNAcβ-Sp0	148	100	50	68
185	GlcAβ1-3Galβ-Sp8	148	74	37	50
140	Galβ1-4[6OSO3]Glcβ-Sp8	147	99	49	67
231	Neu5Acα2-3Galβ1-4(Fuca1-3)GlcNAcβ-Sp8	146	24	12	16
203	NeuAca2-8NeuAca2-8NeuAca2-8NeuAca2-3(GalNAcβ1-4)Galβ1-4Glcβ-Sp0	146	60	30	41
138	Galβ1-4(Fuca1-3)GlcNAcβ1-4Galβ1-4(Fuca1-3)GlcNAcβ1-4Galβ1-4(Fuca1-3)GlcNAcβ-Sp0	146	24	12	17
178	Glcα1-4Glcα-Sp8	145	87	43	60
90	GalNAcβ1-3Galα1-4Galβ1-4GlcNAcβ-Sp0	144	47	24	33
37	[3OSO3]Galβ1-4GlcNAcβ-Sp8	143	34	17	24
141	Galβ1-4GalNAcα1-3(Fuca1-2)Galβ1-4GlcNAcβ-Sp8	143	52	26	37
49	9NAcNeu5Acα2-6Galβ1-4GlcNAcβ-Sp8	141	90	45	64
186	GlcAβ1-6Galβ-Sp8	140	30	15	22
268	[3OSO3]Galβ1-4[Fuca1-3]GlcNAc-Sp0	140	91	46	65
261	Neu5Gcα2-3Galβ1-4Glcβ-Sp0	137	73	37	53
209	Neu5Acα2-3(GalNAcβ1-4)Galβ1-4GlcNAcβ-Sp0	137	124	62	91
89	GalNAcβ1-3(Fuca1-2)Galβ-Sp8	135	83	42	62

35	[3OSO3]Galβ1-4[6OSO3]GlcNAcβ-Sp8	135	72	36	53
177	Glcα1-4Glcβ-Sp8	134	55	27	41
101	Galα1-3GalNAcα-Sp8	134	136	68	102
56	Fucα1-2Galβ1-3GalNAcβ1-3Galα1-4Galβ1-4Glcβ-Sp9	133	73	36	55
228	Neu5Acα2-3Galβ1-4(Fuca1-3)(6OSO3)GlcNAcβ-Sp8	133	64	32	48
183	GlcAa-Sp8	132	88	44	67
274	Galβ1-3(Fuca1-4)GlcNAcβ1-3Galβ1-3(Fuca1-4)GlcNAcβ-Sp0	132	83	41	63
121	Galβ1-3(GlcNAcβ1-6)GalNAcα-Sp8	130	50	25	38
236	Neu5Acα2-3Galβ1-4GlcNAcβ-Sp0	130	75	38	58
48	9NAcNeu5Acα-Sp8	130	60	30	46
11	α-L-Fuc-Sp8	128	105	52	82
22	β-GlcNAc-Sp8	127	121	60	95
19	β-D-Man-Sp8	126	133	66	105
1	Neu5Acα2-8Neu5Acα-Sp8	126	50	25	39
123	Galβ1-3(Neu5Acβ2-6)GalNAcα-Sp8	126	44	22	35
255	Neu5Acβ2-6Galβ1-4GlcNAcβ-Sp8	125	42	21	33
257	Neu5Gca2-3Galβ1-3(Fuca1-4)GlcNAcβ-Sp0	125	60	30	48
266	[3OSO3]Galβ1-4(Fuca1-3)Glc-Sp0	121	71	36	59
234	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-4(Fuca1-3)GlcNAc-Sp0	120	45	22	37
221	Neu5Acα2-3Galβ1-3(Neu5Acα2-6)GalNAcα-Sp8	120	40	20	33
124	Galβ1-3(Neu5Acα2-6)GlcNAcβ1-4Galβ1-4Glcβ-Sp10	118	53	27	45
316	Neu5Acα2-3Galβ1-3(Neu5Acα2-6)GalNAc-Sp14	118	52	26	44
298	Galβ1-4GlcNAcα1-6Galβ1-4GlcNAcβ-Sp0	117	74	37	63
200	Manβ1-4GlcNAcβ-Sp0	117	65	32	56
273	Fucα1-2-Galβ1-4[6OSO3]Glc-Sp0	116	48	24	42
240	Neu5Acα2-3Galβ1-4Glcβ-Sp8	116	37	19	32
21	β-GlcNAc-Sp0	114	66	33	58
43	[6OSO3]Galβ1-4Glcβ-Sp8	112	38	19	34
206	Neu5Acα2-8Neu5Acα2-3(GalNAcβ1-4)Galβ1-4Glcβ-Sp0	111	96	48	86
181	Glcβ1-6Glcβ-Sp8	111	45	22	40
131	Galβ1-3GlcNAcβ1-3Galβ1-4GlcNAcβ-Sp0	110	55	28	50
214	Neu5Acα2-3GalNAcα-Sp8	110	15	7	13

294	Galβ1-3Galβ1-4GlcNAcβ-Sp8	110	95	47	86
291	Galα1-3GalNAcα-Sp16	110	85	43	78
223	Neu5Acα2-3Galβ1-3GalNAcβ1-3Galα1-4Galβ1-4Glcβ-Sp0	109	24	12	22
317	Neu5Acα2-3Galβ1-3GalNAc-Sp14	109	60	30	55
242	Neu5Acα2-6GalNAcα-Sp8	109	63	31	58
179	Glcα1-6Glcα1-6Glcβ-Sp8	109	52	26	47
233	Neu5Acα2-3Galβ1-4(Fuca1-3)GlcNAcβ1-3Galβ1-4GlcNAcβ-Sp8	105	49	24	46
102	Galα1-3GalNAcβ-Sp8	105	75	38	71
180	Glcβ1-4Glcβ-Sp8	104	55	28	53
152	Galβ1-4GlcNAcβ-Sp0	103	54	27	52
248	Neu5Acα2-6Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-Sp0	103	28	14	27
33	[3OSO3]Galβ1-3GlcNAcβ-Sp8	103	29	15	28
29	[3OSO3]Galβ1-4(6OSO3)Glcβ-Sp0	101	17	9	17
147	Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-Sp0	99	52	26	52
227	Neu5Acα2-3Galβ1-4[6OSO3]GlcNAcβ-Sp8	98	59	29	60
259	Neu5Gca2-3Galβ1-4(Fuca1-3)GlcNAcβ-Sp0	97	40	20	41
16	β-Neu5Ac-Sp8	96	45	22	46
244	Neu5Acα2-6Galβ1-4[6OSO3]GlcNAcβ-Sp8	96	30	15	32
212	Neu5Acα2-3(Neu5Acα2-3Galβ1-3GalNAcβ1-4)Galβ1-4Glcβ-Sp0	96	95	47	99
55	Fuca1-2Galβ1-3GalNAcβ1-3Galα-Sp9	95	59	30	62
208	Neu5Acα2-3(6-O-Su)Galβ1-4(Fuca1-3)GlcNAcβ-Sp8	95	27	14	29
285	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-3GlcNAcβ-Sp0	94	19	10	20
278	Galβ1-3GalNAc-Sp14	94	60	30	64
30	[3OSO3]Galβ1-4(6OSO3)Glcβ-Sp8	93	81	40	87
225	Neu5Acα2-3Galβ1-3GlcNAcβ-Sp0	93	55	28	59
303	GlcAβ1-3GlcNAcβ-Sp8	92	61	31	67
215	Neu5Acα2-3GalNAcβ1-4GlcNAcβ-Sp0	92	54	27	59
127	Galβ1-3GalNAcβ1-3Galα1-4Galβ1-4Glcβ-Sp0	91	49	25	54
4	Neu5Gcβ2-6Galβ1-4GlcNAc-Sp8	91	35	18	39
18	β-D-Glc-Sp8	90	44	22	49
153	Galβ1-4GlcNAcβ-Sp8	90	47	23	52
216	Neu5Acα2-3Galβ1-3(6OSO3)GlcNAc-Sp8	89	49	25	55

73	Fuca1-2Galβ1-4Glcβ-Sp0	88	60	30	68
254	Neu5Acβ2-6GalNAcα-Sp8	87	60	30	69
3	Neu5Acα2-8Neu5Acα2-8Neu5Acβ-Sp8	87	49	24	56
283	Galβ1-4GlcNAcβ1-3Galβ1-3GlcNAcβ-Sp0	86	6	3	7
211	Neu5Acα2-3(GalNAcβ1-4)Galβ1-4Glcβ-Sp0	84	39	20	47
239	Neu5Acα2-3Galβ1-4Glcβ-Sp0	81	81	40	100
116	Galβ1-3(Fuca1-4)GlcNAcβ1-3Galβ1-4GlcNAcβ-Sp0	81	25	13	32
119	Galβ1-3(Fuca1-4)GlcNAcβ-Sp8	81	63	31	78
41	6-H2PO3Mana-Sp8	80	64	32	80
282	Galβ1-4(Fuca1-3)GlcNAcβ1-3Galβ1-3(Fuca1-4)GlcNAcβ-Sp0	80	39	19	49
25	GlcNAcβ1-3(GlcNAcβ1-4)(GlcNAcβ1-6)GlcNAc-Sp8	80	18	9	22
315	Neu5Acα2-3Galβ1-3(Neu5Acα2-3Galβ1-4GlcNAcβ1-6)GalNAc-Sp14	80	21	11	26
279	Galβ1-3GlcNAcβ1-3Galβ1-3GlcNAcβ-Sp0	79	41	20	52
38	[3OSO3]Galβ-Sp8	79	18	9	22
78	Fucβ1-3GlcNAcβ-Sp8	78	34	17	43
306	GlcNAcβ1-3Man-Sp10	77	27	13	35
42	[6OSO3]Galβ1-4Glcβ-Sp0	77	92	46	120
144	Galβ1-4GlcNAcβ1-3GalNAcα-Sp8	76	19	9	25
27	[3OSO3][6OSO3]Galβ1-4GlcNAcβ-Sp0	76	41	20	54
117	Galβ1-3(Fuca1-4)GlcNAc-Sp0	75	8	4	11
220	Neu5Acα2-3Galβ1-3[6OSO3]GalNAcα-Sp8	73	38	19	53
296	Galβ1-4GlcNAcβ1-3(Galβ1-4GlcNAcβ1-6)Galβ1-4GlcNAc-Sp0	72	23	12	32
207	Neu5Acα2-8Neu5Acα2-8Neu5Acα-Sp8	72	40	20	55
60	Fuca1-2Galβ1-3GalNAcβ1-4(Neu5Acα2-3)Galβ1-4Glcβ-Sp9	71	25	13	35
245	Neu5Acα2-6Galβ1-4GlcNAcβ-Sp0	71	35	17	49
149	Galβ1-4GlcNAcβ1-3Galβ1-4Glcβ-Sp8	71	82	41	116
8	α-D-Glc-Sp8	70	70	35	100
277	Galβ1-3-(Neu5Aa2-3Galβ1-4GlcNAcβ1-6)GalNAc-Sp14	67	44	22	65
9	α-D-Man-Sp8	67	27	13	40
125	Galβ1-3GalNAcα-Sp8	66	99	50	150
53	Neu5Acα2-6Galβ1-4GlcNAcβ1-2Mana1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-2Mana1-6)Manβ1-4GlcNAcβ1-4GlcNAcβ-Sp13	66	32	16	49

210	Neu5Ac α 2-3(GalNAc β 1-4)Gal β 1-4GlcNAc β -Sp8	64	25	12	39
146	Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp0	63	26	13	42
46	NeuAc α 2-3[6OSO3]Gal β 1-4GlcNAc β -Sp8	63	57	29	91
13	α -L-Rh α -Sp8	63	29	14	46
275	Gal β 1-3-(Gal β 1-4GlcNAc β 1-6)GalNAc-Sp14	62	35	18	57
284	Neu5Ac α 2-3Gal β 1-3GlcNAc β 1-3Gal β 1-3GlcNAc β -Sp0	60	26	13	43
289	6-H2PO3Glc β -Sp10	57	46	23	81
213	Neu5Ac α 2-3(Neu5Ac α 2-6)GalNAc α -Sp8	56	26	13	46
204	Neu5Ac α 2-8Neu5Ac α 2-8Neu5Ac α 2-3(GalNAc β 1-4)Gal β 1-4Glc β -Sp0	55	4	2	7
15	α -Neu5Ac-Sp11	51	41	20	79
253	Neu5Ac α 2-8Neu5Ac α 2-3Gal β 1-4Glc β -Sp0	48	36	18	74
286	[3OSO3]Gal β 1-4[6OSO3]GlcNAc β -Sp0	46	29	14	63
262	Neu5Gc α 2-6GalNAc α -Sp0	44	18	9	41
252	Neu5Ac α 2-8Neu5Ac α -Sp8	41	8	4	19
205	Neu5Ac α 2-8Neu5Ac α 2-8Neu5Ac α 2-3Gal β 1-4Glc β -Sp0	40	8	4	19
238	Neu5Ac α 2-3Gal β 1-4GlcNAc β 1-3Gal β 1-4GlcNAc β -Sp0	33	59	29	176
250	Neu5Ac α 2-6Gal β 1-4Glc β -Sp8	30	26	13	88
77	Fuc α 1-4GlcNAc β -Sp8	24	27	14	112

Supplementary Table S2: List of best hits ($E < 0.01$) of a BLASTp search using the deduced sequence of LECEEA as a query.

Proteins with a single domain equivalent to EEA		Score	E-value
ref NP_001060668.1	Os07g0684000 [Oryza sativa] (=osr40g3)	129	5e-29
emb CAO23507.1	unnamed protein product [Vitis vinifera]	129	7e-29
gb AA444603.1	stress responsive protein [Triticum aestivum]	126	3e-28
gb ABK95474.1	unknown [Populus trichocarpa]	120	3e-26
ref NP_565899.1	hydroxyproline-rich glycoprotein family Arabidopsis thaliana ((At2g39050)	120	4e-26
ref NP_001041764.1	Os01g0104400 [Oryza sativa (japonica cult...	107	2e-22
gb ABK27004.1	unknown [Picea sitchensis]	100	3e-20
gb ABK22768.1	unknown [Picea sitchensis]	99.0	8e-20
gb ABK23910.1	unknown [Picea sitchensis]	97.1	3e-19
gb EDQ82581.1	predicted protein [Physcomitrella patens subsp. p	94.7	2e-18
gb EDQ69990.1	predicted protein [Physcomitrella patens subsp. p	94.4	2e-18
gb EAY89839.1	hypothetical protein OsI_011072 [Oryza sativa ...	92.0	9e-18
gb ABK23307.1	unknown [Picea sitchensis]	87.4	3e-16
gb ABK21966.1	unknown [Picea sitchensis]	86.7	4e-16
gb ABK22123.1	unknown [Picea sitchensis] >gb ABK27146.1 unk...	85.9	7e-16
gb ABK24175.1	unknown [Picea sitchensis] >gb ABK27037.1 unk...	84.7	1e-15
gb EDQ73918.1	predicted protein [Physcomitrella patens subsp. p	60.5	3e-08
emb CAH59433.1	lectin-like protein 1 [Plantago major]	58.9	9e-08
emb CAH59435.1	lectin-like protein 2 [Plantago major]	56.2	5e-07
Proteins with two in tandem arrayed domains equivalent to EEA			
ref NP_001060666.1	Os07g0683600 [Oryza sativa (japonica cult...	119	8e-26
ref NP_001060667.1	Os07g0683900 [Oryza sativa (japonica cult...	116	4e-25
ref NP_001049995.1	Os03g0327600 [Oryza sativa (japonica cult...	114	2e-24
gb EDQ82427.1	predicted protein [Physcomitrella patens subsp. p	102	7e-21
gb ABK25355.1	unknown [Picea sitchensis]	102	9e-21
gb ABK24374.1	unknown [Picea sitchensis]	96.3	5e-19

Supplementary Table S3: List of top 50 hits of a tBLASTn search using the deduced sequence of LECEEA as a query (EST database).

Proteins with a single domain equivalent to EEA	Score	E-value
gb DV449251.1	CV01027A2A02.f1 CV01-normalized library Maniho...	137 3e-31
gb CA800954.1	sau22c12.y1 Gm-cl062 Glycine max cDNA clone SO...	134 2e-30
gb EV240086.1	VV_PED0010g08.bl Vitis vinifera cv. perlette L...	134 2e-30
gb BM890680.1	sam06f06.y1 Gm-cl063 Glycine max cDNA clone SO...	134 2e-30
gb EC987124.1	WIN1129.C21_M02 Muscat Hamburg pre-veraison be...	134 3e-30
gb CN141603.1	OX1_52_E09.g1_A002 Oxidatively-stressed leaves...	133 4e-30
gb EV240087.1	VV_PED0010g08.g1 Vitis vinifera cv. perlette L...	132 7e-30
gb DN141919.1	5036_F02_L03 Switchgrass crown cDNA library Pa...	132 9e-30
gb CX635247.1	UCRPT02_10F01_b Poncirus trifoliata Roots with...	132 1e-29
gb CD573822.1	UCRPT01_02_D04_T7 Poncirus trifoliata CTV-chal...	132 1e-29
gb CV705291.1	UCRPT01_0006K15_f Poncirus trifoliata CTV-chal...	132 1e-29
gb DW224105.1	GH_HYPS_01-01-04R_H12_InvR_13Apr04_082_F Stem ...	132 1e-29
gb CX635248.1	UCRPT02_10F01_g Poncirus trifoliata Roots with...	132 1e-29
gb CX047385.1	UCRCS09_13G12_b Ruby Orange Developing Seed cd...	132 1e-29
gb CV708290.1	UCRPT01_0011B11_f Poncirus trifoliata CTV-chal...	132 1e-29
gb CN187922.1	UCRCS05_0005D18_f Washington Navel Orange Stor...	131 1e-29
gb CN186672.1	UCRCS05_0003E09_f Washington Navel Orange Stor...	131 2e-29
gb CX667274.1	UCRCP01_030_C07_T3 Swingle citrumelo nematode-...	131 2e-29
gb CA162130.1	SCQSRZ3037H04.b RZ3 Saccharum officinarum cDNA...	131 2e-29
gb CA109368.1	SCSGHR1070B01.b HR1 Saccharum officinarum cDNA...	131 2e-29
gb EE021146.2	ZM_BFc0074M13.r ZM_BFc Zea mays cDNA clone ZM_...	131 2e-29
dbj CJ767152.1	CJ767152 Ipomoea nil shoot 8-days old seedlin...	131 2e-29
gb CD432710.1	ETH1_25_E11.g1_A002 Ethylene-treated seedlings...	131 2e-29
gb CX050821.1	UCRCS09_34G05_b Ruby Orange Developing Seed cd...	131 2e-29
gb CN151340.1	WOUND1_74_H03.g1_A002 Wounded leaves Sorghum b...	131 2e-29
gb CN128191.1	RHOH1_27_D12.g1_A002 Acid- and alkaline-treate...	131 2e-29
gb CD431221.1	ETH1_7_C10.g1_A002 Ethylene-treated seedlings ...	131 2e-29
gb CN144638.1	WOUND1_23_C09.g1_A002 Wounded leaves Sorghum b...	131 2e-29
gb CN147712.1	WOUND1_51_D08.g1_A002 Wounded leaves Sorghum b...	130 2e-29
gb CX620548.1	GABR1_52_C01.g1_A002 GA- or brassinolide-treat...	130 3e-29
gb CB290392.1	UCRCS01_01bb10_b1 Washington Navel orange cold...	130 3e-29
gb DV862750.1	CRP2482 Creeping bentgrass EST Agrostis stolon...	130 4e-29
gb EE180130.2	ZM_BFc0162E12.r ZM_BFc Zea mays cDNA clone ZM_...	130 4e-29
gb EE040416.2	ZM_BFc0105N12.f ZM_BFc Zea mays cDNA clone ZM_...	130 4e-29
gb CX109197.1	RECM0573 A normalized whole-life-cycle cDNA li...	130 4e-29
gb DV861049.1	CRP781 Creeping bentgrass EST Agrostis stloni...	130 4e-29
gb CD431884.1	ETH1_11_D11.g1_A002 Ethylene-treated seedlings...	130 4e-29
gb EE181047.2	ZM_BFc0163K11.f ZM_BFc Zea mays cDNA clone ZM_...	130 5e-29
gb EE190900.2	ZM_BFc0190H04.f ZM_BFc Zea mays cDNA clone ZM_...	130 5e-29
gb EC903704.2	ZM_BFc0052M17.r ZM_BFc Zea mays cDNA clone ZM_...	130 5e-29
gb EE190286.2	ZM_BFc0188A03.r ZM_BFc Zea mays cDNA clone ZM_...	129 5e-29
gb EE040417.2	ZM_BFc0105N12.r ZM_BFc Zea mays cDNA clone ZM_...	129 5e-29
gb EG664831.1	RCLGP49TP Castor bean cDNA library from leaves...	129 5e-29
gb EE190924.2	ZM_BFc0190H20.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29
gb EE294911.2	ZM_BFc0189N20.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29
gb EE294025.2	ZM_BFc0188A03.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29
gb EE180129.2	ZM_BFc0162E12.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29
gb EE173587.2	ZM_BFc0151M14.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29
gb EE169896.2	ZM_BFc0145L03.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29
gb EE160134.2	ZM_BFc0129K03.f ZM_BFc Zea mays cDNA clone ZM_...	129 6e-29

SUPPLEMENTARY FIGURES

Supplementary Figure S1: Genomic sequence of EEA. Intron sequences are shown in *italic*, the start- and stopcodon are underlined. The amino acid sequence corresponding to the N-terminal sequence of EEA is shown in **bold**.

ATGGCTTCAACAATCATCGCAACAGGACCCACTTATAGGGTGTACTGCAGG
M A S T I I A T G P T Y R V Y C R

GCCGCCCCCAACTACAATATGACCGTCGGTAAAGGGGTGGCCTTTCTTGCC
A A P N Y N M T V G K G V A F L A

CCTATTGATGAAACAAATGAGCTTCAGGTTTATTCATCAAAGACGATCTAT
P I D E T N E L Q

TAATTTCTTTTATCTTTTATTTATGTCAAAGTGCATGTTTTCATGATCT

TCATCCGTTCTTAAGGATTGTATGCGTATAATTTACAATGAGTTAGCATAT

TCTAGTGTGTATATATATATATTAATTTTTTGTGTTGTGGCAGTATTGGTACA
Y W Y K

AAGATGACACGTACAGCTATATCAAGGACGAAGCGGGCCTTCCTGCATTTT
D D T Y S Y I K D E A G L P A F S

CTCTAGTTAATAAAGCAACTGGTCTAACCCCTAAAACATTCAAATCATCACC
L V N K A T G L T L K H S N H H P

CTGTTCCCTGTAAGAATTCTACGACCTTAACACTGCAGGCTTTCTTAACTTG
V P

TCATTTATACAATTACCGATAGCATTGTAACCTTTTTTTTTTTGTGGAAATTT

*ATCATACATGTAGGTGAAATTGGTGA*CTTACAATCCAAATGTTGTTGATGA
V K L V T Y N P N V V D E

GTCTGTCTTATGGTCACAAGCAGACGATCGCGGTGACGGTTACTCGGCCAT
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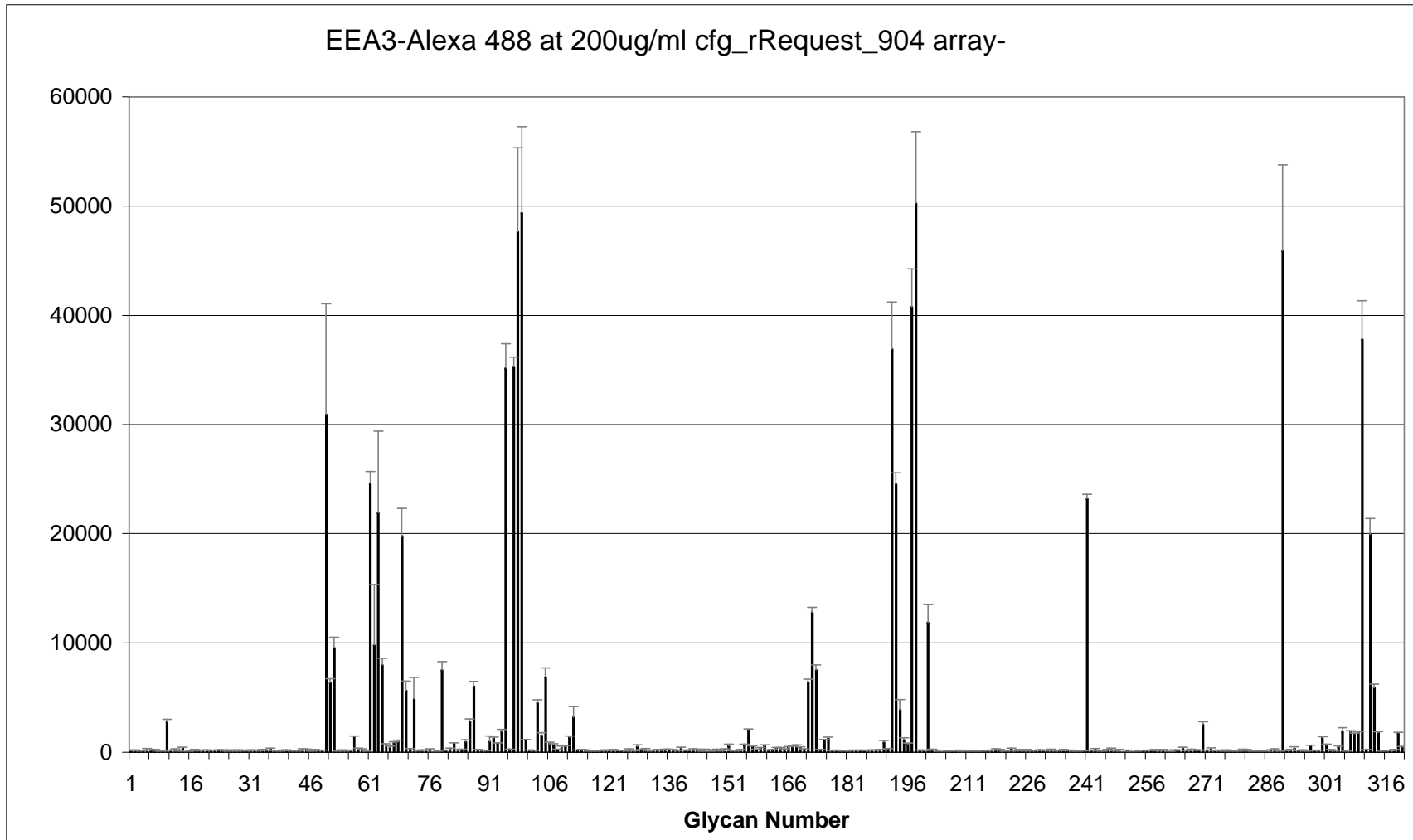
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N Q Q W K I E P H

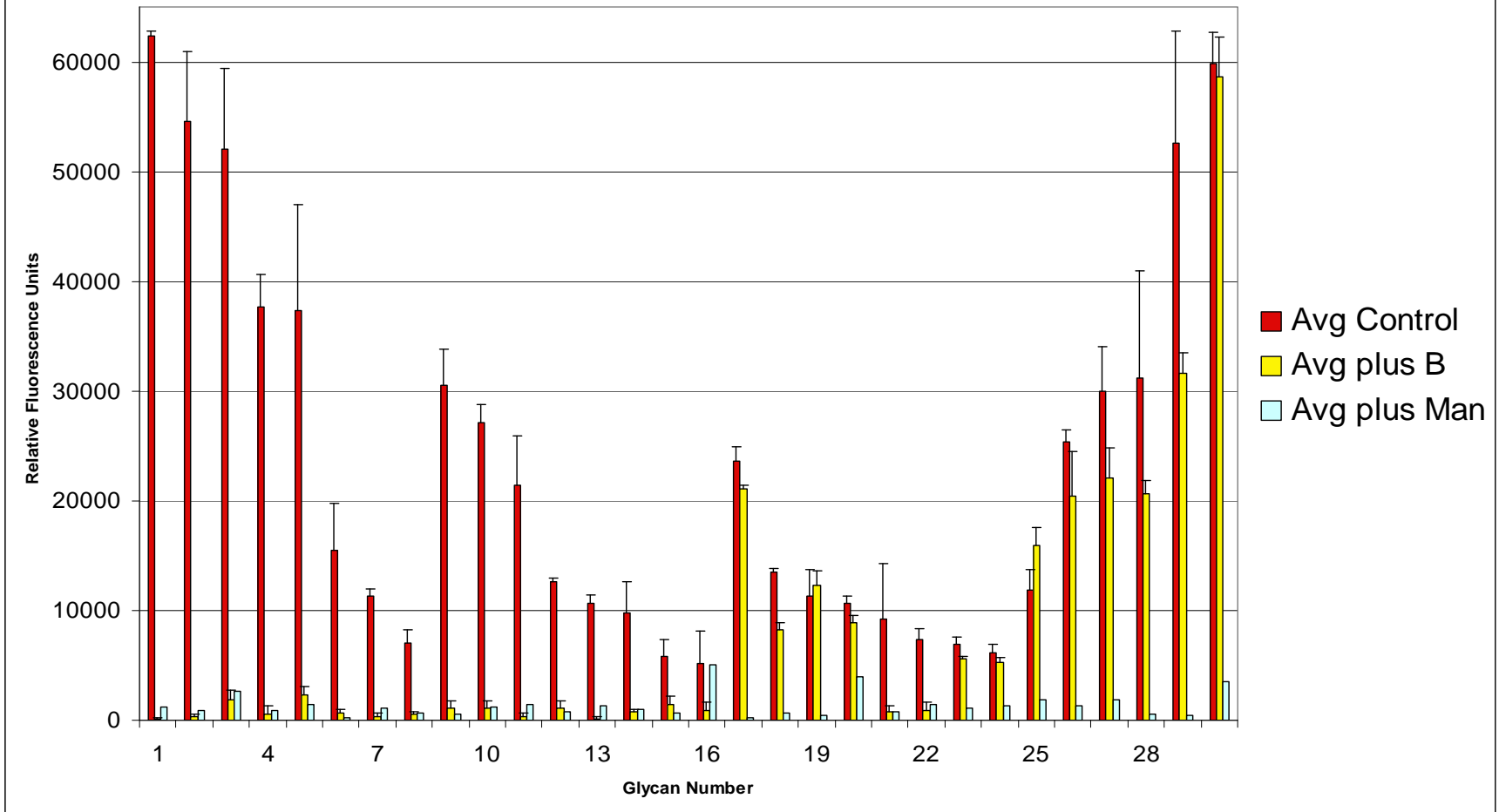
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TTTCCAATCATGAATGCAGCAGGTTGA
T G *



Supplementary Figure S2: Determination of the specificity of EEA by screening on the printed array v3 of the Consortium for Functional Glycomics. Error bars represent mean \pm standard error of the mean. The entire glycan array version is available at <https://www.functionalglycomics.org/static/consortium/resources/resourcecoreh8.shtml>

Summary of EEA Inhibition by B-active Oligosaccharide and RNase B Glycopeptides



Supplementary Figure S3: Summary of EEA inhibition by B-active oligosaccharides and RNase B glycopeptides. Glycan numbers refer to numbers of selected glycans in Table 2. Avg Control = average relative fluorescence units for control (EEA without addition of inhibitor), Avg plus B = average relative fluorescence units for EEA in the presence of blood group B tetrasaccharide, Avg plus Man = average relative fluorescence units for EEA in the presence of a mixture of glycopeptides derived from RNase B.

Supplementary Figure S4: Alignment of the amino acid sequences of *osr40g3* (CAA70175.1; Os07g0684000) and the individual ricin-B domains of *Ricinus communis* agglutinin (AAA33869.1)

A. Alignment of *osr40g3* (residues 45-204) and the N-terminal ricin-B domain of AAA33869.1 (covering residues 309-440)

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Osr40g3      CGRTLPPQPPTVKVYCRANPNYAMTARNGAVVLAPANPKDEYQHWIKDMRWSTSİKDEEGY
RicinBn      -----PEPIVRIVGRNGLCVDVTG-----EEFFDGNPIQLWP---CKSNTDWNQLWT
              *: * *:: * . :*: . : * * * . : :
Osr40g3      PAFALVNKATGQAIKHSLGQSHPVRLVPYNPEVMDESVLWTESRDVGNDFRCIRMVNNIY
RicinBn      LRKDSİRSNGKCLTISK-SSPRQQVVIYNCSTATVGATRQIWDN---RTIINPRSGL
              . : : * : : . * . * : : * * . . . . : * * * . .
Osr40g3      LNFDAFHGDKYHGGVVDGTDIVLWKWCEGDNQRWKIQPY
RicinBn      VLAATSGNSGTKLTVQTNİYAVSQGWLPTNNTQ-----
              : : . . : * : . * * : * :

```

B. Alignment of *osr40g3* (residues 45-204) and the C-terminal ricin-B domain of AAA33869.1 (covering residues 441-564)

```

Osr40g3      CGRTLPPQPPTVKVYCRANPNYAMTARNGAVVLAPANPKDEYQHWIKDMRWSTSİKDEEGY
RicinBc      -----PFVTTIVGLYG---MCLQANSKGVWLEDCTSEKAEQQWALYADGSİRP-----
              * * . * . : : * . * * * . . . : : * : *
Osr40g3      PAFALVNKATGQAIKHSLGQSHPVRLVPYNPEVMDESVLWTESRDVGNDFRCIRMVNNIY
RicinBc      -----QQRNDNCLTİDANİKGTVVKILSCGPASSGQRWWMFKNDGTI
              * : . . : : : : . * . . . . * * : : .
Osr40g3      LNFDAFHGDKYHGGVVDGTDIVLWKWCEGDNQRWKIQPY
RicinBc      LNLYNGLVLDVRRSDPSLKQIIVHPFHGNLNQIWLPLF--
              ** : . : . . : * : : : . * * *

```

Supplementary Figure S5: Sequence alignment of EEA domains retrieved from NCBI database

Sequences retrieved by Blastp search in NCBI database
(redundant sequences have been omitted)

Arabidopsis thaliana

>Arath: [ref|NP_565899.1|](#) hydroxyproline-rich glycoprotein family protein (At2g39050)

Plantago major

>Plama1: [gi|53748491|emb|CAH59433.1|](#) lectin-like protein 1

>Plama2: [gi|53748493|emb|CAH59435.1|](#) lectin-like protein 2

Populus trichocarpa

>Poptr: [gb|ABK95474.1|](#) unknown

Vitis vinifera

>Vitvi: [emb|CAO23507.1|](#) unnamed protein product

Triticum aestivum

>Triae: [gb|AAAY44603.1|](#) stress responsive protein

Oryza sativa

Orysa1: [ref|NP_001060668.1|](#) Os07g0684000

Orysa2: [ref|NP_001041764.1|](#) Os01g0104400

Orysa3: [ref|NP_001049995.1|](#) Os03g0327600

Orysa4: [ref|NP_001060666.1|](#) Os07g0683600 annotated seq incorrect*

Orysa5: [ref|NP_001060667.1|](#) Os07g0683900

The next 2 sequences are not included in the analysis (because they apparently corresponds to pseudogenes)

Orysa6: [ref|NP_001049986.1|](#) Os03g0325700 annotated seq incorrect

Orysa7: [ref|NP_001049987.1|](#) Os03g0325900 annotated seq incorrect

Physcomitrella patens

>Physco1: [ref|XP_001752923.1|](#) predicted protein

>EDQ82427 annotated seq is incomplete*

>Physco2: [ref|XP_001752710.1|](#) predicted protein

>EDQ82581 annotated seq is incomplete*

>Physco3: [ref|XP_001765262.1|](#) predicted protein

>EDQ69990 annotated seq is incomplete*

>Physco4: [ref|XP_001761196.1](#) predicted protein
>EDQ73918 annotated seq comprises extra N-term

Picea sitchensis

>Picsi1: [gb|ABK27004.1](#) unknown [Picea sitchensis]
>Picsi2: [gb|ABK22768.1](#) unknown [Picea sitchensis]
>Picsi3: [gb|ABK22123.1](#) unknown [Picea sitchensis]
>Picsi4: [gb|ABK24175.1](#) unknown [Picea sitchensis]
>Picsi5: [gb|ABK23307.1](#) unknown [Picea sitchensis]
>Picsi6: [gb|ABK21966.1](#) unknown [Picea sitchensis]
>Picsi7: [gb|ABK23910.1](#) unknown [Picea sitchensis]
>Picsi8: [gb|ABK25355.1](#) unknown [Picea sitchensis]
>Picsi9: [gb|ABK24374.1](#) unknown [Picea sitchensis]

*Incorrect and incomplete annotated sequences have been corrected and completed.

Sequences of EEA domains used to construct dendrogram

>EEA

PTYRVYCRAAPNYNMIVGKGVAF LAPIDETNELQYWKDDTYSYIKD
EAGLPAFSLVNKATGLTLKHSNHHPVPVKLVTYNPNVVDESVLWSQA
DDRGDGYSAIRSLTNPASHLEAAPLNDWSYNGAIIMGGVWIDAYNQQ
WKIEPHTG

>Arath

ATVKVYSKAEPNYNLTIRDGKVILAPADPSDEAQHWYKDEKYSTKVK
DADGHPCFALVNKATGEAMKHSV GATHPVHLIRYVPDKLDESVLWT
ESKDFGDGYRTIRMVNNTRLNVDAYHGDSKSGGV RDGTTIVLWDWN
KGDNQLWKIFPF

>Plama1

ESYRLYCKRQGQAGGNYCVTARQGGKLYLTHPNGADCNQIWYKVGND
KVGVI MLVHKATGMVVKHSTTG VQLQLVKKPSGCADKSVLWAESAD
VSGYRFLKTQTD TNYVMDAWTGIINEGTIISIYPNCINDSNRNAENQ
LWKLAP

>Plama2

ESYRLYCKRQGQAGGNYCVTARQGGKLYLTHPNGADCNQIWYKVGND
KVGVI MLVHKATGMVVKHSTTG VQLQLVKKPSGCADKSVLWAESAD
VSGYRFLKTQDD TNYVMDAWTGIINEGTIISIYPNCINDSNRNAENQ
LWKLAP

>Poptr

PSFKVYSKAQPEFHLTIRGGKVILAPSNPSDEFQNWYKDEKYSTRVKD
SEGCPAFALVNKATGQAMKHSIGE AHPVQLIPYNPDVLDESILWTESK
DLGDGFRAVRMVNNTHLNVD AFHGDKKSGGVHDGTSIVLWKWNKG
DNQRWKIIPTRY

>Vitvi

PTVRVFCKAKPNHSLTILDGKVYLAPSDKTDMLQHWIKDEKYSTSVK
DEEGFPSFALVNKATGQAMKHSIGASHPVQLIPYNPDVLDDESVLWTES
KDLGDNFRSIRMINNIHLNVDALHGDRSHGSHVDCTTIVLNKWKKGDN
QLWKISLY

>Triae

PTVKIYCRANPNYAMSVRNGKVVLAPANPKDDYQHWIKDMRWSTSI
KDEEGYPAFAMVNKATGQAIAKHSGLGQSHPVRLVPYNPDYLDDESVLWT
ESRDVGNGFRCVRMVNNIYLNFDALNGDKYHGGVRDGTTEVVLWKC
EGDNQRWKLQPY

>Orysa1

PTVKVYCRANPNYAMTARNGAVVLAPANPKDEYQHWIKDMRWSTSI
KDEEGYPAFALVNKATGQAIAKHSGLGQSHPVRLVPYNPEVMDESVLWT
ESRDVGNGFRCIRMVNNIYLNFDALFHGDKYHGGVRDGTDIVLWKC
EGDNQRWKIQPY

>Orysa2

VTHRIYCKAGEDNYSLAVRDGKVCLVRSRDRDDHTQHWVKDMKYSTR
VKDEEGYPAMALVNKATGDALKHSIGQSHPVRLVRYNPEYMDDESVL
WTESRDVGSFRCIRMVNNIYLNFDALHGDKDHGGVRDGTTLVLWE
WCEGDNQRWKIVPW

>Orysa3N

PTFKIFCRADEGYCVAVREGNVVLAPTNPDRDEHQHWYKDMRFSKIK
DEEGNPAFALVNKATGLAIKHSGLGQGHVPKLPFNPEYPDESVLWTE
SGDVGKSFRCIRMLNIRLNFDALFHGDKDHGGVHDGTTIVLWEWAKG
DNQCWKILPW

>Orysa3C

PTVRIFCKADEGFSVTVRGGSVCLAPTNPDRDEYQHWIKDMRHSNSIKD
EEGYPAFALVNRVTGEAIAKHSQGEHPVKLPYNPGYQDESVLWTES
RDVGHGFRCIRMVNNIYLNFDALHGDKDHGGVRDGTVALWKC
DNQRWKIVPW

>Orysa4N

PTFKIFCRADEGYCLTVRHDAVVLAPTNPDRDCQHWYKDMRHSTRV
KDEEGHPAFALVNRATGLAVKHSGLGQSHPVKLPYNPEYQDESVLWT
ESKDVGHGFRCIRMVNNIYLNLDALFHGDKSHGGVHDGTTVVLWEWC
KGDNQCWKILPW

>Orysa4C

EPTVRILCRADEAYSCLTVRNGAVCLAPTNPDRDFQHWVKDMRHSTSI
KDEEGYPAFALVNKATGEAIAKHSGLGQSHPVRLVPYNPEYLDDESVLWT
ESKDVGHGFRCVRMVNNIYLNFDALFHGDKDHGGVHDGTTVVLWEWC
KGDNQRWKLIPW

>Orysa5N

QIFKIFCRANENYCLTVRDSAVVLAPVNPKDEHQHWFKDMRFSTKVK
DGEGMPAFALVNKATGLAVKHSGLGQSHPVKLPFNPEYEDASVLWTE
SKDVGKGFRCIRMVNNTRLNLDAFHGDKDHGGVRDGTTVVLWEWCK
GDNQSWKILPW

>Orysa5C

VHTVRVFS AAGEDYCLTVRNGTACLAPKNPRDDYQHWIKDMRHSNK
IRDEEGYPAFALVNKVTGEAIKHSTGQGHPVKLVPYNPEYQDESVLW
TESKDVGKGFRCIRMVNNIYLNFD AFHGDKDHGGIHDGTEIVLWKWC
EGDNQRWKILPW

>Physco1N

EAVRLHCRADPNFCLAAIPGQGPVMPNNESDAYQVWYKDESMSNR
VKDESGAHAFSLINKATGECLRHPEDLQQCLLVVYEPNAQDESVLW
TMSEDMGQGYRCIRVVT SITRNLDVLRGDKKSGGMKNGSSVITFAWK
NQDNQVWKMPV

>Physco1C

HAVRLHCRADPNFSIAVIPGQGTIMVPTNASDAHQIWYRDESMSNRV
TDESGAHAFALINKVTGECLRHPEDLKQCLLADYEPNGLDESVLWT
MSEDMGQGYRCIRVVT SITRNLDVLRGDKKSGGVKTGSPLITFAWKN
QDNQVWKMPA

>Physco2

HPVRIHCKADPSYNLAVVPGQGPVMPVPTDISDDYQVWYKDETISTRV
TDETGASAFSLINKATGQALRHAPEDLKQCLLTQYEPNGLDDTIWWT
MSEDMGQGYHCIRLATDITRNMDVLRGDKKSGGVKEGSPVITFAWKK
QDNQIWKMPA

>Physco3

LPVRLHCKADPNFNLA AVPGQGPVMPVFPSPNDDFQVWYKDVTMSTR
VKDETGSSAFSLINKATGQALRHAPEDLAQCLLADYDSNALDQTVLW
TMSEDMGQGYCCIRLASQITRNLDVLRGDKKSGGVKEGSPVITFAWK
KQDNQIWKMITA

>Physco4

ETVRIHSKANANYNVA VRGTVGHGTCIVMADDDTSSQLWLKDDKMA
WTFDKKGGFSIVHKDTMKAIRVAPEEGKVLLADYDPRKLD ESLIY
QSSNRGRNYHTIYNGTSETVLHALRCTQCELMQPCTEGNAHMKENTL
VVVMKDRTKKDDPATVAMNQLWKLTPS

>Picsi1

GQVVRVFTKANPDFSLAIRNGSAVLVHANAHDKHQWVNDETYSTK
VKDEANCPFSFLVNKATGQALKHGLGETQPVLLTEYQLNTFDESILW
TMSGDMGQGYRTIRLVNNIHLNLDAFHGDKKSGGIKDGPNPVVLSW
KKGDNQLWKIVPY

>Picsi2

GQVVRVLTKANPDFSLAIRNGSAVLVHANANDKHQQWVMDETYSTK
VKDEASCPSFSLVNKATGQVLKHGLGETQPVLLTEYQLNTFDESILWT
MSGDMGQGYRTIRLVNNIHLNLDAFHGDKKSGGIKDGPNPVVLSWK
KGDNQLWKIVPY

>Picsi3

GQIVRVCSKANPDYALAIRDGRAVMVFYNPNDPTMQWVKDESWSNQ
VRDQVGHPAFALVNKATGQALRHATAECQEVLLTQYEGASTYDENV
LWSESEDMGYGYRTVRMANNIGLNLDAFQGGRRNGGIRDGTRAVLW
KWNKQDNQLWKLSPCY

>Picsi4

GQIVRVCSKANPDYALAIRDGRAVMVFYNPNDPTMQWVKDESWSNQ
VRDQVGHPAFALVNKATGQALRHAIAECQEVLLTQYEGASTYDENVL
WSESEDMGYGYRTVRMANNIGLNLD AFQGDRRNGGIRDGTRAVLWK
WNKQDNQLWKLSPCY

>Picsi5

GQIVRVCSKANPDYALAIRDGRAVMVFYNPNDPTMQWVKDESWSNQ
VRDQVGHPAFALVNKATGQALRHAIAESQEVLLTQYKGPSTYDENIL
WSESEDMGYGYRTVRMANNIGLNLD AFQGDRRNGGIRDGTRAVLWK
WNKQDNQLWKLSPCY

>Picsi6

GQIVRVCSKANPDYALAIRDGRAVMVFYNPNDPTMQWVKDESWSNQ
VRDQVGHPAFALVNKATGQALRHAIAESHEVLLTQYEGPSTYDENIL
WSESEDMGYGYRTVRMANNIGLNLD AFQGDRRNGGIRDGTRAVLWK
WNKQDNQLWKLSPCY

>Picsi7

GETVKIYCEANPDFLLASRNESVVMVPANESDPSQQWIMDTSSVKA
KDDAGFP AFALVNKATGQALRHGRSEKDKVTLGPHYHPDDLNEAVLFT
QSADV GKG YQCIRPVNNTHLNLDASAGDDKHHV ALSEGTEIVLCKWN
K KESQKWKISPI

>Picsi8N

GEIVKIYCEANPEYYLTAKEDSVV L APGDES NPYQQWIIDGTWGIRVK
DSAGFP AFALINKATRQALRHGKEEKEKVHTCPYSKDELNEVVLWTQ
SDDVGN GYK CIRPVDNTDLNLDANHGDPESGGIQDGTDLILFKWKKQ
ENQKWKILPIS

>Picsi8C

GQSVRIYCEQSPEYFLTVRDGEVVLTPGDADDVSQHWIKVDEWGNKI
RDEVGFPAFALVSKATL KALKHGSQEWDRVELSYNENDLDESVLWT
QSADVGRGYQCIRPVGNIHLNIDAKLADGKHGNVEDGNELILFSWKK
QKNQKWKMLPVD

>Picsi9N

GETVKIYCEANPDFLLASRNESVVMVPANESDPSQQWIMDTSSSVKA
KDDAGFP AFALVNKATGQALRHGRSEKDKVTLGPHYHPDDLNEAVLFT
QSADV GKG YQCIRPVNNTHLNLDASAGDDKHHV ALSEGTEIVLCKWN
K KESQKWKISPIL

>Picsi9C

GSTVRIHCEANPEFFLAARGDVAVLAPENPRDPHQQWIKVDSWGLRV
KDEAGFP AFALVNKATRHALKHGDK EWDQIYLADYNHDKAEQSVLW
TLSADVGN GYQCLRPVNNINLNMDAKAADGHVGGIRDGNELILFEWK
KQSNQKWKLPVH

Sequence alignment of EEA domains**

CLUSTAL 2.0.3 multiple sequence alignment

```
Orysa4N      -PTFKIFCRADEG-YCLTVRHDA-VVLAPTNPRDDCQHWYKDMRHSTRVKDEEGHPAFAL 57
Orysa5N      -QIFKIFCRANEN-YCLTVRDSA-VVLAPVNPKDEHQHWFKDMRFSTKVKDGEGMPAFAL 57
Orysa3N      -PTFKIFCRADEG-YCVAVREGN-VVLAPTNPRDEHQHWYKDMRFSAKIKDEEGNPAFAL 57
Orysa4C      EPTVRIILCRADEA-YSLTVRNGA-VCLAPTNPRDDFQHWVKDMRHSTS IKDEEGYPAFAL 58
Orysa3C      -PTVRIIFCKADEG-FSVTVRGGG-VCLAPTNPRDEYQHWIKDMRHSNSIKDEEGYPAFAL 57
Orysa5C      VHTVRFVSAAGED-YCLTVRNGT-ACLAPKNPRDDYQHWIKDMRHSNKIRDEEGYPAFAL 58
Triae        -PTVKIYCRANPN-YAMSVRNGK-VVLAPANPKDDYQHWIKDMRWSTS IKDEEGYPAFAM 57
Orysa1       -PTVKVYCRANPN-YAMTARNGA-VVLAPANPKDEYQHWIKDMRWSTS IKDEEGYPAFAL 57
Orysa2       -VTHRIYCKAGEDNYS LAVRDGK-VCLVRSDDRDDHTQHWVKDMKYSTRVKDEEGYPAMAL 58
Arath        -ATVKVYSKAEPN-YNLTIRDGK-VILAPADPSDEAQHWYKDEKYSTRVKDADGHPCFAL 57
Poptr        -PSFKVYSKAQPE-FHLTIRGGK-VILAPSNPSDEFQNWYKDEKYSTRVKDSEGCPAFAL 57
Vitvi        -PTVRFVCKAKPN-HSLTILDGK-VYLAPSDKTDLQHWIKDEKYSTS VKDEEGFPFSL 57
EEA          -PTYRVYCRAAPN-YNMIVGKGV-AFLAPIDETNELQYWKDDTYS-YIKDEAGLPFSL 56
Picsi7       GETVKIYCEANPD-FLLASRNES-VVMVPANESDPSQQWIMDTSSVVKAKDDAGFPFAL 58
Picsi9N      GETVKIYCEANPD-FLLASRNES-VVMVPANESDPSQQWIMDTSSVVKAKDDAGFPFAL 58
Picsi8N      GEIVKIYCEANPE-YLTAKEDS-VVLAPGDESNPYQQWIIDGTWGI RVKDSAGFPFAL 58
Picsi8C      GQSVRIYCEQSPE-YFLTVRDGE-VVLT PGDADDVSQHWIKVDEWGNKIRDEVGFPFAL 58
Picsi9C      GSTVRIHCEANPE-FFLAARGDV-AVLAPENRPDPHQWIKVDSWGLRVKDEAGFPFAL 58
Physco1N     -EAVRLHCRADPN-FCLAAIPGQG PVMVPNNESDAYQVWYKDESMSNRVKDESGAHAFSL 58
Physco1C     -HAVRLHCRADPN-FSIAVIPGQGTIMVPTNASDAHQIWYRDESMSNRVTDESGAHAFAL 58
Physco2      -HPVRIHCKADPS-YNLAVVPGQG PVMVPTDISDDYQVWYKDETI STRVTDET GASAFSL 58
Physco3      -LPVRLHCKADPN-FNLAAVPGQG PVMVPFSPNDDFQVWYKDVTMSTRVKDET GSSAFSL 58
Picsi1       GQVVRVFTKANPD-FSLAIRNGS-AVLVHANAHDKHQQVWVNDETYSTKVKDEANCPSFSL 58
Picsi2       GQVVRVLTKANPD-FSLAIRNGS-AVLVHANANDKHQQQVWVMDETYSTKVKDEASCPSFSL 58
Picsi3       GQIVRVCSKANPD-YALAIRDGR-AVMVFYNPNDPTMQVWKDESWSNQVRDQVGHPAFAL 58
Picsi4       GQIVRVCSKANPD-YALAIRDGR-AVMVFYNPNDPTMQVWKDESWSNQVRDQVGHPAFAL 58
Picsi5       GQIVRVCSKANPD-YALAIRDGR-AVMVFYNPNDPTMQVWKDESWSNQVRDQVGHPAFAL 58
Picsi6       GQIVRVCSKANPD-YALAIRDGR-AVMVFYNPNDPTMQVWKDESWSNQVRDQVGHPAFAL 58
          ::          . :          :. . :          *          .          *          . . : : :
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Orysa4N VN RATGLAVKHS LGQSHPVKLV PYN-PEYQDESVLWTESKDVGHGFRCIRMVNNIYLNLD 116
Orysa5N VN KATGLAVKHS LGQSHPVKLV PNFN-PEYEDASVLWTESKDVGKGFRCIRMVNNTRLNLD 116
Orysa3N VN KATGLAIKHS LGQGHVPV K LAPFN-PEYPDESVLWTESG DVGKSFRCIRMLNNI RL NFD 116
Orysa4C VN KATGEAIKHS LGQSHPVRLV PYN-PEYLDDESVLWTESKDVGHGFRCVRMVNNIYLNFD 117
Orysa3C VN RVTGEAIKHS QGEGHPV KLV PYN-PGYQDESVLWTESR DVGHGFRCIRMVNNIYLNFD 116
Orysa5C VN KVTGEAIKHS TGQGHVPV KLV PYN-PEYQDESVLWTESKDVGKGFRCIRMVNNIYLNFD 117
Triae VN KATGQAIKHS LGQSHPVRLV PYN-PDYLDDESVLWTESR DVGNGFRCVRMVNNIYLNFD 116
Orysa1 VN KATGQAIKHS LGQSHPVRLV PYN-PEVMDESVLWTESR DVGNGFRCIRMVNNIYLNFD 116
Orysa2 VN KATGDALKHS IGQSHPVRLV RYN-PEYMDDESVLWTESR DVGSGFRCIRMVNNIYLNFD 117
Arath VN KATGEAMKHS V GATHPVHLIR YV-PDKLDESVLWTESKDFGDGYRTIRMVNNTRLNVD 116
Poptr VN KATGQAMKHS IGEAHPVQLIP YN-PDVLDESILWTESKDLGDFRAVRMVNNTHLNVD 116
Vitvi VN KATGQAMKHS IGASHPVQLIP YN-PDVLDESVLWTESKDLGDNFRSIRMINNIHLNVD 116
EEA VN KATGLTLKHS NHHPVPV KLV TYN-PNVVDESVLWSQADDRGDGYSAIRSLTNPASHLE 115
Picsi7 VN KATGQALRHGRSEKDKVTLG PYH-PDDLNEAVLFTQSADVGKGYQCIRPVNNTHLNLD 117
Picsi9N VN KATGQALRHGRSEKDKVTLG PYH-PDDLNEAVLFTQSADVGKGYQCIRPVNNTHLNLD 117
Picsi8N IN KATRQALRHGKKEEKEKVHTCPYS-KDELNEVVLWTQSDDVGNGYKCIRPVDNTDLNLD 117
Picsi8C VSKATLKALKHGSQEWDRVELSYYN-ENDLDESVLWTQSADVGRGYQCIRPVGNIHLNID 117
Picsi9C VN KATRHALKHGDKEDQIYLADYN-HDKAEQSVLWTL SADVGNQYQCLRPVNNINLNM 117
PhyscolN IN KATGECLRHPPEDLQCLLVVYE-PNAQDESVLWTMS EDMGQGYRCIRVVTSITRNL 117
PhyscolC IN KVTGECLRHPPEDLKQCLLADYE-PNGLDESVLWTMS EDMGQGYRCIRVVTSITRNL 117
Physco2 IN KATGQALRHAPEDLKQCLLADYE-PNGLDDTIWWTMS EDMGQGYHCIRLATDITRNM 117
Physco3 IN KATGQALRHAPEDLKQCLLADYD-SNALDQTVLWTMS EDMGQGYCCIRLASQITRNL 117
Picsi1 VN KATGQALKHGLGETQP VLLTEYQ-LNTFDESILWTMSGDMQGYRTIRLVNNIHLNLD 117
Picsi2 VN KATGQVLKHGLGETQP VLLTEYQ-LNTFDESILWTMSGDMQGYRTIRLVNNIHLNLD 117
Picsi3 VN KATGQALRHATAECQEVLLTQYEGASTYDENVLWSESEDMGYGYRTVRMANNIGLNLD 118
Picsi4 VN KATGQALRHAI AECQEVLLTQYEGASTYDENVLWSESEDMGYGYRTVRMANNIGLNLD 118
Picsi5 VN KATGQALRHAI AESQEVLLTQYKGPSTYDENILWSESEDMGYGYRTVRMANNIGLNLD 118
Picsi6 VN KATGQALRHAI AESHEVLLTQYEGPSTYDENILWSESEDMGYGYRTVRMANNIGLNLD 118
: . : * : : * : : : : * * . : : * . : :

Orysa4N AFHGD-KSHGGVHDGTTVVLEW ECKGDNQCWKILPW-- 151
Orysa5N AFHGD-KDHGGVRDGT T VVLEW ECKGDNQSWKILPW-- 151
Orysa3N AFHGD-KDHGGVHDGTTIVLEW EAKGDNQCWKILPW-- 151
Orysa4C AFHGD-KDHGGVHDGTTVVLEW ECKGDNQRWKILPW-- 152
Orysa3C ALHGD-KDHGGVRDGT T VALWKWCEGDNQRWKIVPW-- 151
Orysa5C AFHGD-KDHGGIHDGTEIVLWKWCEGDNQRWKILPW-- 152
Triae ALNGD-KYHGGVRDGT E VVLEW ECKGDNQRWKLQPY-- 152
Orysal AFHGD-KYHGGVRDGT DIVLWKWCEGDNQRWKIQPY-- 152

Orysa2	ALHGD-KDHGGVVDGTTLVLWLEWCEGDNQRWKIVPW--	152
Arath	AYHGD-SKSGGVRDGTITVLWDWNKGDNLWKIFPF--	151
Poptr	AFHGD-KKSGGVHDGTSIVLWKWNKGDNRWKIIPTRY	153
Vitvi	ALHGD-RSHGSVHDCTTIVLNKWKKGDNQLWKISLY--	151
EEA	AAPLN-DWS---YNGAIIMGVWIDAYNQWQKIEPHTG	149
Picsi7	ASAGDDKHHVALSEGTEIVLCKWNKESQKWKISPI--	153
Picsi9N	ASAGDDKHHVALSEGTEIVLCKWNKESQKWKISPIL-	154
Picsi8N	ANHGD-PESGGIQDGTDLILFKWKKQENQWKILPIS-	153
Picsi8C	AKLAD-GKHGNVEDGNELILFSWKKQKNQKWKMLPVD-	153
Picsi9C	AKAAD-GHVGGIRDGNELILFEWKKQSNQKWKLPVH-	153
Physco1N	VLRGD-KKSGGMKNGSSVITFAWKNQDNQVWKMPV--	152
Physco1C	VLRGD-KKSGGVKTGSPLITFAWKNQDNQVWKMPA--	152
Physco2	VLRGD-KKSGGVKEGSPVITFAWKKQDNQIWKMPA--	152
Physco3	VLRGD-KKSGGVKEGSPVITFAWKKQDNQIWKMITA--	152
Picsi1	AFHGD-KKSGGIKDGNPVVLWSWKKGDNLWKIVPY--	152
Picsi2	AFHGD-KKSGGIKDGNPVVLWSWKKGDNLWKIVPY--	152
Picsi3	AFQGD-RRNGGIRDGTRAVLWKWNKQDNQLWKLSPCY-	154
Picsi4	AFQGD-RRNGGIRDGTRAVLWKWNKQDNQLWKLSPCY-	154
Picsi5	AFQGD-RRNGGIRDGTRAVLWKWNKQDNQLWKLSPCY-	154
Picsi6	AFQGD-RRNGGIRDGTRAVLWKWNKQDNQLWKLSPCY-	154

**Alignment of all sequences except Plama1, Plama2 and Physco4. The latter sequences were omitted to get a better alignment of EEA with other proteins with EUL domain(s).